Supplemental Information

Supplemental Table 2 MS/MS spectral data of proteins with single peptide identification

This table included MS/MS spectral data for protein identified with single significant peptide in TCDD treated and control zebrafish heart samples.

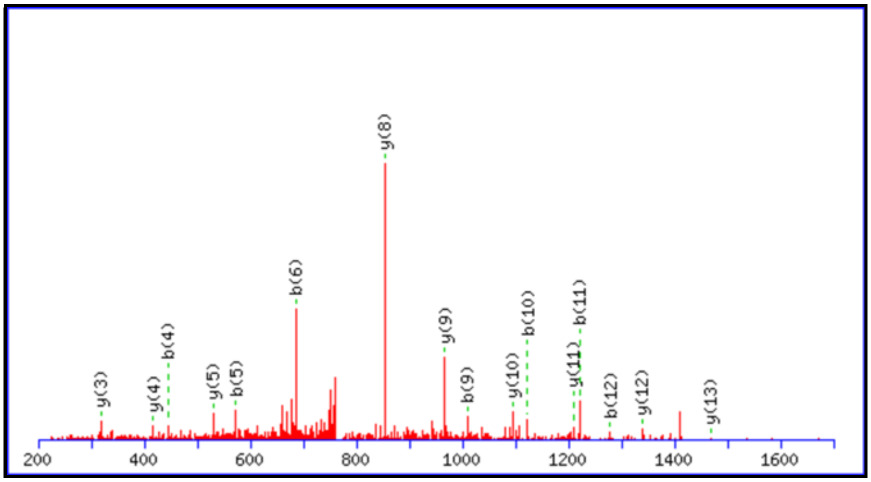
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEEDKIPLLLVGNK**
Found in **gi|57528846|ref|NP_001003649.1|**, hypothetical protein LOC445255 [Danio rerio]

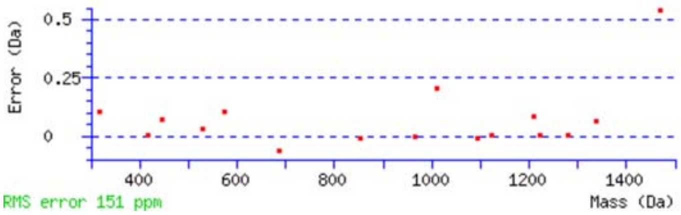
Match to Query 24320: 1538.262724 from(770.138638,2+) index(44561)
Data file TCDD_0530.dta

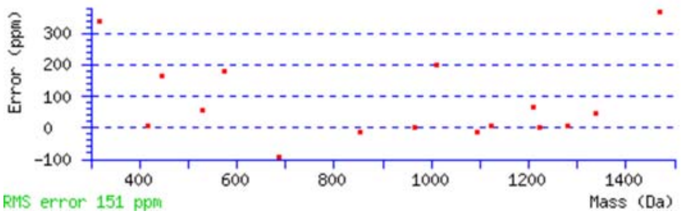
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1537.8715
Ions Score: 65 **Expect:** 7.5e-005
Matches : 16/126 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							14
2	201.0870	101.0471			183.0764	92.0418	E	***1467.8417***	734.4245	1450.8152	725.9112	1449.8312	725.4192	13
3	330.1296	165.5684			312.1190	156.5631	E	***1338.7991***	669.9032	1321.7726	661.3899	1320.7886	660.8979	12
4	**445.1565**	223.0819			427.1460	214.0766	D	***1209.7565***	605.3819	1192.7300	596.8686	1191.7460	596.3766	11
5	**573.2515**	287.1294	556.2249	278.6161	555.2409	278.1241	K	***1094.7296***	547.8684	1077.7030	539.3552			10
6	**686.3355**	343.6714	669.3090	335.1581	668.3250	334.6661	I	***966.6346***	483.8210	949.6081	475.3077			9
7	783.3883	392.1978	766.3618	383.6845	765.3777	383.1925	P	***853.5506***	427.2789	836.5240	418.7656			8
8	896.4724	448.7398	879.4458	440.2266	878.4618	439.7345	L	756.4978	378.7525	739.4713	370.2393			7
9	**1009.5564**	505.2819	992.5299	496.7686	991.5459	496.2766	L	643.4137	322.2105	626.3872	313.6972			6
10	**1122.6405**	561.8239	1105.6140	553.3106	1104.6299	552.8186	L	***530.3297***	265.6685	513.3031	257.1552			5
11	**1221.7089**	611.3581	1204.6824	602.8448	1203.6984	602.3528	V	***417.2456***	209.1264	400.2191	200.6132			4
12	**1278.7304**	639.8688	1261.7038	631.3556	1260.7198	630.8635	G	***318.1772***	159.5922	301.1506	151.0790			3
13	1392.7733	696.8903	1375.7468	688.3770	1374.7627	687.8850	N	261.1557	131.0815	244.1292	122.5682			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AEEDKIPLLLVGNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.4	1537.8715	0.3912	AEEDKIPLLLVGNK
15.7	1536.9351	1.3276	AKESLRPNGVIIIK
13.6	1537.7776	0.4851	KVYYDPSSPGALGGK
8.9	1537.6791	0.5836	MQGSQGDQKSSSGGGK
7.0	1538.6770	-0.4143	ETVSDESDQVCLSK
4.6	1537.7736	0.4891	RISGESSEYLVNGK
4.0	1537.7485	0.5142	GNQGEPGGEPGLKGNK
3.8	1538.7001	-0.4374	QFSSFEAGAQNEPK
3.7	1537.7386	0.5241	QGGSLHNQGNVWGGK
3.6	1538.7221	-0.4594	AETPPLNMEHLCK

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

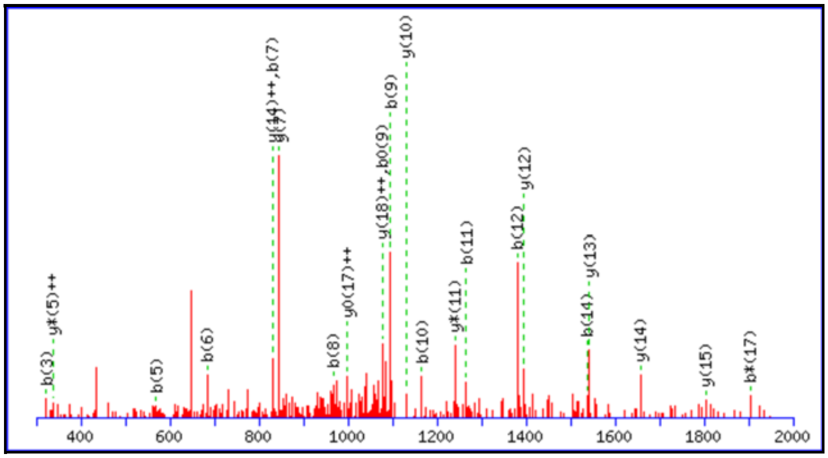
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AHIVFDFHQAVDGVQEQER**
Found in **gi|62955581|ref|NP_001017804.1|**, hypothetical protein LOC550502 [Danio rerio]

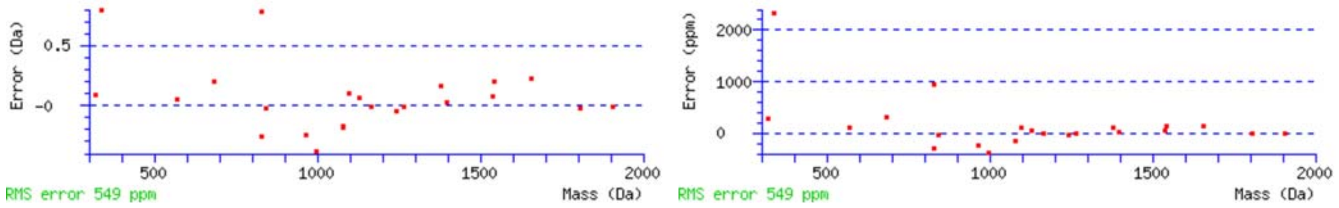
Match to Query 67963: 2224.762724 from(1113.388638,2+) index(45652)
Data file TCDD_0530.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2224.0661
Ions Score: 41 **Expect:** 0.016
Matches : 23/188 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							19
2	209.1033	105.0553					H	2154.0363	1077.5218	2137.0097	1069.0085	2136.0257	1068.5165	18
3	***322.1874***	161.5973					I	2016.9774	1008.9923	1999.9508	1000.4791	1998.9668	999.9870	17
4	421.2558	211.1315					V	1903.8933	952.4503	1886.8668	943.9370	1885.8828	943.4450	16
5	***568.3242***	284.6657					F	**1804.8249**	902.9161	1787.7984	894.4028	1786.8143	893.9108	15
6	***683.3511***	342.1792			665.3406	333.1739	D	**1657.7565**	829.3819	1640.7299	820.8686	1639.7459	820.3766	14
7	***830.4196***	415.7134			812.4090	406.7081	F	**1542.7295**	771.8684	1525.7030	763.3551	1524.7190	762.8631	13
8	***967.4785***	484.2429			949.4679	475.2376	H	**1395.6611**	698.3342	1378.6346	689.8209	1377.6506	689.3289	12
9	***1095.5370***	548.2722	1078.5105	539.7589	1077.5265	539.2669	Q	1258.6022	629.8047	1241.5757	621.2915	1240.5917	620.7995	11
10	***1166.5742***	583.7907	1149.5476	575.2774	1148.5636	574.7854	A	**1130.5436**	565.7755	1113.5171	557.2622	1112.5331	556.7702	10
11	***1265.6426***	633.3249	1248.6160	624.8116	1247.6320	624.3196	V	1059.5065	530.2569	1042.4800	521.7436	1041.4960	521.2516	9
12	***1380.6695***	690.8384	1363.6430	682.3251	1362.6589	681.8331	D	960.4381	480.7227	943.4116	472.2094	942.4276	471.7174	8
13	1437.6910	719.3491	1420.6644	710.8359	1419.6804	710.3438	G	**845.4112**	423.2092	828.3846	414.6959	827.4006	414.2039	7
14	***1536.7594***	768.8833	1519.7328	760.3701	1518.7488	759.8781	V	788.3897	394.6985	771.3632	386.1852	770.3791	385.6932	6
15	1664.8180	832.9126	1647.7914	824.3993	1646.8074	823.9073	Q	689.3213	345.1643	672.2947	336.6510	671.3107	336.1590	5
16	1793.8606	897.4339	1776.8340	888.9206	1775.8500	888.4286	E	561.2627	281.1350	544.2362	272.6217	543.2522	272.1297	4
17	1921.9191	961.4632	1904.8926	952.9499	1903.9086	952.4579	Q	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
18	2050.9617	1025.9845	2033.9352	1017.4712	2032.9512	1016.9792	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
19							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of AHIVFDFHQAVDGVQEQER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.0	2224.0661	0.6966	AHIVFDFHQAVDGVQEQER
4.5	2223.1214	1.6414	HNPLVMENEACKPVILSAMK
2.4	2224.9994	-0.2367	HCSVFASNDVFSDPCVGTRK
0.1	2223.0421	1.7206	ADVCKCGALCLCSILAHYAR

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

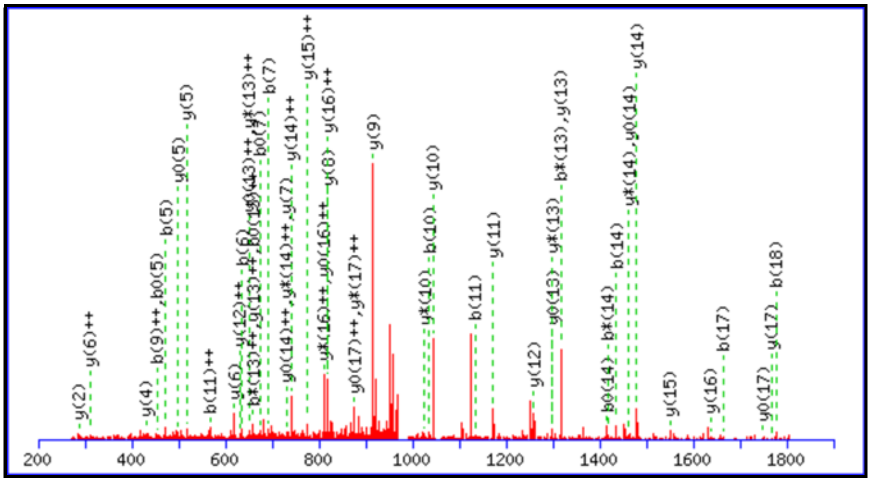
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALESAYGSEKPSLTSAAIR**
Found in **gi|50539806|ref|NP_001002369.1|**, hypothetical protein LOC436642 [Danio rerio]

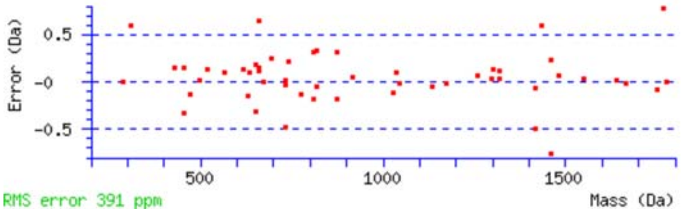
Match to Query 44301: 1950.692724 from(976.353638,2+) index(36523)
Data file TCDD_0530.dta

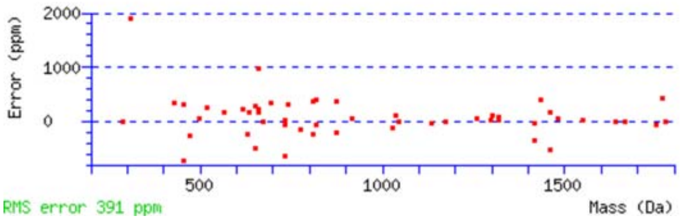
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1950.0058
Ions Score: 49  Expect: 0.0027
Matches : 53/186 fragment ions using 160 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							19
2	185.1285	93.0679					L	1879.9760	940.4916	1862.9494	931.9784	1861.9654	931.4863	18
3	314.1710	157.5892			296.1605	148.5839	E	***1766.8919***	883.9496	1749.8654	875.4363	1748.8814	874.9443	17
4	401.2031	201.1052			383.1925	192.0999	S	***1637.8493***	819.4283	1620.8228	810.9150	1619.8388	810.4230	16
5	**472.2402**	236.6237			454.2296	227.6184	A	***1550.8173***	775.9123	1533.7907	767.3990	1532.8067	766.9070	15
6	**635.3035**	318.1554			617.2930	309.1501	Y	***1479.7802***	740.3937	1462.7536	731.8805	1461.7696	731.3884	14
7	**692.3250**	346.6661			674.3144	337.6608	G	***1316.7169***	658.8621	1299.6903	650.3488	1298.7063	649.8568	13
8	779.3570	390.1821			761.3464	381.1769	S	***1259.6954***	630.3513	1242.6688	621.8381	1241.6848	621.3461	12
9	908.3996	454.7034			890.3890	445.6982	E	***1172.6634***	586.8353	1155.6368	578.3220	1154.6528	577.8300	11
10	**1036.4946**	518.7509	1019.4680	510.2376	1018.4840	509.7456	K	***1043.6208***	522.3140	1026.5942	513.8007	1025.6102	513.3087	10
11	**1133.5473**	567.2773	1116.5208	558.7640	1115.5368	558.2720	P	***915.5258***	458.2665	898.4993	449.7533	897.5152	449.2613	9
12	1220.5794	610.7933	1203.5528	602.2800	1202.5688	601.7880	S	***818.4730***	409.7402	801.4465	401.2269	800.4625	400.7349	8
13	1333.6634	667.3353	1316.6369	658.8221	1315.6529	658.3301	L	***731.4410***	366.2241	714.4145	357.7109	713.4304	357.2189	7
14	**1434.7111**	717.8592	1417.6846	709.3459	1416.7005	708.8539	T	***618.3570***	309.6821	601.3304	301.1688	600.3464	300.6768	6
15	1521.7431	761.3752	1504.7166	752.8619	1503.7326	752.3699	S	***517.3093***	259.1583	500.2827	250.6450	499.2987	250.1530	5
16	1592.7802	796.8938	1575.7537	788.3805	1574.7697	787.8885	A	***430.2772***	215.6423	413.2507	207.1290			4
17	**1663.8174**	832.4123	1646.7908	823.8990	1645.8068	823.4070	A	359.2401	180.1237	342.2136	171.6104			3
18	**1776.9014**	888.9543	1759.8749	880.4411	1758.8909	879.9491	I	***288.2030***	144.6051	271.1765	136.0919			2
19							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ALESAYGSEKPSLTSAAIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.8	1950.0058	0.6870	ALESAYGSEKPSLTSAAIR
1.6	1950.0244	0.6683	SLLNAAADAVERIMVSYK
1.1	1952.9592	-2.2664	YYEREGIQLDPSQISR

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

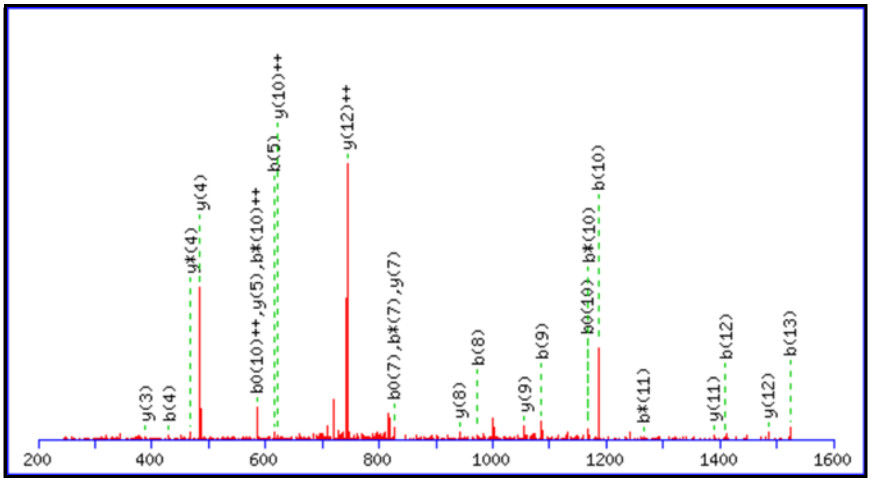
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALPFWNDEIVPQIK**
Found in **gi|38488700|ref|NP_942099.1|**, phosphoglycerate mutase 1 [Danio rerio]

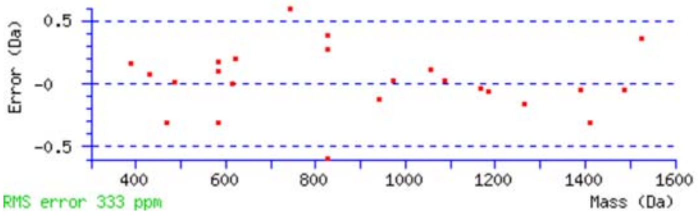
Match to Query 28552: 1669.222724 from(835.618638,2+) index(107246)
Data file TCDD_0530.dta

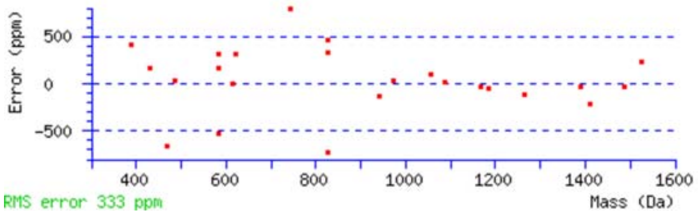
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1668.8875
Ions Score: 47 **Expect:** 0.0056
Matches : 25/122 fragment ions using 52 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							14
2	185.1285	93.0679					L	1598.8577	799.9325	1581.8312	791.4192	1580.8471	790.9272	13
3	282.1812	141.5942					P	***1485.7736***	743.3905	1468.7471	734.8772	1467.7631	734.3852	12
4	***429.2496***	215.1285					F	***1388.7209***	694.8641	1371.6943	686.3508	1370.7103	685.8588	11
5	***615.3289***	308.1681					W	1241.6525	621.3299	1224.6259	612.8166	1223.6419	612.3246	10
6	729.3719	365.1896	712.3453	356.6763			N	***1055.5732***	528.2902	1038.5466	519.7769	1037.5626	519.2849	9
7	844.3988	422.7030	827.3723	414.1898	826.3882	413.6978	D	***941.5302***	471.2688	924.5037	462.7555	923.5197	462.2635	8
8	***973.4414***	487.2243	956.4149	478.7111	955.4308	478.2191	E	***826.5033***	413.7553	809.4767	405.2420	808.4927	404.7500	7
9	***1086.5255***	543.7664	1069.4989	535.2531	1068.5149	534.7611	I	697.4607	349.2340	680.4341	340.7207			6
10	***1185.5939***	593.3006	1168.5673	584.7873	1167.5833	584.2953	V	***584.3766***	292.6920	567.3501	284.1787			5
11	1282.6466	641.8270	1265.6201	633.3137	1264.6361	632.8217	P	***485.3082***	243.1577	468.2817	234.6445			4
12	***1410.7052***	705.8563	1393.6787	697.3430	1392.6947	696.8510	Q	***388.2554***	194.6314	371.2289	186.1181			3
13	***1523.7893***	762.3983	1506.7627	753.8850	1505.7787	753.3930	I	260.1969	130.6021	243.1703	122.0888			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ALPFWNDEIVPQIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.5	1668.8875	0.3352	ALPFWNDEIVPQIK
14.6	1669.8538	-0.6311	FYGYPDGKPCILIK
14.3	1669.9515	-0.7288	KIPFIGASIQNQLNK
11.1	1670.9025	-1.6798	LAAETVSRGGIMIPEK
9.8	1669.8159	-0.5931	EVKEDQLVPEDQNK
9.3	1668.0338	1.1889	ISIIGLKSFAPGKPLK
7.9	1669.8709	-0.6482	EGKTSLPMPGVAENLK
7.8	1668.9464	0.2763	TGRNFLHFVILQPK
7.7	1669.9403	-0.7176	DLLSFHEKSQLLLK
6.8	1669.8675	-0.6448	SEAVVEYVFSGSRLK

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

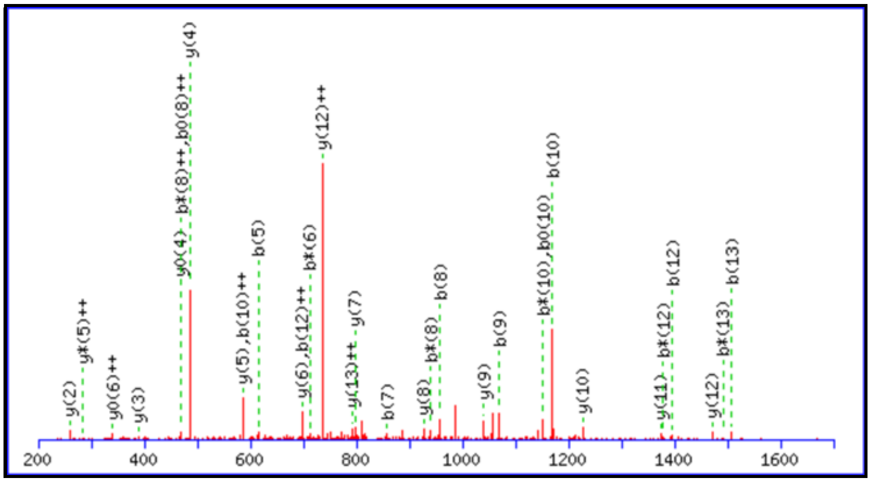
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALPFWNEVIVPEIK**
Found in **gi|41056123|ref|NP_957318.1|**, phosphoglycerate mutase 2 (muscle) [Danio rerio]

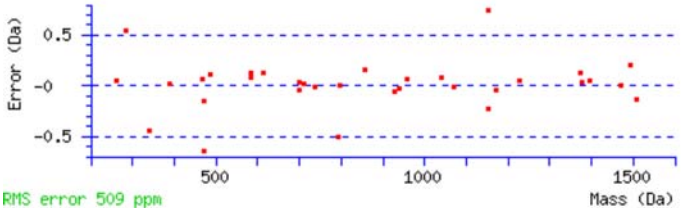
Match to Query 27868: 1653.582724 from(827.798638,2+) index(22790)
Data file TCDD_0530.dta

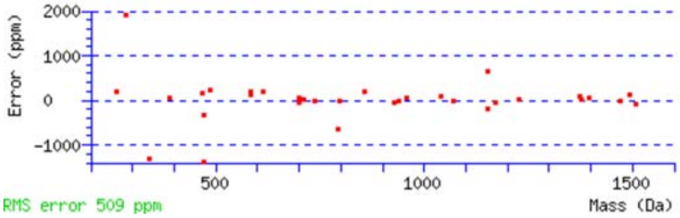
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1653.9130
Ions Score: 70 **Expect:** 2.2e-005
Matches : 33/130 fragment ions using 53 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							14
2	185.1285	93.0679					L	1583.8832	792.4452	1566.8566	783.9320	1565.8726	783.4400	13
3	282.1812	141.5942					P	***1470.7991***	735.9032	1453.7726	727.3899	1452.7886	726.8979	12
4	429.2496	215.1285					F	***1373.7464***	687.3768	1356.7198	678.8635	1355.7358	678.3715	11
5	**615.3289**	308.1681					W	***1226.6780***	613.8426	1209.6514	605.3293	1208.6674	604.8373	10
6	729.3719	365.1896	712.3453	356.6763			N	***1040.5986***	520.8030	1023.5721	512.2897	1022.5881	511.7977	9
7	**858.4145**	429.7109	841.3879	421.1976	840.4039	420.7056	E	***926.5557***	463.7815	909.5292	455.2682	908.5451	454.7762	8
8	**957.4829**	479.2451	940.4563	470.7318	939.4723	470.2398	V	***797.5131***	399.2602	780.4866	390.7469	779.5026	390.2549	7
9	**1070.5669**	535.7871	1053.5404	527.2738	1052.5564	526.7818	I	***698.4447***	349.7260	681.4182	341.2127	680.4341	340.7207	6
10	**1169.6354**	585.3213	1152.6088	576.8080	1151.6248	576.3160	V	***585.3606***	293.1840	568.3341	284.6707	567.3501	284.1787	5
11	1266.6881	633.8477	1249.6616	625.3344	1248.6776	624.8424	P	***486.2922***	243.6498	469.2657	235.1365	468.2817	234.6445	4
12	**1395.7307**	698.3690	1378.7042	689.8557	1377.7201	689.3637	E	***389.2395***	195.1234	372.2129	186.6101	371.2289	186.1181	3
13	**1508.8148**	754.9110	1491.7882	746.3978	1490.8042	745.9057	I	***260.1969***	130.6021	243.1703	122.0888			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ALPFWNEVIVPEIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.4	1653.9130	-0.3303	ALPFWNEVIVPEIK
13.3	1655.8591	-2.2763	GGKENVSLAEALNQAR
10.4	1653.9049	-0.3222	NLNQELQAQVKELK
7.7	1654.7733	-1.1906	EKVEGGVECLDGAHR
6.7	1655.8115	-2.2287	LIISSLGSDDGEHASR
6.2	1655.8016	-2.2189	GEQPSADSGAGIRHFK
5.9	1652.8192	0.7635	LKGDALHQSPDCEIK
5.7	1655.8096	-2.2269	SVAPQFSAFYAGFHK
5.7	1653.8573	-0.2746	RSLEPESSDTPVLPK
5.6	1653.8180	-0.2353	YMCEVMVLSLPELK

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

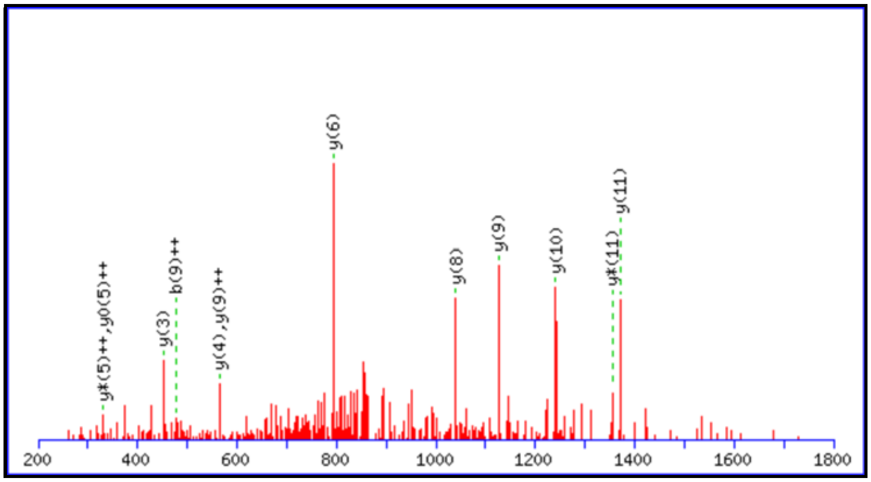
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AMGIMNSFVNDIFER**
Found in **gi|41152402|ref|NP_956411.1|**, histone 2, H2, like [Danio rerio]

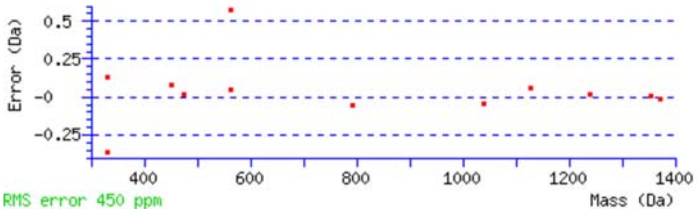
Match to Query 32288: 1742.392724 from(872.203638,2+) index(15278)
Data file TCDD_0530.dta

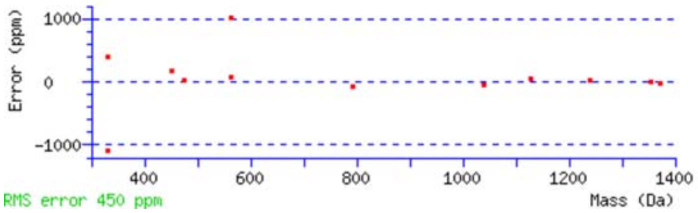
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1742.8120
Ions Score: 43 **Expect:** 0.014
Matches : 12/144 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							15
2	203.0849	102.0461					M	1672.7822	836.8947	1655.7556	828.3815	1654.7716	827.8894	14
3	260.1063	130.5568					G	1541.7417	771.3745	1524.7151	762.8612	1523.7311	762.3692	13
4	373.1904	187.0988					I	1484.7202	742.8638	1467.6937	734.3505	1466.7097	733.8585	12
5	504.2309	252.6191					M	***1371.6362***	686.3217	1354.6096	677.8084	1353.6256	677.3164	11
6	618.2738	309.6405	601.2473	301.1273			N	***1240.5957***	620.8015	1223.5691	612.2882	1222.5851	611.7962	10
7	705.3058	353.1566	688.2793	344.6433	687.2953	344.1513	S	***1126.5527***	563.7800	1109.5262	555.2667	1108.5422	554.7747	9
8	852.3743	426.6908	835.3477	418.1775	834.3637	417.6855	F	***1039.5207***	520.2640	1022.4942	511.7507	1021.5102	511.2587	8
9	951.4427	476.2250	934.4161	467.7117	933.4321	467.2197	V	892.4523	446.7298	875.4258	438.2165	874.4417	437.7245	7
10	1065.4856	533.2464	1048.4590	524.7332	1047.4750	524.2412	N	***793.3839***	397.1956	776.3573	388.6823	775.3733	388.1903	6
11	1180.5125	590.7599	1163.4860	582.2466	1162.5020	581.7546	D	679.3410	340.1741	662.3144	331.6608	661.3304	331.1688	5
12	1293.5966	647.3019	1276.5701	638.7887	1275.5860	638.2967	I	***564.3140***	282.6606	547.2875	274.1474	546.3035	273.6554	4
13	1440.6650	720.8361	1423.6385	712.3229	1422.6545	711.8309	F	***451.2300***	226.1186	434.2034	217.6053	433.2194	217.1133	3
14	1569.7076	785.3574	1552.6811	776.8442	1551.6970	776.3522	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
15							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AMGIMNSFVNDIFER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.6	1742.8120	-0.4193	AMGIMNSFVNDIFER
4.6	1741.9574	0.4354	GNLSLLEKAIALESER
4.5	1741.9032	0.4895	SEASTSPDVPRIMKPK
3.4	1740.8505	1.5422	DNQTVFASYTLMVPR
2.8	1743.8250	-1.4323	SSRCAIATYIDEPYR
2.2	1739.9491	2.4436	VTSTSLLMPSGAAPPLAK

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

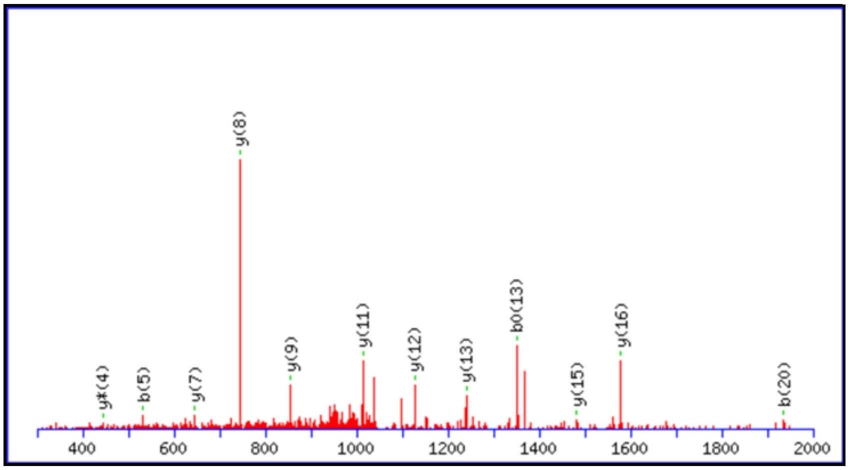
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AQFGQPEILLGTIPGAGGTQR**
Found in **gi|52218912|ref|NP_001004529.1|**, enoyl Coenzyme A hydratase, short chain, 1, mitochondrial [Danio rerio]

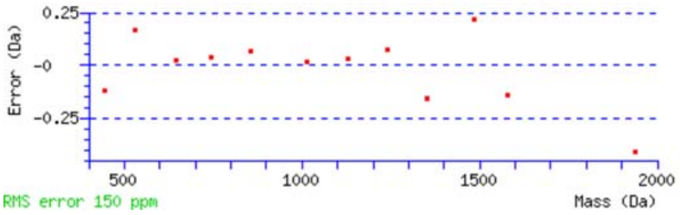
Match to Query 53789: 2111.362724 from(1056.688638,2+) index(253)
Data file TCDD_0530.dta

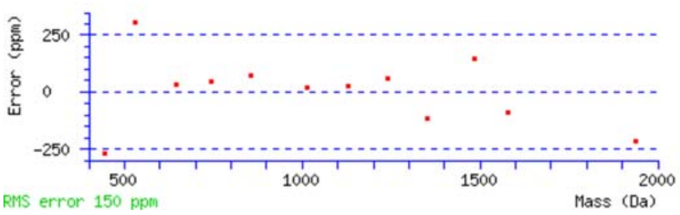
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2110.1171
Ions Score: 53 **Expect:** 0.001
Matches : 12/222 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							21
2	200.1030	100.5551	183.0764	92.0418			Q	2040.0873	1020.5473	2023.0607	1012.0340	2022.0767	1011.5420	20
3	347.1714	174.0893	330.1448	165.5761			F	1912.0287	956.5180	1895.0021	948.0047	1894.0181	947.5127	19
4	404.1928	202.6001	387.1663	194.0868			G	1764.9603	882.9838	1747.9337	874.4705	1746.9497	873.9785	18
5	**532.2514**	266.6294	515.2249	258.1161			Q	1707.9388	854.4730	1690.9123	845.9598	1689.9282	845.4678	17
6	629.3042	315.1557	612.2776	306.6425			P	***1579.8802***	790.4438	1562.8537	781.9305	1561.8697	781.4385	16
7	758.3468	379.6770	741.3202	371.1638	740.3362	370.6717	E	***1482.8275***	741.9174	1465.8009	733.4041	1464.8169	732.9121	15
8	871.4308	436.2191	854.4043	427.7058	853.4203	427.2138	I	1353.7849	677.3961	1336.7583	668.8828	1335.7743	668.3908	14
9	984.5149	492.7611	967.4884	484.2478	966.5043	483.7558	L	***1240.7008***	620.8540	1223.6743	612.3408	1222.6902	611.8488	13
10	1097.5990	549.3031	1080.5724	540.7899	1079.5884	540.2978	L	***1127.6167***	564.3120	1110.5902	555.7987	1109.6062	555.3067	12
11	1154.6204	577.8139	1137.5939	569.3006	1136.6099	568.8086	G	***1014.5327***	507.7700	997.5061	499.2567	996.5221	498.7647	11
12	1255.6681	628.3377	1238.6416	619.8244	1237.6576	619.3324	T	957.5112	479.2592	940.4847	470.7460	939.5007	470.2540	10
13	1368.7522	684.8797	1351.7256	676.3665	1350.7416	675.8744	I	***856.4635***	428.7354	839.4370	420.2221	838.4530	419.7301	9
14	1465.8049	733.4061	1448.7784	724.8928	1447.7944	724.4008	P	***743.3795***	372.1934	726.3529	363.6801	725.3689	363.1881	8
15	1522.8264	761.9168	1505.7999	753.4036	1504.8158	752.9116	G	***646.3267***	323.6670	629.3002	315.1537	628.3161	314.6617	7
16	1593.8635	797.4354	1576.8370	788.9221	1575.8530	788.4301	A	589.3053	295.1563	572.2787	286.6430	571.2947	286.1510	6
17	1650.8850	825.9461	1633.8584	817.4329	1632.8744	816.9408	G	518.2681	259.6377	501.2416	251.1244	500.2576	250.6324	5
18	1707.9064	854.4569	1690.8799	845.9436	1689.8959	845.4516	G	461.2467	231.1270	444.2201	222.6137	443.2361	222.1217	4
19	1808.9541	904.9807	1791.9276	896.4674	1790.9436	895.9754	T	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	3
20	**1937.0127**	969.0100	1919.9862	960.4967	1919.0021	960.0047	Q	303.1775	152.0924	286.1510	143.5791			2
21							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AQFGQPEILLGTIPGAGGTQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.0	2110.1171	1.2456	AQFGQPEILLGTIPGAGGTQR
13.5	2110.1211	1.2416	GVSSWILRDLLEFIYSGR
10.1	2109.0087	2.3540	SGTDTALPTSTHTPPQQNTR
7.0	2110.0957	1.2670	MSRVLILCLLLLSMSCCR
6.7	2110.0957	1.2670	MSRVLILCLLLLSMSCCR
6.4	2110.1245	1.2382	ACFSATFKPTNSIRLIDVK
5.8	2109.0967	2.2660	YGNPTDAHTLLAIQQQALR
5.7	2109.0062	2.3566	SGSVPCPGGNGRYEFISLNR
4.5	2109.8956	1.4671	IDSCGHENDAGVICHDNVR
3.8	2109.9288	1.4339	ELCEFLSYWNGSSFICR

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

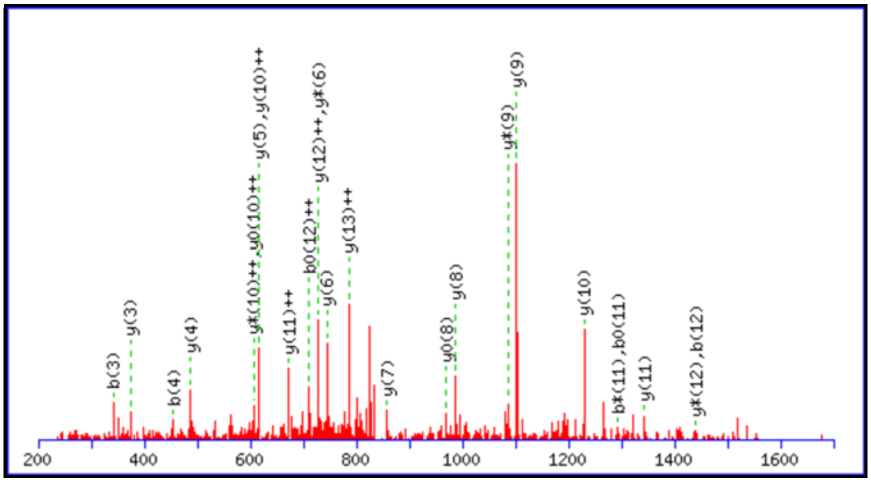
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DILLKDELEEIQAR**
Found in **gi|41055688|ref|NP_956483.1|**, diaphorase (NADH) (cytochrome b-5 reductase) [Danio rerio]

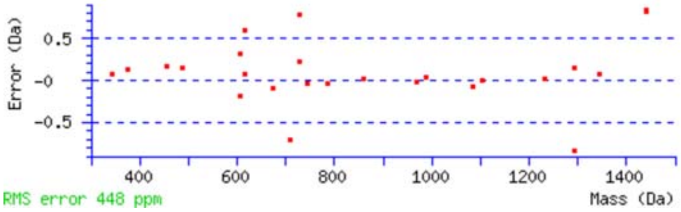
Match to Query 30979: 1683.882724 from(842.948638,2+) index(103312)
Data file TCDD_0531.dta

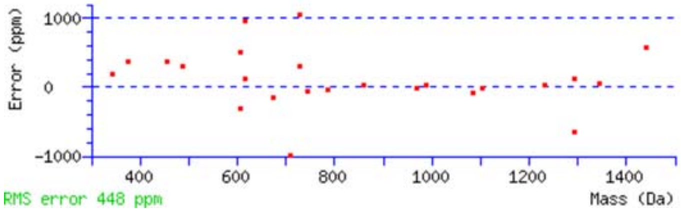
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1683.9043
Ions Score: 48 **Expect:** 0.0037
Matches : 25/140 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	**D**							**14**
2	229.1183	115.0628			211.1077	106.0575	**I**	1569.8846	785.4460	1552.8581	776.9327	1551.8741	776.4407	**13**
3	**342.2023**	171.6048			324.1918	162.5995	**L**	1456.8006	728.9039	1439.7740	720.3907	1438.7900	719.8986	**12**
4	**455.2864**	228.1468			437.2758	219.1416	**L**	***1343.7165***	672.3619	1326.6900	663.8486	1325.7060	663.3566	**11**
5	583.3814	292.1943	566.3548	283.6811	565.3708	283.1890	**K**	***1230.6325***	615.8199	1213.6059	607.3066	1212.6219	606.8146	**10**
6	698.4083	349.7078	681.3818	341.1945	680.3978	340.7025	**D**	***1102.5375***	551.7724	1085.5109	543.2591	1084.5269	542.7671	**9**
7	827.4509	414.2291	810.4244	405.7158	809.4403	405.2238	**E**	***987.5106***	494.2589	970.4840	485.7456	969.5000	485.2536	**8**
8	940.5350	470.7711	923.5084	462.2579	922.5244	461.7658	**L**	***858.4680***	429.7376	841.4414	421.2243	840.4574	420.7323	**7**
9	1069.5776	535.2924	1052.5510	526.7791	1051.5670	526.2871	**E**	***745.3839***	373.1956	728.3573	364.6823	727.3733	364.1903	**6**
10	1198.6202	599.8137	1181.5936	591.3004	1180.6096	590.8084	**E**	***616.3413***	308.6743	599.3148	300.1610	598.3307	299.6690	**5**
11	1311.7042	656.3558	1294.6777	647.8425	1293.6937	647.3505	**I**	***487.2987***	244.1530	470.2722	235.6397			**4**
12	**1439.7628**	720.3850	1422.7363	711.8718	1421.7522	711.3798	**Q**	***374.2146***	187.6110	357.1881	179.0977			**3**
13	1510.7999	755.9036	1493.7734	747.3903	1492.7894	746.8983	**A**	246.1561	123.5817	229.1295	115.0684			**2**
14							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of DILLKDELEEIQAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.3	1683.9043	-0.0215	DILLKDELEEIQAR
14.5	1681.8531	2.0296	KIMPETSAVYAMVSR
12.1	1683.7174	0.1653	GHFWAEDKMFCEK
11.9	1685.8811	-1.9983	EDPLCPFKDALLLR
11.6	1683.8791	0.0036	NILNKPTVNEDSNVK
10.5	1681.8563	2.0264	FLTKALSPFDDSVDK
10.2	1682.8740	1.0087	NLNINVNLTSGYHPK
9.1	1683.8315	0.0512	DNAVSEAPSSSSIVPPK
7.3	1681.8563	2.0264	EDFGTFKELIEQVK
6.8	1682.9032	0.9796	ALPFWNEEIVPQIK

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

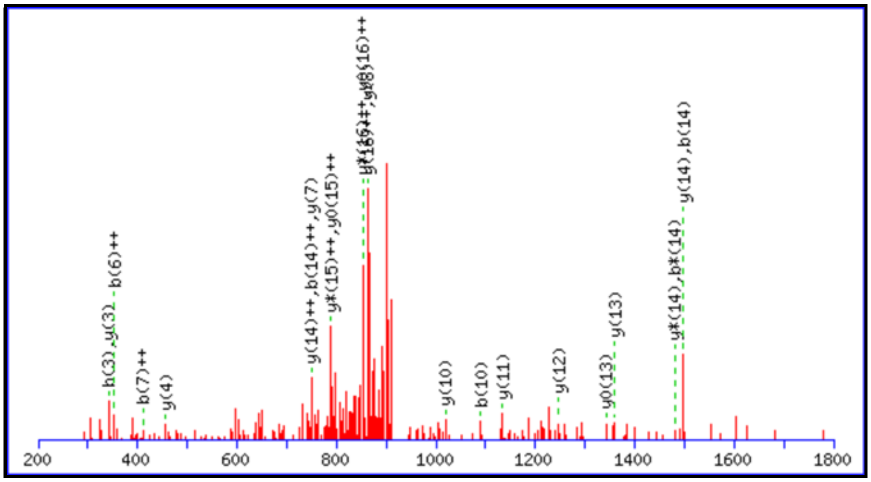
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DKPHLNIGTIGHVDHGK**
Found in **gi|61806580|ref|NP_001013523.1|**, hypothetical protein LOC541378 [Danio rerio]

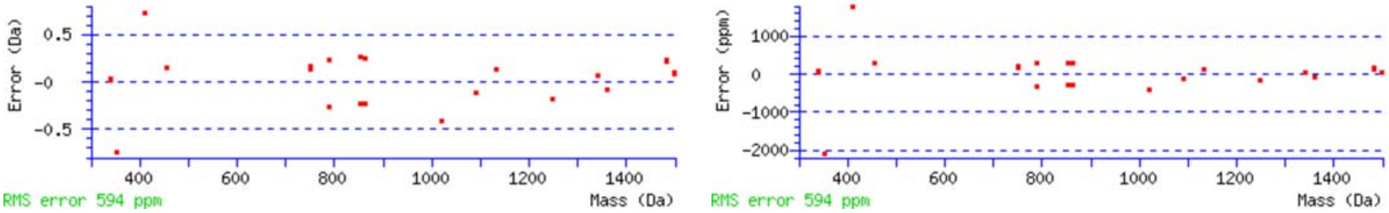
Match to Query 37212: 1838.502724 from(920.258638,2+) index(153564)
Data file TCDD_0530.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1836.9595
Ions Score: 44 **Expect:** 0.0095
Matches : 24/184 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							17
2	244.1292	122.5682	227.1026	114.0550	226.1186	113.5629	K	1722.9398	861.9735	1705.9133	853.4603	1704.9292	852.9683	16
3	**341.1819**	171.0946	324.1554	162.5813	323.1714	162.0893	P	1594.8449	797.9261	1577.8183	789.4128	1576.8343	788.9208	15
4	478.2409	239.6241	461.2143	231.1108	460.2303	230.6188	H	***1497.7921***	749.3997	1480.7655	740.8864	1479.7815	740.3944	14
5	591.3249	296.1661	574.2984	287.6528	573.3144	287.1608	L	***1360.7332***	680.8702	1343.7066	672.3570	1342.7226	671.8649	13
6	705.3678	**353.1876**	688.3413	344.6743	687.3573	344.1823	N	***1247.6491***	624.3282	1230.6226	615.8149	1229.6385	615.3229	12
7	818.4519	**409.7296**	801.4254	401.2163	800.4413	400.7243	I	***1133.6062***	567.3067	1116.5796	558.7935	1115.5956	558.3014	11
8	875.4734	438.2403	858.4468	429.7271	857.4628	429.2350	G	***1020.5221***	510.7647	1003.4956	502.2514	1002.5116	501.7594	10
9	976.5211	488.7642	959.4945	480.2509	958.5105	479.7589	T	963.5007	482.2540	946.4741	473.7407	945.4901	473.2487	9
10	**1089.6051**	545.3062	1072.5786	536.7929	1071.5946	536.3009	I	***862.4530***	431.7301	845.4264	423.2169	844.4424	422.7248	8
11	1146.6266	573.8169	1129.6000	565.3037	1128.6160	564.8116	G	***749.3689***	375.1881	732.3424	366.6748	731.3583	366.1828	7
12	1283.6855	642.3464	1266.6589	633.8331	1265.6749	633.3411	H	692.3474	346.6774	675.3209	338.1641	674.3369	337.6721	6
13	1382.7539	691.8806	1365.7274	683.3673	1364.7433	682.8753	V	555.2885	278.1479	538.2620	269.6346	537.2780	269.1426	5
14	**1497.7809**	**749.3941**	1480.7543	740.8808	1479.7703	740.3888	D	***456.2201***	228.6137	439.1936	220.1004	438.2096	219.6084	4
15	1634.8398	817.9235	1617.8132	809.4102	1616.8292	808.9182	H	***341.1932***	171.1002	324.1666	162.5870			3
16	1691.8612	846.4343	1674.8347	837.9210	1673.8507	837.4290	G	204.1343	102.5708	187.1077	94.0575			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of DKPHLNIGTIGHVDHGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.9	1836.9595	1.5432	DKPHLNIGTIGHVDHGK
7.3	1836.8685	1.6342	IQVADWMKGQTCGLCGK
1.9	1836.9707	1.5320	LNLEHGGHTRITAGPHK
0.0	1836.8069	1.6958	IHSGEKPFTCSQCGMR

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

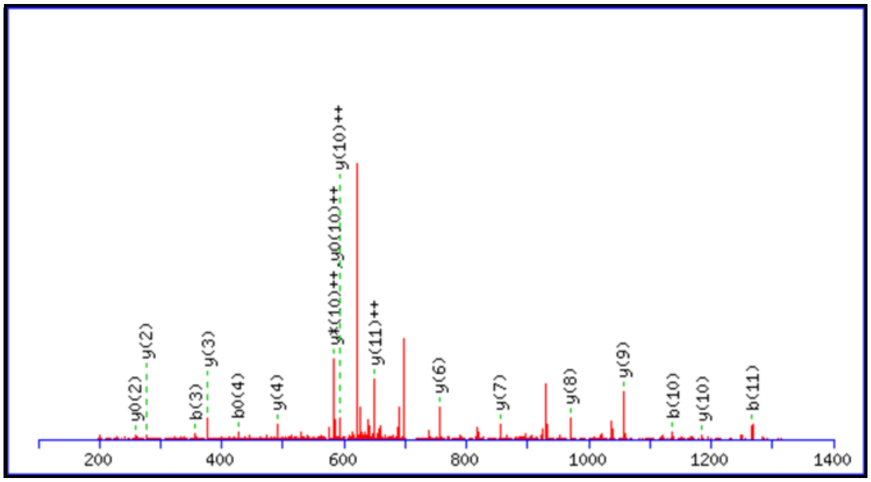
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLQSNVEHLTEK**
Found in **gi|189516256|ref|XP_689914.3|**, PREDICTED: similar to phosphofructokinase, platelet [Danio rerio]

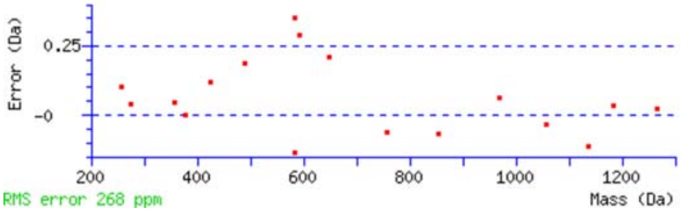
Match to Query 20617: 1412.482724 from(707.248638,2+) index(21463)
Data file TCDD_0530.dta

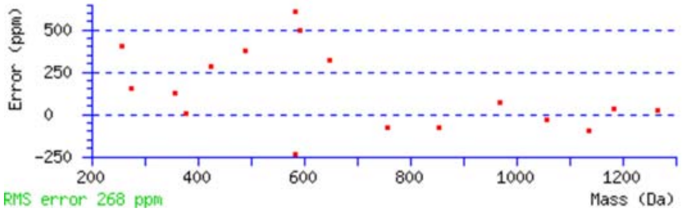
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1411.6943
Ions Score: 59 **Expect:** 0.00035
Matches : 17/126 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							12
2	229.1183	115.0628			211.1077	106.0575	L	1297.6747	649.3410	1280.6481	640.8277	1279.6641	640.3357	11
3	**357.1769**	179.0921	340.1503	170.5788	339.1663	170.0868	Q	***1184.5906***	592.7989	1167.5640	584.2857	1166.5800	583.7937	10
4	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	S	***1056.5320***	528.7696	1039.5055	520.2564	1038.5214	519.7644	9
5	558.2518	279.6295	541.2253	271.1163	540.2413	270.6243	N	***969.5000***	485.2536	952.4734	476.7404	951.4894	476.2483	8
6	657.3202	329.1638	640.2937	320.6505	639.3097	320.1585	V	***855.4571***	428.2322	838.4305	419.7189	837.4465	419.2269	7
7	786.3628	393.6850	769.3363	385.1718	768.3523	384.6798	E	***756.3886***	378.6980	739.3621	370.1847	738.3781	369.6927	6
8	923.4217	462.2145	906.3952	453.7012	905.4112	453.2092	H	627.3461	314.1767	610.3195	305.6634	609.3355	305.1714	5
9	1036.5058	518.7565	1019.4792	510.2433	1018.4952	509.7513	L	***490.2871***	245.6472	473.2606	237.1339	472.2766	236.6419	4
10	**1137.5535**	569.2804	1120.5269	560.7671	1119.5429	560.2751	T	***377.2031***	189.1052	360.1765	180.5919	359.1925	180.0999	3
11	**1266.5961**	633.8017	1249.5695	625.2884	1248.5855	624.7964	E	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of DLQSNVEHLTEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.1	1411.6943	0.7884	DLQSNVEHLTEK
21.8	1411.7558	0.7269	DIKPENILLDDK
17.2	1411.7823	0.7004	QESHSFIPLKVK
16.9	1412.6671	-0.1844	KEVDYSDSLTEK
14.4	1411.7671	0.7157	DERIAAIGLPTEK
13.5	1414.7779	-2.2952	ALSEALLSAKAEGR
12.3	1412.6792	-0.1965	MMNLTVQNTSFK
10.6	1411.8286	0.6541	DLEDLQVLIKVK
9.6	1411.7055	0.7772	LDQAKPTPANSDR
9.6	1412.7010	-0.2183	EFLKQFDEMVK

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

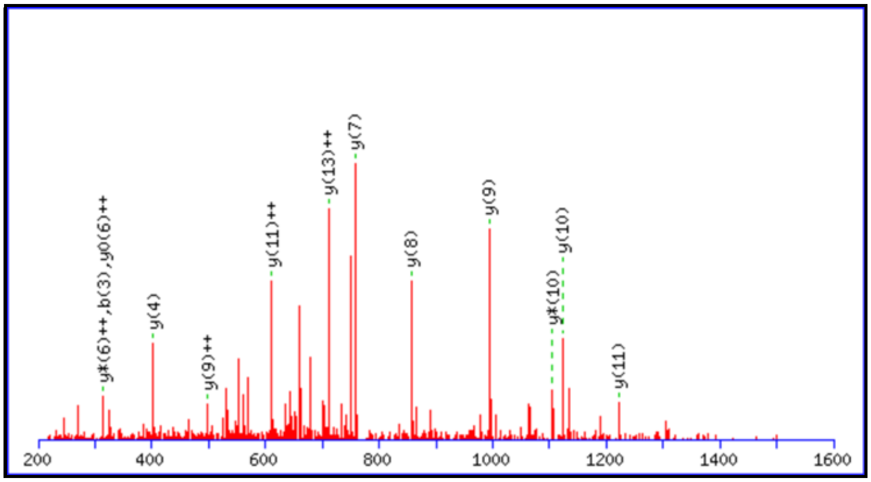
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVVVQHVNIEGLGR**
Found in **gi|55925219|ref|NP_001007344.1|**, sorting and assembly machinery component 50 homolog, like [Danio rerio]

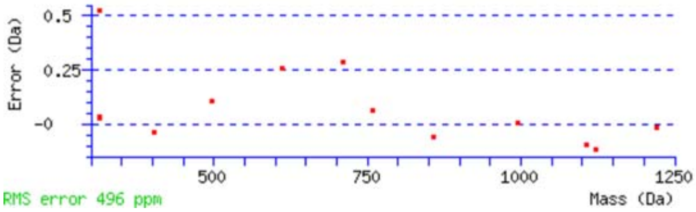
Match to Query 24230: 1535.242724 from(768.628638,2+) index(25671)
Data file TCDD_0530.dta

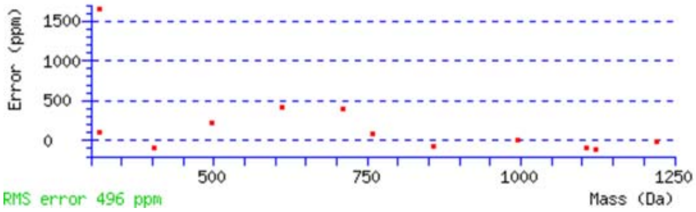
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1600 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1533.8264
Ions Score: 47 **Expect:** 0.0056
Matches : 13/140 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							14
2	215.1026	108.0550			197.0921	99.0497	V	1419.8067	710.4070	1402.7801	701.8937	1401.7961	701.4017	13
3	314.1710	157.5892			296.1605	148.5839	V	1320.7383	660.8728	1303.7117	652.3595	1302.7277	651.8675	12
4	413.2395	207.1234			395.2289	198.1181	V	***1221.6698***	611.3386	1204.6433	602.8253	1203.6593	602.3333	11
5	541.2980	271.1527	524.2715	262.6394	523.2875	262.1474	Q	***1122.6014***	561.8044	1105.5749	553.2911	1104.5909	552.7991	10
6	678.3570	339.6821	661.3304	331.1688	660.3464	330.6768	H	***994.5429***	497.7751	977.5163	489.2618	976.5323	488.7698	9
7	777.4254	389.2163	760.3988	380.7030	759.4148	380.2110	V	***857.4839***	429.2456	840.4574	420.7323	839.4734	420.2403	8
8	891.4683	446.2378	874.4417	437.7245	873.4577	437.2325	N	***758.4155***	379.7114	741.3890	371.1981	740.4050	370.7061	7
9	1004.5524	502.7798	987.5258	494.2665	986.5418	493.7745	I	644.3726	322.6899	627.3461	314.1767	626.3620	313.6847	6
10	1133.5949	567.3011	1116.5684	558.7878	1115.5844	558.2958	E	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	5
11	1190.6164	595.8118	1173.5899	587.2986	1172.6058	586.8066	G	***402.2459***	201.6266	385.2194	193.1133			4
12	1303.7005	652.3539	1286.6739	643.8406	1285.6899	643.3486	L	345.2245	173.1159	328.1979	164.6026			3
13	1360.7219	680.8646	1343.6954	672.3513	1342.7114	671.8593	G	232.1404	116.5738	215.1139	108.0606			2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of DVVVQHVNIEGLGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.8	1533.8264	1.4164	DVVVQHVNIEGLGR
14.4	1532.8021	2.4406	IEAPQMSVEFVRK
12.6	1533.8124	1.4303	SRPALHTEPSGRAR
12.6	1534.7337	0.5090	CKGIEFDAIAPDEK
11.4	1536.8009	-1.5581	GQKGEVGAPGLAGSPGR
8.8	1536.8512	-1.6084	GKSEPQELGVPVVAK
6.9	1533.6994	1.5433	THSSGASPPTPCHQK
6.0	1533.7344	1.5083	LVEAETTEEMINR
4.7	1534.7562	0.4865	MSSKPFTPEEARR
4.4	1535.7579	-0.5152	KEQGGEEVIAYASR

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

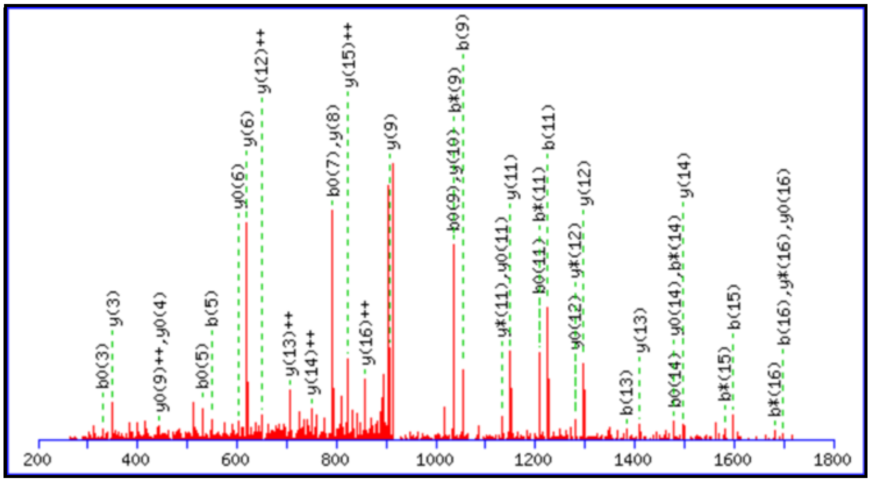
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAFSLFDKDGDGTITTK**
Found in **gi|189532998|ref|XP_001919221.1|**, PREDICTED: similar to calmodulin 2 [Danio rerio]

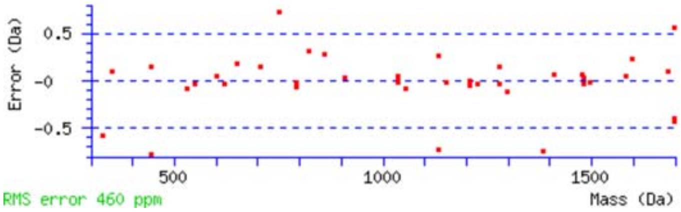
Match to Query 37670: 1845.342724 from(923.678638,2+) index(30592)
Data file TCDD_0530.dta

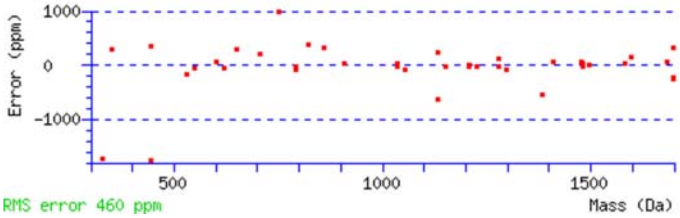
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1843.8840
Ions Score: 54 **Expect:** 0.00095
Matches : 41/176 fragment ions using 60 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	201.0870	101.0471			183.0764	92.0418	A	1715.8487	858.4280	1698.8221	849.9147	1697.8381	849.4227	16
3	348.1554	174.5813			330.1448	165.5761	F	1644.8115	822.9094	1627.7850	814.3961	1626.8010	813.9041	15
4	435.1874	218.0974			417.1769	209.0921	S	***1497.7431***	749.3752	1480.7166	740.8619	1479.7326	740.3699	14
5	***548.2715***	274.6394			530.2609	265.6341	L	***1410.7111***	705.8592	1393.6846	697.3459	1392.7005	696.8539	13
6	695.3399	348.1736			677.3293	339.1683	F	***1297.6270***	649.3172	1280.6005	640.8039	1279.6165	640.3119	12
7	810.3668	405.6871			792.3563	396.6818	D	***1150.5586***	575.7830	1133.5321	567.2697	1132.5481	566.7777	11
8	938.4618	469.7345	921.4353	461.2213	920.4512	460.7293	K	***1035.5317***	518.2695	1018.5051	509.7562	1017.5211	509.2642	10
9	***1053.4888***	527.2480	1036.4622	518.7347	1035.4782	518.2427	D	***907.4367***	454.2220	890.4102	445.7087	889.4262	445.2167	9
10	1110.5102	555.7587	1093.4837	547.2455	1092.4997	546.7535	G	***792.4098***	396.7085	775.3832	388.1953	774.3992	387.7032	8
11	***1225.5372***	613.2722	1208.5106	604.7589	1207.5266	604.2669	D	735.3883	368.1978	718.3618	359.6845	717.3777	359.1925	7
12	1282.5586	641.7829	1265.5321	633.2697	1264.5481	632.7777	G	***620.3614***	310.6843	603.3348	302.1710	602.3508	301.6790	6
13	***1383.6063***	692.3068	1366.5798	683.7935	1365.5957	683.3015	T	563.3399	282.1736	546.3134	273.6603	545.3293	273.1683	5
14	1496.6904	748.8488	1479.6638	740.3355	1478.6798	739.8435	I	462.2922	231.6498	445.2657	223.1365	444.2817	222.6445	4
15	***1597.7380***	799.3727	1580.7115	790.8594	1579.7275	790.3674	T	***349.2082***	175.1077	332.1816	166.5944	331.1976	166.1024	3
16	***1698.7857***	849.8965	1681.7592	841.3832	1680.7752	840.8912	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
17							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EAFSLFDKDGDGTITTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.9	1843.8840	1.4587	EAFSLFDKDGDGTITTK
13.9	1843.9176	1.4251	QAIQSNALNNDKWSAGK
7.9	1842.9087	2.4341	HNFICKYEPESHLVK
7.3	1844.0601	1.2827	KFIFTGVFVGGVYLLGK
7.0	1844.8462	0.4965	SLQLSDSGVYQCTSTEK
6.4	1844.8792	0.4635	QFQSTIPSSSSYPTSTK
5.4	1843.7869	1.5558	YWAQKDMESGQVCDK
4.6	1845.8390	-0.4962	FSTECQDLISQCFIR
3.5	1844.7896	0.5532	CSTKFPDCNCPFADIK
3.4	1843.8887	1.4541	TYGPECDIVLDAAHRK

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

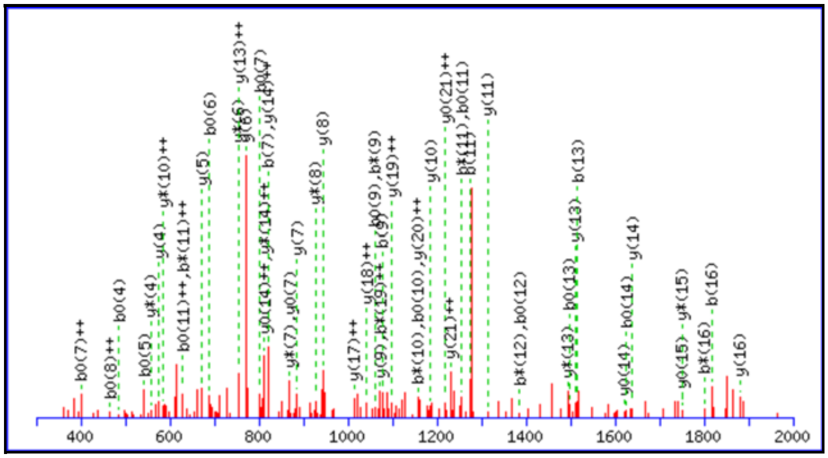
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFLLGFLEQPVEIEGDVPFRPR**
Found in **gi|41055708|ref|NP_956866.1|**, proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 [Danio rerio]

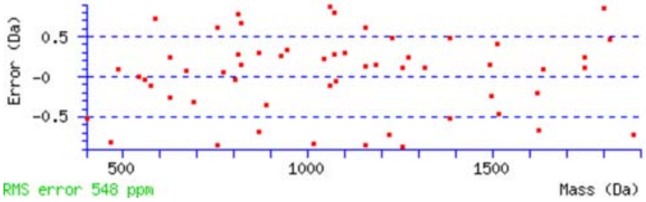
Match to Query 103669: 2587.792724 from(1294.903638,2+) index(28699)
Data file TCDD_0531.dta

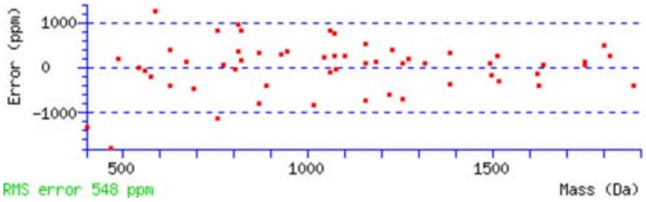
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2586.3482
Ions Score: 41 **Expect:** 0.011
Matches : 56/224 fragment ions using 117 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							22
2	277.1183	139.0628			259.1077	130.0575	F	2458.3129	1229.6601	2441.2864	1221.1468	2440.3023	1220.6548	21
3	390.2023	195.6048			372.1918	186.5995	L	2311.2445	1156.1259	2294.2179	1147.6126	2293.2339	1147.1206	20
4	503.2864	252.1468			485.2758	243.1416	L	2198.1604	1099.5839	2181.1339	1091.0706	2180.1499	1090.5786	19
5	560.3079	280.6576			542.2973	271.6523	G	2085.0764	1043.0418	2068.0498	1034.5285	2067.0658	1034.0365	18
6	707.3763	354.1918			689.3657	345.1865	F	2028.0549	1014.5311	2011.0284	1006.0178	2010.0443	1005.5258	17
7	**820.4604**	410.7338			802.4498	401.7285	L	***1880.9865***	940.9969	1863.9599	932.4836	1862.9759	931.9916	16
8	949.5029	475.2551			931.4924	466.2498	E	1767.9024	884.4549	1750.8759	875.9416	1749.8919	875.4496	15
9	**1077.5615**	539.2844	1060.5350	530.7711	1059.5510	530.2791	Q	***1638.8598***	819.9336	1621.8333	811.4203	1620.8493	810.9283	14
10	1174.6143	587.8108	1157.5877	579.2975	1156.6037	578.8055	P	***1510.8013***	755.9043	1493.7747	747.3910	1492.7907	746.8990	13
11	**1273.6827**	637.3450	1256.6562	628.8317	1255.6721	628.3397	V	1413.7485	707.3779	1396.7219	698.8646	1395.7379	698.3726	12
12	1402.7253	701.8663	1385.6987	693.3530	1384.7147	692.8610	E	***1314.6801***	657.8437	1297.6535	649.3304	1296.6695	648.8384	11
13	**1515.8094**	758.4083	1498.7828	749.8950	1497.7988	749.4030	I	***1185.6375***	593.3224	1168.6109	584.8091	1167.6269	584.3171	10
14	1644.8520	822.9296	1627.8254	814.4163	1626.8414	813.9243	E	***1072.5534***	536.7803	1055.5269	528.2671	1054.5429	527.7751	9
15	1701.8734	851.4403	1684.8469	842.9271	1683.8629	842.4351	G	***943.5108***	472.2591	926.4843	463.7458	925.5003	463.2538	8
16	**1816.9004**	908.9538	1799.8738	900.4405	1798.8898	899.9485	D	***886.4894***	443.7483	869.4628	435.2350	868.4788	434.7430	7
17	1915.9688	958.4880	1898.9422	949.9747	1897.9582	949.4827	V	***771.4624***	386.2348	754.4359	377.7216			6
18	2013.0215	1007.0144	1995.9950	998.5011	1995.0110	998.0091	P	***672.3940***	336.7006	655.3675	328.1874			5
19	2160.0900	1080.5486	2143.0634	1072.0353	2142.0794	1071.5433	F	***575.3412***	288.1743	558.3147	279.6610			4
20	2316.1911	1158.5992	2299.1645	1150.0859	2298.1805	1149.5939	R	428.2728	214.6401	411.2463	206.1268			3
21	2413.2438	1207.1256	2396.2173	1198.6123	2395.2333	1198.1203	P	272.1717	136.5895	255.1452	128.0762			2
22							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of EFLLGFLEQPVEIEGDVPFRPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.3	2586.3482	1.4445	EFLLGFLEQPVEIEGDVPFRPR
7.3	2586.2171	1.5757	DGNNDNRNILQAANEASTLGWGTR
6.2	2586.3047	1.4881	VPADCVLGEVGGGFKVAMNILNNGR
5.4	2589.1368	-1.3440	GYSHNIGTNQAVNSDYKNSDYDK
4.9	2586.2723	1.5205	LSALLMAAGADPHKENCEPLFFR
4.3	2588.2826	-0.4899	LQKLASLDVDCAVLDCEDGVALNK
3.8	2587.2588	0.5339	NIFLTDSGTVKVGDFGSACSLNSAK
3.3	2588.3003	-0.5076	EDGELKELEVNGDITTMVLTNLR
3.0	2587.2642	0.5286	TVHYCLTNNKHFSFPANALPEK
2.4	2585.4078	2.3849	KQIATQTNLTLLQVNNWFINAR

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

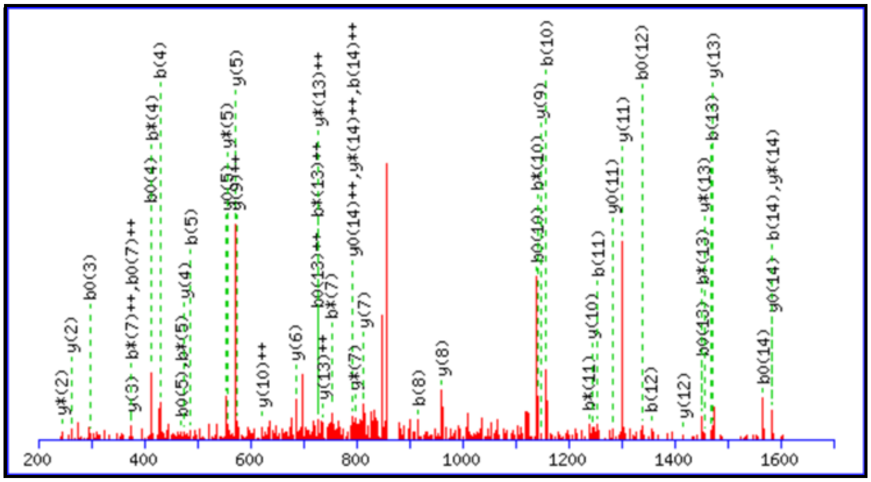
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EKGDGPWFQIPTIDK**
Found in **gi|157743314|ref|NP_001099066.1|**, NADH dehydrogenase (ubiquinone) 1 beta subcomplex 5 [Danio rerio]

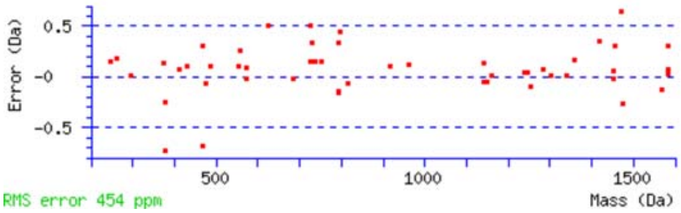
Match to Query 31312: 1730.332724 from(866.173638,2+) index(34002)
Data file TCDD_0530.dta

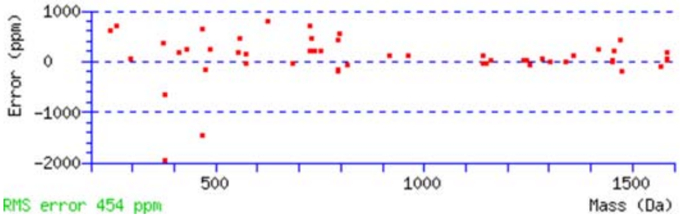
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1729.8675
Ions Score: 46 **Expect:** 0.006
Matches : 52/164 fragment ions using 140 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	**E**							**15**
2	258.1448	129.5761	241.1183	121.0628	240.1343	120.5708	**K**	1601.8322	801.4197	1584.8057	792.9065	1583.8217	792.4145	**14**
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	**G**	***1473.7373***	737.3723	1456.7107	728.8590	1455.7267	728.3670	**13**
4	**430.1932**	215.6003	413.1667	207.0870	412.1827	206.5950	**D**	***1416.7158***	708.8615	1399.6892	700.3483	1398.7052	699.8563	**12**
5	**487.2147**	244.1110	470.1882	235.5977	469.2041	235.1057	**G**	***1301.6889***	651.3481	1284.6623	642.8348	1283.6783	642.3428	**11**
6	584.2675	292.6374	567.2409	284.1241	566.2569	283.6321	**P**	***1244.6674***	622.8373	1227.6408	614.3241	1226.6568	613.8320	**10**
7	770.3468	385.6770	753.3202	377.1638	752.3362	376.6717	**W**	***1147.6146***	574.3109	1130.5881	565.7977	1129.6041	565.3057	**9**
8	**917.4152**	459.2112	900.3886	450.6980	899.4046	450.2060	**F**	***961.5353***	481.2713	944.5088	472.7580	943.5247	472.2660	**8**
9	1045.4738	523.2405	1028.4472	514.7272	1027.4632	514.2352	**Q**	***814.4669***	407.7371	797.4403	399.2238	796.4563	398.7318	**7**
10	**1158.5578**	579.7826	1141.5313	571.2693	1140.5473	570.7773	**I**	***686.4083***	343.7078	669.3818	335.1945	668.3978	334.7025	**6**
11	**1255.6106**	628.3089	1238.5841	619.7957	1237.6000	619.3037	**P**	***573.3243***	287.1658	556.2977	278.6525	555.3137	278.1605	**5**
12	**1356.6583**	678.8328	1339.6317	670.3195	1338.6477	669.8275	**T**	***476.2715***	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
13	**1469.7423**	735.3748	1452.7158	726.8615	1451.7318	726.3695	**I**	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	**3**
14	**1584.7693**	792.8883	1567.7427	784.3750	1566.7587	783.8830	**D**	***262.1397***	131.5735	245.1132	123.0602	244.1292	122.5682	**2**
15							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of EKGDGPWFQIPTIDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.2	1729.8675	0.4652	EKGDGPWFQIPTIDK
8.8	1729.8846	0.4481	SGKSEEAVLLQGVNGDK
7.7	1728.9046	1.4281	VYSQLEHAETVVNIK
7.2	1729.8482	0.4845	DAENLINTAREELDK
6.1	1728.9087	1.4240	TYPPLPDIFLDSVPR
5.7	1728.9622	1.3706	LDEKTVIITGANTGIGK
5.4	1729.8271	0.5056	GDQGSIGYPGSPGKPGEK
5.3	1729.9396	0.3931	TSPQTLSNLCLKINAK
5.2	1728.7737	1.5590	EEPAAACPETVGAQNSR
4.5	1727.9669	2.3659	DESKIIQLSETKPLK

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

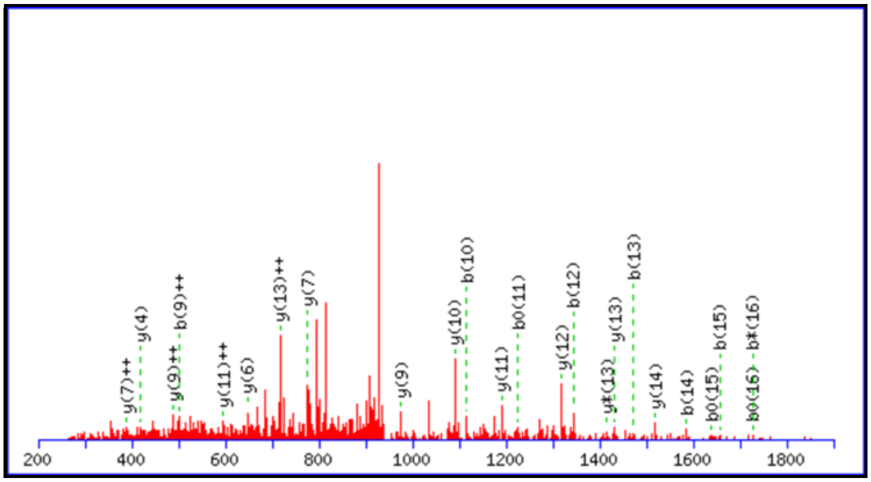
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELESIEVDSIEVENASK**
Found in **gi|47086623|ref|NP_997873.1|**, monocarboxylate transporter 4 [Danio rerio]

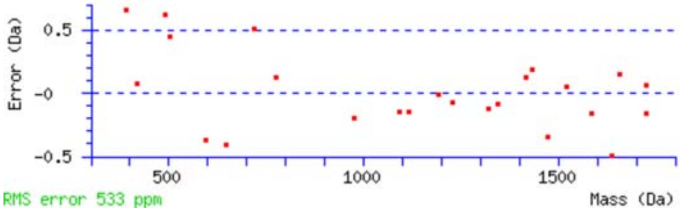
Match to Query 40788: 1891.422724 from(946.718638,2+) index(9247)
Data file TCDD_0530.dta

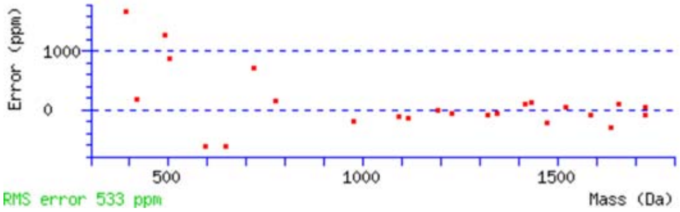
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1889.9105
Ions Score: 46 **Expect:** 0.0051
Matches : 24/164 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	243.1339	122.0706			225.1234	113.0653	L	1761.8753	881.4413	1744.8487	872.9280	1743.8647	872.4360	16
3	372.1765	186.5919			354.1660	177.5866	E	1648.7912	824.8992	1631.7647	816.3860	1630.7806	815.8940	15
4	459.2086	230.1079			441.1980	221.1026	S	***1519.7486***	760.3779	1502.7221	751.8647	1501.7380	751.3727	14
5	572.2926	286.6499			554.2821	277.6447	I	***1432.7166***	716.8619	1415.6900	708.3487	1414.7060	707.8566	13
6	701.3352	351.1712			683.3246	342.1660	E	***1319.6325***	660.3199	1302.6060	651.8066	1301.6220	651.3146	12
7	800.4036	400.7055			782.3931	391.7002	V	***1190.5899***	595.7986	1173.5634	587.2853	1172.5794	586.7933	11
8	915.4306	458.2189			897.4200	449.2136	D	***1091.5215***	546.2644	1074.4950	537.7511	1073.5109	537.2591	10
9	1002.4626	501.7349			984.4520	492.7297	S	***976.4946***	488.7509	959.4680	480.2376	958.4840	479.7456	9
10	***1115.5467***	558.2770			1097.5361	549.2717	I	889.4625	445.2349	872.4360	436.7216	871.4520	436.2296	8
11	1244.5893	622.7983			1226.5787	613.7930	E	***776.3785***	388.6929	759.3519	380.1796	758.3679	379.6876	7
12	***1343.6577***	672.3325			1325.6471	663.3272	V	***647.3359***	324.1716	630.3093	315.6583	629.3253	315.1663	6
13	***1472.7003***	736.8538			1454.6897	727.8485	E	548.2675	274.6374	531.2409	266.1241	530.2569	265.6321	5
14	***1586.7432***	793.8752	1569.7166	785.3620	1568.7326	784.8699	N	***419.2249***	210.1161	402.1983	201.6028	401.2143	201.1108	4
15	***1657.7803***	829.3938	1640.7538	820.8805	1639.7697	820.3885	A	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
16	1744.8123	872.9098	1727.7858	864.3965	1726.8018	863.9045	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
17							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ELESIEVDSIEVENASK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.5	1889.9105	1.5122	ELESIEVDSIEVENASK
5.7	1888.9676	2.4551	LQESNARLCVDVSQSLK
2.5	1890.8993	0.5234	SKLDGSNLLGMLDEDER
2.1	1890.9938	0.4289	ETEEILADTLKVEVFR
0.5	1888.9894	2.4333	QIFEEEIRELQSQIK
0.4	1891.8006	-0.3779	EYERSEDGMNSYASVR

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

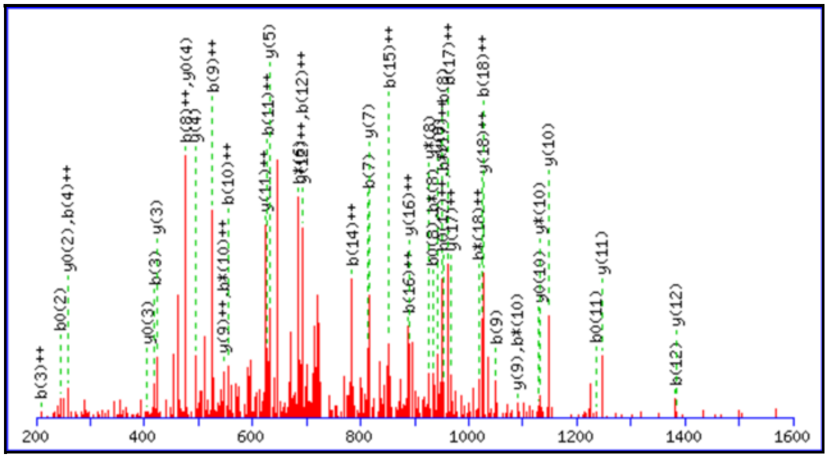
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FDRPGQLHVGFQALHAFEK**
Found in **gi|47085781|ref|NP_998227.1|**, ubiquitin-like modifier activating enzyme 1 [Danio rerio]

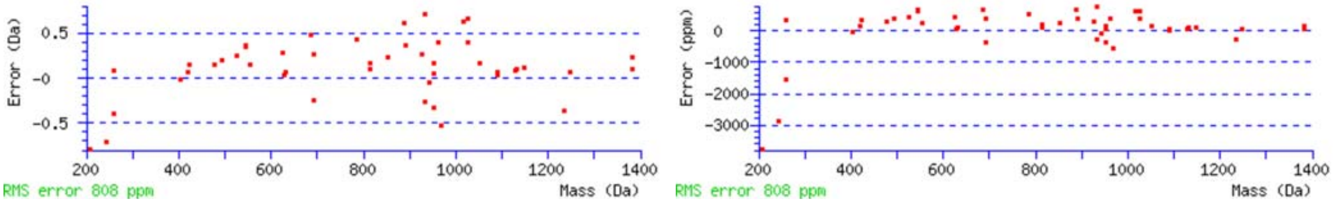
Match to Query 64511: 2196.052725 from(733.024851,3+) index(67910)
Data file TCDD_0530.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2196.1229
Ions Score: 41 **Expect:** 0.015
Matches : 48/208 fragment ions using 110 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415					F							19
2	263.1026	132.0550			245.0921	123.0497	D	2050.0617	1025.5345	2033.0352	1017.0212	2032.0512	1016.5292	18
3	**419.2037**	***210.1055***	402.1772	201.5922	401.1932	201.1002	R	1935.0348	968.0210	1918.0082	959.5078	1917.0242	959.0157	17
4	516.2565	***258.6319***	499.2300	250.1186	498.2459	249.6266	P	1778.9337	889.9705	1761.9071	881.4572	1760.9231	880.9652	16
5	573.2780	287.1426	556.2514	278.6293	555.2674	278.1373	G	1681.8809	841.4441	1664.8544	832.9308	1663.8703	832.4388	15
6	701.3366	351.1719	684.3100	342.6586	683.3260	342.1666	Q	1624.8594	812.9334	1607.8329	804.4201	1606.8489	803.9281	14
7	**814.4206**	407.7139	797.3941	399.2007	796.4100	398.7087	L	1496.8009	748.9041	1479.7743	740.3908	1478.7903	739.8988	13
8	**951.4795**	***476.2434***	934.4530	467.7301	933.4690	467.2381	H	**1383.7168**	692.3620	1366.6902	683.8488	1365.7062	683.3568	12
9	**1050.5479**	***525.7776***	1033.5214	517.2643	1032.5374	516.7723	V	**1246.6579**	623.8326	1229.6313	615.3193	1228.6473	614.8273	11
10	1107.5694	***554.2883***	1090.5429	545.7751	1089.5588	545.2831	G	**1147.5895**	574.2984	1130.5629	565.7851	1129.5789	565.2931	10
11	1254.6378	***627.8225***	1237.6113	619.3093	1236.6273	618.8173	F	**1090.5680**	545.7876	1073.5415	537.2744	1072.5574	536.7824	9
12	**1382.6964**	***691.8518***	1365.6698	683.3386	1364.6858	682.8466	Q	**943.4996**	472.2534	926.4730	463.7402	925.4890	463.2482	8
13	1453.7335	727.3704	1436.7070	718.8571	1435.7229	718.3651	A	**815.4410**	408.2241	798.4145	399.7109	797.4305	399.2189	7
14	1566.8176	***783.9124***	1549.7910	775.3992	1548.8070	774.9071	L	744.4039	372.7056	727.3774	364.1923	726.3933	363.7003	6
15	1703.8765	***852.4419***	1686.8499	843.9286	1685.8659	843.4366	H	**631.3198**	316.1636	614.2933	307.6503	613.3093	307.1583	5
16	1774.9136	***887.9604***	1757.8871	879.4472	1756.9030	878.9552	A	**494.2609**	247.6341	477.2344	239.1208	476.2504	238.6288	4
17	1921.9820	***961.4946***	1904.9555	952.9814	1903.9714	952.4894	F	**423.2238**	212.1155	406.1973	203.6023	405.2132	203.1103	3
18	2051.0246	***1026.0159***	2033.9981	1017.5027	2033.0140	1017.0107	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
19							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of FDRPGQLHVGFQALHAFEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.4	2196.1229	-0.0701	FDRPGQLHVGFQALHAFEK
11.5	2197.1275	-1.0748	NFQLQMCEYLLKIQELK
11.4	2197.2141	-1.1613	VGGKPSMVPVATVDTGASLGVKK
11.0	2198.2158	-2.1630	IANLVLSIQTEEEILTREK
7.5	2197.0004	-0.9477	INESRSHNLPDCTVHSCTK
5.5	2198.0313	-1.9786	NKPNENSYCYQLLQELDK
5.1	2198.2099	-2.1572	QIPLVSSVLNWFSPVQASVK
5.0	2195.0027	1.0500	TATMLCAASGNPDPEISWFK
3.1	2195.9609	0.0918	TGGALNRLCSDELCQCAEEK
3.0	2198.1113	-2.0586	QELSLQTAVCTSPGPRENIR

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

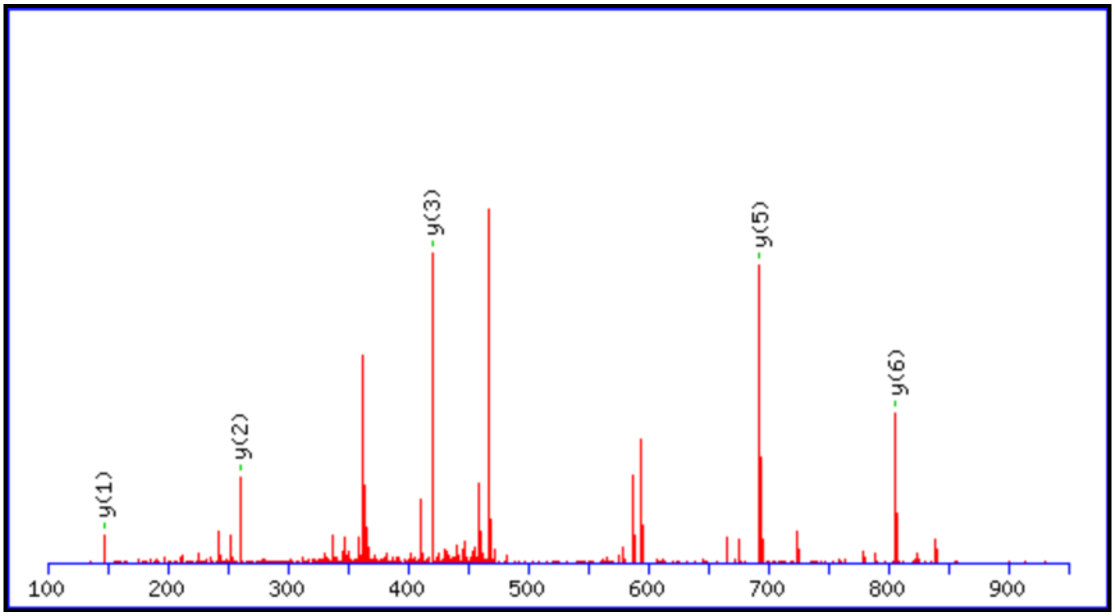
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLLCCLK**
Found in **gi|38564419|ref|NP_942572.1|**, choline transporter-like protein 2 [Danio rerio]

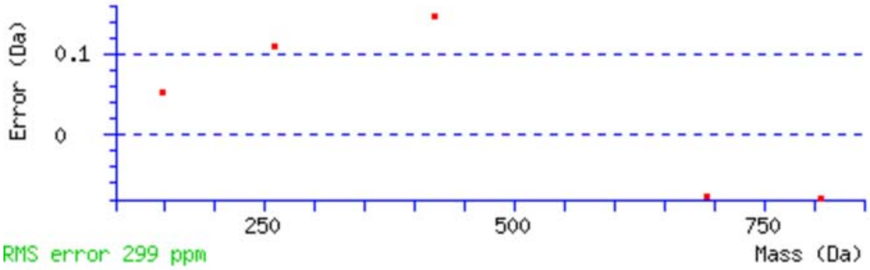
Match to Query 7353: 952.952724 from(477.483638,2+) index(103907)
Data file TCDD_0530.dta

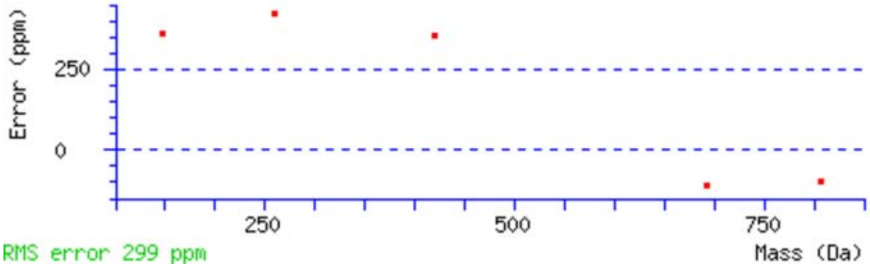
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 952.4874
Variable modifications:
C4 : Carbamidomethyl (C)
C5 : Carbamidomethyl (C)
Ions Score: 41 **Expect:** 0.024
Matches : 5/36 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	148.0757	74.5415	F					7
2	261.1598	131.0835	L	*806.4263*	403.7168	789.3997	395.2035	6
3	374.2438	187.6255	L	*693.3422*	347.1748	676.3157	338.6615	5
4	534.2745	267.6409	C	580.2582	290.6327	563.2316	282.1194	4
5	694.3051	347.6562	C	*420.2275*	210.6174	403.2010	202.1041	3
6	807.3892	404.1982	L	*260.1969*	130.6021	243.1703	122.0888	2
7			K	*147.1128*	74.0600	130.0863	65.5468	1





NCBI **BLAST** search of FLLCCLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.2	952.4874	0.4653	FLLCCLK
28.5	951.5753	1.3774	IHELTVLK
25.5	952.4688	0.4839	FICSENLK
23.3	952.4688	0.4839	LADFGSCLK
22.4	951.5905	1.3622	IYRFLLK
21.5	951.4154	1.5373	DSCGLCLK
21.2	951.5753	1.3774	GPSLIPQIK
20.8	951.3968	1.5560	VCTDGGSEK
19.7	951.5575	1.3952	IHTLMPLK
19.7	951.5753	1.3774	IPPGLNTLK

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

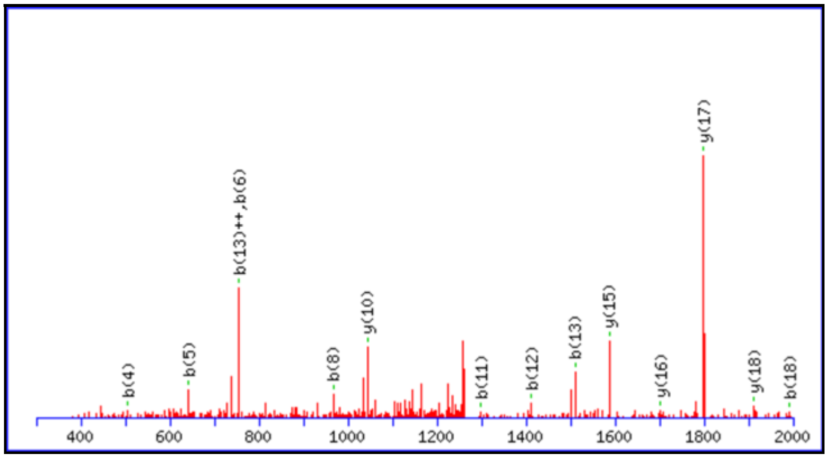
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FNNEHIPDSPFIVPVATLSDDAR**
Found in **gi|189540123|ref|XP_692436.3|**, PREDICTED: similar to Filamin-C (Gamma-filamin) (Filamin-2) (FLN-C) (Actin-binding-like protein) (ABP-L) (ABP-280-like protein) [Danio rerio]

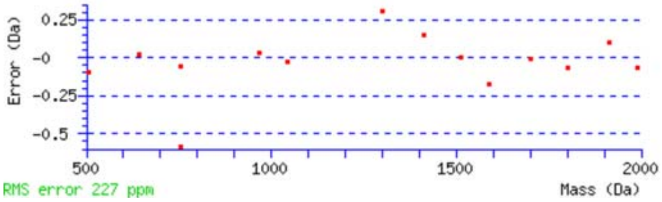
Match to Query 94640: 2553.772724 from(1277.893638,2+) index(106562)
Data file TCDD_0530.dta

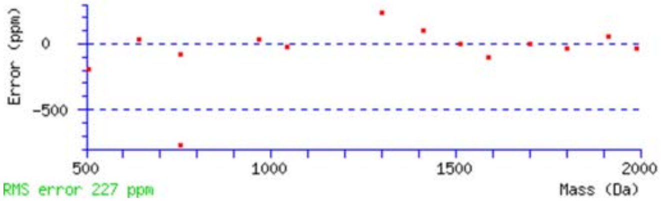
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2553.2500
Ions Score: 57 **Expect:** 0.0003
Matches : 14/252 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							23
2	262.1186	131.5629	245.0921	123.0497			N	2407.1888	1204.0981	2390.1623	1195.5848	2389.1783	1195.0928	22
3	376.1615	188.5844	359.1350	180.0711			N	2293.1459	1147.0766	2276.1194	1138.5633	2275.1353	1138.0713	21
4	***505.2041***	253.1057	488.1776	244.5924	487.1936	244.1004	E	2179.1030	1090.0551	2162.0764	1081.5419	2161.0924	1081.0498	20
5	***642.2630***	321.6352	625.2365	313.1219	624.2525	312.6299	H	2050.0604	1025.5338	2033.0338	1017.0206	2032.0498	1016.5285	19
6	***755.3471***	378.1772	738.3206	369.6639	737.3365	369.1719	I	**1913.0015**	957.0044	1895.9749	948.4911	1894.9909	947.9991	18
7	852.3999	426.7036	835.3733	418.1903	834.3893	417.6983	P	**1799.9174**	900.4623	1782.8909	891.9491	1781.9068	891.4571	17
8	***967.4268***	484.2170	950.4003	475.7038	949.4163	475.2118	D	**1702.8646**	851.9360	1685.8381	843.4227	1684.8541	842.9307	16
9	1054.4588	527.7331	1037.4323	519.2198	1036.4483	518.7278	S	**1587.8377**	794.4225	1570.8112	785.9092	1569.8271	785.4172	15
10	1151.5116	576.2594	1134.4851	567.7462	1133.5010	567.2542	P	1500.8057	750.9065	1483.7791	742.3932	1482.7951	741.9012	14
11	***1298.5800***	649.7937	1281.5535	641.2804	1280.5695	640.7884	F	1403.7529	702.3801	1386.7264	693.8668	1385.7423	693.3748	13
12	***1411.6641***	706.3357	1394.6375	697.8224	1393.6535	697.3304	I	1256.6845	628.8459	1239.6579	620.3326	1238.6739	619.8406	12
13	***1510.7325***	755.8699	1493.7060	747.3566	1492.7219	746.8646	V	1143.6004	572.3039	1126.5739	563.7906	1125.5899	563.2986	11
14	1607.7853	804.3963	1590.7587	795.8830	1589.7747	795.3910	P	**1044.5320**	522.7696	1027.5055	514.2564	1026.5214	513.7644	10
15	1706.8537	853.9305	1689.8271	845.4172	1688.8431	844.9252	V	947.4793	474.2433	930.4527	465.7300	929.4687	465.2380	9
16	1777.8908	889.4490	1760.8642	880.9358	1759.8802	880.4438	A	848.4108	424.7091	831.3843	416.1958	830.4003	415.7038	8
17	1878.9385	939.9729	1861.9119	931.4596	1860.9279	930.9676	T	777.3737	389.1905	760.3472	380.6772	759.3632	380.1852	7
18	***1992.0225***	996.5149	1974.9960	988.0016	1974.0120	987.5096	L	676.3260	338.6667	659.2995	330.1534	658.3155	329.6614	6
19	2079.0546	1040.0309	2062.0280	1031.5176	2061.0440	1031.0256	S	563.2420	282.1246	546.2154	273.6114	545.2314	273.1193	5
20	2194.0815	1097.5444	2177.0550	1089.0311	2176.0709	1088.5391	D	476.2100	238.6086	459.1834	230.0953	458.1994	229.6033	4
21	2309.1085	1155.0579	2292.0819	1146.5446	2291.0979	1146.0526	D	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
22	2380.1456	1190.5764	2363.1190	1182.0631	2362.1350	1181.5711	A	246.1561	123.5817	229.1295	115.0684			2
23							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of FNNEHIPDSPFIVPVATLSDDAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.1	2553.2500	0.5228	FNNEHIPDSPFIVPVATLSDDAR
24.6	2554.2340	-0.4613	FNDEHIPDSPFIVPIASLSDDAR
1.5	2553.2249	0.5479	ADIRPADHPVADFDFDVVVGADGR
0.7	2553.2745	0.4983	EEPVRGSDGLCVEAAPGETGLLVAK
0.0	2553.3650	0.4077	KPVDTTIINLDVSEKPTGSTVPSR

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

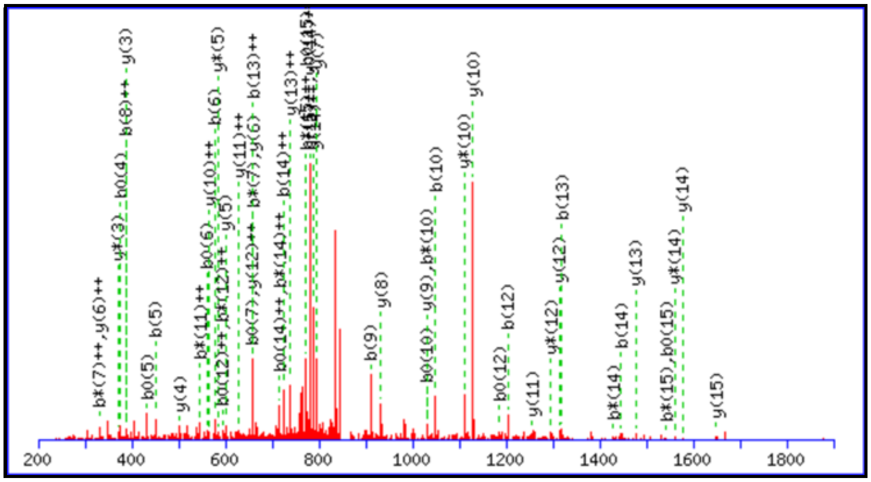
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GATYGKPVHHGVNQIK**
Found in **gi|51010975|ref|NP_001003447.1|**, hypothetical protein LOC445053 [Danio rerio]

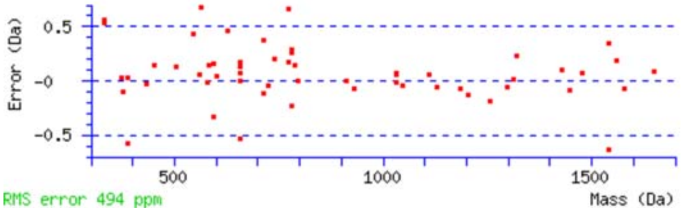
Match to Query 30240: 1705.422724 from(853.718638,2+) index(83179)
Data file TCDD_0530.dta

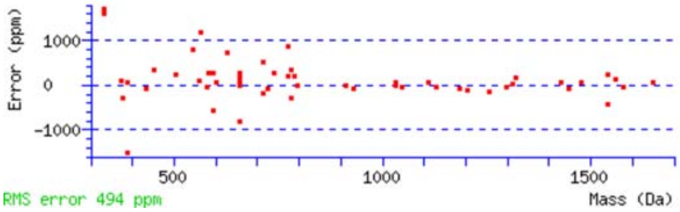
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1704.9060
Ions Score: 54 **Expect:** 0.0012
Matches : 56/140 fragment ions using 138 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							16
2	129.0659	65.0366					A	***1648.8918***	824.9495	1631.8653	816.4363	1630.8812	815.9443	15
3	230.1135	115.5604			212.1030	106.5551	T	***1577.8547***	789.4310	1560.8281	780.9177	1559.8441	780.4257	14
4	393.1769	197.0921			375.1663	188.0868	Y	***1476.8070***	738.9071	1459.7805	730.3939			13
5	**450.1983**	225.6028			432.1878	216.5975	G	***1313.7437***	657.3755	1296.7171	648.8622			12
6	**578.2933**	289.6503	561.2667	281.1370	560.2827	280.6450	K	***1256.7222***	628.8647	1239.6957	620.3515			11
7	675.3461	338.1767	658.3195	329.6634	657.3355	329.1714	P	***1128.6273***	564.8173	1111.6007	556.3040			10
8	774.4145	387.7109	757.3879	379.1976	756.4039	378.7056	V	***1031.5745***	516.2909	1014.5479	507.7776			9
9	**911.4734**	456.2403	894.4468	447.7271	893.4628	447.2350	H	***932.5061***	466.7567	915.4795	458.2434			8
10	**1048.5323**	524.7698	1031.5057	516.2565	1030.5217	515.7645	H	***795.4472***	398.2272	778.4206	389.7139			7
11	1105.5538	553.2805	1088.5272	544.7672	1087.5432	544.2752	G	***658.3883***	329.6978	641.3617	321.1845			6
12	**1204.6222**	602.8147	1187.5956	594.3014	1186.6116	593.8094	V	***601.3668***	301.1870	584.3402	292.6738			5
13	**1318.6651**	659.8362	1301.6385	651.3229	1300.6545	650.8309	N	***502.2984***	251.6528	485.2718	243.1395			4
14	**1446.7237**	723.8655	1429.6971	715.3522	1428.7131	714.8602	Q	***388.2554***	194.6314	371.2289	186.1181			3
15	1559.8077	780.4075	1542.7812	771.8942	1541.7972	771.4022	I	260.1969	130.6021	243.1703	122.0888			2
16							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GATYGKPVHHGVNQIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.9	1704.9060	0.5167	GATYGKPVHHGVNQIK
14.9	1705.9073	-0.4845	MELREFEALVTQIK
11.4	1705.8028	-0.3801	KTCACAHGYLAQDGLR
9.9	1704.6364	0.7863	CDVYGEACADCCLAR
8.9	1705.8271	-0.4044	EVEREFDSGIIAGER
7.8	1705.8370	-0.4143	SDGGDLLSIESKTEQK
7.7	1705.8378	-0.4151	QMLEKECQLSQELK
7.3	1704.9338	0.4889	EFSITEVVPFPISLK
7.3	1705.9073	-0.4845	MSEQLKFIVEQLNK
6.8	1705.8743	-0.4515	LICQGDTVLKEATMK

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

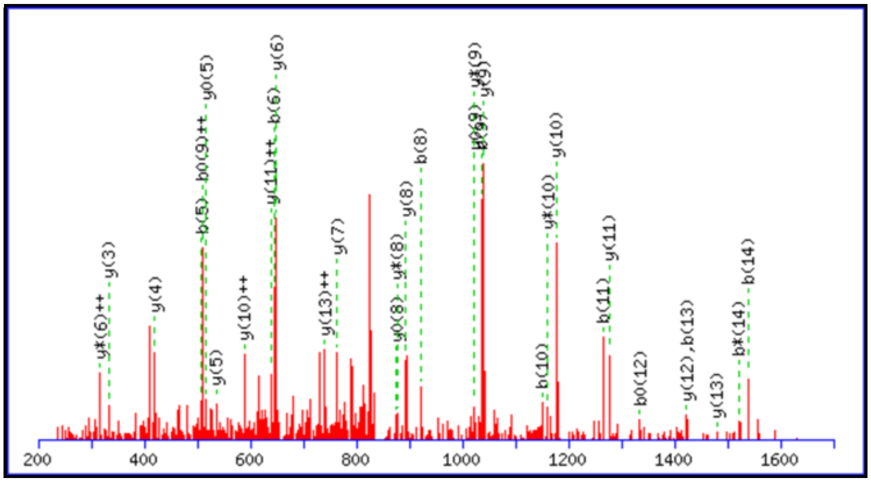
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFGFVHFEDNDSADK**
Found in **gi|47550715|ref|NP_999871.1|**, heterogeneous nuclear ribonucleoprotein A0 [Danio rerio]

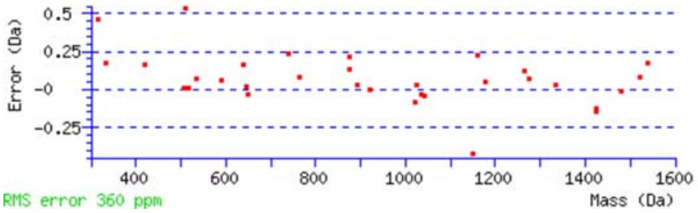
Match to Query 29328: 1685.232724 from(843.623638,2+) index(43746)
Data file TCDD_0530.dta

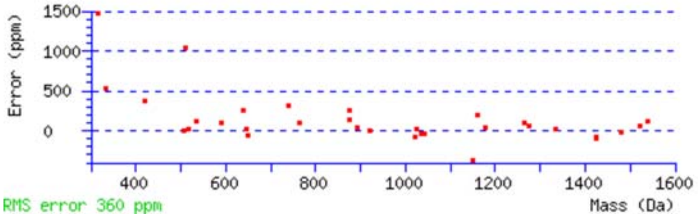
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1683.7165
Ions Score: 53 **Expect:** 0.0014
Matches : 32/134 fragment ions using 70 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							15
2	205.0972	103.0522					F	1627.7023	814.3548	1610.6758	805.8415	1609.6918	805.3495	14
3	262.1186	131.5629					G	***1480.6339***	740.8206	1463.6074	732.3073	1462.6233	731.8153	13
4	409.1870	205.0972					F	***1423.6124***	712.3099	1406.5859	703.7966	1405.6019	703.3046	12
5	**508.2554**	254.6314					V	***1276.5440***	638.7757	1259.5175	630.2624	1258.5335	629.7704	11
6	**645.3144**	323.1608					H	***1177.4756***	589.2414	1160.4491	580.7282	1159.4651	580.2362	10
7	792.3828	396.6950					F	***1040.4167***	520.7120	1023.3902	512.1987	1022.4061	511.7067	9
8	**921.4254**	461.2163			903.4148	452.2110	E	***893.3483***	447.1778	876.3217	438.6645	875.3377	438.1725	8
9	**1036.4523**	518.7298			1018.4417	509.7245	D	***764.3057***	382.6565	747.2792	374.1432	746.2951	373.6512	7
10	**1150.4952**	575.7513	1133.4687	567.2380	1132.4847	566.7460	N	***649.2788***	325.1430	632.2522	316.6297	631.2682	316.1377	6
11	**1265.5222**	633.2647	1248.4956	624.7515	1247.5116	624.2594	D	***535.2358***	268.1216	518.2093	259.6083	517.2253	259.1163	5
12	1352.5542	676.7807	1335.5277	668.2675	1334.5436	667.7755	S	***420.2089***	210.6081	403.1823	202.0948	402.1983	201.6028	4
13	**1423.5913**	712.2993	1406.5648	703.7860	1405.5808	703.2940	A	***333.1769***	167.0921	316.1503	158.5788	315.1663	158.0868	3
14	**1538.6183**	769.8128	1521.5917	761.2995	1520.6077	760.8075	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GFGFVHFEDNDSADK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.5	1683.7165	1.5162	GFGFVHFEDNDSADK
10.7	1684.7913	0.4415	CDVCSREFTLSANLK
6.3	1684.8315	0.4012	HSTAGALKAGQSAEVCR
4.2	1683.9600	1.2727	FFVDTSIILFLNKK
3.4	1683.6729	1.5598	CNYQNRCPNGSDEK
2.8	1683.7021	1.5306	GSTYVCCQHFAPEDK
1.8	1685.7726	-0.5398	EHLKNMANAAGQSCR
0.1	1682.9468	2.2860	VRYSQLLGLHEQIK

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

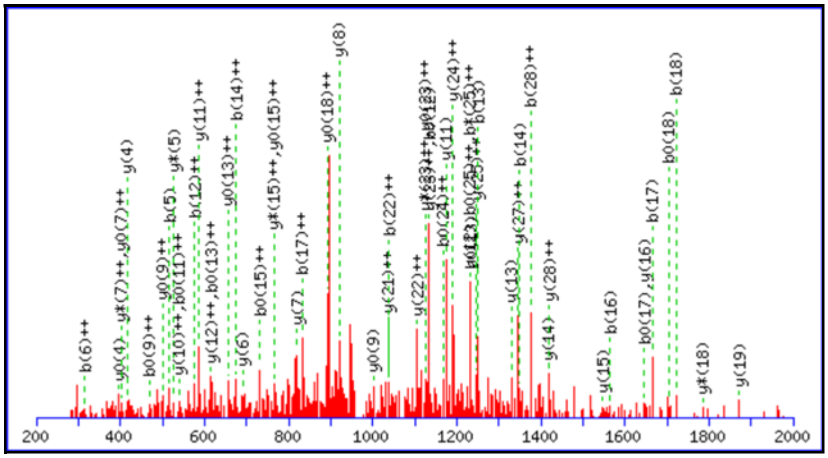
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFPTILGHEAAGVVESVGPGVTEFKPGDK**
Found in **gi|44917595|ref|NP_982285.1|**, alcohol dehydrogenase 8b [Danio rerio]

Match to Query 106233: 2895.252723 from(966.091517,3+) index(35265)
Data file TCDD_0530.dta

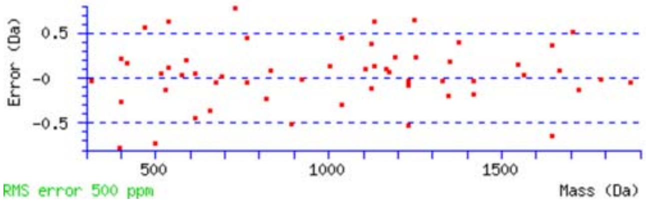
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

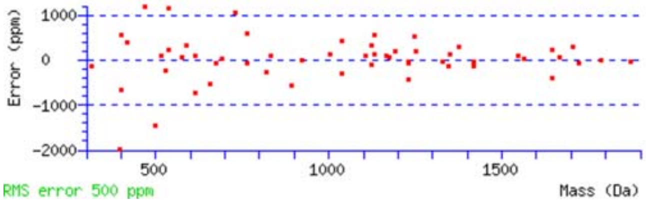


Monoisotopic mass of neutral peptide Mr(calc): 2894.4815
Ions Score: 43 **Expect:** 0.0066
Matches : 57/280 fragment ions using 129 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					**G**							**29**
2	205.0972	103.0522					**F**	2838.4672	1419.7373	2821.4407	1411.2240	2820.4567	1410.7320	**28**
3	302.1499	151.5786					**P**	2691.3988	1346.2031	2674.3723	1337.6898	2673.3883	1337.1978	**27**
4	403.1976	202.1024			385.1870	193.0972	**T**	2594.3461	1297.6767	2577.3195	1289.1634	2576.3355	1288.6714	**26**
5	**516.2817**	258.6445			498.2711	249.6392	**I**	2493.2984	1247.1528	2476.2718	1238.6396	2475.2878	1238.1475	**25**
6	629.3657	**315.1865**			611.3552	306.1812	**L**	2380.2143	1190.6108	2363.1878	1182.0975	2362.2038	1181.6055	**24**
7	686.3872	343.6972			668.3766	334.6920	**G**	2267.1303	1134.0688	2250.1037	1125.5555	2249.1197	1125.0635	**23**
8	823.4461	412.2267			805.4355	403.2214	**H**	2210.1088	1105.5580	2193.0822	1097.0448	2192.0982	1096.5528	**22**
9	952.4887	476.7480			934.4781	467.7427	**E**	2073.0499	1037.0286	2056.0233	1028.5153	2055.0393	1028.0233	**21**
10	1023.5258	512.2665			1005.5152	503.2613	**A**	1944.0073	972.5073	1926.9807	963.9940	1925.9967	963.5020	**20**
11	1094.5629	547.7851			1076.5524	538.7798	**A**	***1872.9702***	936.9887	1855.9436	928.4754	1854.9596	927.9834	**19**
12	1151.5844	**576.2958**			1133.5738	567.2905	**G**	1801.9331	901.4702	1784.9065	892.9569	1783.9225	892.4649	**18**
13	**1250.6528**	625.8300			1232.6422	616.8248	**V**	1744.9116	872.9594	1727.8850	864.4462	1726.9010	863.9542	**17**
14	**1349.7212**	**675.3642**			1331.7106	666.3590	**V**	***1645.8432***	823.4252	1628.8166	814.9120	1627.8326	814.4199	**16**
15	1478.7638	739.8855			1460.7532	730.8803	**E**	***1546.7748***	773.8910	1529.7482	765.3777	1528.7642	764.8857	**15**
16	**1565.7958**	783.4016			1547.7853	774.3963	**S**	***1417.7322***	709.3697	1400.7056	700.8564	1399.7216	700.3644	**14**
17	**1664.8642**	**832.9358**			1646.8537	823.9305	**V**	***1330.7001***	665.8537	1313.6736	657.3404	1312.6896	656.8484	**13**
18	**1721.8857**	861.4465			1703.8751	852.4412	**G**	***1231.6317***	616.3195	1214.6052	607.8062	1213.6212	607.3142	**12**
19	1818.9385	909.9729			1800.9279	900.9676	**P**	***1174.6103***	587.8088	1157.5837	579.2955	1156.5997	578.8035	**11**
20	1875.9599	938.4836			1857.9494	929.4783	**G**	1077.5575	539.2824	1060.5310	530.7691	1059.5469	530.2771	**10**
21	1975.0284	988.0178			1957.0178	979.0125	**V**	1020.5360	510.7717	1003.5095	502.2584	1002.5255	501.7664	**9**
22	2076.0760	**1038.5417**			2058.0655	1029.5364	**T**	***921.4676***	461.2374	904.4411	452.7242	903.4571	452.2322	**8**
23	2205.1186	1103.0630			2187.1081	1094.0577	**E**	***820.4199***	410.7136	803.3934	402.2003	802.4094	401.7083	**7**
24	2352.1870	1176.5972			2334.1765	1167.5919	**F**	***691.3774***	346.1923	674.3508	337.6790	673.3668	337.1870	**6**

25	2480.2820	1240.6446	2463.2555	1232.1314	2462.2714	1231.6394	**K**	544.3089	272.6581	527.2824	264.1448	526.2984	263.6528	**5**
26	2577.3348	1289.1710	2560.3082	1280.6577	2559.3242	1280.1657	**P**	***416.2140***	208.6106	399.1874	200.0974	398.2034	199.6053	**4**
27	2634.3562	1317.6818	2617.3297	1309.1685	2616.3457	1308.6765	**G**	319.1612	160.0842	302.1347	151.5710	301.1506	151.0790	**3**
28	2749.3832	**1375.1952**	2732.3566	1366.6820	2731.3726	1366.1899	**D**	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of GFPTILGHEAAGVVESVGPGVTEFKPGDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.0	2894.4815	0.7713	GFPTILGHEAAGVVESVGPGVTEFKPGDK
10.5	2896.4607	-1.2080	GFPVVLGHESAGVVESVGPGVTDYKPGDK
8.9	2896.3563	-1.1036	GLPGPAGPPGPTGAQGAPGDAGDPGPMGSFGPR
5.8	2894.3262	0.9265	SGCEGHPPWPEGICTKCQPSAITLNR
5.1	2895.3167	-0.0640	GCLANQADLDTEWNNFLDSMLGLAER
1.7	2896.4389	-1.1862	NLTSVSETFQHCKADHGVDILDLVQK
1.4	2896.6302	-1.3775	RPRWVVPLACVAIWVLAAAFASPYIK
1.3	2894.3204	0.9324	KDQPCIDFFSWCHLVPQHGVCNHK
0.8	2894.3386	0.9141	VRVSCSAAESSCDSPNAGSSIIVNIEDGK
0.2	2896.3365	-1.0837	ALLADCSLTGQCCESLSSSLQSPNSIR

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

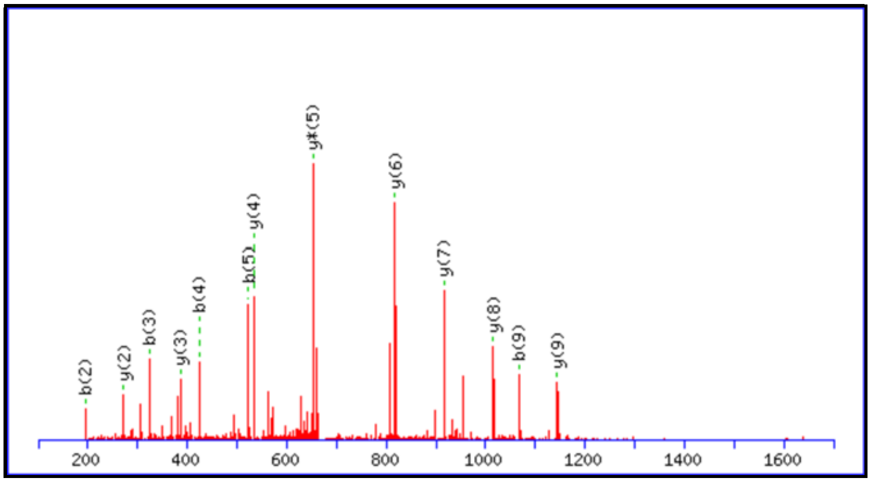
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHEVVFHFNPR**
Found in **gi|125833577|ref|XP_704272.2|**, PREDICTED: similar to Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen) (IgE-binding protein) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Laminin-binding protein) (Lectin L-29) (L-34 galactoside-binding lectin) [Danio rerio]

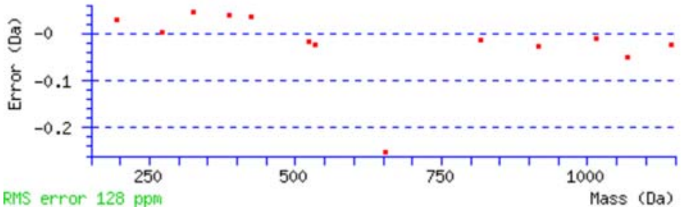
Match to Query 18665: 1339.462724 from(670.738638,2+) index(75416)
Data file TCDD_0530.dta

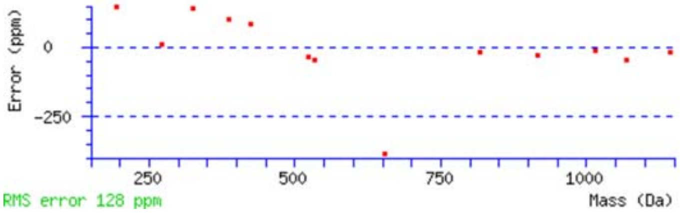
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1337.6629
Ions Score: 45 **Expect:** 0.0091
Matches : 13/84 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					**G**							**11**
2	**195.0877**	98.0475					**H**	1281.6487	641.3280	1264.6222	632.8147	1263.6382	632.3227	**10**
3	**324.1302**	162.5688			306.1197	153.5635	**E**	***1144.5898***	572.7985	1127.5633	564.2853	1126.5792	563.7933	**9**
4	**423.1987**	212.1030			405.1881	203.0977	**V**	***1015.5472***	508.2772	998.5207	499.7640			**8**
5	**522.2671**	261.6372			504.2565	252.6319	**V**	***916.4788***	458.7430	899.4522	450.2298			**7**
6	669.3355	335.1714			651.3249	326.1661	**F**	***817.4104***	409.2088	800.3838	400.6956			**6**
7	806.3944	403.7008			788.3838	394.6956	**H**	670.3420	335.6746	653.3154	327.1613			**5**
8	953.4628	477.2350			935.4522	468.2298	**F**	***533.2831***	267.1452	516.2565	258.6319			**4**
9	**1067.5057**	534.2565	1050.4792	525.7432	1049.4952	525.2512	**N**	***386.2146***	193.6110	369.1881	185.0977			**3**
10	1164.5585	582.7829	1147.5320	574.2696	1146.5479	573.7776	**P**	***272.1717***	136.5895	255.1452	128.0762			**2**
11							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of GHEVVFHFNPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.0	1337.6629	1.7998	GHEVVFHFNPR
8.8	1337.6761	1.7866	YLAGKEVTGNMR
3.0	1338.7044	0.7583	GSSVYASRFLPR
2.9	1337.6220	1.8407	CMTQTGQFLPR
1.1	1337.6398	1.8230	RDIHMEPTDPK
0.4	1340.7201	-1.2574	TLSSRQFFSLR
0.2	1337.6867	1.7760	TVEDPAFGVYLK
0.0	1337.7191	1.7437	STNASLKDVLYK

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

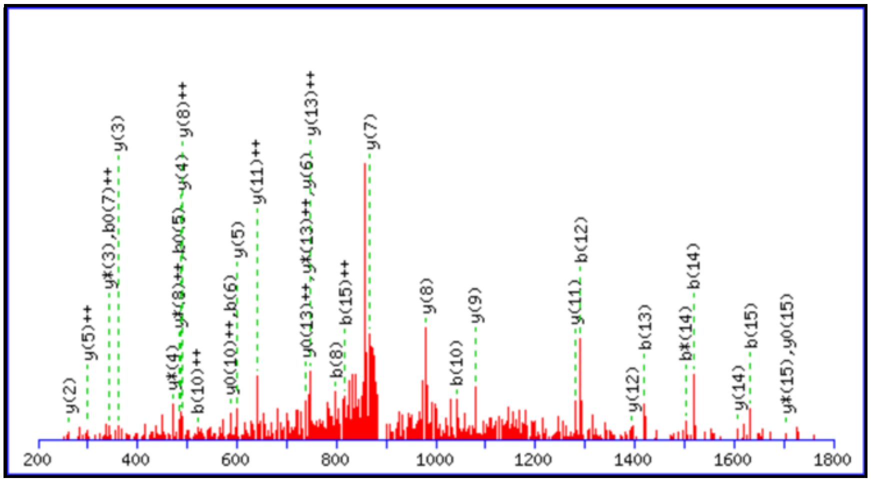
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLDVDSLVIEHIQVNK**
Found in **gi|47086529|ref|NP_997925.1|**, hypothetical protein LOC336641 [Danio rerio]

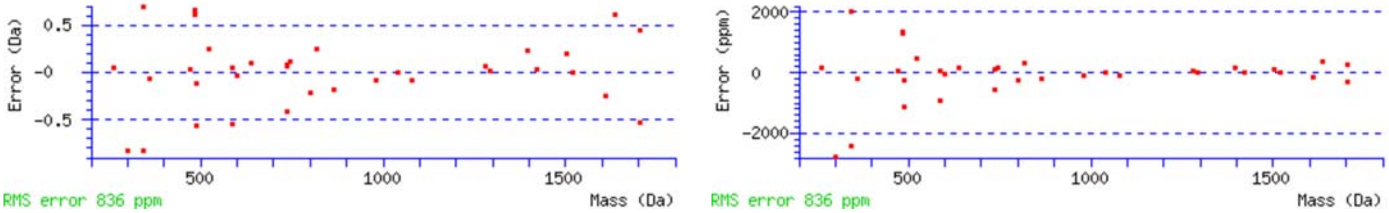
Match to Query 36374: 1780.422724 from(891.218638,2+) index(154400)
Data file TCDD_0531.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1777.9574
Ions Score: 42 **Expect:** 0.015
Matches : 35/140 fragment ions using 76 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							16
2	171.1128	86.0600					L	1721.9432	861.4753	1704.9167	852.9620	1703.9327	852.4700	15
3	286.1397	143.5735			268.1292	134.5682	D	***1608.8592***	804.9332	1591.8326	796.4199	1590.8486	795.9279	14
4	385.2082	193.1077			367.1976	184.1024	V	1493.8322	747.4197	1476.8057	738.9065	1475.8217	738.4145	13
5	500.2351	250.6212			482.2245	241.6159	D	***1394.7638***	697.8855	1377.7373	689.3723	1376.7532	688.8803	12
6	**587.2671**	294.1372			569.2566	285.1319	S	***1279.7369***	640.3721	1262.7103	631.8588	1261.7263	631.3668	11
7	700.3512	350.6792			682.3406	341.6740	L	1192.7048	596.8561	1175.6783	588.3428	1174.6943	587.8508	10
8	**799.4196**	400.2134			781.4090	391.2082	V	***1079.6208***	540.3140	1062.5942	531.8007	1061.6102	531.3087	9
9	912.5037	456.7555			894.4931	447.7502	I	***980.5524***	490.7798	963.5258	482.2665	962.5418	481.7745	8
10	**1041.5463**	521.2768			1023.5357	512.2715	E	***867.4683***	434.2378	850.4417	425.7245	849.4577	425.2325	7
11	1178.6052	589.8062			1160.5946	580.8009	H	***738.4257***	369.7165	721.3991	361.2032			6
12	**1291.6892**	646.3483			1273.6787	637.3430	I	***601.3668***	301.1870	584.3402	292.6738			5
13	**1419.7478**	710.3775	1402.7213	701.8643	1401.7373	701.3723	Q	***488.2827***	244.6450	471.2562	236.1317			4
14	**1518.8162**	759.9118	1501.7897	751.3985	1500.8057	750.9065	V	***360.2241***	180.6157	343.1976	172.1024			3
15	**1632.8592**	816.9332	1615.8326	808.4199	1614.8486	807.9279	N	***261.1557***	131.0815	244.1292	122.5682			2
16							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of GLDVDSLVIEHIQVNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.3	1777.9574	2.4653	GLDVDSLVIEHIQVNK
6.9	1778.8734	1.5494	IGNGGSTLHSLQCLHDK
6.8	1778.0665	2.3562	VLEALQVLRGELTPLK
5.4	1779.9479	0.4748	ATQIEALQHENGTLKK
4.1	1778.8435	1.5792	NQEDNTSKYPDIISR
2.2	1777.9362	2.4865	EAVQAAAKEFLNFVNK
2.2	1777.9583	2.4645	LYLCVREIGGLAMVNK
1.5	1779.9003	0.5225	EQRSTAEQITFETLK
1.3	1778.9719	1.4508	IETHLLAFEIYFRK
0.9	1781.8618	-1.4391	ENDCAIELLPGTTPPR

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

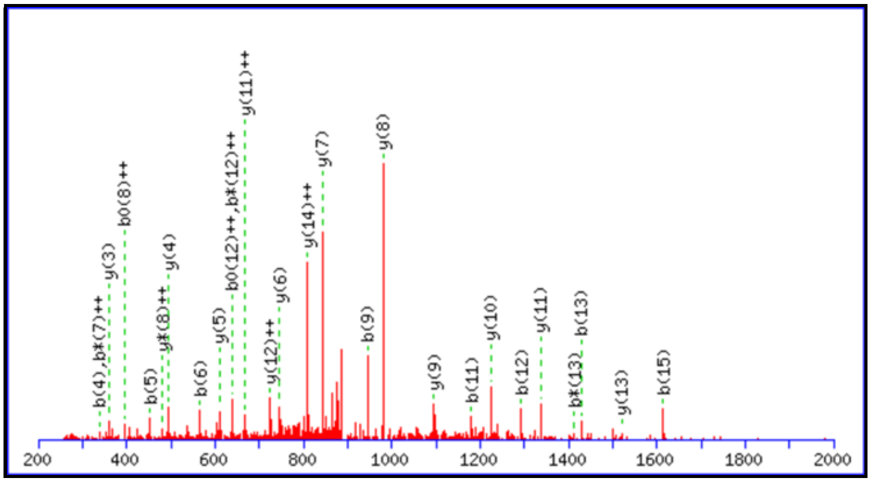
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLPALIQDHPHLHAIR**
Found in **gi|189515773|ref|XP_696194.3|**, PREDICTED: amylo-1, 6-glucosidase, 4-alpha-glucanotransferase [Danio rerio]

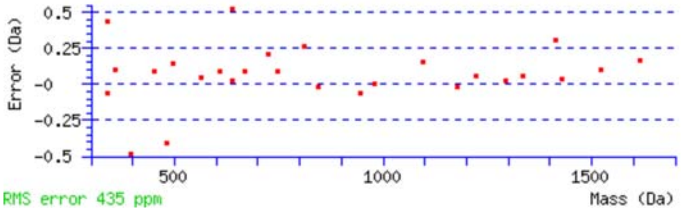
Match to Query 34799: 1787.642724 from(894.828638,2+) index(145649)
Data file TCDD_0530.dta

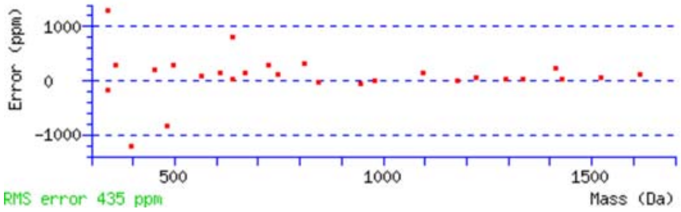
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1786.9955
Ions Score: 63 **Expect:** 0.00012
Matches : 27/138 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							16
2	171.1128	86.0600					L	1730.9813	865.9943	1713.9547	857.4810	1712.9707	856.9890	15
3	268.1656	134.5864					P	1617.8972	809.4522	1600.8707	800.9390	1599.8867	800.4470	14
4	***339.2027***	170.1050					A	***1520.8445***	760.9259	1503.8179	752.4126	1502.8339	751.9206	13
5	***452.2867***	226.6470					L	1449.8073	725.4073	1432.7808	716.8940	1431.7968	716.4020	12
6	***565.3708***	283.1890					I	***1336.7233***	668.8653	1319.6967	660.3520	1318.7127	659.8600	11
7	693.4294	347.2183	676.4028	338.7051			Q	***1223.6392***	612.3232	1206.6127	603.8100	1205.6286	603.3180	10
8	808.4563	404.7318	791.4298	396.2185	790.4458	395.7265	D	***1095.5806***	548.2940	1078.5541	539.7807	1077.5701	539.2887	9
9	***945.5152***	473.2613	928.4887	464.7480	927.5047	464.2560	H	***980.5537***	490.7805	963.5271	482.2672			8
10	1042.5680	521.7876	1025.5415	513.2744	1024.5574	512.7824	P	***843.4948***	422.2510	826.4682	413.7378			7
11	***1179.6269***	590.3171	1162.6004	581.8038	1161.6164	581.3118	H	***746.4420***	373.7246	729.4155	365.2114			6
12	***1292.7110***	646.8591	1275.6844	638.3459	1274.7004	637.8538	L	***609.3831***	305.1952	592.3566	296.6819			5
13	***1429.7699***	715.3886	1412.7433	706.8753	1411.7593	706.3833	H	***496.2990***	248.6532	479.2725	240.1399			4
14	1500.8070	750.9071	1483.7805	742.3939	1482.7964	741.9019	A	***359.2401***	180.1237	342.2136	171.6104			3
15	***1613.8911***	807.4492	1596.8645	798.9359	1595.8805	798.4439	I	288.2030	144.6051	271.1765	136.0919			2
16							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GLPALIQDHPHLHAIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.1	1786.9955	0.6473	GLPALIQDHPHLHAIR
8.8	1787.7212	-0.0784	CQIYGQGCAECCLAR
5.1	1787.8157	-0.1730	FVGYVNEGLLCCVCR
4.8	1786.8638	0.7789	QVFSESQPSPHLFER
4.3	1787.8157	-0.1730	FVGYVNEGLLCCVCR
4.0	1786.8380	0.8047	CVAHTNNKDSVSVGNSR
3.2	1787.7212	-0.0784	CQIYGQGCAECCLAR
3.1	1786.8746	0.7681	DMSDFGIVNVMKYLR
2.6	1787.9391	-0.2963	HNSLSKKPSAAGHTPTR
1.6	1787.7542	-0.1115	VCAHTCVNTAGSFYCR

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

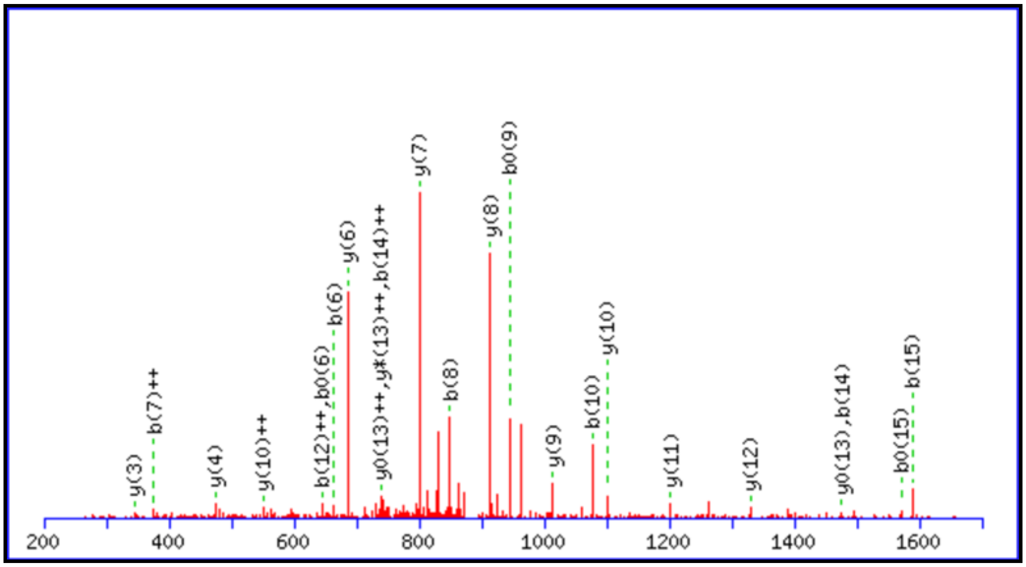
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLVYETSVLDPDEGIR**
Found in **gi|41054571|ref|NP_955892.1|**, citrate synthase [Danio rerio]

Match to Query 33285: 1761.692724 from(881.853638,2+) index(9387)
Data file TCDD_0530.dta

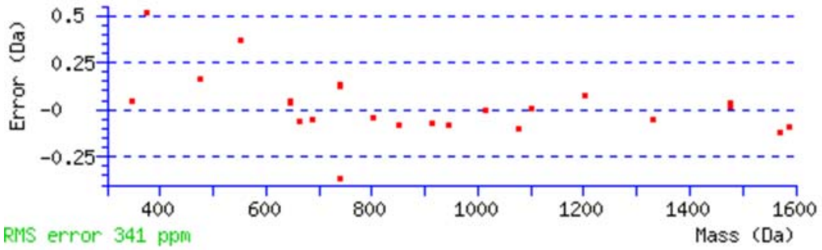
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

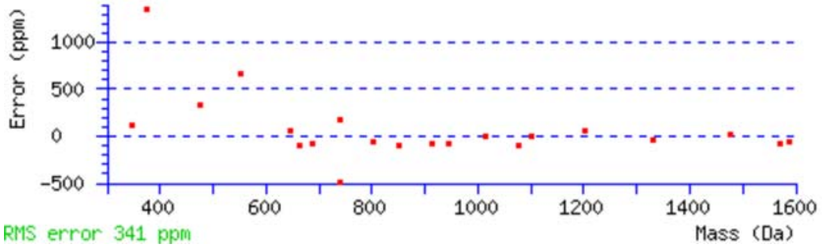


Monoisotopic mass of neutral peptide Mr(calc): 1761.8785
Ions Score: 64 **Expect:** 0.0001
Matches : 24/136 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			**G**							**16**
2	171.1128	86.0600			**L**	1705.8643	853.4358	1688.8378	844.9225	1687.8537	844.4305	**15**
3	270.1812	135.5942			**V**	1592.7802	796.8938	1575.7537	788.3805	1574.7697	787.8885	**14**
4	433.2445	217.1259			**Y**	1493.7118	747.3596	1476.6853	738.8463	1475.7013	738.3543	**13**
5	562.2871	281.6472	544.2766	272.6419	**E**	***1330.6485***	665.8279	1313.6220	657.3146	1312.6379	656.8226	**12**
6	**663.3348**	332.1710	645.3243	323.1658	**T**	***1201.6059***	601.3066	1184.5794	592.7933	1183.5953	592.3013	**11**
7	750.3668	**375.6871**	732.3563	366.6818	**S**	***1100.5582***	550.7828	1083.5317	542.2695	1082.5477	541.7775	**10**
8	**849.4353**	425.2213	831.4247	416.2160	**V**	***1013.5262***	507.2667	996.4997	498.7535	995.5156	498.2615	**9**
9	962.5193	481.7633	944.5088	472.7580	**L**	***914.4578***	457.7325	897.4312	449.2193	896.4472	448.7272	**8**
10	**1077.5463**	539.2768	1059.5357	530.2715	**D**	***801.3737***	401.1905	784.3472	392.6772	783.3632	392.1852	**7**
11	1174.5990	587.8032	1156.5885	578.7979	**P**	***686.3468***	343.6770	669.3202	335.1638	668.3362	334.6717	**6**
12	1289.6260	**645.3166**	1271.6154	636.3113	**D**	589.2940	295.1506	572.2675	286.6374	571.2835	286.1454	**5**
13	1418.6686	709.8379	1400.6580	700.8326	**E**	***474.2671***	237.6372	457.2405	229.1239	456.2565	228.6319	**4**
14	**1475.6900**	**738.3487**	1457.6795	729.3434	**G**	***345.2245***	173.1159	328.1979	164.6026			**3**

15	**1588.7741**	794.8907	1570.7635	785.8854	**I**	288.2030	144.6051	271.1765	136.0919			**2**
16					**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of GLVYETSVLDPDEGIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.3	1761.8785	-0.1858	GLVYETSVLDPDEGIR
19.9	1762.7951	-1.1024	LVTWYDNEFGYSNR
6.4	1761.8911	-0.1983	SSLNHEFFRGKPTSR
5.5	1762.8221	-1.1293	EKPNTESEEGTADKTK
5.3	1761.8931	-0.2004	SGTVEQTDILAVGSMVR
4.9	1761.8356	-0.1428	SPVTDWEEACQTLKR
4.4	1763.8182	-2.1255	DTCEELCLLEQKQR
3.9	1763.0094	-1.3166	GFNTGVILLYLERLR
3.2	1762.9326	-1.2398	QSLETQYLTQRLQR
3.1	1760.8442	0.8485	GQSTLVYHGVESQSNR

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

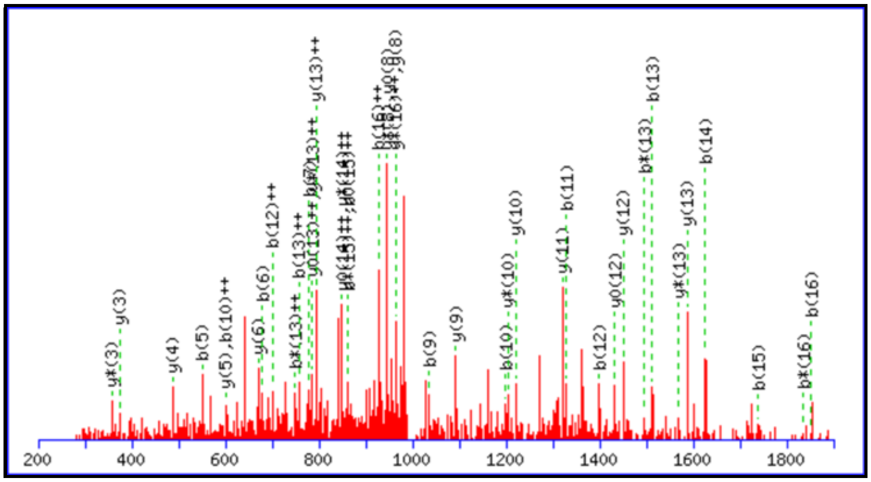
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNIQHQTQEYEALLNIK**
Found in **gi|30410758|ref|NP_848524.1|**, keratin 18 [Danio rerio]

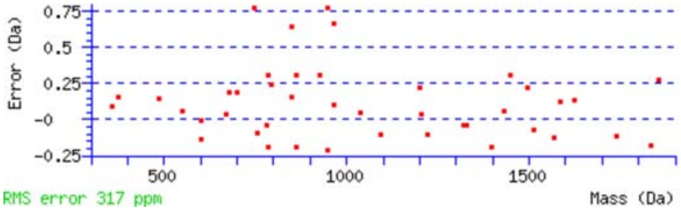
Match to Query 47048: 1997.992724 from(1000.003638,2+) index(33509)
Data file TCDD_0530.dta

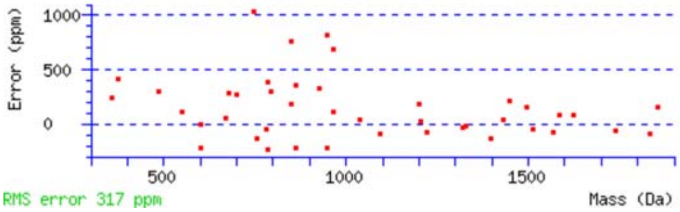
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1998.0170
Ions Score: 50 **Expect:** 0.0022
Matches : 42/166 fragment ions using 83 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							17
2	172.0717	86.5395	155.0451	78.0262			N	1942.0029	971.5051	1924.9763	962.9918	1923.9923	962.4998	16
3	285.1557	143.0815	268.1292	134.5682			I	1827.9599	914.4836	1810.9334	905.9703	1809.9494	905.4783	15
4	413.2143	207.1108	396.1878	198.5975			Q	1714.8759	857.9416	1697.8493	849.4283	1696.8653	848.9363	14
5	***550.2732***	275.6402	533.2467	267.1270			H	***1586.8173***	793.9123	1569.7907	785.3990	1568.8067	784.9070	13
6	***678.3318***	339.6695	661.3053	331.1563			Q	***1449.7584***	725.3828	1432.7318	716.8696	1431.7478	716.3775	12
7	***779.3795***	390.1934	762.3529	381.6801	761.3689	381.1881	T	***1321.6998***	661.3535	1304.6733	652.8403	1303.6892	652.3483	11
8	907.4381	454.2227	890.4115	445.7094	889.4275	445.2174	Q	***1220.6521***	610.8297	1203.6256	602.3164	1202.6416	601.8244	10
9	***1036.4806***	518.7440	1019.4541	510.2307	1018.4701	509.7387	E	***1092.5936***	546.8004	1075.5670	538.2871	1074.5830	537.7951	9
10	***1199.5440***	**600.2756**	1182.5174	591.7624	1181.5334	591.2703	Y	***963.5510***	482.2791	946.5244	473.7658	945.5404	473.2738	8
11	***1328.5866***	664.7969	1311.5600	656.2836	1310.5760	655.7916	E	800.4876	400.7475	783.4611	392.2342	782.4771	391.7422	7
12	***1399.6237***	**700.3155**	1382.5971	691.8022	1381.6131	691.3102	A	***671.4450***	336.2262	654.4185	327.7129			6
13	***1512.7077***	**756.8575**	1495.6812	748.3442	1494.6972	747.8522	L	***600.4079***	300.7076	583.3814	292.1943			5
14	***1625.7918***	813.3995	1608.7653	804.8863	1607.7812	804.3943	L	***487.3239***	244.1656	470.2973	235.6523			4
15	***1739.8347***	870.4210	1722.8082	861.9077	1721.8242	861.4157	N	***374.2398***	187.6235	357.2132	179.1103			3
16	***1852.9188***	**926.9630**	1835.8923	918.4498	1834.9082	917.9578	I	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GNIQHQTQEYEALLNIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.8	1998.0170	-0.0243	GNIQHQTQEYEALLNIK
14.8	1998.9130	-0.9203	LENGEEELDENGALTPNR
9.1	1998.0826	-0.0899	ALETAVYGAYFNVIINLK
4.7	1999.9316	-1.9389	NATSPIWQYFGFTPDEK
4.3	1999.8525	-1.8598	YRHPACFVCSDCGMNLK
4.0	1999.9810	-1.9883	ITATTRDPELANEQQADK
2.6	1998.9907	-0.9980	LFLAGYEMTPTMRDINK
2.2	2000.0546	-2.0619	LMEQLANIAMRQLLDNK
2.2	1998.9706	-0.9778	LLDGEATSVSSSSSSSTTRK
2.0	1999.0093	-1.0166	LLFLILCFQQCSVQCK

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

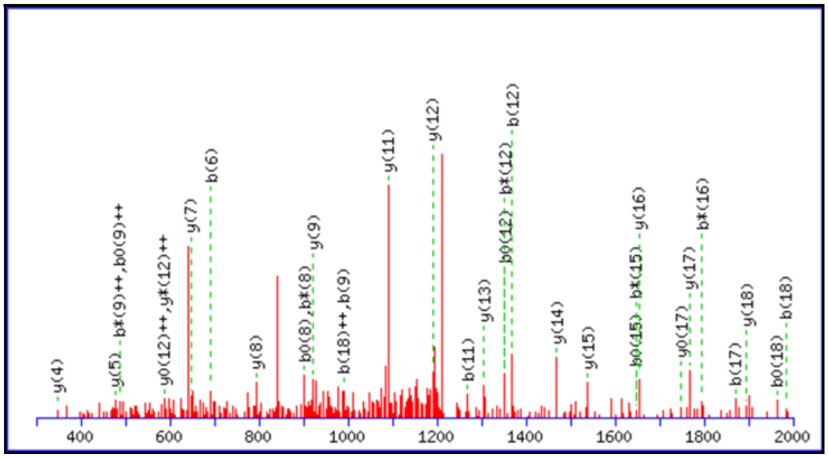
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HAINQEINAYNTPAQFGLEGSGK**
Found in **gi|189533438|ref|XP_696505.3|**, PREDICTED: novel protein similar to vertebrate apolipoprotein B (including Ag(x) antigen) (APOB) [Danio rerio]

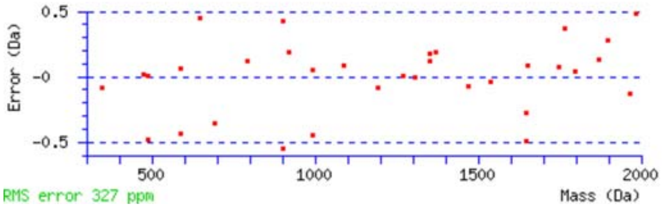
Match to Query 90508: 2458.812724 from(1230.413638,2+) index(44176)
Data file TCDD_0530.dta

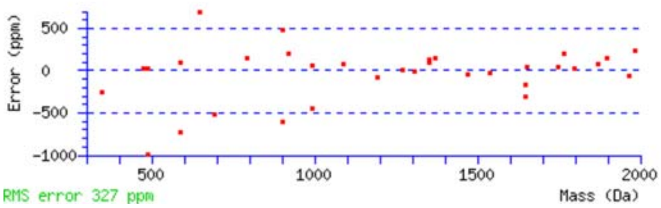
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2458.1877
Ions Score: 62  Expect: 9.8e-005
Matches : 33/244 fragment ions using 67 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367					H							23
2	209.1033	105.0553					A	2322.1361	1161.5717	2305.1095	1153.0584	2304.1255	1152.5664	22
3	322.1874	161.5973					I	2251.0990	1126.0531	2234.0724	1117.5398	2233.0884	1117.0478	21
4	436.2303	218.6188	419.2037	210.1055			N	2138.0149	1069.5111	2120.9883	1060.9978	2120.0043	1060.5058	20
5	564.2889	282.6481	547.2623	274.1348			Q	2023.9720	1012.4896	2006.9454	1003.9763	2005.9614	1003.4843	19
6	**693.3315**	347.1694	676.3049	338.6561	675.3209	338.1641	E	***1895.9134***	948.4603	1878.8868	939.9471	1877.9028	939.4550	18
7	806.4155	403.7114	789.3890	395.1981	788.4050	394.7061	I	***1766.8708***	883.9390	1749.8442	875.4258	1748.8602	874.9338	17
8	920.4585	460.7329	903.4319	452.2196	902.4479	451.7276	N	***1653.7867***	827.3970	1636.7602	818.8837	1635.7762	818.3917	16
9	**991.4956**	496.2514	974.4690	487.7381	973.4850	487.2461	A	***1539.7438***	770.3755	1522.7173	761.8623	1521.7332	761.3703	15
10	1154.5589	577.7831	1137.5323	569.2698	1136.5483	568.7778	Y	***1468.7067***	734.8570	1451.6801	726.3437	1450.6961	725.8517	14
11	**1268.6018**	634.8046	1251.5753	626.2913	1250.5913	625.7993	N	***1305.6434***	653.3253	1288.6168	644.8120	1287.6328	644.3200	13
12	**1369.6495**	685.3284	1352.6230	676.8151	1351.6389	676.3231	T	***1191.6004***	596.3039	1174.5739	587.7906	1173.5899	587.2986	12
13	1466.7023	733.8548	1449.6757	725.3415	1448.6917	724.8495	P	***1090.5528***	545.7800	1073.5262	537.2667	1072.5422	536.7747	11
14	1537.7394	769.3733	1520.7128	760.8601	1519.7288	760.3680	A	993.5000	497.2536	976.4734	488.7404	975.4894	488.2483	10
15	1665.7980	833.4026	1648.7714	824.8893	1647.7874	824.3973	Q	***922.4629***	461.7351	905.4363	453.2218	904.4523	452.7298	9
16	1812.8664	906.9368	1795.8398	898.4236	1794.8558	897.9315	F	***794.4043***	397.7058	777.3777	389.1925	776.3937	388.7005	8
17	**1869.8878**	935.4476	1852.8613	926.9343	1851.8773	926.4423	G	***647.3359***	324.1716	630.3093	315.6583	629.3253	315.1663	7
18	**1982.9719**	991.9896	1965.9454	983.4763	1964.9613	982.9843	L	590.3144	295.6608	573.2879	287.1476	572.3039	286.6556	6
19	2112.0145	1056.5109	2094.9879	1047.9976	2094.0039	1047.5056	E	***477.2304***	239.1188	460.2038	230.6055	459.2198	230.1135	5
20	2169.0360	1085.0216	2152.0094	1076.5083	2151.0254	1076.0163	G	***348.1878***	174.5975	331.1612	166.0842	330.1772	165.5922	4
21	2256.0680	1128.5376	2239.0414	1120.0244	2238.0574	1119.5323	S	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
22	2313.0895	1157.0484	2296.0629	1148.5351	2295.0789	1148.0431	G	204.1343	102.5708	187.1077	94.0575			2
23							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of HAINQEINAYNTPAQFGLEGSGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.1	2458.1877	0.6251	HAINQEINAYNTPAQFGLEGSGK

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

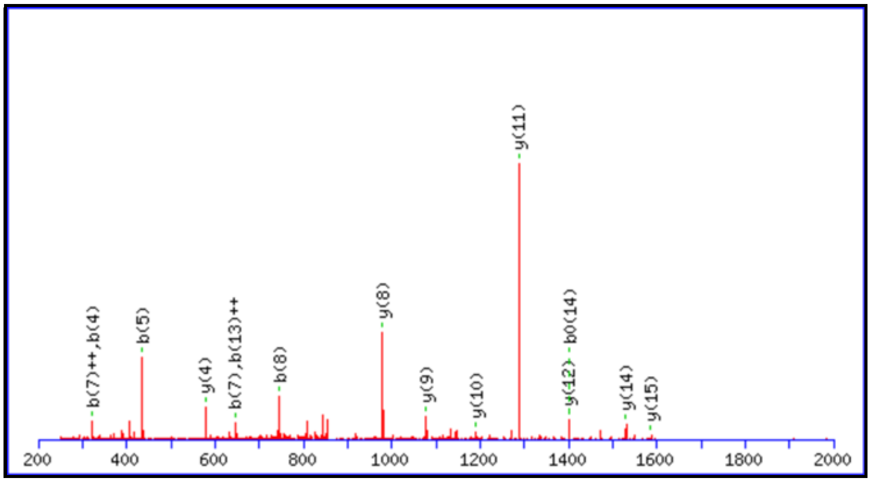
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **HGGAIPIVPTSDFQER**
Found in **gi|47086875|ref|NP_997741.1|**, glutamate dehydrogenase 1a [Danio rerio]

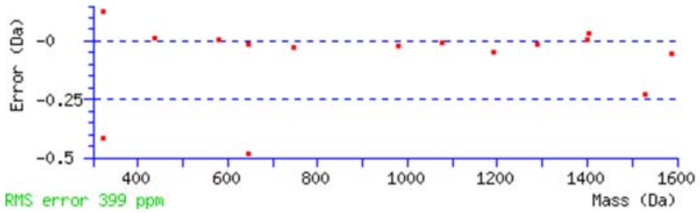
Match to Query 30994: 1722.792724 from(862.403638,2+) index(54838)
Data file TCDD_0530.dta

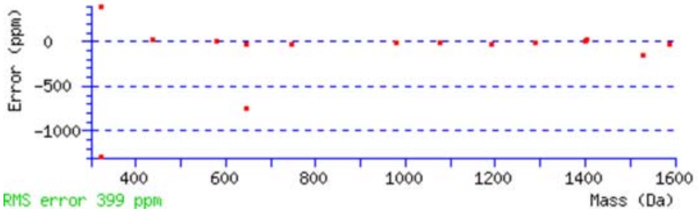
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1722.8689
Ions Score: 47 **Expect:** 0.005
Matches : 15/134 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	138.0662	69.5367					H							16
2	195.0877	98.0475					G	***1586.8173***	793.9123	1569.7908	785.3990	1568.8067	784.9070	15
3	252.1091	126.5582					G	***1529.7958***	765.4016	1512.7693	756.8883	1511.7853	756.3963	14
4	**323.1462**	162.0768					A	1472.7744	736.8908	1455.7478	728.3775	1454.7638	727.8855	13
5	**436.2303**	218.6188					I	***1401.7373***	701.3723	1384.7107	692.8590	1383.7267	692.3670	12
6	533.2831	267.1452					P	***1288.6532***	644.8302	1271.6266	636.3170	1270.6426	635.8250	11
7	**646.3671**	323.6872					I	***1191.6004***	596.3039	1174.5739	587.7906	1173.5899	587.2986	10
8	**745.4355**	373.2214					V	***1078.5164***	539.7618	1061.4898	531.2485	1060.5058	530.7565	9
9	842.4883	421.7478					P	***979.4480***	490.2276	962.4214	481.7143	961.4374	481.2223	8
10	943.5360	472.2716			925.5254	463.2663	T	882.3952	441.7012	865.3686	433.1880	864.3846	432.6959	7
11	1030.5680	515.7876			1012.5574	506.7824	S	781.3475	391.1774	764.3210	382.6641	763.3369	382.1721	6
12	1145.5950	573.3011			1127.5844	564.2958	D	694.3155	347.6614	677.2889	339.1481	676.3049	338.6561	5
13	1292.6634	646.8353			1274.6528	637.8300	F	***579.2885***	290.1479	562.2620	281.6346	561.2780	281.1426	4
14	1420.7219	710.8646	1403.6954	702.3513	1402.7114	701.8593	Q	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
15	1549.7645	775.3859	1532.7380	766.8726	1531.7540	766.3806	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
16							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of HGGAIPIVPTSDFQER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.3	1722.8689	-0.0762	HGGAIPIVPTSDFQER
18.1	1721.9424	0.8503	VQLLHSQNTSLINQK
18.1	1721.9424	0.8503	VQLLHSQNTSLLNQK
4.7	1723.8814	-1.0887	IPENLSDPNVPASLMK
3.3	1724.7940	-2.0013	THYQNDIERMYGAK
3.3	1722.9767	-0.1840	EIEKVLPAVVQEEIK
3.1	1724.7134	-1.9207	ECDWNNQDEKSVMK
2.7	1722.7784	0.0143	HQGLAQQCYDYEIR
2.0	1722.8247	-0.0320	SELNVCPETTAGFLSR
1.9	1720.8567	1.9361	GDDMLITSGRSPFLGR

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

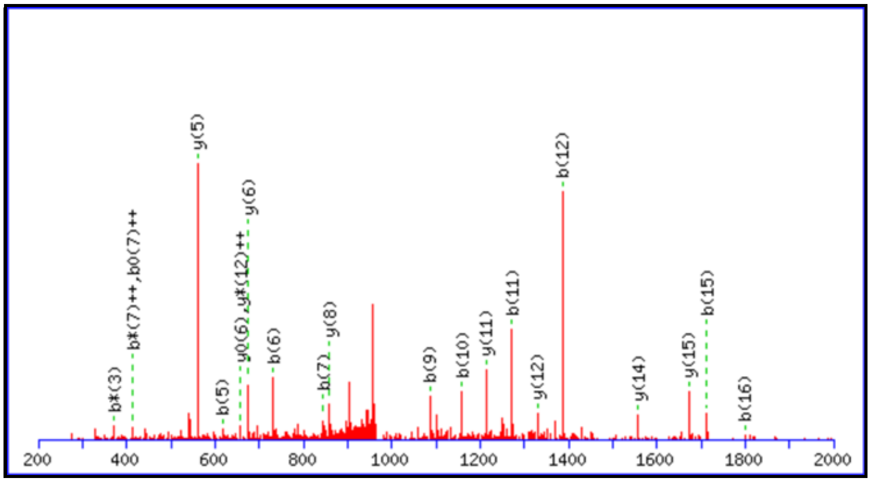
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HHNEVDLLEAIDPNDSK**
Found in **gi|55742591|ref|NP_998335.1|**, telomerase binding protein, p23 [Danio rerio]

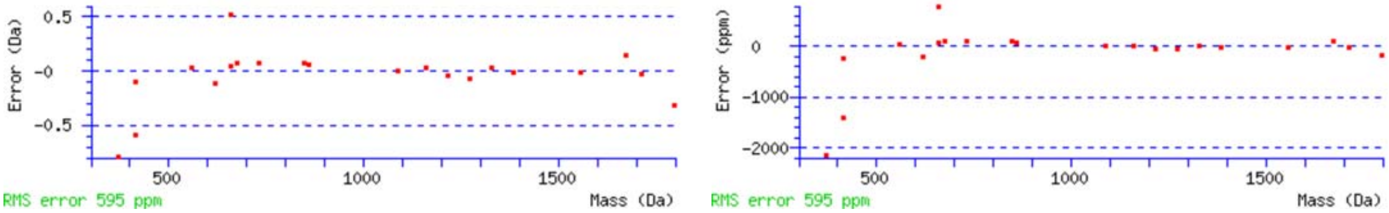
Match to Query 44018: 1946.402724 from(974.208638,2+) index(137877)
Data file TCDD_0530.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1944.9177
Ions Score: 59 **Expect:** 0.00027
Matches : 21/180 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	138.0662	69.5367					**H**							17
2	275.1251	138.0662					**H**	1808.8661	904.9367	1791.8395	896.4234	1790.8555	895.9314	16
3	389.1680	195.0877	372.1415	186.5744			**N**	***1671.8072***	836.4072	1654.7806	827.8940	1653.7966	827.4019	15
4	518.2106	259.6089	501.1841	251.0957	500.2001	250.6037	**E**	***1557.7643***	779.3858	1540.7377	770.8725	1539.7537	770.3805	14
5	***617.2790***	309.1432	600.2525	300.6299	599.2685	300.1379	**V**	1428.7217	714.8645	1411.6951	706.3512	1410.7111	705.8592	13
6	***732.3060***	366.6566	715.2794	358.1434	714.2954	357.6513	**D**	***1329.6533***	665.3303	1312.6267	656.8170	1311.6427	656.3250	12
7	***845.3900***	423.1987	828.3635	414.6854	827.3795	414.1934	**L**	***1214.6263***	607.8168	1197.5998	599.3035	1196.6157	598.8115	11
8	958.4741	479.7407	941.4476	471.2274	940.4635	470.7354	**L**	1101.5422	551.2748	1084.5157	542.7615	1083.5317	542.2695	10
9	***1087.5167***	544.2620	1070.4901	535.7487	1069.5061	535.2567	**E**	988.4582	494.7327	971.4316	486.2195	970.4476	485.7274	9
10	***1158.5538***	579.7805	1141.5273	571.2673	1140.5432	570.7753	**A**	***859.4156***	430.2114	842.3890	421.6982	841.4050	421.2061	8
11	***1271.6379***	636.3226	1254.6113	627.8093	1253.6273	627.3173	**I**	788.3785	394.6929	771.3519	386.1796	770.3679	385.6876	7
12	***1386.6648***	693.8360	1369.6383	685.3228	1368.6543	684.8308	**D**	***675.2944***	338.1508	658.2679	329.6376	657.2838	329.1456	6
13	1483.7176	742.3624	1466.6910	733.8492	1465.7070	733.3571	**P**	***560.2675***	280.6374	543.2409	272.1241	542.2569	271.6321	5
14	1597.7605	799.3839	1580.7340	790.8706	1579.7499	790.3786	**N**	463.2147	232.1110	446.1882	223.5977	445.2041	223.1057	4
15	***1712.7875***	856.8974	1695.7609	848.3841	1694.7769	847.8921	**D**	349.1718	175.0895	332.1452	166.5763	331.1612	166.0842	3
16	***1799.8195***	900.4134	1782.7929	891.9001	1781.8089	891.4081	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
17							**K**	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of HHNEVDLLEAIDPNDSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.0	1944.9177	1.4850	HHNEVDLLEAIDPNDSK
16.2	1945.9857	0.4170	YGKLVNLGGNAGEQGVQDK
5.3	1946.9619	-0.5592	EAQALCTEIVTQTGDLQK
4.4	1945.0675	1.3352	MASVCAVARVLLCLNVVK
3.8	1945.0376	1.3651	GVVIVMNIMQADKSLAEK
3.5	1945.0057	1.3970	QEIADRLNAWIIFNDK
3.0	1944.9727	1.4300	NCFHLTQLDLSDNKLK
2.5	1945.0343	1.3685	REMEVLTDLWLTQALK
2.4	1947.1445	-0.7417	VVELIYIDIVGLAQFKK
1.3	1946.0320	0.3707	GGEGISEAGAKTTVGAVLTTK

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

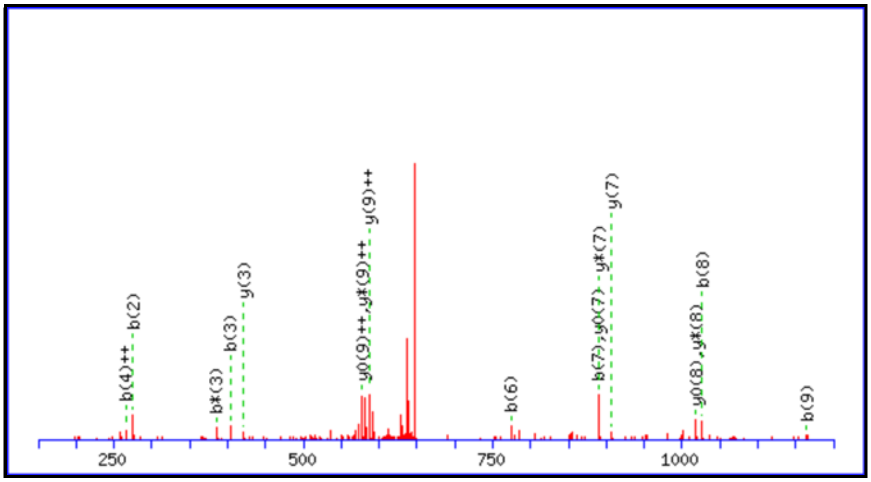
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HHQEEIDHHK**
Found in **gi|113678121|ref|NP_001038324.1|**, ATPase inhibitory factor 1-like [Danio rerio]

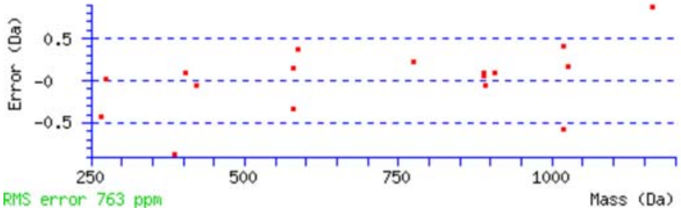
Match to Query 17848: 1309.302724 from(655.658638,2+) index(154868)
Data file TCDD_0531.dta

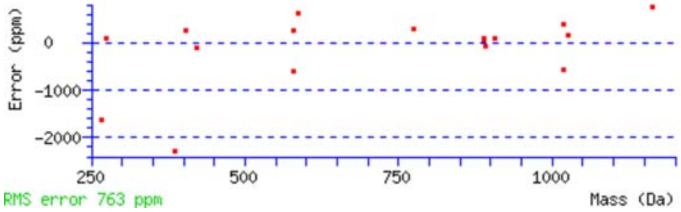
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1308.5959
Ions Score: 44 **Expect:** 0.012
Matches : 17/92 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	138.0662	69.5367					H							10
2	***275.1251***	138.0662					H	1172.5443	586.7758	1155.5178	578.2625	1154.5337	577.7705	9
3	***403.1837***	202.0955	386.1571	193.5822			Q	1035.4854	518.2463	1018.4589	509.7331	1017.4748	509.2411	8
4	532.2263	266.6168	515.1997	258.1035	514.2157	257.6115	E	**907.4268**	454.2170	890.4003	445.7038	889.4163	445.2118	7
5	661.2689	331.1381	644.2423	322.6248	643.2583	322.1328	E	778.3842	389.6958	761.3577	381.1825	760.3737	380.6905	6
6	***774.3529***	387.6801	757.3264	379.1668	756.3424	378.6748	I	649.3416	325.1745	632.3151	316.6612	631.3311	316.1692	5
7	***889.3799***	445.1936	872.3533	436.6803	871.3693	436.1883	D	536.2576	268.6324	519.2310	260.1191	518.2470	259.6271	4
8	***1026.4388***	513.7230	1009.4122	505.2098	1008.4282	504.7177	H	**421.2306**	211.1190	404.2041	202.6057			3
9	***1163.4977***	582.2525	1146.4711	573.7392	1145.4871	573.2472	H	284.1717	142.5895	267.1452	134.0762			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of HHQEEIDHHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.9	1308.5959	0.7068	HHQEEIDHHK
19.3	1308.6561	0.6466	SVESELDFQKK
18.7	1307.6907	1.6120	SGFKNLLLECK
18.1	1308.5793	0.7234	SGLQDGSSSESQK
16.9	1309.5179	-0.2152	HQYNCETCQK
15.6	1307.6721	1.6306	GSFKAGDEGSILK
13.0	1309.6415	-0.3388	DHHFLVGTEAGK
13.0	1309.6336	-0.3309	EYEKMLNDLR
12.9	1309.7354	-0.4327	SHKLAVTAVEQK
12.3	1309.6375	-0.3347	STSQQAQPAHQK

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

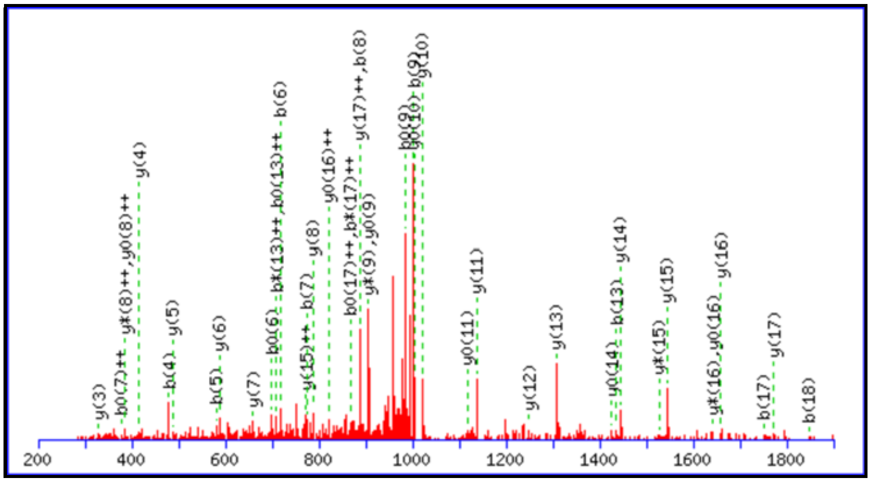
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HILDTHGLDPHQATASGPR**
Found in **gi|41056209|ref|NP_956854.1|**, hypothetical protein LOC393532 [Danio rerio]

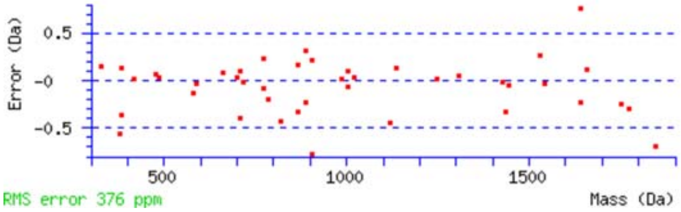
Match to Query 48768: 2023.162724 from(1012.588638,2+) index(64421)
Data file TCDD_0530.dta

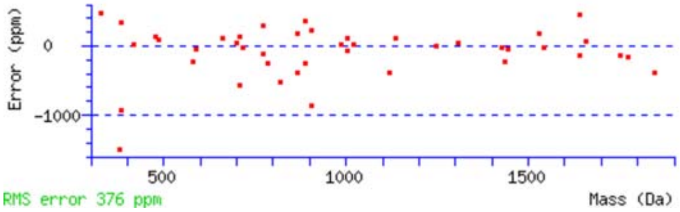
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2022.0031
Ions Score: 56 **Expect:** 0.00059
Matches : 43/182 fragment ions using 112 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	138.0662	69.5367					**H**							**19**
2	251.1503	126.0788					**I**	1885.9515	943.4794	1868.9250	934.9661	1867.9409	934.4741	**18**
3	364.2343	182.6208					**L**	***1772.8674***	886.9374	1755.8409	878.4241	1754.8569	877.9321	**17**
4	**479.2613**	240.1343			461.2507	231.1290	**D**	***1659.7834***	830.3953	1642.7568	821.8821	1641.7728	821.3900	**16**
5	**580.3089**	290.6581			562.2984	281.6528	**T**	***1544.7564***	772.8819	1527.7299	764.3686	1526.7459	763.8766	**15**
6	**717.3678**	359.1876			699.3573	350.1823	**H**	***1443.7088***	722.3580	1426.6822	713.8447	1425.6982	713.3527	**14**
7	**774.3893**	387.6983			756.3787	378.6930	**G**	***1306.6498***	653.8286	1289.6233	645.3153	1288.6393	644.8233	**13**
8	**887.4734**	444.2403			869.4628	435.2350	**L**	***1249.6284***	625.3178	1232.6018	616.8046	1231.6178	616.3125	**12**
9	**1002.5003**	501.7538			984.4898	492.7485	**D**	***1136.5443***	568.7758	1119.5178	560.2625	1118.5337	559.7705	**11**
10	1099.5531	550.2802			1081.5425	541.2749	**P**	***1021.5174***	511.2623	1004.4908	502.7490	1003.5068	502.2570	**10**
11	1236.6120	618.8096			1218.6014	609.8044	**H**	924.4646	462.7359	907.4381	454.2227	906.4540	453.7307	**9**
12	1364.6706	682.8389	1347.6440	674.3257	1346.6600	673.8336	**Q**	***787.4057***	394.2065	770.3791	385.6932	769.3951	385.2012	**8**
13	**1435.7077**	718.3575	1418.6811	709.8442	1417.6971	709.3522	**A**	***659.3471***	330.1772	642.3206	321.6639	641.3365	321.1719	**7**
14	1536.7554	768.8813	1519.7288	760.3680	1518.7448	759.8760	**T**	***588.3100***	294.6586	571.2835	286.1454	570.2994	285.6534	**6**
15	1607.7925	804.3999	1590.7659	795.8866	1589.7819	795.3946	**A**	***487.2623***	244.1348	470.2358	235.6215	469.2518	235.1295	**5**
16	1694.8245	847.9159	1677.7980	839.4026	1676.8139	838.9106	**S**	***416.2252***	208.6162	399.1987	200.1030	398.2146	199.6110	**4**
17	**1751.8460**	876.4266	1734.8194	867.9134	1733.8354	867.4213	**G**	***329.1932***	165.1002	312.1666	156.5870			**3**
18	**1848.8987**	924.9530	1831.8722	916.4397	1830.8882	915.9477	**P**	272.1717	136.5895	255.1452	128.0762			**2**
19							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of HILDTHGLDPHQATASGPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.5	2022.0031	1.1596	HILDTHGLDPHQATASGPR
6.9	2020.9856	2.1771	CILIVNCTCTAGISINNGR
3.3	2020.9854	2.1773	FSKVITNPQGHFSTDESK
3.0	2021.9039	1.2589	DGEGQWTSSTSVEQARER

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

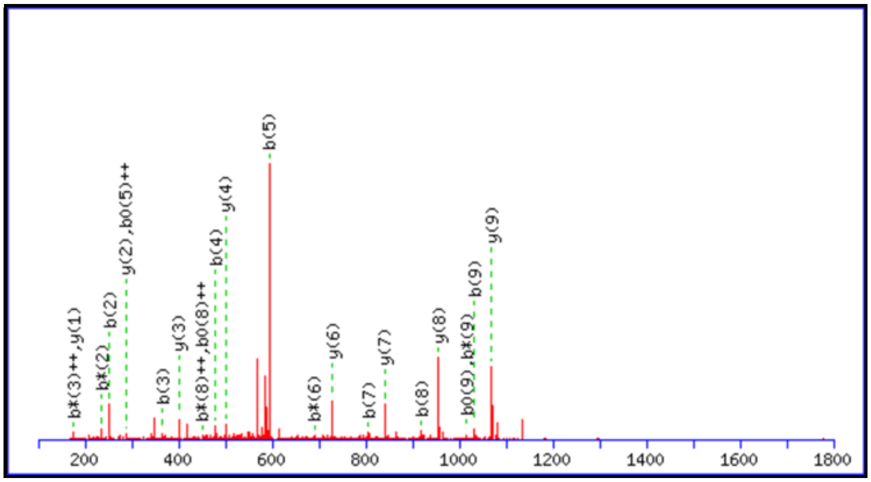
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **HNNLDLVIIR**
Found in **gi|50344970|ref|NP_001002157.1|**, hypothetical protein LOC415247 [Danio rerio]

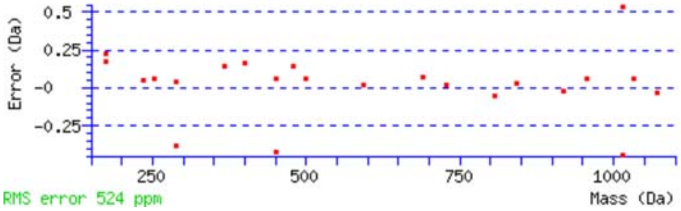
Match to Query 13510: 1207.632724 from(604.823638,2+) index(55204)
Data file TCDD_0530.dta

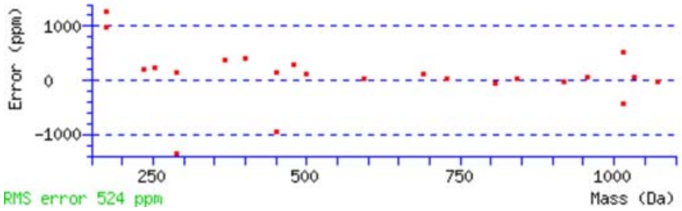
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1205.6880
Ions Score: 48 **Expect:** 0.0046
Matches : 23/88 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367					**H**							**10**
2	**252.1091**	126.5582	235.0826	118.0449			**N**	***1069.6364***	535.3218	1052.6099	526.8086	1051.6259	526.3166	**9**
3	**366.1520**	183.5797	349.1255	175.0664			**N**	***955.5935***	478.3004	938.5669	469.7871	937.5829	469.2951	**8**
4	**479.2361**	240.1217	462.2096	231.6084			**L**	***841.5506***	421.2789	824.5240	412.7656	823.5400	412.2736	**7**
5	**594.2630**	297.6352	577.2365	289.1219	576.2525	288.6299	**D**	***728.4665***	364.7369	711.4400	356.2236	710.4559	355.7316	**6**
6	707.3471	354.1772	690.3206	345.6639	689.3365	345.1719	**L**	613.4396	307.2234	596.4130	298.7101			**5**
7	**806.4155**	403.7114	789.3890	395.1981	788.4050	394.7061	**V**	***500.3555***	250.6814	483.3289	242.1681			**4**
8	**919.4996**	460.2534	902.4730	451.7402	901.4890	451.2482	**I**	***401.2871***	201.1472	384.2605	192.6339			**3**
9	**1032.5837**	516.7955	1015.5571	508.2822	1014.5731	507.7902	**I**	***288.2030***	144.6051	271.1765	136.0919			**2**
10							**R**	***175.1190***	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of HNNLDLVIIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.4	1205.6880	1.9447	HNNLDLVIIR
13.9	1205.7244	1.9083	HLDALLKQIR
13.9	1206.6357	0.9970	GITEGHIVEPR
13.1	1207.6197	0.0130	SSDINQYIIR
10.9	1205.7972	1.8355	LINRPILVLR
10.9	1205.7972	1.8355	LINRPLIVLR
10.8	1206.6431	0.9897	LIDFGCASIIR
9.7	1206.5856	1.0472	HLDFFEMLR
9.2	1206.6179	1.0148	LCAGAFAQTLR
8.6	1206.6469	0.9858	GSVRGIASSFAR

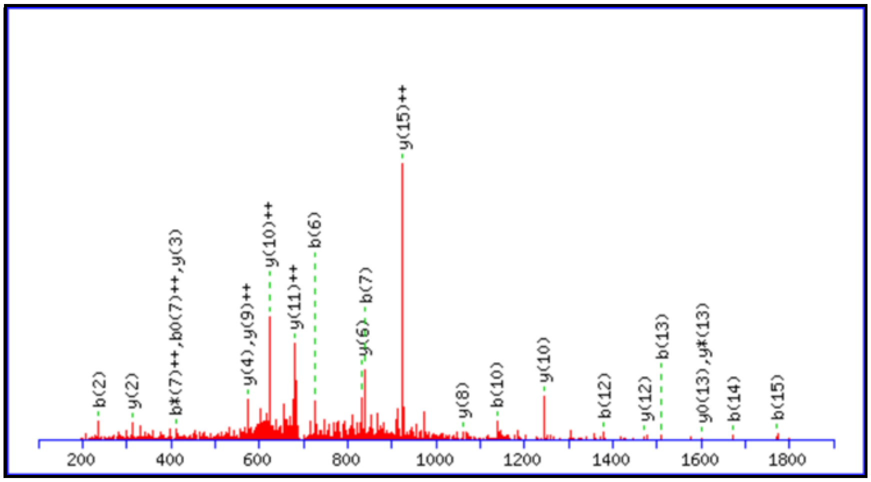
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **HVINFDLPSDIEEYVHR**
Found in **gi|125995404|ref|NP_001075099.1|**, DEAD (Asp-Glu-Ala-Asp) box polypeptide 3 [Danio rerio]

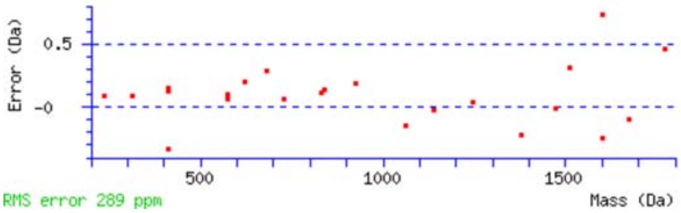
Match to Query 51635: 2082.302724 from(695.108184,3+) index(47145)
Data file TCDD_0530.dta

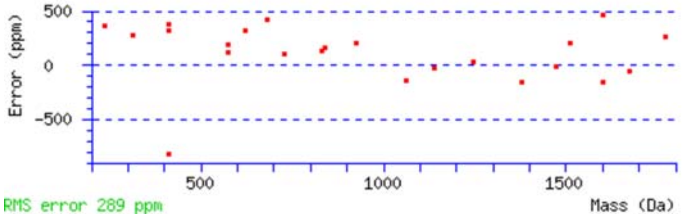
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2082.0170
Ions Score: 50 **Expect:** 0.002
Matches : 23/168 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367					H							17
2	***237.1346***	119.0709					V	1945.9654	973.4863	1928.9389	964.9731	1927.9549	964.4811	16
3	350.2187	175.6130					I	1846.8970	923.9521	1829.8705	915.4389	1828.8864	914.9469	15
4	464.2616	232.6344	447.2350	224.1212			N	1733.8129	867.4101	1716.7864	858.8968	1715.8024	858.4048	14
5	611.3300	306.1686	594.3035	297.6554			F	1619.7700	810.3886	1602.7435	801.8754	1601.7594	801.3834	13
6	***726.3569***	363.6821	709.3304	355.1688	708.3464	354.6768	D	***1472.7016***	736.8544	1455.6751	728.3412	1454.6910	727.8492	12
7	***839.4410***	420.2241	822.4145	411.7109	821.4304	411.2189	L	1357.6747	679.3410	1340.6481	670.8277	1339.6641	670.3357	11
8	936.4938	468.7505	919.4672	460.2373	918.4832	459.7452	P	***1244.5906***	622.7989	1227.5640	614.2857	1226.5800	613.7937	10
9	1023.5258	512.2665	1006.4993	503.7533	1005.5152	503.2613	S	1147.5378	574.2726	1130.5113	565.7593	1129.5273	565.2673	9
10	***1138.5527***	569.7800	1121.5262	561.2667	1120.5422	560.7747	D	***1060.5058***	530.7565	1043.4793	522.2433	1042.4952	521.7513	8
11	1251.6368	626.3220	1234.6103	617.8088	1233.6262	617.3168	I	945.4789	473.2431	928.4523	464.7298	927.4683	464.2378	7
12	***1380.6794***	690.8433	1363.6529	682.3301	1362.6688	681.8381	E	***832.3948***	416.7010	815.3682	408.1878	814.3842	407.6958	6
13	***1509.7220***	755.3646	1492.6955	746.8514	1491.7114	746.3594	E	703.3522	352.1797	686.3257	343.6665	685.3416	343.1745	5
14	***1672.7853***	836.8963	1655.7588	828.3830	1654.7748	827.8910	Y	***574.3096***	287.6584	557.2831	279.1452			4
15	***1771.8537***	886.4305	1754.8272	877.9172	1753.8432	877.4252	V	***411.2463***	206.1268	394.2197	197.6135			3
16	1908.9127	954.9600	1891.8861	946.4467	1890.9021	945.9547	H	***312.1779***	156.5926	295.1513	148.0793			2
17							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of HVINFDLPSDIEEYVHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.2	2082.0170	0.2857	HVINFDLPSDIEEYVHR
9.4	2082.9858	-0.6831	VHSSYFEGKQVSLTDDGSK
6.7	2084.0223	-1.7196	MWGHLSEGYGKLCSIYLK
4.9	2081.0000	1.3027	LKYTVTADGCSKPNGEWGR
4.8	2082.9979	-0.6952	THEIIHTGEKPFACNVCGK
4.8	2082.0858	0.2169	GSPGPDGPLGLAGAPGPPGVIGSR
3.2	2079.9201	2.3826	NGCTDVKEGPVSDMSTLDR
2.0	2081.0841	1.2187	GHAVCPVNLPPTTDVVIHR
1.6	2080.1317	2.1711	FIRNFSQLAAPLTSLTSSK
1.6	2084.0572	-1.7545	GETLLTLLHSPSITDNMSR

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

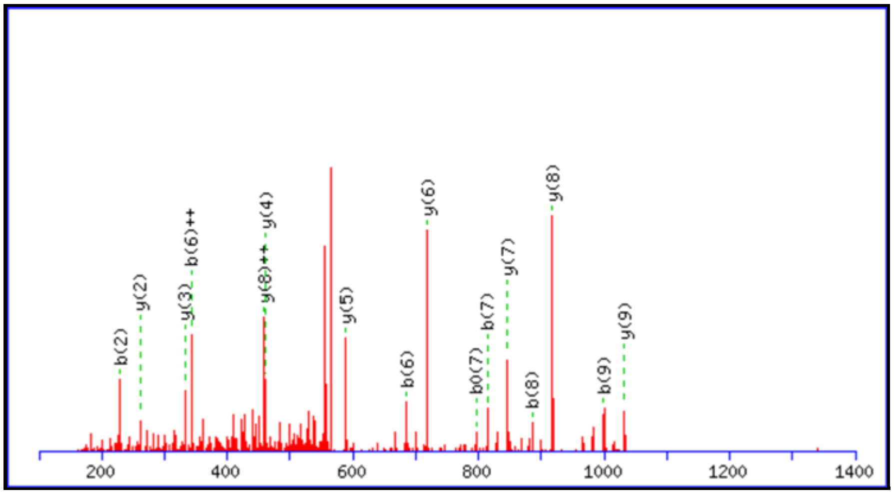
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDAQEQEANK**
Found in **gi|41152334|ref|NP_956996.1|**, ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d [Danio rerio]

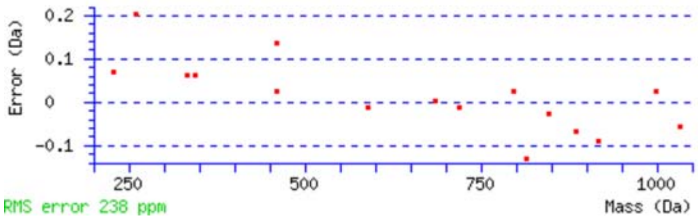
Match to Query 11005: 1144.852724 from(573.433638,2+) index(8256)
Data file TCDD_0530.dta

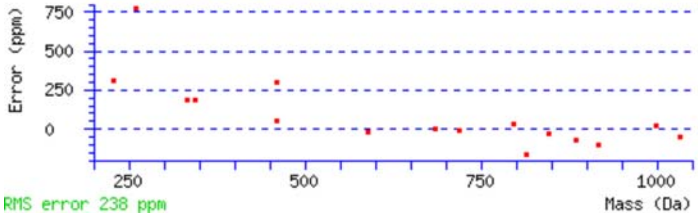
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1144.5360
Ions Score: 64 **Expect:** 0.00013
Matches : 16/94 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							10
2	**229.1183**	115.0628			211.1077	106.0575	D	***1032.4592***	516.7333	1015.4327	508.2200	1014.4487	507.7280	9
3	300.1554	150.5813			282.1448	141.5761	A	***917.4323***	459.2198	900.4058	450.7065	899.4217	450.2145	8
4	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	Q	***846.3952***	423.7012	829.3686	415.1880	828.3846	414.6959	7
5	557.2566	279.1319	540.2300	270.6186	539.2460	270.1266	E	***718.3366***	359.6719	701.3101	351.1587	700.3260	350.6667	6
6	**685.3151**	343.1612	668.2886	334.6479	667.3046	334.1559	Q	***589.2940***	295.1506	572.2675	286.6374	571.2835	286.1454	5
7	**814.3577**	407.6825	797.3312	399.1692	796.3472	398.6772	E	***461.2354***	231.1214	444.2089	222.6081	443.2249	222.1161	4
8	**885.3949**	443.2011	868.3683	434.6878	867.3843	434.1958	A	***332.1928***	166.6001	315.1663	158.0868			3
9	**999.4378**	500.2225	982.4112	491.7093	981.4272	491.2172	N	***261.1557***	131.0815	244.1292	122.5682			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IDAQEQEANK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.4	1144.5360	0.3167	IDAQEQEANK
16.6	1145.5677	-0.7149	NADRLDTVDK
16.2	1145.5425	-0.6898	DLNRADEASR
13.5	1143.6499	1.2028	SNILQESLIK
13.1	1144.6339	0.2188	LELTDLKADK
12.7	1143.4979	1.3548	VEETCVGHDR
12.6	1144.6240	0.2287	QQGLYPAAGLK
12.5	1144.6339	0.2188	LNSLTEELVK
11.9	1142.6594	2.1933	LICAVKQVGR
11.8	1145.5789	-0.7261	DLNNRAQTSK

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

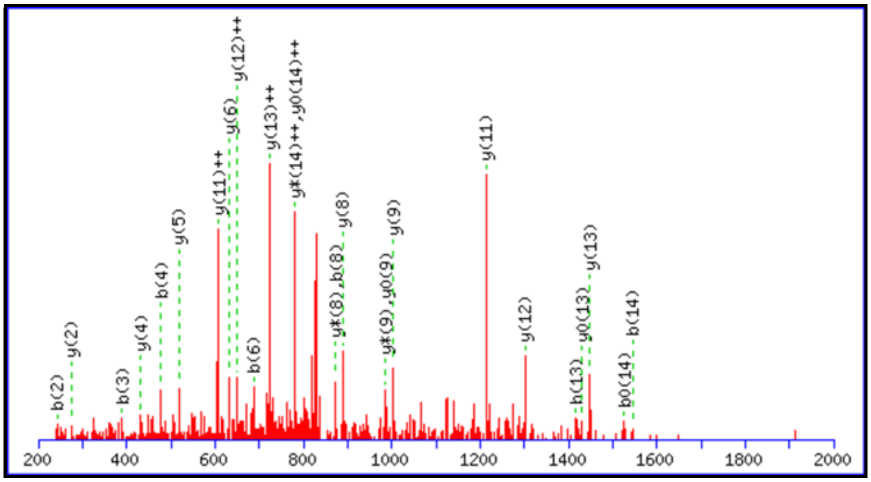
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEFSPLDAWNSGVQK**
Found in **gi|113678245|ref|NP_001038338.1|**, hypothetical protein LOC558738 [Danio rerio]

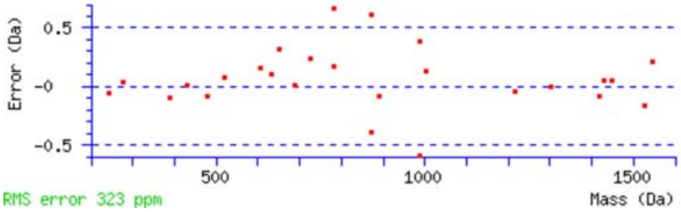
Match to Query 29531: 1690.452724 from(846.233638,2+) index(20092)
Data file TCDD_0530.dta

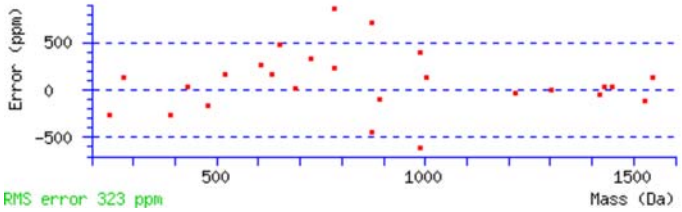
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1689.8362
Ions Score: 57 **Expect:** 0.00055
Matches : 26/140 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							15
2	***243.1339***	122.0706			225.1234	113.0653	E	1577.7594	789.3834	1560.7329	780.8701	1559.7489	780.3781	14
3	***390.2023***	195.6048			372.1918	186.5995	F	***1448.7169***	724.8621	1431.6903	716.3488	1430.7063	715.8568	13
4	***477.2344***	239.1208			459.2238	230.1155	S	***1301.6484***	651.3279	1284.6219	642.8146	1283.6379	642.3226	12
5	574.2871	287.6472			556.2766	278.6419	P	***1214.6164***	607.8118	1197.5899	599.2986	1196.6058	598.8066	11
6	***687.3712***	344.1892			669.3606	335.1840	L	1117.5636	559.2855	1100.5371	550.7722	1099.5531	550.2802	10
7	802.3981	401.7027			784.3876	392.6974	D	***1004.4796***	502.7434	987.4530	494.2302	986.4690	493.7381	9
8	***873.4353***	437.2213			855.4247	428.2160	A	***889.4526***	445.2300	872.4261	436.7167	871.4421	436.2247	8
9	1059.5146	530.2609			1041.5040	521.2556	W	818.4155	409.7114	801.3890	401.1981	800.4050	400.7061	7
10	1173.5575	587.2824	1156.5310	578.7691	1155.5469	578.2771	N	***632.3362***	316.6717	615.3097	308.1585	614.3257	307.6665	6
11	1260.5895	630.7984	1243.5630	622.2851	1242.5790	621.7931	S	***518.2933***	259.6503	501.2667	251.1370	500.2827	250.6450	5
12	1317.6110	659.3091	1300.5844	650.7959	1299.6004	650.3039	G	***431.2613***	216.1343	414.2347	207.6210			4
13	***1416.6794***	708.8433	1399.6529	700.3301	1398.6688	699.8381	V	374.2398	187.6235	357.2132	179.1103			3
14	***1544.7380***	772.8726	1527.7114	764.3594	1526.7274	763.8673	Q	***275.1714***	138.0893	258.1448	129.5761			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IEFSPLDAWNSGVQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.9	1689.8362	0.6165	IEFSPLDAWNSGVQK
14.1	1690.7468	-0.2941	ELFSASSTDSCSRSSK
10.7	1692.7923	-2.3396	MLEGGPRSSSAVSCQK
9.8	1688.8403	1.6124	ELMEEQINKSVAGNK
7.3	1688.9475	1.5053	QLFVTPHPQRITPR
6.5	1690.8236	-0.3708	ELEQASWAKMELEK
6.4	1688.7853	1.6674	ELEDNDPNISSSITR
5.6	1688.9308	1.5219	LERLNLSSTSLSEIK
4.3	1688.8733	1.5794	KIFVGGLNPETTEER
4.2	1689.8243	0.6284	ELEETLKQLENNCK

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

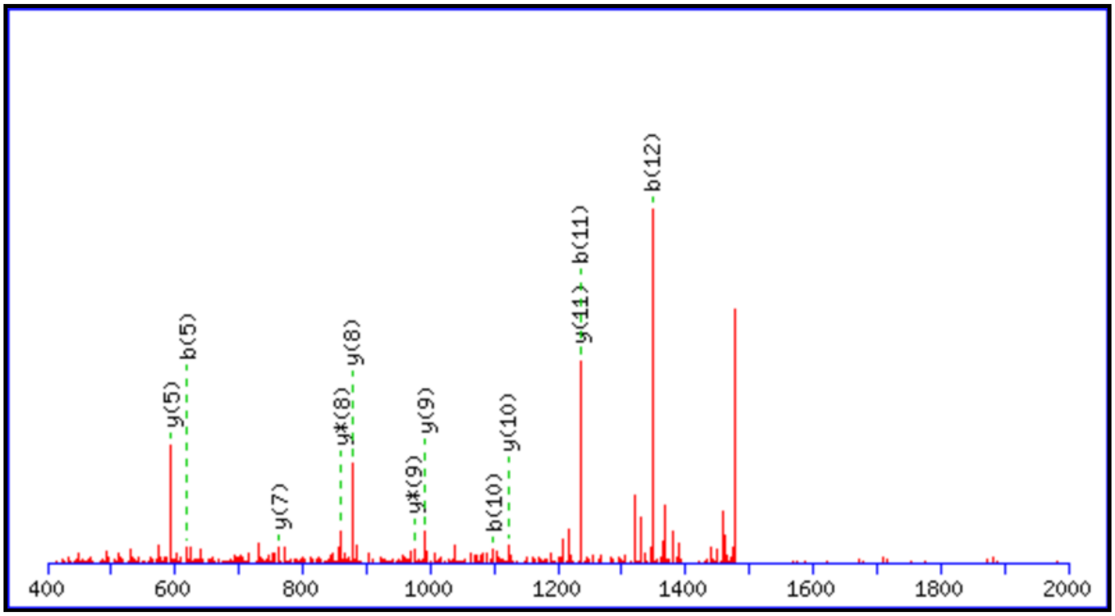
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFLEDNGLPVHIK**
Found in **gi|68379126|ref|XP_693548.1|**, PREDICTED: hypothetical protein LOC767664 [Danio rerio]

Match to Query 22902: 1493.862724 from(1494.870000,1+) index(45309)
Data file TCDD_0530.dta

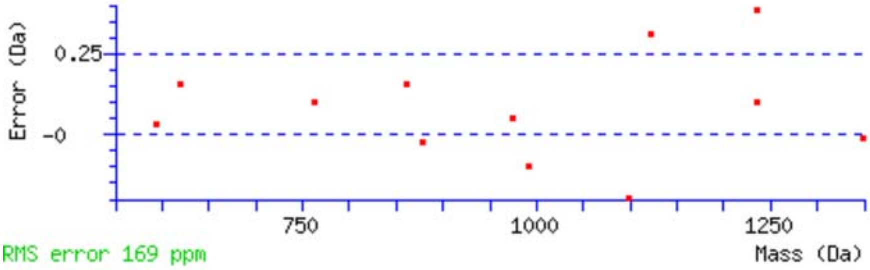
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

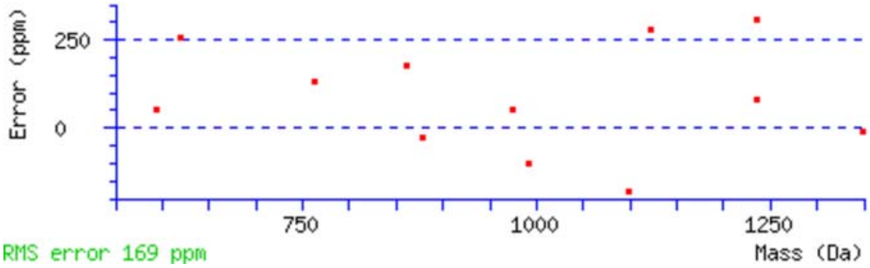


Monoisotopic mass of neutral peptide Mr(calc): 1493.8242
Ions Score: 43 **Expect:** 0.013
Matches : 12/56 fragment ions using 22 most intense peaks (help)

#	b	b*	b^0	Seq.	y	y*	y^0	#
1	114.0913			I				13
2	261.1598			F	1381.7474	1364.7209	1363.7369	12
3	374.2438			L	*1234.6790*	1217.6525	1216.6684	11
4	503.2864		485.2758	E	*1121.5949*	1104.5684	1103.5844	10
5	*618.3134*		600.3028	D	*992.5524*	975.5258	974.5418	9
6	732.3563	715.3297	714.3457	N	*877.5254*	860.4989		8
7	789.3777	772.3512	771.3672	G	*763.4825*	746.4559		7
8	902.4618	885.4353	884.4512	L	706.4610	689.4345		6
9	999.5146	982.4880	981.5040	P	*593.3770*	576.3504		5
10	*1098.5830*	1081.5564	1080.5724	V	496.3242	479.2976		4

11	*1235.6419*	1218.6154	1217.6313	**H**	397.2558	380.2292		**3**
12	*1348.7260*	1331.6994	1330.7154	**I**	260.1969	243.1703		**2**
13				**K**	147.1128	130.0863		**1**





NCBI **BLAST** search of IFLEDNGLPVHIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.1	1493.8242	0.0385	IFLEDNGLPVHIK
17.6	1493.8136	0.0491	QHLNRNDIMLLK
15.3	1493.8031	0.0596	DGFAKVHYGFILK
15.1	1494.7354	-0.8727	DLAFEEGVINFNK
10.3	1493.6901	0.1726	LTGTCMRNSVPCR
10.2	1493.6780	0.1847	ENCSSLSREVENK
9.8	1493.7031	0.1596	QMNELSSELQTSK
8.3	1494.7215	-0.8588	FLAFNNRENQDK
8.3	1493.7734	0.0893	RMCELVLGEFLK
8.1	1493.8354	0.0273	GHDAIVTLLKHYK

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

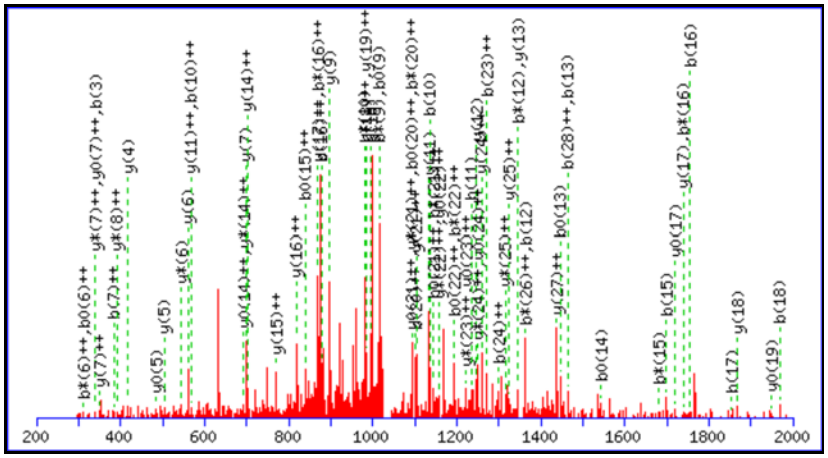
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLDQGQEHTVETPHGVLHVTVHGSGNAR**
Found in **gi|56693257|ref|NP_001008593.1|**, hypothetical protein LOC494050 [Danio rerio]

Match to Query 111155: 3102.352725 from(1035.124851,3+) index(66976)
Data file TCDD_0530.dta

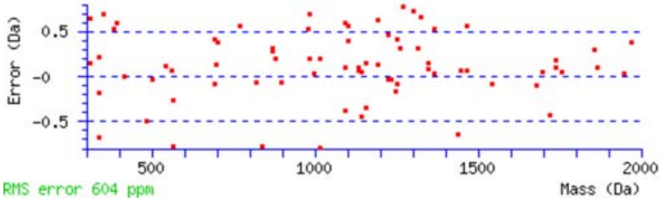
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

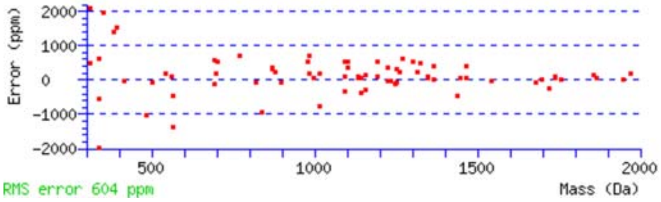


```
Monoisotopic mass of neutral peptide Mr(calc): 3100.5803
Ions Score: 39  Expect: 0.014
Matches : 76/314 fragment ions using 169 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					**I**							29
2	227.1754	114.0913					**L**	2988.5035	1494.7554	2971.4769	1486.2421	2970.4929	1485.7501	28
3	**340.2595**	170.6334					**L**	2875.4194	1438.2133	2858.3928	1429.7001	2857.4088	1429.2081	27
4	455.2864	228.1468			437.2758	219.1416	**D**	2762.3353	1381.6713	2745.3088	1373.1580	2744.3248	1372.6660	26
5	583.3450	292.1761	566.3184	283.6629	565.3344	283.1709	**Q**	2647.3084	1324.1578	2630.2818	1315.6446	2629.2978	1315.1525	25
6	640.3665	320.6869	623.3399	312.1736	622.3559	311.6816	**G**	2519.2498	1260.1285	2502.2233	1251.6153	2501.2392	1251.1233	24
7	768.4250	**384.7162**	751.3985	376.2029	750.4145	375.7109	**Q**	2462.2283	1231.6178	2445.2018	1223.1045	2444.2178	1222.6125	23
8	897.4676	449.2375	880.4411	440.7242	879.4571	440.2322	**E**	2334.1698	1167.5885	2317.1432	1159.0752	2316.1592	1158.5832	22
9	1034.5265	517.7669	1017.5000	509.2536	1016.5160	508.7616	**H**	2205.1272	1103.0672	2188.1006	1094.5540	2187.1166	1094.0619	21
10	**1135.5742**	**568.2907**	1118.5477	559.7775	1117.5637	559.2855	**T**	2068.0683	1034.5378	2051.0417	1026.0245	2050.0577	1025.5325	20
11	**1234.6426**	617.8250	1217.6161	609.3117	1216.6321	608.8197	**V**	1967.0206	984.0139	1949.9940	975.5007	1949.0100	975.0086	19
12	**1363.6852**	682.3462	1346.6587	673.8330	1345.6747	673.3410	**E**	***1867.9522***	934.4797	1850.9256	925.9664	1849.9416	925.4744	18
13	**1464.7329**	732.8701	1447.7064	724.3568	1446.7223	723.8648	**T**	***1738.9096***	869.9584	1721.8830	861.4452	1720.8990	860.9531	17
14	1561.7857	781.3965	1544.7591	772.8832	1543.7751	772.3912	**P**	1637.8619	819.4346	1620.8353	810.9213	1619.8513	810.4293	16
15	**1698.8446**	849.9259	1681.8180	841.4127	1680.8340	840.9206	**H**	1540.8091	770.9082	1523.7826	762.3949	1522.7986	761.9029	15
16	**1755.8660**	**878.4367**	1738.8395	869.9234	1737.8555	869.4314	**G**	1403.7502	702.3787	1386.7237	693.8655	1385.7397	693.3735	14
17	**1854.9345**	927.9709	1837.9079	919.4576	1836.9239	918.9656	**V**	***1346.7288***	673.8680	1329.7022	665.3547	1328.7182	664.8627	13
18	**1968.0185**	**984.5129**	1950.9920	975.9996	1950.0080	975.5076	**L**	***1247.6603***	624.3338	1230.6338	615.8205	1229.6498	615.3285	12
19	2105.0774	1053.0424	2088.0509	1044.5291	2087.0669	1044.0371	**H**	***1134.5763***	567.7918	1117.5497	559.2785	1116.5657	558.7865	11
20	2204.1458	**1102.5766**	2187.1193	1094.0633	2186.1353	1093.5713	**V**	***997.5174***	499.2623	980.4908	490.7490	979.5068	490.2570	10
21	2305.1935	1153.1004	2288.1670	1144.5871	2287.1830	1144.0951	**T**	***898.4490***	449.7281	881.4224	441.2148	880.4384	440.7228	9
22	2404.2619	1202.6346	2387.2354	1194.1213	2386.2514	1193.6293	**V**	797.4013	399.2043	780.3747	390.6910	779.3907	390.1990	8
23	2541.3208	**1271.1641**	2524.2943	1262.6508	2523.3103	1262.1588	**H**	***698.3329***	349.6701	681.3063	341.1568	680.3223	340.6648	7
24	2598.3423	**1299.6748**	2581.3158	1291.1615	2580.3317	1290.6695	**G**	***561.2739***	281.1406	544.2474	272.6273	543.2634	272.1353	6

25	2685.3743	1343.1908	2668.3478	1334.6775	2667.3638	1334.1855	**S**	***504.2525***	252.6299	487.2259	244.1166	486.2419	243.6246	**5**
26	2742.3958	1371.7015	2725.3693	1363.1883	2724.3852	1362.6963	**G**	***417.2205***	209.1139	400.1939	200.6006			**4**
27	2856.4387	1428.7230	2839.4122	1420.2097	2838.4282	1419.7177	**N**	360.1990	180.6031	343.1724	172.0899			**3**
28	2927.4758	**1464.2416**	2910.4493	1455.7283	2909.4653	1455.2363	**A**	246.1561	123.5817	229.1295	115.0684			**2**
29							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of ILLDQGQEHTVETPHGVLHVTVHGSGNAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.3	3100.5803	1.7724	ILLDQGQEHTVETPHGVLHVTVHGSGNAR
4.3	3101.5348	0.8180	SPLYQNCMLACVESRPLPSIGTPEPKSK
2.2	3104.5025	-2.1498	NMFIIDQHSGEVSLNGLVDFEKANHYK
1.6	3101.5348	0.8180	SPLYQNCMLACVESRPLPSIGTPEPKSK

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

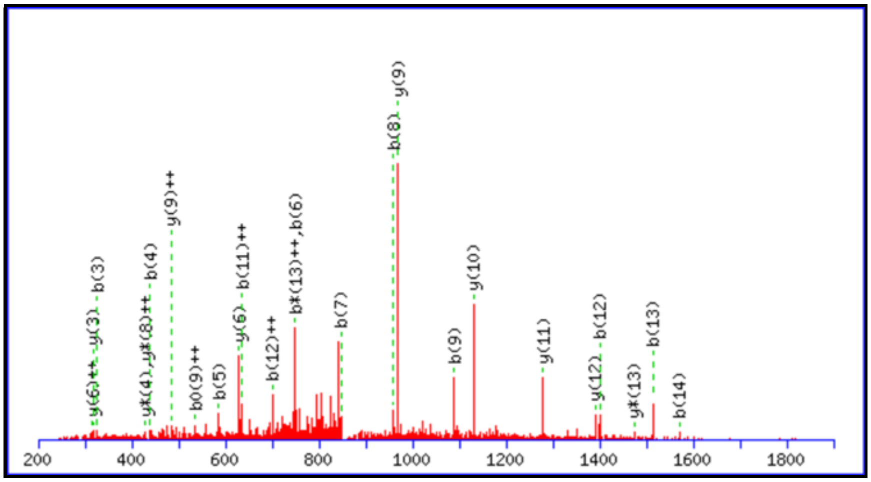
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILVLFYPLEPSQIGK**
Found in **gi|50344950|ref|NP_001002147.1|**, hypothetical protein LOC415237 [Danio rerio]

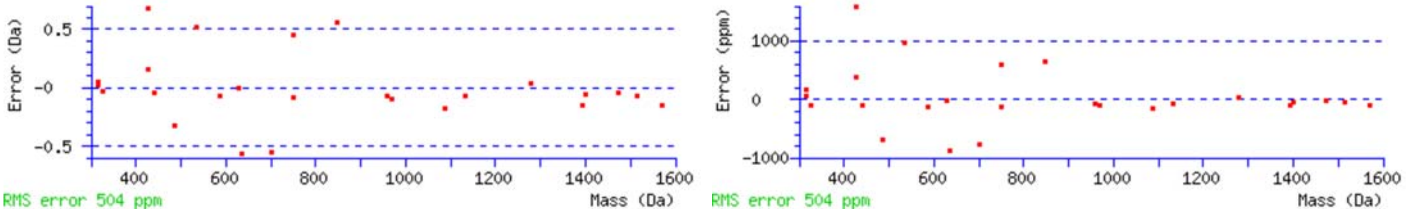
Match to Query 30632: 1716.362724 from(859.188638,2+) index(107543)
Data file TCDD_0530.dta

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1715.9862
Ions Score: 55 **Expect:** 0.00083
Matches : 25/122 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					**I**							**15**
2	227.1754	114.0913					**L**	1603.9094	802.4583	1586.8829	793.9451	1585.8988	793.4531	**14**
3	***326.2438***	163.6255					**V**	1490.8253	745.9163	1473.7988	737.4030	1472.8148	736.9110	**13**
4	***439.3279***	220.1676					**L**	**1391.7569**	696.3821	1374.7304	687.8688	1373.7464	687.3768	**12**
5	***586.3963***	293.7018					**F**	**1278.6729**	639.8401	1261.6463	631.3268	1260.6623	630.8348	**11**
6	***749.4596***	375.2335					**Y**	**1131.6045**	566.3059	1114.5779	557.7926	1113.5939	557.3006	**10**
7	***846.5124***	423.7598					**P**	**968.5411**	484.7742	951.5146	476.2609	950.5306	475.7689	**9**
8	***959.5965***	480.3019					**L**	871.4884	436.2478	854.4618	427.7345	853.4778	427.2425	**8**
9	***1088.6390***	544.8232			1070.6285	535.8179	**E**	758.4043	379.7058	741.3777	371.1925	740.3937	370.7005	**7**
10	1185.6918	593.3495			1167.6812	584.3443	**P**	**629.3617**	315.1845	612.3352	306.6712	611.3511	306.1792	**6**
11	1272.7238	636.8656			1254.7133	627.8603	**S**	532.3089	266.6581	515.2824	258.1448	514.2984	257.6528	**5**
12	***1400.7824***	700.8948	1383.7559	692.3816	1382.7719	691.8896	**Q**	445.2769	223.1421	428.2504	214.6288			**4**
13	***1513.8665***	757.4369	1496.8399	748.9236	1495.8559	748.4316	**I**	**317.2183**	159.1128	300.1918	150.5995			**3**
14	***1570.8879***	785.9476	1553.8614	777.4343	1552.8774	776.9423	**G**	204.1343	102.5708	187.1077	94.0575			**2**
15							**K**	147.1128	74.0600	130.0863	65.5468			**1**



NCBI **BLAST** search of ILVLFYPLEPSQIGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.0	1715.9862	0.3765	ILVLFYPLEPSQIGK
7.0	1716.8278	-0.4651	NLSPSSNASKPEQSSGK
3.5	1717.9106	-1.5479	QMGADVMLSLSLINVK
2.5	1715.7560	0.6067	TSSYSCESVGPETLEK
2.3	1716.6728	-0.3101	CGNGACIMQDFVCDGK
2.2	1717.9587	-1.5960	AQIDAHNINVGIRAVK
1.8	1716.8683	-0.5055	HVTKIQFSEISEDGK
1.7	1715.9651	0.3976	FIFTGVFVGGVYLLGK
1.4	1716.7914	-0.4287	QAEEEDGSQGGVNKAAK
0.8	1717.0073	-0.6446	RLGVLAFLVLGTCSLR

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

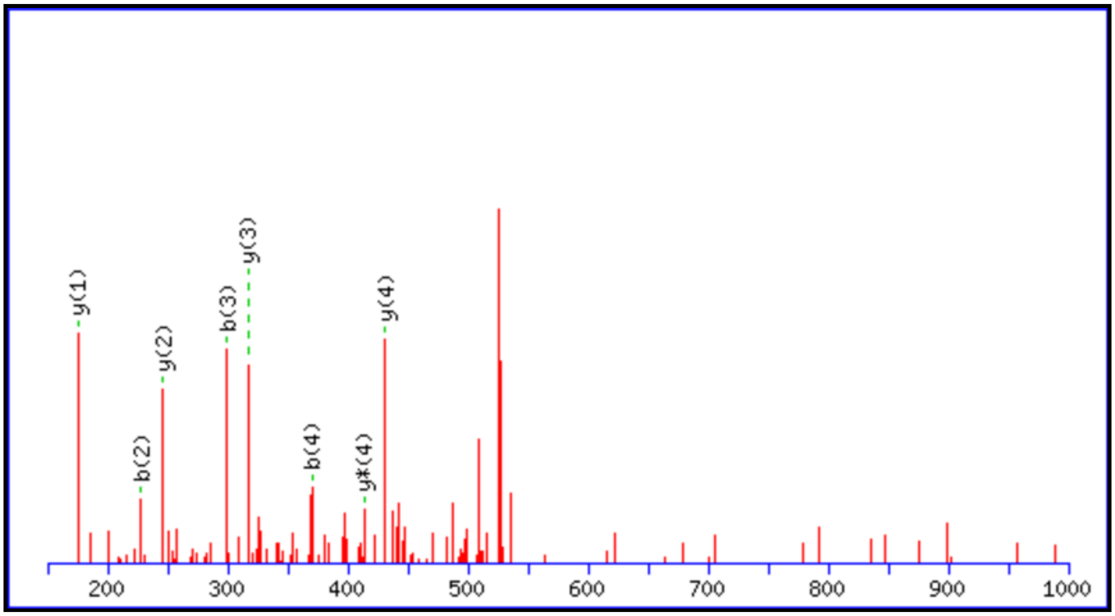
Mascot Search Results

Peptide View

MS/MS Fragmentation of **INAAR**
Found in **gi|131889079|ref|NP_001076537.1|**, hypothetical protein LOC100034487 [Danio rerio]

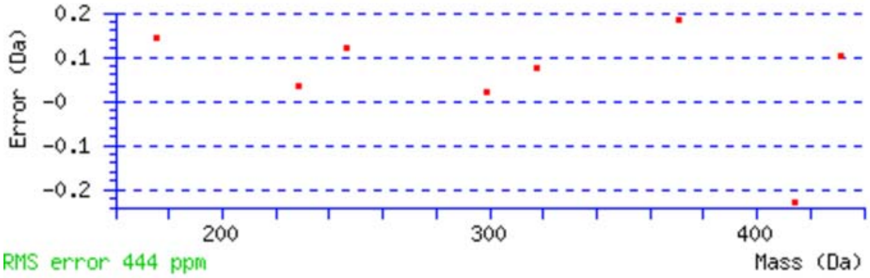
Match to Query 4376: 543.262724 from(544.270000,1+) index(33707)
Data file TCDD_0530.dta

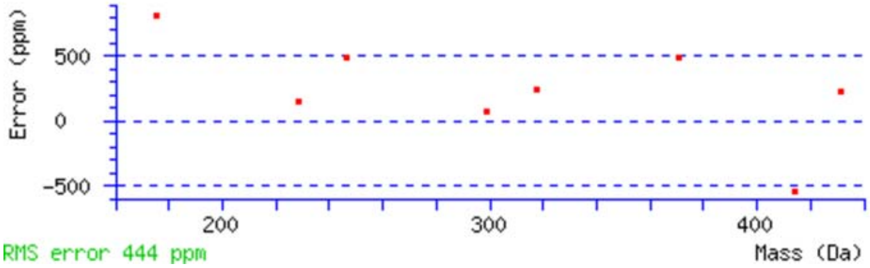
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 543.3129
Ions Score: 42 **Expect:** 0.034
Matches : 8/15 fragment ions using 12 most intense peaks (help)

#	b	b*	Seq.	y	y*	#
1	114.0913		I			5
2	**228.1343**	211.1077	N	***431.2361***	414.2096	4
3	**299.1714**	282.1448	A	***317.1932***	300.1666	3
4	**370.2085**	353.1819	A	***246.1561***	229.1295	2
5			R	***175.1190***	158.0924	1





NCBI **BLAST** search of INAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.9	543.3129	-0.0501	INAAR
41.9	543.3129	-0.0501	LNAAR
28.7	544.2717	-1.0090	NNAAR
25.7	543.3129	-0.0501	NLAAR
24.0	542.2812	0.9815	EPAAR
23.3	543.3241	-0.0614	ARAAR
23.3	543.3493	-0.0865	KVAAR
23.3	543.3241	-0.0614	RAAAR
23.3	543.3493	-0.0865	VKAAR
23.3	543.3129	-0.0502	VQAAR

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

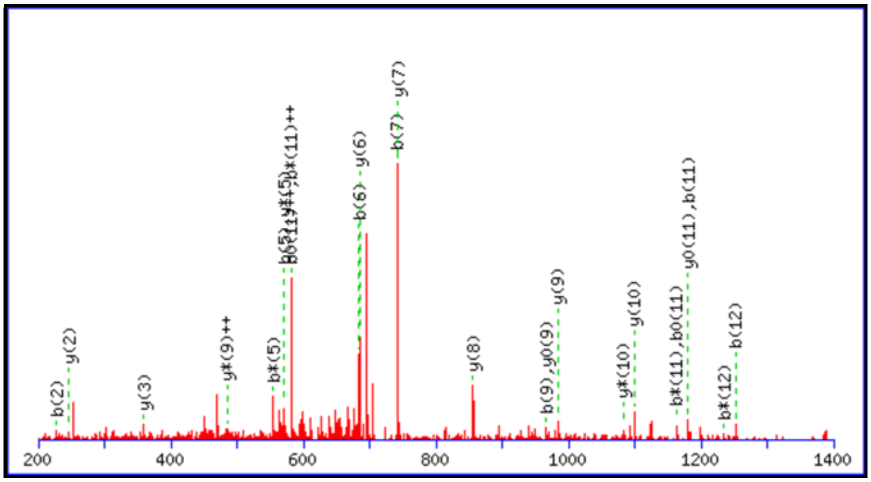
Mascot Search Results

Peptide View

MS/MS Fragmentation of **INVDEIGPQTLAR**
Found in **gi|189517523|ref|XP_001918449.1|**, PREDICTED: hypothetical protein [Danio rerio]

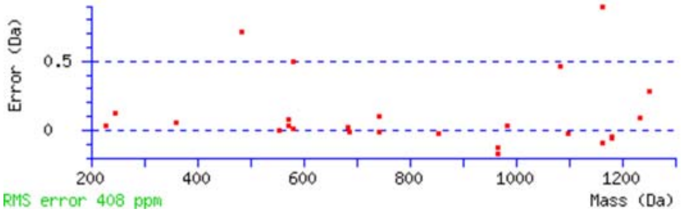
Match to Query 21625: 1425.462724 from(713.738638,2+) index(19603)
Data file TCDD_0531.dta

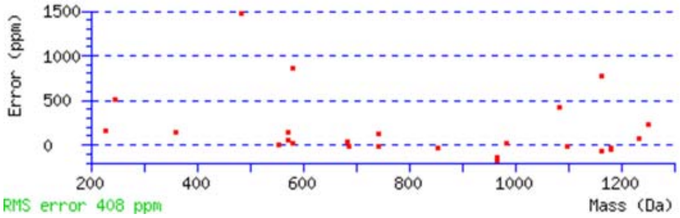
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1424.7623
Ions Score: 44 **Expect:** 0.012
Matches : 25/130 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							13
2	***228.1343***	114.5708	211.1077	106.0575			N	1312.6856	656.8464	1295.6590	648.3331	1294.6750	647.8411	12
3	327.2027	164.1050	310.1761	155.5917			V	1198.6426	599.8250	1181.6161	591.3117	1180.6321	590.8197	11
4	442.2296	221.6185	425.2031	213.1052	424.2191	212.6132	D	***1099.5742***	550.2907	1082.5477	541.7775	1081.5637	541.2855	10
5	***571.2722***	286.1397	554.2457	277.6265	553.2617	277.1345	E	***984.5473***	492.7773	967.5207	484.2640	966.5367	483.7720	9
6	***684.3563***	342.6818	667.3297	334.1685	666.3457	333.6765	I	***855.5047***	428.2560	838.4781	419.7427	837.4941	419.2507	8
7	***741.3777***	371.1925	724.3512	362.6792	723.3672	362.1872	G	***742.4206***	371.7139	725.3941	363.2007	724.4100	362.7087	7
8	838.4305	419.7189	821.4040	411.2056	820.4199	410.7136	P	***685.3992***	343.2032	668.3726	334.6899	667.3886	334.1979	6
9	***966.4891***	483.7482	949.4625	475.2349	948.4785	474.7429	Q	588.3464	294.6768	571.3198	286.1636	570.3358	285.6715	5
10	1067.5368	534.2720	1050.5102	525.7587	1049.5262	525.2667	T	460.2878	230.6475	443.2613	222.1343	442.2772	221.6423	4
11	***1180.6208***	590.8141	1163.5943	582.3008	1162.6103	581.8088	L	***359.2401***	180.1237	342.2136	171.6104			3
12	***1251.6579***	626.3326	1234.6314	617.8193	1233.6474	617.3273	A	***246.1561***	123.5817	229.1295	115.0684			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of INVDEIGPQTLAR

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.0	1424.7623	0.7004	INVDEIGPQTLAR
16.4	1424.6428	0.8199	GGEPAGICLACSYK
12.8	1424.8463	0.6164	RALTIQEIAALAR
11.6	1425.7504	-0.2877	GEVVSVTAYGAFVK
11.5	1426.7391	-1.2764	AQKTGSLCLFFR
10.2	1424.7235	0.7392	GGVVKLCDFGFAR
10.0	1425.8456	-0.3829	LPLRFNDALVLR
9.7	1424.6718	0.7909	NALKSVECYDAR
8.8	1425.7841	-0.3213	HSALDFAIRQLR
7.8	1424.7736	0.6892	THTERLVETLAR

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

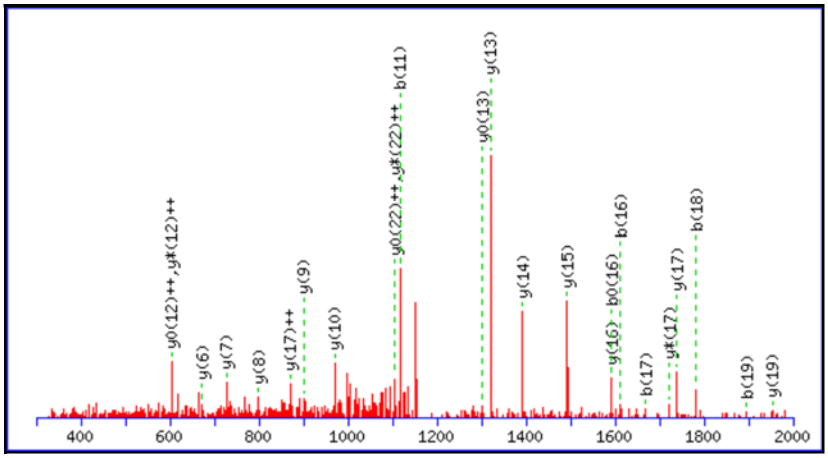
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISGETIFVTAPHDATAGIIGVNR**
Found in **gi|53292609|ref|NP_001005391.1|**, clathrin, heavy polypeptide a (Hc) [Danio rerio]

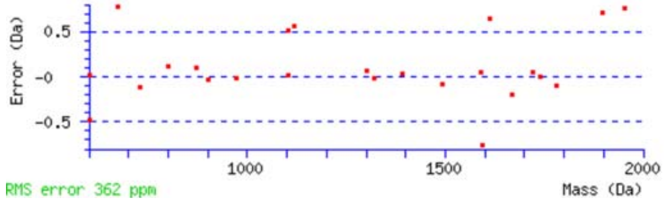
Match to Query 80378: 2339.482724 from(1170.748638,2+) index(19853)
Data file TCDD_0530.dta

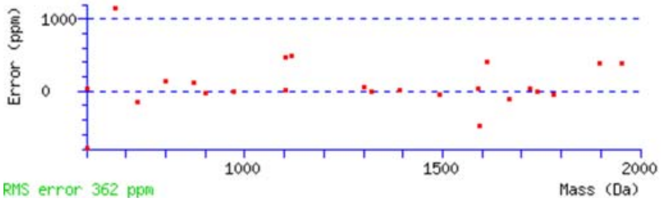
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2338.2281
Ions Score: 48 **Expect:** 0.0027
Matches : 24/204 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					**I**							**23**
2	201.1234	101.0653			183.1128	92.0600	**S**	2226.1513	1113.5793	2209.1248	1105.0660	2208.1408	1104.5740	**22**
3	258.1448	129.5761			240.1343	120.5708	**G**	2139.1193	1070.0633	2122.0927	1061.5500	2121.1087	1061.0580	**21**
4	387.1874	194.0974			369.1769	185.0921	**E**	2082.0978	1041.5526	2065.0713	1033.0393	2064.0873	1032.5473	**20**
5	488.2351	244.6212			470.2245	235.6159	**T**	***1953.0552***	977.0313	1936.0287	968.5180	1935.0447	968.0260	**19**
6	601.3192	301.1632			583.3086	292.1579	**I**	1852.0076	926.5074	1834.9810	917.9941	1833.9970	917.5021	**18**
7	748.3876	374.6974			730.3770	365.6921	**F**	***1738.9235***	869.9654	1721.8969	861.4521	1720.9129	860.9601	**17**
8	847.4560	424.2316			829.4454	415.2264	**V**	***1591.8551***	796.4312	1574.8285	787.9179	1573.8445	787.4259	**16**
9	948.5037	474.7555			930.4931	465.7502	**T**	***1492.7867***	746.8970	1475.7601	738.3837	1474.7761	737.8917	**15**
10	1019.5408	510.2740			1001.5302	501.2687	**A**	***1391.7390***	696.3731	1374.7124	687.8599	1373.7284	687.3678	**14**
11	**1116.5936**	558.8004			1098.5830	549.7951	**P**	***1320.7019***	660.8546	1303.6753	652.3413	1302.6913	651.8493	**13**
12	1253.6525	627.3299			1235.6419	618.3246	**H**	1223.6491	612.3282	1206.6226	603.8149	1205.6385	603.3229	**12**
13	1368.6794	684.8433			1350.6688	675.8381	**D**	1086.5902	543.7987	1069.5636	535.2855	1068.5796	534.7935	**11**
14	1439.7165	720.3619			1421.7060	711.3566	**A**	***971.5633***	486.2853	954.5367	477.7720	953.5527	477.2800	**10**
15	1540.7642	770.8857			1522.7536	761.8805	**T**	***900.5261***	450.7667	883.4996	442.2534	882.5156	441.7614	**9**
16	**1611.8013**	806.4043			1593.7907	797.3990	**A**	***799.4785***	400.2429	782.4519	391.7296			**8**
17	**1668.8228**	834.9150			1650.8122	825.9097	**G**	***728.4413***	364.7243	711.4148	356.2110			**7**
18	**1781.9068**	891.4571			1763.8963	882.4518	**I**	***671.4199***	336.2136	654.3933	327.7003			**6**
19	**1894.9909**	947.9991			1876.9803	938.9938	**I**	558.3358	279.6715	541.3093	271.1583			**5**
20	1952.0124	976.5098			1934.0018	967.5045	**G**	445.2518	223.1295	428.2252	214.6162			**4**
21	2051.0808	1026.0440			2033.0702	1017.0387	**V**	388.2303	194.6188	371.2037	186.1055			**3**
22	2165.1237	1083.0655	2148.0972	1074.5522	2147.1131	1074.0602	**N**	289.1619	145.0846	272.1353	136.5713			**2**
23							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of ISGETIFVTAPHDATAGIIGVNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.3	2338.2281	1.2546	ISGETIFVTAPHDATAGIIGVNR
4.0	2338.0396	1.4431	GASSAFPENSAKGAHNFSACSNGK
2.7	2341.1775	-1.6947	LDRLHNTTFQPSNISDSIQR
1.8	2338.0673	1.4154	EVNSQDEEFELGKSLNGSSNR
0.8	2339.0894	0.3933	DTLGCSLLQKNMCPCFLSPR
0.8	2339.0894	0.3933	DTLGCSLLQKNMCPCFLSPR
0.8	2341.0070	-1.5242	AQGFPAASCWEWTTQTERES

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

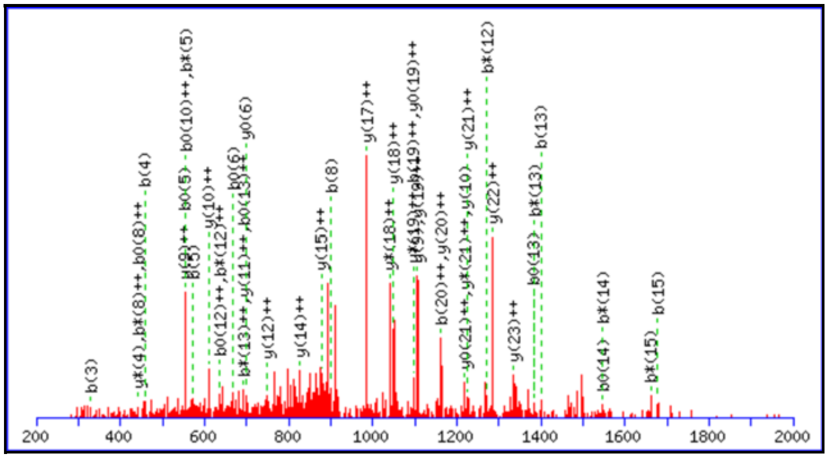
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITDENLQSQTTGLYIPEYEEALKK**
Found in **gi|52219050|ref|NP_001004598.1|**, hypothetical protein LOC447859 [Danio rerio]

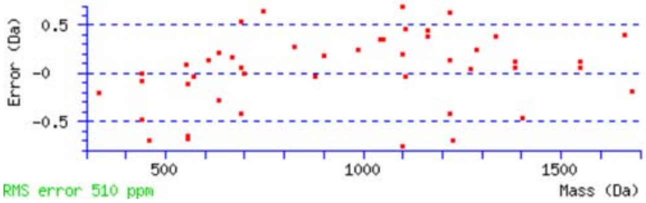
Match to Query 103017: 2783.722725 from(928.914851,3+) index(19748)
Data file TCDD_0530.dta

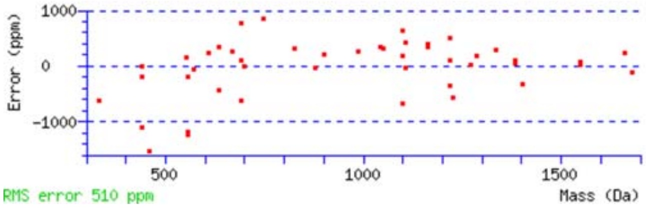
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2782.3912
Ions Score: 45 **Expect:** 0.0048
Matches : 46/258 fragment ions using 80 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							24
2	215.1390	108.0731			197.1285	99.0679	T	2670.3145	1335.6609	2653.2879	1327.1476	2652.3039	1326.6556	23
3	**330.1660**	165.5866			312.1554	156.5813	D	2569.2668	1285.1370	2552.2403	1276.6238	2551.2562	1276.1318	22
4	**459.2086**	230.1079			441.1980	221.1026	E	2454.2399	1227.6236	2437.2133	1219.1103	2436.2293	1218.6183	21
5	**573.2515**	287.1294	556.2249	278.6161	555.2409	278.1241	N	2325.1973	1163.1023	2308.1707	1154.5890	2307.1867	1154.0970	20
6	686.3355	343.6714	669.3090	335.1581	668.3250	334.6661	L	2211.1543	1106.0808	2194.1278	1097.5675	2193.1438	1097.0755	19
7	814.3941	407.7007	797.3676	399.1874	796.3836	398.6954	Q	2098.0703	1049.5388	2081.0437	1041.0255	2080.0597	1040.5335	18
8	**901.4262**	451.2167	884.3996	442.7034	883.4156	442.2114	S	1970.0117	985.5095	1952.9852	976.9962	1952.0011	976.5042	17
9	1029.4847	515.2460	1012.4582	506.7327	1011.4742	506.2407	Q	1882.9797	941.9935	1865.9531	933.4802	1864.9691	932.9882	16
10	1130.5324	565.7698	1113.5059	557.2566	1112.5218	556.7646	T	1754.9211	877.9642	1737.8945	869.4509	1736.9105	868.9589	15
11	1231.5801	616.2937	1214.5535	607.7804	1213.5695	607.2884	T	1653.8734	827.4403	1636.8469	818.9271	1635.8629	818.4351	14
12	1288.6016	644.8044	1271.5750	636.2911	1270.5910	635.7991	G	1552.8257	776.9165	1535.7992	768.4032	1534.8152	767.9112	13
13	**1401.6856**	701.3464	1384.6591	692.8332	1383.6751	692.3412	L	1495.8043	748.4058	1478.7777	739.8925	1477.7937	739.4005	12
14	1564.7489	782.8781	1547.7224	774.3648	1546.7384	773.8728	Y	1382.7202	691.8637	1365.6937	683.3505	1364.7096	682.8585	11
15	**1677.8330**	839.4201	1660.8065	830.9069	1659.8224	830.4149	I	1219.6569	610.3321	1202.6303	601.8188	1201.6463	601.3268	10
16	1774.8858	887.9465	1757.8592	879.4332	1756.8752	878.9412	P	1106.5728	553.7900	1089.5463	545.2768	1088.5623	544.7848	9
17	1903.9284	952.4678	1886.9018	943.9545	1885.9178	943.4625	E	1009.5201	505.2637	992.4935	496.7504	991.5095	496.2584	8
18	2066.9917	1033.9995	2049.9651	1025.4862	2048.9811	1024.9942	Y	880.4775	440.7424	863.4509	432.2291	862.4669	431.7371	7
19	2196.0343	1098.5208	2179.0077	1090.0075	2178.0237	1089.5155	E	717.4141	359.2107	700.3876	350.6974	699.4036	350.2054	6
20	2325.0769	1163.0421	2308.0503	1154.5288	2307.0663	1154.0368	E	588.3715	294.6894	571.3450	286.1761	570.3610	285.6841	5
21	2396.1140	1198.5606	2379.0874	1190.0474	2378.1034	1189.5554	A	459.3289	230.1681	442.3024	221.6548			4
22	2509.1981	1255.1027	2492.1715	1246.5894	2491.1875	1246.0974	L	388.2918	194.6496	371.2653	186.1363			3
23	2637.2930	1319.1501	2620.2665	1310.6369	2619.2825	1310.1449	K	275.2078	138.1075	258.1812	129.5942			2
24							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ITDENLQSQTTGLYIPEYEEALKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.8	2782.3912	1.3315	ITDENLQSQTTGLYIPEYEEALKK
5.5	2783.3932	0.3295	FSLSHRNTWISFGGSYAGALSAWLR
5.4	2784.3211	-0.5984	EINVFEMDGALCADLDVNRPNPAPK
5.2	2784.4844	-0.7616	MLIKAEQHLDLSALPTPESTPLQPR
4.1	2785.3026	-1.5799	ASDDGESVGNCPFCQRLFMILWLK
4.0	2783.1681	0.5546	IEGPPQAPGHPRPNTCCLCWCGCCK
3.0	2783.4440	0.2787	TLDEILREIEEQAVIDEQTLAEVK
2.8	2785.4181	-1.6954	EGHLEHLLARELVPGDTVCLSVGER
1.8	2784.4116	-0.6888	NEEGDSALVAAIKHDQYDMALLLLR
0.9	2782.4429	1.2798	ITQLIDDVDPSTTFVLLNAVYFNGK

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

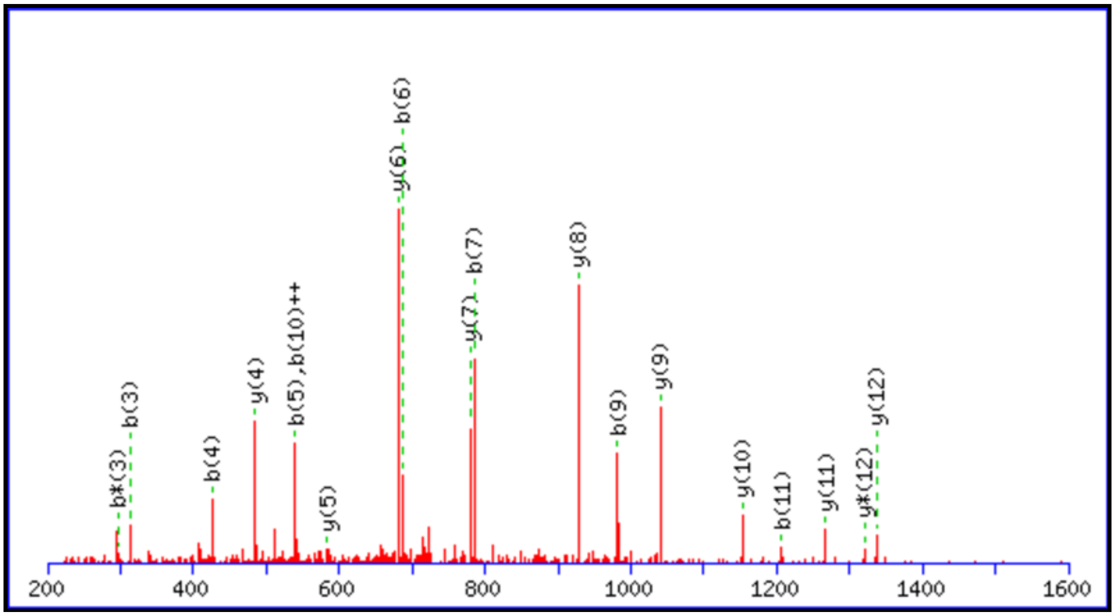
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KAIIIFVPVPQLK**
Found in **gi|41152175|ref|NP_957046.1|**, ribosomal protein S7 [Danio rerio]

Match to Query 22048: 1464.932724 from(733.473638,2+) index(57904)
Data file TCDD_0530.dta

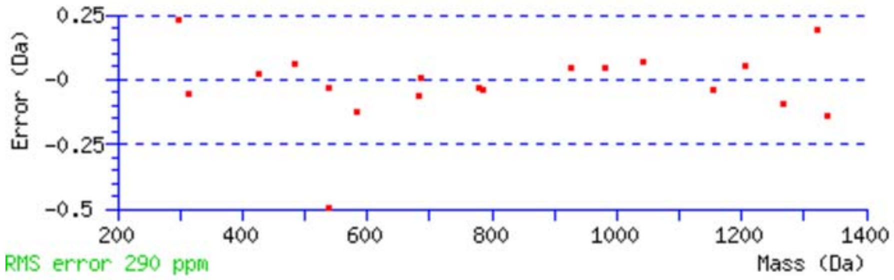
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

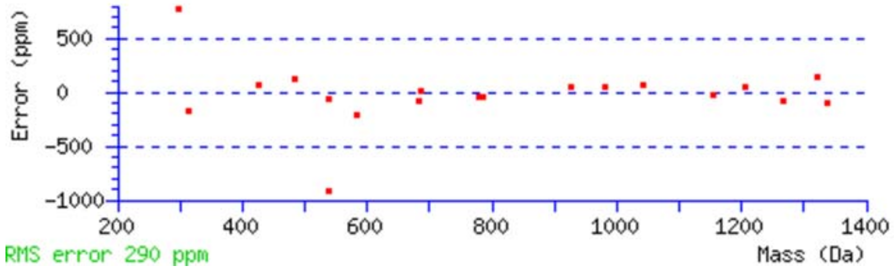


Monoisotopic mass of neutral peptide Mr(calc): 1464.9432
Ions Score: 52 **Expect:** 0.0018
Matches : 19/96 fragment ions using 37 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	129.1022	65.0548	112.0757	56.5415	**K**					**13**
2	200.1394	100.5733	183.1128	92.0600	**A**	***1337.8555***	669.4314	1320.8290	660.9181	**12**
3	**313.2234**	157.1153	296.1969	148.6021	**I**	***1266.8184***	633.9128	1249.7919	625.3996	**11**
4	**426.3075**	213.6574	409.2809	205.1441	**I**	***1153.7343***	577.3708	1136.7078	568.8575	**10**
5	**539.3915**	270.1994	522.3650	261.6861	**I**	***1040.6503***	520.8288	1023.6237	512.3155	**9**
6	**686.4600**	343.7336	669.4334	335.2203	**F**	***927.5662***	464.2867	910.5397	455.7735	**8**
7	**785.5284**	393.2678	768.5018	384.7545	**V**	***780.4978***	390.7525	763.4713	382.2393	**7**
8	882.5811	441.7942	865.5546	433.2809	**P**	***681.4294***	341.2183	664.4028	332.7051	**6**
9	**981.6496**	491.3284	964.6230	482.8151	**V**	***584.3766***	292.6919	567.3501	284.1787	**5**
10	1078.7023	539.8548	1061.6758	531.3415	**P**	***485.3082***	243.1577	468.2817	234.6445	**4**

11	1206.7609	603.8841	1189.7343	595.3708	**Q**	388.2554	194.6314	371.2289	186.1181	**3**
12	1319.8450	660.4261	1302.8184	651.9128	**L**	260.1969	130.6021	243.1703	122.0888	**2**
13					**K**	147.1128	74.0600	130.0863	65.5468	**1**





NCBI **BLAST** search of KAIIIFVPVPQLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.8	1464.9432	-0.0105	KAIIIFVPVPQLK
16.6	1464.7395	0.1933	QALLEMYNTLNR
9.2	1465.7275	-0.7948	LQANFFEMEIPK
5.8	1465.7273	-0.7946	GAADKEGGLQIHDR
5.0	1466.7188	-1.7860	EHCLEPQSLIGGK
4.6	1464.8300	0.1027	KAILAIDSSPTPPR
4.5	1462.7701	2.1626	SSTTSMTSVPKPLK
4.0	1465.7785	-0.8458	KPLSLSAFTLCMR
3.1	1462.6585	2.2743	CGVKPPEPGECYK
3.0	1466.6976	-1.7649	EAERATFWCLNK

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

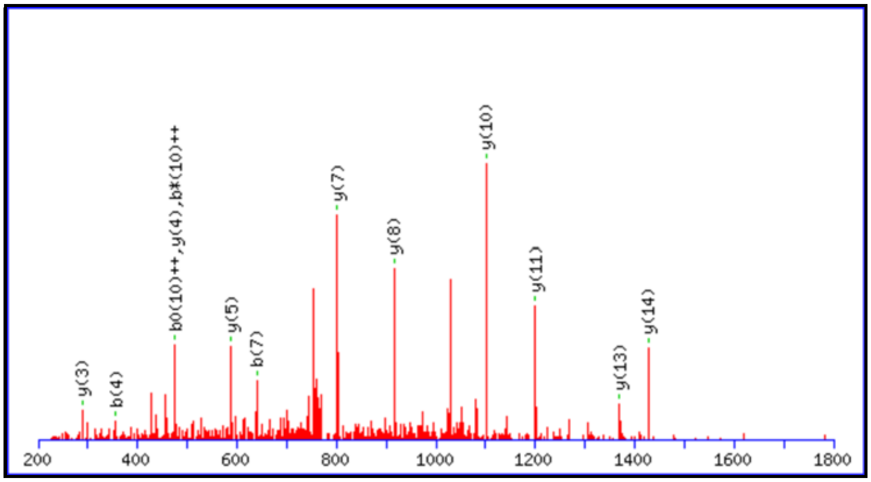
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGGIVAIDNVLWGGR**
Found in **gi|68389723|ref|XP_696495.1|**, PREDICTED: catechol-O-methyltransferase domain containing 1 [Danio rerio]

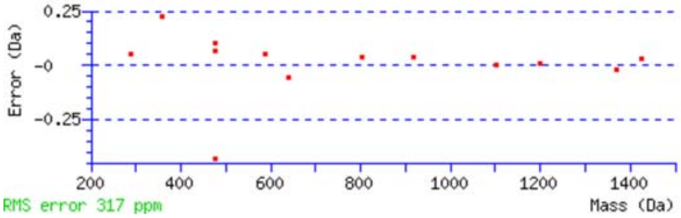
Match to Query 24721: 1554.792724 from(778.403638,2+) index(46302)
Data file TCDD_0530.dta

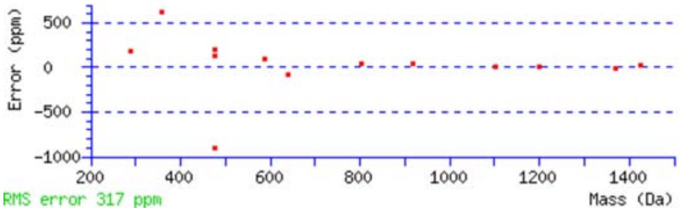
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1800] Da [Full range]
Label all possible matches ○   Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1553.8678
Ions Score: 77 **Expect:** 5.5e-006
Matches : 13/140 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							15
2	186.1237	93.5655	169.0972	85.0522			G	***1426.7801***	713.8937	1409.7536	705.3804	1408.7696	704.8884	14
3	243.1452	122.0762	226.1186	113.5629			G	***1369.7587***	685.3830	1352.7321	676.8697	1351.7481	676.3777	13
4	**356.2292**	178.6183	339.2027	170.1050			I	1312.7372	656.8722	1295.7106	648.3590	1294.7266	647.8670	12
5	455.2976	228.1525	438.2711	219.6392			V	***1199.6531***	600.3302	1182.6266	591.8169	1181.6426	591.3249	11
6	526.3348	263.6710	509.3082	255.1577			A	***1100.5847***	550.7960	1083.5582	542.2827	1082.5742	541.7907	10
7	**639.4188**	320.2130	622.3923	311.6998			I	1029.5476	515.2774	1012.5211	506.7642	1011.5370	506.2722	9
8	754.4458	377.7265	737.4192	369.2132	736.4352	368.7212	D	***916.4635***	458.7354	899.4370	450.2221	898.4530	449.7301	8
9	868.4887	434.7480	851.4621	426.2347	850.4781	425.7427	N	***801.4366***	401.2219	784.4100	392.7087			7
10	967.5571	484.2822	950.5306	475.7689	949.5465	475.2769	V	687.3937	344.2005	670.3671	335.6872			6
11	1080.6412	540.8242	1063.6146	532.3109	1062.6306	531.8189	L	***588.3253***	294.6663	571.2987	286.1530			5
12	1266.7205	633.8639	1249.6939	625.3506	1248.7099	624.8586	W	***475.2412***	238.1242	458.2146	229.6110			4
13	1323.7419	662.3746	1306.7154	653.8613	1305.7314	653.3693	G	***289.1619***	145.0846	272.1353	136.5713			3
14	1380.7634	690.8853	1363.7369	682.3721	1362.7528	681.8801	G	232.1404	116.5738	215.1139	108.0606			2
15							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of KGGIVAIDNVLWGGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.0	1553.8678	0.9249	KGGIVAIDNVLWGGR
7.8	1554.7824	0.0103	SVPATPTTRGPSCPGK
5.8	1554.8704	-0.0777	HLSVVCYVKAALPR
4.2	1554.7752	0.0175	IGAGGLDGYIIEFCK
3.8	1554.7750	0.0177	NADGAPLDTPTTARR
2.4	1554.7687	0.0241	CYSTALFLKNHMK
1.6	1554.8195	-0.0267	AGVWFRSLLTDYK
0.6	1555.7590	-0.9663	ELNNAQDLIAADNR
0.6	1554.8770	-0.0842	QLINNIQEFVIPK

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

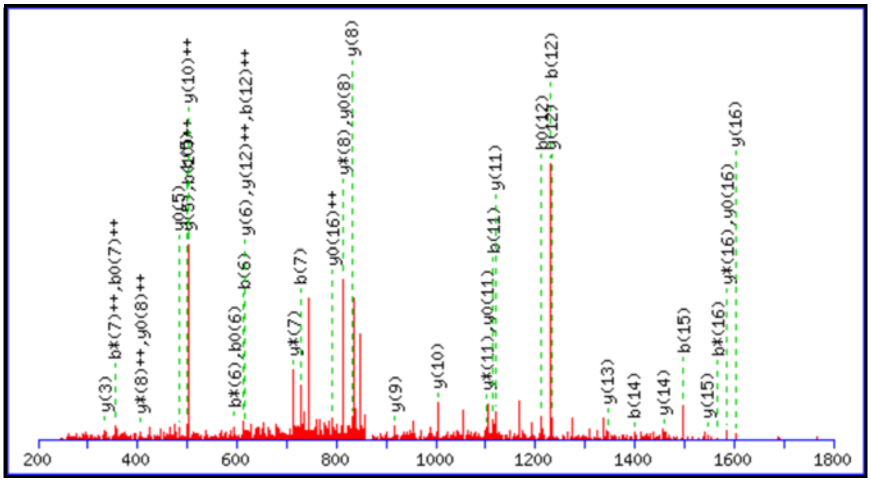
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGSLLIDSSTIDPAVSK**
Found in **gi|41055658|ref|NP_957454.1|**, 3-hydroxyisobutyrate dehydrogenase b [Danio rerio]

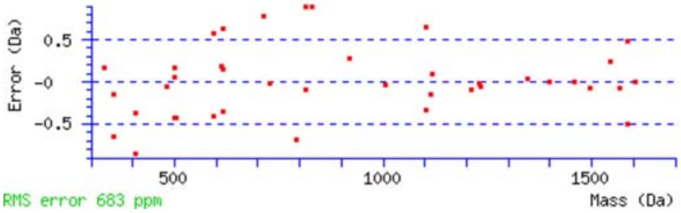
Match to Query 33174: 1729.952724 from(865.983638,2+) index(33999)
Data file TCDD_0531.dta

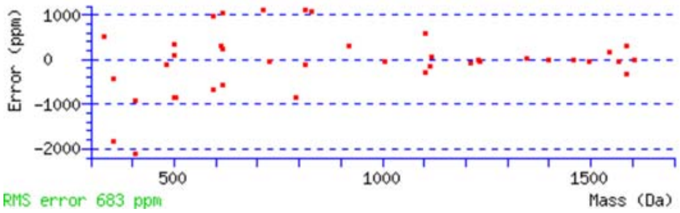
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1729.9462
Ions Score: 46 **Expect:** 0.0056
Matches : 42/186 fragment ions using 100 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							17
2	186.1237	93.5655	169.0972	85.0522			G	***1602.8585***	801.9329	1585.8319	793.4196	1584.8479	792.9276	16
3	273.1557	137.0815	256.1292	128.5682	255.1452	128.0762	S	***1545.8370***	773.4222	1528.8105	764.9089	1527.8265	764.4169	15
4	386.2398	193.6235	369.2132	185.1103	368.2292	184.6183	L	***1458.8050***	729.9061	1441.7785	721.3929	1440.7944	720.9009	14
5	**499.3239**	250.1656	482.2973	241.6523	481.3133	241.1603	L	***1345.7209***	673.3641	1328.6944	664.8508	1327.7104	664.3588	13
6	**612.4079**	306.7076	595.3814	298.1943	594.3974	297.7023	I	***1232.6369***	616.8221	1215.6103	608.3088	1214.6263	607.8168	12
7	**727.4349**	364.2211	710.4083	355.7078	709.4243	355.2158	D	***1119.5528***	560.2800	1102.5263	551.7668	1101.5422	551.2748	11
8	814.4669	407.7371	797.4403	399.2238	796.4563	398.7318	S	***1004.5259***	502.7666	987.4993	494.2533	986.5153	493.7613	10
9	901.4989	451.2531	884.4724	442.7398	883.4884	442.2478	S	***917.4938***	459.2506	900.4673	450.7373	899.4833	450.2453	9
10	1002.5466	501.7769	985.5201	493.2637	984.5360	492.7717	T	***830.4618***	415.7345	813.4353	407.2213	812.4512	406.7293	8
11	**1115.6307**	558.3190	1098.6041	549.8057	1097.6201	549.3137	I	729.4141	365.2107	712.3876	356.6974	711.4036	356.2054	7
12	**1230.6576**	615.8324	1213.6311	607.3192	1212.6470	606.8272	D	***616.3301***	308.6687	599.3035	300.1554	598.3195	299.6634	6
13	1327.7104	664.3588	1310.6838	655.8455	1309.6998	655.3535	P	***501.3031***	251.1552	484.2766	242.6419	483.2926	242.1499	5
14	**1398.7475**	699.8774	1381.7209	691.3641	1380.7369	690.8721	A	404.2504	202.6288	387.2238	194.1155	386.2398	193.6235	4
15	**1497.8159**	749.4116	1480.7894	740.8983	1479.8053	740.4063	V	***333.2132***	167.1103	316.1867	158.5970	315.2027	158.1050	3
16	**1584.8479**	792.9276	1567.8214	784.4143	1566.8374	783.9223	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
17							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of KGSLLIDSSTIDPAVSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.5	1729.9462	0.0066	KGSLLIDSSTIDPAVSK
13.0	1730.9930	-1.0403	KPEKPPVVEEPKGGLK
9.1	1730.8549	-0.9022	VTGKDLATAFDLSCYK
8.6	1731.8792	-1.9264	EGFQSVDSREPLQIK
8.1	1729.9098	0.0430	QEEIQVLNETLSLSK
7.7	1730.9144	-0.9617	LYQHAVEYFLHAIK
6.2	1730.7959	-0.8431	SALETGAVEEASHTDSK
5.6	1730.7505	-0.7978	IMYCTDPGHVDHSTR
5.5	1730.8953	-0.9426	LFELLEMEILYYR
5.2	1728.9621	0.9906	EGLAKITVNISDITQK

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

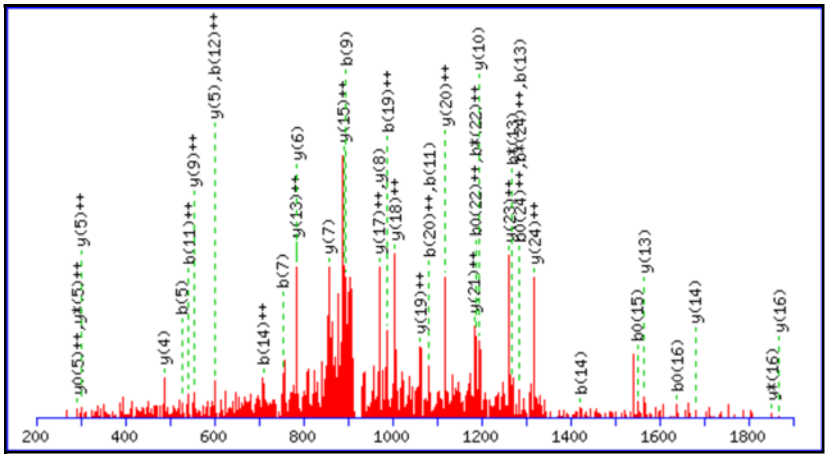
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KIGVELIAASTDSHFSHLAWINTPR**
Found in **gi|50539996|ref|NP_001002468.1|**, peroxiredoxin 2 [Danio rerio]

Match to Query 102374: 2764.512723 from(922.511517,3+) index(90201)
Data file TCDD_0530.dta

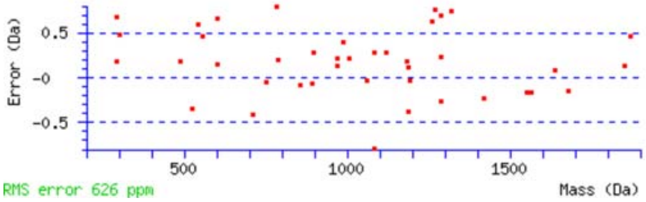
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●

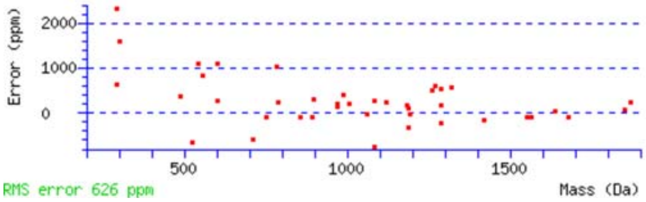


Monoisotopic mass of neutral peptide Mr(calc): 2762.4504
Ions Score: 44 **Expect:** 0.0062
Matches : 41/276 fragment ions using 96 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			**K**							**25**
2	242.1863	121.5968	225.1598	113.0835			**I**	2635.3627	1318.1850	2618.3362	1309.6717	2617.3521	1309.1797	**24**
3	299.2078	150.1075	282.1812	141.5942			**G**	2522.2786	1261.6430	2505.2521	1253.1297	2504.2681	1252.6377	**23**
4	398.2762	199.6417	381.2496	191.1285			**V**	2465.2572	1233.1322	2448.2306	1224.6190	2447.2466	1224.1269	**22**
5	**527.3188**	264.1630	510.2922	255.6498	509.3082	255.1577	**E**	2366.1888	1183.5980	2349.1622	1175.0847	2348.1782	1174.5927	**21**
6	640.4028	320.7051	623.3763	312.1918	622.3923	311.6998	**L**	2237.1462	1119.0767	2220.1196	1110.5635	2219.1356	1110.0714	**20**
7	**753.4869**	377.2471	736.4604	368.7338	735.4763	368.2418	**I**	2124.0621	1062.5347	2107.0356	1054.0214	2106.0515	1053.5294	**19**
8	824.5240	412.7656	807.4975	404.2524	806.5135	403.7604	**A**	2010.9780	1005.9927	1993.9515	997.4794	1992.9675	996.9874	**18**
9	**895.5611**	448.2842	878.5346	439.7709	877.5506	439.2789	**A**	1939.9409	970.4741	1922.9144	961.9608	1921.9304	961.4688	**17**
10	982.5932	491.8002	965.5666	483.2869	964.5826	482.7949	**S**	***1868.9038***	934.9555	1851.8773	926.4423	1850.8933	925.9503	**16**
11	**1083.6408**	**542.3241**	1066.6143	533.8108	1065.6303	533.3188	**T**	1781.8718	891.4395	1764.8452	882.9263	1763.8612	882.4343	**15**
12	1198.6678	**599.8375**	1181.6412	591.3243	1180.6572	590.8322	**D**	***1680.8241***	840.9157	1663.7976	832.4024	1662.8135	831.9104	**14**
13	**1285.6998**	643.3535	1268.6733	634.8403	1267.6892	634.3483	**S**	***1565.7972***	783.4022	1548.7706	774.8889	1547.7866	774.3969	**13**
14	**1422.7587**	**711.8830**	1405.7322	703.3697	1404.7482	702.8777	**H**	1478.7651	739.8862	1461.7386	731.3729	1460.7546	730.8809	**12**
15	1569.8271	785.4172	1552.8006	776.9039	1551.8166	776.4119	**F**	1341.7062	671.3568	1324.6797	662.8435	1323.6957	662.3515	**11**
16	1656.8592	828.9332	1639.8326	820.4199	1638.8486	819.9279	**S**	***1194.6378***	597.8225	1177.6113	589.3093	1176.6273	588.8173	**10**
17	1793.9181	897.4627	1776.8915	888.9494	1775.9075	888.4574	**H**	1107.6058	554.3065	1090.5792	545.7933	1089.5952	545.3012	**9**
18	1907.0021	954.0047	1889.9756	945.4914	1888.9916	944.9994	**L**	***970.5469***	485.7771	953.5203	477.2638	952.5363	476.7718	**8**
19	1978.0393	**989.5233**	1961.0127	981.0100	1960.0287	980.5180	**A**	***857.4628***	429.2350	840.4363	420.7218	839.4522	420.2298	**7**
20	2164.1186	**1082.5629**	2147.0920	1074.0496	2146.1080	1073.5576	**W**	***786.4257***	393.7165	769.3991	385.2032	768.4151	384.7112	**6**
21	2277.2026	1139.1050	2260.1761	1130.5917	2259.1921	1130.0997	**I**	***600.3464***	300.6768	583.3198	292.1636	582.3358	291.6715	**5**
22	2391.2456	1196.1264	2374.2190	1187.6131	2373.2350	1187.1211	**N**	***487.2623***	244.1348	470.2358	235.6215	469.2518	235.1295	**4**
23	2492.2932	1246.6503	2475.2667	1238.1370	2474.2827	1237.6450	**T**	373.2194	187.1133	356.1928	178.6001	355.2088	178.1081	**3**
24	2589.3460	1295.1766	2572.3194	1286.6634	2571.3354	1286.1714	**P**	272.1717	136.5895	255.1452	128.0762			**2**

25							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of KIGVELIAASTDSHFSHLAWINTPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.6	2762.4504	2.0623	KIGVELIAASTDSHFSHLAWINTPR
6.4	2764.3537	0.1590	QNQRSMFDHLSYLLQNSGIGLGMR
5.6	2765.4647	-0.9520	VRVTHVTSPGNICVQLLQFDNQLK
3.1	2764.5594	-0.0467	LISADSKANVLHGLSILELCLIIAMK
0.8	2766.1995	-1.6868	EMMQIADPGNFHHCQNHSCKNLR
0.7	2765.2160	-0.7033	MSGSPNCQTFSSSTVISYSSTDPGTPK

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

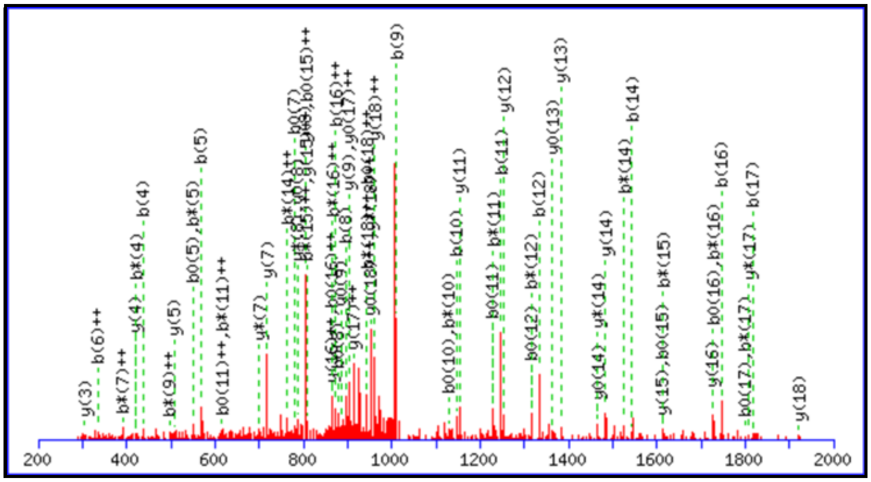
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVLETEVNHVSPLSDASK**
Found in **gi|57770449|ref|NP_001009895.1|**, hypothetical protein LOC393165 isoform 1 [Danio rerio]

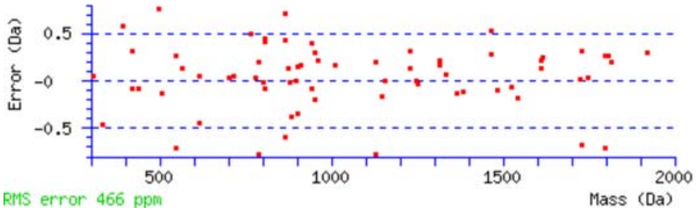
Match to Query 50085: 2049.362724 from(1025.688638,2+) index(51507)
Data file TCDD_0530.dta

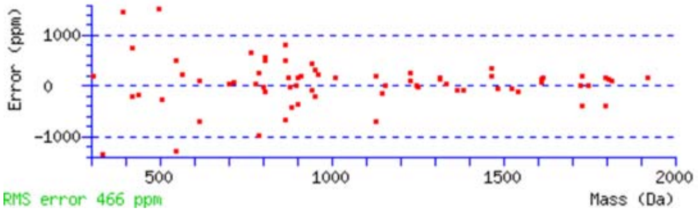
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2049.0742
Ions Score: 42   Expect: 0.014
Matches : 70/206 fragment ions using 164 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			**K**							**19**
2	226.1550	113.5811	209.1285	105.0679			**P**	***1921.9865***	961.4969	1904.9600	952.9836	1903.9760	952.4916	**18**
3	325.2234	163.1153	308.1969	154.6021			**V**	1824.9338	912.9705	1807.9072	904.4573	1806.9232	903.9652	**17**
4	**438.3075**	219.6574	421.2809	211.1441			**L**	***1725.8654***	863.4363	1708.8388	854.9230	1707.8548	854.4310	**16**
5	**567.3501**	284.1787	550.3235	275.6654	549.3395	275.1734	**E**	***1612.7813***	806.8943	1595.7548	798.3810	1594.7707	797.8890	**15**
6	668.3978	334.7025	651.3712	326.1892	650.3872	325.6972	**T**	***1483.7387***	742.3730	1466.7122	733.8597	1465.7281	733.3677	**14**
7	797.4403	399.2238	780.4138	390.7105	779.4298	390.2185	**E**	***1382.6910***	691.8492	1365.6645	683.3359	1364.6805	682.8439	**13**
8	**896.5088**	448.7580	879.4822	440.2447	878.4982	439.7527	**V**	***1253.6484***	627.3279	1236.6219	618.8146	1235.6379	618.3226	**12**
9	**1010.5517**	505.7795	993.5251	497.2662	992.5411	496.7742	**N**	***1154.5800***	577.7937	1137.5535	569.2804	1136.5695	568.7884	**11**
10	**1147.6106**	574.3089	1130.5841	565.7957	1129.6000	565.3037	**H**	1040.5371	520.7722	1023.5106	512.2589	1022.5265	511.7669	**10**
11	**1246.6790**	623.8431	1229.6525	615.3299	1228.6684	614.8379	**V**	***903.4782***	452.2427	886.4516	443.7295	885.4676	443.2374	**9**
12	**1333.7110**	667.3592	1316.6845	658.8459	1315.7005	658.3539	**S**	***804.4098***	402.7085	787.3832	394.1953	786.3992	393.7032	**8**
13	1430.7638	715.8855	1413.7373	707.3723	1412.7532	706.8803	**P**	***717.3777***	359.1925	700.3512	350.6792	699.3672	350.1872	**7**
14	**1543.8479**	772.4276	1526.8213	763.9143	1525.8373	763.4223	**L**	620.3250	310.6661	603.2984	302.1529	602.3144	301.6608	**6**
15	1630.8799	815.9436	1613.8533	807.4303	1612.8693	806.9383	**S**	***507.2409***	254.1241	490.2144	245.6108	489.2304	245.1188	**5**
16	**1745.9068**	873.4571	1728.8803	864.9438	1727.8963	864.4518	**D**	***420.2089***	210.6081	403.1823	202.0948	402.1983	201.6028	**4**
17	**1816.9440**	908.9756	1799.9174	900.4623	1798.9334	899.9703	**A**	***305.1819***	153.0946	288.1554	144.5813	287.1714	144.0893	**3**
18	1903.9760	952.4916	1886.9494	943.9784	1885.9654	943.4863	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
19							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of KPVLETEVNHVSPLSDASK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.9	2049.0742	0.2885	KPVLETEVNHVSPLSDASK
7.7	2049.1510	0.2117	LIQLVSLYGDKSWSIISK
7.2	2048.0902	1.2725	QEISITFQQQTKLLSER
4.2	2049.9160	-0.5533	QTEIEAERCGESEVVDEK
2.5	2048.9871	0.3757	ELLSCISLSSPDGLTCAQR
1.0	2050.9135	-1.5508	HMLVHTGEKTHQCDQCGK
0.4	2050.8916	-1.5288	EQGLHSPGWGNDPGCPTSR
0.2	2048.9374	0.4253	ICSEHFSPEDFRAVNGNK

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

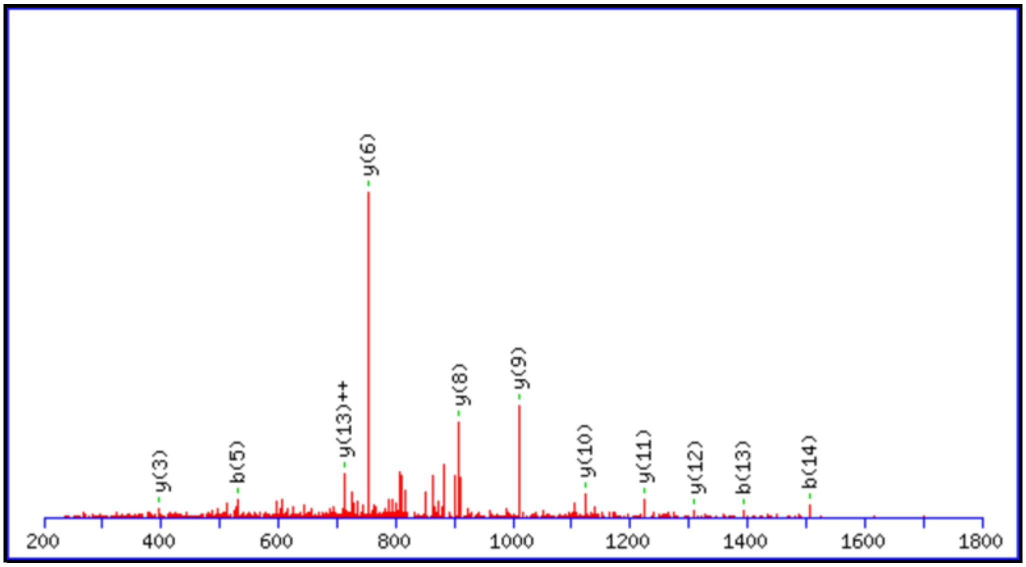
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDISTLTGVPEEHIK**
Found in **gi|66472400|ref|NP_001018512.1|**, NADH dehydrogenase (ubiquinone) Fe-S protein 4, (NADH-coenzyme Q reductase) [Danio rerio]

Match to Query 27811: 1652.172724 from(827.093638,2+) index(33332)
Data file TCDD_0530.dta

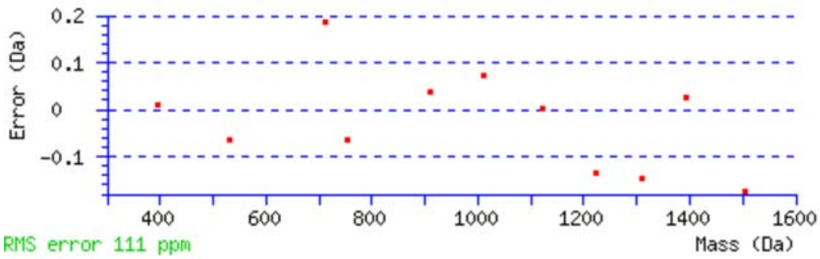
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

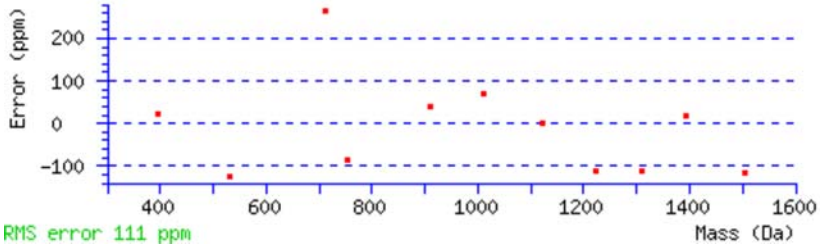


```
Monoisotopic mass of neutral peptide Mr(calc): 1650.8828
Ions Score: 54   Expect: 0.00097
Matches : 11/132 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							15
2	229.1183	115.0628	211.1077	106.0575	D	1538.8061	769.9067	1521.7795	761.3934	1520.7955	760.9014	14
3	342.2023	171.6048	324.1918	162.5995	I	1423.7791	712.3932	1406.7526	703.8799	1405.7686	703.3879	13
4	429.2344	215.1208	411.2238	206.1155	S	***1310.6951***	655.8512	1293.6685	647.3379	1292.6845	646.8459	12
5	**530.2821**	265.6447	512.2715	256.6394	T	***1223.6630***	612.3352	1206.6365	603.8219	1205.6525	603.3299	11
6	643.3661	322.1867	625.3556	313.1814	L	***1122.6154***	561.8113	1105.5888	553.2980	1104.6048	552.8060	10
7	744.4138	372.7105	726.4032	363.7053	T	***1009.5313***	505.2693	992.5047	496.7560	991.5207	496.2640	9
8	801.4353	401.2213	783.4247	392.2160	G	***908.4836***	454.7454	891.4571	446.2322	890.4730	445.7402	8
9	900.5037	450.7555	882.4931	441.7502	V	851.4621	426.2347	834.4356	417.7214	833.4516	417.2294	7
10	997.5564	499.2819	979.5459	490.2766	P	***752.3937***	376.7005	735.3672	368.1872	734.3832	367.6952	6
11	1126.5990	563.8032	1108.5885	554.7979	E	655.3410	328.1741	638.3144	319.6608	637.3304	319.1688	5
12	1255.6416	628.3245	1237.6311	619.3192	E	526.2984	263.6528	509.2718	255.1395	508.2878	254.6475	4
13	**1392.7005**	696.8539	1374.6900	687.8486	H	***397.2558***	199.1315	380.2292	190.6183			3

14	**1505.7846**	753.3959	1487.7740	744.3907	**I**	260.1969	130.6021	243.1703	122.0888			**2**
15					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LDISTLTGVPEEHIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.1	1650.8828	1.2899	LDISTLTGVPEEHIK
8.0	1650.8399	1.3328	ITDFGLSRVAENVCK
4.8	1650.6840	1.4887	EFVCSECERSFMK
3.0	1653.7338	-1.5611	DLDKSSTGVSNCPTCK
2.8	1650.8366	1.3361	WTGDPGVNITVHDLK
1.4	1650.8617	1.3110	FLESQEFQPSIAKK
0.9	1653.9202	-1.7475	RDFNSLAVLEIHLK
0.8	1650.7274	1.4453	EKEQQQEDEFWR
0.8	1649.7296	2.4431	FWEKCYFSQEQR
0.7	1651.8610	0.3117	FLATWQGPYTVLEK

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

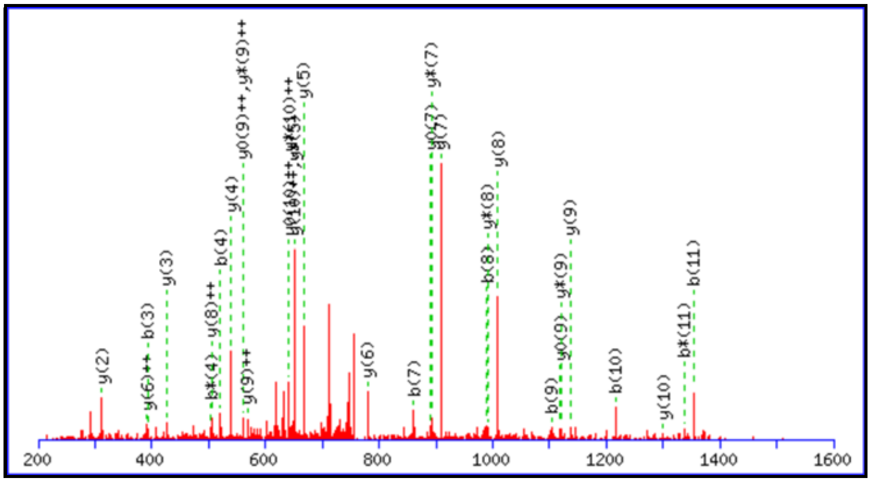
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDYQVELQNLHR**
Found in **gi|54400426|ref|NP_001005960.1|**, ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 [Danio rerio]

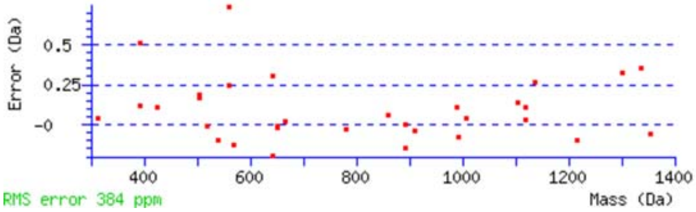
Match to Query 24030: 1526.872724 from(764.443638,2+) index(42802)
Data file TCDD_0530.dta

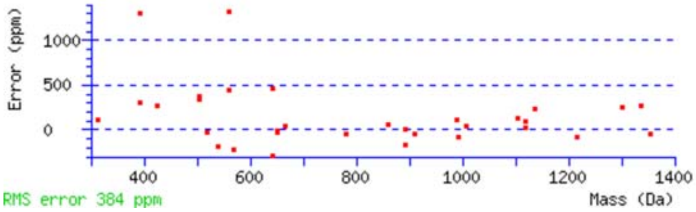
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1526.7841
Ions Score: 50 **Expect:** 0.0028
Matches : 32/112 fragment ions using 62 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							12
2	229.1183	115.0628			211.1077	106.0575	D	1414.7074	707.8573	1397.6808	699.3440	1396.6968	698.8520	11
3	**392.1816**	196.5944			374.1710	187.5892	Y	***1299.6804***	650.3438	1282.6539	641.8306	1281.6698	641.3386	10
4	**520.2402**	260.6237	503.2136	252.1105	502.2296	251.6185	Q	***1136.6171***	568.8122	1119.5905	560.2989	1118.6065	559.8069	9
5	619.3086	310.1579	602.2821	301.6447	601.2980	301.1527	V	***1008.5585***	504.7829	991.5320	496.2696	990.5479	495.7776	8
6	748.3512	374.6792	731.3246	366.1660	730.3406	365.6740	E	***909.4901***	455.2487	892.4635	446.7354	891.4795	446.2434	7
7	**861.4353**	431.2213	844.4087	422.7080	843.4247	422.2160	L	***780.4475***	390.7274	763.4209	382.2141			6
8	**989.4938**	495.2506	972.4673	486.7373	971.4833	486.2453	Q	***667.3634***	334.1854	650.3369	325.6721			5
9	**1103.5368**	552.2720	1086.5102	543.7587	1085.5262	543.2667	N	***539.3049***	270.1561	522.2783	261.6428			4
10	**1216.6208**	608.8141	1199.5943	600.3008	1198.6103	599.8088	L	***425.2619***	213.1346	408.2354	204.6213			3
11	**1353.6797**	677.3435	1336.6532	668.8302	1335.6692	668.3382	H	***312.1779***	156.5926	295.1513	148.0793			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LDYQVELQNLHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.8	1526.7841	0.0886	LDYQVELQNLHR
10.8	1526.8052	0.0675	TPLLNGAEDSKLNR
9.3	1524.6063	2.2664	DGSEEKSSDAEEDK
6.7	1526.7486	0.1241	FLHKHDMDLICR
6.1	1526.7108	0.1619	NYMIKMNELEDK
6.0	1526.7043	0.1684	APGSCKLYEMLCR
4.6	1525.7816	1.0911	INYPEITLSWYK
4.2	1527.7902	-0.9174	AMSTLVPQGGPVLCR
4.2	1527.8144	-0.9417	AIEIIKSDPTEQGK
4.1	1526.7841	0.0886	VEYPINTDAPPRR

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

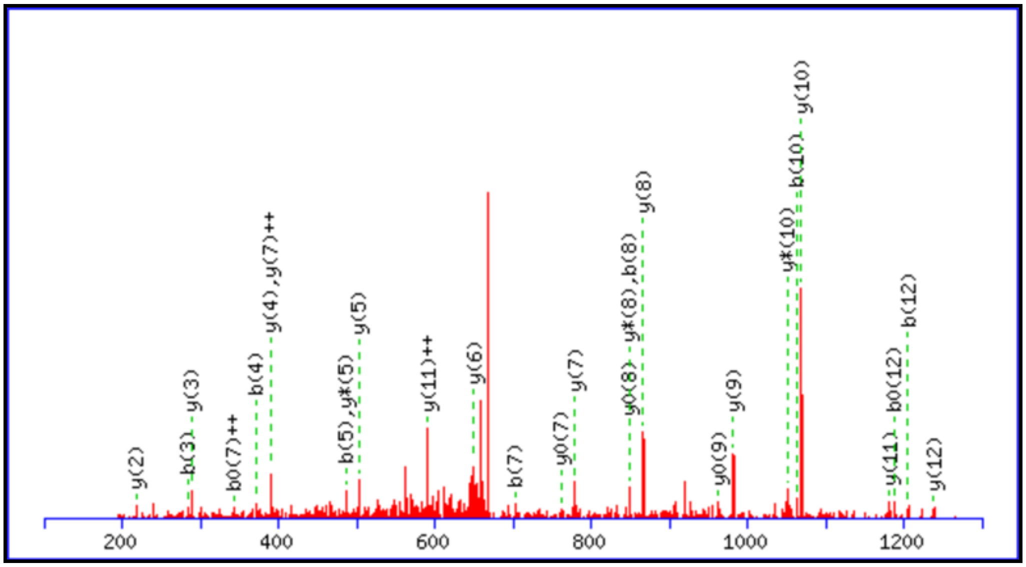
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGISDSEFLTAAK**
Found in **gi|50344731|ref|NP_001002039.1|**, fibrinogen alpha chain [Danio rerio]

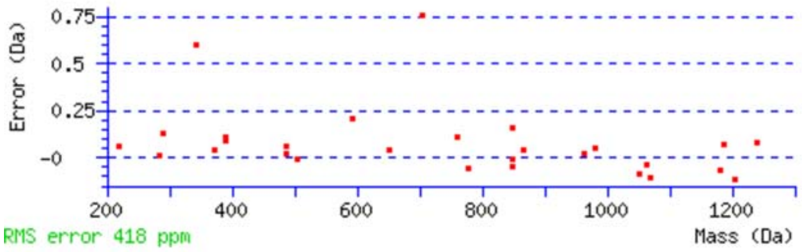
Match to Query 18967: 1352.212724 from(677.113638,2+) index(9147)
Data file TCDD_0530.dta

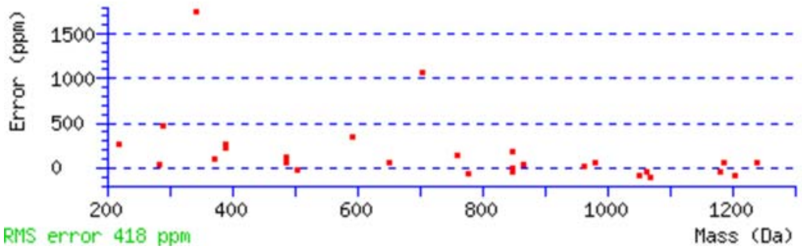
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1350.7031
Ions Score: 74 **Expect:** 1.1e-005
Matches : 28/108 fragment ions using 55 most intense peaks (help)

#	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	114.0913	57.5493			**L**							**13**
2	171.1128	86.0600			**G**	***1238.6263***	619.8168	1221.5998	611.3035	1220.6157	610.8115	**12**
3	**284.1969**	142.6021			**I**	***1181.6048***	591.3061	1164.5783	582.7928	1163.5943	582.3008	**11**
4	**371.2289**	186.1181	353.2183	177.1128	**S**	***1068.5208***	534.7640	1051.4942	526.2508	1050.5102	525.7587	**10**
5	**486.2558**	243.6316	468.2453	234.6263	**D**	***981.4888***	491.2480	964.4622	482.7347	963.4782	482.2427	**9**
6	573.2879	287.1476	555.2773	278.1423	**S**	***866.4618***	433.7345	849.4353	425.2213	848.4512	424.7293	**8**
7	**702.3305**	351.6689	684.3199	342.6636	**E**	***779.4298***	390.2185	762.4032	381.7053	761.4192	381.2132	**7**
8	**849.3989**	425.2031	831.3883	416.1978	**F**	***650.3872***	325.6972	633.3606	317.1840	632.3766	316.6920	**6**
9	962.4829	481.7451	944.4724	472.7398	**L**	***503.3188***	252.1630	486.2922	243.6498	485.3082	243.1577	**5**
10	**1063.5306**	532.2689	1045.5201	523.2637	**T**	***390.2347***	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
11	1134.5677	567.7875	1116.5572	558.7822	**A**	***289.1870***	145.0972	272.1605	136.5839			**3**
12	**1205.6048**	603.3061	1187.5943	594.3008	**A**	***218.1499***	109.5786	201.1234	101.0653			**2**
13					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LGISDSEFLTAAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.1	1350.7031	1.5096	LGISDSEFLTAAK
12.3	1350.7329	1.4798	AVRCYESLILK
10.7	1350.6271	1.5856	QSQAASMELMQK
10.1	1351.7096	0.5032	EGPSDLLGPSPKR
9.7	1351.6224	0.5903	EKTGACIQCSAK
9.4	1354.6993	-2.4866	FQSRLAYDSLR
8.9	1351.7136	0.4992	ELKGYYIPNQK
8.4	1350.6965	1.5162	SELRQFAEMLK
7.6	1351.7401	0.4726	FPQIKAHPWTK
6.8	1352.6031	-0.3903	EVGCDFGINSNAK

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

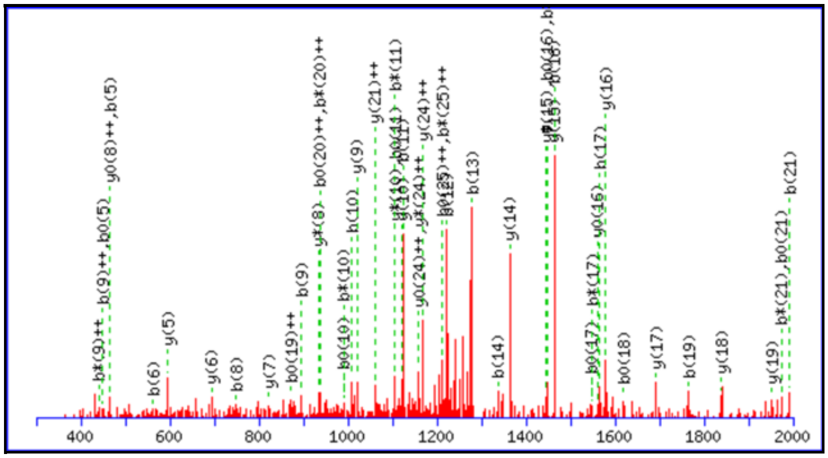
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LHGGTPANFLDVGGGATAQQVTEAFK**
Found in **gi|54261767|ref|NP_998191.1|**, succinate-CoA ligase, ADP-forming, beta subunit [Danio rerio]

Match to Query 96079: 2586.302724 from(1294.158638,2+) index(34622)
Data file TCDD_0530.dta

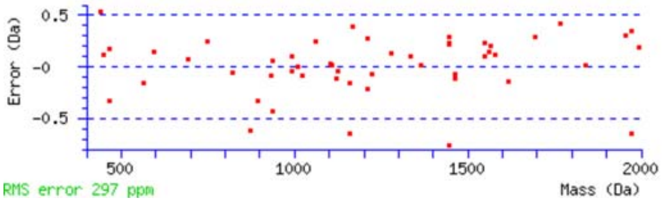
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

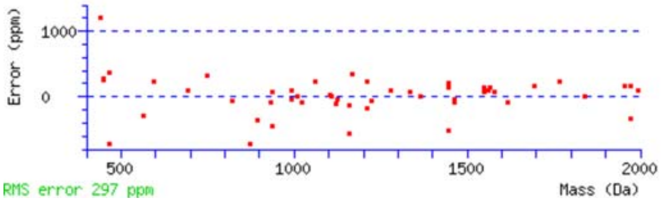


Monoisotopic mass of neutral peptide Mr(calc): 2585.2874
Ions Score: 48 **Expect:** 0.0022
Matches : 53/272 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							26
2	251.1503	126.0788					H	2473.2106	1237.1090	2456.1841	1228.5957	2455.2001	1228.1037	25
3	308.1717	154.5895					G	2336.1517	1168.5795	2319.1252	1160.0662	2318.1412	1159.5742	24
4	365.1932	183.1002					G	2279.1303	1140.0688	2262.1037	1131.5555	2261.1197	1131.0635	23
5	***466.2409***	233.6241			448.2303	224.6188	T	2222.1088	1111.5580	2205.0822	1103.0448	2204.0982	1102.5528	22
6	***563.2936***	282.1504			545.2831	273.1452	P	2121.0611	1061.0342	2104.0346	1052.5209	2103.0505	1052.0289	21
7	634.3307	317.6690			616.3202	308.6637	A	2024.0083	1012.5078	2006.9818	1003.9945	2005.9978	1003.5025	20
8	***748.3737***	374.6905	731.3471	366.1772	730.3631	365.6852	N	***1952.9712***	976.9893	1935.9447	968.4760	1934.9607	967.9840	19
9	***895.4421***	448.2247	878.4155	439.7114	877.4315	439.2194	F	***1838.9283***	919.9678	1821.9018	911.4545	1820.9177	910.9625	18
10	***1008.5261***	504.7667	991.4996	496.2534	990.5156	495.7614	L	***1691.8599***	846.4336	1674.8333	837.9203	1673.8493	837.4283	17
11	***1123.5531***	562.2802	1106.5265	553.7669	1105.5425	553.2749	D	***1578.7758***	789.8916	1561.7493	781.3783	1560.7653	780.8863	16
12	***1222.6215***	611.8144	1205.5950	603.3011	1204.6109	602.8091	V	***1463.7489***	732.3781	1446.7223	723.8648	1445.7383	723.3728	15
13	***1279.6430***	640.3251	1262.6164	631.8118	1261.6324	631.3198	G	***1364.6805***	682.8439	1347.6539	674.3306	1346.6699	673.8386	14
14	***1336.6644***	668.8359	1319.6379	660.3226	1318.6539	659.8306	G	1307.6590	654.3331	1290.6325	645.8199	1289.6484	645.3279	13
15	1393.6859	697.3466	1376.6593	688.8333	1375.6753	688.3413	G	1250.6375	625.8224	1233.6110	617.3091	1232.6270	616.8171	12
16	***1464.7230***	732.8651	1447.6965	724.3519	1446.7124	723.8599	A	1193.6161	597.3117	1176.5895	588.7984	1175.6055	588.3064	11
17	***1565.7707***	783.3890	1548.7441	774.8757	1547.7601	774.3837	T	***1122.5790***	561.7931	1105.5524	553.2798	1104.5684	552.7878	10
18	1636.8078	818.9075	1619.7812	810.3943	1618.7972	809.9023	A	***1021.5313***	511.2693	1004.5047	502.7560	1003.5207	502.2640	9
19	***1764.8664***	882.9368	1747.8398	874.4236	1746.8558	873.9315	Q	950.4942	475.7507	933.4676	467.2375	932.4836	466.7454	8
20	1892.9250	946.9661	1875.8984	938.4528	1874.9144	937.9608	Q	***822.4356***	411.7214	805.4090	403.2082	804.4250	402.7162	7
21	***1991.9934***	996.5003	1974.9668	987.9870	1973.9828	987.4950	V	***694.3770***	347.6921	677.3505	339.1789	676.3665	338.6869	6
22	2093.0410	1047.0242	2076.0145	1038.5109	2075.0305	1038.0189	T	***595.3086***	298.1579	578.2821	289.6447	577.2980	289.1527	5
23	2222.0836	1111.5455	2205.0571	1103.0322	2204.0731	1102.5402	E	494.2609	247.6341	477.2344	239.1208	476.2504	238.6288	4
24	2293.1208	1147.0640	2276.0942	1138.5507	2275.1102	1138.0587	A	365.2183	183.1128	348.1918	174.5995			3

25	2440.1892	1220.5982	2423.1626	1212.0849	2422.1786	1211.5929	**F**	294.1812	147.5942	277.1547	139.0810			**2**
26							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LHGGTPANFLDVGGGATAQQVTEAFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.2	2585.2874	1.0153	LHGGTPANFLDVGGGATAQQVTEAFK
5.0	2588.3268	-2.0241	EVNSGTLQTCLPPTPPNSQKVPPK
0.4	2588.3755	-2.0728	MIKDVLLCLCLFVAPIWCAPVK
0.4	2588.3755	-2.0728	MIKDVLLCLCLFVAPIWCAPVK

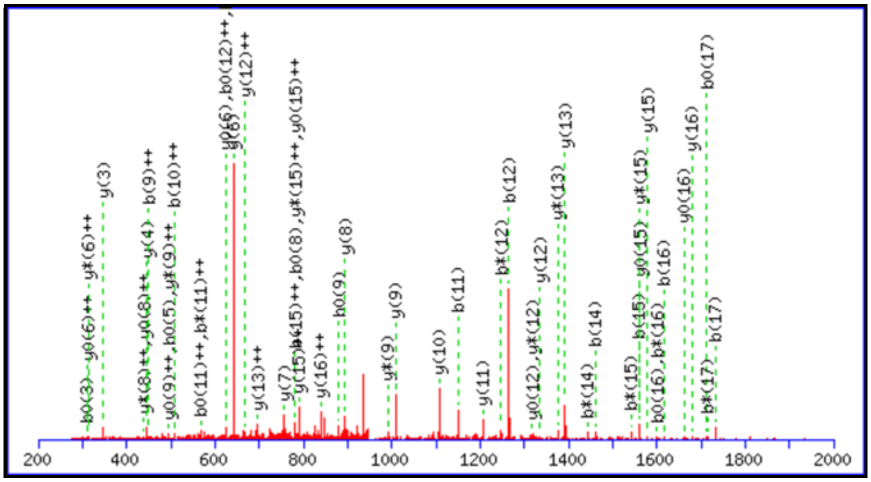
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LITSVGEVVNHDPVVGDR**
Found in **gi|136256027|ref|NP_997974.2|**, phosphorylase, glycogen; brain [Danio rerio]

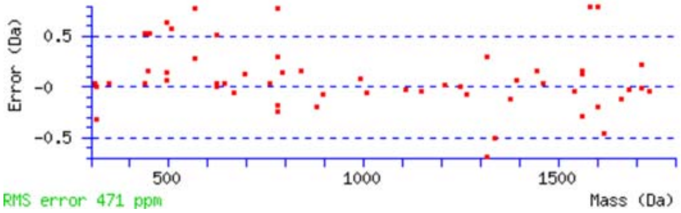
Match to Query 41754: 1906.992724 from(954.503638,2+) index(115408)
Data file TCDD_0530.dta

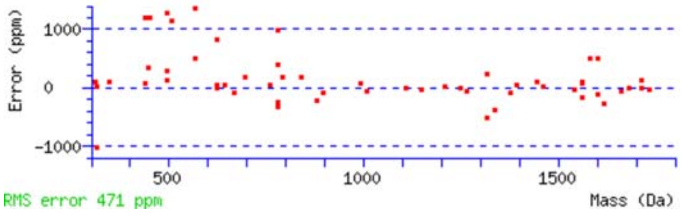
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1904.9956
Ions Score: 57   Expect: 0.00049
Matches : 56/180 fragment ions using 95 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							18
2	227.1754	114.0913					I	1792.9188	896.9630	1775.8923	888.4498	1774.9082	887.9578	17
3	328.2231	164.6152			310.2125	155.6099	T	***1679.8347***	840.4210	1662.8082	831.9077	1661.8242	831.4157	16
4	415.2551	208.1312			397.2445	199.1259	S	***1578.7871***	789.8972	1561.7605	781.3839	1560.7765	780.8919	15
5	514.3235	257.6654			496.3130	248.6601	V	1491.7550	746.3812	1474.7285	737.8679	1473.7445	737.3759	14
6	571.3450	286.1761			553.3344	277.1709	G	***1392.6866***	696.8469	1375.6601	688.3337	1374.6761	687.8417	13
7	700.3876	350.6974			682.3770	341.6921	E	***1335.6652***	668.3362	1318.6386	659.8229	1317.6546	659.3309	12
8	799.4560	400.2316			781.4454	391.2264	V	***1206.6226***	603.8149	1189.5960	595.3016	1188.6120	594.8096	11
9	898.5244	449.7658			880.5138	440.7606	V	***1107.5541***	554.2807	1090.5276	545.7674	1089.5436	545.2754	10
10	1012.5673	506.7873	995.5408	498.2740	994.5568	497.7820	N	***1008.4857***	504.7465	991.4592	496.2332	990.4752	495.7412	9
11	**1149.6262**	575.3168	1132.5997	566.8035	1131.6157	566.3115	H	***894.4428***	447.7250	877.4163	439.2118	876.4322	438.7198	8
12	**1264.6532**	632.8302	1247.6266	624.3170	1246.6426	623.8250	D	***757.3839***	379.1956	740.3573	370.6823	739.3733	370.1903	7
13	1361.7060	681.3566	1344.6794	672.8433	1343.6954	672.3513	P	***642.3570***	321.6821	625.3304	313.1688	624.3464	312.6768	6
14	**1460.7744**	730.8908	1443.7478	722.3775	1442.7638	721.8855	V	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	5
15	**1559.8428**	780.4250	1542.8162	771.9118	1541.8322	771.4197	V	***446.2358***	223.6215	429.2092	215.1083	428.2252	214.6162	4
16	**1616.8642**	808.9358	1599.8377	800.4225	1598.8537	799.9305	G	***347.1674***	174.0873	330.1408	165.5740	329.1568	165.0820	3
17	**1731.8912**	866.4492	1714.8646	857.9360	1713.8806	857.4440	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
18							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LITSVGEVVNHDPVVGDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.6	1904.9956	1.9971	LITSVGEVVNHDPVVGDR
8.8	1904.7806	2.2121	NSSPQENCADIDEGVGDR
5.6	1904.9666	2.0261	ELNVSVAGVTFQVPASCK
2.4	1904.9129	2.0798	EQQWEGHLQQQPNGVK
1.7	1904.9843	2.0084	SADLLAATPDLSSAAALYR
1.6	1905.9560	1.0367	HYQNVFVCTGPLYLPR
1.4	1906.0007	0.9920	SLQLTVDGESVKSTISSR
1.0	1904.9374	2.0553	TPSVTRVCSEAQATVSGR
0.7	1906.0245	0.9682	GAVGRGQANIKPDRPNTR
0.4	1904.9891	2.0036	QTSVLLQISPVSHCHTR

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

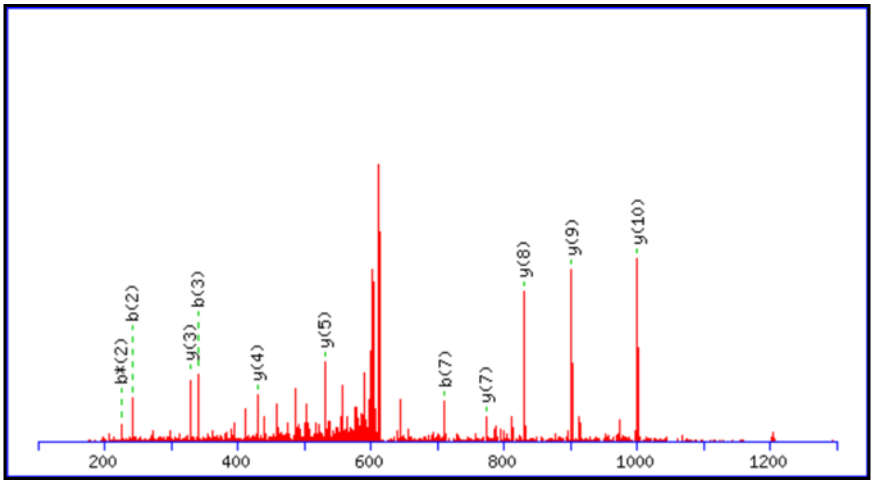
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQVAGEITTGPR**
Found in **gi|189532637|ref|XP_693717.3|**, PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin) [Danio rerio]

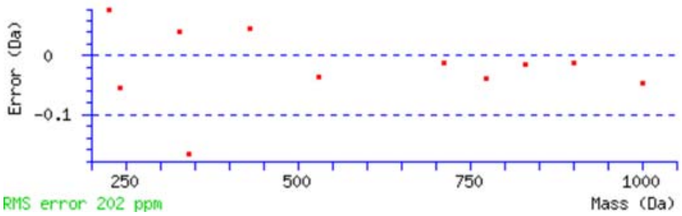
Match to Query 14962: 1243.162724 from(622.588638,2+) index(7988)
Data file TCDD_0530.dta

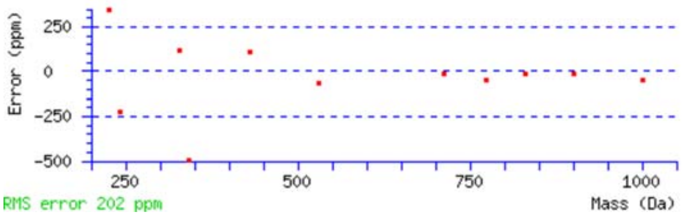
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1240.6776
Ions Score: 45 **Expect:** 0.01
Matches : 11/114 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							12
2	**242.1499**	121.5786	225.1234	113.0653			Q	1128.6008	564.8040	1111.5742	556.2907	1110.5902	555.7987	11
3	**341.2183**	171.1128	324.1918	162.5995			V	***1000.5422***	500.7747	983.5156	492.2615	982.5316	491.7694	10
4	412.2554	206.6314	395.2289	198.1181			A	***901.4738***	451.2405	884.4472	442.7273	883.4632	442.2352	9
5	469.2769	235.1421	452.2504	226.6288			G	***830.4367***	415.7220	813.4101	407.2087	812.4261	406.7167	8
6	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	E	***773.4152***	387.2112	756.3886	378.6980	755.4046	378.2060	7
7	**711.4036**	356.2054	694.3770	347.6921	693.3930	347.2001	I	644.3726	322.6899	627.3461	314.1767	626.3620	313.6847	6
8	812.4512	406.7293	795.4247	398.2160	794.4407	397.7240	T	***531.2885***	266.1479	514.2620	257.6346	513.2780	257.1426	5
9	913.4989	457.2531	896.4724	448.7398	895.4884	448.2478	T	***430.2409***	215.6241	413.2143	207.1108	412.2303	206.6188	4
10	970.5204	485.7638	953.4938	477.2506	952.5098	476.7586	G	***329.1932***	165.1002	312.1666	156.5870			3
11	1067.5732	534.2902	1050.5466	525.7769	1049.5626	525.2849	P	272.1717	136.5895	255.1452	128.0762			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LQVAGEITTGPR

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.2	1240.6776	2.4852	LQVAGEITTGPR
13.5	1242.7183	0.4444	TSQIGILLSSPK
12.9	1241.6000	1.5627	EDPKSPGTAANR
12.8	1242.6503	0.5125	QLGICEPATRR
11.0	1243.6846	-0.5219	QISDLMSLIPK
8.8	1243.6408	-0.4781	KEAQASSEPAVK
8.5	1242.5952	0.5675	QNSNPERSSPK
8.2	1242.6318	0.5309	IELGPMPFDPK
6.8	1241.6728	1.4899	VLEQQITNAAR
6.5	1241.5313	1.6314	EDPAFSGGYSGR

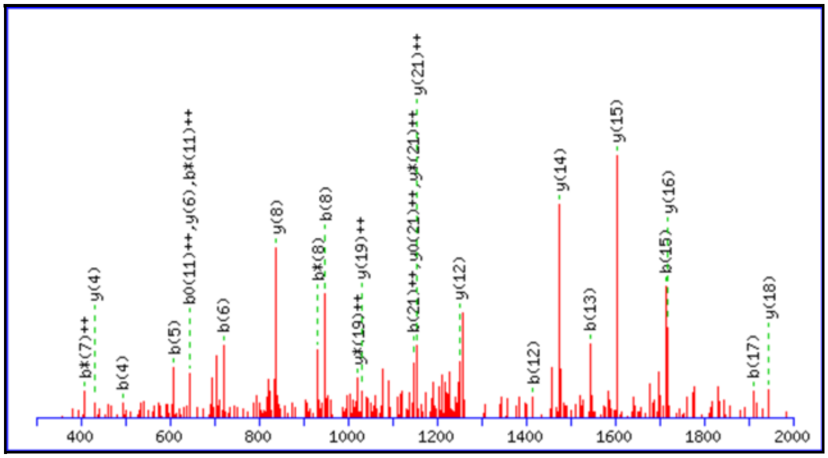
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NELHNLLDKPQLQGIPVLVLGNK**
Found in **gi|45387563|ref|NP_991129.1|**, ADP-ribosylation factor-like 8Ba [Danio rerio]

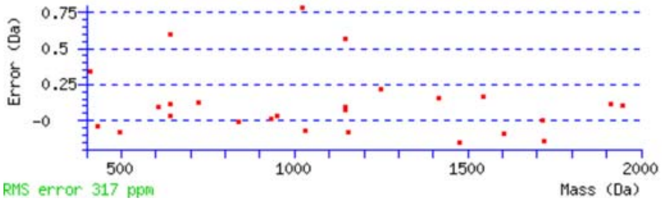
Match to Query 94575: 2551.832724 from(1276.923638,2+) index(130318)
Data file TCDD_0530.dta

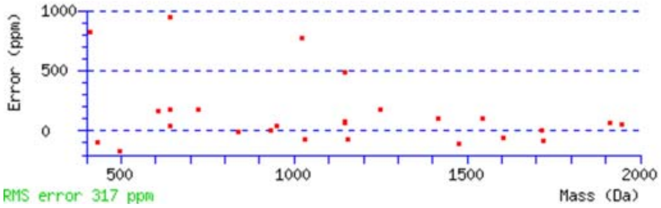
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2551.4486
Ions Score: 61 **Expect:** 0.00012
Matches : 26/232 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							23
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	E	2438.4130	1219.7101	2421.3864	1211.1968	2420.4024	1210.7048	22
3	357.1769	179.0921	340.1503	170.5788	339.1663	170.0868	L	2309.3704	1155.1888	2292.3438	1146.6755	2291.3598	1146.1835	21
4	***494.2358***	247.6215	477.2092	239.1082	476.2252	238.6162	H	2196.2863	1098.6468	2179.2598	1090.1335	2178.2757	1089.6415	20
5	***608.2787***	304.6430	591.2522	296.1297	590.2681	295.6377	N	2059.2274	1030.1173	2042.2008	1021.6041	2041.2168	1021.1120	19
6	***721.3628***	361.1850	704.3362	352.6717	703.3522	352.1797	L	***1945.1845***	973.0959	1928.1579	964.5826	1927.1739	964.0906	18
7	834.4468	417.7271	817.4203	409.2138	816.4363	408.7218	L	1832.1004	916.5538	1815.0738	908.0406	1814.0898	907.5486	17
8	***949.4738***	475.2405	932.4472	466.7272	931.4632	466.2352	D	***1719.0163***	860.0118	1701.9898	851.4985	1701.0058	851.0065	16
9	1077.5687	539.2880	1060.5422	530.7747	1059.5582	530.2827	K	***1603.9894***	802.4983	1586.9628	793.9851			15
10	1174.6215	587.8144	1157.5949	579.3011	1156.6109	578.8091	P	***1475.8944***	738.4509	1458.8679	729.9376			14
11	1302.6801	651.8437	1285.6535	643.3304	1284.6695	642.8384	Q	1378.8417	689.9245	1361.8151	681.4112			13
12	***1415.7641***	708.3857	1398.7376	699.8724	1397.7536	699.3804	L	***1250.7831***	625.8952	1233.7565	617.3819			12
13	***1543.8227***	772.4150	1526.7962	763.9017	1525.8122	763.4097	Q	1137.6990	569.3531	1120.6725	560.8399			11
14	1600.8442	800.9257	1583.8176	792.4125	1582.8336	791.9204	G	1009.6404	505.3239	992.6139	496.8106			10
15	***1713.9282***	857.4678	1696.9017	848.9545	1695.9177	848.4625	I	952.6190	476.8131	935.5924	468.2999			9
16	1810.9810	905.9941	1793.9545	897.4809	1792.9704	896.9889	P	***839.5349***	420.2711	822.5084	411.7578			8
17	***1910.0494***	955.5283	1893.0229	947.0151	1892.0389	946.5231	V	742.4822	371.7447	725.4556	363.2314			7
18	2023.1335	1012.0704	2006.1069	1003.5571	2005.1229	1003.0651	L	***643.4137***	322.2105	626.3872	313.6972			6
19	2122.2019	1061.6046	2105.1754	1053.0913	2104.1913	1052.5993	V	530.3297	265.6685	513.3031	257.1552			5
20	2235.2860	1118.1466	2218.2594	1109.6333	2217.2754	1109.1413	L	***431.2613***	216.1343	414.2347	207.6210			4
21	2292.3074	1146.6574	2275.2809	1138.1441	2274.2969	1137.6521	G	318.1772	159.5922	301.1506	151.0790			3
22	2406.3504	1203.6788	2389.3238	1195.1655	2388.3398	1194.6735	N	261.1557	131.0815	244.1292	122.5682			2
23							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of NELHNLLDKPQLQGIPVLVLGNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.2	2551.4486	0.3841	NELHNLLDKPQLQGIPVLVLGNK
8.5	2552.2693	-0.4366	RWTLIQNSCSLDNTVTIFENAK
2.5	2553.2798	-1.4471	KVHNLEPIHMFLSGASAPYSEAR
2.4	2553.0579	-1.2252	QCWSCKTTCFLSAVTCSCSPER
2.2	2552.2071	-0.3744	ELEAYGDGPPSDPAERLSFFIDK
1.1	2554.1461	-2.3134	ADIYFLLDESGSISYPDFEDMK
0.5	2551.0600	0.7727	CIDDCITGNPSFTCSCLAGFTGR
0.5	2551.0600	0.7727	CIDDCITGNPSFTCSCLAGFTGR

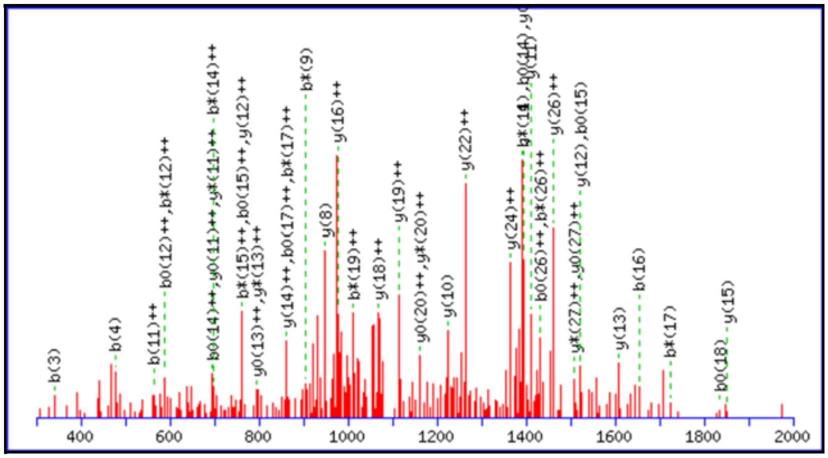
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NIIHGSDSVDSANTEISLWFKPEELVSFK**
Found in **gi|18859107|ref|NP_571001.1|**, non-metastatic cells 2, protein (NM23B) expressed in [Danio rerio]

Match to Query 122002: 3263.402724 from(1088.808184,3+) index(149211)
Data file TCDD_0530.dta

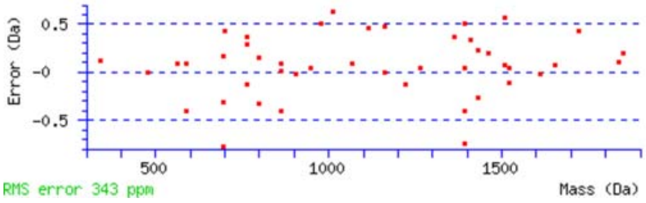
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

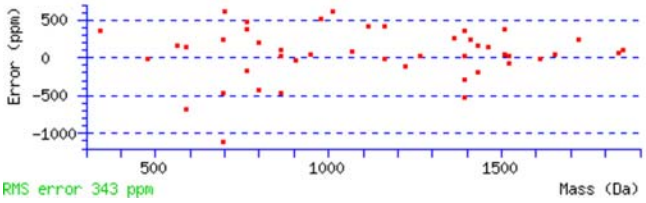


Monoisotopic mass of neutral peptide Mr(calc): 3261.6194
Ions Score: 49 **Expect:** 0.0013
Matches : 45/322 fragment ions using 49 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							29
2	228.1343	114.5708	211.1077	106.0575			I	3148.5837	1574.7955	3131.5572	1566.2822	3130.5732	1565.7902	28
3	**341.2183**	171.1128	324.1918	162.5995			I	3035.4997	1518.2535	3018.4731	1509.7402	3017.4891	1509.2482	27
4	**478.2772**	239.6423	461.2507	231.1290			H	2922.4156	1461.7114	2905.3890	1453.1982	2904.4050	1452.7062	26
5	535.2987	268.1530	518.2722	259.6397			G	2785.3567	1393.1820	2768.3301	1384.6687	2767.3461	1384.1767	25
6	622.3307	311.6690	605.3042	303.1557	604.3202	302.6637	S	2728.3352	1364.6712	2711.3087	1356.1580	2710.3247	1355.6660	24
7	737.3577	369.1825	720.3311	360.6692	719.3471	360.1772	D	2641.3032	1321.1552	2624.2766	1312.6420	2623.2926	1312.1499	23
8	824.3897	412.6985	807.3632	404.1852	806.3791	403.6932	S	2526.2762	1263.6418	2509.2497	1255.1285	2508.2657	1254.6365	22
9	923.4581	462.2327	906.4316	453.7194	905.4476	453.2274	V	2439.2442	1220.1257	2422.2177	1211.6125	2421.2337	1211.1205	21
10	1038.4851	519.7462	1021.4585	511.2329	1020.4745	510.7409	D	2340.1758	1170.5915	2323.1493	1162.0783	2322.1652	1161.5863	20
11	1125.5171	563.2622	1108.4905	554.7489	1107.5065	554.2569	S	2225.1489	1113.0781	2208.1223	1104.5648	2207.1383	1104.0728	19
12	1196.5542	598.7807	1179.5277	590.2675	1178.5436	589.7755	A	2138.1168	1069.5621	2121.0903	1061.0488	2120.1063	1060.5568	18
13	1310.5971	655.8022	1293.5706	647.2889	1292.5866	646.7969	N	2067.0797	1034.0435	2050.0532	1025.5302	2049.0692	1025.0382	17
14	1411.6448	706.3260	1394.6183	697.8128	1393.6342	697.3208	T	1953.0368	977.0220	1936.0102	968.5088	1935.0262	968.0168	16
15	1540.6874	770.8473	1523.6609	762.3341	1522.6768	761.8421	E	***1851.9891***	926.4982	1834.9626	917.9849	1833.9785	917.4929	15
16	**1653.7715**	827.3894	1636.7449	818.8761	1635.7609	818.3841	I	1722.9465	861.9769	1705.9200	853.4636	1704.9360	852.9716	14
17	1740.8035	870.9054	1723.7769	862.3921	1722.7929	861.9001	S	***1609.8625***	805.4349	1592.8359	796.9216	1591.8519	796.4296	13
18	1853.8876	927.4474	1836.8610	918.9341	1835.8770	918.4421	L	***1522.8304***	761.9189	1505.8039	753.4056	1504.8199	752.9136	12
19	2039.9669	1020.4871	2022.9403	1011.9738	2021.9563	1011.4818	W	***1409.7464***	705.3768	1392.7198	696.8635	1391.7358	696.3715	11
20	2187.0353	1094.0213	2170.0087	1085.5080	2169.0247	1085.0160	F	***1223.6671***	612.3372	1206.6405	603.8239	1205.6565	603.3319	10
21	2315.1302	1158.0688	2298.1037	1149.5555	2297.1197	1149.0635	K	1076.5986	538.8030	1059.5721	530.2897	1058.5881	529.7977	9
22	2412.1830	1206.5951	2395.1565	1198.0819	2394.1724	1197.5899	P	***948.5037***	474.7555	931.4771	466.2422	930.4931	465.7502	8
23	2541.2256	1271.1164	2524.1991	1262.6032	2523.2150	1262.1112	E	851.4509	426.2291	834.4244	417.7158	833.4403	417.2238	7
24	2670.2682	1335.6377	2653.2417	1327.1245	2652.2576	1326.6325	E	722.4083	361.7078	705.3818	353.1945	704.3978	352.7025	6

25	2783.3523	1392.1798	2766.3257	1383.6665	2765.3417	1383.1745	**L**	593.3657	297.1865	576.3392	288.6732	575.3552	288.1812	**5**
26	2882.4207	1441.7140	2865.3941	1433.2007	2864.4101	1432.7087	**V**	480.2817	240.6445	463.2551	232.1312	462.2711	231.6392	**4**
27	2969.4527	1485.2300	2952.4262	1476.7167	2951.4421	1476.2247	**S**	381.2132	191.1103	364.1867	182.5970	363.2027	182.1050	**3**
28	3116.5211	1558.7642	3099.4946	1550.2509	3098.5106	1549.7589	**F**	294.1812	147.5942	277.1547	139.0810			**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of NIIHGSDSVDSANTEISLWFKPEELVSFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.2	3261.6194	1.7834	NIIHGSDSVDSANTEISLWFKPEELVSFK
4.2	3264.4018	-0.9991	YHVLGEMFVTEDCAQSCECTKTGAVCQAK
3.5	3264.4018	-0.9991	YHVLGEMFVTEDCAQSCECTKTGAVCQAK
3.3	3263.5153	-0.1126	GYNSNANKNTLETVQYGVEGSTAFLECQAR
1.6	3261.3925	2.0102	SCLDSSSDANPKPNHVVMEETDDLEEESK
0.3	3265.5885	-2.1858	HHGLIVETEGSHSSDSSTVSSALQMLQSLTK
0.0	3261.6034	1.7993	SIPLVPELSLQNSQTSSAGDLSTEMSSAASVR
0.0	3261.5646	1.8382	SSNSIPPSPLACNPSSQPLSPQCSPSSLTGPPK

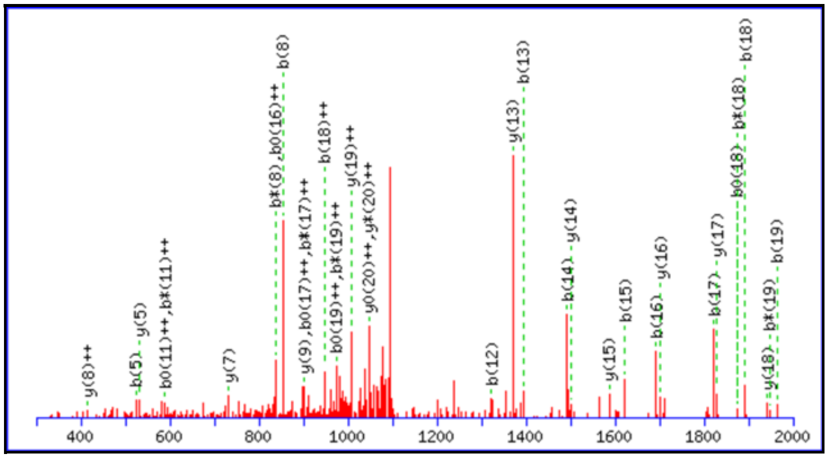
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPALQNSEPENQAVEAEAAEN**
Found in **gi|150378483|ref|NP_001092897.1|**, heat shock protein, alpha-crystallin-related, b11 [Danio rerio]

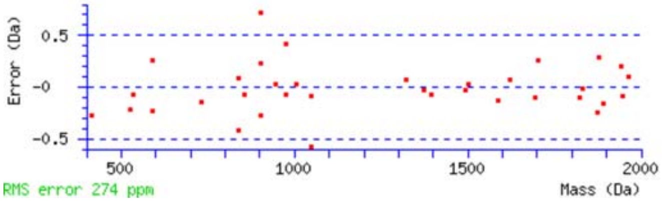
Match to Query 67886: 2224.312724 from(1113.163638,2+) index(8053)
Data file TCDD_0530.dta

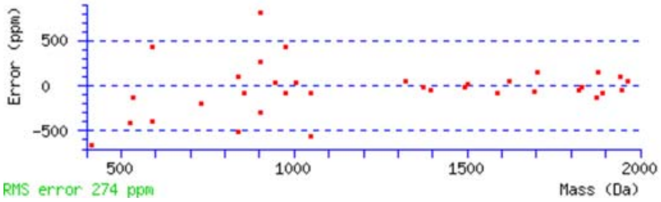
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2223.9879
Ions Score: 64 **Expect:** 7e-005
Matches : 36/226 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			**N**							**21**
2	212.1030	106.5551	195.0764	98.0418			**P**	2110.9523	1055.9798	2093.9258	1047.4665	2092.9418	1046.9745	**20**
3	283.1401	142.0737	266.1135	133.5604			**A**	2013.8996	1007.4534	1996.8730	998.9402	1995.8890	998.4481	**19**
4	396.2241	198.6157	379.1976	190.1024			**L**	***1942.8625***	971.9349	1925.8359	963.4216	1924.8519	962.9296	**18**
5	***524.2827***	262.6450	507.2562	254.1317			**Q**	***1829.7784***	915.3928	1812.7519	906.8796	1811.7678	906.3876	**17**
6	638.3257	319.6665	621.2991	311.1532			**N**	***1701.7198***	851.3636	1684.6933	842.8503	1683.7093	842.3583	**16**
7	725.3577	363.1825	708.3311	354.6692	707.3471	354.1772	**S**	***1587.6769***	794.3421	1570.6504	785.8288	1569.6663	785.3368	**15**
8	***854.4003***	427.7038	837.3737	419.1905	836.3897	418.6985	**E**	***1500.6449***	750.8261	1483.6183	742.3128	1482.6343	741.8208	**14**
9	951.4530	476.2302	934.4265	467.7169	933.4425	467.2249	**P**	***1371.6023***	686.3048	1354.5757	677.7915	1353.5917	677.2995	**13**
10	1080.4956	540.7515	1063.4691	532.2382	1062.4851	531.7462	**E**	1274.5495	637.7784	1257.5230	629.2651	1256.5390	628.7731	**12**
11	1194.5386	597.7729	1177.5120	589.2596	1176.5280	588.7676	**N**	1145.5069	573.2571	1128.4804	564.7438	1127.4964	564.2518	**11**
12	***1322.5971***	661.8022	1305.5706	653.2889	1304.5866	652.7969	**Q**	1031.4640	516.2356	1014.4374	507.7224	1013.4534	507.2304	**10**
13	***1393.6342***	697.3208	1376.6077	688.8075	1375.6237	688.3155	**A**	***903.4054***	452.2063	886.3789	443.6931	885.3949	443.2011	**9**
14	***1492.7027***	746.8550	1475.6761	738.3417	1474.6921	737.8497	**V**	832.3683	416.6878	815.3418	408.1745	814.3577	407.6825	**8**
15	***1621.7453***	811.3763	1604.7187	802.8630	1603.7347	802.3710	**E**	***733.2999***	367.1536	716.2733	358.6403	715.2893	358.1483	**7**
16	***1692.7824***	846.8948	1675.7558	838.3815	1674.7718	837.8895	**A**	604.2573	302.6323	587.2307	294.1190	586.2467	293.6270	**6**
17	***1821.8250***	911.4161	1804.7984	902.9028	1803.8144	902.4108	**E**	***533.2202***	267.1137	516.1936	258.6005	515.2096	258.1084	**5**
18	***1892.8621***	946.9347	1875.8355	938.4214	1874.8515	937.9294	**A**	404.1776	202.5924	387.1510	194.0792	386.1670	193.5872	**4**
19	***1963.8992***	982.4532	1946.8726	973.9400	1945.8886	973.4479	**A**	333.1405	167.0739	316.1139	158.5606	315.1299	158.0686	**3**
20	2092.9418	1046.9745	2075.9152	1038.4613	2074.9312	1037.9692	**E**	262.1034	131.5553	245.0768	123.0420	244.0928	122.5500	**2**
21							**N**	133.0608	67.0340	116.0342	58.5207			**1**





NCBI **BLAST** search of NPALQNSEPENQAVEAEAAEN
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.4	2223.9879	0.3248	NPALQNSEPENQAVEAEAAEN
4.0	2223.9848	0.3279	NTSDPQKTTINCPACGSSASSR
2.8	2224.0681	0.2446	SVLQSEIDASSPLMYGTPSSR
1.6	2222.1088	2.2039	GIYSCPQCRQTFSPRPALAK
1.6	2222.1088	2.2039	IYSCPQCRQSFTPRPALAK
0.5	2224.0244	0.2883	GPAFEVEDTEQDSSLTTRSR
0.3	2224.1447	0.1680	ANNPADLANLANITDEVVRSK
0.1	2223.2296	1.0831	MTASAAAELPHSKLLLSAVSVK

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

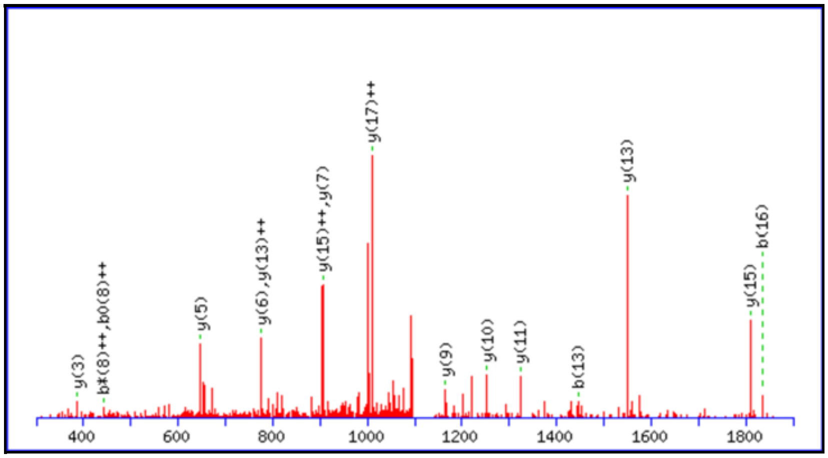
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSPLPYPEASYPEEPYPDR**
Found in **gi|54400460|ref|NP_001005979.1|**, fibulin 5 [Danio rerio]

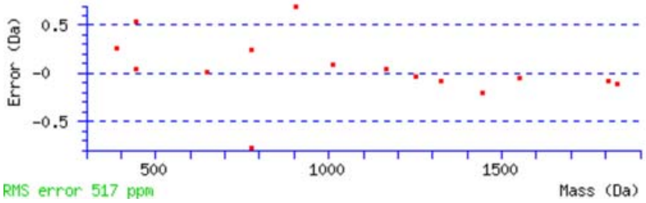
Match to Query 67464: 2220.842724 from(1111.428638,2+) index(8961)
Data file TCDD_0530.dta

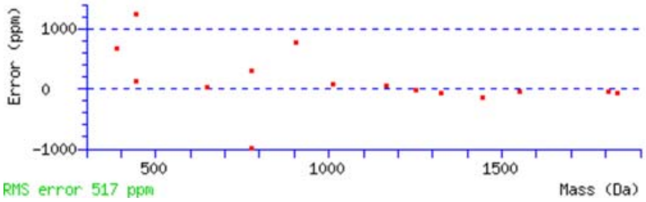
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2220.0011
Ions Score: 74 **Expect:** 7.1e-006
Matches : 16/212 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							19
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	S	2106.9655	1053.9864	2089.9389	1045.4731	2088.9549	1044.9811	18
3	299.1350	150.0711	282.1084	141.5579	281.1244	141.0659	P	2019.9335	1010.4704	2002.9069	1001.9571	2001.9229	1001.4651	17
4	412.2191	206.6132	395.1925	198.0999	394.2085	197.6079	L	1922.8807	961.9440	1905.8541	953.4307	1904.8701	952.9387	16
5	509.2718	255.1395	492.2453	246.6263	491.2613	246.1343	P	***1809.7966***	905.4019	1792.7701	896.8887	1791.7861	896.3967	15
6	672.3352	336.6712	655.3086	328.1579	654.3246	327.6659	Y	1712.7439	856.8756	1695.7173	848.3623	1694.7333	847.8703	14
7	769.3879	385.1976	752.3614	376.6843	751.3774	376.1923	P	***1549.6805***	775.3439	1532.6540	766.8306	1531.6700	766.3386	13
8	898.4305	449.7189	881.4040	441.2056	880.4199	440.7136	E	1452.6278	726.8175	1435.6012	718.3042	1434.6172	717.8122	12
9	969.4676	485.2374	952.4411	476.7242	951.4571	476.2322	A	***1323.5852***	662.2962	1306.5586	653.7830	1305.5746	653.2909	11
10	1056.4997	528.7535	1039.4731	520.2402	1038.4891	519.7482	S	***1252.5481***	626.7777	1235.5215	618.2644	1234.5375	617.7724	10
11	1219.5630	610.2851	1202.5364	601.7719	1201.5524	601.2798	Y	***1165.5160***	583.2617	1148.4895	574.7484	1147.5055	574.2564	9
12	1316.6157	658.8115	1299.5892	650.2982	1298.6052	649.8062	P	1002.4527	501.7300	985.4262	493.2167	984.4421	492.7247	8
13	**1445.6583**	723.3328	1428.6318	714.8195	1427.6478	714.3275	E	***905.3999***	453.2036	888.3734	444.6903	887.3894	444.1983	7
14	1574.7009	787.8541	1557.6744	779.3408	1556.6904	778.8488	E	***776.3573***	388.6823	759.3308	380.1690	758.3468	379.6770	6
15	1671.7537	836.3805	1654.7271	827.8672	1653.7431	827.3752	P	***647.3148***	324.1610	630.2882	315.6477	629.3042	315.1557	5
16	**1834.8170**	917.9121	1817.7905	909.3989	1816.8065	908.9069	Y	550.2620	275.6346	533.2354	267.1214	532.2514	266.6293	4
17	1931.8698	966.4385	1914.8432	957.9253	1913.8592	957.4332	P	***387.1987***	194.1030	370.1721	185.5897	369.1881	185.0977	3
18	2046.8967	1023.9520	2029.8702	1015.4387	2028.8862	1014.9467	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
19							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of NSPLPYPEASYPEEPYPDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.3	2220.0011	0.8416	NSPLPYPEASYPEEPYPDR
8.3	2222.0533	-1.2106	YSDCTCCIIKPHAISEALAGK
2.3	2221.0970	-0.2543	LVCGDEGKGAMAEVSTIVDTVK
1.3	2219.9762	0.8665	KAMMDDAGQIFCHTPSTDPR
0.7	2221.1201	-0.2774	SVDEEDRPFALGMQFVLLR
0.5	2222.0777	-1.2349	QMTDTTTAVLTGLDKYSSYK
0.4	2221.0838	-0.2410	VEQGFTDKPYQDQLPMVAR
0.1	2223.1906	-2.3479	SAQQHRSVQLSAASLAVVLCR
0.1	2219.0793	1.7634	SLQWGVASPILRCDDAFER

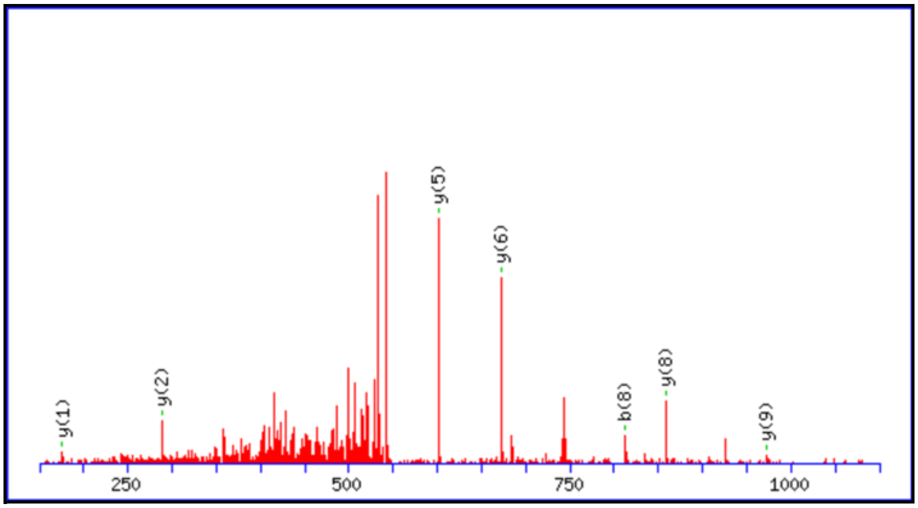
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLADALKANR**
Found in **gi|125832496|ref|XP_699375.2|**, PREDICTED: similar to mCG2694 [Danio rerio]

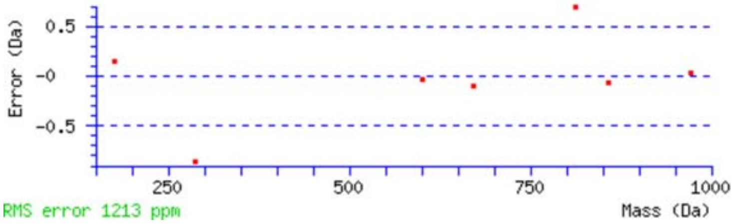
Match to Query 9074: 1100.252724 from(551.133638,2+) index(88961)
Data file TCDD_0531.dta

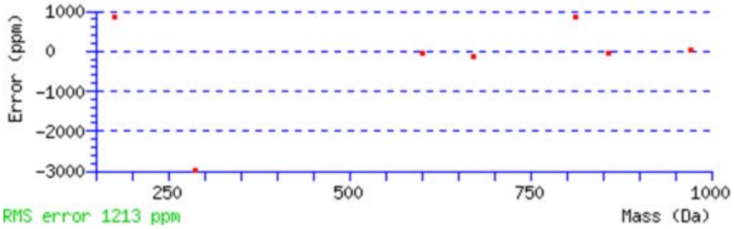
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1098.6145
Ions Score: 46 **Expect:** 0.0083
Matches : 7/90 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							10
2	242.1499	121.5786	225.1234	113.0653			L	***971.5633***	486.2853	954.5367	477.7720	953.5527	477.2800	9
3	313.1870	157.0972	296.1605	148.5839			A	***858.4792***	429.7432	841.4526	421.2300	840.4686	420.7380	8
4	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	D	787.4421	394.2247	770.4155	385.7114	769.4315	385.2194	7
5	499.2511	250.1292	482.2245	241.6159	481.2405	241.1239	A	***672.4151***	336.7112	655.3886	328.1979			6
6	612.3352	306.6712	595.3086	298.1579	594.3246	297.6659	L	***601.3780***	301.1926	584.3515	292.6794			5
7	740.4301	370.7187	723.4036	362.2054	722.4196	361.7134	K	488.2940	244.6506	471.2674	236.1373			4
8	811.4672	406.2373	794.4407	397.7240	793.4567	397.2320	A	360.1990	180.6031	343.1724	172.0899			3
9	925.5102	463.2587	908.4836	454.7454	907.4996	454.2534	N	***289.1619***	145.0846	272.1353	136.5713			2
10							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of QLADALKANR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.3	1098.5782	1.6746	AGLDAAGQGALR
46.5	1098.6145	1.6382	QLADALKANR
29.6	1098.6145	1.6382	KLNEAQQLR
29.6	1098.6761	1.5767	QLLSLEKIR
20.6	1098.6397	1.6130	LESVLNVGLR
20.6	1098.6145	1.6382	LQGELDRLR
20.3	1099.5370	0.7157	SSGLANAPNNR
20.2	1098.6761	1.5767	LKELLSQLR
19.4	1098.6397	1.6130	LELAAAVVSAR
19.2	1101.4938	-1.2411	DEDAAVPTER

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

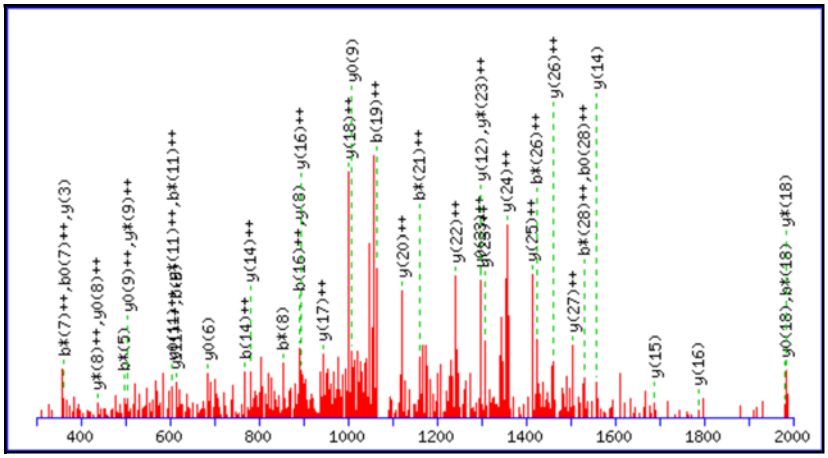
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSSVIVQEIIQNVVENFAEAHGEQNVSEK**
Found in **gi|189533132|ref|XP_001923741.1|**, PREDICTED: A kinase anchor protein 12 [Danio rerio]

Match to Query 118802: 3224.862723 from(1075.961517,3+) index(25679)
Data file TCDD_0530.dta

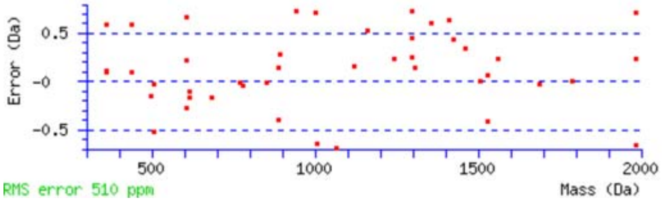
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

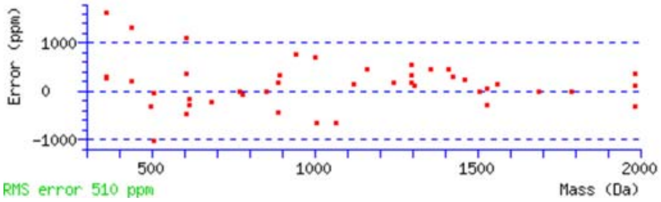


Monoisotopic mass of neutral peptide Mr(calc): 3224.5949
Ions Score: 43 **Expect:** 0.0053
Matches : 44/332 fragment ions using 65 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			**Q**							29
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	**S**	3097.5436	1549.2755	3080.5171	1540.7622	3079.5331	1540.2702	28
3	303.1299	152.0686	286.1034	143.5553	285.1193	143.0633	**S**	3010.5116	1505.7594	2993.4851	1497.2462	2992.5011	1496.7542	27
4	402.1983	201.6028	385.1718	193.0895	384.1878	192.5975	**V**	2923.4796	1462.2434	2906.4530	1453.7302	2905.4690	1453.2382	26
5	515.2824	258.1448	498.2558	249.6316	497.2718	249.1395	**I**	2824.4112	1412.7092	2807.3846	1404.1960	2806.4006	1403.7039	25
6	614.3508	307.6790	597.3243	299.1658	596.3402	298.6738	**V**	2711.3271	1356.1672	2694.3006	1347.6539	2693.3165	1347.1619	24
7	742.4094	371.7083	725.3828	363.1951	724.3988	362.7030	**Q**	2612.2587	1306.6330	2595.2322	1298.1197	2594.2481	1297.6277	23
8	871.4520	436.2296	854.4254	427.7164	853.4414	427.2243	**E**	2484.2001	1242.6037	2467.1736	1234.0904	2466.1896	1233.5984	22
9	984.5360	492.7717	967.5095	484.2584	966.5255	483.7664	**I**	2355.1575	1178.0824	2338.1310	1169.5691	2337.1470	1169.0771	21
10	1097.6201	549.3137	1080.5936	540.8004	1079.6095	540.3084	**I**	2242.0735	1121.5404	2225.0469	1113.0271	2224.0629	1112.5351	20
11	1225.6787	613.3430	1208.6521	604.8297	1207.6681	604.3377	**Q**	2128.9894	1064.9983	2111.9629	1056.4851	2110.9788	1055.9931	19
12	1339.7216	670.3644	1322.6951	661.8512	1321.7110	661.3592	**N**	2000.9308	1000.9690	1983.9043	992.4558	1982.9203	991.9638	18
13	1438.7900	719.8986	1421.7635	711.3854	1420.7795	710.8934	**V**	1886.8879	943.9476	1869.8613	935.4343	1868.8773	934.9423	17
14	1537.8584	769.4329	1520.8319	760.9196	1519.8479	760.4276	**V**	***1787.8195***	894.4134	1770.7929	885.9001	1769.8089	885.4081	16
15	1666.9010	833.9542	1649.8745	825.4409	1648.8905	824.9489	**E**	***1688.7511***	844.8792	1671.7245	836.3659	1670.7405	835.8739	15
16	1780.9440	890.9756	1763.9174	882.4623	1762.9334	881.9703	**N**	***1559.7085***	780.3579	1542.6819	771.8446	1541.6979	771.3526	14
17	1928.0124	964.5098	1910.9858	955.9965	1910.0018	955.5045	**F**	1445.6655	723.3364	1428.6390	714.8231	1427.6550	714.3311	13
18	1999.0495	1000.0284	1982.0229	991.5151	1981.0389	991.0231	**A**	***1298.5971***	649.8022	1281.5706	641.2889	1280.5866	640.7969	12
19	2128.0921	1064.5497	2111.0655	1056.0364	2110.0815	1055.5444	**E**	1227.5600	614.2836	1210.5335	605.7704	1209.5495	605.2784	11
20	2199.1292	1100.0682	2182.1026	1091.5550	2181.1186	1091.0630	**A**	1098.5174	549.7624	1081.4909	541.2491	1080.5069	540.7571	10
21	2336.1881	1168.5977	2319.1616	1160.0844	2318.1775	1159.5924	**H**	1027.4803	514.2438	1010.4538	505.7305	1009.4697	505.2385	9
22	2393.2096	1197.1084	2376.1830	1188.5951	2375.1990	1188.1031	**G**	***890.4214***	445.7143	873.3949	437.2011	872.4108	436.7091	8
23	2522.2522	1261.6297	2505.2256	1253.1164	2504.2416	1252.6244	**E**	833.3999	417.2036	816.3734	408.6903	815.3894	408.1983	7
24	2650.3107	1325.6590	2633.2842	1317.1457	2632.3002	1316.6537	**Q**	704.3573	352.6823	687.3308	344.1690	686.3468	343.6770	6

25	2764.3537	1382.6805	2747.3271	1374.1672	2746.3431	1373.6752	**N**	576.2988	288.6530	559.2722	280.1397	558.2882	279.6477	**5**
26	2863.4221	1432.2147	2846.3955	1423.7014	2845.4115	1423.2094	**V**	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	**4**
27	2950.4541	1475.7307	2933.4276	1467.2174	2932.4435	1466.7254	**S**	***363.1874***	182.0974	346.1609	173.5841	345.1769	173.0921	**3**
28	3079.4967	1540.2520	3062.4701	1531.7387	3061.4861	1531.2467	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of QSSVIVQEIIQNVVENFAEAHGEQNVSEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.3	3224.5949	0.2678	QSSVIVQEIIQNVVENFAEAHGEQNVSEK
2.8	3223.5628	1.2999	TLSVIMGVFVCCWLPFFILNCMVPFCK
2.2	3225.3702	-0.5075	HLQQHENAVEGESCYYHCVLCNYSTK
2.0	3222.6732	2.1895	LQLGSHTGSLTITNSRISDSGLYTVTSISSK
1.5	3226.6413	-1.7786	FTCVSLALLLCVQGSHSQLNVCGLAPLNNR
1.1	3223.5628	1.2999	TLSVIMGVFVCCWLPFFILNCMVPFCK
0.9	3223.5628	1.2999	TLSVIMGVFVCCWLPFFILNCMVPFCK
0.2	3223.4575	1.4052	ADGNDSDSSSYSSVSTTGTYNMLSAIVNRPK
0.1	3224.6870	0.1757	STINVDILISEFLHNAGVFFTYKDVNIR
0.1	3222.7987	2.0641	VAMYAVMVLMILTTVFGNLLVIISISHFK

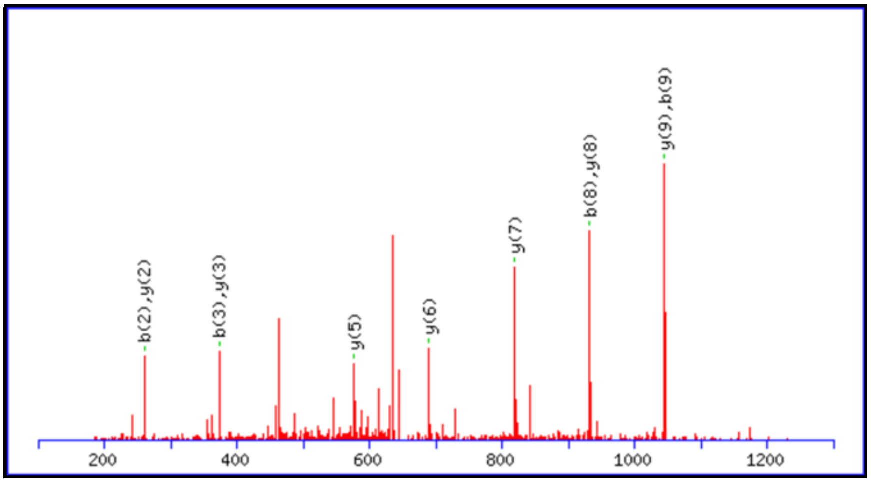
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RCLIEIFGILK**
Found in **gi|189532432|ref|XP_696565.3|**, PREDICTED: novel protein similar to vertebrate AT rich interactive domain containing protein family [Danio rerio]

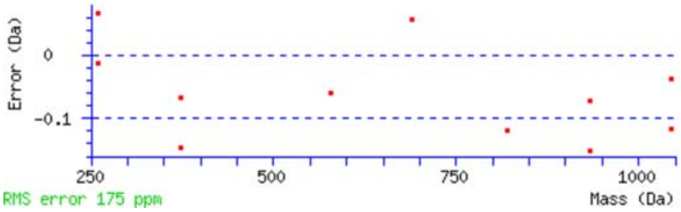
Match to Query 17595: 1304.162724 from(653.088638,2+) index(183)
Data file TCDD_0530.dta

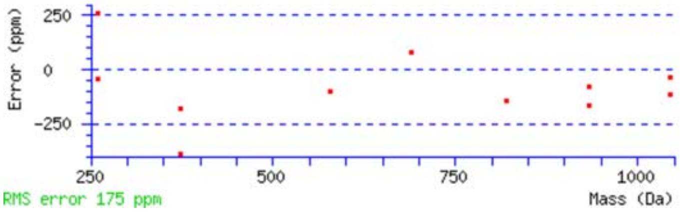
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1303.7686
Ions Score: 58 **Expect:** 0.00054
Matches : 11/100 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							11
2	**260.1176**	130.5624	243.0910	122.0491			C	1148.6748	574.8410	1131.6482	566.3278	1130.6642	565.8357	10
3	**373.2016**	187.1045	356.1751	178.5912			L	***1045.6656***	523.3364	1028.6390	514.8232	1027.6550	514.3312	9
4	486.2857	243.6465	469.2592	235.1332			I	***932.5815***	466.7944	915.5550	458.2811	914.5710	457.7891	8
5	615.3283	308.1678	598.3017	299.6545	597.3177	299.1625	E	***819.4975***	410.2524	802.4709	401.7391	801.4869	401.2471	7
6	728.4124	364.7098	711.3858	356.1965	710.4018	355.7045	I	***690.4549***	345.7311	673.4283	337.2178			6
7	875.4808	438.2440	858.4542	429.7307	857.4702	429.2387	F	***577.3708***	289.1890	560.3443	280.6758			5
8	**932.5022**	466.7548	915.4757	458.2415	914.4917	457.7495	G	430.3024	215.6548	413.2758	207.1416			4
9	**1045.5863**	523.2968	1028.5598	514.7835	1027.5757	514.2915	I	***373.2809***	187.1441	356.2544	178.6308			3
10	1158.6704	579.8388	1141.6438	571.3255	1140.6598	570.8335	L	***260.1969***	130.6021	243.1703	122.0888			2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of RCLIEIFGILK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.1	1303.7057	0.4570	MQLLEIITTDK
57.8	1303.7686	0.3941	RCLIEIFGILK
35.4	1303.6871	0.4756	DTSSDALELLIK
18.4	1302.7296	1.4332	FLKIAEVGAGGNK
18.1	1301.6762	2.4866	KQLIQDVCGNK
18.1	1304.6832	-0.5205	EIMELLMKGNK
16.9	1302.6918	1.4709	ELIEELTESLK
16.4	1303.7023	0.4604	LKFPSDLDELK
16.4	1303.7170	0.4458	DSGLKLLCTGLK
15.9	1302.7031	1.4597	EQDLSEKTLLK

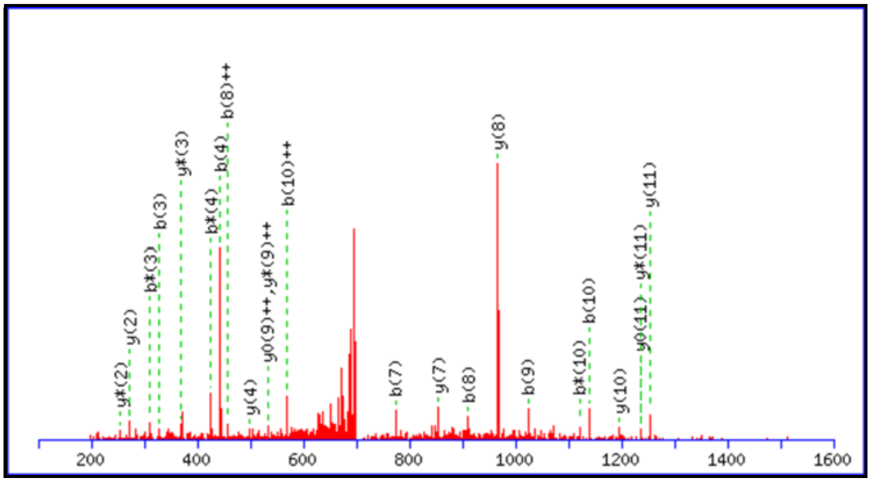
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **RGNDIAFHINPR**
Found in **gi|83523754|ref|NP_999858.2|**, chimera galectin Gal3 [Danio rerio]

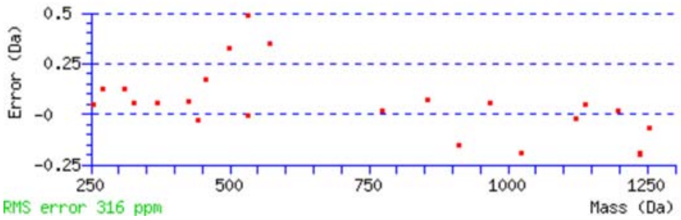
Match to Query 20530: 1409.532724 from(705.773638,2+) index(74556)
Data file TCDD_0530.dta

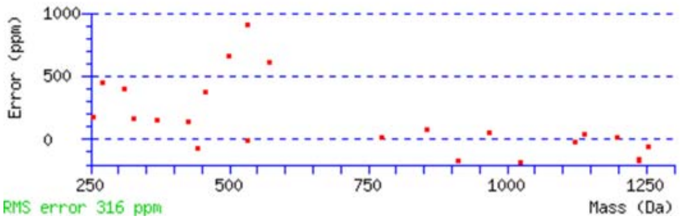
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



`Monoisotopic mass of neutral peptide Mr(calc):` 1408.7324
`Ions Score:` `43` **`Expect:`** `0.016`
`Matches :` `24/110 fragment ions using 48 most intense peaks   (help)`

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							12
2	214.1299	107.5686	197.1033	99.0553			G	***1253.6385***	627.3229	1236.6120	618.8096	1235.6280	618.3176	11
3	***328.1728***	164.5900	311.1462	156.0768			N	***1196.6171***	598.8122	1179.5905	590.2989	1178.6065	589.8069	10
4	***443.1997***	222.1035	426.1732	213.5902	425.1892	213.0982	D	1082.5742	541.7907	1065.5476	533.2774	1064.5636	532.7854	9
5	556.2838	278.6455	539.2572	270.1323	538.2732	269.6402	I	***967.5472***	484.2772	950.5207	475.7640			8
6	627.3209	314.1641	610.2944	305.6508	609.3103	305.1588	A	***854.4631***	427.7352	837.4366	419.2219			7
7	***774.3893***	387.6983	757.3628	379.1850	756.3787	378.6930	F	783.4260	392.2167	766.3995	383.7034			6
8	***911.4482***	456.2278	894.4217	447.7145	893.4377	447.2225	H	636.3576	318.6824	619.3311	310.1692			5
9	***1024.5323***	512.7698	1007.5057	504.2565	1006.5217	503.7645	I	***499.2987***	250.1530	482.2722	241.6397			4
10	***1138.5752***	569.7912	1121.5487	561.2780	1120.5647	560.7860	N	386.2146	193.6110	369.1881	185.0977			3
11	***1235.6280***	618.3176	1218.6014	609.8044	1217.6174	609.3123	P	***272.1717***	136.5895	255.1452	128.0762			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of RGNDIAFHINPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.5	1408.7324	0.8004	RGNDIAFHINPR
12.1	1408.7020	0.8307	ESIICVGSSYVPR
11.9	1408.7899	0.7428	GVGLVAANAGARTPR
11.7	1407.8085	1.7242	EELAQIVALGIPR
9.4	1409.7892	-0.2564	WQAGLPVAGSRLR
6.9	1408.7786	0.7541	ASLPQLSGLDPRR
6.8	1408.7952	0.7375	RPPHLRPFHPR
6.7	1409.6609	-0.1282	DEPAPLNLACDPR
6.3	1409.7449	-0.2122	HCASSLLLGSLPR
5.6	1410.7150	-1.1823	ALRCLASHNPSSR

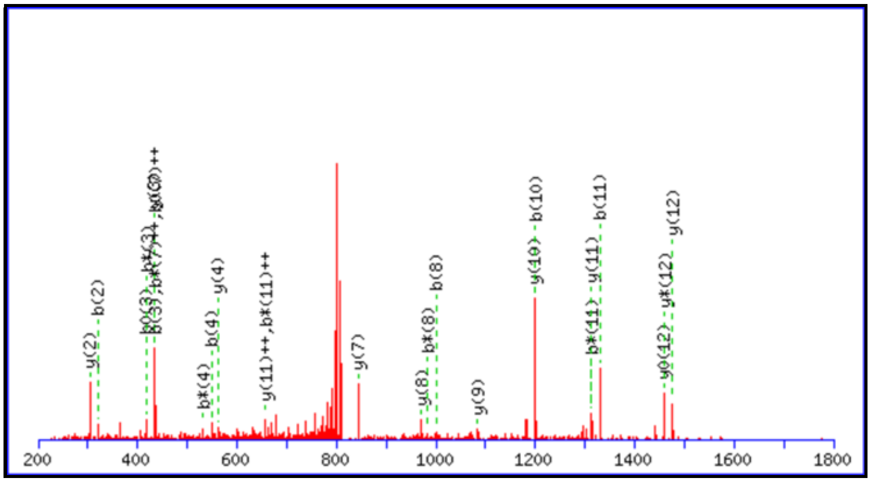
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **RYDNLKPIAEEER**
Found in **gi|148596955|ref|NP_001091951.1|**, ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E [Danio rerio]

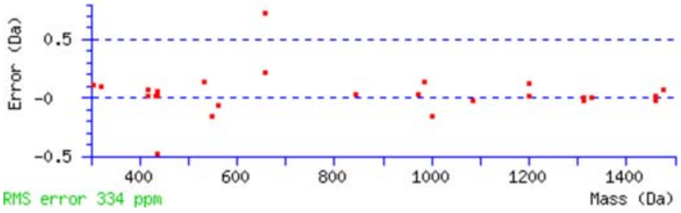
Match to Query 27076: 1632.732724 from(817.373638,2+) index(55788)
Data file TCDD_0530.dta

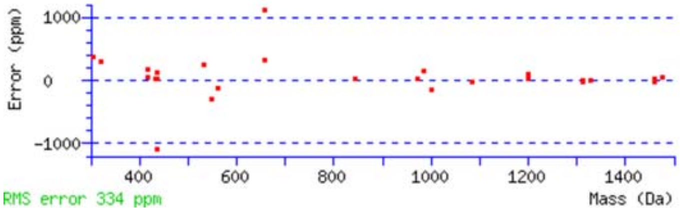
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1631.8267
Ions Score: 60 **Expect:** 0.00025
Matches : 27/138 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							13
2	***320.1717***	160.5895	303.1452	152.0762			Y	***1476.7329***	738.8701	1459.7064	730.3568	1458.7223	729.8648	12
3	***435.1987***	218.1030	418.1721	209.5897	417.1881	209.0977	D	***1313.6696***	657.3384	1296.6430	648.8251	1295.6590	648.3331	11
4	***549.2416***	275.1244	532.2150	266.6112	531.2310	266.1191	N	***1198.6426***	599.8250	1181.6161	591.3117	1180.6321	590.8197	10
5	662.3257	331.6665	645.2991	323.1532	644.3151	322.6612	L	***1084.5997***	542.8035	1067.5732	534.2902	1066.5891	533.7982	9
6	790.4206	395.7139	773.3941	387.2007	772.4100	386.7087	K	***971.5156***	486.2615	954.4891	477.7482	953.5051	477.2562	8
7	887.4734	444.2403	870.4468	435.7271	869.4628	435.2350	P	***843.4207***	422.2140	826.3941	413.7007	825.4101	413.2087	7
8	***1000.5574***	500.7824	983.5309	492.2691	982.5469	491.7771	I	746.3679	373.6876	729.3414	365.1743	728.3573	364.6823	6
9	1071.5946	536.3009	1054.5680	527.7876	1053.5840	527.2956	A	633.2838	317.1456	616.2573	308.6323	615.2733	308.1403	5
10	***1200.6371***	600.8222	1183.6106	592.3089	1182.6266	591.8169	E	***562.2467***	281.6270	545.2202	273.1137	544.2362	272.6217	4
11	***1329.6797***	665.3435	1312.6532	656.8302	1311.6692	656.3382	E	***433.2041***	217.1057	416.1776	208.5924	415.1936	208.1004	3
12	***1458.7223***	729.8648	1441.6958	721.3515	1440.7118	720.8595	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of RYDNLKPIAEEER

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.4	1631.8267	0.9060	RYDNLKPIAEEER
25.8	1631.7937	0.9391	EKNLEQLTQNMER
9.6	1631.8379	0.8948	GGFRAAAIGAVEAASER
8.6	1631.8089	0.9238	MISDKTSHANLPYR
7.6	1633.7737	-1.0409	SPHDDTEAFTVFLR
7.5	1631.9246	0.8081	SIYAELILQKALDR
6.7	1631.7209	1.0118	KQAGTDCENGPVEER
6.4	1633.7770	-1.0442	EADPLFEREIMER
6.3	1630.7627	1.9700	GFNDDQKEQYFIK
6.0	1630.8146	1.9181	DLCTHICWILMRK

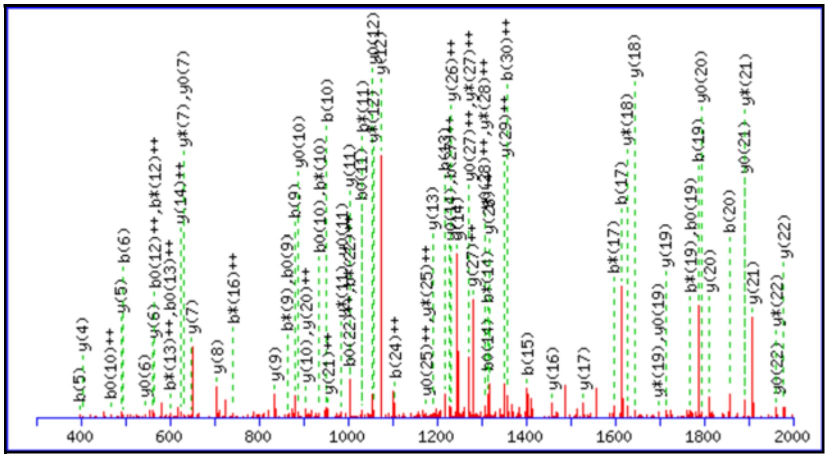
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAAAPPKEEAPPANAPDGDAPAEGSASAGEK**
Found in **gi|189525434|ref|XP_686365.3|**, PREDICTED: im:7157373 [Danio rerio]

Match to Query 105450: 2859.952724 from(1430.983638,2+) index(30085)
Data file TCDD_0530.dta

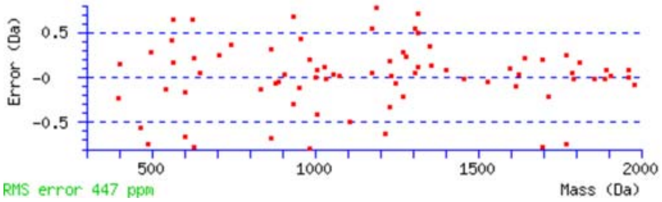
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

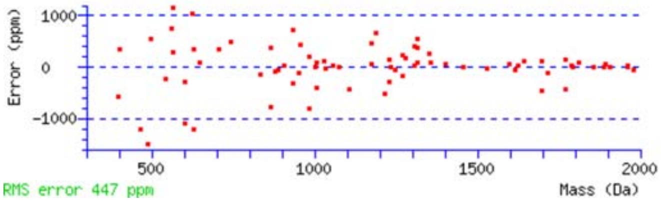


Monoisotopic mass of neutral peptide Mr(calc): 2859.3158
Ions Score: 67 **Expect:** 2.7e-005
Matches : 79/346 fragment ions using 161 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							31
2	159.0764	80.0418			141.0659	71.0366	A	2773.2911	1387.1492	2756.2646	1378.6359	2755.2806	1378.1439	30
3	230.1135	115.5604			212.1030	106.5551	A	2702.2540	1351.6306	2685.2275	1343.1174	2684.2434	1342.6254	29
4	301.1506	151.0790			283.1401	142.0737	A	2631.2169	1316.1121	2614.1903	1307.5988	2613.2063	1307.1068	28
5	**398.2034**	199.6053			380.1928	190.6001	P	2560.1798	1280.5935	2543.1532	1272.0803	2542.1692	1271.5882	27
6	**495.2562**	248.1317			477.2456	239.1264	P	2463.1270	1232.0671	2446.1005	1223.5539	2445.1165	1223.0619	26
7	623.3511	312.1792	606.3246	303.6659	605.3406	303.1739	K	2366.0743	1183.5408	2349.0477	1175.0275	2348.0637	1174.5355	25
8	752.3937	376.7005	735.3672	368.1872	734.3832	367.6952	E	2237.9793	1119.4933	2220.9527	1110.9800	2219.9687	1110.4880	24
9	**881.4363**	441.2218	864.4098	432.7085	863.4258	432.2165	E	2108.9367	1054.9720	2091.9101	1046.4587	2090.9261	1045.9667	23
10	**952.4734**	476.7404	935.4469	468.2271	934.4629	467.7351	A	***1979.8941***	990.4507	1962.8676	981.9374	1961.8835	981.4454	22
11	1049.5262	525.2667	1032.4997	516.7535	1031.5156	516.2615	P	***1908.8570***	954.9321	1891.8304	946.4189	1890.8464	945.9269	21
12	1146.5790	573.7931	1129.5524	565.2798	1128.5684	564.7878	P	***1811.8042***	906.4058	1794.7777	897.8925	1793.7937	897.4005	20
13	**1217.6161**	609.3117	1200.5895	600.7984	1199.6055	600.3064	A	***1714.7515***	857.8794	1697.7249	849.3661	1696.7409	848.8741	19
14	1331.6590	666.3331	1314.6325	657.8199	1313.6484	657.3279	N	***1643.7143***	822.3608	1626.6878	813.8475	1625.7038	813.3555	18
15	**1402.6961**	701.8517	1385.6696	693.3384	1384.6856	692.8464	A	***1529.6714***	765.3393	1512.6449	756.8261	1511.6609	756.3341	17
16	1499.7489	750.3781	1482.7223	741.8648	1481.7383	741.3728	P	***1458.6343***	729.8208	1441.6078	721.3075	1440.6237	720.8155	16
17	**1614.7758**	807.8916	1597.7493	799.3783	1596.7653	798.8863	D	1361.5815	681.2944	1344.5550	672.7811	1343.5710	672.2891	15
18	1671.7973	836.4023	1654.7707	827.8890	1653.7867	827.3970	G	***1246.5546***	623.7809	1229.5281	615.2677	1228.5440	614.7757	14
19	**1786.8242**	893.9158	1769.7977	885.4025	1768.8137	884.9105	D	***1189.5331***	595.2702	1172.5066	586.7569	1171.5226	586.2649	13
20	**1857.8613**	929.4343	1840.8348	920.9210	1839.8508	920.4290	A	***1074.5062***	537.7567	1057.4796	529.2435	1056.4956	528.7515	12
21	1954.9141	977.9607	1937.8876	969.4474	1936.9035	968.9554	P	***1003.4691***	502.2382	986.4425	493.7249	985.4585	493.2329	11
22	2025.9512	1013.4793	2008.9247	1004.9660	2007.9407	1004.4740	A	***906.4163***	453.7118	889.3898	445.1985	888.4058	444.7065	10
23	2154.9938	1078.0005	2137.9673	1069.4873	2136.9833	1068.9953	E	***835.3792***	418.1932	818.3527	409.6800	817.3686	409.1880	9
24	2212.0153	1106.5113	2194.9887	1097.9980	2194.0047	1097.5060	G	***706.3366***	353.6719	689.3101	345.1587	688.3260	344.6667	8

25	2299.0473	1150.0273	2282.0208	1141.5140	2281.0367	1141.0220	**S**	***649.3151***	325.1612	632.2886	316.6479	631.3046	316.1559	**7**
26	2370.0844	1185.5459	2353.0579	1177.0326	2352.0739	1176.5406	**A**	***562.2831***	281.6452	545.2566	273.1319	544.2726	272.6399	**6**
27	2457.1165	1229.0619	2440.0899	1220.5486	2439.1059	1220.0566	**S**	***491.2460***	246.1266	474.2195	237.6134	473.2354	237.1214	**5**
28	2528.1536	1264.5804	2511.1270	1256.0671	2510.1430	1255.5751	**A**	***404.2140***	202.6106	387.1874	194.0974	386.2034	193.6053	**4**
29	2585.1750	1293.0912	2568.1485	1284.5779	2567.1645	1284.0859	**G**	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	**3**
30	2714.2176	1357.6125	2697.1911	1349.0992	2696.2071	1348.6072	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
31							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of SAAAPPKEEAPPANAPDGDAPAEGSASAGEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.1	2859.3158	0.6369	SAAAPPKEEAPPANAPDGDAPAEGSASAGEK
2.8	2862.3728	-2.4201	CLVRMGYQCTFGVLQAGQYGVAQTR

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

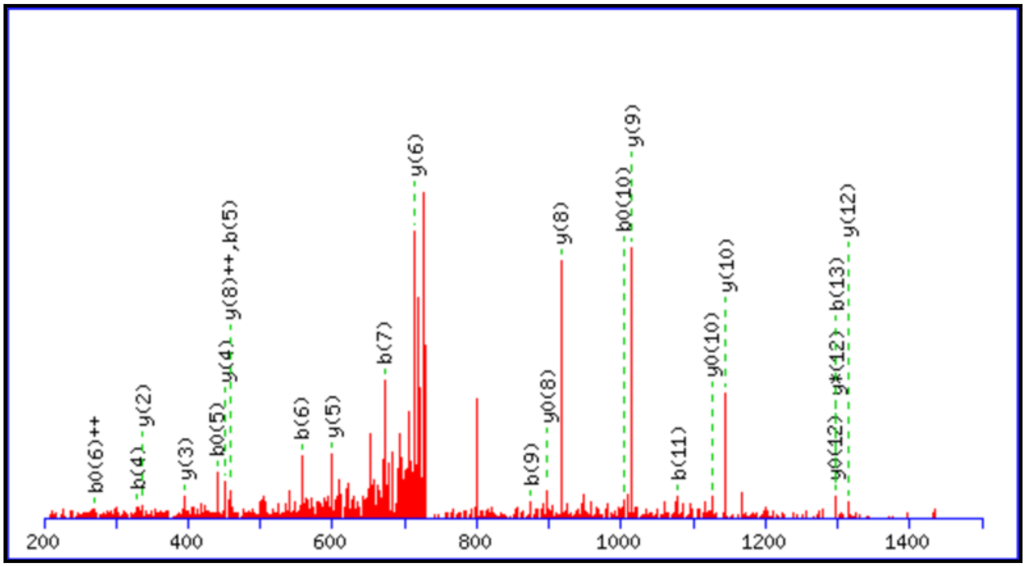
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAGLEVDSDFGGYR**
Found in **gi|41056175|ref|NP_956396.1|**, programmed cell death 8 (apoptosis-inducing factor) [Danio rerio]

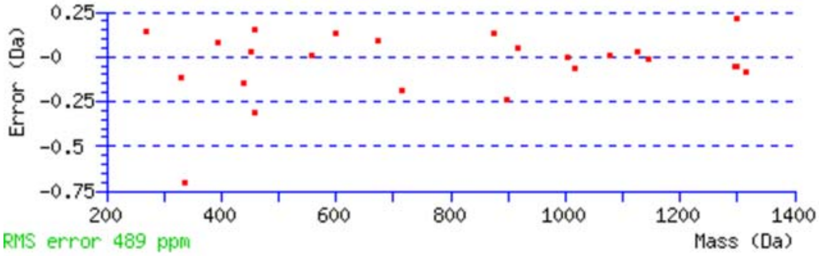
Match to Query 22199: 1471.282724 from(736.648638,2+) index(8657)
Data file TCDD_0530.dta

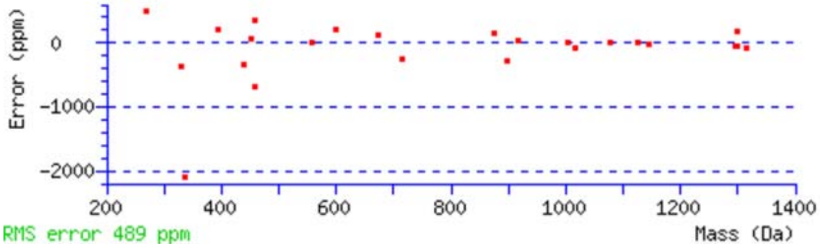
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1471.6579
Ions Score: 62 **Expect:** 0.00018
Matches : 24/120 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	S							14
2	159.0764	80.0418	141.0659	71.0366	A	1385.6332	693.3202	1368.6066	684.8070	1367.6226	684.3149	13
3	216.0979	108.5526	198.0873	99.5473	G	***1314.5961***	657.8017	1297.5695	649.2884	1296.5855	648.7964	12
4	***329.1819***	165.0946	311.1714	156.0893	L	1257.5746	629.2909	1240.5481	620.7777	1239.5640	620.2857	11
5	***458.2245***	229.6159	440.2140	220.6106	E	***1144.4905***	572.7489	1127.4640	564.2356	1126.4800	563.7436	10
6	***557.2930***	279.1501	539.2824	270.1448	V	***1015.4480***	508.2276	998.4214	499.7143	997.4374	499.2223	9
7	***672.3199***	336.6636	654.3093	327.6583	D	***916.3795***	458.6934	899.3530	450.1801	898.3690	449.6881	8
8	759.3519	380.1796	741.3414	371.1743	S	801.3526	401.1799	784.3260	392.6667	783.3420	392.1747	7
9	***874.3789***	437.6931	856.3683	428.6878	D	***714.3206***	357.6639	697.2940	349.1506	696.3100	348.6586	6
10	1021.4473	511.2273	1003.4367	502.2220	F	***599.2936***	300.1504	582.2671	291.6372			5
11	***1078.4687***	539.7380	1060.4582	530.7327	G	***452.2252***	226.6162	435.1987	218.1030			4
12	1135.4902	568.2487	1117.4796	559.2435	G	***395.2037***	198.1055	378.1772	189.5922			3
13	***1298.5535***	649.7804	1280.5430	640.7751	Y	***338.1823***	169.5948	321.1557	161.0815			2
14					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of SAGLEVDSDFGGYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.0	1471.6579	-0.3752	SAGLEVDSDFGGYR
10.5	1471.7994	-0.5167	SIAGEVVSLKGQER
9.6	1470.7678	0.5149	KAQEVDALINENK
7.0	1469.8640	1.4188	VALLASLMDVIGLR
6.1	1469.8388	1.4439	RDGLLCDVILVVR
5.9	1469.8282	1.4545	TLQIVFNLFFTK
5.5	1473.7722	-2.4895	NCGKVLSTAAGIQR
5.3	1469.8242	1.4585	APEPPLTLPPPVSR
4.7	1471.8762	-0.5935	WTAVLLTLLSLSR
4.5	1471.8511	-0.5684	VFQDVAQKVVAIR

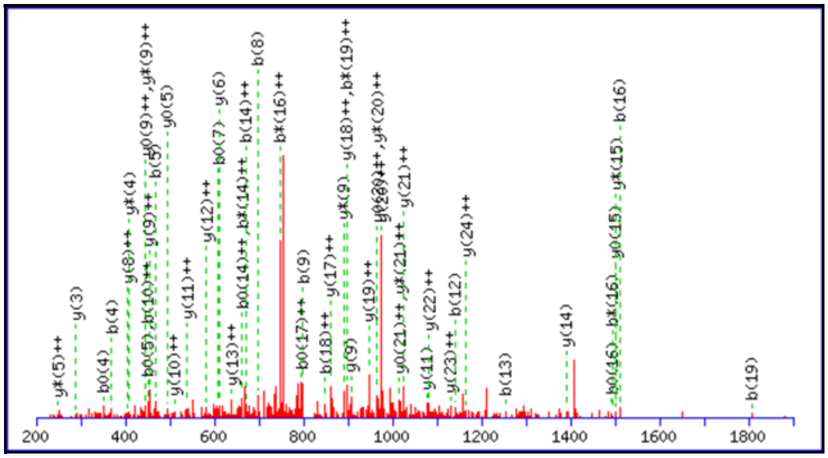
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAPLVGTATTQLISGLPSLPSHGGR**
Found in **gi|61651682|ref|NP_001013279.1|**, fibronectin 1b [Danio rerio]

Match to Query 87432: 2417.172723 from(806.731517,3+) index(34867)
Data file TCDD_0530.dta

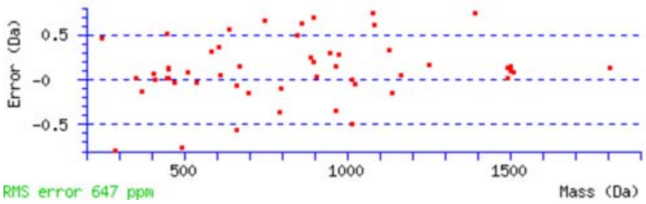
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●

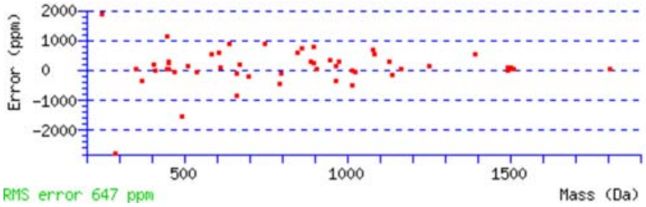


Monoisotopic mass of neutral peptide Mr(calc): 2416.3074
Ions Score: 41 **Expect:** 0.013
Matches : 52/260 fragment ions using 133 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	**S**							**25**
2	159.0764	80.0418			141.0659	71.0366	**A**	2330.2827	1165.6450	2313.2561	1157.1317	2312.2721	1156.6397	**24**
3	256.1292	128.5682			238.1186	119.5629	**P**	2259.2456	1130.1264	2242.2190	1121.6131	2241.2350	1121.1211	**23**
4	**369.2132**	185.1103			351.2027	176.1050	**L**	2162.1928	1081.6000	2145.1662	1073.0868	2144.1822	1072.5948	**22**
5	**468.2817**	234.6445			450.2711	225.6392	**V**	2049.1087	1025.0580	2032.0822	1016.5447	2031.0982	1016.0527	**21**
6	525.3031	263.1552			507.2926	254.1499	**G**	1950.0403	975.5238	1933.0138	967.0105	1932.0298	966.5185	**20**
7	626.3508	313.6790			608.3402	304.6738	**T**	1893.0189	947.0131	1875.9923	938.4998	1875.0083	938.0078	**19**
8	**697.3879**	349.1976			679.3774	340.1923	**A**	1791.9712	896.4892	1774.9446	887.9760	1773.9606	887.4839	**18**
9	**798.4356**	399.7214			780.4250	390.7162	**T**	1720.9341	860.9707	1703.9075	852.4574	1702.9235	851.9654	**17**
10	899.4833	450.2453			881.4727	441.2400	**T**	1619.8864	810.4468	1602.8598	801.9336	1601.8758	801.4415	**16**
11	1027.5419	514.2746	1010.5153	505.7613	1009.5313	505.2693	**Q**	1518.8387	759.9230	1501.8122	751.4097	1500.8281	750.9177	**15**
12	**1140.6259**	570.8166	1123.5994	562.3033	1122.6154	561.8113	**L**	**1390.7801**	695.8937	1373.7536	687.3804	1372.7696	686.8884	**14**
13	**1253.7100**	627.3586	1236.6834	618.8454	1235.6994	618.3533	**I**	1277.6961	639.3517	1260.6695	630.8384	1259.6855	630.3464	**13**
14	1340.7420	670.8746	1323.7155	662.3614	1322.7314	661.8694	**S**	1164.6120	582.8096	1147.5854	574.2964	1146.6014	573.8044	**12**
15	1397.7635	699.3854	1380.7369	690.8721	1379.7529	690.3801	**G**	**1077.5800**	539.2936	1060.5534	530.7803	1059.5694	530.2883	**11**
16	**1510.8475**	755.9274	1493.8210	747.4141	1492.8370	746.9221	**L**	1020.5585	510.7829	1003.5320	502.2696	1002.5479	501.7776	**10**
17	1607.9003	804.4538	1590.8738	795.9405	1589.8897	795.4485	**P**	**907.4744**	454.2409	890.4479	445.7276	889.4639	445.2356	**9**
18	1694.9323	847.9698	1677.9058	839.4565	1676.9218	838.9645	**S**	810.4217	405.7145	793.3951	397.2012	792.4111	396.7092	**8**
19	**1808.0164**	904.5118	1790.9898	895.9986	1790.0058	895.5066	**L**	723.3896	362.1985	706.3631	353.6852	705.3791	353.1932	**7**
20	1905.0692	953.0382	1888.0426	944.5249	1887.0586	944.0329	**P**	**610.3056**	305.6564	593.2790	297.1432	592.2950	296.6511	**6**
21	1992.1012	996.5542	1975.0746	988.0410	1974.0906	987.5489	**S**	513.2528	257.1300	496.2263	248.6168	495.2423	248.1248	**5**
22	2129.1601	1065.0837	2112.1335	1056.5704	2111.1495	1056.0784	**H**	426.2208	213.6140	409.1942	205.1008			**4**
23	2186.1816	1093.5944	2169.1550	1085.0811	2168.1710	1084.5891	**G**	**289.1619**	145.0846	272.1353	136.5713			**3**
24	2243.2030	1122.1052	2226.1765	1113.5919	2225.1925	1113.0999	**G**	232.1404	116.5738	215.1139	108.0606			**2**

25							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of SAPLVGTATTQLISGLPSLPSHGGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.1	2416.3074	0.8653	SAPLVGTATTQLISGLPSLPSHGGR
4.4	2415.1754	1.9973	NVLGHMQQGGTPTPFDRNFATK
4.0	2419.2305	-2.0578	EKLVISEDCELVTVVDVYPGR
1.9	2419.1091	-1.9364	CVVLLLSCTTAWPNCCAIHCR
1.5	2416.1805	0.9922	IIIQRAANGGQECPDTLFEER
1.3	2415.1190	2.0537	DEVKHGVELADLSEDPEYSQR
1.0	2417.9271	-0.7544	AGYRLNADGCGCDDVDECASDR
0.8	2419.4429	-2.2702	IIAGGMVIGSLIVGLLFALLFFR
0.6	2419.0573	-1.8845	THTGEKPYKCEYCDYAAAQK
0.6	2418.1146	-0.9419	LDNLPSLQIEISRDGSNGSDSDS

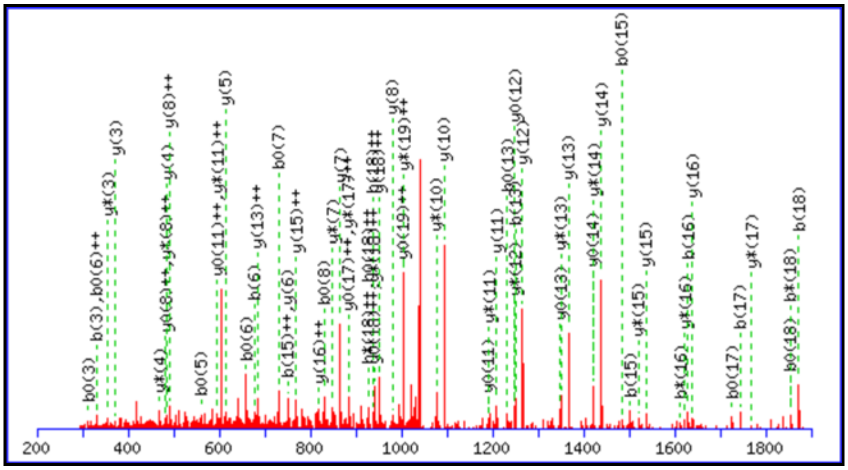
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SELFTVATGDGGDNHQNQPK**
Found in **gi|52219158|ref|NP_001004661.1|**, aquaporin 8 [Danio rerio]

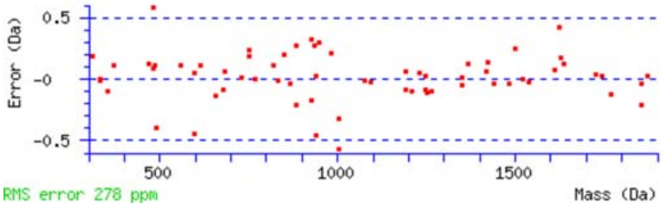
Match to Query 54189: 2115.262724 from(1058.638638,2+) index(19538)
Data file TCDD_0530.dta

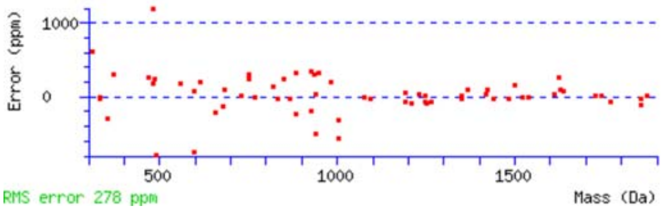
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2113.9665
Ions Score: 49 **Expect:** 0.0024
Matches : 66/188 fragment ions using 144 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	**S**							**20**
2	217.0819	109.0446			199.0713	100.0393	**E**	2027.9417	1014.4745	2010.9152	1005.9612	2009.9312	1005.4692	**19**
3	**330.1660**	165.5866			312.1554	156.5813	**L**	1898.8991	949.9532	1881.8726	941.4399	1880.8886	940.9479	**18**
4	477.2344	239.1208			459.2238	230.1155	**F**	1785.8151	893.4112	1768.7885	884.8979	1767.8045	884.4059	**17**
5	578.2821	289.6447			560.2715	280.6394	**T**	***1638.7467***	819.8770	1621.7201	811.3637	1620.7361	810.8717	**16**
6	**677.3505**	339.1789			659.3399	330.1736	**V**	***1537.6990***	769.3531	1520.6724	760.8399	1519.6884	760.3478	**15**
7	748.3876	374.6974			730.3770	365.6921	**A**	***1438.6306***	719.8189	1421.6040	711.3056	1420.6200	710.8136	**14**
8	849.4353	425.2213			831.4247	416.2160	**T**	***1367.5934***	684.3004	1350.5669	675.7871	1349.5829	675.2951	**13**
9	906.4567	453.7320			888.4462	444.7267	**G**	***1266.5458***	633.7765	1249.5192	625.2632	1248.5352	624.7712	**12**
10	1021.4837	511.2455			1003.4731	502.2402	**D**	***1209.5243***	605.2658	1192.4978	596.7525	1191.5137	596.2605	**11**
11	1078.5051	539.7562			1060.4946	530.7509	**G**	***1094.4974***	547.7523	1077.4708	539.2390	1076.4868	538.7470	**10**
12	1135.5266	568.2669			1117.5160	559.2617	**G**	1037.4759	519.2416	1020.4493	510.7283	1019.4653	510.2363	**9**
13	**1250.5535**	625.7804			1232.5430	616.7751	**D**	***980.4544***	490.7309	963.4279	482.2176	962.4439	481.7256	**8**
14	1364.5965	682.8019	1347.5699	674.2886	1346.5859	673.7966	**N**	***865.4275***	433.2174	848.4009	424.7041			**7**
15	**1501.6554**	751.3313	1484.6288	742.8181	1483.6448	742.3260	**H**	***751.3846***	376.1959	734.3580	367.6826			**6**
16	**1629.7140**	815.3606	1612.6874	806.8473	1611.7034	806.3553	**Q**	***614.3257***	307.6665	597.2991	299.1532			**5**
17	**1743.7569**	872.3821	1726.7303	863.8688	1725.7463	863.3768	**N**	***486.2671***	243.6372	469.2405	235.1239			**4**
18	**1871.8155**	936.4114	1854.7889	927.8981	1853.8049	927.4061	**Q**	***372.2241***	186.6157	355.1976	178.1024			**3**
19	1968.8682	984.9378	1951.8417	976.4245	1950.8577	975.9325	**P**	244.1656	122.5864	227.1390	114.0731			**2**
20							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of SELFTVATGDGGDNHQNQPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.3	2113.9665	1.2962	SELFTVATGDGGDNHQNQPK
6.4	2116.9809	-1.7182	TDILKYLCECQFDDNLK
5.1	2116.0510	-0.7883	MELIVYTQDGTYSQSLLR
3.3	2112.9845	2.2782	AQMIQSGSSTSTSTVATEAEK
2.3	2117.0726	-1.8099	LTNGHGSAAGDLVHQERLSR
1.1	2112.9746	2.2882	MAPPSPSTNSSSHSAAEQLSK
0.8	2115.1589	0.1038	LFEVPDPNKPQKLGLHQR

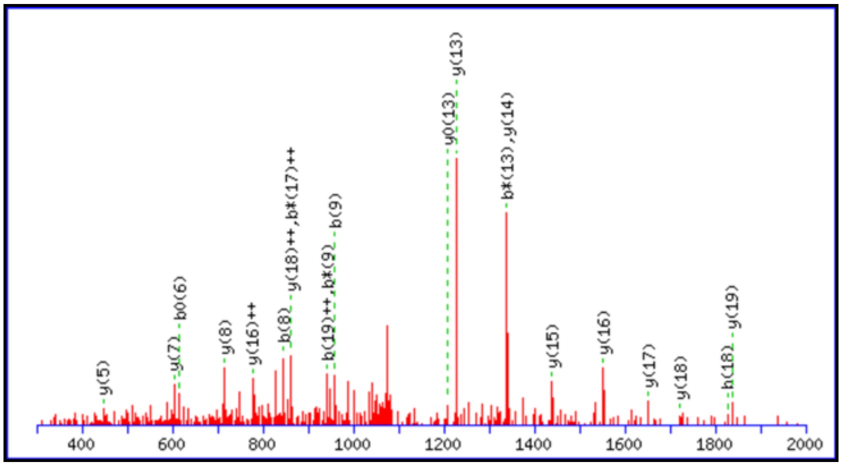
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFLDAVNVIKPTAIIGVSGAGR**
Found in **gi|57525624|ref|NP_001003627.1|**, malic enzyme 2, NAD(+)-dependent, mitochondrial [Danio rerio]

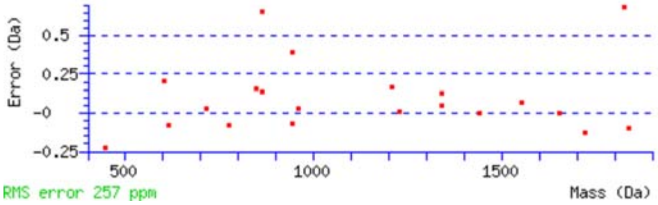
Match to Query 63241: 2185.542724 from(1093.778638,2+) index(35756)
Data file TCDD_0530.dta

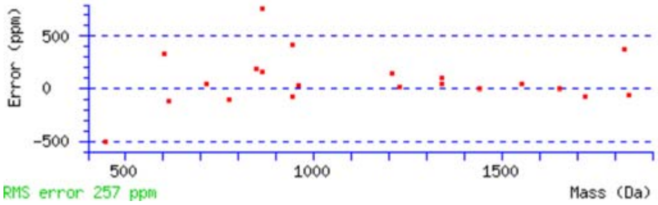
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2184.2267
Ions Score: 54  Expect: 0.00081
Matches : 21/232 fragment ions using 34 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	**S**							**22**
2	235.1077	118.0575			217.0972	109.0522	**F**	2098.2019	1049.6046	2081.1754	1041.0913	2080.1913	1040.5993	**21**
3	348.1918	174.5995			330.1812	165.5942	**L**	1951.1335	976.0704	1934.1069	967.5571	1933.1229	967.0651	**20**
4	463.2187	232.1130			445.2082	223.1077	**D**	***1838.0494***	919.5283	1821.0229	911.0151	1820.0389	910.5231	**19**
5	534.2558	267.6316			516.2453	258.6263	**A**	***1723.0225***	862.0149	1705.9959	853.5016	1705.0119	853.0096	**18**
6	633.3243	317.1658			615.3137	308.1605	**V**	***1651.9854***	826.4963	1634.9588	817.9830	1633.9748	817.4910	**17**
7	747.3672	374.1872	730.3406	365.6740	729.3566	365.1819	**N**	***1552.9170***	776.9621	1535.8904	768.4488	1534.9064	767.9568	**16**
8	**846.4356**	423.7214	829.4090	415.2082	828.4250	414.7162	**V**	***1438.8740***	719.9407	1421.8475	711.4274	1420.8635	710.9354	**15**
9	**959.5197**	480.2635	942.4931	471.7502	941.5091	471.2582	**I**	***1339.8056***	670.4064	1322.7791	661.8932	1321.7950	661.4012	**14**
10	1087.6146	544.3109	1070.5881	535.7977	1069.6041	535.3057	**K**	***1226.7215***	613.8644	1209.6950	605.3511	1208.7110	604.8591	**13**
11	1184.6674	592.8373	1167.6408	584.3241	1166.6568	583.8320	**P**	1098.6266	549.8169	1081.6000	541.3037	1080.6160	540.8116	**12**
12	1285.7151	643.3612	1268.6885	634.8479	1267.7045	634.3559	**T**	1001.5738	501.2905	984.5473	492.7773	983.5633	492.2853	**11**
13	1356.7522	678.8797	1339.7256	670.3665	1338.7416	669.8744	**A**	900.5261	450.7667	883.4996	442.2534	882.5156	441.7614	**10**
14	1469.8362	735.4218	1452.8097	726.9085	1451.8257	726.4165	**I**	829.4890	415.2482	812.4625	406.7349	811.4785	406.2429	**9**
15	1582.9203	791.9638	1565.8938	783.4505	1564.9097	782.9585	**I**	***716.4050***	358.7061	699.3784	350.1928	698.3944	349.7008	**8**
16	1639.9418	820.4745	1622.9152	811.9612	1621.9312	811.4692	**G**	***603.3209***	302.1641	586.2944	293.6508	585.3103	293.1588	**7**
17	1739.0102	870.0087	1721.9836	861.4955	1720.9996	861.0034	**V**	546.2994	273.6534	529.2729	265.1401	528.2889	264.6481	**6**
18	**1826.0422**	913.5247	1809.0157	905.0115	1808.0316	904.5195	**S**	***447.2310***	224.1191	430.2045	215.6059	429.2205	215.1139	**5**
19	1883.0637	942.0355	1866.0371	933.5222	1865.0531	933.0302	**G**	360.1990	180.6031	343.1724	172.0899			**4**
20	1954.1008	977.5540	1937.0742	969.0408	1936.0902	968.5488	**A**	303.1775	152.0924	286.1510	143.5791			**3**
21	2011.1223	1006.0648	1994.0957	997.5515	1993.1117	997.0595	**G**	232.1404	116.5738	215.1139	108.0606			**2**
22							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of SFLDAVNVIKPTAIIGVSGAGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.0	2184.2267	1.3161	SFLDAVNVIKPTAIIGVSGAGR
8.3	2184.1031	1.4396	IMDQAMLVGAPVIGLNDSGGAR
5.3	2187.9830	-2.4403	TFQVCNVMEYSQNNWLR
4.7	2185.0175	0.5252	NLDDIYTDLYVVENETGGR
1.7	2186.0500	-0.5073	LDMFLDLLQSYRDLCER

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

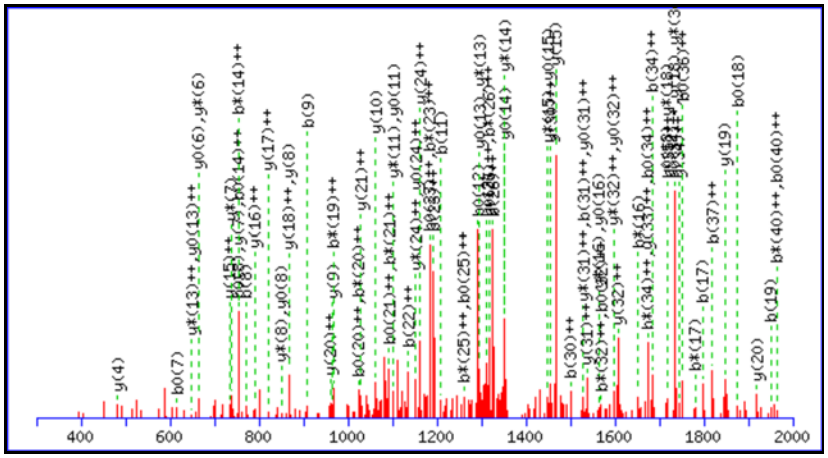
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGTPGFSHHHYTTNSGQPGLHALPGLPGPPGPPDASISYGR**
Found in **gi|68448495|ref|NP_001020335.1|**, hypothetical protein LOC100003906 isoform 1 [Danio rerio]

Match to Query 172990: 4118.892723 from(1373.971517,3+) index(67406)
Data file TCDD_0531.dta

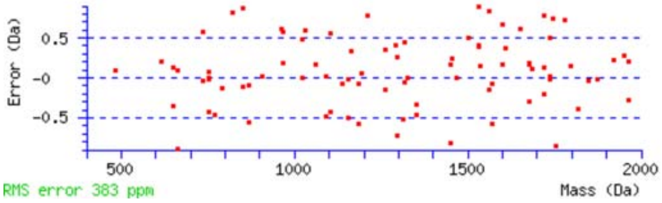
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

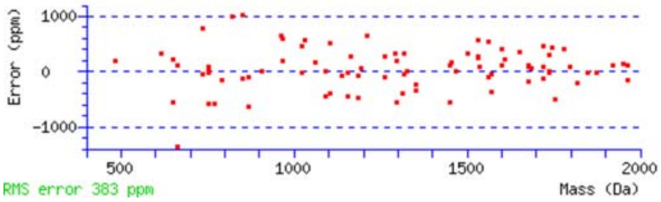


Monoisotopic mass of neutral peptide Mr(calc): 4117.9784
Ions Score: 43 **Expect:** 0.0032
Matches : 88/448 fragment ions using 136 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							41
2	145.0608	73.0340			127.0502	64.0287	G	4031.9536	2016.4804	4014.9270	2007.9672	4013.9430	2007.4751	40
3	246.1084	123.5579			228.0979	114.5526	T	3974.9321	1987.9697	3957.9056	1979.4564	3956.9215	1978.9644	39
4	343.1612	172.0842			325.1506	163.0790	P	3873.8844	1937.4459	3856.8579	1928.9326	3855.8739	1928.4406	38
5	400.1827	200.5950			382.1721	191.5897	G	3776.8317	1888.9195	3759.8051	1880.4062	3758.8211	1879.9142	37
6	547.2511	274.1292			529.2405	265.1239	F	3719.8102	1860.4087	3702.7837	1851.8955	3701.7996	1851.4035	36
7	634.2831	317.6452			616.2726	308.6399	S	3572.7418	1786.8745	3555.7152	1778.3613	3554.7312	1777.8693	35
8	**771.3420**	386.1747			753.3315	377.1694	H	3485.7098	1743.3585	3468.6832	1734.8452	3467.6992	1734.3532	34
9	**908.4009**	454.7041			890.3904	445.6988	H	3348.6509	1674.8291	3331.6243	1666.3158	3330.6403	1665.8238	33
10	1045.4599	523.2336			1027.4493	514.2283	H	3211.5919	1606.2996	3194.5654	1597.7863	3193.5814	1597.2943	32
11	**1208.5232**	604.7652			1190.5126	595.7599	Y	3074.5330	1537.7702	3057.5065	1529.2569	3056.5225	1528.7649	31
12	1309.5709	655.2891			1291.5603	646.2838	T	2911.4697	1456.2385	2894.4432	1447.7252	2893.4591	1447.2332	30
13	1410.6185	705.8129			1392.6080	696.8076	T	2810.4220	1405.7146	2793.3955	1397.2014	2792.4115	1396.7094	29
14	1524.6615	762.8344	1507.6349	754.3211	1506.6509	753.8291	N	2709.3743	1355.1908	2692.3478	1346.6775	2691.3638	1346.1855	28
15	1611.6935	806.3504	1594.6669	797.8371	1593.6829	797.3451	S	2595.3314	1298.1693	2578.3049	1289.6561	2577.3208	1289.1641	27
16	1668.7150	834.8611	1651.6884	826.3478	1650.7044	825.8558	G	2508.2994	1254.6533	2491.2728	1246.1401	2490.2888	1245.6480	26
17	**1796.7735**	898.8904	1779.7470	890.3771	1778.7630	889.8851	Q	2451.2779	1226.1426	2434.2514	1217.6293	2433.2674	1217.1373	25
18	1893.8263	947.4168	1876.7998	938.9035	1875.8157	938.4115	P	2323.2193	1162.1133	2306.1928	1153.6000	2305.2088	1153.1080	24
19	**1950.8478**	975.9275	1933.8212	967.4142	1932.8372	966.9222	G	2226.1666	1113.5869	2209.1400	1105.0737	2208.1560	1104.5816	23
20	2063.9318	1032.4696	2046.9053	1023.9563	2045.9213	1023.4643	L	2169.1451	1085.0762	2152.1186	1076.5629	2151.1346	1076.0709	22
21	2200.9907	1100.9990	2183.9642	1092.4857	2182.9802	1091.9937	H	2056.0611	1028.5342	2039.0345	1020.0209	2038.0505	1019.5289	21
22	2272.0279	**1136.5176**	2255.0013	1128.0043	2254.0173	1127.5123	A	***1919.0021***	960.0047	1901.9756	951.4914	1900.9916	950.9994	20
23	2385.1119	**1193.0596**	2368.0854	1184.5463	2367.1014	1184.0543	L	***1847.9650***	924.4862	1830.9385	915.9729	1829.9545	915.4809	19
24	2482.1647	1241.5860	2465.1381	1233.0727	2464.1541	1232.5807	P	***1734.8810***	867.9441	1717.8544	859.4308	1716.8704	858.9388	18

25	2539.1861	1270.0967	2522.1596	1261.5834	2521.1756	1261.0914	**G**	1637.8282	819.4177	1620.8016	810.9045	1619.8176	810.4125	**17**
26	2652.2702	**1326.6387**	2635.2437	1318.1255	2634.2596	1317.6335	**L**	1580.8067	790.9070	1563.7802	782.3937	1562.7962	781.9017	**16**
27	2749.3230	1375.1651	2732.2964	1366.6519	2731.3124	1366.1598	**P**	***1467.7227***	734.3650	1450.6961	725.8517	1449.7121	725.3597	**15**
28	2806.3444	1403.6759	2789.3179	1395.1626	2788.3339	1394.6706	**G**	1370.6699	685.8386	1353.6434	677.3253	1352.6593	676.8333	**14**
29	2903.3972	1452.2022	2886.3707	1443.6890	2885.3866	1443.1970	**P**	***1313.6484***	657.3279	1296.6219	648.8146	1295.6379	648.3226	**13**
30	3000.4500	**1500.7286**	2983.4234	1492.2153	2982.4394	1491.7233	**P**	1216.5957	608.8015	1199.5691	600.2882	1198.5851	599.7962	**12**
31	3057.4714	**1529.2394**	3040.4449	1520.7261	3039.4609	1520.2341	**G**	1119.5429	560.2751	1102.5164	551.7618	1101.5323	551.2698	**11**
32	3154.5242	1577.7657	3137.4976	1569.2525	3136.5136	1568.7605	**P**	***1062.5215***	531.7644	1045.4949	523.2511	1044.5109	522.7591	**10**
33	3251.5770	1626.2921	3234.5504	1617.7788	3233.5664	1617.2868	**P**	***965.4687***	483.2380	948.4421	474.7247	947.4581	474.2327	**9**
34	3366.6039	**1683.8056**	3349.5774	1675.2923	3348.5933	1674.8003	**D**	***868.4159***	434.7116	851.3894	426.1983	850.4054	425.7063	**8**
35	3437.6410	**1719.3241**	3420.6145	1710.8109	3419.6305	1710.3189	**A**	***753.3890***	377.1981	736.3624	368.6849	735.3784	368.1928	**7**
36	3524.6730	1762.8402	3507.6465	1754.3269	3506.6625	1753.8349	**S**	682.3519	341.6796	665.3253	333.1663	664.3413	332.6743	**6**
37	3637.7571	**1819.3822**	3620.7306	1810.8689	3619.7465	1810.3769	**I**	595.3198	298.1636	578.2933	289.6503	577.3093	289.1583	**5**
38	3724.7891	1862.8982	3707.7626	1854.3849	3706.7786	1853.8929	**S**	***482.2358***	241.6215	465.2092	233.1083	464.2252	232.6162	**4**
39	3887.8525	1944.4299	3870.8259	1935.9166	3869.8419	1935.4246	**Y**	395.2037	198.1055	378.1772	189.5922			**3**
40	3944.8739	1972.9406	3927.8474	1964.4273	3926.8634	1963.9353	**G**	232.1404	116.5738	215.1139	108.0606			**2**
41							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of SGTPGFSHHHYTTNSGQPGLHALPGLPGPPGPPDASISYGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.0	4117.9784	0.9144	SGTPGFSHHHYTTNSGQPGLHALPGLPGPPGPPDASISYGR
8.6	4119.7889	-0.8961	CFGPSICCGEGIGCLVGSPETLRCLEEDFLPSPCEMSGK
8.6	4119.8088	-0.9161	VQAFTGEETGSSGGCDTTAPQRTLYTAVSDSDTEDPDVR
8.2	4117.1479	1.7448	DINTVLLAVLMENGDVVVWQFSLPLNGKESVVSCSTIK
7.9	4119.9848	-1.0921	MSGAVATGGAQSAGLGAAAAGCCSSASGAGSAALLSAGSGIAGRLPSR
7.8	4119.9848	-1.0921	MSGAVATGGAQSAGLGAAAAGCCSSASGAGSAALLSAGSGIAGRLPSR
7.6	4119.7707	-0.8780	LTESGEPACHCQPGYSGPTCETALTCEGEAVRDYLYR
4.5	4119.7707	-0.8780	LTESGEPACHCQPGYSGPTCETALTCEGEAVRDYLYR
3.0	4117.1089	1.7838	VPIDKPVVKIVSGNDHLVMLTAHGELYTSGCGEQGQLGR
2.1	4119.3468	-0.4541	SVKLVNINIPDILEGKPSIILGLIWTIILHCHVCVTR

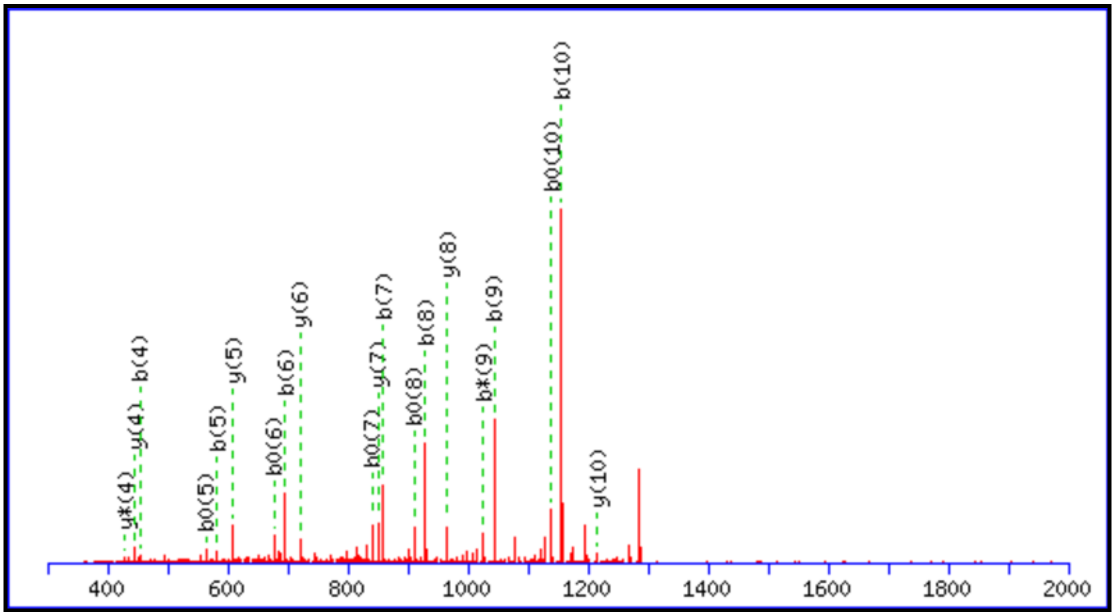
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SHIDELYANIK**
Found in **gi|57525836|ref|NP_001003569.1|**, hypothetical protein LOC445175 [Danio rerio]

Match to Query 17520: 1301.952724 from(1302.960000,1+) index(38927)
Data file TCDD_0530.dta

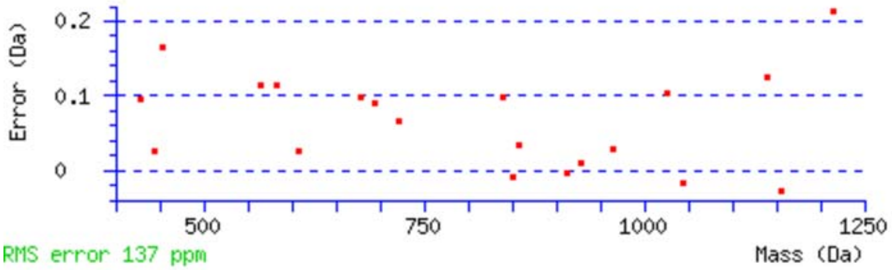
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

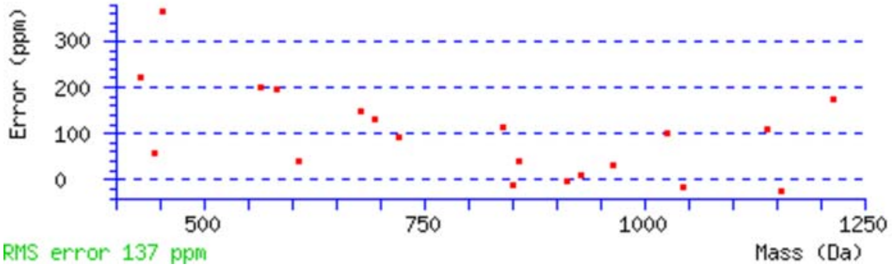


Monoisotopic mass of neutral peptide Mr(calc): 1301.6615
Ions Score: 60 **Expect:** 0.00032
Matches : 20/46 fragment ions using 30 most intense peaks (help)

#	b	b*	b^0	Seq.	y	y*	y^0	#
1	88.0393		70.0287	**S**				**11**
2	225.0982		207.0877	**H**	***1215.6368***	1198.6103	1197.6262	**10**
3	338.1823		320.1717	**I**	1078.5779	1061.5514	1060.5673	**9**
4	***453.2092***		435.1987	**D**	***965.4938***	948.4673	947.4833	**8**
5	***582.2518***		564.2413	**E**	***850.4669***	833.4403	832.4563	**7**
6	***695.3359***		677.3253	**L**	***721.4243***	704.3978		**6**
7	***858.3992***		840.3886	**Y**	***608.3402***	591.3137		**5**
8	***929.4363***		911.4258	**A**	***445.2769***	428.2504		**4**
9	***1043.4793***	1026.4527	1025.4687	**N**	374.2398	357.2132		**3**
10	***1156.5633***	1139.5368	1138.5527	**I**	260.1969	243.1703		**2**

11				**K**	147.1128	130.0863		**1**





NCBI **BLAST** search of SHIDELYANIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.9	1301.6615	0.2912	SHIDELYANIK
17.4	1301.7568	0.1959	QHLKIHTAGGLK
12.9	1302.7296	-0.7768	FLKIAEVGAGGNK
12.7	1301.7125	0.2402	KCAVVGNSGNLLK
10.5	1301.7667	0.1861	RLSATSLSLNLK
10.2	1301.6689	0.2838	LYVMTSINFSK
10.1	1302.6891	-0.7364	DSLLRTATANNK
9.7	1302.6642	-0.7115	ECLAVVWALDK
9.7	1302.6642	-0.7115	ECLAVVWAVEK
9.6	1301.7377	0.2150	NTMLAEVVGKLK

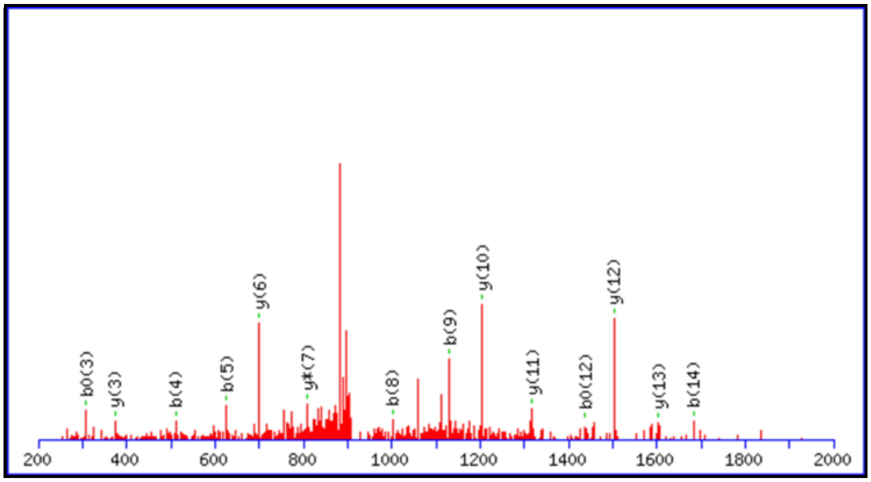
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SHTWLFETQPLDNIK**
Found in **gi|59933260|ref|NP_001012377.1|**, cardiomyopathy associated 1 [Danio rerio]

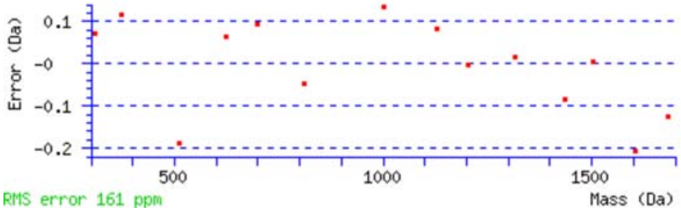
Match to Query 36886: 1829.892724 from(915.953638,2+) index(46293)
Data file TCDD_0530.dta

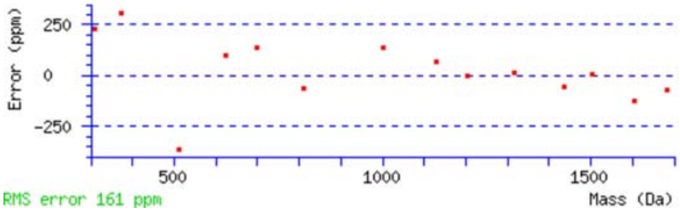
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1827.9155
Ions Score: 51 **Expect:** 0.002
Matches : 14/146 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							15
2	225.0982	113.0527			207.0877	104.0475	H	1741.8908	871.4490	1724.8642	862.9358	1723.8802	862.4438	14
3	326.1459	163.5766			308.1353	154.5713	T	***1604.8319***	802.9196	1587.8053	794.4063	1586.8213	793.9143	13
4	***512.2252***	256.6162			494.2146	247.6110	W	***1503.7842***	752.3957	1486.7577	743.8825	1485.7736	743.3905	12
5	***625.3093***	313.1583			607.2987	304.1530	L	***1317.7049***	659.3561	1300.6783	650.8428	1299.6943	650.3508	11
6	772.3777	386.6925			754.3671	377.6872	F	***1204.6208***	602.8141	1187.5943	594.3008	1186.6103	593.8088	10
7	901.4203	451.2138			883.4097	442.2085	E	1057.5524	529.2798	1040.5259	520.7666	1039.5419	520.2746	9
8	***1002.4680***	501.7376			984.4574	492.7323	T	928.5098	464.7585	911.4833	456.2453	910.4993	455.7533	8
9	***1130.5265***	565.7669	1113.5000	557.2536	1112.5160	556.7616	Q	827.4621	414.2347	810.4356	405.7214	809.4516	405.2294	7
10	1227.5793	614.2933	1210.5528	605.7800	1209.5687	605.2880	P	***699.4036***	350.2054	682.3770	341.6921	681.3930	341.2001	6
11	1340.6634	670.8353	1323.6368	662.3220	1322.6528	661.8300	L	602.3508	301.6790	585.3243	293.1658	584.3402	292.6738	5
12	1455.6903	728.3488	1438.6638	719.8355	1437.6797	719.3435	D	489.2667	245.1370	472.2402	236.6237	471.2562	236.1317	4
13	1569.7332	785.3703	1552.7067	776.8570	1551.7227	776.3650	N	***374.2398***	187.6235	357.2132	179.1103			3
14	***1682.8173***	841.9123	1665.7907	833.3990	1664.8067	832.9070	I	260.1969	130.6021	243.1703	122.0888			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SHTWLFETQPLDNIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.8	1827.9155	1.9772	SHTWLFETQPLDNIK
7.3	1827.9077	1.9850	NAMGVGLVFEADLYTTK
4.8	1829.6808	0.2120	CDPSCFNGSCWGTGPDK
1.6	1832.0495	-2.1567	AAAVRALGVYILFPCLR
0.2	1828.0054	1.8873	TGPSERAVTQSILSVVGK
0.1	1827.9876	1.9051	LAIAQMAQALLGSEERK

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

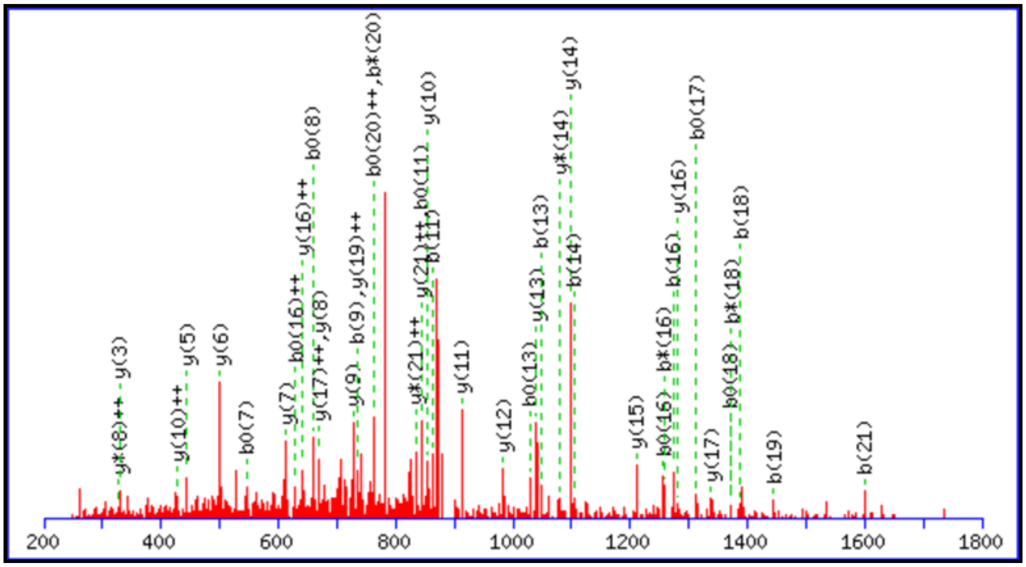
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYGGAGALGGAGQGGIGGGPGR**
Found in **gi|114326248|ref|NP_001041529.1|**, elastin b [Danio rerio]

Match to Query 34118: 1775.192724 from(888.603638,2+) index(32312)
Data file TCDD_0530.dta

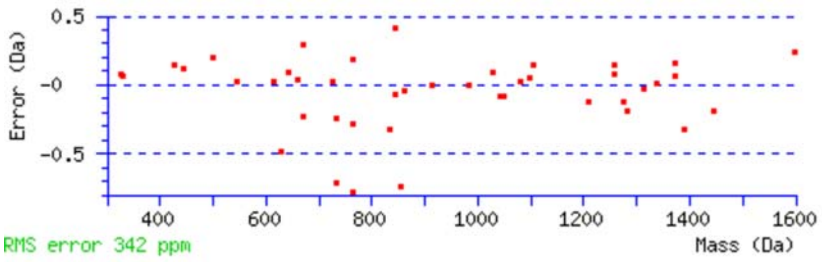
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

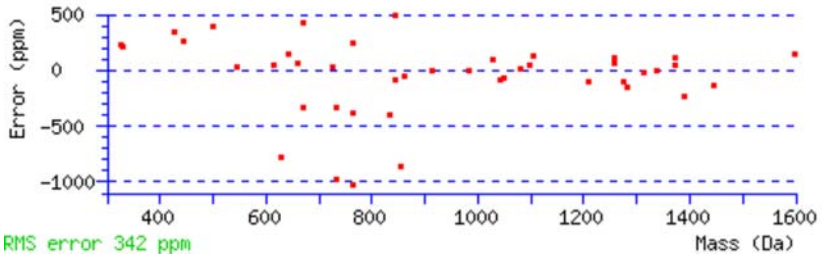


Monoisotopic mass of neutral peptide Mr(calc): 1772.8554
Ions Score: 52 **Expect:** 0.0015
Matches : 43/186 fragment ions using 114 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	88.0393	44.5233			70.0287	35.5180	S					22
2	251.1026	126.0550			233.0921	117.0497	Y	1686.8307	843.9190	1669.8041	835.4057	21
3	308.1241	154.5657			290.1135	145.5604	G	1523.7673	762.3873	1506.7408	753.8740	20
4	365.1456	183.0764			347.1350	174.0711	G	1466.7459	733.8766	1449.7193	725.3633	19
5	436.1827	218.5950			418.1721	209.5897	A	1409.7244	705.3658	1392.6979	696.8526	18
6	493.2041	247.1057			475.1936	238.1004	G	***1338.6873***	669.8473	1321.6607	661.3340	17
7	564.2413	282.6243			546.2307	273.6190	A	***1281.6658***	641.3366	1264.6393	632.8233	16
8	677.3253	339.1663			659.3148	330.1610	L	***1210.6287***	605.8180	1193.6022	597.3047	15
9	**734.3468**	367.6770			716.3362	358.6717	G	***1097.5446***	549.2760	1080.5181	540.7627	14
10	791.3682	396.1878			773.3577	387.1825	G	***1040.5232***	520.7652	1023.4966	512.2520	13
11	**862.4054**	431.7063			844.3948	422.7010	A	***983.5017***	492.2545	966.4752	483.7412	12
12	919.4268	460.2170			901.4163	451.2118	G	***912.4646***	456.7359	895.4381	448.2227	11
13	**1047.4854**	524.2463	1030.4589	515.7331	1029.4748	515.2411	Q	***855.4431***	428.2252	838.4166	419.7119	10
14	**1104.5069**	552.7571	1087.4803	544.2438	1086.4963	543.7518	G	***727.3846***	364.1959	710.3580	355.6826	9

15	1161.5283	581.2678	1144.5018	572.7545	1143.5178	572.2625	**G**	***670.3631***	335.6852	653.3366	327.1719	**8**
16	**1274.6124**	637.8098	1257.5858	629.2966	1256.6018	628.8046	**I**	***613.3416***	307.1745	596.3151	298.6612	**7**
17	1331.6339	666.3206	1314.6073	657.8073	1313.6233	657.3153	**G**	***500.2576***	250.6324	483.2310	242.1191	**6**
18	**1388.6553**	694.8313	1371.6288	686.3180	1370.6448	685.8260	**G**	***443.2361***	222.1217	426.2096	213.6084	**5**
19	**1445.6768**	723.3420	1428.6502	714.8288	1427.6662	714.3367	**G**	386.2146	193.6110	369.1881	185.0977	**4**
20	1542.7295	771.8684	1525.7030	763.3551	1524.7190	762.8631	**P**	***329.1932***	165.1002	312.1666	156.5870	**3**
21	**1599.7510**	800.3791	1582.7245	791.8659	1581.7404	791.3739	**G**	232.1404	116.5738	215.1139	108.0606	**2**
22							**R**	175.1190	88.0631	158.0924	79.5498	**1**





NCBI **BLAST** search of SYGGAGALGGAGQGGIGGGPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	**Mr(calc):**	**Delta**	**Sequence**
52.4	1772.8554	2.3373	SYGGAGALGGAGQGGIGGGPGR
7.0	1772.7280	2.4647	CISAAYVCDGINDCR
4.2	1775.8723	-0.6796	LEEAGGATSAQIEMNKK
3.3	1773.8356	1.3572	NSLKSYVLSNDECFR
3.2	1773.8931	1.2996	ITDLAIVGEAGQCGKDK
3.1	1772.8904	2.3023	ILESGKLETEQGQEGR
2.4	1774.8836	0.3091	TVQELVSDLLSAEDEK
2.2	1772.9420	2.2507	NALSNGIDKAYLEIPR
1.0	1776.7261	-1.5334	NQTDTFADFDTMTDR
1.0	1773.8390	1.3538	DPKVTSDEVCGCPLVR

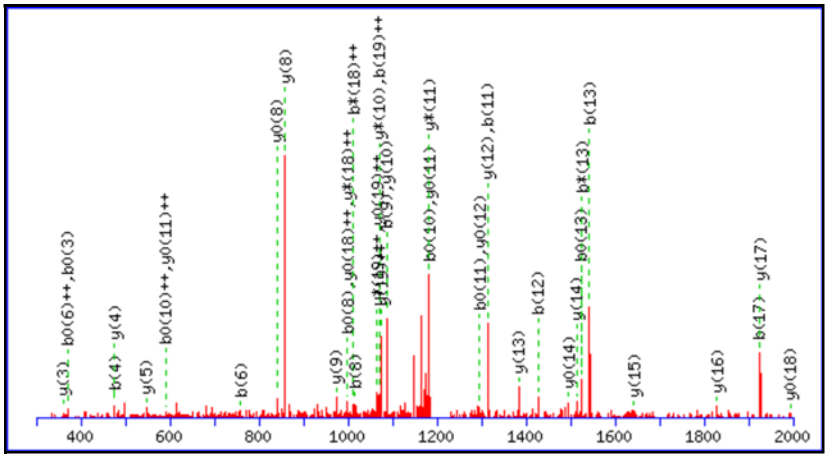
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYHSPWEEAIINDPTLADTLK**
Found in **gi|41053611|ref|NP_957148.1|**, hypothetical protein LOC393828 [Danio rerio]

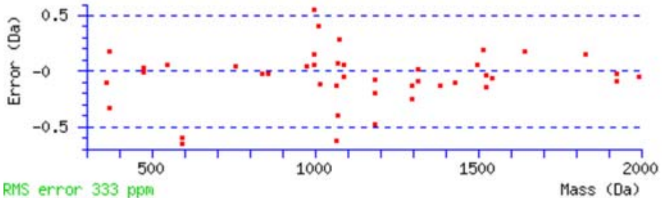
Match to Query 85634: 2398.672724 from(1200.343638,2+) index(119595)
Data file TCDD_0530.dta

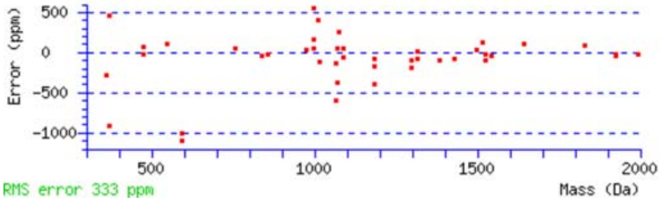
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2399.1645
Ions Score: 56 **Expect:** 0.00041
Matches : 43/214 fragment ions using 68 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	**S**							**21**
2	251.1026	126.0550			233.0921	117.0497	**Y**	2313.1398	1157.0735	2296.1132	1148.5602	2295.1292	1148.0682	**20**
3	388.1615	194.5844			370.1510	185.5791	**H**	2150.0764	1075.5419	2133.0499	1067.0286	2132.0659	1066.5366	**19**
4	**475.1936**	238.1004			457.1830	229.0951	**S**	2013.0175	1007.0124	1995.9910	998.4991	1995.0069	998.0071	**18**
5	572.2463	286.6268			554.2358	277.6215	**P**	***1925.9855***	963.4964	1908.9589	954.9831	1907.9749	954.4911	**17**
6	**758.3257**	379.6665			740.3151	370.6612	**W**	***1828.9327***	914.9700	1811.9062	906.4567	1810.9222	905.9647	**16**
7	887.3682	444.1878			869.3577	435.1825	**E**	***1642.8534***	821.9303	1625.8269	813.4171	1624.8428	812.9251	**15**
8	**1016.4108**	508.7091			998.4003	499.7038	**E**	***1513.8108***	757.4090	1496.7843	748.8958	1495.8003	748.4038	**14**
9	**1087.4480**	544.2276			1069.4374	535.2223	**A**	***1384.7682***	692.8877	1367.7417	684.3745	1366.7577	683.8825	**13**
10	1200.5320	600.7696			1182.5214	591.7644	**I**	***1313.7311***	657.3692	1296.7046	648.8559	1295.7205	648.3639	**12**
11	**1313.6161**	657.3117			1295.6055	648.3064	**I**	1200.6470	600.8272	1183.6205	592.3139	1182.6365	591.8219	**11**
12	**1427.6590**	714.3331	1410.6325	705.8199	1409.6484	705.3279	**N**	***1087.5630***	544.2851	1070.5364	535.7719	1069.5524	535.2798	**10**
13	**1542.6859**	771.8466	1525.6594	763.3333	1524.6754	762.8413	**D**	***973.5201***	487.2637	956.4935	478.7504	955.5095	478.2584	**9**
14	1639.7387	820.3730	1622.7122	811.8597	1621.7281	811.3677	**P**	***858.4931***	429.7502	841.4666	421.2369	840.4825	420.7449	**8**
15	1740.7864	870.8968	1723.7598	862.3836	1722.7758	861.8916	**T**	761.4403	381.2238	744.4138	372.7105	743.4298	372.2185	**7**
16	1853.8705	927.4389	1836.8439	918.9256	1835.8599	918.4336	**L**	660.3927	330.7000	643.3661	322.1867	642.3821	321.6947	**6**
17	**1924.9076**	962.9574	1907.8810	954.4441	1906.8970	953.9521	**A**	***547.3086***	274.1579	530.2821	265.6447	529.2980	265.1527	**5**
18	2039.9345	1020.4709	2022.9080	1011.9576	2021.9239	1011.4656	**D**	***476.2715***	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
19	2140.9822	1070.9947	2123.9556	1062.4815	2122.9716	1061.9895	**T**	***361.2445***	181.1259	344.2180	172.6126	343.2340	172.1206	**3**
20	2254.0663	1127.5368	2237.0397	1119.0235	2236.0557	1118.5315	**L**	260.1969	130.6021	243.1703	122.0888			**2**
21							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of SYHSPWEEAIINDPTLADTLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.2	2399.1645	-0.4918	SYHSPWEEAIINDPTLADTLK
4.6	2400.0396	-1.3669	LPRDCGCDLAEDTLDPAAMSPP
3.4	2398.2712	0.4015	TLNMVTPTLRVEDCSIALLPR
2.5	2398.2137	0.4590	LIQFLFSQMQSNSPSTVGMKR
0.5	2397.2470	1.4257	LCKPQISDVIVDPMCGTGAIPLK

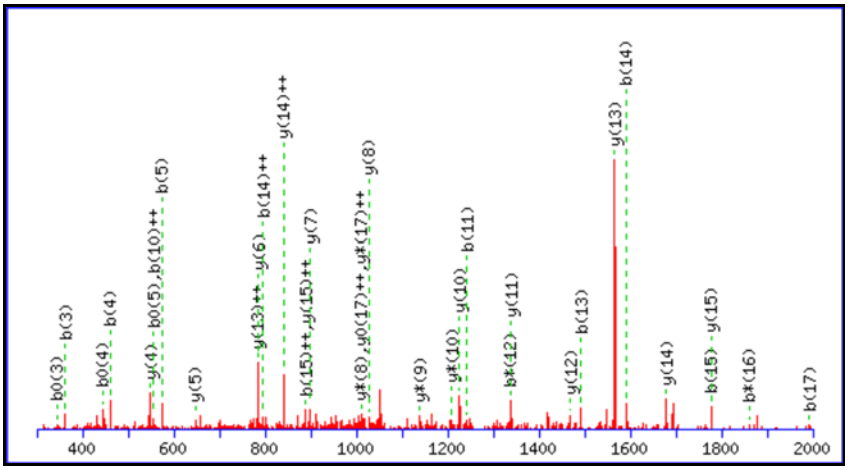
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFLVIPELAQELHVWTDK**
Found in **gi|121583986|ref|NP_001073435.1|**, hypothetical protein LOC557972 [Danio rerio]

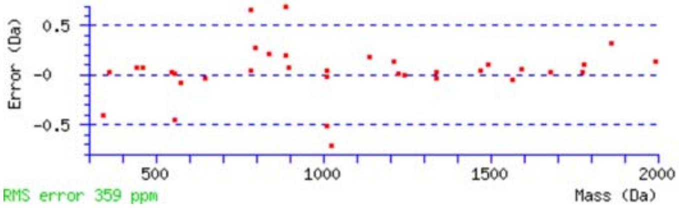
Match to Query 57897: 2140.482724 from(1071.248638,2+) index(38206)
Data file TCDD_0530.dta

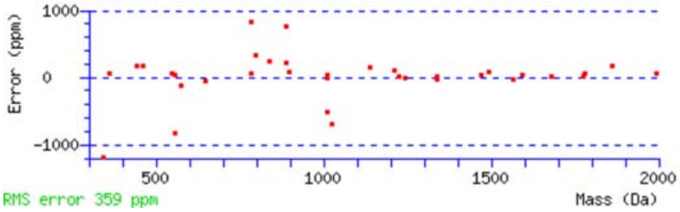
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



`Monoisotopic mass of neutral peptide Mr(calc):` 2138.1412
Ions Score: 48 **Expect:** 0.0033
Matches : 35/184 fragment ions using 68 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	**T**							**18**
2	249.1234	125.0653			231.1128	116.0600	**F**	2038.1008	1019.5540	2021.0742	1011.0408	2020.0902	1010.5488	**17**
3	**362.2074**	181.6074			344.1969	172.6021	**L**	1891.0324	946.0198	1874.0058	937.5066	1873.0218	937.0145	**16**
4	**461.2758**	231.1416			443.2653	222.1363	**V**	***1777.9483***	889.4778	1760.9218	880.9645	1759.9377	880.4725	**15**
5	**574.3599**	287.6836			556.3493	278.6783	**I**	***1678.8799***	839.9436	1661.8534	831.4303	1660.8693	830.9383	**14**
6	671.4127	336.2100			653.4021	327.2047	**P**	***1565.7958***	783.4016	1548.7693	774.8883	1547.7853	774.3963	**13**
7	800.4553	400.7313			782.4447	391.7260	**E**	***1468.7431***	734.8752	1451.7165	726.3619	1450.7325	725.8699	**12**
8	913.5393	457.2733			895.5288	448.2680	**L**	***1339.7005***	670.3539	1322.6739	661.8406	1321.6899	661.3486	**11**
9	984.5764	492.7919			966.5659	483.7866	**A**	***1226.6164***	613.8118	1209.5899	605.2986	1208.6058	604.8066	**10**
10	1112.6350	556.8211	1095.6085	548.3079	1094.6245	547.8159	**Q**	1155.5793	578.2933	1138.5528	569.7800	1137.5687	569.2880	**9**
11	**1241.6776**	621.3424	1224.6511	612.8292	1223.6671	612.3372	**E**	***1027.5207***	514.2640	1010.4942	505.7507	1009.5102	505.2587	**8**
12	1354.7617	677.8845	1337.7351	669.3712	1336.7511	668.8792	**L**	***898.4781***	449.7427	881.4516	441.2294	880.4676	440.7374	**7**
13	**1491.8206**	746.4139	1474.7940	737.9007	1473.8100	737.4087	**H**	***785.3941***	393.2007	768.3675	384.6874	767.3835	384.1954	**6**
14	**1590.8890**	795.9481	1573.8625	787.4349	1572.8784	786.9429	**V**	***648.3352***	324.6712	631.3086	316.1579	630.3246	315.6659	**5**
15	**1776.9683**	888.9878	1759.9418	880.4745	1758.9578	879.9825	**W**	***549.2667***	275.1370	532.2402	266.6237	531.2562	266.1317	**4**
16	1878.0160	939.5116	1860.9895	930.9984	1860.0054	930.5064	**T**	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	**3**
17	**1993.0429**	997.0251	1976.0164	988.5118	1975.0324	988.0198	**D**	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	**2**
18							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of TFLVIPELAQELHVWTDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.0	2138.1412	2.3415	TFLVIPELAQELHVWTDK
8.3	2139.9669	0.5159	GVEGRSSQNSEAEVSGSDAFK
6.4	2139.1106	1.3721	ENPINRDIVLTVMALDGGGR
5.3	2139.1510	1.3317	LREILVPGSVQWMGLQGEK
5.2	2139.1535	1.3292	ELSVQGLTQISLSLHTASQK
4.3	2139.0881	1.3946	YAMKGAGTTEDTLIEILASR
4.0	2139.0668	1.4159	RPLLAENGSINSQQGDVDAR
3.9	2138.0855	2.3972	HSTEVDINTTLQLLGSPGEK
2.8	2138.9473	1.5354	CLMDEHKNHEAVTAEAER
2.5	2140.0477	0.4350	FNADDGVYEKVVTEWLQK

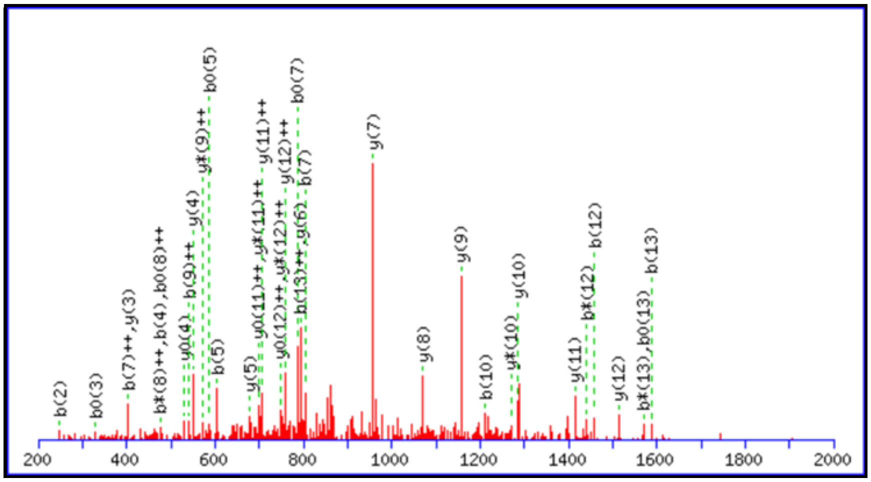
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFVQESIYDEFVER**
Found in **gi|51571951|ref|NP_998466.2|**, aldehyde dehydrogenase 2b [Danio rerio]

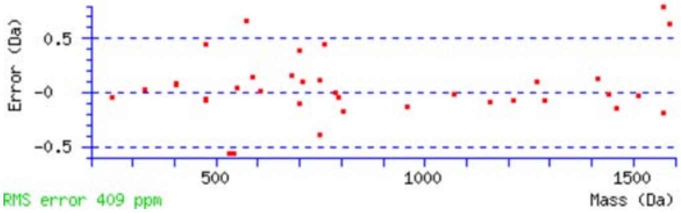
Match to Query 33260: 1761.192724 from(881.603638,2+) index(14670)
Data file TCDD_0530.dta

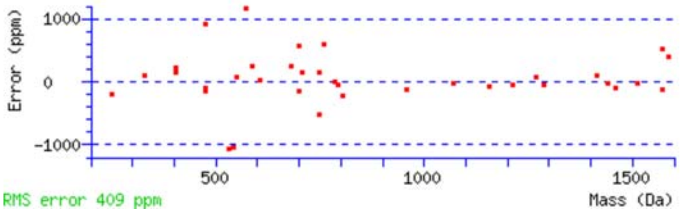
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1760.8257
Ions Score: 55 **Expect:** 0.00092
Matches : 37/148 fragment ions using 57 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							14
2	**249.1234**	125.0653			231.1128	116.0600	F	1660.7853	830.8963	1643.7588	822.3830	1642.7748	821.8910	13
3	348.1918	174.5995			330.1812	165.5942	V	***1513.7169***	757.3621	1496.6904	748.8488	1495.7064	748.3568	12
4	**476.2504**	238.6288	459.2238	230.1155	458.2398	229.6235	Q	***1414.6485***	707.8279	1397.6220	699.3146	1396.6379	698.8226	11
5	**605.2930**	303.1501	588.2664	294.6368	587.2824	294.1448	E	***1286.5899***	643.7986	1269.5634	635.2853	1268.5794	634.7933	10
6	692.3250	346.6661	675.2984	338.1529	674.3144	337.6608	S	***1157.5473***	579.2773	1140.5208	570.7640	1139.5368	570.2720	9
7	**805.4090**	**403.2082**	788.3825	394.6949	787.3985	394.2029	I	***1070.5153***	535.7613	1053.4888	527.2480	1052.5047	526.7560	8
8	968.4724	484.7398	951.4458	476.2266	950.4618	475.7345	Y	***957.4312***	479.2193	940.4047	470.7060	939.4207	470.2140	7
9	1083.4993	**542.2533**	1066.4728	533.7400	1065.4888	533.2480	D	***794.3679***	397.6876	777.3414	389.1743	776.3573	388.6823	6
10	**1212.5419**	606.7746	1195.5154	598.2613	1194.5313	597.7693	E	***679.3410***	340.1741	662.3144	331.6608	661.3304	331.1688	5
11	1359.6103	680.3088	1342.5838	671.7955	1341.5998	671.3035	F	***550.2984***	275.6528	533.2718	267.1396	532.2878	266.6475	4
12	**1458.6787**	729.8430	1441.6522	721.3297	1440.6682	720.8377	V	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
13	**1587.7213**	**794.3643**	1570.6948	785.8510	1569.7108	785.3590	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TFVQESIYDEFVER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.7	1760.8257	0.3670	TFVQESIYDEFVER
10.1	1760.9131	0.2797	YSQLLALPALCEIGDR
10.1	1761.8985	-0.7058	TFVIQGFGNVGLHSMR
7.4	1760.9001	0.2927	LKRPGFVCGPCCTKPR
5.3	1759.9291	1.2636	RPCDILTPEGFKTVK
5.0	1758.9298	2.2629	QLKGDTNTVEALLMAR
4.2	1759.8965	1.2962	AEFRTSLRPDNADLR
4.0	1760.8879	0.3048	IGCNSLIGSIWGKEER
4.0	1761.7814	-0.5887	FPCANDTSVCLPPER
3.9	1758.9087	2.2840	FLSLSGCHQITDLGLR

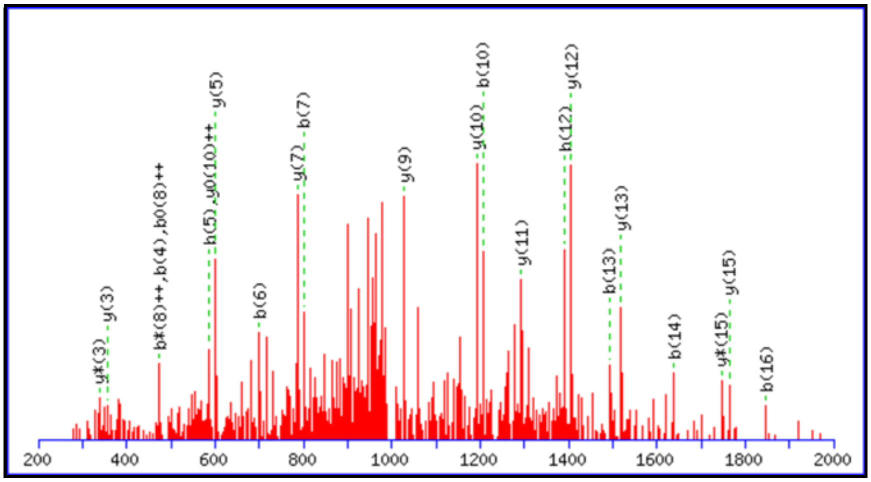
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TKEDILTYEIADVFHAK**
Found in **gi|41055939|ref|NP_956436.1|**, sorting and assembly machinery component 50 homolog [Danio rerio]

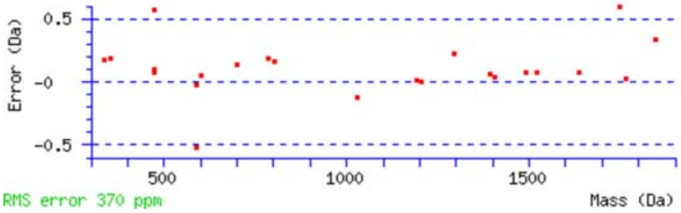
Match to Query 46829: 1993.702724 from(997.858638,2+) index(47199)
Data file TCDD_0530.dta

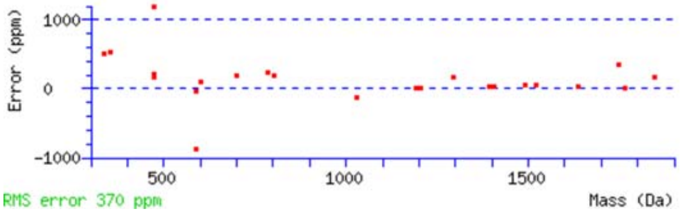
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1992.0204
Ions Score: 63 **Expect:** 0.0001
Matches : 23/180 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							17
2	230.1499	115.5786	213.1234	107.0653	212.1394	106.5733	K	1891.9800	946.4936	1874.9535	937.9804	1873.9694	937.4884	16
3	359.1925	180.0999	342.1660	171.5866	341.1819	171.0946	E	***1763.8850***	882.4462	1746.8585	873.9329	1745.8745	873.4409	15
4	***474.2195***	237.6134	457.1929	229.1001	456.2089	228.6081	D	1634.8425	817.9249	1617.8159	809.4116	1616.8319	808.9196	14
5	***587.3035***	294.1554	570.2770	285.6421	569.2930	285.1501	I	***1519.8155***	760.4114	1502.7890	751.8981	1501.8049	751.4061	13
6	***700.3876***	350.6974	683.3610	342.1842	682.3770	341.6921	L	***1406.7314***	703.8694	1389.7049	695.3561	1388.7209	694.8641	12
7	***801.4353***	401.2213	784.4087	392.7080	783.4247	392.2160	T	***1293.6474***	647.3273	1276.6208	638.8141	1275.6368	638.3220	11
8	964.4986	482.7529	947.4720	474.2397	946.4880	473.7477	Y	***1192.5997***	596.8035	1175.5732	588.2902	1174.5891	587.7982	10
9	1093.5412	547.2742	1076.5146	538.7610	1075.5306	538.2689	E	***1029.5364***	515.2718	1012.5098	506.7585	1011.5258	506.2665	9
10	***1206.6252***	603.8163	1189.5987	595.3030	1188.6147	594.8110	I	900.4938	450.7505	883.4672	442.2373	882.4832	441.7452	8
11	1277.6624	639.3348	1260.6358	630.8215	1259.6518	630.3295	A	***787.4097***	394.2085	770.3832	385.6952	769.3992	385.2032	7
12	***1392.6893***	696.8483	1375.6628	688.3350	1374.6787	687.8430	D	716.3726	358.6899	699.3461	350.1767	698.3620	349.6847	6
13	***1491.7577***	746.3825	1474.7312	737.8692	1473.7472	737.3772	V	***601.3457***	301.1765	584.3191	292.6632			5
14	***1638.8261***	819.9167	1621.7996	811.4034	1620.8156	810.9114	F	502.2772	251.6423	485.2507	243.1290			4
15	1775.8850	888.4462	1758.8585	879.9329	1757.8745	879.4409	H	***355.2088***	178.1081	338.1823	169.5948			3
16	***1846.9222***	923.9647	1829.8956	915.4514	1828.9116	914.9594	A	218.1499	109.5786	201.1234	101.0653			2
17							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TKEDILTYEIADVFHAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.2	1992.0204	1.6823	TKEDILTYEIADVFHAK
8.1	1992.0384	1.6643	LKLQGSCTSCPSSIITLK
7.3	1992.9727	0.7300	LLDNMLHQEISNFYTR
6.3	1991.9808	1.7219	CALELEAIVNSPLNMYR
5.6	1993.0628	0.6399	VNMTGVIETTMTFLPLVK
5.2	1992.9973	0.7055	ITSTSCCIQNIQIAVGTK
4.8	1993.8404	-0.1377	HSMCNSQSTCTPTLNTR
4.3	1992.9442	0.7585	NFGPKGFGYGQGAGALSHTQ
3.9	1992.9584	0.7444	AALVFTCAVCRSQMPDPK
3.0	1992.0164	1.6864	NALPDILGSTAGPGAADLPDK

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

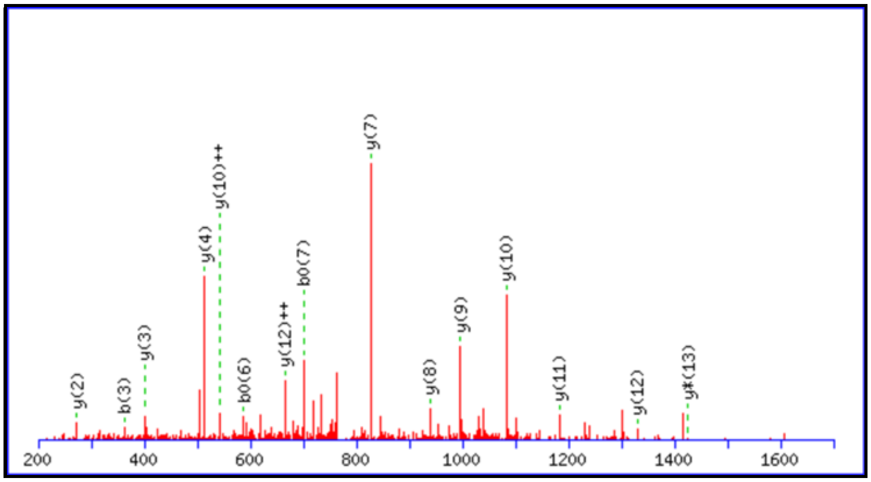
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLFVSGLPTDIKPR**
Found in **gi|41053746|ref|NP_956553.1|**, RNA binding protein with multiple splicing 2 [Danio rerio]

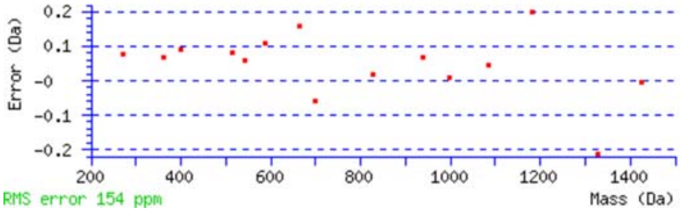
Match to Query 24466: 1543.362724 from(772.688638,2+) index(44801)
Data file TCDD_0530.dta

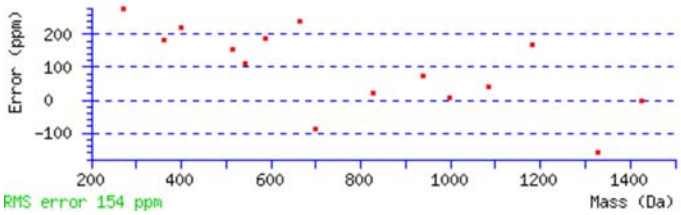
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1542.8770
Ions Score: 56 **Expect:** 0.00061
Matches : 15/126 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							14
2	215.1390	108.0731			197.1285	99.0679	L	1442.8366	721.9219	1425.8100	713.4087	1424.8260	712.9166	13
3	362.2074	181.6074			344.1969	172.6021	F	***1329.7525***	665.3799	1312.7260	656.8666	1311.7419	656.3746	12
4	461.2758	231.1416			443.2653	222.1363	V	***1182.6841***	591.8457	1165.6576	583.3324	1164.6735	582.8404	11
5	548.3079	274.6576			530.2973	265.6523	S	***1083.6157***	542.3115	1066.5891	533.7982	1065.6051	533.3062	10
6	605.3293	303.1683			587.3188	294.1630	G	***996.5837***	498.7955	979.5571	490.2822	978.5731	489.7902	9
7	718.4134	359.7103			700.4028	350.7051	L	***939.5622***	470.2847	922.5356	461.7715	921.5516	461.2795	8
8	815.4662	408.2367			797.4556	399.2314	P	***826.4781***	413.7427	809.4516	405.2294	808.4676	404.7374	7
9	916.5138	458.7606			898.5033	449.7553	T	729.4254	365.2163	712.3988	356.7030	711.4148	356.2110	6
10	1031.5408	516.2740			1013.5302	507.2688	D	628.3777	314.6925	611.3511	306.1792	610.3671	305.6872	5
11	1144.6249	572.8161			1126.6143	563.8108	I	***513.3507***	257.1790	496.3242	248.6657			4
12	1272.7198	636.8635	1255.6933	628.3503	1254.7093	627.8583	K	***400.2667***	200.6370	383.2401	192.1237			3
13	1369.7726	685.3899	1352.7460	676.8767	1351.7620	676.3846	P	***272.1717***	136.5895	255.1452	128.0762			2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TLFVSGLPTDIKPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.5	1542.8770	0.4857	TLFVSGLPTDIKPR
47.8	1542.8253	0.5374	KLAEQELLDVTER
10.3	1543.8570	-0.4943	QNIDVKQTVGTTLK
9.3	1541.9446	1.4181	LLQFGKIIIGVWR
9.1	1544.7082	-1.3455	FSEVSLSQFWCR
7.9	1543.7590	-0.3963	EAAAGALQNITAGDSR
6.3	1543.8206	-0.4579	VGKSGNIPAGTTVDTK
5.2	1544.6790	-1.3163	ERNHEFSMDGPAR
4.8	1544.8198	-1.4571	KPPAPKATYETNTK
4.7	1543.8107	-0.4480	LFSNGSLHITATQR

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

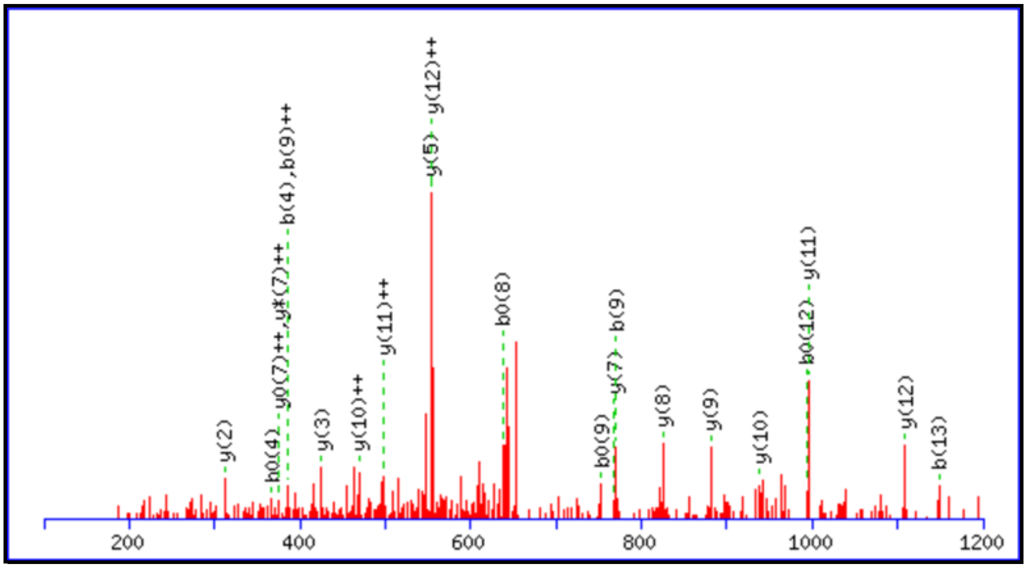
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLLGGGGVDGAIHR**
Found in **gi|52218992|ref|NP_001004573.1|**, hypothetical protein LOC447834 [Danio rerio]

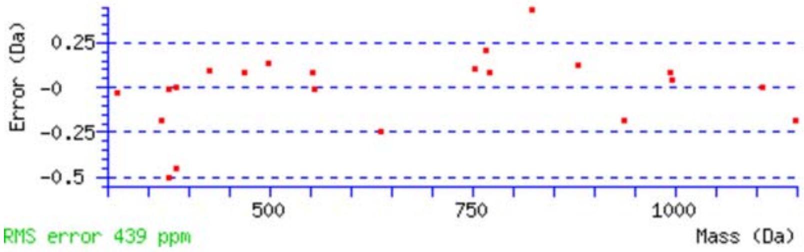
Match to Query 18201: 1322.702724 from(662.358638,2+) index(35559)
Data file TCDD_0530.dta

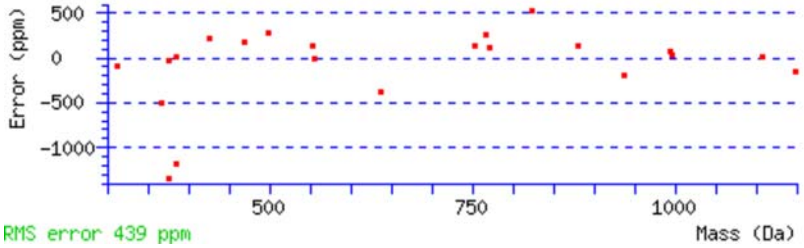
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1321.7103
Ions Score: 40  Expect: 0.027
Matches : 22/120 fragment ions using 62 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	**T**							**14**
2	215.1390	108.0731	197.1285	99.0679	**L**	1221.6698	611.3386	1204.6433	602.8253	1203.6593	602.3333	**13**
3	328.2231	164.6152	310.2125	155.6099	**L**	***1108.5858***	554.7965	1091.5592	546.2833	1090.5752	545.7912	**12**
4	**385.2445**	193.1259	367.2340	184.1206	**G**	***995.5017***	498.2545	978.4752	489.7412	977.4912	489.2492	**11**
5	442.2660	221.6366	424.2554	212.6314	**G**	***938.4803***	469.7438	921.4537	461.2305	920.4697	460.7385	**10**
6	499.2875	250.1474	481.2769	241.1421	**G**	***881.4588***	441.2330	864.4322	432.7198	863.4482	432.2278	**9**
7	556.3089	278.6581	538.2984	269.6528	**G**	***824.4373***	412.7223	807.4108	404.2090	806.4268	403.7170	**8**
8	655.3774	328.1923	637.3668	319.1870	**V**	***767.4159***	384.2116	750.3893	375.6983	749.4053	375.2063	**7**
9	**770.4043**	385.7058	752.3937	376.7005	**D**	668.3474	334.6774	651.3209	326.1641	650.3369	325.6721	**6**
10	827.4258	414.2165	809.4152	405.2112	**G**	***553.3205***	277.1639	536.2940	268.6506			**5**
11	898.4629	449.7351	880.4523	440.7298	**A**	496.2990	248.6532	479.2725	240.1399			**4**
12	1011.5469	506.2771	993.5364	497.2718	**I**	***425.2619***	213.1346	408.2354	204.6213			**3**
13	**1148.6058**	574.8066	1130.5953	565.8013	**H**	***312.1779***	156.5926	295.1513	148.0793			**2**
14					**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of TLLGGGGVDGAIHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.3	1321.7103	0.9925	TLLGGGGVDGAIHR
14.2	1322.6653	0.0375	EPRVCSPDPVPK
9.5	1322.6466	0.0561	NVLIQDSESYR
9.4	1321.8194	0.8833	TLILIGAPGVGRR
6.4	1321.7102	0.9925	QQGLAALQQTHK
5.8	1322.6839	0.0188	VVENIKCLFCR
5.7	1322.6289	0.0738	EGVVDIYNCVR
5.0	1322.6877	0.0150	MPPVQSQPAGRR
4.9	1323.5552	-0.8525	HDSDDAESHRR
4.5	1320.6357	2.0670	GRIFCGDVGQNR

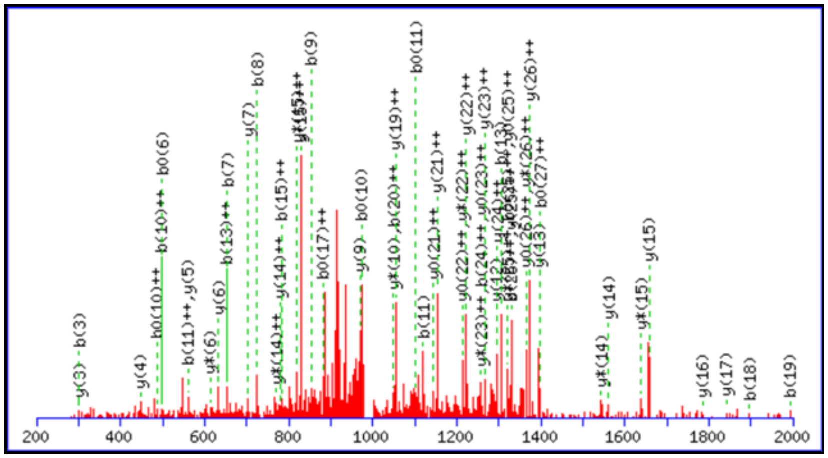
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLSAGSHAEHEGKPYCNNPCYAALFGPK**
Found in **gi|125842393|ref|XP_001333107.1|**, PREDICTED: zgc:103738 [Danio rerio]

Match to Query 107632: 2959.962723 from(987.661517,3+) index(137287)
Data file TCDD_0530.dta

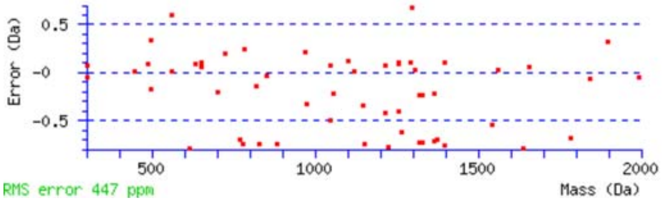
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

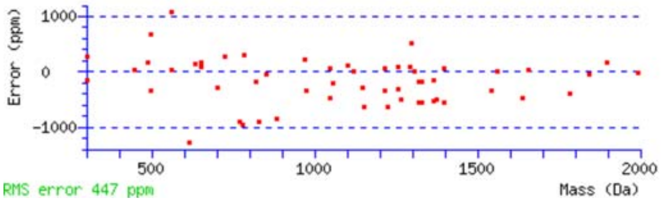


Monoisotopic mass of neutral peptide Mr(calc): 2961.3538
Ions Score: 43 **Expect:** 0.0069
Matches : 58/266 fragment ions using 135 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	**T**							**28**
2	215.1390	108.0731			197.1285	99.0679	**L**	2861.3134	1431.1603	2844.2868	1422.6471	2843.3028	1422.1551	**27**
3	**302.1710**	151.5892			284.1605	142.5839	**S**	2748.2293	1374.6183	2731.2028	1366.1050	2730.2188	1365.6130	**26**
4	373.2082	187.1077			355.1976	178.1024	**A**	2661.1973	1331.1023	2644.1708	1322.5890	2643.1867	1322.0970	**25**
5	430.2296	215.6185			412.2191	206.6132	**G**	2590.1602	1295.5837	2573.1336	1287.0705	2572.1496	1286.5785	**24**
6	517.2617	259.1345			499.2511	250.1292	**S**	2533.1387	1267.0730	2516.1122	1258.5597	2515.1282	1258.0677	**23**
7	**654.3206**	327.6639			636.3100	318.6586	**H**	2446.1067	1223.5570	2429.0801	1215.0437	2428.0961	1214.5517	**22**
8	**725.3577**	363.1825			707.3471	354.1772	**A**	2309.0478	1155.0275	2292.0212	1146.5143	2291.0372	1146.0222	**21**
9	**854.4003**	427.7038			836.3897	418.6985	**E**	2238.0107	1119.5090	2220.9841	1110.9957	2220.0001	1110.5037	**20**
10	991.4592	**496.2332**			973.4486	487.2279	**H**	2108.9681	1054.9877	2091.9415	1046.4744	2090.9575	1045.9824	**19**
11	**1120.5018**	**560.7545**			1102.4912	551.7492	**E**	1971.9092	986.4582	1954.8826	977.9449	1953.8986	977.4529	**18**
12	1177.5232	589.2653			1159.5127	580.2600	**G**	***1842.8666***	921.9369	1825.8400	913.4237			**17**
13	**1305.6182**	**653.3127**	1288.5917	644.7995	1287.6076	644.3075	**K**	***1785.8451***	893.4262	1768.8186	884.9129			**16**
14	1402.6710	701.8391	1385.6444	693.3258	1384.6604	692.8338	**P**	***1657.7501***	829.3787	1640.7236	820.8654			**15**
15	1565.7343	**783.3708**	1548.7077	774.8575	1547.7237	774.3655	**Y**	***1560.6974***	780.8523	1543.6708	772.3391			**14**
16	1668.7435	834.8754	1651.7169	826.3621	1650.7329	825.8701	**C**	***1397.6341***	699.3207	1380.6075	690.8074			**13**
17	1782.7864	891.8968	1765.7599	883.3836	1764.7758	882.8916	**N**	***1294.6249***	647.8161	1277.5983	639.3028			**12**
18	**1896.8293**	948.9183	1879.8028	940.4050	1878.8188	939.9130	**N**	1180.5819	590.7946	1163.5554	582.2813			**11**
19	**1993.8821**	997.4447	1976.8556	988.9314	1975.8715	988.4394	**P**	1066.5390	533.7731	1049.5125	525.2599			**10**
20	2096.8913	**1048.9493**	2079.8647	1040.4360	2078.8807	1039.9440	**C**	***969.4863***	485.2468	952.4597	476.7335			**9**
21	2259.9546	1130.4809	2242.9281	1121.9677	2241.9440	1121.4757	**Y**	866.4771	433.7422	849.4505	425.2289			**8**
22	2330.9917	1165.9995	2313.9652	1157.4862	2312.9812	1156.9942	**A**	***703.4137***	352.2105	686.3872	343.6972			**7**
23	2402.0288	1201.5181	2385.0023	1193.0048	2384.0183	1192.5128	**A**	***632.3766***	316.6920	615.3501	308.1787			**6**
24	2515.1129	**1258.0601**	2498.0864	1249.5468	2497.1023	1249.0548	**L**	***561.3395***	281.1734	544.3130	272.6601			**5**

25	2662.1813	**1331.5943**	2645.1548	1323.0810	2644.1708	1322.5890	**F**	***448.2554***	224.6314	431.2289	216.1181			**4**
26	2719.2028	1360.1050	2702.1762	1351.5918	2701.1922	1351.0997	**G**	***301.1870***	151.0972	284.1605	142.5839			**3**
27	2816.2555	1408.6314	2799.2290	1400.1181	2798.2450	1399.6261	**P**	244.1656	122.5864	227.1390	114.0731			**2**
28							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of TLSAGSHAEHEGKPYCNNPCYAALFGPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.6	2961.3538	-1.3910	TLSAGSHAEHEGKPYCNNPCYAALFGPK
14.4	2961.3080	-1.3452	SDVAQNILEIAGACAEAEGACAGEAEGEAGR
4.5	2959.4862	0.4765	TCTVINVEGDAYGAGLLQYLIDRHPNK
2.4	2959.5497	0.4130	HAILSSNPKHFYYPGAGAWVLSLLYR
0.7	2958.6021	1.3606	QLPQISVPWIHPGFGLPYWRADLLR
0.3	2958.4851	1.4776	AFCFLPLSLETGLPFHVNGHFALDSAR

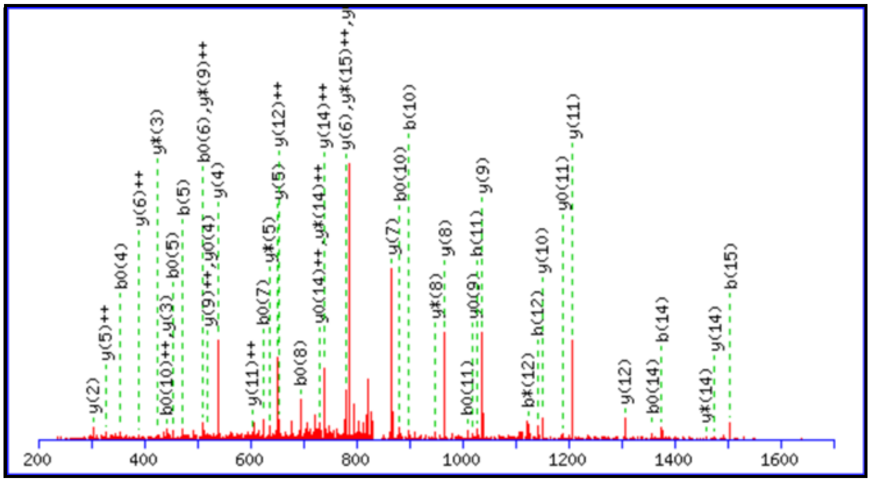
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTGLVGLAVSQNPHER**
Found in **gi|61806484|ref|NP_001013474.1|**, hypothetical protein LOC541328 [Danio rerio]

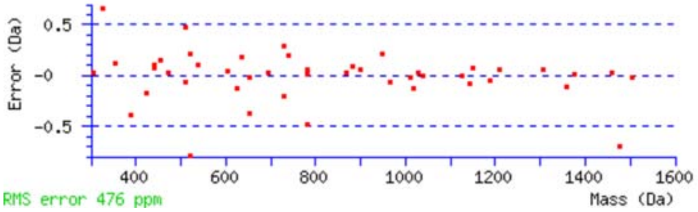
Match to Query 29046: 1677.522724 from(839.768638,2+) index(35969)
Data file TCDD_0530.dta

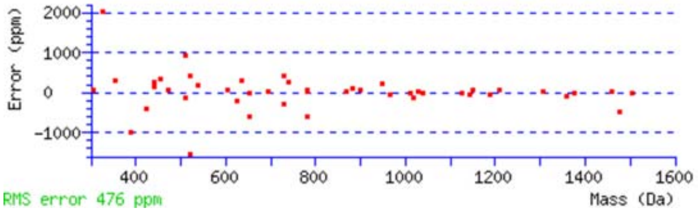
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1677.8798
Ions Score: 58 **Expect:** 0.00045
Matches : 46/158 fragment ions using 95 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	**T**							**16**
2	203.1026	102.0550			185.0921	93.0497	**T**	1577.8394	789.4234	1560.8129	780.9101	1559.8289	780.4181	**15**
3	260.1241	130.5657			242.1135	121.5604	**G**	***1476.7918***	738.8995	1459.7652	730.3862	1458.7812	729.8942	**14**
4	373.2082	187.1077			355.1976	178.1024	**L**	1419.7703	710.3888	1402.7437	701.8755	1401.7597	701.3835	**13**
5	**472.2766**	236.6419			454.2660	227.6366	**V**	***1306.6862***	653.8467	1289.6597	645.3335	1288.6757	644.8415	**12**
6	529.2980	265.1527			511.2875	256.1474	**G**	***1207.6178***	604.3125	1190.5913	595.7993	1189.6072	595.3073	**11**
7	642.3821	321.6947			624.3715	312.6894	**L**	***1150.5963***	575.8018	1133.5698	567.2885	1132.5858	566.7965	**10**
8	713.4192	357.2132			695.4087	348.2080	**A**	***1037.5123***	519.2598	1020.4857	510.7465	1019.5017	510.2545	**9**
9	812.4876	406.7475			794.4771	397.7422	**V**	***966.4752***	483.7412	949.4486	475.2279	948.4646	474.7359	**8**
10	**899.5197**	450.2635			881.5091	441.2582	**S**	***867.4068***	434.2070	850.3802	425.6937	849.3962	425.2017	**7**
11	**1027.5782**	514.2928	1010.5517	505.7795	1009.5677	505.2875	**Q**	***780.3747***	390.6910	763.3482	382.1777	762.3642	381.6857	**6**
12	**1141.6212**	571.3142	1124.5946	562.8009	1123.6106	562.3089	**N**	***652.3161***	326.6617	635.2896	318.1484	634.3056	317.6564	**5**
13	1238.6739	619.8406	1221.6474	611.3273	1220.6634	610.8353	**P**	***538.2732***	269.6402	521.2467	261.1270	520.2627	260.6350	**4**
14	**1375.7328**	688.3701	1358.7063	679.8568	1357.7223	679.3648	**H**	***441.2205***	221.1139	424.1939	212.6006	423.2099	212.1086	**3**
15	**1504.7754**	752.8914	1487.7489	744.3781	1486.7649	743.8861	**E**	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
16							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of TTGLVGLAVSQNPHER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.8	1677.8798	-0.3571	TTGLVGLAVSQNPHER
6.1	1677.8322	-0.3095	TDSKLPEIQEHPER
4.6	1675.9482	1.5746	RPGAEINADLLRPVR
4.2	1678.8461	-1.3233	QAPLKPHCLSAETER
2.7	1677.7814	-0.2587	ELGLCDRCLSLDER
2.1	1677.6615	-0.1388	EGWGSGEDGEAGGGGGSGR
1.1	1677.7569	-0.2342	FTFRCSDGINFSER

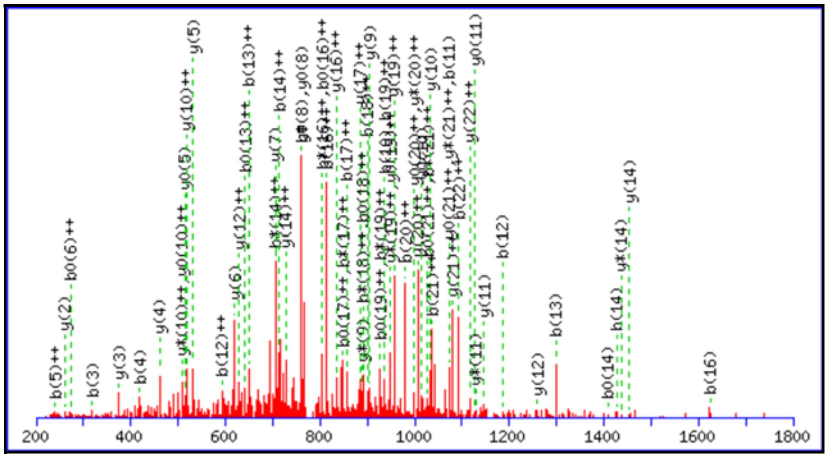
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAFTGSTDVGHLIQQASSASNLK**
Found in **gi|189538766|ref|XP_001921117.1|**, PREDICTED: similar to mitogen-activated protein kinase-activated protein kinase 5 [Danio rerio]

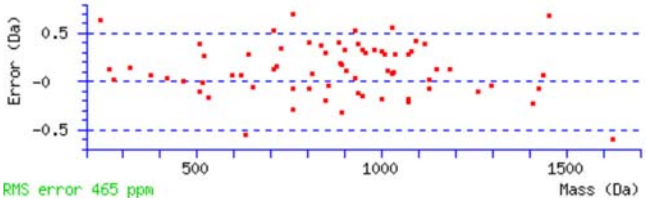
Match to Query 79710: 2331.082725 from(778.034851,3+) index(20350)
Data file TCDD_0530.dta

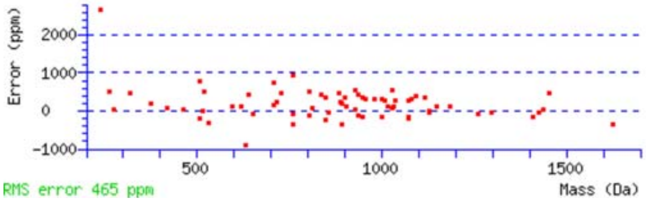
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2330.1866
Ions Score: 59 **Expect:** 0.00021
Matches : 70/226 fragment ions using 134 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					**V**							**23**
2	171.1128	86.0600					**A**	2232.1255	1116.5664	2215.0990	1108.0531	2214.1149	1107.5611	**22**
3	**318.1812**	159.5942					**F**	2161.0884	1081.0478	2144.0618	1072.5346	2143.0778	1072.0425	**21**
4	**419.2289**	210.1181			401.2183	201.1128	**T**	2014.0200	1007.5136	1996.9934	999.0004	1996.0094	998.5083	**20**
5	476.2504	***238.6288***			458.2398	229.6235	**G**	1912.9723	956.9898	1895.9457	948.4765	1894.9617	947.9845	**19**
6	563.2824	282.1448			545.2718	273.1396	**S**	1855.9508	928.4791	1838.9243	919.9658	1837.9403	919.4738	**18**
7	664.3301	332.6687			646.3195	323.6634	**T**	1768.9188	884.9630	1751.8923	876.4498	1750.9082	875.9578	**17**
8	779.3570	390.1821			761.3464	381.1769	**D**	1667.8711	834.4392	1650.8446	825.9259	1649.8606	825.4339	**16**
9	878.4254	439.7164			860.4149	430.7111	**V**	1552.8442	776.9257	1535.8176	768.4125	1534.8336	767.9204	**15**
10	**935.4469**	468.2271			917.4363	459.2218	**G**	**1453.7758**	727.3915	1436.7492	718.8782	1435.7652	718.3862	**14**
11	**1072.5058**	536.7565			1054.4952	527.7513	**H**	1396.7543	698.8808	1379.7278	690.3675	1378.7437	689.8755	**13**
12	**1185.5899**	***593.2986***			1167.5793	584.2933	**L**	**1259.6954**	630.3513	1242.6688	621.8381	1241.6848	621.3461	**12**
13	**1298.6739**	***649.8406***			1280.6634	640.8353	**I**	**1146.6113**	573.8093	1129.5848	565.2960	1128.6008	564.8040	**11**
14	**1426.7325**	***713.8699***	1409.7060	705.3566	1408.7219	704.8646	**Q**	**1033.5273**	517.2673	1016.5007	508.7540	1015.5167	508.2620	**10**
15	1554.7911	777.8992	1537.7645	769.3859	1536.7805	768.8939	**Q**	**905.4687**	453.2380	888.4421	444.7247	887.4581	444.2327	**9**
16	**1625.8282**	***813.4177***	1608.8017	804.9045	1607.8176	804.4125	**A**	777.4101	389.2087	760.3836	380.6954	759.3995	380.2034	**8**
17	1712.8602	***856.9338***	1695.8337	848.4205	1694.8497	847.9285	**S**	**706.3730**	353.6901	689.3464	345.1769	688.3624	344.6849	**7**
18	1799.8923	***900.4498***	1782.8657	891.9365	1781.8817	891.4445	**S**	**619.3410**	310.1741	602.3144	301.6608	601.3304	301.1688	**6**
19	1870.9294	***935.9683***	1853.9028	927.4550	1852.9188	926.9630	**A**	**532.3089**	266.6581	515.2824	258.1448	514.2984	257.6528	**5**
20	1957.9614	***979.4843***	1940.9348	970.9711	1939.9508	970.4791	**S**	**461.2718**	231.1395	444.2453	222.6263	443.2613	222.1343	**4**
21	2072.0043	***1036.5058***	2054.9778	1027.9925	2053.9938	1027.5005	**N**	**374.2398**	187.6235	357.2132	179.1103			**3**
22	2185.0884	***1093.0478***	2168.0618	1084.5346	2167.0778	1084.0425	**L**	**260.1969**	130.6021	243.1703	122.0888			**2**
23							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of VAFTGSTDVGHLIQQASSASNLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.5	2330.1866	0.8961	VAFTGSTDVGHLIQQASSASNLK
9.6	2331.9011	-0.8184	QECQCGTGGICNQTTGECVCK
8.0	2330.1729	0.9098	CESVLSIWSSGFFSNRSIALK
7.1	2331.0506	0.0321	MEGLLDTEEFCCSICLDLLK
6.7	2331.1324	-0.0497	GNPADFLWWPEAELAFNNLK
5.5	2331.2297	-0.1470	FRSGFLICFLISLSSEASVQK
5.3	2331.1053	-0.0226	TFELQSTNITFTNMVSVDER
4.8	2331.0506	0.0321	MEGLLDTEEFCCSICLDLLK
4.8	2328.9951	2.0876	YSCHASNDVGKDSCSTEVSVK
4.5	2333.0924	-2.0097	FRQIWTEHSDLNTSEDLDK

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

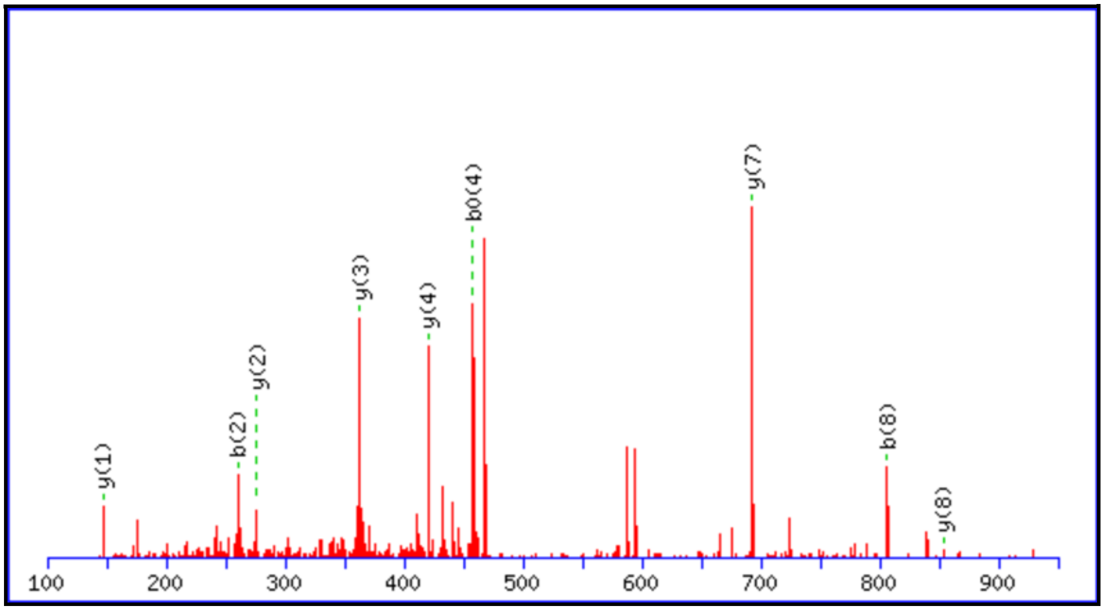
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VCTDGGSEK**
Found in **gi|125815320|ref|XP_697137.2|**, PREDICTED: similar to Cystine/glutamate transporter (Amino acid transport system xc-) (xCT) (Solute carrier family 7 member 11) (Calcium channel blocker resistance protein CCBR1) [Danio rerio]

Match to Query 7340: 951.282724 from(476.648638,2+) index(108604)
Data file TCDD_0530.dta

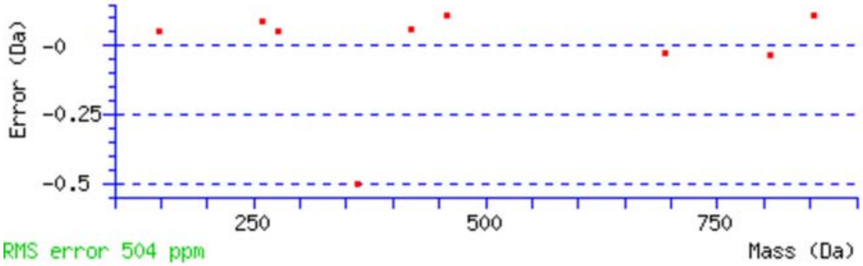
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

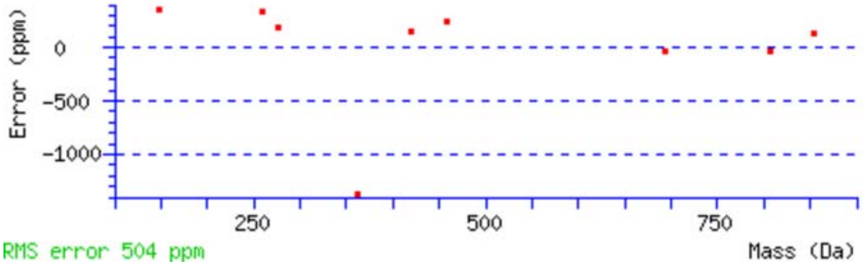


Monoisotopic mass of neutral peptide Mr(calc): 951.3968
Variable modifications:
C2 : Carbamidomethyl (C)
Ions Score: 45 **Expect:** 0.011
Matches : 9/74 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415			V							9
2	**260.1063**	130.5568			C	***853.3356***	427.1715	836.3091	418.6582	835.3251	418.1662	8
3	361.1540	181.0806	343.1435	172.0754	T	***693.3050***	347.1561	676.2784	338.6429	675.2944	338.1508	7
4	476.1810	238.5941	458.1704	229.5888	D	592.2573	296.6323	575.2307	288.1190	574.2467	287.6270	6
5	533.2024	267.1049	515.1919	258.0996	G	477.2304	239.1188	460.2038	230.6055	459.2198	230.1135	5
6	590.2239	295.6156	572.2133	286.6103	G	***420.2089***	210.6081	403.1823	202.0948	402.1983	201.6028	4
7	677.2559	339.1316	659.2454	330.1263	S	***363.1874***	182.0974	346.1609	173.5841	345.1769	173.0921	3
8	**806.2985**	403.6529	788.2879	394.6476	E	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	2

9					**K**	*147.1128*	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of VCTDGGSEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.6	951.3968	-0.1141	VCTDGGSEK
25.9	952.4874	-1.2047	FLLCCLK
24.6	952.4688	-1.1861	FICSENLK
20.2	951.4154	-0.1327	DSCGLCLK
19.0	951.4154	-0.1327	VCEKCEK
18.6	952.4721	-1.1894	MKMSLSEK
18.4	951.4518	-0.1690	DKTMNCIK
18.4	951.5753	-0.2926	ELHSLLLK
18.4	951.4661	-0.1834	FSQSENLK
18.4	951.5211	-0.2384	KYACNLLK

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

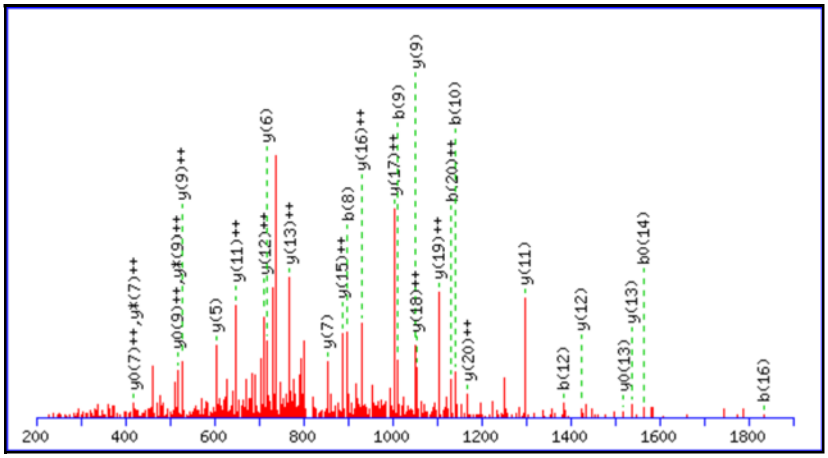
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VETVFSHVLKPFPTHITQAER**
Found in **gi|37497110|ref|NP_922916.1|**, ribophorin I [Danio rerio]

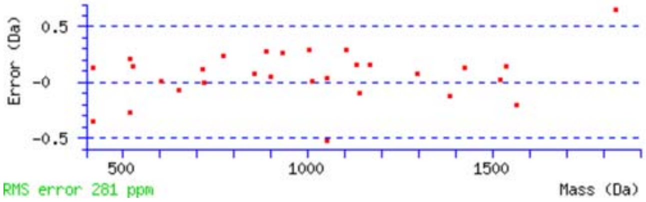
Match to Query 88984: 2435.792724 from(812.938184,3+) index(138078)
Data file TCDD_0530.dta

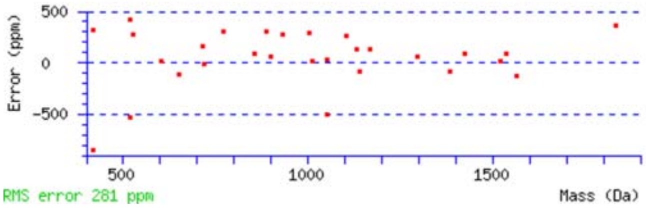
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2435.2961
Ions Score: 53 **Expect:** 0.00075
Matches : 29/218 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							21
2	229.1183	115.0628			211.1077	106.0575	E	2337.2350	1169.1211	2320.2084	1160.6079	2319.2244	1160.1159	20
3	330.1660	165.5866			312.1554	156.5813	T	2208.1924	1104.5998	2191.1659	1096.0866	2190.1818	1095.5946	19
4	429.2344	215.1208			411.2238	206.1155	V	2107.1447	1054.0760	2090.1182	1045.5627	2089.1342	1045.0707	18
5	576.3028	288.6550			558.2922	279.6498	F	2008.0763	1004.5418	1991.0498	996.0285	1990.0657	995.5365	17
6	663.3348	332.1710			645.3243	323.1658	S	1861.0079	931.0076	1843.9813	922.4943	1842.9973	922.0023	16
7	800.3937	400.7005			782.3832	391.6952	H	1773.9759	887.4916	1756.9493	878.9783	1755.9653	878.4863	15
8	**899.4621**	450.2347			881.4516	441.2294	V	1636.9170	818.9621	1619.8904	810.4488	1618.9064	809.9568	14
9	**1012.5462**	506.7767			994.5356	497.7715	L	***1537.8485***	769.4279	1520.8220	760.9146	1519.8380	760.4226	13
10	**1140.6412**	570.8242	1123.6146	562.3109	1122.6306	561.8189	K	***1424.7645***	712.8859	1407.7379	704.3726	1406.7539	703.8806	12
11	1237.6939	619.3506	1220.6674	610.8373	1219.6834	610.3453	P	***1296.6695***	648.8384	1279.6430	640.3251	1278.6589	639.8331	11
12	**1384.7623**	692.8848	1367.7358	684.3715	1366.7518	683.8795	F	1199.6167	600.3120	1182.5902	591.7987	1181.6062	591.3067	10
13	1481.8151	741.4112	1464.7886	732.8979	1463.8045	732.4059	P	***1052.5483***	526.7778	1035.5218	518.2645	1034.5378	517.7725	9
14	1582.8628	791.9350	1565.8362	783.4218	1564.8522	782.9298	T	955.4956	478.2514	938.4690	469.7381	937.4850	469.2461	8
15	1719.9217	860.4645	1702.8952	851.9512	1701.9111	851.4592	H	***854.4479***	427.7276	837.4213	419.2143	836.4373	418.7223	7
16	**1833.0058**	917.0065	1815.9792	908.4932	1814.9952	908.0012	I	***717.3890***	359.1981	700.3624	350.6849	699.3784	350.1928	6
17	1934.0534	967.5304	1917.0269	959.0171	1916.0429	958.5251	T	***604.3049***	302.6561	587.2784	294.1428	586.2944	293.6508	5
18	2062.1120	1031.5597	2045.0855	1023.0464	2044.1015	1022.5544	Q	503.2572	252.1323	486.2307	243.6190	485.2467	243.1270	4
19	2133.1491	1067.0782	2116.1226	1058.5649	2115.1386	1058.0729	A	375.1987	188.1030	358.1721	179.5897	357.1881	179.0977	3
20	2262.1917	1131.5995	2245.1652	1123.0862	2244.1812	1122.5942	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
21							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VETVFSHVLKPFPTHITQAER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.3	2435.2961	0.4966	VETVFSHVLKPFPTHITQAER
4.8	2438.2765	-2.4838	QTPANEQSSQPQELKATLSLLR
4.4	2438.1471	-2.3544	TQSSGPCHSFHAQPLSLPCSLK
4.2	2437.1002	-1.3075	EMCGISALPPGNASPPEGAGSPGER
4.0	2436.1202	-0.3275	VGDHSSPYGLQEYRPQMDMVK
3.3	2437.1123	-1.3196	MSSCPHVSPAGILCVADQCHGLR
2.9	2435.1477	0.6451	VEVSAPFTFCGMDCFGPFVVKR
1.5	2435.0699	0.7228	GDPNCSQYYGGPELEPPTAQQK

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

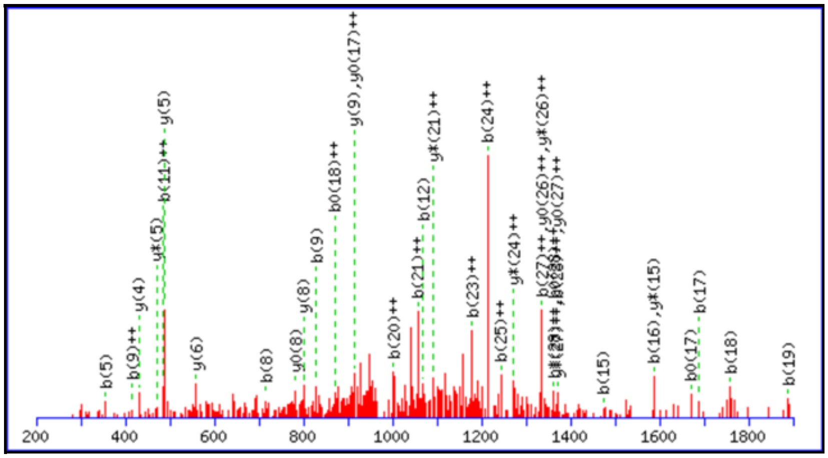
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGAGAPVYLAAVLEYLTAEILELAGNAAR**
Found in **gi|41055102|ref|NP_957367.1|**, H2A histone family, member X [Danio rerio]

Match to Query 106568: 2914.652724 from(972.558184,3+) index(16305)
Data file TCDD_0530.dta

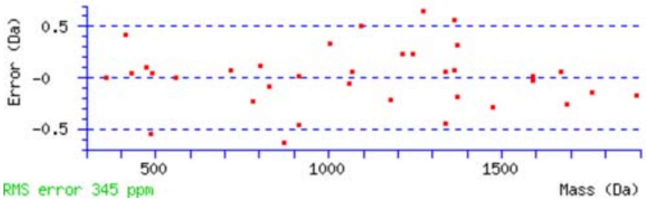
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●

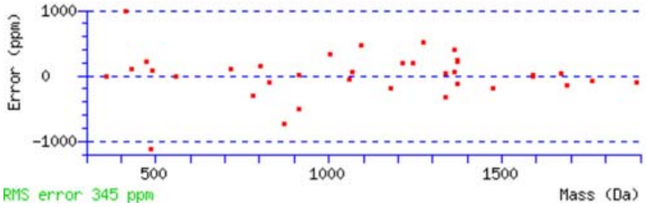


Monoisotopic mass of neutral peptide Mr(calc): 2914.5804
Ions Score: 41 **Expect:** 0.01
Matches : 37/246 fragment ions using 80 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							29
2	157.0972	79.0522					G	2816.5193	1408.7633	2799.4927	1400.2500	2798.5087	1399.7580	28
3	228.1343	114.5708					A	2759.4978	1380.2525	2742.4713	1371.7393	2741.4872	1371.2473	27
4	285.1557	143.0815					G	2688.4607	1344.7340	2671.4341	1336.2207	2670.4501	1335.7287	26
5	***356.1928***	178.6001					A	2631.4392	1316.2233	2614.4127	1307.7100	2613.4287	1307.2180	25
6	453.2456	227.1264					P	2560.4021	1280.7047	2543.3756	1272.1914	2542.3916	1271.6994	24
7	552.3140	276.6607					V	2463.3494	1232.1783	2446.3228	1223.6650	2445.3388	1223.1730	23
8	***715.3774***	358.1923					Y	2364.2809	1182.6441	2347.2544	1174.1308	2346.2704	1173.6388	22
9	***828.4614***	***414.7343***					L	2201.2176	1101.1124	2184.1911	1092.5992	2183.2070	1092.1072	21
10	899.4985	450.2529					A	2088.1335	1044.5704	2071.1070	1036.0571	2070.1230	1035.5651	20
11	970.5356	***485.7715***					A	2017.0964	1009.0519	2000.0699	1000.5386	1999.0859	1000.0466	19
12	***1069.6041***	535.3057					V	1946.0593	973.5333	1929.0328	965.0200	1928.0488	964.5280	18
13	1182.6881	591.8477					L	1846.9909	923.9991	1829.9644	915.4858	1828.9803	914.9938	17
14	1311.7307	656.3690			1293.7202	647.3637	E	1733.9068	867.4571	1716.8803	858.9438	1715.8963	858.4518	16
15	***1474.7940***	737.9007			1456.7835	728.8954	Y	1604.8642	802.9358	1587.8377	794.4225	1586.8537	793.9305	15
16	***1587.8781***	794.4427			1569.8675	785.4374	L	1441.8009	721.4041	1424.7744	712.8908	1423.7904	712.3988	14
17	***1688.9258***	844.9665			1670.9152	835.9612	T	1328.7169	664.8621	1311.6903	656.3488	1310.7063	655.8568	13
18	***1759.9629***	880.4851			1741.9523	871.4798	A	1227.6692	614.3382	1210.6426	605.8250	1209.6586	605.3329	12
19	***1889.0055***	945.0064			1870.9949	936.0011	E	1156.6321	578.8197	1139.6055	570.3064	1138.6215	569.8144	11
20	2002.0896	***1001.5484***			1984.0790	992.5431	I	1027.5895	514.2984	1010.5629	505.7851	1009.5789	505.2931	10
21	2115.1736	***1058.0904***			2097.1631	1049.0852	L	**914.5054**	457.7563	897.4789	449.2431	896.4948	448.7511	9
22	2244.2162	1122.6117			2226.2057	1113.6065	E	**801.4213**	401.2143	784.3948	392.7010	783.4108	392.2090	8
23	2357.3003	***1179.1538***			2339.2897	1170.1485	L	672.3787	336.6930	655.3522	328.1797			7
24	2428.3374	***1214.6723***			2410.3268	1205.6671	A	**559.2947**	280.1510	542.2681	271.6377			6

25	2485.3589	***1243.1831***			2467.3483	1234.1778	**G**	**488.2576**	244.6324	471.2310	236.1191			**5**
26	2599.4018	1300.2045	2582.3752	1291.6913	2581.3912	1291.1992	**N**	**431.2361**	216.1217	414.2096	207.6084			**4**
27	2670.4389	***1335.7231***	2653.4123	1327.2098	2652.4283	1326.7178	**A**	317.1932	159.1002	300.1666	150.5870			**3**
28	2741.4760	***1371.2416***	2724.4495	1362.7284	2723.4654	1362.2364	**A**	246.1561	123.5817	229.1295	115.0684			**2**
29							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of VGAGAPVYLAAVLEYLTAEILELAGNAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.1	2914.5804	0.0724	VGAGAPVYLAAVLEYLTAEILELAGNAAR
14.1	2914.4295	0.2232	SSDVDLPSASLKTDIQTPDASLDSPDLK
6.3	2915.2688	-0.6161	MFCSFVFICFCCSCLFGVFADSGVVK
2.5	2915.3306	-0.6778	QYPVALMCDVEKMFHQFHVDHADR
2.2	2912.4226	2.2302	ELDLSENNLGDFGVKLLSAGLEDPHCK
2.0	2916.4480	-1.7953	FPDKHVFSDLEIVPDHEPVLNNMPK
1.9	2915.2688	-0.6161	MFCSFVFICFCCSCLFGVFADSGVVK
1.9	2915.2688	-0.6161	MFCSFVFICFCCSCLFGVFADSGVVK
1.9	2915.2688	-0.6161	MFCSFVFICFCCSCLFGVFADSGVVK
0.7	2916.3283	-1.6756	KTIVCFAQHPCFSNESHENQAENVK

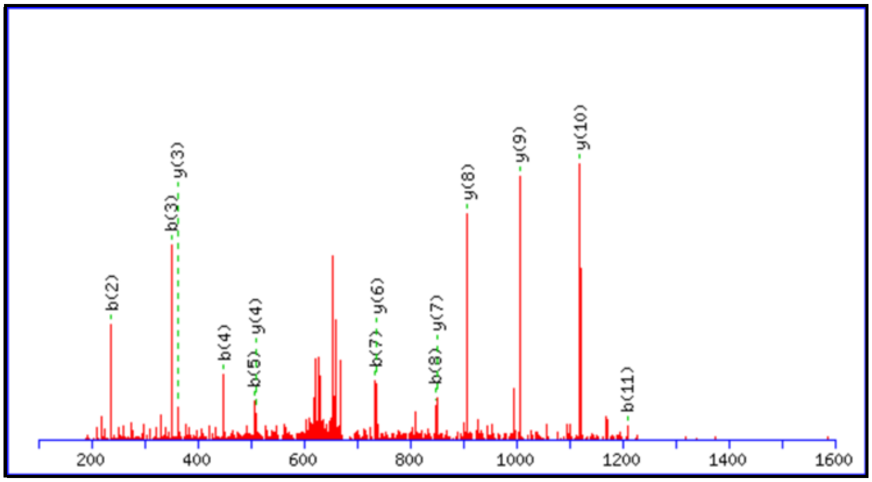
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VHLVGIDIFTNK**
Found in **gi|47085971|ref|NP_998350.1|**, eukaryotic translation initiation factor 5A [Danio rerio]

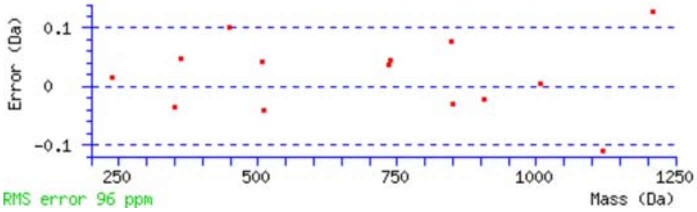
Match to Query 19008: 1354.702724 from(678.358638,2+) index(128942)
Data file TCDD_0530.dta

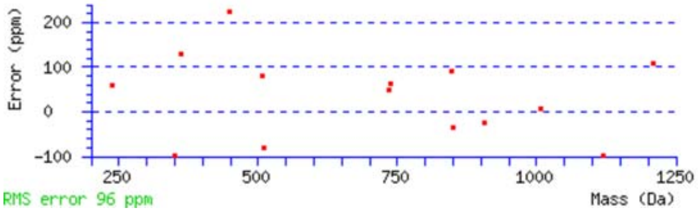
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1354.7609
Ions Score: 54 **Expect:** 0.0011
Matches : 14/96 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							12
2	***237.1346***	119.0709					H	1256.6997	628.8535	1239.6732	620.3402	1238.6892	619.8482	11
3	***350.2187***	175.6130					L	***1119.6408***	560.3241	1102.6143	551.8108	1101.6303	551.3188	10
4	***449.2871***	225.1472					V	***1006.5568***	503.7820	989.5302	495.2688	988.5462	494.7767	9
5	***506.3085***	253.6579					G	***907.4884***	454.2478	890.4618	445.7345	889.4778	445.2425	8
6	619.3926	310.1999					I	***850.4669***	425.7371	833.4403	417.2238	832.4563	416.7318	7
7	***734.4196***	367.7134			716.4090	358.7081	D	***737.3828***	369.1951	720.3563	360.6818	719.3723	360.1898	6
8	***847.5036***	424.2554			829.4930	415.2502	I	622.3559	311.6816	605.3293	303.1683	604.3453	302.6763	5
9	994.5720	497.7897			976.5615	488.7844	F	***509.2718***	255.1395	492.2453	246.6263	491.2613	246.1343	4
10	1095.6197	548.3135			1077.6091	539.3082	T	***362.2034***	181.6053	345.1769	173.0921	344.1928	172.6001	3
11	***1209.6626***	605.3350	1192.6361	596.8217	1191.6521	596.3297	N	261.1557	131.0815	244.1292	122.5682			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VHLVGIDIFTNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.0	1354.7609	-0.0582	VHLVGIDIFTNK
8.9	1354.7027	0.0000	DINMKPTPNGIR
7.7	1354.7027	-0.0000	HVLKGQDTGCLK
7.1	1354.6737	0.0290	DYAVVMCRLGTK
5.9	1355.6391	-0.9364	VHPDSSVTLCEL
4.3	1355.6429	-0.9402	RYTTAGNSGSSAGK
4.2	1354.5823	0.1204	FDVDSACAGESVR
2.6	1356.5326	-1.8299	DCEESLNFLCQ
2.3	1356.5148	-1.8121	MECQECPEGFK
2.3	1355.6027	-0.9000	NEYAEKDCASVK

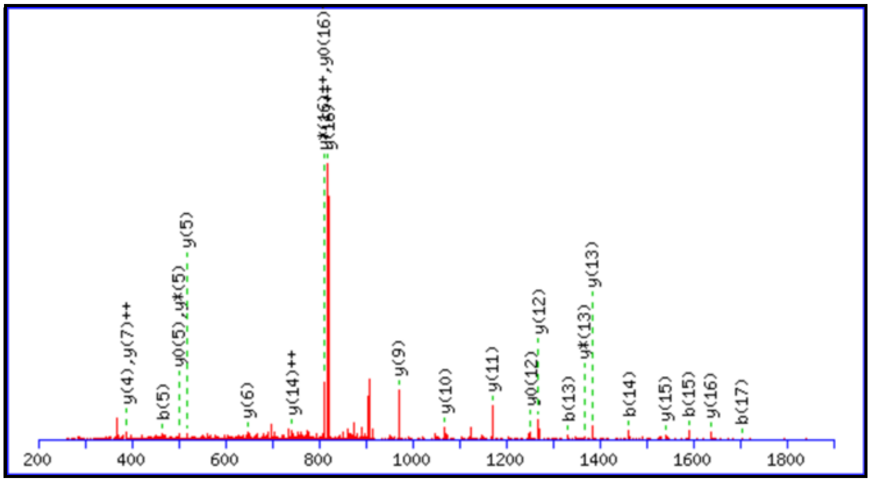
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLPGVDVTVGHEEEQGGK**
Found in **gi|62955301|ref|NP_001017662.1|**, hypothetical protein LOC550355 [Danio rerio]

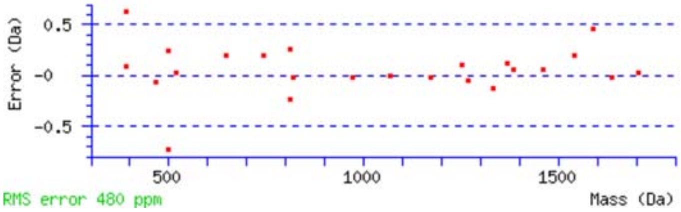
Match to Query 37936: 1849.322724 from(925.668638,2+) index(19397)
Data file TCDD_0530.dta

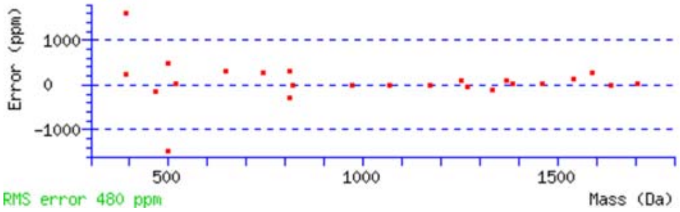
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1848.9218
Ions Score: 53 **Expect:** 0.0011
Matches : 24/158 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					**V**							**18**
2	213.1598	107.0835					**L**	1750.8606	875.9339	1733.8341	867.4207	1732.8501	866.9287	**17**
3	310.2125	155.6099					**P**	***1637.7766***	819.3919	1620.7500	810.8786	1619.7660	810.3866	**16**
4	367.2340	184.1206					**G**	***1540.7238***	770.8655	1523.6972	762.3523	1522.7132	761.8603	**15**
5	**466.3024**	233.6548					**V**	1483.7023	742.3548	1466.6758	733.8415	1465.6918	733.3495	**14**
6	581.3293	291.1683			563.3188	282.1630	**D**	***1384.6339***	692.8206	1367.6074	684.3073	1366.6234	683.8153	**13**
7	680.3978	340.7025			662.3872	331.6972	**V**	***1269.6070***	635.3071	1252.5804	626.7938	1251.5964	626.3018	**12**
8	781.4454	391.2264			763.4349	382.2211	**T**	***1170.5386***	585.7729	1153.5120	577.2596	1152.5280	576.7676	**11**
9	880.5138	440.7606			862.5033	431.7553	**V**	***1069.4909***	535.2491	1052.4643	526.7358	1051.4803	526.2438	**10**
10	937.5353	469.2713			919.5247	460.2660	**G**	***970.4225***	485.7149	953.3959	477.2016	952.4119	476.7096	**9**
11	1074.5942	537.8007			1056.5837	528.7955	**H**	913.4010	457.2041	896.3745	448.6909	895.3904	448.1989	**8**
12	1203.6368	602.3220			1185.6263	593.3168	**E**	776.3421	388.6747	759.3155	380.1614	758.3315	379.6694	**7**
13	**1332.6794**	666.8433			1314.6688	657.8381	**E**	***647.2995***	324.1534	630.2729	315.6401	629.2889	315.1481	**6**
14	**1461.7220**	731.3646			1443.7114	722.3594	**E**	***518.2569***	259.6321	501.2304	251.1188	500.2463	250.6268	**5**
15	**1589.7806**	795.3939	1572.7540	786.8807	1571.7700	786.3886	**Q**	***389.2143***	195.1108	372.1878	186.5975			**4**
16	1646.8020	823.9047	1629.7755	815.3914	1628.7915	814.8994	**G**	261.1557	131.0815	244.1292	122.5682			**3**
17	**1703.8235**	852.4154	1686.7970	843.9021	1685.8129	843.4101	**G**	204.1343	102.5708	187.1077	94.0575			**2**
18							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of VLPGVDVTVGHEEEQGGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.2	1848.9218	0.4009	VLPGVDVTVGHEEEQGGK
3.0	1848.8936	0.4291	LVMKPIHECTYCDIK
3.0	1849.9760	-0.6533	FCQFINEQSPVKLLK
2.9	1850.0010	-0.6783	DVTREAATNGVLLHLNK
2.9	1850.8745	-1.5518	IDSSDTTVSLNEDTINK
2.8	1850.8283	-1.5056	NDDHVVGVTDNPPTEDK
2.8	1848.8936	0.4291	LVMKPIHECTYCDIK
2.7	1850.8152	-1.4925	VCWVCNGSGSRLNDER
1.8	1846.9247	2.3980	EEKCTYELSAVLIHR
1.4	1849.9648	-0.6421	ELFQPFGKVVECDIVK

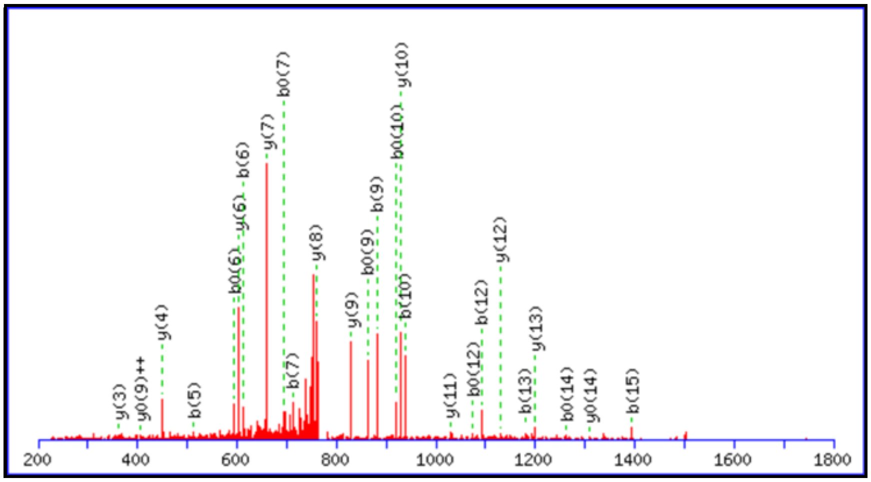
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLQATVVAVGPGSTNK**
Found in **gi|55926092|ref|NP_571601.1|**, heat shock 10kD protein 1 (chaperonin 10) [Danio rerio]

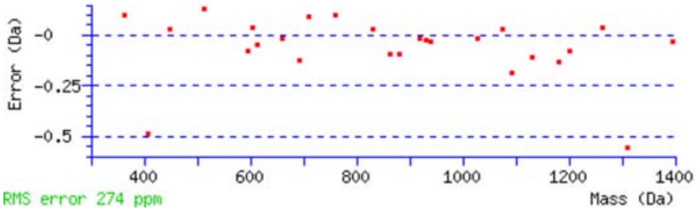
Match to Query 24348: 1539.542724 from(770.778638,2+) index(7983)
Data file TCDD_0530.dta

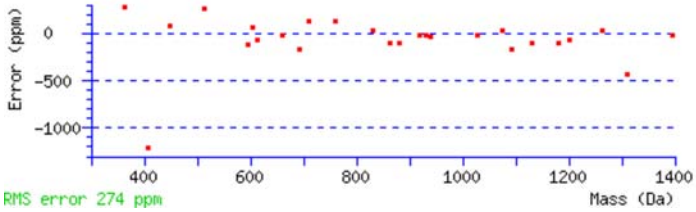
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1539.8621
Ions Score: 48 **Expect:** 0.0038
Matches : 26/164 fragment ions using 65 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					**V**							**16**
2	213.1598	107.0835					**L**	1441.8009	721.4041	1424.7744	712.8908	1423.7904	712.3988	**15**
3	341.2183	171.1128	324.1918	162.5995			**Q**	1328.7169	664.8621	1311.6903	656.3488	1310.7063	655.8568	**14**
4	412.2554	206.6314	395.2289	198.1181			**A**	***1200.6583***	600.8328	1183.6317	592.3195	1182.6477	591.8275	**13**
5	**513.3031**	257.1552	496.2766	248.6419	495.2926	248.1499	**T**	***1129.6212***	565.3142	1112.5946	556.8009	1111.6106	556.3089	**12**
6	**612.3715**	306.6894	595.3450	298.1761	594.3610	297.6841	**V**	***1028.5735***	514.7904	1011.5469	506.2771	1010.5629	505.7851	**11**
7	**711.4400**	356.2236	694.4134	347.7103	693.4294	347.2183	**V**	***929.5051***	465.2562	912.4785	456.7429	911.4945	456.2509	**10**
8	782.4771	391.7422	765.4505	383.2289	764.4665	382.7369	**A**	***830.4367***	415.7220	813.4101	407.2087	812.4261	406.7167	**9**
9	**881.5455**	441.2764	864.5189	432.7631	863.5349	432.2711	**V**	***759.3995***	380.2034	742.3730	371.6901	741.3890	371.1981	**8**
10	**938.5669**	469.7871	921.5404	461.2738	920.5564	460.7818	**G**	***660.3311***	330.6692	643.3046	322.1559	642.3206	321.6639	**7**
11	1035.6197	518.3135	1018.5932	509.8002	1017.6091	509.3082	**P**	***603.3097***	302.1585	586.2831	293.6452	585.2991	293.1532	**6**
12	**1092.6412**	546.8242	1075.6146	538.3109	1074.6306	537.8189	**G**	506.2569	253.6321	489.2304	245.1188	488.2463	244.6268	**5**
13	**1179.6732**	590.3402	1162.6467	581.8270	1161.6626	581.3350	**S**	***449.2354***	225.1214	432.2089	216.6081	431.2249	216.1161	**4**
14	1280.7209	640.8641	1263.6943	632.3508	1262.7103	631.8588	**T**	***362.2034***	181.6053	345.1769	173.0921	344.1928	172.6001	**3**
15	**1394.7638**	697.8855	1377.7373	689.3723	1376.7532	688.8803	**N**	261.1557	131.0815	244.1292	122.5682			**2**
16							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of VLQATVVAVGPGSTNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.4	1539.8621	-0.3194	VLQATVVAVGPGSTNK
24.6	1539.8079	-0.2652	VLAATTCTPAHLNTK
15.4	1539.7351	-0.1924	EESCYVTAGNALRK
12.1	1539.7893	-0.2466	TSITSLGTSFRDQK
6.9	1537.7493	1.7934	DIRQFVAACSVCAR
5.8	1538.8417	0.7011	TTGSGAQEPVVPKLR
5.0	1538.9396	0.6032	VLKVLSGALANVDIK
4.6	1539.7834	-0.2407	TFITFSALFSHNR
4.2	1537.7922	1.7505	YLECSALTQRGLK
3.6	1537.6388	1.9039	DADNPESSQMTICK

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

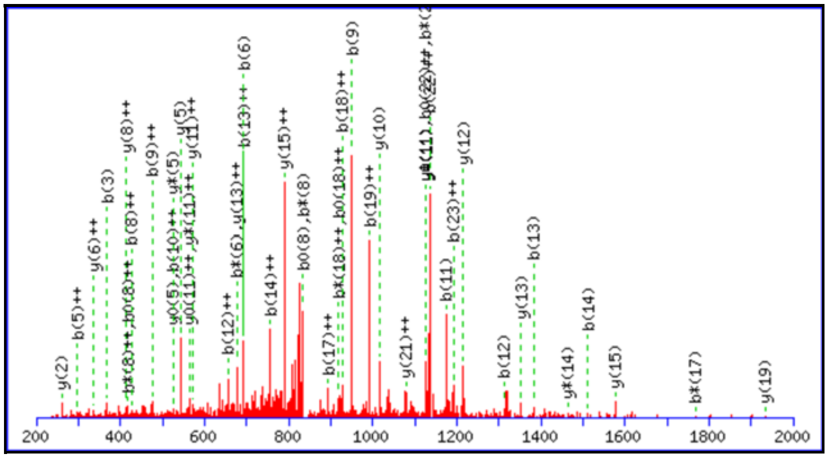
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLRPQVSAVPQHAQGESAEPADLK**
Found in **gi|112363126|ref|NP_001036210.1|**, dynein, cytoplasmic 1, heavy chain 1 [Danio rerio]

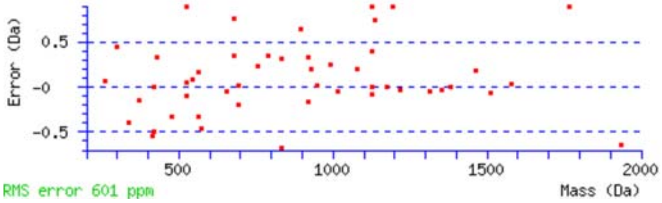
Match to Query 101044: 2527.162725 from(843.394851,3+) index(36511)
Data file TCDD_0531.dta

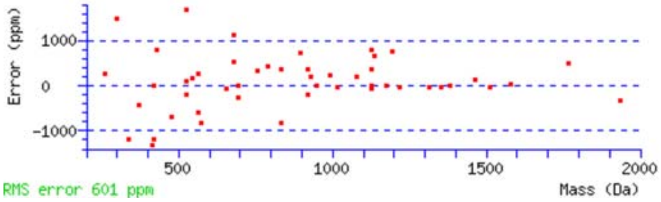
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2526.3190
Ions Score: 41 **Expect:** 0.013
Matches : 49/256 fragment ions using 107 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415					V							24
2	213.1598	107.0835					L	2428.2579	1214.6326	2411.2314	1206.1193	2410.2473	1205.6273	23
3	**369.2609**	185.1341	352.2343	176.6208			R	2315.1738	1158.0906	2298.1473	1149.5773	2297.1633	1149.0853	22
4	466.3136	233.6605	449.2871	225.1472			P	2159.0727	1080.0400	2142.0462	1071.5267	2141.0622	1071.0347	21
5	594.3722	***297.6897***	577.3457	289.1765			Q	2062.0200	1031.5136	2044.9934	1023.0004	2044.0094	1022.5083	20
6	**693.4406**	347.2239	676.4141	338.7107			V	**1933.9614**	967.4843	1916.9348	958.9711	1915.9508	958.4791	19
7	780.4726	390.7400	763.4461	382.2267	762.4621	381.7347	S	1834.8930	917.9501	1817.8664	909.4369	1816.8824	908.9448	18
8	851.5098	***426.2585***	834.4832	417.7452	833.4992	417.2532	A	1747.8610	874.4341	1730.8344	865.9208	1729.8504	865.4288	17
9	**950.5782**	***475.7927***	933.5516	467.2795	932.5676	466.7874	V	1676.8238	838.9156	1659.7973	830.4023	1658.8133	829.9103	16
10	1047.6309	***524.3191***	1030.6044	515.8058	1029.6204	515.3138	P	**1577.7554**	789.3814	1560.7289	780.8681	1559.7449	780.3761	15
11	**1175.6895**	588.3484	1158.6630	579.8351	1157.6790	579.3431	Q	1480.7027	740.8550	1463.6761	732.3417	1462.6921	731.8497	14
12	**1312.7484**	***656.8779***	1295.7219	648.3646	1294.7379	647.8726	H	**1352.6441**	676.8257	1335.6175	668.3124	1334.6335	667.8204	13
13	**1383.7855**	***692.3964***	1366.7590	683.8831	1365.7750	683.3911	A	**1215.5852**	608.2962	1198.5586	599.7830	1197.5746	599.2909	12
14	**1511.8441**	***756.4257***	1494.8176	747.9124	1493.8336	747.4204	Q	1144.5481	572.7777	1127.5215	564.2644	1126.5375	563.7724	11
15	1568.8656	784.9364	1551.8390	776.4232	1550.8550	775.9311	G	**1016.4895**	508.7484	999.4629	500.2351	998.4789	499.7431	10
16	1697.9082	849.4577	1680.8816	840.9445	1679.8976	840.4524	E	959.4680	480.2376	942.4415	471.7244	941.4575	471.2324	9
17	1784.9402	***892.9737***	1767.9137	884.4605	1766.9296	883.9685	S	830.4254	415.7164	813.3989	407.2031	812.4149	406.7111	8
18	1855.9773	***928.4923***	1838.9508	919.9790	1837.9668	919.4870	A	743.3934	372.2003	726.3668	363.6871	725.3828	363.1951	7
19	1985.0199	***993.0136***	1967.9934	984.5003	1967.0093	984.0083	E	672.3563	336.6818	655.3297	328.1685	654.3457	327.6765	6
20	2082.0727	1041.5400	2065.0461	1033.0267	2064.0621	1032.5347	P	**543.3137**	272.1605	526.2871	263.6472	525.3031	263.1552	5
21	2153.1098	1077.0585	2136.0832	1068.5453	2135.0992	1068.0533	A	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
22	2268.1367	***1134.5720***	2251.1102	1126.0587	2250.1262	1125.5667	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
23	2381.2208	***1191.1140***	2364.1943	1182.6008	2363.2102	1182.1088	L	**260.1969**	130.6021	243.1703	122.0888			2
24							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VLRPQVSAVPQHAQGESAEPADLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.9	2526.3190	0.8437	VLRPQVSAVPQHAQGESAEPADLK
9.1	2527.0818	0.0810	CNMDHEYFGLDVPQEMSLNTK
7.9	2527.9760	-0.8132	DPCLCPVCEGCQFNGRDCGNGER
5.9	2529.0757	-1.9129	CVSCKPGFQLLDGQCQDVDECSR
5.2	2525.2081	1.9546	TAKNMTSVPGVNGSPHSALDYSHR
4.6	2526.2691	0.8936	CVYLFSFAMIFNGIADILGSFAK
4.5	2528.0939	-0.9312	NPGVIFDDQTQHNDADEEDEIK
4.5	2527.1433	0.0194	MAGSAGEWCLMESDPGVFTELIK
4.5	2529.2542	-2.0915	AGFIAQSCLAQGLSTMLANLFSMR
4.2	2526.3289	0.8338	TAEEVTQKLQIAAETEIQINAAR

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

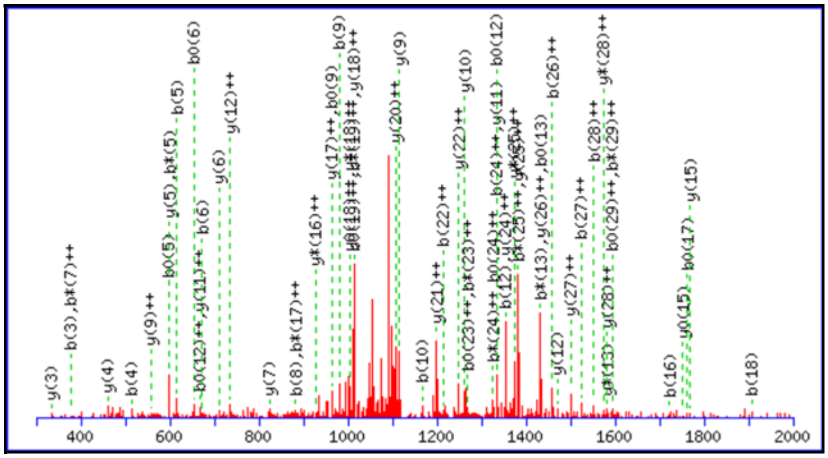
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNYHTGPIVWGEPGTNGQHAFYQLIHQGTR**
Found in **gi|21426837|ref|NP_658910.1|**, glucose phosphate isomerase b [Danio rerio]

Match to Query 132237: 3378.582723 from(1127.201517,3+) index(147366)
Data file TCDD_0530.dta

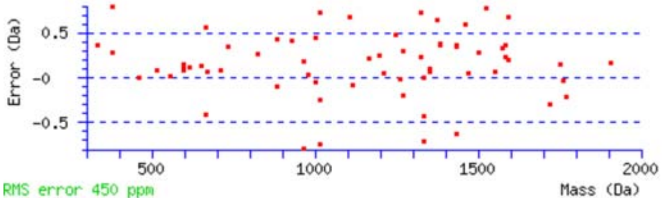
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

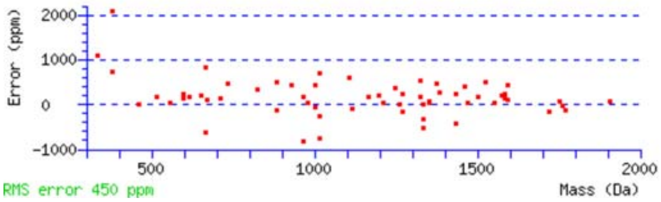


Monoisotopic mass of neutral peptide Mr(calc): 3376.6490
Ions Score: 45 **Expect:** 0.0031
Matches : 65/336 fragment ions using 133 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415					V							30
2	214.1186	107.5629	197.0921	99.0497			N	3278.5879	1639.7976	3261.5613	1631.2843	3260.5773	1630.7923	29
3	**377.1819**	189.0946	360.1554	180.5813			Y	3164.5449	1582.7761	3147.5184	1574.2628	3146.5344	1573.7708	28
4	**514.2409**	257.6241	497.2143	249.1108			H	3001.4816	1501.2444	2984.4551	1492.7312	2983.4710	1492.2392	27
5	**615.2885**	308.1479	598.2620	299.6346	597.2780	299.1426	T	2864.4227	1432.7150	2847.3961	1424.2017	2846.4121	1423.7097	26
6	**672.3100**	336.6586	655.2835	328.1454	654.2994	327.6534	G	2763.3750	1382.1911	2746.3485	1373.6779	2745.3644	1373.1859	25
7	769.3628	385.1850	752.3362	376.6717	751.3522	376.1797	P	2706.3535	1353.6804	2689.3270	1345.1671	2688.3430	1344.6751	24
8	**882.4468**	441.7271	865.4203	433.2138	864.4363	432.7218	I	2609.3008	1305.1540	2592.2742	1296.6408	2591.2902	1296.1487	23
9	**981.5152**	491.2613	964.4887	482.7480	963.5047	482.2560	V	2496.2167	1248.6120	2479.1902	1240.0987	2478.2062	1239.6067	22
10	**1167.5946**	584.3009	1150.5680	575.7876	1149.5840	575.2956	W	2397.1483	1199.0778	2380.1218	1190.5645	2379.1377	1190.0725	21
11	1224.6160	612.8116	1207.5895	604.2984	1206.6055	603.8064	G	2211.0690	1106.0381	2194.0424	1097.5249	2193.0584	1097.0329	20
12	**1353.6586**	677.3329	1336.6321	668.8197	1335.6480	668.3277	E	2154.0475	1077.5274	2137.0210	1069.0141	2136.0370	1068.5221	19
13	1450.7114	725.8593	1433.6848	717.3461	1432.7008	716.8540	P	2025.0049	1013.0061	2007.9784	1004.4928	2006.9944	1004.0008	18
14	1507.7328	754.3701	1490.7063	745.8568	1489.7223	745.3648	G	1927.9522	964.4797	1910.9256	955.9664	1909.9416	955.4744	17
15	1608.7805	804.8939	1591.7540	796.3806	1590.7700	795.8886	T	1870.9307	935.9690	1853.9042	927.4557	1852.9201	926.9637	16
16	**1722.8234**	861.9154	1705.7969	853.4021	1704.8129	852.9101	N	***1769.8830***	885.4452	1752.8565	876.9319	1751.8725	876.4399	15
17	1779.8449	890.4261	1762.8184	881.9128	1761.8343	881.4208	G	1655.8401	828.4237	1638.8136	819.9104	1637.8295	819.4184	14
18	**1907.9035**	954.4554	1890.8769	945.9421	1889.8929	945.4501	Q	1598.8186	799.9130	1581.7921	791.3997	1580.8081	790.9077	13
19	2044.9624	1022.9848	2027.9359	1014.4716	2026.9518	1013.9796	H	***1470.7601***	735.8837	1453.7335	727.3704	1452.7495	726.8784	12
20	2115.9995	1058.5034	2098.9730	1049.9901	2097.9889	1049.4981	A	***1333.7011***	667.3542	1316.6746	658.8409	1315.6906	658.3489	11
21	2263.0679	1132.0376	2246.0414	1123.5243	2245.0574	1123.0323	F	***1262.6640***	631.8357	1245.6375	623.3224	1244.6535	622.8304	10
22	2426.1313	**1213.5693**	2409.1047	1205.0560	2408.1207	1204.5640	Y	***1115.5956***	558.3014	1098.5691	549.7882	1097.5851	549.2962	9
23	2554.1898	1277.5986	2537.1633	1269.0853	2536.1793	1268.5933	Q	952.5323	476.7698	935.5057	468.2565	934.5217	467.7645	8
24	2667.2739	**1334.1406**	2650.2474	1325.6273	2649.2633	1325.1353	L	***824.4737***	412.7405	807.4472	404.2272	806.4631	403.7352	7

25	2780.3580	1390.6826	2763.3314	1382.1693	2762.3474	1381.6773	**I**	***711.3896***	356.1985	694.3631	347.6852	693.3791	347.1932	**6**
26	2917.4169	**1459.2121**	2900.3903	1450.6988	2899.4063	1450.2068	**H**	***598.3056***	299.6564	581.2790	291.1432	580.2950	290.6511	**5**
27	3045.4755	**1523.2414**	3028.4489	1514.7281	3027.4649	1514.2361	**Q**	***461.2467***	231.1270	444.2201	222.6137	443.2361	222.1217	**4**
28	3102.4969	**1551.7521**	3085.4704	1543.2388	3084.4864	1542.7468	**G**	***333.1881***	167.0977	316.1615	158.5844	315.1775	158.0924	**3**
29	3203.5446	1602.2759	3186.5180	1593.7627	3185.5340	1593.2707	**T**	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	**2**
30							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of VNYHTGPIVWGEPGTNGQHAFYQLIHQGTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.0	3376.6490	1.9337	VNYHTGPIVWGEPGTNGQHAFYQLIHQGTR
2.1	3376.3868	2.1959	APAVDCGKGHLFCWECLGDAHEPCDCETWK
1.2	3380.4260	-1.8433	HNTYCEEGITHASRCVSIWWCCPTWPST
0.7	3378.6264	-0.0437	MAVGALLAAADVDAALAACQAADSFDYKSFFAK
0.7	3380.8582	-2.2755	EADTVEEVLLEELQVFKVPVPITEILISTK
0.5	3378.7260	-0.1433	HTSTIGPVIGIILSVFVMGGMCFVCQRVVCR
0.1	3376.3868	2.1959	APAVDCGKGHLFCWECLGDAHEPCDCETWK
0.0	3380.4418	-1.8591	GGQDCGVIEVSGTWDDGNCGDIRPIICEIDM

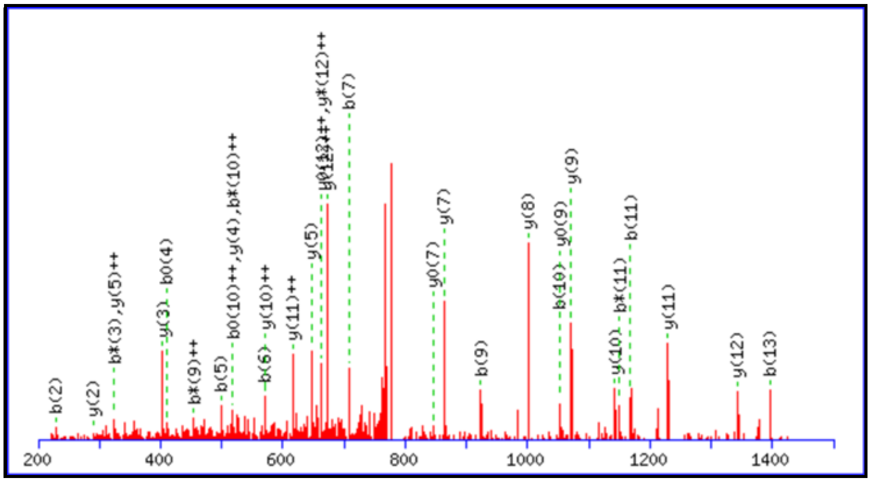
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQISAAHTDEDIDR**
Found in **gi|189517050|ref|XP_701260.3|**, PREDICTED: glycine C-acetyltransferase [Danio rerio]

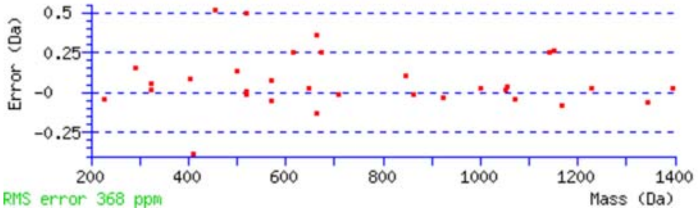
Match to Query 25148: 1569.522724 from(785.768638,2+) index(30738)
Data file TCDD_0530.dta

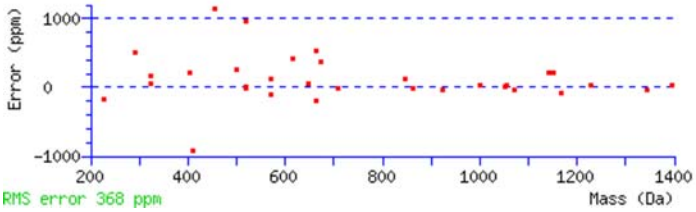
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1568.7431
Ions Score: 68 **Expect:** 4.6e-005
Matches : 32/146 fragment ions using 49 most intense peaks (help)

#	**b**	**b^{++}**	**b***	**b^{*++}**	**b^0**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^0**	**y^{0++}**	**#**
1	100.0757	50.5415					**V**							**14**
2	**228.1343**	114.5708	211.1077	106.0575			**Q**	1470.6819	735.8446	1453.6554	727.3313	1452.6714	726.8393	**13**
3	341.2183	171.1128	324.1918	162.5995			**I**	***1342.6233***	671.8153	1325.5968	663.3020	1324.6128	662.8100	**12**
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	**S**	***1229.5393***	615.2733	1212.5127	606.7600	1211.5287	606.2680	**11**
5	**499.2875**	250.1474	482.2609	241.6341	481.2769	241.1421	**A**	***1142.5073***	571.7573	1125.4807	563.2440	1124.4967	562.7520	**10**
6	**570.3246**	285.6659	553.2980	277.1527	552.3140	276.6606	**A**	***1071.4701***	536.2387	1054.4436	527.7254	1053.4596	527.2334	**9**
7	**707.3835**	354.1954	690.3570	345.6821	689.3729	345.1901	**H**	***1000.4330***	500.7202	983.4065	492.2069	982.4225	491.7149	**8**
8	808.4312	404.7192	791.4046	396.2060	790.4206	395.7139	**T**	***863.3741***	432.1907	846.3476	423.6774	845.3636	423.1854	**7**
9	**923.4581**	462.2327	906.4316	453.7194	905.4476	453.2274	**D**	762.3264	381.6669	745.2999	373.1536	744.3159	372.6616	**6**
10	**1052.5007**	526.7540	1035.4742	518.2407	1034.4901	517.7487	**E**	***647.2995***	324.1534	630.2729	315.6401	629.2889	315.1481	**5**
11	**1167.5277**	584.2675	1150.5011	575.7542	1149.5171	575.2622	**D**	***518.2569***	259.6321	501.2304	251.1188	500.2463	250.6268	**4**
12	1280.6117	640.8095	1263.5852	632.2962	1262.6012	631.8042	**I**	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	**3**
13	**1395.6387**	698.3230	1378.6121	689.8097	1377.6281	689.3177	**D**	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	**2**
14							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of VQISAAHTDEDIDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.8	1568.7431	0.7797	VQISAAHTDEDIDR
12.7	1570.8315	-1.3088	QVLTLLGVTENNDR
10.4	1569.8614	-0.3387	GDVVKAVVLDVDVDK
9.9	1568.6591	0.8637	GQTQEYTDEDVER
8.9	1568.7731	0.7496	NLLTQCMFFPVEK
8.2	1570.8077	-1.2849	AHGHAVVQDRAASPR
7.8	1569.8614	-0.3386	LNLDIGLLSLDQEK
7.8	1568.7729	0.7498	LINGPDPCSGRVER
7.5	1569.6956	-0.1729	YCVFSHEELVCK
7.1	1568.7332	0.7896	DAHPPPADLSQEHR

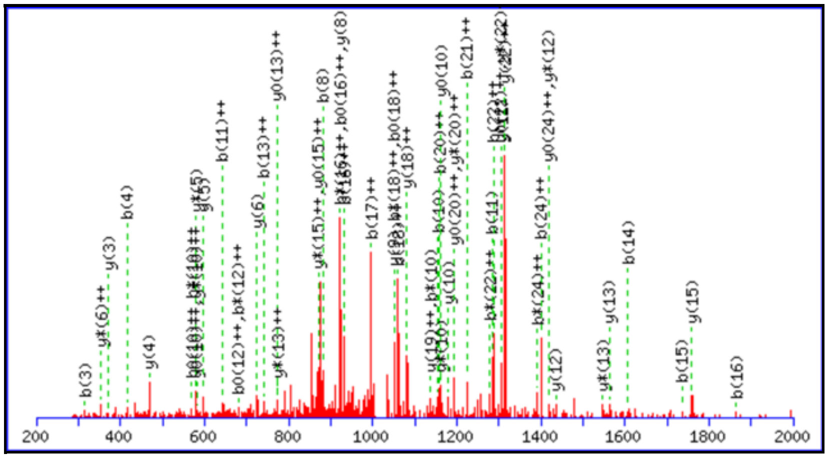
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSEVPQQIHHQPVQQQQQPTQQPQPK**
Found in **gi|57525959|ref|NP_001003533.1|**, BCL2-associated athanogene 3 [Danio rerio]

Match to Query 109896: 3043.752723 from(1015.591517,3+) index(43429)
Data file TCDD_0530.dta

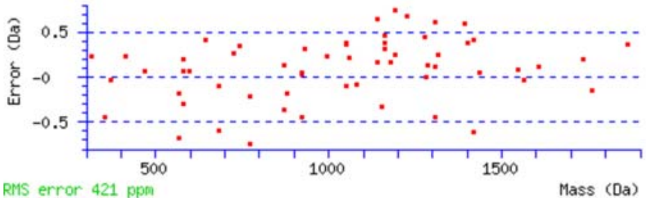
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

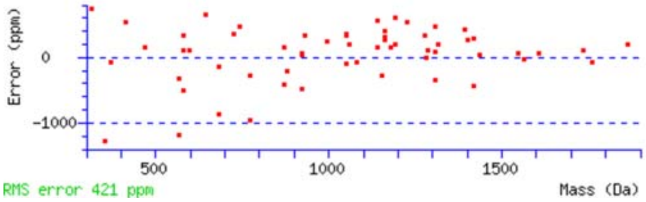


Monoisotopic mass of neutral peptide Mr(calc): 3041.5432
Ions Score: 41 **Expect:** 0.0095
Matches : 59/276 fragment ions using 100 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							26
2	187.1077	94.0575			169.0972	85.0522	S	2943.4820	1472.2446	2926.4554	1463.7314	2925.4714	1463.2394	25
3	***316.1503***	158.5788			298.1397	149.5735	E	2856.4500	1428.7286	2839.4234	1420.2153	2838.4394	1419.7233	24
4	***415.2187***	208.1130			397.2082	199.1077	V	2727.4074	1364.2073	2710.3808	1355.6941	2709.3968	1355.2020	23
5	512.2715	256.6394			494.2609	247.6341	P	2628.3390	1314.6731	2611.3124	1306.1598	2610.3284	1305.6678	22
6	640.3301	320.6687	623.3035	312.1554	622.3195	311.6634	Q	2531.2862	1266.1467	2514.2597	1257.6335	2513.2756	1257.1415	21
7	768.3886	384.6980	751.3621	376.1847	750.3781	375.6927	Q	2403.2276	1202.1174	2386.2011	1193.6042	2385.2171	1193.1122	20
8	***881.4727***	441.2400	864.4462	432.7267	863.4621	432.2347	I	2275.1690	1138.0882	2258.1425	1129.5749	2257.1585	1129.0829	19
9	1018.5316	509.7694	1001.5051	501.2562	1000.5211	500.7642	H	2162.0850	1081.5461	2145.0584	1073.0329	2144.0744	1072.5408	18
10	***1155.5905***	578.2989	1138.5640	569.7856	1137.5800	569.2936	H	2025.0261	1013.0167	2007.9995	1004.5034	2007.0155	1004.0114	17
11	***1283.6491***	**642.3282**	1266.6226	633.8149	1265.6385	633.3229	Q	1887.9672	944.4872	1870.9406	935.9739	1869.9566	935.4819	16
12	1380.7019	690.8546	1363.6753	682.3413	1362.6913	681.8493	P	***1759.9086***	880.4579	1742.8820	871.9447	1741.8980	871.4526	15
13	1479.7703	**740.3888**	1462.7437	731.8755	1461.7597	731.3835	V	1662.8558	831.9315	1645.8293	823.4183	1644.8452	822.9263	14
14	***1607.8289***	804.4181	1590.8023	795.9048	1589.8183	795.4128	Q	***1563.7874***	782.3973	1546.7609	773.8841	1545.7768	773.3921	13
15	***1735.8874***	868.4474	1718.8609	859.9341	1717.8769	859.4421	Q	***1435.7288***	718.3680	1418.7023	709.8548	1417.7183	709.3628	12
16	***1863.9460***	**932.4766**	1846.9195	923.9634	1845.9355	923.4714	Q	***1307.6702***	654.3388	1290.6437	645.8255	1289.6597	645.3335	11
17	1992.0046	**996.5059**	1974.9781	987.9927	1973.9940	987.5007	Q	***1179.6117***	590.3095	1162.5851	581.7962	1161.6011	581.3042	10
18	2120.0632	**1060.5352**	2103.0366	1052.0220	2102.0526	1051.5299	Q	***1051.5531***	526.2802	1034.5265	517.7669	1033.5425	517.2749	9
19	2217.1159	1109.0616	2200.0894	1100.5483	2199.1054	1100.0563	P	***923.4945***	462.2509	906.4680	453.7376	905.4839	453.2456	8
20	2318.1636	**1159.5854**	2301.1371	1151.0722	2300.1531	1150.5802	T	826.4417	413.7245	809.4152	405.2112	808.4312	404.7192	7
21	2446.2222	**1223.6147**	2429.1957	1215.1015	2428.2116	1214.6095	Q	***725.3941***	363.2007	708.3675	354.6874			6
22	2574.2808	**1287.6440**	2557.2542	1279.1308	2556.2702	1278.6387	Q	***597.3355***	299.1714	580.3089	290.6581			5
23	2671.3335	1336.1704	2654.3070	1327.6571	2653.3230	1327.1651	P	***469.2769***	235.1421	452.2504	226.6288			4
24	2799.3921	**1400.1997**	2782.3656	1391.6864	2781.3816	1391.1944	Q	***372.2241***	186.6157	355.1976	178.1024			3

25	2896.4449	1448.7261	2879.4183	1440.2128	2878.4343	1439.7208	**P**	244.1656	122.5864	227.1390	114.0731			**2**
26							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of VSEVPQQIHHQPVQQQQQPTQQPQPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.9	3041.5432	2.2096	VSEVPQQIHHQPVQQQQQPTQQPQPK
2.9	3045.5892	-1.8364	LFRHMEELLSPAGLAPCSLQQLQHSIK
1.9	3045.5350	-1.7823	IDSYSRICFPLAYVLFNLIYWSIYS
1.0	3043.4777	0.2751	AKSENTMTTIMDPTVMPAAASVPPAQTQR

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

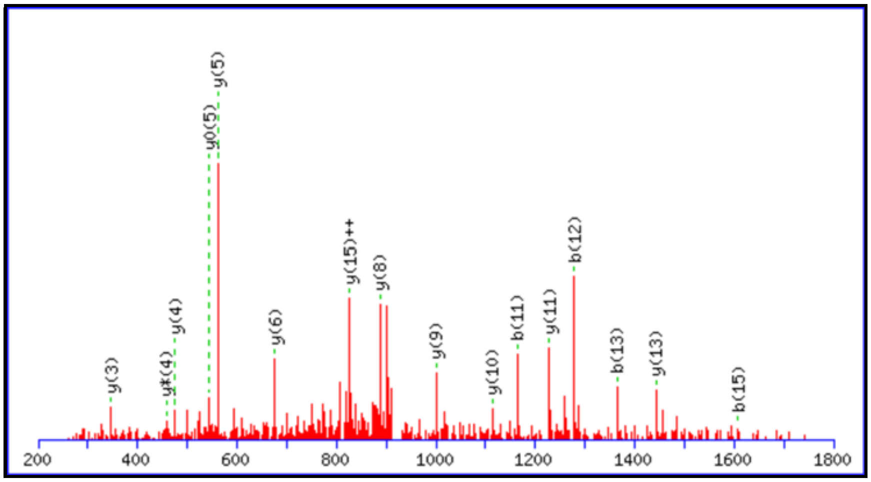
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSPITINLINVLSENGR**
Found in **gi|51467909|ref|NP_001003843.1|**, ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit [Danio rerio]

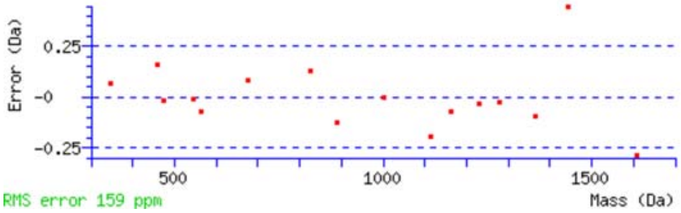
Match to Query 37246: 1839.302724 from(920.658638,2+) index(1901)
Data file TCDD_0530.dta

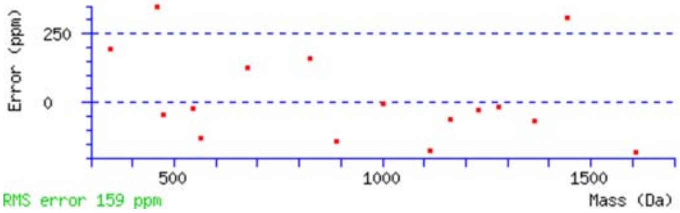
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1838.0261
Ions Score: 51 **Expect:** 0.0018
Matches : 16/172 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					**V**							**17**
2	187.1077	94.0575			169.0972	85.0522	**S**	1739.9650	870.4861	1722.9385	861.9729	1721.9545	861.4809	**16**
3	284.1605	142.5839			266.1499	133.5786	**P**	1652.9330	826.9701	1635.9064	818.4569	1634.9224	817.9649	**15**
4	397.2445	199.1259			379.2340	190.1206	**I**	1555.8802	778.4438	1538.8537	769.9305	1537.8697	769.4385	**14**
5	498.2922	249.6498			480.2817	240.6445	**T**	***1442.7962***	721.9017	1425.7696	713.3884	1424.7856	712.8964	**13**
6	611.3763	306.1918			593.3657	297.1865	**I**	1341.7485	671.3779	1324.7219	662.8646	1323.7379	662.3726	**12**
7	725.4192	363.2132	708.3927	354.7000	707.4087	354.2080	**N**	***1228.6644***	614.8358	1211.6379	606.3226	1210.6539	605.8306	**11**
8	838.5033	419.7553	821.4767	411.2420	820.4927	410.7500	**L**	***1114.6215***	557.8144	1097.5949	549.3011	1096.6109	548.8091	**10**
9	951.5873	476.2973	934.5608	467.7840	933.5768	467.2920	**I**	***1001.5374***	501.2724	984.5109	492.7591	983.5269	492.2671	**9**
10	1065.6303	533.3188	1048.6037	524.8055	1047.6197	524.3135	**N**	***888.4534***	444.7303	871.4268	436.2170	870.4428	435.7250	**8**
11	**1164.6987**	582.8530	1147.6721	574.3397	1146.6881	573.8477	**V**	774.4104	387.7089	757.3839	379.1956	756.3999	378.7036	**7**
12	**1277.7827**	639.3950	1260.7562	630.8817	1259.7722	630.3897	**L**	***675.3420***	338.1747	658.3155	329.6614	657.3315	329.1694	**6**
13	**1364.8148**	682.9110	1347.7882	674.3978	1346.8042	673.9057	**S**	***562.2580***	281.6326	545.2314	273.1193	544.2474	272.6273	**5**
14	1493.8574	747.4323	1476.8308	738.9190	1475.8468	738.4270	**E**	***475.2259***	238.1166	458.1994	229.6033	457.2154	229.1113	**4**
15	**1607.9003**	804.4538	1590.8737	795.9405	1589.8897	795.4485	**N**	***346.1833***	173.5953	329.1568	165.0820			**3**
16	1664.9218	832.9645	1647.8952	824.4512	1646.9112	823.9592	**G**	232.1404	116.5738	215.1139	108.0606			**2**
17							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of VSPITINLINVLSENGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.0	1838.0261	1.2766	VSPITINLINVLSENGR
17.7	1837.8958	1.4069	ENGFNIYVSNNIALDR

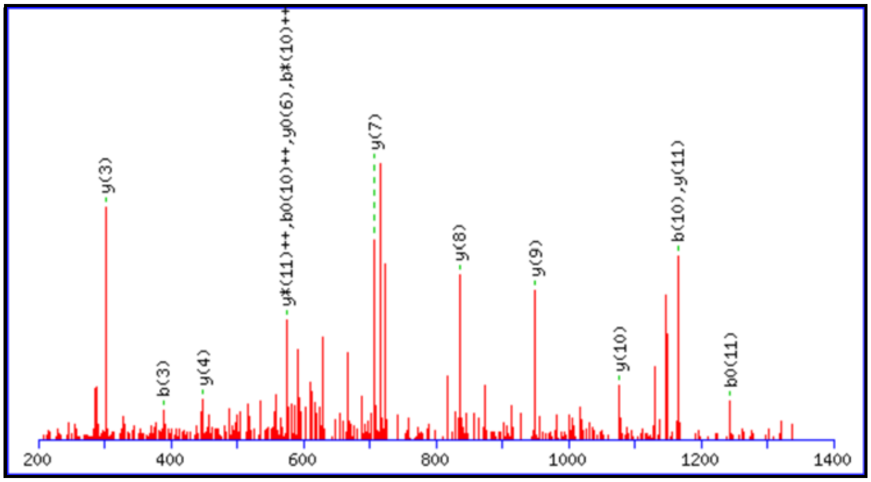
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDSQIEDGSFPGK**
Found in **gi|41055614|ref|NP_956800.1|**, hypothetical protein LOC393478 [Danio rerio]

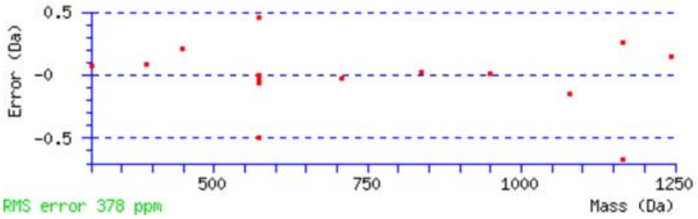
Match to Query 22052: 1465.282724 from(733.648638,2+) index(21486)
Data file TCDD_0530.dta

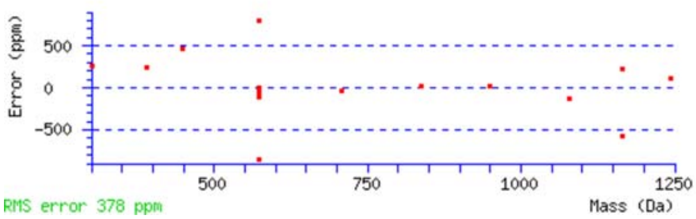
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1464.6521
Ions Score: 62 **Expect:** 0.00018
Matches : 15/128 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	187.0866	94.0469					W							13
2	302.1135	151.5604			284.1030	142.5551	D	1279.5801	640.2937	1262.5535	631.7804	1261.5695	631.2884	12
3	**389.1456**	195.0764			371.1350	186.0711	S	***1164.5531***	582.7802	1147.5266	574.2669	1146.5426	573.7749	11
4	517.2041	259.1057	500.1776	250.5924	499.1936	250.1004	Q	***1077.5211***	539.2642	1060.4946	530.7509	1059.5106	530.2589	10
5	630.2882	315.6477	613.2617	307.1345	612.2776	306.6425	I	***949.4625***	475.2349	932.4360	466.7216	931.4520	466.2296	9
6	759.3308	380.1690	742.3042	371.6558	741.3202	371.1638	E	***836.3785***	418.6929	819.3519	410.1796	818.3679	409.6876	8
7	874.3577	437.6825	857.3312	429.1692	856.3472	428.6772	D	***707.3359***	354.1716	690.3093	345.6583	689.3253	345.1663	7
8	931.3792	466.1932	914.3527	457.6800	913.3686	457.1880	G	592.3089	296.6581	575.2824	288.1448	574.2984	287.6528	6
9	1018.4112	509.7093	1001.3847	501.1960	1000.4007	500.7040	S	535.2875	268.1474	518.2609	259.6341	517.2769	259.1421	5
10	**1165.4796**	583.2435	1148.4531	574.7302	1147.4691	574.2382	F	***448.2554***	224.6314	431.2289	216.1181			4
11	1262.5324	631.7698	1245.5059	623.2566	1244.5218	622.7646	P	***301.1870***	151.0972	284.1605	142.5839			3
12	1319.5539	660.2806	1302.5273	651.7673	1301.5433	651.2753	G	204.1343	102.5708	187.1077	94.0575			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of WDSQIEDGSFPGK

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.8	1464.6521	0.6306	WDSQIEDGSFPGK
12.5	1465.6330	-0.3503	CVCNPGFELGADGK
12.0	1464.7096	0.5731	ALDSFLTNSESPGK
11.9	1462.7892	2.4935	HQQLEAEIQVLR
10.9	1464.7316	0.5511	AMVSVAVGTEATVCK
10.9	1466.7188	-1.4361	GVFSQINGCISTGK
9.7	1464.7283	0.5545	ITDFGCNTILSPGK
9.1	1463.7005	1.5823	ATQQSLSDQFPSR
8.4	1464.6490	0.6338	WLSENSTCPICR
7.4	1464.8452	0.4375	RYVAAYLLAALGGK

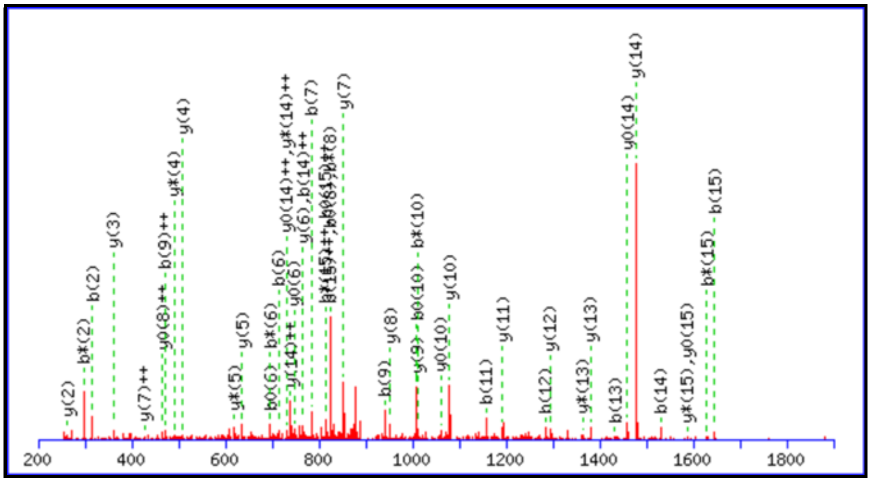
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WKPSTLAGVSEQFVDK**
Found in **gi|62122813|ref|NP_001014338.1|**, 3-hydroxyisobutyryl-Coenzyme A hydrolase [Danio rerio]

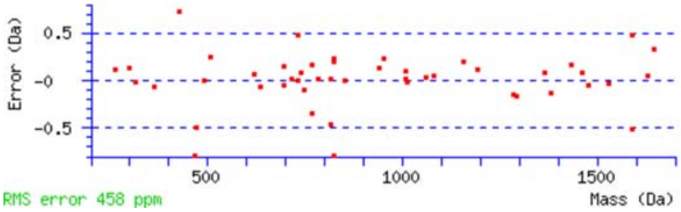
Match to Query 35084: 1792.912724 from(897.463638,2+) index(45500)
Data file TCDD_0530.dta

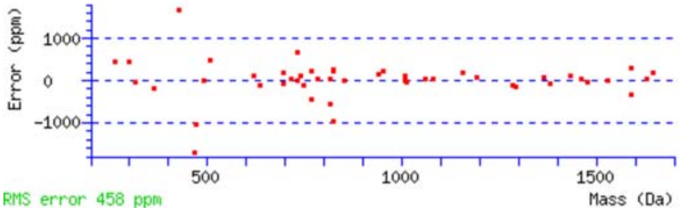
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1790.9203
Ions Score: 63 **Expect:** 0.00013
Matches : 48/170 fragment ions using 99 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	187.0866	94.0469					**W**							16
2	**315.1816**	158.0944	298.1550	149.5811			**K**	1605.8483	803.4278	1588.8217	794.9145	1587.8377	794.4225	15
3	412.2343	206.6208	395.2078	198.1075			**P**	***1477.7533***	739.3803	1460.7268	730.8670	1459.7427	730.3750	14
4	499.2663	250.1368	482.2398	241.6235	481.2558	241.1315	**S**	***1380.7005***	690.8539	1363.6740	682.3406	1362.6900	681.8486	13
5	600.3140	300.6606	583.2875	292.1474	582.3035	291.6554	**T**	***1293.6685***	647.3379	1276.6420	638.8246	1275.6579	638.3326	12
6	**713.3981**	357.2027	696.3715	348.6894	695.3875	348.1974	**L**	***1192.6208***	596.8141	1175.5943	588.3008	1174.6103	587.8088	11
7	**784.4352**	392.7212	767.4087	384.2080	766.4246	383.7160	**A**	***1079.5368***	540.2720	1062.5102	531.7587	1061.5262	531.2667	10
8	841.4567	421.2320	824.4301	412.7187	823.4461	412.2267	**G**	***1008.4997***	504.7535	991.4731	496.2402	990.4891	495.7482	9
9	**940.5251**	470.7662	923.4985	462.2529	922.5145	461.7609	**V**	***951.4782***	476.2427	934.4516	467.7295	933.4676	467.2374	8
10	1027.5571	514.2822	1010.5306	505.7689	1009.5465	505.2769	**S**	***852.4098***	426.7085	835.3832	418.1953	834.3992	417.7032	7
11	**1156.5997**	578.8035	1139.5732	570.2902	1138.5891	569.7982	**E**	***765.3777***	383.1925	748.3512	374.6792	747.3672	374.1872	6
12	**1284.6583**	642.8328	1267.6317	634.3195	1266.6477	633.8275	**Q**	***636.3352***	318.6712	619.3086	310.1579	618.3246	309.6659	5
13	**1431.7267**	716.3670	1414.7001	707.8537	1413.7161	707.3617	**F**	***508.2766***	254.6419	491.2500	246.1287	490.2660	245.6366	4
14	**1530.7951**	765.9012	1513.7686	757.3879	1512.7845	756.8959	**V**	***361.2082***	181.1077	344.1816	172.5944	343.1976	172.1024	3
15	**1645.8220**	823.4147	1628.7955	814.9014	1627.8115	814.4094	**D**	***262.1397***	131.5735	245.1132	123.0602	244.1292	122.5682	2
16							**K**	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of WKPSTLAGVSEQFVDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.0	1790.9203	1.9924	WKPSTLAGVSEQFVDK
11.7	1790.9825	1.9302	EANALCHRLPVLNTLK
10.1	1791.9591	0.9536	SANVRKPQTSSQPPPAK
3.8	1791.7280	1.1847	HCWNCYHVLDCTK
3.1	1791.8688	1.0439	CAWIPVQYPVISECK
2.7	1791.7693	1.1434	DRELGNVDAGENSADCK
2.1	1790.7539	2.1589	NGYCTVCTGKCHYTK
1.9	1791.9731	0.9397	SPIHVKVEPSVDTSGIK
1.7	1792.7430	0.1697	CSGLIDCMDLESNEHK
1.6	1791.8275	1.0852	ESVHTANSTQEEYVAK

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

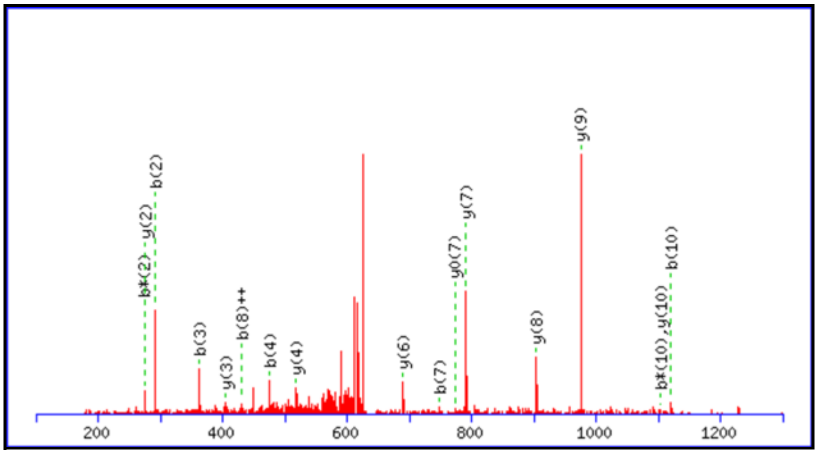
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YQAITATLEEK**
Found in **gi|47086477|ref|NP_997949.1|**, ribosomal protein L13a [Danio rerio]

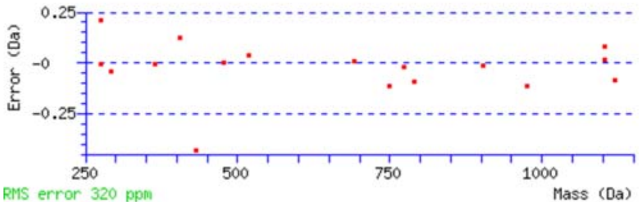
Match to Query 15930: 1267.492724 from(634.753638,2+) index(8104)
Data file TCDD_0530.dta

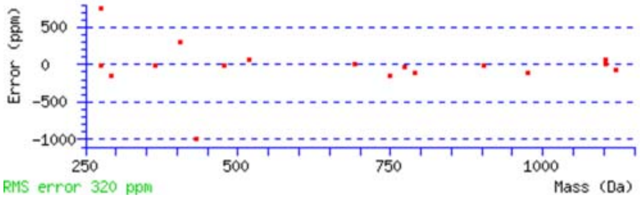
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1265.6503
Ions Score: 41 **Expect:** 0.022
Matches : 17/108 fragment ions using 44 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							11
2	**292.1292**	146.5682	275.1026	138.0550			Q	***1103.5943***	552.3008	1086.5677	543.7875	1085.5837	543.2955	10
3	**363.1663**	182.0868	346.1397	173.5735			A	***975.5357***	488.2715	958.5092	479.7582	957.5251	479.2662	9
4	**476.2504**	238.6288	459.2238	230.1155			I	***904.4986***	452.7529	887.4720	444.2397	886.4880	443.7477	8
5	577.2980	289.1527	560.2715	280.6394	559.2875	280.1474	T	***791.4145***	396.2109	774.3880	387.6976	773.4040	387.2056	7
6	648.3352	324.6712	631.3086	316.1579	630.3246	315.6659	A	***690.3668***	345.6871	673.3403	337.1738	672.3563	336.6818	6
7	**749.3828**	375.1951	732.3563	366.6818	731.3723	366.1898	T	619.3297	310.1685	602.3032	301.6552	601.3192	301.1632	5
8	862.4669	431.7371	845.4403	423.2238	844.4563	422.7318	L	***518.2821***	259.6447	501.2555	251.1314	500.2715	250.6394	4
9	991.5095	496.2584	974.4829	487.7451	973.4989	487.2531	E	***405.1980***	203.1026	388.1714	194.5894	387.1874	194.0974	3
10	**1120.5521**	560.7797	1103.5255	552.2664	1102.5415	551.7744	E	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YQAITATLEEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.5	1265.6503	1.8424	YQAITATLEEK

18.4	1265.6404	1.8523	KFEGGHYTSLK
16.6	1265.5677	1.9251	YHFEDVAGSNK
14.2	1265.6463	1.8464	SSLSSGPSTTSKK
13.3	1265.6000	1.8927	YALQSNNSNQK
13.3	1265.6364	1.8563	KSFLNSAEASGR
12.9	1265.7132	1.7795	GSFILRVFAEK
12.2	1266.5914	0.9013	KFDQCLAEEK
11.6	1265.5259	1.9668	SSTDEPGTEESK
11.5	1265.5281	1.9646	CMANEKGDWR

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

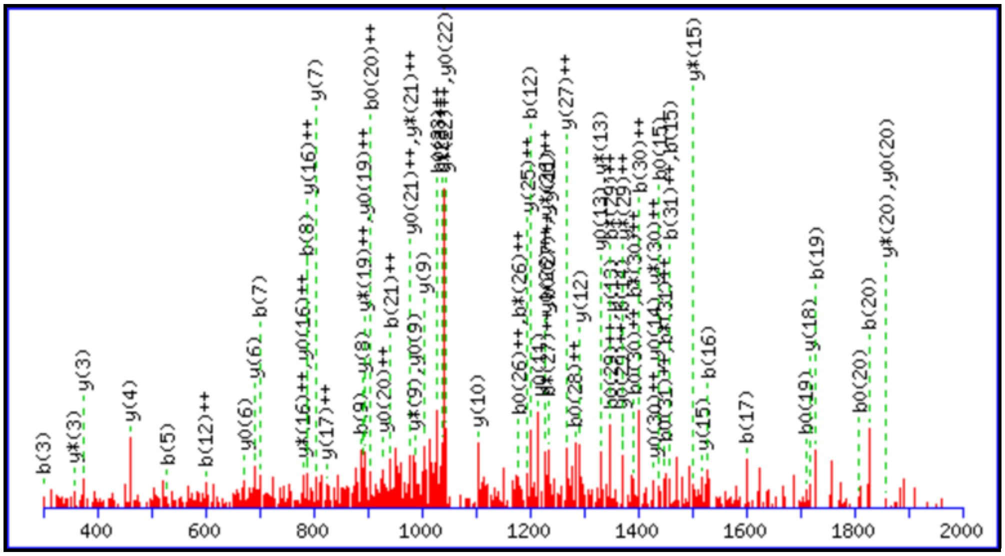
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAVDDLGSTLAEVASAAGAVGGMVNSITQSINK**
Found in **gi|57222259|ref|NP_001009560.1|**, talin 1 [Danio rerio]

Match to Query 123661: 3175.712724 from(1059.578184,3+) index(6009)
Data file TCDD_0531.dta

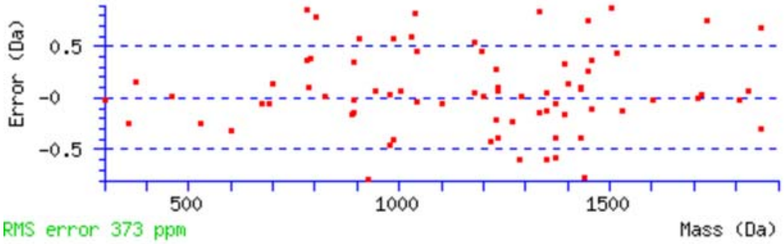
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

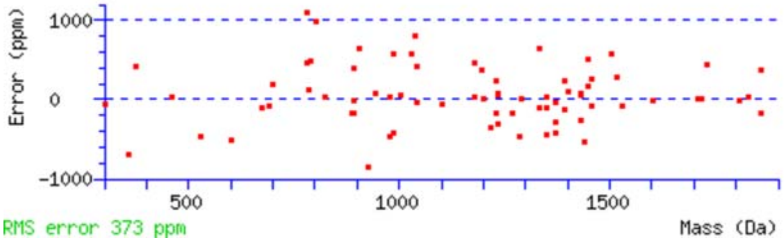


Monoisotopic mass of neutral peptide Mr(calc): 3174.5714
Ions Score: 42 **Expect:** 0.0066
Matches : 75/330 fragment ions using 164 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}
1	130.0499	65.5286			112.0393	56.5233	E				
2	201.0870	101.0471			183.0764	92.0418	A	3046.5361	1523.7717	3029.5096	1515.2584
3	***300.1554***	150.5813			282.1448	141.5761	V	2975.4990	1488.2531	2958.4725	1479.7399
4	415.1823	208.0948			397.1718	199.0895	D	2876.4306	1438.7189	2859.4040	1430.2057
5	***530.2093***	265.6083			512.1987	256.6030	D	2761.4037	1381.2055	2744.3771	1372.6922
6	643.2933	322.1503			625.2828	313.1450	L	2646.3767	1323.6920	2629.3502	1315.1787
7	***700.3148***	350.6610			682.3042	341.6558	G	2533.2926	1267.1500	2516.2661	1258.6367
8	***787.3468***	394.1771			769.3363	385.1718	S	2476.2712	1238.6392	2459.2446	1230.1260
9	***888.3945***	444.7009			870.3840	435.6956	T	2389.2392	1195.1232	2372.2126	1186.6099
10	1001.4786	501.2429			983.4680	492.2376	L	2288.1915	1144.5994	2271.1649	1136.0861
11	1072.5157	536.7615			1054.5051	527.7562	A	2175.1074	1088.0573	2158.0809	1079.5441
12	***1201.5583***	601.2828			1183.5477	592.2775	E	2104.0703	1052.5388	2087.0437	1044.0255
13	1300.6267	650.8170			1282.6161	641.8117	V	1975.0277	988.0175	1958.0012	979.5042
14	***1371.6638***	686.3355			1353.6533	677.3303	A	1875.9593	938.4833	1858.9327	929.9700
15	***1458.6958***	729.8516			1440.6853	720.8463	S	1804.9222	902.9647	1787.8956	894.4515

16	***1529.7330***	765.3701			1511.7224	756.3648	A	***1717.8901***	859.4487	1700.8636	850.9354
17	***1600.7701***	800.8887			1582.7595	791.8834	A	1646.8530	823.9302	1629.8265	815.4169
18	1657.7915	829.3994			1639.7810	820.3941	G	1575.8159	788.4116	1558.7894	779.8983
19	***1728.8287***	864.9180			1710.8181	855.9127	A	***1518.7945***	759.9009	1501.7679	751.3876
20	***1827.8971***	914.4522			1809.8865	905.4469	V	1447.7573	724.3823	1430.7308	715.8690
21	1884.9185	942.9629			1866.9080	933.9576	G	***1348.6889***	674.8481	1331.6624	666.3348
22	1941.9400	971.4736			1923.9294	962.4684	G	***1291.6675***	646.3374	1274.6409	637.8241
23	2072.9805	1036.9939			2054.9699	1027.9886	M	***1234.6460***	617.8266	1217.6194	609.3134
24	2172.0489	1086.5281			2154.0383	1077.5228	V	***1103.6055***	552.3064	1086.5790	543.7931
25	2286.0918	1143.5495	2269.0653	1135.0363	2268.0813	1134.5443	N	***1004.5371***	502.7722	987.5106	494.2589
26	2373.1238	1187.0656	2356.0973	1178.5523	2355.1133	1178.0603	S	***890.4942***	445.7507	873.4676	437.2374
27	2486.2079	1243.6076	2469.1814	1235.0943	2468.1973	1234.6023	I	***803.4621***	402.2347	786.4356	393.7214
28	2587.2556	1294.1314	2570.2290	1285.6182	2569.2450	1285.1262	T	***690.3781***	345.6927	673.3515	337.1794
29	2715.3142	1358.1607	2698.2876	1349.6474	2697.3036	1349.1554	Q	589.3304	295.1688	572.3039	286.6556
30	2802.3462	1401.6767	2785.3196	1393.1635	2784.3356	1392.6715	S	***461.2718***	231.1395	444.2453	222.6263
31	2915.4303	1458.2188	2898.4037	1449.7055	2897.4197	1449.2135	I	***374.2398***	187.6235	357.2132	179.1103
32	3029.4732	1515.2402	3012.4466	1506.7270	3011.4626	1506.2349	N	261.1557	131.0815	244.1292	122.5682
33							K	147.1128	74.0600	130.0863	65.5468





NCBI **BLAST** search of EAVDDLGSTLAEVASAAGAVGGMVNSITQSINK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.5	3174.5714	1.1413	EAVDDLGSTLAEVASAAGAVGGMVNSITQSINK
5.2	3173.6721	2.0407	ALDLSAGLKHTLAQFTLSSQSSLGGPAAFSAK
4.5	3175.4139	0.2988	DEEDFSELEPDEQLVCSVTEITEHLGR
3.8	3175.4532	0.2595	VYSNADCNNICHGRITPNMICAGTRPGGK
3.8	3176.4966	-0.7838	AEEDSPCVVTLQCSPGSASAISSLQVVSEAR
3.3	3177.4212	-1.7085	SPHSSVHEHVLGALCCLVEDSPRGMSDCR

2.5	3175.6639	0.0488	TIQHLHNGASPGFAPLGEIELTIRHSPQR
2.0	3174.3910	1.3217	SGVEAGFESGPEEDFLNLGAEACNFMQAQK
1.5	3173.3138	2.3990	QESGYMNPPSASQSHACHSHSYPMNPSSR
0.8	3174.4467	1.2660	HMMIHTGEKPHTCTQCGKSFTQSSSLNK

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

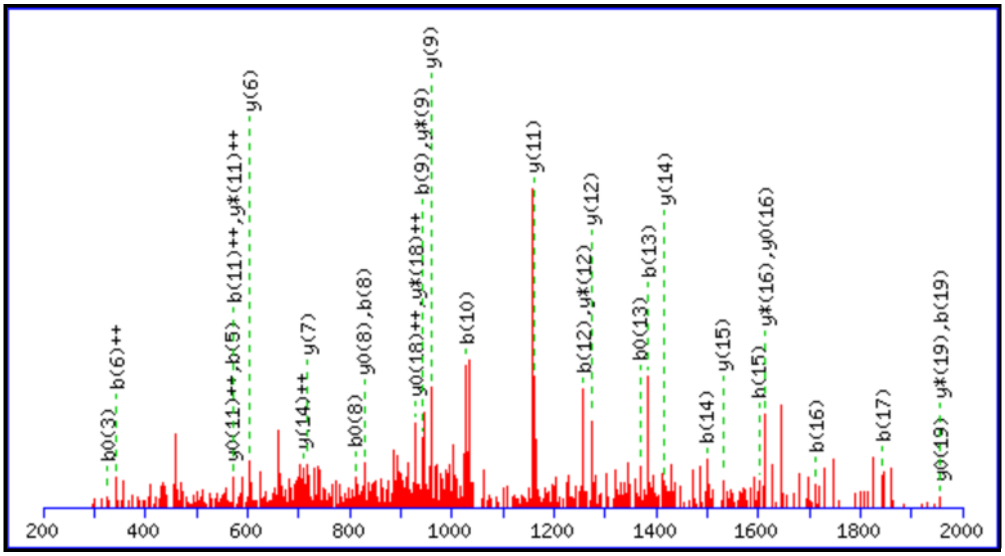
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVDEVDAALSDLEITLEGGK**
Found in **gi|189531190|ref|XP_685536.2|**, PREDICTED: im:7145859 isoform 1 [Danio rerio]

Match to Query 56997: 2102.922724 from(1052.468638,2+) index(4044)
Data file TCDD_0531.dta

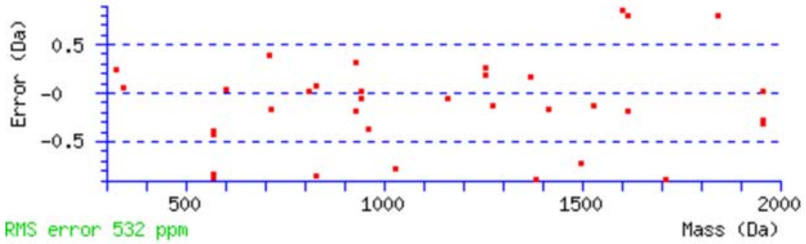
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

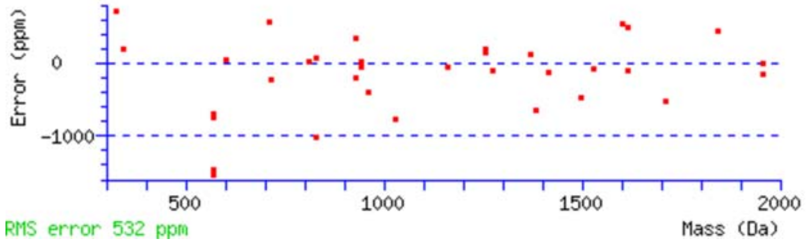


```
Monoisotopic mass of neutral peptide Mr(calc): 2102.0267
Ions Score: 42  Expect: 0.012
Matches : 36/184 fragment ions using 85 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	**E**							**20**
2	229.1183	115.0628	211.1077	106.0575	**V**	1973.9914	987.4993	1956.9648	978.9860	1955.9808	978.4940	**19**
3	***344.1452***	172.5763	326.1347	163.5710	**D**	1874.9229	937.9651	1857.8964	929.4518	1856.9124	928.9598	**18**
4	473.1878	237.0975	455.1773	228.0923	**E**	1759.8960	880.4516	1742.8695	871.9384	1741.8854	871.4464	**17**
5	***572.2562***	286.6318	554.2457	277.6265	**V**	1630.8534	815.9303	1613.8269	807.4171	1612.8428	806.9251	**16**
6	687.2832	344.1452	669.2726	335.1399	**D**	**1531.7850**	766.3961	1514.7584	757.8829	1513.7744	757.3909	**15**
7	758.3203	379.6638	740.3097	370.6585	**A**	**1416.7581**	708.8827	1399.7315	700.3694	1398.7475	699.8774	**14**
8	***829.3574***	415.1823	811.3468	406.1771	**A**	1345.7209	673.3641	1328.6944	664.8508	1327.7104	664.3588	**13**
9	***942.4415***	471.7244	924.4309	462.7191	**L**	**1274.6838**	637.8455	1257.6573	629.3323	1256.6733	628.8403	**12**
10	***1029.4735***	515.2404	1011.4629	506.2351	**S**	**1161.5998**	581.3035	1144.5732	572.7902	1143.5892	572.2982	**11**
11	1144.5004	572.7539	1126.4899	563.7486	**D**	1074.5677	537.7875	1057.5412	529.2742	1056.5572	528.7822	**10**
12	***1257.5845***	629.2959	1239.5739	620.2906	**L**	**959.5408**	480.2740	942.5142	471.7608	941.5302	471.2687	**9**
13	***1386.6271***	693.8172	1368.6165	684.8119	**E**	846.4567	423.7320	829.4302	415.2187	828.4462	414.7267	**8**
14	***1499.7112***	750.3592	1481.7006	741.3539	**I**	**717.4141**	359.2107	700.3876	350.6974	699.4036	350.2054	**7**

15	*1600.7588*	800.8831	1582.7483	791.8778	**T**	**604.3301**	302.6687	587.3035	294.1554	586.3195	293.6634	**6**
16	*1713.8429*	857.4251	1695.8323	848.4198	**L**	503.2824	252.1448	486.2558	243.6316	485.2718	243.1395	**5**
17	*1842.8855*	921.9464	1824.8749	912.9411	**E**	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	**4**
18	1899.9070	950.4571	1881.8964	941.4518	**G**	261.1557	131.0815	244.1292	122.5682			**3**
19	*1956.9284*	978.9678	1938.9179	969.9626	**G**	204.1343	102.5708	187.1077	94.0575			**2**
20					**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of EVDEVDAALSDLEITLEGGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.4	2104.0689	-1.1461	FTGSVDIQVVGDDLTVTNPK
42.3	2102.0267	0.8961	EVDEVDAALSDLEITLEGGK
8.7	2101.9651	0.9576	DEITQQTEQAEKPDDVEK
7.1	2103.0452	-0.1225	VETLEGAQVNAQQMGCKGLK
6.6	2105.0869	-2.1642	QVCVCVCVSLALNLCIALK
6.6	2105.0869	-2.1642	QVCVCVCVSLALNLCIALK
5.9	2104.1568	-1.2341	QTKPTFKSYLPPLQTDLK
4.3	2102.0506	0.8721	VCAINKAGAGPYSDVSIFYK
3.9	2105.0715	-2.1487	SSGVFELKVLSFTSTSSVCK
3.8	2101.0990	1.8237	ILETFKINSDNGHLTLMR

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

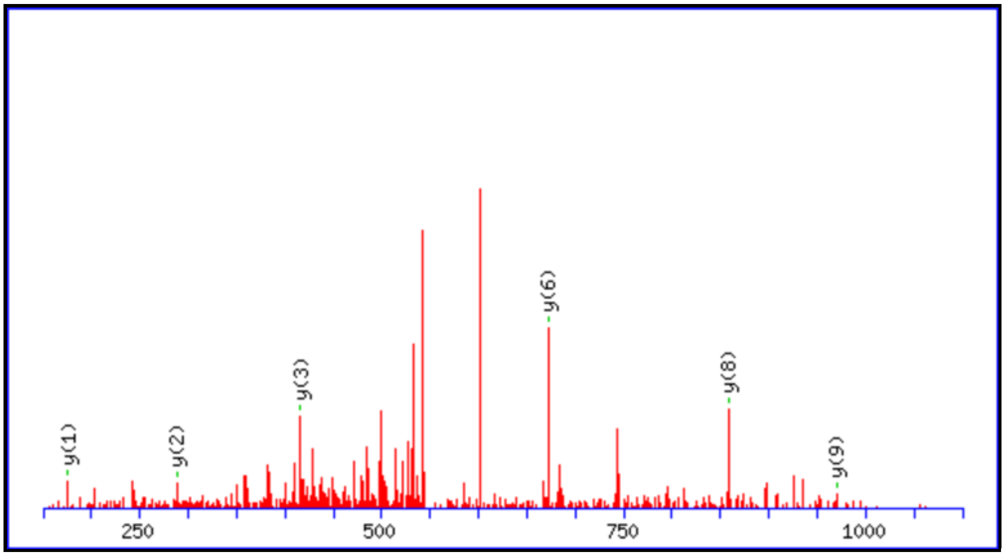
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLADAIAKLR**
Found in **gi|189530625|ref|XP_001920330.1|**, PREDICTED: similar to spectrin repeat containing, nuclear envelope 1 [Danio rerio]

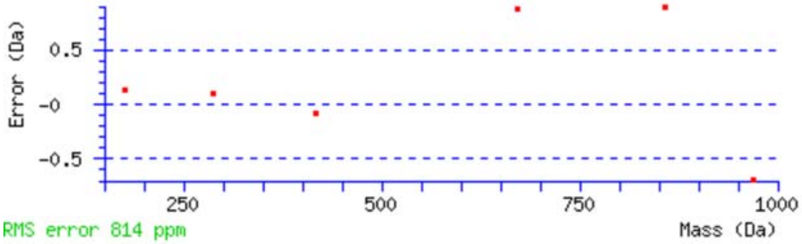
Match to Query 9013: 1098.742724 from(550.378638,2+) index(21937)
Data file TCDD_0531.dta

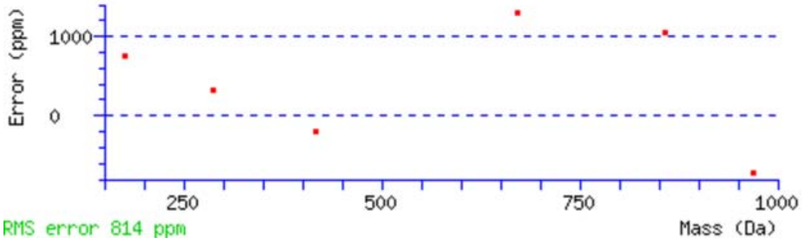
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): `1097.6557`
Ions Score: `45` **Expect:** `0.01`
Matches : `6/90 fragment ions using 10 most intense peaks` (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	
1	129.0659	65.0366	112.0393	56.5233			Q						
2	242.1499	121.5786	225.1234	113.0653			L	*970.6044*	485.8058	953.5778	477.2926	952.5938	47
3	313.1870	157.0972	296.1605	148.5839			A	*857.5203*	429.2638	840.4938	420.7505	839.5098	42
4	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	D	786.4832	393.7452	769.4567	385.2320	768.4726	38
5	499.2511	250.1292	482.2245	241.6159	481.2405	241.1239	A	*671.4563*	336.2318	654.4297	327.7185		
6	612.3352	306.6712	595.3086	298.1579	594.3246	297.6659	I	600.4192	300.7132	583.3926	292.1999		
7	683.3723	342.1898	666.3457	333.6765	665.3617	333.1845	A	487.3351	244.1712	470.3085	235.6579		
8	811.4672	406.2373	794.4407	397.7240	793.4567	397.2320	K	*416.2980*	208.6526	399.2714	200.1394		
9	924.5513	462.7793	907.5247	454.2660	906.5407	453.7740	L	*288.2030*	144.6051	271.1765	136.0919		
10							R	*175.1190*	88.0631	158.0924	79.5498		





NCBI **BLAST** search of QLADAIAKLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.0	1098.5782	0.1646	AGLDAAGQGALR
45.3	1097.6557	1.0871	QLADAIAKLR
36.5	1098.6145	0.1282	QLADALKANR
25.6	1099.5370	-0.7943	SSGLANAPNNR
23.1	1098.6145	0.1282	KLNEAQQLR
23.1	1098.6761	0.0667	QLLSLEKIR
22.8	1098.6145	0.1282	LQGELDRLR
21.3	1098.6397	0.1031	LKQELAELR
19.8	1098.6761	0.0667	LKELLSQLR
19.8	1097.6556	1.0871	EILAANAIRK

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

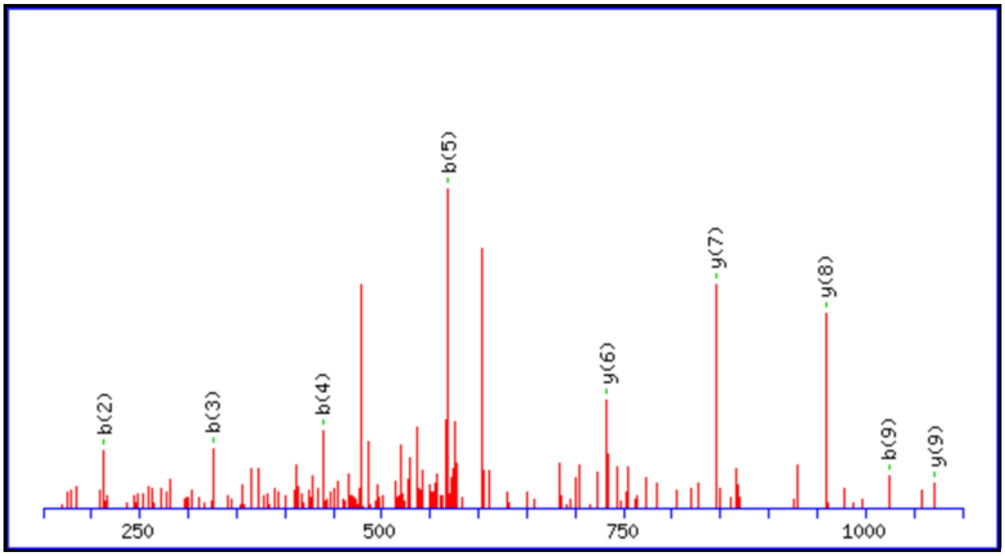
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILIQEQLSK**
Found in **gi|125843259|ref|XP_690811.2|**, PREDICTED: polymerase (RNA) III (DNA directed) polypeptide B [Danio rerio]

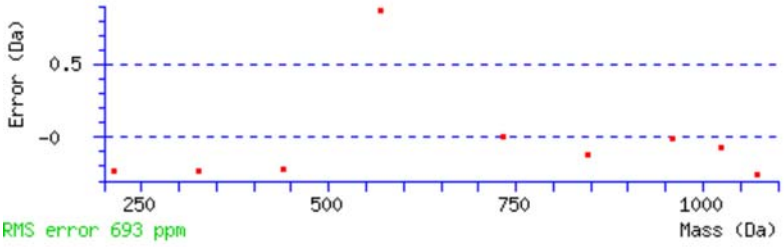
Match to Query 11544: 1169.292724 from(585.653638,2+) index(9496)
Data file TCDD_0531.dta

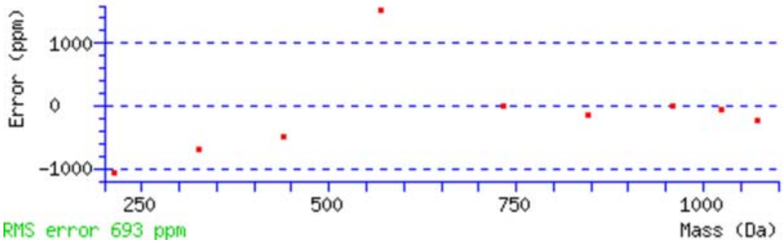
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1169.7019
Ions Score: 45 **Expect:** 0.011
Matches : 9/88 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}
1	100.0757	50.5415					**V**					
2	***213.1598***	107.0835					**I**	***1071.6408***	536.3241	1054.6143	527.8108	1053.6
3	***326.2438***	163.6255					**L**	***958.5568***	479.7820	941.5302	471.2688	940.5
4	***439.3279***	220.1676					**I**	***845.4727***	423.2400	828.4462	414.7267	827.4
5	***567.3865***	284.1969	550.3599	275.6836			**Q**	***732.3886***	366.6980	715.3621	358.1847	714.3
6	696.4291	348.7182	679.4025	340.2049	678.4185	339.7129	**E**	604.3301	302.6687	587.3035	294.1554	586.3
7	824.4876	412.7475	807.4611	404.2342	806.4771	403.7422	**Q**	475.2875	238.1474	458.2609	229.6341	457.2
8	937.5717	469.2895	920.5451	460.7762	919.5611	460.2842	**L**	347.2289	174.1181	330.2023	165.6048	329.2
9	***1024.6037***	512.8055	1007.5772	504.2922	1006.5932	503.8002	**S**	234.1448	117.5761	217.1183	109.0628	216.1
10							**K**	147.1128	74.0600	130.0863	65.5468	





NCBI **BLAST** search of VILIQEQLSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.6	1169.7019	-0.4092	VILIQEQLSK
36.5	1169.6656	-0.3728	VLLLIDDQNK
30.1	1169.6656	-0.3728	LVILEGELER
26.7	1169.7132	-0.4205	IVLLGDRSIGK
23.3	1169.6669	-0.3742	VLNHVLGGPHK
23.1	1169.6404	-0.3477	NPNLQTSGVLK
14.7	1171.6812	-2.3885	TLIELQKEAK
12.1	1169.7132	-0.4205	LVLTNGKLQGK
12.1	1169.6656	-0.3728	VLLVELEEAR
10.1	1168.6492	0.6435	VIEGSFVYKK

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