

MATRIX
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Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQSYLENPTSYHLQQSQHQKVR**
Found in **ch06usp|P19484|TFEB_HUMAN** in **uni_human_nru**, Transcription factor EB OS=Homo sapiens GN=TFEB PE=1 SV=3 CH=ch06u

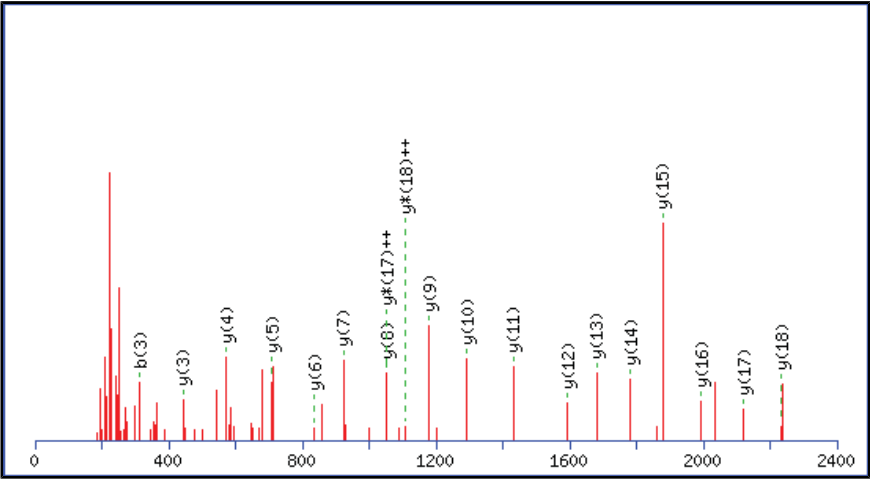
Match to Query 13887: 2711.332216 from(678.840330,4+) index(6959)
Title: Spectrum25099 scans:7922,
Data file File Name: 160611_TFEB_C.raw

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches ☐ Label matches used for scoring ☒

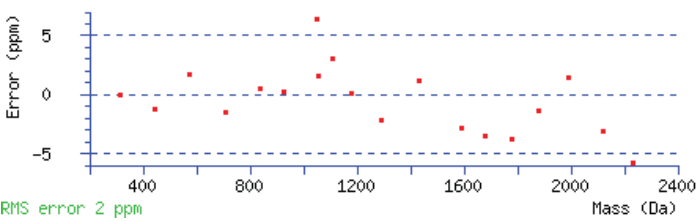
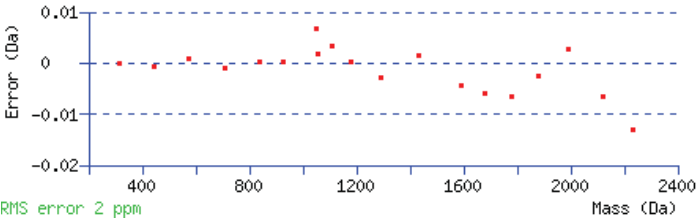
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2711.3416
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications: **K20** : Acetyl (K)
Ions Score: 120 Expect: 1.5e-010
Matches : 19/248 fragment ions using 34 most intense peaks ([help](#))

#	a	a ⁺⁺	a [*]	a ^{*++}	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	72.0808	36.5440			100.0757	50.5415			V					22
2	200.1394	100.5733	183.1128	92.0600	228.1343	114.5708	211.1077	106.0575	Q	2613.2804	1307.1439	2596.2539	1298.6306	21
3	287.1714	144.0893	270.1448	135.5761	315.1663	158.0868	298.1397	149.5735	S	2485.2219	1243.1146	2468.1953	1234.6013	20
4	450.2347	225.6210	433.2082	217.1077	478.2296	239.6185	461.2031	231.1052	Y	2398.1898	1199.5986	2381.1633	1191.0853	19
5	563.3188	282.1630	546.2922	273.6498	591.3137	296.1605	574.2871	287.6472	L	2235.1265	1118.0669	2218.1000	1109.5536	18
6	692.3614	346.6843	675.3348	338.1710	720.3563	360.6818	703.3297	352.1685	E	2122.0424	1061.5249	2105.0159	1053.0116	17
7	806.4043	403.7058	789.3777	395.1925	834.3992	417.7032	817.3727	409.1900	N	1992.9998	997.0036	1975.9733	988.4903	16
8	903.4571	452.2322	886.4305	443.7189	931.4520	466.2296	914.4254	457.7164	P	1878.9569	939.9821	1861.9304	931.4688	15
9	1004.5047	502.7560	987.4782	494.2427	1032.4997	516.7535	1015.4731	508.2402	T	1781.9042	891.4557	1764.8776	882.9424	14
10	1091.5368	546.2720	1074.5102	537.7587	1119.5317	560.2695	1102.5051	551.7562	S	1680.8565	840.9319	1663.8299	832.4186	13
11	1254.6001	627.8037	1237.5735	619.2904	1282.5950	641.8011	1265.5685	633.2879	Y	1593.8245	797.4159	1576.7979	788.9026	12
12	1391.6590	696.3331	1374.6325	687.8199	1419.6539	710.3306	1402.6274	701.8173	H	1430.7611	715.8842	1413.7346	707.3709	11
13	1504.7431	752.8752	1487.7165	744.3619	1532.7380	766.8726	1515.7114	758.3594	L	1293.7022	647.3547	1276.6757	638.8415	10
14	1632.8016	816.9045	1615.7751	808.3912	1660.7966	830.9019	1643.7700	822.3886	Q	1180.6181	590.8127	1163.5916	582.2994	9
15	1760.8602	880.9338	1743.8337	872.4205	1788.8551	894.9312	1771.8286	886.4179	Q	1052.5596	526.7834	1035.5330	518.2701	8
16	1847.8923	924.4498	1830.8657	915.9365	1875.8872	938.4472	1858.8606	929.9339	S	924.5010	462.7541	907.4744	454.2409	7
17	1975.9508	988.4791	1958.9243	979.9658	2003.9457	1002.4765	1986.9192	993.9632	Q	837.4690	419.2381	820.4424	410.7248	6
18	2113.0097	1057.0085	2095.9832	1048.4952	2141.0047	1071.0060	2123.9781	1062.4927	H	709.4104	355.2088	692.3838	346.6956	5

19	2241.0683	1121.0378	2224.0418	1112.5245	2269.0632	1135.0353	2252.0367	1126.5220	Q	572.3515	286.6794	555.3249	278.1661	4
20	2411.1739	1206.0906	2394.1473	1197.5773	2439.1688	1220.0880	2422.1422	1211.5747	K	444.2929	222.6501	427.2663	214.1368	3
21	2510.2423	1255.6248	2493.2157	1247.1115	2538.2372	1269.6222	2521.2106	1261.1090	V	274.1874	137.5973	257.1608	129.0840	2
22									R	175.1190	88.0631	158.0924	79.5498	1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
120.1	2711.3416	-0.0093	VQSYLENPTSYHLQSQHQKVR

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

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Mascot Search Results

Peptide View

MS/MS Fragmentation of **EYLSETYGNKFAAHISPAQGSPKPPPAASPGVR**
Found in **ch06usp|P19484|TFEB_HUMAN** in **uni_human_nru**, Transcription factor EB OS=Homo sapiens GN=TFEB PE=1 SV=3 CH=ch06u

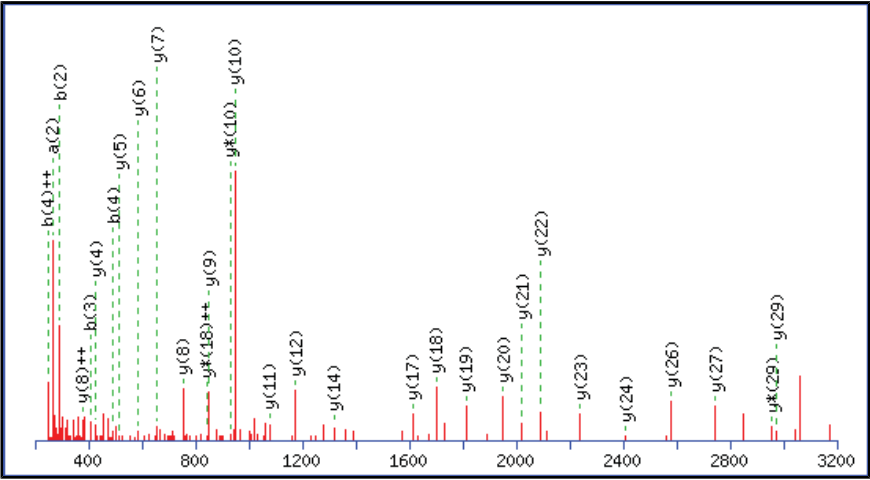
Match to Query 16386: 3465.732376 from(867.440370,4+) index(11693)
Title: Spectrum29434 scans:13137,
Data file File Name: 160611_TFEB_B.raw

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches ☐ Label matches used for scoring ☒

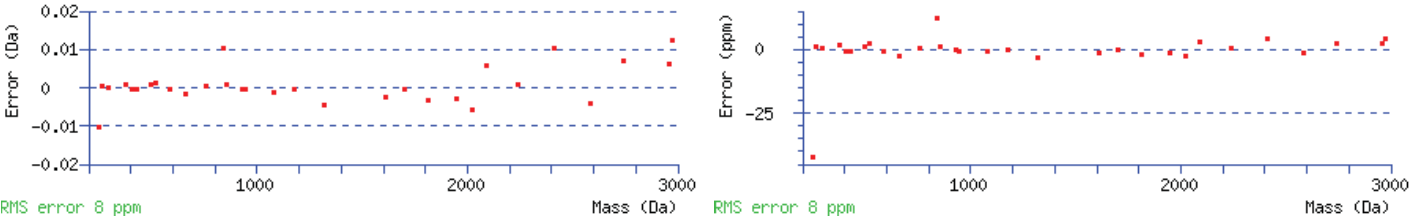
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 3465.7317
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K10 : Acetyl (K)
Ions Score: 120 Expect: 1.5e-010
Matches : 30/352 fragment ions using 79 most intense peaks ([help](#))

#	a	a ⁺⁺	a [*]	a ^{*++}	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	102.0550	51.5311			130.0499	65.5286			E					33
2	265.1183	133.0628			293.1132	147.0602			Y	3337.6964	1669.3518	3320.6699	1660.8386	32
3	378.2023	189.6048			406.1973	203.6023			L	3174.6331	1587.8202	3157.6065	1579.3069	31
4	465.2344	233.1208			493.2293	247.1183			S	3061.5490	1531.2781	3044.5225	1522.7649	30
5	594.2770	297.6421			622.2719	311.6396			E	2974.5170	1487.7621	2957.4904	1479.2489	29
6	695.3246	348.1660			723.3196	362.1634			T	2845.4744	1423.2408	2828.4478	1414.7276	28
7	858.3880	429.6976			886.3829	443.6951			Y	2744.4267	1372.7170	2727.4002	1364.2037	27
8	915.4094	458.2084			943.4044	472.2058			G	2581.3634	1291.1853	2564.3368	1282.6721	26
9	1029.4524	515.2298	1012.4258	506.7165	1057.4473	529.2273	1040.4207	520.7140	N	2524.3419	1262.6746	2507.3154	1254.1613	25
10	1199.5579	600.2826	1182.5313	591.7693	1227.5528	614.2800	1210.5263	605.7668	K	2410.2990	1205.6531	2393.2724	1197.1399	24
11	1346.6263	673.8168	1329.5998	665.3035	1374.6212	687.8143	1357.5947	679.3010	F	2240.1935	1120.6004	2223.1669	1112.0871	23
12	1417.6634	709.3353	1400.6369	700.8221	1445.6583	723.3328	1428.6318	714.8195	A	2093.1250	1047.0662	2076.0985	1038.5529	22
13	1488.7005	744.8539	1471.6740	736.3406	1516.6955	758.8514	1499.6689	750.3381	A	2022.0879	1011.5476	2005.0614	1003.0343	21
14	1625.7594	813.3834	1608.7329	804.8701	1653.7544	827.3808	1636.7278	818.8675	H	1951.0508	976.0290	1934.0243	967.5158	20
15	1738.8435	869.9254	1721.8170	861.4121	1766.8384	883.9229	1749.8119	875.4096	I	1813.9919	907.4996	1796.9654	898.9863	19
16	1825.8755	913.4414	1808.8490	904.9281	1853.8705	927.4389	1836.8439	918.9256	S	1700.9078	850.9576	1683.8813	842.4443	18
17	1922.9283	961.9678	1905.9018	953.4545	1950.9232	975.9652	1933.8967	967.4520	P	1613.8758	807.4415	1596.8493	798.9283	17
18	1993.9654	997.4863	1976.9389	988.9731	2021.9603	1011.4838	2004.9338	1002.9705	A	1516.8231	758.9152	1499.7965	750.4019	16

19	2122.0240	1061.5156	2104.9974	1053.0024	2150.0189	1075.5131	2132.9924	1066.9998	Q	1445.7859	723.3966	1428.7594	714.8833	15
20	2179.0455	1090.0264	2162.0189	1081.5131	2207.0404	1104.0238	2190.0138	1095.5106	G	1317.7274	659.3673	1300.7008	650.8540	14
21	2266.0775	1133.5424	2249.0509	1125.0291	2294.0724	1147.5398	2277.0459	1139.0266	S	1260.7059	630.8566	1243.6793	622.3433	13
22	2363.1303	1182.0688	2346.1037	1173.5555	2391.1252	1196.0662	2374.0986	1187.5529	P	1173.6739	587.3406	1156.6473	578.8273	12
23	2491.2252	1246.1162	2474.1987	1237.6030	2519.2201	1260.1137	2502.1936	1251.6004	K	1076.6211	538.8142	1059.5946	530.3009	11
24	2588.2780	1294.6426	2571.2514	1286.1294	2616.2729	1308.6401	2599.2463	1300.1268	P	948.5261	474.7667	931.4996	466.2534	10
25	2685.3307	1343.1690	2668.3042	1334.6557	2713.3257	1357.1665	2696.2991	1348.6532	P	851.4734	426.2403	834.4468	417.7271	9
26	2782.3835	1391.6954	2765.3570	1383.1821	2810.3784	1405.6928	2793.3519	1397.1796	P	754.4206	377.7139	737.3941	369.2007	8
27	2853.4206	1427.2139	2836.3941	1418.7007	2881.4155	1441.2114	2864.3890	1432.6981	A	657.3679	329.1876	640.3413	320.6743	7
28	2924.4577	1462.7325	2907.4312	1454.2192	2952.4527	1476.7300	2935.4261	1468.2167	A	586.3307	293.6690	569.3042	285.1557	6
29	3011.4898	1506.2485	2994.4632	1497.7352	3039.4847	1520.2460	3022.4581	1511.7327	S	515.2936	258.1504	498.2671	249.6372	5
30	3108.5425	1554.7749	3091.5160	1546.2616	3136.5374	1568.7724	3119.5109	1560.2591	P	428.2616	214.6344	411.2350	206.1212	4
31	3165.5640	1583.2856	3148.5374	1574.7724	3193.5589	1597.2831	3176.5324	1588.7698	G	331.2088	166.1081	314.1823	157.5948	3
32	3264.6324	1632.8198	3247.6059	1624.3066	3292.6273	1646.8173	3275.6008	1638.3040	V	274.1874	137.5973	257.1608	129.0840	2
33									R	175.1190	88.0631	158.0924	79.5498	1



NCBI BLAST search of [EYLSETYGNKFAAHISPAQGSPPPAASPGVR](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
119.5	3465.7317	0.0007	EYLSETYGNKFAAHISPAQGSPPPAASPGVR	Acetyl K10 100.00%
26.9	3465.7317	0.0007	EYLSETYGNKFAAHISPAQGSPPPAASPGVR	Acetyl K23 0.00%

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

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Mascot Search Results

Peptide View

MS/MS Fragmentation of **FAAHISPAQGSPKPPPAASPGVR**
Found in **ch06usp|P19484|TFEB_HUMAN** in **uni_human_nru**, Transcription factor EB OS=Homo sapiens GN=TFEB PE=1 SV=3 CH=ch06u

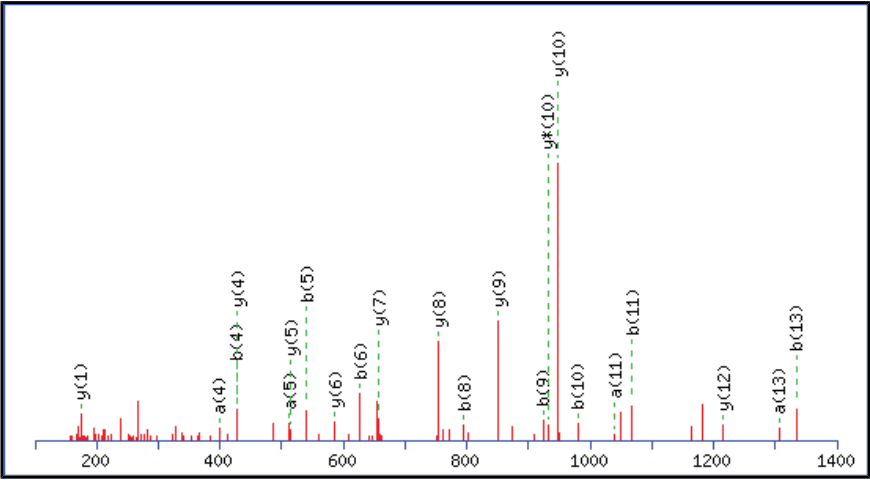
Match to Query 11491: 2281.195452 from(761.405760,3+) index(7286)
Title: Spectrum25027 scans:8284,
Data file File Name: 160611_TFEB_B.raw

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches ☐ Label matches used for scoring ☒

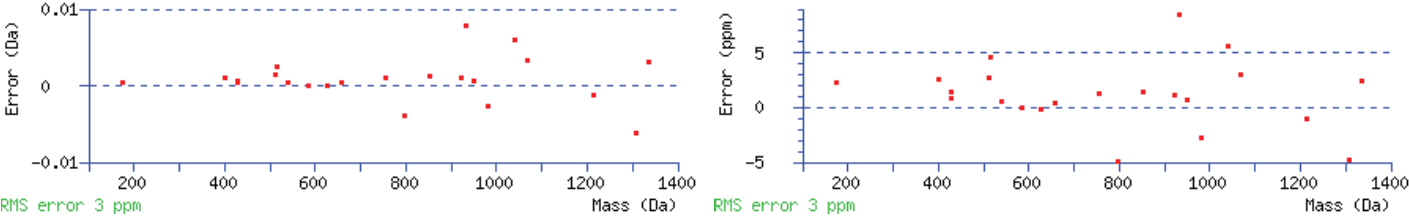
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2281.1967
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K13 : Acetyl (K)
Ions Score: 70 Expect: 9.8e-006
Matches : 22/232 fragment ions using 41 most intense peaks ([help](#))

#	a	a ⁺⁺	a [*]	a ^{*++}	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	120.0808	60.5440			148.0757	74.5415			F					23
2	191.1179	96.0626			219.1128	110.0600			A	2135.1356	1068.0714	2118.1091	1059.5582	22
3	262.1550	131.5811			290.1499	145.5786			A	2064.0985	1032.5529	2047.0720	1024.0396	21
4	399.2139	200.1106			427.2088	214.1081			H	1993.0614	997.0343	1976.0348	988.5211	20
5	512.2980	256.6526			540.2929	270.6501			I	1856.0025	928.5049	1838.9759	919.9916	19
6	599.3300	300.1686			627.3249	314.1661			S	1742.9184	871.9628	1725.8919	863.4496	18
7	696.3828	348.6950			724.3777	362.6925			P	1655.8864	828.4468	1638.8598	819.9336	17
8	767.4199	384.2136			795.4148	398.2110			A	1558.8336	779.9204	1541.8071	771.4072	16
9	895.4785	448.2429	878.4519	439.7296	923.4734	462.2403	906.4468	453.7271	Q	1487.7965	744.4019	1470.7700	735.8886	15
10	952.4999	476.7536	935.4734	468.2403	980.4948	490.7511	963.4683	482.2378	G	1359.7379	680.3726	1342.7114	671.8593	14
11	1039.5320	520.2696	1022.5054	511.7563	1067.5269	534.2671	1050.5003	525.7538	S	1302.7165	651.8619	1285.6899	643.3486	13
12	1136.5847	568.7960	1119.5582	560.2827	1164.5796	582.7935	1147.5531	574.2802	P	1215.6844	608.3459	1198.6579	599.8326	12
13	1306.6902	653.8488	1289.6637	645.3355	1334.6852	667.8462	1317.6586	659.3329	K	1118.6317	559.8195	1101.6051	551.3062	11
14	1403.7430	702.3751	1386.7165	693.8619	1431.7379	716.3726	1414.7114	707.8593	P	948.5261	474.7667	931.4996	466.2534	10
15	1500.7958	750.9015	1483.7692	742.3883	1528.7907	764.8990	1511.7641	756.3857	P	851.4734	426.2403	834.4468	417.7271	9
16	1597.8485	799.4279	1580.8220	790.9146	1625.8435	813.4254	1608.8169	804.9121	P	754.4206	377.7139	737.3941	369.2007	8
17	1668.8857	834.9465	1651.8591	826.4332	1696.8806	848.9439	1679.8540	840.4306	A	657.3679	329.1876	640.3413	320.6743	7
18	1739.9228	870.4650	1722.8962	861.9517	1767.9177	884.4625	1750.8911	875.9492	A	586.3307	293.6690	569.3042	285.1557	6

19	1826.9548	913.9810	1809.9282	905.4678	1854.9497	927.9785	1837.9232	919.4652	S	515.2936	258.1504	498.2671	249.6372	5
20	1924.0076	962.5074	1906.9810	953.9941	1952.0025	976.5049	1934.9759	967.9916	P	428.2616	214.6344	411.2350	206.1212	4
21	1981.0290	991.0181	1964.0025	982.5049	2009.0239	1005.0156	1991.9974	996.5023	G	331.2088	166.1081	314.1823	157.5948	3
22	2080.0974	1040.5524	2063.0709	1032.0391	2108.0924	1054.5498	2091.0658	1046.0365	V	274.1874	137.5973	257.1608	129.0840	2
23									R	175.1190	88.0631	158.0924	79.5498	1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.3	2281.1967	-0.0013	FAAHISPAQGSPKPPPAASPGVR
4.1	2281.1790	0.0165	PRPRWSGPPCLLPEPNLPR

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

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Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDEGPPGYEPLAPGHGSPFPSLSKK**
Found in **ch06usp|P19484|TFEB_HUMAN** in **uni_human_nru**, Transcription factor EB OS=Homo sapiens GN=TFEB PE=1 SV=3 CH=ch06u

Match to Query 13951: 2731.297272 from(911.439700,3+) index(13253)
Title: Spectrum30915 scans:14898,
Data file File Name: 160611_TFEB_D.raw

Click mouse within plot area to zoom in by factor of two about that point

Or,

Plot from

0

 to

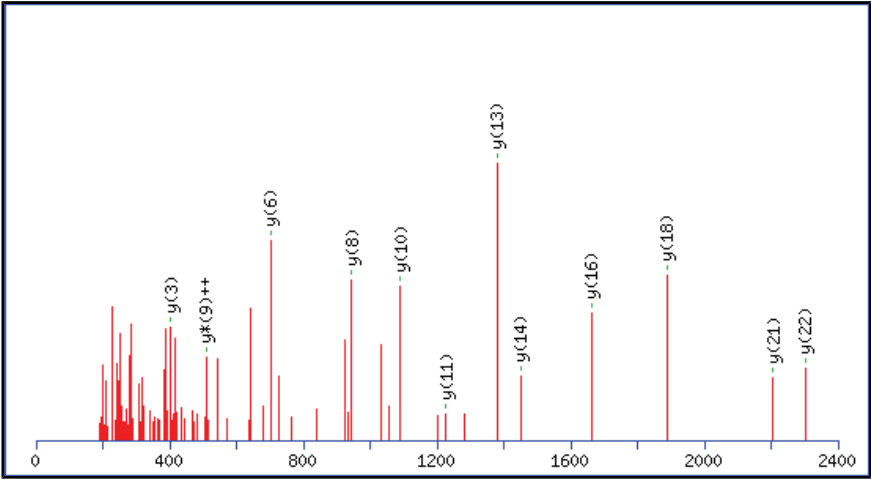
2400

 Da

Full range

Label all possible matches ☐ Label matches used for scoring ☒

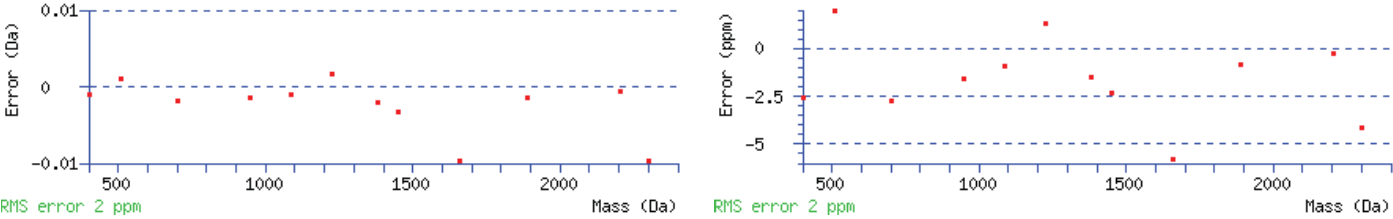
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2731.3129
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications: **K26** : Acetyl (K)
Ions Score: 84 Expect: 5.5e-007
Matches : 12/204 fragment ions using 16 most intense peaks ([help](#))

#	a	a ⁺⁺	a [*]	a ^{*++}	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	102.0550	51.5311			130.0499	65.5286			E					26
2	217.0819	109.0446			245.0768	123.0420			D	2603.2776	1302.1425	2586.2511	1293.6292	25
3	346.1245	173.5659			374.1194	187.5633			E	2488.2507	1244.6290	2471.2242	1236.1157	24
4	403.1460	202.0766			431.1409	216.0741			G	2359.2081	1180.1077	2342.1816	1171.5944	23
5	500.1987	250.6030			528.1936	264.6005			P	2302.1866	1151.5970	2285.1601	1143.0837	22
6	597.2515	299.1294			625.2464	313.1268			P	2205.1339	1103.0706	2188.1073	1094.5573	21
7	654.2729	327.6401			682.2679	341.6376			G	2108.0811	1054.5442	2091.0546	1046.0309	20
8	817.3363	409.1718			845.3312	423.1692			Y	2051.0597	1026.0335	2034.0331	1017.5202	19
9	914.3890	457.6982			942.3840	471.6956			P	1887.9963	944.5018	1870.9698	935.9885	18
10	1043.4316	522.2195			1071.4265	536.2169			E	1790.9436	895.9754	1773.9170	887.4621	17
11	1140.4844	570.7458			1168.4793	584.7433			P	1661.9010	831.4541	1644.8744	822.9408	16
12	1253.5685	627.2879			1281.5634	641.2853			L	1564.8482	782.9277	1547.8217	774.4145	15
13	1324.6056	662.8064			1352.6005	676.8039			A	1451.7641	726.3857	1434.7376	717.8724	14
14	1421.6583	711.3328			1449.6533	725.3303			P	1380.7270	690.8672	1363.7005	682.3539	13
15	1478.6798	739.8435			1506.6747	753.8410			G	1283.6743	642.3408	1266.6477	633.8275	12
16	1615.7387	808.3730			1643.7336	822.3705			H	1226.6528	613.8300	1209.6262	605.3168	11
17	1672.7602	836.8837			1700.7551	850.8812			G	1089.5939	545.3006	1072.5673	536.7873	10
18	1759.7922	880.3997			1787.7871	894.3972			S	1032.5724	516.7898	1015.5459	508.2766	9

19	1856.8450	928.9261			1884.8399	942.9236			P	945.5404	473.2738	928.5138	464.7606	8
20	2003.9134	1002.4603			2031.9083	1016.4578			F	848.4876	424.7475	831.4611	416.2342	7
21	2100.9661	1050.9867			2128.9611	1064.9842			P	701.4192	351.2132	684.3927	342.7000	6
22	2187.9982	1094.5027			2215.9931	1108.5002			S	604.3665	302.6869	587.3399	294.1736	5
23	2301.0822	1151.0448			2329.0772	1165.0422			L	517.3344	259.1709	500.3079	250.6576	4
24	2388.1143	1194.5608			2416.1092	1208.5582			S	404.2504	202.6288	387.2238	194.1155	3
25	2516.2092	1258.6083	2499.1827	1250.0950	2544.2041	1272.6057	2527.1776	1264.0924	K	317.2183	159.1128	300.1918	150.5995	2
26									K	189.1234	95.0653	172.0968	86.5520	1



NCBI BLAST search of [EDEGPPGYPEPLAPGHGSPFPSLSKK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
84.3	2731.3129	-0.0157	EDEGPPGYPEPLAPGHGSPFPSLSKK	Acetyl K26 50.00%
84.3	2731.3129	-0.0157	EDEGPPGYPEPLAPGHGSPFPSLSKK	Acetyl K25 50.00%

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