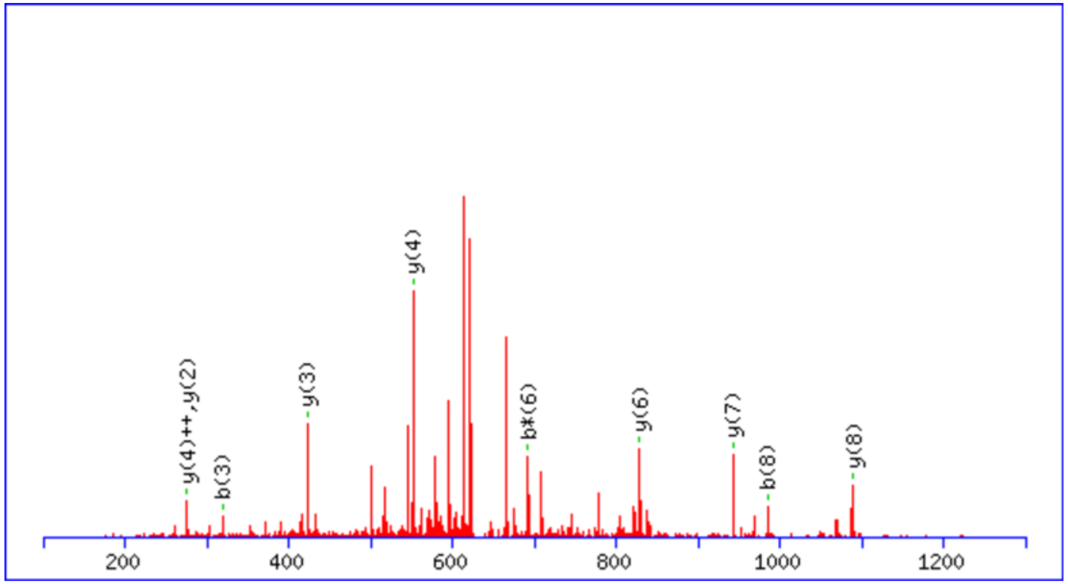
Peptide View

MS/MS Fragmentation of **GNFNYIEFTR**
Found in **IPI00033494**, Tax_Id=9606 Gene_Symbol=MYL12B Myosin regulatory light chain 12B
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 6033: 1259.593648 from(630.804100,2+)
Title: OECHL100310_13.15722.15722.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1259.593475**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53 **Expect:** 0.00059**Matches :** 10/92 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	58.028740	29.518008					**G**						
2	172.071667	86.539471	155.045118	78.026197			**N**	1203.579299	602.293288	1186.552750	593.780013	1185.568734	593.2880
3	**319.140081**	160.073678	302.113532	151.560404			**F**	***1089.536372***	545.271824	1072.509823	536.758549	1071.525807	536.2665
4	433.183008	217.095142	416.156459	208.581867			**N**	***942.467958***	471.737617	925.441409	463.224342	924.457393	462.7323
5	596.246337	298.626807	579.219788	290.113532			**Y**	***828.425031***	414.716154	811.398482	406.202879	810.414466	405.7108
6	709.330401	355.168839	692.303852	346.655564			**I**	665.361702	333.184489	648.335153	324.671214	647.351137	324.1792
7	838.372994	419.690135	821.346445	411.176861	820.362429	410.684853	**E**	***552.277638***	276.642457	535.251089	268.129182	534.267073	267.6371
8	**985.441408**	493.224342	968.414859	484.711068	967.430843	484.219060	**F**	***423.235045***	212.121160	406.208496	203.607886	405.224480	203.1158
9	1086.489087	543.748181	1069.462538	535.234907	1068.478522	534.742899	**T**	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.5816
10							**R**	175.118952	88.063114	158.092403	79.549839		



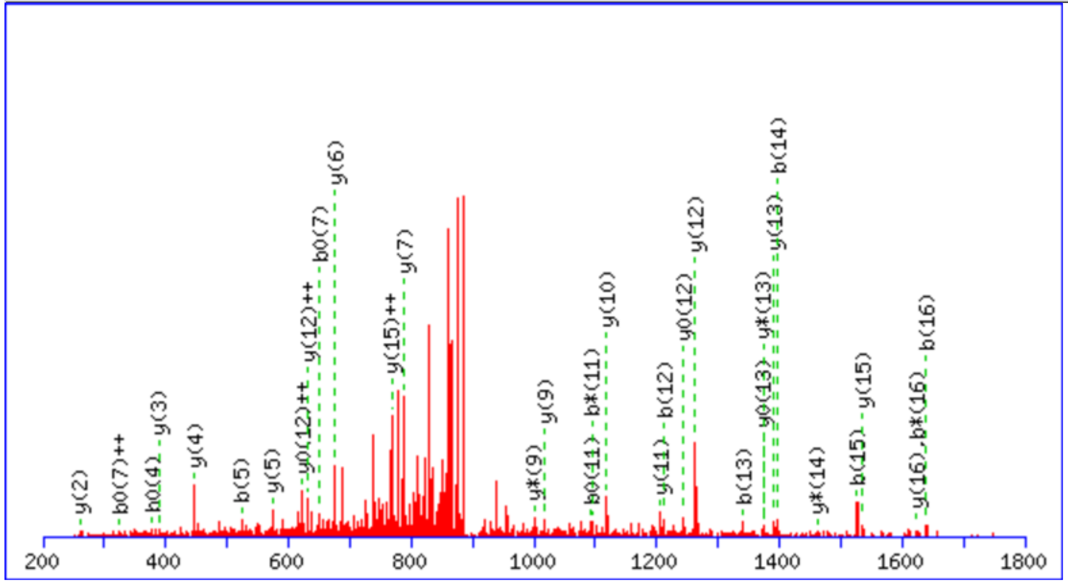
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 11652: 1784.879648 from(893.447100,2+)
Title: OECHL100310_13.7733.7733.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60 **Expect:** 0.00014**Matches :** 33/170 fragment ions using 89 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	164.070605	82.538940					Y						
2	251.102633	126.054954			233.092068	117.049672	S	***1622.823172***	811.915224	1605.796623	803.401950	1604.812607	802.9099
3	308.124097	154.565687			290.113532	145.560404	G	***1535.791144***	768.399210	1518.764595	759.885936	1517.780579	759.3939
4	395.156125	198.081701			377.145560	189.076418	S	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.8831
5	**524.198718**	262.602997			506.188153	253.597715	E	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.3671

6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.8458
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.3351
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.8191
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.2952
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.2660
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.7421
12	**1212.537889**	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.2001
13	**1340.632852**	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.6762
14	**1397.654316**	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.6288
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	***389.239461***	195.123368	372.212912	186.610094	371.228896	186.1180
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		



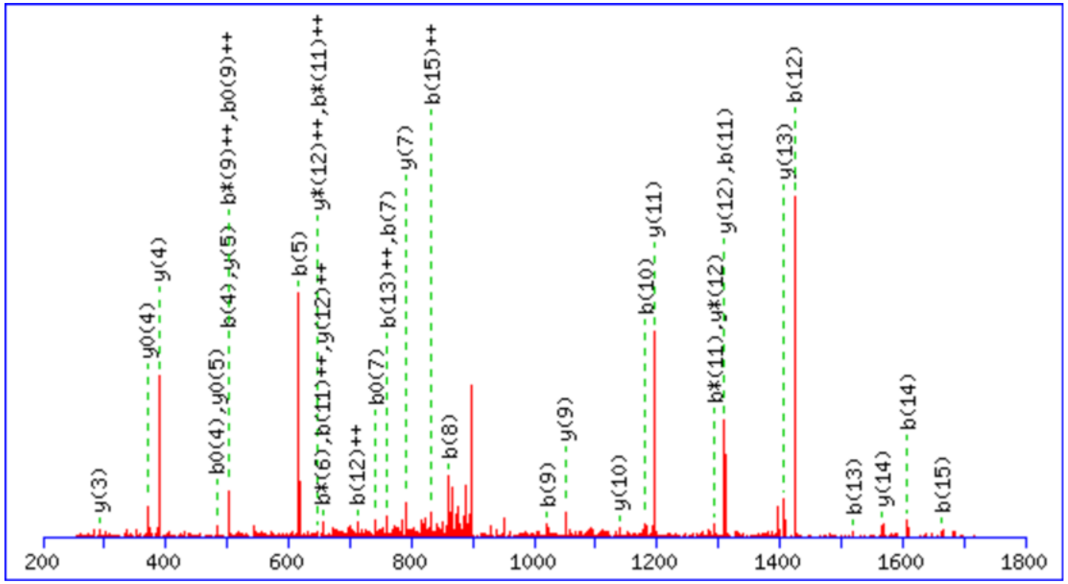
Peptide View

MS/MS Fragmentation of **SRCPDGSTCCELPSGK**

Found in **IPI00182138**, Tax_Id=9606 Gene_Symbol=GRN Isoform 2 of Granulins
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 11860: 1809.746448 from(905.880500,2+)
Title: OECHL100310_13.4915.4915.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1809.744415**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70 **Expect:** 3e-006**Matches :** 37/174 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	88.039304	44.523290			70.028739	35.518008	**S**						
2	244.140415	122.573845	227.113866	114.060571	226.129850	113.568563	**R**	1723.719653	862.363465	1706.693104	853.850190	1705.709088	853.3581
3	404.171064	202.589170	387.144515	194.075896	386.160499	193.583888	**C**	***1567.618542***	784.312909	1550.591993	775.799635	1549.607977	775.3076
4	***501.223828***	251.115552	484.197279	242.602277	483.213263	242.110269	**P**	***1407.587893***	704.297585	1390.561344	695.784310	1389.577328	695.2923
5	***616.250771***	308.629024	599.224222	300.115749	598.240206	299.623741	**D**	***1310.535129***	655.771203	1293.508580	647.257928	1292.524564	646.7659
6	673.272235	337.139756	656.245686	328.626481	655.261670	328.134473	**G**	***1195.508186***	598.257731	1178.481637	589.744457	1177.497621	589.2524
7	***760.304263***	380.655770	743.277714	372.142495	742.293698	371.650487	**S**	***1138.486722***	569.746999	1121.460173	561.233725	1120.476157	560.7417
8	***861.351942***	431.179609	844.325393	422.666335	843.341377	422.174327	**T**	***1051.454694***	526.230985	1034.428145	517.717711	1033.444129	517.2257
9	***1021.382591***	511.194934	1004.356042	502.681659	1003.372026	502.189651	**C**	950.407015	475.707146	933.380466	467.193871	932.396450	466.7018
10	***1181.413240***	591.210258	1164.386691	582.696984	1163.402675	582.204976	**C**	***790.376366***	395.691821	773.349817	387.178547	772.365801	386.6865
11	***1310.455833***	**655.731555**	1293.429284	647.218280	1292.445268	646.726272	**E**	630.345717	315.676497	613.319168	307.163222	612.335152	306.6712
12	***1423.539897***	**712.273587**	1406.513348	703.760312	1405.529332	703.268304	**L**	***501.303124***	251.155200	484.276575	242.641925	483.292559	242.1499
13	***1520.592661***	**760.799969**	1503.566112	752.286694	1502.582096	751.794686	**P**	***388.219060***	194.613168	371.192511	186.099894	370.208495	185.6078
14	***1607.624689***	804.315983	1590.598140	795.802708	1589.614124	795.310700	**S**	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.0815
15	***1664.646153***	**832.826715**	1647.619604	824.313440	1646.635588	823.821432	**G**	204.134268	102.570772	187.107719	94.057497		
16							**K**	147.112804	74.060040	130.086255	65.546765		



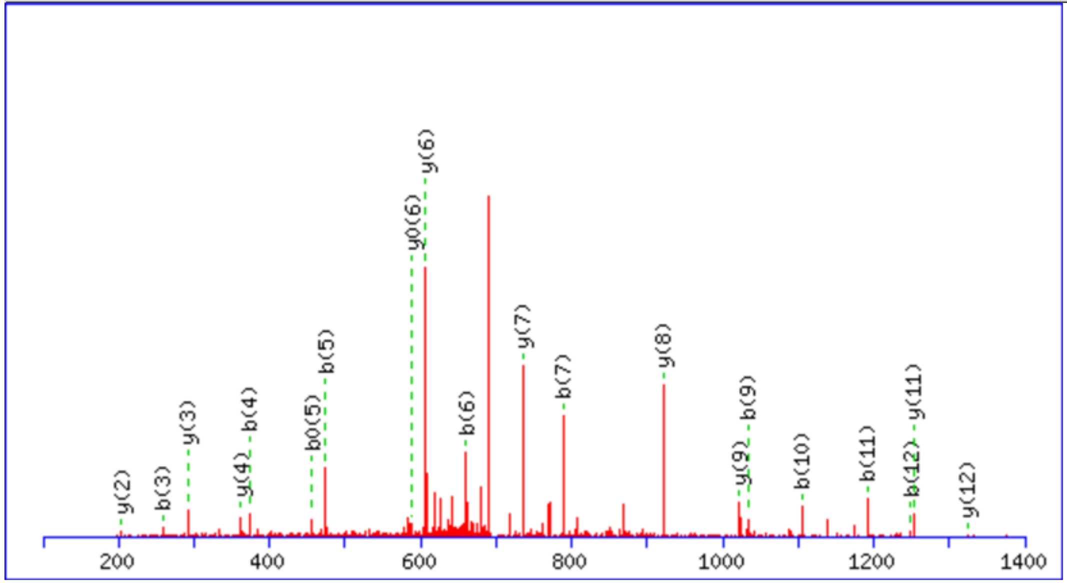
Peptide View

MS/MS Fragmentation of **AADDTWEPFASGK**
Found in **IPI00022432**, Tax_Id=9606 Gene_Symbol=TTR Transthyretin
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 7500: 1393.614848 from(697.814700,2+)
Title: OECHL100310_13.14428.14428.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1393.615005**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70 **Expect:** 6.1e-006**Matches :** 20/112 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							13
2	143.081504	72.044390			A	***1323.585173***	662.296225	1306.558624	653.782950	1305.574608	653.290942	12
3	***258.108447***	129.557862	240.097882	120.552579	D	***1252.548059***	626.777668	1235.521510	618.264393	1234.537494	617.772385	11
4	***373.135390***	187.071333	355.124825	178.066051	D	1137.521116	569.264196	1120.494567	560.750922	1119.510551	560.258914	10
5	***474.183069***	237.595173	456.172504	228.589890	T	***1022.494173***	511.750725	1005.467624	503.237450	1004.483608	502.745442	9

6	***660.262382***	330.634829	642.251817	321.629547	**W**	***921.446494***	461.226885	904.419945	452.713611	903.435929	452.221603	**8**
7	***789.304975***	395.156126	771.294410	386.150843	**E**	***735.367181***	368.187229	718.340632	359.673954	717.356616	359.181946	**7**
8	886.357739	443.682508	868.347174	434.677225	**P**	***606.324588***	303.665932	589.298039	295.152658	588.314023	294.660650	**6**
9	***1033.426153***	517.216715	1015.415588	508.211432	**F**	509.271824	255.139550	492.245275	246.626275	491.261259	246.134267	**5**
10	***1104.463267***	552.735272	1086.452702	543.729989	**A**	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	**4**
11	***1191.495295***	596.251286	1173.484730	587.246003	**S**	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	**3**
12	***1248.516759***	624.762018	1230.506194	615.756735	**G**	***204.134268***	102.570772	187.107719	94.057497			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**



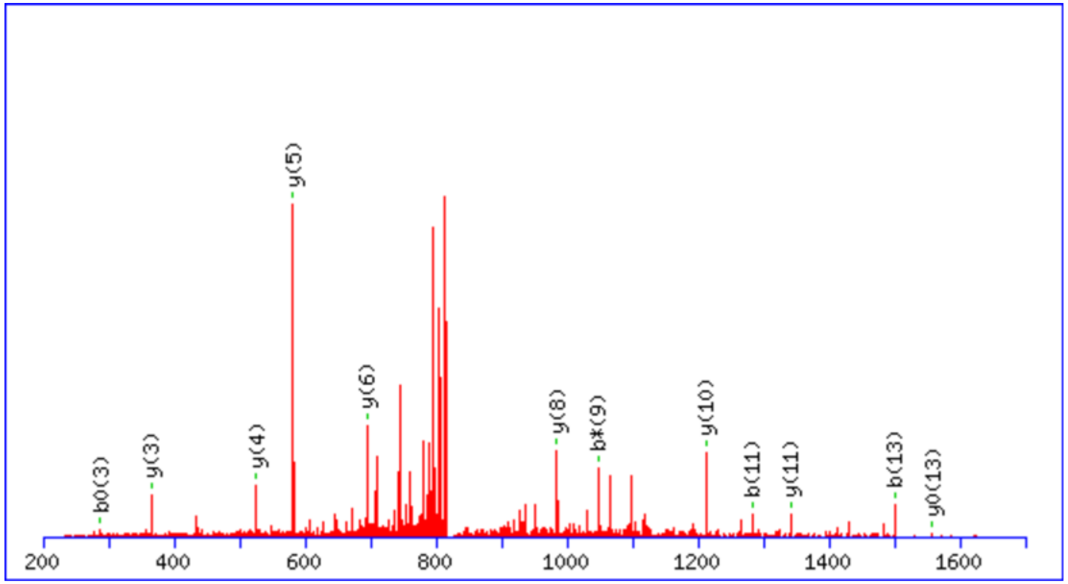
Peptide View

MS/MS Fragmentation of **ASFENNCEIGCFAK**
Found in **IPI00010105**, Tax_Id=9606 Gene_Symbol=EIF6 Eukaryotic translation initiation factor 6
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 10343: 1645.687048 from(823.850800,2+)
Title: OECHL100310_13.12993.12993.2.dta

Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1645.686462**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56 **Expect:** 7.7e-005**Matches :** 12/134 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	72.044390	36.525833					**A**						
2	159.076418	80.041847			141.065853	71.036564	**S**	1575.656640	788.331958	1558.630091	779.818684	1557.646075	779.3266
3	306.144832	153.576054			288.134267	144.570772	**F**	1488.624612	744.815944	1471.598063	736.302670	1470.614047	735.8106
4	435.187425	218.097351			417.176860	209.092068	**E**	***1341.556198***	671.281737	1324.529649	662.768463	1323.545633	662.2764
5	549.230352	275.118814	532.203803	266.605540	531.219787	266.113532	**N**	***1212.513605***	606.760441	1195.487056	598.247166	1194.503040	597.7551
6	663.273279	332.140278	646.246730	323.627003	645.262714	323.134995	**N**	1098.470678	549.738977	1081.444129	541.225703	1080.460113	540.7336
7	823.303928	412.155602	806.277379	403.642328	805.293363	403.150320	**C**	***984.427751***	492.717514	967.401202	484.204239	966.417186	483.7122
8	952.346521	476.676899	935.319972	468.163624	934.335956	467.671616	**E**	824.397102	412.702189	807.370553	404.188915	806.386537	403.6969
9	1065.430585	533.218931	1048.404036	524.705656	1047.420020	524.213648	**I**	***695.354509***	348.180893	678.327960	339.667618		
10	1122.452049	561.729663	1105.425500	553.216388	1104.441484	552.724380	**G**	***582.270445***	291.638861	565.243896	283.125586		
11	**1282.482698**	641.744987	1265.456149	633.231713	1264.472133	632.739705	**C**	***525.248981***	263.128129	508.222432	254.614854		
12	1429.551112	715.279194	1412.524563	706.765920	1411.540547	706.273912	**F**	***365.218332***	183.112804	348.191783	174.599530		
13	**1500.588226**	750.797751	1483.561677	742.284477	1482.577661	741.792469	**A**	218.149918	109.578597	201.123369	101.065322		
14							**K**	147.112804	74.060040	130.086255	65.546765		



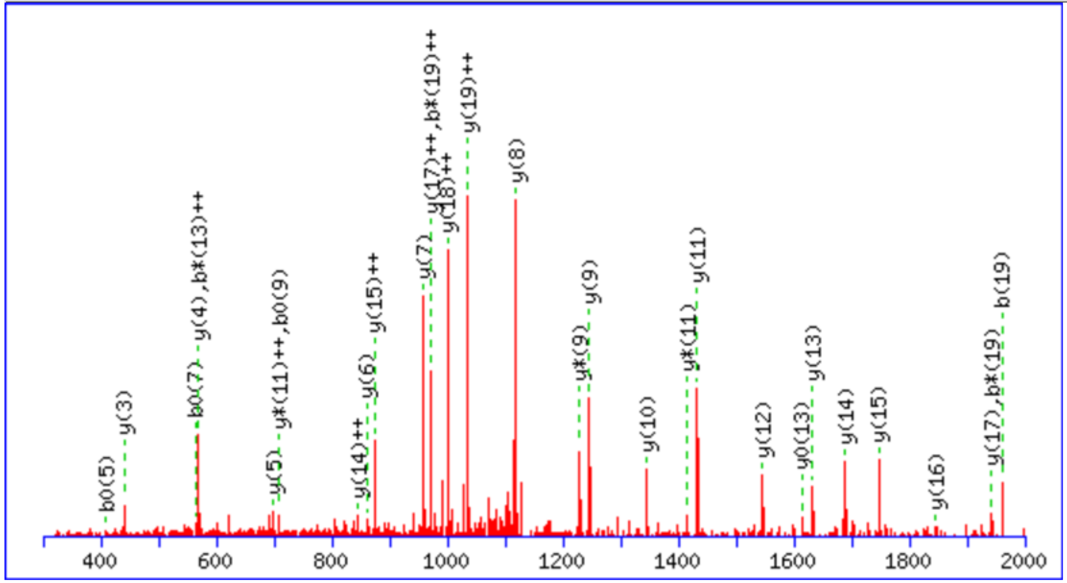
Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 14381: 2270.109448 from(1136.062000,2+)
Title: OECHL100310_13.10018.10018.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 95 **Expect:** 6.4e-008**Matches :** 31/212 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	
1	102.054955	51.531116			84.044390	42.525833	**T**						
2	201.123369	101.065322			183.112804	92.060040	**V**	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400	10
3	272.160483	136.583879			254.149918	127.578597	**A**	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986	10
4	329.181947	165.094611			311.171382	156.089329	**G**	1999.965437	1000.486357	1982.938888	991.973082	1981.954872	9
5	426.234711	213.620994			408.224146	204.615711	**P**	***1942.943973***	971.975625	1925.917424	963.462350	1924.933408	9

6	525.303125	263.155201			507.292560	254.149918	**V**	***1845.891209***	923.449243	1828.864660	914.935968	1827.880644	9
7	582.324589	291.665933			564.314024	282.660650	**G**	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230	8
8	639.346053	320.176665			621.335488	311.171382	**G**	***1689.801331***	845.404304	1672.774782	836.891029	1671.790766	8
9	726.378081	363.692679			708.367516	354.687396	**S**	***1632.779867***	816.893572	1615.753318	808.380297	1614.769302	8
10	839.462145	420.234711			821.451580	411.229428	**L**	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274	7
11	926.494173	463.750725			908.483608	454.745442	**S**	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210	7
12	1025.562587	513.284932			1007.552022	504.279649	**V**	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182	6
13	1153.621165	577.314221	1136.594616	568.800946	1135.610600	568.308938	**Q**	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768	6
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	**C**	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190	5
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	**P**	***958.474106***	479.740691	941.447557	471.227417	940.463541	4
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	**Y**	***861.421342***	431.214309	844.394793	422.701035	843.410777	4
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	**E**	***698.358013***	349.682645	681.331464	341.169370	680.347448	3
18	1830.905463	915.956370	1813.878914	907.443095	1812.894898	906.951087	**K**	***569.315420***	285.161348	552.288871	276.648074	551.304855	2
19	1959.948056	980.477666	1942.921507	971.964392	1941.937491	971.472384	**E**	***441.220457***	221.113867	424.193908	212.600592	423.209892	2
20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	**H**	312.177864	156.592570	295.151315	148.079295		
21							**R**	175.118952	88.063114	158.092403	79.549839		



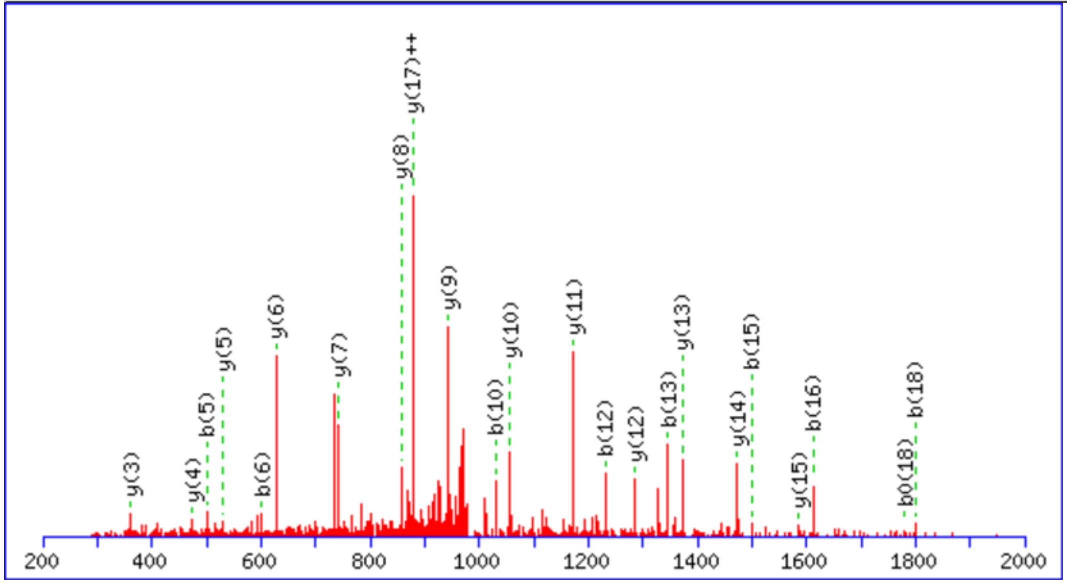
Peptide View

MS/MS Fragmentation of **AFPALTSLDLSDNPGLGER**
Found in **IPI00029260**, Tax_Id=9606 Gene_Symbol=CD14 Monocyte differentiation antigen CD14
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 12942: 1971.991248 from(987.002900,2+)
Title: OECHL100310_13.18049.18049.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1971.990158**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 104 **Expect:** 5.5e-009**Matches :** 23/180 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	72.044390	36.525833					A						
2	219.112804	110.060040					F	1901.960333	951.483805	1884.933784	942.970530	1883.949768	942.4785
3	316.165568	158.586422					P	1754.891919	877.949597	1737.865370	869.436323	1736.881354	868.9443
4	387.202682	194.104979					A	1657.839155	829.423215	1640.812606	820.909941	1639.828590	820.4179
5	**500.286746**	250.647011					L	***1586.802041***	793.904659	1569.775492	785.391384	1568.791476	784.8993
6	**601.334425**	301.170851			583.323860	292.165568	T	***1473.717977***	737.362627	1456.691428	728.849352	1455.707412	728.3573
7	688.366453	344.686865			670.355888	335.681582	S	***1372.670298***	686.838787	1355.643749	678.325513	1354.659733	677.8335
8	801.450517	401.228897			783.439952	392.223614	L	***1285.638270***	643.322773	1268.611721	634.809499	1267.627705	634.3174
9	916.477460	458.742368			898.466895	449.737085	D	***1172.554206***	586.780741	1155.527657	578.267467	1154.543641	577.7754
10	**1029.561524**	515.284400			1011.550959	506.279117	L	***1057.527263***	529.267270	1040.500714	520.753995	1039.516698	520.2619
11	1116.593552	558.800414			1098.582987	549.795132	S	***944.443199***	472.725238	927.416650	464.211963	926.432634	463.7199
12	**1231.620495**	616.313886			1213.609930	607.308603	D	***857.411171***	429.209224	840.384622	420.695949	839.400606	420.2039
13	**1345.663422**	673.335349	1328.636873	664.822075	1327.652857	664.330067	N	***742.384228***	371.695752	725.357679	363.182477	724.373663	362.6904
14	1442.716186	721.861731	1425.689637	713.348457	1424.705621	712.856449	P	***628.341301***	314.674288	611.314752	306.161014	610.330736	305.6690
15	**1499.737650**	750.372463	1482.711101	741.859189	1481.727085	741.367181	G	***531.288537***	266.147906	514.261988	257.634632	513.277972	257.1426
16	**1612.821714**	806.914495	1595.795165	798.401221	1594.811149	797.909212	L	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.6318
17	1669.843178	835.425227	1652.816629	826.911952	1651.832613	826.419944	G	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.0898
18	**1798.885771**	899.946524	1781.859222	891.433249	1780.875206	890.941241	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.5791

19							**R**	175.118952	88.063114	158.092403	79.549839		



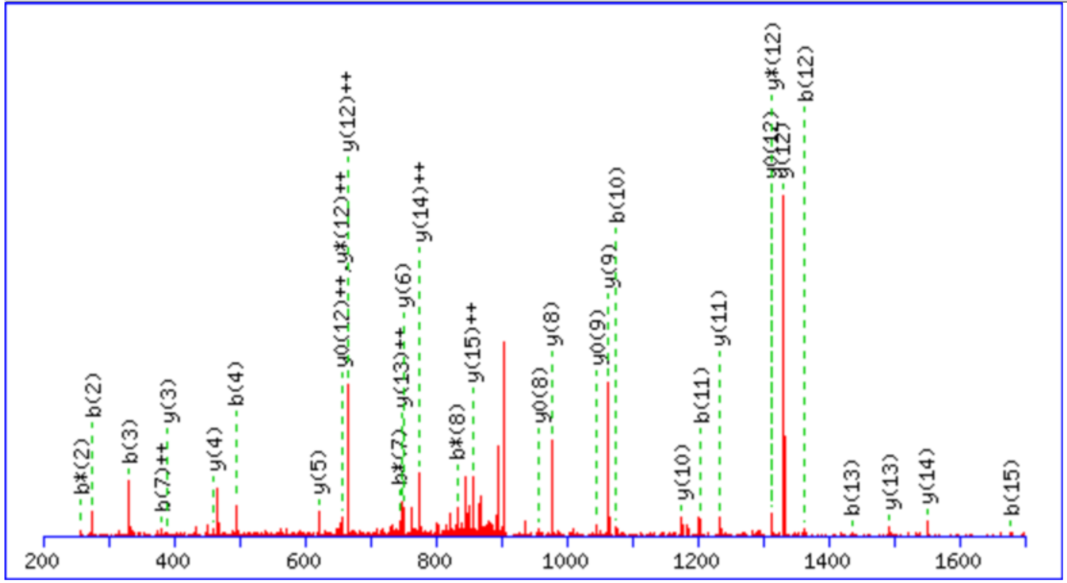
Peptide View

MS/MS Fragmentation of **NCGYPGISPEECASRK**
Found in **IPI00010675**, Tax_Id=9606 Gene_Symbol=TFF2 Trefoil factor 2
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 11960: 1823.794448 from(912.904500,2+)
Title: OECHL100310_13.8023.8023.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1823.793045**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 51 **Expect:** 0.00053**Matches :** 33/162 fragment ions using 75 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}
1	115.050203	58.028740	98.023654	49.515465			**N**						
2	**275.080852**	138.044064	258.054303	129.530790			**C**	1710.757418	855.882347	1693.730869	847.369073	1692.746853	846.8770
3	**332.102316**	166.554796	315.075767	158.041521			**G**	***1550.726769***	775.867023	1533.700220	767.353748	1532.716204	766.8617
4	**495.165645**	248.086460	478.139096	239.573186			**Y**	***1493.705305***	747.356291	1476.678756	738.843016	1475.694740	738.3510

5	592.218409	296.612843	575.191860	288.099568			**P**	***1330.641976***	665.824626	1313.615427	657.311352	1312.631411	656.8193
6	649.239873	325.123575	632.213324	316.610300			**G**	***1233.589212***	617.298244	1216.562663	608.784970	1215.578647	608.2929
7	762.323937	381.665607	745.297388	373.152332			**I**	***1176.567748***	588.787512	1159.541199	580.274238	1158.557183	579.7822
8	849.355965	425.181621	832.329416	416.668346	831.345400	416.176338	**S**	***1063.483684***	532.245480	1046.457135	523.732206	1045.473119	523.2401
9	946.408729	473.708003	929.382180	465.194728	928.398164	464.702720	**P**	***976.451656***	488.729466	959.425107	480.216192	958.441091	479.7241
10	**1075.451322**	538.229299	1058.424773	529.716025	1057.440757	529.224017	**E**	879.398892	440.203084	862.372343	431.689810	861.388327	431.1978
11	**1204.493915**	602.750596	1187.467366	594.237321	1186.483350	593.745313	**E**	***750.356299***	375.681788	733.329750	367.168513	732.345734	366.6765
12	**1364.524564**	682.765920	1347.498015	674.252646	1346.513999	673.760638	**C**	***621.313706***	311.160491	604.287157	302.647217	603.303141	302.1552
13	**1435.561678**	718.284477	1418.535129	709.771203	1417.551113	709.279195	**A**	***461.283057***	231.145166	444.256508	222.631892	443.272492	222.1398
14	1522.593706	761.800491	1505.567157	753.287217	1504.583141	752.795209	**S**	***390.245943***	195.626610	373.219394	187.113335	372.235378	186.6213
15	**1678.694817**	839.851047	1661.668268	831.337772	1660.684252	830.845764	**R**	303.213915	152.110595	286.187366	143.597321		
16							**K**	147.112804	74.060040	130.086255	65.546765		



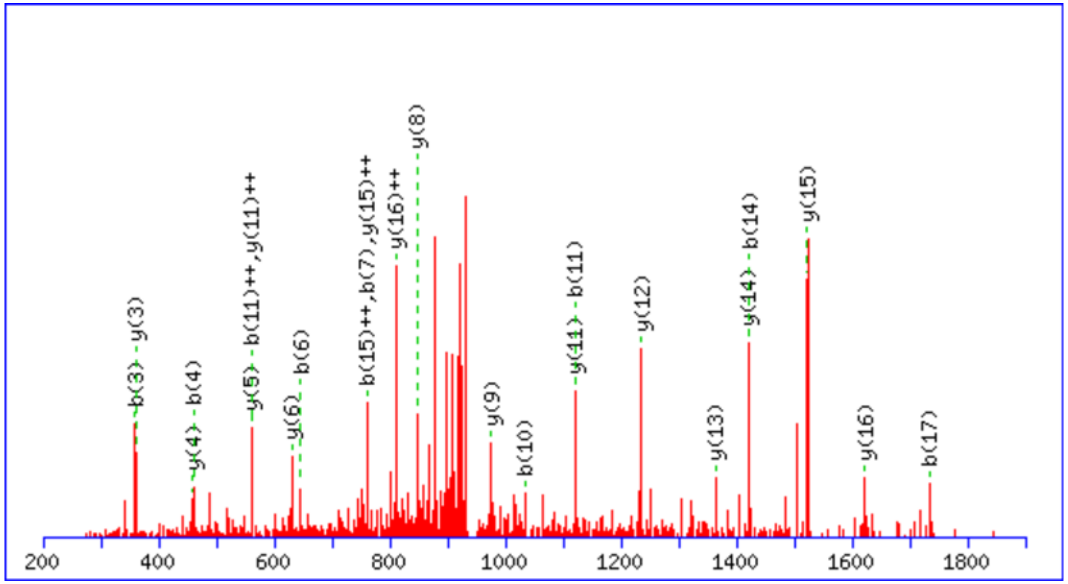
Peptide View

MS/MS Fragmentation of **CVVTGEDGSESEATVNVK**

Found in **IPI00385035**, Tax_Id=9606 Gene_Symbol=NCAM1 Neural cell adhesion molecule (Fragment)
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 12417: 1879.850248 from(940.932400,2+)
Title: OECHL100310_13.8354.8354.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1879.846954**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 95 **Expect:** 3.3e-008**Matches :** 25/160 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}
1	161.037925	81.022600					C						
2	260.106339	130.556807					V	1720.823565	860.915421	1703.797016	852.402146	1702.813000	851.9101
3	**359.174753**	180.091015					V	***1621.755151***	811.381214	1604.728602	802.867939	1603.744586	802.3759
4	**460.222432**	230.614854			442.211867	221.609572	T	***1522.686737***	761.847007	1505.660188	753.333732	1504.676172	752.8417
5	517.243896	259.125586			499.233331	250.120304	G	***1421.639058***	711.323167	1404.612509	702.809893	1403.628493	702.3178
6	**646.286489**	323.646883			628.275924	314.641600	E	***1364.617594***	682.812435	1347.591045	674.299161	1346.607029	673.8071
7	**761.313432**	381.160354			743.302867	372.155072	D	***1235.575001***	618.291139	1218.548452	609.777864	1217.564436	609.2858
8	818.334896	409.671086			800.324331	400.665804	G	***1120.548058***	560.777667	1103.521509	552.264393	1102.537493	551.7723
9	905.366924	453.187100			887.356359	444.181818	S	1063.526594	532.266935	1046.500045	523.753661	1045.516029	523.2616
10	**1034.409517**	517.708397			1016.398952	508.703114	E	***976.494566***	488.750921	959.468017	480.237647	958.484001	479.7456
11	**1121.441545**	**561.224411**			1103.430980	552.219128	S	***847.451973***	424.229625	830.425424	415.716350	829.441408	415.2243
12	1250.484138	625.745707			1232.473573	616.740425	E	760.419945	380.713611	743.393396	372.200336	742.409380	371.7083
13	1321.521252	661.264264			1303.510687	652.258982	A	***631.377352***	316.192314	614.350803	307.679040	613.366787	307.1870
14	**1422.568931**	711.788104			1404.558366	702.782821	T	***560.340238***	280.673757	543.313689	272.160483	542.329673	271.6684
15	1521.637345	**761.322311**			1503.626780	752.317028	V	***459.292559***	230.149918	442.266010	221.636643		
16	1635.680272	818.343774	1618.653723	809.830500	1617.669707	809.338492	N	***360.224145***	180.615711	343.197596	172.102436		
17	**1734.748686**	867.877981	1717.722137	859.364707	1716.738121	858.872699	V	246.181218	123.594247	229.154669	115.080973		
18							K	147.112804	74.060040	130.086255	65.546765		



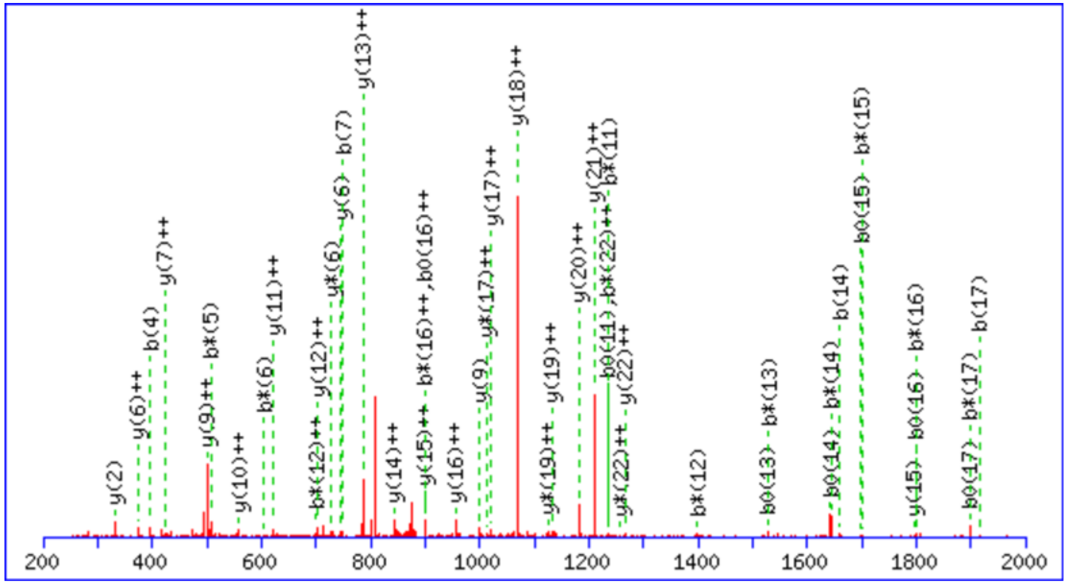
Peptide View

MS/MS Fragmentation of **QLGPQPQDIIYYEDGVVPTTDRR**
Found in **IPI00015199**, Tax_Id=9606 Gene_Symbol=CD7 T-cell antigen CD7
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 15475: 2659.326372 from(887.449400,3+)
Title: OECHL100310_13.16195.16195.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 2659.324203**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 65 **Expect:** 6.5e-005**Matches :** 47/246 fragment ions using 120 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	
1	129.065854	65.036565	112.039305	56.523291			Q						
2	242.149918	121.578597	225.123369	113.065323			L	2532.272897	1266.640086	2515.246348	1258.126812	2514.262332	12
3	299.171382	150.089329	282.144833	141.576055			G	2419.188833	1210.098054	2402.162284	1201.584780	2401.178268	12
4	**396.224146**	198.615711	379.197597	190.102436			P	2362.167369	1181.587322	2345.140820	1173.074048	2344.156804	11
5	524.282724	262.645000	507.256175	254.131726			Q	2265.114605	1133.060940	2248.088056	1124.547666	2247.104040	11

6	621.335488	311.171382	604.308939	302.658108			**P**	2137.056027	1069.031651	2120.029478	1060.518377	2119.045462	10
7	**749.394066**	375.200671	732.367517	366.687397			**Q**	2040.003263	1020.505269	2022.976714	1011.991995	2021.992698	10
8	864.421009	432.714143	847.394460	424.200868	846.410444	423.708860	**D**	1911.944685	956.475980	1894.918136	947.962706	1893.934120	9
9	977.505073	489.256175	960.478524	480.742900	959.494508	480.250892	**I**	**1796.917742**	898.962509	1779.891193	890.449234	1778.907177	8
10	1090.589137	545.798206	1073.562588	537.284932	1072.578572	536.792924	**I**	1683.833678	842.420477	1666.807129	833.907202	1665.823113	8
11	1253.652466	627.329871	1236.625917	618.816597	1235.641901	618.324589	**Y**	1570.749614	785.878445	1553.723065	777.365170	1552.739049	7
12	1416.715795	708.861536	1399.689246	700.348261	1398.705230	699.856253	**Y**	1407.686285	704.346780	1390.659736	695.833506	1389.675720	6
13	1545.758388	773.382832	1528.731839	764.869558	1527.747823	764.377549	**E**	1244.622956	622.815116	1227.596407	614.301841	1226.612391	6
14	**1660.785331**	830.896304	1643.758782	822.383029	1642.774766	821.891021	**D**	1115.580363	558.293819	1098.553814	549.780545	1097.569798	5
15	1717.806795	859.407036	1700.780246	850.893761	1699.796230	850.401753	**G**	**1000.553420**	500.780348	983.526871	492.267073	982.542855	4
16	1816.875209	908.941243	1799.848660	900.427968	1798.864644	899.935960	**V**	943.531956	472.269616	926.505407	463.756341	925.521391	4
17	**1915.943623**	958.475450	1898.917074	949.962175	1897.933058	949.470167	**V**	844.463542	422.735409	827.436993	414.222134	826.452977	4
18	2012.996387	1007.001832	1995.969838	998.488557	1994.985822	997.996549	**P**	**745.395128**	373.201202	728.368579	364.687927	727.384563	3
19	2114.044066	1057.525671	2097.017517	1049.012396	2096.033501	1048.520388	**T**	648.342364	324.674820	631.315815	316.161545	630.331799	3
20	2215.091745	1108.049510	2198.065196	1099.536236	2197.081180	1099.044228	**T**	547.294685	274.150980	530.268136	265.637706	529.284120	2
21	2330.118688	1165.562982	2313.092139	1157.049707	2312.108123	1156.557699	**D**	446.247006	223.627141	429.220457	215.113866	428.236441	2
22	2486.219799	1243.613537	2469.193250	1235.100263	2468.209234	1234.608255	**R**	**331.220063**	166.113669	314.193514	157.600395		
23							**R**	175.118952	88.063114	158.092403	79.549839		



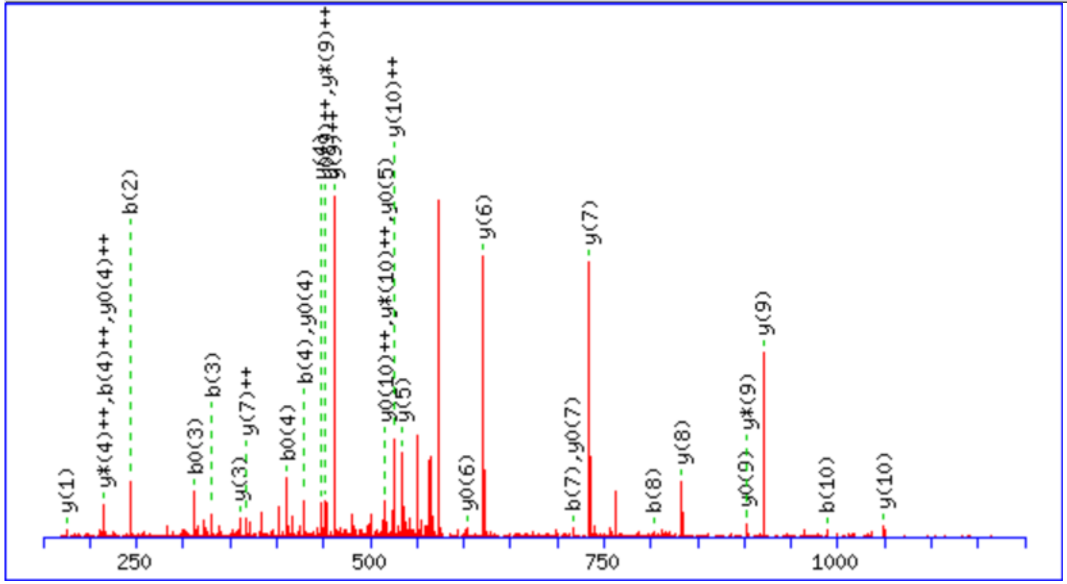
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 4434: 1161.635048 from(581.824800,2+)
Title: OECHL100310_13.5197.5197.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55 **Expect:** 0.00021**Matches :** 33/94 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	114.091340	57.549308					I						
2	**243.133933**	122.070605			225.123368	113.065322	E	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637
3	**330.165961**	165.586618			312.155396	156.581336	S	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340
4	**429.234375**	215.120826			411.223810	206.115543	V	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326
5	542.318439	271.662858			524.307874	262.657575	L	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119

6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087
7	**716.382495**	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073
8	**803.414523**	402.210899			785.403958	393.205617	**S**	***447.267407***	224.137342	430.240858	215.624067	429.256842	215.132059
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053		
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321		
11							**R**	***175.118952***	88.063114	158.092403	79.549840		

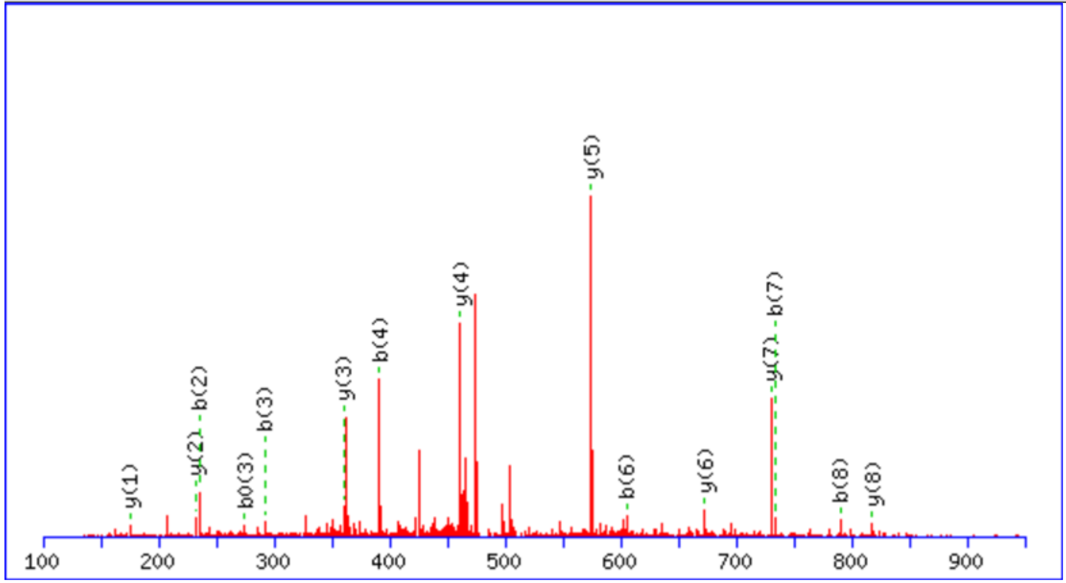


Peptide View

MS/MS Fragmentation of **FSGVITQGR**
Found in **IPI00220588**, Tax_Id=9606 Gene_Symbol=CPXM1 39 kDa protein
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 1930: 963.513848 from(482.764200,2+)
Title: OECHL100310_13.8048.8048.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 963.513794**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55 **Expect:** 0.0002**Matches :** 15/76 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.075690	74.541483					**F**							**9**
2	**235.107718**	118.057497			217.097153	109.052214	**S**	***817.452643***	409.229960	800.426094	400.716685	799.442078	400.224677	**8**
3	**292.129182**	146.568229			274.118617	137.562946	**G**	***730.420615***	365.713946	713.394066	357.200671	712.410050	356.708663	**7**
4	**391.197596**	196.102436			373.187031	187.097153	**V**	***673.399151***	337.203214	656.372602	328.689939	655.388586	328.197931	**6**
5	504.281660	252.644468			486.271095	243.639186	**I**	***574.330737***	287.669007	557.304188	279.155732	556.320172	278.663724	**5**
6	**605.329339**	303.168308			587.318774	294.163025	**T**	***461.246673***	231.126975	444.220124	222.613700	443.236108	222.121692	**4**
7	**733.387917**	367.197597	716.361368	358.684322	715.377352	358.192314	**Q**	***360.198994***	180.603135	343.172445	172.089861			**3**
8	**790.409381**	395.708329	773.382832	387.195054	772.398816	386.703046	**G**	***232.140416***	116.573846	215.113867	108.060572			**2**
9							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**

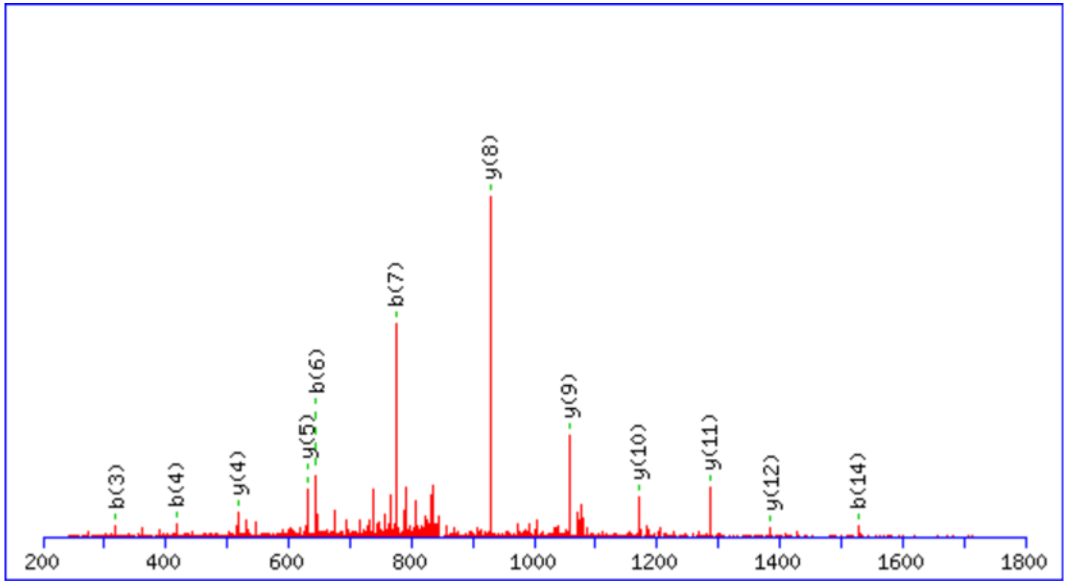


Peptide View

MS/MS Fragmentation of **AVFVDLEPTVIDEVR**
Found in **IPI00166768**, Tax_Id=9606 Gene_Symbol=TUBA1C TUBA1C protein
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 10962: 1700.898648 from(851.456600,2+)
Title: OECHL100310_13.18064.18064.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1700.898514**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54 **Expect:** 0.00045**Matches :** 12/128 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**15**
2	171.112804	86.060040			**V**	1630.868665	815.937971	1613.842116	807.424696	1612.858100	806.932688	**14**
3	***318.181218***	159.594247			**F**	1531.800251	766.403764	1514.773702	757.890489	1513.789686	757.398481	**13**
4	***417.249632***	209.128454			**V**	***1384.731837***	692.869557	1367.705288	684.356282	1366.721272	683.864274	**12**
5	532.276575	266.641926	514.266010	257.636643	**D**	***1285.663423***	643.335350	1268.636874	634.822075	1267.652858	634.330067	**11**
6	***645.360639***	323.183958	627.350074	314.178675	**L**	***1170.636480***	585.821878	1153.609931	577.308604	1152.625915	576.816596	**10**
7	***774.403232***	387.705254	756.392667	378.699972	**E**	***1057.552416***	529.279846	1040.525867	520.766572	1039.541851	520.274564	**9**
8	871.455996	436.231636	853.445431	427.226354	**P**	***928.509823***	464.758550	911.483274	456.245275	910.499258	455.753267	**8**
9	972.503675	486.755476	954.493110	477.750193	**T**	831.457059	416.232168	814.430510	407.718893	813.446494	407.226885	**7**
10	1071.572089	536.289683	1053.561524	527.284400	**V**	730.409380	365.708328	713.382831	357.195054	712.398815	356.703046	**6**
11	1184.656153	592.831715	1166.645588	583.826432	**I**	***631.340966***	316.174121	614.314417	307.660846	613.330401	307.168838	**5**
12	1299.683096	650.345186	1281.672531	641.339904	**D**	***518.256902***	259.632089	501.230353	251.118815	500.246337	250.626807	**4**
13	1428.725689	714.866483	1410.715124	705.861200	**E**	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	**3**
14	***1527.794103***	764.400690	1509.783538	755.395407	**V**	274.187366	137.597321	257.160817	129.084047			**2**
15					**R**	175.118952	88.063114	158.092403	79.549839			**1**



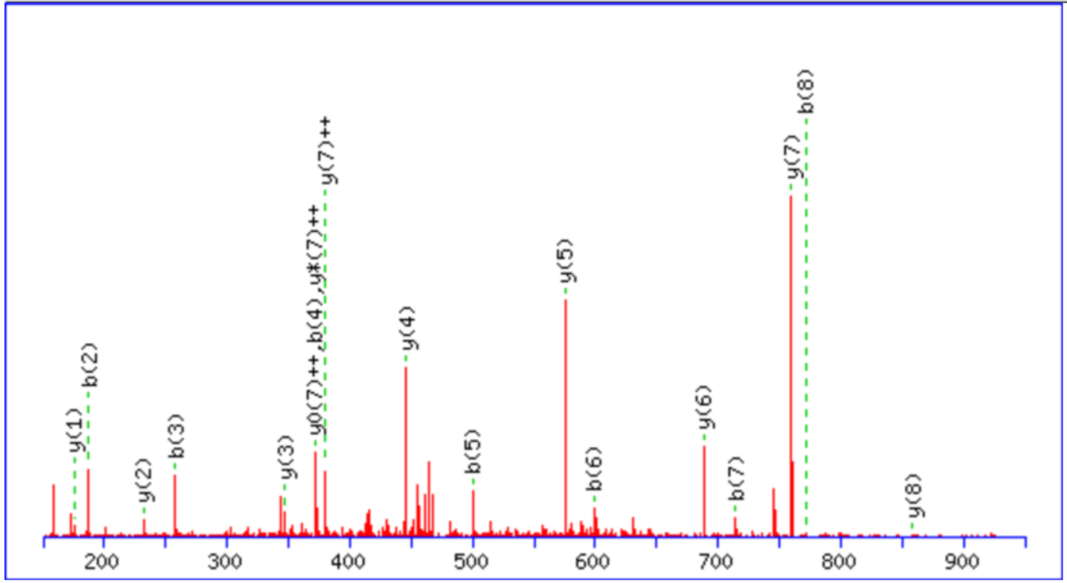
Peptide View

MS/MS Fragmentation of **SVAIEVDGR**
Found in **IPI00297252**, Tax_Id=9606 Gene_Symbol=SULF2 Isoform 1 of Extracellular sulfatase Sulf-2
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 1577: 944.492848 from(473.253700,2+)
Title: OECHL100310_13.8229.8229.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 944.492706**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52 **Expect:** 0.00093**Matches :** 18/76 fragment ions using 40 most intense peaks (help)

#	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y^{*}**	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	88.039304	44.523290	70.028739	35.518008	**S**							**9**
2	**187.107718**	94.057497	169.097153	85.052214	**V**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
3	**258.144832**	129.576054	240.134267	120.570772	**A**	***759.399544***	380.203410	742.372995	371.690136	741.388979	371.198128	**7**
4	**371.228896**	186.118086	353.218331	177.112804	**I**	***688.362430***	344.684853	671.335881	336.171579	670.351865	335.679571	**6**
5	**500.271489**	250.639383	482.260924	241.634100	**E**	***575.278366***	288.142821	558.251817	279.629547	557.267801	279.137539	**5**

6	**599.339903**	300.173590	581.329338	291.168307	**V**	***446.235773***	223.621524	429.209224	215.108250	428.225208	214.616242	**4**
7	**714.366846**	357.687061	696.356281	348.681779	**D**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
8	**771.388310**	386.197793	753.377745	377.192511	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
9					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



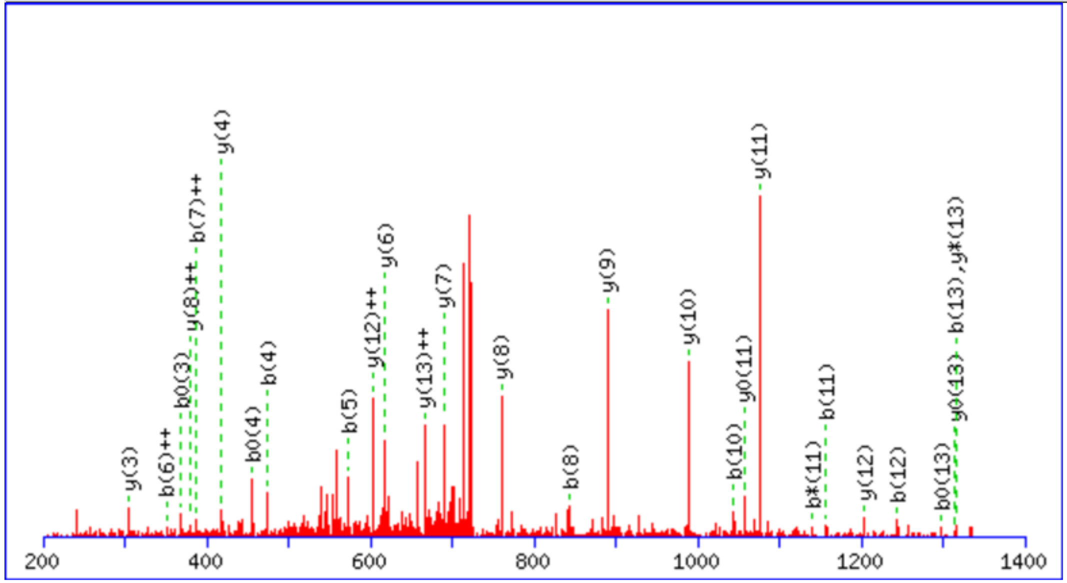
Peptide View

MS/MS Fragmentation of **SEKSVEAAAELSAK**
Found in **IPI00550020**, Tax_Id=9606 Gene_Symbol=PTMS Parathymosin
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 8087: 1460.733648 from(731.374100,2+)
Title: OECHL100310_13.11245.11245.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1460.735794**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 58 **Expect:** 0.00021**Matches :** 29/148 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	130.049869	65.528572			112.039304	56.523290	**S**						

2	259.092462	130.049869			241.081897	121.044586	**E**	1332.700536	666.853906	1315.673987	658.340631	1314.689971	657.8486
3	***387.187425***	194.097350	370.160876	185.584076	369.176860	185.092068	**K**	***1203.657943***	602.332609	1186.631394	593.819335	1185.647378	593.3273
4	***474.219453***	237.613364	457.192904	229.100090	456.208888	228.608082	**S**	***1075.562980***	538.285128	1058.536431	529.771854	1057.552415	529.2798
5	***573.287867***	287.147571	556.261318	278.634297	555.277302	278.142289	**V**	***988.530952***	494.769114	971.504403	486.255839	970.520387	485.7638
6	702.330460	351.668868	685.303911	343.155593	684.319895	342.663585	**E**	***889.462538***	445.234907	872.435989	436.721633	871.451973	436.2296
7	773.367574	387.187425	756.341025	378.674150	755.357009	378.182142	**A**	***760.419945***	380.713611	743.393396	372.200336	742.409380	371.7083
8	***844.404688***	422.705982	827.378139	414.192707	826.394123	413.700699	**A**	***689.382831***	345.195054	672.356282	336.681779	671.372266	336.1897
9	915.441802	458.224539	898.415253	449.711264	897.431237	449.219256	**A**	***618.345717***	309.676497	601.319168	301.163222	600.335152	300.6712
10	***1044.484395***	522.745836	1027.457846	514.232561	1026.473830	513.740553	**E**	547.308603	274.157940	530.282054	265.644665	529.298038	265.1526
11	***1157.568459***	579.287867	1140.541910	570.774593	1139.557894	570.282585	**L**	***418.266010***	209.636643	401.239461	201.123368	400.255445	200.6313
12	***1244.600487***	622.803881	1227.573938	614.290607	1226.589922	613.798599	**S**	***305.181946***	153.094611	288.155397	144.581337	287.171381	144.0893
13	***1315.637601***	658.322438	1298.611052	649.809164	1297.627036	649.317156	**A**	218.149918	109.578597	201.123369	101.065322		
14							**K**	147.112804	74.060040	130.086255	65.546765		

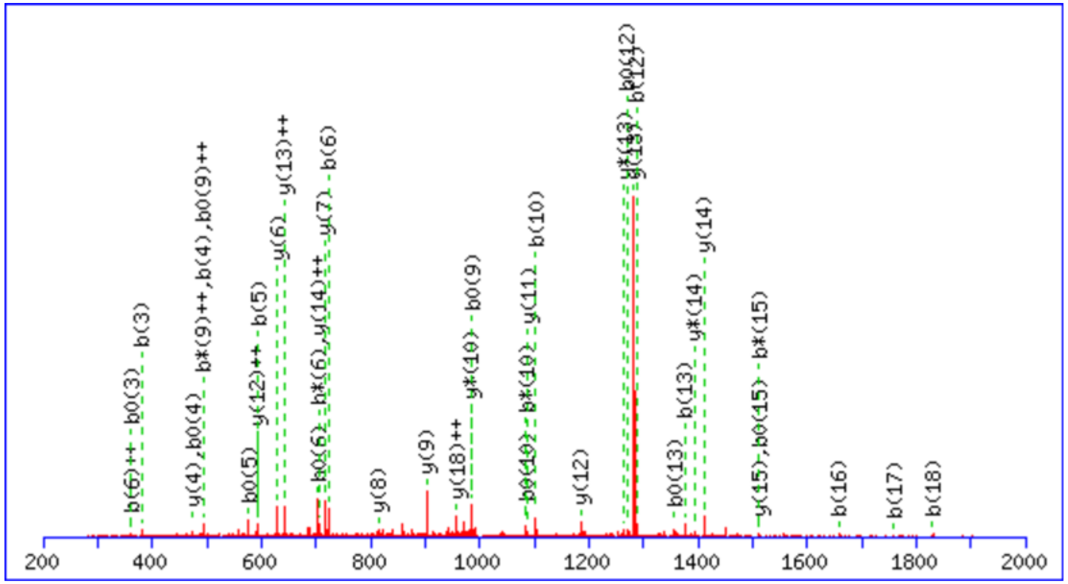


Peptide View

MS/MS Fragmentation of **SYELTQPPSVSVSPGQTAR**
Found in **IPI00382440**, Tax_Id=9606 Gene_Symbol=- Ig lambda chain V-IV region Hil
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 13109: 2003.001448 from(1002.508000,2+)
Title: OECHL100310_13.12568.12568.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 2002.995987**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53 **Expect:** 0.001**Matches :** 42/202 fragment ions using 82 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	88.039304	44.523290			70.028739	35.518008	**S**						
2	251.102633	126.054954			233.092068	117.049672	**Y**	1916.971234	958.989255	1899.944685	950.475981	1898.960669	949.9839
3	***380.145226***	190.576251			362.134661	181.570969	**E**	1753.907905	877.457591	1736.881356	868.944316	1735.897340	868.4523
4	***493.229290***	247.118283			475.218725	238.113001	**L**	1624.865312	812.936294	1607.838763	804.423020	1606.854747	803.9310
5	***594.276969***	297.642123			576.266404	288.636840	**T**	***1511.781248***	756.394262	1494.754699	747.880988	1493.770683	747.3889
6	***722.335547***	361.671412	705.308998	353.158137	704.324982	352.666129	**Q**	***1410.733569***	705.870423	1393.707020	697.357148	1392.723004	696.8651
7	819.388311	410.197794	802.361762	401.684519	801.377746	401.192511	**P**	***1282.674991***	641.841134	1265.648442	633.327859	1264.664426	632.8358
8	916.441075	458.724176	899.414526	450.210901	898.430510	449.718893	**P**	***1185.622227***	593.314752	1168.595678	584.801477	1167.611662	584.3094
9	1003.473103	502.240190	986.446554	493.726915	985.462538	493.234907	**S**	***1088.569463***	544.788370	1071.542914	536.275095	1070.558898	535.7830
10	***1102.541517***	551.774397	1085.514968	543.261122	1084.530952	542.769114	**V**	1001.537435	501.272356	984.510886	492.759081	983.526870	492.2670
11	1189.573545	595.290411	1172.546996	586.777136	1171.562980	586.285128	**S**	***902.469021***	451.738149	885.442472	443.224874	884.458456	442.7328
12	***1288.641959***	644.824618	1271.615410	636.311343	1270.631394	635.819335	**V**	***815.436993***	408.222135	798.410444	399.708860	797.426428	399.2168
13	***1375.673987***	688.340632	1358.647438	679.827357	1357.663422	679.335349	**S**	***716.368579***	358.687928	699.342030	350.174653	698.358014	349.6826
14	1472.726751	736.867014	1455.700202	728.353739	1454.716186	727.861731	**P**	***629.336551***	315.171914	612.310002	306.658639	611.325986	306.1666
15	1529.748215	765.377746	1512.721666	756.864471	1511.737650	756.372463	**G**	532.283787	266.645532	515.257238	258.132257	514.273222	257.6402
16	***1657.806793***	829.407035	1640.780244	820.893760	1639.796228	820.401752	**Q**	***475.262323***	238.134800	458.235774	229.621525	457.251758	229.1295
17	***1758.854472***	879.930874	1741.827923	871.417600	1740.843907	870.925592	**T**	347.203745	174.105510	330.177196	165.592236	329.193180	165.1002
18	***1829.891586***	915.449431	1812.865037	906.936157	1811.881021	906.444149	**A**	246.156066	123.581671	229.129517	115.068396		
19							**R**	175.118952	88.063114	158.092403	79.549839		



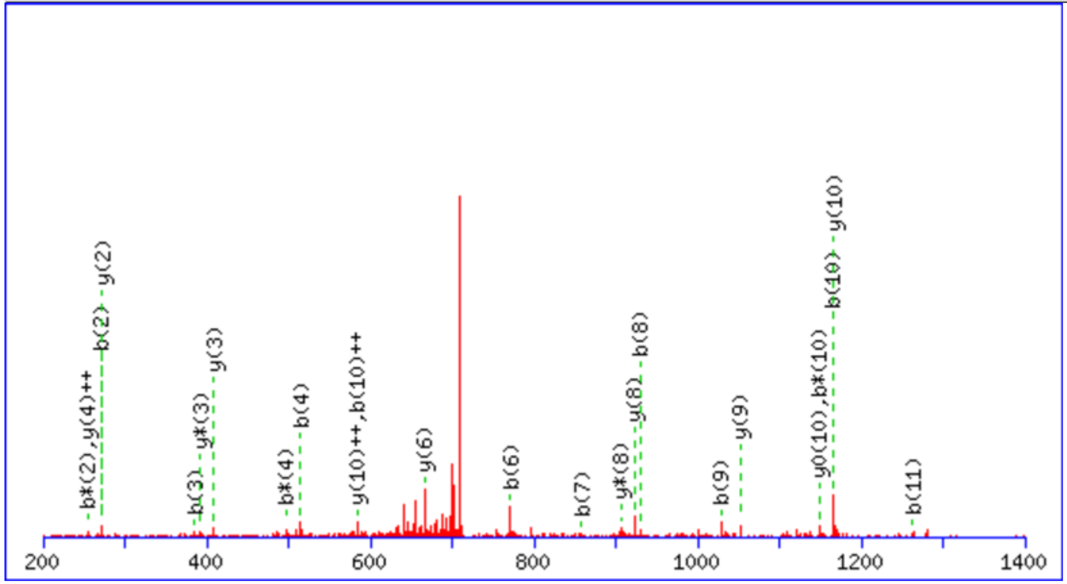
Peptide View

MS/MS Fragmentation of **NRNEQESAVHPR**
Found in **IPI00396437**, Tax_Id=9606 Gene_Symbol=DBNL Isoform 2 of Drebrin-like protein
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 7839: 1435.694848 from(718.854700,2+)
Title: OECHL100310_13.1694.1694.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1435.691605**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52 **Expect:** 0.00074**Matches :** 24/116 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	115.050203	58.028740	98.023654	49.515465			**N**						
2	***271.151314***	136.079295	254.124765	127.566021			**R**	1322.655986	661.831631	1305.629437	653.318357	1304.645421	652.8263
3	***385.194241***	193.100759	368.167692	184.587484			**N**	**1166.554875**	583.781076	1149.528326	575.267801	1148.544310	574.7757
4	***514.236834***	257.622055	497.210285	249.108781	496.226269	248.616773	**E**	**1052.511948**	526.759612	1035.485399	518.246337	1034.501383	517.7543
5	642.295412	321.651344	625.268863	313.138070	624.284847	312.646062	**Q**	**923.469355**	462.238316	906.442806	453.725041	905.458790	453.2330

6	***771.338005***	386.172641	754.311456	377.659366	753.327440	377.167358	**E**	795.410777	398.209026	778.384228	389.695752	777.400212	389.2037
7	***858.370033***	429.688655	841.343484	421.175380	840.359468	420.683372	**S**	**666.368184**	333.687730	649.341635	325.174455	648.357619	324.6824
8	***929.407147***	465.207212	912.380598	456.693937	911.396582	456.201929	**A**	579.336156	290.171716	562.309607	281.658441		
9	***1028.475561***	514.741419	1011.449012	506.228144	1010.464996	505.736136	**V**	508.299042	254.653159	491.272493	246.139884		
10	***1165.534473***	583.270874	1148.507924	574.757600	1147.523908	574.265592	**H**	**409.230628**	205.118952	392.204079	196.605677		
11	***1262.587237***	631.797257	1245.560688	623.283982	1244.576672	622.791974	**P**	**272.171716**	136.589496	255.145167	128.076221		
12							**R**	175.118952	88.063114	158.092403	79.549839		



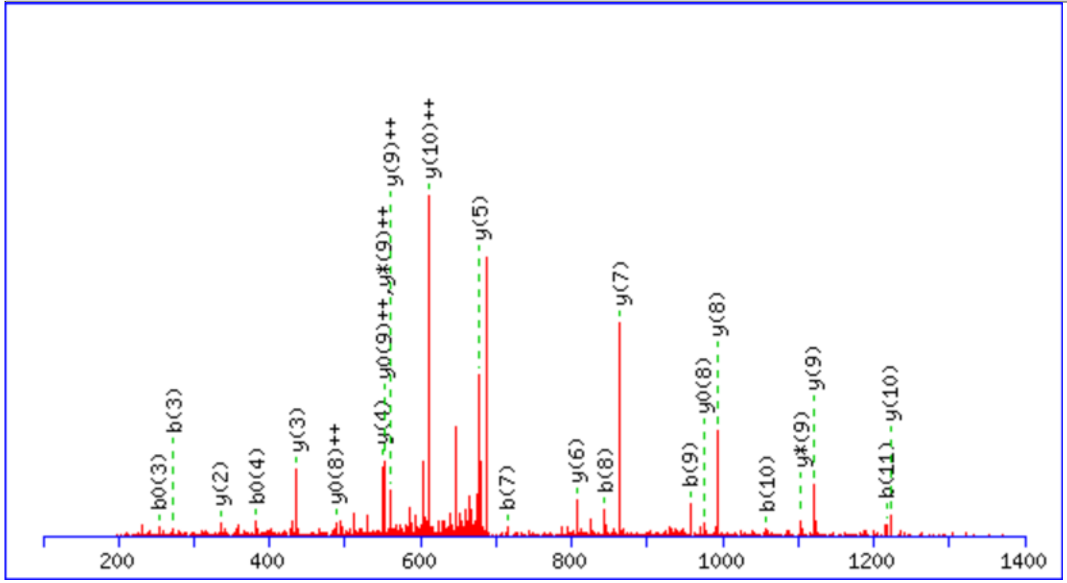
Peptide View

MS/MS Fragmentation of **VATQEGKEITCR**
Found in **IPI00031564**, Tax_Id=9606 Gene_Symbol=GGCT Isoform 1 of Gamma-glutamylcyclotransferase
Experiment: 49 - PyB-1 **Fraction:** PyB-1

Match to Query 7485: 1390.687248 from(696.350900,2+)
Title: OECHL100310_13.3589.3589.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1390.687454**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**

Score: 51 **Expect:** 0.00097**Matches :** 24/118 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	100.075690	50.541483					V						
2	171.112804	86.060040					A	1292.626328	646.816802	1275.599779	638.303528	1274.615763	637.8115
3	**272.160483**	136.583879			254.149918	127.578597	T	***1221.589214***	611.298245	1204.562665	602.784971	1203.578649	602.2929
4	400.219061	200.613169	383.192512	192.099894	382.208496	191.607886	Q	***1120.541535***	560.774406	1103.514986	552.261131	1102.530970	551.7691
5	529.261654	265.134465	512.235105	256.621191	511.251089	256.129183	E	***992.482957***	496.745117	975.456408	488.231842	974.472392	487.7398
6	586.283118	293.645197	569.256569	285.131923	568.272553	284.639915	G	***863.440364***	432.223820	846.413815	423.710546	845.429799	423.2185
7	**714.378081**	357.692679	697.351532	349.179404	696.367516	348.687396	K	***806.418900***	403.713088	789.392351	395.199814	788.408335	394.7078
8	**843.420674**	422.213975	826.394125	413.700701	825.410109	413.208693	E	***678.323937***	339.665607	661.297388	331.152332	660.313372	330.6603
9	**956.504738**	478.756007	939.478189	470.242733	938.494173	469.750725	I	***549.281344***	275.144310	532.254795	266.631036	531.270779	266.1390
10	**1057.552417**	529.279847	1040.525868	520.766572	1039.541852	520.274564	T	***436.197280***	218.602278	419.170731	210.089003	418.186715	209.5969
11	**1217.583066**	609.295171	1200.556517	600.781897	1199.572501	600.289889	C	***335.149601***	168.078438	318.123052	159.565164		
12							R	175.118952	88.063114	158.092403	79.549839		



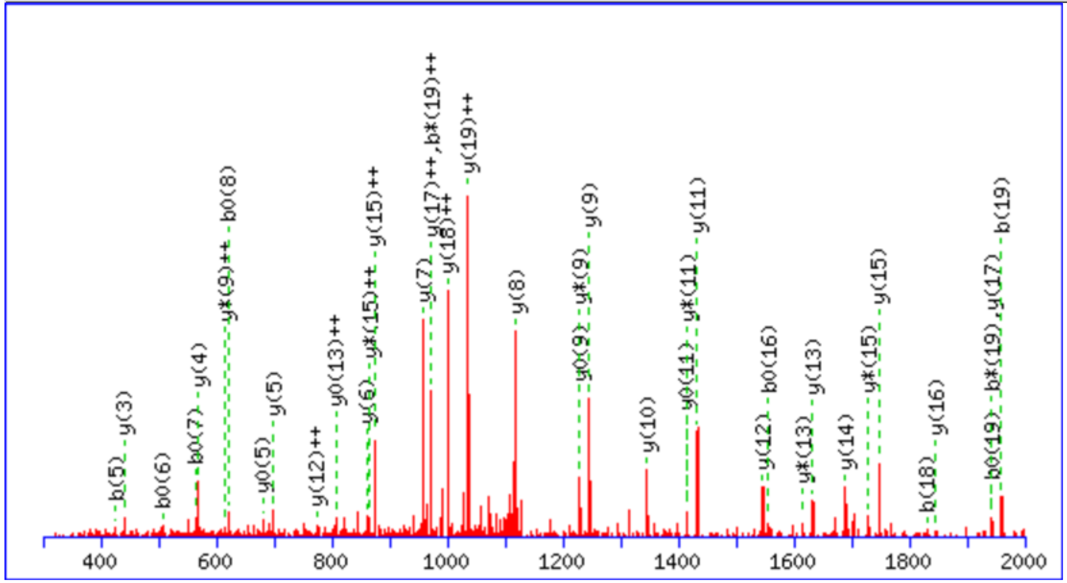
Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 19 - NOPB1 **Fraction:** NOPB1

Match to Query 13649: 2270.113448 from(1136.064000,2+)
Title: OECHL100310_11.10021.10021.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 81 **Expect:** 1.6e-006**Matches :** 40/212 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	
1	102.054955	51.531116			84.044390	42.525833	**T**						
2	201.123369	101.065322			183.112804	92.060040	**V**	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400	10
3	272.160483	136.583879			254.149918	127.578597	**A**	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986	10
4	329.181947	165.094611			311.171382	156.089329	**G**	1999.965437	1000.486357	1982.938888	991.973082	1981.954872	9
5	**426.234711**	213.620994			408.224146	204.615711	**P**	***1942.943973***	971.975625	1925.917424	963.462350	1924.933408	9
6	525.303125	263.155201			507.292560	254.149918	**V**	***1845.891209***	923.449243	1828.864660	914.935968	1827.880644	9
7	582.324589	291.665933			564.314024	282.660650	**G**	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230	8
8	639.346053	320.176665			621.335488	311.171382	**G**	***1689.801331***	845.404304	1672.774782	836.891029	1671.790766	8
9	726.378081	363.692679			708.367516	354.687396	**S**	***1632.779867***	816.893572	1615.753318	808.380297	1614.769302	8
10	839.462145	420.234711			821.451580	411.229428	**L**	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274	7
11	926.494173	463.750725			908.483608	454.745442	**S**	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210	7
12	1025.562587	513.284932			1007.552022	504.279649	**V**	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182	6
13	1153.621165	577.314221	1136.594616	568.800946	1135.610600	568.308938	**Q**	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768	6
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	**C**	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190	5
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	**P**	***958.474106***	479.740691	941.447557	471.227417	940.463541	4
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	**Y**	***861.421342***	431.214309	844.394793	422.701035	843.410777	4
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	**E**	***698.358013***	349.682645	681.331464	341.169370	680.347448	3
18	**1830.905463**	915.956370	1813.878914	907.443095	1812.894898	906.951087	**K**	***569.315420***	285.161348	552.288871	276.648074	551.304855	2
19	**1959.948056**	980.477666	1942.921507	971.964392	1941.937491	971.472384	**E**	***441.220457***	221.113867	424.193908	212.600592	423.209892	2

20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	**H**	312.177864	156.592570	295.151315	148.079295		
21							**R**	175.118952	88.063114	158.092403	79.549839		



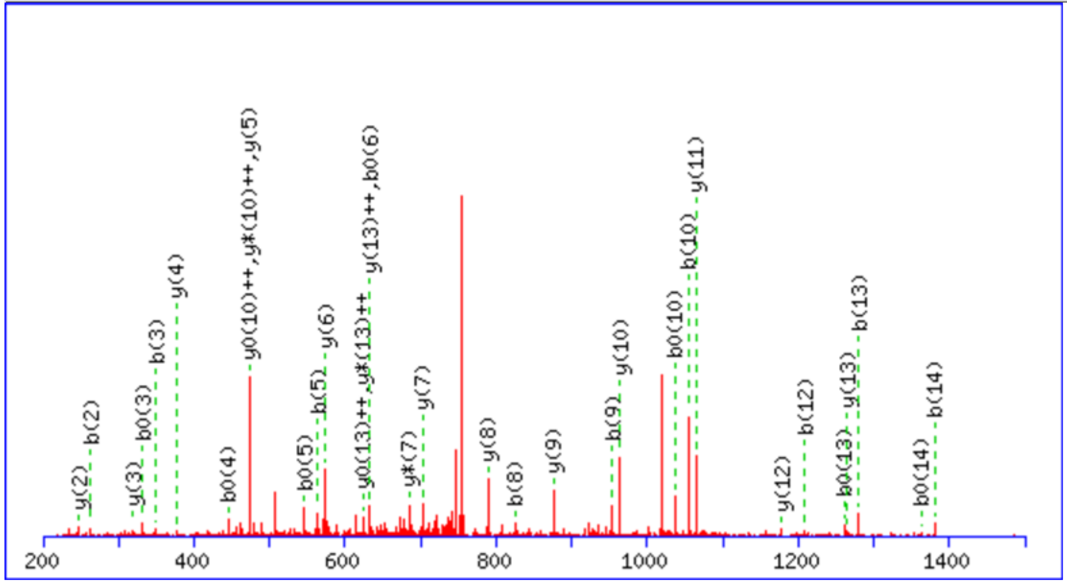
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 19 - NOPB1 **Fraction:** NOPB1

Match to Query 9302: 1525.726448 from(763.870500,2+)
Title: OECHL100310_11.10407.10407.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 94 **Expect:** 4.1e-008**Matches :** 34/150 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	116.034219	58.520748			98.023654	49.515465	**D**						
2	**263.102633**	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.3515
3	**350.134661**	175.570968			332.124096	166.565686	**S**	***1264.637937***	632.822607	1247.611388	624.309332	1246.627372	623.8173

4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.3013
5	**564.266404**	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.7592
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.2354
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.7194
8	**825.362488**	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.2034
9	**953.421066**	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.6873
10	**1054.468745**	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.6581
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.1342
12	**1208.542973**	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.6078
13	**1279.580087**	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	***319.197597***	160.102436	302.171048	151.589162	301.187032	151.0971
14	**1380.627766**	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.5785
15							**K**	147.112804	74.060040	130.086255	65.546765		



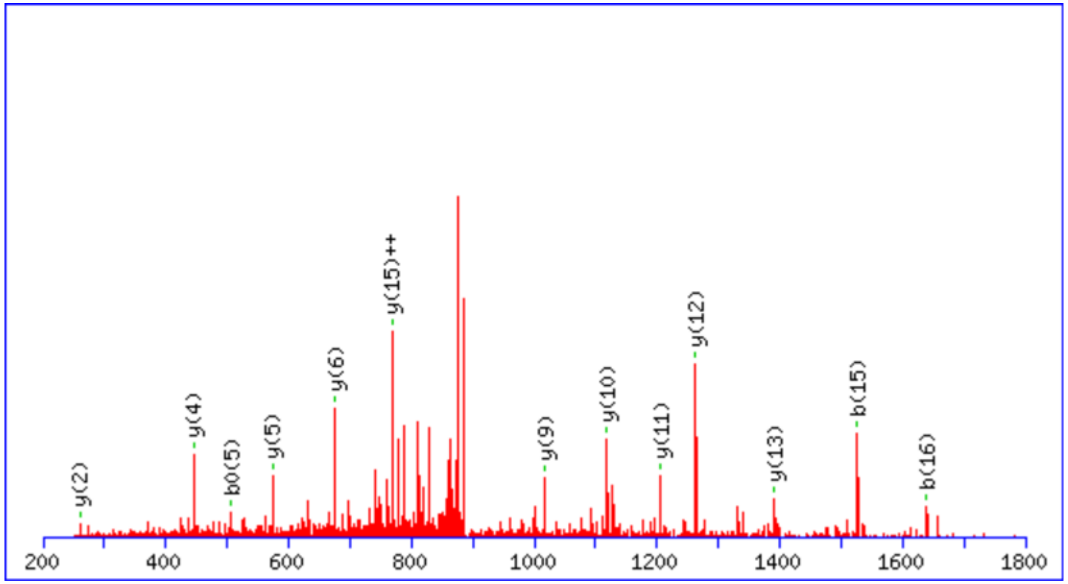
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**

Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 19 - NOPB1 **Fraction:** NOPB1

Match to Query 11533: 1784.881248 from(893.447900,2+)
Title: OECHL100310_11.7197.7197.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 75 **Expect:** 5.1e-006**Matches :** 13/170 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	164.070605	82.538940					**Y**						
2	251.102633	126.054954			233.092068	117.049672	**S**	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.9099
3	308.124097	154.565687			290.113532	145.560404	**G**	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.3939
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.8831
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.3671
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.8458
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.3351
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.8191
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.2952
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.2660
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	788.487631	394.747453	771.461082	386.234179	770.477066	385.7421
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.2001
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.6762
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.6288
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.1180
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		



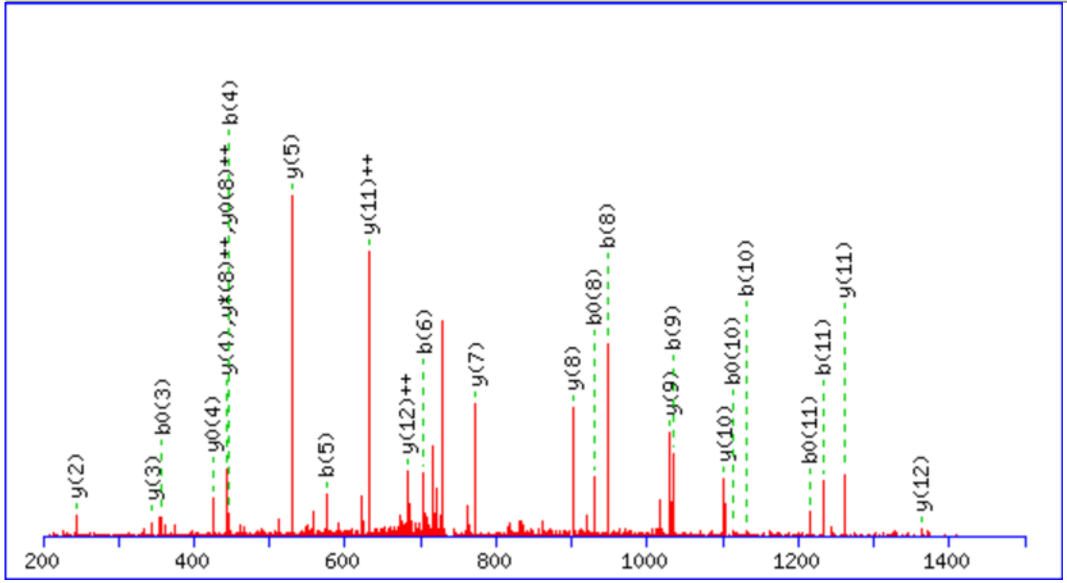
Peptide View

MS/MS Fragmentation of **ITCAEEGWSPTPK**
Found in **IPI00006154**, Tax_Id=9606 Gene_Symbol=CFHR2 Isoform Long of Complement factor H-related protein 2
Experiment: 19 - NOPB1 **Fraction:** NOPB1

Match to Query 8790: 1474.677248 from(738.345900,2+)
Title: OECHL100310_11.9756.9756.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1474.676224**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 79 **Expect:** 1.4e-006**Matches :** 26/114 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**I**							**13**
2	215.139019	108.073147	197.128454	99.067865	**T**	***1362.599444***	681.803360	1345.572895	673.290086	1344.588879	672.798078	**12**
3	375.169668	188.088472	357.159103	179.083190	**C**	***1261.551765***	631.279521	1244.525216	622.766246	1243.541200	622.274238	**11**
4	**446.206782**	223.607029	428.196217	214.601747	**A**	***1101.521116***	551.264196	1084.494567	542.750922	1083.510551	542.258914	**10**
5	**575.249375**	288.128326	557.238810	279.123043	**E**	***1030.484002***	515.745639	1013.457453	507.232365	1012.473437	506.740357	**9**

6	**704.291968**	352.649622	686.281403	343.644340	**E**	***901.441409***	451.224343	884.414860	442.711068	883.430844	442.219060	**8**
7	761.313432	381.160354	743.302867	372.155072	**G**	***772.398816***	386.703046	755.372267	378.189772	754.388251	377.697764	**7**
8	**947.392745**	474.200011	929.382180	465.194728	**W**	715.377352	358.192314	698.350803	349.679040	697.366787	349.187032	**6**
9	**1034.424773**	517.716025	1016.414208	508.710742	**S**	***529.298039***	265.152658	512.271490	256.639383	511.287474	256.147375	**5**
10	**1131.477537**	566.242407	1113.466972	557.237124	**P**	***442.266011***	221.636644	425.239462	213.123369	424.255446	212.631361	**4**
11	**1232.525216**	616.766246	1214.514651	607.760964	**T**	***345.213247***	173.110262	328.186698	164.596987	327.202682	164.104979	**3**
12	1329.577980	665.292628	1311.567415	656.287346	**P**	***244.165568***	122.586422	227.139019	114.073148			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**



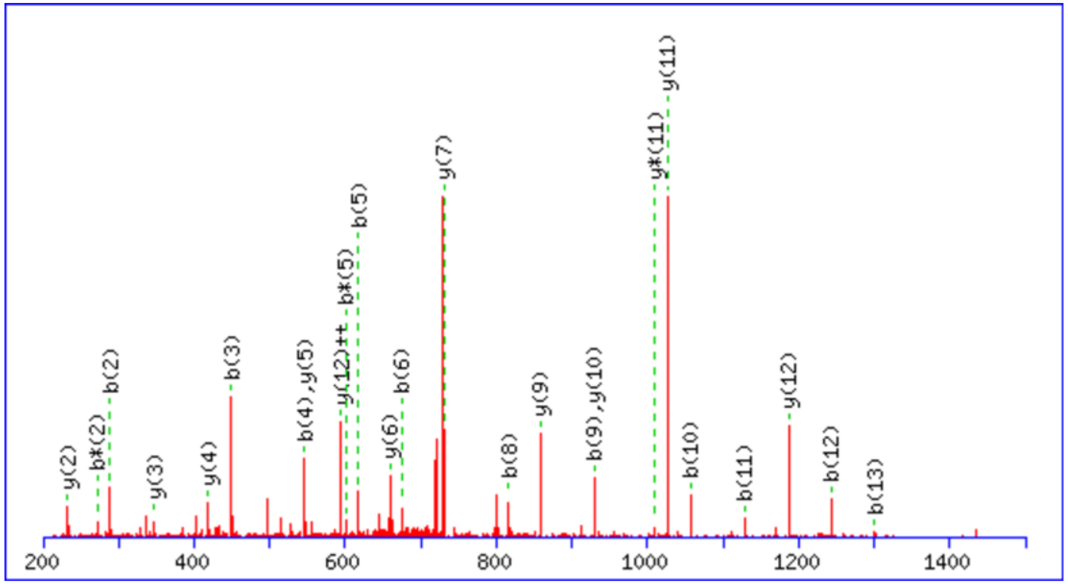
Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 19 - NOPB1 **Fraction:** NOPB1

Match to Query 8770: 1473.646048 from(737.830300,2+)
Title: OECHL100310_11.7122.7122.2.dta

Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 86 **Expect:** 1.4e-007**Matches :** 25/128 fragment ions using 38 most intense peaks (help)

#	**b**	**b^{++}**	**b***	**b^{*++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**
1	161.037925	81.022600					**C**						
2	***289.096503***	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.8093
3	***449.127152***	225.067214	432.100603	216.553940			**C**	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.7800
4	***546.179916***	273.593596	529.153367	265.080322			**P**	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.7646
5	***617.217030***	309.112153	600.190481	300.598879			**A**	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.2383
6	***674.238494***	337.622885	657.211945	329.109611			**G**	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.7197
7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.2090
8	***816.312722***	408.659999	799.286173	400.146725			**A**	**730.384229**	365.695753	713.357680	357.182478	712.373664	356.6904
9	***929.396786***	465.202031	912.370237	456.688757			**L**	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.1719
10	***1057.455364***	529.231320	1040.428815	520.718046			**Q**	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.6298
11	***1128.492478***	564.749877	1111.465929	556.236603			**A**	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.6005
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	**347.167359**	174.087317	330.140810	165.574043	329.156794	165.0820
13	***1300.540885***	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	**232.140416**	116.573846	215.113867	108.060571		
14							**R**	175.118952	88.063114	158.092403	79.549839		



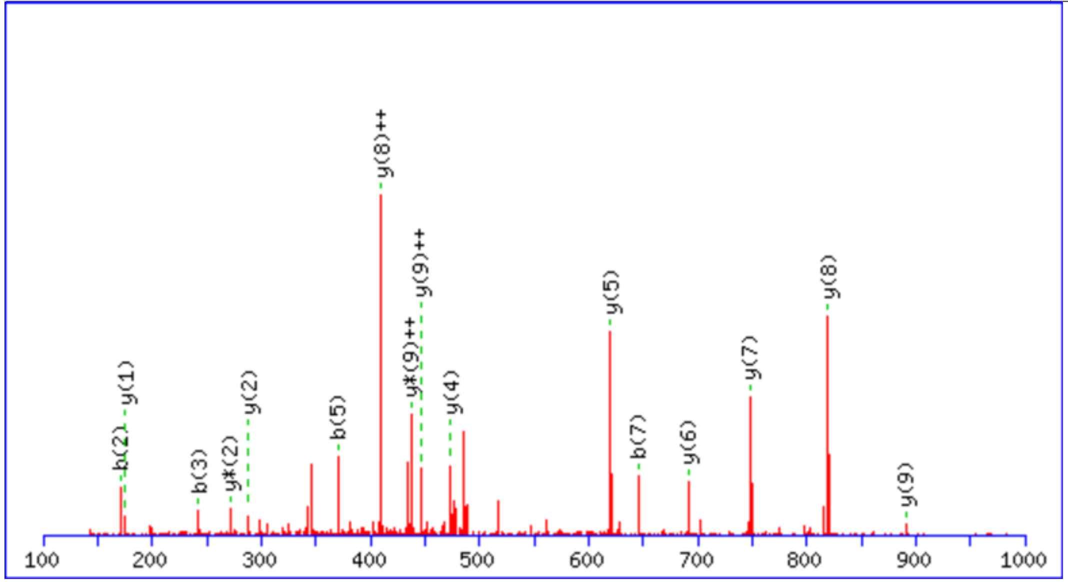
Peptide View

MS/MS Fragmentation of **VAAGAFQGLR**
Found in **IPI00022417**, Tax_Id=9606 Gene_Symbol=LRG1 Leucine-rich alpha-2-glycoprotein
Experiment: 19 - NOPB1 **Fraction:** NOPB1

Match to Query 2410: 988.545448 from(495.280000,2+)
Title: OECHL100310_11.10764.10764.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 988.545410**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66 **Expect:** 1.9e-005**Matches :** 16/60 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	100.075690	50.541483			**V**					**10**
2	**171.112804**	86.060040			**A**	***890.484278***	445.745777	873.457729	437.232503	**9**
3	**242.149918**	121.578597			**A**	***819.447164***	410.227220	802.420615	401.713946	**8**
4	299.171382	150.089329			**G**	***748.410050***	374.708663	731.383501	366.195389	**7**
5	**370.208496**	185.607886			**A**	***691.388586***	346.197931	674.362037	337.684657	**6**

6	517.276910	259.142093			**F**	***620.351472***	310.679374	603.324923	302.166100	**5**
7	**645.335488**	323.171382	628.308939	314.658108	**Q**	***473.283058***	237.145167	456.256509	228.631893	**4**
8	702.356952	351.682114	685.330403	343.168840	**G**	345.224480	173.115878	328.197931	164.602604	**3**
9	815.441016	408.224146	798.414467	399.710872	**L**	***288.203016***	144.605146	271.176467	136.091872	**2**
10					**R**	***175.118952***	88.063114	158.092403	79.549840	**1**



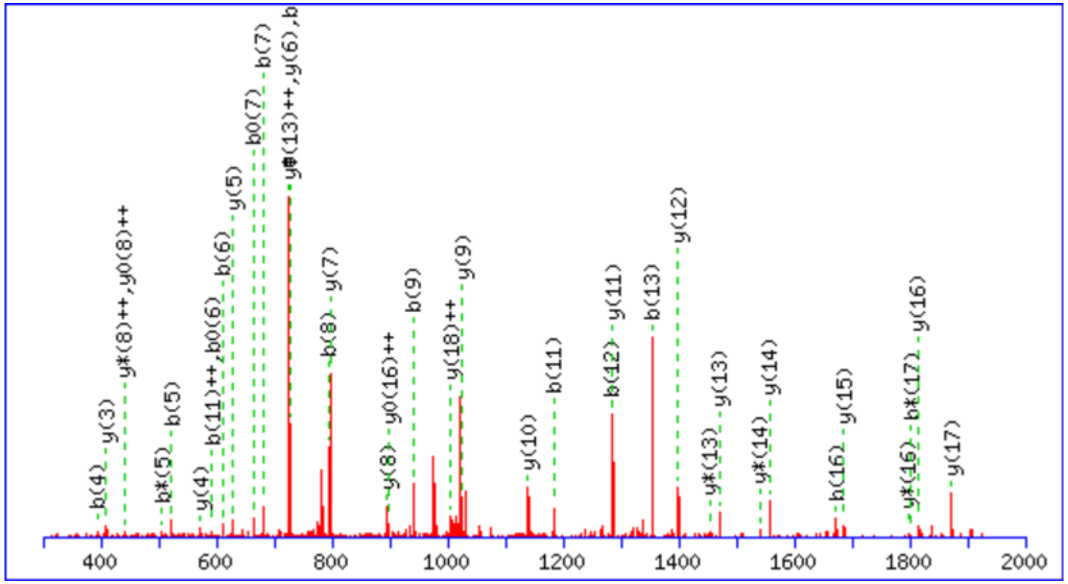
Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 19 - NOPB1 **Fraction:** NOPB1

Match to Query 13046: 2078.987448 from(1040.501000,2+)
Title: OECHL100310_11.16532.16532.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 102 **Expect:** 9.9e-009**Matches :** 40/200 fragment ions using 66 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}

1	72.044390	36.525833					**A**						
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444
4	**394.183344**	197.595310	377.156795	189.082035			**Q**	***1814.870790***	907.939033	1797.844241	899.425759	1796.860225	898.933
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904
6	**610.257965**	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383
7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867
8	**794.379143**	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676
15	1508.712833	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	***572.282723***	286.645000	555.256174	278.131725	554.272158	277.639
17	1818.844576	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108
18	1905.876604	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573
19							**R**	175.118952	88.063114	158.092403	79.549840		



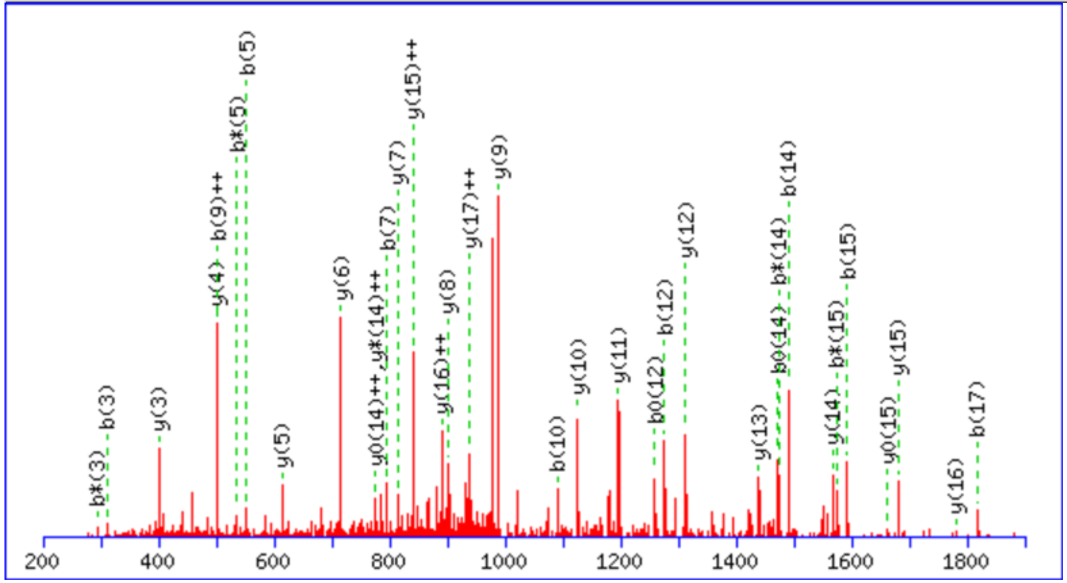
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 19 - NOPB1 **Fraction:** NOPB1

Match to Query 12690: 1990.022248 from(996.018400,2+)
Title: OECHL100310_11.9321.9321.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 91 **Expect:** 1.1e-007**Matches :** 35/186 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	115.050203	58.028740	98.023654	49.515465			**N**						
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.9921
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.4657
4	424.255445	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.9315
5	**552.314023**	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.3895

6	680.372601	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.3602
7	**795.399544**	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.3309
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.8174
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.2989
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.7694
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.2534
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.7374
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.2032
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.6793
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.1373
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510		
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128		
18							**R**	175.118952	88.063114	158.092403	79.549839		

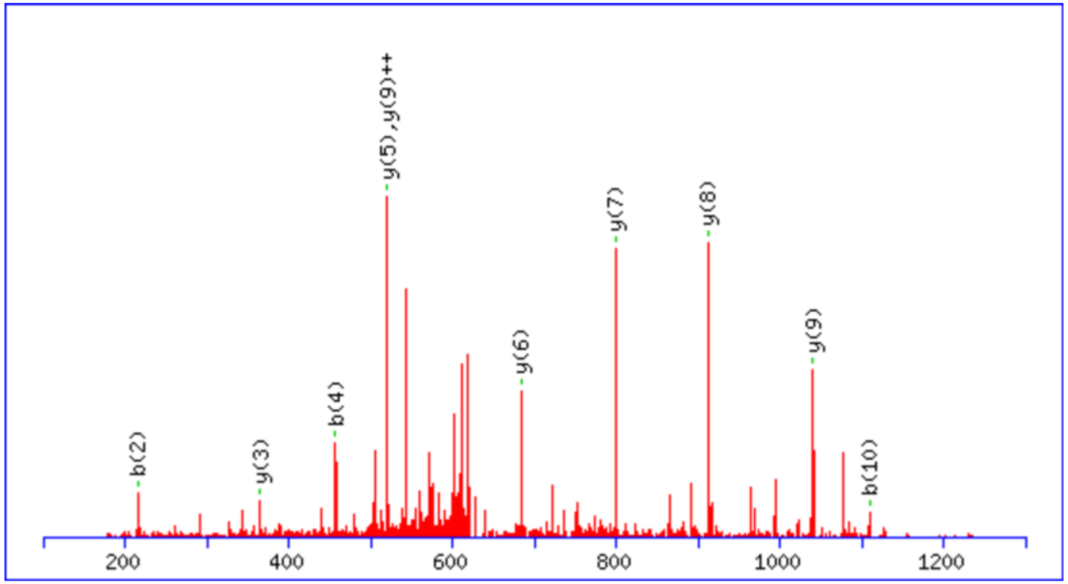


Peptide View

MS/MS Fragmentation of **SQKIDYGVFAK**
Found in **IPI00020990**, Tax_Id=9606 Gene_Symbol=OMD Osteomodulin
Experiment: 19 - NOPB1 **Fraction:** NOPB1

Match to Query 6337: 1254.660848 from(628.337700,2+)
Title: OECHL100310_11.10912.10912.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1254.660828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 54 **Expect:** 0.00035**Matches :** 10/106 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	88.039304	44.523290			70.028739	35.518008	**S**						
2	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	**Q**	1168.636087	584.821682	1151.609538	576.308407	1150.625522	575.8163
3	344.192845	172.600060	327.166296	164.086786	326.182280	163.594778	**K**	***1040.577509***	520.792393	1023.550960	512.279118	1022.566944	511.7871
4	**457.276909**	229.142092	440.250360	220.628818	439.266344	220.136810	**I**	***912.482546***	456.744911	895.455997	448.231637	894.471981	447.7396
5	572.303852	286.655564	555.277303	278.142290	554.293287	277.650282	**D**	***799.398482***	400.202879	782.371933	391.689605	781.387917	391.1975
6	735.367181	368.187229	718.340632	359.673954	717.356616	359.181946	**Y**	***684.371539***	342.689408	667.344990	334.176133		
7	792.388645	396.697961	775.362096	388.184686	774.378080	387.692678	**G**	***521.308210***	261.157743	504.281661	252.644469		
8	891.457059	446.232168	874.430510	437.718893	873.446494	437.226885	**V**	464.286746	232.647011	447.260197	224.133737		
9	1038.525473	519.766375	1021.498924	511.253100	1020.514908	510.761092	**F**	***365.218332***	183.112804	348.191783	174.599530		
10	**1109.562587**	555.284932	1092.536038	546.771657	1091.552022	546.279649	**A**	218.149918	109.578597	201.123369	101.065322		
11							**K**	147.112804	74.060040	130.086255	65.546765		



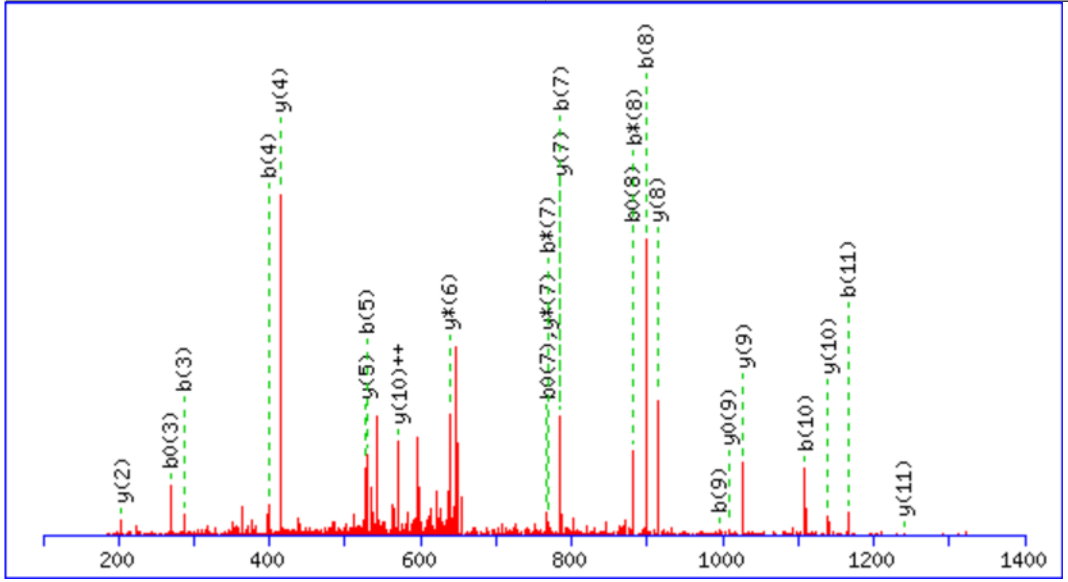
Peptide View

MS/MS Fragmentation of **ATLLEEQLPLGK**
Found in **IPI00414542**, Tax_Id=9606 Gene_Symbol=PDCD1LG2 Isoform 1 of Programmed cell death 1 ligand 2
Experiment: 19 - NOPB1 **Fraction:** NOPB1

Match to Query 7145: 1310.745048 from(656.379800,2+)
Title: OECHL100310_11.16403.16403.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1310.744537**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 55 **Expect:** 0.00013**Matches :** 25/106 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	72.044390	36.525833					**A**						
2	173.092069	87.049672			155.081504	78.044390	**T**	***1240.714731***	620.861004	1223.688182	612.347729	1222.704166	611.8557
3	***286.176133***	143.591704			268.165568	134.586422	**L**	***1139.667052***	570.337164	1122.640503	561.823890	1121.656487	561.3318
4	***399.260197***	200.133737			381.249632	191.128454	**L**	***1026.582988***	513.795132	1009.556439	505.281858	1008.572423	504.7898
5	***528.302790***	264.655033			510.292225	255.649751	**E**	***913.498924***	457.253100	896.472375	448.739825	895.488359	448.2478

6	657.345383	329.176330			639.334818	320.171047	**E**	***784.456331***	392.731804	767.429782	384.218529	766.445766	383.7265
7	***785.403961***	393.205619	768.377412	384.692344	767.393396	384.200336	**Q**	655.413738	328.210507	638.387189	319.697232		
8	***898.488025***	449.747651	881.461476	441.234376	880.477460	440.742368	**L**	***527.355160***	264.181218	510.328611	255.667943		
9	***995.540789***	498.274033	978.514240	489.760758	977.530224	489.268750	**P**	***414.271096***	207.639186	397.244547	199.125911		
10	***1108.624853***	554.816065	1091.598304	546.302790	1090.614288	545.810782	**L**	317.218332	159.112804	300.191783	150.599529		
11	***1165.646317***	583.326797	1148.619768	574.813522	1147.635752	574.321514	**G**	***204.134268***	102.570772	187.107719	94.057497		
12							**K**	147.112804	74.060040	130.086255	65.546765		



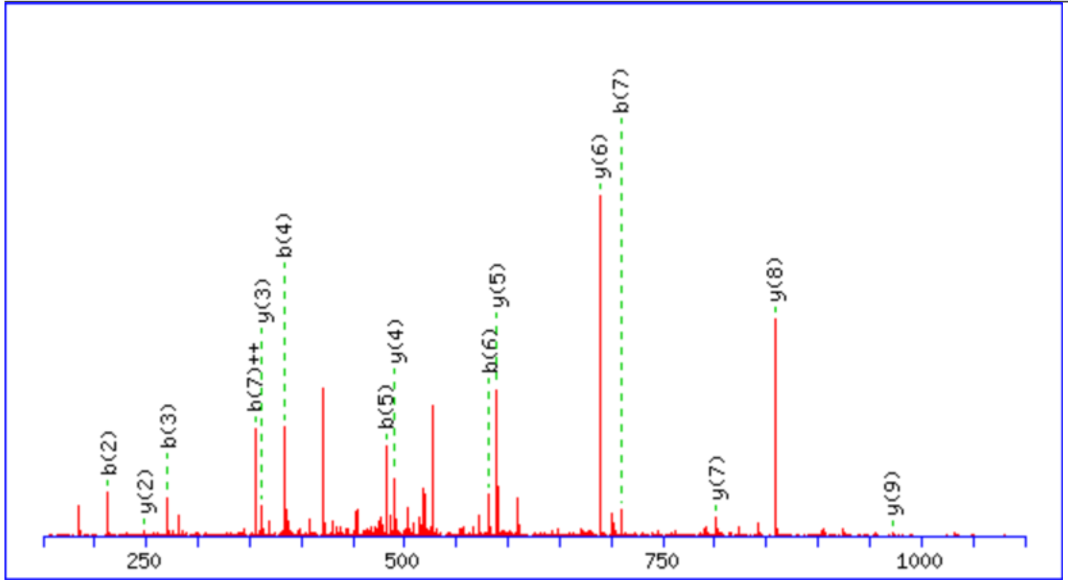
Peptide View

MS/MS Fragmentation of **VLGIVVQNTK**
Found in **IPI00397949**, Tax_Id=9606 Gene_Symbol=GPR56 Isoform 2 of G-protein coupled receptor 56
Experiment: 19 - NOPB1 **Fraction:** NOPB1

Match to Query 3619: 1069.649248 from(535.831900,2+)
Title: OECHL100310_11.11186.11186.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1069.649551**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**

Score: 59 **Expect:** 3.6e-005**Matches :** 15/78 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	100.075690	50.541483					**V**							**10**
2	**213.159754**	107.083515					**L**	***971.588408***	486.297842	954.561859	477.784568	953.577843	477.292560	**9**
3	**270.181218**	135.594247					**G**	***858.504344***	429.755810	841.477795	421.242536	840.493779	420.750528	**8**
4	**383.265282**	192.136279					**I**	***801.482880***	401.245078	784.456331	392.731804	783.472315	392.239796	**7**
5	**482.333696**	241.670486					**V**	***688.398816***	344.703046	671.372267	336.189772	670.388251	335.697764	**6**
6	**581.402110**	291.204693					**V**	***589.330402***	295.168839	572.303853	286.655565	571.319837	286.163557	**5**
7	**709.460688**	355.233982	692.434139	346.720708			**Q**	***490.261988***	245.634632	473.235439	237.121357	472.251423	236.629349	**4**
8	823.503615	412.255446	806.477066	403.742171			**N**	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	**3**
9	924.551294	462.779285	907.524745	454.266011	906.540729	453.774003	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
10							**K**	147.112804	74.060040	130.086255	65.546765			**1**



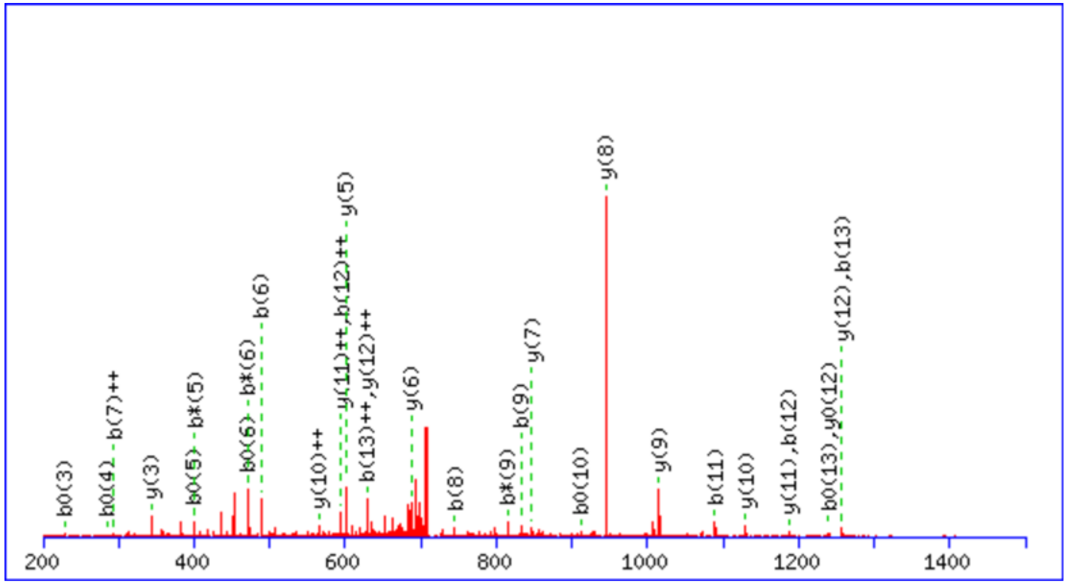
Peptide View

MS/MS Fragmentation of **SSAGNAPCSPCPAR**

Found in **IPI00005222**, Tax_Id=9606 Gene_Symbol=EPHB6 ephrin receptor EphB6 precursor
Experiment: 19 - NOPB1 **Fraction:** NOPB1

Match to Query 8348: 1430.604248 from(716.309400,2+)
Title: OECHL100310_11.3012.3012.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1430.603073**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 56 **Expect:** 7.6e-005**Matches :** 31/138 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	88.039304	44.523290			70.028739	35.518008	S						
2	175.071332	88.039304			157.060767	79.034021	S	1344.578331	672.792803	1327.551782	664.279529	1326.567766	663.7875
3	246.108446	123.557861			228.097881	114.552578	A	***1257.546303***	629.276790	1240.519754	620.763515	1239.535738	620.2715
4	303.129910	152.068593			285.119345	143.063311	G	***1186.509189***	593.758233	1169.482640	585.244958	1168.498624	584.7529
5	417.172837	209.090057	400.146288	200.576782	399.162272	200.084774	N	***1129.487725***	565.247501	1112.461176	556.734226	1111.477160	556.2422
6	**488.209951**	244.608613	471.183402	236.095339	470.199386	235.603331	A	***1015.444798***	508.226037	998.418249	499.712763	997.434233	499.2207
7	585.262715	**293.134996**	568.236166	284.621721	567.252150	284.129713	P	***944.407684***	472.707480	927.381135	464.194206	926.397119	463.7021
8	**745.293364**	373.150320	728.266815	364.637046	727.282799	364.145038	C	***847.354920***	424.181098	830.328371	415.667824	829.344355	415.1758
9	**832.325392**	416.666334	815.298843	408.153060	814.314827	407.661052	S	***687.324271***	344.165774	670.297722	335.652499	669.313706	335.1604
10	929.378156	465.192716	912.351607	456.679442	911.367591	456.187434	P	***600.292243***	300.649760	583.265694	292.136485		
11	**1089.408805**	545.208041	1072.382256	536.694766	1071.398240	536.202758	C	503.239479	252.123377	486.212930	243.610103		
12	**1186.461569**	**593.734423**	1169.435020	585.221148	1168.451004	584.729140	P	***343.208830***	172.108053	326.182281	163.594778		
13	**1257.498683**	**629.252980**	1240.472134	620.739705	1239.488118	620.247697	A	246.156066	123.581671	229.129517	115.068396		
14							R	175.118952	88.063114	158.092403	79.549839		



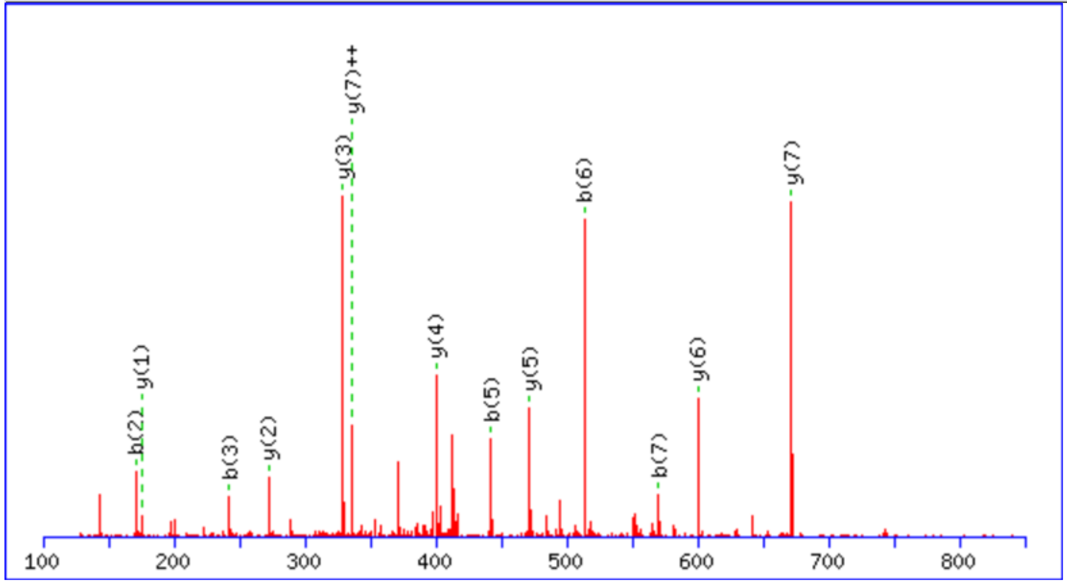
Peptide View

MS/MS Fragmentation of **GLAEAAGPR**
Found in **IPI00290826**, Tax_Id=9606 Gene_Symbol=FAM174A Membrane protein FAM174A
Experiment: 19 - NOPB1 **Fraction:** NOPB1

Match to Query 1046: 840.445048 from(421.229800,2+)
Title: OECHL100310_11.3890.3890.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 840.445343**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52 **Expect:** 0.00034**Matches :** 13/64 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008			**G**							**9**
2	**171.112804**	86.060040			**L**	784.431179	392.719228	767.404630	384.205953	766.420614	383.713945	**8**
3	**242.149918**	121.578597			**A**	***671.347115***	336.177196	654.320566	327.663921	653.336550	327.171913	**7**
4	371.192511	186.099894	353.181946	177.094611	**E**	***600.310001***	300.658639	583.283452	292.145364	582.299436	291.653356	**6**
5	**442.229625**	221.618450	424.219060	212.613168	**A**	***471.267408***	236.137342	454.240859	227.624067			**5**

6	**513.266739**	257.137008	495.256174	248.131725	**A**	***400.230294***	200.618785	383.203745	192.105510			**4**
7	**570.288203**	285.647740	552.277638	276.642457	**G**	***329.193180***	165.100228	312.166631	156.586953			**3**
8	667.340967	334.174122	649.330402	325.168839	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
9					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



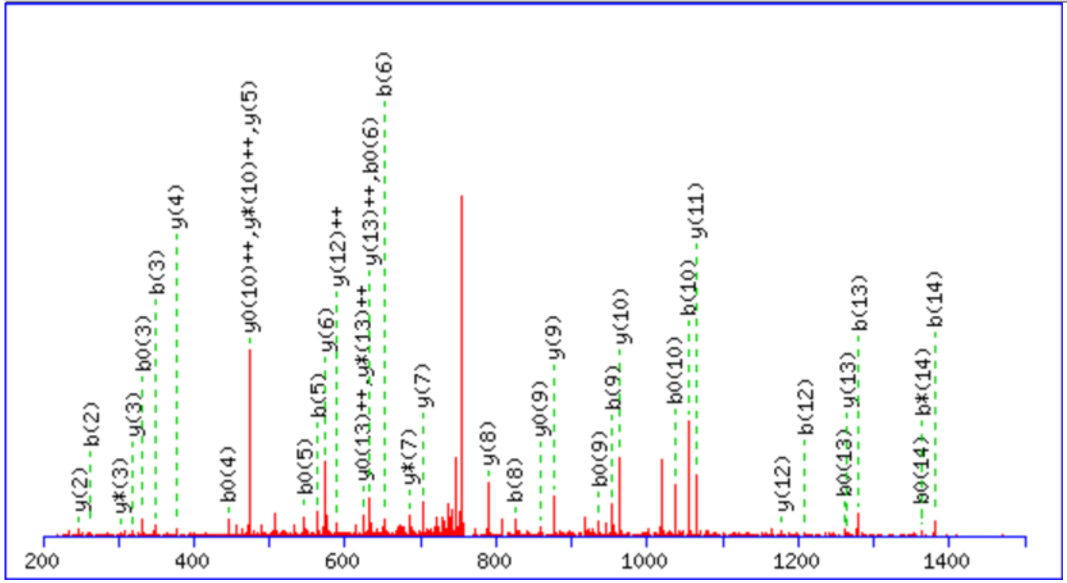
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 9898: 1525.725848 from(763.870200,2+)
Title: OECHL100310_09.10760.10760.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 86 **Expect:** 2.6e-007**Matches :** 40/150 fragment ions using 61 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	116.034219	58.520748			98.023654	49.515465	**D**						

2	**263.102633**	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.3515
3	**350.134661**	175.570968			332.124096	166.565686	**S**	***1264.637937***	632.822607	1247.611388	624.309332	1246.627372	623.8173
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.3013
5	**564.266404**	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.7592
6	**651.298432**	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.2354
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.7194
8	**825.362488**	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.2034
9	**953.421066**	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.6873
10	**1054.468745**	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.6581
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.1342
12	**1208.542973**	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.6078
13	**1279.580087**	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	***319.197597***	160.102436	302.171048	151.589162	301.187032	151.0971
14	**1380.627766**	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.5785
15							**K**	147.112804	74.060040	130.086255	65.546765		

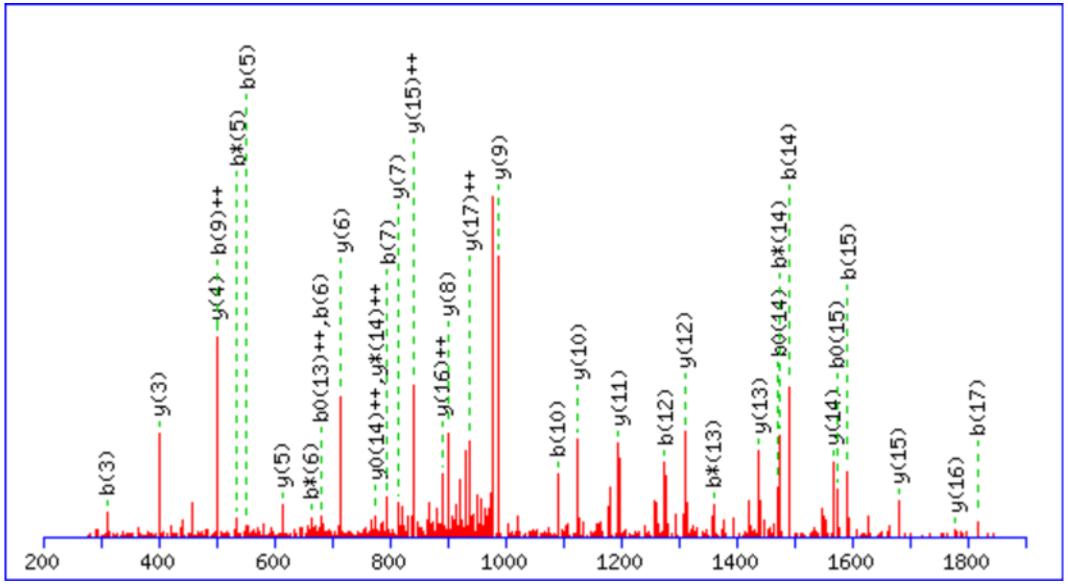


Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 13745: 1990.023848 from(996.019200,2+)
Title: OECHL100310_09.9739.9739.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 92 **Expect:** 7.9e-008**Matches :** 36/186 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	115.050203	58.028740	98.023654	49.515465			**N**						
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.9921
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.4657
4	424.255445	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.9315
5	**552.314023**	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.3895
6	**680.372601**	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.3602
7	**795.399544**	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.3309
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.8174
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.2989
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.7694
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.2534
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.7374
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.2032
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.6793
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.1373
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510		
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128		
18							**R**	175.118952	88.063114	158.092403	79.549839		



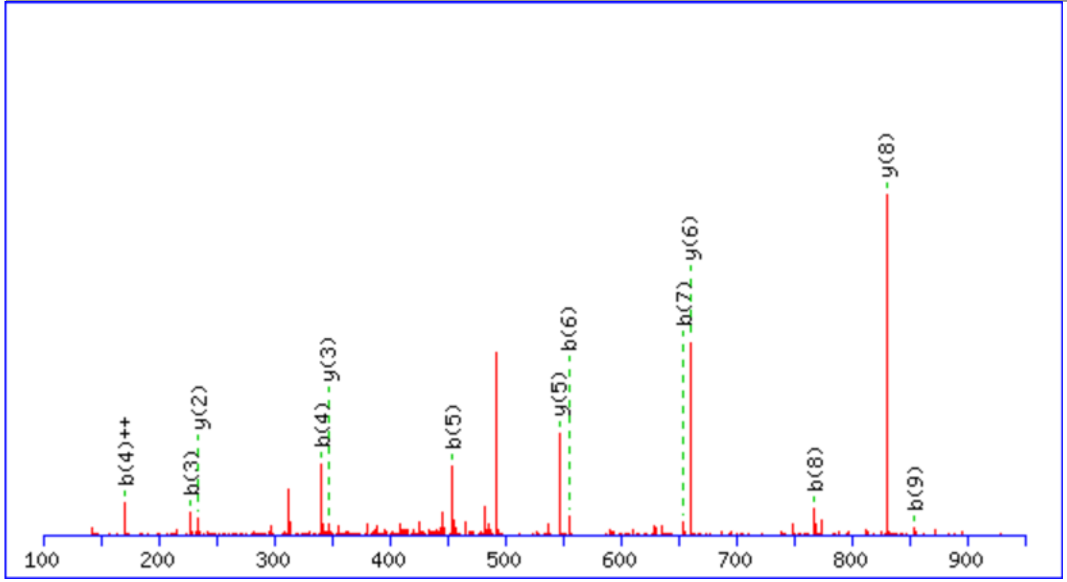
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 2880: 999.634448 from(500.824500,2+)
Title: OECHL100310_09.16992.16992.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65 **Expect:** 3.9e-006**Matches :** 14/78 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**

6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



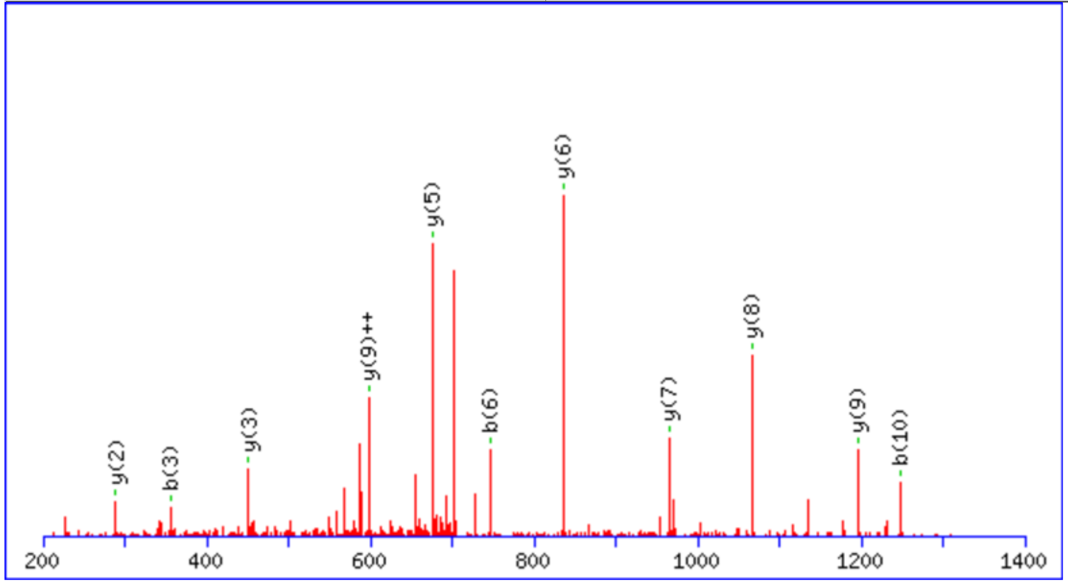
Peptide View

MS/MS Fragmentation of **LLETECPQYIR**
Found in **IPI00007047**, Tax_Id=9606 Gene_Symbol=S100A8 Protein S100-A8
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 8738: 1420.702448 from(711.358500,2+)
Title: OECHL100310_09.12192.12192.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1420.702026**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66 **Expect:** 3.1e-005**Matches :** 11/90 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	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1308.625265	654.816271	1291.598716	646.302996	1290.614700	645.8109
3	**356.217997**	178.612637			338.207432	169.607354	**E**	***1195.541201***	598.274239	1178.514652	589.760964	1177.530636	589.2689
4	457.265676	229.136476			439.255111	220.131194	**T**	***1066.498608***	533.752942	1049.472059	525.239668	1048.488043	524.7476
5	586.308269	293.657773			568.297704	284.652490	**E**	***965.450929***	483.229103	948.424380	474.715828	947.440364	474.2238
6	**746.338918**	373.673097			728.328353	364.667815	**C**	***836.408336***	418.707806	819.381787	410.194531		
7	843.391682	422.199479			825.381117	413.194197	**P**	***676.377687***	338.692481	659.351138	330.179207		
8	971.450260	486.228768	954.423711	477.715494	953.439695	477.223486	**Q**	579.324923	290.166099	562.298374	281.652825		
9	1134.513589	567.760433	1117.487040	559.247158	1116.503024	558.755150	**Y**	***451.266345***	226.136810	434.239796	217.623536		
10	**1247.597653**	624.302465	1230.571104	615.789190	1229.587088	615.297182	**I**	***288.203016***	144.605146	271.176467	136.091871		
11							**R**	175.118952	88.063114	158.092403	79.549839		



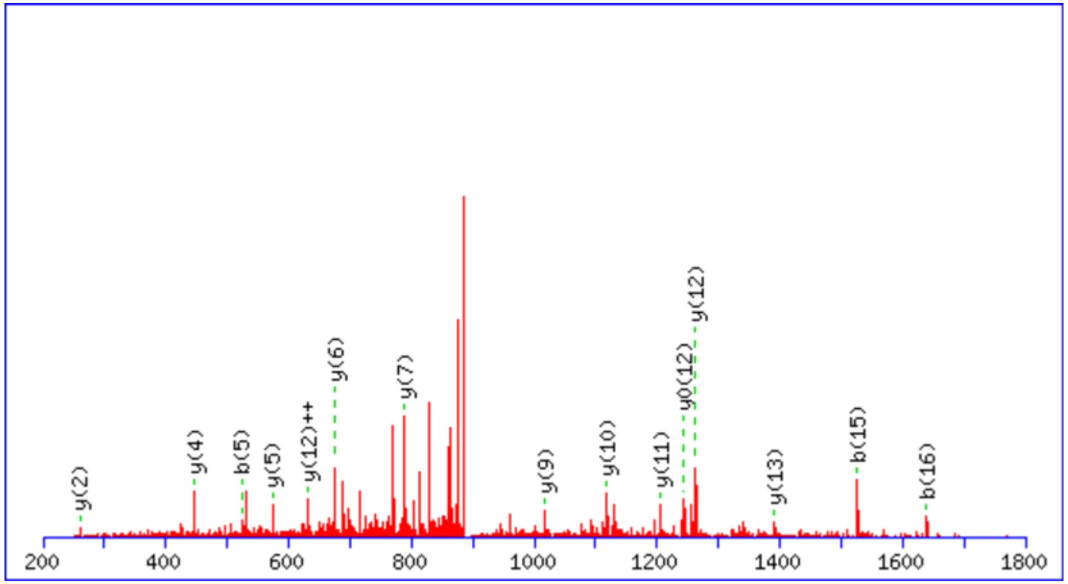
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P

Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 12365: 1784.879248 from(893.446900,2+)
Title: OECHL100310_09.7433.7433.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 60 **Expect:** 0.00017**Matches :** 15/170 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}
1	164.070605	82.538940					Y						
2	251.102633	126.054954			233.092068	117.049672	S	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.9099
3	308.124097	154.565687			290.113532	145.560404	G	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.3939
4	395.156125	198.081701			377.145560	189.076418	S	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.8831
5	**524.198718**	262.602997			506.188153	253.597715	E	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.3671
6	581.220182	291.113729			563.209617	282.108447	G	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.8458
7	668.252210	334.629743			650.241645	325.624461	S	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.3351
8	769.299889	385.153583			751.289324	376.148300	T	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.8191
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	Q	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.2952
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	T	889.535310	445.271293	872.508761	436.758018	871.524745	436.2660
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	L	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.7421
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	T	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.2001
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	K	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.6762
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	G	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.6288
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	E	389.239461	195.123368	372.212912	186.610094	371.228896	186.1180
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	L	***260.196868***	130.602072	243.170319	122.088797		
17							K	147.112804	74.060040	130.086255	65.546765		



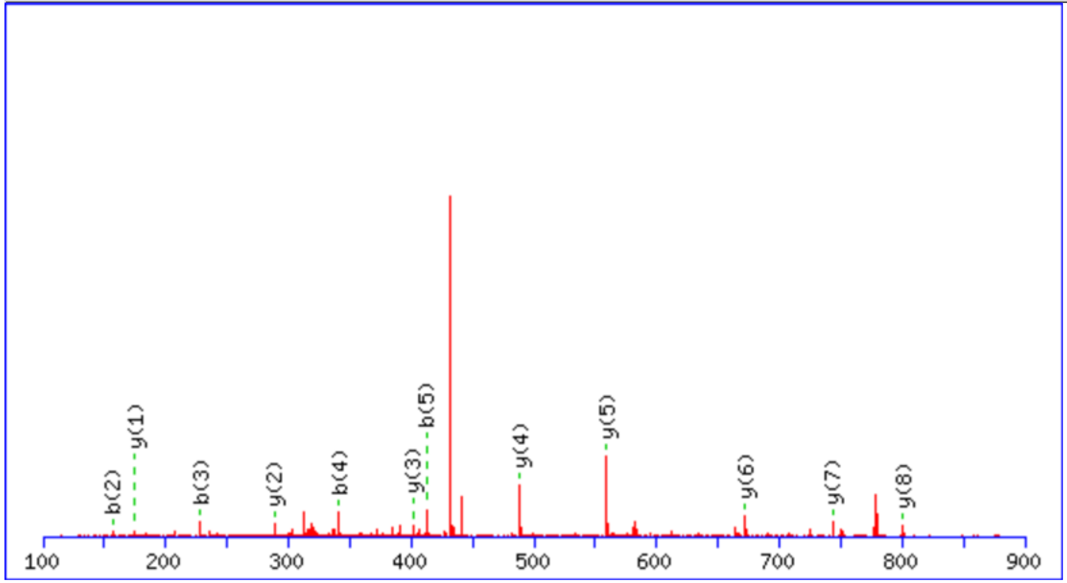
Peptide View

MS/MS Fragmentation of **VGALASLIR**
Found in **IPI00005794**, Tax_Id=9606 Gene_Symbol=PGCP Putative uncharacterized protein ENSP00000323500
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 1488: 898.560448 from(450.287500,2+)
Title: OECHL100310_09.15481.15481.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 898.559982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51 **Expect:** 0.00039**Matches :** 12/64 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.075690	50.541483			**V**							**9**
2	**157.097154**	79.052215			**G**	***800.498864***	400.753070	783.472315	392.239796	782.488299	391.747788	**8**
3	**228.134268**	114.570772			**A**	***743.477400***	372.242338	726.450851	363.729064	725.466835	363.237056	**7**
4	**341.218332**	171.112804			**L**	***672.440286***	336.723781	655.413737	328.210507	654.429721	327.718499	**6**
5	**412.255446**	206.631361			**A**	***559.356222***	280.181749	542.329673	271.668475	541.345657	271.176467	**5**

6	499.287474	250.147375	481.276909	241.142092	**S**	***488.319108***	244.663192	471.292559	236.149917	470.308543	235.657909	**4**
7	612.371538	306.689407	594.360973	297.684125	**L**	***401.287080***	201.147178	384.260531	192.633903			**3**
8	725.455602	363.231439	707.445037	354.226157	**I**	***288.203016***	144.605146	271.176467	136.091871			**2**
9					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



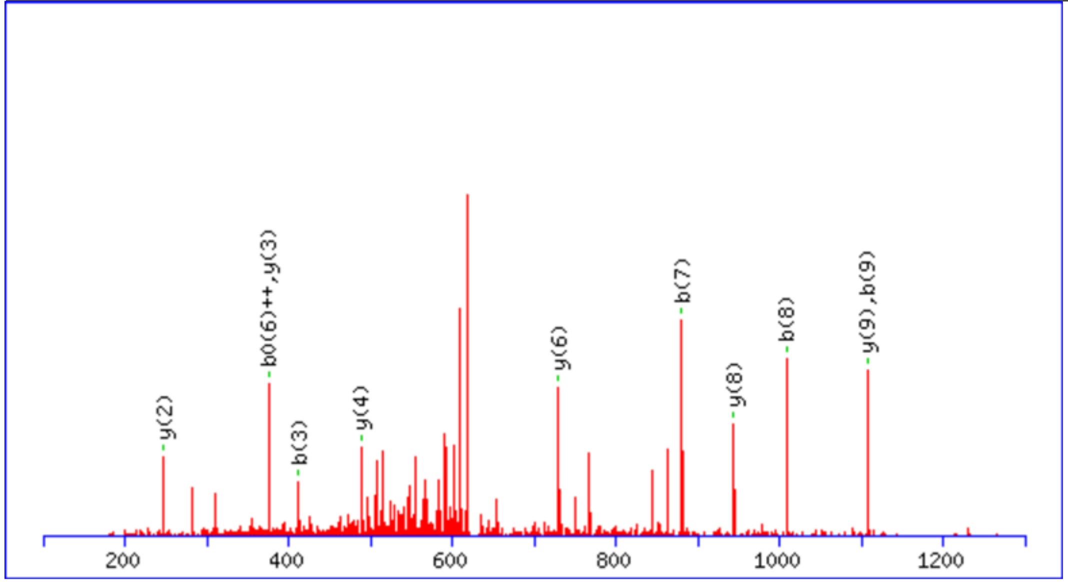
Peptide View

MS/MS Fragmentation of **FYTIEILKVE**
Found in **IPI00022974**, Tax_Id=9606 Gene_Symbol=PIP Prolactin-inducible protein
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 6788: 1253.691048 from(627.852800,2+)
Title: OECHL100310_09.18767.18767.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1253.690720**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54 **Expect:** 0.00018**Matches :** 11/86 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	148.075690	74.541483					**F**						

2	311.139019	156.073148					**Y**	***1107.629604***	554.318440	1090.603055	545.805166	1089.619039	545.3131
3	**412.186698**	206.596987			394.176133	197.591705	**T**	***944.566275***	472.786776	927.539726	464.273501	926.555710	463.7814
4	525.270762	263.139019			507.260197	254.133737	**I**	843.518596	422.262936	826.492047	413.749662	825.508031	413.2576
5	654.313355	327.660316			636.302790	318.655033	**E**	***730.434532***	365.720904	713.407983	357.207630	712.423967	356.7156
6	767.397419	384.202348			749.386854	375.197065	**I**	601.391939	301.199608	584.365390	292.686333	583.381374	292.1943
7	**880.481483**	440.744380			862.470918	431.739097	**L**	***488.307875***	244.657576	471.281326	236.144301	470.297310	235.6522
8	**1008.576446**	504.791861	991.549897	496.278587	990.565881	495.786579	**K**	***375.223811***	188.115544	358.197262	179.602269	357.213246	179.1102
9	**1107.644860**	554.326068	1090.618311	545.812794	1089.634295	545.320786	**V**	***247.128848***	124.068062			229.118283	115.0627
10							**E**	148.060434	74.533855			130.049869	65.5285



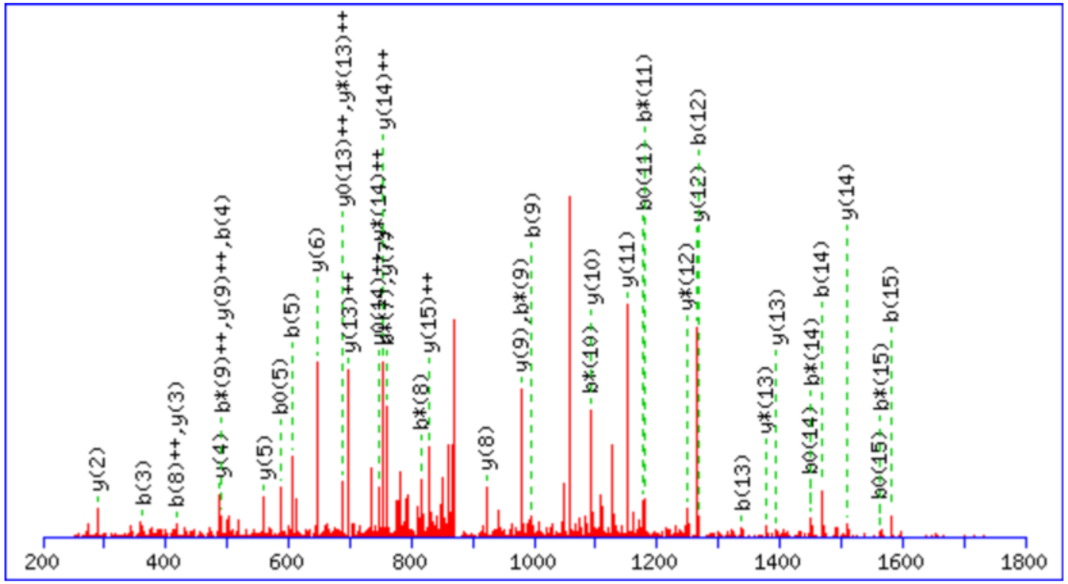
Peptide View

MS/MS Fragmentation of **VFDKDGNGYISAAELR**
Found in **IPI00075248**, Tax_Id=9606 Gene_Symbol=CALM3;CALM2;CALM1 Calmodulin
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 12047: 1753.864448 from(877.939500,2+)

Title: OECHL100310_09.13369.13369.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1753.863495**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 69 **Expect:** 1.6e-005**Matches :** 44/166 fragment ions using 90 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	100.075690	50.541483					**V**						
2	247.144104	124.075690					**F**	1655.802376	828.404826	1638.775827	819.891551	1637.791811	819.3995
3	**362.171047**	181.589161			344.160482	172.583879	**D**	***1508.733962***	754.870619	1491.707413	746.357345	1490.723397	745.8653
4	**490.266010**	245.636643	473.239461	237.123369	472.255445	236.631361	**K**	***1393.707019***	697.357148	1376.680470	688.843873	1375.696454	688.3518
5	**605.292953**	303.150115	588.266404	294.636840	587.282388	294.144832	**D**	***1265.612056***	633.309666	1248.585507	624.796392	1247.601491	624.3043
6	662.314417	331.660847	645.287868	323.147572	644.303852	322.655564	**G**	***1150.585113***	575.796194	1133.558564	567.282920	1132.574548	566.7909
7	776.357344	388.682310	759.330795	380.169036	758.346779	379.677028	**N**	***1093.563649***	547.285462	1076.537100	538.772188	1075.553084	538.2801
8	833.378808	417.193042	816.352259	408.679768	815.368243	408.187760	**G**	***979.520722***	490.263999	962.494173	481.750724	961.510157	481.2587
9	**996.442137**	498.724707	979.415588	490.211432	978.431572	489.719424	**Y**	***922.499258***	461.753267	905.472709	453.239992	904.488693	452.7479
10	1109.526201	555.266738	1092.499652	546.753464	1091.515636	546.261456	**I**	***759.435929***	380.221603	742.409380	371.708328	741.425364	371.2163
11	1196.558229	598.782753	1179.531680	590.269478	1178.547664	589.777470	**S**	***646.351865***	323.679571	629.325316	315.166296	628.341300	314.6742
12	**1267.595343**	634.301310	1250.568794	625.788035	1249.584778	625.296027	**A**	***559.319837***	280.163557	542.293288	271.650282	541.309272	271.1582
13	**1338.632457**	669.819866	1321.605908	661.306592	1320.621892	660.814584	**A**	***488.282723***	244.644999	471.256174	236.131725	470.272158	235.6397
14	**1467.675050**	734.341163	1450.648501	725.827889	1449.664485	725.335881	**E**	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.1211
15	**1580.759114**	790.883195	1563.732565	782.369921	1562.748549	781.877912	**L**	***288.203016***	144.605146	271.176467	136.091871		
16							**R**	175.118952	88.063114	158.092403	79.549839		



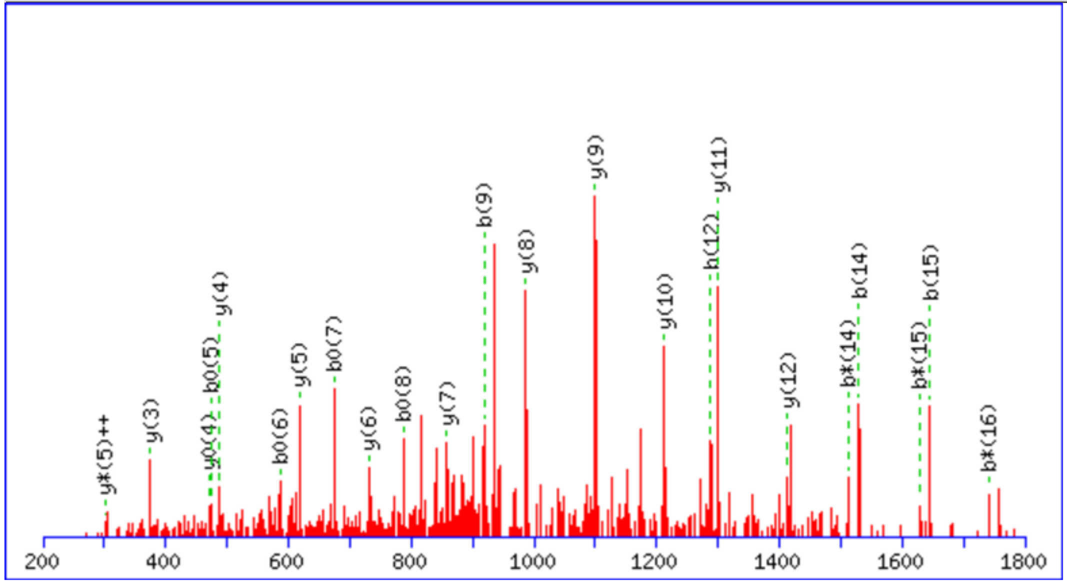
Peptide View

MS/MS Fragmentation of **TATFAISILQQIELDLK**
Found in **IPI00025491**, Tax_Id=9606 Gene_Symbol=EIF4A1;SNORA67 Eukaryotic initiation factor 4A-I
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 13283: 1903.068448 from(952.541500,2+)
Title: OECHL100310_09.21487.21487.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1903.066605**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53 **Expect:** 0.00017**Matches :** 23/170 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}
1	102.054955	51.531116			84.044390	42.525833	T						
2	173.092069	87.049672			155.081504	78.044390	A	1803.026229	902.016752	1785.999680	893.503478	1785.015664	893.0114
3	274.139748	137.573512			256.129183	128.568230	T	1731.989115	866.498195	1714.962566	857.984921	1713.978550	857.4929
4	421.208162	211.107719			403.197597	202.102436	F	1630.941436	815.974356	1613.914887	807.461081	1612.930871	806.9690
5	492.245276	246.626276			474.234711	237.620993	A	1483.873022	742.440149	1466.846473	733.926875	1465.862457	733.4348

6	605.329340	303.168308			587.318775	294.163026	**I**	***1412.835908***	706.921592	1395.809359	698.408317	1394.825343	697.9163
7	692.361368	346.684322			674.350803	337.679039	**S**	***1299.751844***	650.379560	1282.725295	641.866286	1281.741279	641.3742
8	805.445432	403.226354			787.434867	394.221071	**I**	***1212.719816***	606.863546	1195.693267	598.350272	1194.709251	597.8582
9	**918.529496**	459.768386			900.518931	450.763104	**L**	***1099.635752***	550.321514	1082.609203	541.808240	1081.625187	541.3162
10	1046.588074	523.797675	1029.561525	515.284401	1028.577509	514.792393	**Q**	***986.551688***	493.779482	969.525139	485.266207	968.541123	484.7741
11	1174.646652	587.826964	1157.620103	579.313690	1156.636087	578.821682	**Q**	***858.493110***	429.750193	841.466561	421.236918	840.482545	420.7449
12	**1287.730716**	644.368996	1270.704167	635.855722	1269.720151	635.363714	**I**	***730.434532***	365.720904	713.407983	357.207629	712.423967	356.7156
13	1416.773309	708.890292	1399.746760	700.377018	1398.762744	699.885010	**E**	***617.350468***	309.178872	600.323919	300.665597	599.339903	300.1735
14	**1529.857373**	765.432324	1512.830824	756.919050	1511.846808	756.427042	**L**	***488.307875***	244.657575	471.281326	236.144301	470.297310	235.6522
15	**1644.884316**	822.945796	1627.857767	814.432522	1626.873751	813.940513	**D**	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.1102
16	1757.968380	879.487828	1740.941831	870.974553	1739.957815	870.482545	**L**	260.196868	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		



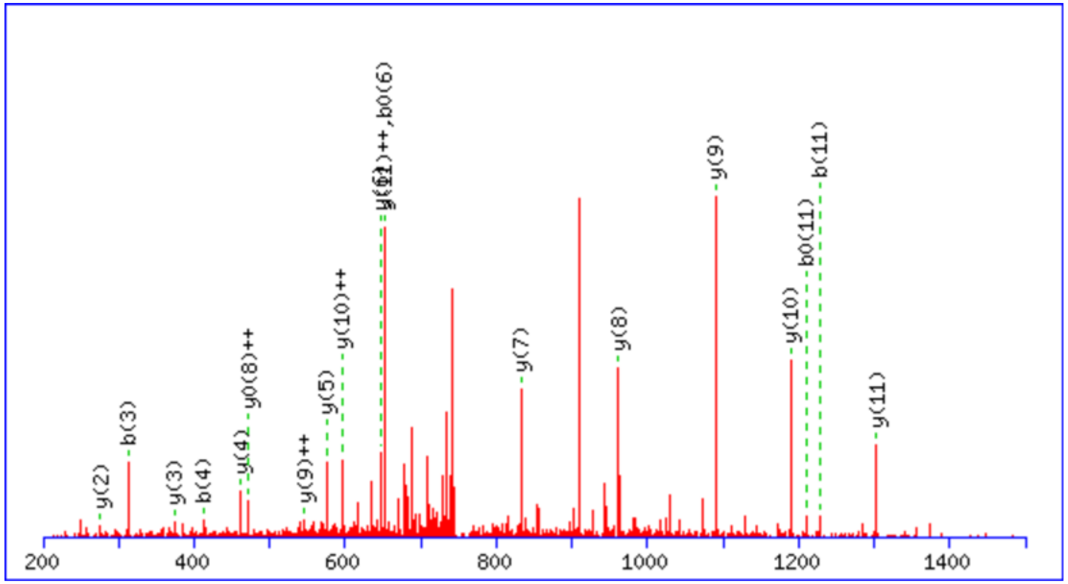
Peptide View

MS/MS Fragmentation of **AQLVEEWANSVKK**

Found in **IPI00016150**, Tax_Id=9606 Gene_Symbol=SERPINI1 Neuroserpin
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 9602: 1500.793648 from(751.404100,2+)
Title: OECHL100310_09.14186.14186.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1500.793610**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 63 **Expect:** 4.9e-005**Matches :** 19/128 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}
1	72.044390	36.525833					**A**						
2	200.102968	100.555122	183.076419	92.041848			**Q**	1430.763805	715.885541	1413.737256	707.372266	1412.753240	706.8802
3	**313.187032**	157.097154	296.160483	148.583879			**L**	***1302.705227***	651.856252	1285.678678	643.342977	1284.694662	642.8509
4	**412.255446**	206.631361	395.228897	198.118087			**V**	***1189.621163***	595.314220	1172.594614	586.800945	1171.610598	586.3089
5	541.298039	271.152658	524.271490	262.639383	523.287474	262.147375	**E**	***1090.552749***	545.780013	1073.526200	537.266738	1072.542184	536.7747
6	670.340632	335.673954	653.314083	327.160680	652.330067	326.668672	**E**	***961.510156***	481.258716	944.483607	472.745442	943.499591	472.2534
7	856.419945	428.713611	839.393396	420.200336	838.409380	419.708328	**W**	***832.467563***	416.737420	815.441014	408.224145	814.456998	407.7321
8	927.457059	464.232168	910.430510	455.718893	909.446494	455.226885	**A**	***646.388250***	323.697763	629.361701	315.184489	628.377685	314.6924
9	1041.499986	521.253631	1024.473437	512.740357	1023.489421	512.248349	**N**	***575.351136***	288.179206	558.324587	279.665932	557.340571	279.1739
10	1128.532014	564.769645	1111.505465	556.256371	1110.521449	555.764363	**S**	***461.308209***	231.157743	444.281660	222.644468	443.297644	222.1524
11	**1227.600428**	614.303852	1210.573879	605.790578	1209.589863	605.298570	**V**	***374.276181***	187.641729	357.249632	179.128454		
12	1355.695391	678.351334	1338.668842	669.838059	1337.684826	669.346051	**K**	***275.207767***	138.107521	258.181218	129.594247		
13							**K**	147.112804	74.060040	130.086255	65.546765		



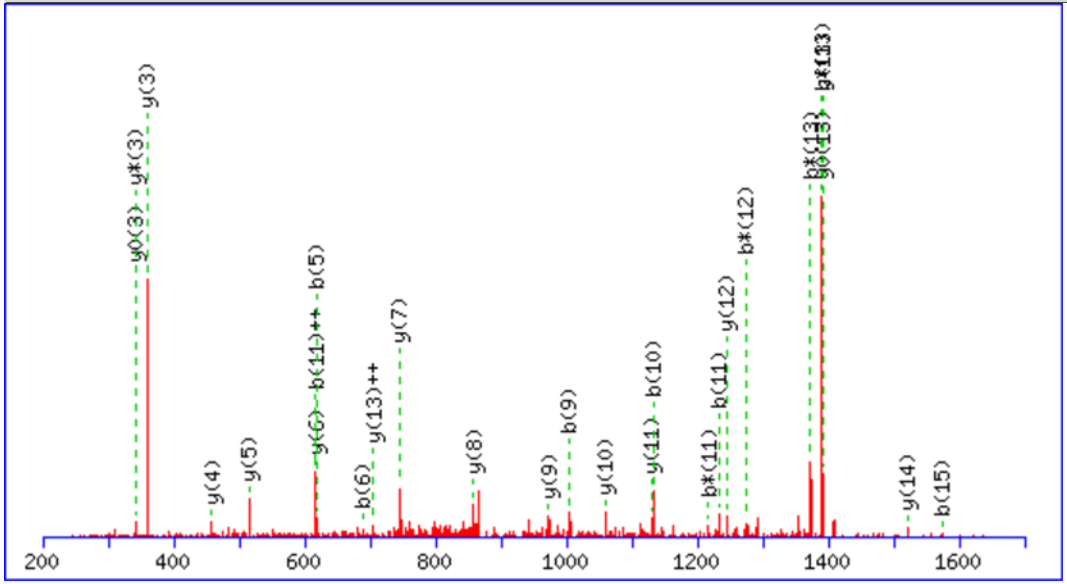
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 11975: 1746.916848 from(874.465700,2+)
Title: OECHL100310_09.16728.16728.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 62 **Expect:** 6.1e-005**Matches :** 27/156 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018

6	**689.386854**	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	1290.657609	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							**R**	175.118952	88.063114	158.092403	79.549839		



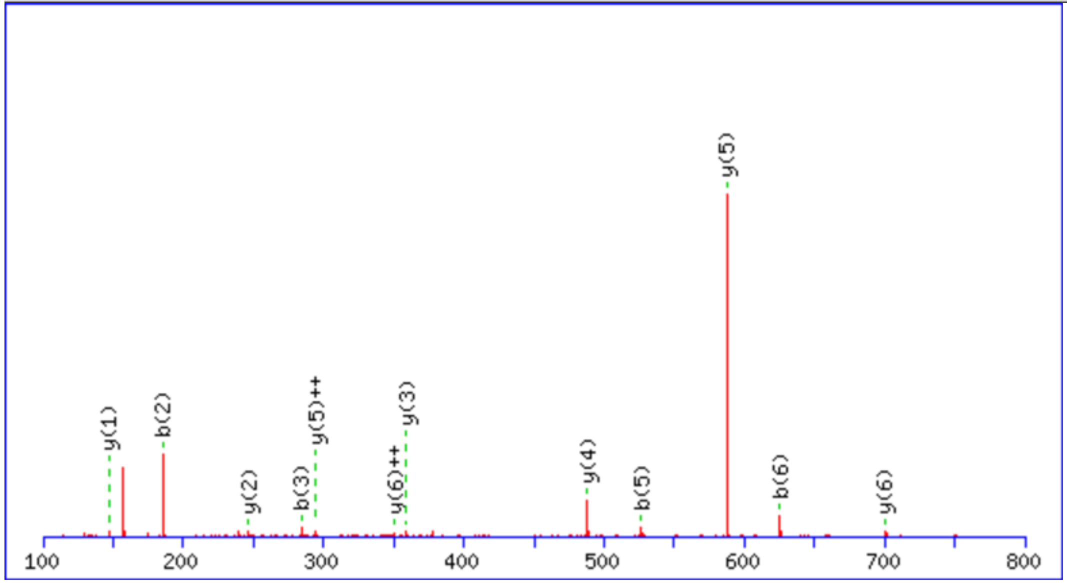
Peptide View

MS/MS Fragmentation of **ALVQIVK**
Found in **IPI00216569**, Tax_Id=9606 Gene_Symbol=CST7 Cystatin-F precursor

Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 727: 770.490248 from(386.252400,2+)
Title: OECHL100310_09.11669.11669.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 770.490173**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: Q4 :** Deamidated (NQ)**Ions Score:** 51 **Expect:** 0.00032**Matches :** 12/42 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			**A**					**7**
2	**185.128454**	93.067865			**L**	***700.460354***	350.733815	683.433805	342.220541	**6**
3	**284.196868**	142.602072			**V**	***587.376290***	294.191783	570.349741	285.678509	**5**
4	413.239462	207.123369	396.212913	198.610095	**Q**	***488.307876***	244.657576	471.281327	236.144301	**4**
5	**526.323526**	263.665401	509.296977	255.152127	**I**	***359.265282***	180.136279	342.238733	171.623004	**3**
6	**625.391940**	313.199608	608.365391	304.686333	**V**	***246.181218***	123.594247	229.154669	115.080972	**2**
7					**K**	***147.112804***	74.060040	130.086255	65.546765	**1**

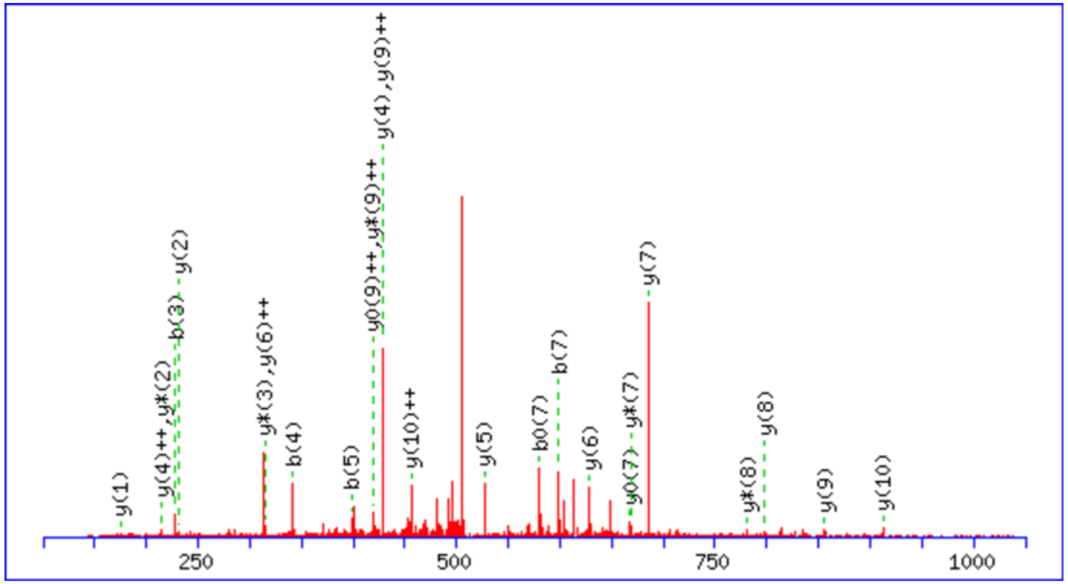


Peptide View

MS/MS Fragmentation of **IGGIGTVPVGR**
Found in **IPI00014424**, Tax_Id=9606 Gene_Symbol=EEF1A2 Elongation factor 1-alpha 2
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 3233: 1024.603248 from(513.308900,2+)
Title: OECHL100310_09.10897.10897.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1024.602951**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59 **Expect:** 3.6e-005**Matches :** 25/80 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**I**							**11**
2	171.112804	86.060040			**G**	***912.526143***	456.766710	895.499594	448.253435	894.515578	447.761427	**10**
3	**228.134268**	114.570772			**G**	***855.504679***	428.255978	838.478130	419.742703	837.494114	419.250695	**9**
4	**341.218332**	171.112804			**I**	***798.483215***	399.745246	781.456666	391.231971	780.472650	390.739963	**8**
5	**398.239796**	199.623536			**G**	***685.399151***	343.203214	668.372602	334.689939	667.388586	334.197931	**7**
6	499.287475	250.147375	481.276910	241.142093	**T**	***628.377687***	314.692482	611.351138	306.179207	610.367122	305.687199	**6**
7	**598.355889**	299.681583	580.345324	290.676300	**V**	***527.330008***	264.168642	510.303459	255.655368			**5**
8	695.408653	348.207965	677.398088	339.202682	**P**	***428.261594***	214.634435	411.235045	206.121161			**4**
9	794.477067	397.742172	776.466502	388.736889	**V**	331.208830	166.108053	314.182281	157.594779			**3**
10	851.498531	426.252904	833.487966	417.247621	**G**	***232.140416***	116.573846	215.113867	108.060572			**2**
11					**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



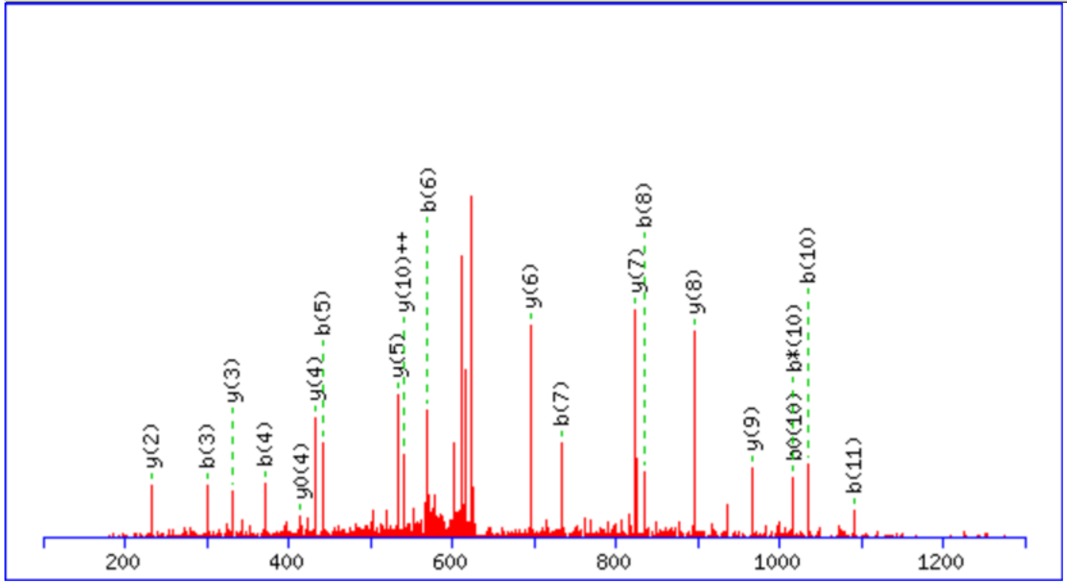
Peptide View

MS/MS Fragmentation of **ADLAAQYTTVGR**
Found in **IPI00019988**, Tax_Id=9606 Gene_Symbol=SGSH N-sulphoglucosamine sulphohydrolase
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 6912: 1264.641448 from(633.328000,2+)
Title: OECHL100310_09.10654.10654.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1264.641159**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57 **Expect:** 0.00015**Matches :** 20/114 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	72.044390	36.525833					**A**						
2	187.071333	94.039304			169.060768	85.034022	**D**	1194.611330	597.809303	1177.584781	589.296029	1176.600765	588.8040
3	***300.155397***	150.581336			282.144832	141.576054	**L**	1079.584387	540.295832	1062.557838	531.782557	1061.573822	531.2905
4	***371.192511***	186.099894			353.181946	177.094611	**A**	***966.500323***	483.753800	949.473774	475.240525	948.489758	474.7485
5	***442.229625***	221.618450			424.219060	212.613168	**A**	***895.463209***	448.235243	878.436660	439.721968	877.452644	439.2299

6	***570.288203***	285.647740	553.261654	277.134465	552.277638	276.642457	**Q**	***824.426095***	412.716686	807.399546	404.203411	806.415530	403.7114
7	***733.351532***	367.179404	716.324983	358.666130	715.340967	358.174122	**Y**	***696.367517***	348.687397	679.340968	340.174122	678.356952	339.6821
8	***834.399211***	417.703244	817.372662	409.189969	816.388646	408.697961	**T**	***533.304188***	267.155732	516.277639	258.642458	515.293623	258.1504
9	935.446890	468.227083	918.420341	459.713809	917.436325	459.221801	**T**	***432.256509***	216.631892	415.229960	208.118618	414.245944	207.6266
10	***1034.515304***	517.761290	1017.488755	509.248016	1016.504739	508.756008	**V**	***331.208830***	166.108053	314.182281	157.594778		
11	***1091.536768***	546.272022	1074.510219	537.758748	1073.526203	537.266740	**G**	***232.140416***	116.573846	215.113867	108.060571		
12							**R**	175.118952	88.063114	158.092403	79.549839		



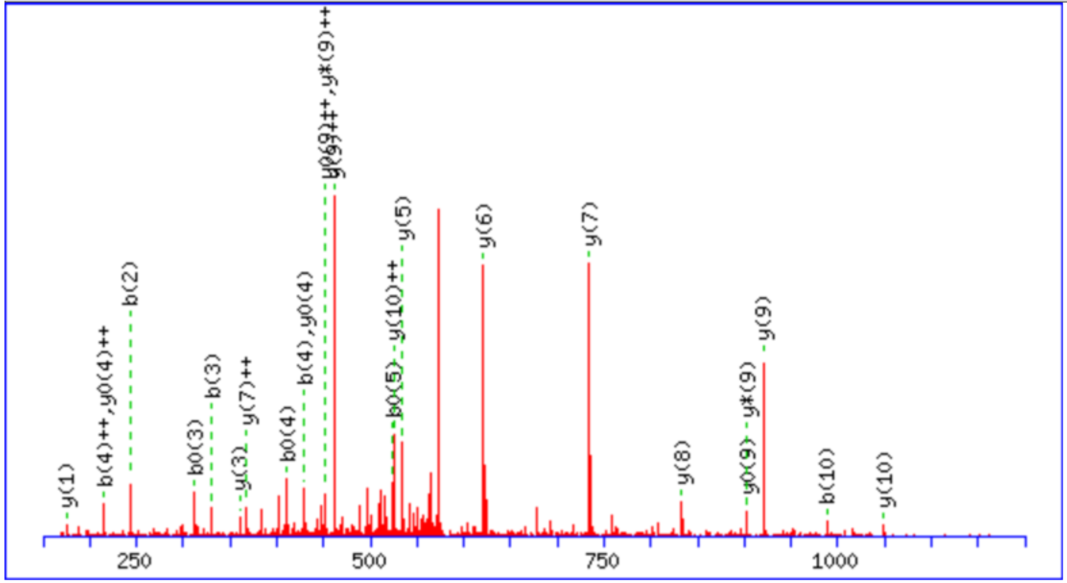
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 5316: 1161.635648 from(581.825100,2+)
Title: OECHL100310_09.5341.5341.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**

Score: 55 **Expect:** 0.0002**Matches :** 25/94 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	114.091340	57.549308					**I**						
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637
3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340
4	**429.234375**	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087
7	716.382495	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073
8	803.414523	402.210899			785.403958	393.205617	**S**	447.267407	224.137342	430.240858	215.624067	429.256842	215.132059
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053		
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321		
11							**R**	***175.118952***	88.063114	158.092403	79.549840		

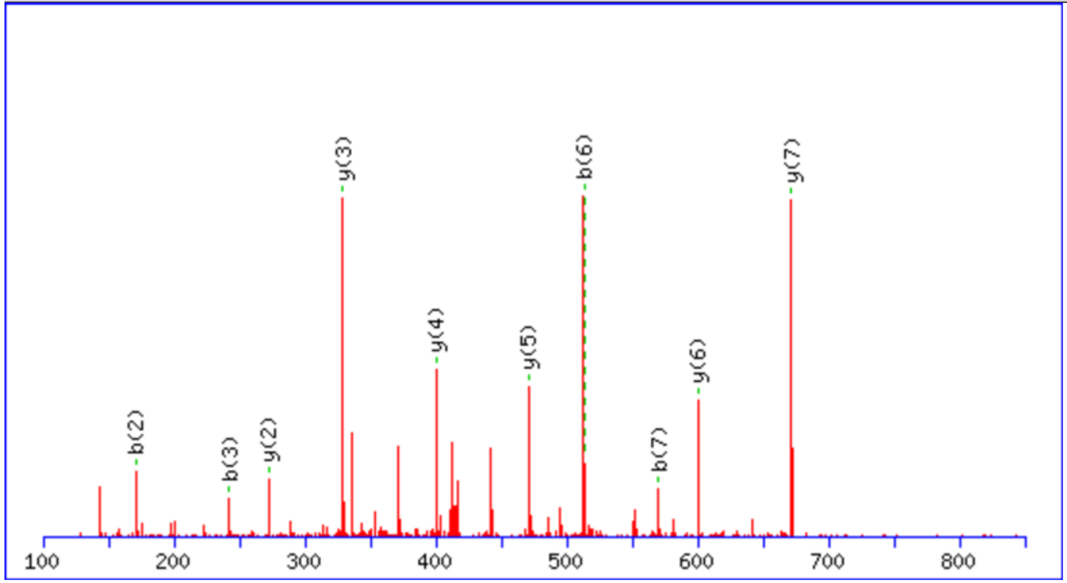


Peptide View

MS/MS Fragmentation of **GLAEAAGPR**
Found in **IPI00290826**, Tax_Id=9606 Gene_Symbol=FAM174A Membrane protein FAM174A
Experiment: 01 - S_A-1 **Fraction:** S_A-1

Match to Query 1135: 840.445048 from(421.229800,2+)
Title: OECHL100310_09.4013.4013.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 840.445343**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51 **Expect:** 0.00045**Matches :** 10/64 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							9
2	**171.112804**	86.060040			L	784.431179	392.719228	767.404630	384.205953	766.420614	383.713945	8
3	**242.149918**	121.578597			A	***671.347115***	336.177196	654.320566	327.663921	653.336550	327.171913	7
4	371.192511	186.099894	353.181946	177.094611	E	***600.310001***	300.658639	583.283452	292.145364	582.299436	291.653356	6
5	442.229625	221.618450	424.219060	212.613168	A	***471.267408***	236.137342	454.240859	227.624067			5
6	**513.266739**	257.137008	495.256174	248.131725	A	***400.230294***	200.618785	383.203745	192.105510			4
7	**570.288203**	285.647740	552.277638	276.642457	G	***329.193180***	165.100228	312.166631	156.586953			3
8	667.340967	334.174122	649.330402	325.168839	P	***272.171716***	136.589496	255.145167	128.076221			2
9					R	175.118952	88.063114	158.092403	79.549839			1

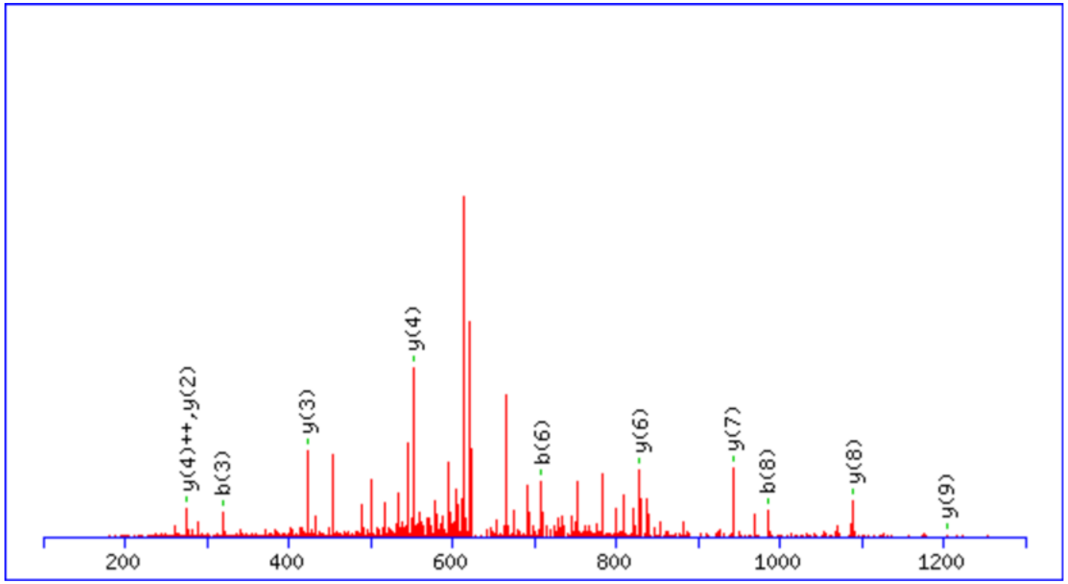


Peptide View

MS/MS Fragmentation of **GNFNYIEFTR**
Found in **IPI00033494**, Tax_Id=9606 Gene_Symbol=MYL12B Myosin regulatory light chain 12B
Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 7313: 1259.594848 from(630.804700,2+)
Title: OECHL100312_24.15561.15561.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 1259.593475**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71 **Expect:** 8.8e-006**Matches :** 11/92 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	58.028740	29.518008					**G**						
2	172.071667	86.539471	155.045118	78.026197			**N**	***1203.579299***	602.293288	1186.552750	593.780013	1185.568734	593.2880
3	**319.140081**	160.073678	302.113532	151.560404			**F**	***1089.536372***	545.271824	1072.509823	536.758549	1071.525807	536.2665
4	433.183008	217.095142	416.156459	208.581867			**N**	***942.467958***	471.737617	925.441409	463.224342	924.457393	462.7323
5	596.246337	298.626807	579.219788	290.113532			**Y**	***828.425031***	414.716154	811.398482	406.202879	810.414466	405.7108
6	**709.330401**	355.168839	692.303852	346.655564			**I**	665.361702	333.184489	648.335153	324.671214	647.351137	324.1792
7	838.372994	419.690135	821.346445	411.176861	820.362429	410.684853	**E**	***552.277638***	276.642457	535.251089	268.129182	534.267073	267.6371
8	**985.441408**	493.224342	968.414859	484.711068	967.430843	484.219060	**F**	***423.235045***	212.121160	406.208496	203.607886	405.224480	203.1158
9	1086.489087	543.748181	1069.462538	535.234907	1068.478522	534.742899	**T**	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.5816
10							**R**	175.118952	88.063114	158.092403	79.549839		



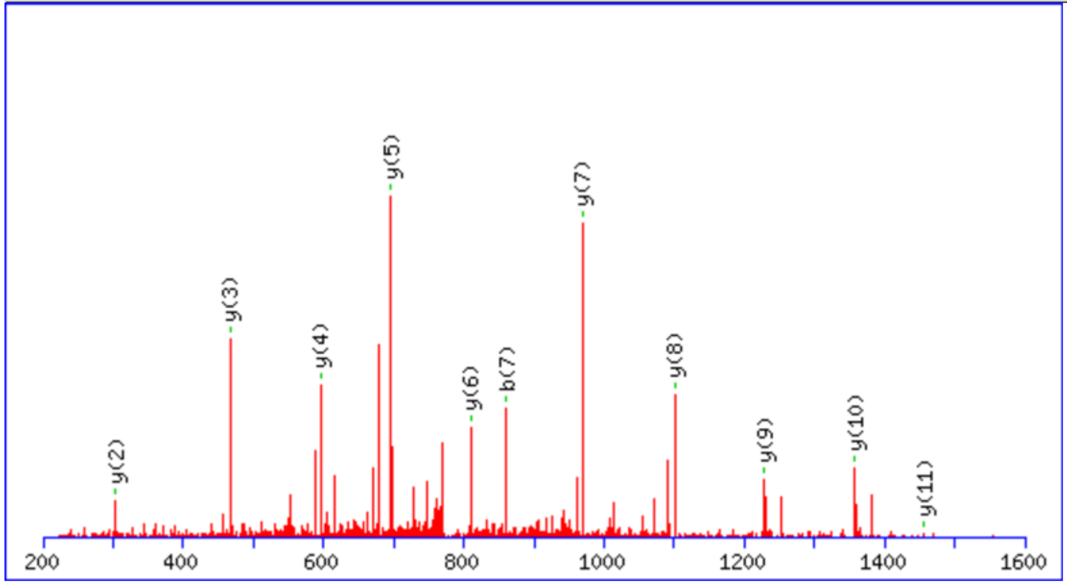
Peptide View

MS/MS Fragmentation of **VVEQMCITQYER**
Found in **IPI00022284**, Tax_Id=9606 Gene_Symbol=PRNP Major prion protein
Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 10360: 1554.717648 from(778.366100,2+)
Title: OECHL100312_24.12705.12705.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 1554.717041**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 91 **Expect:** 7.7e-008**Matches :** 11/120 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	100.075690	50.541483					**V**						
2	199.144104	100.075690					**V**	***1456.655914***	728.831595	1439.629365	720.318321	1438.645349	719.8263
3	328.186697	164.596987			310.176132	155.591704	**E**	***1357.587500***	679.297388	1340.560951	670.784114	1339.576935	670.2921
4	456.245275	228.626276	439.218726	220.113001	438.234710	219.620993	**Q**	***1228.544907***	614.776092	1211.518358	606.262817	1210.534342	605.7708
5	587.285760	294.146518	570.259211	285.633244	569.275195	285.141236	**M**	***1100.486329***	550.746803	1083.459780	542.233528	1082.475764	541.7415

6	747.316409	374.161843	730.289860	365.648568	729.305844	365.156560	**C**	***969.445844***	485.226560	952.419295	476.713286	951.435279	476.2212
7	860.400473	430.703875	843.373924	422.190600	842.389908	421.698592	**I**	***809.415195***	405.211236	792.388646	396.697961	791.404630	396.2059
8	961.448152	481.227714	944.421603	472.714440	943.437587	472.222432	**T**	***696.331131***	348.669204	679.304582	340.155929	678.320566	339.6639
9	1089.506730	545.257003	1072.480181	536.743729	1071.496165	536.251721	**Q**	***595.283452***	298.145364	578.256903	289.632090	577.272887	289.1400
10	1252.570059	626.788668	1235.543510	618.275393	1234.559494	617.783385	**Y**	***467.224874***	234.116075	450.198325	225.602801	449.214309	225.1107
11	1381.612652	691.309964	1364.586103	682.796690	1363.602087	682.304682	**E**	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.5791
12							**R**	175.118952	88.063114	158.092403	79.549839		



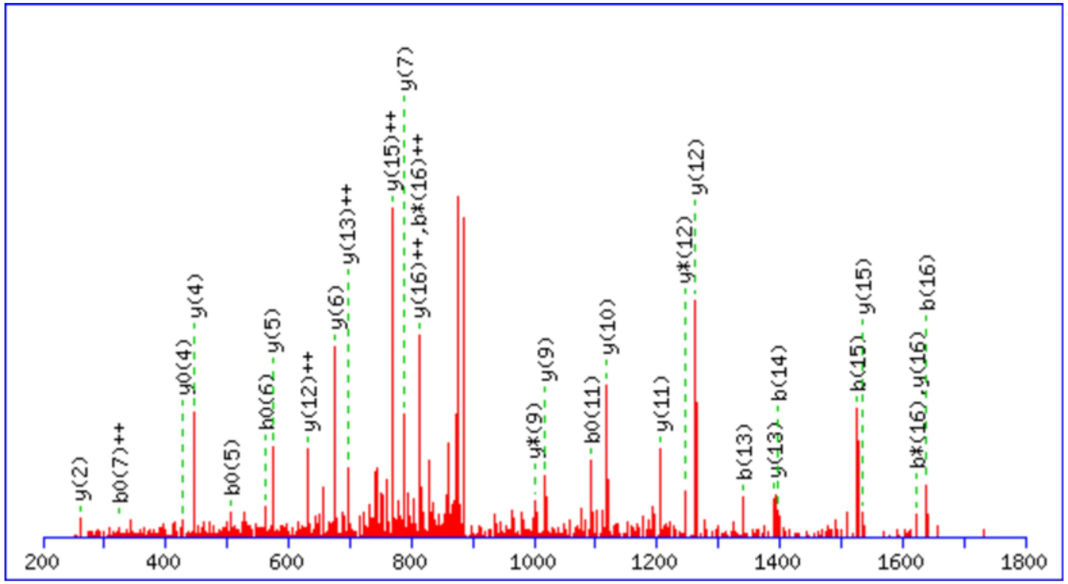
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 12335: 1784.880048 from(893.447300,2+)
Title: OECHL100312_24.8103.8103.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**

Score: 89 **Expect:** 1.8e-007**Matches :** 29/170 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	164.070605	82.538940					**Y**						
2	251.102633	126.054954			233.092068	117.049672	**S**	***1622.823172***	811.915224	1605.796623	803.401950	1604.812607	802.9099
3	308.124097	154.565687			290.113532	145.560404	**G**	***1535.791144***	768.399210	1518.764595	759.885936	1517.780579	759.3939
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.8831
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.3671
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.8458
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.3351
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.8191
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.2952
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.2660
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.7421
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.2001
13	**1340.632852**	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.6762
14	**1397.654316**	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.6288
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.1180
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		



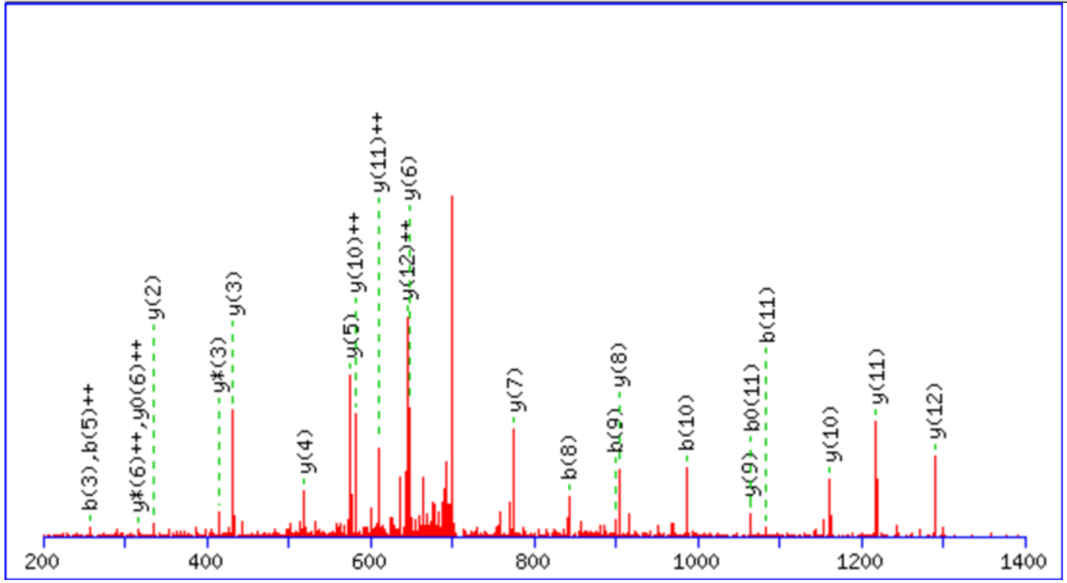
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 8739: 1416.624048 from(709.319300,2+)
Title: OECHL100312_24.2306.2306.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 92 **Expect:** 3.7e-008**Matches :** 24/128 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	129.102239	65.054757	112.075690	56.541483			K						
2	200.139353	100.573315	183.112804	92.060040			A	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.2664
3	**257.160817**	129.084047	240.134268	120.570772			G	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.7478
4	354.213581	177.610429	337.187032	169.097154			P	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.2371
5	514.244230	257.625753	497.217681	249.112479			C	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.7107

6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.6954
7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.1741
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.1448
9	**899.403979**	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.6262
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.1155
11	**1083.488771**	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546		
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164		
13							**R**	175.118952	88.063114	158.092403	79.549839		



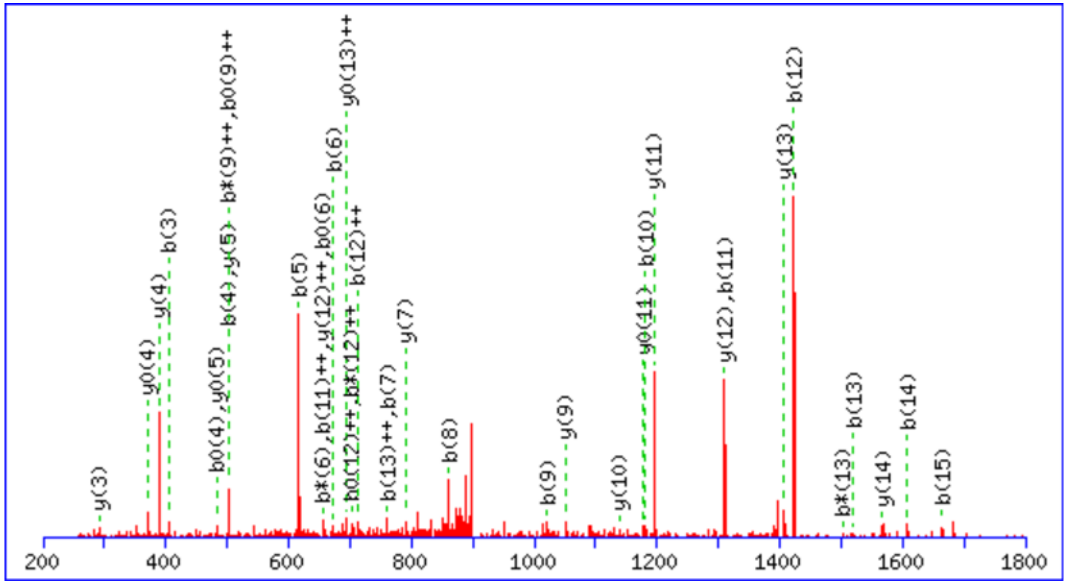
Peptide View

MS/MS Fragmentation of **SRCPDGSTCCELPSGK**
Found in **IPI00182138**, Tax_Id=9606 Gene_Symbol=GRN Isoform 2 of Granulins
Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 12452: 1809.745848 from(905.880200,2+)
Title: OECHL100312_24.5543.5543.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 1809.744415**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66 **Expect:** 7.2e-006**Matches :** 39/174 fragment ions using 79 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	88.039304	44.523290			70.028739	35.518008	**S**						
2	244.140415	122.573845	227.113866	114.060571	226.129850	113.568563	**R**	1723.719653	862.363465	1706.693104	853.850190	1705.709088	853.3581
3	***404.171064***	202.589170	387.144515	194.075896	386.160499	193.583888	**C**	**1567.618542**	784.312909	1550.591993	775.799635	1549.607977	775.3076
4	***501.223828***	251.115552	484.197279	242.602277	483.213263	242.110269	**P**	**1407.587893**	704.297585	1390.561344	695.784310	1389.577328	695.2923
5	***616.250771***	308.629024	599.224222	300.115749	598.240206	299.623741	**D**	**1310.535129**	655.771203	1293.508580	647.257928	1292.524564	646.7659
6	***673.272235***	337.139756	656.245686	328.626481	655.261670	328.134473	**G**	**1195.508186**	598.257731	1178.481637	589.744457	1177.497621	589.2524
7	***760.304263***	380.655770	743.277714	372.142495	742.293698	371.650487	**S**	**1138.486722**	569.746999	1121.460173	561.233725	1120.476157	560.7417
8	***861.351942***	431.179609	844.325393	422.666335	843.341377	422.174327	**T**	**1051.454694**	526.230985	1034.428145	517.717711	1033.444129	517.2257
9	***1021.382591***	511.194934	1004.356042	502.681659	1003.372026	502.189651	**C**	950.407015	475.707146	933.380466	467.193871	932.396450	466.7018
10	***1181.413240***	591.210258	1164.386691	582.696984	1163.402675	582.204976	**C**	**790.376366**	395.691821	773.349817	387.178547	772.365801	386.6865
11	***1310.455833***	**655.731555**	1293.429284	647.218280	1292.445268	646.726272	**E**	630.345717	315.676497	613.319168	307.163222	612.335152	306.6712
12	***1423.539897***	**712.273587**	1406.513348	703.760312	1405.529332	703.268304	**L**	**501.303124**	251.155200	484.276575	242.641925	483.292559	242.1499
13	***1520.592661***	**760.799969**	1503.566112	752.286694	1502.582096	751.794686	**P**	**388.219060**	194.613168	371.192511	186.099894	370.208495	185.6078
14	***1607.624689***	804.315983	1590.598140	795.802708	1589.614124	795.310700	**S**	**291.166296**	146.086786	274.139747	137.573512	273.155731	137.0815
15	***1664.646153***	832.826715	1647.619604	824.313440	1646.635588	823.821432	**G**	204.134268	102.570772	187.107719	94.057497		
16							**K**	147.112804	74.060040	130.086255	65.546765		



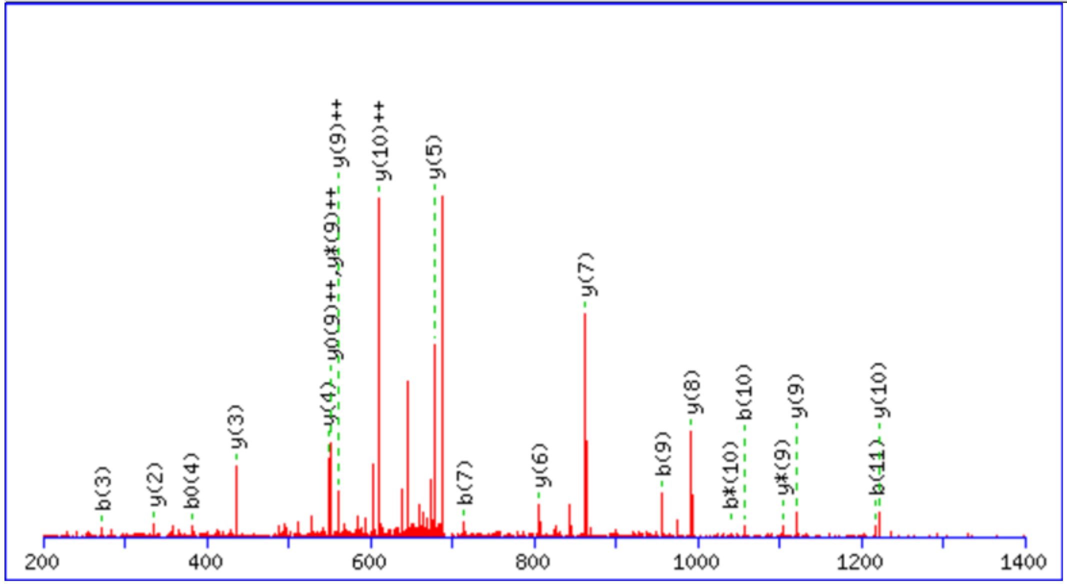
Peptide View

MS/MS Fragmentation of **VATQEGKEITCR**
Found in **IPI00031564**, Tax_Id=9606 Gene_Symbol=GGCT Isoform 1 of Gamma-glutamylcyclotransferase
Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 8576: 1390.687848 from(696.351200,2+)
Title: OECHL100312_24.4278.4278.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 1390.687454**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61 **Expect:** 9e-005**Matches :** 21/118 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	100.075690	50.541483					**V**						
2	171.112804	86.060040					**A**	1292.626328	646.816802	1275.599779	638.303528	1274.615763	637.8115
3	**272.160483**	136.583879			254.149918	127.578597	**T**	***1221.589214***	611.298245	1204.562665	602.784971	1203.578649	602.2929
4	400.219061	200.613169	383.192512	192.099894	382.208496	191.607886	**Q**	***1120.541535***	560.774406	1103.514986	552.261131	1102.530970	551.7691
5	529.261654	265.134465	512.235105	256.621191	511.251089	256.129183	**E**	***992.482957***	496.745117	975.456408	488.231842	974.472392	487.7398

6	586.283118	293.645197	569.256569	285.131923	568.272553	284.639915	**G**	***863.440364***	432.223820	846.413815	423.710546	845.429799	423.2185
7	**714.378081**	357.692679	697.351532	349.179404	696.367516	348.687396	**K**	***806.418900***	403.713088	789.392351	395.199814	788.408335	394.7078
8	843.420674	422.213975	826.394125	413.700701	825.410109	413.208693	**E**	***678.323937***	339.665607	661.297388	331.152332	660.313372	330.6603
9	**956.504738**	478.756007	939.478189	470.242733	938.494173	469.750725	**I**	***549.281344***	275.144310	532.254795	266.631036	531.270779	266.1390
10	**1057.552417**	529.279847	1040.525868	520.766572	1039.541852	520.274564	**T**	***436.197280***	218.602278	419.170731	210.089003	418.186715	209.5969
11	**1217.583066**	609.295171	1200.556517	600.781897	1199.572501	600.289889	**C**	***335.149601***	168.078438	318.123052	159.565164		
12							**R**	175.118952	88.063114	158.092403	79.549839		



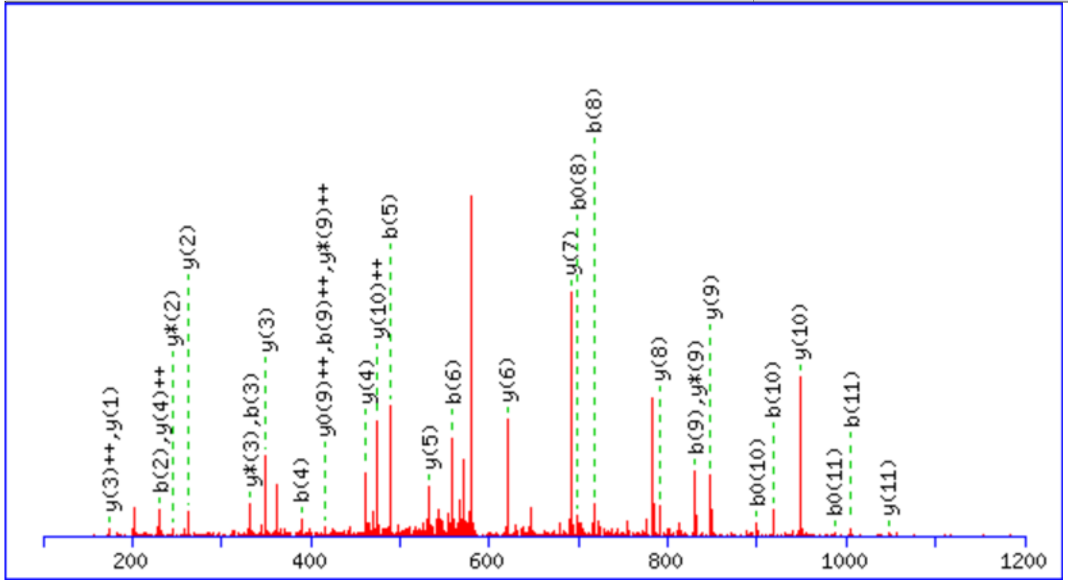
Peptide View

MS/MS Fragmentation of **MVTGVASALSSR**
Found in **IPI00554676**, Tax_Id=9606 Gene_Symbol=HBG2 Hemoglobin subunit gamma-2
Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 5996: 1177.612248 from(589.813400,2+)
Title: OECHL100312_24.11493.11493.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 1177.612503**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**

Score: 84 **Expect:** 3.6e-007**Matches :** 32/104 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518			**M**							**12**
2	**231.116175**	116.061725			**V**	***1047.579299***	524.293288	1030.552750	515.780013	1029.568734	515.288005	**11**
3	**332.163854**	166.585565	314.153289	157.580283	**T**	***948.510885***	474.759080	931.484336	466.245806	930.500320	465.753798	**10**
4	**389.185318**	195.096297	371.174753	186.091015	**G**	***847.463206***	424.235241	830.436657	415.721966	829.452641	415.229958	**9**
5	**488.253732**	244.630504	470.243167	235.625222	**V**	***790.441742***	395.724509	773.415193	387.211234	772.431177	386.719226	**8**
6	**559.290846**	280.149061	541.280281	271.143779	**A**	***691.373328***	346.190302	674.346779	337.677027	673.362763	337.185019	**7**
7	646.322874	323.665075	628.312309	314.659793	**S**	***620.336214***	310.671745	603.309665	302.158470	602.325649	301.666462	**6**
8	**717.359988**	359.183632	699.349423	350.178350	**A**	***533.304186***	267.155731	516.277637	258.642456	515.293621	258.150448	**5**
9	**830.444052**	415.725664	812.433487	406.720382	**L**	***462.267072***	231.637174	445.240523	223.123899	444.256507	222.631891	**4**
10	**917.476080**	459.241678	899.465515	450.236396	**S**	***349.183008***	175.095142	332.156459	166.581867	331.172443	166.089859	**3**
11	**1004.508108**	502.757692	986.497543	493.752410	**S**	***262.150980***	131.579128	245.124431	123.065853	244.140415	122.573845	**2**
12					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**

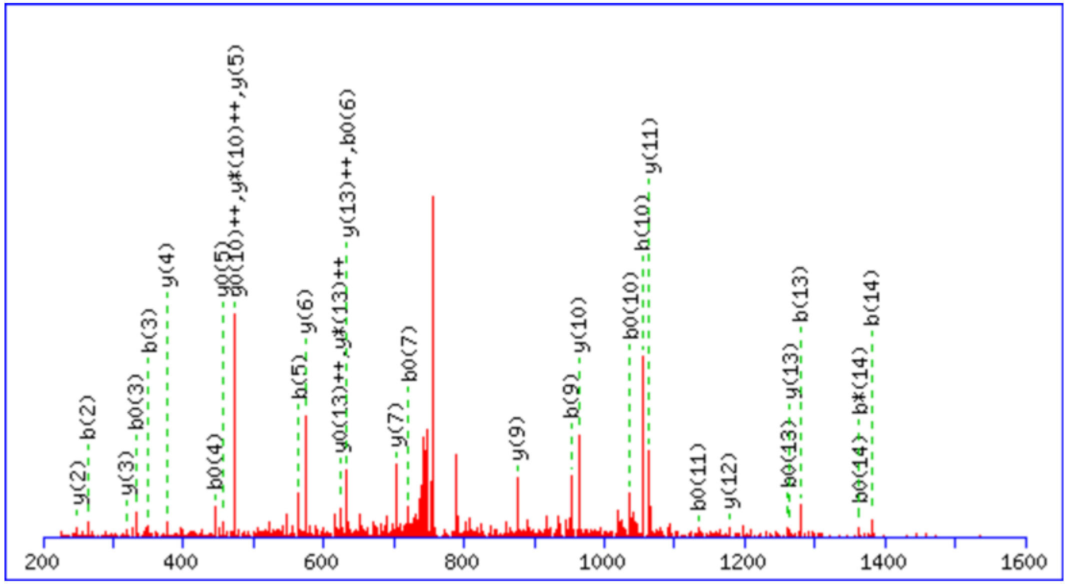


Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 9860: 1525.726848 from(763.870700,2+)
Title: OECHL100312_24.10733.10733.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 76 **Expect:** 2.9e-006**Matches :** 33/150 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	116.034219	58.520748			98.023654	49.515465	**D**						
2	**263.102633**	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.3515
3	**350.134661**	175.570968			332.124096	166.565686	**S**	***1264.637937***	632.822607	1247.611388	624.309332	1246.627372	623.8173
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.3013
5	**564.266404**	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.7592
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.2354
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.7194
8	825.362488	413.184882			807.351923	404.179599	**S**	789.410110	395.208693	772.383561	386.695418	771.399545	386.2034
9	**953.421066**	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.6873
10	**1054.468745**	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.6581
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.1342
12	1208.542973	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.6078
13	**1279.580087**	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	***319.197597***	160.102436	302.171048	151.589162	301.187032	151.0971
14	**1380.627766**	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.5785
15							**K**	147.112804	74.060040	130.086255	65.546765		



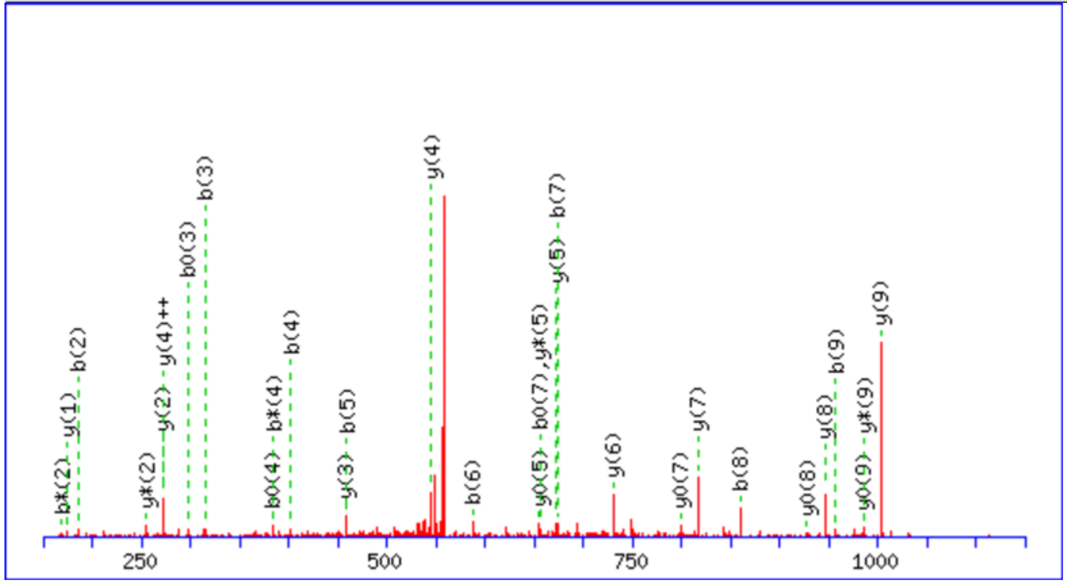
Peptide View

MS/MS Fragmentation of **KGESGQSWPR**
Found in **IPI00015029**, Tax_Id=9606 Gene_Symbol=PTGES3 Prostaglandin E synthase 3
Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 5277: 1130.546648 from(566.280600,2+)
Title: OECHL100312_24.4760.4760.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 1130.546860**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 73 **Expect:** 5.2e-006**Matches :** 30/98 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							**10**
2	**186.123703**	93.565489	169.097154	85.052215			**G**	***1003.459184***	502.233230	986.432635	493.719956	985.448619	493.227948	**9**
3	**315.166296**	158.086786	298.139747	149.573512	297.155731	149.081504	**E**	***946.437720***	473.722498	929.411171	465.209224	928.427155	464.717216	**8**
4	**402.198324**	201.602800	385.171775	193.089526	384.187759	192.597518	**S**	***817.395127***	409.201202	800.368578	400.687927	799.384562	400.195919	**7**
5	**459.219788**	230.113532	442.193239	221.600258	441.209223	221.108250	**G**	***730.363099***	365.685188	713.336550	357.171913	712.352534	356.679905	**6**

6	**587.278366**	294.142821	570.251817	285.629547	569.267801	285.137539	**Q**	***673.341635***	337.174456	656.315086	328.661181	655.331070	328.169173	**5**
7	**674.310394**	337.658835	657.283845	329.145560	656.299829	328.653552	**S**	***545.283057***	273.145167	528.256508	264.631892	527.272492	264.139884	**4**
8	**860.389707**	430.698492	843.363158	422.185217	842.379142	421.693209	**W**	***458.251029***	229.629153	441.224480	221.115878			**3**
9	**957.442471**	479.224874	940.415922	470.711599	939.431906	470.219591	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
10							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



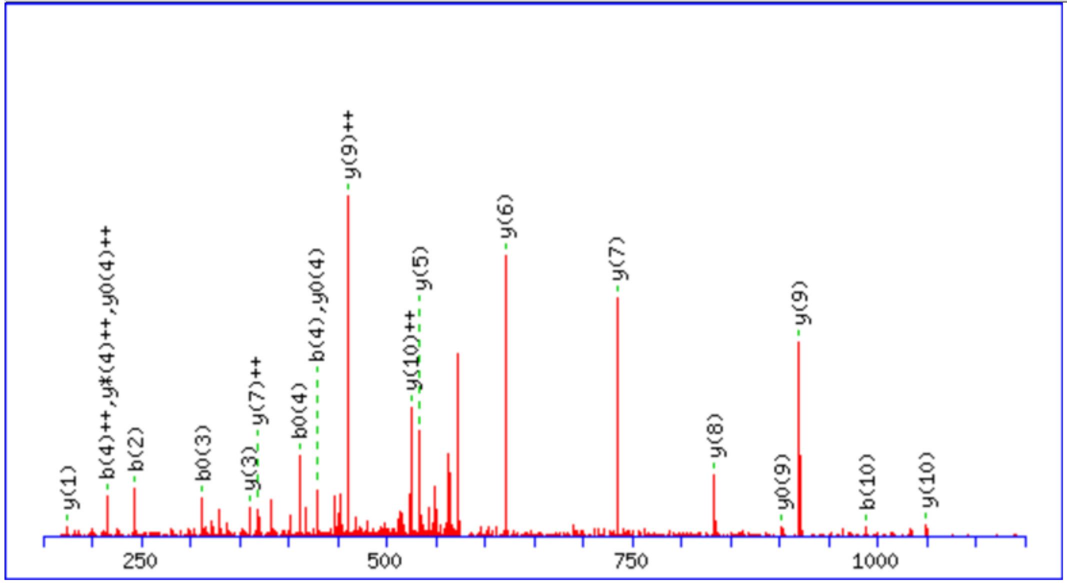
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 5751: 1161.633848 from(581.824200,2+)
Title: OECHL100312_24.5842.5842.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64 **Expect:** 3.1e-005**Matches :** 21/94 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	114.091340	57.549308					**I**						
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637
3	330.165961	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340
4	**429.234375**	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087
7	716.382495	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073
8	803.414523	402.210899			785.403958	393.205617	**S**	447.267407	224.137342	430.240858	215.624067	429.256842	215.132059
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053		
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321		
11							**R**	***175.118952***	88.063114	158.092403	79.549840		



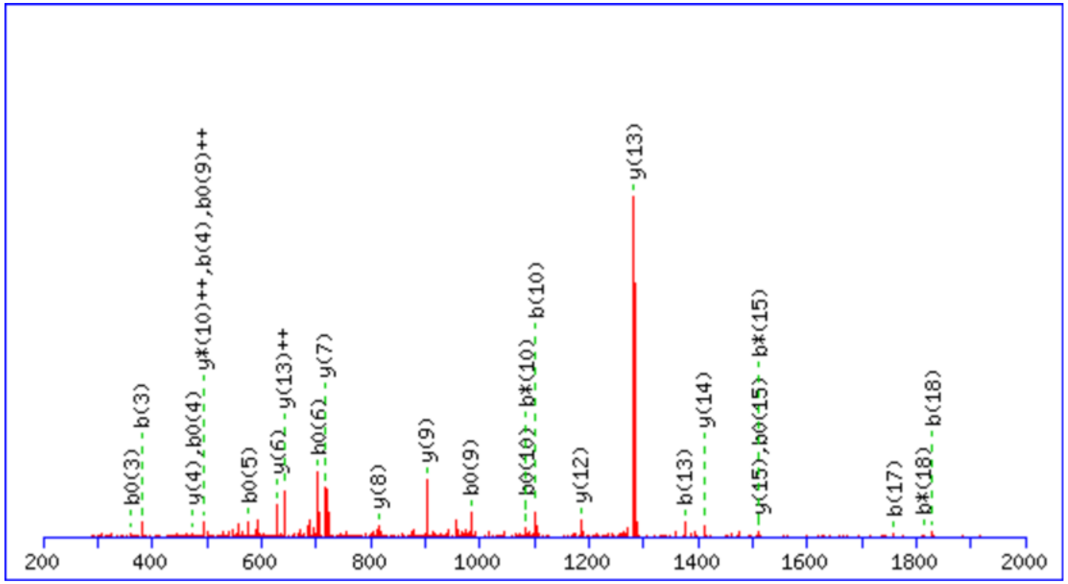
Peptide View

MS/MS Fragmentation of **SYELTQPPSVSVSPGQTAR**
Found in **IPI00382440**, Tax_Id=9606 Gene_Symbol=- Ig lambda chain V-IV region Hil

Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 13386: 2002.995448 from(1002.505000,2+)
Title: OECHL100312_24.12788.12788.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 2002.995987**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 64 **Expect:** 7e-005**Matches :** 28/202 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	88.039304	44.523290			70.028739	35.518008	S						
2	251.102633	126.054954			233.092068	117.049672	Y	1916.971234	958.989255	1899.944685	950.475981	1898.960669	949.9839
3	***380.145226***	190.576251			362.134661	181.570969	E	1753.907905	877.457591	1736.881356	868.944316	1735.897340	868.4523
4	***493.229290***	247.118283			475.218725	238.113001	L	1624.865312	812.936294	1607.838763	804.423020	1606.854747	803.9310
5	594.276969	297.642123			576.266404	288.636840	T	***1511.781248***	756.394262	1494.754699	747.880988	1493.770683	747.3889
6	722.335547	361.671412	705.308998	353.158137	704.324982	352.666129	Q	***1410.733569***	705.870423	1393.707020	697.357148	1392.723004	696.8651
7	819.388311	410.197794	802.361762	401.684519	801.377746	401.192511	P	***1282.674991***	641.841134	1265.648442	633.327859	1264.664426	632.8358
8	916.441075	458.724176	899.414526	450.210901	898.430510	449.718893	P	***1185.622227***	593.314752	1168.595678	584.801477	1167.611662	584.3094
9	1003.473103	502.240190	986.446554	493.726915	985.462538	493.234907	S	1088.569463	544.788370	1071.542914	536.275095	1070.558898	535.7830
10	***1102.541517***	551.774397	1085.514968	543.261122	1084.530952	542.769114	V	1001.537435	501.272356	984.510886	492.759081	983.526870	492.2670
11	1189.573545	595.290411	1172.546996	586.777136	1171.562980	586.285128	S	***902.469021***	451.738149	885.442472	443.224874	884.458456	442.7328
12	1288.641959	644.824618	1271.615410	636.311343	1270.631394	635.819335	V	***815.436993***	408.222135	798.410444	399.708860	797.426428	399.2168
13	***1375.673987***	688.340632	1358.647438	679.827357	1357.663422	679.335349	S	***716.368579***	358.687928	699.342030	350.174653	698.358014	349.6826
14	1472.726751	736.867014	1455.700202	728.353739	1454.716186	727.861731	P	***629.336551***	315.171914	612.310002	306.658639	611.325986	306.1666
15	1529.748215	765.377746	1512.721666	756.864471	1511.737650	756.372463	G	532.283787	266.645532	515.257238	258.132257	514.273222	257.6402
16	1657.806793	829.407035	1640.780244	820.893760	1639.796228	820.401752	Q	***475.262323***	238.134800	458.235774	229.621525	457.251758	229.1295
17	***1758.854472***	879.930874	1741.827923	871.417600	1740.843907	870.925592	T	347.203745	174.105510	330.177196	165.592236	329.193180	165.1002
18	***1829.891586***	915.449431	1812.865037	906.936157	1811.881021	906.444149	A	246.156066	123.581671	229.129517	115.068396		
19							R	175.118952	88.063114	158.092403	79.549839		



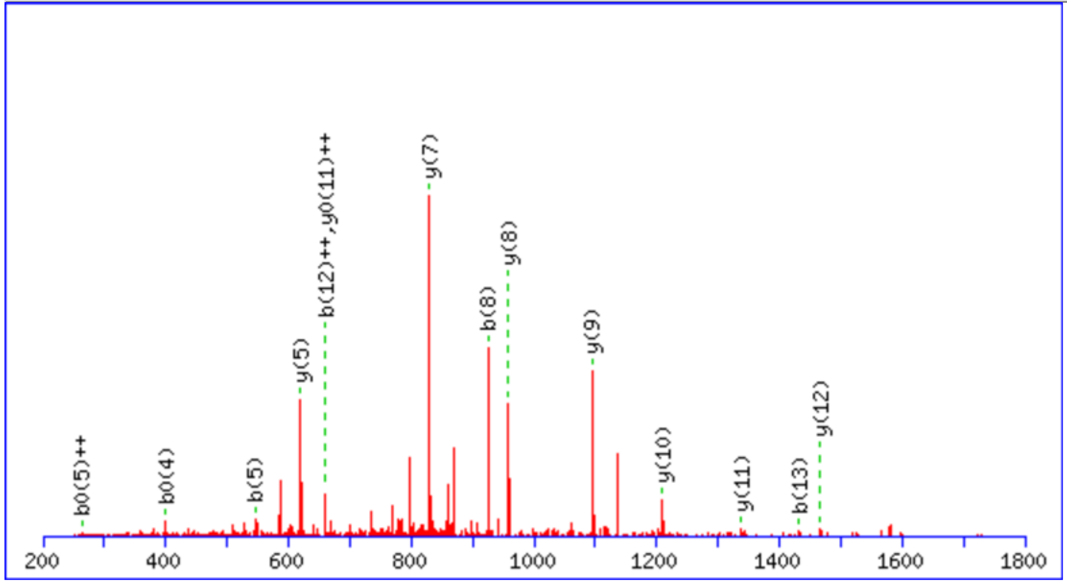
Peptide View

MS/MS Fragmentation of **STVEELHEPIPSLFR**
Found in **IPI00410487**, Tax_Id=9606 Gene_Symbol=TWSG1 Isoform 1 of Twisted gastrulation protein homolog 1
Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 12145: 1752.903448 from(877.459000,2+)
Title: OECHL100312_24.16366.16366.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 1752.904633**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58 **Expect:** 0.0002**Matches :** 14/134 fragment ions using 15 most intense peaks   (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**15**
2	189.086983	95.047129	171.076418	86.041847	**T**	1666.879898	833.943587	1649.853349	825.430313	1648.869333	824.938304	**14**
3	288.155397	144.581336	270.144832	135.576054	**V**	1565.832219	783.419748	1548.805670	774.906473	1547.821654	774.414465	**13**
4	417.197990	209.102633	399.187425	200.097351	**E**	***1466.763805***	733.885541	1449.737256	725.372266	1448.753240	724.880258	**12**
5	**546.240583**	273.623930	528.230018	264.618647	**E**	***1337.721212***	669.364244	1320.694663	660.850970	1319.710647	660.358961	**11**

6	659.324647	330.165962	641.314082	321.160679	**L**	***1208.678619***	604.842948	1191.652070	596.329673	1190.668054	595.837665	**10**
7	796.383559	398.695418	778.372994	389.690135	**H**	***1095.594555***	548.300915	1078.568006	539.787641	1077.583990	539.295633	**9**
8	**925.426152**	463.216714	907.415587	454.211432	**E**	***958.535643***	479.771460	941.509094	471.258185	940.525078	470.766177	**8**
9	1022.478916	511.743096	1004.468351	502.737814	**P**	***829.493050***	415.250163	812.466501	406.736889	811.482485	406.244881	**7**
10	1135.562980	568.285128	1117.552415	559.279845	**I**	732.440286	366.723781	715.413737	358.210507	714.429721	357.718499	**6**
11	1232.615744	616.811510	1214.605179	607.806227	**P**	***619.356222***	310.181749	602.329673	301.668475	601.345657	301.176467	**5**
12	1319.647772	660.327524	1301.637207	651.322242	**S**	522.303458	261.655367	505.276909	253.142093	504.292893	252.650085	**4**
13	**1432.731836**	716.869556	1414.721271	707.864273	**L**	435.271430	218.139353	418.244881	209.626078			**3**
14	1579.800250	790.403763	1561.789685	781.398481	**F**	322.187366	161.597321	305.160817	153.084047			**2**
15					**R**	175.118952	88.063114	158.092403	79.549839			**1**

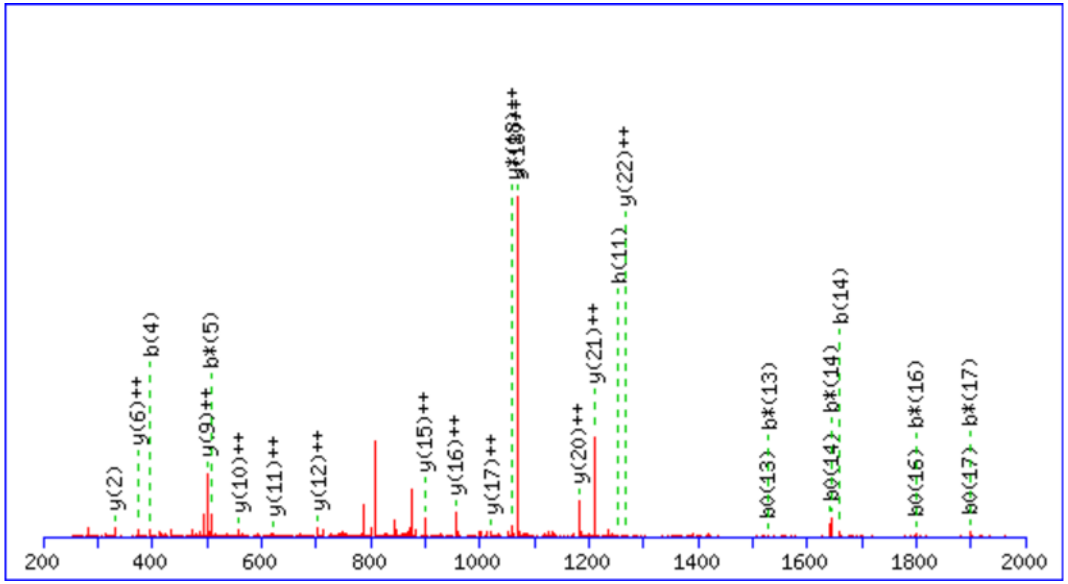


Peptide View

MS/MS Fragmentation of **QLGPQPQDIIYYEDGVVPTTDRR**
Found in **IPI00015199**, Tax_Id=9606 Gene_Symbol=CD7 T-cell antigen CD7
Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 15135: 2659.328472 from(887.450100,3+)
Title: OECHL100312_24.16256.16256.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 2659.324203**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 57 **Expect:** 0.00036**Matches :** 26/246 fragment ions using 52 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	
1	129.065854	65.036565	112.039305	56.523291			**Q**						
2	242.149918	121.578597	225.123369	113.065323			**L**	2532.272897	1266.640086	2515.246348	1258.126812	2514.262332	12
3	299.171382	150.089329	282.144833	141.576055			**G**	2419.188833	1210.098054	2402.162284	1201.584780	2401.178268	12
4	**396.224146**	198.615711	379.197597	190.102436			**P**	2362.167369	1181.587322	2345.140820	1173.074048	2344.156804	11
5	524.282724	262.645000	507.256175	254.131726			**Q**	2265.114605	1133.060940	2248.088056	1124.547666	2247.104040	11
6	621.335488	311.171382	604.308939	302.658108			**P**	2137.056027	1069.031651	2120.029478	1060.518377	2119.045462	10
7	749.394066	375.200671	732.367517	366.687397			**Q**	2040.003263	1020.505269	2022.976714	1011.991995	2021.992698	10
8	864.421009	432.714143	847.394460	424.200868	846.410444	423.708860	**D**	1911.944685	956.475980	1894.918136	947.962706	1893.934120	9
9	977.505073	489.256175	960.478524	480.742900	959.494508	480.250892	**I**	1796.917742	898.962509	1779.891193	890.449234	1778.907177	8
10	1090.589137	545.798206	1073.562588	537.284932	1072.578572	536.792924	**I**	1683.833678	842.420477	1666.807129	833.907202	1665.823113	8
11	**1253.652466**	627.329871	1236.625917	618.816597	1235.641901	618.324589	**Y**	1570.749614	785.878445	1553.723065	777.365170	1552.739049	7
12	1416.715795	708.861536	1399.689246	700.348261	1398.705230	699.856253	**Y**	1407.686285	704.346780	1390.659736	695.833506	1389.675720	6
13	1545.758388	773.382832	1528.731839	764.869558	1527.747823	764.377549	**E**	1244.622956	622.815116	1227.596407	614.301841	1226.612391	6
14	**1660.785331**	830.896304	1643.758782	822.383029	1642.774766	821.891021	**D**	1115.580363	558.293819	1098.553814	549.780545	1097.569798	5
15	1717.806795	859.407036	1700.780246	850.893761	1699.796230	850.401753	**G**	1000.553420	500.780348	983.526871	492.267073	982.542855	4
16	1816.875209	908.941243	1799.848660	900.427968	1798.864644	899.935960	**V**	943.531956	472.269616	926.505407	463.756341	925.521391	4
17	1915.943623	958.475450	1898.917074	949.962175	1897.933058	949.470167	**V**	844.463542	422.735409	827.436993	414.222134	826.452977	4
18	2012.996387	1007.001832	1995.969838	998.488557	1994.985822	997.996549	**P**	745.395128	373.201202	728.368579	364.687927	727.384563	3
19	2114.044066	1057.525671	2097.017517	1049.012396	2096.033501	1048.520388	**T**	648.342364	324.674820	631.315815	316.161545	630.331799	3
20	2215.091745	1108.049510	2198.065196	1099.536236	2197.081180	1099.044228	**T**	547.294685	274.150980	530.268136	265.637706	529.284120	2
21	2330.118688	1165.562982	2313.092139	1157.049707	2312.108123	1156.557699	**D**	446.247006	223.627141	429.220457	215.113866	428.236441	2
22	2486.219799	1243.613537	2469.193250	1235.100263	2468.209234	1234.608255	**R**	331.220063	166.113669	314.193514	157.600395		
23							**R**	175.118952	88.063114	158.092403	79.549839		



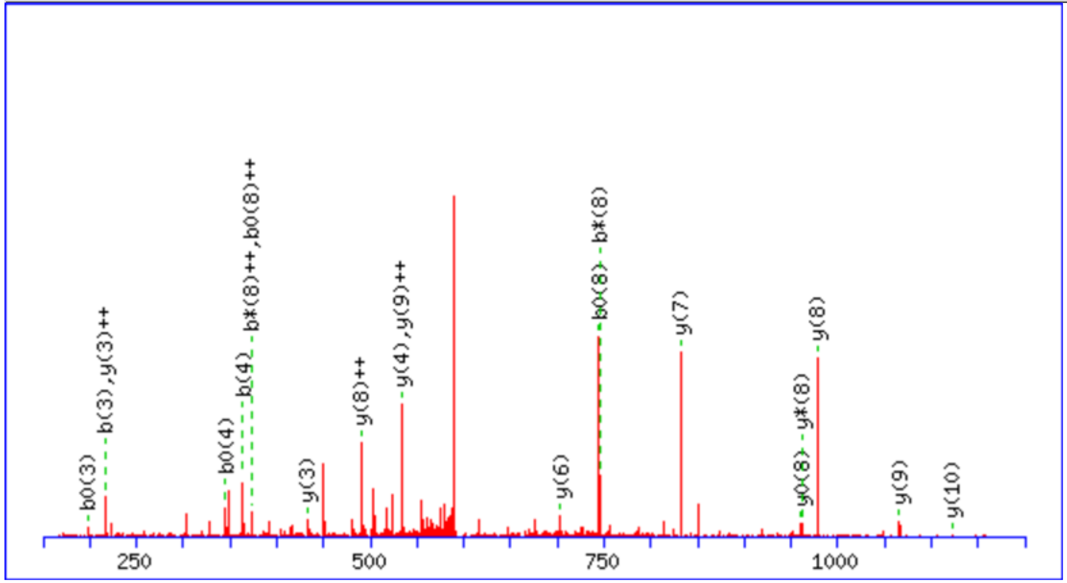
Peptide View

MS/MS Fragmentation of **AGSFKVATQER**
Found in **IPI00643388**, Tax_Id=9606 Gene_Symbol=RGL4 RGL4 protein
Experiment: 50 - PyB-2 **Fraction:** PyB-2

Match to Query 6171: 1192.620648 from(597.317600,2+)
Title: OECHL100312_24.2452.2452.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_24.raw
Monoisotopic mass of neutral peptide Mr(calc): 1192.620026**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50 **Expect:** 0.00078**Matches :** 20/106 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	72.044390	36.525833					**A**						
2	129.065854	65.036565					**G**	***1122.590199***	561.798738	1105.563650	553.285463	1104.579634	552.7934
3	**216.097882**	108.552579			198.087317	99.547296	**S**	***1065.568735***	533.288006	1048.542186	524.774731	1047.558170	524.2827
4	**363.166296**	182.086786			345.155731	173.081504	**F**	***978.536707***	489.771992	961.510158	481.258717	960.526142	480.7667
5	491.261259	246.134267	474.234710	237.620993	473.250694	237.128985	**K**	***831.468293***	416.237785	814.441744	407.724510	813.457728	407.2325

6	590.329673	295.668475	573.303124	287.155200	572.319108	286.663192	**V**	***703.373330***	352.190303	686.346781	343.677029	685.362765	343.1850
7	661.366787	331.187032	644.340238	322.673757	643.356222	322.181749	**A**	604.304916	302.656096	587.278367	294.142822	586.294351	293.6508
8	762.414466	381.710871	745.387917	373.197597	744.403901	372.705589	**T**	***533.267802***	267.137539	516.241253	258.624265	515.257237	258.1322
9	890.473044	445.740160	873.446495	437.226886	872.462479	436.734878	**Q**	***432.220123***	216.613700	415.193574	208.100425	414.209558	207.6084
10	1019.515637	510.261457	1002.489088	501.748182	1001.505072	501.256174	**E**	304.161545	152.584411	287.134996	144.071136	286.150980	143.5791
11							**R**	175.118952	88.063114	158.092403	79.549840		

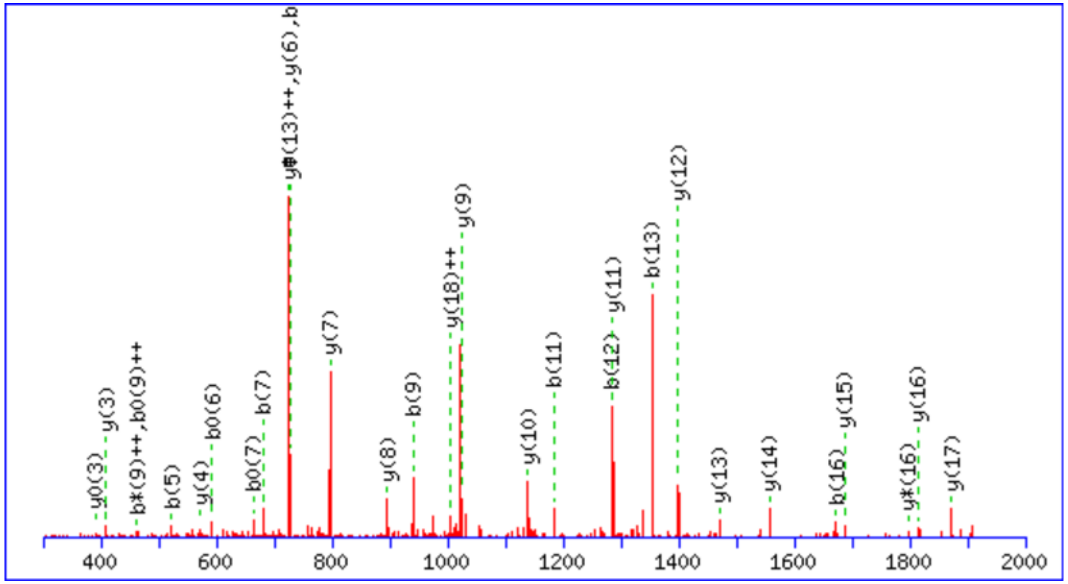


Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 32 - OPA-2 **Fraction:** OPA-2

Match to Query 13554: 2078.985448 from(1040.500000,2+)
Title: OECHL100312_11.16815.16815.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 100 **Expect:** 1.6e-008**Matches :** 31/200 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	72.044390	36.525833					**A**						
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444
4	394.183344	197.595310	377.156795	189.082035			**Q**	***1814.870790***	907.939033	1797.844241	899.425759	1796.860225	898.933
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904
6	610.257965	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383
7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867
8	794.379143	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676
15	1508.712833	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	629.304187	315.155732	612.277638	306.642457	611.293622	306.150
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	***572.282723***	286.645000	555.256174	278.131725	554.272158	277.639
17	1818.844576	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108
18	1905.876604	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573
19							**R**	175.118952	88.063114	158.092403	79.549840		



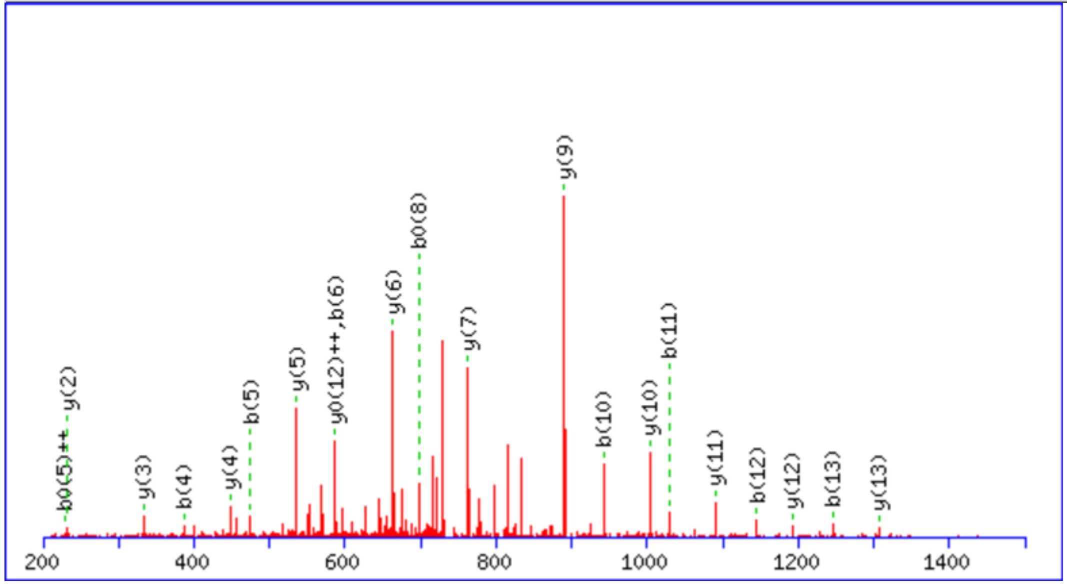
Peptide View

MS/MS Fragmentation of **GLDTSLGAVQSDTGR**
Found in **IPI00289931**, Tax_Id=9606 Gene_Symbol=MADCAM1 MADCAM1 protein
Experiment: 32 - OPA-2 **Fraction:** OPA-2

Match to Query 8995: 1475.721448 from(738.868000,2+)
Title: OECHL100312_11.11085.11085.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1475.721619**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 102 **Expect:** 9.3e-009**Matches :** 21/142 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	58.028740	29.518008					G						
2	171.112804	86.060040					L	1419.707414	710.357345	1402.680865	701.844071	1401.696849	701.3520
3	286.139747	143.573512			268.129182	134.568229	D	***1306.623350***	653.815313	1289.596801	645.302039	1288.612785	644.8100
4	**387.187426**	194.097351			369.176861	185.092069	T	***1191.596407***	596.301842	1174.569858	587.788567	1173.585842	587.2965
5	**474.219454**	237.613365			456.208889	228.608082	S	***1090.548728***	545.778002	1073.522179	537.264728	1072.538163	536.7727

6	**587.303518**	294.155397			569.292953	285.150115	**L**	***1003.516700***	502.261988	986.490151	493.748714	985.506135	493.2567
7	644.324982	322.666129			626.314417	313.660847	**G**	***890.432636***	445.719956	873.406087	437.206682	872.422071	436.7146
8	715.362096	358.184686			697.351531	349.179404	**A**	833.411172	417.209224	816.384623	408.695950	815.400607	408.2039
9	814.430510	407.718893			796.419945	398.713611	**V**	***762.374058***	381.690667	745.347509	373.177393	744.363493	372.6853
10	**942.489088**	471.748182	925.462539	463.234908	924.478523	462.742900	**Q**	***663.305644***	332.156460	646.279095	323.643186	645.295079	323.1511
11	**1029.521116**	515.264196	1012.494567	506.750922	1011.510551	506.258914	**S**	***535.247066***	268.127171	518.220517	259.613897	517.236501	259.1218
12	**1144.548059**	572.777668	1127.521510	564.264393	1126.537494	563.772385	**D**	***448.215038***	224.611157	431.188489	216.097882	430.204473	215.6058
13	**1245.595738**	623.301507	1228.569189	614.788233	1227.585173	614.296225	**T**	***333.188095***	167.097685	316.161546	158.584411	315.177530	158.0924
14	1302.617202	651.812239	1285.590653	643.298965	1284.606637	642.806957	**G**	***232.140416***	116.573846	215.113867	108.060571		
15							**R**	175.118952	88.063114	158.092403	79.549839		

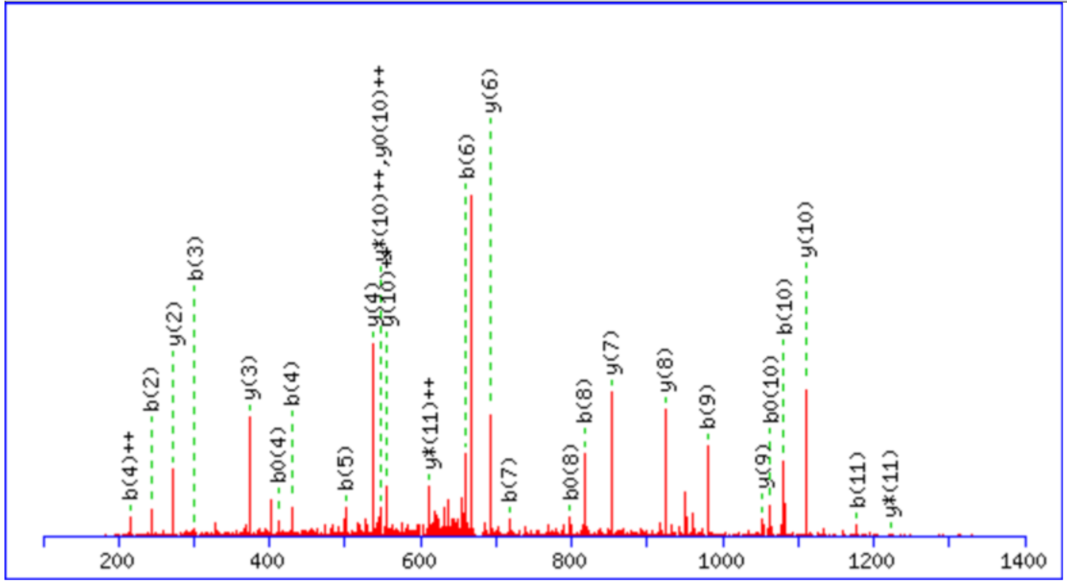


Peptide View

MS/MS Fragmentation of **LEGEACGVYTPR**
Found in **IPI00297284**, Tax_Id=9606 Gene_Symbol=IGFBP2 Insulin-like growth factor-binding protein 2
Experiment: 32 - OPA-2 **Fraction:** OPA-2

Match to Query 7746: 1350.626248 from(676.320400,2+)
Title: OECHL100312_11.8496.8496.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1350.623795**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 56 **Expect:** 0.00025**Matches :** 27/104 fragment ions using 60 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							**12**
2	***243.133933***	122.070605	225.123368	113.065322	**E**	1238.547015	619.777146	1221.520466	611.263871	1220.536450	610.771863	**11**
3	***300.155397***	150.581336	282.144832	141.576054	**G**	**1109.504422**	555.255849	1092.477873	546.742575	1091.493857	546.250567	**10**
4	***429.197990***	215.102633	411.187425	206.097351	**E**	**1052.482958**	526.745117	1035.456409	518.231843	1034.472393	517.739835	**9**
5	***500.235104***	250.621190	482.224539	241.615908	**A**	**923.440365**	462.223821	906.413816	453.710546	905.429800	453.218538	**8**
6	***660.265753***	330.636515	642.255188	321.631232	**C**	**852.403251**	426.705264	835.376702	418.191989	834.392686	417.699981	**7**
7	***717.287217***	359.147247	699.276652	350.141964	**G**	**692.372602**	346.689939	675.346053	338.176665	674.362037	337.684657	**6**
8	***816.355631***	408.681454	798.345066	399.676171	**V**	635.351138	318.179207	618.324589	309.665933	617.340573	309.173925	**5**
9	***979.418960***	490.213118	961.408395	481.207836	**Y**	**536.282724**	268.645000	519.256175	260.131726	518.272159	259.639718	**4**
10	***1080.466639***	540.736958	1062.456074	531.731675	**T**	**373.219395**	187.113335	356.192846	178.600061	355.208830	178.108053	**3**
11	***1177.519403***	589.263340	1159.508838	580.258057	**P**	**272.171716**	136.589496	255.145167	128.076221			**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**

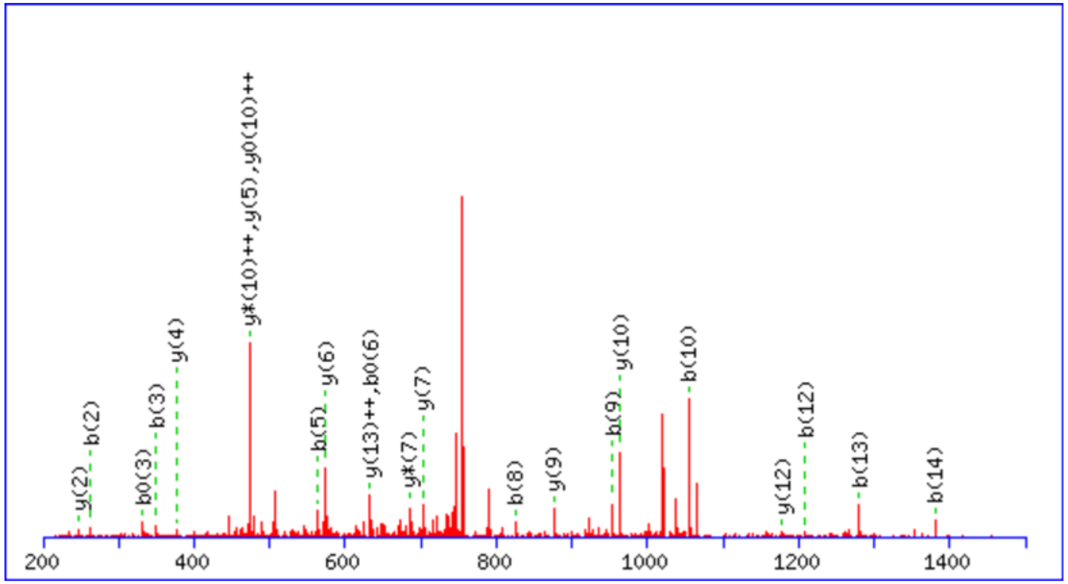


Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 32 - OPA-2 **Fraction:** OPA-2

Match to Query 9514: 1525.726848 from(763.870700,2+)
Title: OECHL100312_11.10705.10705.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62 **Expect:** 7e-005**Matches :** 23/150 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	116.034219	58.520748			98.023654	49.515465	**D**						
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.3515
3	***350.134661***	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.8173
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.3013
5	***564.266404***	282.636840			546.255839	273.631558	**T**	1064.521845	532.764561	1047.495296	524.251286	1046.511280	523.7592
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.2354
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.7194
8	***825.362488***	413.184882			807.351923	404.179599	**S**	789.410110	395.208693	772.383561	386.695418	771.399545	386.2034
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.6873
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.6581
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.1342
12	***1208.542973***	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.6078
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.0971
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.5785
15							**K**	147.112804	74.060040	130.086255	65.546765		



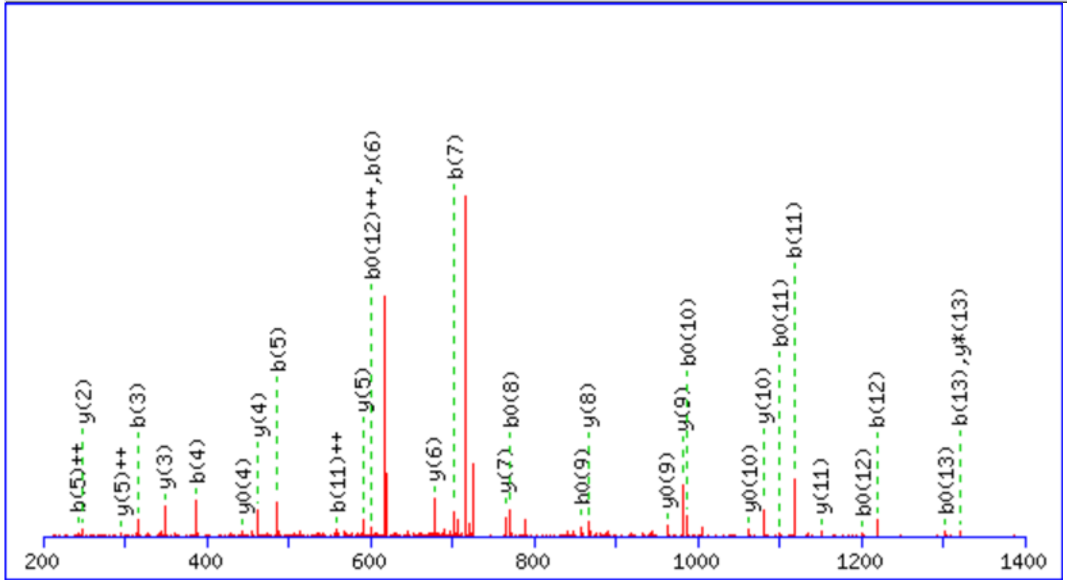
Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 32 - OPA-2 **Fraction:** OPA-2

Match to Query 8844: 1465.677048 from(733.845800,2+)
Title: OECHL100312_11.9693.9693.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 67 **Expect:** 1.5e-005**Matches :** 32/128 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	1337.643082	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	**316.113926**	158.560601	298.103361	149.555319	**A**	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	**387.151040**	194.079158	369.140475	185.073875	**A**	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	**486.219454**	243.613365	468.208889	234.608082	**V**	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**

6	**601.246397**	301.126837	583.235832	292.121554	**D**	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	**9**
7	**702.294076**	351.650676	684.283511	342.645394	**T**	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	***765.398875***	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	876.358132	438.682704	858.347567	429.677421	**S**	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	1005.400725	503.204001	987.390160	494.198718	**E**	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	**1118.484789**	559.746033	1100.474224	550.740750	**I**	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	**1219.532468**	610.269872	1201.521903	601.264590	**T**	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	**1320.580147**	660.793712	1302.569582	651.788429	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**



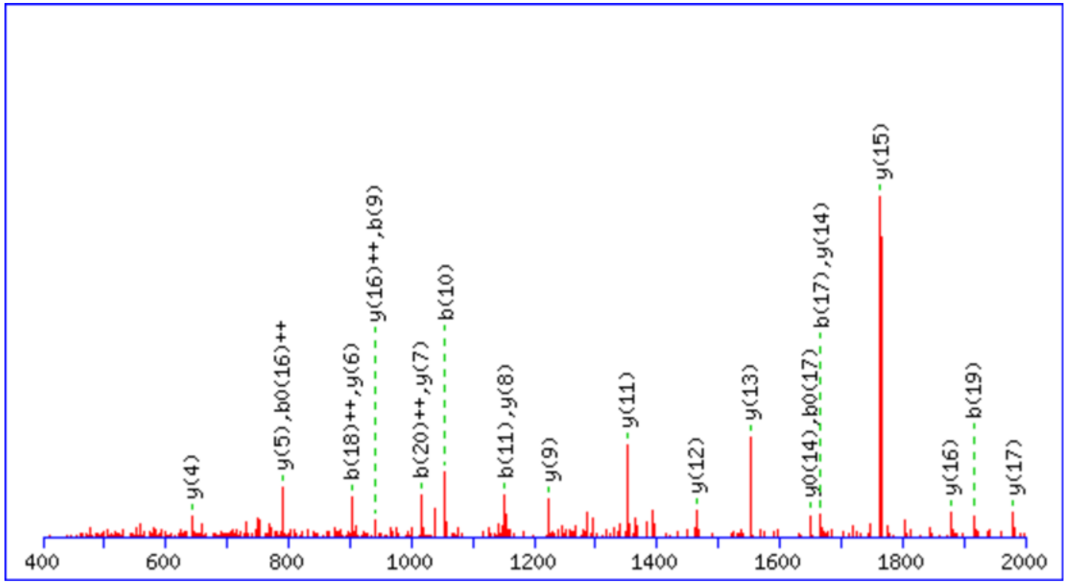
Peptide View

MS/MS Fragmentation of **SCSSSCVATDPDSIGAAHLIFCCFR**
Found in **IPI00022620**, Tax_Id=9606 Gene_Symbol=SLURP1 Secreted Ly-6/uPAR-related protein 1
Experiment: 32 - OPA-2 **Fraction:** OPA-2

Match to Query 15924: 2817.197448 from(1409.606000,2+)

Title: OECHL100312_11.18623.18623.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 2817.197922**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 77 **Expect:** 1.1e-006**Matches :** 24/216 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**25**
2	248.069953	124.538614	230.059388	115.533332	**C**	2731.173141	1366.090208	2714.146592	1357.576934	2713.162576	1357.084926	**24**
3	335.101981	168.054628	317.091416	159.049346	**S**	2571.142492	1286.074884	2554.115943	1277.561609	2553.131927	1277.069601	**23**
4	422.134009	211.570642	404.123444	202.565360	**S**	2484.110464	1242.558870	2467.083915	1234.045595	2466.099899	1233.553587	**22**
5	509.166037	255.086656	491.155472	246.081374	**S**	2397.078436	1199.042856	2380.051887	1190.529581	2379.067871	1190.037573	**21**
6	669.196686	335.101981	651.186121	326.096699	**C**	2310.046408	1155.526842	2293.019859	1147.013567	2292.035843	1146.521559	**20**
7	768.265100	384.636188	750.254535	375.630905	**V**	2150.015759	1075.511517	2132.989210	1066.998243	2132.005194	1066.506235	**19**
8	839.302214	420.154745	821.291649	411.149462	**A**	2050.947345	1025.977310	2033.920796	1017.464036	2032.936780	1016.972028	**18**
9	**940.349893**	470.678585	922.339328	461.673302	**T**	***1979.910231***	990.458753	1962.883682	981.945479	1961.899666	981.453471	**17**
10	**1055.376836**	528.192056	1037.366271	519.186773	**D**	***1878.862552***	939.934914	1861.836003	931.421639	1860.851987	930.929631	**16**
11	**1152.429600**	576.718438	1134.419035	567.713155	**P**	***1763.835609***	882.421442	1746.809060	873.908168	1745.825044	873.416160	**15**
12	1267.456543	634.231910	1249.445978	625.226627	**D**	***1666.782845***	833.895060	1649.756296	825.381786	1648.772280	824.889778	**14**
13	1354.488571	677.747924	1336.478006	668.742641	**S**	***1551.755902***	776.381589	1534.729353	767.868314	1533.745337	767.376306	**13**
14	1467.572635	734.289956	1449.562070	725.284673	**I**	***1464.723874***	732.865575	1447.697325	724.352300			**12**
15	1524.594099	762.800687	1506.583534	753.795405	**G**	***1351.639810***	676.323543	1334.613261	667.810268			**11**
16	1595.631213	798.319244	1577.620648	789.313962	**A**	1294.618346	647.812811	1277.591797	639.299536			**10**
17	**1666.668327**	833.837801	1648.657762	824.832519	**A**	***1223.581232***	612.294254	1206.554683	603.780979			**9**
18	1803.727239	**902.367257**	1785.716674	893.361975	**H**	***1152.544118***	576.775697	1135.517569	568.262422			**8**
19	**1916.811303**	958.909289	1898.800738	949.904007	**L**	***1015.485206***	508.246241	998.458657	499.732966			**7**
20	2029.895367	**1015.451321**	2011.884802	1006.446039	**I**	***902.401142***	451.704209	885.374593	443.190934			**6**
21	2176.963781	1088.985528	2158.953216	1079.980246	**F**	***789.317078***	395.162177	772.290529	386.648902			**5**
22	2336.994430	1169.000853	2318.983865	1159.995570	**C**	***642.248664***	321.627970	625.222115	313.114695			**4**
23	2497.025079	1249.016177	2479.014514	1240.010895	**C**	482.218015	241.612645	465.191466	233.099371			**3**
24	2644.093493	1322.550384	2626.082928	1313.545102	**F**	322.187366	161.597321	305.160817	153.084046			**2**
25					**R**	175.118952	88.063114	158.092403	79.549839			**1**



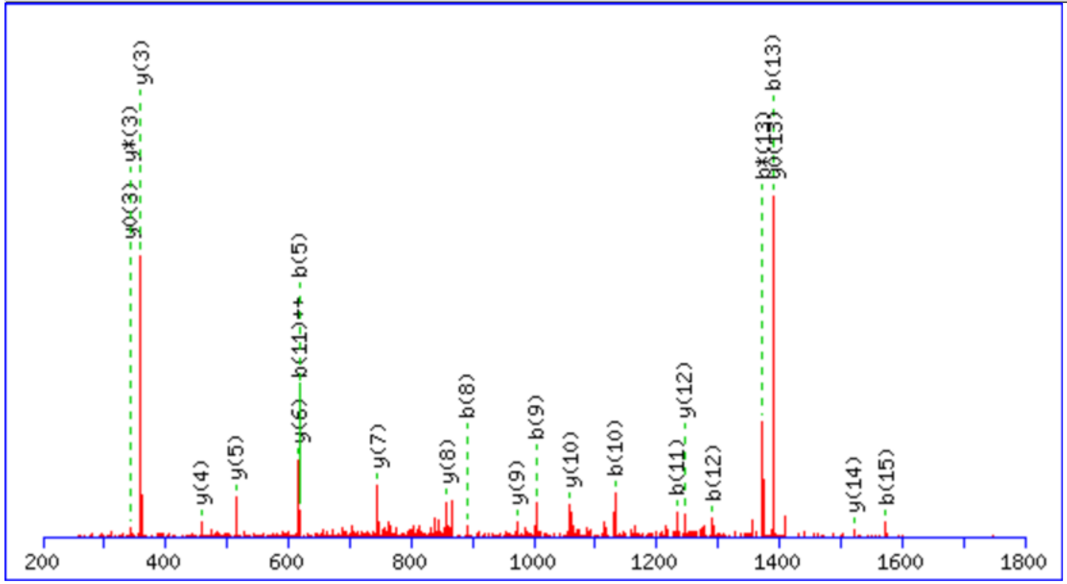
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 32 - OPA-2 **Fraction:** OPA-2

Match to Query 11600: 1746.916848 from(874.465700,2+)
Title: OECHL100312_11.16524.16524.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 67 **Expect:** 2e-005**Matches :** 23/156 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	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	***618.349740***	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018

6	689.386854	345.197065			671.376289	336.191782	A	1130.580027	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	S	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	***890.461809***	445.734542	873.435260	437.221268	872.451244	436.729260	N	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	L	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	E	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	T	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	G	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	V	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							R	175.118952	88.063114	158.092403	79.549839		



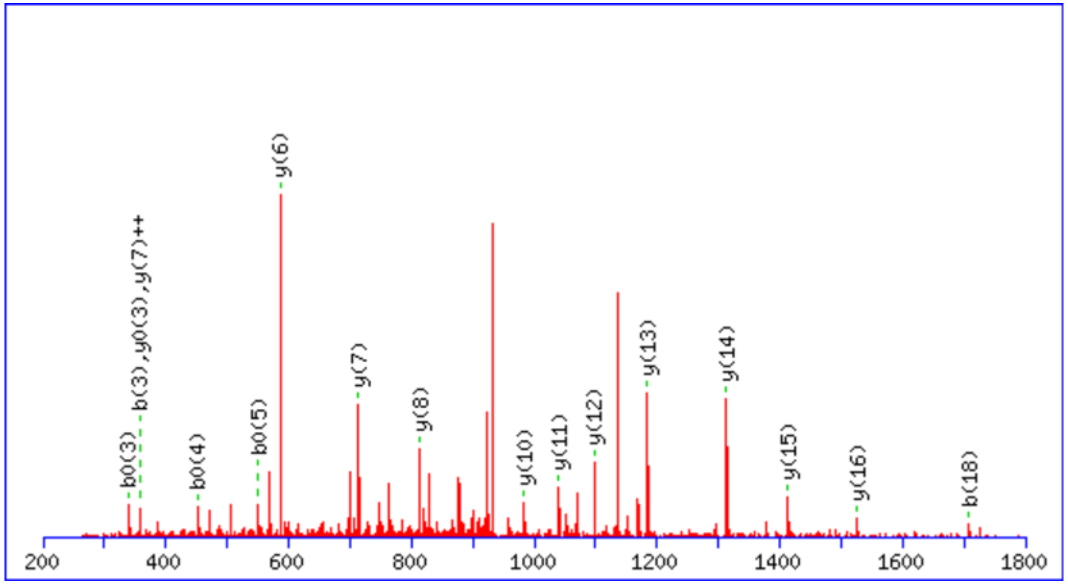
Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**
Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)

Experiment: 32 - OPA-2 **Fraction:** OPA-2

Match to Query 12562: 1881.033248 from(941.523900,2+)
Title: OECHL100312_11.13367.13367.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 59 **Expect:** 6e-005**Matches :** 17/208 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	130.049869	65.528572			112.039304	56.523290	**E**						
2	229.118283	115.062780			211.107718	106.057497	**V**	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.9966
3	**357.176861**	179.092069	340.150312	170.578794	339.166296	170.086786	**Q**	1653.928246	827.467761	1636.901697	818.954487	1635.917681	818.4624
4	470.260925	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.4331
5	569.329339	285.168308	552.302790	276.655033	551.318774	276.163025	**V**	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.8911
6	698.371932	349.689604	681.345383	341.176330	680.361367	340.684322	**E**	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.3569
7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	**S**	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.8356
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	**G**	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.3196
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	**G**	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.8089
10	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	**G**	***983.599641***	492.303459	966.573092	483.790184	965.589076	483.2981
11	1069.552416	535.279846	1052.525867	526.766572	1051.541851	526.274564	**L**	926.578177	463.792727	909.551628	455.279452	908.567612	454.7874
12	1168.620830	584.814053	1151.594281	576.300779	1150.610265	575.808771	**V**	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.2454
13	1296.715793	648.861535	1279.689244	640.348260	1278.705228	639.856252	**K**	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.7112
14	1393.768557	697.387917	1376.742008	688.874642	1375.757992	688.382634	**P**	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.6637
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	**G**	489.277972	245.142624	472.251423	236.629349	471.267407	236.1373
16	1507.811485	754.409381	1490.784936	745.896106	1489.800920	745.404098	**G**	432.256508	216.631892	415.229959	208.118617	414.245943	207.6266
17	1594.843513	797.925395	1577.816964	789.412120	1576.832948	788.920112	**S**	375.235044	188.121160	358.208495	179.607885	357.224479	179.1158
18	**1707.927577**	854.467427	1690.901028	845.954152	1689.917012	845.462144	**L**	288.203016	144.605146	271.176467	136.091871		
19							**R**	175.118952	88.063114	158.092403	79.549839		



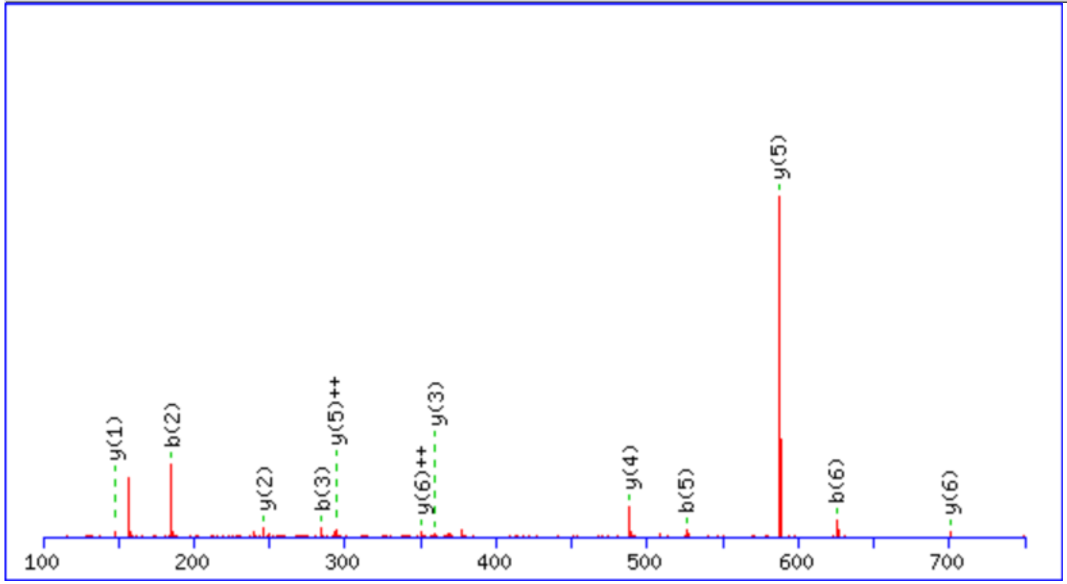
Peptide View

MS/MS Fragmentation of **ALVQIVK**
Found in **IPI00216569**, Tax_Id=9606 Gene_Symbol=CST7 Cystatin-F precursor
Experiment: 32 - OPA-2 **Fraction:** OPA-2

Match to Query 770: 770.489848 from(386.252200,2+)
Title: OECHL100312_11.11549.11549.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 770.490173**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: Q4 :** Deamidated (NQ)**Ions Score:** 53 **Expect:** 0.00021**Matches :** 12/42 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	72.044390	36.525833			**A**					**7**
2	**185.128454**	93.067865			**L**	***700.460354***	350.733815	683.433805	342.220541	**6**
3	**284.196868**	142.602072			**V**	***587.376290***	294.191783	570.349741	285.678509	**5**
4	413.239462	207.123369	396.212913	198.610095	**Q**	***488.307876***	244.657576	471.281327	236.144301	**4**
5	**526.323526**	263.665401	509.296977	255.152127	**I**	***359.265282***	180.136279	342.238733	171.623004	**3**

6	**625.391940**	313.199608	608.365391	304.686333	**V**	***246.181218***	123.594247	229.154669	115.080972	**2**
7					**K**	***147.112804***	74.060040	130.086255	65.546765	**1**



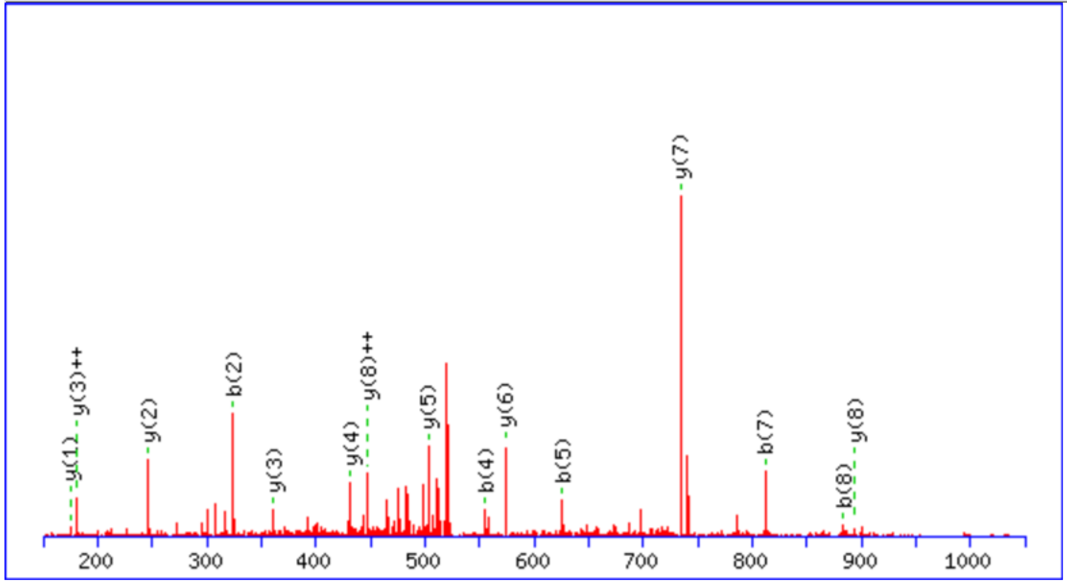
Peptide View

MS/MS Fragmentation of **YCCAAADAR**
Found in **IPI00455600**, Tax_Id=9606 Gene_Symbol=SHISA3 Protein shisa-3 homolog
Experiment: 32 - OPA-2 **Fraction:** OPA-2

Match to Query 3663: 1056.411048 from(529.212800,2+)
Title: OECHL100312_11.2993.2993.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1056.411682**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52 **Expect:** 3.9e-005**Matches :** 15/64 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			**Y**							**9**
2	**324.101254**	162.554265			**C**	***894.355649***	447.681462	877.329100	439.168188	876.345084	438.676180	**8**
3	484.131903	242.569590			**C**	***734.325000***	367.666138	717.298451	359.152863	716.314435	358.660855	**7**

4	**555.169017**	278.088147			**A**	***574.294351***	287.650813	557.267802	279.137539	556.283786	278.645531	**6**
5	**626.206131**	313.606704			**A**	***503.257237***	252.132256	486.230688	243.618982	485.246672	243.126974	**5**
6	697.243245	349.125261			**A**	***432.220123***	216.613699	415.193574	208.100425	414.209558	207.608417	**4**
7	**812.270188**	406.638732	794.259623	397.633449	**D**	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	**3**
8	**883.307302**	442.157289	865.296737	433.152006	**A**	***246.156066***	123.581671	229.129517	115.068396			**2**
9					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**

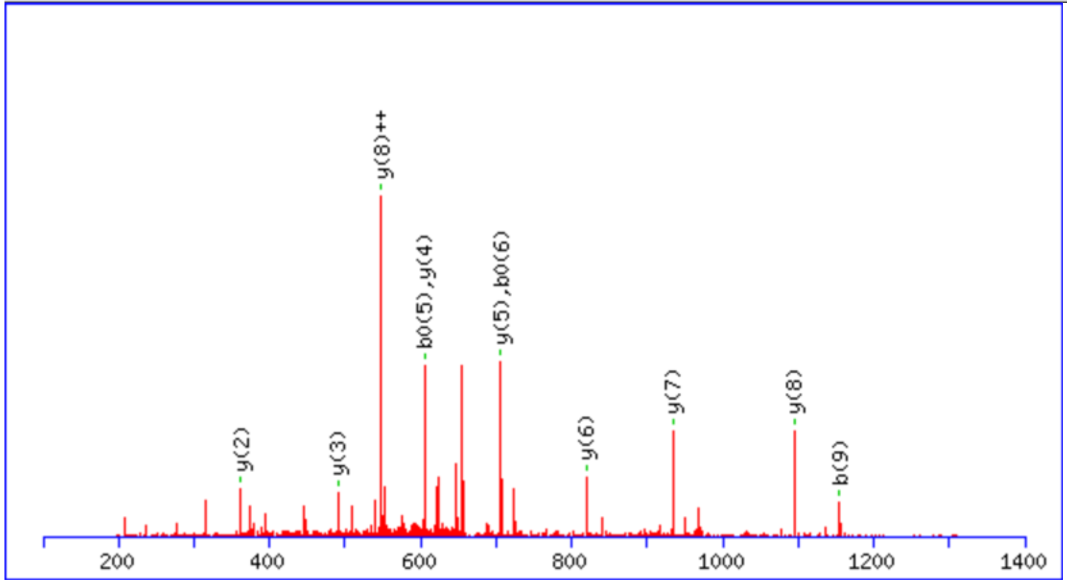


Peptide View

MS/MS Fragmentation of **SFCDLTDEWR**
Found in **IPI00010193**, Tax_Id=9606 Gene_Symbol=IFNAR2 Isoform 1 of Interferon-alpha/beta receptor beta chain
Experiment: 32 - OPA-2 **Fraction:** OPA-2

Match to Query 7573: 1327.550848 from(664.782700,2+)
Title: OECHL100312_11.16479.16479.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1327.550308**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51 **Expect:** 0.00019**Matches :** 11/86 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**10**
2	235.107718	118.057497	217.097153	109.052214	**F**	1241.525550	621.266413	1224.499001	612.753138	1223.514985	612.261130	**9**
3	395.138367	198.072821	377.127802	189.067539	**C**	***1094.457136***	547.732206	1077.430587	539.218932	1076.446571	538.726924	**8**
4	510.165310	255.586293	492.154745	246.581010	**D**	***934.426487***	467.716882	917.399938	459.203607	916.415922	458.711599	**7**
5	623.249374	312.128325	605.238809	303.123043	**L**	***819.399544***	410.203410	802.372995	401.690135	801.388979	401.198127	**6**
6	724.297053	362.652165	706.286488	353.646882	**T**	***706.315480***	353.661378	689.288931	345.148103	688.304915	344.656095	**5**
7	839.323996	420.165636	821.313431	411.160353	**D**	***605.267801***	303.137539	588.241252	294.624264	587.257236	294.132256	**4**
8	968.366589	484.686933	950.356024	475.681650	**E**	***490.240858***	245.624067	473.214309	237.110792	472.230293	236.618784	**3**
9	1154.445902	577.726589	1136.435337	568.721306	**W**	***361.198265***	181.102770	344.171716	172.589496			**2**
10					**R**	175.118952	88.063114	158.092403	79.549839			**1**



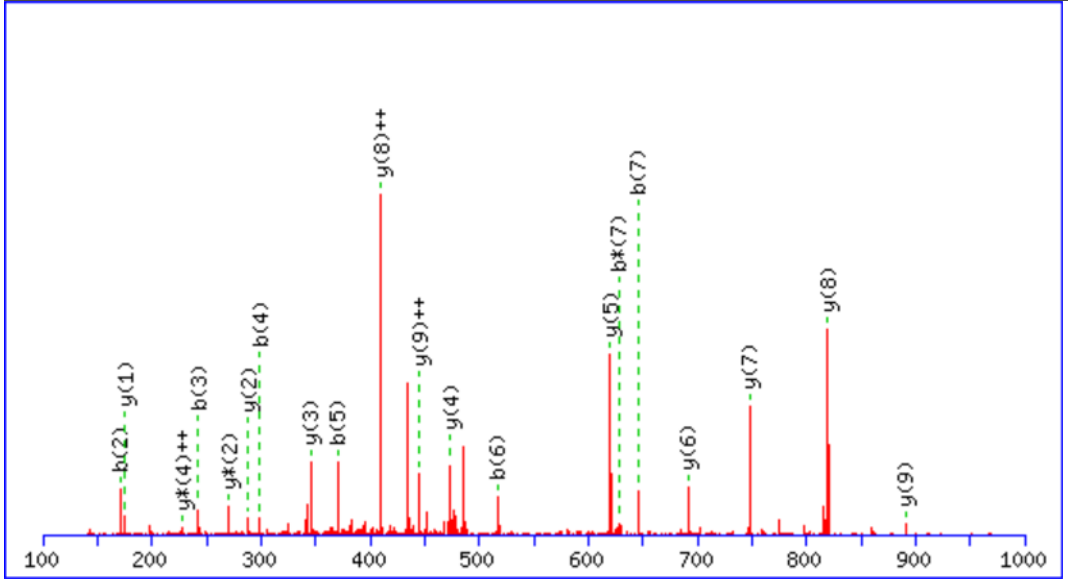
Peptide View

MS/MS Fragmentation of **VAAGAFQGLR**
Found in **IPI00022417**, Tax_Id=9606 Gene_Symbol=LRG1 Leucine-rich alpha-2-glycoprotein

Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 2662: 988.546648 from(495.280600,2+)
Title: OECHL100312_07.10941.10941.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 988.545410**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70 **Expect:** 5.6e-006**Matches :** 20/60 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	100.075690	50.541483			**V**					**10**
2	**171.112804**	86.060040			**A**	***890.484278***	445.745777	873.457729	437.232503	**9**
3	**242.149918**	121.578597			**A**	***819.447164***	410.227220	802.420615	401.713946	**8**
4	**299.171382**	150.089329			**G**	***748.410050***	374.708663	731.383501	366.195389	**7**
5	**370.208496**	185.607886			**A**	***691.388586***	346.197931	674.362037	337.684657	**6**
6	**517.276910**	259.142093			**F**	***620.351472***	310.679374	603.324923	302.166100	**5**
7	**645.335488**	323.171382	628.308939	314.658108	**Q**	***473.283058***	237.145167	456.256509	228.631893	**4**
8	702.356952	351.682114	685.330403	343.168840	**G**	***345.224480***	173.115878	328.197931	164.602604	**3**
9	815.441016	408.224146	798.414467	399.710872	**L**	***288.203016***	144.605146	271.176467	136.091872	**2**
10					**R**	***175.118952***	88.063114	158.092403	79.549840	**1**

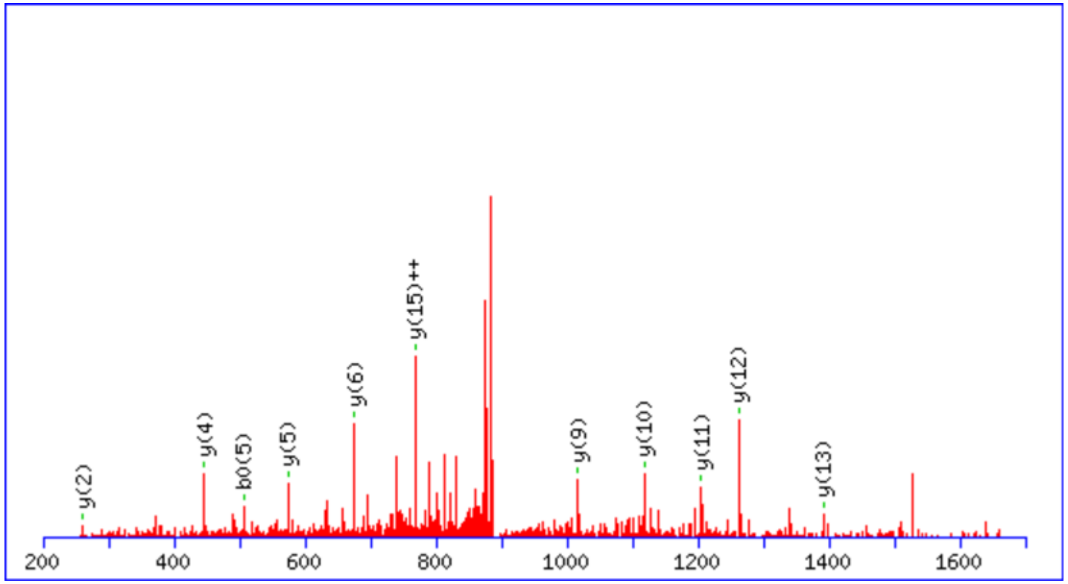


Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 12338: 1784.880048 from(893.447300,2+)
Title: OECHL100312_07.7592.7592.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 66 **Expect:** 3.5e-005**Matches :** 11/170 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	164.070605	82.538940					**Y**						
2	251.102633	126.054954			233.092068	117.049672	**S**	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.9099
3	308.124097	154.565687			290.113532	145.560404	**G**	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.3939
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.8831
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.3671
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.8458
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.3351
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.8191
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.2952
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.2660
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	788.487631	394.747453	771.461082	386.234179	770.477066	385.7421
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.2001
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.6762
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.6288
15	1526.696909	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.1180
16	1639.780973	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		



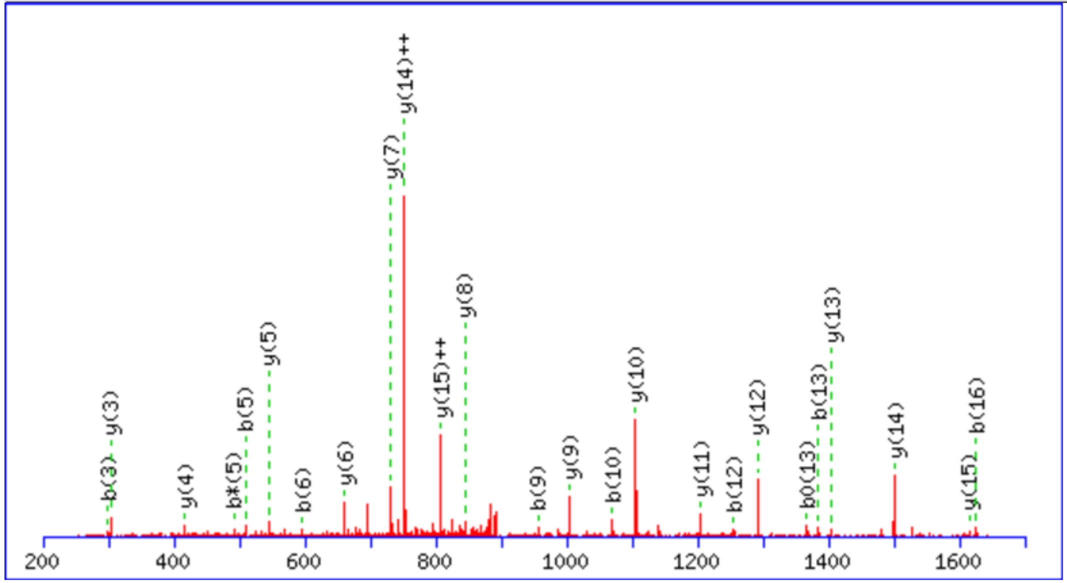
Peptide View

MS/MS Fragmentation of **GQLPISVTCIADEIGAR**
Found in **IPI00240345**, Tax_Id=9606 Gene_Symbol=CLEC14A C-type lectin domain family 14 member A
Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 12441: 1798.927448 from(900.471000,2+)
Title: OECHL100312_07.19475.19475.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1798.924728**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 101 **Expect:** 1e-008**Matches :** 25/172 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	58.028740	29.518008					**G**						
2	186.087318	93.547297	169.060769	85.034023			**Q**	1742.910548	871.958912	1725.883999	863.445638	1724.899983	862.9536
3	**299.171382**	150.089329	282.144833	141.576055			**L**	***1614.851970***	807.929623	1597.825421	799.416349	1596.841405	798.9243
4	396.224146	198.615711	379.197597	190.102436			**P**	***1501.767906***	751.387591	1484.741357	742.874317	1483.757341	742.3823
5	**509.308210**	255.157743	492.281661	246.644468			**I**	***1404.715142***	702.861209	1387.688593	694.347935	1386.704577	693.8559

6	**596.340238**	298.673757	579.313689	290.160483	578.329673	289.668475	**S**	***1291.631078***	646.319177	1274.604529	637.805903	1273.620513	637.3138
7	695.408652	348.207964	678.382103	339.694689	677.398087	339.202681	**V**	***1204.599050***	602.803163	1187.572501	594.289889	1186.588485	593.7978
8	796.456331	398.731804	779.429782	390.218529	778.445766	389.726521	**T**	***1105.530636***	553.268956	1088.504087	544.755682	1087.520071	544.2636
9	**956.486980**	478.747128	939.460431	470.233854	938.476415	469.741846	**C**	***1004.482957***	502.745117	987.456408	494.231842	986.472392	493.7398
10	**1069.571044**	535.289160	1052.544495	526.775886	1051.560479	526.283878	**I**	***844.452308***	422.729792	827.425759	414.216518	826.441743	413.7245
11	1140.608158	570.807717	1123.581609	562.294443	1122.597593	561.802435	**A**	***731.368244***	366.187760	714.341695	357.674486	713.357679	357.1824
12	**1255.635101**	628.321189	1238.608552	619.807914	1237.624536	619.315906	**D**	***660.331130***	330.669203	643.304581	322.155929	642.320565	321.6639
13	**1384.677694**	692.842485	1367.651145	684.329211	1366.667129	683.837203	**E**	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.1504
14	1497.761758	749.384517	1480.735209	740.871243	1479.751193	740.379235	**I**	***416.261594***	208.634435	399.235045	200.121160		
15	1554.783222	777.895249	1537.756673	769.381975	1536.772657	768.889967	**G**	***303.177530***	152.092403	286.150981	143.579128		
16	**1625.820336**	813.413806	1608.793787	804.900532	1607.809771	804.408524	**A**	246.156066	123.581671	229.129517	115.068396		
17							**R**	175.118952	88.063114	158.092403	79.549839		



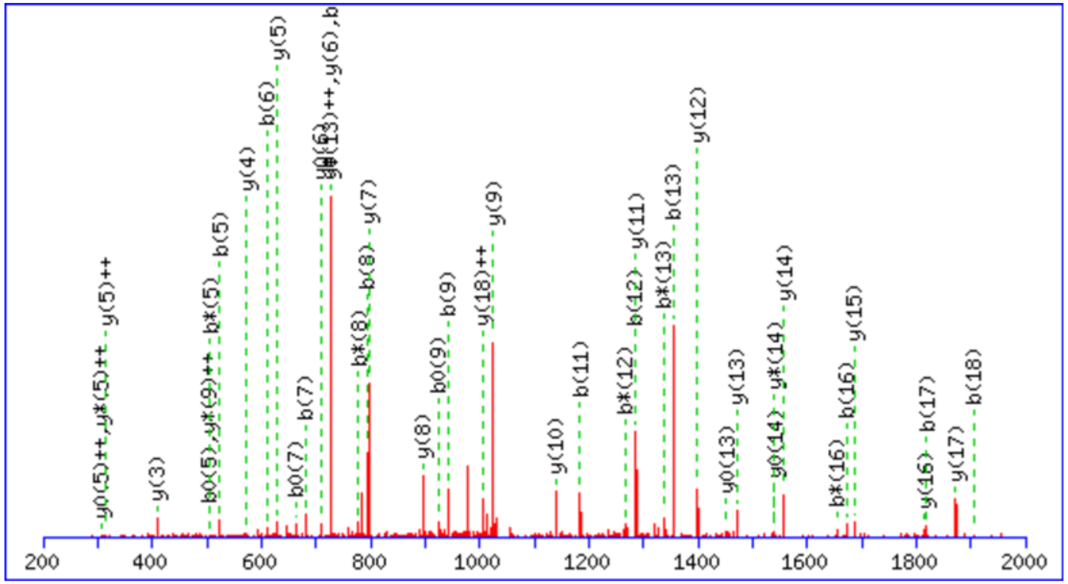
Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**

Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 14081: 2078.983448 from(1040.499000,2+)
Title: OECHL100312_07.17030.17030.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 92 **Expect:** 1.1e-007**Matches :** 46/200 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	72.044390	36.525833					A						
2	209.103302	105.055289					H	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973
3	266.124766	133.566021					G	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444
4	394.183344	197.595310	377.156795	189.082035			Q	***1814.870790***	907.939033	1797.844241	899.425759	1796.860225	898.933
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	E	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904
6	**610.257965**	305.632621	593.231416	297.119346	592.247400	296.627338	S	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383
7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	A	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867
8	**794.379143**	397.693210	777.352594	389.179935	776.368578	388.687927	I	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	F	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	N	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	E	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	V	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	A	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	P	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676
15	1508.712833	754.860054	1491.686284	746.346780	1490.702268	745.854772	G	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	Y	***572.282723***	286.645000	555.256174	278.131725	554.272158	277.639
17	**1818.844576**	909.925926	1801.818027	901.412652	1800.834011	900.920643	F	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108
18	**1905.876604**	953.441940	1888.850055	944.928666	1887.866039	944.436658	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573
19							R	175.118952	88.063114	158.092403	79.549840		



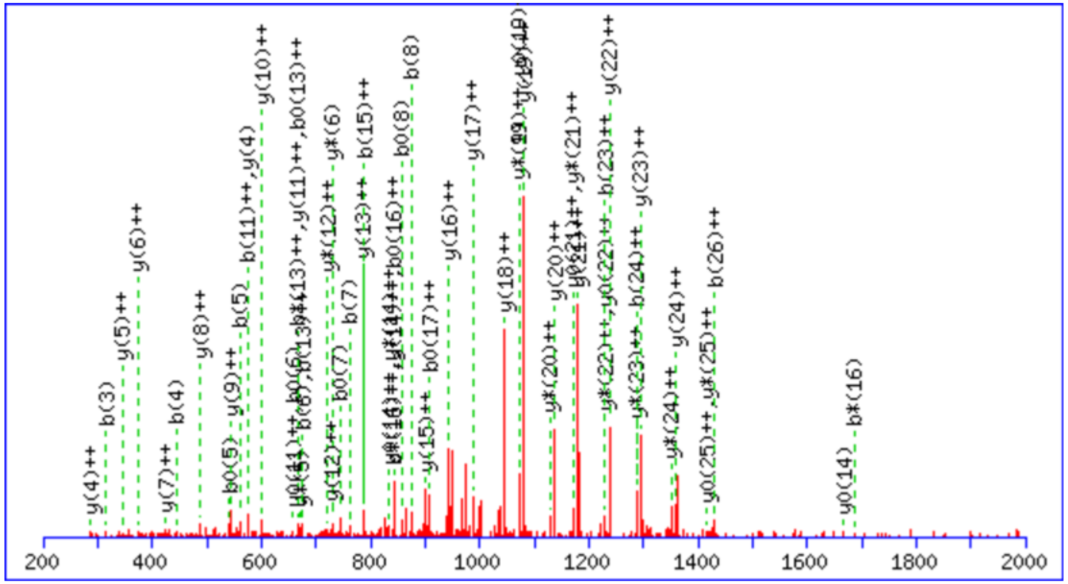
Peptide View

MS/MS Fragmentation of **DAEEDDSLANSSDLLKELLETGDNRER**
Found in **IPI00000828**, Tax_Id=9606 Gene_Symbol=PENK Proenkephalin-A
Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 17191: 3033.404172 from(1012.142000,3+)
Title: OECHL100312_07.19854.19854.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 3033.401001**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 85 **Expect:** 6.5e-007**Matches :** 64/292 fragment ions using 131 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	
1	116.034219	58.520748			98.023654	49.515465	**D**						
2	187.071333	94.039304			169.060768	85.034022	**A**	2919.381392	1460.194334	2902.354843	1451.681059	2901.370827	14
3	**316.113926**	158.560601			298.103361	149.555319	**E**	2848.344278	1424.675777	2831.317729	1416.162502	2830.333713	14
4	**445.156519**	223.081898			427.145954	214.076615	**E**	2719.301685	1360.154480	2702.275136	1351.641206	2701.291120	13
5	**560.183462**	280.595369			542.172897	271.590087	**D**	2590.259092	1295.633184	2573.232543	1287.119909	2572.248527	12

6	**675.210405**	338.108841			657.199840	329.103558	**D**	2475.232149	1238.119712	2458.205600	1229.606438	2457.221584	12
7	**762.242433**	381.624855			744.231868	372.619572	**S**	2360.205206	1180.606241	2343.178657	1172.092966	2342.194641	11
8	**875.326497**	438.166887			857.315932	429.161604	**L**	2273.173178	1137.090227	2256.146629	1128.576952	2255.162613	11
9	946.363611	473.685444			928.353046	464.680161	**A**	2160.089114	1080.548195	2143.062565	1072.034920	2142.078549	10
10	1060.406538	530.706907	1043.379989	522.193633	1042.395973	521.701624	**N**	2089.052000	1045.029638	2072.025451	1036.516363	2071.041435	10
11	1147.438566	**574.222921**	1130.412017	565.709647	1129.428001	565.217639	**S**	1975.009073	988.008174	1957.982524	979.494900	1956.998508	9
12	1234.470594	617.738935	1217.444045	609.225661	1216.460029	608.733653	**S**	1887.977045	944.492160	1870.950496	935.978886	1869.966480	9
13	1349.497537	**675.252407**	1332.470988	666.739132	1331.486972	666.247124	**D**	1800.945017	900.976146	1783.918468	892.462872	1782.934452	8
14	1462.581601	731.794439	1445.555052	723.281164	1444.571036	722.789156	**L**	1685.918074	843.462675	1668.891525	834.949400	1667.907509	8
15	1575.665665	**788.336471**	1558.639116	779.823196	1557.655100	779.331188	**L**	1572.834010	786.920643	1555.807461	778.407368	1554.823445	7
16	1703.760628	852.383952	1686.734079	843.870678	1685.750063	843.378670	**K**	1459.749946	730.378611	1442.723397	721.865336	1441.739381	7
17	1832.803221	916.905248	1815.776672	908.391974	1814.792656	907.899966	**E**	1331.654983	666.331129	1314.628434	657.817855	1313.644418	6
18	1945.887285	973.447280	1928.860736	964.934006	1927.876720	964.441998	**L**	1202.612390	601.809833	1185.585841	593.296558	1184.601825	5
19	2058.971349	1029.989312	2041.944800	1021.476038	2040.960784	1020.984030	**L**	1089.528326	545.267801	1072.501777	536.754526	1071.517761	5
20	2188.013942	1094.510609	2170.987393	1085.997334	2170.003377	1085.505326	**E**	976.444262	488.725769	959.417713	480.212494	958.433697	4
21	2289.061621	1145.034448	2272.035072	1136.521174	2271.051056	1136.029166	**T**	847.401669	424.204472	830.375120	415.691198	829.391104	4
22	2346.083085	1173.545180	2329.056536	1165.031906	2328.072520	1164.539898	**G**	746.353990	373.680633	729.327441	365.167358	728.343425	3
23	2461.110028	**1231.058652**	2444.083479	1222.545377	2443.099463	1222.053369	**D**	689.332526	345.169901	672.305977	336.656626	671.321961	3
24	2575.152955	**1288.080115**	2558.126406	1279.566841	2557.142390	1279.074833	**N**	574.305583	287.656430	557.279034	279.143155	556.295018	2
25	2731.254066	1366.130671	2714.227517	1357.617396	2713.243501	1357.125388	**R**	460.262656	230.634966	443.236107	222.121692	442.252091	2
26	2860.296659	**1430.651967**	2843.270110	1422.138693	2842.286094	1421.646685	**E**	304.161545	152.584411	287.134996	144.071136	286.150980	1
27							**R**	175.118952	88.063114	158.092403	79.549839		



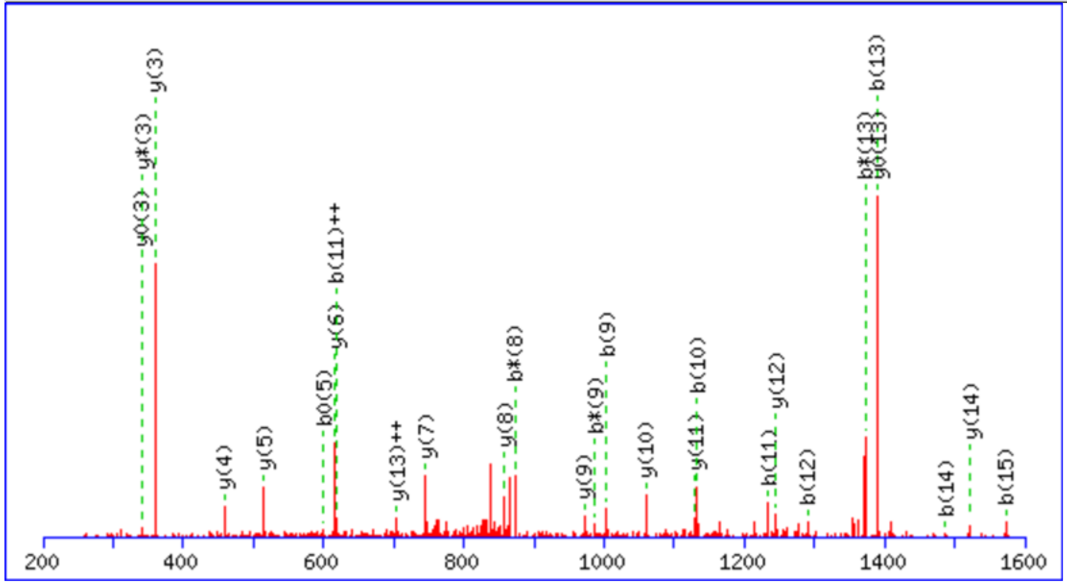
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 12037: 1746.917648 from(874.466100,2+)
Title: OECHL100312_07.16831.16831.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 82 **Expect:** 6.1e-007**Matches :** 27/156 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	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	618.349740	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018

6	689.386854	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	**1486.778787**	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							**R**	175.118952	88.063114	158.092403	79.549839		



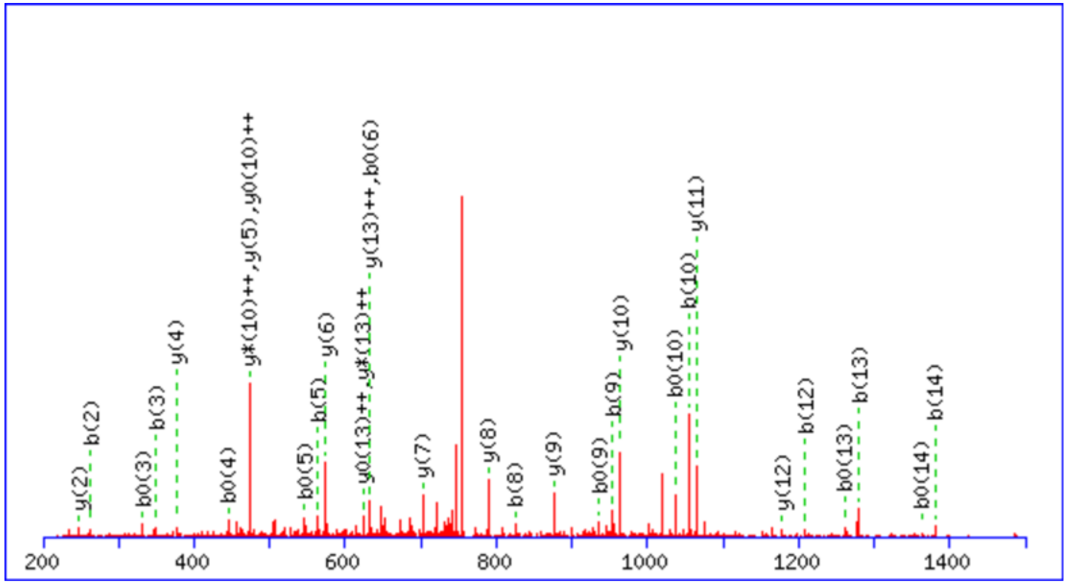
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2

Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 9811: 1525.726848 from(763.870700,2+)
Title: OECHL100312_07.10689.10689.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 75 **Expect:** 3.8e-006**Matches :** 32/150 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	116.034219	58.520748			98.023654	49.515465	**D**						
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.3515
3	***350.134661***	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.8173
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.3013
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.7592
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.2354
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.7194
8	***825.362488***	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.2034
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.6873
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.6581
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.1342
12	***1208.542973***	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.6078
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.0971
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.5785
15							**K**	147.112804	74.060040	130.086255	65.546765		



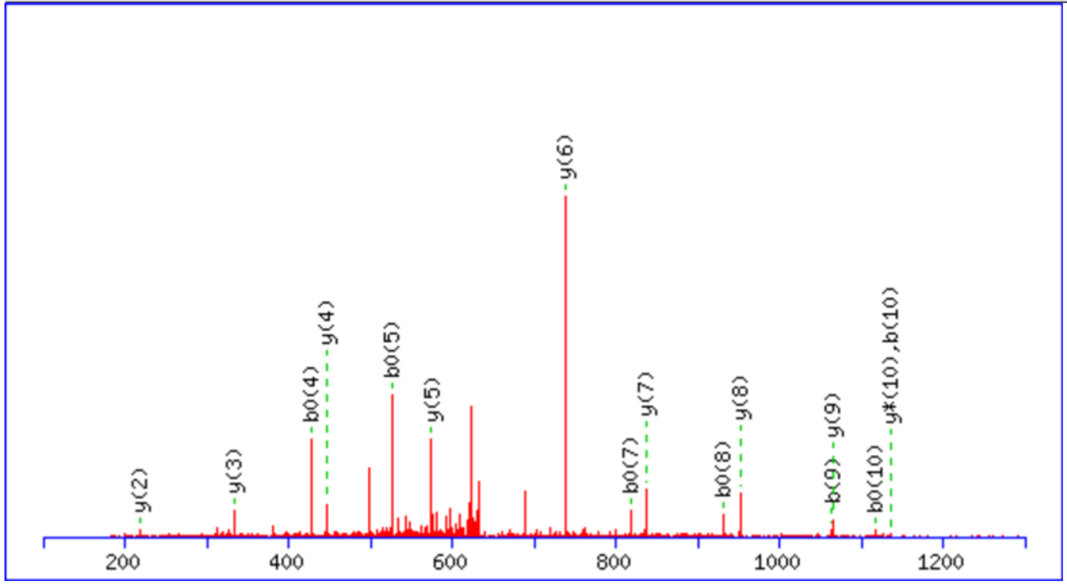
Peptide View

MS/MS Fragmentation of **ESLDVYELDAK**
Found in **IPI00013698**, Tax_Id=9606 Gene_Symbol=ASAH1 Isoform 1 of Acid ceramidase
Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 7129: 1280.613848 from(641.314200,2+)
Title: OECHL100312_07.14236.14236.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1280.613586**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 69 **Expect:** 1.1e-005**Matches :** 16/96 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							11
2	217.081897	109.044586	199.071332	100.039304	S	1152.578296	576.792786	1135.551747	568.279512	1134.567731	567.787504	10
3	330.165961	165.586618	312.155396	156.581336	L	***1065.546268***	533.276772	1048.519719	524.763498	1047.535703	524.271490	9
4	445.192904	223.100090	427.182339	214.094808	D	***952.462204***	476.734740	935.435655	468.221466	934.451639	467.729458	8
5	544.261318	272.634297	526.250753	263.629015	V	***837.435261***	419.221269	820.408712	410.707994	819.424696	410.215986	7

6	707.324647	354.165962	689.314082	345.160679	**Y**	***738.366847***	369.687062	721.340298	361.173787	720.356282	360.681779	**6**
7	836.367240	418.687258	818.356675	409.681976	**E**	***575.303518***	288.155397	558.276969	279.642123	557.292953	279.150115	**5**
8	949.451304	475.229290	931.440739	466.224008	**L**	***446.260925***	223.634101	429.234376	215.120826	428.250360	214.628818	**4**
9	**1064.478247**	532.742762	1046.467682	523.737479	**D**	***333.176861***	167.092069	316.150312	158.578794	315.166296	158.086786	**3**
10	**1135.515361**	568.261319	1117.504796	559.256036	**A**	***218.149918***	109.578597	201.123369	101.065322			**2**
11					**K**	147.112804	74.060040	130.086255	65.546765			**1**

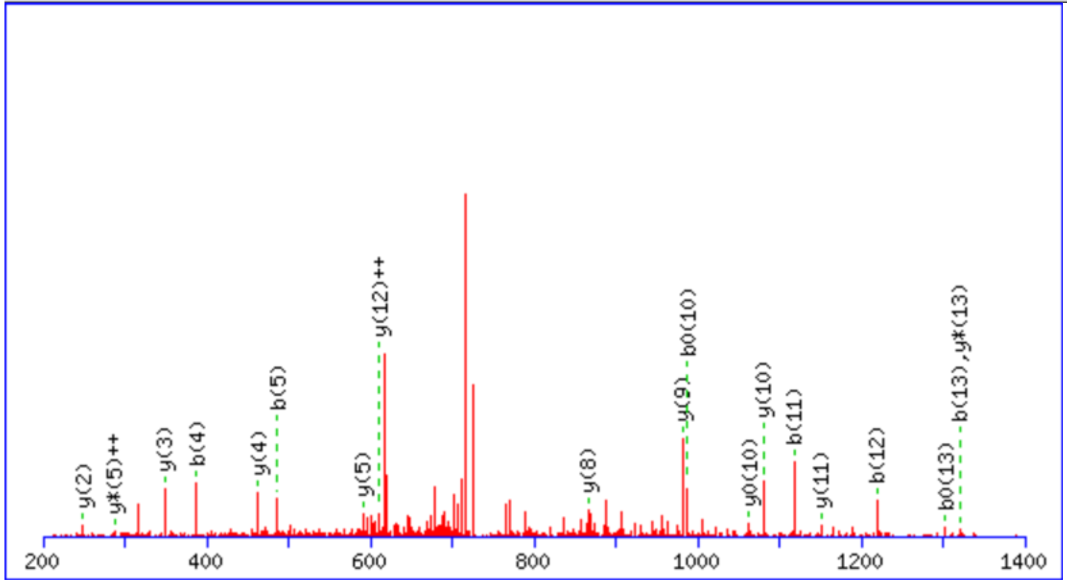


Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 9086: 1465.679648 from(733.847100,2+)
Title: OECHL100312_07.9745.9745.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 64 **Expect:** 2.8e-005**Matches :** 19/128 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	1337.643082	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	316.113926	158.560601	298.103361	149.555319	**A**	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	**387.151040**	194.079158	369.140475	185.073875	**A**	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	**486.219454**	243.613365	468.208889	234.608082	**V**	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**
6	601.246397	301.126837	583.235832	292.121554	**D**	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	**9**
7	702.294076	351.650676	684.283511	342.645394	**T**	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	765.398875	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	876.358132	438.682704	858.347567	429.677421	**S**	678.366847	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	1005.400725	503.204001	987.390160	494.198718	**E**	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	**1118.484789**	559.746033	1100.474224	550.740750	**I**	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	**1219.532468**	610.269872	1201.521903	601.264590	**T**	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	**1320.580147**	660.793712	1302.569582	651.788429	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**

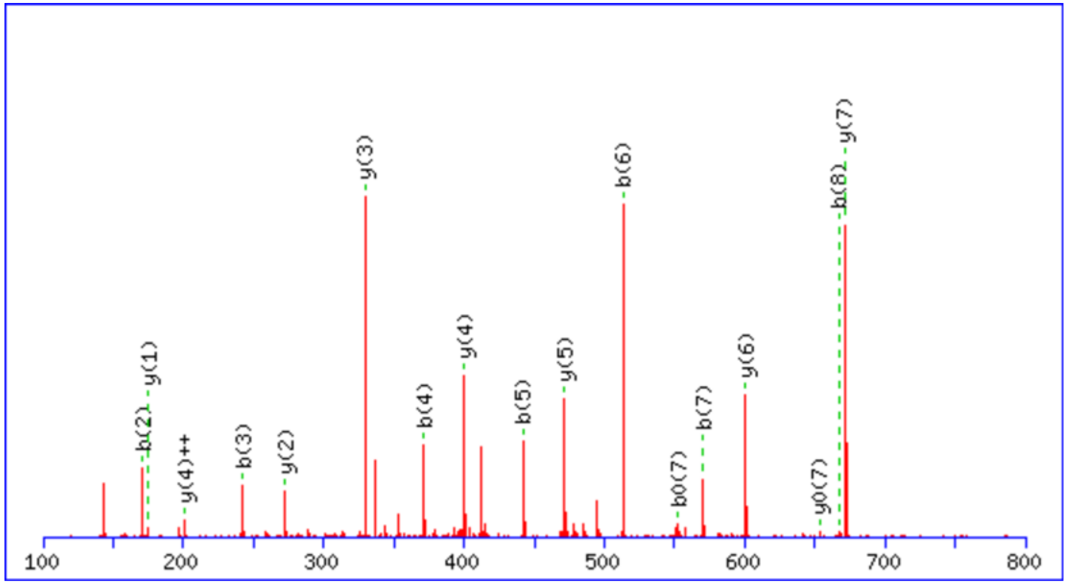


Peptide View

MS/MS Fragmentation of **GLAEAAGPR**
Found in **IPI00290826**, Tax_Id=9606 Gene_Symbol=FAM174A Membrane protein FAM174A
Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 1103: 840.446848 from(421.230700,2+)
Title: OECHL100312_07.3974.3974.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 840.445343**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53 **Expect:** 0.00031**Matches :** 17/64 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			**G**							**9**
2	***171.112804***	86.060040			**L**	784.431179	392.719228	767.404630	384.205953	766.420614	383.713945	**8**
3	***242.149918***	121.578597			**A**	**671.347115**	336.177196	654.320566	327.663921	653.336550	327.171913	**7**
4	***371.192511***	186.099894	353.181946	177.094611	**E**	**600.310001**	300.658639	583.283452	292.145364	582.299436	291.653356	**6**
5	***442.229625***	221.618450	424.219060	212.613168	**A**	**471.267408**	236.137342	454.240859	227.624067			**5**
6	***513.266739***	257.137008	495.256174	248.131725	**A**	**400.230294**	200.618785	383.203745	192.105510			**4**
7	***570.288203***	285.647740	552.277638	276.642457	**G**	**329.193180**	165.100228	312.166631	156.586953			**3**
8	***667.340967***	334.174122	649.330402	325.168839	**P**	**272.171716**	136.589496	255.145167	128.076221			**2**
9					**R**	**175.118952**	88.063114	158.092403	79.549839			**1**



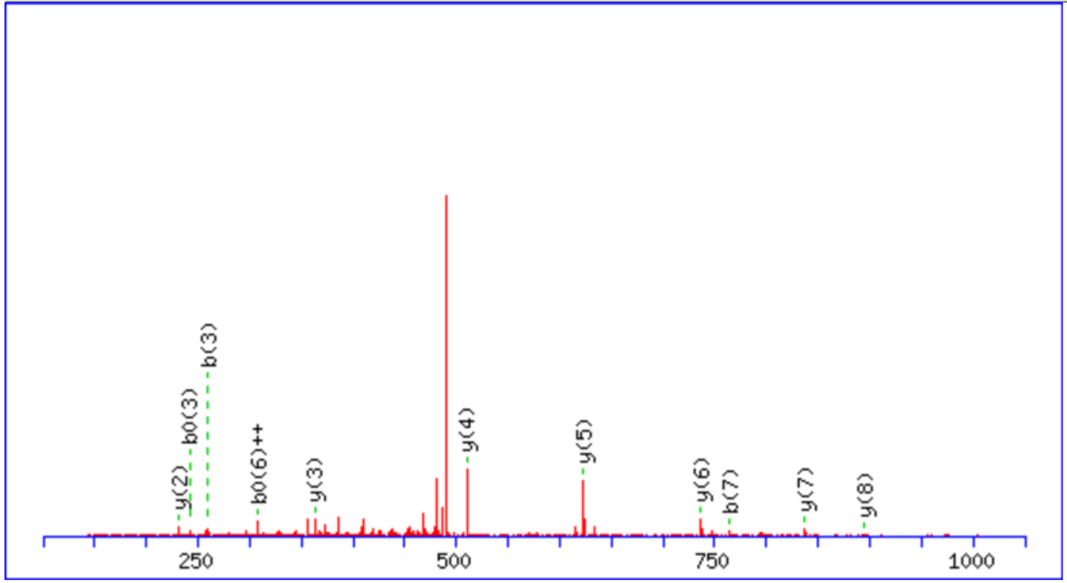
Peptide View

MS/MS Fragmentation of **TGTILFMGR**
Found in **IPI00016150**, Tax_Id=9606 Gene_Symbol=SERPINI1 Neuroserpin
Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 2729: 994.526048 from(498.270300,2+)
Title: OECHL100312_07.15619.15619.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 994.526993**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59 **Expect:** 5.3e-005**Matches :** 11/68 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							**9**
2	159.076419	80.041847	141.065854	71.036565	**G**	***894.486586***	447.746931	877.460037	439.233657	876.476021	438.741649	**8**
3	**260.124098**	130.565687	242.113533	121.560405	**T**	***837.465122***	419.236199	820.438573	410.722925	819.454557	410.230917	**7**
4	373.208162	187.107719	355.197597	178.102437	**I**	***736.417443***	368.712360	719.390894	360.199085			**6**
5	486.292226	243.649751	468.281661	234.644469	**L**	***623.333379***	312.170328	606.306830	303.657053			**5**

6	633.360640	317.183958	615.350075	308.178676	**F**	***510.249315***	255.628296	493.222766	247.115021			**4**
7	**764.401125**	382.704201	746.390560	373.698918	**M**	***363.180901***	182.094089	346.154352	173.580814			**3**
8	821.422589	411.214933	803.412024	402.209650	**G**	***232.140416***	116.573846	215.113867	108.060572			**2**
9					**R**	175.118952	88.063114	158.092403	79.549840			**1**



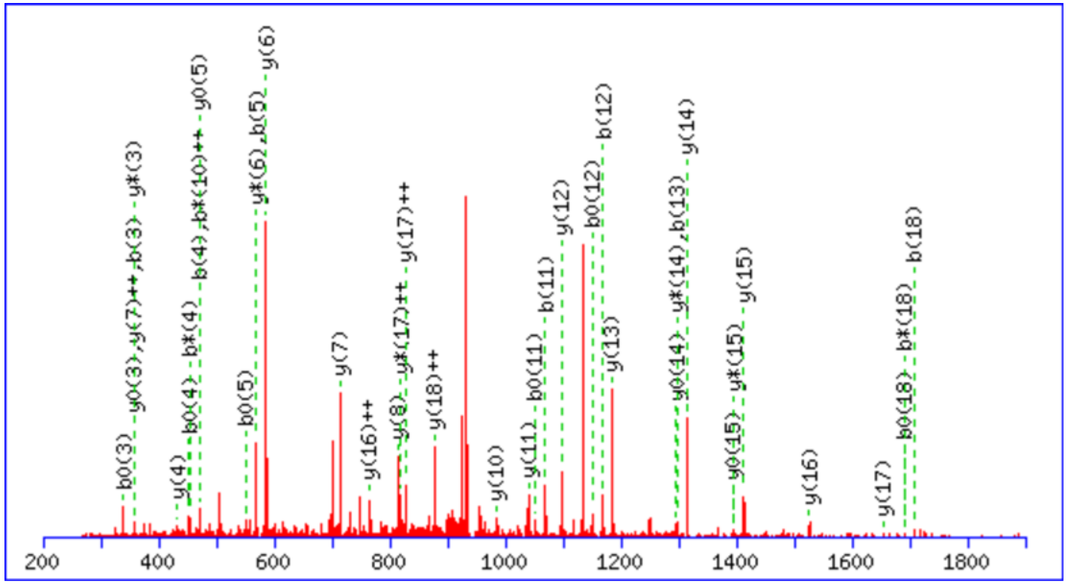
Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**
Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 12985: 1881.034848 from(941.524700,2+)
Title: OECHL100312_07.13589.13589.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58 **Expect:** 7.9e-005**Matches :** 41/208 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	130.049869	65.528572			112.039304	56.523290	**E**						

2	229.118283	115.062780			211.107718	106.057497	**V**	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.9966
3	**357.176861**	179.092069	340.150312	170.578794	339.166296	170.086786	**Q**	***1653.928246***	827.467761	1636.901697	818.954487	1635.917681	818.4624
4	**470.260925**	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.4331
5	**569.329339**	285.168308	552.302790	276.655033	551.318774	276.163025	**V**	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.8911
6	698.371932	349.689604	681.345383	341.176330	680.361367	340.684322	**E**	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.3569
7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	**S**	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.8356
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	**G**	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.3196
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	**G**	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.8089
10	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	**G**	***983.599641***	492.303459	966.573092	483.790184	965.589076	483.2981
11	**1069.552416**	535.279846	1052.525867	526.766572	1051.541851	526.274564	**L**	926.578177	463.792727	909.551628	455.279452	908.567612	454.7874
12	**1168.620830**	584.814053	1151.594281	576.300779	1150.610265	575.808771	**V**	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.2454
13	**1296.715793**	648.861535	1279.689244	640.348260	1278.705228	639.856252	**K**	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.7112
14	1393.768557	697.387917	1376.742008	688.874642	1375.757992	688.382634	**P**	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.6637
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	**G**	489.277972	245.142624	472.251423	236.629349	471.267407	236.1373
16	1507.811485	754.409381	1490.784936	745.896106	1489.800920	745.404098	**G**	***432.256508***	216.631892	415.229959	208.118617	414.245943	207.6266
17	1594.843513	797.925395	1577.816964	789.412120	1576.832948	788.920112	**S**	375.235044	188.121160	358.208495	179.607885	357.224479	179.1158
18	**1707.927577**	854.467427	1690.901028	845.954152	1689.917012	845.462144	**L**	288.203016	144.605146	271.176467	136.091871		
19							**R**	175.118952	88.063114	158.092403	79.549839		



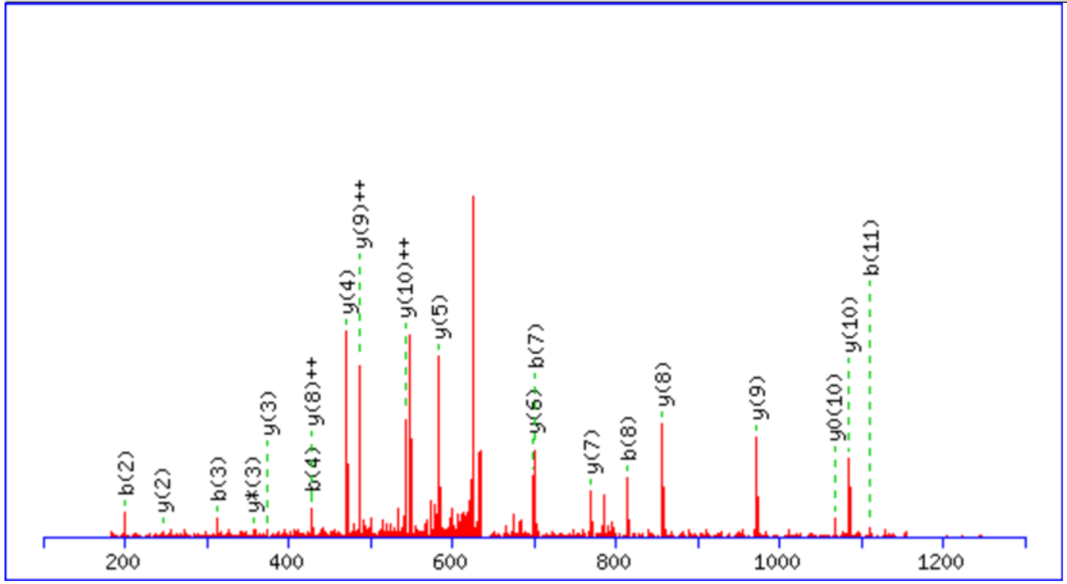
Peptide View

MS/MS Fragmentation of **AQLDSADIPKAR**
Found in **IPI00026303**, Tax_Id=9606 Gene_Symbol=PI15 Peptidase inhibitor 15
Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 7161: 1283.683448 from(642.849000,2+)
Title: OECHL100312_07.7738.7738.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1283.683334**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55 **Expect:** 0.00026**Matches :** 20/114 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	72.044390	36.525833					A						
2	**200.102968**	100.555122	183.076419	92.041848			Q	1213.653527	607.330402	1196.626978	598.817127	1195.642962	598.3251
3	**313.187032**	157.097154	296.160483	148.583879			L	***1085.594949***	543.301113	1068.568400	534.787838	1067.584384	534.2958
4	**428.213975**	214.610626	411.187426	206.097351	410.203410	205.605343	D	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
5	515.246003	258.126640	498.219454	249.613365	497.235438	249.121357	S	***857.483942***	429.245609	840.457393	420.732335	839.473377	420.2403

6	586.283117	293.645197	569.256568	285.131922	568.272552	284.639914	A	***770.451914***	385.729595	753.425365	377.216321	752.441349	376.7243
7	**701.310060**	351.158668	684.283511	342.645394	683.299495	342.153386	D	***699.414800***	350.211038	682.388251	341.697764	681.404235	341.2057
8	**814.394124**	407.700700	797.367575	399.187426	796.383559	398.695418	I	***584.387857***	292.697567	567.361308	284.184292		
9	911.446888	456.227082	894.420339	447.713808	893.436323	447.221800	P	***471.303793***	236.155535	454.277244	227.642260		
10	1039.541851	520.274564	1022.515302	511.761289	1021.531286	511.269281	K	***374.251029***	187.629153	357.224480	179.115878		
11	**1110.578965**	555.793121	1093.552416	547.279846	1092.568400	546.787838	A	***246.156066***	123.581671	229.129517	115.068396		
12							R	175.118952	88.063114	158.092403	79.549839		



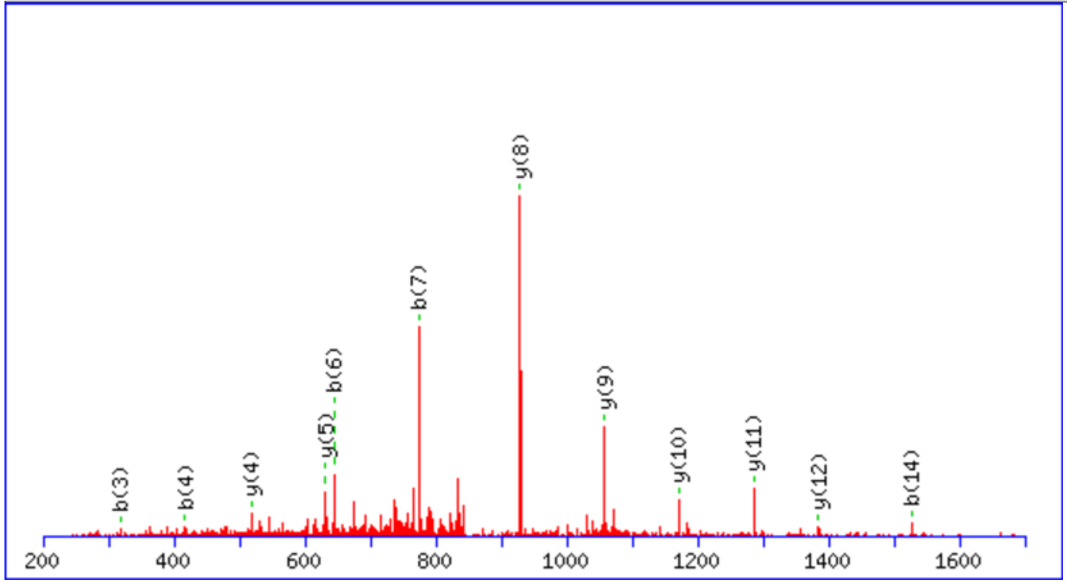
Peptide View

MS/MS Fragmentation of **AVFVDLEPTVIDEVR**
Found in **IPI00166768**, Tax_Id=9606 Gene_Symbol=TUBA1C TUBA1C protein
Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 11530: 1700.899648 from(851.457100,2+)
Title: OECHL100312_07.19141.19141.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1700.898514**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**

Score: 54 **Expect:** 0.00045**Matches :** 12/128 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							15
2	171.112804	86.060040			V	1630.868665	815.937971	1613.842116	807.424696	1612.858100	806.932688	14
3	***318.181218***	159.594247			F	1531.800251	766.403764	1514.773702	757.890489	1513.789686	757.398481	13
4	***417.249632***	209.128454			V	***1384.731837***	692.869557	1367.705288	684.356282	1366.721272	683.864274	12
5	532.276575	266.641926	514.266010	257.636643	D	***1285.663423***	643.335350	1268.636874	634.822075	1267.652858	634.330067	11
6	***645.360639***	323.183958	627.350074	314.178675	L	***1170.636480***	585.821878	1153.609931	577.308604	1152.625915	576.816596	10
7	***774.403232***	387.705254	756.392667	378.699972	E	***1057.552416***	529.279846	1040.525867	520.766572	1039.541851	520.274564	9
8	871.455996	436.231636	853.445431	427.226354	P	***928.509823***	464.758550	911.483274	456.245275	910.499258	455.753267	8
9	972.503675	486.755476	954.493110	477.750193	T	831.457059	416.232168	814.430510	407.718893	813.446494	407.226885	7
10	1071.572089	536.289683	1053.561524	527.284400	V	730.409380	365.708328	713.382831	357.195054	712.398815	356.703046	6
11	1184.656153	592.831715	1166.645588	583.826432	I	***631.340966***	316.174121	614.314417	307.660846	613.330401	307.168838	5
12	1299.683096	650.345186	1281.672531	641.339904	D	***518.256902***	259.632089	501.230353	251.118815	500.246337	250.626807	4
13	1428.725689	714.866483	1410.715124	705.861200	E	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
14	***1527.794103***	764.400690	1509.783538	755.395407	V	274.187366	137.597321	257.160817	129.084047			2
15					R	175.118952	88.063114	158.092403	79.549839			1

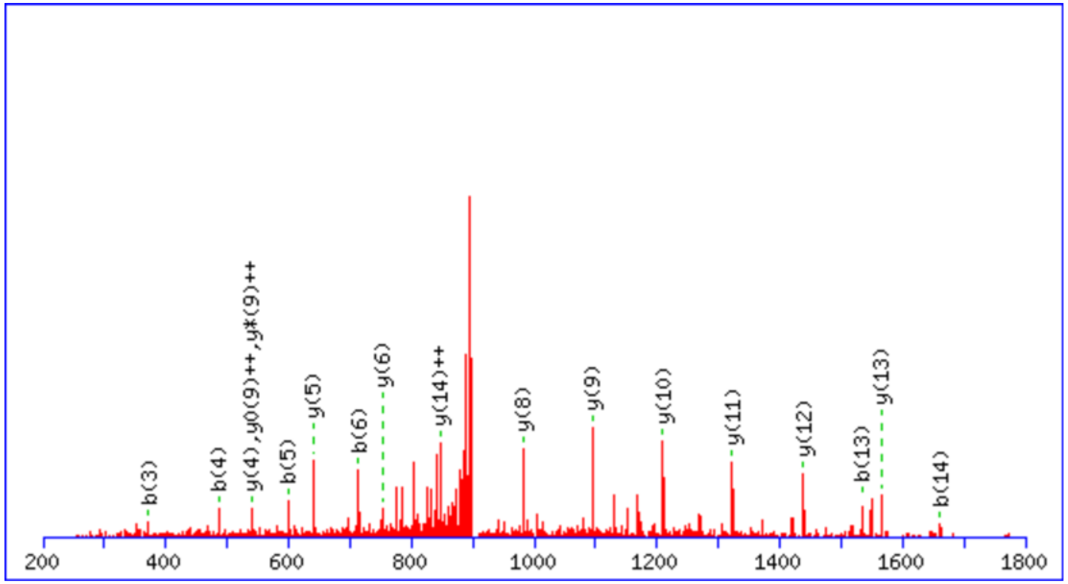


Peptide View

MS/MS Fragmentation of **NKQDLDINNITTYKK**
Found in **IPI00220361**, Tax_Id=9606 Gene_Symbol=CALB1 Calbindin
Experiment: 17 - NOPA2 **Fraction:** NOPA2

Match to Query 12486: 1806.949248 from(904.481900,2+)
Title: OECHL100312_07.10137.10137.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1806.947540**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50 **Expect:** 0.00094**Matches :** 18/156 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	115.050203	58.028740	98.023654	49.515465			N						
2	243.145166	122.076221	226.118617	113.562947			K	1693.911927	847.459602	1676.885378	838.946327	1675.901362	838.4543
3	***371.203744***	186.105510	354.177195	177.592236			Q	***1565.816964***	783.412120	1548.790415	774.898846	1547.806399	774.4068
4	***486.230687***	243.618982	469.204138	235.105707	468.220122	234.613699	D	***1437.758386***	719.382831	1420.731837	710.869557	1419.747821	710.3775
5	***599.314751***	300.161014	582.288202	291.647739	581.304186	291.155731	L	***1322.731443***	661.869359	1305.704894	653.356085	1304.720878	652.8640
6	***714.341694***	357.674485	697.315145	349.161211	696.331129	348.669203	D	***1209.647379***	605.327328	1192.620830	596.814053	1191.636814	596.3220
7	827.425758	414.216517	810.399209	405.703243	809.415193	405.211235	I	***1094.620436***	547.813856	1077.593887	539.300582	1076.609871	538.8085
8	941.468685	471.237981	924.442136	462.724706	923.458120	462.232698	N	***981.536372***	491.271824	964.509823	482.758550	963.525807	482.2665
9	1055.511612	528.259444	1038.485063	519.746170	1037.501047	519.254162	N	867.493445	434.250361	850.466896	425.737086	849.482880	425.2450
10	1168.595676	584.801476	1151.569127	576.288202	1150.585111	575.796193	I	***753.450518***	377.228897	736.423969	368.715623	735.439953	368.2236
11	1269.643355	635.325315	1252.616806	626.812041	1251.632790	626.320033	T	***640.366454***	320.686865	623.339905	312.173591	622.355889	311.6815
12	1370.691034	685.849155	1353.664485	677.335881	1352.680469	676.843872	T	***539.318775***	270.163026	522.292226	261.649751	521.308210	261.1577
13	***1533.754363***	767.380820	1516.727814	758.867545	1515.743798	758.375537	Y	438.271096	219.639186	421.244547	211.125912		
14	***1661.849326***	831.428301	1644.822777	822.915027	1643.838761	822.423019	K	275.207767	138.107521	258.181218	129.594247		
15							K	147.112804	74.060040	130.086255	65.546765		



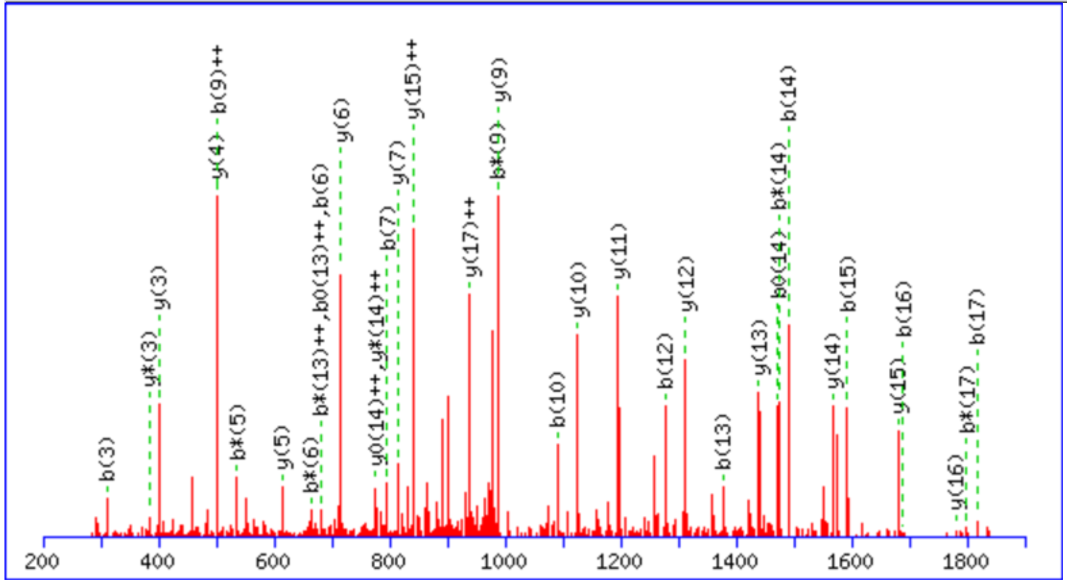
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 14401: 1990.026048 from(996.020300,2+)
Title: OECHL100312_01.9458.9458.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 105 **Expect:** 4e-009**Matches :** 37/186 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	115.050203	58.028740	98.023654	49.515465			N						
2	212.102967	106.555121	195.076418	98.041847			P	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.9921
3	***311.171381***	156.089328	294.144832	147.576054			V	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.4657
4	424.255445	212.631361	407.228896	204.118086			L	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.9315
5	552.314023	276.660650	535.287474	268.147375			Q	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.3895

6	***680.372601***	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.3602
7	***795.399544***	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.3309
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.8174
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.2989
10	***1090.527598***	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.7694
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	901.510158	451.258717	884.483609	442.745443	883.499593	442.2534
12	***1276.628040***	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.7374
13	***1377.675719***	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.2032
14	***1490.759783***	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.6793
15	***1591.807462***	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.1373
16	***1688.860226***	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510		
17	***1816.918804***	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128		
18							**R**	175.118952	88.063114	158.092403	79.549839		

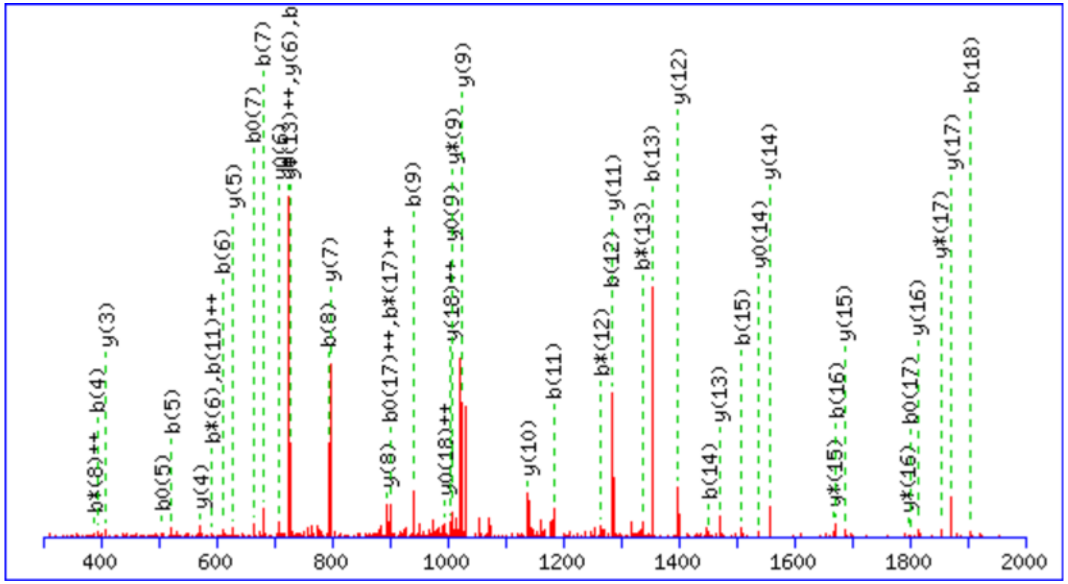


Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 15008: 2078.983448 from(1040.499000,2+)
Title: OECHL100312_01.16920.16920.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 86 **Expect:** 4.5e-007**Matches :** 50/200 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	72.044390	36.525833					**A**						
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444
4	**394.183344**	197.595310	377.156795	189.082035			**Q**	***1814.870790***	907.939033	1797.844241	899.425759	1796.860225	898.933
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904
6	**610.257965**	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383
7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867
8	**794.379143**	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195
14	**1451.691369**	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676
15	**1508.712833**	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	***572.282723***	286.645000	555.256174	278.131725	554.272158	277.639
17	1818.844576	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108
18	**1905.876604**	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573
19							**R**	175.118952	88.063114	158.092403	79.549840		



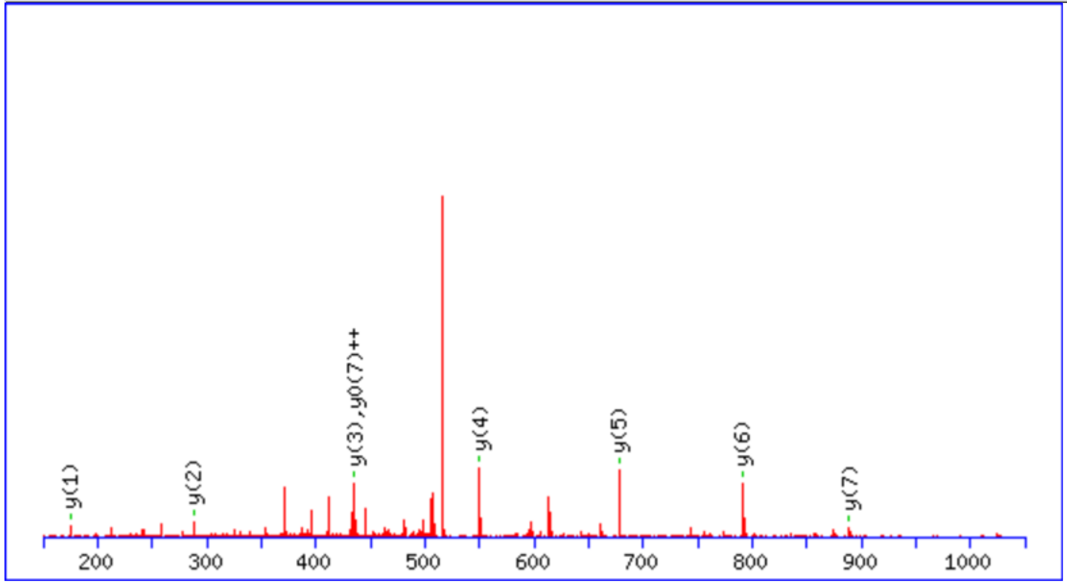
Peptide View

MS/MS Fragmentation of **CPLQDFLR**
Found in **IPI00003807**, Tax_Id=9606 Gene_Symbol=ACP2 Lysosomal acid phosphatase
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 3790: 1047.516848 from(524.765700,2+)
Title: OECHL100312_01.16558.16558.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1047.517151**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71 **Expect:** 7.2e-006**Matches :** 8/64 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	161.037925	81.022600					C							8
2	258.090689	129.548982					P	***888.493779***	444.750528	871.467230	436.237253	870.483214	435.745245	7
3	371.174753	186.091015					L	***791.441015***	396.224146	774.414466	387.710871	773.430450	387.218863	6
4	499.233331	250.120304	482.206782	241.607029			Q	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	5
5	614.260274	307.633775	597.233725	299.120501	596.249709	298.628493	D	***550.298373***	275.652825	533.271824	267.139550	532.287808	266.647542	4

6	761.328688	381.167982	744.302139	372.654708	743.318123	372.162700	**F**	***435.271430***	218.139353	418.244881	209.626079			**3**
7	874.412752	437.710014	857.386203	429.196740	856.402187	428.704732	**L**	***288.203016***	144.605146	271.176467	136.091872			**2**
8							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



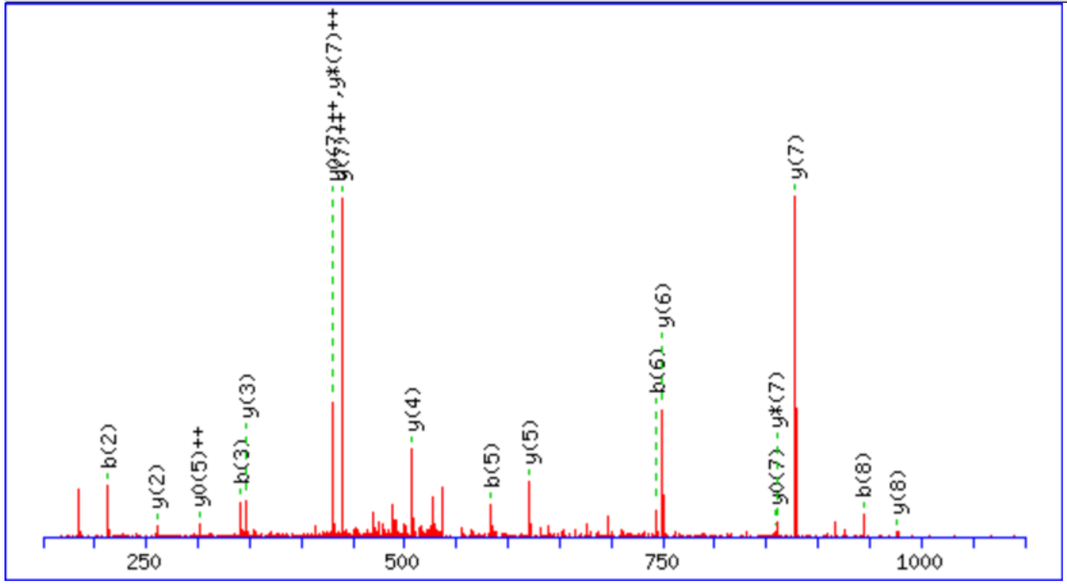
Peptide View

MS/MS Fragmentation of **LVQELCSLK**
Found in **IPI00018275**, Tax_Id=9606 Gene_Symbol=PRND Prion-like protein doppel
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 4295: 1088.591248 from(545.302900,2+)
Title: OECHL100312_01.11359.11359.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1088.589966**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54 **Expect:** 0.0003**Matches :** 18/82 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	114.091340	57.549308					**L**							**9**
2	**213.159754**	107.083515					**V**	***976.513194***	488.760235	959.486645	480.246961	958.502629	479.754953	**8**

3	**341.218332**	171.112804	324.191783	162.599529			**Q**	***877.444780***	439.226028	860.418231	430.712754	859.434215	430.220746	**7**
4	470.260925	235.634100	453.234376	227.120826	452.250360	226.628818	**E**	***749.386202***	375.196739	732.359653	366.683465	731.375637	366.191457	**6**
5	**583.344989**	292.176133	566.318440	283.662858	565.334424	283.170850	**L**	***620.343609***	310.675443	603.317060	302.162168	602.333044	301.670160	**5**
6	**743.375638**	372.191457	726.349089	363.678183	725.365073	363.186175	**C**	***507.259545***	254.133410	490.232996	245.620136	489.248980	245.128128	**4**
7	830.407666	415.707471	813.381117	407.194197	812.397101	406.702189	**S**	***347.228896***	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
8	**943.491730**	472.249503	926.465181	463.736229	925.481165	463.244221	**L**	***260.196868***	130.602072	243.170319	122.088797			**2**
9							**K**	147.112804	74.060040	130.086255	65.546765			**1**



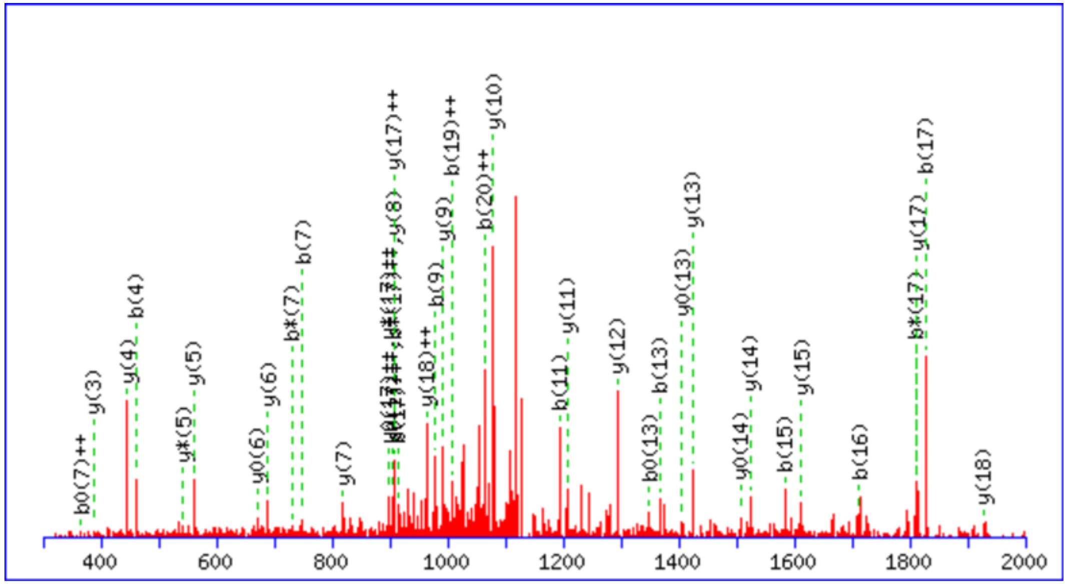
Peptide View

MS/MS Fragmentation of **SKEDSNSTESKSSSEEDGQLK**
Found in **IPI00012734**, Tax_Id=9606 Gene_Symbol=DMP1 Isoform 1 of Dentin matrix acidic phosphoprotein 1
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 16056: 2270.999448 from(1136.507000,2+)
Title: OECHL100312_01.2069.2069.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.998581**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**

Score: 77 **Expect:** 2e-006**Matches :** 40/230 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	
1	88.039304	44.523290			70.028739	35.518008	**S**						
2	216.134267	108.570771	199.107718	100.057497	198.123702	99.565489	**K**	2184.973868	1092.990572	2167.947319	1084.477297	2166.963303	10
3	345.176860	173.092068	328.150311	164.578793	327.166295	164.086785	**E**	2056.878905	1028.943090	2039.852356	1020.429816	2038.868340	10
4	**460.203803**	230.605539	443.177254	222.092265	442.193238	221.600257	**D**	***1927.836312***	964.421794	1910.809763	955.908520	1909.825747	9
5	547.235831	274.121554	530.209282	265.608279	529.225266	265.116271	**S**	***1812.809369***	906.908323	1795.782820	898.395048	1794.798804	8
6	661.278758	331.143017	644.252209	322.629743	643.268193	322.137735	**N**	1725.777341	863.392309	1708.750792	854.879034	1707.766776	8
7	**748.310786**	374.659031	731.284237	366.145757	730.300221	365.653749	**S**	***1611.734414***	806.370845	1594.707865	797.857571	1593.723849	7
8	849.358465	425.182871	832.331916	416.669596	831.347900	416.177588	**T**	***1524.702386***	762.854831	1507.675837	754.341557	1506.691821	7
9	**978.401058**	489.704167	961.374509	481.190893	960.390493	480.698885	**E**	***1423.654707***	712.330992	1406.628158	703.817717	1405.644142	7
10	1065.433086	533.220181	1048.406537	524.706907	1047.422521	524.214899	**S**	***1294.612114***	647.809695	1277.585565	639.296421	1276.601549	6
11	**1193.528049**	597.267663	1176.501500	588.754388	1175.517484	588.262380	**K**	***1207.580086***	604.293681	1190.553537	595.780407	1189.569521	5
12	1280.560077	640.783677	1263.533528	632.270402	1262.549512	631.778394	**S**	***1079.485123***	540.246200	1062.458574	531.732925	1061.474558	5
13	**1367.592105**	684.299691	1350.565556	675.786416	1349.581540	675.294408	**S**	***992.453095***	496.730186	975.426546	488.216911	974.442530	4
14	1454.624133	727.815705	1437.597584	719.302430	1436.613568	718.810422	**S**	***905.421067***	453.214172	888.394518	444.700897	887.410502	4
15	**1583.666726**	792.337001	1566.640177	783.823727	1565.656161	783.331719	**E**	***818.389039***	409.698158	801.362490	401.184883	800.378474	4
16	**1712.709319**	856.858298	1695.682770	848.345023	1694.698754	847.853015	**E**	***689.346446***	345.176861	672.319897	336.663587	671.335881	3
17	**1827.736262**	**914.371769**	1810.709713	905.858495	1809.725697	905.366487	**D**	***560.303853***	280.655565	543.277304	272.142290	542.293288	2
18	1884.757726	942.882501	1867.731177	934.369227	1866.747161	933.877219	**G**	***445.276910***	223.142093	428.250361	214.628818		
19	2012.816304	**1006.911790**	1995.789755	998.398516	1994.805739	997.906508	**Q**	***388.255446***	194.631361	371.228897	186.118087		
20	2125.900368	**1063.453822**	2108.873819	1054.940547	2107.889803	1054.448539	**L**	260.196868	130.602072	243.170319	122.088798		
21							**K**	147.112804	74.060040	130.086255	65.546765		



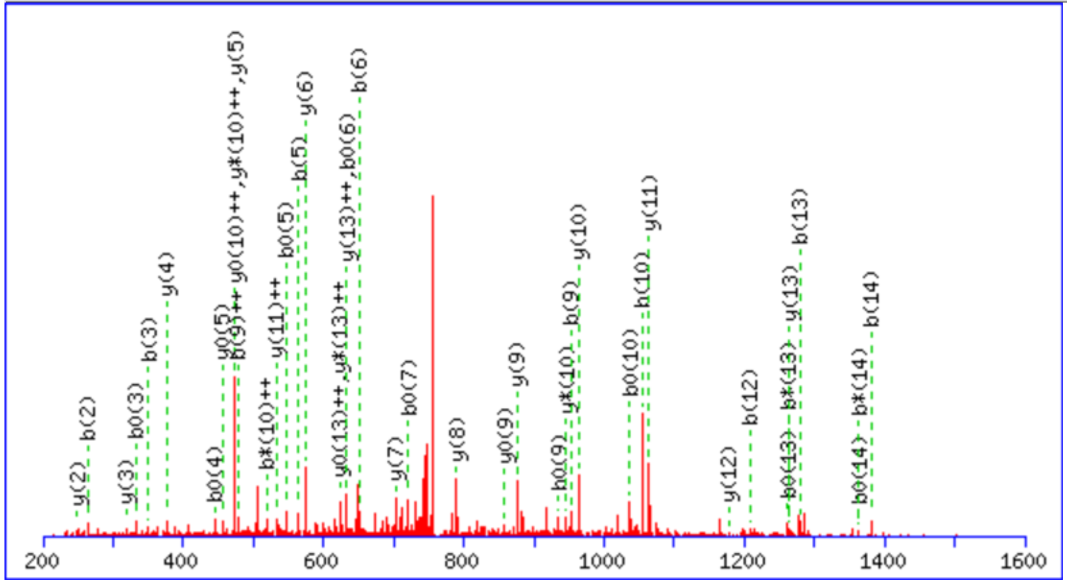
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 9986: 1525.728248 from(763.871400,2+)
Title: OECHL100312_01.10402.10402.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 65 **Expect:** 3.6e-005**Matches :** 43/150 fragment ions using 88 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	116.034219	58.520748			98.023654	49.515465	**D**						
2	**263.102633**	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.3515
3	**350.134661**	175.570968			332.124096	166.565686	**S**	***1264.637937***	632.822607	1247.611388	624.309332	1246.627372	623.8173
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.3013
5	**564.266404**	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.7592

6	**651.298432**	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.2354
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.7194
8	825.362488	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.2034
9	**953.421066**	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.6873
10	**1054.468745**	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.6581
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.1342
12	**1208.542973**	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.6078
13	**1279.580087**	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	***319.197597***	160.102436	302.171048	151.589162	301.187032	151.0971
14	**1380.627766**	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.5785
15							**K**	147.112804	74.060040	130.086255	65.546765		

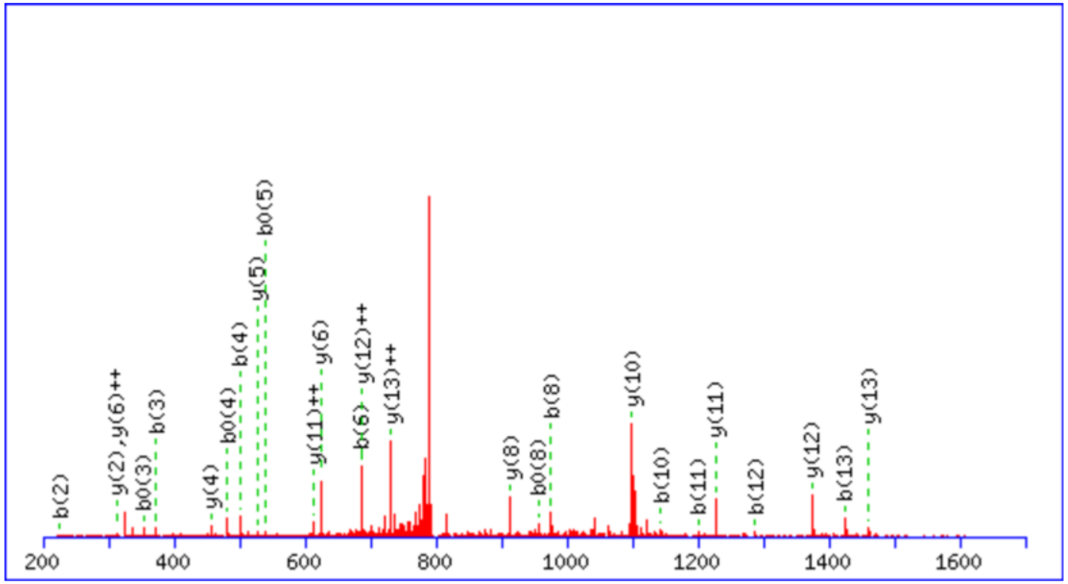


Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 10739: 1597.705848 from(799.860200,2+)
Title: OECHL100312_01.2072.2072.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67 **Expect:** 1.2e-005**Matches :** 26/144 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	138.066188	69.536732					**H**						
2	***225.098216***	113.052746			207.087651	104.047463	**S**	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.3253
3	***372.166630***	186.586953			354.156065	177.581671	**F**	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.8093
4	***500.261593***	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.2751
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.2276
6	***686.325650***	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	1042.437069	521.722173	1025.410520	513.208898	1024.426504	512.7168
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.1955
8	***975.398892***	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	784.351883	392.679580	767.325334	384.166305	766.341318	383.6742
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.6589
10	***1143.488770***	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.1325
11	***1200.510234***	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.6140
12	***1287.542262***	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	399.209892	200.108584	382.183343	191.595309	381.199327	191.1033
13	***1424.601174***	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	***312.177864***	156.592570	295.151315	148.079295		
14							**R**	175.118952	88.063114	158.092403	79.549839		



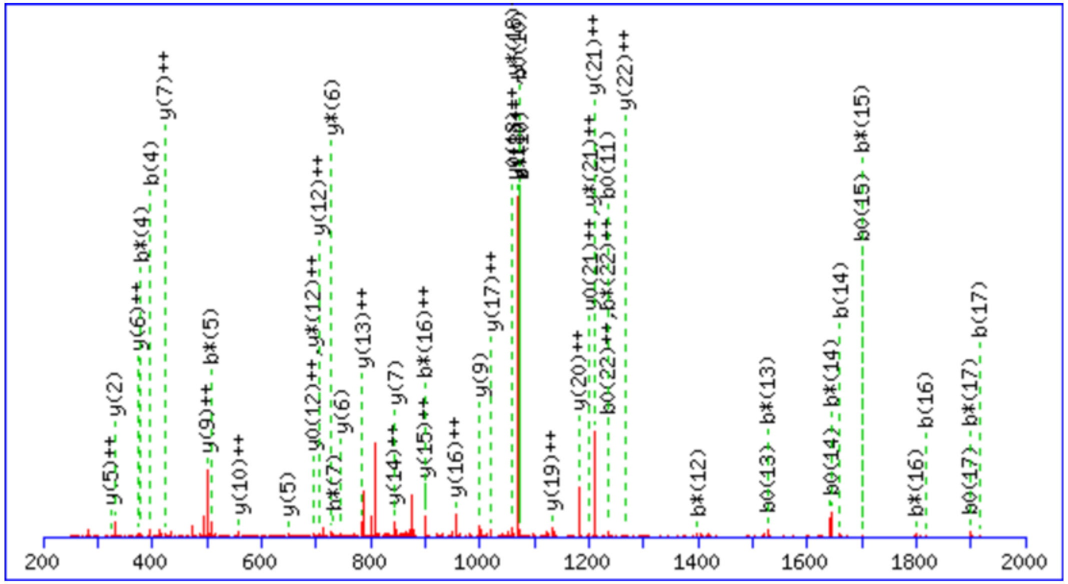
Peptide View

MS/MS Fragmentation of **QLGPQPQDIIYYEDGVVPTTDRR**
Found in **IPI00015199**, Tax_Id=9606 Gene_Symbol=CD7 T-cell antigen CD7
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 17782: 2659.330872 from(887.450900,3+)
Title: OECHL100312_01.17152.17152.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 2659.324203**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 68 **Expect:** 2.8e-005**Matches :** 51/246 fragment ions using 118 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	
1	129.065854	65.036565	112.039305	56.523291			Q						
2	242.149918	121.578597	225.123369	113.065323			L	2532.272897	1266.640086	2515.246348	1258.126812	2514.262332	125
3	299.171382	150.089329	282.144833	141.576055			G	2419.188833	1210.098054	2402.162284	1201.584780	2401.178268	12
4	396.224146	198.615711	379.197597	190.102436			P	2362.167369	1181.587322	2345.140820	1173.074048	2344.156804	11
5	524.282724	262.645000	507.256175	254.131726			Q	2265.114605	1133.060940	2248.088056	1124.547666	2247.104040	11

6	621.335488	311.171382	604.308939	302.658108			**P**	2137.056027	1069.031651	2120.029478	1060.518377	2119.045462	10
7	749.394066	375.200671	732.367517	366.687397			**Q**	2040.003263	1020.505269	2022.976714	1011.991995	2021.992698	10
8	864.421009	432.714143	847.394460	424.200868	846.410444	423.708860	**D**	1911.944685	956.475980	1894.918136	947.962706	1893.934120	9
9	977.505073	489.256175	960.478524	480.742900	959.494508	480.250892	**I**	1796.917742	898.962509	1779.891193	890.449234	1778.907177	8
10	1090.589137	545.798206	1073.562588	537.284932	1072.578572	536.792924	**I**	1683.833678	842.420477	1666.807129	833.907202	1665.823113	8
11	1253.652466	627.329871	1236.625917	618.816597	1235.641901	618.324589	**Y**	1570.749614	785.878445	1553.723065	777.365170	1552.739049	7
12	1416.715795	708.861536	1399.689246	700.348261	1398.705230	699.856253	**Y**	1407.686285	704.346780	1390.659736	695.833506	1389.675720	6
13	1545.758388	773.382832	1528.731839	764.869558	1527.747823	764.377549	**E**	1244.622956	622.815116	1227.596407	614.301841	1226.612391	6
14	**1660.785331**	830.896304	1643.758782	822.383029	1642.774766	821.891021	**D**	1115.580363	558.293819	1098.553814	549.780545	1097.569798	5
15	1717.806795	859.407036	1700.780246	850.893761	1699.796230	850.401753	**G**	**1000.553420**	500.780348	983.526871	492.267073	982.542855	4
16	**1816.875209**	908.941243	1799.848660	900.427968	1798.864644	899.935960	**V**	943.531956	472.269616	926.505407	463.756341	925.521391	4
17	**1915.943623**	958.475450	1898.917074	949.962175	1897.933058	949.470167	**V**	**844.463542**	422.735409	827.436993	414.222134	826.452977	4
18	2012.996387	1007.001832	1995.969838	998.488557	1994.985822	997.996549	**P**	**745.395128**	373.201202	728.368579	364.687927	727.384563	3
19	2114.044066	1057.525671	2097.017517	1049.012396	2096.033501	1048.520388	**T**	**648.342364**	324.674820	631.315815	316.161545	630.331799	3
20	2215.091745	1108.049510	2198.065196	1099.536236	2197.081180	1099.044228	**T**	547.294685	274.150980	530.268136	265.637706	529.284120	2
21	2330.118688	1165.562982	2313.092139	1157.049707	2312.108123	1156.557699	**D**	446.247006	223.627141	429.220457	215.113866	428.236441	2
22	2486.219799	1243.613537	2469.193250	1235.100263	2468.209234	1234.608255	**R**	**331.220063**	166.113669	314.193514	157.600395		
23							**R**	175.118952	88.063114	158.092403	79.549839		



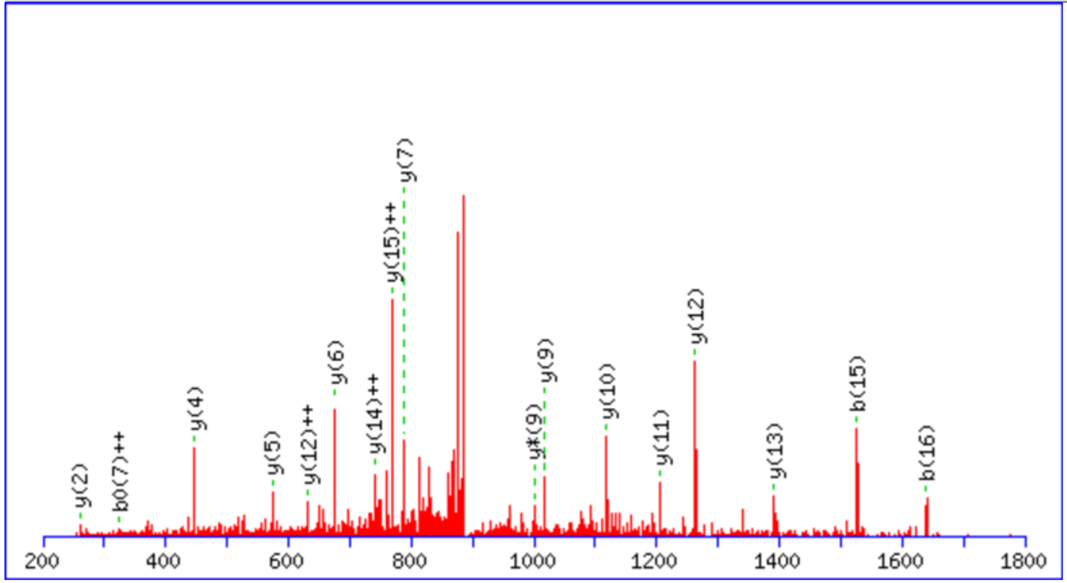
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 12826: 1784.882848 from(893.448700,2+)
Title: OECHL100312_01.7158.7158.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67 **Expect:** 3e-005**Matches :** 17/170 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	164.070605	82.538940					**Y**						
2	251.102633	126.054954			233.092068	117.049672	**S**	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.9099
3	308.124097	154.565687			290.113532	145.560404	**G**	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.3939
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.8831
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.3671

6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.8458
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.3351
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.8191
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.2952
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.2660
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.7421
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.2001
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.6762
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.6288
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.1180
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		



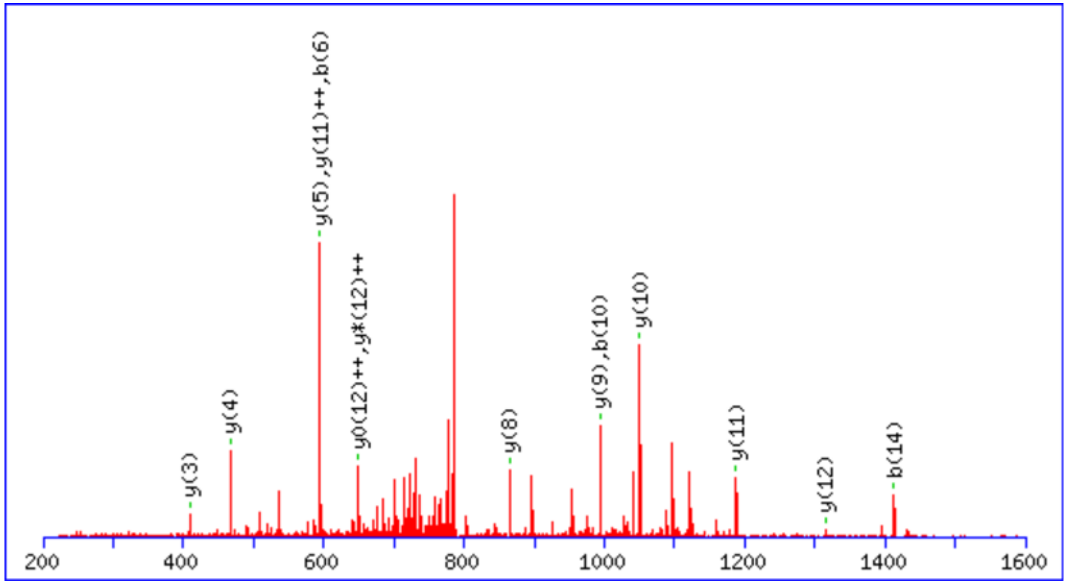
Peptide View

MS/MS Fragmentation of **ASLQHGQAAEKGPHR**

Found in **IPI00165044**, Tax_Id=9606 Gene_Symbol=FAM198B Isoform 2 of Protein ENED
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 10641: 1585.808848 from(793.911700,2+)
Title: OECHL100312_01.1701.1701.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1585.807312**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70 **Expect:** 1.2e-005**Matches :** 14/150 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	72.044390	36.525833					**A**						
2	159.076418	80.041847			141.065853	71.036564	**S**	1515.777500	758.392388	1498.750951	749.879114	1497.766935	749.3871
3	272.160482	136.583879			254.149917	127.578597	**L**	1428.745472	714.876374	1411.718923	706.363100	1410.734907	705.8710
4	400.219060	200.613168	383.192511	192.099894	382.208495	191.607886	**Q**	***1315.661408***	658.334342	1298.634859	649.821068	1297.650843	649.3290
5	537.277972	269.142624	520.251423	260.629350	519.267407	260.137342	**H**	***1187.602830***	594.305053	1170.576281	585.791779	1169.592265	585.2997
6	**594.299436**	297.653356	577.272887	289.140082	576.288871	288.648074	**G**	***1050.543918***	525.775597	1033.517369	517.262323	1032.533353	516.7703
7	722.358014	361.682645	705.331465	353.169371	704.347449	352.677363	**Q**	***993.522454***	497.264865	976.495905	488.751591	975.511889	488.2595
8	793.395128	397.201202	776.368579	388.687928	775.384563	388.195920	**A**	***865.463876***	433.235576	848.437327	424.722302	847.453311	424.2302
9	864.432242	432.719759	847.405693	424.206485	846.421677	423.714477	**A**	794.426762	397.717019	777.400213	389.203745	776.416197	388.7117
10	**993.474835**	497.241056	976.448286	488.727781	975.464270	488.235773	**E**	723.389648	362.198462	706.363099	353.685188	705.379083	353.1931
11	1121.569798	561.288537	1104.543249	552.775263	1103.559233	552.283255	**K**	***594.347055***	297.677166	577.320506	289.163891		
12	1178.591262	589.799269	1161.564713	581.285995	1160.580697	580.793987	**G**	***466.252092***	233.629684	449.225543	225.116409		
13	1275.644026	638.325651	1258.617477	629.812377	1257.633461	629.320369	**P**	***409.230628***	205.118952	392.204079	196.605677		
14	**1412.702938**	706.855107	1395.676389	698.341833	1394.692373	697.849825	**H**	312.177864	156.592570	295.151315	148.079295		
15							**R**	175.118952	88.063114	158.092403	79.549839		



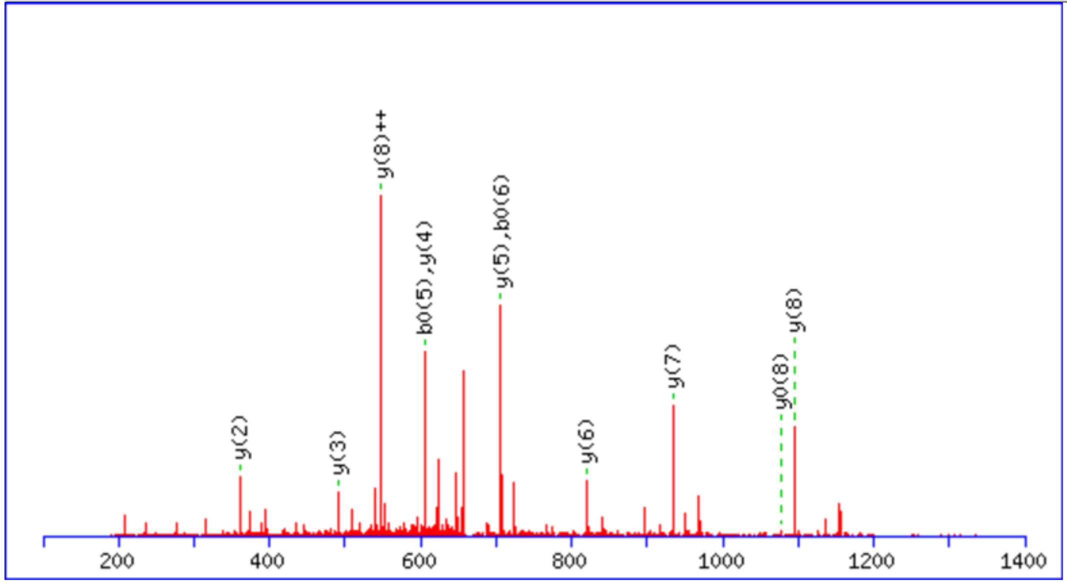
Peptide View

MS/MS Fragmentation of **SFCDLTDEWR**
Found in **IPI00010193**, Tax_Id=9606 Gene_Symbol=IFNAR2 Isoform 1 of Interferon-alpha/beta receptor beta chain
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 7840: 1327.550848 from(664.782700,2+)
Title: OECHL100312_01.16507.16507.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1327.550308**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 55 **Expect:** 7.6e-005**Matches :** 11/86 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**10**
2	235.107718	118.057497	217.097153	109.052214	**F**	1241.525550	621.266413	1224.499001	612.753138	1223.514985	612.261130	**9**
3	395.138367	198.072821	377.127802	189.067539	**C**	***1094.457136***	547.732206	1077.430587	539.218932	1076.446571	538.726924	**8**
4	510.165310	255.586293	492.154745	246.581010	**D**	***934.426487***	467.716882	917.399938	459.203607	916.415922	458.711599	**7**
5	623.249374	312.128325	605.238809	303.123043	**L**	***819.399544***	410.203410	802.372995	401.690135	801.388979	401.198127	**6**

6	724.297053	362.652165	706.286488	353.646882	**T**	***706.315480***	353.661378	689.288931	345.148103	688.304915	344.656095	**5**
7	839.323996	420.165636	821.313431	411.160353	**D**	***605.267801***	303.137539	588.241252	294.624264	587.257236	294.132256	**4**
8	968.366589	484.686933	950.356024	475.681650	**E**	***490.240858***	245.624067	473.214309	237.110792	472.230293	236.618784	**3**
9	1154.445902	577.726589	1136.435337	568.721306	**W**	***361.198265***	181.102770	344.171716	172.589496			**2**
10					**R**	175.118952	88.063114	158.092403	79.549839			**1**



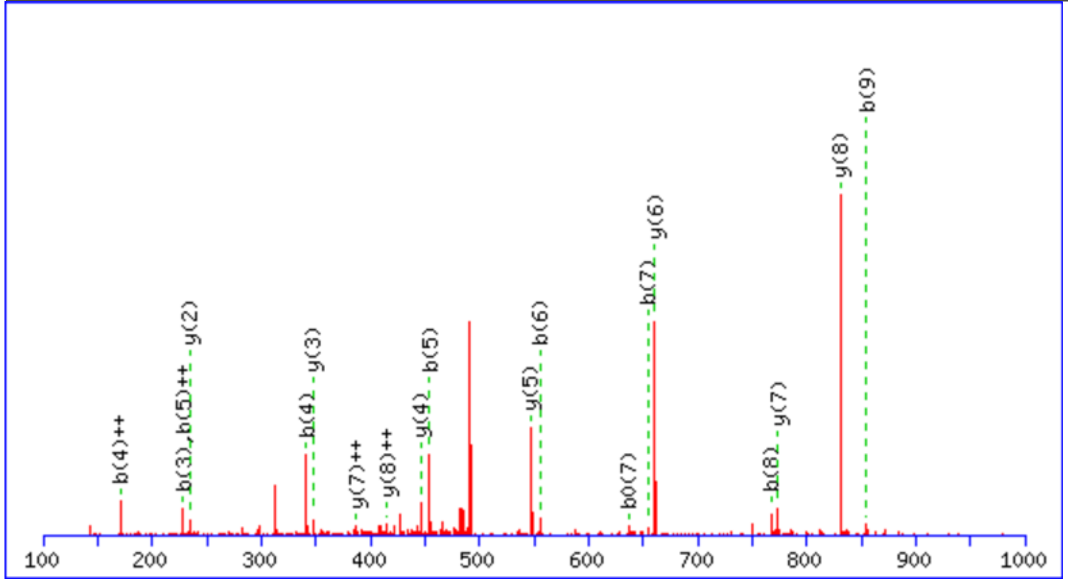
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 3053: 999.632848 from(500.823700,2+)
Title: OECHL100312_01.16747.16747.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60 **Expect:** 1.1e-005**Matches :** 20/78 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#

1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	**171.112804**			**L**	**773.513117**	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	**227.654836**			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	**446.297310**	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**

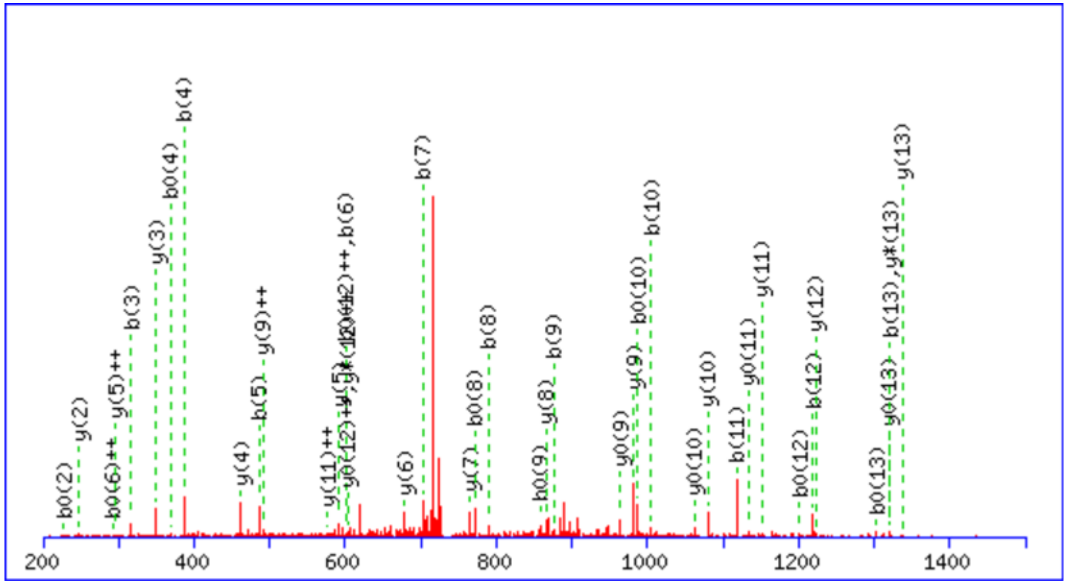


Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 9202: 1465.680448 from(733.847500,2+)
Title: OECHL100312_01.9363.9363.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 56 **Expect:** 0.00024**Matches :** 42/128 fragment ions using 109 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	S							14
2	245.076812	123.042044	227.066247	114.036761	D	***1337.643082***	669.325179	1320.616533	660.811905	1319.632517	660.319897	13
3	**316.113926**	158.560601	298.103361	149.555319	A	***1222.616139***	611.811708	1205.589590	603.298433	1204.605574	602.806425	12
4	**387.151040**	194.079158	369.140475	185.073875	A	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	11
5	**486.219454**	243.613365	468.208889	234.608082	V	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	10
6	**601.246397**	301.126837	583.235832	292.121554	D	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	9
7	**702.294076**	351.650676	684.283511	342.645394	T	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	8
8	**789.326104**	395.166690	771.315539	386.161408	S	***765.398875***	383.203076	748.372326	374.689801	747.388310	374.197793	7
9	**876.358132**	438.682704	858.347567	429.677421	S	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	6
10	**1005.400725**	503.204001	987.390160	494.198718	E	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	5
11	**1118.484789**	559.746033	1100.474224	550.740750	I	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	4
12	**1219.532468**	610.269872	1201.521903	601.264590	T	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	3
13	**1320.580147**	660.793712	1302.569582	651.788429	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
14					K	147.112804	74.060040	130.086255	65.546765			1



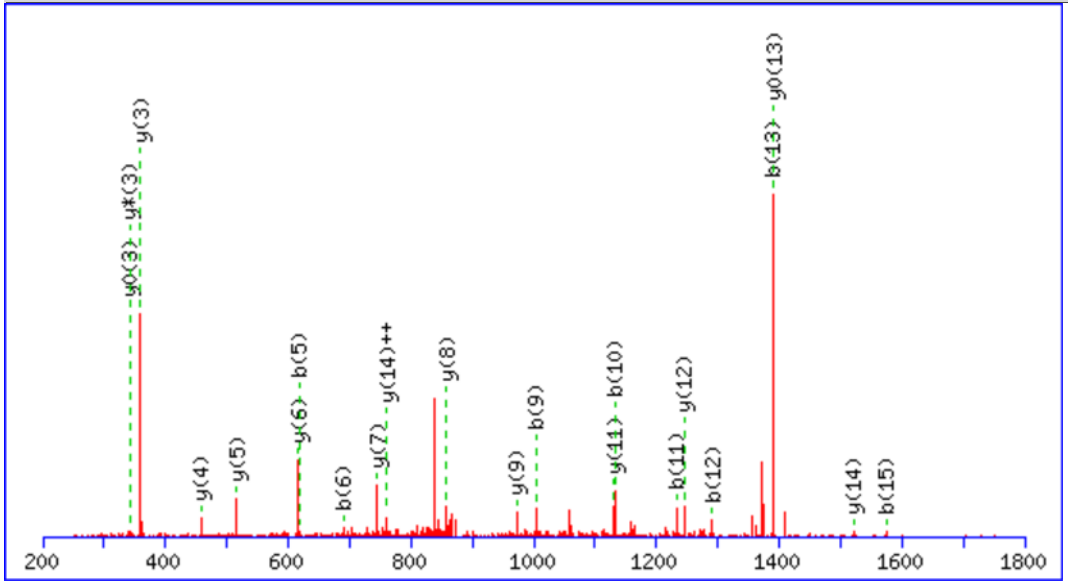
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 12476: 1746.915448 from(874.465000,2+)
Title: OECHL100312_01.16576.16576.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 83 **Expect:** 5.3e-007**Matches :** 22/156 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	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	***618.349740***	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018

6	689.386854	345.197065			671.376289	336.191782	A	1130.580027	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	S	1059.542913	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	972.510885	486.759081	955.484336	478.245806	954.500320	477.7537
9	1003.545873	502.276574	986.519324	493.763300	985.535308	493.271292	L	858.467958	429.737617	841.441409	421.224343	840.457393	420.7323
10	1132.588466	566.797871	1115.561917	558.284597	1114.577901	557.792588	E	745.383894	373.195585	728.357345	364.682311	727.373329	364.1903
11	1233.636145	617.321710	1216.609596	608.808436	1215.625580	608.316428	T	616.341301	308.674289	599.314752	300.161014	598.330736	299.6690
12	1290.657609	645.832442	1273.631060	637.319168	1272.647044	636.827160	G	515.293622	258.150449	498.267073	249.637175	497.283057	249.1451
13	1389.726023	695.366649	1372.699474	686.853375	1371.715458	686.361367	V	458.272158	229.639717	441.245609	221.126443	440.261593	220.6344
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	P	359.203744	180.105510	342.177195	171.592236	341.193179	171.1002
15	1573.810815	787.409046	1556.784266	778.895771	1555.800250	778.403763	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							R	175.118952	88.063114	158.092403	79.549839		



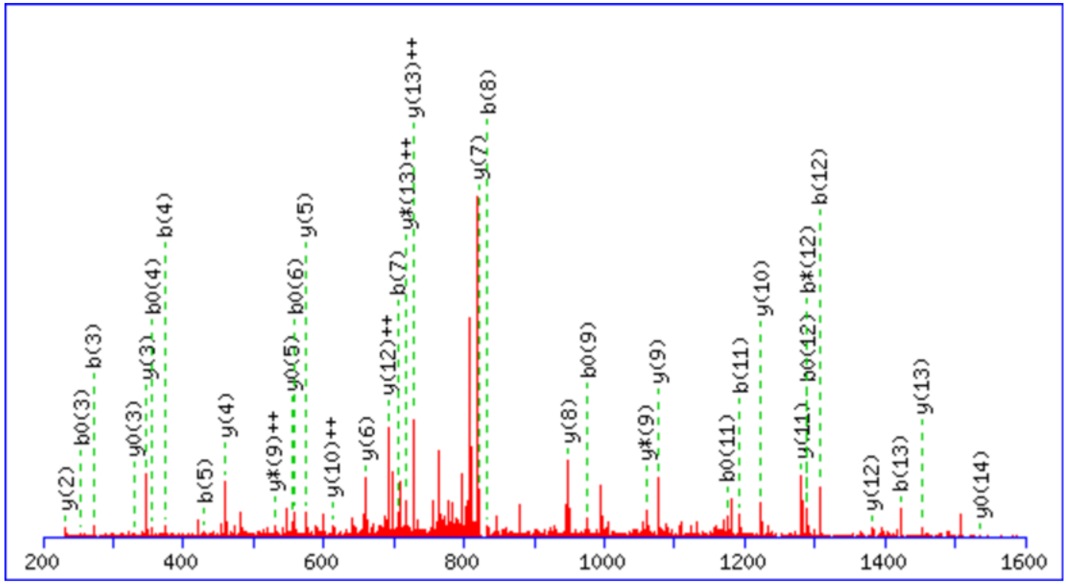
Peptide View

MS/MS Fragmentation of **VTATGFQQCSLIDGR**
Found in **IPI00333140**, Tax_Id=9606 Gene_Symbol=DNER Delta and Notch-like epidermal growth factor-related receptor

Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 11348: 1651.796248 from(826.905400,2+)
Title: OECHL100312_01.13430.13430.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1651.798828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 57 **Expect:** 0.00023**Matches :** 36/150 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	100.075690	50.541483					V						
2	201.123369	101.065322			183.112804	92.060040	T	1553.737670	777.372473	1536.711121	768.859198	1535.727105	768.3671
3	**272.160483**	136.583879			254.149918	127.578597	A	***1452.689991***	726.848633	1435.663442	718.335359	1434.679426	717.8433
4	**373.208162**	187.107719			355.197597	178.102437	T	***1381.652877***	691.330076	1364.626328	682.816802	1363.642312	682.3247
5	**430.229626**	215.618451			412.219061	206.613169	G	***1280.605198***	640.806237	1263.578649	632.292962	1262.594633	631.8009
6	577.298040	289.152658			559.287475	280.147376	F	***1223.583734***	612.295505	1206.557185	603.782230	1205.573169	603.2902
7	**705.356618**	353.181947	688.330069	344.668673	687.346053	344.176665	Q	***1076.515320***	538.761298	1059.488771	530.248023	1058.504755	529.7560
8	**833.415196**	417.211236	816.388647	408.697962	815.404631	408.205954	Q	***948.456742***	474.732009	931.430193	466.218734	930.446177	465.7267
9	993.445845	497.226561	976.419296	488.713286	975.435280	488.221278	C	***820.398164***	410.702720	803.371615	402.189445	802.387599	401.6974
10	1080.477873	540.742575	1063.451324	532.229300	1062.467308	531.737292	S	***660.367515***	330.687395	643.340966	322.174121	642.356950	321.6821
11	**1193.561937**	597.284607	1176.535388	588.771332	1175.551372	588.279324	L	***573.335487***	287.171381	556.308938	278.658107	555.324922	278.1660
12	**1306.646001**	653.826638	1289.619452	645.313364	1288.635436	644.821356	I	***460.251423***	230.629349	443.224874	222.116075	442.240858	221.6240
13	**1421.672944**	711.340110	1404.646395	702.826836	1403.662379	702.334827	D	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.0820
14	1478.694408	739.850842	1461.667859	731.337567	1460.683843	730.845559	G	***232.140416***	116.573846	215.113867	108.060571		
15							R	175.118952	88.063114	158.092403	79.549839		



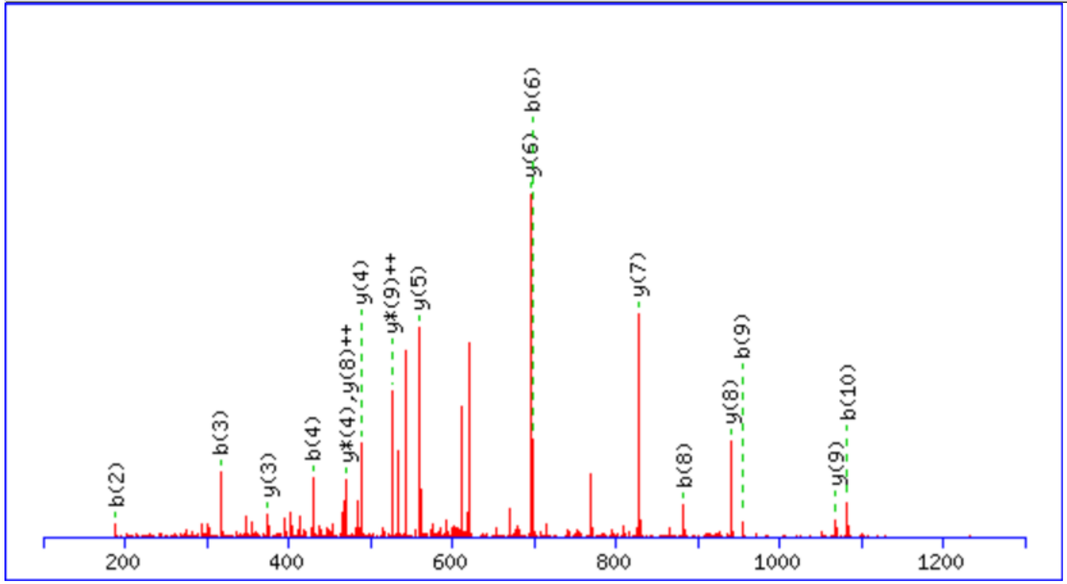
Peptide View

MS/MS Fragmentation of **GMQLMHANAQR**
Found in **IPI00007853**, Tax_Id=9606 Gene_Symbol=IFI30 Gamma-interferon-inducible lysosomal thiol reductase
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 6882: 1255.590848 from(628.802700,2+)
Title: OECHL100312_01.5521.5521.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1255.591370**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51 **Expect:** 0.00051**Matches :** 17/76 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.028740	29.518008			**G**					**11**
2	***189.069225***	95.038250			**M**	1199.577209	600.292243	1182.550660	591.778968	**10**
3	***317.127803***	159.067540	300.101254	150.554265	**Q**	***1068.536724***	534.772000	1051.510175	526.258726	**9**
4	***430.211867***	215.609572	413.185318	207.096297	**L**	***940.478146***	470.742711	923.451597	462.229436	**8**
5	561.252352	281.129814	544.225803	272.616540	**M**	***827.394082***	414.200679	810.367533	405.687404	**7**

6	***698.311264***	349.659270	681.284715	341.145996	**H**	***696.353597***	348.680436	679.327048	340.167162	**6**
7	769.348378	385.177827	752.321829	376.664553	**A**	***559.294685***	280.150981	542.268136	271.637706	**5**
8	***883.391305***	442.199291	866.364756	433.686016	**N**	***488.257571***	244.632423	471.231022	236.119149	**4**
9	***954.428419***	477.717848	937.401870	469.204573	**A**	***374.214644***	187.610960	357.188095	179.097685	**3**
10	***1082.486997***	541.747137	1065.460448	533.233862	**Q**	303.177530	152.092403	286.150981	143.579128	**2**
11					**R**	175.118952	88.063114	158.092403	79.549839	**1**

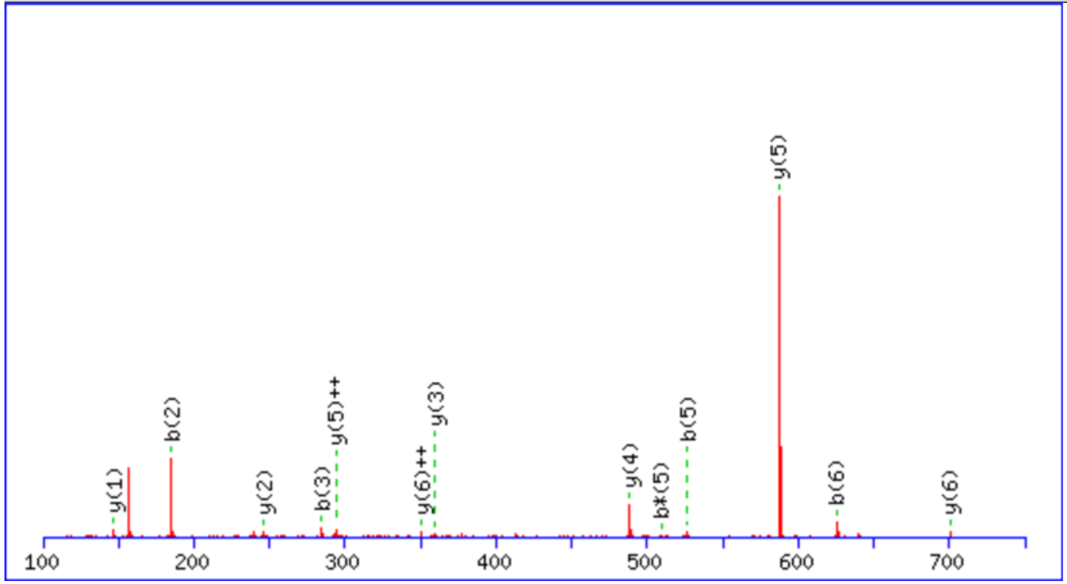


Peptide View

MS/MS Fragmentation of **ALVQIVK**
Found in **IPI00216569**, Tax_Id=9606 Gene_Symbol=CST7 Cystatin-F precursor
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 643: 770.490848 from(386.252700,2+)
Title: OECHL100312_01.11350.11350.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 770.490173**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: Q4 :** Deamidated (NQ)**Ions Score:** 58 **Expect:** 7e-005**Matches :** 13/42 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			**A**					**7**
2	**185.128454**	93.067865			**L**	***700.460354***	350.733815	683.433805	342.220541	**6**
3	**284.196868**	142.602072			**V**	***587.376290***	294.191783	570.349741	285.678509	**5**
4	413.239462	207.123369	396.212913	198.610095	**Q**	***488.307876***	244.657576	471.281327	236.144301	**4**
5	**526.323526**	263.665401	509.296977	255.152127	**I**	***359.265282***	180.136279	342.238733	171.623004	**3**
6	**625.391940**	313.199608	608.365391	304.686333	**V**	***246.181218***	123.594247	229.154669	115.080972	**2**
7					**K**	***147.112804***	74.060040	130.086255	65.546765	**1**



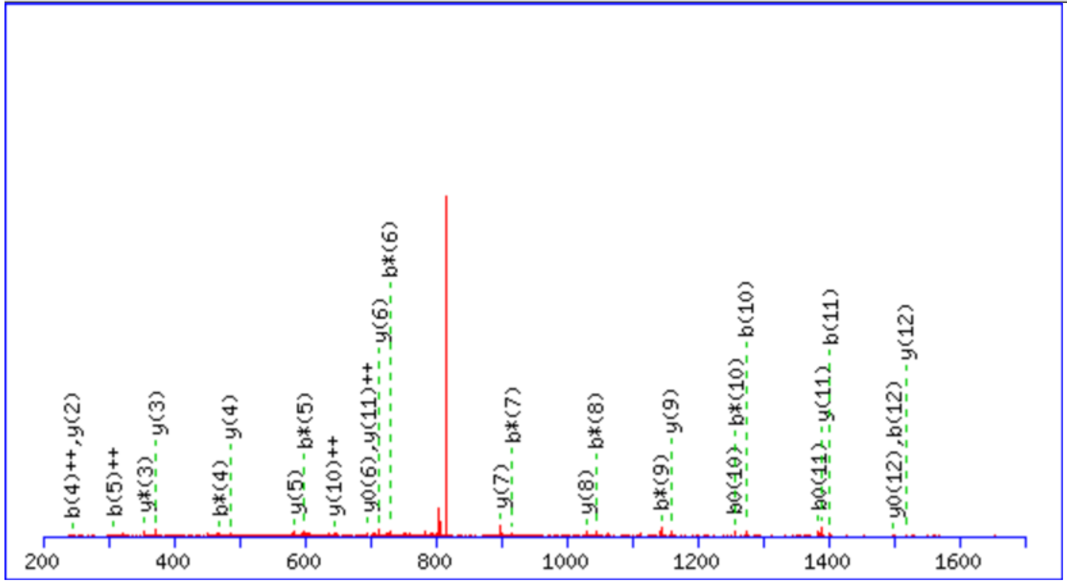
Peptide View

MS/MS Fragmentation of **QQTEEMWEVLKPK**
Found in **IPI00007778**, Tax_Id=9606 Gene_Symbol=CTBS Di-N-acetylchitobiase
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 11228: 1644.819648 from(823.417100,2+)
Title: OECHL100312_01.15426.15426.2.dta

Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1644.818115**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54 **Expect:** 0.00057**Matches :** 29/130 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	129.065854	65.036565	112.039305	56.523291			**Q**						
2	257.124432	129.065854	240.097883	120.552580			**Q**	***1517.766843***	759.387060	1500.740294	750.873785	1499.756278	750.3817
3	358.172111	179.589694	341.145562	171.076419	340.161546	170.584411	**T**	***1389.708265***	695.357771	1372.681716	686.844496	1371.697700	686.3524
4	487.214704	244.110990	470.188155	235.597716	469.204139	235.105708	**E**	1288.660586	644.833931	1271.634037	636.320657	1270.650021	635.8286
5	616.257297	308.632287	599.230748	300.119012	598.246732	299.627004	**E**	***1159.617993***	580.312635	1142.591444	571.799360	1141.607428	571.3073
6	747.297782	374.152529	730.271233	365.639255	729.287217	365.147247	**M**	***1030.575400***	515.791338	1013.548851	507.278064	1012.564835	506.7860
7	933.377095	467.192186	916.350546	458.678911	915.366530	458.186903	**W**	***899.534915***	450.271096	882.508366	441.757821	881.524350	441.2658
8	1062.419688	531.713482	1045.393139	523.200208	1044.409123	522.708200	**E**	***713.455602***	357.231439	696.429053	348.718165	695.445037	348.2261
9	1161.488102	581.247689	1144.461553	572.734415	1143.477537	572.242407	**V**	***584.413009***	292.710143	567.386460	284.196868		
10	**1274.572166**	637.789721	1257.545617	629.276447	1256.561601	628.784439	**L**	***485.344595***	243.175935	468.318046	234.662661		
11	**1402.667129**	701.837203	1385.640580	693.323928	1384.656564	692.831920	**K**	***372.260531***	186.633904	355.233982	178.120629		
12	**1499.719893**	750.363585	1482.693344	741.850310	1481.709328	741.358302	**P**	***244.165568***	122.586422	227.139019	114.073148		
13							**K**	147.112804	74.060040	130.086255	65.546765		

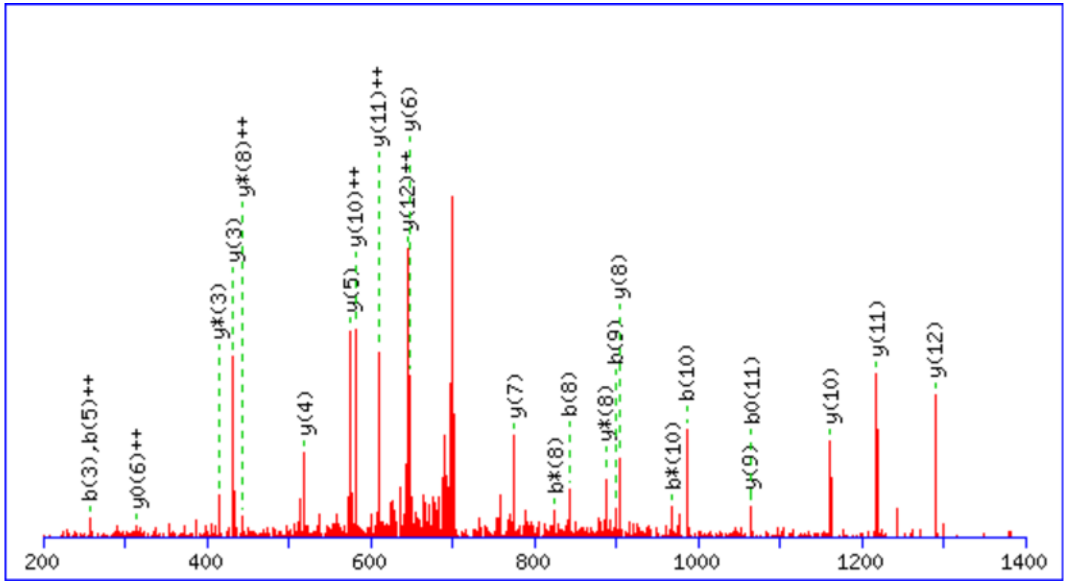


Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 8660: 1416.625248 from(709.319900,2+)
Title: OECHL100312_01.1955.1955.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67 **Expect:** 1.2e-005**Matches :** 25/128 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	129.102239	65.054757	112.075690	56.541483			**K**						
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.2664
3	**257.160817**	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.7478
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.2371
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.7107
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.6954
7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.1741
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.1448
9	**899.403979**	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.6262
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.1155
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546		
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	335.149601	168.078438	318.123052	159.565164		
13							**R**	175.118952	88.063114	158.092403	79.549839		



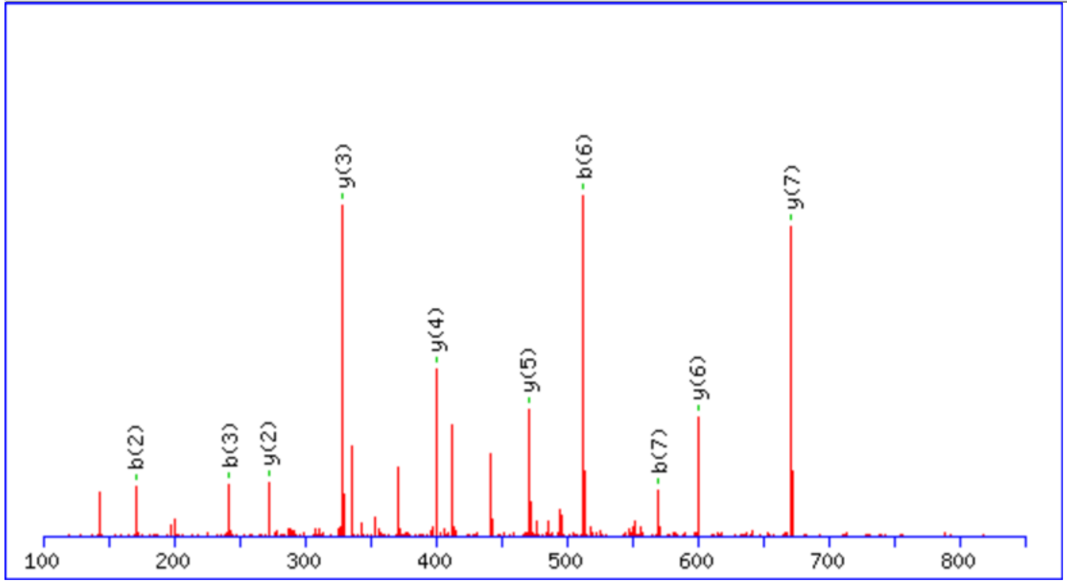
Peptide View

MS/MS Fragmentation of **GLAEAAGPR**
Found in **IPI00290826**, Tax_Id=9606 Gene_Symbol=FAM174A Membrane protein FAM174A
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 1079: 840.445448 from(421.230000,2+)
Title: OECHL100312_01.3741.3741.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 840.445343**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51 **Expect:** 0.00053**Matches :** 10/64 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.028740	29.518008			**G**							**9**
2	**171.112804**	86.060040			**L**	784.431179	392.719228	767.404630	384.205953	766.420614	383.713945	**8**
3	**242.149918**	121.578597			**A**	***671.347115***	336.177196	654.320566	327.663921	653.336550	327.171913	**7**
4	371.192511	186.099894	353.181946	177.094611	**E**	***600.310001***	300.658639	583.283452	292.145364	582.299436	291.653356	**6**
5	442.229625	221.618450	424.219060	212.613168	**A**	***471.267408***	236.137342	454.240859	227.624067			**5**

6	**513.266739**	257.137008	495.256174	248.131725	**A**	***400.230294***	200.618785	383.203745	192.105510			**4**
7	**570.288203**	285.647740	552.277638	276.642457	**G**	***329.193180***	165.100228	312.166631	156.586953			**3**
8	667.340967	334.174122	649.330402	325.168839	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
9					**R**	175.118952	88.063114	158.092403	79.549839			**1**



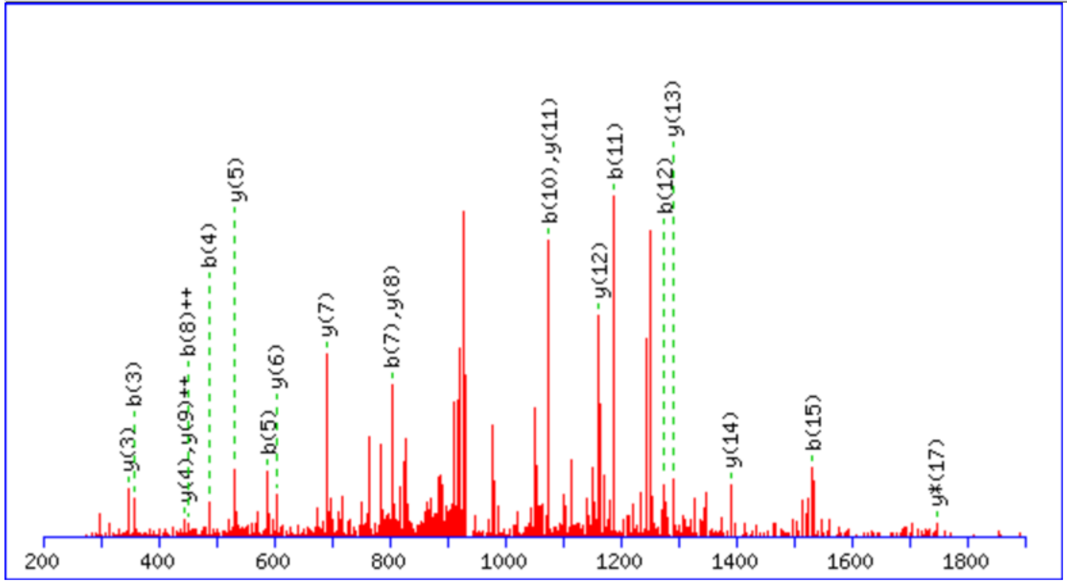
Peptide View

MS/MS Fragmentation of **NIEMTQSPSSLSASVGDR**
Found in **IPI00387025**, Tax_Id=9606 Gene_Symbol=- Ig kappa chain V-I region DEE
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 13589: 1877.879048 from(939.946800,2+)
Title: OECHL100312_01.12702.12702.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1877.878891**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60 **Expect:** 0.00015**Matches :** 21/198 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	115.050203	58.028740	98.023654	49.515465			**N**						

2	228.134267	114.570771	211.107718	106.057497			**I**	1764.843254	882.925265	1747.816705	874.411991	1746.832689	873.9199
3	**357.176860**	179.092068	340.150311	170.578793	339.166295	170.086785	**E**	1651.759190	826.383233	1634.732641	817.869959	1633.748625	817.3779
4	**488.217345**	244.612310	471.190796	236.099036	470.206780	235.607028	**M**	1522.716597	761.861937	1505.690048	753.348662	1504.706032	752.8566
5	**589.265024**	295.136150	572.238475	286.622876	571.254459	286.130868	**T**	***1391.676112***	696.341694	1374.649563	687.828420	1373.665547	687.3364
6	717.323602	359.165439	700.297053	350.652165	699.313037	350.160157	**Q**	***1290.628433***	645.817855	1273.601884	637.304580	1272.617868	636.8125
7	**804.355630**	402.681453	787.329081	394.168179	786.345065	393.676171	**S**	***1162.569855***	581.788566	1145.543306	573.275291	1144.559290	572.7832
8	901.408394	451.207835	884.381845	442.694561	883.397829	442.202553	**P**	***1075.537827***	538.272552	1058.511278	529.759277	1057.527262	529.2672
9	988.440422	494.723849	971.413873	486.210575	970.429857	485.718567	**S**	978.485063	489.746170	961.458514	481.232895	960.474498	480.7408
10	**1075.472450**	538.239863	1058.445901	529.726589	1057.461885	529.234580	**S**	891.453035	446.230156	874.426486	437.716881	873.442470	437.2248
11	**1188.556514**	594.781895	1171.529965	586.268621	1170.545949	585.776612	**L**	***804.421007***	402.714142	787.394458	394.200867	786.410442	393.7088
12	**1275.588542**	638.297909	1258.561993	629.784635	1257.577977	629.292626	**S**	***691.336943***	346.172110	674.310394	337.658835	673.326378	337.1668
13	1346.625656	673.816466	1329.599107	665.303192	1328.615091	664.811183	**A**	***604.304915***	302.656096	587.278366	294.142821	586.294350	293.6508
14	1433.657684	717.332480	1416.631135	708.819206	1415.647119	708.327198	**S**	***533.267801***	267.137539	516.241252	258.624264	515.257236	258.1322
15	**1532.726098**	766.866687	1515.699549	758.353413	1514.715533	757.861405	**V**	***446.235773***	223.621524	429.209224	215.108250	428.225208	214.6162
16	1589.747562	795.377419	1572.721013	786.864145	1571.736997	786.372137	**G**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.0820
17	1704.774505	852.890891	1687.747956	844.377616	1686.763940	843.885608	**D**	290.145895	145.576585	273.119346	137.063311	272.135330	136.5713
18							**R**	175.118952	88.063114	158.092403	79.549839		

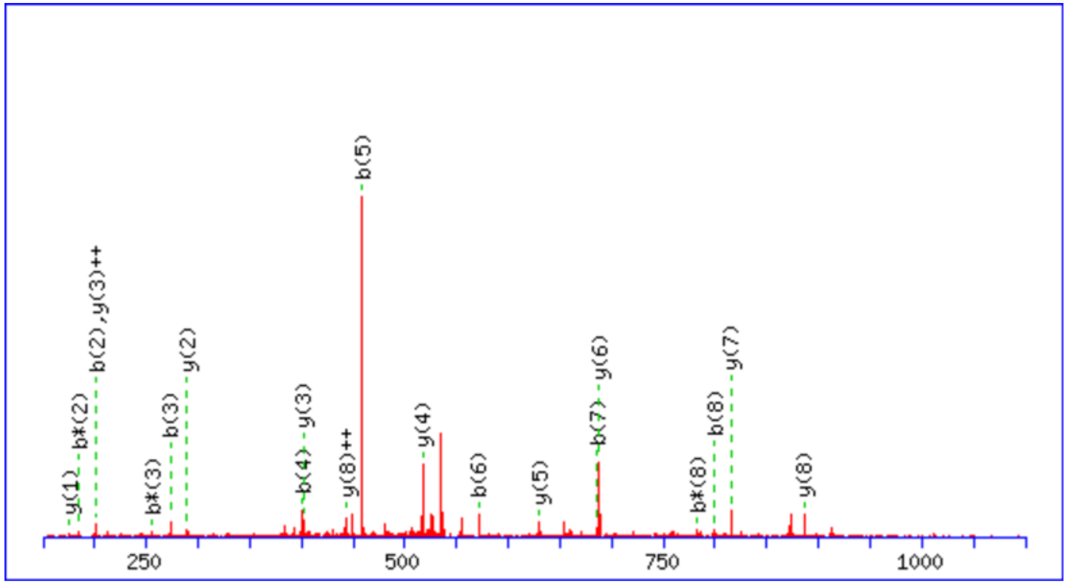


Peptide View

MS/MS Fragmentation of **SNAQGIDLNR**
Found in **IPI00031121**, Tax_Id=9606 Gene_Symbol=CPE Carboxypeptidase E precursor
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 4263: 1086.545048 from(544.279800,2+)
Title: OECHL100312_01.5733.5733.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1086.541763**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55 **Expect:** 0.00038**Matches :** 20/100 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	$b*^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	**S**							**10**
2	**202.082231**	101.544753	185.055682	93.031479	184.071666	92.539471	**N**	1000.517033	500.762155	983.490484	492.248880	982.506468	491.756872	**9**
3	**273.119345**	137.063311	256.092796	128.550036	255.108780	128.058028	**A**	***886.474106***	443.740691	869.447557	435.227416	868.463541	434.735408	**8**
4	**401.177923**	201.092600	384.151374	192.579325	383.167358	192.087317	**Q**	***815.436992***	408.222134	798.410443	399.708859	797.426427	399.216851	**7**
5	**458.199387**	229.603332	441.172838	221.090057	440.188822	220.598049	**G**	***687.378414***	344.192845	670.351865	335.679570	669.367849	335.187562	**6**
6	**571.283451**	286.145364	554.256902	277.632089	553.272886	277.140081	**I**	***630.356950***	315.682113	613.330401	307.168838	612.346385	306.676830	**5**
7	**686.310394**	343.658835	669.283845	335.145560	668.299829	334.653552	**D**	***517.272886***	259.140081	500.246337	250.626806	499.262321	250.134798	**4**
8	**799.394458**	400.200867	782.367909	391.687592	781.383893	391.195585	**L**	***402.245943***	201.626609	385.219394	193.113335			**3**
9	913.437385	457.222331	896.410836	448.709056	895.426820	448.217048	**N**	***289.161879***	145.084577	272.135330	136.571303			**2**
10							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



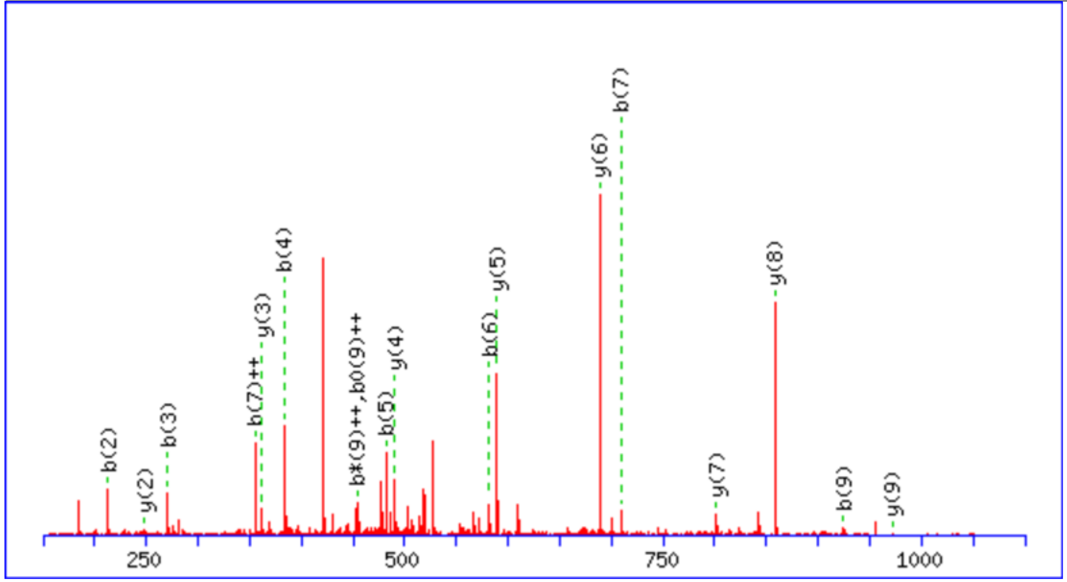
Peptide View

MS/MS Fragmentation of **VLGIVVQNTK**
Found in **IPI00397949**, Tax_Id=9606 Gene_Symbol=GPR56 Isoform 2 of G-protein coupled receptor 56
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 4019: 1069.650648 from(535.832600,2+)
Title: OECHL100312_01.11128.11128.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1069.649551**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52 **Expect:** 0.00016**Matches :** 18/78 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							10
2	**213.159754**	107.083515					L	***971.588408***	486.297842	954.561859	477.784568	953.577843	477.292560	9
3	**270.181218**	135.594247					G	***858.504344***	429.755810	841.477795	421.242536	840.493779	420.750528	8
4	**383.265282**	192.136279					I	***801.482880***	401.245078	784.456331	392.731804	783.472315	392.239796	7
5	**482.333696**	241.670486					V	***688.398816***	344.703046	671.372267	336.189772	670.388251	335.697764	6

6	**581.402110**	291.204693					**V**	***589.330402***	295.168839	572.303853	286.655565	571.319837	286.163557	**5**
7	**709.460688**	355.233982	692.434139	346.720708			**Q**	***490.261988***	245.634632	473.235439	237.121357	472.251423	236.629349	**4**
8	823.503615	412.255446	806.477066	403.742171			**N**	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	**3**
9	**924.551294**	462.779285	907.524745	454.266011	906.540729	453.774003	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
10							**K**	147.112804	74.060040	130.086255	65.546765			**1**



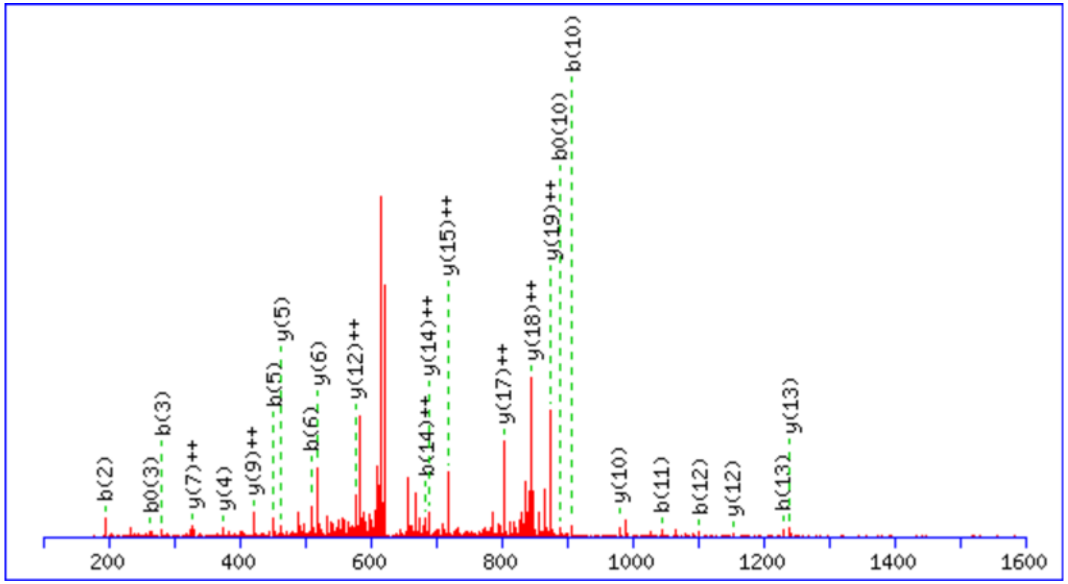
Peptide View

MS/MS Fragmentation of **HGSGLGHSSSHGQHGSGSGR**
Found in **IPI00398625**, Tax_Id=9606 Gene_Symbol=HRNR Hornerin
Experiment: 47 - PyA-2 **Fraction:** PyA-2

Match to Query 13653: 1884.832872 from(629.284900,3+)
Title: OECHL100312_01.1168.1168.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1884.832413**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50 **Expect:** 0.0008**Matches :** 25/196 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	138.066188	69.536732					**H**						
2	***195.087652***	98.047464					**G**	1748.780746	874.894011	1731.754197	866.380736	1730.770181	865.8887
3	***282.119680***	141.563478			264.109115	132.558195	**S**	1691.759282	846.383279	1674.732733	837.870004	1673.748717	837.3779
4	339.141144	170.074210			321.130579	161.068927	**G**	1604.727254	802.867265	1587.700705	794.353990	1586.716689	793.8619
5	***452.225208***	226.616242			434.214643	217.610959	**L**	1547.705790	774.356533	1530.679241	765.843258	1529.695225	765.3512
6	***509.246672***	255.126974			491.236107	246.121691	**G**	1434.621726	717.814501	1417.595177	709.301226	1416.611161	708.8092
7	646.305584	323.656430			628.295019	314.651147	**H**	1377.600262	689.303769	1360.573713	680.790494	1359.589697	680.2984
8	733.337612	367.172444			715.327047	358.167161	**S**	***1240.541350***	620.774313	1223.514801	612.261038	1222.530785	611.7690
9	820.369640	410.688458			802.359075	401.683175	**S**	***1153.509322***	577.258299	1136.482773	568.745024	1135.498757	568.2530
10	***907.401668***	454.204472			889.391103	445.199189	**S**	1066.477294	533.742285	1049.450745	525.229010	1048.466729	524.7370
11	***1044.460580***	522.733928			1026.450015	513.728645	**H**	***979.445266***	490.226271	962.418717	481.712996	961.434701	481.2209
12	***1101.482044***	551.244660			1083.471479	542.239377	**G**	842.386354	421.696815	825.359805	413.183540	824.375789	412.6915
13	***1229.540622***	615.273949	1212.514073	606.760674	1211.530057	606.268666	**Q**	785.364890	393.186083	768.338341	384.672808	767.354325	384.1808
14	1366.599534	683.803405	1349.572985	675.290130	1348.588969	674.798122	**H**	657.306312	329.156794	640.279763	320.643519	639.295747	320.1515
15	1423.620998	712.314137	1406.594449	703.800862	1405.610433	703.308854	**G**	***520.247400***	260.627338	503.220851	252.114063	502.236835	251.6220
16	1510.653026	755.830151	1493.626477	747.316876	1492.642461	746.824868	**S**	***463.225936***	232.116606	446.199387	223.603331	445.215371	223.1113
17	1567.674490	784.340883	1550.647941	775.827608	1549.663925	775.335600	**G**	***376.193908***	188.600592	359.167359	180.087317	358.183343	179.5953
18	1654.706518	827.856897	1637.679969	819.343622	1636.695953	818.851614	**S**	319.172444	160.089860	302.145895	151.576585	301.161879	151.0845
19	1711.727982	856.367629	1694.701433	847.854354	1693.717417	847.362346	**G**	232.140416	116.573846	215.113867	108.060571		
20							**R**	175.118952	88.063114	158.092403	79.549839		



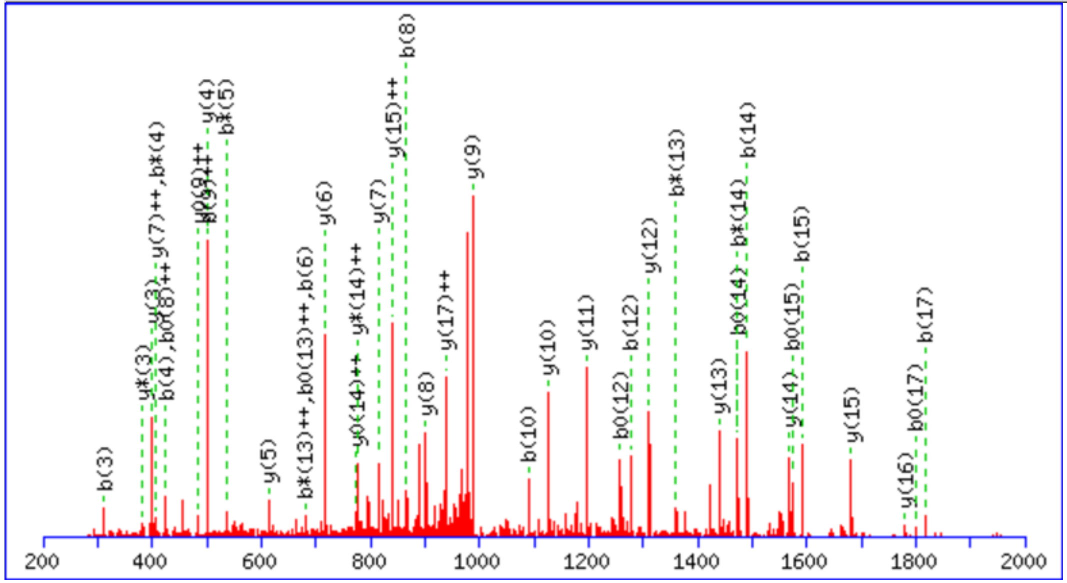
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 14631: 1990.025248 from(996.019900,2+)
Title: OECHL100310_07.9358.9358.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 97 **Expect:** 3e-008**Matches :** 42/186 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	115.050203	58.028740	98.023654	49.515465			**N**						
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.9921
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.4657
4	**424.255445**	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.9315
5	552.314023	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.3895

6	**680.372601**	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.3602
7	795.399544	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.3309
8	**866.436658**	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.8174
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.2989
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.7694
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.2534
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.7374
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.2032
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.6793
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.1373
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510		
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128		
18							**R**	175.118952	88.063114	158.092403	79.549839		

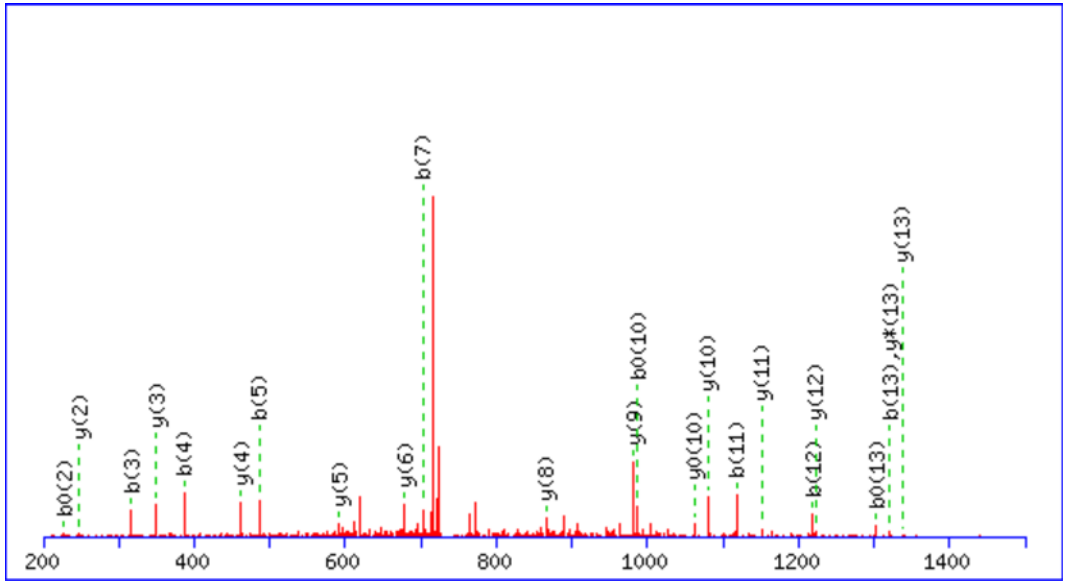


Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 9394: 1465.678648 from(733.846600,2+)
Title: OECHL100310_07.9397.9397.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 85 **Expect:** 2.7e-007**Matches :** 23/128 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	***1337.643082***	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	**316.113926**	158.560601	298.103361	149.555319	**A**	***1222.616139***	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	**387.151040**	194.079158	369.140475	185.073875	**A**	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	**486.219454**	243.613365	468.208889	234.608082	**V**	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**
6	601.246397	301.126837	583.235832	292.121554	**D**	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	**9**
7	**702.294076**	351.650676	684.283511	342.645394	**T**	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	765.398875	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	876.358132	438.682704	858.347567	429.677421	**S**	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	1005.400725	503.204001	987.390160	494.198718	**E**	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	**1118.484789**	559.746033	1100.474224	550.740750	**I**	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	**1219.532468**	610.269872	1201.521903	601.264590	**T**	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	**1320.580147**	660.793712	1302.569582	651.788429	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**



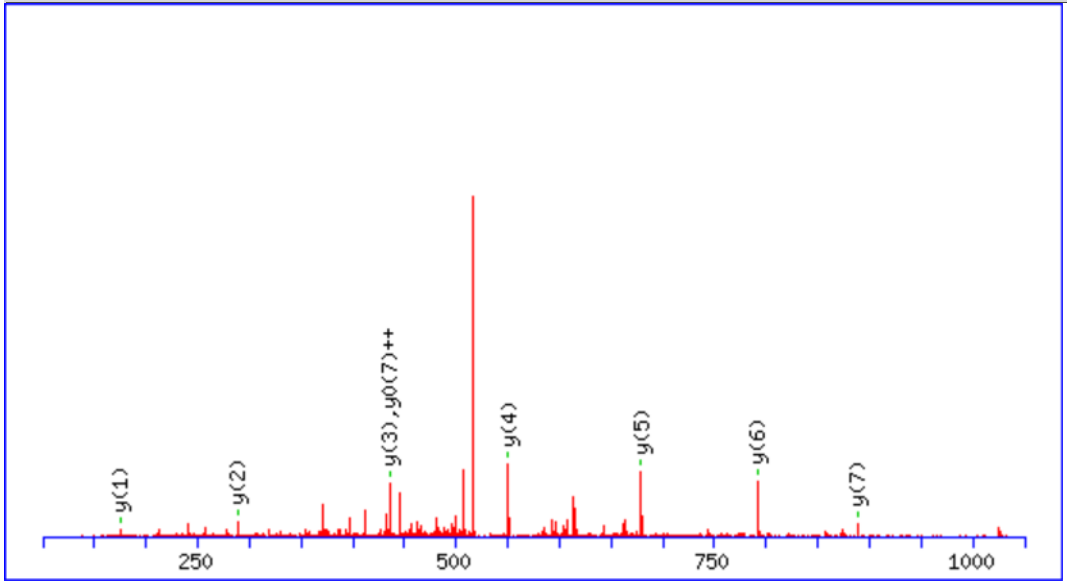
Peptide View

MS/MS Fragmentation of **CPLQDFLR**
Found in **IPI00003807**, Tax_Id=9606 Gene_Symbol=ACP2 Lysosomal acid phosphatase
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 4049: 1047.516248 from(524.765400,2+)
Title: OECHL100310_07.16473.16473.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1047.517151**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71 **Expect:** 7.6e-006**Matches :** 8/64 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	161.037925	81.022600					**C**							**8**
2	258.090689	129.548982					**P**	***888.493779***	444.750528	871.467230	436.237253	870.483214	435.745245	**7**
3	371.174753	186.091015					**L**	***791.441015***	396.224146	774.414466	387.710871	773.430450	387.218863	**6**
4	499.233331	250.120304	482.206782	241.607029			**Q**	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	**5**
5	614.260274	307.633775	597.233725	299.120501	596.249709	298.628493	**D**	***550.298373***	275.652825	533.271824	267.139550	532.287808	266.647542	**4**

6	761.328688	381.167982	744.302139	372.654708	743.318123	372.162700	F	*435.271430*	218.139353	418.244881	209.626079			3
7	874.412752	437.710014	857.386203	429.196740	856.402187	428.704732	L	*288.203016*	144.605146	271.176467	136.091872			2
8							R	*175.118952*	88.063114	158.092403	79.549840			1



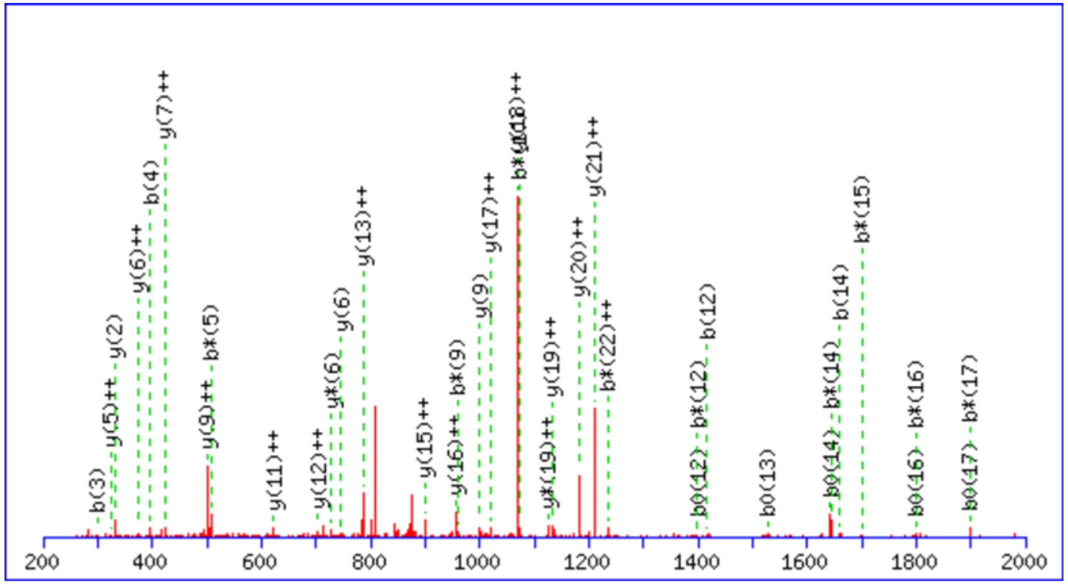
Peptide View

MS/MS Fragmentation of **QLGPQPQDIIYYEDGVVPTTDRR**
Found in **IPI00015199**, Tax_Id=9606 Gene_Symbol=CD7 T-cell antigen CD7
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 18029: 2659.324872 from(887.448900,3+)
Title: OECHL100310_07.17060.17060.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 2659.324203**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63 **Expect:** 0.0001**Matches :** 37/246 fragment ions using 86 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	
1	129.065854	65.036565	112.039305	56.523291			Q						
2	242.149918	121.578597	225.123369	113.065323			L	2532.272897	1266.640086	2515.246348	1258.126812	2514.262332	12

3	**299.171382**	150.089329	282.144833	141.576055			**G**	2419.188833	1210.098054	2402.162284	1201.584780	2401.178268	12
4	**396.224146**	198.615711	379.197597	190.102436			**P**	2362.167369	1181.587322	2345.140820	1173.074048	2344.156804	11
5	524.282724	262.645000	507.256175	254.131726			**Q**	2265.114605	1133.060940	2248.088056	1124.547666	2247.104040	11
6	621.335488	311.171382	604.308939	302.658108			**P**	2137.056027	1069.031651	2120.029478	1060.518377	2119.045462	10
7	749.394066	375.200671	732.367517	366.687397			**Q**	2040.003263	1020.505269	2022.976714	1011.991995	2021.992698	10
8	864.421009	432.714143	847.394460	424.200868	846.410444	423.708860	**D**	1911.944685	956.475980	1894.918136	947.962706	1893.934120	9
9	977.505073	489.256175	960.478524	480.742900	959.494508	480.250892	**I**	1796.917742	898.962509	1779.891193	890.449234	1778.907177	8
10	1090.589137	545.798206	1073.562588	537.284932	1072.578572	536.792924	**I**	1683.833678	842.420477	1666.807129	833.907202	1665.823113	8
11	1253.652466	627.329871	1236.625917	618.816597	1235.641901	618.324589	**Y**	1570.749614	785.878445	1553.723065	777.365170	1552.739049	7
12	**1416.715795**	708.861536	1399.689246	700.348261	1398.705230	699.856253	**Y**	1407.686285	704.346780	1390.659736	695.833506	1389.675720	6
13	1545.758388	773.382832	1528.731839	764.869558	1527.747823	764.377549	**E**	1244.622956	622.815116	1227.596407	614.301841	1226.612391	6
14	**1660.785331**	830.896304	1643.758782	822.383029	1642.774766	821.891021	**D**	1115.580363	558.293819	1098.553814	549.780545	1097.569798	5
15	1717.806795	859.407036	1700.780246	850.893761	1699.796230	850.401753	**G**	**1000.553420**	500.780348	983.526871	492.267073	982.542855	4
16	1816.875209	908.941243	1799.848660	900.427968	1798.864644	899.935960	**V**	943.531956	472.269616	926.505407	463.756341	925.521391	4
17	1915.943623	958.475450	1898.917074	949.962175	1897.933058	949.470167	**V**	844.463542	422.735409	827.436993	414.222134	826.452977	4
18	2012.996387	1007.001832	1995.969838	998.488557	1994.985822	997.996549	**P**	**745.395128**	373.201202	728.368579	364.687927	727.384563	3
19	2114.044066	1057.525671	2097.017517	1049.012396	2096.033501	1048.520388	**T**	648.342364	324.674820	631.315815	316.161545	630.331799	3
20	2215.091745	1108.049510	2198.065196	1099.536236	2197.081180	1099.044228	**T**	547.294685	274.150980	530.268136	265.637706	529.284120	2
21	2330.118688	1165.562982	2313.092139	1157.049707	2312.108123	1156.557699	**D**	446.247006	223.627141	429.220457	215.113866	428.236441	2
22	2486.219799	1243.613537	2469.193250	1235.100263	2468.209234	1234.608255	**R**	**331.220063**	166.113669	314.193514	157.600395		
23							**R**	175.118952	88.063114	158.092403	79.549839		



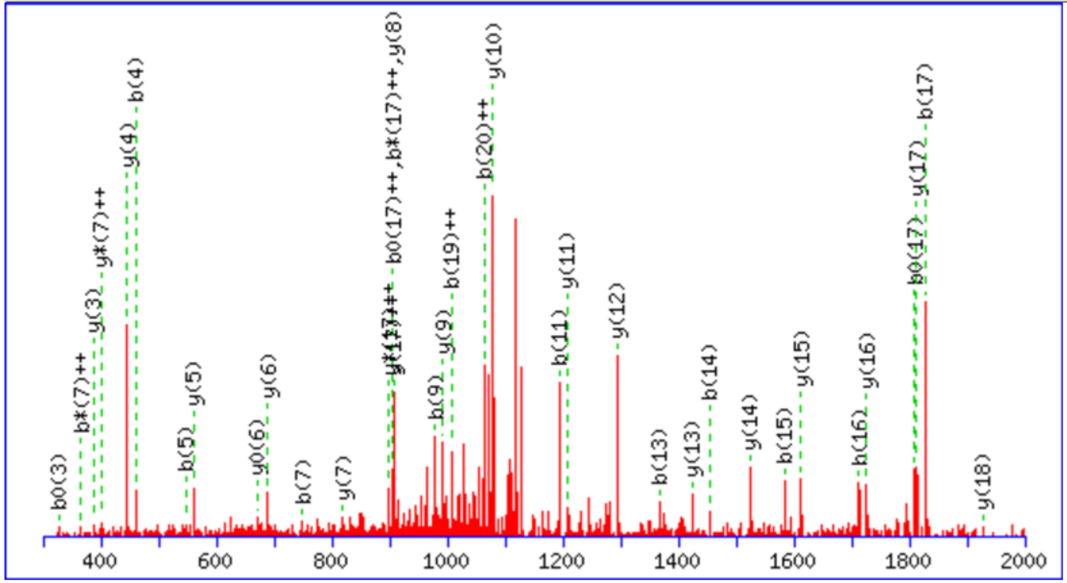
Peptide View

MS/MS Fragmentation of **SKEDSNSTESKSSSEEDGQLK**
Found in **IPI00012734**, Tax_Id=9606 Gene_Symbol=DMP1 Isoform 1 of Dentin matrix acidic phosphoprotein 1
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 16232: 2270.999448 from(1136.507000,2+)
Title: OECHL100310_07.2094.2094.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.998581**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 100 **Expect:** 9.9e-009**Matches :** 37/230 fragment ions using 68 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	
1	88.039304	44.523290			70.028739	35.518008	**S**						
2	216.134267	108.570771	199.107718	100.057497	198.123702	99.565489	**K**	2184.973868	1092.990572	2167.947319	1084.477297	2166.963303	108
3	345.176860	173.092068	328.150311	164.578793	327.166295	164.086785	**E**	2056.878905	1028.943090	2039.852356	1020.429816	2038.868340	10
4	**460.203803**	230.605539	443.177254	222.092265	442.193238	221.600257	**D**	***1927.836312***	964.421794	1910.809763	955.908520	1909.825747	9
5	**547.235831**	274.121554	530.209282	265.608279	529.225266	265.116271	**S**	***1812.809369***	906.908323	1795.782820	898.395048	1794.798804	8

6	661.278758	331.143017	644.252209	322.629743	643.268193	322.137735	**N**	***1725.777341***	863.392309	1708.750792	854.879034	1707.766776	85
7	**748.310786**	374.659031	731.284237	366.145757	730.300221	365.653749	**S**	***1611.734414***	806.370845	1594.707865	797.857571	1593.723849	79
8	849.358465	425.182871	832.331916	416.669596	831.347900	416.177588	**T**	***1524.702386***	762.854831	1507.675837	754.341557	1506.691821	75
9	**978.401058**	489.704167	961.374509	481.190893	960.390493	480.698885	**E**	***1423.654707***	712.330992	1406.628158	703.817717	1405.644142	70
10	1065.433086	533.220181	1048.406537	524.706907	1047.422521	524.214899	**S**	***1294.612114***	647.809695	1277.585565	639.296421	1276.601549	63
11	**1193.528049**	597.267663	1176.501500	588.754388	1175.517484	588.262380	**K**	***1207.580086***	604.293681	1190.553537	595.780407	1189.569521	59
12	1280.560077	640.783677	1263.533528	632.270402	1262.549512	631.778394	**S**	***1079.485123***	540.246200	1062.458574	531.732925	1061.474558	53
13	**1367.592105**	684.299691	1350.565556	675.786416	1349.581540	675.294408	**S**	***992.453095***	496.730186	975.426546	488.216911	974.442530	48
14	**1454.624133**	727.815705	1437.597584	719.302430	1436.613568	718.810422	**S**	***905.421067***	453.214172	888.394518	444.700897	887.410502	44
15	**1583.666726**	792.337001	1566.640177	783.823727	1565.656161	783.331719	**E**	***818.389039***	409.698158	801.362490	401.184883	800.378474	40
16	**1712.709319**	856.858298	1695.682770	848.345023	1694.698754	847.853015	**E**	***689.346446***	345.176861	672.319897	336.663587	671.335881	33
17	**1827.736262**	914.371769	1810.709713	905.858495	1809.725697	905.366487	**D**	***560.303853***	280.655565	543.277304	272.142290	542.293288	27
18	1884.757726	942.882501	1867.731177	934.369227	1866.747161	933.877219	**G**	***445.276910***	223.142093	428.250361	214.628818		
19	2012.816304	1006.911790	1995.789755	998.398516	1994.805739	997.906508	**Q**	***388.255446***	194.631361	371.228897	186.118087		
20	2125.900368	1063.453822	2108.873819	1054.940547	2107.889803	1054.448539	**L**	260.196868	130.602072	243.170319	122.088798		
21							**K**	147.112804	74.060040	130.086255	65.546765		



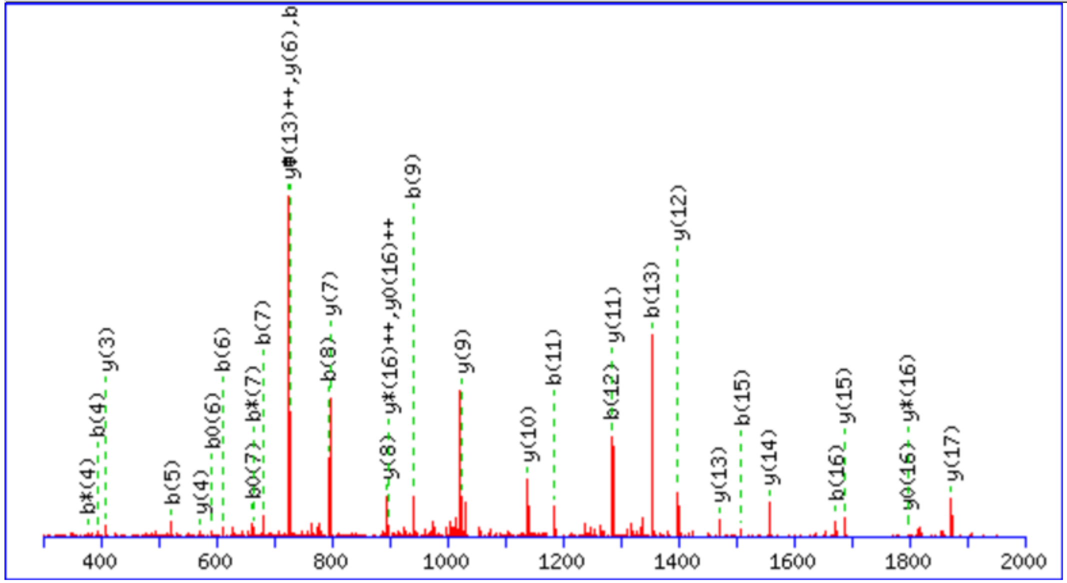
Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 15146: 2078.981448 from(1040.498000,2+)
Title: OECHL100310_07.16719.16719.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 74 **Expect:** 7.3e-006**Matches :** 35/200 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	72.044390	36.525833					**A**						
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444
4	**394.183344**	197.595310	377.156795	189.082035			**Q**	1814.870790	907.939033	1797.844241	899.425759	1796.860225	898.933
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904
6	**610.257965**	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383
7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867
8	**794.379143**	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676
15	**1508.712833**	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	629.304187	315.155732	612.277638	306.642457	611.293622	306.150
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	***572.282723***	286.645000	555.256174	278.131725	554.272158	277.639
17	1818.844576	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108
18	1905.876604	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573

19							**R**	175.118952	88.063114	158.092403	79.549840		



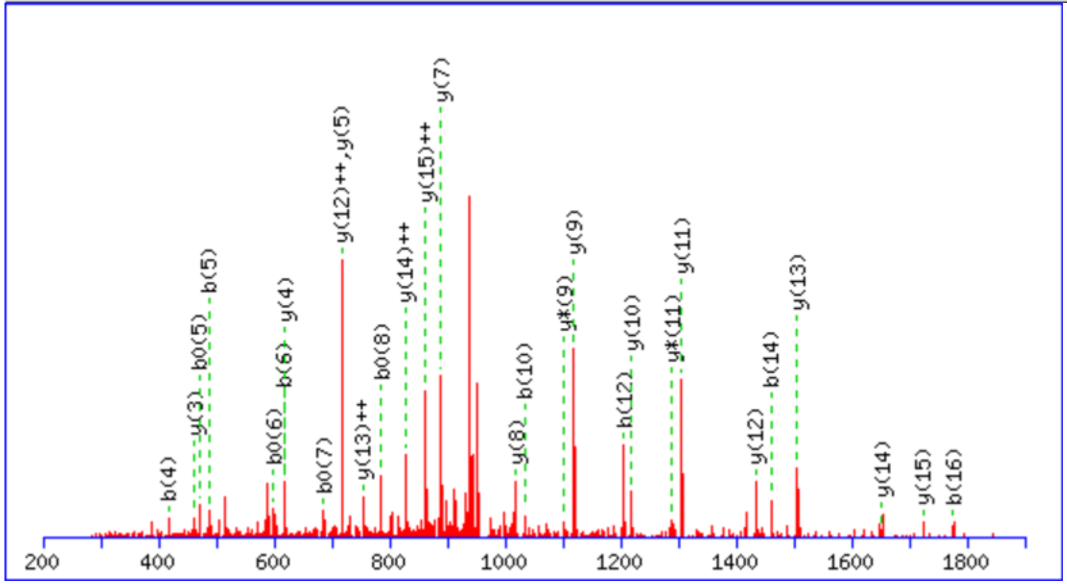
Peptide View

MS/MS Fragmentation of **TPAFAESVTEGDVRWEK**
Found in **IPI00384016**, Tax_Id=9606 Gene_Symbol=DLSTP;DLST Full-length cDNA 5-PRIME end of clone CS0DJ009YL13 of T cells (Jurkat cell line) of Homo sapiens (Fragment)
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 14064: 1920.923248 from(961.468900,2+)
Title: OECHL100310_07.14707.14707.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1920.921753**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63 **Expect:** 8.2e-005**Matches :** 29/164 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	102.054955	51.531116			84.044390	42.525833	**T**						
2	199.107719	100.057497			181.097154	91.052215	**P**	1820.881355	910.944316	1803.854806	902.431041	1802.870790	901.9390
3	270.144833	135.576055			252.134268	126.570772	**A**	***1723.828591***	862.417934	1706.802042	853.904659	1705.818026	853.4126

4	**417.213247**	209.110261			399.202682	200.104979	**F**	***1652.791477***	826.899377	1635.764928	818.386102	1634.780912	817.8940
5	**488.250361**	244.628818			470.239796	235.623536	**A**	***1505.723063***	753.365170	1488.696514	744.851895	1487.712498	744.3598
6	**617.292954**	309.150115			599.282389	300.144833	**E**	***1434.685949***	717.846612	1417.659400	709.333338	1416.675384	708.8413
7	704.324982	352.666129			686.314417	343.660846	**S**	***1305.643356***	653.325316	1288.616807	644.812042	1287.632791	644.3200
8	803.393396	402.200336			785.382831	393.195053	**V**	***1218.611328***	609.809302	1201.584779	601.296028	1200.600763	600.8040
9	904.441075	452.724176			886.430510	443.718893	**T**	***1119.542914***	560.275095	1102.516365	551.761821	1101.532349	551.2698
10	**1033.483668**	517.245472			1015.473103	508.240190	**E**	***1018.495235***	509.751256	1001.468686	501.237981	1000.484670	500.7459
11	1090.505132	545.756204			1072.494567	536.750922	**G**	***889.452642***	445.229959	872.426093	436.716684	871.442077	436.2246
12	**1205.532075**	603.269676			1187.521510	594.264393	**D**	832.431178	416.719227	815.404629	408.205953	814.420613	407.7139
13	1304.600489	652.803883			1286.589924	643.798600	**V**	***717.404235***	359.205756	700.377686	350.692481	699.393670	350.2004
14	**1460.701600**	730.854438	1443.675051	722.341164	1442.691035	721.849156	**R**	***618.335821***	309.671548	601.309272	301.158274	600.325256	300.6662
15	1646.780913	823.894095	1629.754364	815.380820	1628.770348	814.888812	**W**	***462.234710***	231.620993	445.208161	223.107718	444.224145	222.6157
16	**1775.823506**	888.415391	1758.796957	879.902117	1757.812941	879.410108	**E**	276.155397	138.581336	259.128848	130.068062	258.144832	129.5760
17							**K**	147.112804	74.060040	130.086255	65.546765		



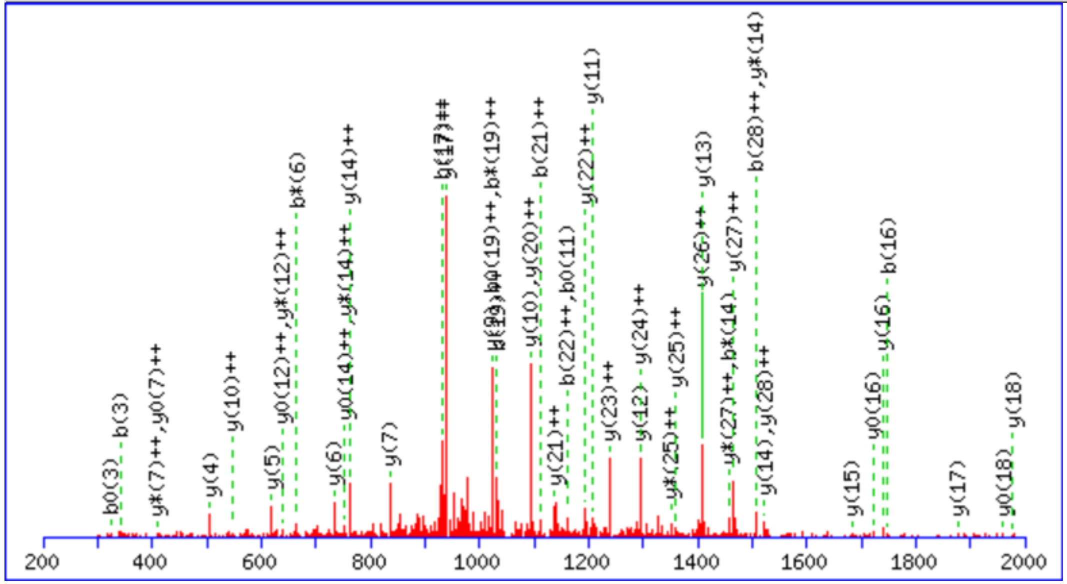
Peptide View

MS/MS Fragmentation of **LLDPQNSNSPLTHGCLDSLASTTDICQAK**
Found in **IPI00011899**, Tax_Id=9606 Gene_Symbol=BAMBI BMP and activin membrane-bound inhibitor homolog
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 19305: 3155.489172 from(1052.837000,3+)
Title: OECHL100310_07.16519.16519.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 3155.486328**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67 **Expect:** 3.9e-005**Matches :** 50/314 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	
1	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	3043.409542	1522.208409	3026.382993	1513.695134	3025.398977	15
3	342.202347	171.604811			324.191782	162.599529	**D**	2930.325478	1465.666377	2913.298929	1457.153102	2912.314913	14
4	439.255111	220.131193			421.244546	211.125911	**P**	2815.298535	1408.152905	2798.271986	1399.639631	2797.287970	13
5	567.313689	284.160483	550.287140	275.647208	549.303124	275.155200	**Q**	2718.245771	1359.626523	2701.219222	1351.113249	2700.235206	13
6	681.356616	341.181946	664.330067	332.668672	663.346051	332.176664	**N**	2590.187193	1295.597234	2573.160644	1287.083960	2572.176628	12
7	768.388644	384.697960	751.362095	376.184686	750.378079	375.692678	**S**	2476.144266	1238.575771	2459.117717	1230.062496	2458.133701	12
8	882.431571	441.719424	865.405022	433.206149	864.421006	432.714141	**N**	2389.112238	1195.059757	2372.085689	1186.546482	2371.101673	11
9	969.463599	485.235437	952.437050	476.722163	951.453034	476.230155	**S**	2275.069311	1138.038293	2258.042762	1129.525019	2257.058746	11
10	1066.516363	533.761820	1049.489814	525.248545	1048.505798	524.756537	**P**	2188.037283	1094.522279	2171.010734	1086.009005	2170.026718	10
11	1179.600427	590.303851	1162.573878	581.790577	1161.589862	581.298569	**L**	2090.984519	1045.995897	2073.957970	1037.482623	2072.973954	10
12	1280.648106	640.827691	1263.621557	632.314416	1262.637541	631.822408	**T**	***1977.900455***	989.453866	1960.873906	980.940591	1959.889890	9
13	1417.707018	709.357147	1400.680469	700.843872	1399.696453	700.351864	**H**	***1876.852776***	938.930026	1859.826227	930.416752	1858.842211	9
14	1474.728482	737.867879	1457.701933	729.354604	1456.717917	728.862596	**G**	***1739.793864***	870.400570	1722.767315	861.887296	1721.783299	8
15	1634.759131	817.883203	1617.732582	809.369929	1616.748566	808.877921	**C**	***1682.772400***	841.889838	1665.745851	833.376564	1664.761835	8
16	1747.843195	874.425235	1730.816646	865.911961	1729.832630	865.419953	**L**	***1522.741751***	761.874514	1505.715202	753.361239	1504.731186	7
17	1862.870138	**931.938707**	1845.843589	923.425432	1844.859573	922.933424	**D**	***1409.657687***	705.332482	1392.631138	696.819207	1391.647122	6
18	1949.902166	975.454721	1932.875617	966.941446	1931.891601	966.449438	**S**	***1294.630744***	647.819010	1277.604195	639.305736	1276.620179	6
19	2062.986230	**1031.996753**	2045.959681	1023.483478	2044.975665	1022.991470	**L**	***1207.598716***	604.302996	1190.572167	595.789722	1189.588151	5
20	2134.023344	1067.515310	2116.996795	1059.002035	2116.012779	1058.510027	**A**	***1094.514652***	547.760964	1077.488103	539.247690	1076.504087	5

21	2221.055372	**1111.031324**	2204.028823	1102.518049	2203.044807	1102.026041	**S**	***1023.477538***	512.242407	1006.450989	503.729132	1005.466973	5
22	2322.103051	**1161.555163**	2305.076502	1153.041889	2304.092486	1152.549881	**T**	936.445510	468.726393	919.418961	460.213118	918.434945	4
23	2423.150730	1212.079003	2406.124181	1203.565728	2405.140165	1203.073720	**T**	***835.397831***	418.202554	818.371282	409.689279	817.387266	4
24	2538.177673	1269.592474	2521.151124	1261.079200	2520.167108	1260.587192	**D**	***734.350152***	367.678714	717.323603	359.165440	716.339587	3
25	2651.261737	1326.134506	2634.235188	1317.621232	2633.251172	1317.129224	**I**	***619.323209***	310.165243	602.296660	301.651968		
26	2811.292386	1406.149831	2794.265837	1397.636556	2793.281821	1397.144548	**C**	***506.239145***	253.623211	489.212596	245.109936		
27	2939.350964	1470.179120	2922.324415	1461.665845	2921.340399	1461.173837	**Q**	346.208496	173.607886	329.181947	165.094612		
28	3010.388078	**1505.697677**	2993.361529	1497.184402	2992.377513	1496.692394	**A**	218.149918	109.578597	201.123369	101.065323		
29							**K**	147.112804	74.060040	130.086255	65.546765		



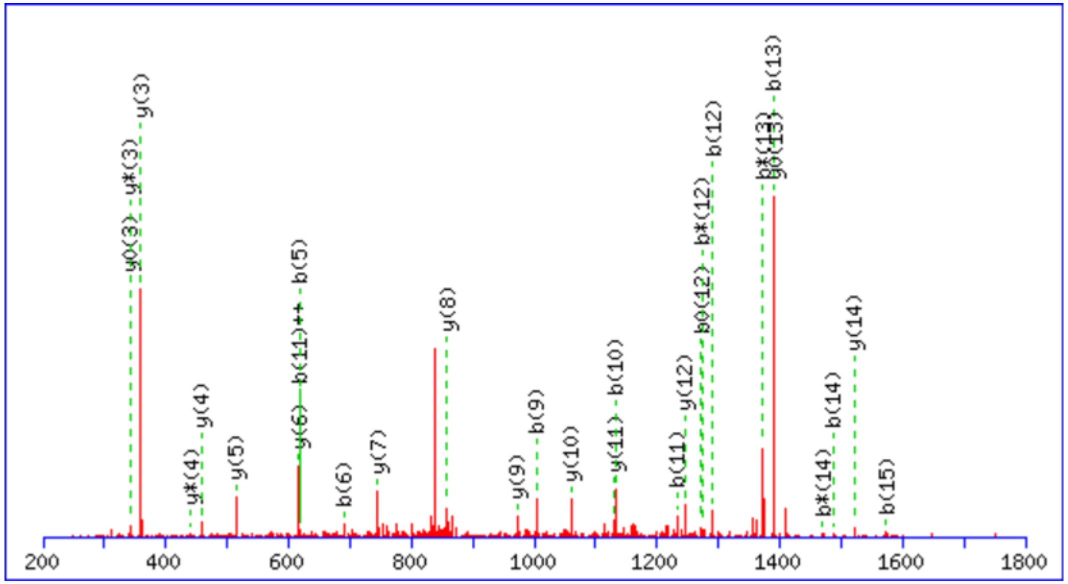
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 12624: 1746.916248 from(874.465400,2+)

Title: OECHL100310_07.16607.16607.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 88 **Expect:** 1.6e-007**Matches :** 29/156 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	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	***618.349740***	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018
6	***689.386854***	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							**R**	175.118952	88.063114	158.092403	79.549839		



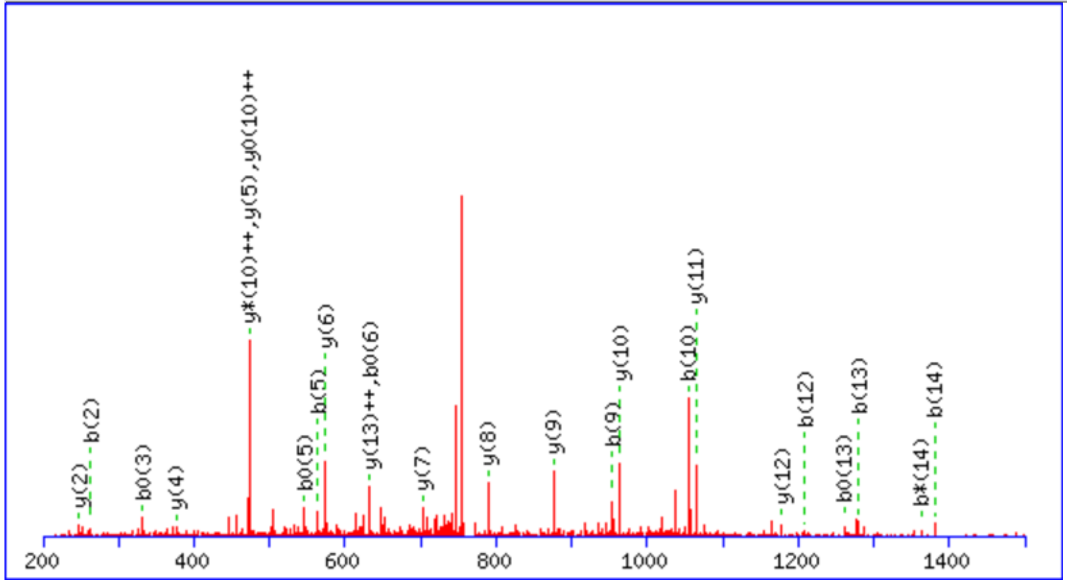
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 10153: 1525.725048 from(763.869800,2+)
Title: OECHL100310_07.10304.10304.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 74 **Expect:** 3.9e-006**Matches :** 25/150 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}
1	116.034219	58.520748			98.023654	49.515465	**D**						
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.3515
3	350.134661	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.8173
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.3013
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.7592

6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.2354
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.7194
8	825.362488	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.2034
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.6873
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.6581
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.1342
12	***1208.542973***	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.6078
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.0971
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.5785
15							**K**	147.112804	74.060040	130.086255	65.546765		

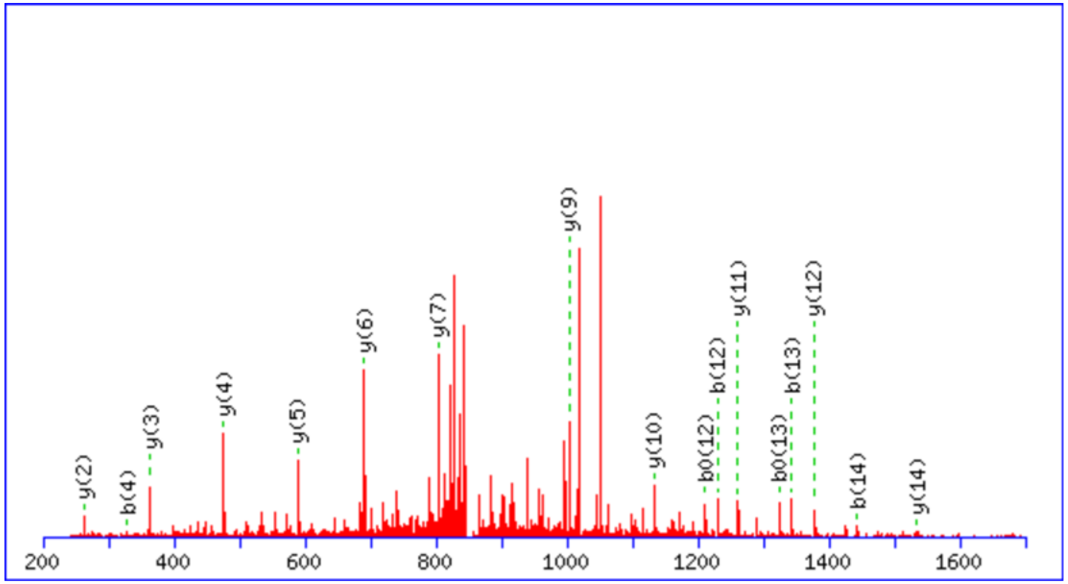


Peptide View

MS/MS Fragmentation of **GLGTDEESILTLLTSR**
Found in **IPI00329801**, Tax_Id=9606 Gene_Symbol=ANXA5 Annexin A5
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 12151: 1703.890448 from(852.952500,2+)
Title: OECHL100310_07.22309.22309.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1703.894135**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 77 **Expect:** 2.2e-006**Matches :** 17/142 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							16
2	171.112804	86.060040			L	1647.879958	824.443617	1630.853409	815.930343	1629.869393	815.438335	15
3	228.134268	114.570772			G	***1534.795894***	767.901585	1517.769345	759.388310	1516.785329	758.896302	14
4	**329.181947**	165.094611	311.171382	156.089329	T	1477.774430	739.390853	1460.747881	730.877579	1459.763865	730.385570	13
5	444.208890	222.608083	426.198325	213.602801	D	***1376.726751***	688.867013	1359.700202	680.353739	1358.716186	679.861731	12
6	573.251483	287.129380	555.240918	278.124097	E	***1261.699808***	631.353542	1244.673259	622.840267	1243.689243	622.348259	11
7	702.294076	351.650676	684.283511	342.645394	E	***1132.657215***	566.832246	1115.630666	558.318971	1114.646650	557.826963	10
8	789.326104	395.166690	771.315539	386.161408	S	***1003.614622***	502.310949	986.588073	493.797674	985.604057	493.305666	9
9	902.410168	451.708722	884.399603	442.703440	I	916.582594	458.794935	899.556045	450.281660	898.572029	449.789652	8
10	1015.494232	508.250754	997.483667	499.245472	L	***803.498530***	402.252903	786.471981	393.739628	785.487965	393.247620	7
11	1116.541911	558.774594	1098.531346	549.769311	T	***690.414466***	345.710871	673.387917	337.197596	672.403901	336.705588	6
12	**1229.625975**	615.316625	1211.615410	606.311343	L	***589.366787***	295.187031	572.340238	286.673757	571.356222	286.181749	5
13	**1342.710039**	671.858657	1324.699474	662.853375	L	***476.282723***	238.644999	459.256174	230.131725	458.272158	229.639717	4
14	**1443.757718**	722.382497	1425.747153	713.377214	T	***363.198659***	182.102968	346.172110	173.589693	345.188094	173.097685	3
15	1530.789746	765.898511	1512.779181	756.893228	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
16					R	175.118952	88.063114	158.092403	79.549839			1



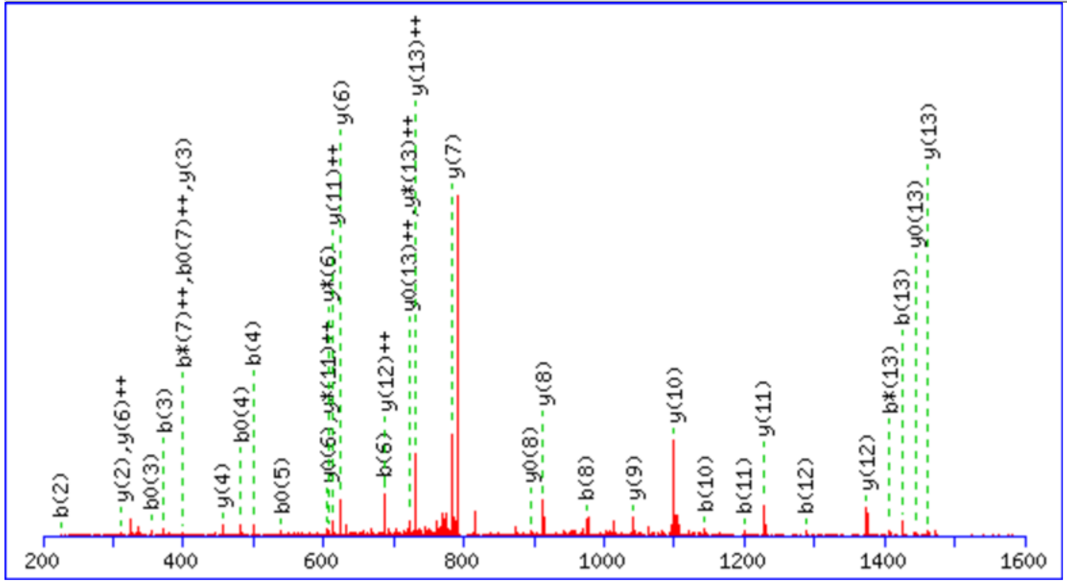
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 10898: 1597.706848 from(799.860700,2+)
Title: OECHL100310_07.2099.2099.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 62 **Expect:** 3.9e-005**Matches :** 37/144 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	138.066188	69.536732					H						
2	**225.098216**	113.052746			207.087651	104.047463	S	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.3253
3	**372.166630**	186.586953			354.156065	177.581671	F	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.8093
4	**500.261593**	250.634435	483.235044	242.121160	482.251028	241.629152	K	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.2751
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	G	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.2276

6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	E	***1042.437069***	521.722173	1025.410520	513.208898	1024.426504	512.7168
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	E	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.1955
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	C	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.6742
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	P	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.6589
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	A	527.268470	264.137873	510.241921	255.624598	509.257905	255.1325
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	G	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.6140
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	S	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.1033
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	H	***312.177864***	156.592570	295.151315	148.079295		
14							R	175.118952	88.063114	158.092403	79.549839		



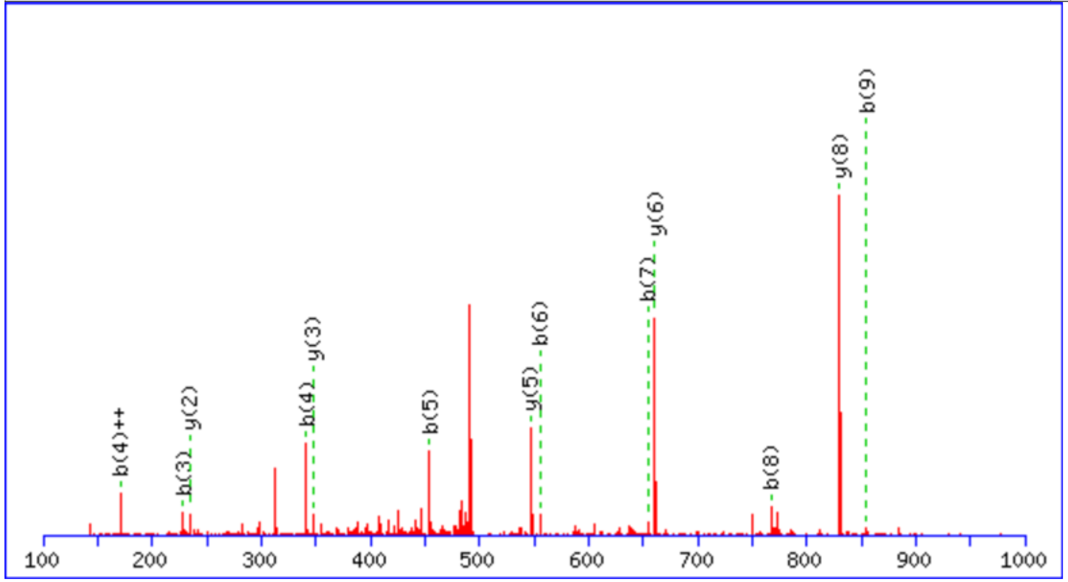
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 3266: 999.633848 from(500.824200,2+)

Title: OECHL100310_07.16737.16737.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61 **Expect:** 9.3e-006**Matches :** 14/78 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**

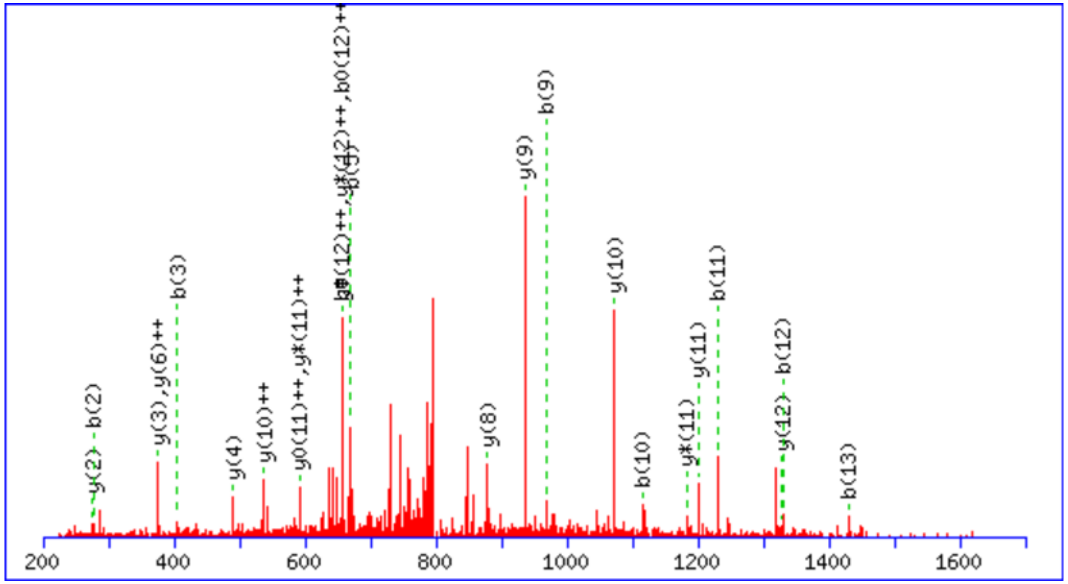


Peptide View

MS/MS Fragmentation of **LYQQHGAGLFDVTR**
Found in **IPI00554538**, Tax_Id=9606 Gene_Symbol=TPP1 Putative uncharacterized protein TPP1
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 10995: 1603.812448 from(802.913500,2+)
Title: OECHL100310_07.13251.13251.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1603.810699**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49 **Expect:** 0.0015**Matches :** 25/130 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	114.091340	57.549308					**L**						
2	***277.154669***	139.080973					**Y**	1491.733905	746.370591	1474.707356	737.857316	1473.723340	737.3653
3	***405.213247***	203.110262	388.186698	194.596987			**Q**	***1328.670576***	664.838926	1311.644027	656.325652	1310.660011	655.8336
4	533.271825	267.139551	516.245276	258.626276			**Q**	***1200.611998***	600.809637	1183.585449	592.296363	1182.601433	591.8043
5	***670.330737***	335.669007	653.304188	327.155732			**H**	***1072.553420***	536.780348	1055.526871	528.267074	1054.542855	527.7750
6	727.352201	364.179739	710.325652	355.666464			**G**	***935.494508***	468.250892	918.467959	459.737618	917.483943	459.2456
7	798.389315	399.698296	781.362766	391.185021			**A**	***878.473044***	439.740160	861.446495	431.226886	860.462479	430.7348
8	855.410779	428.209028	838.384230	419.695753			**G**	807.435930	404.221603	790.409381	395.708329	789.425365	395.2163
9	***968.494843***	484.751060	951.468294	476.237785			**L**	750.414466	375.710871	733.387917	367.197597	732.403901	366.7055
10	***1115.563257***	558.285267	1098.536708	549.771992			**F**	637.330402	319.168839	620.303853	310.655565	619.319837	310.1635
11	***1230.590200***	615.798738	1213.563651	607.285464	1212.579635	606.793456	**D**	***490.261988***	245.634632	473.235439	237.121358	472.251423	236.6293
12	***1329.658614***	665.332945	1312.632065	656.819671	1311.648049	656.327663	**V**	***375.235045***	188.121161	358.208496	179.607886	357.224480	179.1158
13	***1430.706293***	715.856785	1413.679744	707.343510	1412.695728	706.851502	**T**	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.5816
14							**R**	175.118952	88.063114	158.092403	79.549839		



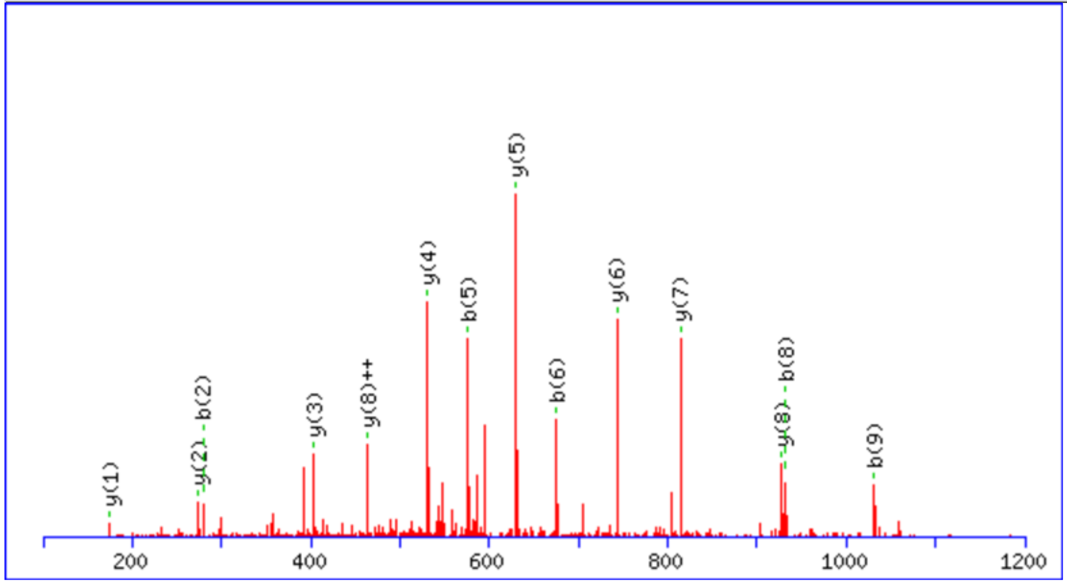
Peptide View

MS/MS Fragmentation of **YDIALVQEVR**
Found in **IPI00031065**, Tax_Id=9606 Gene_Symbol=DNASE1 Deoxyribonuclease-1
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 6090: 1204.646248 from(603.330400,2+)
Title: OECHL100310_07.15169.15169.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1204.645172**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62 **Expect:** 4.3e-005**Matches :** 14/90 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	164.070605	82.538940					Y						
2	**279.097548**	140.052412			261.086983	131.047130	D	1042.589136	521.798206	1025.562587	513.284932	1024.578571	512.7929
3	392.181612	196.594444			374.171047	187.589162	I	***927.562193***	464.284735	910.535644	455.771460	909.551628	455.2794
4	463.218726	232.113001			445.208161	223.107719	A	***814.478129***	407.742703	797.451580	399.229428	796.467564	398.7374
5	**576.302790**	288.655033			558.292225	279.649751	L	***743.441015***	372.224146	726.414466	363.710871	725.430450	363.2188

6	**675.371204**	338.189240			657.360639	329.183958	**V**	***630.356951***	315.682114	613.330402	307.168839	612.346386	306.6768
7	803.429782	402.218529	786.403233	393.705255	785.419217	393.213247	**Q**	***531.288537***	266.147907	514.261988	257.634632	513.277972	257.1426
8	**932.472375**	466.739826	915.445826	458.226551	914.461810	457.734543	**E**	***403.229959***	202.118618	386.203410	193.605343	385.219394	193.1133
9	**1031.540789**	516.274033	1014.514240	507.760758	1013.530224	507.268750	**V**	***274.187366***	137.597321	257.160817	129.084047		
10							**R**	***175.118952***	88.063114	158.092403	79.549839		



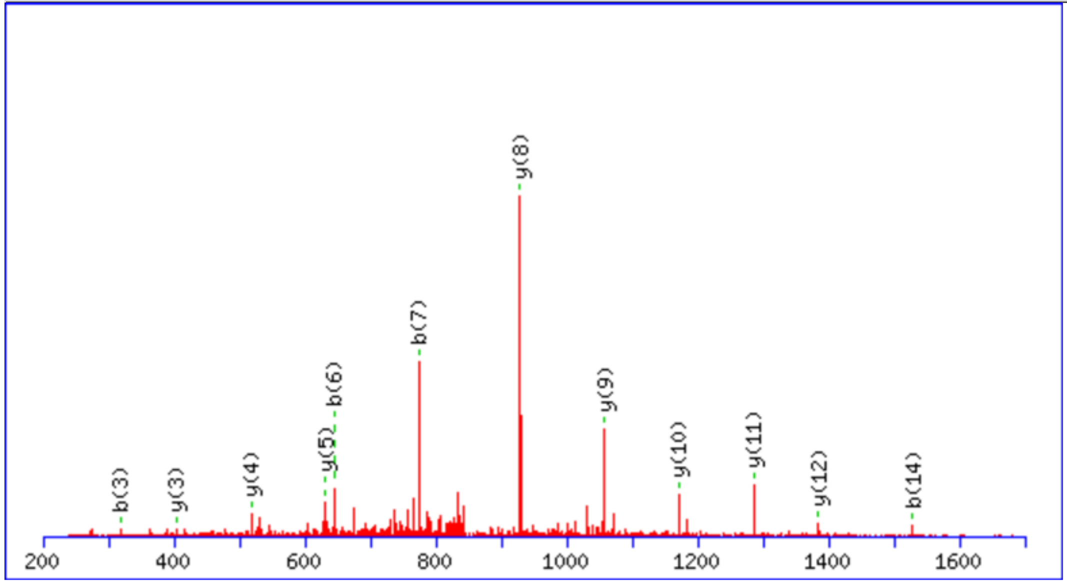
Peptide View

MS/MS Fragmentation of **AVFVDLEPTVIDEVR**
Found in **IPI00166768**, Tax_Id=9606 Gene_Symbol=TUBA1C TUBA1C protein
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 12134: 1700.900848 from(851.457700,2+)
Title: OECHL100310_07.19268.19268.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1700.898514**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66 **Expect:** 3e-005**Matches :** 12/128 fragment ions using 15 most intense peaks (help)

#	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y^{*}**	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**

1	72.044390	36.525833			**A**							**15**
2	171.112804	86.060040			**V**	1630.868665	815.937971	1613.842116	807.424696	1612.858100	806.932688	**14**
3	**318.181218**	159.594247			**F**	1531.800251	766.403764	1514.773702	757.890489	1513.789686	757.398481	**13**
4	417.249632	209.128454			**V**	***1384.731837***	692.869557	1367.705288	684.356282	1366.721272	683.864274	**12**
5	532.276575	266.641926	514.266010	257.636643	**D**	***1285.663423***	643.335350	1268.636874	634.822075	1267.652858	634.330067	**11**
6	**645.360639**	323.183958	627.350074	314.178675	**L**	***1170.636480***	585.821878	1153.609931	577.308604	1152.625915	576.816596	**10**
7	**774.403232**	387.705254	756.392667	378.699972	**E**	***1057.552416***	529.279846	1040.525867	520.766572	1039.541851	520.274564	**9**
8	871.455996	436.231636	853.445431	427.226354	**P**	***928.509823***	464.758550	911.483274	456.245275	910.499258	455.753267	**8**
9	972.503675	486.755476	954.493110	477.750193	**T**	831.457059	416.232168	814.430510	407.718893	813.446494	407.226885	**7**
10	1071.572089	536.289683	1053.561524	527.284400	**V**	730.409380	365.708328	713.382831	357.195054	712.398815	356.703046	**6**
11	1184.656153	592.831715	1166.645588	583.826432	**I**	***631.340966***	316.174121	614.314417	307.660846	613.330401	307.168838	**5**
12	1299.683096	650.345186	1281.672531	641.339904	**D**	***518.256902***	259.632089	501.230353	251.118815	500.246337	250.626807	**4**
13	1428.725689	714.866483	1410.715124	705.861200	**E**	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	**3**
14	**1527.794103**	764.400690	1509.783538	755.395407	**V**	274.187366	137.597321	257.160817	129.084047			**2**
15					**R**	175.118952	88.063114	158.092403	79.549839			**1**

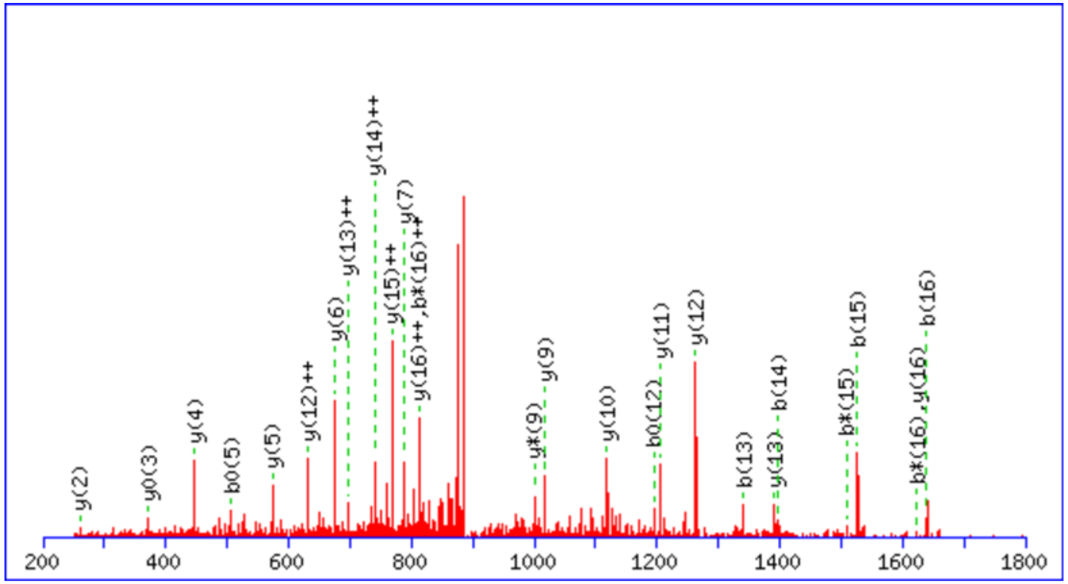


Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 12953: 1784.880448 from(893.447500,2+)
Title: OECHL100310_07.7289.7289.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 72 **Expect:** 9.3e-006**Matches :** 27/170 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	164.070605	82.538940					**Y**						
2	251.102633	126.054954			233.092068	117.049672	**S**	***1622.823172***	811.915224	1605.796623	803.401950	1604.812607	802.9099
3	308.124097	154.565687			290.113532	145.560404	**G**	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.3939
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.8831
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.3671
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.8458
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.3351
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.8191
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.2952
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.2660
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.7421
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.2001
13	**1340.632852**	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.6762
14	**1397.654316**	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.6288
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.1180
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		



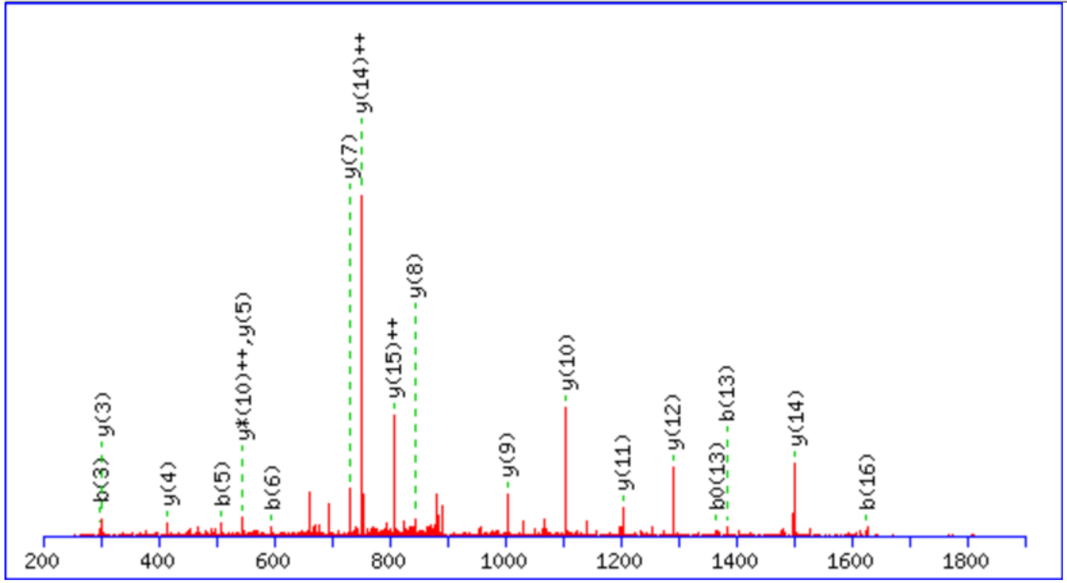
Peptide View

MS/MS Fragmentation of **GQLPISVTCIADEIGAR**
Found in **IPI00240345**, Tax_Id=9606 Gene_Symbol=CLEC14A C-type lectin domain family 14 member A
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 13072: 1798.924848 from(900.469700,2+)
Title: OECHL100310_07.19904.19904.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1798.924728**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70 **Expect:** 1.3e-005**Matches :** 19/172 fragment ions using 31 most intense peaks   (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}
1	58.028740	29.518008					**G**						
2	186.087318	93.547297	169.060769	85.034023			**Q**	1742.910548	871.958912	1725.883999	863.445638	1724.899983	862.9536
3	**299.171382**	150.089329	282.144833	141.576055			**L**	1614.851970	807.929623	1597.825421	799.416349	1596.841405	798.9243
4	396.224146	198.615711	379.197597	190.102436			**P**	***1501.767906***	751.387591	1484.741357	742.874317	1483.757341	742.3823
5	**509.308210**	255.157743	492.281661	246.644468			**I**	1404.715142	702.861209	1387.688593	694.347935	1386.704577	693.8559

6	**596.340238**	298.673757	579.313689	290.160483	578.329673	289.668475	**S**	***1291.631078***	646.319177	1274.604529	637.805903	1273.620513	637.3138
7	695.408652	348.207964	678.382103	339.694689	677.398087	339.202681	**V**	***1204.599050***	602.803163	1187.572501	594.289889	1186.588485	593.7978
8	796.456331	398.731804	779.429782	390.218529	778.445766	389.726521	**T**	***1105.530636***	553.268956	1088.504087	544.755682	1087.520071	544.2636
9	956.486980	478.747128	939.460431	470.233854	938.476415	469.741846	**C**	***1004.482957***	502.745117	987.456408	494.231842	986.472392	493.7398
10	1069.571044	535.289160	1052.544495	526.775886	1051.560479	526.283878	**I**	***844.452308***	422.729792	827.425759	414.216518	826.441743	413.7245
11	1140.608158	570.807717	1123.581609	562.294443	1122.597593	561.802435	**A**	***731.368244***	366.187760	714.341695	357.674486	713.357679	357.1824
12	1255.635101	628.321189	1238.608552	619.807914	1237.624536	619.315906	**D**	660.331130	330.669203	643.304581	322.155929	642.320565	321.6639
13	**1384.677694**	692.842485	1367.651145	684.329211	1366.667129	683.837203	**E**	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.1504
14	1497.761758	749.384517	1480.735209	740.871243	1479.751193	740.379235	**I**	***416.261594***	208.634435	399.235045	200.121160		
15	1554.783222	777.895249	1537.756673	769.381975	1536.772657	768.889967	**G**	***303.177530***	152.092403	286.150981	143.579128		
16	**1625.820336**	813.413806	1608.793787	804.900532	1607.809771	804.408524	**A**	246.156066	123.581671	229.129517	115.068396		
17							**R**	175.118952	88.063114	158.092403	79.549839		



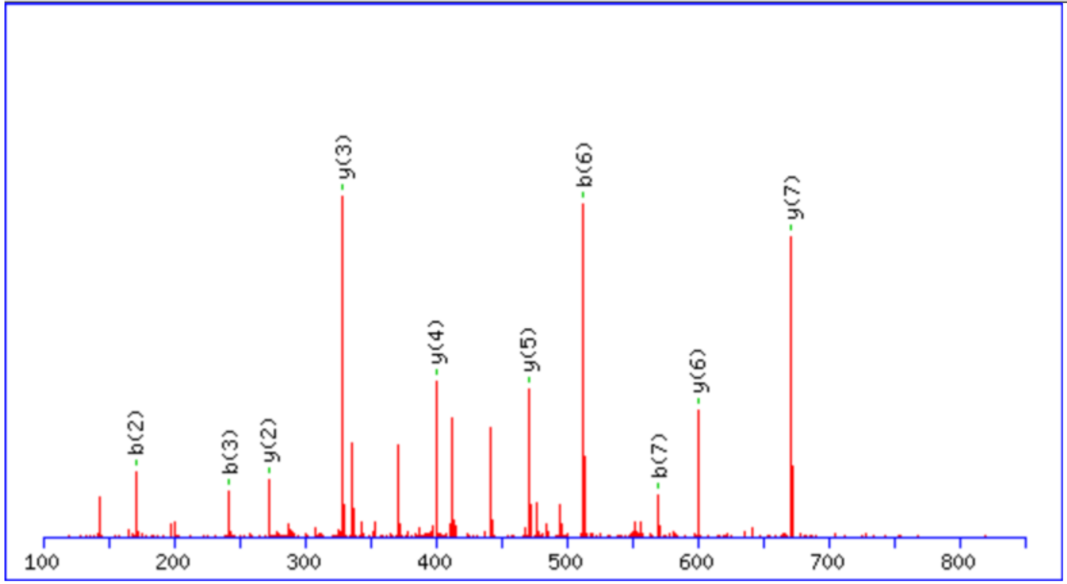
Peptide View

MS/MS Fragmentation of **GLAEAAGPR**

Found in **IPI00290826**, Tax_Id=9606 Gene_Symbol=FAM174A Membrane protein FAM174A
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 1202: 840.445848 from(421.230200,2+)
Title: OECHL100310_07.3767.3767.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 840.445343**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51 **Expect:** 0.00053**Matches :** 10/64 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			**G**							**9**
2	**171.112804**	86.060040			**L**	784.431179	392.719228	767.404630	384.205953	766.420614	383.713945	**8**
3	**242.149918**	121.578597			**A**	***671.347115***	336.177196	654.320566	327.663921	653.336550	327.171913	**7**
4	371.192511	186.099894	353.181946	177.094611	**E**	***600.310001***	300.658639	583.283452	292.145364	582.299436	291.653356	**6**
5	442.229625	221.618450	424.219060	212.613168	**A**	***471.267408***	236.137342	454.240859	227.624067			**5**
6	**513.266739**	257.137008	495.256174	248.131725	**A**	***400.230294***	200.618785	383.203745	192.105510			**4**
7	**570.288203**	285.647740	552.277638	276.642457	**G**	***329.193180***	165.100228	312.166631	156.586953			**3**
8	667.340967	334.174122	649.330402	325.168839	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
9					**R**	175.118952	88.063114	158.092403	79.549839			**1**

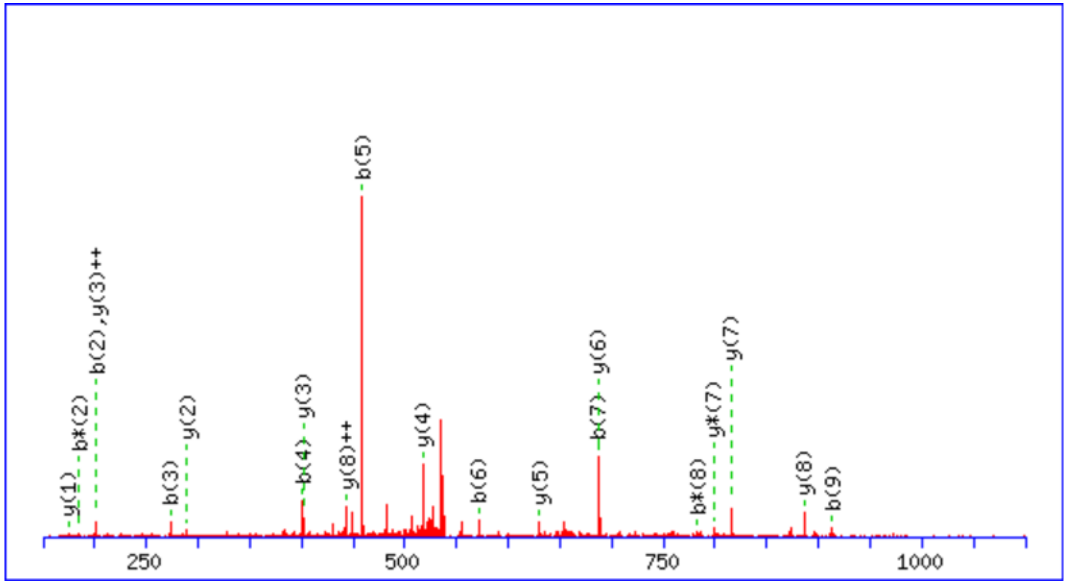


Peptide View

MS/MS Fragmentation of **SNAQGIDLNR**
Found in **IPI00031121**, Tax_Id=9606 Gene_Symbol=CPE Carboxypeptidase E precursor
Experiment: 46 - PyA-1 **Fraction:** PyA-1

Match to Query 4561: 1086.541648 from(544.278100,2+)
Title: OECHL100310_07.5840.5840.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1086.541763**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58 **Expect:** 0.00016**Matches :** 20/100 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	**S**							**10**
2	**202.082231**	101.544753	185.055682	93.031479	184.071666	92.539471	**N**	1000.517033	500.762155	983.490484	492.248880	982.506468	491.756872	**9**
3	**273.119345**	137.063311	256.092796	128.550036	255.108780	128.058028	**A**	***886.474106***	443.740691	869.447557	435.227416	868.463541	434.735408	**8**
4	**401.177923**	201.092600	384.151374	192.579325	383.167358	192.087317	**Q**	***815.436992***	408.222134	798.410443	399.708859	797.426427	399.216851	**7**
5	**458.199387**	229.603332	441.172838	221.090057	440.188822	220.598049	**G**	***687.378414***	344.192845	670.351865	335.679570	669.367849	335.187562	**6**
6	**571.283451**	286.145364	554.256902	277.632089	553.272886	277.140081	**I**	***630.356950***	315.682113	613.330401	307.168838	612.346385	306.676830	**5**
7	**686.310394**	343.658835	669.283845	335.145560	668.299829	334.653552	**D**	***517.272886***	259.140081	500.246337	250.626806	499.262321	250.134798	**4**
8	799.394458	400.200867	782.367909	391.687592	781.383893	391.195585	**L**	***402.245943***	201.626609	385.219394	193.113335			**3**
9	**913.437385**	457.222331	896.410836	448.709056	895.426820	448.217048	**N**	***289.161879***	145.084577	272.135330	136.571303			**2**
10							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



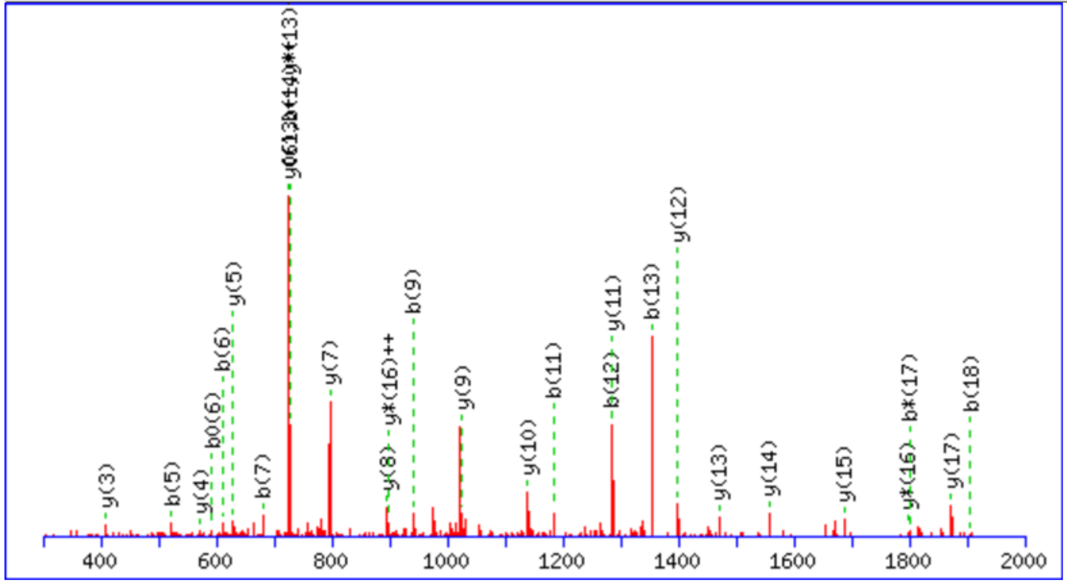
Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 31 - OPA-1 **Fraction:** OPA-1

Match to Query 14266: 2078.983448 from(1040.499000,2+)
Title: OECHL100310_05.17036.17036.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 94 **Expect:** 5.8e-008**Matches :** 29/200 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	72.044390	36.525833					**A**						
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444
4	394.183344	197.595310	377.156795	189.082035			**Q**	1814.870790	907.939033	1797.844241	899.425759	1796.860225	898.933
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904

6	**610.257965**	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383
7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867
8	794.379143	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676
15	1508.712833	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150
16	1671.776162	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	***572.282723***	286.645000	555.256174	278.131725	554.272158	277.639
17	1818.844576	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108
18	**1905.876604**	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573
19							**R**	175.118952	88.063114	158.092403	79.549840		



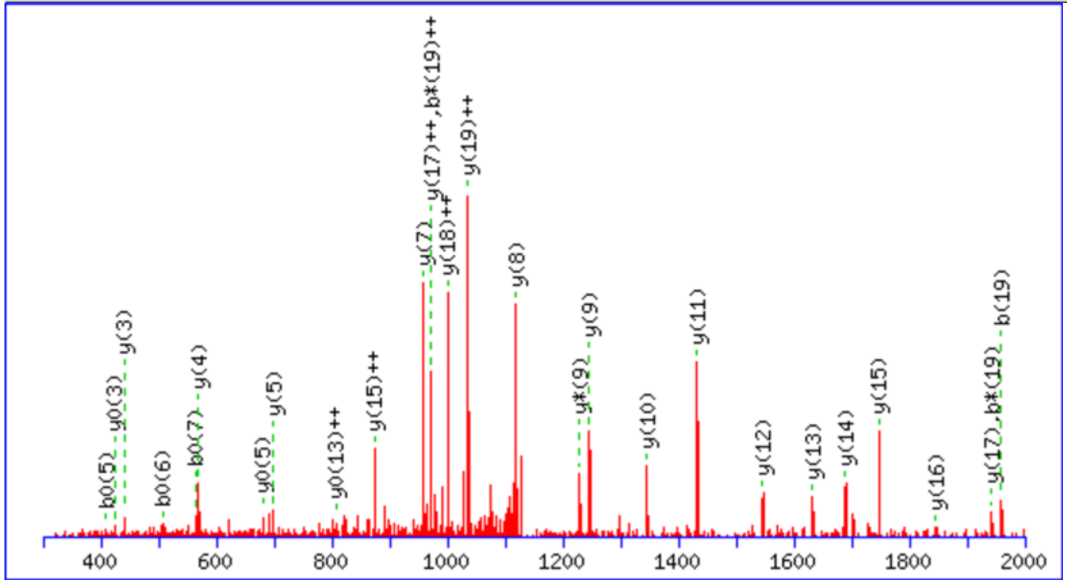
Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 31 - OPA-1 **Fraction:** OPA-1

Match to Query 15149: 2270.111448 from(1136.063000,2+)
Title: OECHL100310_05.10513.10513.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 80 **Expect:** 2.4e-006**Matches :** 28/212 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0
1	102.054955	51.531116			84.044390	42.525833	**T**					
2	201.123369	101.065322			183.112804	92.060040	**V**	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400
3	272.160483	136.583879			254.149918	127.578597	**A**	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986
4	329.181947	165.094611			311.171382	156.089329	**G**	1999.965437	1000.486357	1982.938888	991.973082	1981.954872
5	426.234711	213.620994			408.224146	204.615711	**P**	***1942.943973***	971.975625	1925.917424	963.462350	1924.933408
6	525.303125	263.155201			507.292560	254.149918	**V**	***1845.891209***	923.449243	1828.864660	914.935968	1827.880644
7	582.324589	291.665933			564.314024	282.660650	**G**	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230
8	639.346053	320.176665			621.335488	311.171382	**G**	***1689.801331***	845.404304	1672.774782	836.891029	1671.790766
9	726.378081	363.692679			708.367516	354.687396	**S**	***1632.779867***	816.893572	1615.753318	808.380297	1614.769302
10	839.462145	420.234711			821.451580	411.229428	**L**	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274
11	926.494173	463.750725			908.483608	454.745442	**S**	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210
12	1025.562587	513.284932			1007.552022	504.279649	**V**	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182
13	1153.621165	577.314221	1136.594616	568.800946	1135.610600	568.308938	**Q**	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	**C**	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	**P**	***958.474106***	479.740691	941.447557	471.227417	940.463541
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	**Y**	861.421342	431.214309	844.394793	422.701035	843.410777
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	**E**	***698.358013***	349.682645	681.331464	341.169370	680.347448
18	1830.905463	915.956370	1813.878914	907.443095	1812.894898	906.951087	**K**	***569.315420***	285.161348	552.288871	276.648074	551.304855
19	1959.948056	980.477666	1942.921507	971.964392	1941.937491	971.472384	**E**	***441.220457***	221.113867	424.193908	212.600592	423.209892

20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	**H**	312.177864	156.592570	295.151315	148.079295		
21							**R**	175.118952	88.063114	158.092403	79.549839		



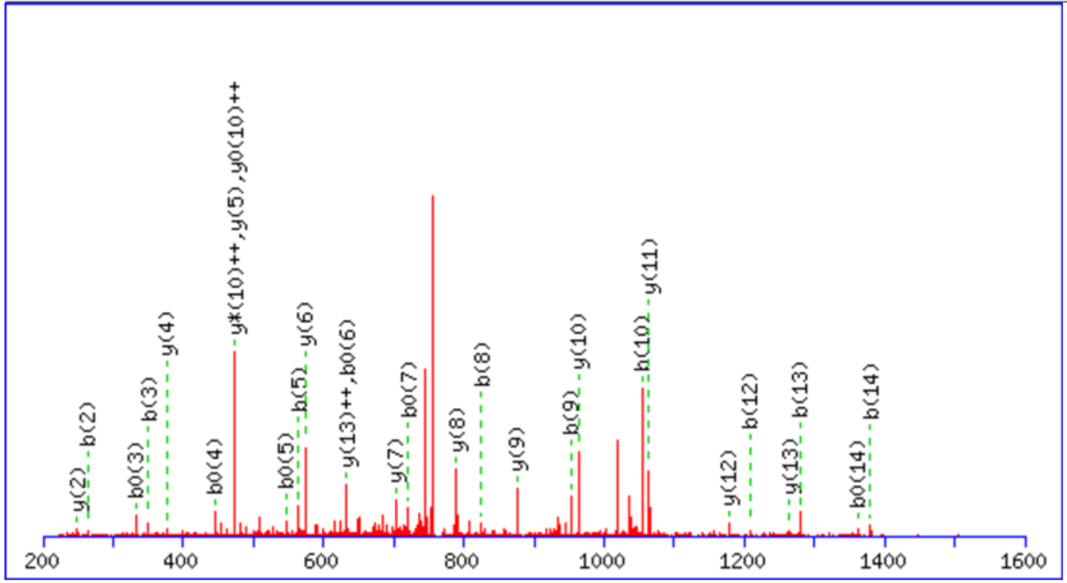
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 31 - OPA-1 **Fraction:** OPA-1

Match to Query 9977: 1525.725648 from(763.870100,2+)
Title: OECHL100310_05.10808.10808.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 94 **Expect:** 3.9e-008**Matches :** 29/150 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	116.034219	58.520748			98.023654	49.515465	**D**						
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.3515
3	***350.134661***	175.570968			332.124096	166.565686	**S**	***1264.637937***	632.822607	1247.611388	624.309332	1246.627372	623.8173

4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.3013
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.7592
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.2354
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.7194
8	***825.362488***	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.2034
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.6873
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.6581
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.1342
12	***1208.542973***	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.6078
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.0971
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.5785
15							**K**	147.112804	74.060040	130.086255	65.546765		



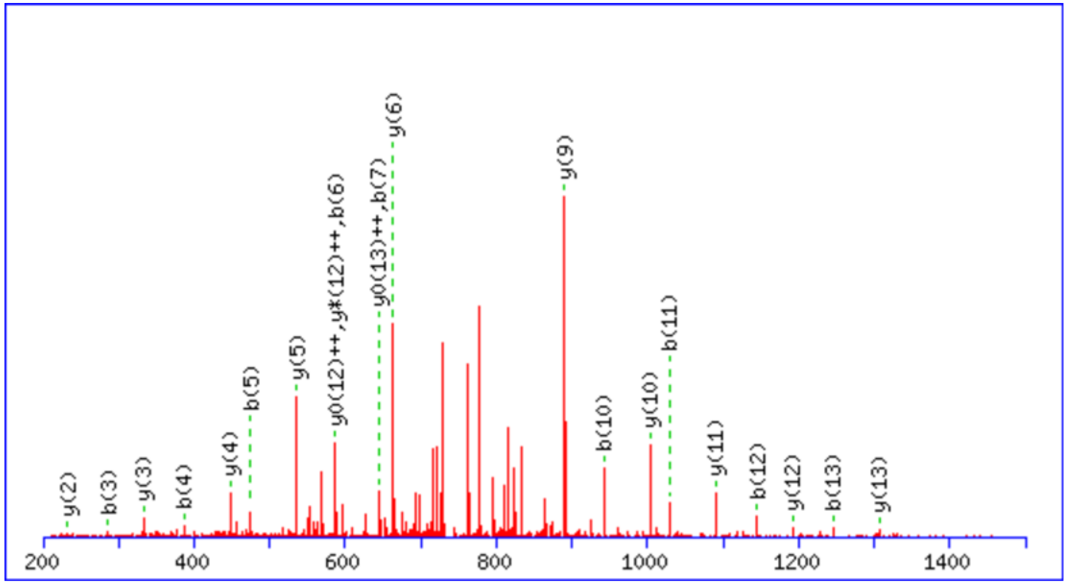
Peptide View

MS/MS Fragmentation of **GLDTSLGAVQSDTGR**

Found in **IPI00289931**, Tax_Id=9606 Gene_Symbol=MADCAM1 MADCAM1 protein
Experiment: 31 - OPA-1 **Fraction:** OPA-1

Match to Query 9423: 1475.722248 from(738.868400,2+)
Title: OECHL100310_05.11297.11297.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1475.721619**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 87 **Expect:** 3.2e-007**Matches :** 22/142 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	58.028740	29.518008					**G**						
2	171.112804	86.060040					**L**	1419.707414	710.357345	1402.680865	701.844071	1401.696849	701.3520
3	***286.139747***	143.573512			268.129182	134.568229	**D**	***1306.623350***	653.815313	1289.596801	645.302039	1288.612785	644.8100
4	***387.187426***	194.097351			369.176861	185.092069	**T**	***1191.596407***	596.301842	1174.569858	587.788567	1173.585842	587.2965
5	***474.219454***	237.613365			456.208889	228.608082	**S**	***1090.548728***	545.778002	1073.522179	537.264728	1072.538163	536.7727
6	***587.303518***	294.155397			569.292953	285.150115	**L**	***1003.516700***	502.261988	986.490151	493.748714	985.506135	493.2567
7	***644.324982***	322.666129			626.314417	313.660847	**G**	***890.432636***	445.719956	873.406087	437.206682	872.422071	436.7146
8	715.362096	358.184686			697.351531	349.179404	**A**	833.411172	417.209224	816.384623	408.695950	815.400607	408.2039
9	814.430510	407.718893			796.419945	398.713611	**V**	762.374058	381.690667	745.347509	373.177393	744.363493	372.6853
10	***942.489088***	471.748182	925.462539	463.234908	924.478523	462.742900	**Q**	***663.305644***	332.156460	646.279095	323.643186	645.295079	323.1511
11	***1029.521116***	515.264196	1012.494567	506.750922	1011.510551	506.258914	**S**	***535.247066***	268.127171	518.220517	259.613897	517.236501	259.1218
12	***1144.548059***	572.777668	1127.521510	564.264393	1126.537494	563.772385	**D**	***448.215038***	224.611157	431.188489	216.097882	430.204473	215.6058
13	***1245.595738***	623.301507	1228.569189	614.788233	1227.585173	614.296225	**T**	***333.188095***	167.097685	316.161546	158.584411	315.177530	158.0924
14	1302.617202	651.812239	1285.590653	643.298965	1284.606637	642.806957	**G**	***232.140416***	116.573846	215.113867	108.060571		
15							**R**	175.118952	88.063114	158.092403	79.549839		



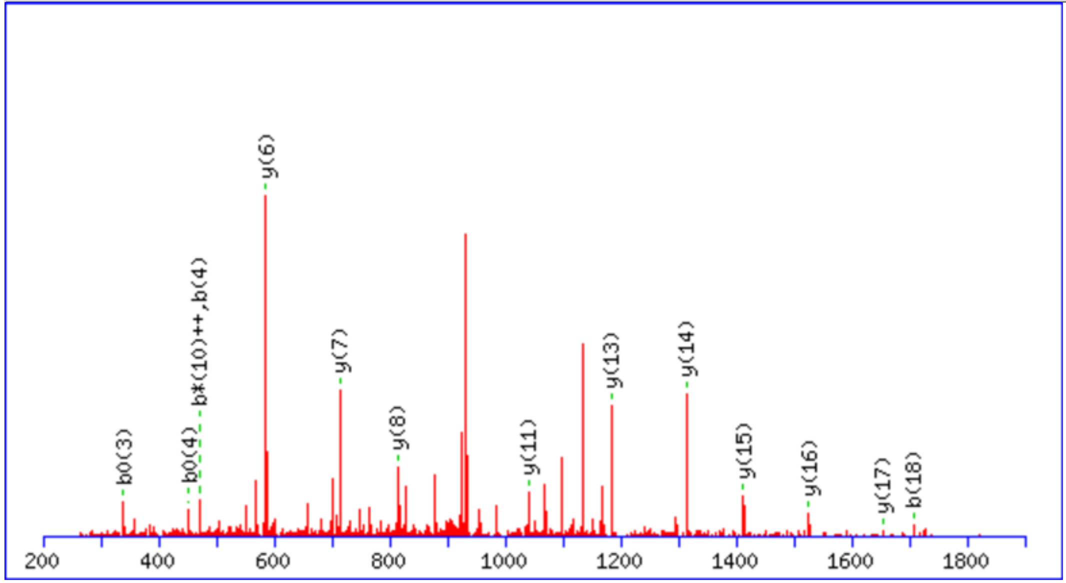
Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**
Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
Experiment: 31 - OPA-1 **Fraction:** OPA-1

Match to Query 13178: 1881.032448 from(941.523500,2+)
Title: OECHL100310_05.13675.13675.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77 **Expect:** 1e-006**Matches :** 14/208 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	130.049869	65.528572			112.039304	56.523290	E						
2	229.118283	115.062780			211.107718	106.057497	V	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.9966
3	357.176861	179.092069	340.150312	170.578794	339.166296	170.086786	Q	***1653.928246***	827.467761	1636.901697	818.954487	1635.917681	818.4624
4	**470.260925**	235.634101	453.234376	227.120826	452.250360	226.628818	L	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.4331
5	569.329339	285.168308	552.302790	276.655033	551.318774	276.163025	V	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.8911

6	698.371932	349.689604	681.345383	341.176330	680.361367	340.684322	**E**	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.3569
7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	**S**	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.8356
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	**G**	1097.642569	549.324923	1080.616020	540.811648	1079.632004	540.3196
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	**G**	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.8089
10	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	**G**	983.599641	492.303459	966.573092	483.790184	965.589076	483.2981
11	1069.552416	535.279846	1052.525867	526.766572	1051.541851	526.274564	**L**	926.578177	463.792727	909.551628	455.279452	908.567612	454.7874
12	1168.620830	584.814053	1151.594281	576.300779	1150.610265	575.808771	**V**	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.2454
13	1296.715793	648.861535	1279.689244	640.348260	1278.705228	639.856252	**K**	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.7112
14	1393.768557	697.387917	1376.742008	688.874642	1375.757992	688.382634	**P**	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.6637
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	**G**	489.277972	245.142624	472.251423	236.629349	471.267407	236.1373
16	1507.811485	754.409381	1490.784936	745.896106	1489.800920	745.404098	**G**	432.256508	216.631892	415.229959	208.118617	414.245943	207.6266
17	1594.843513	797.925395	1577.816964	789.412120	1576.832948	788.920112	**S**	375.235044	188.121160	358.208495	179.607885	357.224479	179.1158
18	**1707.927577**	854.467427	1690.901028	845.954152	1689.917012	845.462144	**L**	288.203016	144.605146	271.176467	136.091871		
19							**R**	175.118952	88.063114	158.092403	79.549839		

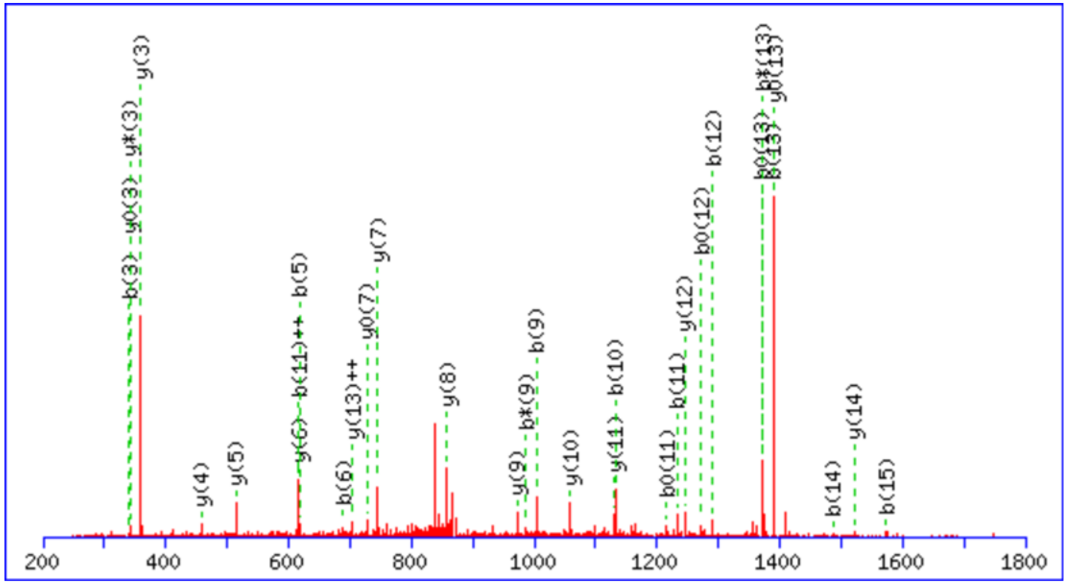


Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 31 - OPA-1 **Fraction:** OPA-1

Match to Query 12123: 1746.916048 from(874.465300,2+)
Title: OECHL100310_05.16859.16859.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 74 **Expect:** 4e-006**Matches :** 32/156 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	114.091340	57.549308					L						
2	227.175404	114.091340					L	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	***340.259468***	170.633372					I	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	503.322797	252.165036					Y	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	***618.349740***	309.678508			600.339175	300.673226	D	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018
6	***689.386854***	345.197065			671.376289	336.191782	A	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	S	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	L	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	E	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	T	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	G	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	V	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							R	175.118952	88.063114	158.092403	79.549839		



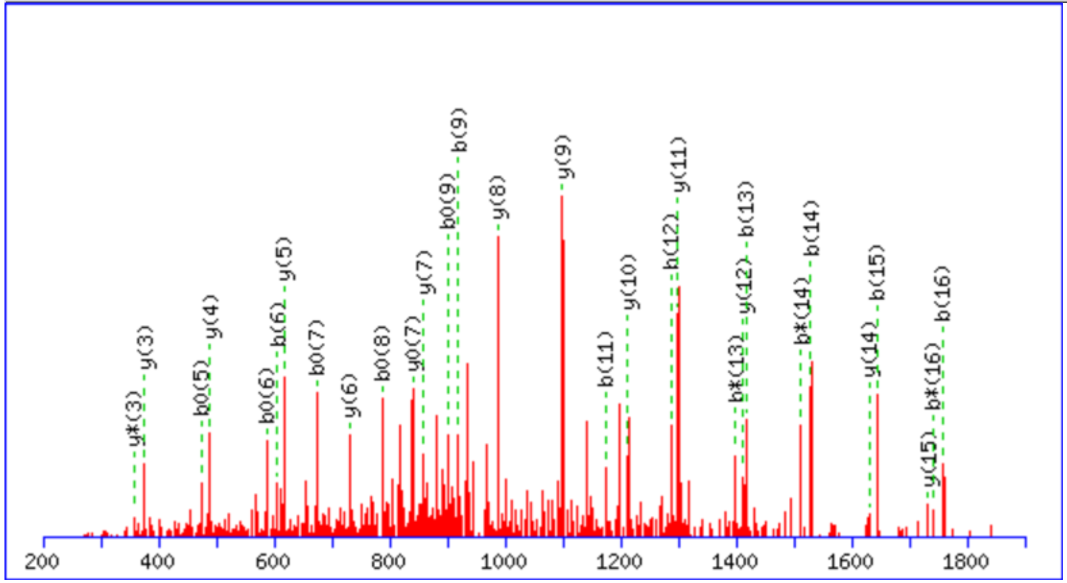
Peptide View

MS/MS Fragmentation of **TATFAISILQQIELDLK**
Found in **IPI00025491**, Tax_Id=9606 Gene_Symbol=EIF4A1;SNORA67 Eukaryotic initiation factor 4A-I
Experiment: 31 - OPA-1 **Fraction:** OPA-1

Match to Query 13334: 1903.068048 from(952.541300,2+)
Title: OECHL100310_05.21831.21831.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1903.066605**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 54 **Expect:** 0.0001**Matches :** 30/170 fragment ions using 78 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	102.054955	51.531116			84.044390	42.525833	**T**						
2	173.092069	87.049672			155.081504	78.044390	**A**	1803.026229	902.016752	1785.999680	893.503478	1785.015664	893.0114
3	274.139748	137.573512			256.129183	128.568230	**T**	***1731.989115***	866.498195	1714.962566	857.984921	1713.978550	857.4929
4	421.208162	211.107719			403.197597	202.102436	**F**	***1630.941436***	815.974356	1613.914887	807.461081	1612.930871	806.9690
5	492.245276	246.626276			474.234711	237.620993	**A**	1483.873022	742.440149	1466.846473	733.926875	1465.862457	733.4348

6	**605.329340**	303.168308			587.318775	294.163026	**I**	***1412.835908***	706.921592	1395.809359	698.408317	1394.825343	697.9163
7	692.361368	346.684322			674.350803	337.679039	**S**	***1299.751844***	650.379560	1282.725295	641.866286	1281.741279	641.3742
8	805.445432	403.226354			787.434867	394.221071	**I**	***1212.719816***	606.863546	1195.693267	598.350272	1194.709251	597.8582
9	**918.529496**	459.768386			900.518931	450.763104	**L**	***1099.635752***	550.321514	1082.609203	541.808240	1081.625187	541.3162
10	1046.588074	523.797675	1029.561525	515.284401	1028.577509	514.792393	**Q**	***986.551688***	493.779482	969.525139	485.266207	968.541123	484.7741
11	**1174.646652**	587.826964	1157.620103	579.313690	1156.636087	578.821682	**Q**	***858.493110***	429.750193	841.466561	421.236918	840.482545	420.7449
12	**1287.730716**	644.368996	1270.704167	635.855722	1269.720151	635.363714	**I**	***730.434532***	365.720904	713.407983	357.207629	712.423967	356.7156
13	**1416.773309**	708.890292	1399.746760	700.377018	1398.762744	699.885010	**E**	***617.350468***	309.178872	600.323919	300.665597	599.339903	300.1735
14	**1529.857373**	765.432324	1512.830824	756.919050	1511.846808	756.427042	**L**	***488.307875***	244.657575	471.281326	236.144301	470.297310	235.6522
15	**1644.884316**	822.945796	1627.857767	814.432522	1626.873751	813.940513	**D**	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.1102
16	**1757.968380**	879.487828	1740.941831	870.974553	1739.957815	870.482545	**L**	260.196868	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		



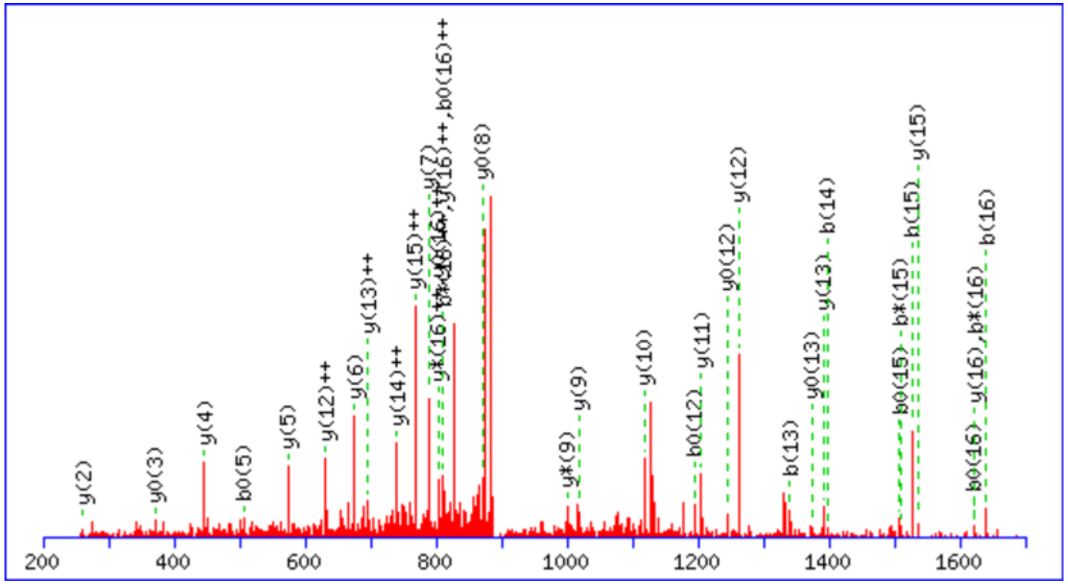
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**

Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 31 - OPA-1 **Fraction:** OPA-1

Match to Query 12436: 1784.879648 from(893.447100,2+)
Title: OECHL100310_05.7496.7496.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62 **Expect:** 9.2e-005**Matches :** 36/170 fragment ions using 74 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	164.070605	82.538940					**Y**						
2	251.102633	126.054954			233.092068	117.049672	**S**	***1622.823172***	811.915224	1605.796623	803.401950	1604.812607	802.9099
3	308.124097	154.565687			290.113532	145.560404	**G**	***1535.791144***	768.399210	1518.764595	759.885936	1517.780579	759.3939
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.8831
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.3671
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.8458
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.3351
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.8191
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.2952
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.2660
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.7421
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.2001
13	**1340.632852**	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.6762
14	**1397.654316**	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.6288
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.1180
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		



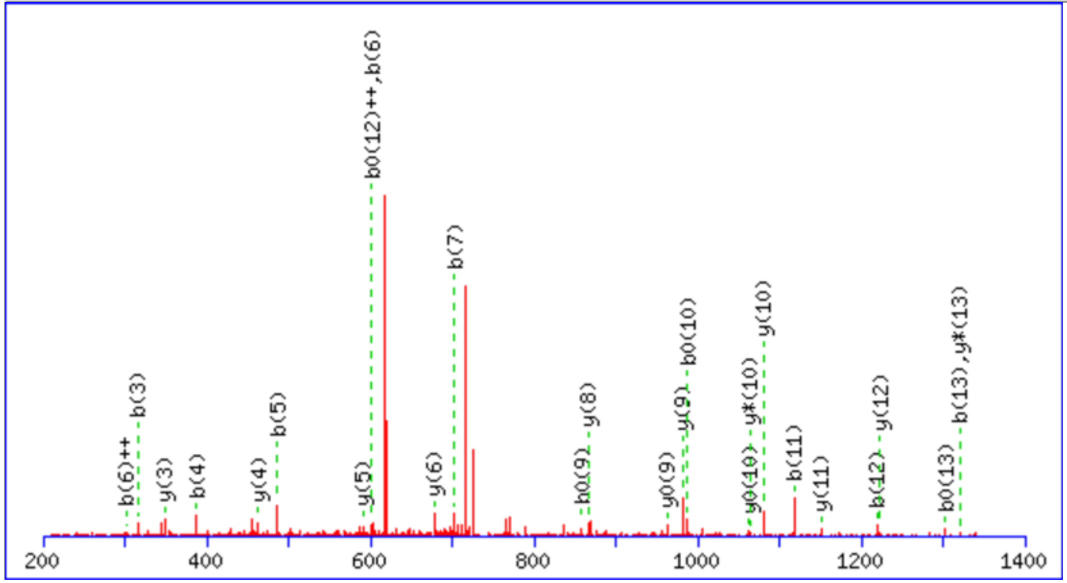
Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 31 - OPA-1 **Fraction:** OPA-1

Match to Query 9262: 1465.679248 from(733.846900,2+)
Title: OECHL100310_05.9549.9549.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 60 **Expect:** 7.7e-005**Matches :** 26/128 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	1337.643082	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	***316.113926***	158.560601	298.103361	149.555319	**A**	***1222.616139***	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	***387.151040***	194.079158	369.140475	185.073875	**A**	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	***486.219454***	243.613365	468.208889	234.608082	**V**	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**

6	***601.246397***	301.126837	583.235832	292.121554	**D**	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	**9**
7	***702.294076***	351.650676	684.283511	342.645394	**T**	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	765.398875	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	876.358132	438.682704	858.347567	429.677421	**S**	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	1005.400725	503.204001	987.390160	494.198718	**E**	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	***1118.484789***	559.746033	1100.474224	550.740750	**I**	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	***1219.532468***	610.269872	1201.521903	601.264590	**T**	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	***1320.580147***	660.793712	1302.569582	651.788429	**T**	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**



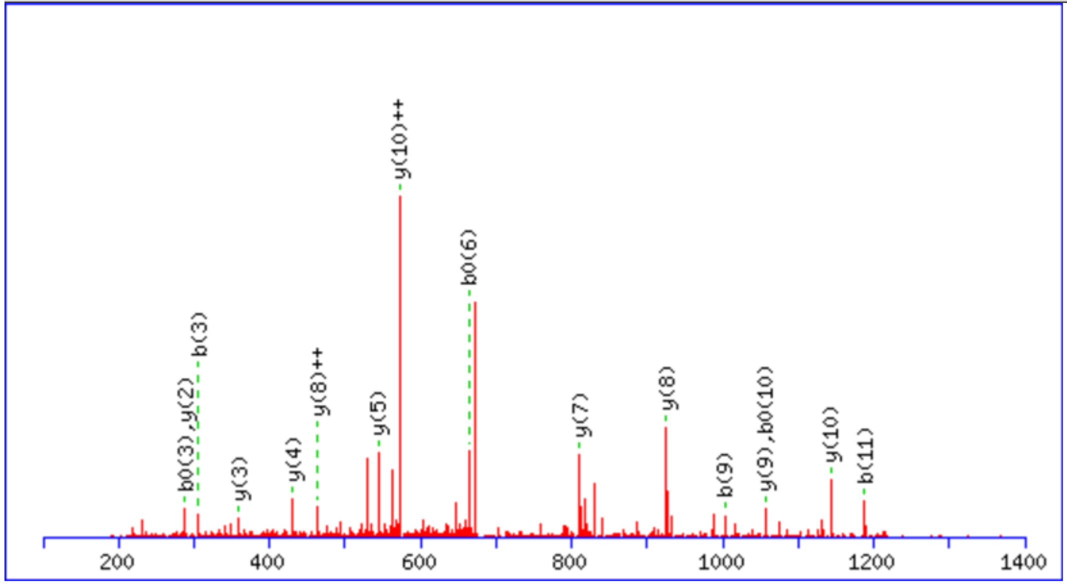
Peptide View

MS/MS Fragmentation of **AFSMDEHNAALR**
Found in **IPI00008239**, Tax_Id=9606 Gene_Symbol=GPRC5B cDNA FLJ55176, highly similar to G-protein coupled receptor family C group 5 member B
Experiment: 31 - OPA-1 **Fraction:** OPA-1

Match to Query 8248: 1360.619048 from(681.316800,2+)

Title: OECHL100310_05.9380.9380.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1360.619354**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59 **Expect:** 8.1e-005**Matches :** 16/102 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	72.044390	36.525833					**A**						
2	219.112804	110.060040					**F**	1290.589546	645.798411	1273.562997	637.285137	1272.578981	636.7931
3	**306.144832**	153.576054			288.134267	144.570772	**S**	***1143.521132***	572.264204	1126.494583	563.750929	1125.510567	563.2589
4	437.185317	219.096296			419.174752	210.091014	**M**	***1056.489104***	528.748190	1039.462555	520.234916	1038.478539	519.7429
5	552.212260	276.609768			534.201695	267.604486	**D**	***925.448619***	463.227947	908.422070	454.714673	907.438054	454.2226
6	681.254853	341.131065			663.244288	332.125782	**E**	***810.421676***	405.714476	793.395127	397.201201	792.411111	396.7091
7	818.313765	409.660521			800.303200	400.655238	**H**	681.379083	341.193179	664.352534	332.679905		
8	932.356692	466.681984	915.330143	458.168709	914.346127	457.676701	**N**	***544.320171***	272.663724	527.293622	264.150449		
9	**1003.393806**	502.200541	986.367257	493.687266	985.383241	493.195258	**A**	***430.277244***	215.642260	413.250695	207.128985		
10	1074.430920	537.719098	1057.404371	529.205824	1056.420355	528.713816	**A**	***359.240130***	180.123703	342.213581	171.610428		
11	**1187.514984**	594.261130	1170.488435	585.747856	1169.504419	585.255847	**L**	***288.203016***	144.605146	271.176467	136.091871		
12							**R**	175.118952	88.063114	158.092403	79.549839		

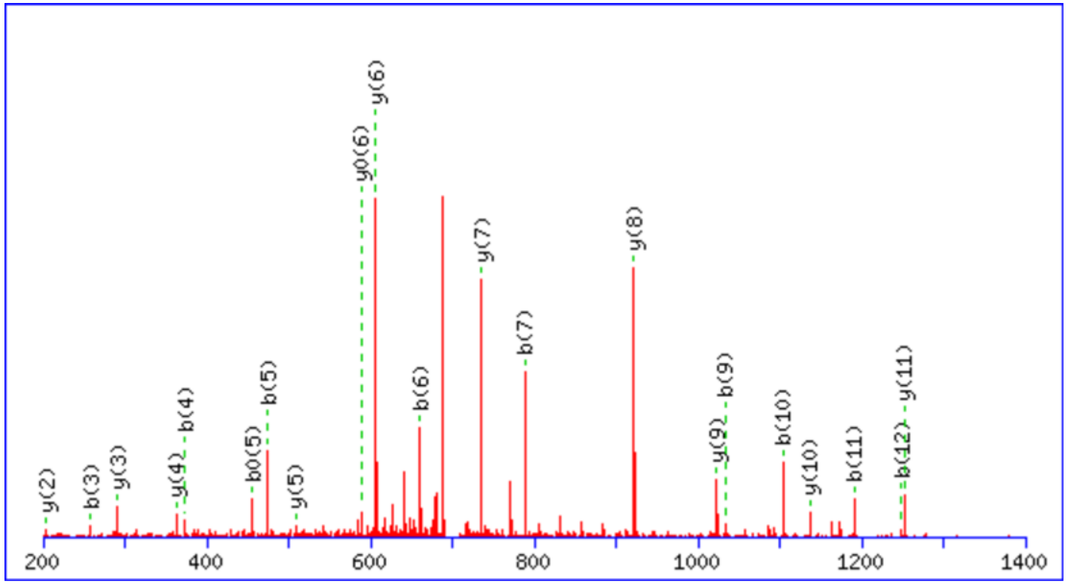


Peptide View

MS/MS Fragmentation of **AADDTWEPFASGK**
Found in **IPI00022432**, Tax_Id=9606 Gene_Symbol=TTR Transthyretin
Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 8673: 1393.615048 from(697.814800,2+)
Title: OECHL100310_03.15117.15117.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1393.615005**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77 **Expect:** 1.2e-006**Matches :** 21/112 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**13**
2	143.081504	72.044390			**A**	1323.585173	662.296225	1306.558624	653.782950	1305.574608	653.290942	**12**
3	**258.108447**	129.557862	240.097882	120.552579	**D**	***1252.548059***	626.777668	1235.521510	618.264393	1234.537494	617.772385	**11**
4	**373.135390**	187.071333	355.124825	178.066051	**D**	***1137.521116***	569.264196	1120.494567	560.750922	1119.510551	560.258914	**10**
5	**474.183069**	237.595173	456.172504	228.589890	**T**	***1022.494173***	511.750725	1005.467624	503.237450	1004.483608	502.745442	**9**
6	**660.262382**	330.634829	642.251817	321.629547	**W**	***921.446494***	461.226885	904.419945	452.713611	903.435929	452.221603	**8**
7	**789.304975**	395.156126	771.294410	386.150843	**E**	***735.367181***	368.187229	718.340632	359.673954	717.356616	359.181946	**7**
8	886.357739	443.682508	868.347174	434.677225	**P**	***606.324588***	303.665932	589.298039	295.152658	588.314023	294.660650	**6**
9	**1033.426153**	517.216715	1015.415588	508.211432	**F**	***509.271824***	255.139550	492.245275	246.626275	491.261259	246.134267	**5**
10	**1104.463267**	552.735272	1086.452702	543.729989	**A**	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	**4**
11	**1191.495295**	596.251286	1173.484730	587.246003	**S**	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	**3**
12	**1248.516759**	624.762018	1230.506194	615.756735	**G**	***204.134268***	102.570772	187.107719	94.057497			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**



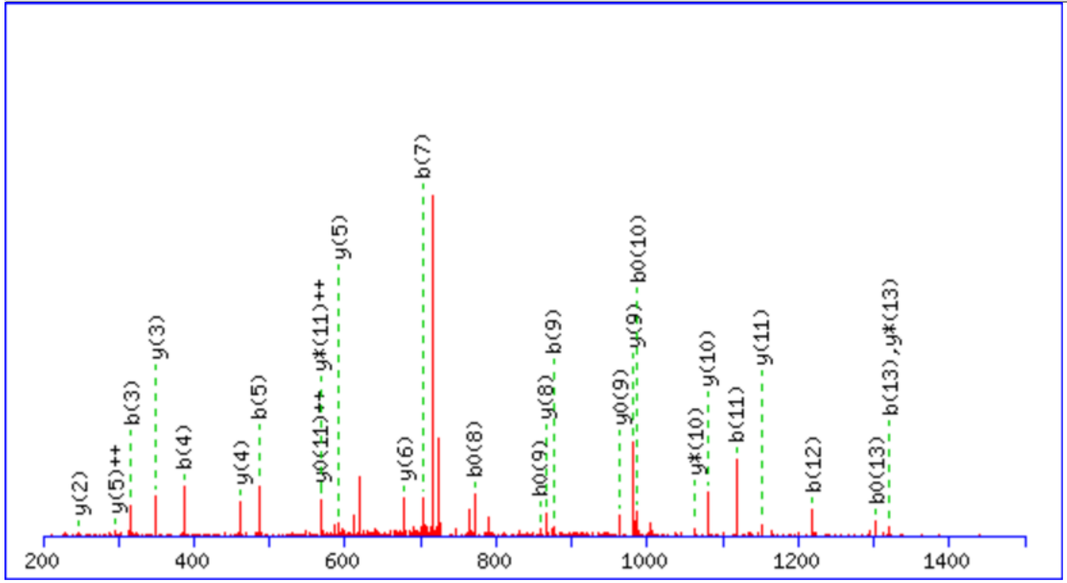
Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 9428: 1465.678448 from(733.846500,2+)
Title: OECHL100310_03.9986.9986.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications:** **N-term :** Acetyl (N-term)**Ions Score:** 73 **Expect:** 3.8e-006**Matches :** 27/128 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	1337.643082	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	***316.113926***	158.560601	298.103361	149.555319	**A**	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	***387.151040***	194.079158	369.140475	185.073875	**A**	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	***486.219454***	243.613365	468.208889	234.608082	**V**	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**

6	601.246397	301.126837	583.235832	292.121554	**D**	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	**9**
7	***702.294076***	351.650676	684.283511	342.645394	**T**	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	765.398875	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	***876.358132***	438.682704	858.347567	429.677421	**S**	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	1005.400725	503.204001	987.390160	494.198718	**E**	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	***1118.484789***	559.746033	1100.474224	550.740750	**I**	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	***1219.532468***	610.269872	1201.521903	601.264590	**T**	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	***1320.580147***	660.793712	1302.569582	651.788429	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**



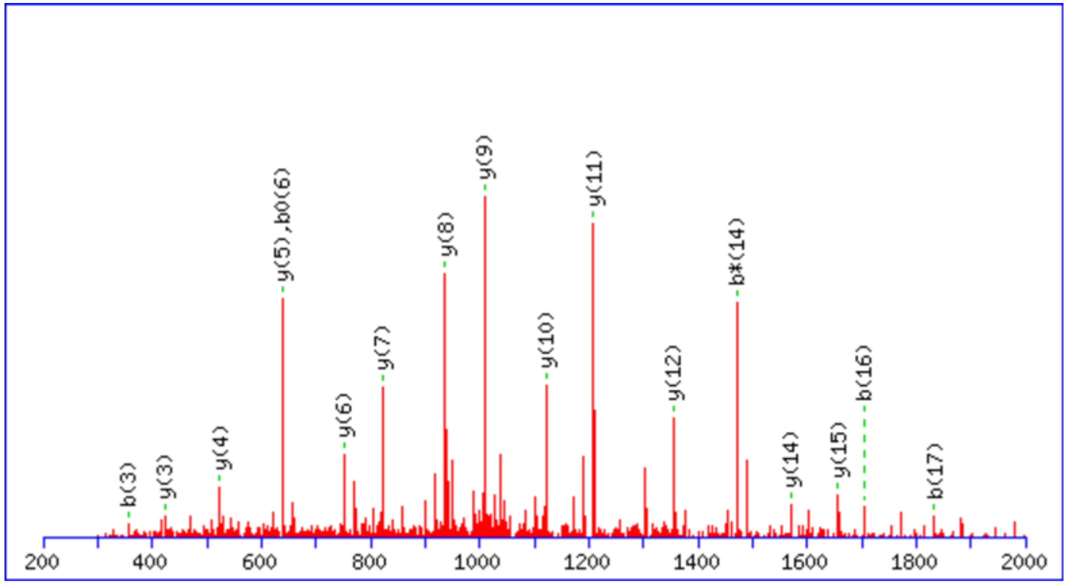
Peptide View

MS/MS Fragmentation of **LLQDSVDFSLADAINTEFK**
Found in **IPI00418471**, Tax_Id=9606 Gene_Symbol=VIM Vimentin
Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 14687: 2125.057448 from(1063.536000,2+)

Title: OECHL100310_03.20847.20847.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 2125.057907**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 114 **Expect:** 7.2e-010**Matches :** 17/202 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0+}
1	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	2012.981128	1006.994202	1995.954579	998.480928	1994.970563	997.988
3	**355.233982**	178.120629	338.207433	169.607355			**Q**	1899.897064	950.452170	1882.870515	941.938896	1881.886499	941.446
4	470.260925	235.634101	453.234376	227.120826	452.250360	226.628818	**D**	1771.838486	886.422881	1754.811937	877.909607	1753.827921	877.417
5	557.292953	279.150115	540.266404	270.636840	539.282388	270.144832	**S**	***1656.811543***	828.909410	1639.784994	820.396135	1638.800978	819.904
6	656.361367	328.684322	639.334818	320.171047	638.350802	319.679039	**V**	***1569.779515***	785.393396	1552.752966	776.880121	1551.768950	776.388
7	771.388310	386.197793	754.361761	377.684519	753.377745	377.192511	**D**	1470.711101	735.859189	1453.684552	727.345914	1452.700536	726.853
8	918.456724	459.732000	901.430175	451.218726	900.446159	450.726718	**F**	***1355.684158***	678.345717	1338.657609	669.832443	1337.673593	669.340
9	1005.488752	503.248014	988.462203	494.734739	987.478187	494.242731	**S**	***1208.615744***	604.811510	1191.589195	596.298236	1190.605179	595.806
10	1118.572816	559.790046	1101.546267	551.276772	1100.562251	550.784763	**L**	***1121.583716***	561.295496	1104.557167	552.782222	1103.573151	552.290
11	1189.609930	595.308603	1172.583381	586.795328	1171.599365	586.303320	**A**	***1008.499652***	504.753464	991.473103	496.240190	990.489087	495.748
12	1304.636873	652.822074	1287.610324	644.308800	1286.626308	643.816792	**D**	***937.462538***	469.234907	920.435989	460.721633	919.451973	460.229
13	1375.673987	688.340631	1358.647438	679.827357	1357.663422	679.335349	**A**	***822.435595***	411.721436	805.409046	403.208161	804.425030	402.716
14	1488.758051	744.882663	1471.731502	736.369389	1470.747486	735.877381	**I**	***751.398481***	376.202879	734.371932	367.689604	733.387916	367.197
15	1602.800978	801.904127	1585.774429	793.390852	1584.790413	792.898844	**N**	***638.314417***	319.660847	621.287868	311.147572	620.303852	310.655
16	**1703.848657**	852.427966	1686.822108	843.914692	1685.838092	843.422684	**T**	***524.271490***	262.639383	507.244941	254.126109	506.260925	253.634
17	**1832.891250**	916.949263	1815.864701	908.435989	1814.880685	907.943980	**E**	***423.223811***	212.115544	406.197262	203.602269	405.213246	203.110
18	1979.959664	990.483470	1962.933115	981.970196	1961.949099	981.478187	**F**	294.181218	147.594247	277.154669	139.080973		
19							**K**	147.112804	74.060040	130.086255	65.546766		



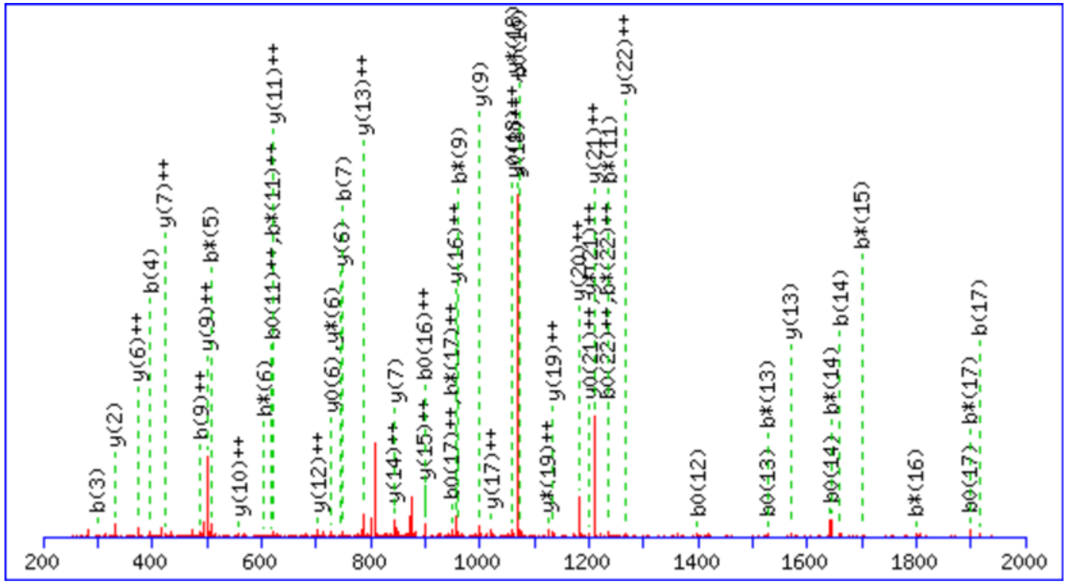
Peptide View

MS/MS Fragmentation of **QLGPQPQDIIYYEDGVVPTTDRR**
Found in **IPI00015199**, Tax_Id=9606 Gene_Symbol=CD7 T-cell antigen CD7
Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 16799: 2659.328472 from(887.450100,3+)
Title: OECHL100310_03.17368.17368.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 2659.324203**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 70 **Expect:** 2e-005**Matches :** 55/246 fragment ions using 119 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	
1	129.065854	65.036565	112.039305	56.523291			**Q**						
2	242.149918	121.578597	225.123369	113.065323			**L**	2532.272897	1266.640086	2515.246348	1258.126812	2514.262332	12
3	**299.171382**	150.089329	282.144833	141.576055			**G**	2419.188833	1210.098054	2402.162284	1201.584780	2401.178268	12
4	**396.224146**	198.615711	379.197597	190.102436			**P**	2362.167369	1181.587322	2345.140820	1173.074048	2344.156804	11
5	524.282724	262.645000	507.256175	254.131726			**Q**	2265.114605	1133.060940	2248.088056	1124.547666	2247.104040	11

6	621.335488	311.171382	604.308939	302.658108			**P**	2137.056027	1069.031651	2120.029478	1060.518377	2119.045462	10
7	**749.394066**	375.200671	732.367517	366.687397			**Q**	2040.003263	1020.505269	2022.976714	1011.991995	2021.992698	10
8	864.421009	432.714143	847.394460	424.200868	846.410444	423.708860	**D**	1911.944685	956.475980	1894.918136	947.962706	1893.934120	9
9	977.505073	489.256175	960.478524	480.742900	959.494508	480.250892	**I**	1796.917742	898.962509	1779.891193	890.449234	1778.907177	8
10	1090.589137	545.798206	1073.562588	537.284932	1072.578572	536.792924	**I**	1683.833678	842.420477	1666.807129	833.907202	1665.823113	8
11	1253.652466	627.329871	1236.625917	618.816597	1235.641901	618.324589	**Y**	**1570.749614**	785.878445	1553.723065	777.365170	1552.739049	7
12	1416.715795	708.861536	1399.689246	700.348261	1398.705230	699.856253	**Y**	1407.686285	704.346780	1390.659736	695.833506	1389.675720	6
13	1545.758388	773.382832	1528.731839	764.869558	1527.747823	764.377549	**E**	1244.622956	622.815116	1227.596407	614.301841	1226.612391	6
14	**1660.785331**	830.896304	1643.758782	822.383029	1642.774766	821.891021	**D**	1115.580363	558.293819	1098.553814	549.780545	1097.569798	5
15	1717.806795	859.407036	1700.780246	850.893761	1699.796230	850.401753	**G**	**1000.553420**	500.780348	983.526871	492.267073	982.542855	4
16	1816.875209	908.941243	1799.848660	900.427968	1798.864644	899.935960	**V**	943.531956	472.269616	926.505407	463.756341	925.521391	4
17	**1915.943623**	958.475450	1898.917074	949.962175	1897.933058	949.470167	**V**	**844.463542**	422.735409	827.436993	414.222134	826.452977	4
18	2012.996387	1007.001832	1995.969838	998.488557	1994.985822	997.996549	**P**	**745.395128**	373.201202	728.368579	364.687927	727.384563	3
19	2114.044066	1057.525671	2097.017517	1049.012396	2096.033501	1048.520388	**T**	648.342364	324.674820	631.315815	316.161545	630.331799	3
20	2215.091745	1108.049510	2198.065196	1099.536236	2197.081180	1099.044228	**T**	547.294685	274.150980	530.268136	265.637706	529.284120	2
21	2330.118688	1165.562982	2313.092139	1157.049707	2312.108123	1156.557699	**D**	446.247006	223.627141	429.220457	215.113866	428.236441	2
22	2486.219799	1243.613537	2469.193250	1235.100263	2468.209234	1234.608255	**R**	**331.220063**	166.113669	314.193514	157.600395		
23							**R**	175.118952	88.063114	158.092403	79.549839		



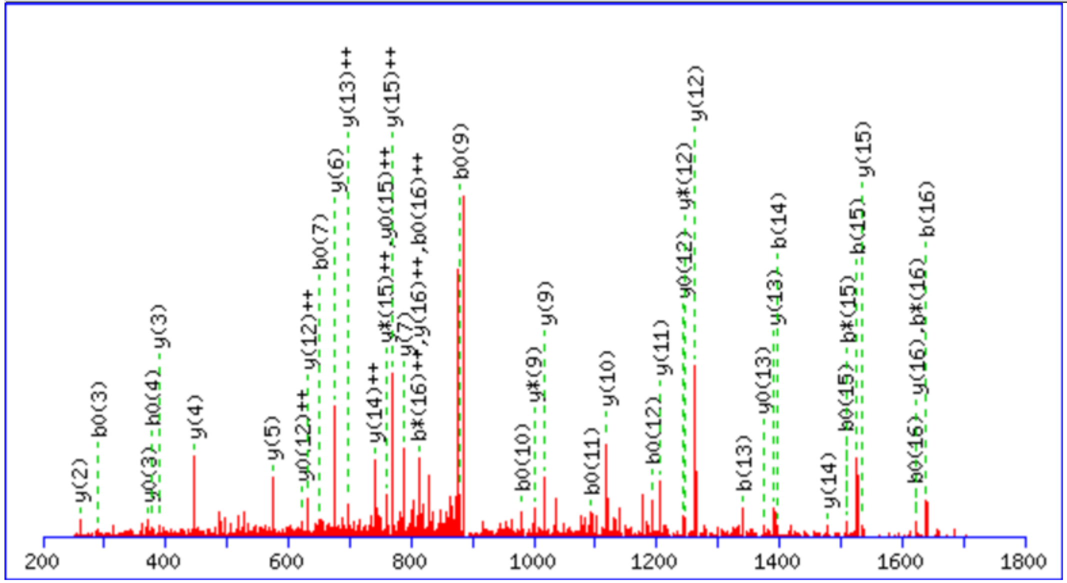
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 12652: 1784.880048 from(893.447300,2+)
Title: OECHL100310_03.7728.7728.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 80 **Expect:** 1.5e-006**Matches :** 44/170 fragment ions using 90 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	164.070605	82.538940					**Y**						
2	251.102633	126.054954			233.092068	117.049672	**S**	***1622.823172***	811.915224	1605.796623	803.401950	1604.812607	802.9099
3	308.124097	154.565687			290.113532	145.560404	**G**	***1535.791144***	768.399210	1518.764595	759.885936	1517.780579	759.3939
4	395.156125	198.081701			377.145560	189.076418	**S**	***1478.769680***	739.888478	1461.743131	731.375204	1460.759115	730.8831
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.3671

6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.8458
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.3351
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.8191
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.2952
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.2660
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.7421
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.2001
13	**1340.632852**	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.6762
14	**1397.654316**	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.6288
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	***389.239461***	195.123368	372.212912	186.610094	371.228896	186.1180
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		



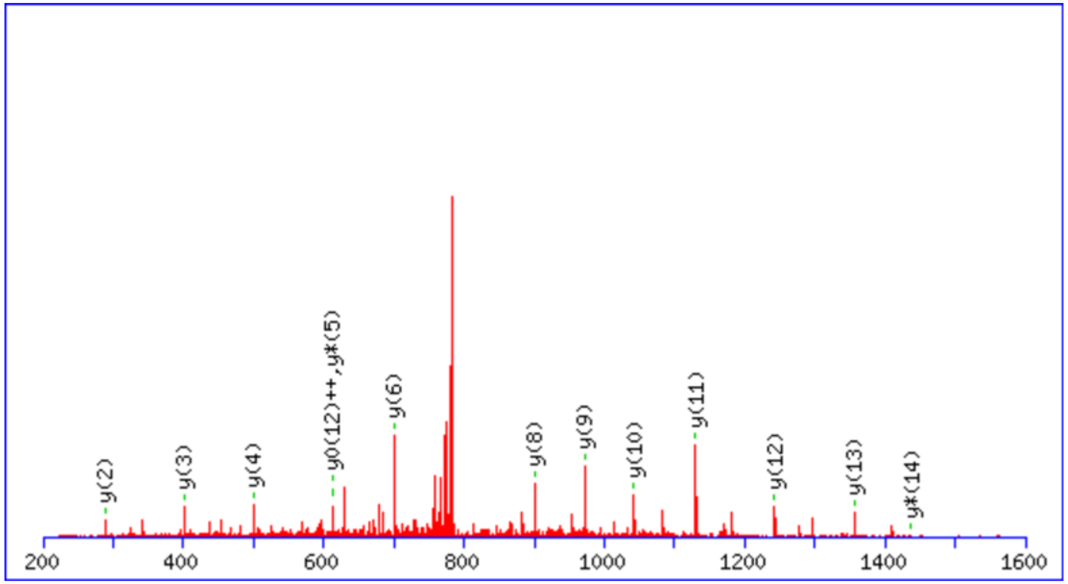
Peptide View

MS/MS Fragmentation of **QVLLSAAEAAEVILR**

Found in **IPI00297779**, Tax_Id=9606 Gene_Symbol=CCT2 T-complex protein 1 subunit beta
Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 10722: 1581.905648 from(791.960100,2+)
Title: OECHL100310_03.20896.20896.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1581.908966**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 101 **Expect:** 3e-009**Matches :** 14/152 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	129.065854	65.036565	112.039305	56.523291			**Q**						
2	228.134268	114.570772	211.107719	106.057498			**V**	1454.857706	727.932491	1437.831157	719.419217	1436.847141	718.9272
3	341.218332	171.112804	324.191783	162.599530			**L**	***1355.789292***	678.398284	1338.762743	669.885010	1337.778727	669.3930
4	454.302396	227.654836	437.275847	219.141562			**L**	***1242.705228***	621.856252	1225.678679	613.342977	1224.694663	612.8509
5	541.334424	271.170850	524.307875	262.657576	523.323859	262.165568	**S**	***1129.621164***	565.314220	1112.594615	556.800946	1111.610599	556.3089
6	612.371538	306.689407	595.344989	298.176133	594.360973	297.684125	**A**	***1042.589136***	521.798206	1025.562587	513.284931	1024.578571	512.7929
7	683.408652	342.207964	666.382103	333.694690	665.398087	333.202682	**A**	***971.552022***	486.279649	954.525473	477.766374	953.541457	477.2743
8	812.451245	406.729261	795.424696	398.215986	794.440680	397.723978	**E**	***900.514908***	450.761092	883.488359	442.247817	882.504343	441.7558
9	883.488359	442.247818	866.461810	433.734543	865.477794	433.242535	**A**	771.472315	386.239795	754.445766	377.726521	753.461750	377.2345
10	954.525473	477.766375	937.498924	469.253100	936.514908	468.761092	**A**	***700.435201***	350.721238	683.408652	342.207964	682.424636	341.7159
11	1083.568066	542.287671	1066.541517	533.774397	1065.557501	533.282389	**E**	629.398087	315.202681	612.371538	306.689407	611.387522	306.1973
12	1182.636480	591.821878	1165.609931	583.308604	1164.625915	582.816596	**V**	***500.355494***	250.681385	483.328945	242.168110		
13	1295.720544	648.363910	1278.693995	639.850636	1277.709979	639.358628	**I**	***401.287080***	201.147178	384.260531	192.633903		
14	1408.804608	704.905942	1391.778059	696.392668	1390.794043	695.900659	**L**	***288.203016***	144.605146	271.176467	136.091871		
15							**R**	175.118952	88.063114	158.092403	79.549839		



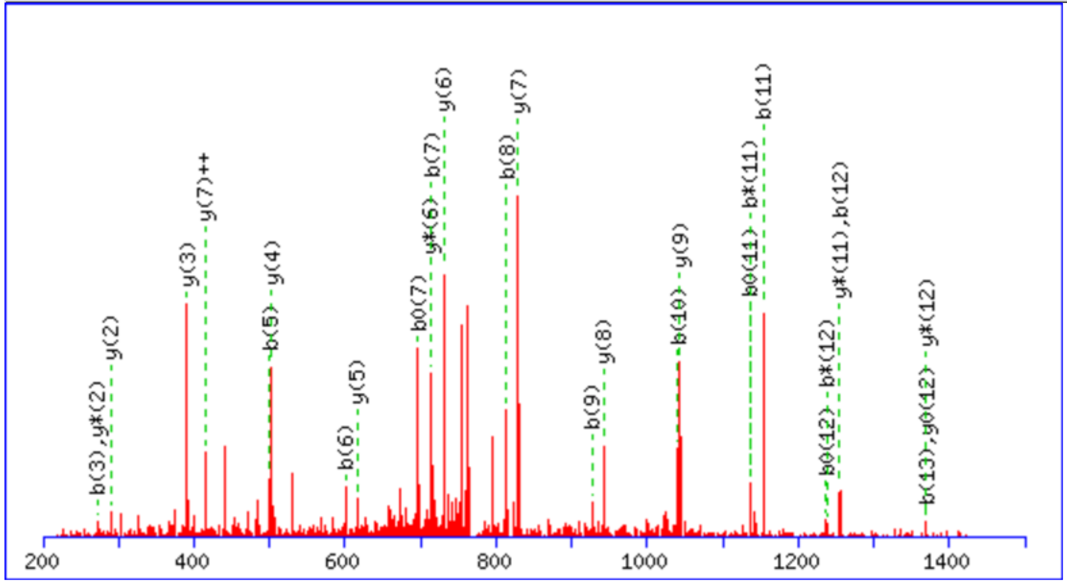
Peptide View

MS/MS Fragmentation of **GVDEVTIVNILTNR**
Found in **IPI00909509**, Tax_Id=9606 Gene_Symbol=- cDNA FLJ59138, highly similar to Annexin A2
Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 10284: 1541.841048 from(771.927800,2+)
Title: OECHL100310_03.20229.20229.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1541.841324**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63 **Expect:** 3.7e-005**Matches :** 29/132 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	58.028740	29.518008					G						
2	157.097154	79.052215					V	1485.827134	743.417205	1468.800585	734.903931	1467.816569	734.4119
3	***272.124097***	136.565687			254.113532	127.560404	D	1386.758720	693.882998	1369.732171	685.369723	1368.748155	684.8777
4	401.166690	201.086983			383.156125	192.081701	E	1271.731777	636.369526	1254.705228	627.856252	1253.721212	627.3642
5	***500.235104***	250.621190			482.224539	241.615908	V	1142.689184	571.848230	1125.662635	563.334955	1124.678619	562.8429

6	***601.282783***	301.145030			583.272218	292.139747	**T**	**1043.620770**	522.314023	1026.594221	513.800748	1025.610205	513.3087
7	***714.366847***	357.687062			696.356282	348.681779	**I**	**942.573091**	471.790183	925.546542	463.276909	924.562526	462.7849
8	***813.435261***	407.221269			795.424696	398.215986	**V**	**829.489027**	415.248151	812.462478	406.734877	811.478462	406.2428
9	***927.478188***	464.242732	910.451639	455.729458	909.467623	455.237450	**N**	**730.420613**	365.713944	713.394064	357.200670	712.410048	356.7086
10	***1040.562252***	520.784764	1023.535703	512.271489	1022.551687	511.779481	**I**	**616.377686**	308.692481	599.351137	300.179206	598.367121	299.6871
11	***1153.646316***	577.326796	1136.619767	568.813521	1135.635751	568.321513	**L**	**503.293622**	252.150449	486.267073	243.637174	485.283057	243.1451
12	***1254.693995***	627.850635	1237.667446	619.337361	1236.683430	618.845353	**T**	**390.209558**	195.608417	373.183009	187.095142	372.198993	186.6031
13	***1368.736922***	684.872099	1351.710373	676.358824	1350.726357	675.866816	**N**	**289.161879**	145.084577	272.135330	136.571303		
14							**R**	175.118952	88.063114	158.092403	79.549839		



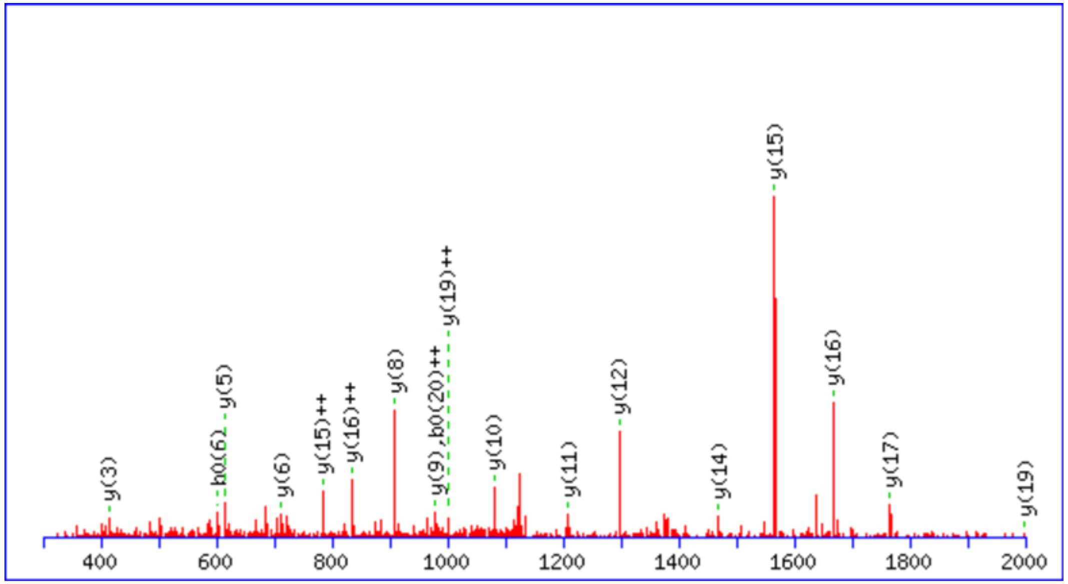
Peptide View

MS/MS Fragmentation of **TSVAYVTPGDSETAPVVTVTHR**
Found in **IPI00022039**, Tax_Id=9606 Gene_Symbol=CD84 Isoform 3 of SLAM family member 5
Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 15362: 2286.147448 from(1144.081000,2+)

Title: OECHL100310_03.12668.12668.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 2286.149231**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77 **Expect:** 3.5e-006**Matches :** 18/206 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							**22**
2	189.086983	95.047129	171.076418	86.041847	**S**	2186.108791	1093.558034	2169.082242	1085.044759	2168.098226	1084.552751	**21**
3	288.155397	144.581336	270.144832	135.576054	**V**	2099.076763	1050.042019	2082.050214	1041.528745	2081.066198	1041.036737	**20**
4	359.192511	180.099894	341.181946	171.094611	**A**	***2000.008349***	1000.507813	1982.981800	991.994538	1981.997784	991.502530	**19**
5	522.255840	261.631558	504.245275	252.626276	**Y**	1928.971235	964.989256	1911.944686	956.475981	1910.960670	955.983973	**18**
6	621.324254	311.165765	603.313689	302.160483	**V**	***1765.907906***	883.457591	1748.881357	874.944317	1747.897341	874.452309	**17**
7	722.371933	361.689605	704.361368	352.684322	**T**	***1666.839492***	833.923384	1649.812943	825.410110	1648.828927	824.918102	**16**
8	819.424697	410.215987	801.414132	401.210704	**P**	***1565.791813***	783.399545	1548.765264	774.886270	1547.781248	774.394262	**15**
9	876.446161	438.726719	858.435596	429.721436	**G**	***1468.739049***	734.873163	1451.712500	726.359888	1450.728484	725.867880	**14**
10	991.473104	496.240190	973.462539	487.234908	**D**	1411.717585	706.362431	1394.691036	697.849156	1393.707020	697.357148	**13**
11	1078.505132	539.756204	1060.494567	530.750922	**S**	***1296.690642***	648.848959	1279.664093	640.335685	1278.680077	639.843677	**12**
12	1207.547725	604.277501	1189.537160	595.272218	**E**	***1209.658614***	605.332945	1192.632065	596.819671	1191.648049	596.327663	**11**
13	1308.595404	654.801340	1290.584839	645.796058	**T**	***1080.616021***	540.811649	1063.589472	532.298374	1062.605456	531.806366	**10**
14	1379.632518	690.319897	1361.621953	681.314615	**A**	***979.568342***	490.287809	962.541793	481.774535	961.557777	481.282527	**9**
15	1476.685282	738.846279	1458.674717	729.840997	**P**	***908.531228***	454.769252	891.504679	446.255978	890.520663	445.763970	**8**
16	1575.753696	788.380486	1557.743131	779.375204	**V**	811.478464	406.242870	794.451915	397.729596	793.467899	397.237588	**7**
17	1674.822110	837.914693	1656.811545	828.909411	**V**	***712.410050***	356.708663	695.383501	348.195389	694.399485	347.703381	**6**
18	1775.869789	888.438533	1757.859224	879.433250	**T**	***613.341636***	307.174456	596.315087	298.661182	595.331071	298.169174	**5**
19	1874.938203	937.972740	1856.927638	928.967457	**V**	512.293957	256.650617	495.267408	248.137342	494.283392	247.645334	**4**
20	1975.985882	988.496579	1957.975317	979.491297	**T**	***413.225543***	207.116410	396.198994	198.603135	395.214978	198.111127	**3**
21	2113.044794	1057.026035	2095.034229	1048.020753	**H**	312.177864	156.592570	295.151315	148.079296			**2**
22					**R**	175.118952	88.063114	158.092403	79.549839			**1**



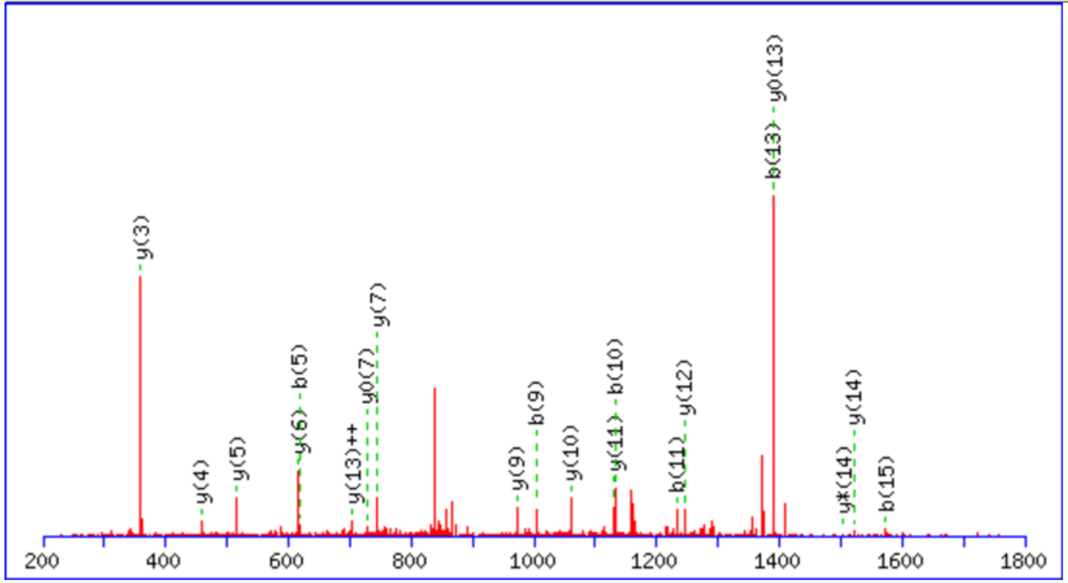
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 12362: 1746.914848 from(874.464700,2+)
Title: OECHL100310_03.16888.16888.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 72 **Expect:** 6.4e-006**Matches :** 20/156 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018

6	689.386854	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	858.467958	429.737617	841.441409	421.224343	840.457393	420.7323
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	1290.657609	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							**R**	175.118952	88.063114	158.092403	79.549839		



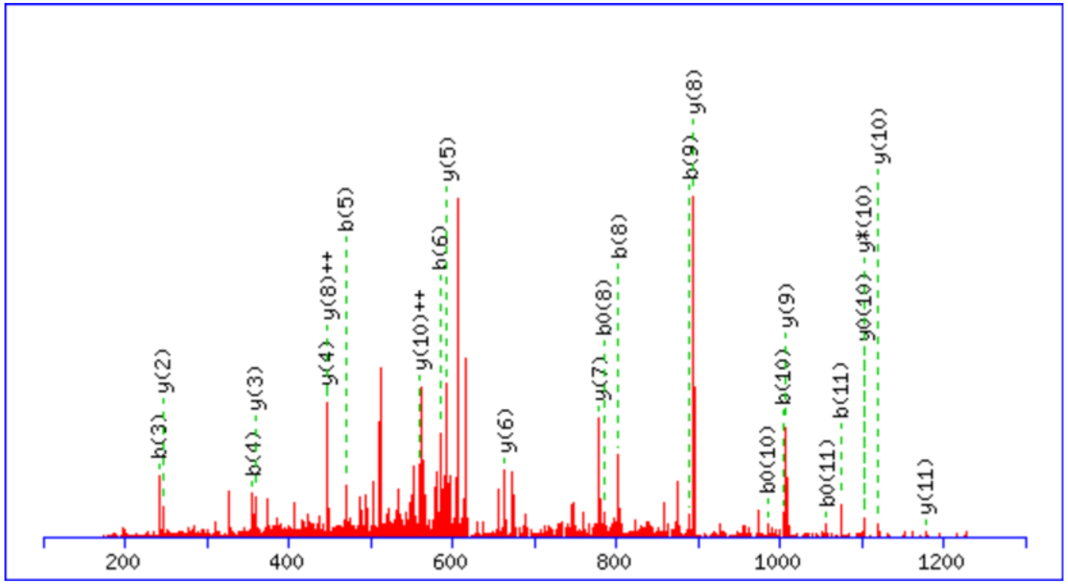
Peptide View

MS/MS Fragmentation of **AGLIDDAFSLAR**
Found in **IPI00007798**, Tax_Id=9606 Gene_Symbol=TRHDE Thyrotropin-releasing hormone-degrading ectoenzyme

Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 6999: 1247.650648 from(624.832600,2+)
Title: OECHL100310_03.19329.19329.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1247.650986**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 51 **Expect:** 0.00095**Matches :** 25/96 fragment ions using 66 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**12**
2	129.065854	65.036565			**G**	***1177.621164***	589.314220	1160.594615	580.800946	1159.610599	580.308938	**11**
3	**242.149918**	121.578597			**L**	***1120.599700***	560.803488	1103.573151	552.290214	1102.589135	551.798205	**10**
4	**355.233982**	178.120629			**I**	***1007.515636***	504.261456	990.489087	495.748182	989.505071	495.256174	**9**
5	**470.260925**	235.634101	452.250360	226.628818	**D**	***894.431572***	447.719424	877.405023	439.206150	876.421007	438.714142	**8**
6	**585.287868**	293.147572	567.277303	284.142290	**D**	***779.404629***	390.205953	762.378080	381.692678	761.394064	381.200670	**7**
7	656.324982	328.666129	638.314417	319.660847	**A**	***664.377686***	332.692481	647.351137	324.179207	646.367121	323.687199	**6**
8	**803.393396**	402.200336	785.382831	393.195054	**F**	***593.340572***	297.173924	576.314023	288.660650	575.330007	288.168642	**5**
9	**890.425424**	445.716350	872.414859	436.711068	**S**	***446.272158***	223.639717	429.245609	215.126443	428.261593	214.634435	**4**
10	**1003.509488**	502.258382	985.498923	493.253100	**L**	***359.240130***	180.123703	342.213581	171.610429			**3**
11	**1074.546602**	537.776939	1056.536037	528.771657	**A**	***246.156066***	123.581671	229.129517	115.068397			**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**



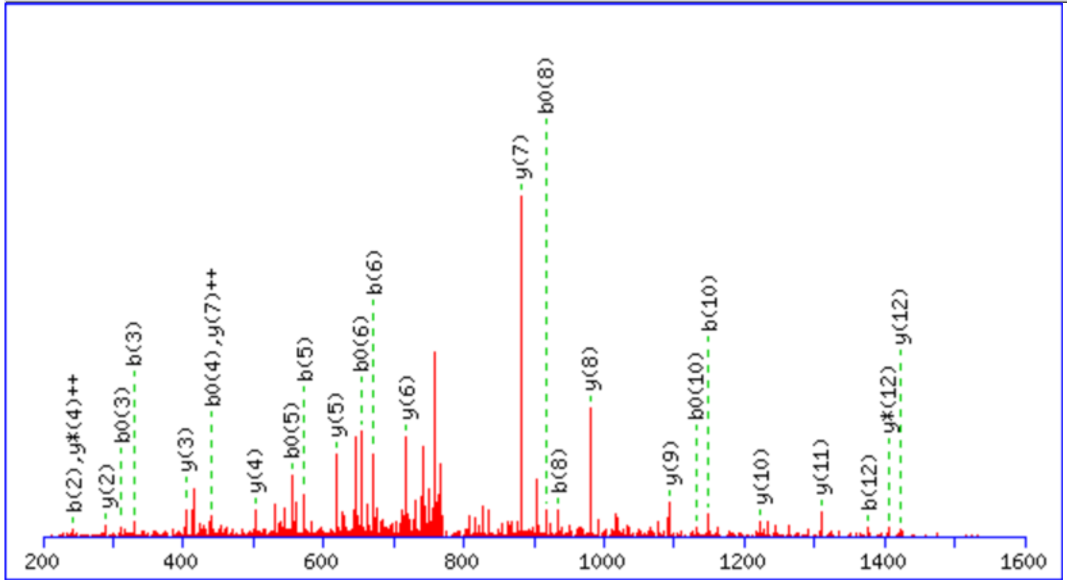
Peptide View

MS/MS Fragmentation of **ELSELVYTDVLDR**
Found in **IPI00102821**, Tax_Id=9606 Gene_Symbol=MGC29506 Isoform 1 of Proapoptotic caspase adapter protein
Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 10441: 1550.786048 from(776.400300,2+)
Title: OECHL100310_03.18643.18643.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1550.782791**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 65 **Expect:** 3.1e-005**Matches :** 27/118 fragment ions using 55 most intense peaks   (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**E**							**13**
2	**243.133933**	122.070605	225.123368	113.065322	**L**	***1422.747487***	711.877382	1405.720938	703.364107	1404.736922	702.872099	**12**
3	**330.165961**	165.586618	312.155396	156.581336	**S**	***1309.663423***	655.335350	1292.636874	646.822075	1291.652858	646.330067	**11**
4	459.208554	230.107915	441.197989	221.102633	**E**	***1222.631395***	611.819336	1205.604846	603.306061	1204.620830	602.814053	**10**
5	**572.292618**	286.649947	554.282053	277.644665	**L**	***1093.588802***	547.298039	1076.562253	538.784765	1075.578237	538.292757	**9**

6	**671.361032**	336.184154	653.350467	327.178872	**V**	***980.504738***	490.756007	963.478189	482.242733	962.494173	481.750725	**8**
7	834.424361	417.715819	816.413796	408.710536	**Y**	***881.436324***	441.221800	864.409775	432.708526	863.425759	432.216518	**7**
8	**935.472040**	468.239658	917.461475	459.234376	**T**	***718.372995***	359.690136	701.346446	351.176861	700.362430	350.684853	**6**
9	1050.498983	525.753130	1032.488418	516.747847	**D**	***617.325316***	309.166296	600.298767	300.653022	599.314751	300.161014	**5**
10	**1149.567397**	575.287337	1131.556832	566.282054	**V**	***502.298373***	251.652824	485.271824	243.139550	484.287808	242.647542	**4**
11	1262.651461	631.829369	1244.640896	622.824086	**L**	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	**3**
12	**1377.678404**	689.342840	1359.667839	680.337558	**D**	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	**2**
13					**R**	175.118952	88.063114	158.092403	79.549839			**1**



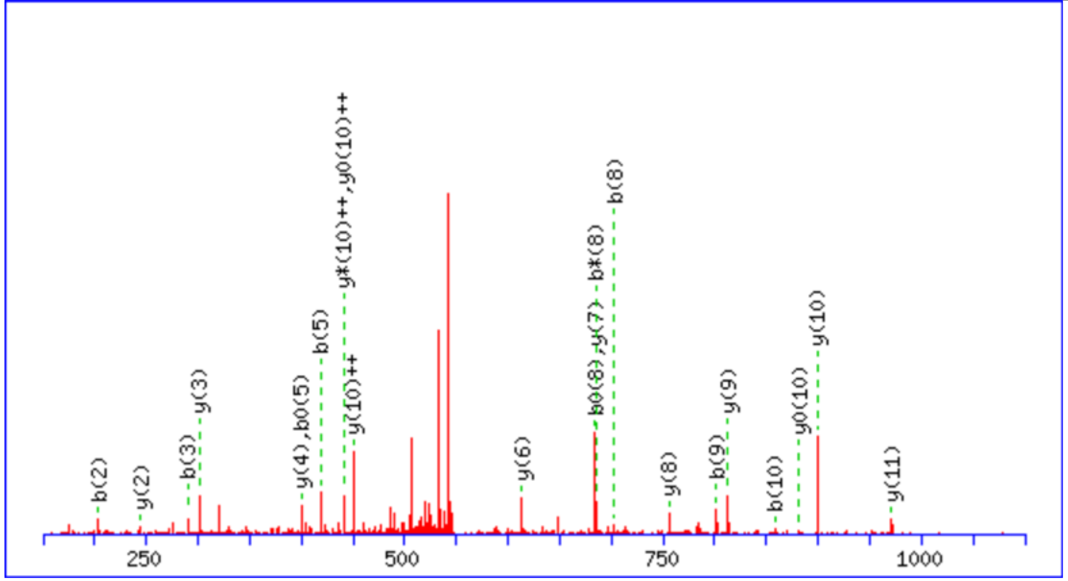
Peptide View

MS/MS Fragmentation of **MASGAANVVGPK**
Found in **IPI00334282**, Tax_Id=9606 Gene_Symbol=FAM3C Protein FAM3C
Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 4681: 1100.563248 from(551.288900,2+)
Title: OECHL100310_03.5239.5239.2.dta

Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1100.564819**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 61 **Expect:** 7e-005**Matches :** 22/98 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					**M**							**12**
2	**203.084875**	102.046075					**A**	***970.531621***	485.769448	953.505072	477.256174	952.521056	476.764166	**11**
3	**290.116903**	145.562089			272.106338	136.556807	**S**	***899.494507***	450.250891	882.467958	441.737617	881.483942	441.245609	**10**
4	347.138367	174.072821			329.127802	165.067539	**G**	***812.462479***	406.734877	795.435930	398.221603			**9**
5	**418.175481**	209.591378			400.164916	200.586096	**A**	***755.441015***	378.224145	738.414466	369.710871			**8**
6	489.212595	245.109935			471.202030	236.104653	**A**	***684.403901***	342.705588	667.377352	334.192314			**7**
7	603.255522	302.131399	586.228973	293.618124	585.244957	293.126116	**N**	***613.366787***	307.187031	596.340238	298.673757			**6**
8	**702.323936**	351.665606	685.297387	343.152331	684.313371	342.660323	**V**	499.323860	250.165568	482.297311	241.652293			**5**
9	**801.392350**	401.199813	784.365801	392.686538	783.381785	392.194530	**V**	***400.255446***	200.631361	383.228897	192.118086			**4**
10	**858.413814**	429.710545	841.387265	421.197270	840.403249	420.705262	**G**	***301.187032***	151.097154	284.160483	142.583879			**3**
11	955.466578	478.236927	938.440029	469.723652	937.456013	469.231644	**P**	***244.165568***	122.586422	227.139019	114.073147			**2**
12							**K**	147.112804	74.060040	130.086255	65.546765			**1**



Peptide View

MS/MS Fragmentation of **LFIGGLSFETTEESLR**

Found in **IPI00396378**, Tax_Id=9606 Gene_Symbol=HNRNPA2B1 Isoform B1 of Heterogeneous nuclear ribonucleoproteins A2/B1

Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 12770: 1797.914848 from(899.964700,2+)

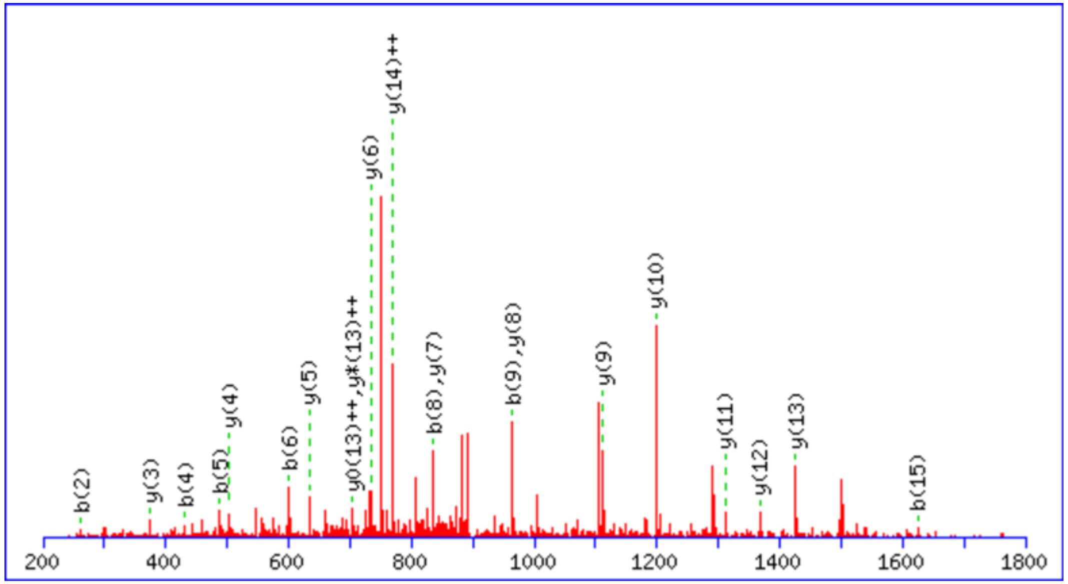
Title: OECHL100310_03.19925.19925.2.dta

Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw

Monoisotopic mass of neutral peptide Mr(calc): 1797.914871**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**

Score: 55 **Expect:** 0.00045**Matches :** 21/134 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							**16**
2	**261.159754**	131.083515			**F**	1685.838093	843.422685	1668.811544	834.909410	1667.827528	834.417402	**15**
3	374.243818	187.625547			**I**	1538.769679	769.888478	1521.743130	761.375203	1520.759114	760.883195	**14**
4	**431.265282**	216.136279			**G**	***1425.685615***	713.346446	1408.659066	704.833171	1407.675050	704.341163	**13**
5	**488.286746**	244.647011			**G**	***1368.664151***	684.835714	1351.637602	676.322439	1350.653586	675.830431	**12**
6	**601.370810**	301.189043			**L**	***1311.642687***	656.324982	1294.616138	647.811707	1293.632122	647.319699	**11**
7	688.402838	344.705057	670.392273	335.699774	**S**	***1198.558623***	599.782950	1181.532074	591.269675	1180.548058	590.777667	**10**
8	**835.471252**	418.239264	817.460687	409.233981	**F**	***1111.526595***	556.266936	1094.500046	547.753661	1093.516030	547.261653	**9**
9	**964.513845**	482.760561	946.503280	473.755278	**E**	***964.458181***	482.732729	947.431632	474.219454	946.447616	473.727446	**8**
10	1065.561524	533.284400	1047.550959	524.279117	**T**	***835.415588***	418.211432	818.389039	409.698158	817.405023	409.206150	**7**
11	1166.609203	583.808240	1148.598638	574.802957	**T**	***734.367909***	367.687593	717.341360	359.174318	716.357344	358.682310	**6**
12	1295.651796	648.329536	1277.641231	639.324253	**E**	***633.320230***	317.163753	616.293681	308.650479	615.309665	308.158471	**5**
13	1424.694389	712.850833	1406.683824	703.845550	**E**	***504.277637***	252.642457	487.251088	244.129182	486.267072	243.637174	**4**
14	1511.726417	756.366847	1493.715852	747.361564	**S**	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	**3**
15	**1624.810481**	812.908879	1606.799916	803.903596	**L**	288.203016	144.605146	271.176467	136.091871			**2**
16					**R**	175.118952	88.063114	158.092403	79.549839			**1**



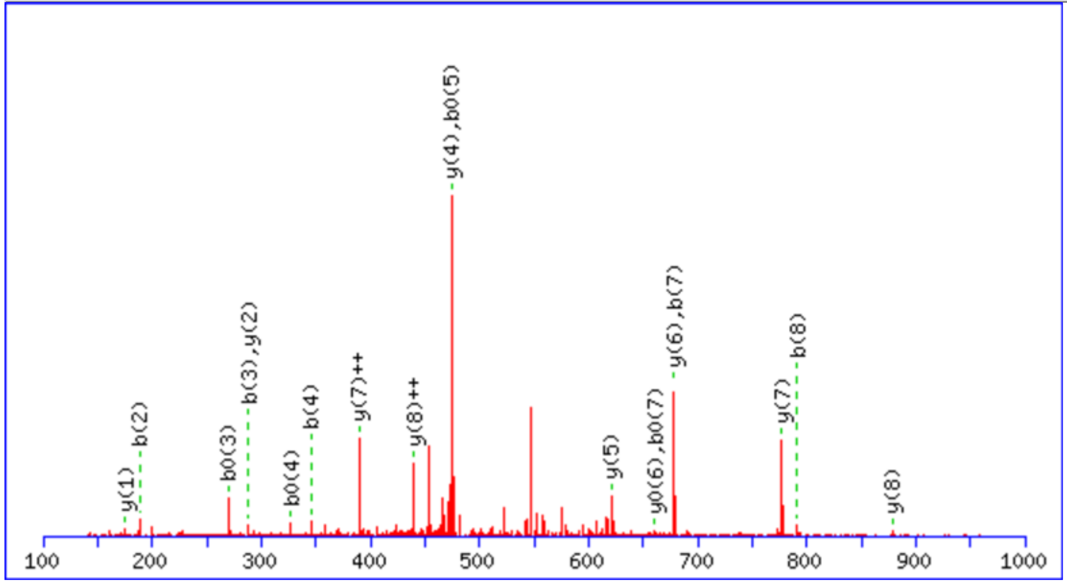
Peptide View

MS/MS Fragmentation of **STVGFDAIR**
Found in **IPI00012842**, Tax_Id=9606 Gene_Symbol=SLC26A4 Pendrin
Experiment: 16 - NOPA1 **Fraction:** NOPA1

Match to Query 2497: 964.496648 from(483.255600,2+)
Title: OECHL100310_03.11502.11502.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 964.497803**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49 **Expect:** 0.00077**Matches :** 19/74 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**9**
2	**189.086983**	95.047129	171.076418	86.041847	**T**	***878.473044***	439.740160	861.446495	431.226885	860.462479	430.734877	**8**
3	**288.155397**	144.581336	270.144832	135.576054	**V**	***777.425365***	389.216320	760.398816	380.703046	759.414800	380.211038	**7**
4	**345.176861**	173.092068	327.166296	164.086786	**G**	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	**6**
5	492.245275	246.626275	474.234710	237.620993	**F**	***621.335487***	311.171382	604.308938	302.658107	603.324922	302.166099	**5**

6	607.272218	304.139747	589.261653	295.134464	**D**	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.631892	**4**
7	**678.309332**	339.658304	660.298767	330.653021	**A**	359.240130	180.123703	342.213581	171.610428			**3**
8	**791.393396**	396.200336	773.382831	387.195053	**I**	***288.203016***	144.605146	271.176467	136.091871			**2**
9					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**

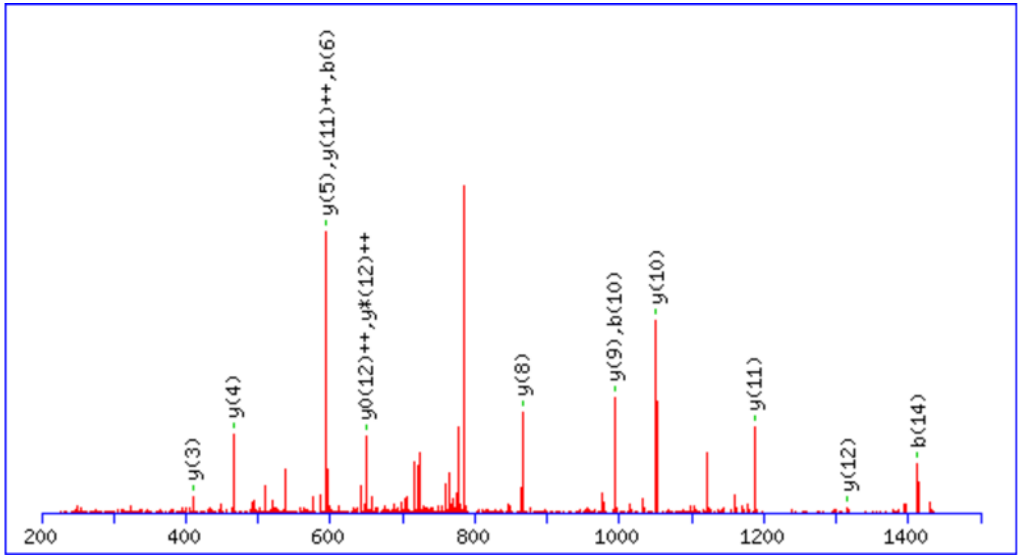


Peptide View

MS/MS Fragmentation of **ASLQHGQAAEKGPHR**
Found in **IPI00165044**, Tax_Id=9606 Gene_Symbol=FAM198B Isoform 2 of Protein ENED
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 10909: 1585.809248 from(793.911900,2+)
Title: OECHL100310_33.1719.1719.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1585.807312**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71
Expect: 1e-005**Matches :** 14/150 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	72.044390	36.525833					A							15
2	159.076418	80.041847			141.065853	71.036564	S	1515.777500	758.392388	1498.750951	749.879114	1497.766935	749.387106	14
3	272.160482	136.583879			254.149917	127.578597	L	1428.745472	714.876374	1411.718923	706.363100	1410.734907	705.871092	13
4	400.219060	200.613168	383.192511	192.099894	382.208495	191.607886	Q	***1315.661408***	658.334342	1298.634859	649.821068	1297.650843	649.329060	12
5	537.277972	269.142624	520.251423	260.629350	519.267407	260.137342	H	***1187.602830***	594.305053	1170.576281	585.791779	1169.592265	585.299771	11
6	**594.299436**	297.653356	577.272887	289.140082	576.288871	288.648074	G	***1050.543918***	525.775597	1033.517369	517.262323	1032.533353	516.770315	10
7	722.358014	361.682645	705.331465	353.169371	704.347449	352.677363	Q	***993.522454***	497.264865	976.495905	488.751591	975.511889	488.259583	9
8	793.395128	397.201202	776.368579	388.687928	775.384563	388.195920	A	***865.463876***	433.235576	848.437327	424.722302	847.453311	424.230294	8
9	864.432242	432.719759	847.405693	424.206485	846.421677	423.714477	A	794.426762	397.717019	777.400213	389.203745	776.416197	388.711737	7
10	**993.474835**	497.241056	976.448286	488.727781	975.464270	488.235773	E	723.389648	362.198462	706.363099	353.685188	705.379083	353.193180	6
11	1121.569798	561.288537	1104.543249	552.775263	1103.559233	552.283255	K	***594.347055***	297.677166	577.320506	289.163891			5
12	1178.591262	589.799269	1161.564713	581.285995	1160.580697	580.793987	G	***466.252092***	233.629684	449.225543	225.116409			4
13	1275.644026	638.325651	1258.617477	629.812377	1257.633461	629.320369	P	***409.230628***	205.118952	392.204079	196.605677			3
14	**1412.702938**	706.855107	1395.676389	698.341833	1394.692373	697.849825	H	312.177864	156.592570	295.151315	148.079295			2
15							R	175.118952	88.063114	158.092403	79.549839			1



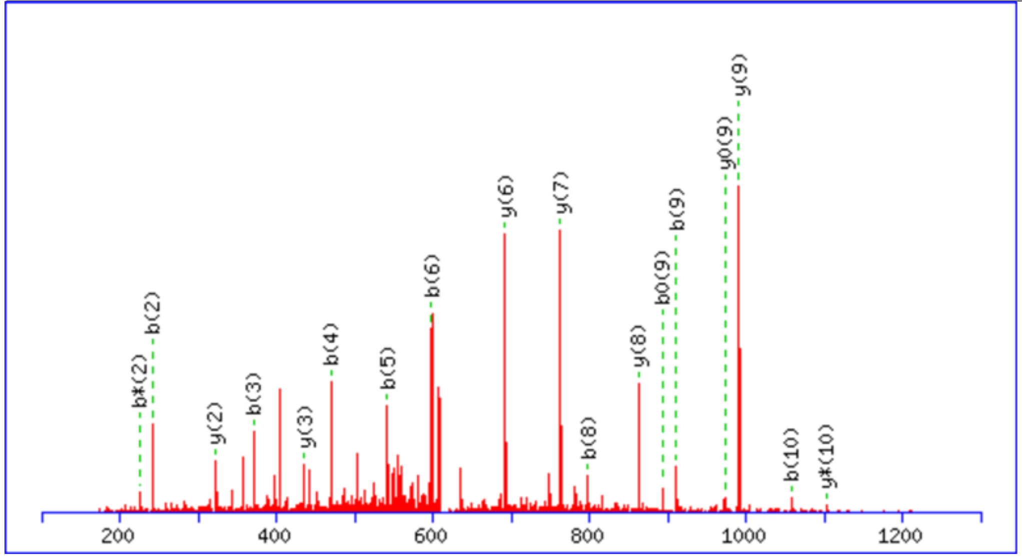
Peptide View

MS/MS Fragmentation of **IQEVAGSLIFR**
Found in **IPI00006988**, Tax_Id=9606 Gene_Symbol=RETN Resistin
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 6507: 1231.692248 from(616.853400,2+)
Title: OECHL100310_33.16799.16799.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1231.692459**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 0.00017**Matches :** 18/106 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	114.091340	57.549308					**I**							**11**
2	***242.149918***	121.578597	225.123369	113.065323			**Q**	1119.615685	560.311481	1102.589136	551.798206	1101.605120	551.306198	**10**
3	***371.192511***	186.099894	354.165962	177.586619	353.181946	177.094611	**E**	**991.557107**	496.282192	974.530558	487.768917	973.546542	487.276909	**9**
4	***470.260925***	235.634101	453.234376	227.120826	452.250360	226.628818	**V**	**862.514514**	431.760895	845.487965	423.247621	844.503949	422.755613	**8**
5	***541.298039***	271.152658	524.271490	262.639383	523.287474	262.147375	**A**	**763.446100**	382.226688	746.419551	373.713414	745.435535	373.221406	**7**
6	***598.319503***	299.663390	581.292954	291.150115	580.308938	290.658107	**G**	**692.408986**	346.708131	675.382437	338.194857	674.398421	337.702849	**6**

7	685.351531	343.179404	668.324982	334.666129	667.340966	334.174121	**S**	635.387522	318.197399	618.360973	309.684125	617.376957	309.192117	**5**
8	***798.435595***	399.721436	781.409046	391.208161	780.425030	390.716153	**L**	548.355494	274.681385	531.328945	266.168111			**4**
9	***911.519659***	456.263468	894.493110	447.750193	893.509094	447.258185	**I**	**435.271430**	218.139353	418.244881	209.626078			**3**
10	***1058.588073***	529.797675	1041.561524	521.284400	1040.577508	520.792392	**F**	**322.187366**	161.597321	305.160817	153.084046			**2**
11							**R**	175.118952	88.063114	158.092403	79.549839			**1**



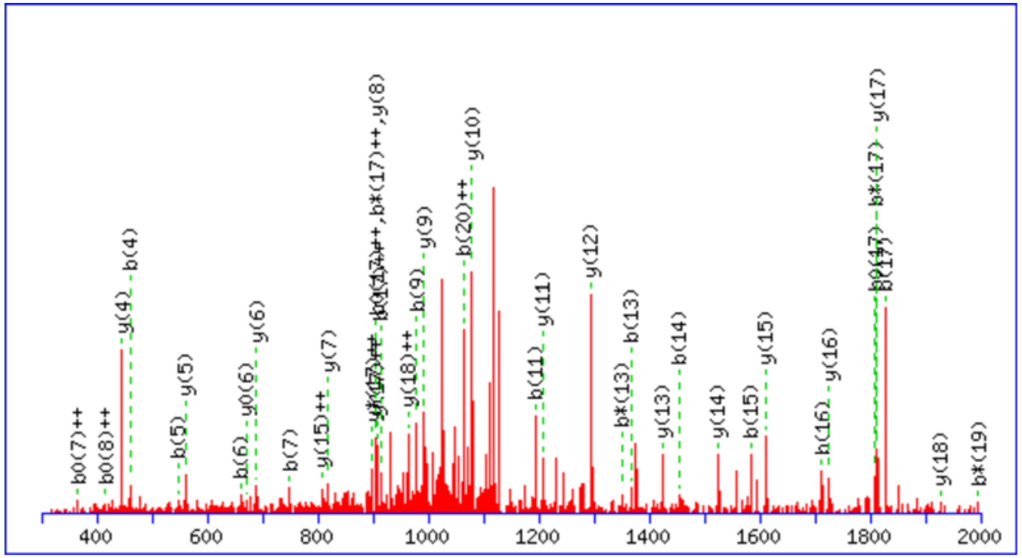
Peptide View

MS/MS Fragmentation of **SKEDSNSTESKSSSEEDGQLK**
Found in **IPI00012734**, Tax_Id=9606 Gene_Symbol=DMP1 Isoform 1 of Dentin matrix acidic phosphoprotein 1
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 15123: 2271.001448 from(1136.508000,2+)
Title: OECHL100310_33.2137.2137.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.998581**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 79
Expect: 1.2e-006**Matches :** 41/230 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}
1	88.039304	44.523290			70.028739	35.518008	**S**						

2	216.134267	108.570771	199.107718	100.057497	198.123702	99.565489	**K**	2184.973868	1092.990572	2167.947319	1084.477297	2166.963303	1083.9852
3	345.176860	173.092068	328.150311	164.578793	327.166295	164.086785	**E**	2056.878905	1028.943090	2039.852356	1020.429816	2038.868340	1019.9378
4	**460.203803**	230.605539	443.177254	222.092265	442.193238	221.600257	**D**	***1927.836312***	964.421794	1910.809763	955.908520	1909.825747	955.4165
5	**547.235831**	274.121554	530.209282	265.608279	529.225266	265.116271	**S**	***1812.809369***	906.908323	1795.782820	898.395048	1794.798804	897.9030
6	**661.278758**	331.143017	644.252209	322.629743	643.268193	322.137735	**N**	***1725.777341***	863.392309	1708.750792	854.879034	1707.766776	854.3870
7	**748.310786**	374.659031	731.284237	366.145757	730.300221	365.653749	**S**	***1611.734414***	806.370845	1594.707865	797.857571	1593.723849	797.3655
8	849.358465	425.182871	832.331916	416.669596	831.347900	416.177588	**T**	***1524.702386***	762.854831	1507.675837	754.341557	1506.691821	753.8495
9	**978.401058**	489.704167	961.374509	481.190893	960.390493	480.698885	**E**	***1423.654707***	712.330992	1406.628158	703.817717	1405.644142	703.3257
10	1065.433086	533.220181	1048.406537	524.706907	1047.422521	524.214899	**S**	***1294.612114***	647.809695	1277.585565	639.296421	1276.601549	638.8044
11	**1193.528049**	597.267663	1176.501500	588.754388	1175.517484	588.262380	**K**	***1207.580086***	604.293681	1190.553537	595.780407	1189.569521	595.2883
12	1280.560077	640.783677	1263.533528	632.270402	1262.549512	631.778394	**S**	***1079.485123***	540.246200	1062.458574	531.732925	1061.474558	531.2409
13	**1367.592105**	684.299691	1350.565556	675.786416	1349.581540	675.294408	**S**	***992.453095***	496.730186	975.426546	488.216911	974.442530	487.7249
14	**1454.624133**	727.815705	1437.597584	719.302430	1436.613568	718.810422	**S**	***905.421067***	453.214172	888.394518	444.700897	887.410502	444.2088
15	**1583.666726**	792.337001	1566.640177	783.823727	1565.656161	783.331719	**E**	***818.389039***	409.698158	801.362490	401.184883	800.378474	400.6928
16	**1712.709319**	856.858298	1695.682770	848.345023	1694.698754	847.853015	**E**	***689.346446***	345.176861	672.319897	336.663587	671.335881	336.1715
17	**1827.736262**	914.371769	1810.709713	905.858495	1809.725697	905.366487	**D**	***560.303853***	280.655565	543.277304	272.142290	542.293288	271.6502
18	1884.757726	942.882501	1867.731177	934.369227	1866.747161	933.877219	**G**	***445.276910***	223.142093	428.250361	214.628818		
19	2012.816304	1006.911790	1995.789755	998.398516	1994.805739	997.906508	**Q**	388.255446	194.631361	371.228897	186.118087		
20	2125.900368	1063.453822	2108.873819	1054.940547	2107.889803	1054.448539	**L**	260.196868	130.602072	243.170319	122.088798		
21							**K**	147.112804	74.060040	130.086255	65.546765		



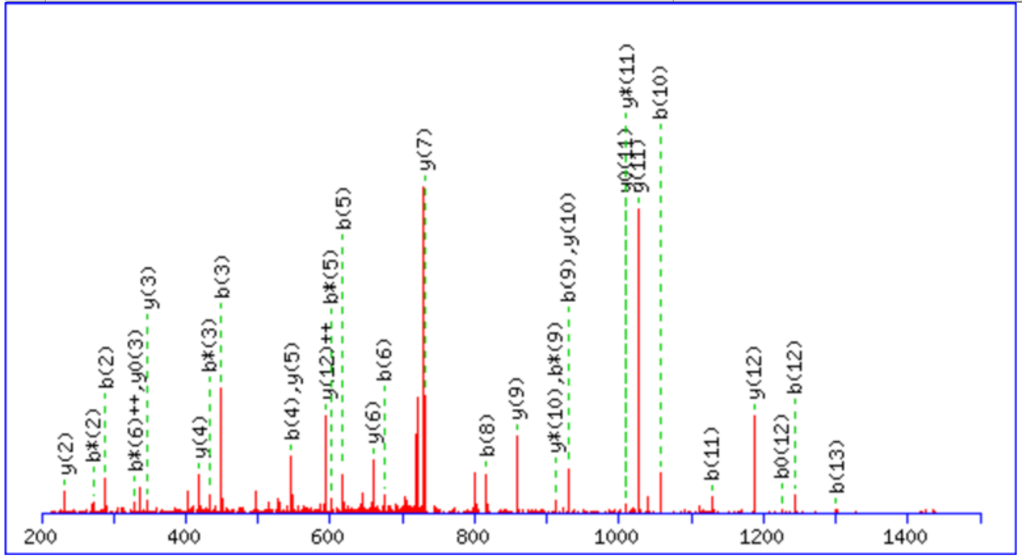
Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 9666: 1473.646048 from(737.830300,2+)
Title: OECHL100310_33.7572.7572.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 80
Expect: 4.6e-007**Matches :** 32/128 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	161.037925	81.022600					**C**							**14**
2	***289.096503***	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.809312	**13**
3	***449.127152***	225.067214	432.100603	216.553940			**C**	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.780023	**12**
4	***546.179916***	273.593596	529.153367	265.080322			**P**	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.764698	**11**
5	***617.217030***	309.112153	600.190481	300.598879			**A**	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.238316	**10**
6	***674.238494***	337.622885	657.211945	329.109611			**G**	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.719759	**9**

7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
8	***816.312722***	408.659999	799.286173	400.146725			**A**	**730.384229**	365.695753	713.357680	357.182478	712.373664	356.690470	**7**
9	***929.396786***	465.202031	912.370237	456.688757			**L**	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.171913	**6**
10	***1057.455364***	529.231320	1040.428815	520.718046			**Q**	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.629881	**5**
11	***1128.492478***	564.749877	1111.465929	556.236603			**A**	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.600592	**4**
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	**347.167359**	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
13	***1300.540885***	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	**232.140416**	116.573846	215.113867	108.060571			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



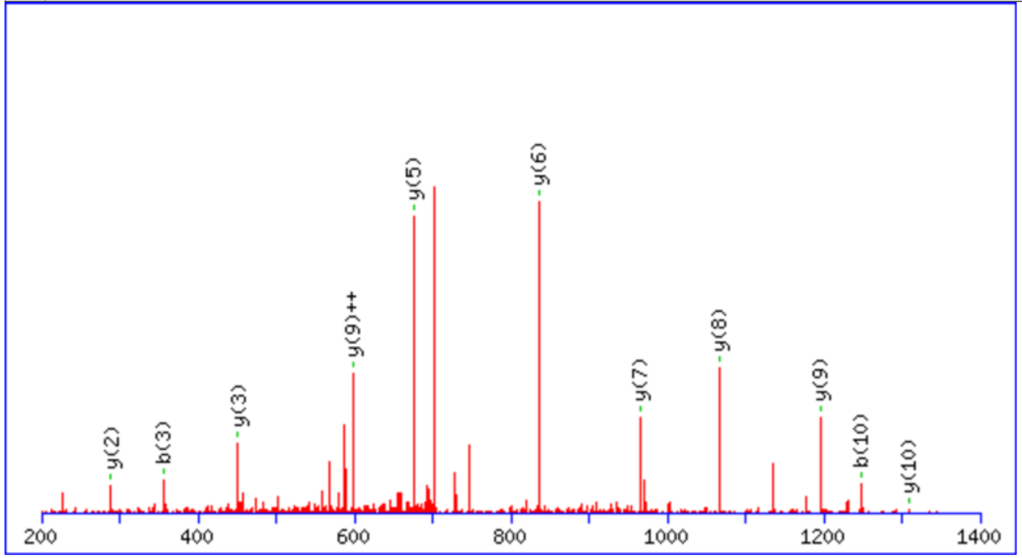
Peptide View

MS/MS Fragmentation of **LLETECPQYIR**
Found in **IPI00007047**, Tax_Id=9606 Gene_Symbol=S100A8 Protein S100-A8
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 9007: 1420.703448 from(711.359000,2+)
Title: OECHL100310_33.12328.12328.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1420.702026**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 79

Expect: 1.4e-006**Matches :** 11/90 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	114.091340	57.549308					**L**							**11**
2	227.175404	114.091340					**L**	***1308.625265***	654.816271	1291.598716	646.302996	1290.614700	645.810988	**10**
3	**356.217997**	178.612637			338.207432	169.607354	**E**	***1195.541201***	598.274239	1178.514652	589.760964	1177.530636	589.268956	**9**
4	457.265676	229.136476			439.255111	220.131194	**T**	***1066.498608***	533.752942	1049.472059	525.239668	1048.488043	524.747660	**8**
5	586.308269	293.657773			568.297704	284.652490	**E**	***965.450929***	483.229103	948.424380	474.715828	947.440364	474.223820	**7**
6	746.338918	373.673097			728.328353	364.667815	**C**	***836.408336***	418.707806	819.381787	410.194531			**6**
7	843.391682	422.199479			825.381117	413.194197	**P**	***676.377687***	338.692481	659.351138	330.179207			**5**
8	971.450260	486.228768	954.423711	477.715494	953.439695	477.223486	**Q**	579.324923	290.166099	562.298374	281.652825			**4**
9	1134.513589	567.760433	1117.487040	559.247158	1116.503024	558.755150	**Y**	***451.266345***	226.136810	434.239796	217.623536			**3**
10	**1247.597653**	624.302465	1230.571104	615.789190	1229.587088	615.297182	**I**	***288.203016***	144.605146	271.176467	136.091871			**2**
11							**R**	175.118952	88.063114	158.092403	79.549839			**1**



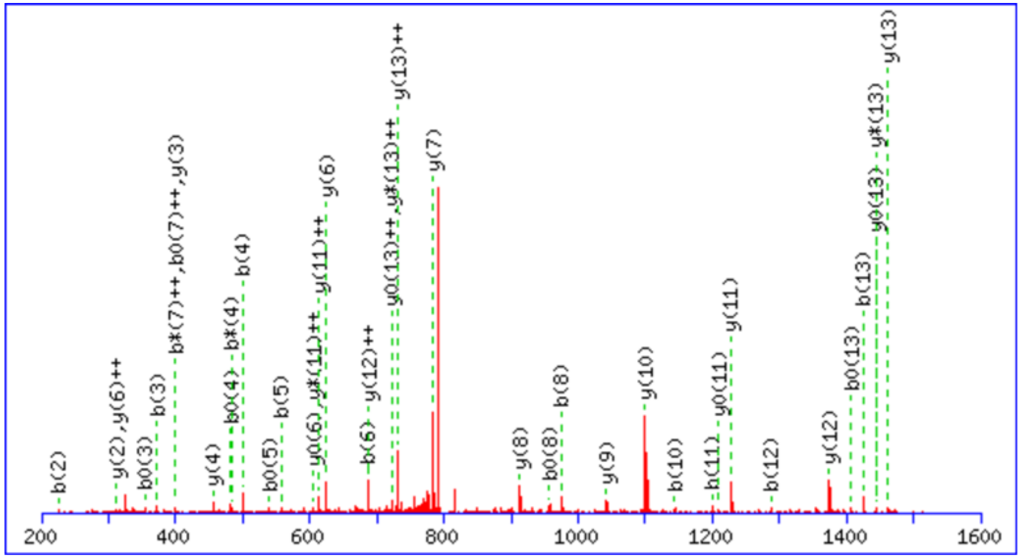
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**

Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 10991: 1597.707448 from(799.861000,2+)
Title: OECHL100310_33.2165.2165.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 69
Expect: 8.9e-006**Matches :** 40/144 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	138.066188	69.536732					**H**							**14**
2	**225.098216**	113.052746			207.087651	104.047463	**S**	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.325325	**13**
3	**372.166630**	186.586953			354.156065	177.581671	**F**	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.809311	**12**
4	**500.261593**	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	**11**
5	**557.283057**	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	**10**
6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	***1042.437069***	521.722173	1025.410520	513.208898	1024.426504	512.716890	**9**
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	527.268470	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	***312.177864***	156.592570	295.151315	148.079295			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



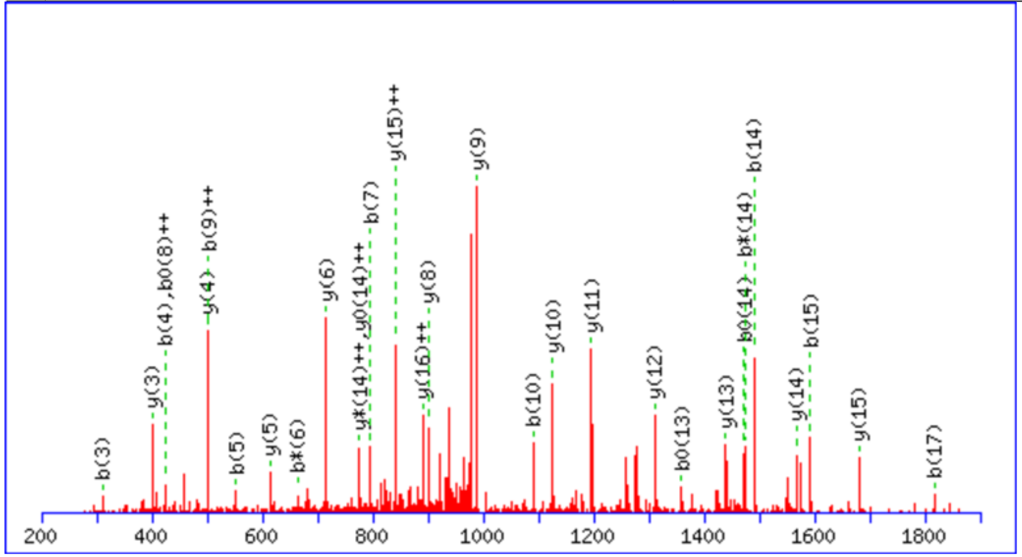
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 13993: 1990.024448 from(996.019500,2+)
Title: OECHL100310_33.9859.9859.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 2.8e-006**Matches :** 30/186 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	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	1779.934789	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	**424.255445**	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	**552.314023**	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	680.372601	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**

7	**795.399544**	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	1276.628040	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	814.478130	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510			**3**
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**

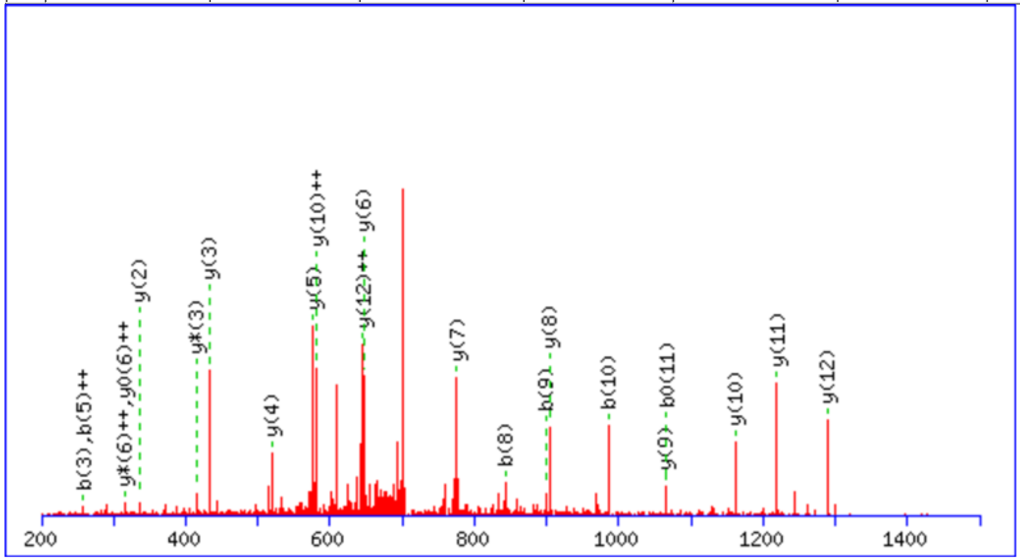


Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 8945: 1416.624248 from(709.319400,2+)
Title: OECHL100310_33.1970.1970.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 88
Expect: 1.1e-007**Matches :** 22/128 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							**13**
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	**12**
3	**257.160817**	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	**11**
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	**10**
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	**9**
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	**8**
7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	**899.403979**	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

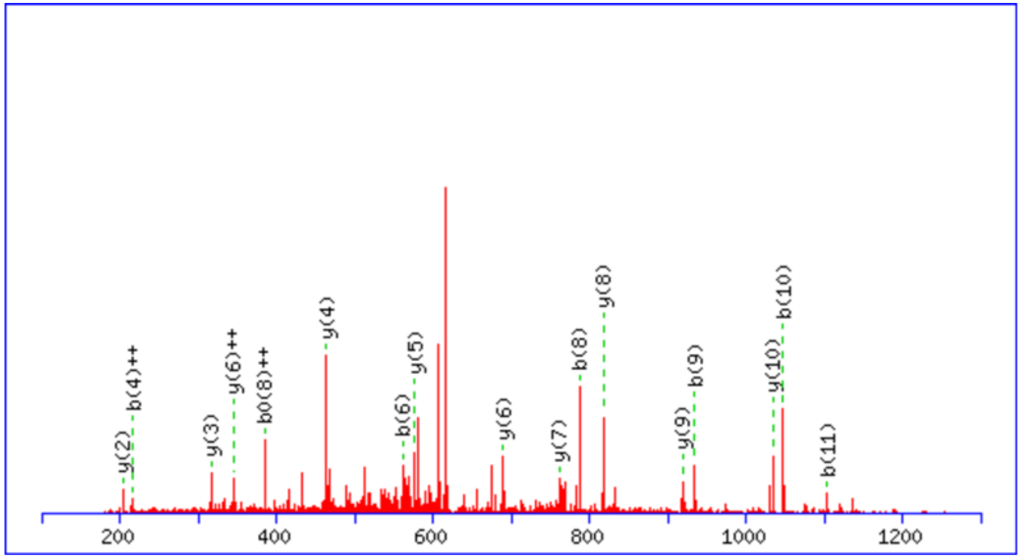


Peptide View

MS/MS Fragmentation of **DTDTGALLFIGK**
Found in **IPI00006114**, Tax_Id=9606 Gene_Symbol=SERPINF1 Pigment epithelium-derived factor
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 6757: 1249.654248 from(625.834400,2+)
Title: OECHL100310_33.17588.17588.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1249.655426**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 84
Expect: 3.4e-007**Matches :** 18/94 fragment ions using 22 most intense peaks (help)

#	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	116.034219	58.520748	98.023654	49.515465	**D**							**12**
2	**217.081898**	109.044587	199.071333	100.039304	**T**	1135.635753	568.321514	1118.609204	559.808240	1117.625188	559.316232	**11**
3	332.108841	166.558058	314.098276	157.552776	**D**	***1034.588074***	517.797675	1017.561525	509.284401	1016.577509	508.792393	**10**
4	433.156520	217.081898	415.145955	208.076616	**T**	***919.561131***	460.284203	902.534582	451.770929	901.550566	451.278921	**9**
5	490.177984	245.592630	472.167419	236.587347	**G**	***818.513452***	409.760364	801.486903	401.247089			**8**
6	**561.215098**	281.111187	543.204533	272.105905	**A**	***761.491988***	381.249632	744.465439	372.736357			**7**
7	674.299162	337.653219	656.288597	328.647937	**L**	***690.454874***	345.731075	673.428325	337.217800			**6**
8	**787.383226**	394.195251	769.372661	385.189969	**L**	***577.370810***	289.189043	560.344261	280.675768			**5**
9	**934.451640**	467.729458	916.441075	458.724176	**F**	***464.286746***	232.647011	447.260197	224.133736			**4**
10	**1047.535704**	524.271490	1029.525139	515.266207	**I**	***317.218332***	159.112804	300.191783	150.599529			**3**
11	**1104.557168**	552.782222	1086.546603	543.776939	**G**	***204.134268***	102.570772	187.107719	94.057497			**2**
12					**K**	147.112804	74.060040	130.086255	65.546765			**1**



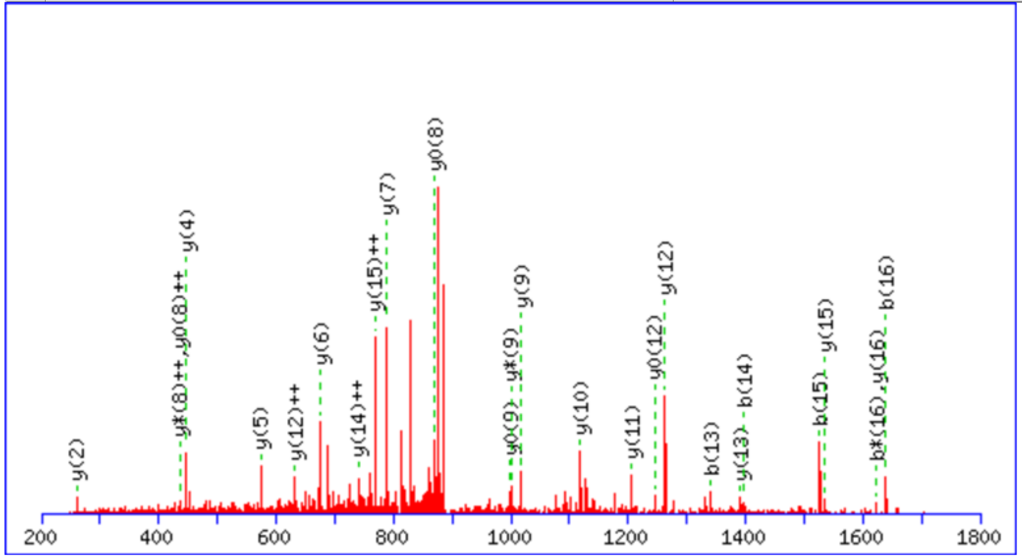
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 12757: 1784.882648 from(893.448600,2+)
Title: OECHL100310_33.7708.7708.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 81
Expect: 1.2e-006**Matches :** 26/170 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	164.070605	82.538940					**Y**							**17**
2	251.102633	126.054954			233.092068	117.049672	**S**	***1622.823172***	811.915224	1605.796623	803.401950	1604.812607	802.909941	**16**
3	308.124097	154.565687			290.113532	145.560404	**G**	***1535.791144***	768.399210	1518.764595	759.885936	1517.780579	759.393928	**15**
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.883195	**14**
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.367182	**13**
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.845885	**12**

7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.335153	**11**
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.819139	**10**
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.295299	**9**
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.266010	**8**
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.742171	**7**
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.200139	**6**
13	**1340.632852**	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.676299	**5**
14	**1397.654316**	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	**4**
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**

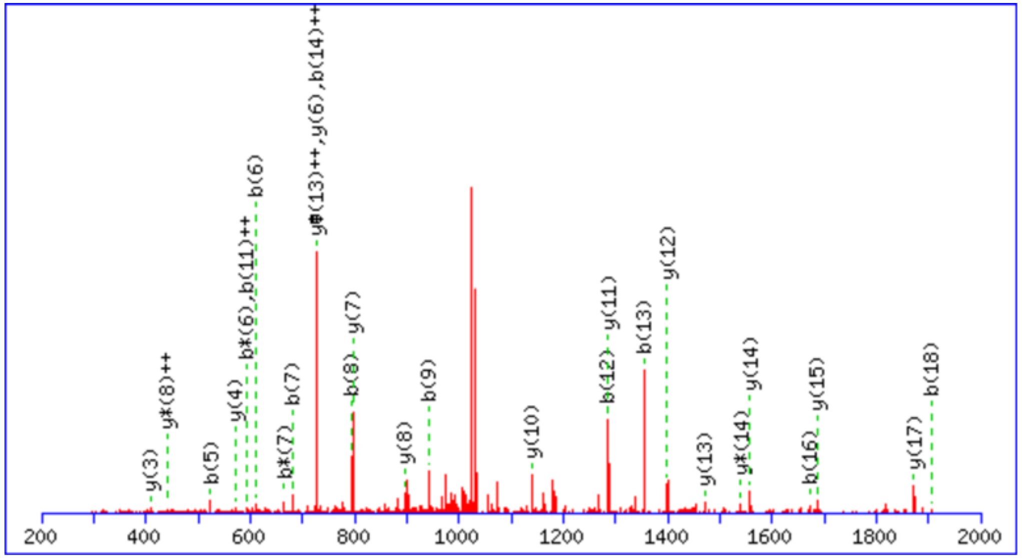


Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 14431: 2078.983448 from(1040.499000,2+)
Title: OECHL100310_33.17106.17106.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 76
Expect: 4.1e-006**Matches :** 29/200 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**19**
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973939	**18**
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444483	**17**
4	394.183344	197.595310	377.156795	189.082035			**Q**	1814.870790	907.939033	1797.844241	899.425759	1796.860225	898.933751	**16**
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904462	**15**
6	**610.257965**	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383165	**14**
7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867151	**13**
8	**794.379143**	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348594	**12**
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806562	**11**
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272355	**10**
11	1184.533077	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	1025.505072	513.256174	1008.478523	504.742900	1007.494507	504.250892	**9**
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729595	**8**
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195388	**7**
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676831	**6**
15	1508.712833	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	629.304187	315.155732	612.277638	306.642457	611.293622	306.150449	**5**
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	***572.282723***	286.645000	555.256174	278.131725	554.272158	277.639717	**4**
17	1818.844576	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	**3**
18	**1905.876604**	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
19							**R**	175.118952	88.063114	158.092403	79.549840			**1**



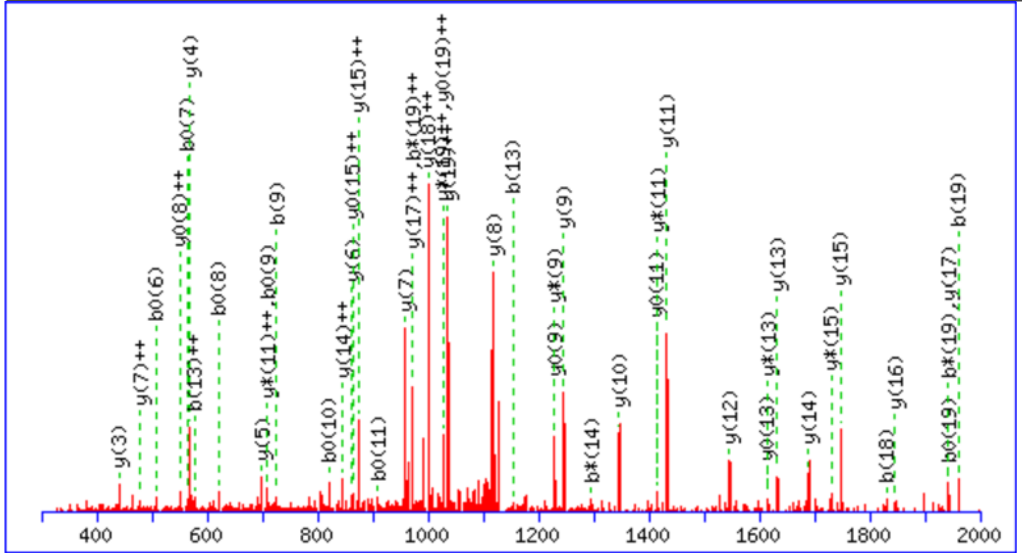
Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 15120: 2270.113448 from(1136.064000,2+)
Title: OECHL100310_33.10563.10563.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72
Expect: 1.1e-005**Matches :** 48/212 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	102.054955	51.531116			84.044390	42.525833	T						
2	201.123369	101.065322			183.112804	92.060040	V	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400	1076.5338
3	272.160483	136.583879			254.149918	127.578597	A	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986	1026.9996
4	329.181947	165.094611			311.171382	156.089329	G	1999.965437	1000.486357	1982.938888	991.973082	1981.954872	991.4810
5	426.234711	213.620994			408.224146	204.615711	P	***1942.943973***	971.975625	1925.917424	963.462350	1924.933408	962.9703
6	525.303125	263.155201			507.292560	254.149918	V	***1845.891209***	923.449243	1828.864660	914.935968	1827.880644	914.4439

7	582.324589	291.665933			564.314024	282.660650	**G**	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230	864.9097
8	639.346053	320.176665			621.335488	311.171382	**G**	***1689.801331***	845.404304	1672.774782	836.891029	1671.790766	836.3990
9	**726.378081**	363.692679			708.367516	354.687396	**S**	***1632.779867***	816.893572	1615.753318	808.380297	1614.769302	807.8882
10	839.462145	420.234711			821.451580	411.229428	**L**	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274	764.3722
11	926.494173	463.750725			908.483608	454.745442	**S**	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210	707.8302
12	1025.562587	513.284932			1007.552022	504.279649	**V**	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182	664.3142
13	**1153.621165**	577.314221	1136.594616	568.800946	1135.610600	568.308938	**Q**	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768	614.7800
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	**C**	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190	550.7507
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	**P**	***958.474106***	479.740691	941.447557	471.227417	940.463541	470.7354
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	**Y**	***861.421342***	431.214309	844.394793	422.701035	843.410777	422.2090
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	**E**	***698.358013***	349.682645	681.331464	341.169370	680.347448	340.6773
18	**1830.905463**	915.956370	1813.878914	907.443095	1812.894898	906.951087	**K**	***569.315420***	285.161348	552.288871	276.648074	551.304855	276.1560
19	**1959.948056**	980.477666	1942.921507	971.964392	1941.937491	971.472384	**E**	***441.220457***	221.113867	424.193908	212.600592	423.209892	212.1085
20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	**H**	312.177864	156.592570	295.151315	148.079295		
21							**R**	175.118952	88.063114	158.092403	79.549839		

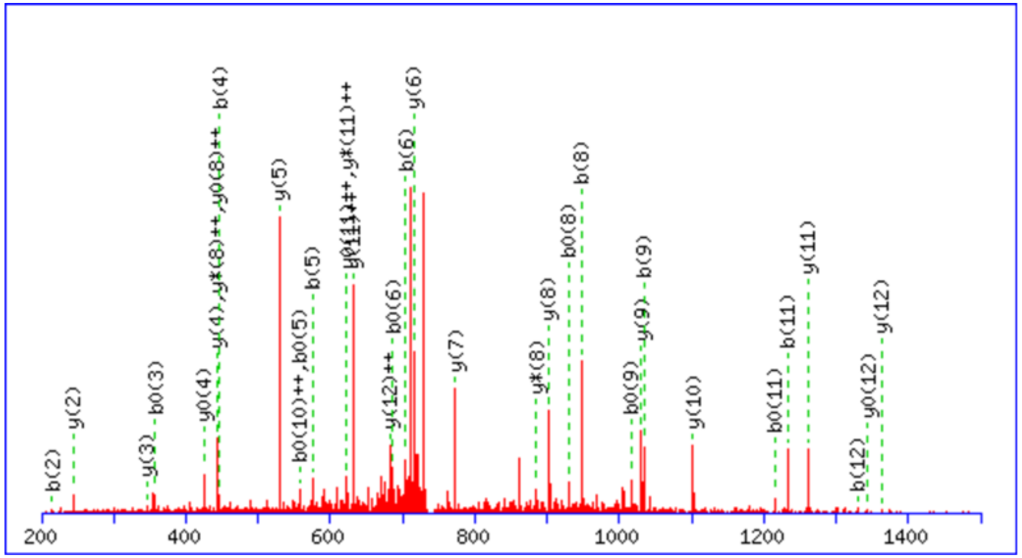


Peptide View

MS/MS Fragmentation of **ITCAEEGWSPTPK**
Found in **IPI00006154**, Tax_Id=9606 Gene_Symbol=CFHR2 Isoform Long of Complement factor H-related protein 2
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 9685: 1474.676848 from(738.345700,2+)
Title: OECHL100310_33.10337.10337.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1474.676224**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63
Expect: 5e-005**Matches :** 35/114 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**I**							**13**
2	**215.139019**	108.073147	197.128454	99.067865	**T**	***1362.599444***	681.803360	1345.572895	673.290086	1344.588879	672.798078	**12**
3	375.169668	188.088472	357.159103	179.083190	**C**	***1261.551765***	631.279521	1244.525216	622.766246	1243.541200	622.274238	**11**
4	**446.206782**	223.607029	428.196217	214.601747	**A**	***1101.521116***	551.264196	1084.494567	542.750922	1083.510551	542.258914	**10**
5	**575.249375**	288.128326	557.238810	279.123043	**E**	***1030.484002***	515.745639	1013.457453	507.232365	1012.473437	506.740357	**9**
6	**704.291968**	352.649622	686.281403	343.644340	**E**	***901.441409***	451.224343	884.414860	442.711068	883.430844	442.219060	**8**
7	761.313432	381.160354	743.302867	372.155072	**G**	***772.398816***	386.703046	755.372267	378.189772	754.388251	377.697764	**7**
8	**947.392745**	474.200011	929.382180	465.194728	**W**	***715.377352***	358.192314	698.350803	349.679040	697.366787	349.187032	**6**
9	**1034.424773**	517.716025	1016.414208	508.710742	**S**	***529.298039***	265.152658	512.271490	256.639383	511.287474	256.147375	**5**
10	1131.477537	566.242407	1113.466972	557.237124	**P**	***442.266011***	221.636644	425.239462	213.123369	424.255446	212.631361	**4**
11	**1232.525216**	616.766246	1214.514651	607.760964	**T**	***345.213247***	173.110262	328.186698	164.596987	327.202682	164.104979	**3**
12	**1329.577980**	665.292628	1311.567415	656.287346	**P**	***244.165568***	122.586422	227.139019	114.073148			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**



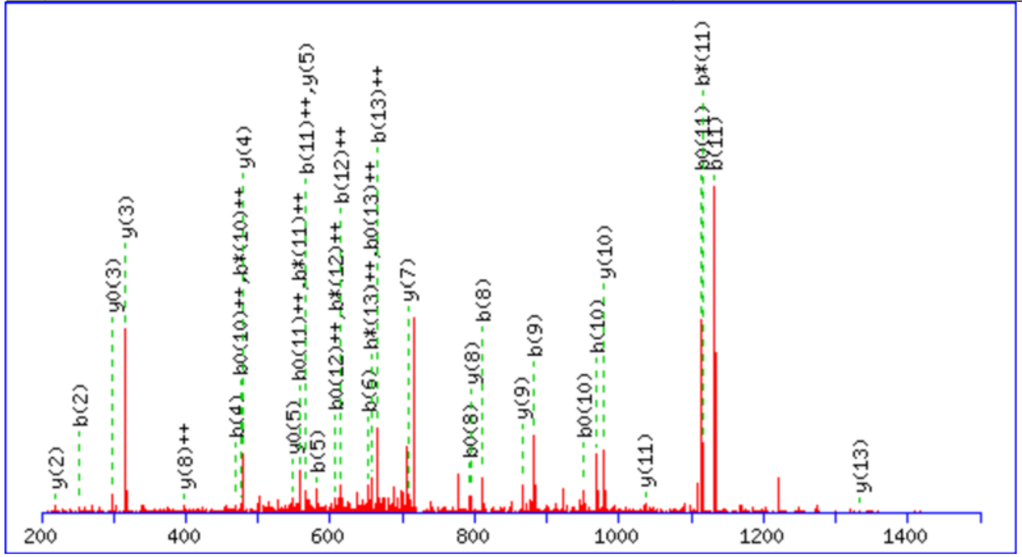
Peptide View

MS/MS Fragmentation of **NHCGIASAASYPTV**
Found in **IPI00012887**, Tax_Id=9606 Gene_Symbol=CTSL1 Cathepsin L1
Experiment: 25 - NOPD1 **Fraction:** NOPD1

Match to Query 9301: 1446.656248 from(724.335400,2+)
Title: OECHL100310_33.11819.11819.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1446.656158**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00065**Matches :** 36/116 fragment ions using 74 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**					**14**
2	*252.109115*	126.558195	235.082566	118.044921			**H**	*1333.620514*	667.313895	1315.609949	658.308612	**13**
3	412.139764	206.573520	395.113215	198.060245			**C**	1196.561602	598.784439	1178.551037	589.779157	**12**
4	*469.161228*	235.084252	452.134679	226.570977			**G**	*1036.530953*	518.769115	1018.520388	509.763832	**11**
5	*582.245292*	291.626284	565.218743	283.113009			**I**	*979.509489*	490.258383	961.498924	481.253100	**10**
6	*653.282406*	327.144841	636.255857	318.631566			**A**	*866.425425*	433.716351	848.414860	424.711068	**9**

7	740.314434	370.660855	723.287885	362.147580	722.303869	361.655572	**S**	***795.388311***	398.197794	777.377746	389.192511	**8**
8	***811.351548***	406.179412	794.324999	397.666137	793.340983	397.174129	**A**	***708.356283***	354.681780	690.345718	345.676497	**7**
9	***882.388662***	441.697969	865.362113	433.184694	864.378097	432.692686	**A**	637.319169	319.163223	619.308604	310.157940	**6**
10	***969.420690***	485.213983	952.394141	476.700708	951.410125	476.208700	**S**	***566.282055***	283.644666	548.271490	274.639383	**5**
11	***1132.484019***	**566.745647**	1115.457470	558.232373	1114.473454	557.740365	**Y**	***479.250027***	240.128652	461.239462	231.123369	**4**
12	1229.536783	**615.272029**	1212.510234	606.758755	1211.526218	606.266747	**P**	***316.186698***	158.596987	298.176133	149.591705	**3**
13	1330.584462	**665.795869**	1313.557913	657.282594	1312.573897	656.790586	**T**	***219.133934***	110.070605	201.123369	101.065323	**2**
14							**V**	118.086255	59.546766			**1**



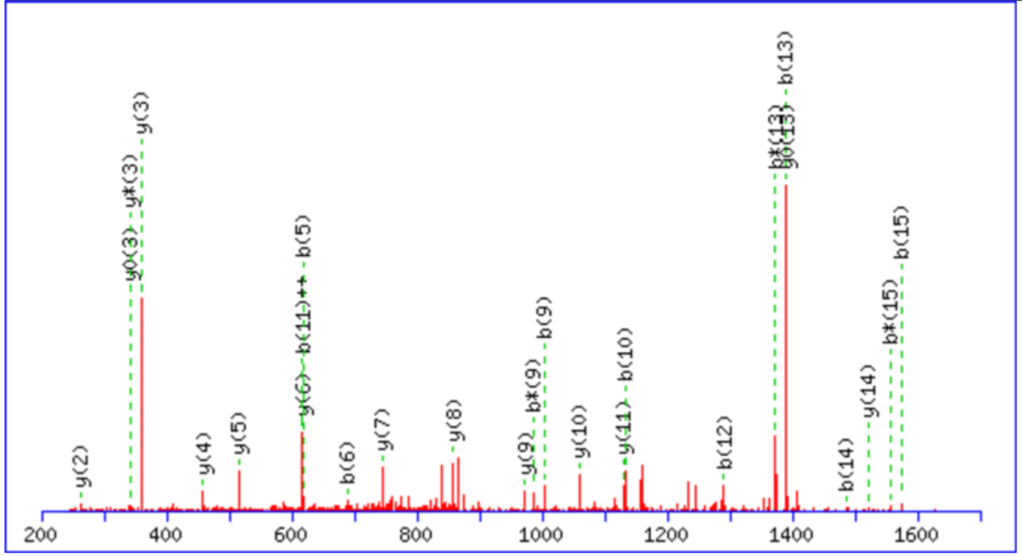
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 13048: 1746.916048 from(874.465300,2+)
Title: OECHL100310_31.16933.16933.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 79

Expect: 1.2e-006**Matches :** 26/156 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	114.091340	57.549308					L							16
2	227.175404	114.091340					L	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	15
3	340.259468	170.633372					I	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	14
4	503.322797	252.165036					Y	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	13
5	**618.349740**	309.678508			600.339175	300.673226	D	1245.606970	623.307123	1228.580421	614.793849	1227.596405	614.301841	12
6	**689.386854**	345.197065			671.376289	336.191782	A	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	11
7	776.418882	388.713079			758.408317	379.707796	S	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	10
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	9
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	L	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	8
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	E	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	7
11	1233.636145	617.321710	1216.609596	608.808436	1215.625580	608.316428	T	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	6
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	G	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	5
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	V	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	4
14	**1486.778787**	743.893032	1469.752238	735.379757	1468.768222	734.887749	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
16							R	175.118952	88.063114	158.092403	79.549839			1

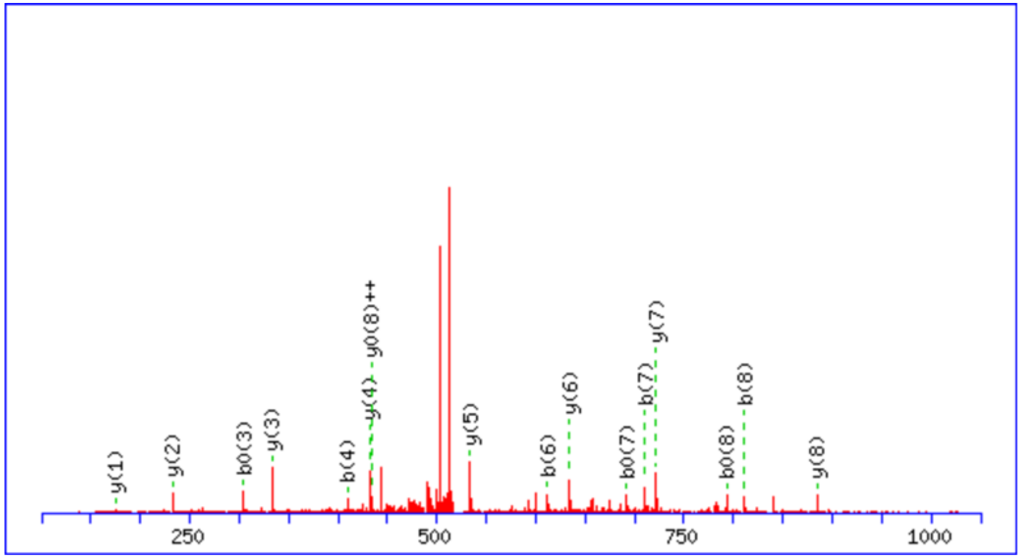


Peptide View

MS/MS Fragmentation of **GTYSTTVTGR**
Found in **IPI00029168**, Tax_Id=9606 Gene_Symbol=LPA Apolipoprotein(a)
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 4031: 1041.511848 from(521.763200,2+)
Title: OECHL100310_31.4162.4162.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1041.509109**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66
Expect: 2.1e-005**Matches :** 16/84 fragment ions using 27 most intense peaks (help)

#	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	58.028740	29.518008			**G**							**10**
2	159.076419	80.041847	141.065854	71.036565	**T**	985.494903	493.251090	968.468354	484.737815	967.484338	484.245807	**9**
3	322.139748	161.573512	304.129183	152.568230	**Y**	***884.447224***	442.727250	867.420675	434.213976	866.436659	433.721968	**8**
4	**409.171776**	205.089526	391.161211	196.084243	**S**	***721.383895***	361.195586	704.357346	352.682311	703.373330	352.190303	**7**
5	510.219455	255.613365	492.208890	246.608083	**T**	***634.351867***	317.679572	617.325318	309.166297	616.341302	308.674289	**6**
6	**611.267134**	306.137205	593.256569	297.131923	**T**	***533.304188***	267.155732	516.277639	258.642458	515.293623	258.150450	**5**
7	**710.335548**	355.671412	692.324983	346.666130	**V**	***432.256509***	216.631893	415.229960	208.118618	414.245944	207.626610	**4**
8	**811.383227**	406.195252	793.372662	397.189969	**T**	***333.188095***	167.097686	316.161546	158.584411	315.177530	158.092403	**3**
9	868.404691	434.705984	850.394126	425.700701	**G**	***232.140416***	116.573846	215.113867	108.060572			**2**
10					**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



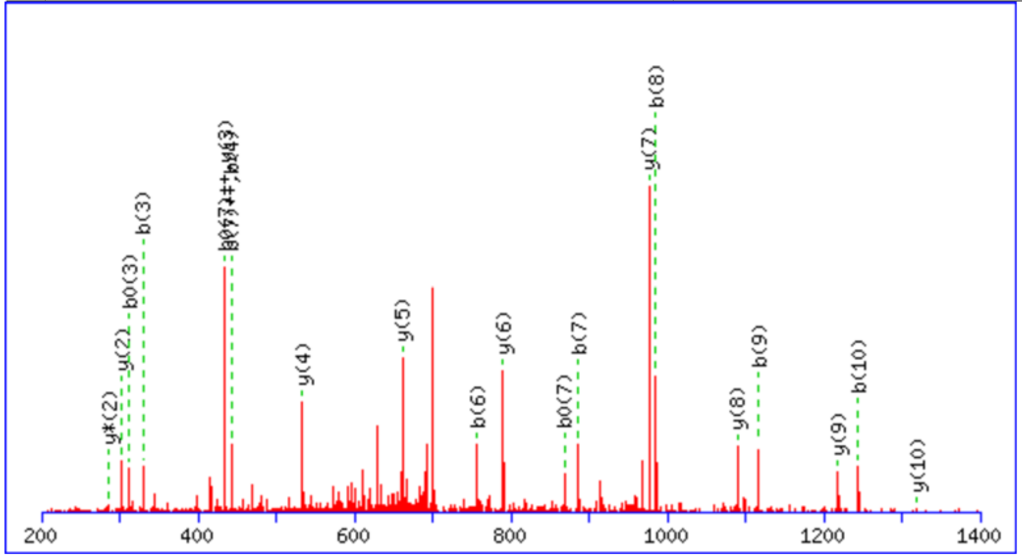
Peptide View

MS/MS Fragmentation of **VTEIWQEVMQR**
Found in **IPI00027827**, Tax_Id=9606 Gene_Symbol=SOD3 Extracellular superoxide dismutase [Cu-Zn]
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 9439: 1417.701848 from(709.858200,2+)
Title: OECHL100310_31.18497.18497.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1417.702377**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 83
Expect: 7.8e-007**Matches :** 21/100 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	100.075690	50.541483					**V**							**11**
2	201.123369	101.065322			183.112804	92.060040	**T**	***1319.641249***	660.324263	1302.614700	651.810988	1301.630684	651.318980	**10**
3	**330.165962**	165.586619			312.155397	156.581336	**E**	***1218.593570***	609.800423	1201.567021	601.287149	1200.583005	600.795141	**9**
4	**443.250026**	222.128651			425.239461	213.123369	**I**	***1089.550977***	545.279127	1072.524428	536.765852	1071.540412	536.273844	**8**
5	629.329339	315.168308			611.318774	306.163025	**W**	***976.466913***	488.737095	959.440364	480.223820	958.456348	479.731812	**7**
6	**757.387917**	379.197597	740.361368	370.684322	739.377352	370.192314	**Q**	***790.387600***	395.697438	773.361051	387.184164	772.377035	386.692156	**6**

7	**886.430510**	443.718893	869.403961	435.205619	868.419945	434.713611	**E**	***662.329022***	331.668149	645.302473	323.154875	644.318457	322.662867	**5**
8	**985.498924**	493.253100	968.472375	484.739826	967.488359	484.247818	**V**	***533.286429***	267.146853	516.259880	258.633578			**4**
9	**1116.539409**	558.773343	1099.512860	550.260068	1098.528844	549.768060	**M**	***434.218015***	217.612646	417.191466	209.099371			**3**
10	**1244.597987**	622.802632	1227.571438	614.289357	1226.587422	613.797349	**Q**	***303.177530***	152.092403	286.150981	143.579129			**2**
11							**R**	175.118952	88.063114	158.092403	79.549839			**1**



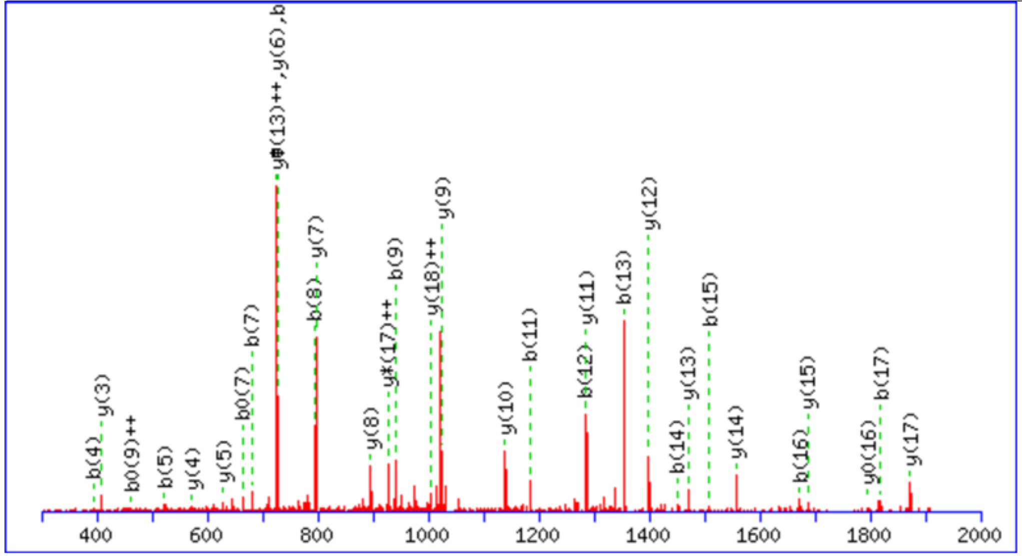
Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 15608: 2078.981448 from(1040.498000,2+)
Title: OECHL100310_31.17174.17174.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 83
Expect: 8.5e-007**Matches :** 34/200 fragment ions using 66 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**19**

2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973939	**18**
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444483	**17**
4	**394.183344**	197.595310	377.156795	189.082035			**Q**	1814.870790	907.939033	1797.844241	899.425759	1796.860225	898.933751	**16**
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904462	**15**
6	610.257965	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383165	**14**
7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867151	**13**
8	**794.379143**	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348594	**12**
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806562	**11**
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272355	**10**
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250892	**9**
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729595	**8**
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195388	**7**
14	**1451.691369**	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676831	**6**
15	**1508.712833**	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150449	**5**
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	***572.282723***	286.645000	555.256174	278.131725	554.272158	277.639717	**4**
17	**1818.844576**	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	**3**
18	1905.876604	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
19							**R**	175.118952	88.063114	158.092403	79.549840			**1**

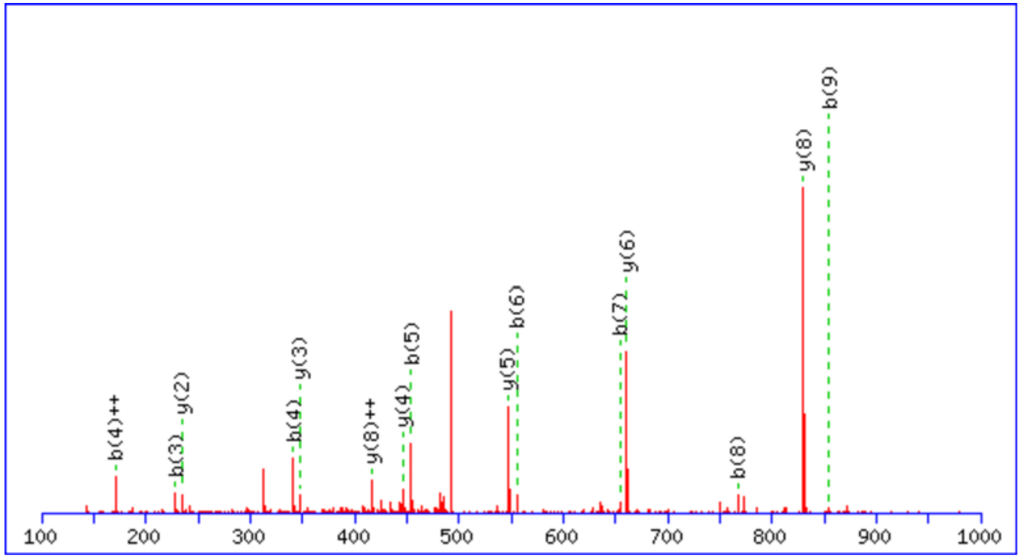


Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 3292: 999.633248 from(500.823900,2+)
Title: OECHL100310_31.17092.17092.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63
Expect: 5.8e-006**Matches :** 16/78 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	**446.297310**	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



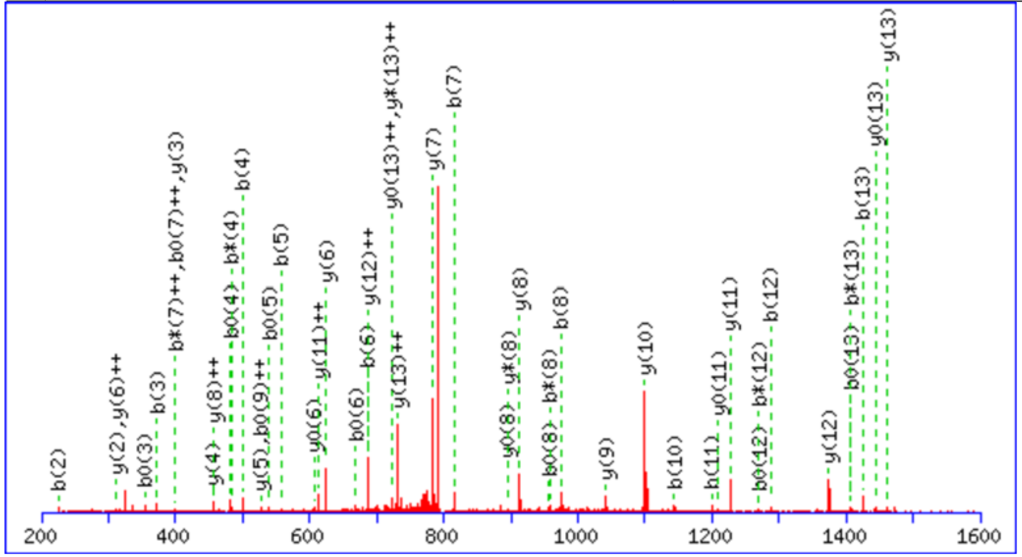
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 11452: 1597.707248 from(799.860900,2+)
Title: OECHL100310_31.2163.2163.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 76
Expect: 1.4e-006**Matches :** 49/144 fragment ions using 84 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					**H**							**14**
2	**225.098216**	113.052746			207.087651	104.047463	**S**	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.325325	**13**
3	**372.166630**	186.586953			354.156065	177.581671	**F**	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.809311	**12**
4	**500.261593**	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	**11**
5	**557.283057**	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	**10**
6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	***1042.437069***	521.722173	1025.410520	513.208898	1024.426504	512.716890	**9**

7	**815.368243**	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	***312.177864***	156.592570	295.151315	148.079295			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



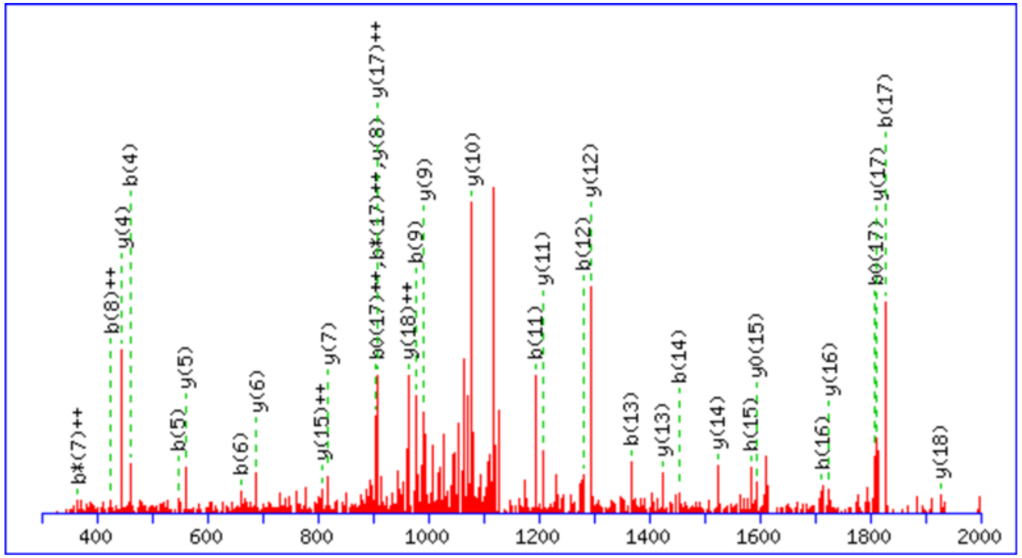
Peptide View

MS/MS Fragmentation of **SKEDSNSTESKSSSEEDGQLK**
Found in **IPI00012734**, Tax_Id=9606 Gene_Symbol=DMP1 Isoform 1 of Dentin matrix acidic phosphoprotein 1
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 16680: 2270.999448 from(1136.507000,2+)
Title: OECHL100310_31.2175.2175.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.998581**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 99

Expect: 1.2e-008**Matches :** 34/230 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	88.039304	44.523290			70.028739	35.518008	S						
2	216.134267	108.570771	199.107718	100.057497	198.123702	99.565489	K	2184.973868	1092.990572	2167.947319	1084.477297	2166.963303	1083.9852
3	345.176860	173.092068	328.150311	164.578793	327.166295	164.086785	E	2056.878905	1028.943090	2039.852356	1020.429816	2038.868340	1019.9378
4	**460.203803**	230.605539	443.177254	222.092265	442.193238	221.600257	D	***1927.836312***	964.421794	1910.809763	955.908520	1909.825747	955.4165
5	**547.235831**	274.121554	530.209282	265.608279	529.225266	265.116271	S	***1812.809369***	906.908323	1795.782820	898.395048	1794.798804	897.9030
6	**661.278758**	331.143017	644.252209	322.629743	643.268193	322.137735	N	***1725.777341***	863.392309	1708.750792	854.879034	1707.766776	854.3870
7	748.310786	374.659031	731.284237	366.145757	730.300221	365.653749	S	1611.734414	806.370845	1594.707865	797.857571	1593.723849	797.3655
8	849.358465	425.182871	832.331916	416.669596	831.347900	416.177588	T	***1524.702386***	762.854831	1507.675837	754.341557	1506.691821	753.8495
9	**978.401058**	489.704167	961.374509	481.190893	960.390493	480.698885	E	***1423.654707***	712.330992	1406.628158	703.817717	1405.644142	703.3257
10	1065.433086	533.220181	1048.406537	524.706907	1047.422521	524.214899	S	***1294.612114***	647.809695	1277.585565	639.296421	1276.601549	638.8044
11	**1193.528049**	597.267663	1176.501500	588.754388	1175.517484	588.262380	K	***1207.580086***	604.293681	1190.553537	595.780407	1189.569521	595.2883
12	**1280.560077**	640.783677	1263.533528	632.270402	1262.549512	631.778394	S	***1079.485123***	540.246200	1062.458574	531.732925	1061.474558	531.2409
13	**1367.592105**	684.299691	1350.565556	675.786416	1349.581540	675.294408	S	***992.453095***	496.730186	975.426546	488.216911	974.442530	487.7249
14	**1454.624133**	727.815705	1437.597584	719.302430	1436.613568	718.810422	S	***905.421067***	453.214172	888.394518	444.700897	887.410502	444.2088
15	**1583.666726**	792.337001	1566.640177	783.823727	1565.656161	783.331719	E	***818.389039***	409.698158	801.362490	401.184883	800.378474	400.6928
16	**1712.709319**	856.858298	1695.682770	848.345023	1694.698754	847.853015	E	***689.346446***	345.176861	672.319897	336.663587	671.335881	336.1715
17	**1827.736262**	914.371769	1810.709713	905.858495	1809.725697	905.366487	D	***560.303853***	280.655565	543.277304	272.142290	542.293288	271.6502
18	1884.757726	942.882501	1867.731177	934.369227	1866.747161	933.877219	G	***445.276910***	223.142093	428.250361	214.628818		
19	2012.816304	1006.911790	1995.789755	998.398516	1994.805739	997.906508	Q	388.255446	194.631361	371.228897	186.118087		
20	2125.900368	1063.453822	2108.873819	1054.940547	2107.889803	1054.448539	L	260.196868	130.602072	243.170319	122.088798		
21							K	147.112804	74.060040	130.086255	65.546765		



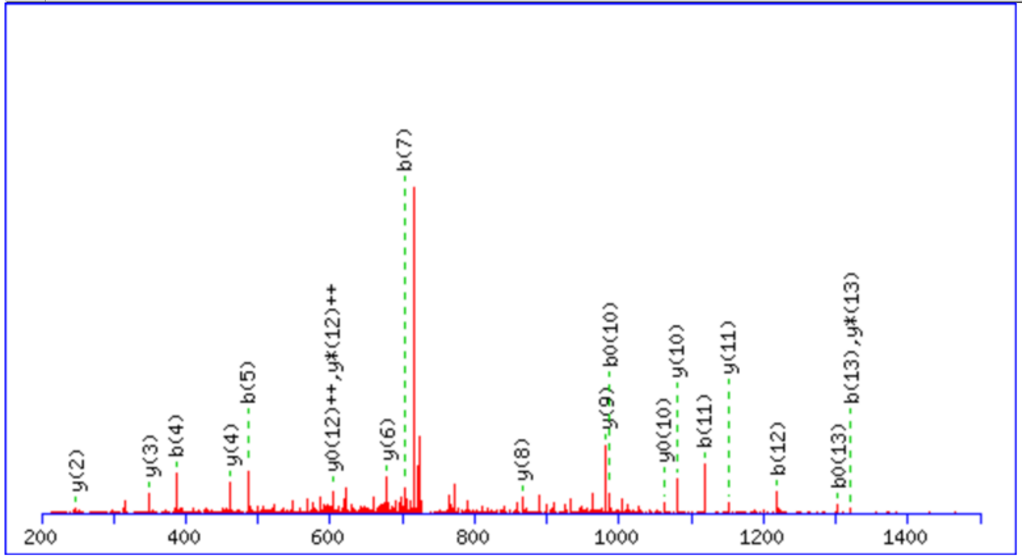
Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 9874: 1465.678648 from(733.846600,2+)
Title: OECHL100310_31.9693.9693.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 64 **Expect:** 3e-005**Matches :** 20/128 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	1337.643082	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	316.113926	158.560601	298.103361	149.555319	**A**	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	***387.151040***	194.079158	369.140475	185.073875	**A**	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	***486.219454***	243.613365	468.208889	234.608082	**V**	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**
6	601.246397	301.126837	583.235832	292.121554	**D**	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	**9**

7	***702.294076***	351.650676	684.283511	342.645394	**T**	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	765.398875	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	876.358132	438.682704	858.347567	429.677421	**S**	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	1005.400725	503.204001	987.390160	494.198718	**E**	591.334819	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	***1118.484789***	559.746033	1100.474224	550.740750	**I**	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	***1219.532468***	610.269872	1201.521903	601.264590	**T**	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	***1320.580147***	660.793712	1302.569582	651.788429	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**



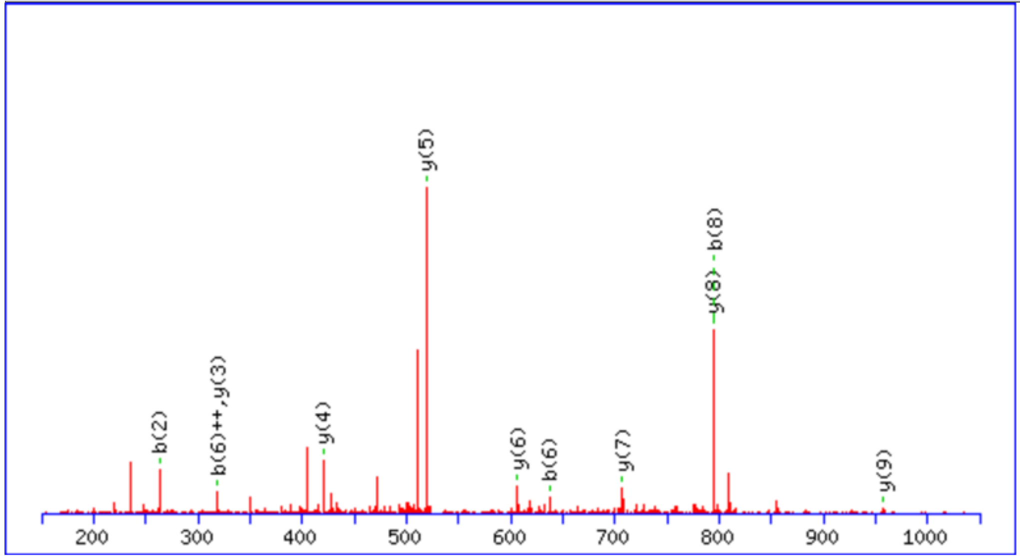
Peptide View

MS/MS Fragmentation of **VYSTSVTGSR**
Found in **IPI00010402**, Tax_Id=9606 Gene_Symbol=SH3BGRL3 Putative uncharacterized protein
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 4255: 1055.524448 from(528.769500,2+)
Title: OECHL100310_31.3907.3907.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1055.524750**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54

Expect: 0.00032**Matches :** 11/84 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							10
2	**263.139019**	132.073148			Y	***957.463601***	479.235439	940.437052	470.722164	939.453036	470.230156	9
3	350.171047	175.589161	332.160482	166.583879	S	***794.400272***	397.703774	777.373723	389.190499	776.389707	388.698491	8
4	451.218726	226.113001	433.208161	217.107719	T	***707.368244***	354.187760	690.341695	345.674486	689.357679	345.182478	7
5	538.250754	269.629015	520.240189	260.623733	S	***606.320565***	303.663921	589.294016	295.150646	588.310000	294.658638	6
6	**637.319168**	319.163222	619.308603	310.157940	V	***519.288537***	260.147907	502.261988	251.634632	501.277972	251.142624	5
7	738.366847	369.687062	720.356282	360.681779	T	***420.220123***	210.613699	403.193574	202.100425	402.209558	201.608417	4
8	**795.388311**	398.197794	777.377746	389.192511	G	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	3
9	882.420339	441.713808	864.409774	432.708525	S	262.150980	131.579128	245.124431	123.065853	244.140415	122.573845	2
10					R	175.118952	88.063114	158.092403	79.549839			1

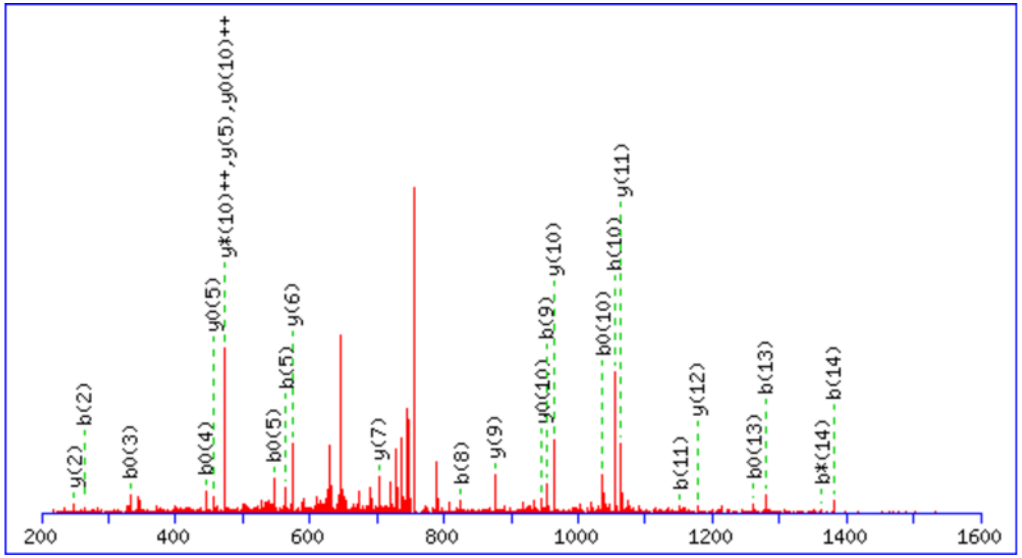


Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 10726: 1525.725048 from(763.869800,2+)
Title: OECHL100310_31.10649.10649.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49
Expect: 0.0013**Matches :** 26/150 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	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	350.134661	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	**9**
8	***825.362488***	413.184882			807.351923	404.179599	**S**	789.410110	395.208693	772.383561	386.695418	771.399545	386.203410	**8**
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	**7**
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	**6**
11	***1151.521509***	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	**5**
12	1208.542973	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	376.219061	188.613168	359.192512	180.099894	358.208496	179.607886	**4**
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	**3**
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



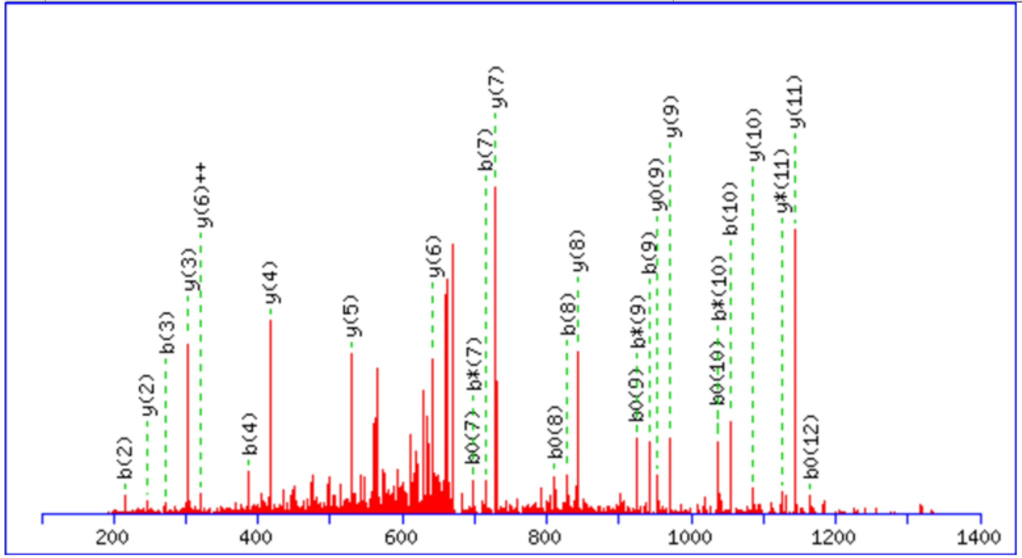
Peptide View

MS/MS Fragmentation of **TLGDQLSLLLGAR**
Found in **IPI00005707**, Tax_Id=9606 Gene_Symbol=MRC2 C-type mannose receptor 2
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 8796: 1355.777648 from(678.896100,2+)
Title: OECHL100310_31.20799.20799.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1355.777252**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60
Expect: 3.3e-005**Matches :** 28/124 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	102.054955	51.531116			84.044390	42.525833	**T**							**13**
2	**215.139019**	108.073147			197.128454	99.067865	**L**	1255.736863	628.372069	1238.710314	619.858795	1237.726298	619.366787	**12**
3	**272.160483**	136.583879			254.149918	127.578597	**G**	***1142.652799***	571.830038	1125.626250	563.316763	1124.642234	562.824755	**11**
4	**387.187426**	194.097351			369.176861	185.092069	**D**	***1085.631335***	543.319305	1068.604786	534.806031	1067.620770	534.314023	**10**
5	515.246004	258.126640	498.219455	249.613366	497.235439	249.121358	**Q**	***970.604392***	485.805834	953.577843	477.292559	952.593827	476.800551	**9**
6	628.330068	314.668672	611.303519	306.155398	610.319503	305.663390	**L**	***842.545814***	421.776545	825.519265	413.263270	824.535249	412.771262	**8**

7	**715.362096**	358.184686	698.335547	349.671412	697.351531	349.179404	**S**	***729.461750***	365.234513	712.435201	356.721238	711.451185	356.229230	**7**
8	**828.446160**	414.726718	811.419611	406.213444	810.435595	405.721436	**L**	***642.429722***	321.718499	625.403173	313.205224			**6**
9	**941.530224**	471.268750	924.503675	462.755476	923.519659	462.263468	**L**	***529.345658***	265.176467	512.319109	256.663192			**5**
10	**1054.614288**	527.810782	1037.587739	519.297508	1036.603723	518.805500	**L**	***416.261594***	208.634435	399.235045	200.121160			**4**
11	1111.635752	556.321514	1094.609203	547.808240	1093.625187	547.316231	**G**	***303.177530***	152.092403	286.150981	143.579128			**3**
12	1182.672866	591.840071	1165.646317	583.326797	1164.662301	582.834788	**A**	***246.156066***	123.581671	229.129517	115.068396			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

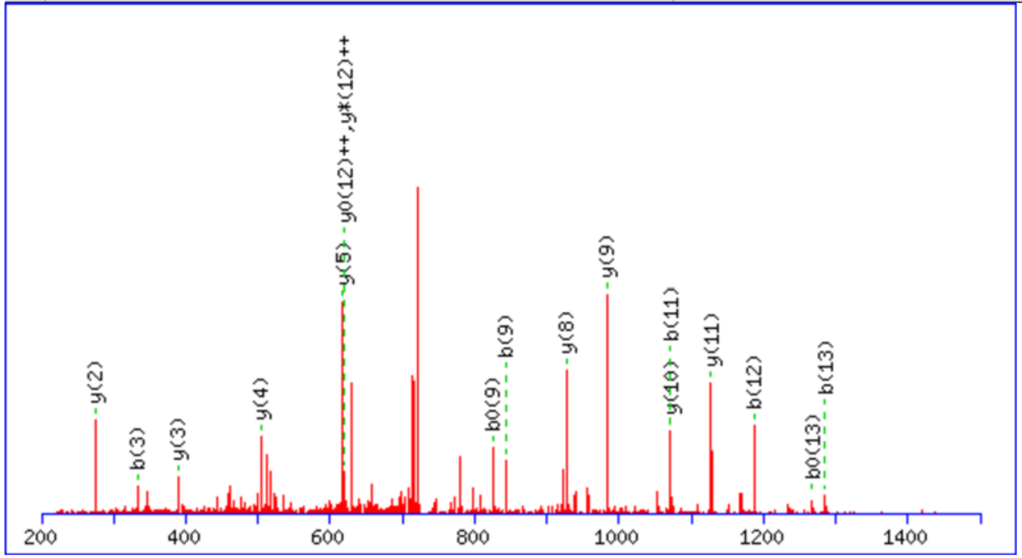


Peptide View

MS/MS Fragmentation of **FGQGSGPIVLDDVR**
Found in **IPI00418512**, Tax_Id=9606 Gene_Symbol=DMBT1 Isoform 4 of Deleted in malignant brain tumors 1 protein
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 9837: 1458.746248 from(730.380400,2+)
Title: OECHL100310_31.15464.15464.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1458.746719**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60
Expect: 0.00011**Matches :** 17/140 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							14
2	205.097154	103.052215					G	1312.685556	656.846416	1295.659007	648.333142	1294.674991	647.841134	13
3	**333.155732**	167.081504	316.129183	158.568230			Q	1255.664092	628.335684	1238.637543	619.822410	1237.653527	619.330402	12
4	390.177196	195.592236	373.150647	187.078961			G	***1127.605514***	564.306395	1110.578965	555.793121	1109.594949	555.301113	11
5	477.209224	239.108250	460.182675	230.594976	459.198659	230.102968	S	***1070.584050***	535.795663	1053.557501	527.282389	1052.573485	526.790381	10
6	534.230688	267.618982	517.204139	259.105708	516.220123	258.613700	G	***983.552022***	492.279649	966.525473	483.766375	965.541457	483.274367	9
7	631.283452	316.145364	614.256903	307.632090	613.272887	307.140082	P	***926.530558***	463.768917	909.504009	455.255643	908.519993	454.763635	8
8	744.367516	372.687396	727.340967	364.174122	726.356951	363.682114	I	829.477794	415.242535	812.451245	406.729261	811.467229	406.237253	7
9	**843.435930**	422.221603	826.409381	413.708329	825.425365	413.216321	V	716.393730	358.700503	699.367181	350.187229	698.383165	349.695221	6
10	956.519994	478.763635	939.493445	470.250361	938.509429	469.758353	L	***617.325316***	309.166296	600.298767	300.653022	599.314751	300.161014	5
11	**1071.546937**	536.277107	1054.520388	527.763832	1053.536372	527.271824	D	***504.241252***	252.624264	487.214703	244.110990	486.230687	243.618982	4
12	**1186.573880**	593.790578	1169.547331	585.277304	1168.563315	584.785296	D	***389.214309***	195.110793	372.187760	186.597518	371.203744	186.105510	3
13	**1285.642294**	643.324785	1268.615745	634.811511	1267.631729	634.319503	V	***274.187366***	137.597321	257.160817	129.084047			2
14							R	175.118952	88.063114	158.092403	79.549839			1

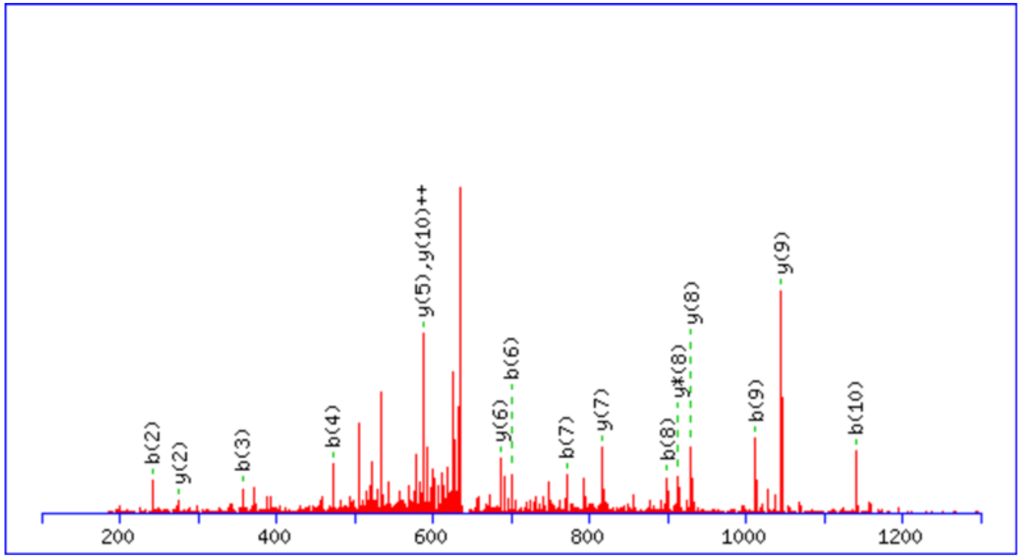


Peptide View

MS/MS Fragmentation of **LKDDEVAQLKK**
Found in **IPI00219217**, Tax_Id=9606 Gene_Symbol=LDHB L-lactate dehydrogenase B chain
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 7784: 1285.724048 from(643.869300,2+)
Title: OECHL100310_31.4431.4431.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1285.724136**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00057**Matches :** 16/102 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	114.091340	57.549308					**L**							**11**
2	***242.186303***	121.596790	225.159754	113.083515			**K**	1173.647379	587.327328	1156.620830	578.814053	1155.636814	578.322045	**10**
3	***357.213246***	179.110261	340.186697	170.596987	339.202681	170.104979	**D**	**1045.552416**	523.279846	1028.525867	514.766572	1027.541851	514.274564	**9**
4	***472.240189***	236.623733	455.213640	228.110458	454.229624	227.618450	**D**	**930.525473**	465.766375	913.498924	457.253100	912.514908	456.761092	**8**
5	601.282782	301.145029	584.256233	292.631755	583.272217	292.139747	**E**	**815.498530**	408.252903	798.471981	399.739629	797.487965	399.247621	**7**
6	***700.351196***	350.679236	683.324647	342.165962	682.340631	341.673954	**V**	**686.455937**	343.731607	669.429388	335.218332			**6**
7	***771.388310***	386.197793	754.361761	377.684519	753.377745	377.192511	**A**	**587.387523**	294.197400	570.360974	285.684125			**5**
8	***899.446888***	450.227082	882.420339	441.713808	881.436323	441.221800	**Q**	516.350409	258.678843	499.323860	250.165568			**4**
9	***1012.530952***	506.769114	995.504403	498.255840	994.520387	497.763832	**L**	388.291831	194.649554	371.265282	186.136279			**3**
10	***1140.625915***	570.816596	1123.599366	562.303321	1122.615350	561.811313	**K**	**275.207767**	138.107521	258.181218	129.594247			**2**
11							**K**	147.112804	74.060040	130.086255	65.546765			**1**



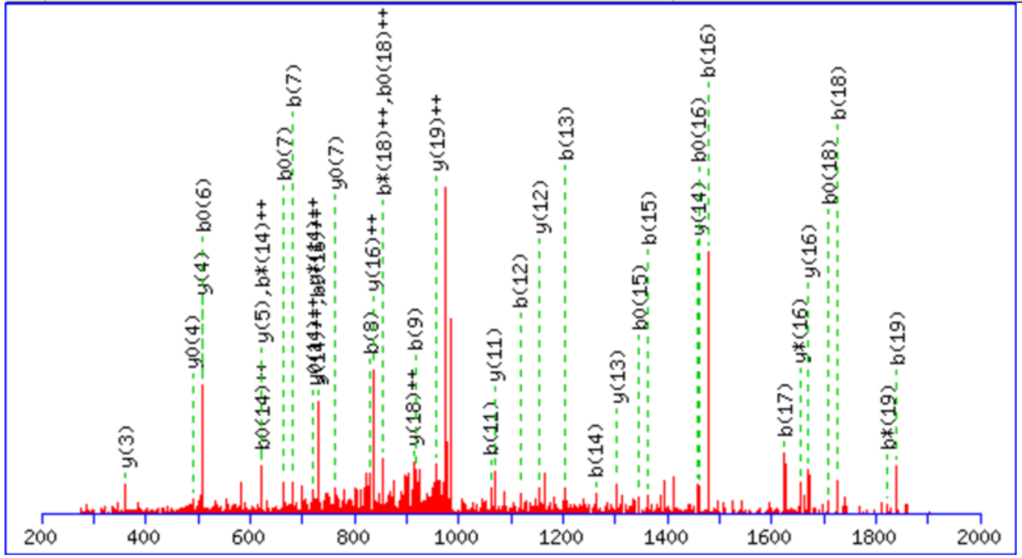
Peptide View

MS/MS Fragmentation of **ASGVPDRFSGSGSGTDFTLK**
Found in **IPI00387107**, Tax_Id=9606 Gene_Symbol=IGKV2-40 Ig kappa chain V-II region Cum
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 15026: 1984.949448 from(993.482000,2+)
Title: OECHL100310_31.13595.13595.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1984.949066**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57
Expect: 0.0003**Matches :** 40/210 fragment ions using 81 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**20**
2	159.076418	80.041847			141.065853	71.036564	**S**	1914.919197	957.963236	1897.892648	949.449962	1896.908632	948.957954	**19**
3	216.097882	108.552579			198.087317	99.547296	**G**	1827.887169	914.447222	1810.860620	905.933948	1809.876604	905.441940	**18**
4	315.166296	158.086786			297.155731	149.081504	**V**	1770.865705	885.936490	1753.839156	877.423216	1752.855140	876.931208	**17**
5	412.219060	206.613168			394.208495	197.607885	**P**	**1671.797291**	836.402283	1654.770742	827.889009	1653.786726	827.397001	**16**
6	527.246003	264.126640			509.235438	255.121357	**D**	1574.744527	787.875902	1557.717978	779.362627	1556.733962	778.870619	**15**

7	***683.347114***	342.177195	666.320565	333.663920	665.336549	333.171912	**R**	**1459.717584**	730.362430	1442.691035	721.849156	1441.707019	721.357148	**14**
8	***830.415528***	415.711402	813.388979	407.198127	812.404963	406.706119	**F**	**1303.616473**	652.311875	1286.589924	643.798600	1285.605908	643.306592	**13**
9	***917.447556***	459.227416	900.421007	450.714141	899.436991	450.222133	**S**	**1156.548059**	578.777668	1139.521510	570.264393	1138.537494	569.772385	**12**
10	974.469020	487.738148	957.442471	479.224873	956.458455	478.732865	**G**	**1069.516031**	535.261654	1052.489482	526.748379	1051.505466	526.256371	**11**
11	***1061.501048***	531.254162	1044.474499	522.740887	1043.490483	522.248879	**S**	1012.494567	506.750922	995.468018	498.237647	994.484002	497.745639	**10**
12	***1118.522512***	559.764894	1101.495963	551.251619	1100.511947	550.759611	**G**	925.462539	463.234908	908.435990	454.721633	907.451974	454.229625	**9**
13	***1205.554540***	603.280908	1188.527991	594.767633	1187.543975	594.275625	**S**	868.441075	434.724176	851.414526	426.210901	850.430510	425.718893	**8**
14	***1262.576004***	631.791640	1245.549455	623.278365	1244.565439	622.786357	**G**	781.409047	391.208162	764.382498	382.694887	763.398482	382.202879	**7**
15	***1363.623683***	682.315479	1346.597134	673.802205	1345.613118	673.310197	**T**	724.387583	362.697430	707.361034	354.184155	706.377018	353.692147	**6**
16	***1478.650626***	739.828951	1461.624077	731.315677	1460.640061	730.823668	**D**	**623.339904**	312.173590	606.313355	303.660316	605.329339	303.168308	**5**
17	***1625.719040***	813.363158	1608.692491	804.849884	1607.708475	804.357875	**F**	**508.312961**	254.660118	491.286412	246.146844	490.302396	245.654836	**4**
18	***1726.766719***	863.886998	1709.740170	855.373723	1708.756154	854.881715	**T**	**361.244547**	181.125911	344.217998	172.612637	343.233982	172.120629	**3**
19	***1839.850783***	920.429029	1822.824234	911.915755	1821.840218	911.423747	**L**	260.196868	130.602072	243.170319	122.088797			**2**
20							**K**	147.112804	74.060040	130.086255	65.546765			**1**

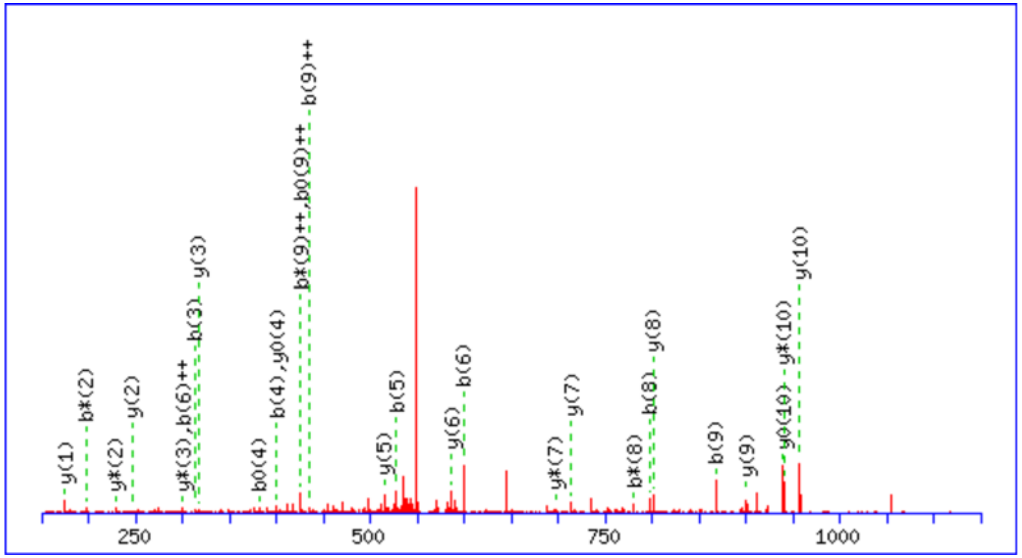


Peptide View

MS/MS Fragmentation of **RGVSQAPTAAR**
Found in **IPI00025365**, Tax_Id=9606 Gene_Symbol=EDN3 Isoform Long of Endothelin-3
Experiment: 10 - S_D-1 **Fraction:** S_D-1

Match to Query 5196: 1112.605048 from(557.309800,2+)
Title: OECHL100310_31.2131.2131.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1112.605042**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00045**Matches :** 29/108 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	157.108387	79.057831	140.081838	70.544557			**R**							**11**
2	214.129851	107.568564	197.103302	99.055289			**G**	***957.511221***	479.259249	940.484672	470.745974	939.500656	470.253966	**10**
3	**313.198265**	157.102770	296.171716	148.589496			**V**	***900.489757***	450.748517	883.463208	442.235242	882.479192	441.743234	**9**
4	**400.230293**	200.618785	383.203744	192.105510	382.219728	191.613502	**S**	***801.421343***	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
5	**528.288871**	264.648074	511.262322	256.134799	510.278306	255.642791	**Q**	***714.389315***	357.698296	697.362766	349.185021	696.378750	348.693013	**7**
6	**599.325985**	300.166631	582.299436	291.653356	581.315420	291.161348	**A**	***586.330737***	293.669007	569.304188	285.155732	568.320172	284.663724	**6**
7	696.378749	348.693013	679.352200	340.179738	678.368184	339.687730	**P**	***515.293623***	258.150450	498.267074	249.637175	497.283058	249.145167	**5**
8	**797.426428**	399.216852	780.399879	390.703578	779.415863	390.211570	**T**	418.240859	209.624068	401.214310	201.110793	400.230294	200.618785	**4**
9	**868.463542**	434.735409	851.436993	426.222135	850.452977	425.730127	**A**	***317.193180***	159.100228	300.166631	150.586953			**3**
10	**939.500656**	470.253966	922.474107	461.740692	921.490091	461.248684	**A**	***246.156066***	123.581671	229.129517	115.068397			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



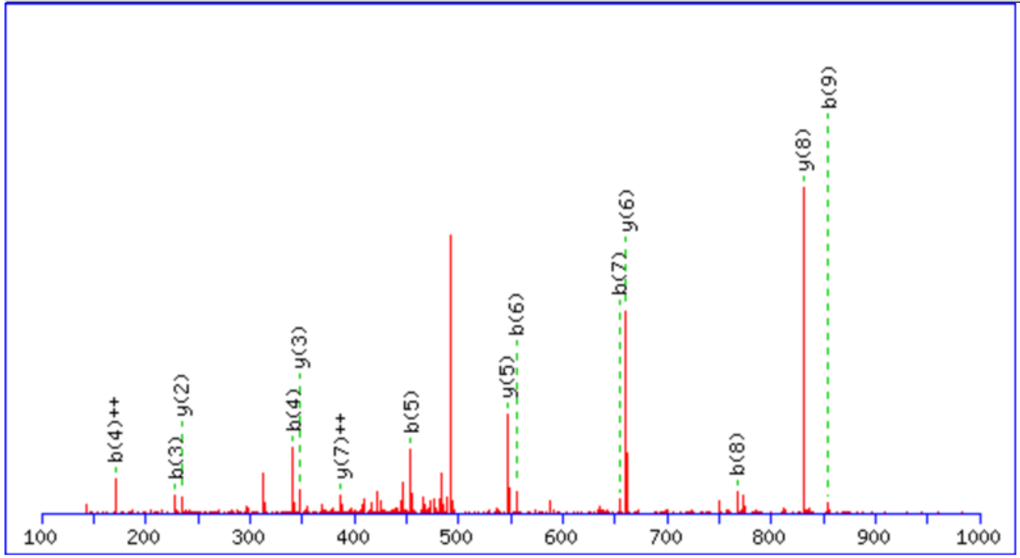
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 2990: 999.633648 from(500.824100,2+)
Title: OECHL100310_29.16908.16908.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62
Expect: 8e-006**Matches :** 15/78 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**

7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



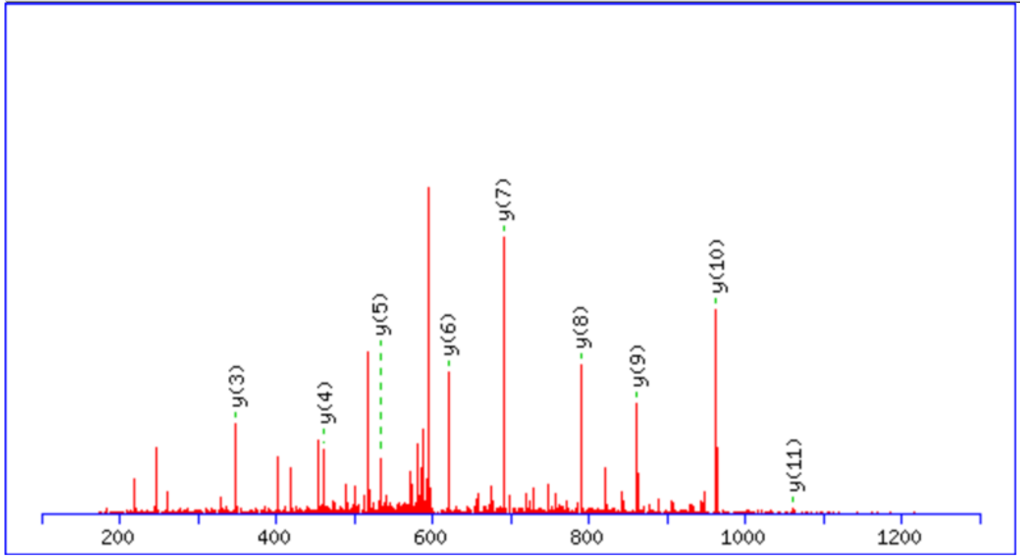
Peptide View

MS/MS Fragmentation of **MVTAVASALSSR**
Found in **IPI00220706**, Tax_Id=9606 Gene_Symbol=HBG2;HBG1 Hemoglobin subunit gamma-1
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 5920: 1207.624448 from(604.819500,2+)
Title: OECHL100310_29.10249.10249.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1207.623062**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: M1 :** Oxidation (M), with neutral loss 63.998285**Ions Score:** 58 **Expect:** 0.00013**Matches :** 9/104 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	84.044391	42.525833			**M**							**12**
2	183.112805	92.060040			**V**	***1061.594949***	531.301113	1044.568400	522.787838	1043.584384	522.295830	**11**

3	284.160484	142.583880	266.149919	133.578598	**T**	***962.526535***	481.766906	945.499986	473.253631	944.515970	472.761623	**10**
4	355.197598	178.102437	337.187033	169.097155	**A**	***861.478856***	431.243066	844.452307	422.729791	843.468291	422.237783	**9**
5	454.266012	227.636644	436.255447	218.631362	**V**	***790.441742***	395.724509	773.415193	387.211234	772.431177	386.719226	**8**
6	525.303126	263.155201	507.292561	254.149919	**A**	***691.373328***	346.190302	674.346779	337.677028	673.362763	337.185020	**7**
7	612.335154	306.671215	594.324589	297.665933	**S**	***620.336214***	310.671745	603.309665	302.158471	602.325649	301.666463	**6**
8	683.372268	342.189772	665.361703	333.184489	**A**	***533.304186***	267.155731	516.277637	258.642457	515.293621	258.150449	**5**
9	796.456332	398.731804	778.445767	389.726521	**L**	***462.267072***	231.637174	445.240523	223.123899	444.256507	222.631891	**4**
10	883.488360	442.247818	865.477795	433.242535	**S**	***349.183008***	175.095142	332.156459	166.581867	331.172443	166.089859	**3**
11	970.520388	485.763832	952.509823	476.758549	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**



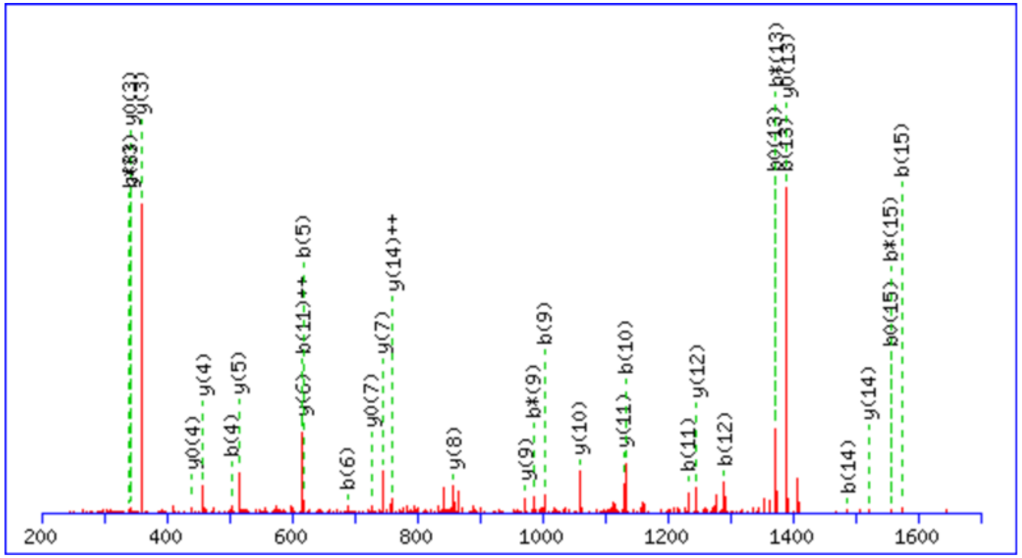
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 12206: 1746.918648 from(874.466600,2+)

Title: OECHL100310_29.16918.16918.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 84
Expect: 4.8e-007**Matches :** 34/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	***340.259468***	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	***503.322797***	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	***618.349740***	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	***689.386854***	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



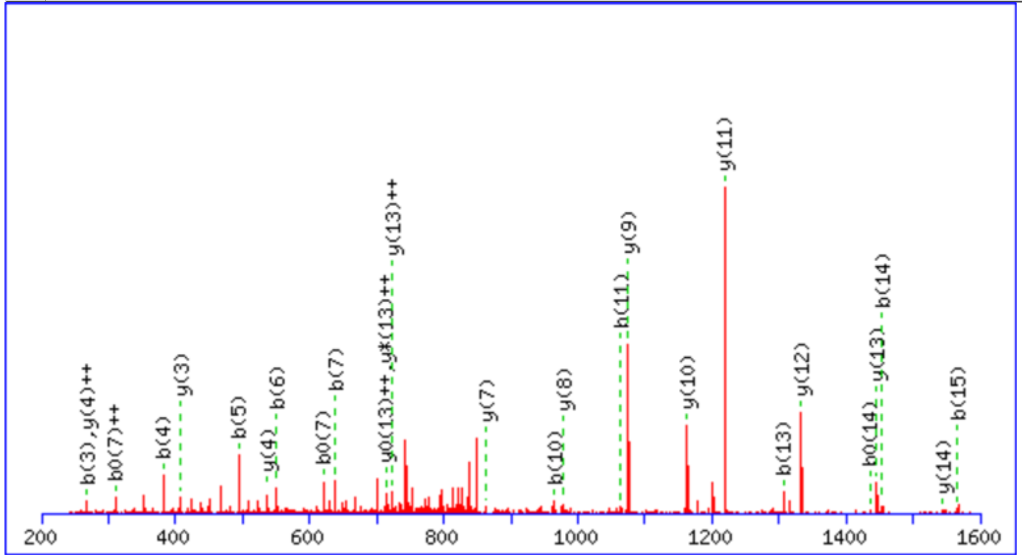
Peptide View

MS/MS Fragmentation of **APVILGSPDDVLEFLK**
Found in **IPI00073772**, Tax_Id=9606 Gene_Symbol=FBP1 Fructose-1,6-bisphosphatase 1
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 11971: 1711.940848 from(856.977700,2+)
Title: OECHL100310_29.22145.22145.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1711.939636**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 89
Expect: 8.8e-008**Matches :** 27/132 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**16**
2	169.097154	85.052215			**P**	1641.909801	821.458538	1624.883252	812.945264	1623.899236	812.453256	**15**
3	***268.165568***	134.586422			**V**	***1544.857037***	772.932156	1527.830488	764.418882	1526.846472	763.926874	**14**
4	***381.249632***	191.128454			**I**	***1445.788623***	723.397949	1428.762074	714.884675	1427.778058	714.392667	**13**
5	***494.333696***	247.670486			**L**	***1332.704559***	666.855917	1315.678010	658.342643	1314.693994	657.850635	**12**
6	***551.355160***	276.181218			**G**	***1219.620495***	610.313885	1202.593946	601.800611	1201.609930	601.308603	**11**

7	***638.387188***	319.697232	620.376623	310.691950	**S**	***1162.599031***	581.803153	1145.572482	573.289879	1144.588466	572.797871	**10**
8	735.439952	368.223614	717.429387	359.218332	**P**	***1075.567003***	538.287139	1058.540454	529.773865	1057.556438	529.281857	**9**
9	850.466895	425.737086	832.456330	416.731803	**D**	***978.514239***	489.760757	961.487690	481.247483	960.503674	480.755475	**8**
10	***965.493838***	483.250557	947.483273	474.245274	**D**	***863.487296***	432.247286	846.460747	423.734011	845.476731	423.242003	**7**
11	***1064.562252***	532.784764	1046.551687	523.779481	**V**	748.460353	374.733814	731.433804	366.220540	730.449788	365.728532	**6**
12	1177.646316	589.326796	1159.635751	580.321513	**L**	649.391939	325.199607	632.365390	316.686333	631.381374	316.194325	**5**
13	***1306.688909***	653.848092	1288.678344	644.842810	**E**	***536.307875***	268.657576	519.281326	260.144301	518.297310	259.652293	**4**
14	***1453.757323***	727.382299	1435.746758	718.377017	**F**	***407.265282***	204.136279	390.238733	195.623004			**3**
15	***1566.841387***	783.924331	1548.830822	774.919049	**L**	260.196868	130.602072	243.170319	122.088797			**2**
16					**K**	147.112804	74.060040	130.086255	65.546765			**1**



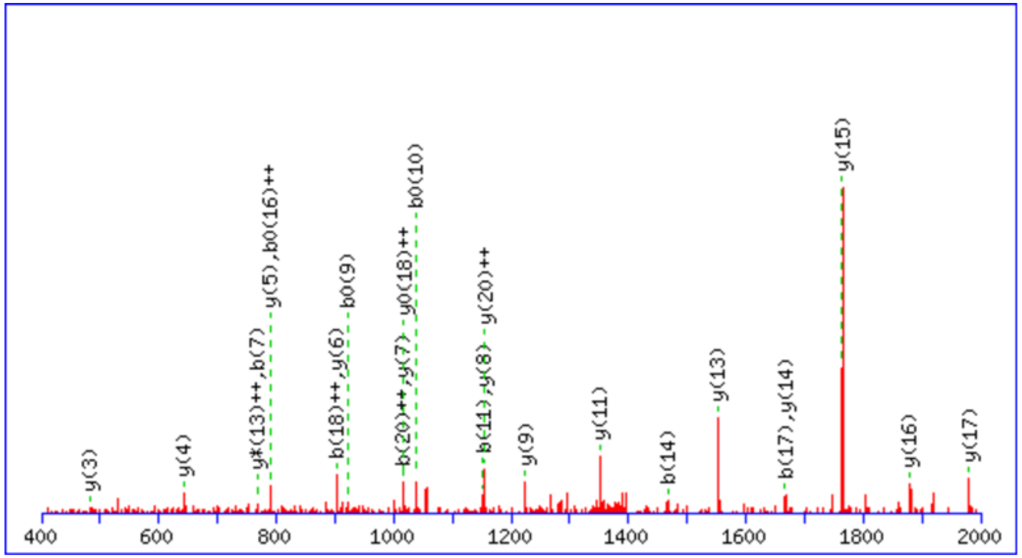
Peptide View

MS/MS Fragmentation of **SCSSSCVATDPDSIGAAHLIFCCFR**
Found in **IPI00022620**, Tax_Id=9606 Gene_Symbol=SLURP1 Secreted Ly-6/uPAR-related protein 1
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 18111: 2817.203448 from(1409.609000,2+)

Title: OECHL100310_29.19251.19251.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 2817.197922**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 0.00029**Matches :** 25/216 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							25
2	248.069953	124.538614	230.059388	115.533332	C	2731.173141	1366.090208	2714.146592	1357.576934	2713.162576	1357.084926	24
3	335.101981	168.054628	317.091416	159.049346	S	2571.142492	1286.074884	2554.115943	1277.561609	2553.131927	1277.069601	23
4	422.134009	211.570642	404.123444	202.565360	S	2484.110464	1242.558870	2467.083915	1234.045595	2466.099899	1233.553587	22
5	509.166037	255.086656	491.155472	246.081374	S	2397.078436	1199.042856	2380.051887	1190.529581	2379.067871	1190.037573	21
6	669.196686	335.101981	651.186121	326.096699	C	2310.046408	1155.526842	2293.019859	1147.013567	2292.035843	1146.521559	20
7	**768.265100**	384.636188	750.254535	375.630905	V	2150.015759	1075.511517	2132.989210	1066.998243	2132.005194	1066.506235	19
8	839.302214	420.154745	821.291649	411.149462	A	2050.947345	1025.977310	2033.920796	1017.464036	2032.936780	1016.972028	18
9	940.349893	470.678585	922.339328	461.673302	T	***1979.910231***	990.458753	1962.883682	981.945479	1961.899666	981.453471	17
10	1055.376836	528.192056	1037.366271	519.186773	D	***1878.862552***	939.934914	1861.836003	931.421639	1860.851987	930.929631	16
11	**1152.429600**	576.718438	1134.419035	567.713155	P	***1763.835609***	882.421442	1746.809060	873.908168	1745.825044	873.416160	15
12	1267.456543	634.231910	1249.445978	625.226627	D	***1666.782845***	833.895060	1649.756296	825.381786	1648.772280	824.889778	14
13	1354.488571	677.747924	1336.478006	668.742641	S	***1551.755902***	776.381589	1534.729353	767.868314	1533.745337	767.376306	13
14	**1467.572635**	734.289956	1449.562070	725.284673	I	1464.723874	732.865575	1447.697325	724.352300			12
15	1524.594099	762.800687	1506.583534	753.795405	G	***1351.639810***	676.323543	1334.613261	667.810268			11
16	1595.631213	798.319244	1577.620648	789.313962	A	1294.618346	647.812811	1277.591797	639.299536			10
17	**1666.668327**	833.837801	1648.657762	824.832519	A	***1223.581232***	612.294254	1206.554683	603.780979			9
18	1803.727239	902.367257	1785.716674	893.361975	H	***1152.544118***	576.775697	1135.517569	568.262422			8
19	1916.811303	958.909289	1898.800738	949.904007	L	***1015.485206***	508.246241	998.458657	499.732966			7
20	2029.895367	1015.451321	2011.884802	1006.446039	I	***902.401142***	451.704209	885.374593	443.190934			6
21	2176.963781	1088.985528	2158.953216	1079.980246	F	***789.317078***	395.162177	772.290529	386.648902			5
22	2336.994430	1169.000853	2318.983865	1159.995570	C	***642.248664***	321.627970	625.222115	313.114695			4
23	2497.025079	1249.016177	2479.014514	1240.010895	C	***482.218015***	241.612645	465.191466	233.099371			3
24	2644.093493	1322.550384	2626.082928	1313.545102	F	322.187366	161.597321	305.160817	153.084046			2
25					R	175.118952	88.063114	158.092403	79.549839			1



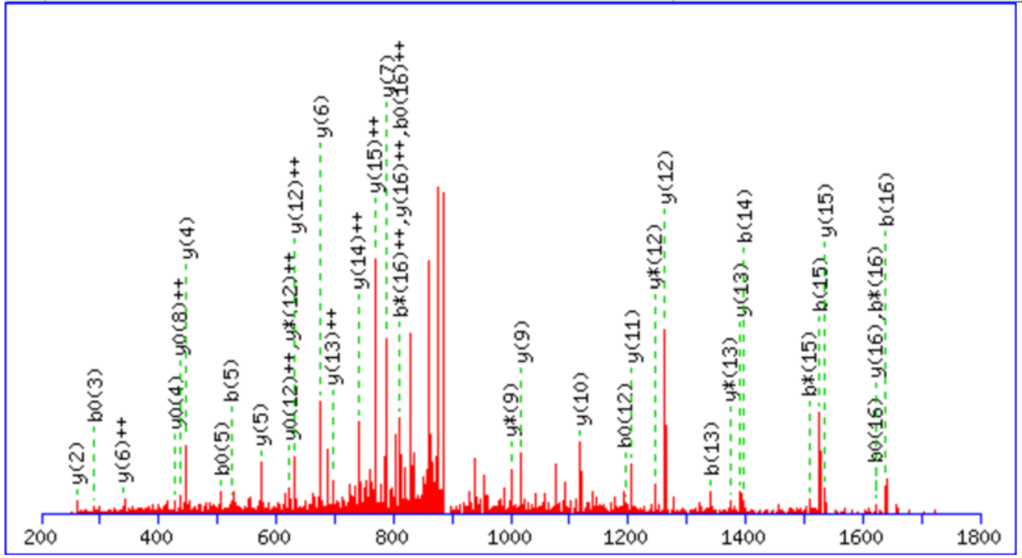
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 12616: 1784.880048 from(893.447300,2+)
Title: OECHL100310_29.7619.7619.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 80
Expect: 1.7e-006**Matches :** 38/170 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	164.070605	82.538940					**Y**							**17**
2	251.102633	126.054954			233.092068	117.049672	**S**	***1622.823172***	811.915224	1605.796623	803.401950	1604.812607	802.909941	**16**
3	308.124097	154.565687			290.113532	145.560404	**G**	***1535.791144***	768.399210	1518.764595	759.885936	1517.780579	759.393928	**15**
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.883195	**14**
5	**524.198718**	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.367182	**13**
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.845885	**12**

7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.335153	**11**
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.819139	**10**
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.295299	**9**
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.266010	**8**
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.742171	**7**
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.200139	**6**
13	**1340.632852**	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.676299	**5**
14	**1397.654316**	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	**4**
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**

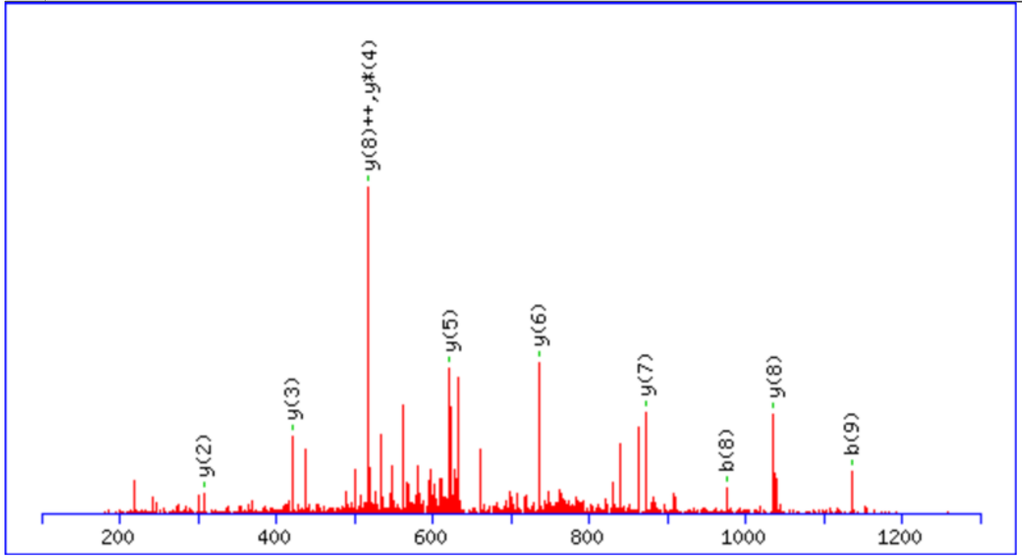


Peptide View

MS/MS Fragmentation of **FVYHLSDLCK**
Found in **IPI00178926**, Tax_Id=9606 Gene_Symbol=IGJ Immunoglobulin J chain
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 7106: 1280.622248 from(641.318400,2+)
Title: OECHL100310_29.13863.13863.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1280.622345**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49
Expect: 0.0011**Matches :** 10/74 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483			**F**							**10**
2	247.144104	124.075690			**V**	1134.561207	567.784242	1117.534658	559.270967	1116.550642	558.778959	**9**
3	410.207433	205.607354			**Y**	***1035.492793***	518.250035	1018.466244	509.736760	1017.482228	509.244752	**8**
4	547.266345	274.136811			**H**	***872.429464***	436.718370	855.402915	428.205096	854.418899	427.713088	**7**
5	660.350409	330.678843			**L**	***735.370552***	368.188914	718.344003	359.675640	717.359987	359.183632	**6**
6	747.382437	374.194857	729.371872	365.189574	**S**	***622.286488***	311.646882	605.259939	303.133608	604.275923	302.641600	**5**
7	862.409380	431.708328	844.398815	422.703045	**D**	535.254460	268.130868	518.227911	259.617594	517.243895	259.125586	**4**
8	**975.493444**	488.250360	957.482879	479.245077	**L**	***420.227517***	210.617397	403.200968	202.104122			**3**
9	**1135.524093**	568.265685	1117.513528	559.260402	**C**	***307.143453***	154.075365	290.116904	145.562090			**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**

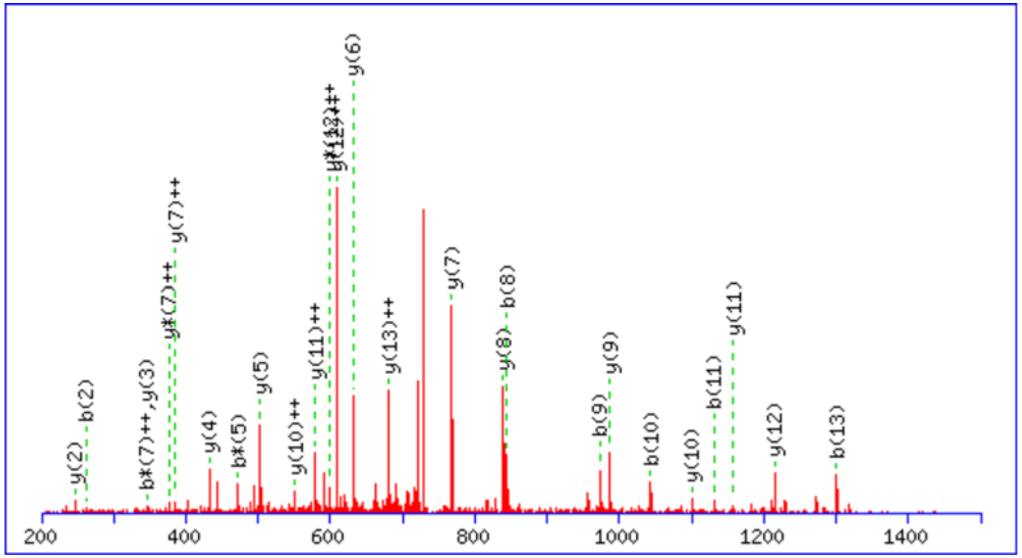


Peptide View

MS/MS Fragmentation of **LFGGNFAHQASVAR**
Found in **IPI00298237**, Tax_Id=9606 Gene_Symbol=TPP1 cDNA FLJ56402, highly similar to Tripeptidyl-peptidase 1
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 9209: 1473.747848 from(737.881200,2+)
Title: OECHL100310_29.11981.11981.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.747696**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 73
Expect: 7.1e-006**Matches :** 26/122 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	114.091340	57.549308					**L**							**14**
2	**261.159754**	131.083515					**F**	1361.670909	681.339093	1344.644360	672.825818	1343.660344	672.333810	**13**
3	318.181218	159.594247					**G**	***1214.602495***	607.804886	1197.575946	599.291611	1196.591930	598.799603	**12**
4	375.202682	188.104979					**G**	***1157.581031***	579.294154	1140.554482	570.780879	1139.570466	570.288871	**11**
5	489.245609	245.126442	472.219060	236.613168			**N**	***1100.559567***	550.783422	1083.533018	542.270147	1082.549002	541.778139	**10**
6	636.314023	318.660650	619.287474	310.147375			**F**	***986.516640***	493.761958	969.490091	485.248684	968.506075	484.756676	**9**
7	707.351137	354.179207	690.324588	345.665932			**A**	***839.448226***	420.227751	822.421677	411.714477	821.437661	411.222469	**8**
8	**844.410049**	422.708663	827.383500	414.195388			**H**	***768.411112***	384.709194	751.384563	376.195920	750.400547	375.703912	**7**
9	**972.468627**	486.737952	955.442078	478.224677			**Q**	***631.352200***	316.179738	614.325651	307.666464	613.341635	307.174456	**6**
10	**1043.505741**	522.256509	1026.479192	513.743234			**A**	***503.293622***	252.150449	486.267073	243.637175	485.283057	243.145167	**5**
11	**1130.537769**	565.772523	1113.511220	557.259248	1112.527204	556.767240	**S**	***432.256508***	216.631892	415.229959	208.118618	414.245943	207.626610	**4**
12	1229.606183	615.306730	1212.579634	606.793455	1211.595618	606.301447	**V**	***345.224480***	173.115878	328.197931	164.602603			**3**
13	**1300.643297**	650.825287	1283.616748	642.312012	1282.632732	641.820004	**A**	***246.156066***	123.581671	229.129517	115.068396			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



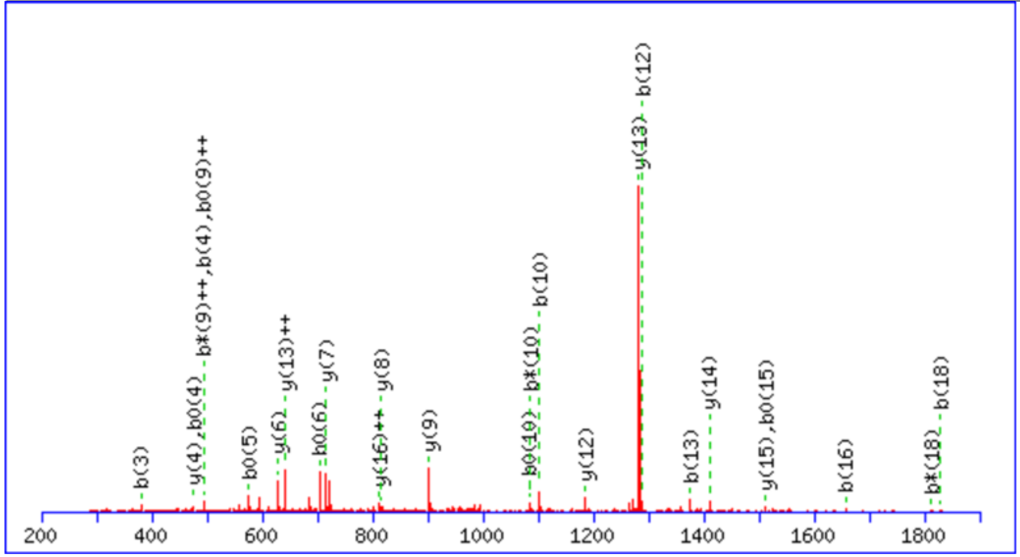
Peptide View

MS/MS Fragmentation of **SYELTQPPSVSVSPGQTAR**
Found in **IPI00382440**, Tax_Id=9606 Gene_Symbol=- Ig lambda chain V-IV region Hil
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 14283: 2002.995448 from(1002.505000,2+)
Title: OECHL100310_29.13257.13257.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 2002.995987**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70
Expect: 1.8e-005**Matches :** 27/202 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	**S**							**19**
2	251.102633	126.054954			233.092068	117.049672	**Y**	1916.971234	958.989255	1899.944685	950.475981	1898.960669	949.983973	**18**
3	***380.145226***	190.576251			362.134661	181.570969	**E**	1753.907905	877.457591	1736.881356	868.944316	1735.897340	868.452308	**17**
4	***493.229290***	247.118283			475.218725	238.113001	**L**	1624.865312	812.936294	1607.838763	804.423020	1606.854747	803.931012	**16**
5	594.276969	297.642123			576.266404	288.636840	**T**	***1511.781248***	756.394262	1494.754699	747.880988	1493.770683	747.388980	**15**
6	722.335547	361.671412	705.308998	353.158137	704.324982	352.666129	**Q**	***1410.733569***	705.870423	1393.707020	697.357148	1392.723004	696.865140	**14**

7	819.388311	410.197794	802.361762	401.684519	801.377746	401.192511	P	***1282.674991***	641.841134	1265.648442	633.327859	1264.664426	632.835851	13
8	916.441075	458.724176	899.414526	450.210901	898.430510	449.718893	P	***1185.622227***	593.314752	1168.595678	584.801477	1167.611662	584.309469	12
9	1003.473103	502.240190	986.446554	493.726915	985.462538	493.234907	S	1088.569463	544.788370	1071.542914	536.275095	1070.558898	535.783087	11
10	***1102.541517***	551.774397	1085.514968	543.261122	1084.530952	542.769114	V	1001.537435	501.272356	984.510886	492.759081	983.526870	492.267073	10
11	1189.573545	595.290411	1172.546996	586.777136	1171.562980	586.285128	S	***902.469021***	451.738149	885.442472	443.224874	884.458456	442.732866	9
12	***1288.641959***	644.824618	1271.615410	636.311343	1270.631394	635.819335	V	***815.436993***	408.222135	798.410444	399.708860	797.426428	399.216852	8
13	***1375.673987***	688.340632	1358.647438	679.827357	1357.663422	679.335349	S	***716.368579***	358.687928	699.342030	350.174653	698.358014	349.682645	7
14	1472.726751	736.867014	1455.700202	728.353739	1454.716186	727.861731	P	***629.336551***	315.171914	612.310002	306.658639	611.325986	306.166631	6
15	1529.748215	765.377746	1512.721666	756.864471	1511.737650	756.372463	G	532.283787	266.645532	515.257238	258.132257	514.273222	257.640249	5
16	***1657.806793***	829.407035	1640.780244	820.893760	1639.796228	820.401752	Q	***475.262323***	238.134800	458.235774	229.621525	457.251758	229.129517	4
17	1758.854472	879.930874	1741.827923	871.417600	1740.843907	870.925592	T	347.203745	174.105510	330.177196	165.592236	329.193180	165.100228	3
18	***1829.891586***	915.449431	1812.865037	906.936157	1811.881021	906.444149	A	246.156066	123.581671	229.129517	115.068396			2
19							R	175.118952	88.063114	158.092403	79.549839			1



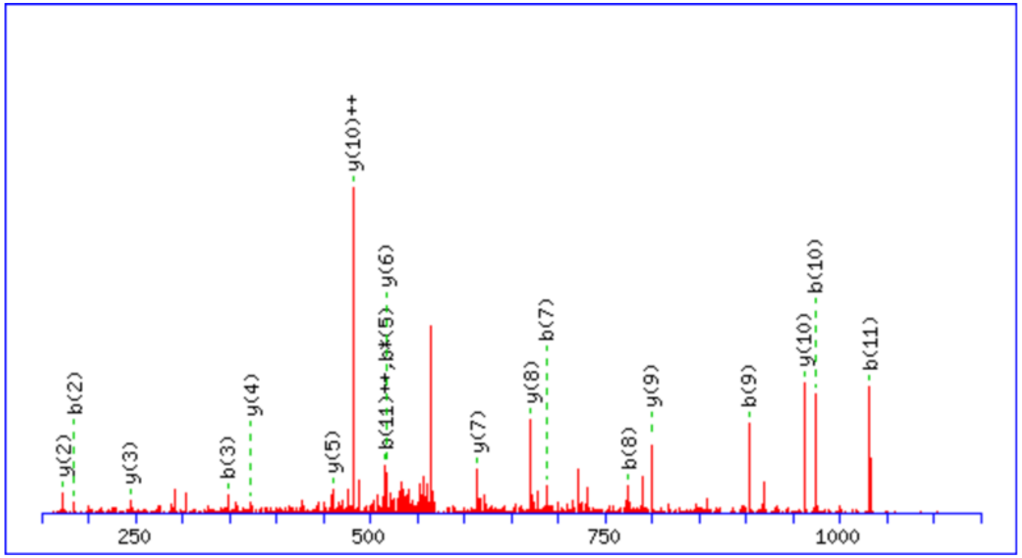
Peptide View

MS/MS Fragmentation of **AIYKGPGSEAGP**

Found in **IPI00011284**, Tax_Id=9606 Gene_Symbol=COMT Isoform Membrane-bound of Catechol O-methyltransferase
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 4931: 1145.571848 from(573.793200,2+)
Title: OECHL100310_29.8086.8086.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1145.571671**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59
Expect: 0.00016**Matches :** 19/90 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							12
2	**185.128454**	93.067865					I	1075.541852	538.274564	1058.515303	529.761290	1057.531287	529.269282	11
3	**348.191783**	174.599529					Y	***962.457788***	481.732532	945.431239	473.219258	944.447223	472.727250	10
4	476.286746	238.647011	459.260197	230.133737			K	***799.394459***	400.200868	782.367910	391.687593	781.383894	391.195585	9
5	533.308210	267.157743	516.281661	258.644469			G	***671.299496***	336.153386			653.288931	327.148104	8
6	630.360974	315.684125	613.334425	307.170851			P	***614.278032***	307.642654			596.267467	298.637372	7
7	**687.382438**	344.194857	670.355889	335.681583			G	***517.225268***	259.116272			499.214703	250.110990	6
8	**774.414466**	387.710871	757.387917	379.197597	756.403901	378.705589	S	***460.203804***	230.605540			442.193239	221.600257	5
9	**903.457059**	452.232168	886.430510	443.718893	885.446494	443.226885	E	***373.171776***	187.089526			355.161211	178.084243	4
10	**974.494173**	487.750725	957.467624	479.237450	956.483608	478.745442	A	***244.129183***	122.568229					3
11	**1031.515637**	516.261457	1014.489088	507.748182	1013.505072	507.256174	G	***173.092069***	87.049672					2
12							P	116.070605	58.538941					1



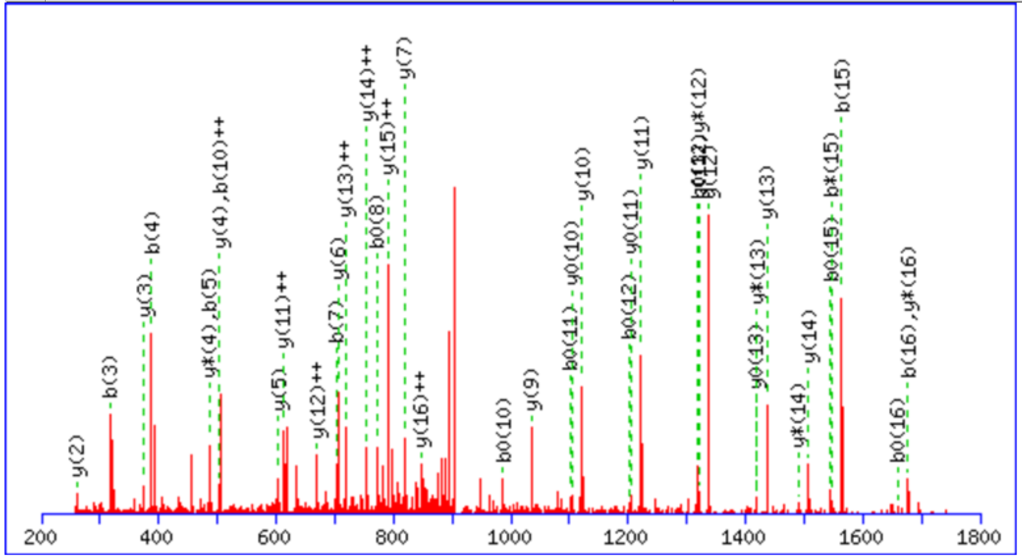
Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTKDLK**
Found in **IPI00455510**, Tax_Id=9606 Gene_Symbol=PTMA;PTMAP5 Isoform 2 of Prothymosin alpha
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 12879: 1821.886048 from(911.950300,2+)
Title: OECHL100310_29.12093.12093.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1821.884354**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 69 **Expect:** 1.9e-005**Matches :** 42/162 fragment ions using 75 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	**S**							**17**
2	245.076812	123.042044			227.066247	114.036761	**D**	1693.849052	847.428164	1676.822503	838.914890	1675.838487	838.422882	**16**
3	**316.113926**	158.560601			298.103361	149.555319	**A**	1578.822109	789.914693	1561.795560	781.401418	1560.811544	780.909410	**15**
4	**387.151040**	194.079158			369.140475	185.073875	**A**	***1507.784995***	754.396136	1490.758446	745.882861	1489.774430	745.390853	**14**
5	**486.219454**	243.613365			468.208889	234.608082	**V**	***1436.747881***	718.877579	1419.721332	710.364304	1418.737316	709.872296	**13**
6	601.246397	301.126837			583.235832	292.121554	**D**	***1337.679467***	669.343372	1320.652918	660.830097	1319.668902	660.338089	**12**

7	**702.294076**	351.650676			684.283511	342.645394	**T**	***1222.652524***	611.829900	1205.625975	603.316626	1204.641959	602.824618	**11**
8	789.326104	395.166690			771.315539	386.161408	**S**	***1121.604845***	561.306061	1104.578296	552.792786	1103.594280	552.300778	**10**
9	876.358132	438.682704			858.347567	429.677421	**S**	***1034.572817***	517.790047	1017.546268	509.276772	1016.562252	508.784764	**9**
10	1005.400725	503.204001			987.390160	494.198718	**E**	947.540789	474.274033	930.514240	465.760758	929.530224	465.268750	**8**
11	1118.484789	559.746033			1100.474224	550.740750	**I**	***818.498196***	409.752736	801.471647	401.239462	800.487631	400.747454	**7**
12	1219.532468	610.269872			1201.521903	601.264590	**T**	***705.414132***	353.210704	688.387583	344.697430	687.403567	344.205422	**6**
13	**1320.580147**	660.793712			1302.569582	651.788429	**T**	***604.366453***	302.686865	587.339904	294.173590	586.355888	293.681582	**5**
14	1448.675110	724.841193	1431.648561	716.327919	1430.664545	715.835911	**K**	***503.318774***	252.163025	486.292225	243.649750	485.308209	243.157742	**4**
15	**1563.702053**	782.354665	1546.675504	773.841390	1545.691488	773.349382	**D**	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	**3**
16	**1676.786117**	838.896697	1659.759568	830.383422	1658.775552	829.891414	**L**	***260.196868***	130.602072	243.170319	122.088797			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**

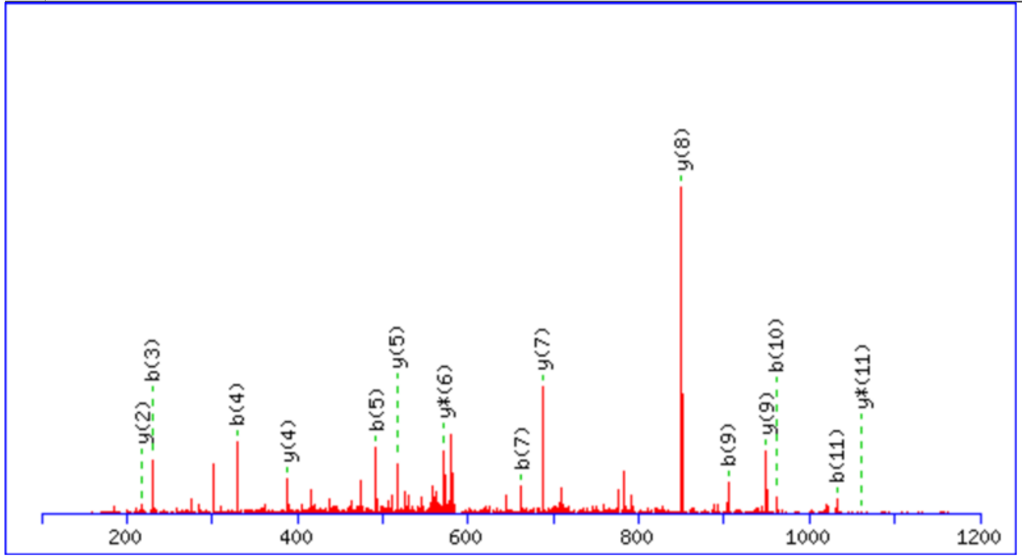


Peptide View

MS/MS Fragmentation of **TGAVYVAEIGAK**
Found in **IPI00552937**, Tax_Id=9606 Gene_Symbol=NHLRC3 NHL repeat-containing protein 3
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 5506: 1177.635448 from(589.825000,2+)
Title: OECHL100310_29.11350.11350.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1177.634277**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 9.9e-005**Matches :** 15/102 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							**12**
2	159.076419	80.041847	141.065854	71.036565	**G**	1077.593888	539.300582	1060.567339	530.787308	1059.583323	530.295300	**11**
3	***230.113533***	115.560404	212.102968	106.555122	**A**	1020.572424	510.789850	1003.545875	502.276576	1002.561859	501.784568	**10**
4	***329.181947***	165.094611	311.171382	156.089329	**V**	***949.535310***	475.271293	932.508761	466.758019	931.524745	466.266011	**9**
5	***492.245276***	246.626276	474.234711	237.620994	**Y**	***850.466896***	425.737086	833.440347	417.223812	832.456331	416.731804	**8**
6	591.313690	296.160483	573.303125	287.155201	**V**	***687.403567***	344.205422	670.377018	335.692147	669.393002	335.200139	**7**
7	***662.350804***	331.679040	644.340239	322.673758	**A**	588.335153	294.671215	571.308604	286.157940	570.324588	285.665932	**6**
8	791.393397	396.200337	773.382832	387.195054	**E**	***517.298039***	259.152658	500.271490	250.639383	499.287474	250.147375	**5**
9	***904.477461***	452.742369	886.466896	443.737086	**I**	***388.255446***	194.631361	371.228897	186.118087			**4**
10	***961.498925***	481.253101	943.488360	472.247818	**G**	275.171382	138.089329	258.144833	129.576055			**3**
11	***1032.536039***	516.771658	1014.525474	507.766375	**A**	***218.149918***	109.578597	201.123369	101.065322			**2**
12					**K**	147.112804	74.060040	130.086255	65.546765			**1**

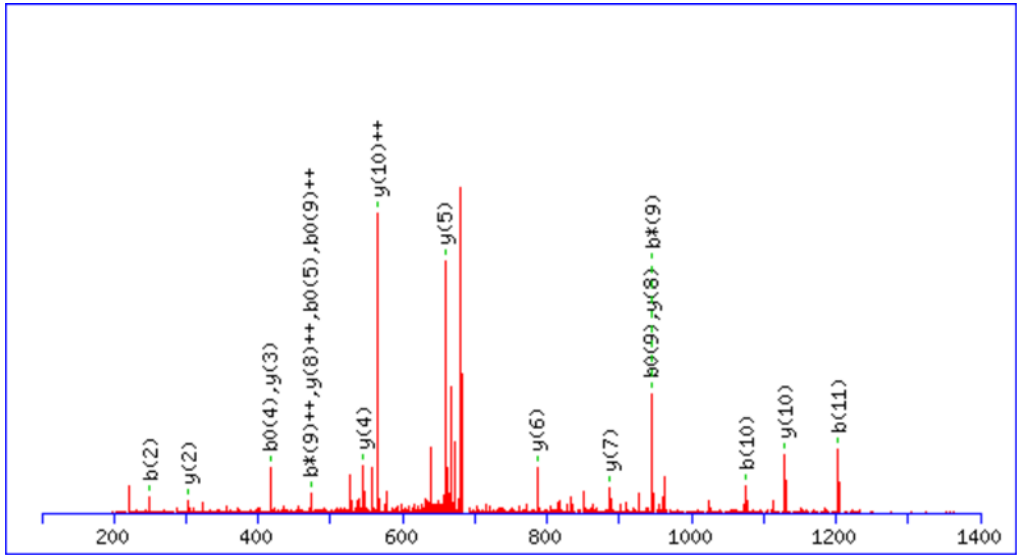


Peptide View

MS/MS Fragmentation of **TFGQGTKLEIKR**
Found in **IPI00827643**, Tax_Id=9606 Gene_Symbol=- HRV Fab 027-VL (Fragment)
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 8199: 1376.778448 from(689.396500,2+)
Title: OECHL100310_29.8043.8043.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1376.777588**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57
Expect: 7.3e-005**Matches :** 19/120 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	102.054955	51.531116			84.044390	42.525833	T							12
2	**249.123369**	125.065322			231.112804	116.060040	F	1276.737198	638.872237	1259.710649	630.358963	1258.726633	629.866955	11
3	306.144833	153.576054			288.134268	144.570772	G	***1129.668784***	565.338030	1112.642235	556.824756	1111.658219	556.332748	10
4	434.203411	217.605343	417.176862	209.092069	416.192846	208.600061	Q	1072.647320	536.827298	1055.620771	528.314024	1054.636755	527.822016	9
5	491.224875	246.116075	474.198326	237.602801	473.214310	237.110793	G	***944.588742***	472.798009	927.562193	464.284735	926.578177	463.792727	8
6	592.272554	296.639915	575.246005	288.126641	574.261989	287.634633	T	***887.567278***	444.287277	870.540729	435.774003	869.556713	435.281995	7
7	720.367517	360.687397	703.340968	352.174122	702.356952	351.682114	K	***786.519599***	393.763438	769.493050	385.250163	768.509034	384.758155	6
8	833.451581	417.229429	816.425032	408.716154	815.441016	408.224146	L	***658.424636***	329.715956	641.398087	321.202682	640.414071	320.710674	5
9	962.494174	481.750725	945.467625	473.237451	944.483609	472.745443	E	***545.340572***	273.173924	528.314023	264.660650	527.330007	264.168642	4
10	**1075.578238**	538.292757	1058.551689	529.779483	1057.567673	529.287475	I	***416.297979***	208.652627	399.271430	200.139353			3
11	**1203.673201**	602.340239	1186.646652	593.826964	1185.662636	593.334956	K	***303.213915***	152.110595	286.187366	143.597321			2
12							R	175.118952	88.063114	158.092403	79.549839			1



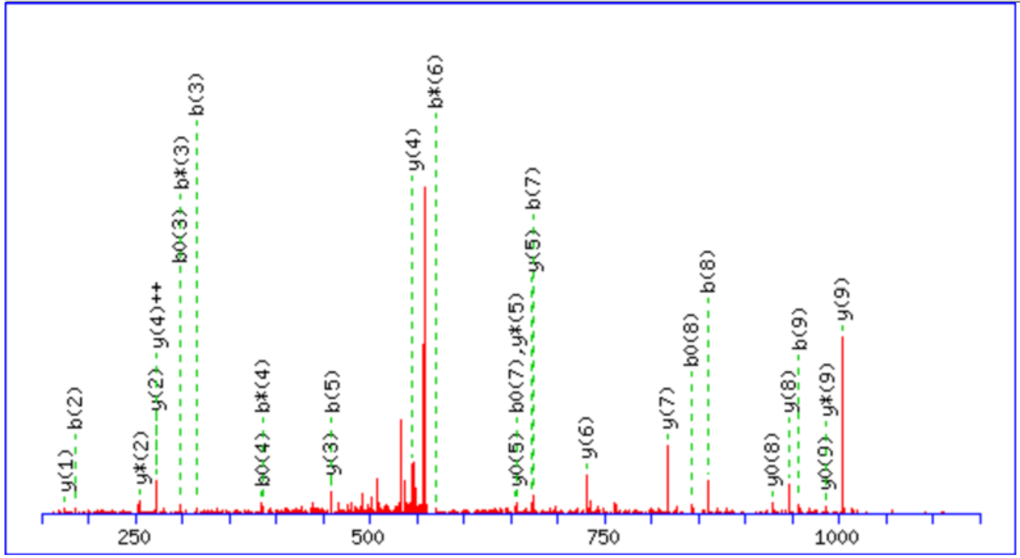
Peptide View

MS/MS Fragmentation of **KGESGQSWPR**
Found in **IPI00015029**, Tax_Id=9606 Gene_Symbol=PTGES3 Prostaglandin E synthase 3
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 4699: 1130.544448 from(566.279500,2+)
Title: OECHL100310_29.3933.3933.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1130.546860**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 0.00028**Matches :** 29/98 fragment ions using 58 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							**10**
2	**186.123703**	93.565489	169.097154	85.052215			**G**	***1003.459184***	502.233230	986.432635	493.719956	985.448619	493.227948	**9**
3	**315.166296**	158.086786	298.139747	149.573512	297.155731	149.081504	**E**	***946.437720***	473.722498	929.411171	465.209224	928.427155	464.717216	**8**
4	402.198324	201.602800	385.171775	193.089526	384.187759	192.597518	**S**	***817.395127***	409.201202	800.368578	400.687927	799.384562	400.195919	**7**
5	**459.219788**	230.113532	442.193239	221.600258	441.209223	221.108250	**G**	***730.363099***	365.685188	713.336550	357.171913	712.352534	356.679905	**6**
6	587.278366	294.142821	570.251817	285.629547	569.267801	285.137539	**Q**	***673.341635***	337.174456	656.315086	328.661181	655.331070	328.169173	**5**

7	**674.310394**	337.658835	657.283845	329.145560	656.299829	328.653552	**S**	***545.283057***	273.145167	528.256508	264.631892	527.272492	264.139884	**4**
8	**860.389707**	430.698492	843.363158	422.185217	842.379142	421.693209	**W**	***458.251029***	229.629153	441.224480	221.115878			**3**
9	**957.442471**	479.224874	940.415922	470.711599	939.431906	470.219591	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
10							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



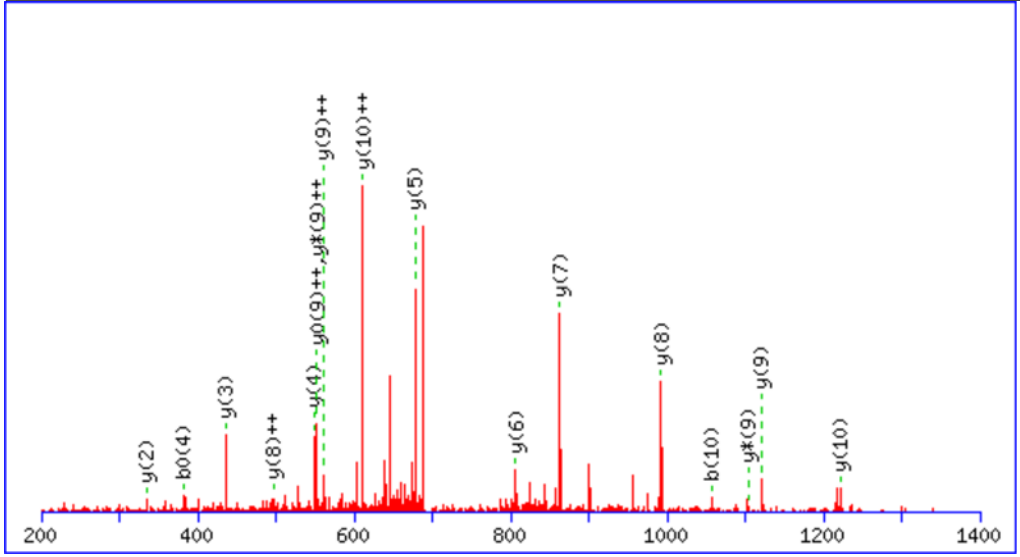
Peptide View

MS/MS Fragmentation of **VATQEGKEITCR**
Found in **IPI00031564**, Tax_Id=9606 Gene_Symbol=GGCT Isoform 1 of Gamma-glutamylcyclotransferase
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 8334: 1390.686848 from(696.350700,2+)
Title: OECHL100310_29.3539.3539.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1390.687454**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.0013**Matches :** 17/118 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					**V**							**12**
2	171.112804	86.060040					**A**	1292.626328	646.816802	1275.599779	638.303528	1274.615763	637.811520	**11**

3	272.160483	136.583879			254.149918	127.578597	**T**	***1221.589214***	611.298245	1204.562665	602.784971	1203.578649	602.292963	**10**
4	400.219061	200.613169	383.192512	192.099894	382.208496	191.607886	**Q**	***1120.541535***	560.774406	1103.514986	552.261131	1102.530970	551.769123	**9**
5	529.261654	265.134465	512.235105	256.621191	511.251089	256.129183	**E**	***992.482957***	496.745117	975.456408	488.231842	974.472392	487.739834	**8**
6	586.283118	293.645197	569.256569	285.131923	568.272553	284.639915	**G**	***863.440364***	432.223820	846.413815	423.710546	845.429799	423.218538	**7**
7	714.378081	357.692679	697.351532	349.179404	696.367516	348.687396	**K**	***806.418900***	403.713088	789.392351	395.199814	788.408335	394.707806	**6**
8	843.420674	422.213975	826.394125	413.700701	825.410109	413.208693	**E**	***678.323937***	339.665607	661.297388	331.152332	660.313372	330.660324	**5**
9	956.504738	478.756007	939.478189	470.242733	938.494173	469.750725	**I**	***549.281344***	275.144310	532.254795	266.631036	531.270779	266.139028	**4**
10	1057.552417	529.279847	1040.525868	520.766572	1039.541852	520.274564	**T**	***436.197280***	218.602278	419.170731	210.089003	418.186715	209.596995	**3**
11	1217.583066	609.295171	1200.556517	600.781897	1199.572501	600.289889	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**



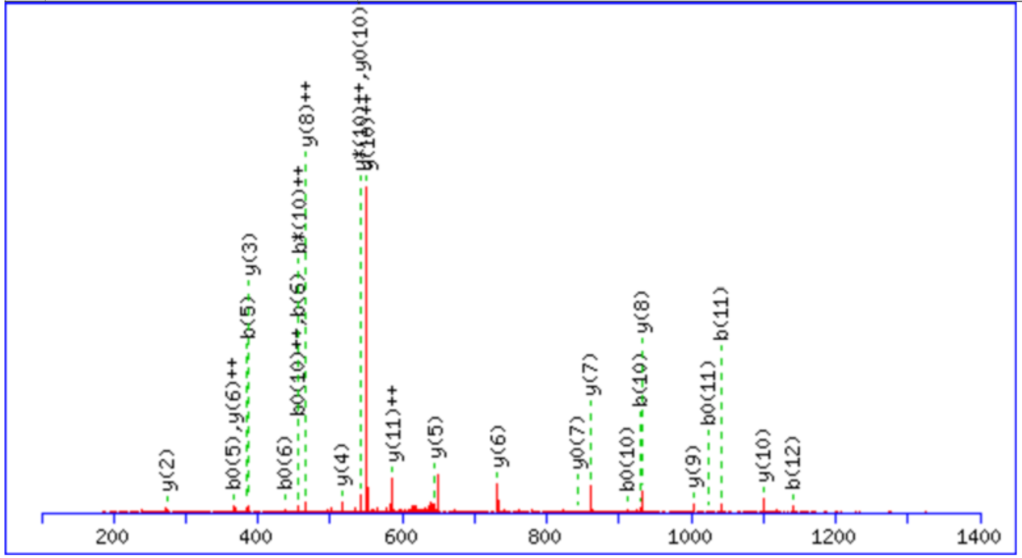
Peptide View

MS/MS Fragmentation of **SGAPAAESKEIVR**
Found in **IPI00299977**, Tax_Id=9606 Gene_Symbol=PHPT1 14 kDa phosphohistidine phosphatase
Experiment: 55 - PyD-1 **Fraction:** PyD-1

Match to Query 7670: 1313.694648 from(657.854600,2+)

Title: OECHL100310_29.4497.4497.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1313.693893**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00086**Matches :** 27/122 fragment ions using 55 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	**S**							**13**
2	145.060768	73.034022			127.050203	64.028740	**G**	1227.669177	614.338227	1210.642628	605.824952	1209.658612	605.332944	**12**
3	216.097882	108.552579			198.087317	99.547296	**A**	1170.647713	585.827495	1153.621164	577.314220	1152.637148	576.822212	**11**
4	313.150646	157.078961			295.140081	148.073679	**P**	***1099.610599***	550.308938	1082.584050	541.795663	1081.600034	541.303655	**10**
5	**384.187760**	192.597518			366.177195	183.592235	**A**	***1002.557835***	501.782556	985.531286	493.269281	984.547270	492.777273	**9**
6	**455.224874**	228.116075			437.214309	219.110792	**A**	***931.520721***	466.263999	914.494172	457.750724	913.510156	457.258716	**8**
7	584.267467	292.637372			566.256902	283.632089	**E**	***860.483607***	430.745442	843.457058	422.232167	842.473042	421.740159	**7**
8	671.299495	336.153386			653.288930	327.148103	**S**	***731.441014***	366.224145	714.414465	357.710871	713.430449	357.218863	**6**
9	799.394458	400.200867	782.367909	391.687592	781.383893	391.195585	**K**	***644.408986***	322.708131	627.382437	314.194857	626.398421	313.702849	**5**
10	**928.437051**	464.722164	911.410502	456.208889	910.426486	455.716881	**E**	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.655367	**4**
11	**1041.521115**	521.264196	1024.494566	512.750921	1023.510550	512.258913	**I**	***387.271430***	194.139353	370.244881	185.626079			**3**
12	**1140.589529**	570.798403	1123.562980	562.285128	1122.578964	561.793120	**V**	***274.187366***	137.597321	257.160817	129.084047			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

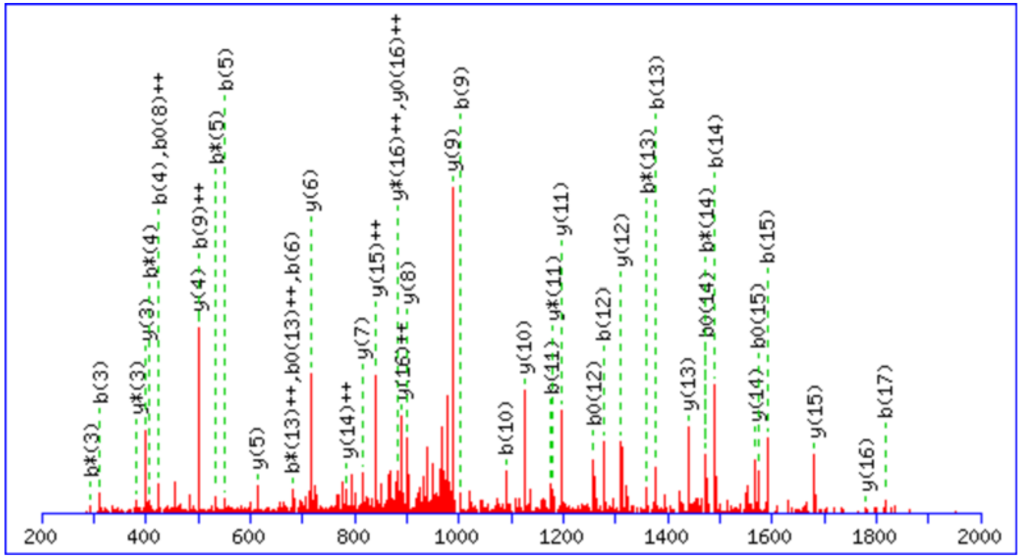


Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 40 - OPD-1 **Fraction:** OPD-1

Match to Query 12071: 1990.022848 from(996.018700,2+)
Title: OECHL100310_27.9367.9367.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 84
Expect: 5e-007**Matches :** 45/186 fragment ions using 81 most intense peaks (help)

#	**b**	**b^{++}**	**b***	**b^{*++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	**424.255445**	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	**552.314023**	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	**680.372601**	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**
7	795.399544	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	**1003.495570**	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	**1177.559626**	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	**1377.675719**	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510			**3**
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**



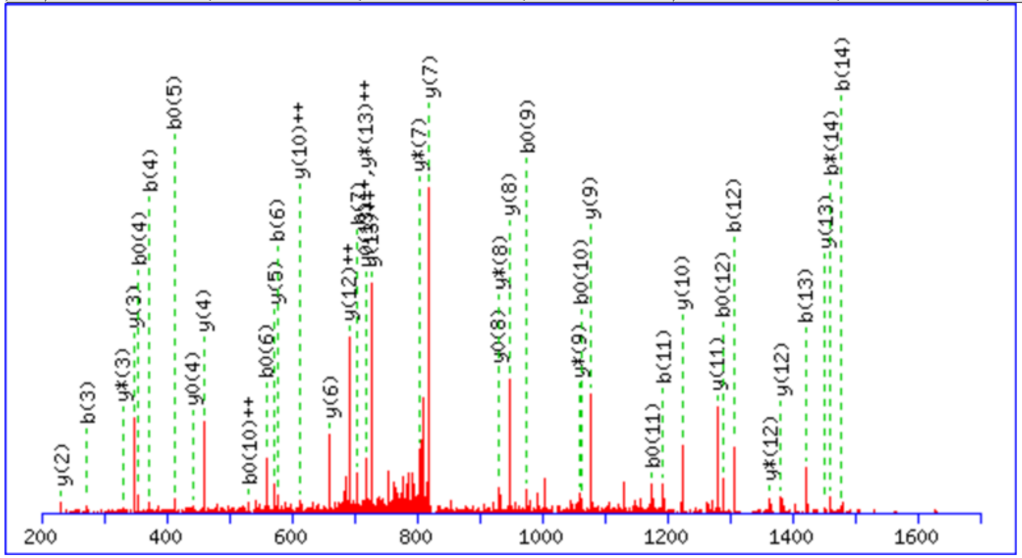
Peptide View

MS/MS Fragmentation of **VTATGFQQCSLIDGR**
Found in **IPI00333140**, Tax_Id=9606 Gene_Symbol=DNER Delta and Notch-like epidermal growth factor-related receptor
Experiment: 40 - OPD-1 **Fraction:** OPD-1

Match to Query 9731: 1651.800848 from(826.907700,2+)
Title: OECHL100310_27.13267.13267.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1651.798828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 84
Expect: 4.9e-007**Matches :** 41/150 fragment ions using 69 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					**V**							**15**
2	201.123369	101.065322			183.112804	92.060040	**T**	1553.737670	777.372473	1536.711121	768.859198	1535.727105	768.367190	**14**
3	**272.160483**	136.583879			254.149918	127.578597	**A**	***1452.689991***	726.848633	1435.663442	718.335359	1434.679426	717.843351	**13**
4	**373.208162**	187.107719			355.197597	178.102437	**T**	***1381.652877***	691.330076	1364.626328	682.816802	1363.642312	682.324794	**12**
5	430.229626	215.618451			412.219061	206.613169	**G**	***1280.605198***	640.806237	1263.578649	632.292962	1262.594633	631.800954	**11**
6	**577.298040**	289.152658			559.287475	280.147376	**F**	***1223.583734***	612.295505	1206.557185	603.782230	1205.573169	603.290222	**10**

7	**705.356618**	353.181947	688.330069	344.668673	687.346053	344.176665	**Q**	***1076.515320***	538.761298	1059.488771	530.248023	1058.504755	529.756015	**9**
8	833.415196	417.211236	816.388647	408.697962	815.404631	408.205954	**Q**	***948.456742***	474.732009	931.430193	466.218734	930.446177	465.726726	**8**
9	993.445845	497.226561	976.419296	488.713286	975.435280	488.221278	**C**	***820.398164***	410.702720	803.371615	402.189445	802.387599	401.697437	**7**
10	1080.477873	540.742575	1063.451324	532.229300	1062.467308	531.737292	**S**	***660.367515***	330.687395	643.340966	322.174121	642.356950	321.682113	**6**
11	**1193.561937**	597.284607	1176.535388	588.771332	1175.551372	588.279324	**L**	***573.335487***	287.171381	556.308938	278.658107	555.324922	278.166099	**5**
12	**1306.646001**	653.826638	1289.619452	645.313364	1288.635436	644.821356	**I**	***460.251423***	230.629349	443.224874	222.116075	442.240858	221.624067	**4**
13	**1421.672944**	711.340110	1404.646395	702.826836	1403.662379	702.334827	**D**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
14	**1478.694408**	739.850842	1461.667859	731.337567	1460.683843	730.845559	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



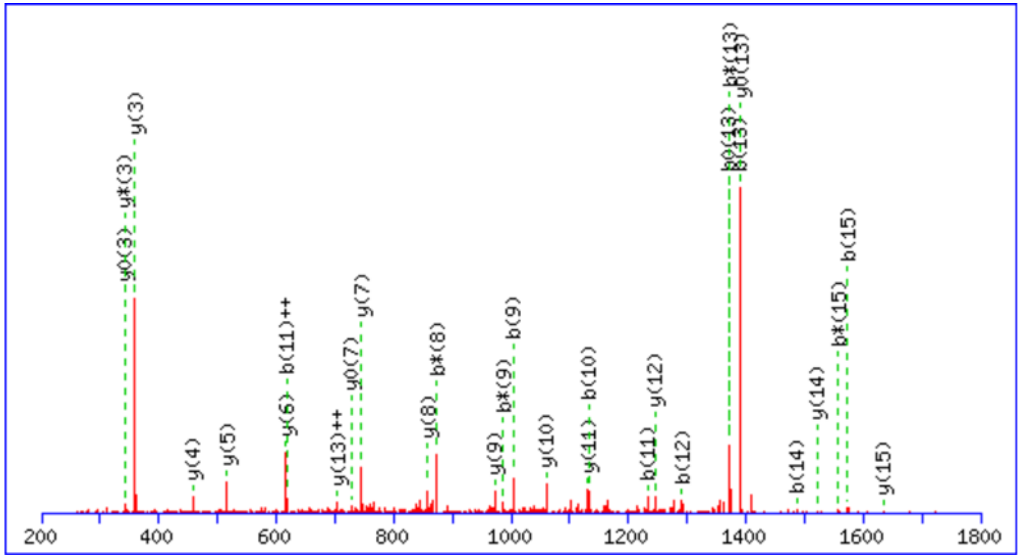
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 40 - OPD-1 **Fraction:** OPD-1

Match to Query 10491: 1746.916848 from(874.465700,2+)
Title: OECHL100310_27.16094.16094.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_27.raw

Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 2e-006**Matches :** 30/156 fragment ions using 58 most intense peaks (help)

#	**b**	**b^{++}**	**b^{*}**	**b^{*++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y^{*}**	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	***1634.838427***	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	618.349740	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	689.386854	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	**1486.778787**	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



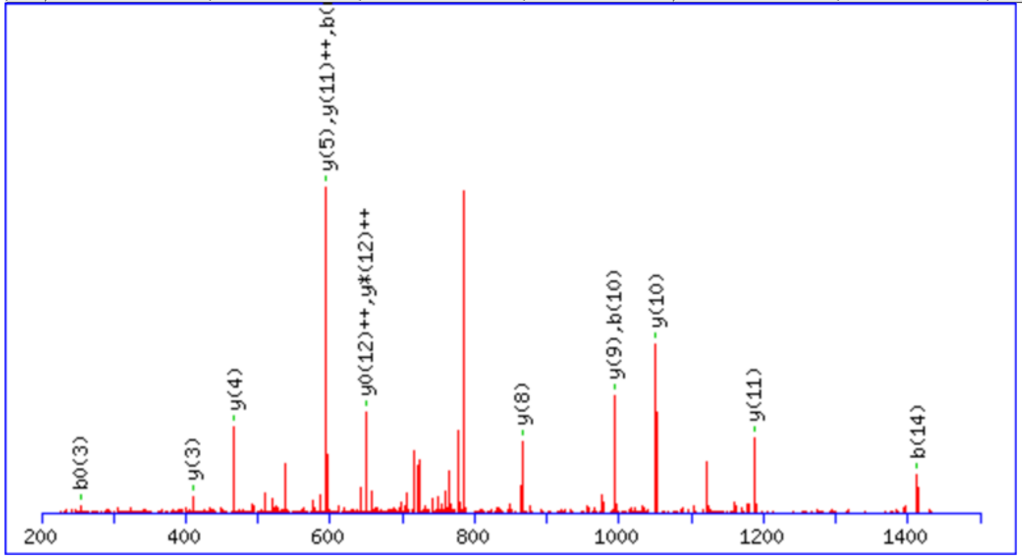
Peptide View

MS/MS Fragmentation of **ASLQHGQAAEKGPHR**
Found in **IPI00165044**, Tax_Id=9606 Gene_Symbol=FAM198B Isoform 2 of Protein ENED
Experiment: 40 - OPD-1 **Fraction:** OPD-1

Match to Query 9224: 1585.808848 from(793.911700,2+)
Title: OECHL100310_27.1671.1671.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1585.807312**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59
Expect: 0.00016**Matches :** 14/150 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	72.044390	36.525833					**A**							**15**
2	159.076418	80.041847			141.065853	71.036564	**S**	1515.777500	758.392388	1498.750951	749.879114	1497.766935	749.387106	**14**
3	272.160482	136.583879			254.149917	127.578597	**L**	1428.745472	714.876374	1411.718923	706.363100	1410.734907	705.871092	**13**
4	400.219060	200.613168	383.192511	192.099894	382.208495	191.607886	**Q**	1315.661408	658.334342	1298.634859	649.821068	1297.650843	649.329060	**12**
5	537.277972	269.142624	520.251423	260.629350	519.267407	260.137342	**H**	***1187.602830***	594.305053	1170.576281	585.791779	1169.592265	585.299771	**11**
6	**594.299436**	297.653356	577.272887	289.140082	576.288871	288.648074	**G**	***1050.543918***	525.775597	1033.517369	517.262323	1032.533353	516.770315	**10**

7	722.358014	361.682645	705.331465	353.169371	704.347449	352.677363	**Q**	***993.522454***	497.264865	976.495905	488.751591	975.511889	488.259583	**9**
8	793.395128	397.201202	776.368579	388.687928	775.384563	388.195920	**A**	***865.463876***	433.235576	848.437327	424.722302	847.453311	424.230294	**8**
9	864.432242	432.719759	847.405693	424.206485	846.421677	423.714477	**A**	794.426762	397.717019	777.400213	389.203745	776.416197	388.711737	**7**
10	**993.474835**	497.241056	976.448286	488.727781	975.464270	488.235773	**E**	723.389648	362.198462	706.363099	353.685188	705.379083	353.193180	**6**
11	1121.569798	561.288537	1104.543249	552.775263	1103.559233	552.283255	**K**	***594.347055***	297.677166	577.320506	289.163891			**5**
12	1178.591262	589.799269	1161.564713	581.285995	1160.580697	580.793987	**G**	***466.252092***	233.629684	449.225543	225.116409			**4**
13	1275.644026	638.325651	1258.617477	629.812377	1257.633461	629.320369	**P**	***409.230628***	205.118952	392.204079	196.605677			**3**
14	**1412.702938**	706.855107	1395.676389	698.341833	1394.692373	697.849825	**H**	312.177864	156.592570	295.151315	148.079295			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



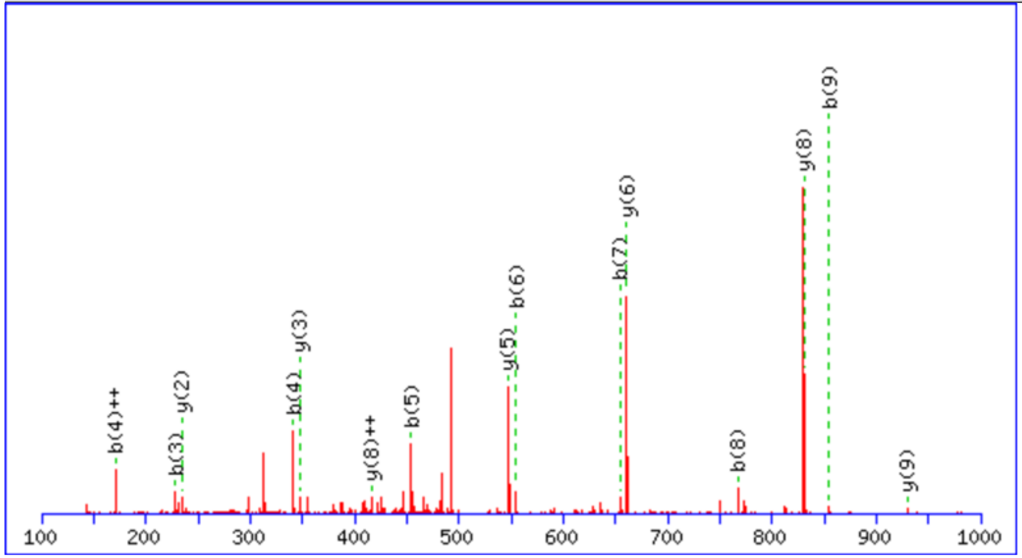
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 40 - OPD-1 **Fraction:** OPD-1

Match to Query 2473: 999.635448 from(500.825000,2+)
Title: OECHL100310_27.16213.16213.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_27.raw

Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63
Expect: 5e-006**Matches :** 16/78 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							10
2	***171.112804***	86.060040			V	**929.602995**	465.305136	912.576446	456.791861	911.592430	456.299853	9
3	***228.134268***	114.570772			G	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	8
4	***341.218332***	171.112804			L	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	7
5	***454.302396***	227.654836			L	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	6
6	***555.350075***	278.178676	537.339510	269.173393	T	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	5
7	***654.418489***	327.712883	636.407924	318.707600	V	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	4
8	***767.502553***	384.254915	749.491988	375.249632	I	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	3
9	***854.534581***	427.770929	836.524016	418.765646	S	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	2
10					K	147.112804	74.060040	130.086255	65.546765			1



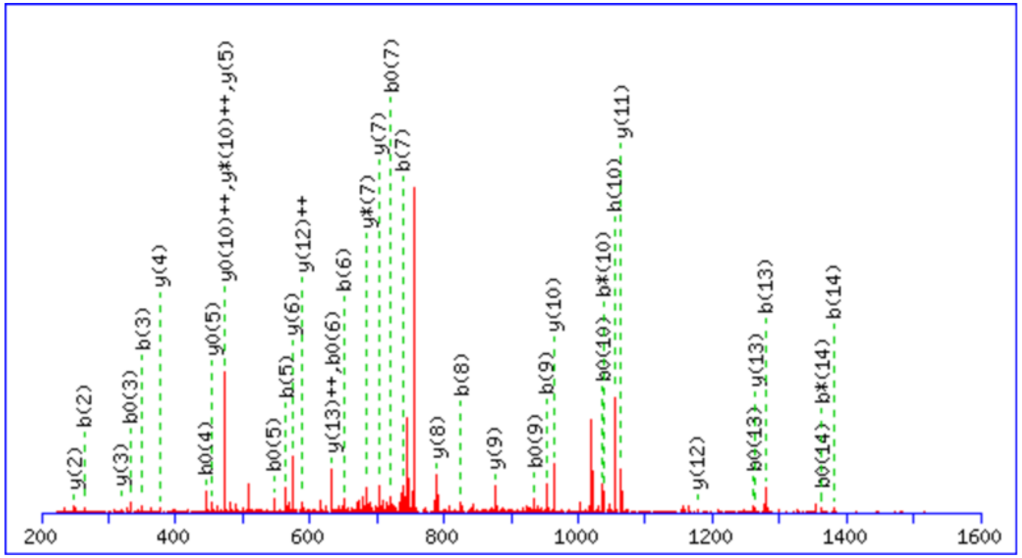
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2

Experiment: 40 - OPD-1 **Fraction:** OPD-1

Match to Query 8676: 1525.726848 from(763.870700,2+)
Title: OECHL100310_27.10434.10434.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60
Expect: 0.0001**Matches :** 39/150 fragment ions using 90 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	**263.102633**	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	**350.134661**	175.570968			332.124096	166.565686	**S**	***1264.637937***	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	**564.266404**	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	**651.298432**	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**
7	**738.330460**	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	**9**
8	**825.362488**	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.203410	**8**
9	**953.421066**	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	**7**
10	**1054.468745**	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	**6**
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	**5**
12	1208.542973	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	**4**
13	**1279.580087**	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	***319.197597***	160.102436	302.171048	151.589162	301.187032	151.097154	**3**
14	**1380.627766**	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



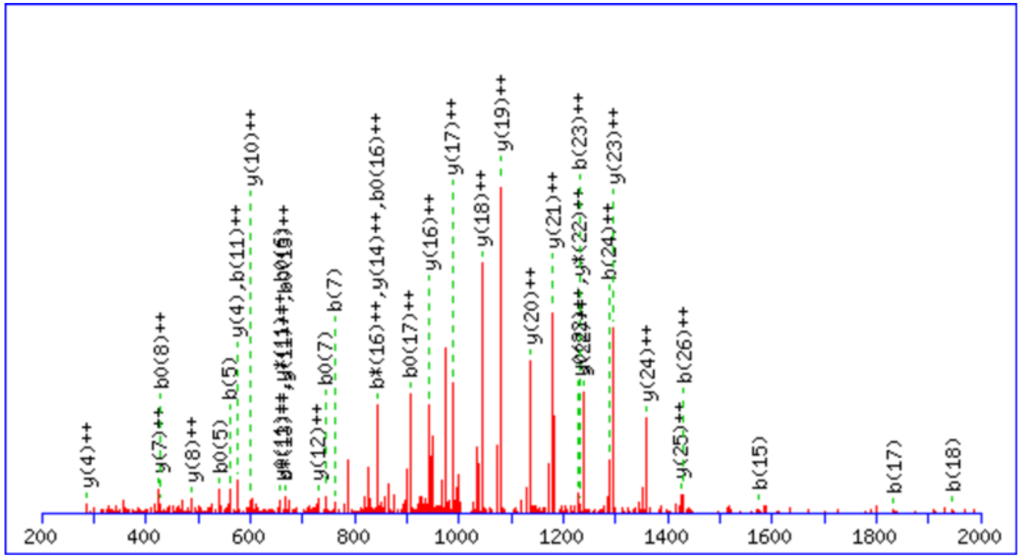
Peptide View

MS/MS Fragmentation of **DAEEDDSLANSSDLLKELLETGDNRER**
Found in **IPI00000828**, Tax_Id=9606 Gene_Symbol=PENK Proenkephalin-A
Experiment: 40 - OPD-1 **Fraction:** OPD-1

Match to Query 15185: 3033.404172 from(1012.142000,3+)
Title: OECHL100310_27.18231.18231.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 3033.401001**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 92
Expect: 1.4e-007**Matches :** 40/292 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	116.034219	58.520748			98.023654	49.515465	D						
2	187.071333	94.039304			169.060768	85.034022	A	2919.381392	1460.194334	2902.354843	1451.681059	2901.370827	1451.1890
3	316.113926	158.560601			298.103361	149.555319	E	2848.344278	1424.675777	2831.317729	1416.162502	2830.333713	1415.6704
4	445.156519	223.081898			427.145954	214.076615	E	2719.301685	1360.154480	2702.275136	1351.641206	2701.291120	1351.1491
5	**560.183462**	280.595369			542.172897	271.590087	D	2590.259092	1295.633184	2573.232543	1287.119909	2572.248527	1286.6279
6	675.210405	338.108841			657.199840	329.103558	D	2475.232149	1238.119712	2458.205600	1229.606438	2457.221584	1229.1144

7	**762.242433**	381.624855			744.231868	372.619572	**S**	2360.205206	1180.606241	2343.178657	1172.092966	2342.194641	1171.6009
8	875.326497	438.166887			857.315932	429.161604	**L**	2273.173178	1137.090227	2256.146629	1128.576952	2255.162613	1128.0849
9	946.363611	473.685444			928.353046	464.680161	**A**	2160.089114	1080.548195	2143.062565	1072.034920	2142.078549	1071.5429
10	1060.406538	530.706907	1043.379989	522.193633	1042.395973	521.701624	**N**	2089.052000	1045.029638	2072.025451	1036.516363	2071.041435	1036.0243
11	1147.438566	**574.222921**	1130.412017	565.709647	1129.428001	565.217639	**S**	1975.009073	988.008174	1957.982524	979.494900	1956.998508	979.0028
12	1234.470594	617.738935	1217.444045	609.225661	1216.460029	608.733653	**S**	1887.977045	944.492160	1870.950496	935.978886	1869.966480	935.4868
13	1349.497537	675.252407	1332.470988	666.739132	1331.486972	666.247124	**D**	1800.945017	900.976146	1783.918468	892.462872	1782.934452	891.9708
14	1462.581601	731.794439	1445.555052	723.281164	1444.571036	722.789156	**L**	1685.918074	843.462675	1668.891525	834.949400	1667.907509	834.4573
15	**1575.665665**	788.336471	1558.639116	779.823196	1557.655100	779.331188	**L**	1572.834010	786.920643	1555.807461	778.407368	1554.823445	777.9153
16	1703.760628	852.383952	1686.734079	843.870678	1685.750063	843.378670	**K**	1459.749946	730.378611	1442.723397	721.865336	1441.739381	721.3733
17	**1832.803221**	916.905248	1815.776672	908.391974	1814.792656	907.899966	**E**	1331.654983	666.331129	1314.628434	657.817855	1313.644418	657.3258
18	**1945.887285**	973.447280	1928.860736	964.934006	1927.876720	964.441998	**L**	1202.612390	601.809833	1185.585841	593.296558	1184.601825	592.8045
19	2058.971349	1029.989312	2041.944800	1021.476038	2040.960784	1020.984030	**L**	1089.528326	545.267801	1072.501777	536.754526	1071.517761	536.2625
20	2188.013942	1094.510609	2170.987393	1085.997334	2170.003377	1085.505326	**E**	976.444262	488.725769	959.417713	480.212494	958.433697	479.7204
21	2289.061621	1145.034448	2272.035072	1136.521174	2271.051056	1136.029166	**T**	847.401669	424.204472	830.375120	415.691198	829.391104	415.1991
22	2346.083085	1173.545180	2329.056536	1165.031906	2328.072520	1164.539898	**G**	746.353990	373.680633	729.327441	365.167358	728.343425	364.6753
23	2461.110028	**1231.058652**	2444.083479	1222.545377	2443.099463	1222.053369	**D**	689.332526	345.169901	672.305977	336.656626	671.321961	336.1646
24	2575.152955	**1288.080115**	2558.126406	1279.566841	2557.142390	1279.074833	**N**	574.305583	287.656430	557.279034	279.143155	556.295018	278.6511
25	2731.254066	1366.130671	2714.227517	1357.617396	2713.243501	1357.125388	**R**	460.262656	230.634966	443.236107	222.121692	442.252091	221.6296
26	2860.296659	**1430.651967**	2843.270110	1422.138693	2842.286094	1421.646685	**E**	304.161545	152.584411	287.134996	144.071136	286.150980	143.5791
27							**R**	175.118952	88.063114	158.092403	79.549839		



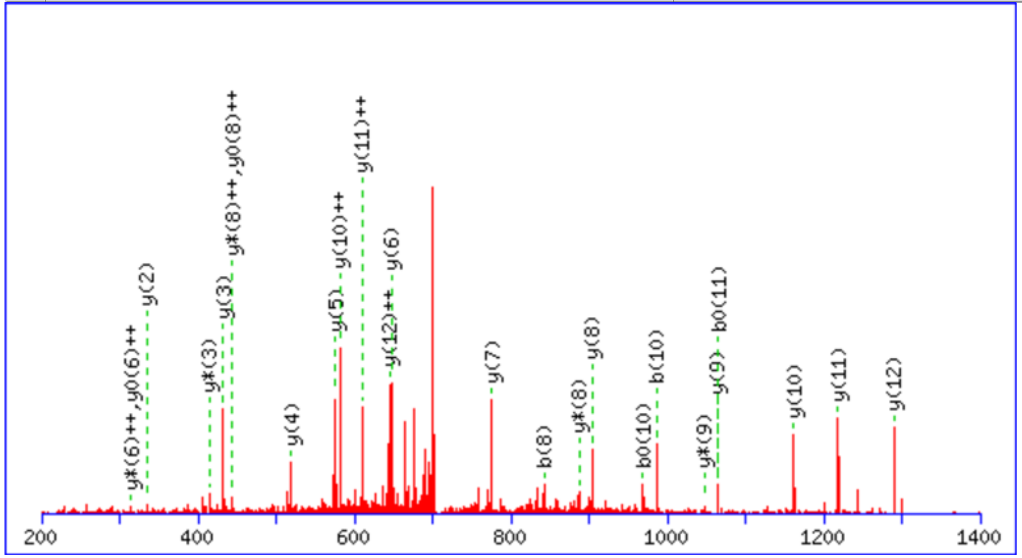
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 40 - OPD-1 **Fraction:** OPD-1

Match to Query 7560: 1416.626048 from(709.320300,2+)
Title: OECHL100310_27.1866.1866.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 92
Expect: 4.3e-008**Matches :** 25/128 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			K							13
2	200.139353	100.573315	183.112804	92.060040			A	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	12
3	257.160817	129.084047	240.134268	120.570772			G	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	11
4	354.213581	177.610429	337.187032	169.097154			P	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	10
5	514.244230	257.625753	497.217681	249.112479			C	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	9
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	E	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	8

7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	899.403979	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

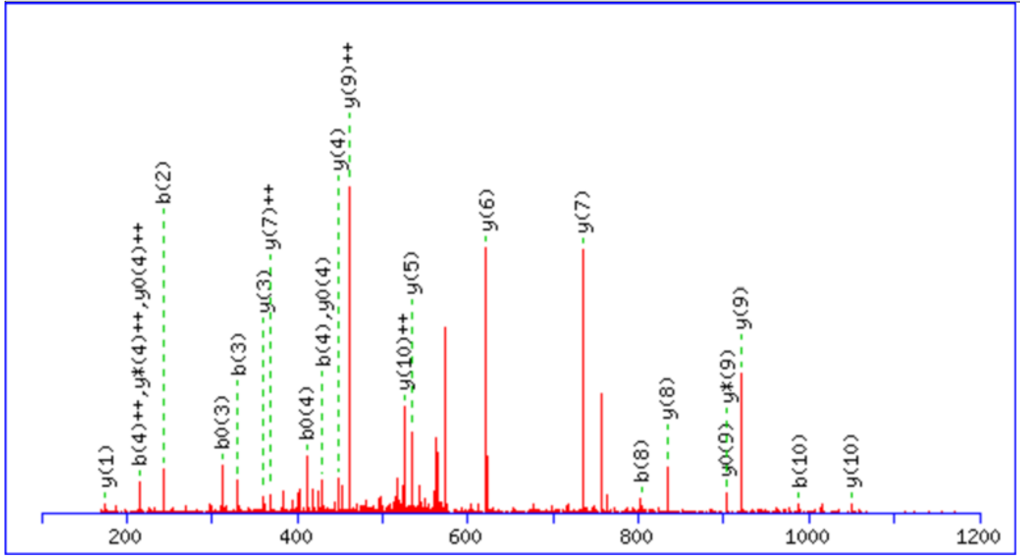


Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 40 - OPD-1 **Fraction:** OPD-1

Match to Query 4581: 1161.635448 from(581.825000,2+)
Title: OECHL100310_27.5100.5100.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70
Expect: 5.9e-006**Matches :** 25/94 fragment ions using 40 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					**I**							**11**
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637	**10**
3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340	**9**
4	**429.234375**	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326	**8**
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119	**7**
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087	**6**
7	716.382495	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073	**5**
8	**803.414523**	402.210899			785.403958	393.205617	**S**	***447.267407***	224.137342	430.240858	215.624067	429.256842	215.132059	**4**
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053			**3**
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



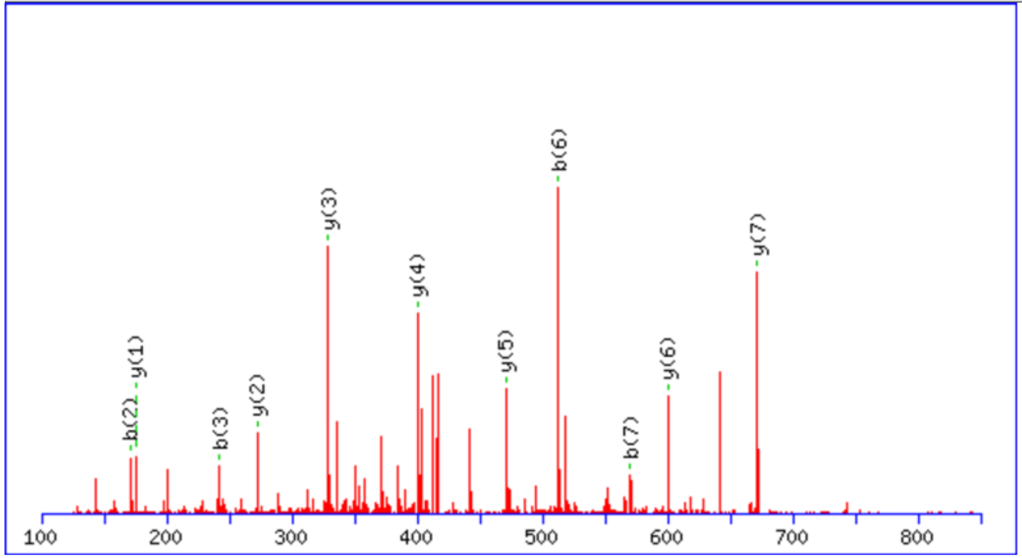
Peptide View

MS/MS Fragmentation of **GLAEAAGPR**
Found in **IPI00290826**, Tax_Id=9606 Gene_Symbol=FAM174A Membrane protein FAM174A

Experiment: 40 - OPD-1 **Fraction:** OPD-1

Match to Query 1010: 840.445248 from(421.229900,2+)
Title: OECHL100310_27.3745.3745.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 840.445343**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63
Expect: 3.4e-005**Matches :** 11/64 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							9
2	**171.112804**	86.060040			L	784.431179	392.719228	767.404630	384.205953	766.420614	383.713945	8
3	**242.149918**	121.578597			A	***671.347115***	336.177196	654.320566	327.663921	653.336550	327.171913	7
4	371.192511	186.099894	353.181946	177.094611	E	***600.310001***	300.658639	583.283452	292.145364	582.299436	291.653356	6
5	442.229625	221.618450	424.219060	212.613168	A	***471.267408***	236.137342	454.240859	227.624067			5
6	**513.266739**	257.137008	495.256174	248.131725	A	***400.230294***	200.618785	383.203745	192.105510			4
7	**570.288203**	285.647740	552.277638	276.642457	G	***329.193180***	165.100228	312.166631	156.586953			3
8	667.340967	334.174122	649.330402	325.168839	P	***272.171716***	136.589496	255.145167	128.076221			2
9					R	***175.118952***	88.063114	158.092403	79.549839			1

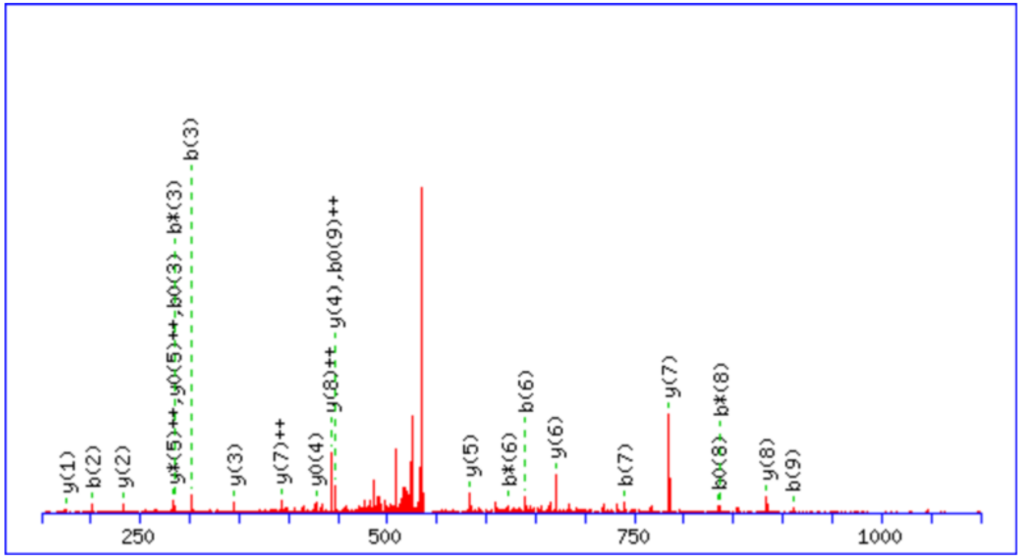


Peptide View

MS/MS Fragmentation of **NSVNSHTIGR**
Found in **IPI00300376**, Tax_Id=9606 Gene_Symbol=TGM3 Protein-glutamine gamma-glutamyltransferase E
Experiment: 40 - OPD-1 **Fraction:** OPD-1

Match to Query 3621: 1083.542048 from(542.778300,2+)
Title: OECHL100310_27.2386.2386.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1083.542114**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60
Expect: 7.6e-005**Matches :** 24/100 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**10**
2	**202.082231**	101.544753	185.055682	93.031479	184.071666	92.539471	**S**	970.506468	485.756872	953.479919	477.243598	952.495903	476.751590	**9**
3	**301.150645**	151.078960	284.124096	142.565686	283.140080	142.073678	**V**	***883.474440***	442.240858	866.447891	433.727584	865.463875	433.235576	**8**
4	415.193572	208.100424	398.167023	199.587150	397.183007	199.095142	**N**	***784.406026***	392.706651	767.379477	384.193377	766.395461	383.701369	**7**
5	502.225600	251.616438	485.199051	243.103164	484.215035	242.611156	**S**	***670.363099***	335.685188	653.336550	327.171913	652.352534	326.679905	**6**
6	**639.284512**	320.145894	622.257963	311.632620	621.273947	311.140612	**H**	***583.331071***	292.169174	566.304522	283.655899	565.320506	283.163891	**5**
7	**740.332191**	370.669734	723.305642	362.156459	722.321626	361.664451	**T**	***446.272159***	223.639718	429.245610	215.126443	428.261594	214.634435	**4**
8	853.416255	427.211766	836.389706	418.698491	835.405690	418.206483	**I**	***345.224480***	173.115878	328.197931	164.602604			**3**
9	**910.437719**	455.722498	893.411170	447.209223	892.427154	446.717215	**G**	***232.140416***	116.573846	215.113867	108.060572			**2**
10							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



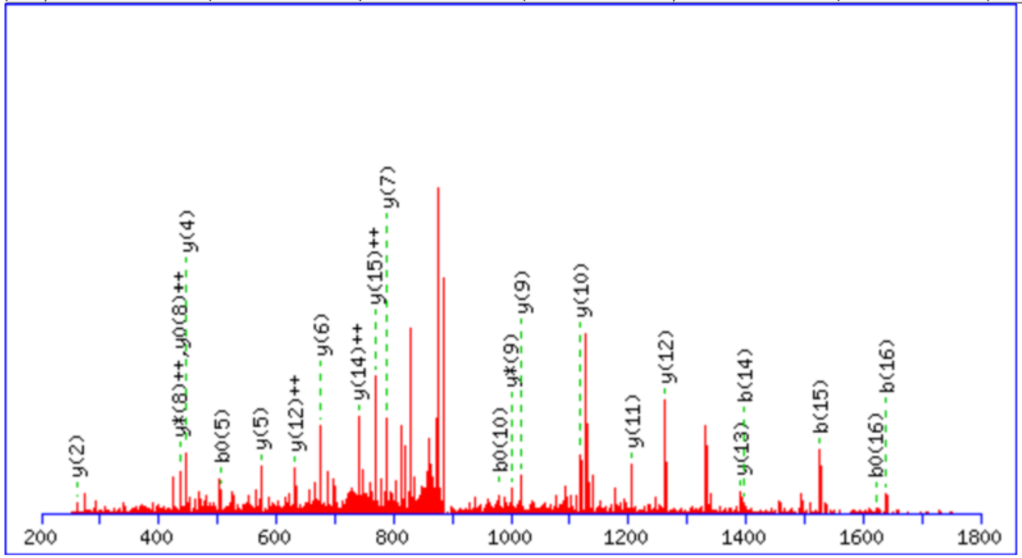
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 40 - OPD-1 **Fraction:** OPD-1

Match to Query 10843: 1784.880648 from(893.447600,2+)
Title: OECHL100310_27.7173.7173.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 0.00027**Matches :** 22/170 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					**Y**							**17**
2	251.102633	126.054954			233.092068	117.049672	**S**	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.909941	**16**
3	308.124097	154.565687			290.113532	145.560404	**G**	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.393928	**15**
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.883195	**14**
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.367182	**13**
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.845885	**12**

7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.335153	**11**
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.819139	**10**
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.295299	**9**
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.266010	**8**
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.742171	**7**
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.200139	**6**
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.676299	**5**
14	**1397.654316**	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	**4**
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**

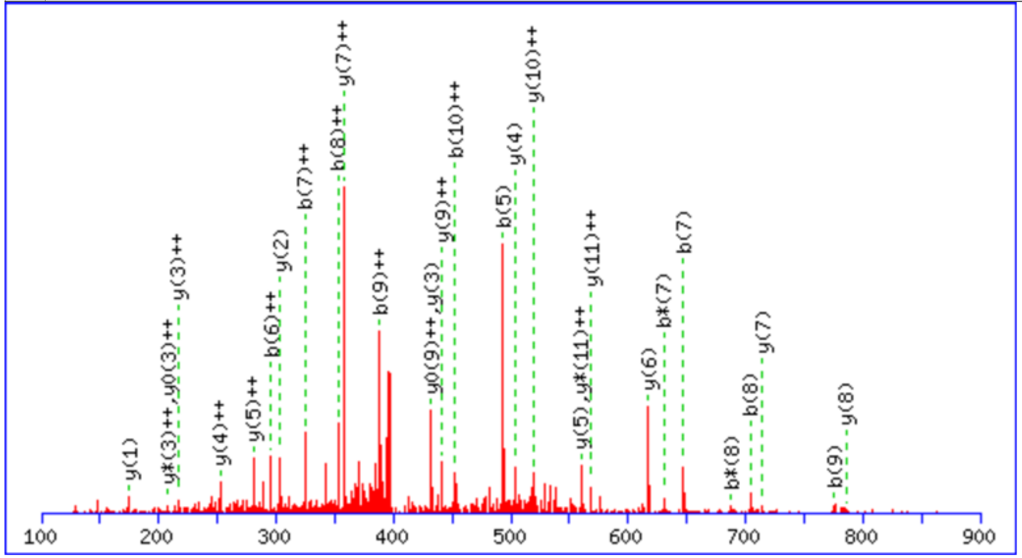


Peptide View

MS/MS Fragmentation of **APRPAPGGAEQR**
Found in **IPI00001952**, Tax_Id=9606 Gene_Symbol=ENDOD1 Endonuclease domain-containing 1 protein
Experiment: 40 - OPD-1 **Fraction:** OPD-1

Match to Query 5160: 1205.626572 from(402.882800,3+)
Title: OECHL100310_27.1760.1760.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1205.626495**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 0.0003**Matches :** 30/106 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	72.044390	36.525833					A							12
2	169.097154	85.052215					P	1135.596682	568.301979	1118.570133	559.788705	1117.586117	559.296697	11
3	325.198265	163.102770	308.171716	154.589496			R	1038.543918	519.775597	1021.517369	511.262323	1020.533353	510.770315	10
4	422.251029	211.629152	405.224480	203.115878			P	882.442807	441.725042	865.416258	433.211767	864.432242	432.719759	9
5	**493.288143**	247.147709	476.261594	238.634435			A	***785.390043***	393.198660	768.363494	384.685385	767.379478	384.193377	8
6	590.340907	**295.674092**	573.314358	287.160817			P	***714.352929***	357.680103	697.326380	349.166828	696.342364	348.674820	7
7	**647.362371**	**324.184824**	630.335822	315.671549			G	***617.300165***	309.153721	600.273616	300.640446	599.289600	300.148438	6
8	**704.383835**	**352.695556**	687.357286	344.182281			G	***560.278701***	280.642989	543.252152	272.129714	542.268136	271.637706	5
9	**775.420949**	**388.214113**	758.394400	379.700838			A	***503.257237***	252.132256	486.230688	243.618982	485.246672	243.126974	4
10	904.463542	**452.735409**	887.436993	444.222135	886.452977	443.730127	E	***432.220123***	216.613699	415.193574	208.100425	414.209558	207.608417	3
11	1032.522120	516.764698	1015.495571	508.251424	1014.511555	507.759416	Q	***303.177530***	152.092403	286.150981	143.579128			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1

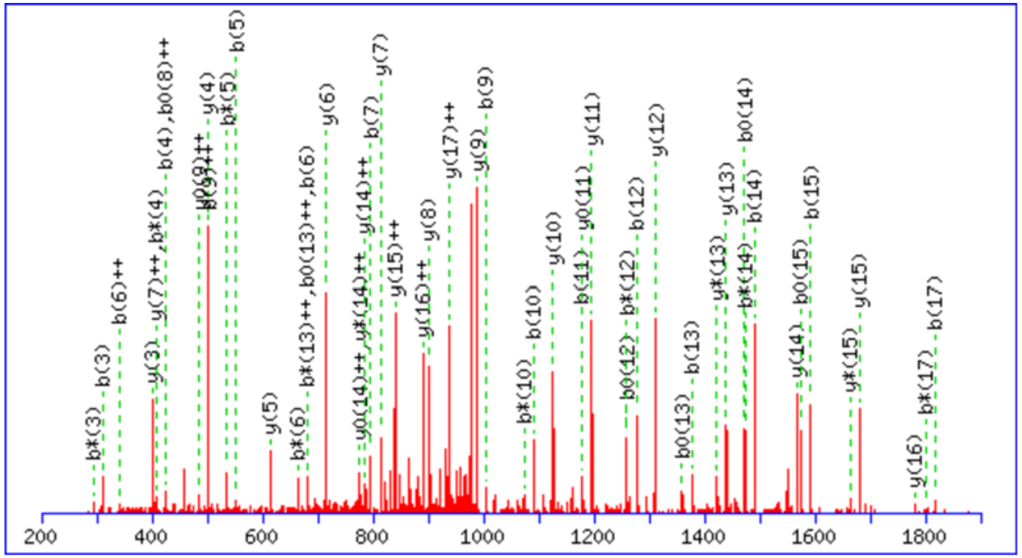


Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 07 - S_C-1 **Fraction:** S_C-1

Match to Query 13185: 1990.024448 from(996.019500,2+)
Title: OECHL100310_25.9483.9483.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 98
Expect: 2.3e-008**Matches :** 55/186 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	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	**424.255445**	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	**552.314023**	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	**680.372601**	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**
7	**795.399544**	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	**1003.495570**	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	**1177.559626**	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	**1377.675719**	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510			**3**
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**



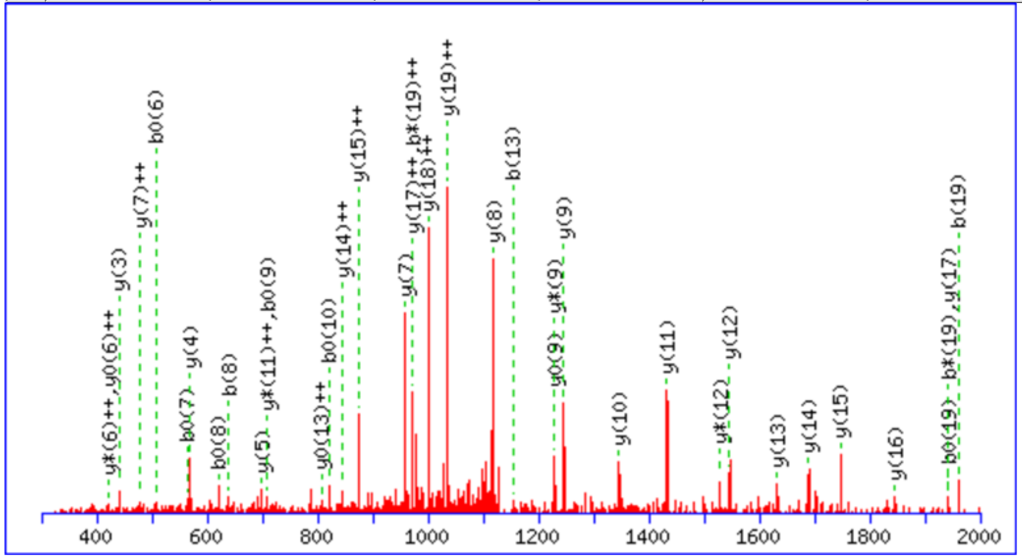
Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 07 - S_C-1 **Fraction:** S_C-1

Match to Query 14358: 2270.113448 from(1136.064000,2+)
Title: OECHL100310_25.10250.10250.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 82
Expect: 1.2e-006**Matches :** 38/212 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	102.054955	51.531116			84.044390	42.525833	T						
2	201.123369	101.065322			183.112804	92.060040	V	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400	1076.5338
3	272.160483	136.583879			254.149918	127.578597	A	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986	1026.9996
4	329.181947	165.094611			311.171382	156.089329	G	1999.965437	1000.486357	1982.938888	991.973082	1981.954872	991.4810
5	426.234711	213.620994			408.224146	204.615711	P	***1942.943973***	971.975625	1925.917424	963.462350	1924.933408	962.9703
6	525.303125	263.155201			507.292560	254.149918	V	***1845.891209***	923.449243	1828.864660	914.935968	1827.880644	914.4439

7	582.324589	291.665933			564.314024	282.660650	**G**	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230	864.9097
8	**639.346053**	320.176665			621.335488	311.171382	**G**	***1689.801331***	845.404304	1672.774782	836.891029	1671.790766	836.3990
9	726.378081	363.692679			708.367516	354.687396	**S**	***1632.779867***	816.893572	1615.753318	808.380297	1614.769302	807.8882
10	839.462145	420.234711			821.451580	411.229428	**L**	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274	764.3722
11	926.494173	463.750725			908.483608	454.745442	**S**	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210	707.8302
12	1025.562587	513.284932			1007.552022	504.279649	**V**	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182	664.3142
13	**1153.621165**	577.314221	1136.594616	568.800946	1135.610600	568.308938	**Q**	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768	614.7800
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	**C**	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190	550.7507
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	**P**	***958.474106***	479.740691	941.447557	471.227417	940.463541	470.7354
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	**Y**	861.421342	431.214309	844.394793	422.701035	843.410777	422.2090
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	**E**	***698.358013***	349.682645	681.331464	341.169370	680.347448	340.6773
18	1830.905463	915.956370	1813.878914	907.443095	1812.894898	906.951087	**K**	***569.315420***	285.161348	552.288871	276.648074	551.304855	276.1560
19	**1959.948056**	980.477666	1942.921507	971.964392	1941.937491	971.472384	**E**	***441.220457***	221.113867	424.193908	212.600592	423.209892	212.1085
20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	**H**	312.177864	156.592570	295.151315	148.079295		
21							**R**	175.118952	88.063114	158.092403	79.549839		

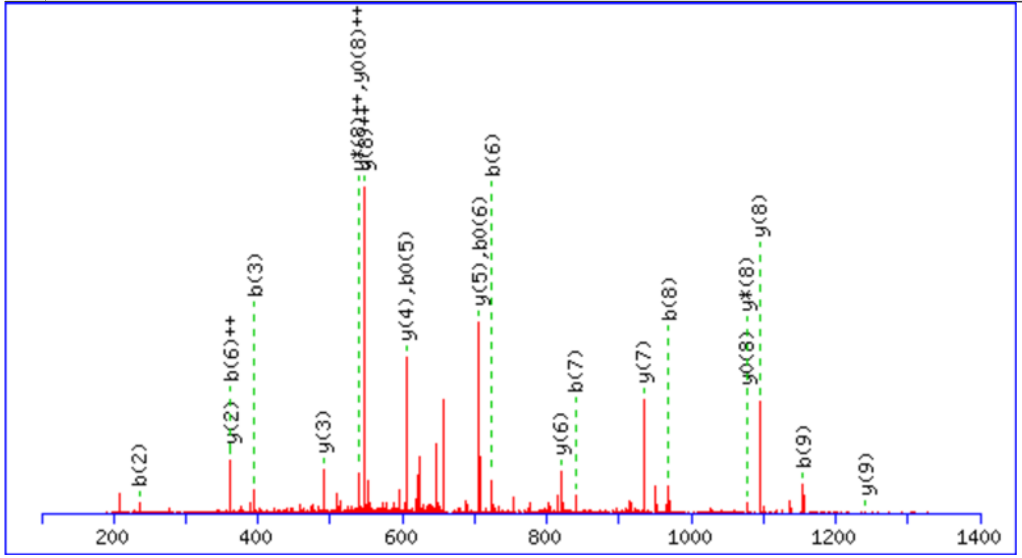


Peptide View

MS/MS Fragmentation of **SFCDLTDEWR**
Found in **IPI00010193**, Tax_Id=9606 Gene_Symbol=IFNAR2 Isoform 1 of Interferon-alpha/beta receptor beta chain
Experiment: 07 - S_C-1 **Fraction:** S_C-1

Match to Query 7774: 1327.549248 from(664.781900,2+)
Title: OECHL100310_25.16064.16064.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1327.550308**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49
Expect: 0.00026**Matches :** 22/86 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							10
2	**235.107718**	118.057497	217.097153	109.052214	F	***1241.525550***	621.266413	1224.499001	612.753138	1223.514985	612.261130	9
3	**395.138367**	198.072821	377.127802	189.067539	C	***1094.457136***	547.732206	1077.430587	539.218932	1076.446571	538.726924	8
4	510.165310	255.586293	492.154745	246.581010	D	***934.426487***	467.716882	917.399938	459.203607	916.415922	458.711599	7
5	623.249374	312.128325	605.238809	303.123043	L	***819.399544***	410.203410	802.372995	401.690135	801.388979	401.198127	6
6	**724.297053**	362.652165	706.286488	353.646882	T	***706.315480***	353.661378	689.288931	345.148103	688.304915	344.656095	5
7	**839.323996**	420.165636	821.313431	411.160353	D	***605.267801***	303.137539	588.241252	294.624264	587.257236	294.132256	4
8	**968.366589**	484.686933	950.356024	475.681650	E	***490.240858***	245.624067	473.214309	237.110792	472.230293	236.618784	3
9	**1154.445902**	577.726589	1136.435337	568.721306	W	***361.198265***	181.102770	344.171716	172.589496			2
10					R	175.118952	88.063114	158.092403	79.549839			1

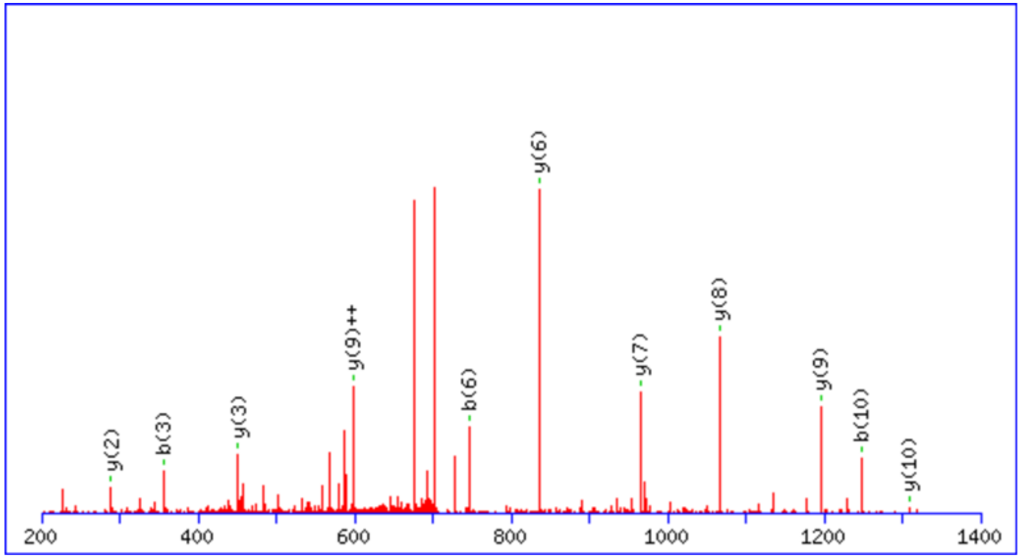


Peptide View

MS/MS Fragmentation of **LLETECPQYIR**
Found in **IPI00007047**, Tax_Id=9606 Gene_Symbol=S100A8 Protein S100-A8
Experiment: 07 - S_C-1 **Fraction:** S_C-1

Match to Query 8683: 1420.703848 from(711.359200,2+)
Title: OECHL100310_25.11775.11775.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1420.702026**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66
Expect: 3.2e-005**Matches :** 11/90 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	114.091340	57.549308					**L**							**11**
2	227.175404	114.091340					**L**	***1308.625265***	654.816271	1291.598716	646.302996	1290.614700	645.810988	**10**
3	**356.217997**	178.612637			338.207432	169.607354	**E**	***1195.541201***	598.274239	1178.514652	589.760964	1177.530636	589.268956	**9**
4	457.265676	229.136476			439.255111	220.131194	**T**	***1066.498608***	533.752942	1049.472059	525.239668	1048.488043	524.747660	**8**
5	586.308269	293.657773			568.297704	284.652490	**E**	***965.450929***	483.229103	948.424380	474.715828	947.440364	474.223820	**7**
6	**746.338918**	373.673097			728.328353	364.667815	**C**	***836.408336***	418.707806	819.381787	410.194531			**6**
7	843.391682	422.199479			825.381117	413.194197	**P**	676.377687	338.692481	659.351138	330.179207			**5**
8	971.450260	486.228768	954.423711	477.715494	953.439695	477.223486	**Q**	579.324923	290.166099	562.298374	281.652825			**4**
9	1134.513589	567.760433	1117.487040	559.247158	1116.503024	558.755150	**Y**	***451.266345***	226.136810	434.239796	217.623536			**3**
10	**1247.597653**	624.302465	1230.571104	615.789190	1229.587088	615.297182	**I**	***288.203016***	144.605146	271.176467	136.091871			**2**
11							**R**	175.118952	88.063114	158.092403	79.549839			**1**



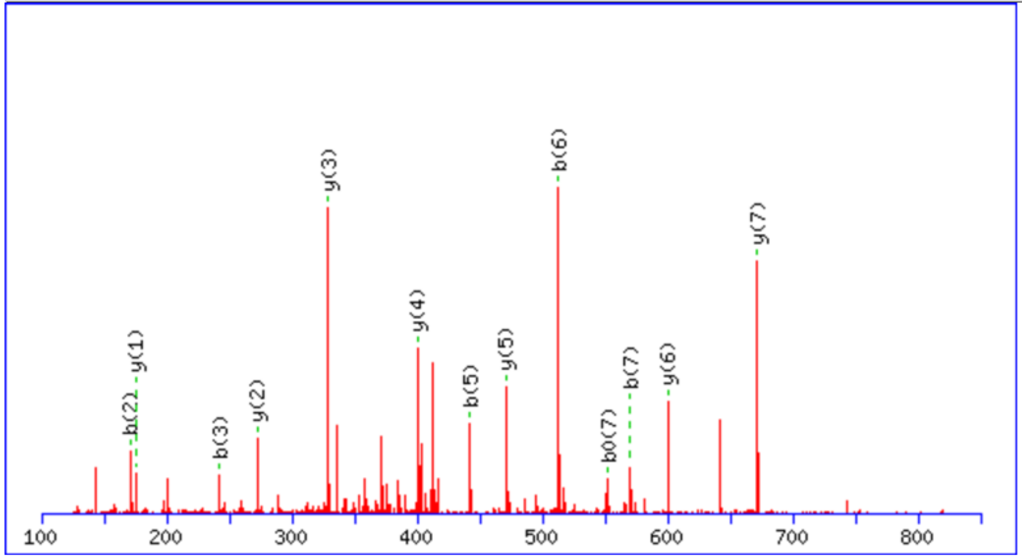
Peptide View

MS/MS Fragmentation of **GLAEAAGPR**
Found in **IPI00290826**, Tax_Id=9606 Gene_Symbol=FAM174A Membrane protein FAM174A
Experiment: 07 - S_C-1 **Fraction:** S_C-1

Match to Query 1124: 840.445048 from(421.229800,2+)
Title: OECHL100310_25.3877.3877.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 840.445343**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 8.1e-005**Matches :** 13/64 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							9
2	**171.112804**	86.060040			L	784.431179	392.719228	767.404630	384.205953	766.420614	383.713945	8
3	**242.149918**	121.578597			A	***671.347115***	336.177196	654.320566	327.663921	653.336550	327.171913	7
4	371.192511	186.099894	353.181946	177.094611	E	***600.310001***	300.658639	583.283452	292.145364	582.299436	291.653356	6
5	**442.229625**	221.618450	424.219060	212.613168	A	***471.267408***	236.137342	454.240859	227.624067			5
6	**513.266739**	257.137008	495.256174	248.131725	A	***400.230294***	200.618785	383.203745	192.105510			4

7	**570.288203**	285.647740	552.277638	276.642457	G	***329.193180***	165.100228	312.166631	156.586953			3
8	667.340967	334.174122	649.330402	325.168839	P	***272.171716***	136.589496	255.145167	128.076221			2
9					R	***175.118952***	88.063114	158.092403	79.549839			1



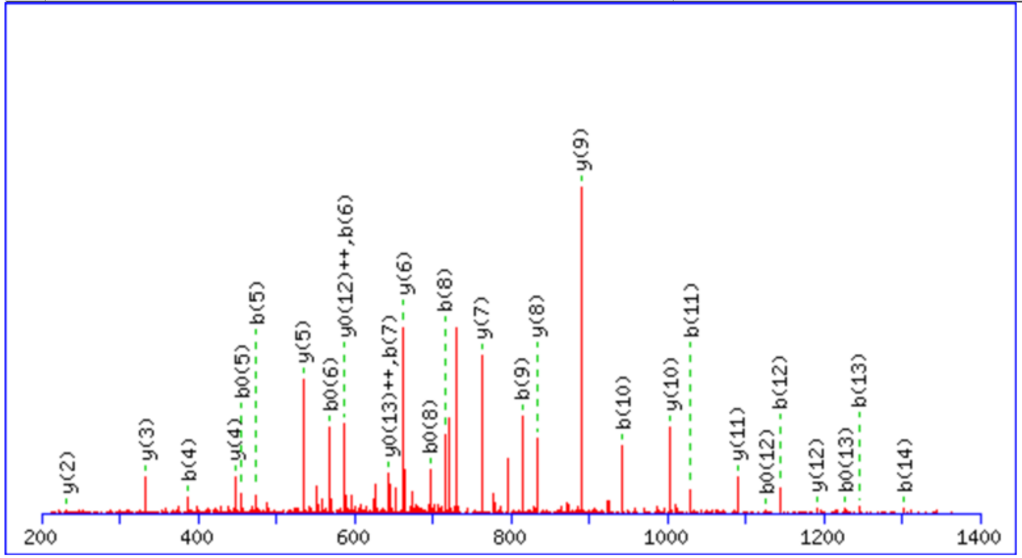
Peptide View

MS/MS Fragmentation of **GLDTSLGAVQSDTGR**
Found in **IPI00289931**, Tax_Id=9606 Gene_Symbol=MADCAM1 MADCAM1 protein
Experiment: 07 - S_C-1 **Fraction:** S_C-1

Match to Query 9338: 1475.722048 from(738.868300,2+)
Title: OECHL100310_25.10938.10938.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1475.721619**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 79
Expect: 1.9e-006**Matches :** 29/142 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	58.028740	29.518008					G							15
2	171.112804	86.060040					L	1419.707414	710.357345	1402.680865	701.844071	1401.696849	701.352063	14
3	286.139747	143.573512			268.129182	134.568229	D	1306.623350	653.815313	1289.596801	645.302039	1288.612785	644.810031	13

4	***387.187426***	194.097351			369.176861	185.092069	**T**	***1191.596407***	596.301842	1174.569858	587.788567	1173.585842	587.296559	**12**
5	***474.219454***	237.613365			456.208889	228.608082	**S**	***1090.548728***	545.778002	1073.522179	537.264728	1072.538163	536.772719	**11**
6	***587.303518***	294.155397			569.292953	285.150115	**L**	***1003.516700***	502.261988	986.490151	493.748714	985.506135	493.256706	**10**
7	***644.324982***	322.666129			626.314417	313.660847	**G**	***890.432636***	445.719956	873.406087	437.206682	872.422071	436.714674	**9**
8	***715.362096***	358.184686			697.351531	349.179404	**A**	***833.411172***	417.209224	816.384623	408.695950	815.400607	408.203942	**8**
9	***814.430510***	407.718893			796.419945	398.713611	**V**	***762.374058***	381.690667	745.347509	373.177393	744.363493	372.685385	**7**
10	***942.489088***	471.748182	925.462539	463.234908	924.478523	462.742900	**Q**	***663.305644***	332.156460	646.279095	323.643186	645.295079	323.151178	**6**
11	***1029.521116***	515.264196	1012.494567	506.750922	1011.510551	506.258914	**S**	***535.247066***	268.127171	518.220517	259.613897	517.236501	259.121889	**5**
12	***1144.548059***	572.777668	1127.521510	564.264393	1126.537494	563.772385	**D**	***448.215038***	224.611157	431.188489	216.097882	430.204473	215.605874	**4**
13	***1245.595738***	623.301507	1228.569189	614.788233	1227.585173	614.296225	**T**	***333.188095***	167.097685	316.161546	158.584411	315.177530	158.092403	**3**
14	***1302.617202***	651.812239	1285.590653	643.298965	1284.606637	642.806957	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**

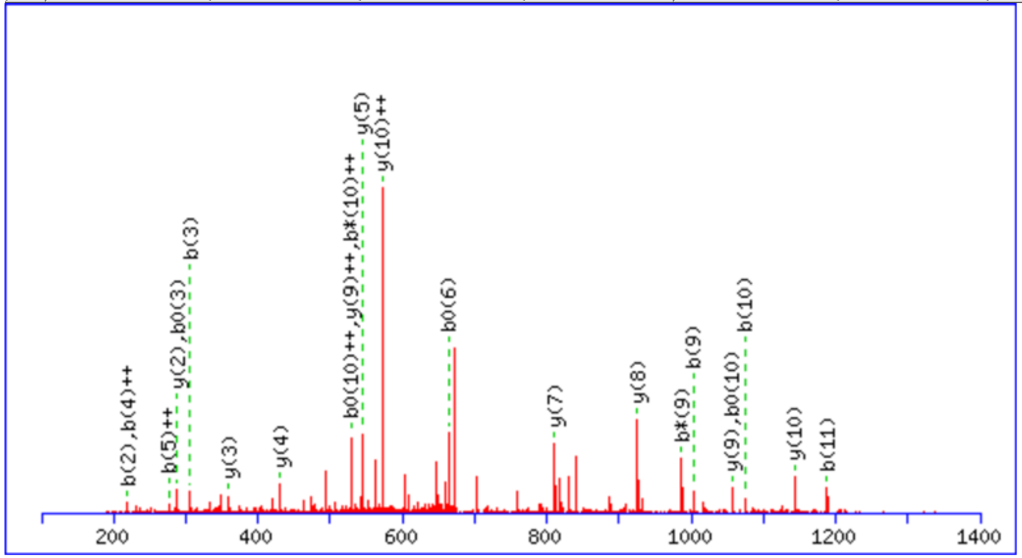


Peptide View

MS/MS Fragmentation of **AFSMDEHNAALR**
Found in **IPI00008239**, Tax_Id=9606 Gene_Symbol=GPRC5B cDNA FLJ55176, highly similar to G-protein coupled receptor family C group 5 member B
Experiment: 07 - S_C-1 **Fraction:** S_C-1

Match to Query 8116: 1360.620248 from(681.317400,2+)
Title: OECHL100310_25.9338.9338.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1360.619354**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00082**Matches :** 23/102 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							12
2	**219.112804**	110.060040					F	1290.589546	645.798411	1273.562997	637.285137	1272.578981	636.793128	11
3	**306.144832**	153.576054			288.134267	144.570772	S	***1143.521132***	572.264204	1126.494583	563.750929	1125.510567	563.258921	10
4	437.185317	**219.096296**			419.174752	210.091014	M	***1056.489104***	528.748190	1039.462555	520.234916	1038.478539	519.742908	9
5	552.212260	**276.609768**			534.201695	267.604486	D	***925.448619***	463.227947	908.422070	454.714673	907.438054	454.222665	8
6	681.254853	341.131065			663.244288	332.125782	E	***810.421676***	405.714476	793.395127	397.201201	792.411111	396.709193	7
7	818.313765	409.660521			800.303200	400.655238	H	681.379083	341.193179	664.352534	332.679905			6
8	932.356692	466.681984	915.330143	458.168709	914.346127	457.676701	N	***544.320171***	272.663724	527.293622	264.150449			5
9	**1003.393806**	502.200541	986.367257	493.687266	985.383241	493.195258	A	***430.277244***	215.642260	413.250695	207.128985			4
10	**1074.430920**	537.719098	1057.404371	529.205824	1056.420355	528.713816	A	***359.240130***	180.123703	342.213581	171.610428			3
11	**1187.514984**	594.261130	1170.488435	585.747856	1169.504419	585.255847	L	***288.203016***	144.605146	271.176467	136.091871			2
12							R	175.118952	88.063114	158.092403	79.549839			1

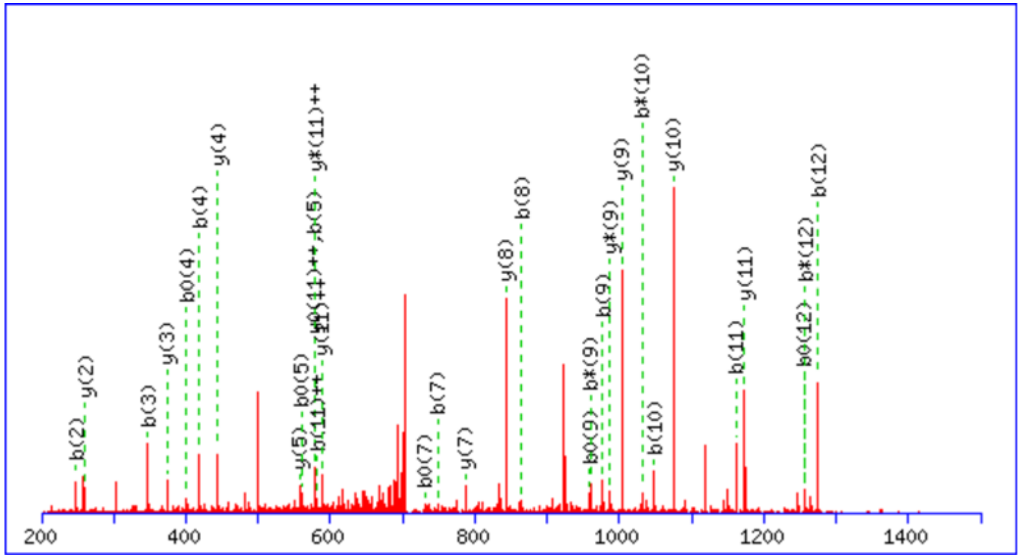


Peptide View

MS/MS Fragmentation of **SCVACGNDIALIK**
Found in **IPI00295663**, Tax_Id=9606 Gene_Symbol=CELA3A Chymotrypsin-like elastase family member 3A
Experiment: 07 - S_C-1 **Fraction:** S_C-1

Match to Query 8677: 1419.685048 from(710.849800,2+)
Title: OECHL100310_25.12423.12423.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1419.685013**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53
Expect: 0.00068**Matches :** 32/122 fragment ions using 73 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	**S**							**13**
2	***248.069953***	124.538614			230.059388	115.533332	**C**	1333.660270	667.333773	1316.633721	658.820498	1315.649705	658.328490	**12**
3	***347.138367***	174.072822			329.127802	165.067539	**V**	**1173.629621**	587.318448	1156.603072	578.805174	1155.619056	578.313166	**11**
4	***418.175481***	209.591379			400.164916	200.586096	**A**	**1074.561207**	537.784242	1057.534658	529.270967	1056.550642	528.778959	**10**
5	***578.206130***	289.606703			560.195565	280.601421	**C**	**1003.524093**	502.265684	986.497544	493.752410	985.513528	493.260402	**9**
6	635.227594	318.117435			617.217029	309.112153	**G**	**843.493444**	422.250360	826.466895	413.737085	825.482879	413.245077	**8**
7	***749.270521***	375.138899	732.243972	366.625624	731.259956	366.133616	**N**	**786.471980**	393.739628	769.445431	385.226353	768.461415	384.734345	**7**
8	***864.297464***	432.652370	847.270915	424.139096	846.286899	423.647088	**D**	672.429053	336.718164	655.402504	328.204890	654.418488	327.712882	**6**
9	***977.381528***	489.194402	960.354979	480.681128	959.370963	480.189120	**I**	**557.402110**	279.204693	540.375561	270.691418			**5**
10	***1048.418642***	524.712959	1031.392093	516.199685	1030.408077	515.707677	**A**	**444.318046**	222.662661	427.291497	214.149386			**4**
11	***1161.502706***	581.254991	1144.476157	572.741717	1143.492141	572.249709	**L**	**373.280932**	187.144104	356.254383	178.630829			**3**
12	***1274.586770***	637.797023	1257.560221	629.283749	1256.576205	628.791740	**I**	**260.196868**	130.602072	243.170319	122.088797			**2**
13							**K**	147.112804	74.060040	130.086255	65.546765			**1**



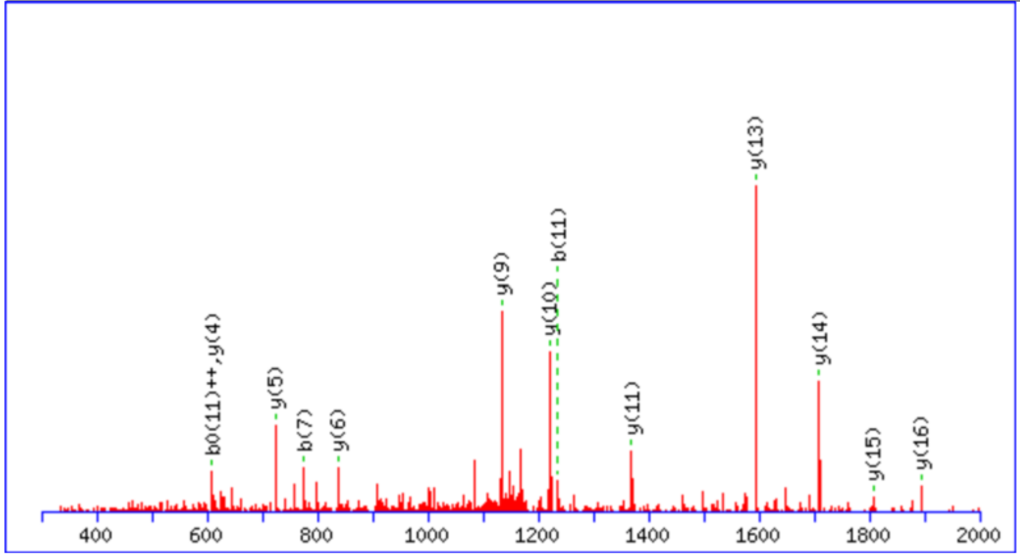
Peptide View

MS/MS Fragmentation of **EAFQSVNPEFSPEALDNCCR**
Found in **IPI00011289**, Tax_Id=9606 Gene_Symbol=SLC28A1 Isoform 1 of Sodium/nucleoside cotransporter 1
Experiment: 07 - S_C-1 **Fraction:** S_C-1

Match to Query 14890: 2369.007448 from(1185.511000,2+)
Title: OECHL100310_25.15941.15941.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 2369.005234**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 73
Expect: 3e-006**Matches :** 13/214 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	130.049869	65.528572			112.039304	56.523290	**E**						
2	201.086983	101.047130			183.076418	92.041847	**A**	2240.969929	1120.988602	2223.943380	1112.475328	2222.959364	1111.9833
3	348.155397	174.581336			330.144832	165.576054	**F**	2169.932815	1085.470045	2152.906266	1076.956771	2151.922250	1076.4647
4	476.213975	238.610626	459.187426	230.097351	458.203410	229.605343	**Q**	2022.864401	1011.935838	2005.837852	1003.422564	2004.853836	1002.9305
5	563.246003	282.126640	546.219454	273.613365	545.235438	273.121357	**S**	***1894.805823***	947.906549	1877.779274	939.393275	1876.795258	938.9012
6	662.314417	331.660847	645.287868	323.147572	644.303852	322.655564	**V**	***1807.773795***	904.390535	1790.747246	895.877261	1789.763230	895.3852

7	**776.357344**	388.682310	759.330795	380.169036	758.346779	379.677028	**N**	***1708.705381***	854.856328	1691.678832	846.343054	1690.694816	845.8510
8	873.410108	437.208692	856.383559	428.695418	855.399543	428.203410	**P**	***1594.662454***	797.834865	1577.635905	789.321590	1576.651889	788.8295
9	1002.452701	501.729989	985.426152	493.216714	984.442136	492.724706	**E**	1497.609690	749.308483	1480.583141	740.795208	1479.599125	740.3032
10	1149.521115	575.264196	1132.494566	566.750921	1131.510550	566.258913	**F**	***1368.567097***	684.787186	1351.540548	676.273912	1350.556532	675.7819
11	**1236.553143**	618.780210	1219.526594	610.266935	1218.542578	609.774927	**S**	***1221.498683***	611.252979	1204.472134	602.739705	1203.488118	602.2476
12	1333.605907	667.306592	1316.579358	658.793317	1315.595342	658.301309	**P**	***1134.466655***	567.736965	1117.440106	559.223691	1116.456090	558.7316
13	1462.648500	731.827888	1445.621951	723.314614	1444.637935	722.822606	**E**	1037.413891	519.210583	1020.387342	510.697309	1019.403326	510.2053
14	1533.685614	767.346445	1516.659065	758.833171	1515.675049	758.341163	**A**	908.371298	454.689287	891.344749	446.176012	890.360733	445.6840
15	1646.769678	823.888477	1629.743129	815.375203	1628.759113	814.883194	**L**	***837.334184***	419.170730	820.307635	410.657455	819.323619	410.1654
16	1761.796621	881.401949	1744.770072	872.888674	1743.786056	872.396666	**D**	***724.250120***	362.628698	707.223571	354.115423	706.239555	353.6234
17	1875.839548	938.423412	1858.812999	929.910138	1857.828983	929.418129	**N**	***609.223177***	305.115226	592.196628	296.601952		
18	2035.870197	1018.438737	2018.843648	1009.925462	2017.859632	1009.433454	**C**	495.180250	248.093763	478.153701	239.580488		
19	2195.900846	1098.454061	2178.874297	1089.940786	2177.890281	1089.448778	**C**	335.149601	168.078438	318.123052	159.565164		
20							**R**	175.118952	88.063114	158.092403	79.549839		

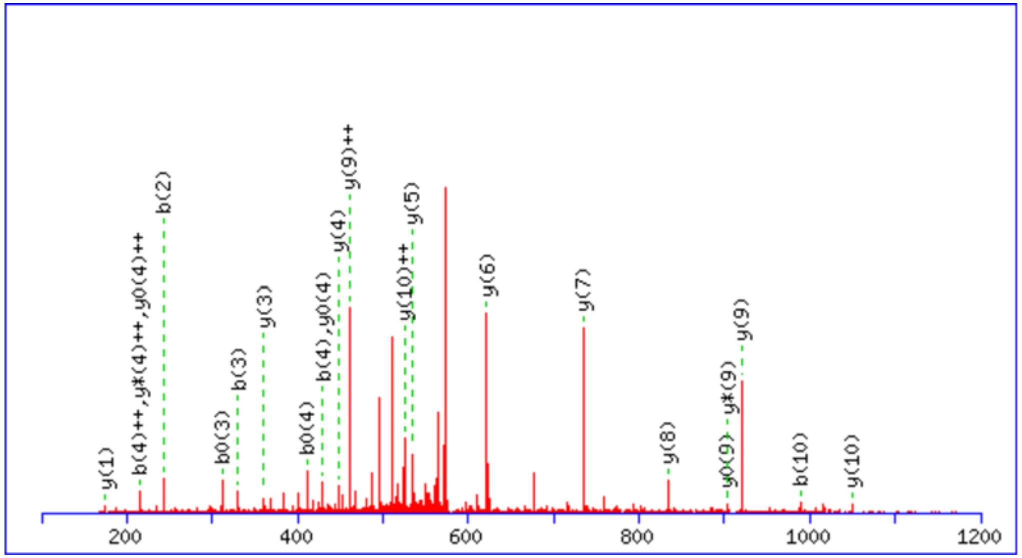


Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 07 - S_C-1 **Fraction:** S_C-1

Match to Query 5295: 1161.635448 from(581.825000,2+)
Title: OECHL100310_25.5315.5315.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00064**Matches :** 23/94 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					**I**							**11**
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637	**10**
3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340	**9**
4	**429.234375**	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326	**8**
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119	**7**
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087	**6**
7	716.382495	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073	**5**
8	803.414523	402.210899			785.403958	393.205617	**S**	***447.267407***	224.137342	430.240858	215.624067	429.256842	215.132059	**4**
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053			**3**
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



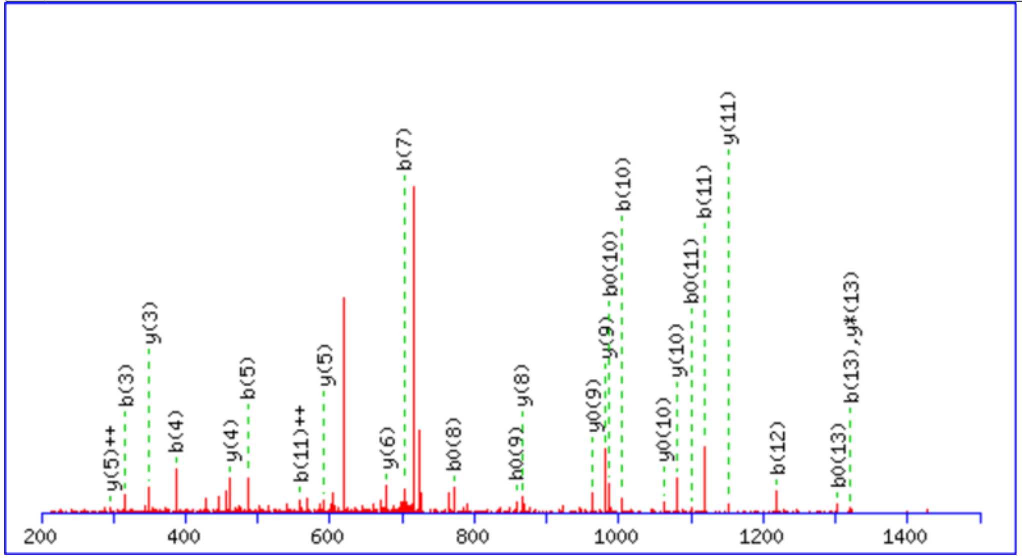
Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 07 - S_C-1 **Fraction:** S_C-1

Match to Query 9119: 1465.679648 from(733.847100,2+)
Title: OECHL100310_25.9372.9372.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 54 **Expect:** 0.00034**Matches :** 26/128 fragment ions using 49 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	1337.643082	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	***316.113926***	158.560601	298.103361	149.555319	**A**	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	***387.151040***	194.079158	369.140475	185.073875	**A**	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	***486.219454***	243.613365	468.208889	234.608082	**V**	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**
6	601.246397	301.126837	583.235832	292.121554	**D**	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	**9**

7	***702.294076***	351.650676	684.283511	342.645394	**T**	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	765.398875	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	876.358132	438.682704	858.347567	429.677421	**S**	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	***1005.400725***	503.204001	987.390160	494.198718	**E**	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	***1118.484789***	559.746033	1100.474224	550.740750	**I**	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	***1219.532468***	610.269872	1201.521903	601.264590	**T**	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	***1320.580147***	660.793712	1302.569582	651.788429	**T**	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**



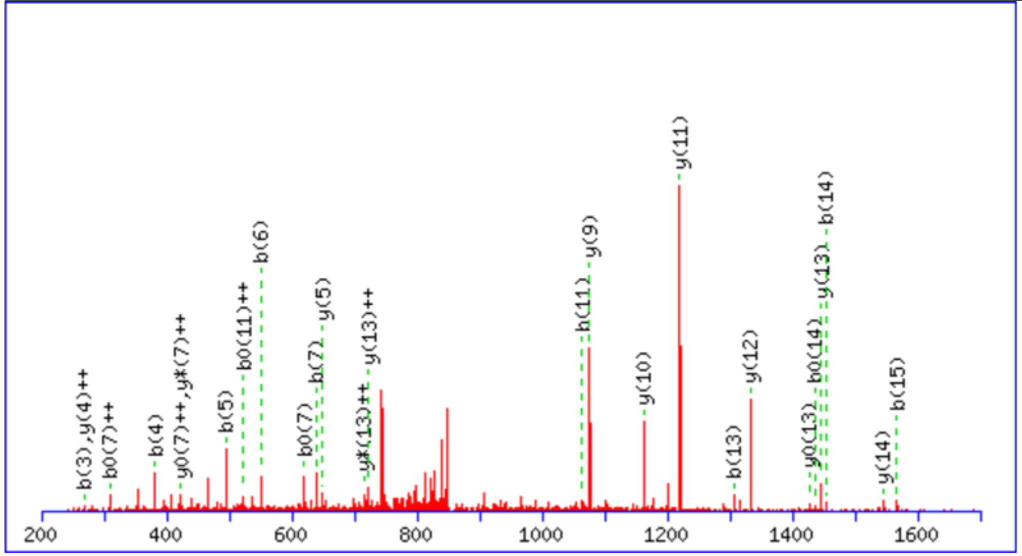
Peptide View

MS/MS Fragmentation of **APVILGSPDDVLEFLK**
Found in **IPI00073772**, Tax_Id=9606 Gene_Symbol=FBP1 Fructose-1,6-bisphosphatase 1
Experiment: 07 - S_C-1 **Fraction:** S_C-1

Match to Query 11325: 1711.936648 from(856.975600,2+)
Title: OECHL100310_25.19856.19856.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1711.939636**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51

Expect: 0.00042**Matches :** 26/132 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**16**
2	169.097154	85.052215			**P**	1641.909801	821.458538	1624.883252	812.945264	1623.899236	812.453256	**15**
3	***268.165568***	134.586422			**V**	**1544.857037**	772.932156	1527.830488	764.418882	1526.846472	763.926874	**14**
4	***381.249632***	191.128454			**I**	**1445.788623**	723.397949	1428.762074	714.884675	1427.778058	714.392667	**13**
5	***494.333696***	247.670486			**L**	**1332.704559**	666.855917	1315.678010	658.342643	1314.693994	657.850635	**12**
6	***551.355160***	276.181218			**G**	**1219.620495**	610.313885	1202.593946	601.800611	1201.609930	601.308603	**11**
7	***638.387188***	319.697232	620.376623	310.691950	**S**	**1162.599031**	581.803153	1145.572482	573.289879	1144.588466	572.797871	**10**
8	735.439952	368.223614	717.429387	359.218332	**P**	**1075.567003**	538.287139	1058.540454	529.773865	1057.556438	529.281857	**9**
9	850.466895	425.737086	832.456330	416.731803	**D**	978.514239	489.760757	961.487690	481.247483	960.503674	480.755475	**8**
10	965.493838	483.250557	947.483273	474.245274	**D**	863.487296	432.247286	846.460747	423.734011	845.476731	423.242003	**7**
11	***1064.562252***	532.784764	1046.551687	523.779481	**V**	748.460353	374.733814	731.433804	366.220540	730.449788	365.728532	**6**
12	1177.646316	589.326796	1159.635751	580.321513	**L**	**649.391939**	325.199607	632.365390	316.686333	631.381374	316.194325	**5**
13	***1306.688909***	653.848092	1288.678344	644.842810	**E**	536.307875	268.657576	519.281326	260.144301	518.297310	259.652293	**4**
14	***1453.757323***	727.382299	1435.746758	718.377017	**F**	407.265282	204.136279	390.238733	195.623004			**3**
15	***1566.841387***	783.924331	1548.830822	774.919049	**L**	260.196868	130.602072	243.170319	122.088797			**2**
16					**K**	147.112804	74.060040	130.086255	65.546765			**1**

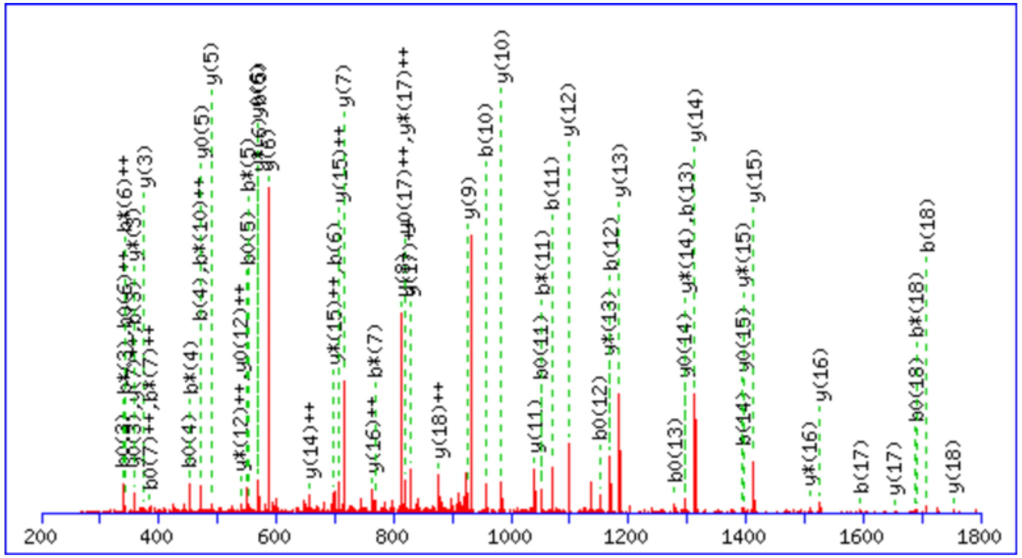


Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**
Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
Experiment: 52 - PyC-1 **Fraction:** PyC-1

Match to Query 14285: 1881.034848 from(941.524700,2+)
Title: OECHL100310_23.13104.13104.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 79
Expect: 6e-007**Matches :** 66/208 fragment ions using 122 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	**E**							**19**
2	229.118283	115.062780			211.107718	106.057497	**V**	***1752.996660***	877.001968	1735.970111	868.488694	1734.986095	867.996686	**18**
3	**357.176861**	179.092069	340.150312	170.578794	339.166296	170.086786	**Q**	***1653.928246***	827.467761	1636.901697	818.954487	1635.917681	818.462479	**17**
4	**470.260925**	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.433190	**16**
5	**569.329339**	285.168308	552.302790	276.655033	551.318774	276.163025	**V**	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.891158	**15**
6	**698.371932**	349.689604	681.345383	341.176330	680.361367	340.684322	**E**	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.356951	**14**
7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	**S**	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.835654	**13**
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	**G**	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.319640	**12**
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	**G**	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.808908	**11**
10	**956.468352**	478.737814	939.441803	470.224540	938.457787	469.732532	**G**	***983.599641***	492.303459	966.573092	483.790184	965.589076	483.298176	**10**
11	**1069.552416**	535.279846	1052.525867	526.766572	1051.541851	526.274564	**L**	***926.578177***	463.792727	909.551628	455.279452	908.567612	454.787444	**9**
12	**1168.620830**	584.814053	1151.594281	576.300779	1150.610265	575.808771	**V**	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.245412	**8**
13	**1296.715793**	648.861535	1279.689244	640.348260	1278.705228	639.856252	**K**	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.711205	**7**
14	**1393.768557**	697.387917	1376.742008	688.874642	1375.757992	688.382634	**P**	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.663723	**6**
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	**G**	***489.277972***	245.142624	472.251423	236.629349	471.267407	236.137341	**5**
16	1507.811485	754.409381	1490.784936	745.896106	1489.800920	745.404098	**G**	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	**4**
17	**1594.843513**	797.925395	1577.816964	789.412120	1576.832948	788.920112	**S**	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	**3**
18	**1707.927577**	854.467427	1690.901028	845.954152	1689.917012	845.462144	**L**	288.203016	144.605146	271.176467	136.091871			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



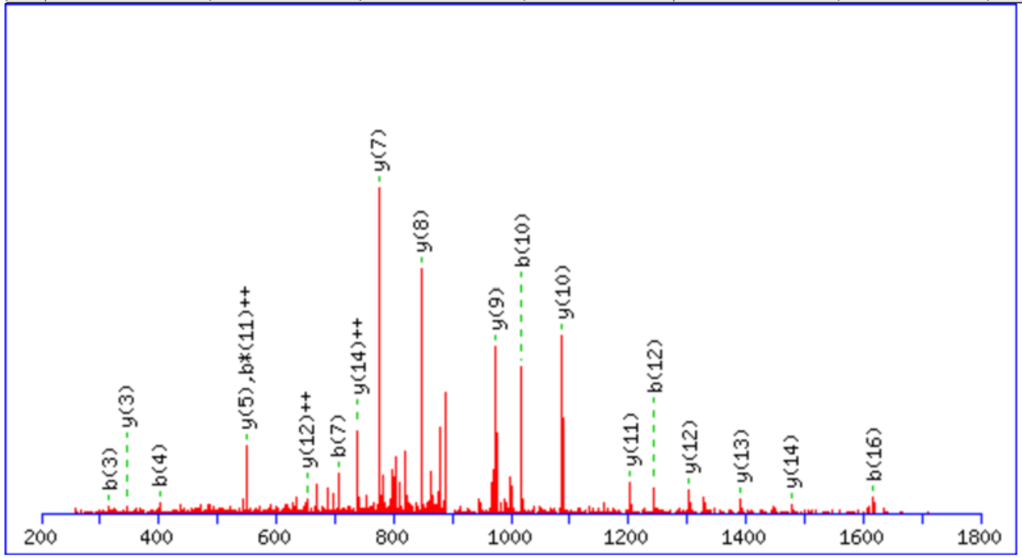
Peptide View

MS/MS Fragmentation of **GQESSTDIKAPEGFAVR**
Found in **IPI00009793**, Tax_Id=9606 Gene_Symbol=C1RL Complement C1r subcomponent-like protein
Experiment: 52 - PyC-1 **Fraction:** PyC-1

Match to Query 13498: 1790.876248 from(896.445400,2+)
Title: OECHL100310_23.10731.10731.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1790.879883**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72
Expect: 1.1e-005**Matches :** 19/176 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	58.028740	29.518008					**G**							**17**
2	186.087318	93.547297	169.060769	85.034023			**Q**	1734.865705	867.936491	1717.839156	859.423216	1716.855140	858.931208	**16**
3	**315.129911**	158.068594	298.103362	149.555319	297.119346	149.063311	**E**	1606.807127	803.907202	1589.780578	795.393927	1588.796562	794.901919	**15**
4	**402.161939**	201.584608	385.135390	193.071333	384.151374	192.579325	**S**	***1477.764534***	739.385905	1460.737985	730.872631	1459.753969	730.380623	**14**
5	489.193967	245.100621	472.167418	236.587347	471.183402	236.095339	**S**	***1390.732506***	695.869891	1373.705957	687.356617	1372.721941	686.864609	**13**
6	590.241646	295.624461	573.215097	287.111187	572.231081	286.619179	**T**	***1303.700478***	652.353877	1286.673929	643.840603	1285.689913	643.348594	**12**

7	**705.268589**	353.137933	688.242040	344.624658	687.258024	344.132650	**D**	***1202.652799***	601.830038	1185.626250	593.316763	1184.642234	592.824755	**11**
8	818.352653	409.679965	801.326104	401.166690	800.342088	400.674682	**I**	***1087.625856***	544.316566	1070.599307	535.803292	1069.615291	535.311284	**10**
9	946.447616	473.727446	929.421067	465.214172	928.437051	464.722164	**K**	***974.541792***	487.774534	957.515243	479.261260	956.531227	478.769252	**9**
10	**1017.484730**	509.246003	1000.458181	500.732729	999.474165	500.240721	**A**	***846.446829***	423.727053	829.420280	415.213778	828.436264	414.721770	**8**
11	1114.537494	557.772385	1097.510945	549.259111	1096.526929	548.767102	**P**	***775.409715***	388.208496	758.383166	379.695221	757.399150	379.203213	**7**
12	**1243.580087**	622.293682	1226.553538	613.780407	1225.569522	613.288399	**E**	678.356951	339.682114	661.330402	331.168839	660.346386	330.676831	**6**
13	1300.601551	650.804414	1283.575002	642.291139	1282.590986	641.799131	**G**	***549.314358***	275.160817	532.287809	266.647543			**5**
14	1447.669965	724.338621	1430.643416	715.825346	1429.659400	715.333338	**F**	492.292894	246.650085	475.266345	238.136811			**4**
15	1518.707079	759.857178	1501.680530	751.343903	1500.696514	750.851895	**A**	***345.224480***	173.115878	328.197931	164.602603			**3**
16	**1617.775493**	809.391385	1600.748944	800.878110	1599.764928	800.386102	**V**	274.187366	137.597321	257.160817	129.084047			**2**
17							**R**	175.118952	88.063114	158.092403	79.549839			**1**

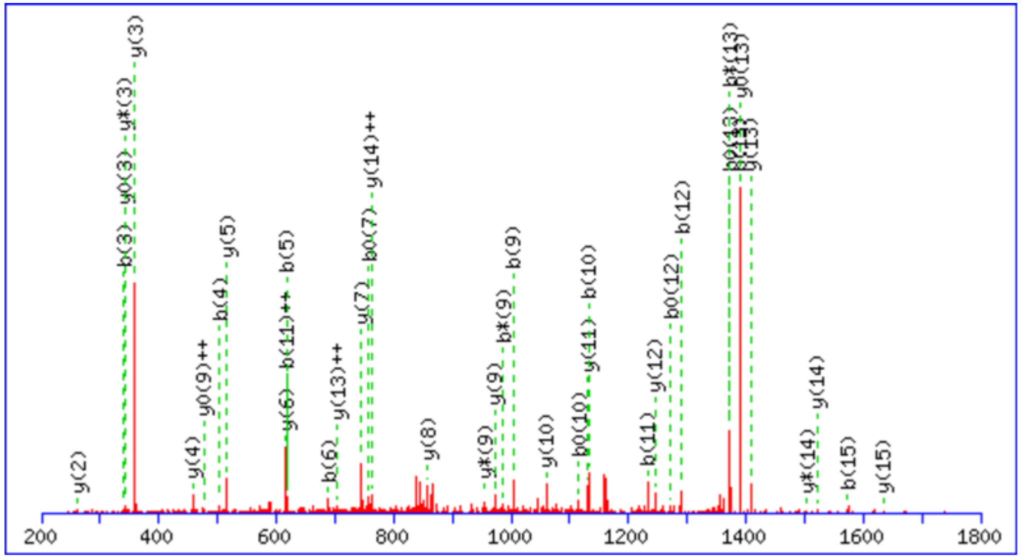


Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 52 - PyC-1 **Fraction:** PyC-1

Match to Query 13137: 1746.914448 from(874.464500,2+)
Title: OECHL100310_23.16283.16283.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 82
Expect: 6.6e-007**Matches :** 39/156 fragment ions using 87 most intense peaks (help)

#	**b**	**b^{++}**	**b^{*}**	**b^{*++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y^{*}**	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	***1634.838427***	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	**340.259468**	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	**503.322797**	252.165036					**Y**	***1408.670299***	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	**689.386854**	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



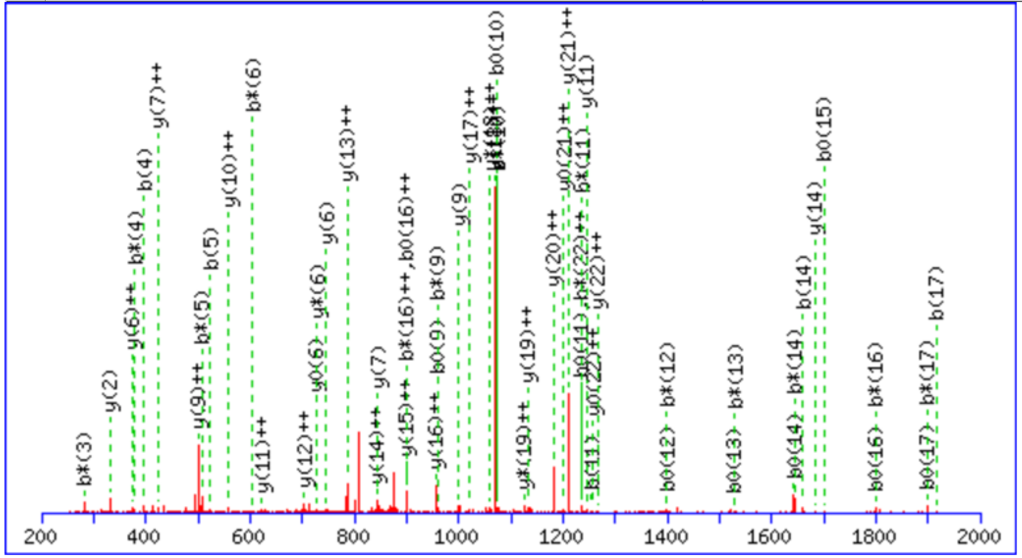
Peptide View

MS/MS Fragmentation of **QLGPQPQDIIYYEDGVVPTTDRR**
Found in **IPI00015199**, Tax_Id=9606 Gene_Symbol=CD7 T-cell antigen CD7
Experiment: 52 - PyC-1 **Fraction:** PyC-1

Match to Query 18655: 2659.328172 from(887.450000,3+)
Title: OECHL100310_23.16660.16660.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 2659.324203**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60
Expect: 0.0002**Matches :** 57/246 fragment ions using 149 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}
1	129.065854	65.036565	112.039305	56.523291			Q						
2	242.149918	121.578597	225.123369	113.065323			L	2532.272897	1266.640086	2515.246348	1258.126812	2514.262332	1257.6348
3	299.171382	150.089329	282.144833	141.576055			G	2419.188833	1210.098054	2402.162284	1201.584780	2401.178268	1201.0927
4	**396.224146**	198.615711	379.197597	190.102436			P	2362.167369	1181.587322	2345.140820	1173.074048	2344.156804	1172.5820
5	**524.282724**	262.645000	507.256175	254.131726			Q	2265.114605	1133.060940	2248.088056	1124.547666	2247.104040	1124.0556
6	621.335488	311.171382	604.308939	302.658108			P	2137.056027	1069.031651	2120.029478	1060.518377	2119.045462	1060.0263

7	749.394066	375.200671	732.367517	366.687397			**Q**	2040.003263	1020.505269	2022.976714	1011.991995	2021.992698	1011.4999
8	864.421009	432.714143	847.394460	424.200868	846.410444	423.708860	**D**	1911.944685	956.475980	1894.918136	947.962706	1893.934120	947.4706
9	977.505073	489.256175	960.478524	480.742900	959.494508	480.250892	**I**	1796.917742	898.962509	1779.891193	890.449234	1778.907177	889.9572
10	1090.589137	545.798206	1073.562588	537.284932	1072.578572	536.792924	**I**	**1683.833678**	842.420477	1666.807129	833.907202	1665.823113	833.4151
11	**1253.652466**	627.329871	1236.625917	618.816597	1235.641901	618.324589	**Y**	1570.749614	785.878445	1553.723065	777.365170	1552.739049	776.8731
12	1416.715795	708.861536	1399.689246	700.348261	1398.705230	699.856253	**Y**	1407.686285	704.346780	1390.659736	695.833506	1389.675720	695.3414
13	1545.758388	773.382832	1528.731839	764.869558	1527.747823	764.377549	**E**	**1244.622956**	622.815116	1227.596407	614.301841	1226.612391	613.8098
14	**1660.785331**	830.896304	1643.758782	822.383029	1642.774766	821.891021	**D**	1115.580363	558.293819	1098.553814	549.780545	1097.569798	549.2885
15	1717.806795	859.407036	1700.780246	850.893761	1699.796230	850.401753	**G**	**1000.553420**	500.780348	983.526871	492.267073	982.542855	491.7750
16	1816.875209	908.941243	1799.848660	900.427968	1798.864644	899.935960	**V**	943.531956	472.269616	926.505407	463.756341	925.521391	463.2643
17	**1915.943623**	958.475450	1898.917074	949.962175	1897.933058	949.470167	**V**	**844.463542**	422.735409	827.436993	414.222134	826.452977	413.7301
18	2012.996387	1007.001832	1995.969838	998.488557	1994.985822	997.996549	**P**	**745.395128**	373.201202	728.368579	364.687927	727.384563	364.1959
19	2114.044066	1057.525671	2097.017517	1049.012396	2096.033501	1048.520388	**T**	648.342364	324.674820	631.315815	316.161545	630.331799	315.6695
20	2215.091745	1108.049510	2198.065196	1099.536236	2197.081180	1099.044228	**T**	547.294685	274.150980	530.268136	265.637706	529.284120	265.1456
21	2330.118688	1165.562982	2313.092139	1157.049707	2312.108123	1156.557699	**D**	446.247006	223.627141	429.220457	215.113866	428.236441	214.6218
22	2486.219799	1243.613537	2469.193250	1235.100263	2468.209234	1234.608255	**R**	**331.220063**	166.113669	314.193514	157.600395		
23							**R**	175.118952	88.063114	158.092403	79.549839		



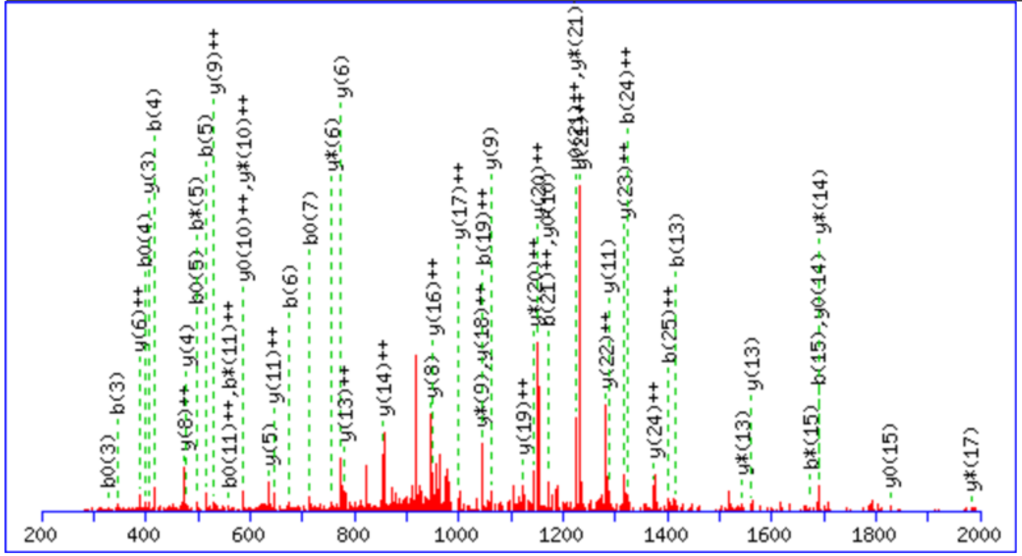
Peptide View

MS/MS Fragmentation of **TENAVCGCSPGHFCIVQDGDHCAACR**
Found in **IPI00024331**, Tax_Id=9606 Gene_Symbol=TNFRSF14 Tumor necrosis factor receptor superfamily member 14
Experiment: 52 - PyC-1 **Fraction:** PyC-1

Match to Query 19602: 2977.181472 from(993.401100,3+)
Title: OECHL100310_23.10262.10262.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 2977.178284**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 4.9e-005**Matches :** 54/284 fragment ions using 120 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}
1	102.054955	51.531116			84.044390	42.525833	**T**						
2	231.097548	116.052412			213.086983	107.047130	**E**	2877.137837	1439.072556	2860.111288	1430.559282	2859.127272	1430.0672
3	**345.140475**	173.073876	328.113926	164.560601	327.129910	164.068593	**N**	2748.095244	1374.551260	2731.068695	1366.037985	2730.084679	1365.5459
4	**416.177589**	208.592433	399.151040	200.079158	398.167024	199.587150	**A**	2634.052317	1317.529796	2617.025768	1309.016522	2616.041752	1308.5245
5	**515.246003**	258.126640	498.219454	249.613365	497.235438	249.121357	**V**	2563.015203	1282.011239	2545.988654	1273.497965	2545.004638	1273.0059
6	**675.276652**	338.141964	658.250103	329.628690	657.266087	329.136682	**C**	2463.946789	1232.477032	2446.920240	1223.963758	2445.936224	1223.4717
7	732.298116	366.652696	715.271567	358.139422	714.287551	357.647414	**G**	2303.916140	1152.461708	2286.889591	1143.948433	2285.905575	1143.4564
8	892.328765	446.668021	875.302216	438.154746	874.318200	437.662738	**C**	2246.894676	1123.950976	2229.868127	1115.437701	2228.884111	1114.9456
9	979.360793	490.184035	962.334244	481.670760	961.350228	481.178752	**S**	2086.864027	1043.935651	2069.837478	1035.422377	2068.853462	1034.9303
10	1076.413557	538.710417	1059.387008	530.197142	1058.402992	529.705134	**P**	1999.831999	1000.419638	1982.805450	991.906363	1981.821434	991.4143
11	1133.435021	567.221149	1116.408472	558.707874	1115.424456	558.215866	**G**	1902.779235	951.893256	1885.752686	943.379981	1884.768670	942.8879
12	1270.493933	635.750605	1253.467384	627.237330	1252.483368	626.745322	**H**	1845.757771	923.382524	1828.731222	914.869249	1827.747206	914.3772
13	**1417.562347**	709.284812	1400.535798	700.771537	1399.551782	700.279529	**F**	1708.698859	854.853068	1691.672310	846.339793	1690.688294	845.8477
14	1577.592996	789.300136	1560.566447	780.786862	1559.582431	780.294854	**C**	**1561.630445**	781.318861	1544.603896	772.805586	1543.619880	772.3135
15	**1690.677060**	845.842168	1673.650511	837.328894	1672.666495	836.836885	**I**	1401.599796	701.303536	1384.573247	692.790262	1383.589231	692.2982
16	1789.745474	895.376375	1772.718925	886.863101	1771.734909	886.371093	**V**	**1288.515732**	644.761504	1271.489183	636.248230	1270.505167	635.7562
17	1917.804052	959.405664	1900.777503	950.892390	1899.793487	950.400382	**Q**	1189.447318	595.227297	1172.420769	586.714023	1171.436753	586.2220
18	2032.830995	1016.919136	2015.804446	1008.405861	2014.820430	1007.913853	**D**	**1061.388740**	531.198008	1044.362191	522.684734	1043.378175	522.1927
19	2089.852459	**1045.429868**	2072.825910	1036.916593	2071.841894	1036.424585	**G**	**946.361797**	473.684537	929.335248	465.171262	928.351232	464.6792
20	2204.879402	1102.943339	2187.852853	1094.430064	2186.868837	1093.938056	**D**	889.340333	445.173804	872.313784	436.660530	871.329768	436.1685
21	2341.938314	**1171.472795**	2324.911765	1162.959520	2323.927749	1162.467512	**H**	**774.313390**	387.660333	757.286841	379.147059		

22	2501.968963	1251.488119	2484.942414	1242.974845	2483.958398	1242.482837	**C**	**637.254478**	319.130877	620.227929	310.617603		
23	2573.006077	1287.006676	2555.979528	1278.493402	2554.995512	1278.001394	**A**	**477.223829**	239.115553	460.197280	230.602278		
24	2644.043191	**1322.525234**	2627.016642	1314.011959	2626.032626	1313.519951	**A**	**406.186715**	203.596995	389.160166	195.083721		
25	2804.073840	**1402.540558**	2787.047291	1394.027283	2786.063275	1393.535275	**C**	335.149601	168.078438	318.123052	159.565164		
26							**R**	175.118952	88.063114	158.092403	79.549839		



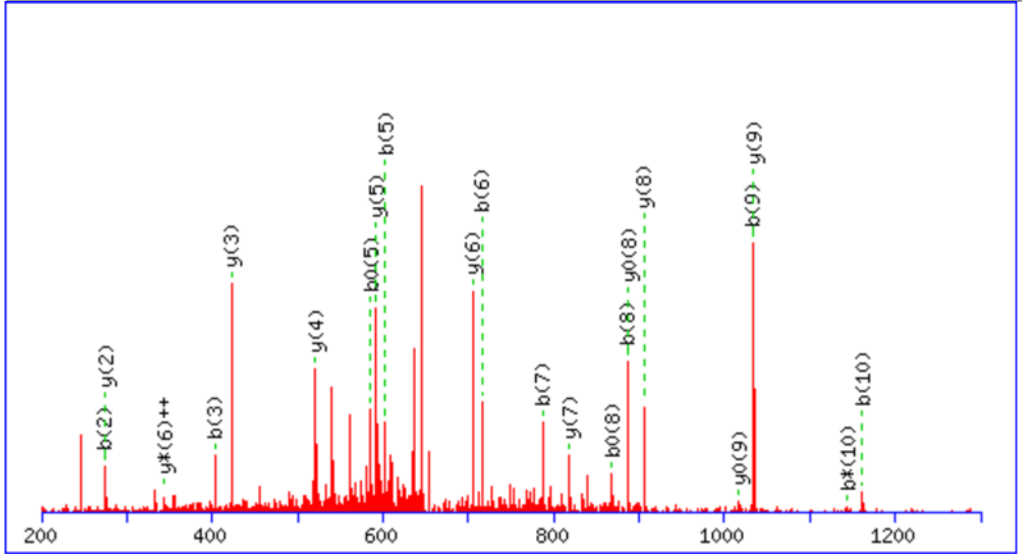
Peptide View

MS/MS Fragmentation of **CIESLIAVFQK**
Found in **IPI00013895**, Tax_Id=9606 Gene_Symbol=S100A11 Protein S100-A11
Experiment: 52 - PyC-1 **Fraction:** PyC-1

Match to Query 8023: 1306.695248 from(654.354900,2+)
Title: OECHL100310_23.19833.19833.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1306.695496**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00064**Matches :** 22/84 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	161.037925	81.022600					**C**							**11**

2	***274.121989***	137.564632					**I**	1147.672137	574.339707	1130.645588	565.826432	1129.661572	565.334424	**10**
3	***403.164582***	202.085929			385.154017	193.080647	**E**	***1034.588073***	517.797675	1017.561524	509.284400	1016.577508	508.792392	**9**
4	490.196610	245.601943			472.186045	236.596661	**S**	***905.545480***	453.276378	888.518931	444.763104	887.534915	444.271096	**8**
5	***603.280674***	302.143975			585.270109	293.138693	**L**	***818.513452***	409.760364	801.486903	401.247090			**7**
6	***716.364738***	358.686007			698.354173	349.680725	**I**	***705.429388***	353.218332	688.402839	344.705058			**6**
7	***787.401852***	394.204564			769.391287	385.199282	**A**	***592.345324***	296.676300	575.318775	288.163026			**5**
8	***886.470266***	443.738771			868.459701	434.733489	**V**	***521.308210***	261.157743	504.281661	252.644469			**4**
9	***1033.538680***	517.272978			1015.528115	508.267696	**F**	***422.239796***	211.623536	405.213247	203.110261			**3**
10	***1161.597258***	581.302267	1144.570709	572.788993	1143.586693	572.296985	**Q**	***275.171382***	138.089329	258.144833	129.576054			**2**
11							**K**	147.112804	74.060040	130.086255	65.546765			**1**



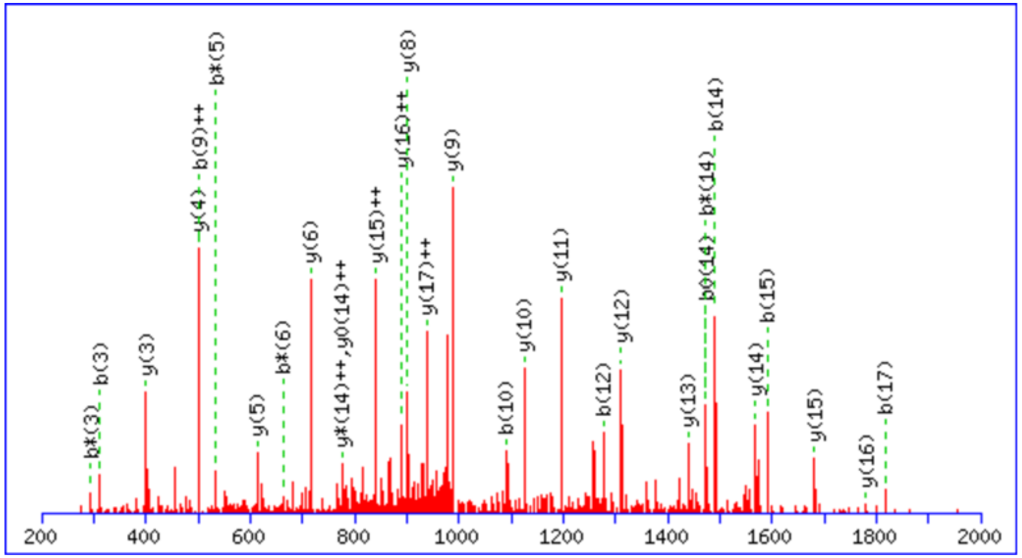
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 52 - PyC-1 **Fraction:** PyC-1

Match to Query 15202: 1990.027048 from(996.020800,2+)

Title: OECHL100310_23.9174.9174.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 94
Expect: 4.7e-008**Matches :** 30/186 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	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	424.255445	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	552.314023	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	680.372601	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**
7	795.399544	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	814.478130	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510			**3**
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**



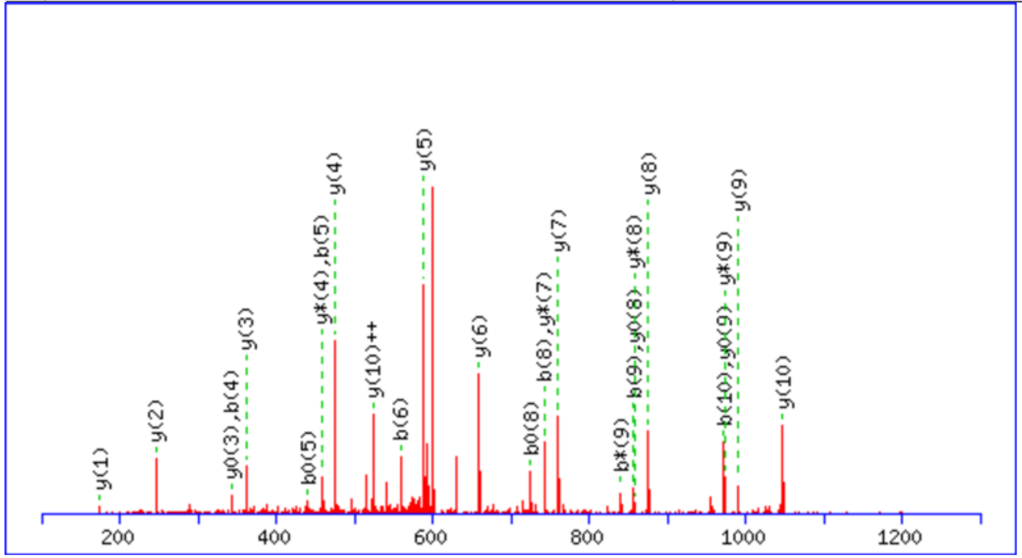
Peptide View

MS/MS Fragmentation of **GLGDDTALNDAR**
Found in **IPI00216914**, Tax_Id=9606 Gene_Symbol=VMO1 Vitelline membrane outer layer protein 1 homolog
Experiment: 52 - PyC-1 **Fraction:** PyC-1

Match to Query 6665: 1216.567648 from(609.291100,2+)
Title: OECHL100310_23.8102.8102.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1216.568390**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 86
Expect: 2.3e-007**Matches :** 27/106 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	58.028740	29.518008					**G**							**12**
2	171.112804	86.060040					**L**	1160.554207	580.780742	1143.527658	572.267467	1142.543642	571.775459	**11**
3	228.134268	114.570772					**G**	***1047.470143***	524.238710	1030.443594	515.725435	1029.459578	515.233427	**10**
4	**343.161211**	172.084243			325.150646	163.078961	**D**	***990.448679***	495.727978	973.422130	487.214703	972.438114	486.722695	**9**
5	**458.188154**	229.597715			440.177589	220.592433	**D**	***875.421736***	438.214506	858.395187	429.701232	857.411171	429.209224	**8**
6	**559.235833**	280.121555			541.225268	271.116272	**T**	***760.394793***	380.701035	743.368244	372.187760	742.384228	371.695752	**7**

7	630.272947	315.640112			612.262382	306.634829	A	***659.347114***	330.177195	642.320565	321.663921	641.336549	321.171913	6
8	**743.357011**	372.182144			725.346446	363.176861	L	***588.310000***	294.658638	571.283451	286.145364	570.299435	285.653356	5
9	**857.399938**	429.203607	840.373389	420.690333	839.389373	420.198325	N	***475.225936***	238.116606	458.199387	229.603331	457.215371	229.111323	4
10	**972.426881**	486.717079	955.400332	478.203804	954.416316	477.711796	D	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	3
11	1043.463995	522.235636	1026.437446	513.722361	1025.453430	513.230353	A	***246.156066***	123.581671	229.129517	115.068397			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1



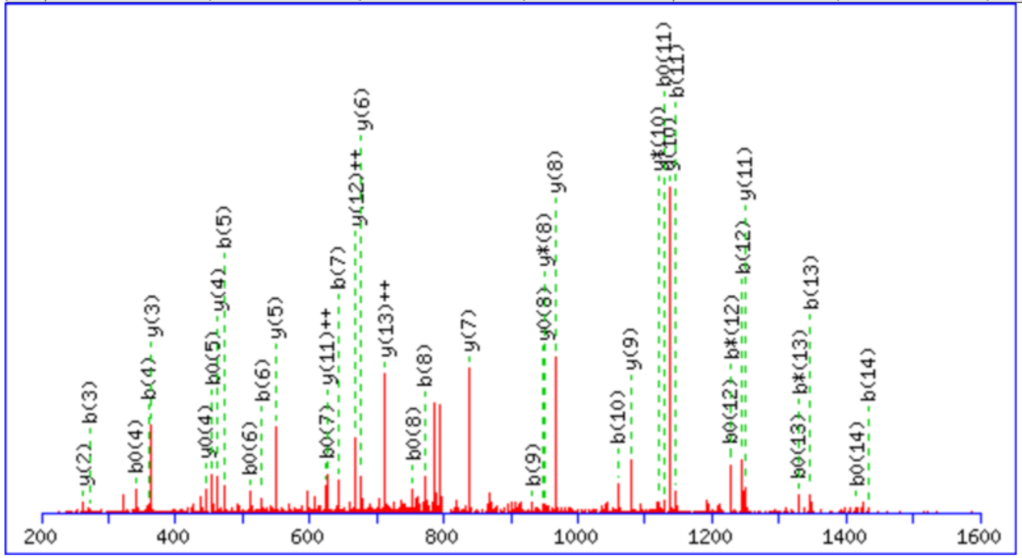
Peptide View

MS/MS Fragmentation of **AISSIGLECQSVTSR**
Found in **IPI00006988**, Tax_Id=9606 Gene_Symbol=RETN Resistin
Experiment: 52 - PyC-1 **Fraction:** PyC-1

Match to Query 11358: 1606.799448 from(804.407000,2+)
Title: OECHL100310_23.11307.11307.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1606.798462**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 73
Expect: 6.6e-006**Matches :** 40/144 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	72.044390	36.525833					A							15
2	185.128454	93.067865					I	1536.768633	768.887955	1519.742084	760.374680	1518.758068	759.882672	14
3	***272.160482***	136.583879			254.149917	127.578596	S	1423.684569	712.345923	1406.658020	703.832648	1405.674004	703.340640	13
4	***359.192510***	180.099893			341.181945	171.094610	S	1336.652541	668.829909	1319.625992	660.316634	1318.641976	659.824626	12
5	***472.276574***	236.641925			454.266009	227.636642	I	**1249.620513**	625.313895	1232.593964	616.800620	1231.609948	616.308612	11
6	***529.298038***	265.152657			511.287473	256.147375	G	**1136.536449**	568.771863	1119.509900	560.258588	1118.525884	559.766580	10
7	***642.382102***	321.694689			624.371537	312.689407	L	**1079.514985**	540.261131	1062.488436	531.747856	1061.504420	531.255848	9
8	***771.424695***	386.215986			753.414130	377.210703	E	**966.430921**	483.719099	949.404372	475.205824	948.420356	474.713816	8
9	***931.455344***	466.231310			913.444779	457.226028	C	**837.388328**	419.197802	820.361779	410.684528	819.377763	410.192520	7
10	***1059.513922***	530.260599	1042.487373	521.747325	1041.503357	521.255317	Q	**677.357679**	339.182478	660.331130	330.669203	659.347114	330.177195	6
11	***1146.545950***	573.776613	1129.519401	565.263339	1128.535385	564.771331	S	**549.299101**	275.153189	532.272552	266.639914	531.288536	266.147906	5
12	***1245.614364***	623.310820	1228.587815	614.797546	1227.603799	614.305538	V	**462.267073**	231.637175	445.240524	223.123900	444.256508	222.631892	4
13	***1346.662043***	673.834660	1329.635494	665.321385	1328.651478	664.829377	T	**363.198659**	182.102968	346.172110	173.589693	345.188094	173.097685	3
14	***1433.694071***	717.350674	1416.667522	708.837399	1415.683506	708.345391	S	**262.150980**	131.579128	245.124431	123.065854	244.140415	122.573846	2
15							R	175.118952	88.063114	158.092403	79.549839			1

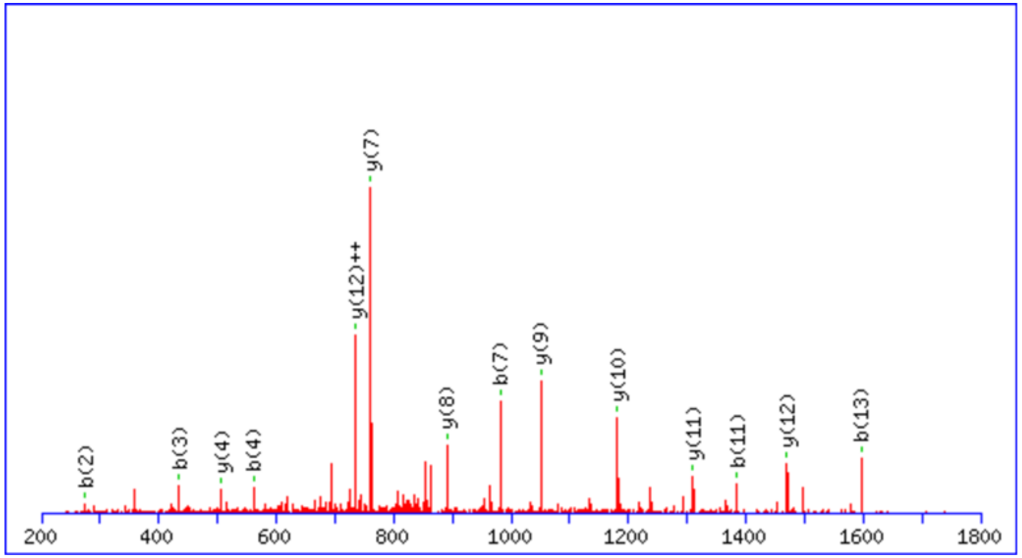


Peptide View

MS/MS Fragmentation of **LCCQMCEPGTFLVK**
Found in **IPI00002435**, Tax_Id=9606 Gene_Symbol=CD27 CD27 antigen
Experiment: 52 - PyC-1 **Fraction:** PyC-1

Match to Query 13121: 1741.767048 from(871.890800,2+)
Title: OECHL100310_23.15292.15292.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1741.766006**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72
Expect: 4.4e-006**Matches :** 14/130 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	114.091340	57.549308					**L**							**14**
2	***274.121989***	137.564632					**C**	1629.689206	815.348241	1612.662657	806.834967	1611.678641	806.342959	**13**
3	***434.152638***	217.579957					**C**	***1469.658557***	735.332917	1452.632008	726.819642	1451.647992	726.327634	**12**
4	***562.211216***	281.609246	545.184667	273.095972			**Q**	***1309.627908***	655.317592	1292.601359	646.804318	1291.617343	646.312310	**11**
5	693.251701	347.129489	676.225152	338.616214			**M**	***1181.569330***	591.288303	1164.542781	582.775029	1163.558765	582.283021	**10**
6	853.282350	427.144813	836.255801	418.631539			**C**	***1050.528845***	525.768061	1033.502296	517.254786	1032.518280	516.762778	**9**
7	***982.324943***	491.666110	965.298394	483.152835	964.314378	482.660827	**E**	***890.498196***	445.752736	873.471647	437.239462	872.487631	436.747454	**8**
8	1079.377707	540.192492	1062.351158	531.679217	1061.367142	531.187209	**P**	***761.455603***	381.231440	744.429054	372.718165	743.445038	372.226157	**7**
9	1136.399171	568.703224	1119.372622	560.189949	1118.388606	559.697941	**G**	664.402839	332.705058	647.376290	324.191783	646.392274	323.699775	**6**
10	1237.446850	619.227063	1220.420301	610.713789	1219.436285	610.221781	**T**	607.381375	304.194326	590.354826	295.681051	589.370810	295.189043	**5**
11	***1384.515264***	692.761270	1367.488715	684.247996	1366.504699	683.755988	**F**	***506.333696***	253.670486	489.307147	245.157212			**4**
12	1497.599328	749.303302	1480.572779	740.790028	1479.588763	740.298020	**L**	359.265282	180.136279	342.238733	171.623004			**3**
13	***1596.667742***	798.837509	1579.641193	790.324235	1578.657177	789.832227	**V**	246.181218	123.594247	229.154669	115.080973			**2**
14							**K**	147.112804	74.060040	130.086255	65.546765			**1**



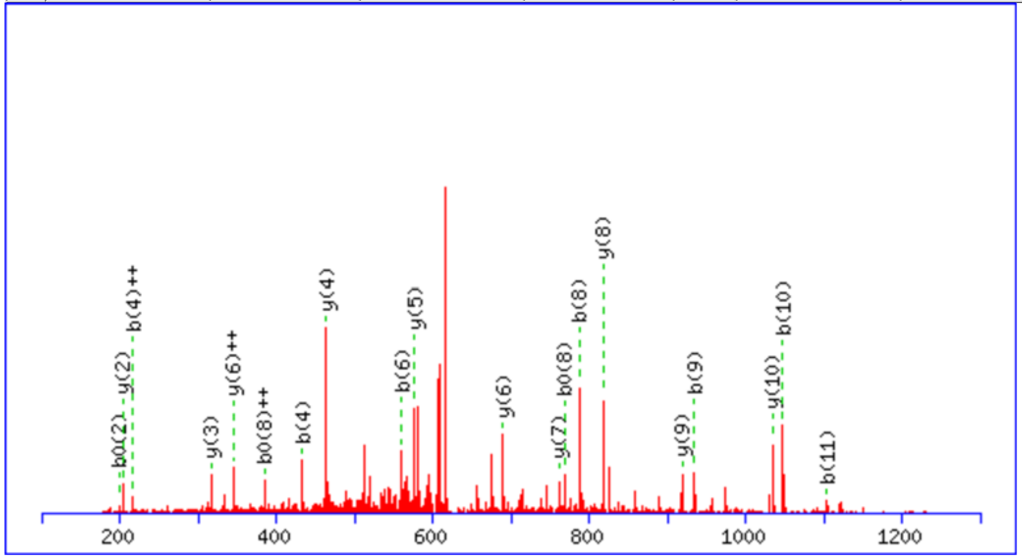
Peptide View

MS/MS Fragmentation of **DTDTGALLFIGK**
Found in **IPI00006114**, Tax_Id=9606 Gene_Symbol=SERPINF1 Pigment epithelium-derived factor
Experiment: 52 - PyC-1 **Fraction:** PyC-1

Match to Query 7350: 1249.656248 from(625.835400,2+)
Title: OECHL100310_23.17104.17104.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1249.655426**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70
Expect: 8e-006**Matches :** 21/94 fragment ions using 33 most intense peaks (help)

#	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y^{*}**	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	116.034219	58.520748	98.023654	49.515465	**D**							**12**
2	**217.081898**	109.044587	199.071333	100.039304	**T**	1135.635753	568.321514	1118.609204	559.808240	1117.625188	559.316232	**11**
3	332.108841	166.558058	314.098276	157.552776	**D**	***1034.588074***	517.797675	1017.561525	509.284401	1016.577509	508.792393	**10**
4	**433.156520**	217.081898	415.145955	208.076616	**T**	***919.561131***	460.284203	902.534582	451.770929	901.550566	451.278921	**9**
5	490.177984	245.592630	472.167419	236.587347	**G**	***818.513452***	409.760364	801.486903	401.247089			**8**
6	**561.215098**	281.111187	543.204533	272.105905	**A**	***761.491988***	381.249632	744.465439	372.736357			**7**

7	674.299162	337.653219	656.288597	328.647937	**L**	***690.454874***	345.731075	673.428325	337.217800			**6**
8	**787.383226**	394.195251	769.372661	385.189969	**L**	***577.370810***	289.189043	560.344261	280.675768			**5**
9	**934.451640**	467.729458	916.441075	458.724176	**F**	***464.286746***	232.647011	447.260197	224.133736			**4**
10	**1047.535704**	524.271490	1029.525139	515.266207	**I**	***317.218332***	159.112804	300.191783	150.599529			**3**
11	**1104.557168**	552.782222	1086.546603	543.776939	**G**	***204.134268***	102.570772	187.107719	94.057497			**2**
12					**K**	147.112804	74.060040	130.086255	65.546765			**1**



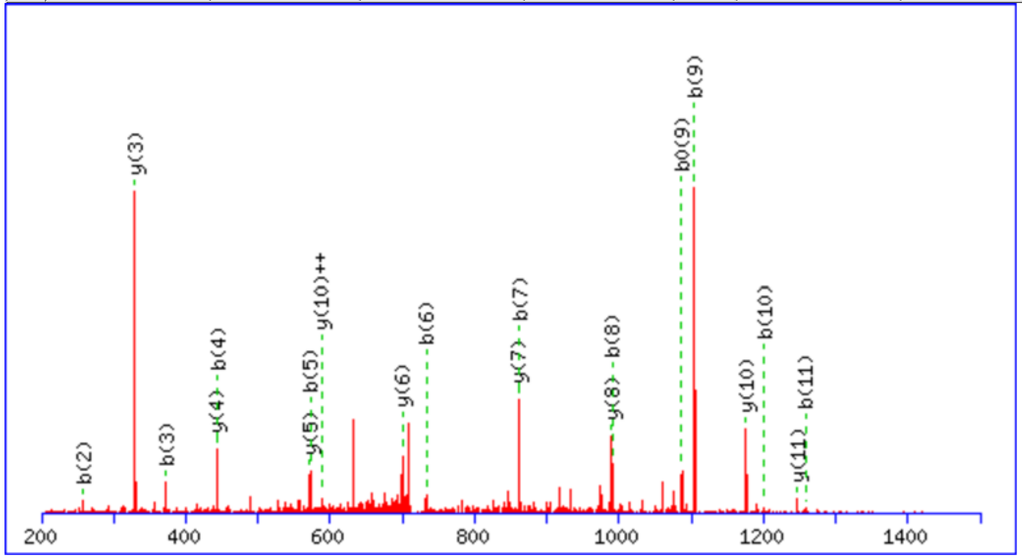
Peptide View

MS/MS Fragmentation of **WADAECEEIPGR**
Found in **IPI00027436**, Tax_Id=9606 Gene_Symbol=NGFR Tumor necrosis factor receptor superfamily member 16
Experiment: 52 - PyC-1 **Fraction:** PyC-1

Match to Query 9228: 1431.610248 from(716.812400,2+)
Title: OECHL100310_23.10332.10332.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1431.608856**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57
Expect: 5.4e-005**Matches :** 20/98 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#

1	187.086589	94.046932			**W**							**12**
2	***258.123703***	129.565490			**A**	**1246.536843**	623.772060	1229.510294	615.258785	1228.526278	614.766777	**11**
3	***373.150646***	187.078961	355.140081	178.073679	**D**	**1175.499729**	588.253502	1158.473180	579.740228	1157.489164	579.248220	**10**
4	***444.187760***	222.597518	426.177195	213.592236	**A**	1060.472786	530.740031	1043.446237	522.226757	1042.462221	521.734749	**9**
5	***573.230353***	287.118815	555.219788	278.113532	**E**	**989.435672**	495.221474	972.409123	486.708199	971.425107	486.216191	**8**
6	***733.261002***	367.134139	715.250437	358.128857	**C**	**860.393079**	430.700178	843.366530	422.186903	842.382514	421.694895	**7**
7	***862.303595***	431.655436	844.293030	422.650153	**E**	**700.362430**	350.684853	683.335881	342.171578	682.351865	341.679570	**6**
8	***991.346188***	496.176732	973.335623	487.171450	**E**	**571.319837**	286.163556	554.293288	277.650282	553.309272	277.158274	**5**
9	***1104.430252***	552.718764	1086.419687	543.713482	**I**	**442.277244**	221.642260	425.250695	213.128985			**4**
10	***1201.483016***	601.245146	1183.472451	592.239864	**P**	**329.193180**	165.100228	312.166631	156.586953			**3**
11	***1258.504480***	629.755878	1240.493915	620.750596	**G**	232.140416	116.573846	215.113867	108.060571			**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**

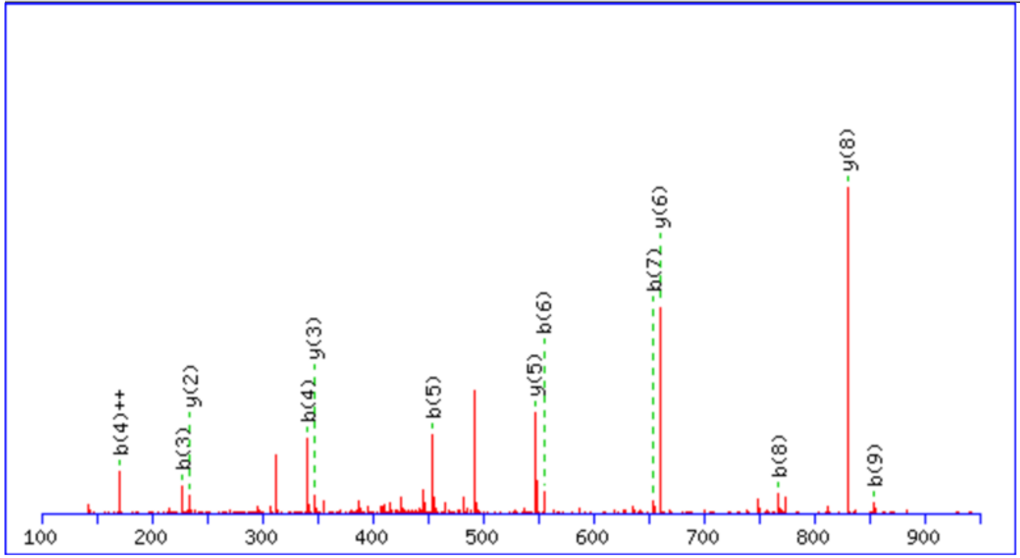


Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 22 - NOPC1 **Fraction:** NOPC1

Match to Query 2694: 999.634248 from(500.824400,2+)
Title: OECHL100310_21.17386.17386.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65
Expect: 4e-006**Matches :** 14/78 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**

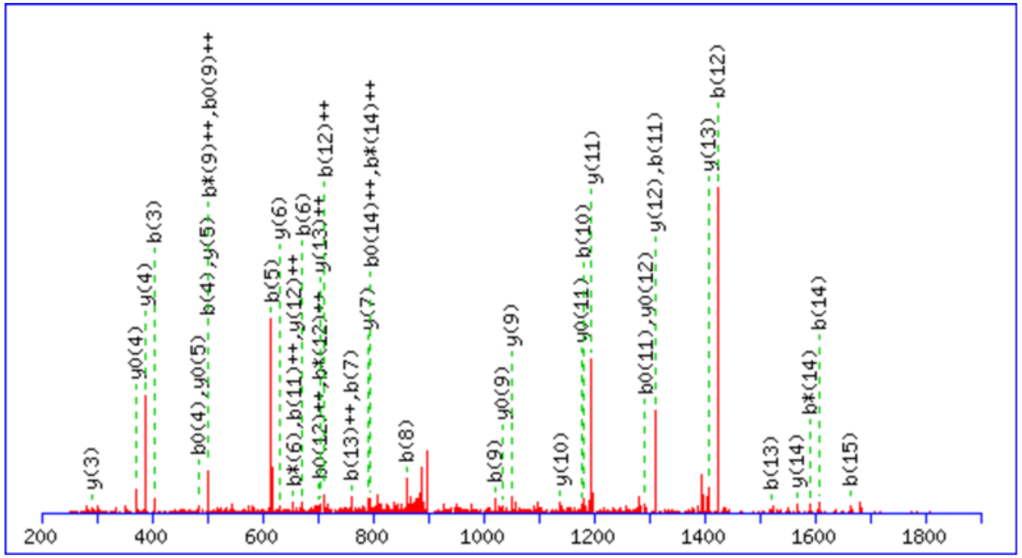


Peptide View

MS/MS Fragmentation of **SRCPDGSTCCELPSGK**
Found in **IPI00182138**, Tax_Id=9606 Gene_Symbol=GRN Isoform 2 of Granulins
Experiment: 22 - NOPC1 **Fraction:** NOPC1

Match to Query 11970: 1809.745048 from(905.879800,2+)
Title: OECHL100310_21.5076.5076.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1809.744415**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63
Expect: 1.5e-005**Matches :** 44/174 fragment ions using 94 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	**S**							**16**
2	244.140415	122.573845	227.113866	114.060571	226.129850	113.568563	**R**	1723.719653	862.363465	1706.693104	853.850190	1705.709088	853.358182	**15**
3	***404.171064***	202.589170	387.144515	194.075896	386.160499	193.583888	**C**	**1567.618542**	784.312909	1550.591993	775.799635	1549.607977	775.307627	**14**
4	***501.223828***	251.115552	484.197279	242.602277	483.213263	242.110269	**P**	**1407.587893**	704.297585	1390.561344	695.784310	1389.577328	695.292302	**13**
5	***616.250771***	308.629024	599.224222	300.115749	598.240206	299.623741	**D**	**1310.535129**	655.771203	1293.508580	647.257928	1292.524564	646.765920	**12**
6	***673.272235***	337.139756	656.245686	328.626481	655.261670	328.134473	**G**	**1195.508186**	598.257731	1178.481637	589.744457	1177.497621	589.252449	**11**
7	***760.304263***	380.655770	743.277714	372.142495	742.293698	371.650487	**S**	**1138.486722**	569.746999	1121.460173	561.233725	1120.476157	560.741717	**10**
8	***861.351942***	431.179609	844.325393	422.666335	843.341377	422.174327	**T**	**1051.454694**	526.230985	1034.428145	517.717711	1033.444129	517.225703	**9**
9	***1021.382591***	511.194934	1004.356042	502.681659	1003.372026	502.189651	**C**	950.407015	475.707146	933.380466	467.193871	932.396450	466.701863	**8**
10	***1181.413240***	591.210258	1164.386691	582.696984	1163.402675	582.204976	**C**	**790.376366**	395.691821	773.349817	387.178547	772.365801	386.686539	**7**
11	***1310.455833***	**655.731555**	1293.429284	647.218280	1292.445268	646.726272	**E**	**630.345717**	315.676497	613.319168	307.163222	612.335152	306.671214	**6**
12	***1423.539897***	**712.273587**	1406.513348	703.760312	1405.529332	703.268304	**L**	**501.303124**	251.155200	484.276575	242.641925	483.292559	242.149917	**5**
13	***1520.592661***	**760.799969**	1503.566112	752.286694	1502.582096	751.794686	**P**	**388.219060**	194.613168	371.192511	186.099894	370.208495	185.607886	**4**
14	***1607.624689***	804.315983	1590.598140	795.802708	1589.614124	795.310700	**S**	**291.166296**	146.086786	274.139747	137.573512	273.155731	137.081504	**3**
15	***1664.646153***	832.826715	1647.619604	824.313440	1646.635588	823.821432	**G**	204.134268	102.570772	187.107719	94.057497			**2**
16							**K**	147.112804	74.060040	130.086255	65.546765			**1**



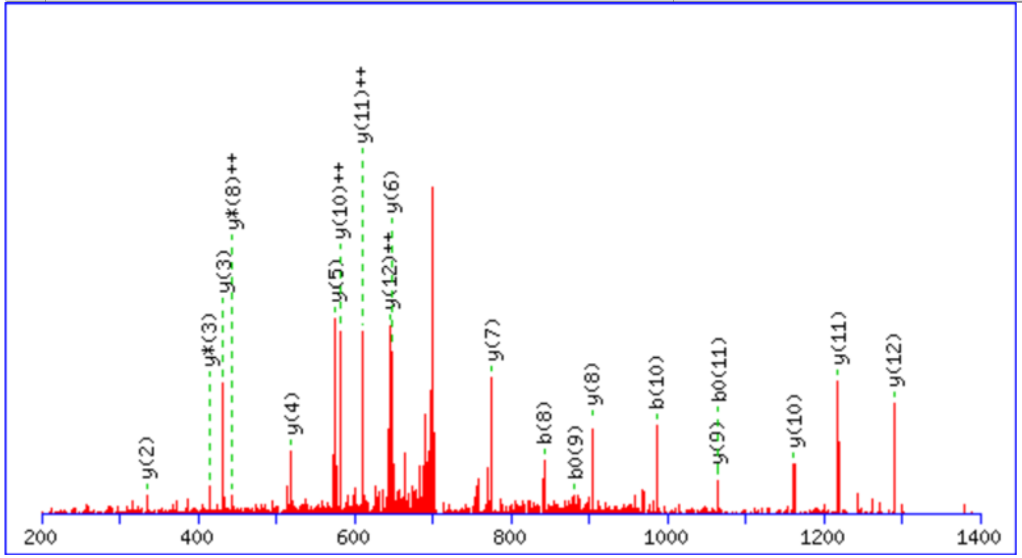
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 22 - NOPC1 **Fraction:** NOPC1

Match to Query 7898: 1416.624648 from(709.319600,2+)
Title: OECHL100310_21.2090.2090.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 87
Expect: 1.1e-007**Matches :** 20/128 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							**13**
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	**12**
3	257.160817	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	**11**
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	**10**
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	**9**
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	**8**

7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	899.403979	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

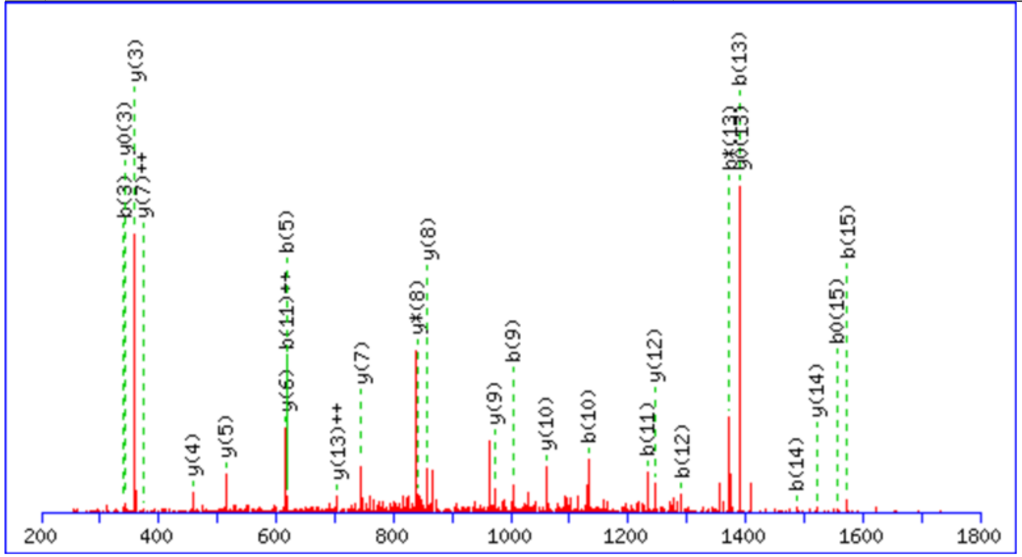


Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 22 - NOPC1 **Fraction:** NOPC1

Match to Query 11389: 1746.917248 from(874.465900,2+)
Title: OECHL100310_21.17095.17095.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 78
Expect: 1.8e-006**Matches :** 27/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	***340.259468***	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	***618.349740***	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	689.386854	345.197065			671.376289	336.191782	**A**	1130.580027	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**

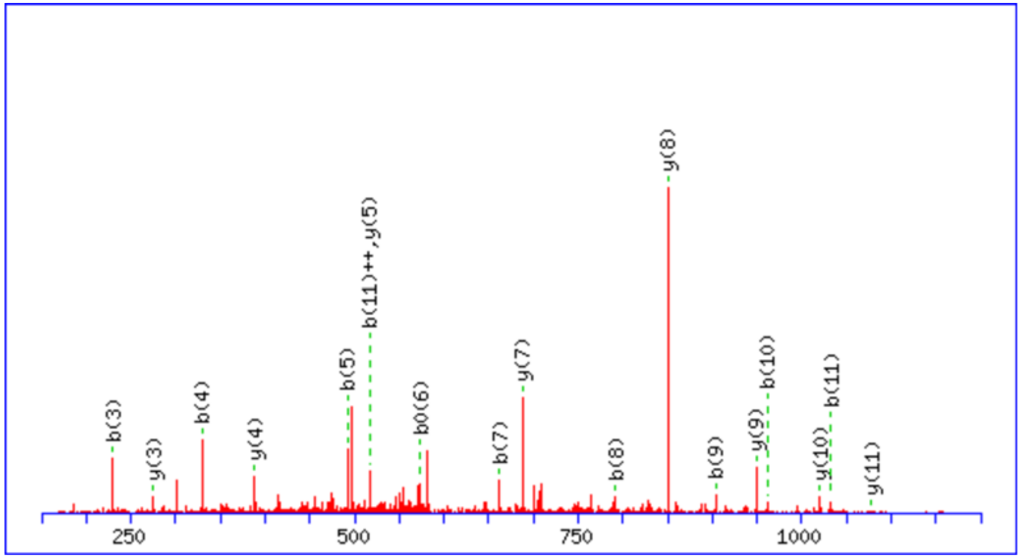


Peptide View

MS/MS Fragmentation of **TGAVYVAEIGAK**
Found in **IPI00552937**, Tax_Id=9606 Gene_Symbol=NHLRC3 NHL repeat-containing protein 3
Experiment: 22 - NOPC1 **Fraction:** NOPC1

Match to Query 4972: 1177.632848 from(589.823700,2+)
Title: OECHL100310_21.11361.11361.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1177.634277**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64
Expect: 2.9e-005**Matches :** 18/102 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							**12**
2	159.076419	80.041847	141.065854	71.036565	**G**	***1077.593888***	539.300582	1060.567339	530.787308	1059.583323	530.295300	**11**
3	***230.113533***	115.560404	212.102968	106.555122	**A**	***1020.572424***	510.789850	1003.545875	502.276576	1002.561859	501.784568	**10**
4	***329.181947***	165.094611	311.171382	156.089329	**V**	***949.535310***	475.271293	932.508761	466.758019	931.524745	466.266011	**9**
5	***492.245276***	246.626276	474.234711	237.620994	**Y**	***850.466896***	425.737086	833.440347	417.223812	832.456331	416.731804	**8**
6	591.313690	296.160483	573.303125	287.155201	**V**	***687.403567***	344.205422	670.377018	335.692147	669.393002	335.200139	**7**
7	***662.350804***	331.679040	644.340239	322.673758	**A**	588.335153	294.671215	571.308604	286.157940	570.324588	285.665932	**6**
8	***791.393397***	396.200337	773.382832	387.195054	**E**	***517.298039***	259.152658	500.271490	250.639383	499.287474	250.147375	**5**
9	***904.477461***	452.742369	886.466896	443.737086	**I**	***388.255446***	194.631361	371.228897	186.118087			**4**
10	***961.498925***	481.253101	943.488360	472.247818	**G**	***275.171382***	138.089329	258.144833	129.576055			**3**
11	***1032.536039***	516.771658	1014.525474	507.766375	**A**	218.149918	109.578597	201.123369	101.065322			**2**
12					**K**	147.112804	74.060040	130.086255	65.546765			**1**



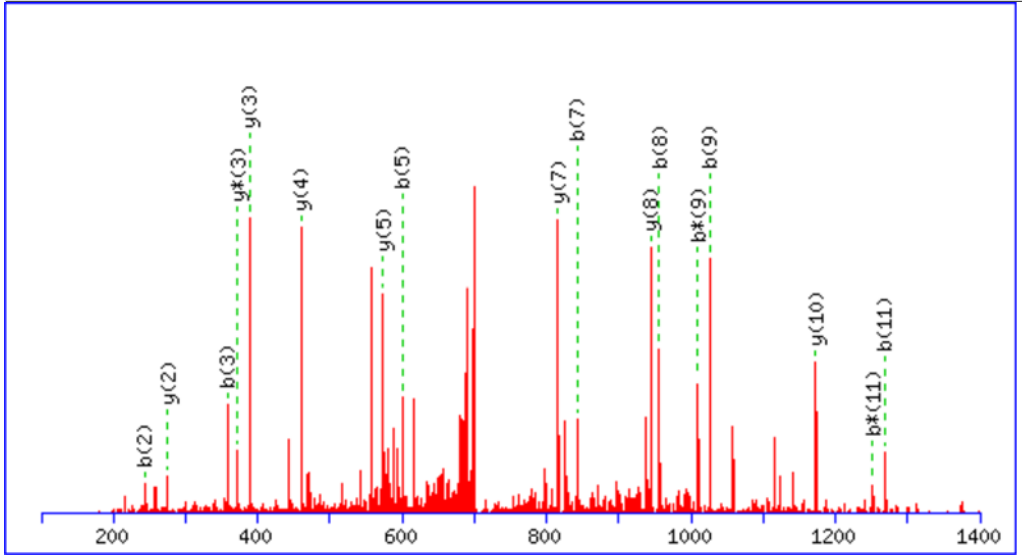
Peptide View

MS/MS Fragmentation of **LEDLENQLANQK**
Found in **IPI00012325**, Tax_Id=9606 Gene_Symbol=MATN4 matrilin 4 isoform 3 precursor
Experiment: 22 - NOPC1 **Fraction:** NOPC1

Match to Query 7872: 1413.709248 from(707.861900,2+)
Title: OECHL100310_21.11795.11795.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1413.709930**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62
Expect: 7.2e-005**Matches :** 17/106 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					**L**							**12**
2	***243.133933***	122.070605			225.123368	113.065322	**E**	1301.633185	651.320231	1284.606636	642.806956	1283.622620	642.314948	**11**
3	***358.160876***	179.584076			340.150311	170.578794	**D**	***1172.590592***	586.798934	1155.564043	578.285660	1154.580027	577.793652	**10**
4	471.244940	236.126108			453.234375	227.120826	**L**	1057.563649	529.285462	1040.537100	520.772188	1039.553084	520.280180	**9**
5	***600.287533***	300.647405			582.276968	291.642122	**E**	***944.479585***	472.743431	927.453036	464.230156	926.469020	463.738148	**8**
6	714.330460	357.668868	697.303911	349.155594	696.319895	348.663586	**N**	***815.436992***	408.222134	798.410443	399.708859			**7**

7	***842.389038***	421.698157	825.362489	413.184883	824.378473	412.692875	Q	701.394065	351.200671	684.367516	342.687396			6
8	***955.473102***	478.240189	938.446553	469.726915	937.462537	469.234907	L	***573.335487***	287.171382	556.308938	278.658107			5
9	***1026.510216***	513.758746	1009.483667	505.245472	1008.499651	504.753464	A	***460.251423***	230.629349	443.224874	222.116075			4
10	1140.553143	570.780210	1123.526594	562.266935	1122.542578	561.774927	N	***389.214309***	195.110792	372.187760	186.597518			3
11	***1268.611721***	634.809499	1251.585172	626.296224	1250.601156	625.804216	Q	***275.171382***	138.089329	258.144833	129.576054			2
12							K	147.112804	74.060040	130.086255	65.546765			1



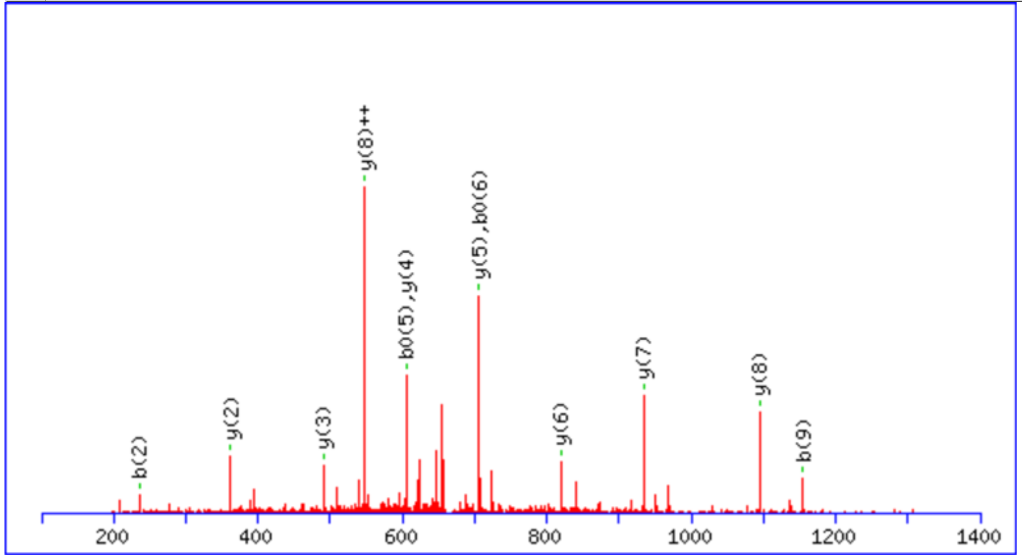
Peptide View

MS/MS Fragmentation of **SFCDLTDEWR**
Found in **IPI00010193**, Tax_Id=9606 Gene_Symbol=IFNAR2 Isoform 1 of Interferon-alpha/beta receptor beta chain
Experiment: 22 - NOPC1 **Fraction:** NOPC1

Match to Query 7166: 1327.551648 from(664.783100,2+)
Title: OECHL100310_21.17075.17075.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1327.550308**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59
Expect: 3.1e-005**Matches :** 12/86 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#

1	88.039304	44.523290	70.028739	35.518008	**S**							**10**
2	**235.107718**	118.057497	217.097153	109.052214	**F**	1241.525550	621.266413	1224.499001	612.753138	1223.514985	612.261130	**9**
3	395.138367	198.072821	377.127802	189.067539	**C**	***1094.457136***	547.732206	1077.430587	539.218932	1076.446571	538.726924	**8**
4	510.165310	255.586293	492.154745	246.581010	**D**	***934.426487***	467.716882	917.399938	459.203607	916.415922	458.711599	**7**
5	623.249374	312.128325	605.238809	303.123043	**L**	***819.399544***	410.203410	802.372995	401.690135	801.388979	401.198127	**6**
6	724.297053	362.652165	706.286488	353.646882	**T**	***706.315480***	353.661378	689.288931	345.148103	688.304915	344.656095	**5**
7	839.323996	420.165636	821.313431	411.160353	**D**	***605.267801***	303.137539	588.241252	294.624264	587.257236	294.132256	**4**
8	968.366589	484.686933	950.356024	475.681650	**E**	***490.240858***	245.624067	473.214309	237.110792	472.230293	236.618784	**3**
9	**1154.445902**	577.726589	1136.435337	568.721306	**W**	***361.198265***	181.102770	344.171716	172.589496			**2**
10					**R**	175.118952	88.063114	158.092403	79.549839			**1**



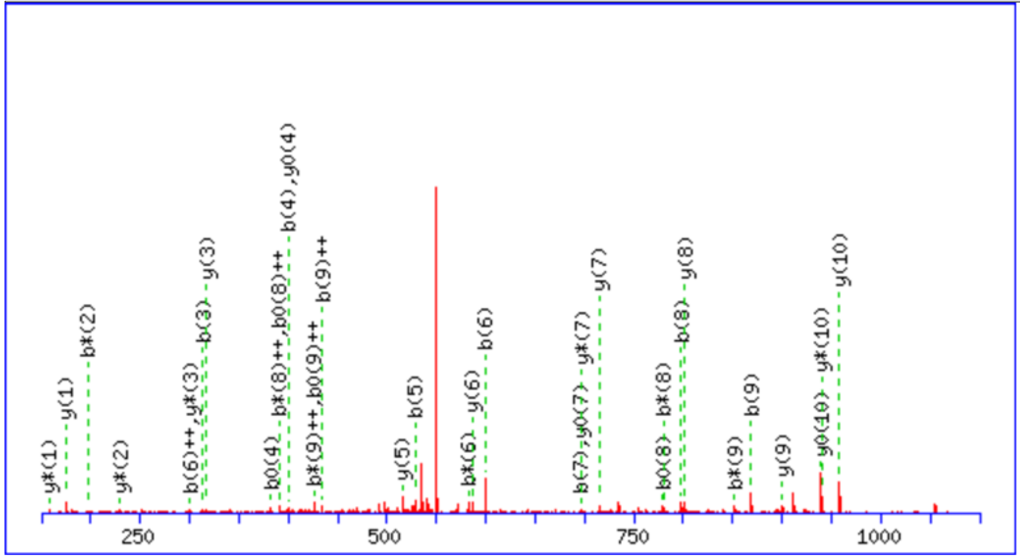
Peptide View

MS/MS Fragmentation of **RGVSQAPTAAR**
Found in **IPI00025365**, Tax_Id=9606 Gene_Symbol=EDN3 Isoform Long of Endothelin-3
Experiment: 22 - NOPC1 **Fraction:** NOPC1

Match to Query 4118: 1112.605248 from(557.309900,2+)

Title: OECHL100310_21.2225.2225.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1112.605042**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 0.00021**Matches :** 36/108 fragment ions using 55 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			**R**							**11**
2	214.129851	107.568564	197.103302	99.055289			**G**	***957.511221***	479.259249	940.484672	470.745974	939.500656	470.253966	**10**
3	***313.198265***	157.102770	296.171716	148.589496			**V**	***900.489757***	450.748517	883.463208	442.235242	882.479192	441.743234	**9**
4	***400.230293***	200.618785	383.203744	192.105510	382.219728	191.613502	**S**	***801.421343***	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
5	***528.288871***	264.648074	511.262322	256.134799	510.278306	255.642791	**Q**	***714.389315***	357.698296	697.362766	349.185021	696.378750	348.693013	**7**
6	***599.325985***	300.166631	582.299436	291.653356	581.315420	291.161348	**A**	***586.330737***	293.669007	569.304188	285.155732	568.320172	284.663724	**6**
7	***696.378749***	348.693013	679.352200	340.179738	678.368184	339.687730	**P**	***515.293623***	258.150450	498.267074	249.637175	497.283058	249.145167	**5**
8	***797.426428***	399.216852	780.399879	390.703578	779.415863	390.211570	**T**	418.240859	209.624068	401.214310	201.110793	400.230294	200.618785	**4**
9	***868.463542***	434.735409	851.436993	426.222135	850.452977	425.730127	**A**	***317.193180***	159.100228	300.166631	150.586953			**3**
10	***939.500656***	470.253966	922.474107	461.740692	921.490091	461.248684	**A**	246.156066	123.581671	229.129517	115.068397			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**

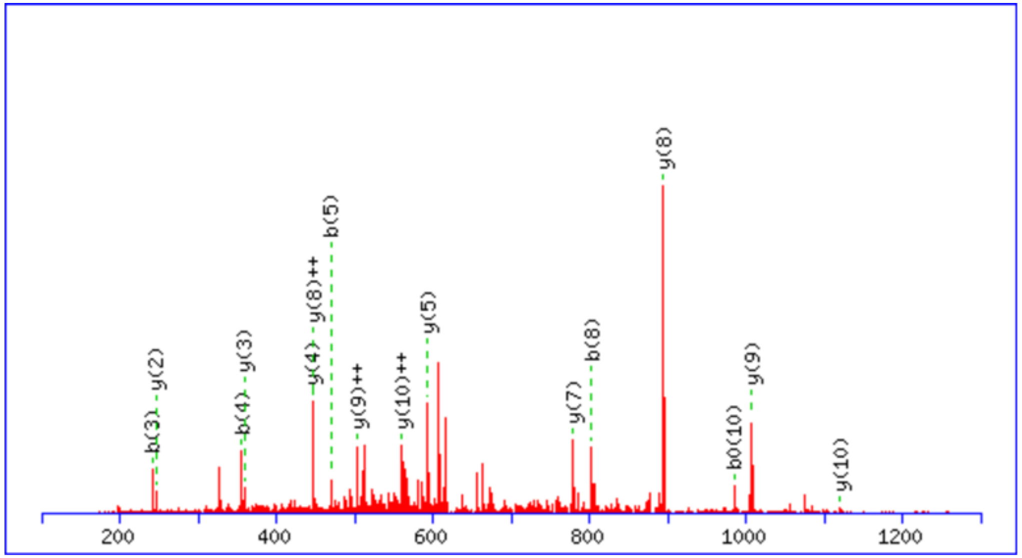


Peptide View

MS/MS Fragmentation of **AGLIDDAFSLAR**
Found in **IPI00007798**, Tax_Id=9606 Gene_Symbol=TRHDE Thyrotropin-releasing hormone-degrading ectoenzyme
Experiment: 22 - NOPC1 **Fraction:** NOPC1

Match to Query 6051: 1247.651448 from(624.833000,2+)
Title: OECHL100310_21.19486.19486.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1247.650986**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00089**Matches :** 16/96 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**12**
2	129.065854	65.036565			**G**	1177.621164	589.314220	1160.594615	580.800946	1159.610599	580.308938	**11**
3	**242.149918**	121.578597			**L**	***1120.599700***	560.803488	1103.573151	552.290214	1102.589135	551.798205	**10**
4	**355.233982**	178.120629			**I**	***1007.515636***	504.261456	990.489087	495.748182	989.505071	495.256174	**9**
5	**470.260925**	235.634101	452.250360	226.628818	**D**	***894.431572***	447.719424	877.405023	439.206150	876.421007	438.714142	**8**
6	585.287868	293.147572	567.277303	284.142290	**D**	***779.404629***	390.205953	762.378080	381.692678	761.394064	381.200670	**7**
7	656.324982	328.666129	638.314417	319.660847	**A**	664.377686	332.692481	647.351137	324.179207	646.367121	323.687199	**6**
8	**803.393396**	402.200336	785.382831	393.195054	**F**	***593.340572***	297.173924	576.314023	288.660650	575.330007	288.168642	**5**
9	890.425424	445.716350	872.414859	436.711068	**S**	***446.272158***	223.639717	429.245609	215.126443	428.261593	214.634435	**4**
10	1003.509488	502.258382	985.498923	493.253100	**L**	***359.240130***	180.123703	342.213581	171.610429			**3**
11	1074.546602	537.776939	1056.536037	528.771657	**A**	***246.156066***	123.581671	229.129517	115.068397			**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**



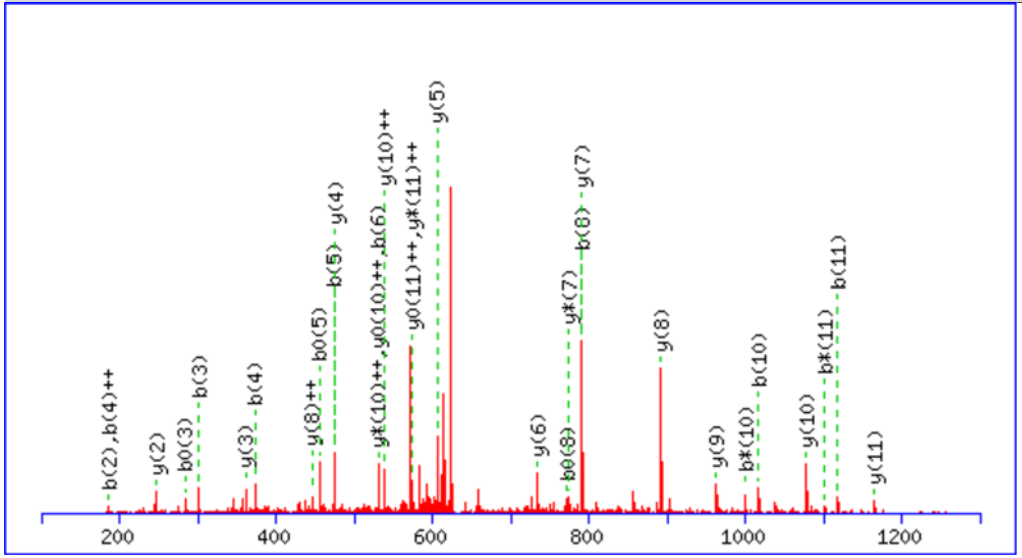
Peptide View

MS/MS Fragmentation of **VSDATGQMNLTK**
Found in **IPI00027341**, Tax_Id=9606 Gene_Symbol=CAPG Macrophage-capping protein
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 6516: 1263.613048 from(632.813800,2+)
Title: OECHL100310_19.7235.7235.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1263.612900**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 79
Expect: 1.5e-006**Matches :** 31/116 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	100.075690	50.541483					**V**							**12**
2	**187.107718**	94.057497			169.097153	85.052214	**S**	***1165.551765***	583.279520	1148.525216	574.766246	1147.541200	574.274238	**11**
3	**302.134661**	151.570968			284.124096	142.565686	**D**	***1078.519737***	539.763507	1061.493188	531.250232	1060.509172	530.758224	**10**
4	**373.171775**	187.089525			355.161210	178.084243	**A**	***963.492794***	482.250035	946.466245	473.736761	945.482229	473.244753	**9**
5	**474.219454**	237.613365			456.208889	228.608082	**T**	***892.455680***	446.731478	875.429131	438.218204	874.445115	437.726196	**8**
6	**531.240918**	266.124097			513.230353	257.118815	**G**	***791.408001***	396.207639	774.381452	387.694364	773.397436	387.202356	**7**

7	659.299496	330.153386	642.272947	321.640112	641.288931	321.148104	Q	***734.386537***	367.696907	717.359988	359.183632	716.375972	358.691624	6
8	**790.339981**	395.673629	773.313432	387.160354	772.329416	386.668346	M	***606.327959***	303.667618	589.301410	295.154343	588.317394	294.662335	5
9	904.382908	452.695092	887.356359	444.181818	886.372343	443.689810	N	***475.287474***	238.147375	458.260925	229.634100	457.276909	229.142092	4
10	**1017.466972**	509.237124	1000.440423	500.723850	999.456407	500.231842	L	***361.244547***	181.125911	344.217998	172.612637	343.233982	172.120629	3
11	**1118.514651**	559.760964	1101.488102	551.247689	1100.504086	550.755681	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
12							K	147.112804	74.060040	130.086255	65.546765			1



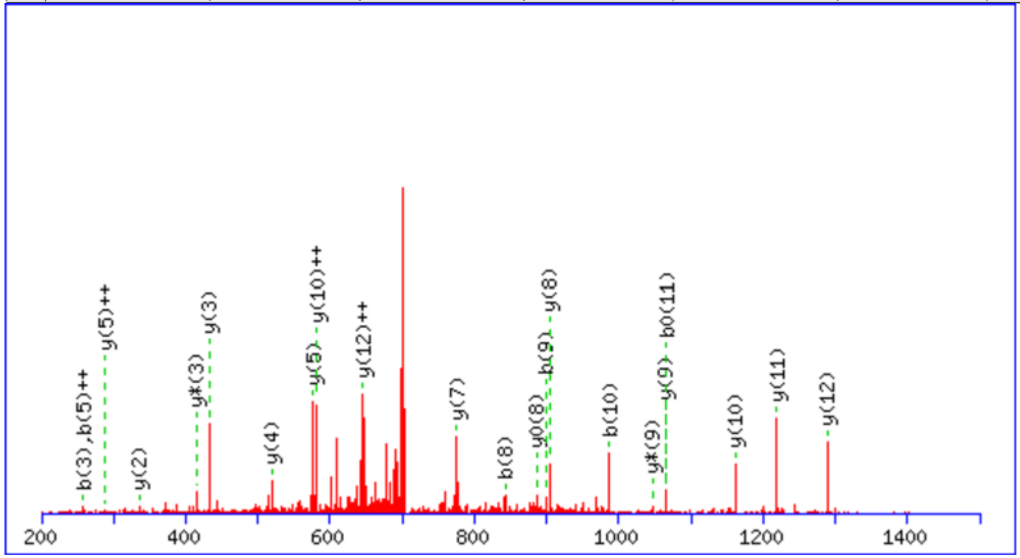
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 8167: 1416.625048 from(709.319800,2+)
Title: OECHL100310_19.2085.2085.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 76
Expect: 1.6e-006**Matches :** 22/128 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#

1	129.102239	65.054757	112.075690	56.541483			**K**							**13**
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	**12**
3	**257.160817**	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	**11**
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	**10**
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	**9**
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	**8**
7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	647.292971	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	**899.403979**	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**



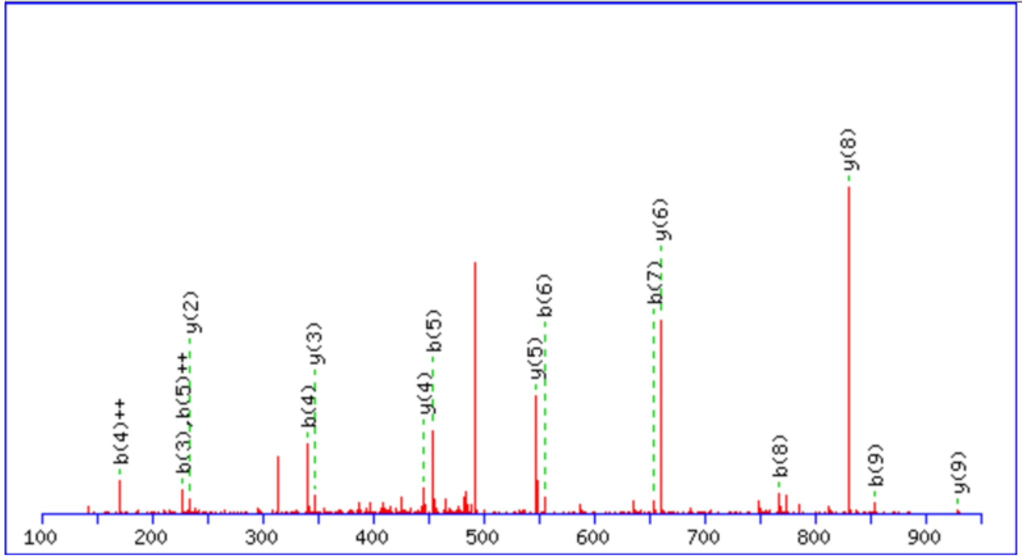
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**

Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 2694: 999.633448 from(500.824000,2+)
Title: OECHL100310_19.16482.16482.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67
Expect: 2.3e-006**Matches :** 17/78 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	**929.602995**	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	**171.112804**			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	**227.654836**			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	**446.297310**	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**

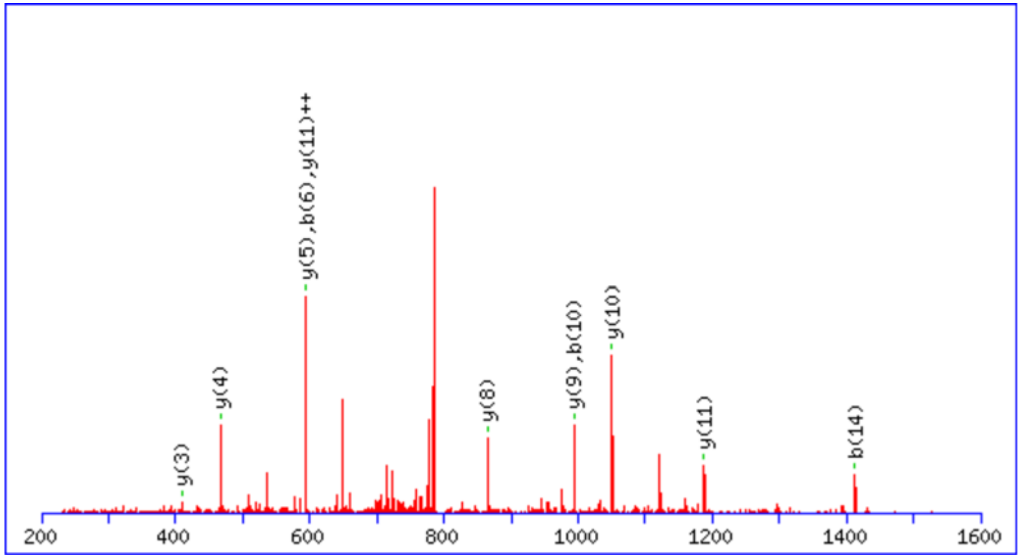


Peptide View

MS/MS Fragmentation of **ASLQHGQAAEKGPHR**
Found in **IPI00165044**, Tax_Id=9606 Gene_Symbol=FAM198B Isoform 2 of Protein ENED
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 10073: 1585.807848 from(793.911200,2+)
Title: OECHL100310_19.1907.1907.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1585.807312**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.0011**Matches :** 11/150 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	72.044390	36.525833					**A**							**15**
2	159.076418	80.041847			141.065853	71.036564	**S**	1515.777500	758.392388	1498.750951	749.879114	1497.766935	749.387106	**14**
3	272.160482	136.583879			254.149917	127.578597	**L**	1428.745472	714.876374	1411.718923	706.363100	1410.734907	705.871092	**13**
4	400.219060	200.613168	383.192511	192.099894	382.208495	191.607886	**Q**	1315.661408	658.334342	1298.634859	649.821068	1297.650843	649.329060	**12**
5	537.277972	269.142624	520.251423	260.629350	519.267407	260.137342	**H**	***1187.602830***	594.305053	1170.576281	585.791779	1169.592265	585.299771	**11**
6	**594.299436**	297.653356	577.272887	289.140082	576.288871	288.648074	**G**	***1050.543918***	525.775597	1033.517369	517.262323	1032.533353	516.770315	**10**
7	722.358014	361.682645	705.331465	353.169371	704.347449	352.677363	**Q**	***993.522454***	497.264865	976.495905	488.751591	975.511889	488.259583	**9**
8	793.395128	397.201202	776.368579	388.687928	775.384563	388.195920	**A**	***865.463876***	433.235576	848.437327	424.722302	847.453311	424.230294	**8**
9	864.432242	432.719759	847.405693	424.206485	846.421677	423.714477	**A**	794.426762	397.717019	777.400213	389.203745	776.416197	388.711737	**7**
10	**993.474835**	497.241056	976.448286	488.727781	975.464270	488.235773	**E**	723.389648	362.198462	706.363099	353.685188	705.379083	353.193180	**6**
11	1121.569798	561.288537	1104.543249	552.775263	1103.559233	552.283255	**K**	***594.347055***	297.677166	577.320506	289.163891			**5**
12	1178.591262	589.799269	1161.564713	581.285995	1160.580697	580.793987	**G**	***466.252092***	233.629684	449.225543	225.116409			**4**
13	1275.644026	638.325651	1258.617477	629.812377	1257.633461	629.320369	**P**	***409.230628***	205.118952	392.204079	196.605677			**3**
14	**1412.702938**	706.855107	1395.676389	698.341833	1394.692373	697.849825	**H**	312.177864	156.592570	295.151315	148.079295			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



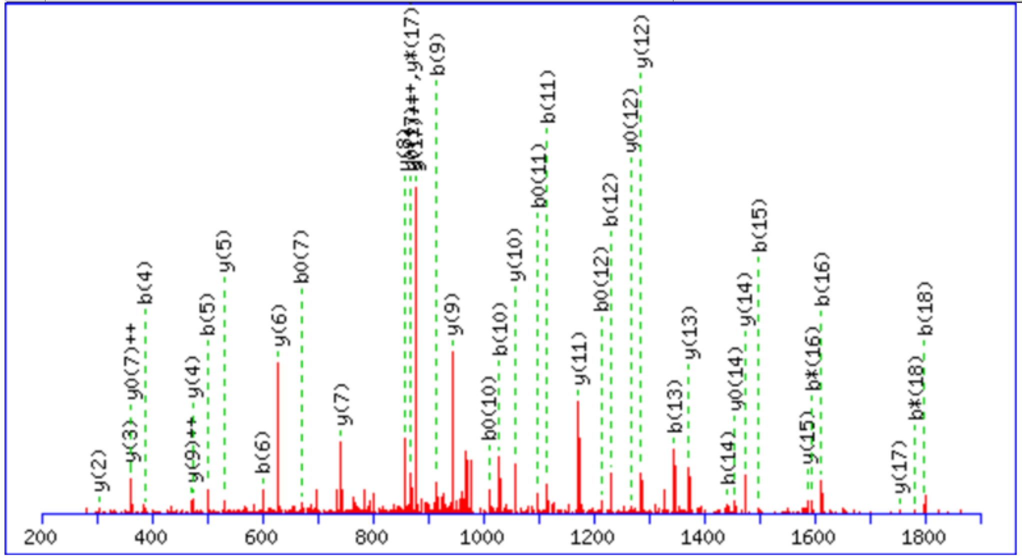
Peptide View

MS/MS Fragmentation of **AFPALTSLDLSDNPGLGER**
Found in **IPI00029260**, Tax_Id=9606 Gene_Symbol=CD14 Monocyte differentiation antigen CD14
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 13759: 1971.990848 from(987.002700,2+)
Title: OECHL100310_19.18714.18714.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1971.990158**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 2.8e-006**Matches :** 40/180 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	72.044390	36.525833					**A**							**19**
2	219.112804	110.060040					**F**	1901.960333	951.483805	1884.933784	942.970530	1883.949768	942.478522	**18**
3	316.165568	158.586422					**P**	***1754.891919***	877.949597	1737.865370	869.436323	1736.881354	868.944315	**17**
4	**387.202682**	194.104979					**A**	1657.839155	829.423215	1640.812606	820.909941	1639.828590	820.417933	**16**
5	**500.286746**	250.647011					**L**	***1586.802041***	793.904659	1569.775492	785.391384	1568.791476	784.899376	**15**
6	**601.334425**	301.170851			583.323860	292.165568	**T**	***1473.717977***	737.362627	1456.691428	728.849352	1455.707412	728.357344	**14**

7	688.366453	344.686865			670.355888	335.681582	S	***1372.670298***	686.838787	1355.643749	678.325513	1354.659733	677.833505	13
8	801.450517	401.228897			783.439952	392.223614	L	***1285.638270***	643.322773	1268.611721	634.809499	1267.627705	634.317491	12
9	**916.477460**	458.742368			898.466895	449.737085	D	***1172.554206***	586.780741	1155.527657	578.267467	1154.543641	577.775459	11
10	**1029.561524**	515.284400			1011.550959	506.279117	L	***1057.527263***	529.267270	1040.500714	520.753995	1039.516698	520.261987	10
11	**1116.593552**	558.800414			1098.582987	549.795132	S	***944.443199***	472.725238	927.416650	464.211963	926.432634	463.719955	9
12	**1231.620495**	616.313886			1213.609930	607.308603	D	***857.411171***	429.209224	840.384622	420.695949	839.400606	420.203941	8
13	**1345.663422**	673.335349	1328.636873	664.822075	1327.652857	664.330067	N	***742.384228***	371.695752	725.357679	363.182477	724.373663	362.690469	7
14	**1442.716186**	721.861731	1425.689637	713.348457	1424.705621	712.856449	P	***628.341301***	314.674288	611.314752	306.161014	610.330736	305.669006	6
15	**1499.737650**	750.372463	1482.711101	741.859189	1481.727085	741.367181	G	***531.288537***	266.147906	514.261988	257.634632	513.277972	257.142624	5
16	**1612.821714**	806.914495	1595.795165	798.401221	1594.811149	797.909212	L	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.631892	4
17	1669.843178	835.425227	1652.816629	826.911952	1651.832613	826.419944	G	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	3
18	**1798.885771**	899.946524	1781.859222	891.433249	1780.875206	890.941241	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
19							R	175.118952	88.063114	158.092403	79.549839			1



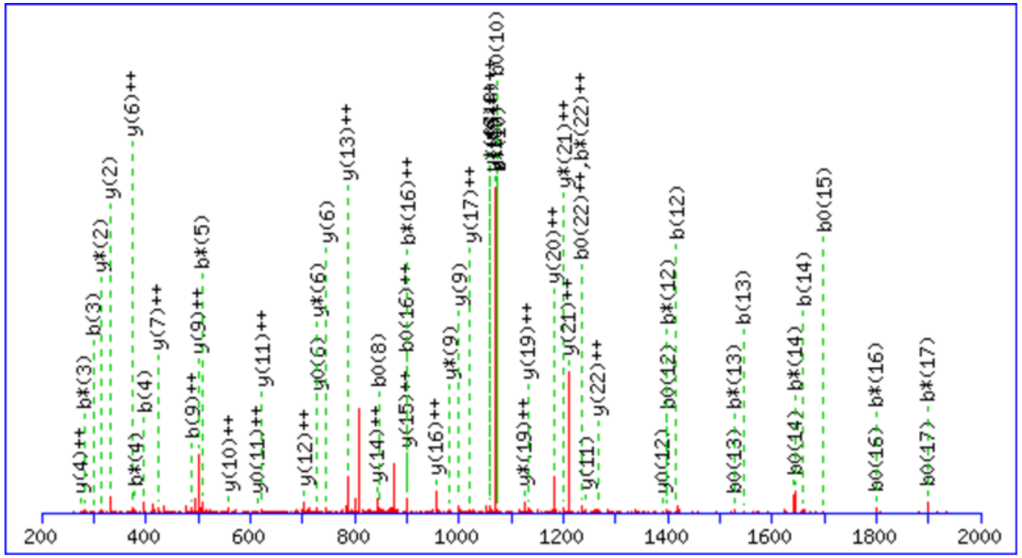
Peptide View

MS/MS Fragmentation of **QLGPQPQDIIYYEDGVVPTTDRR**

Found in **IPI00015199**, Tax_Id=9606 Gene_Symbol=CD7 T-cell antigen CD7
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 16688: 2659.329372 from(887.450400,3+)
Title: OECHL100310_19.16683.16683.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 2659.324203**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71
Expect: 1.7e-005**Matches :** 58/246 fragment ions using 145 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}
1	129.065854	65.036565	112.039305	56.523291			Q						
2	242.149918	121.578597	225.123369	113.065323			L	2532.272897	1266.640086	2515.246348	1258.126812	2514.262332	1257.6348
3	**299.171382**	150.089329	282.144833	141.576055			G	2419.188833	1210.098054	2402.162284	1201.584780	2401.178268	1201.0927
4	**396.224146**	198.615711	379.197597	190.102436			P	2362.167369	1181.587322	2345.140820	1173.074048	2344.156804	1172.5820
5	524.282724	262.645000	507.256175	254.131726			Q	2265.114605	1133.060940	2248.088056	1124.547666	2247.104040	1124.0556
6	621.335488	311.171382	604.308939	302.658108			P	2137.056027	1069.031651	2120.029478	1060.518377	2119.045462	1060.0263
7	749.394066	375.200671	732.367517	366.687397			Q	2040.003263	1020.505269	2022.976714	1011.991995	2021.992698	1011.4999
8	864.421009	432.714143	847.394460	424.200868	846.410444	423.708860	D	1911.944685	956.475980	1894.918136	947.962706	1893.934120	947.4706
9	977.505073	489.256175	960.478524	480.742900	959.494508	480.250892	I	1796.917742	898.962509	1779.891193	890.449234	1778.907177	889.9572
10	1090.589137	545.798206	1073.562588	537.284932	1072.578572	536.792924	I	1683.833678	842.420477	1666.807129	833.907202	1665.823113	833.4151
11	1253.652466	627.329871	1236.625917	618.816597	1235.641901	618.324589	Y	1570.749614	785.878445	1553.723065	777.365170	1552.739049	776.8731
12	**1416.715795**	708.861536	1399.689246	700.348261	1398.705230	699.856253	Y	1407.686285	704.346780	1390.659736	695.833506	1389.675720	695.3414
13	**1545.758388**	773.382832	1528.731839	764.869558	1527.747823	764.377549	E	**1244.622956**	622.815116	1227.596407	614.301841	1226.612391	613.8098
14	**1660.785331**	830.896304	1643.758782	822.383029	1642.774766	821.891021	D	1115.580363	558.293819	1098.553814	549.780545	1097.569798	549.2885
15	1717.806795	859.407036	1700.780246	850.893761	1699.796230	850.401753	G	**1000.553420**	500.780348	983.526871	492.267073	982.542855	491.7750
16	1816.875209	908.941243	1799.848660	900.427968	1798.864644	899.935960	V	943.531956	472.269616	926.505407	463.756341	925.521391	463.2643
17	1915.943623	958.475450	1898.917074	949.962175	1897.933058	949.470167	V	844.463542	422.735409	827.436993	414.222134	826.452977	413.7301
18	2012.996387	1007.001832	1995.969838	998.488557	1994.985822	997.996549	P	**745.395128**	373.201202	728.368579	364.687927	727.384563	364.1959
19	2114.044066	1057.525671	2097.017517	1049.012396	2096.033501	1048.520388	T	648.342364	324.674820	631.315815	316.161545	630.331799	315.6695
20	2215.091745	1108.049510	2198.065196	1099.536236	2197.081180	1099.044228	T	547.294685	274.150980	530.268136	265.637706	529.284120	265.1456
21	2330.118688	1165.562982	2313.092139	1157.049707	2312.108123	1156.557699	D	446.247006	223.627141	429.220457	215.113866	428.236441	214.6218
22	2486.219799	1243.613537	2469.193250	1235.100263	2468.209234	1234.608255	R	**331.220063**	166.113669	314.193514	157.600395		
23							R	175.118952	88.063114	158.092403	79.549839		



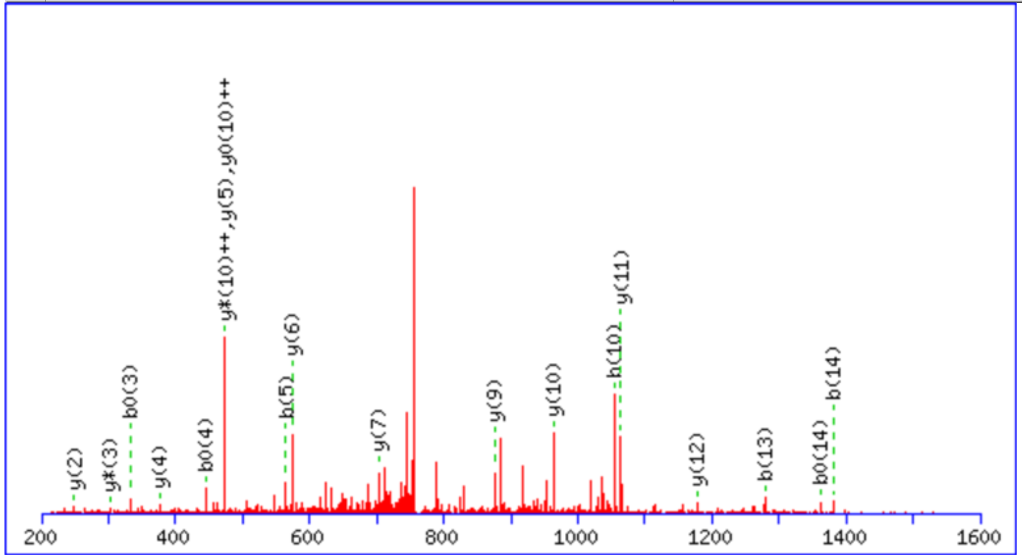
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 9434: 1525.727048 from(763.870800,2+)
Title: OECHL100310_19.10377.10377.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70
Expect: 1.2e-005**Matches :** 19/150 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	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	263.102633	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	350.134661	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	**564.266404**	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**

7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	**9**
8	825.362488	413.184882			807.351923	404.179599	**S**	789.410110	395.208693	772.383561	386.695418	771.399545	386.203410	**8**
9	953.421066	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	**7**
10	**1054.468745**	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	**6**
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	**5**
12	1208.542973	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	**4**
13	**1279.580087**	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	**3**
14	**1380.627766**	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



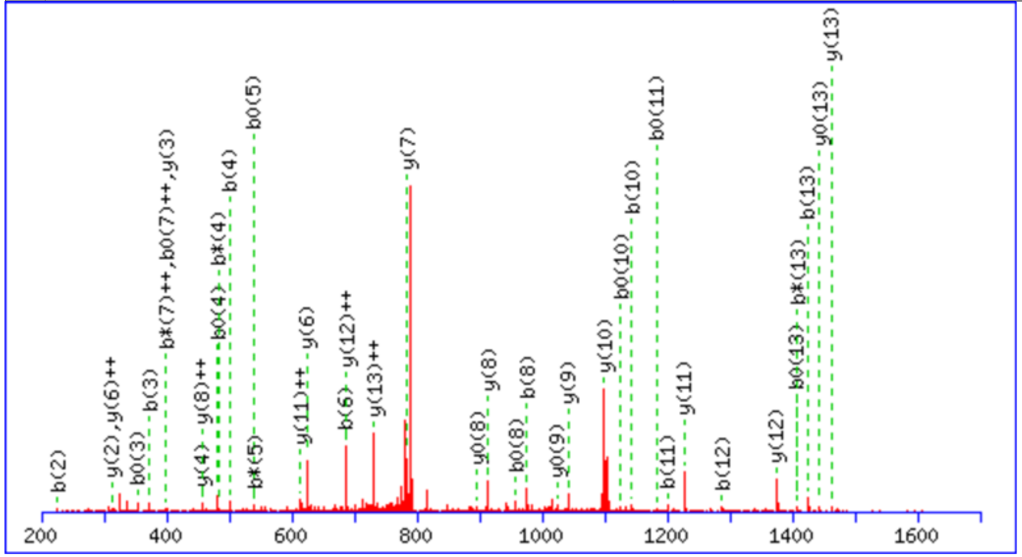
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 10164: 1597.706448 from(799.860500,2+)
Title: OECHL100310_19.2243.2243.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw

Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 8.6e-005**Matches :** 40/144 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	138.066188	69.536732					**H**							**14**
2	**225.098216**	113.052746			207.087651	104.047463	**S**	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.325325	**13**
3	**372.166630**	186.586953			354.156065	177.581671	**F**	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.809311	**12**
4	**500.261593**	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	**11**
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	**10**
6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	***1042.437069***	521.722173	1025.410520	513.208898	1024.426504	512.716890	**9**
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	527.268470	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	***312.177864***	156.592570	295.151315	148.079295			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**

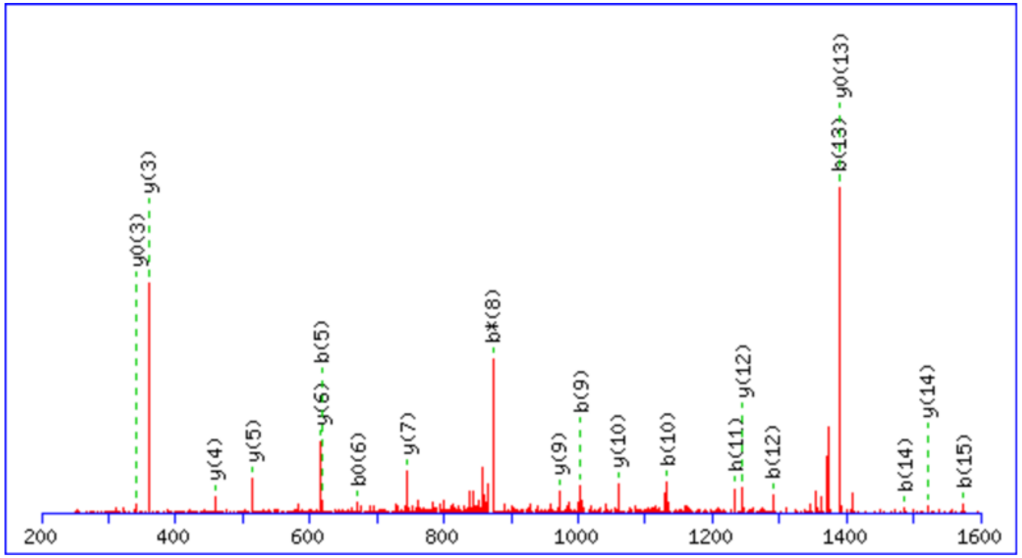


Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 11997: 1746.917048 from(874.465800,2+)
Title: OECHL100310_19.16230.16230.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 85
Expect: 3.2e-007**Matches :** 21/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	***618.349740***	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	689.386854	345.197065			671.376289	336.191782	**A**	1130.580027	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	858.467958	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



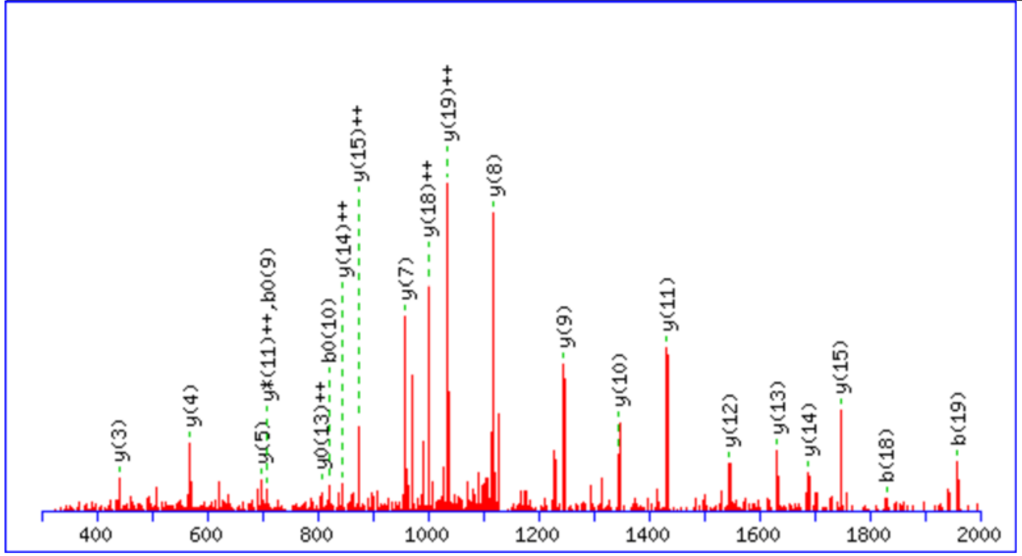
Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 15390: 2270.109448 from(1136.062000,2+)
Title: OECHL100310_19.10003.10003.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 83
Expect: 9.2e-007**Matches :** 22/212 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	102.054955	51.531116			84.044390	42.525833	**T**						
2	201.123369	101.065322			183.112804	92.060040	**V**	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400	1076.5338
3	272.160483	136.583879			254.149918	127.578597	**A**	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986	1026.9996
4	329.181947	165.094611			311.171382	156.089329	**G**	1999.965437	1000.486357	1982.938888	991.973082	1981.954872	991.4810
5	426.234711	213.620994			408.224146	204.615711	**P**	1942.943973	971.975625	1925.917424	963.462350	1924.933408	962.9703
6	525.303125	263.155201			507.292560	254.149918	**V**	1845.891209	923.449243	1828.864660	914.935968	1827.880644	914.4439

7	582.324589	291.665933			564.314024	282.660650	**G**	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230	864.9097
8	639.346053	320.176665			621.335488	311.171382	**G**	***1689.801331***	845.404304	1672.774782	836.891029	1671.790766	836.3990
9	726.378081	363.692679			708.367516	354.687396	**S**	***1632.779867***	816.893572	1615.753318	808.380297	1614.769302	807.8882
10	839.462145	420.234711			821.451580	411.229428	**L**	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274	764.3722
11	926.494173	463.750725			908.483608	454.745442	**S**	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210	707.8302
12	1025.562587	513.284932			1007.552022	504.279649	**V**	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182	664.3142
13	1153.621165	577.314221	1136.594616	568.800946	1135.610600	568.308938	**Q**	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768	614.7800
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	**C**	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190	550.7507
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	**P**	***958.474106***	479.740691	941.447557	471.227417	940.463541	470.7354
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	**Y**	861.421342	431.214309	844.394793	422.701035	843.410777	422.2090
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	**E**	***698.358013***	349.682645	681.331464	341.169370	680.347448	340.6773
18	**1830.905463**	915.956370	1813.878914	907.443095	1812.894898	906.951087	**K**	***569.315420***	285.161348	552.288871	276.648074	551.304855	276.1560
19	**1959.948056**	980.477666	1942.921507	971.964392	1941.937491	971.472384	**E**	***441.220457***	221.113867	424.193908	212.600592	423.209892	212.1085
20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	**H**	312.177864	156.592570	295.151315	148.079295		
21							**R**	175.118952	88.063114	158.092403	79.549839		

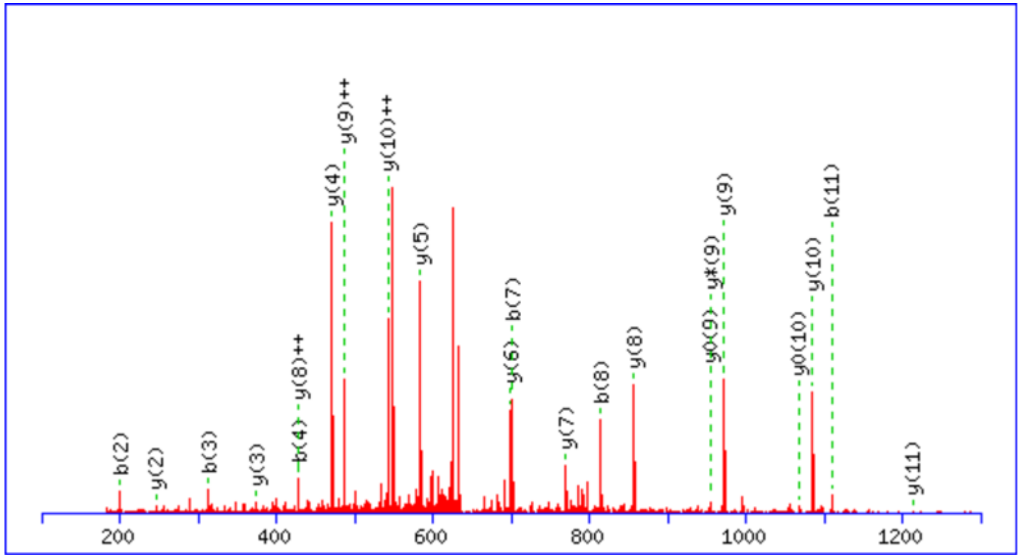


Peptide View

MS/MS Fragmentation of **AQLDSADIPKAR**
Found in **IPI00026303**, Tax_Id=9606 Gene_Symbol=PI15 Peptidase inhibitor 15
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 6731: 1283.684248 from(642.849400,2+)
Title: OECHL100310_19.7840.7840.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1283.683334**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71
Expect: 5.9e-006**Matches :** 22/114 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	72.044390	36.525833					**A**							**12**
2	**200.102968**	100.555122	183.076419	92.041848			**Q**	***1213.653527***	607.330402	1196.626978	598.817127	1195.642962	598.325119	**11**
3	**313.187032**	157.097154	296.160483	148.583879			**L**	***1085.594949***	543.301113	1068.568400	534.787838	1067.584384	534.295830	**10**
4	**428.213975**	214.610626	411.187426	206.097351	410.203410	205.605343	**D**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
5	515.246003	258.126640	498.219454	249.613365	497.235438	249.121357	**S**	***857.483942***	429.245609	840.457393	420.732335	839.473377	420.240327	**8**
6	586.283117	293.645197	569.256568	285.131922	568.272552	284.639914	**A**	***770.451914***	385.729595	753.425365	377.216321	752.441349	376.724313	**7**
7	**701.310060**	351.158668	684.283511	342.645394	683.299495	342.153386	**D**	***699.414800***	350.211038	682.388251	341.697764	681.404235	341.205756	**6**
8	**814.394124**	407.700700	797.367575	399.187426	796.383559	398.695418	**I**	***584.387857***	292.697567	567.361308	284.184292			**5**
9	911.446888	456.227082	894.420339	447.713808	893.436323	447.221800	**P**	***471.303793***	236.155535	454.277244	227.642260			**4**
10	1039.541851	520.274564	1022.515302	511.761289	1021.531286	511.269281	**K**	***374.251029***	187.629153	357.224480	179.115878			**3**
11	**1110.578965**	555.793121	1093.552416	547.279846	1092.568400	546.787838	**A**	***246.156066***	123.581671	229.129517	115.068396			**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**



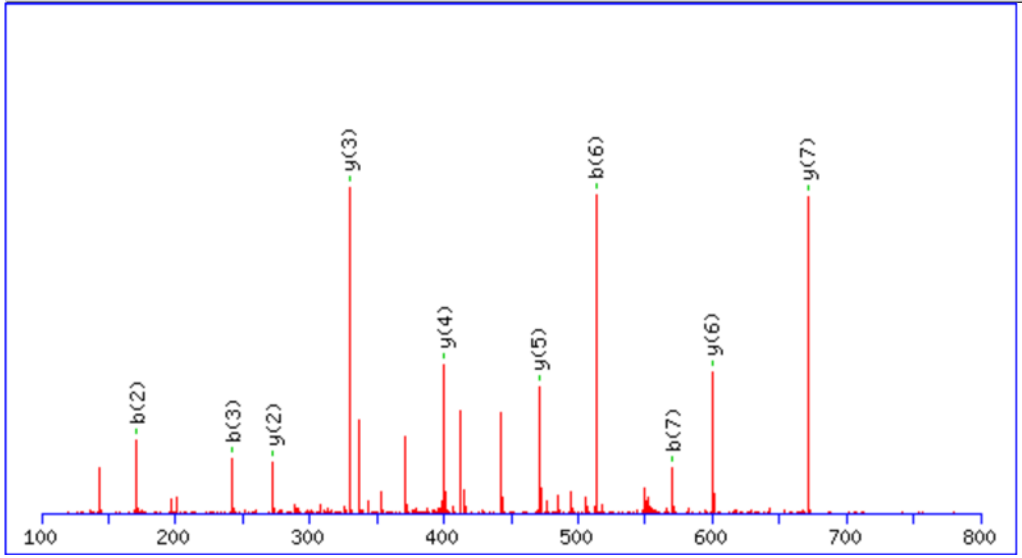
Peptide View

MS/MS Fragmentation of **GLAEAAGPR**
Found in **IPI00290826**, Tax_Id=9606 Gene_Symbol=FAM174A Membrane protein FAM174A
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 962: 840.446048 from(421.230300,2+)
Title: OECHL100310_19.4317.4317.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 840.445343**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00052**Matches :** 10/64 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			**G**							**9**
2	**171.112804**	86.060040			**L**	784.431179	392.719228	767.404630	384.205953	766.420614	383.713945	**8**
3	**242.149918**	121.578597			**A**	***671.347115***	336.177196	654.320566	327.663921	653.336550	327.171913	**7**
4	371.192511	186.099894	353.181946	177.094611	**E**	***600.310001***	300.658639	583.283452	292.145364	582.299436	291.653356	**6**
5	442.229625	221.618450	424.219060	212.613168	**A**	***471.267408***	236.137342	454.240859	227.624067			**5**
6	**513.266739**	257.137008	495.256174	248.131725	**A**	***400.230294***	200.618785	383.203745	192.105510			**4**

7	**570.288203**	285.647740	552.277638	276.642457	**G**	***329.193180***	165.100228	312.166631	156.586953			**3**
8	667.340967	334.174122	649.330402	325.168839	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
9					**R**	175.118952	88.063114	158.092403	79.549839			**1**



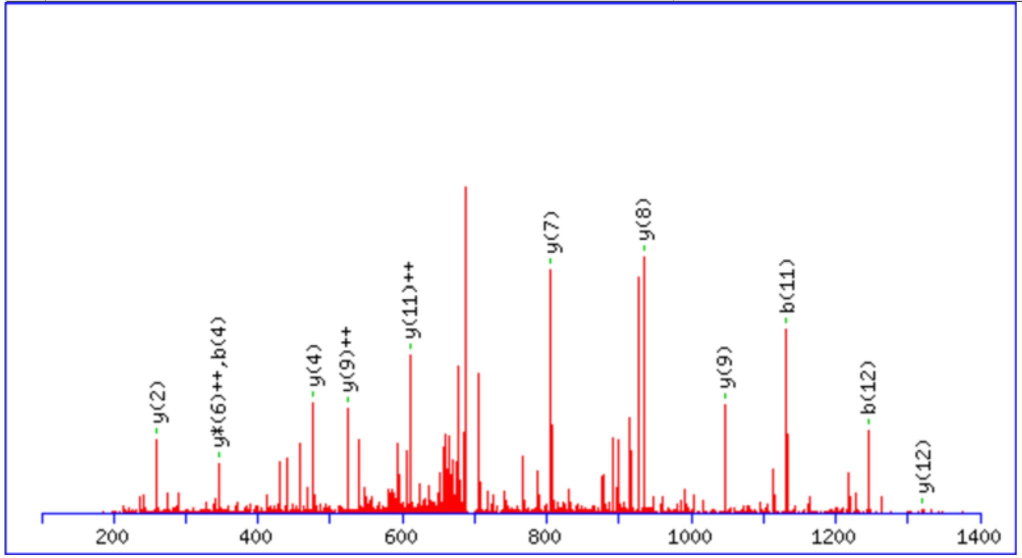
Peptide View

MS/MS Fragmentation of **ATGDIKVTESEIK**
Found in **IPI00302614**, Tax_Id=9606 Gene_Symbol=VTCN1 V-set domain containing T cell activation inhibitor 1
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 7951: 1389.735848 from(695.875200,2+)
Title: OECHL100310_19.8095.8095.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1389.735107**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 0.00016**Matches :** 12/128 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	72.044390	36.525833					**A**							**13**
2	173.092069	87.049672			155.081504	78.044390	**T**	***1319.705288***	660.356282	1302.678739	651.843008	1301.694723	651.350999	**12**
3	230.113533	115.560404			212.102968	106.555122	**G**	1218.657609	609.832442	1201.631060	601.319168	1200.647044	600.827160	**11**

4	**345.140476**	173.073876			327.129911	164.068593	**D**	1161.636145	581.321710	1144.609596	572.808436	1143.625580	572.316428	**10**
5	458.224540	229.615908			440.213975	220.610626	**I**	***1046.609202***	523.808239	1029.582653	515.294964	1028.598637	514.802956	**9**
6	586.319503	293.663390	569.292954	285.150115	568.308938	284.658107	**K**	***933.525138***	467.266207	916.498589	458.752932	915.514573	458.260924	**8**
7	685.387917	343.197597	668.361368	334.684322	667.377352	334.192314	**V**	***805.430175***	403.218725	788.403626	394.705451	787.419610	394.213443	**7**
8	786.435596	393.721436	769.409047	385.208162	768.425031	384.716154	**T**	706.361761	353.684518	689.335212	345.171244	688.351196	344.679236	**6**
9	915.478189	458.242733	898.451640	449.729458	897.467624	449.237450	**E**	605.314082	303.160679	588.287533	294.647404	587.303517	294.155396	**5**
10	1002.510217	501.758747	985.483668	493.245472	984.499652	492.753464	**S**	***476.271489***	238.639382	459.244940	230.126108	458.260924	229.634100	**4**
11	**1131.552810**	566.280043	1114.526261	557.766769	1113.542245	557.274760	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
12	**1244.636874**	622.822075	1227.610325	614.308800	1226.626309	613.816792	**I**	***260.196868***	130.602072	243.170319	122.088797			**2**
13							**K**	147.112804	74.060040	130.086255	65.546765			**1**



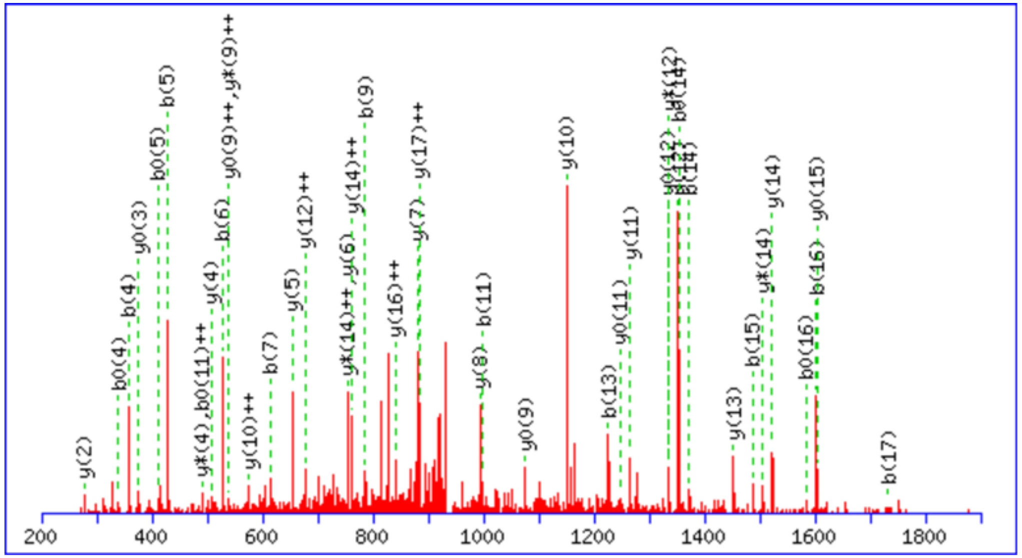
Peptide View

MS/MS Fragmentation of **ASGVAVSDGVIKVFNDMK**
Found in **IPI00012011**, Tax_Id=9606 Gene_Symbol=CFL1 Cofilin-1
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 13101: 1877.955448 from(939.985000,2+)
Title: OECHL100310_19.20025.20025.2.dta

Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1877.955704**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 55 **Expect:** 0.00044**Matches :** 43/176 fragment ions using 91 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.054955	57.531116					**A**							**18**
2	201.086983	101.047130			183.076418	92.041847	**S**	1765.915297	883.461287	1748.888748	874.948012	1747.904732	874.456004	**17**
3	258.108447	129.557861			240.097882	120.552579	**G**	1678.883269	839.945273	1661.856720	831.431998	1660.872704	830.939990	**16**
4	***357.176861***	179.092068			339.166296	170.086786	**V**	1621.861805	811.434541	1604.835256	802.921266	1603.851240	802.429258	**15**
5	***428.213975***	214.610626			410.203410	205.605343	**A**	***1522.793391***	761.900334	1505.766842	753.387059	1504.782826	752.895051	**14**
6	***527.282389***	264.144833			509.271824	255.139550	**V**	***1451.756277***	726.381777	1434.729728	717.868502	1433.745712	717.376494	**13**
7	***614.314417***	307.660847			596.303852	298.655564	**S**	***1352.687863***	676.847570	1335.661314	668.334295	1334.677298	667.842287	**12**
8	729.341360	365.174318			711.330795	356.169036	**D**	***1265.655835***	633.331556	1248.629286	624.818281	1247.645270	624.326273	**11**
9	***786.362824***	393.685050			768.352259	384.679768	**G**	***1150.628892***	575.818084	1133.602343	567.304810	1132.618327	566.812802	**10**
10	885.431238	443.219257			867.420673	434.213975	**V**	1093.607428	547.307352	1076.580879	538.794078	1075.596863	538.302070	**9**
11	***998.515302***	499.761289			980.504737	490.756007	**I**	***994.539014***	497.773145	977.512465	489.259871	976.528449	488.767863	**8**
12	1126.610265	563.808771	1109.583716	555.295496	1108.599700	554.803488	**K**	***881.454950***	441.231113	864.428401	432.717839	863.444385	432.225831	**7**
13	***1225.678679***	613.342978	1208.652130	604.829703	1207.668114	604.337695	**V**	***753.359987***	377.183632	736.333438	368.670357	735.349422	368.178349	**6**
14	***1372.747093***	686.877185	1355.720544	678.363910	1354.736528	677.871902	**F**	***654.291573***	327.649425	637.265024	319.136150	636.281008	318.644142	**5**
15	***1486.790020***	743.898648	1469.763471	735.385374	1468.779455	734.893366	**N**	***507.223159***	254.115218	490.196610	245.601943	489.212594	245.109935	**4**
16	***1601.816963***	801.412120	1584.790414	792.898845	1583.806398	792.406837	**D**	393.180232	197.093754	376.153683	188.580480	375.169667	188.088472	**3**
17	***1732.857448***	866.932362	1715.830899	858.419088	1714.846883	857.927080	**M**	***278.153289***	139.580282	261.126740	131.067008			**2**
18							**K**	147.112804	74.060040	130.086255	65.546765			**1**



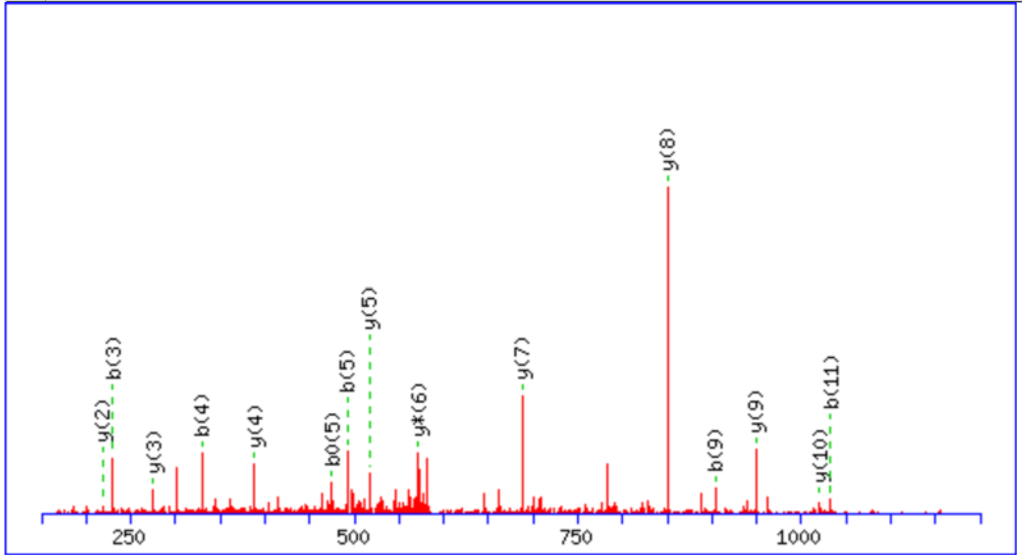
Peptide View

MS/MS Fragmentation of **TGAVYVAEIGAK**
Found in **IPI00552937**, Tax_Id=9606 Gene_Symbol=NHLRC3 NHL repeat-containing protein 3
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 5127: 1177.632848 from(589.823700,2+)
Title: OECHL100310_19.10879.10879.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1177.634277**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53
Expect: 0.00035**Matches :** 15/102 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							**12**
2	159.076419	80.041847	141.065854	71.036565	**G**	1077.593888	539.300582	1060.567339	530.787308	1059.583323	530.295300	**11**
3	**230.113533**	115.560404	212.102968	106.555122	**A**	***1020.572424***	510.789850	1003.545875	502.276576	1002.561859	501.784568	**10**
4	**329.181947**	165.094611	311.171382	156.089329	**V**	***949.535310***	475.271293	932.508761	466.758019	931.524745	466.266011	**9**
5	**492.245276**	246.626276	474.234711	237.620994	**Y**	***850.466896***	425.737086	833.440347	417.223812	832.456331	416.731804	**8**
6	591.313690	296.160483	573.303125	287.155201	**V**	***687.403567***	344.205422	670.377018	335.692147	669.393002	335.200139	**7**

7	662.350804	331.679040	644.340239	322.673758	A	588.335153	294.671215	571.308604	286.157940	570.324588	285.665932	6
8	791.393397	396.200337	773.382832	387.195054	E	***517.298039***	259.152658	500.271490	250.639383	499.287474	250.147375	5
9	**904.477461**	452.742369	886.466896	443.737086	I	***388.255446***	194.631361	371.228897	186.118087			4
10	961.498925	481.253101	943.488360	472.247818	G	***275.171382***	138.089329	258.144833	129.576055			3
11	**1032.536039**	516.771658	1014.525474	507.766375	A	***218.149918***	109.578597	201.123369	101.065322			2
12					K	147.112804	74.060040	130.086255	65.546765			1



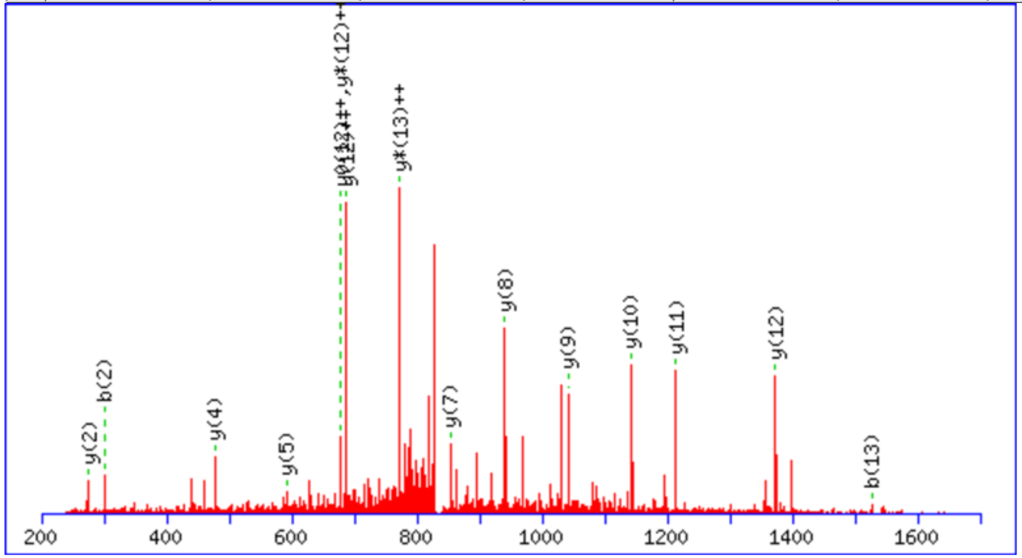
Peptide View

MS/MS Fragmentation of **LWCATTSNFDSDKK**
Found in **IPI00027509**, Tax_Id=9606 Gene_Symbol=MMP9 Matrix metalloproteinase-9
Experiment: 37 - OPC-1 **Fraction:** OPC-1

Match to Query 11151: 1671.756848 from(836.885700,2+)
Title: OECHL100310_19.10306.10306.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1671.756271**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00068**Matches :** 15/130 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#

1	114.091340	57.549308					**L**							**14**
2	**300.170653**	150.588965					**W**	1559.679484	780.343380	1542.652935	771.830106	1541.668919	771.338098	**13**
3	460.201302	230.604289					**C**	***1373.600171***	687.303724	1356.573622	678.790449	1355.589606	678.298441	**12**
4	531.238416	266.122846					**A**	***1213.569522***	607.288399	1196.542973	598.775125	1195.558957	598.283117	**11**
5	632.286095	316.646686			614.275530	307.641403	**T**	***1142.532408***	571.769842	1125.505859	563.256568	1124.521843	562.764560	**10**
6	733.333774	367.170525			715.323209	358.165243	**T**	***1041.484729***	521.246003	1024.458180	512.732728	1023.474164	512.240720	**9**
7	820.365802	410.686539			802.355237	401.681257	**S**	***940.437050***	470.722163	923.410501	462.208889	922.426485	461.716881	**8**
8	934.408729	467.708003	917.382180	459.194728	916.398164	458.702720	**N**	***853.405022***	427.206149	836.378473	418.692875	835.394457	418.200867	**7**
9	1081.477143	541.242210	1064.450594	532.728935	1063.466578	532.236927	**F**	739.362095	370.184686	722.335546	361.671411	721.351530	361.179403	**6**
10	1196.504086	598.755681	1179.477537	590.242407	1178.493521	589.750399	**D**	***592.293681***	296.650479	575.267132	288.137204	574.283116	287.645196	**5**
11	1283.536114	642.271695	1266.509565	633.758421	1265.525549	633.266413	**S**	***477.266738***	239.137007	460.240189	230.623733	459.256173	230.131725	**4**
12	1398.563057	699.785167	1381.536508	691.271892	1380.552492	690.779884	**D**	390.234710	195.620993	373.208161	187.107719	372.224145	186.615711	**3**
13	**1526.658020**	763.832648	1509.631471	755.319374	1508.647455	754.827366	**K**	***275.207767***	138.107521	258.181218	129.594247			**2**
14							**K**	147.112804	74.060040	130.086255	65.546765			**1**

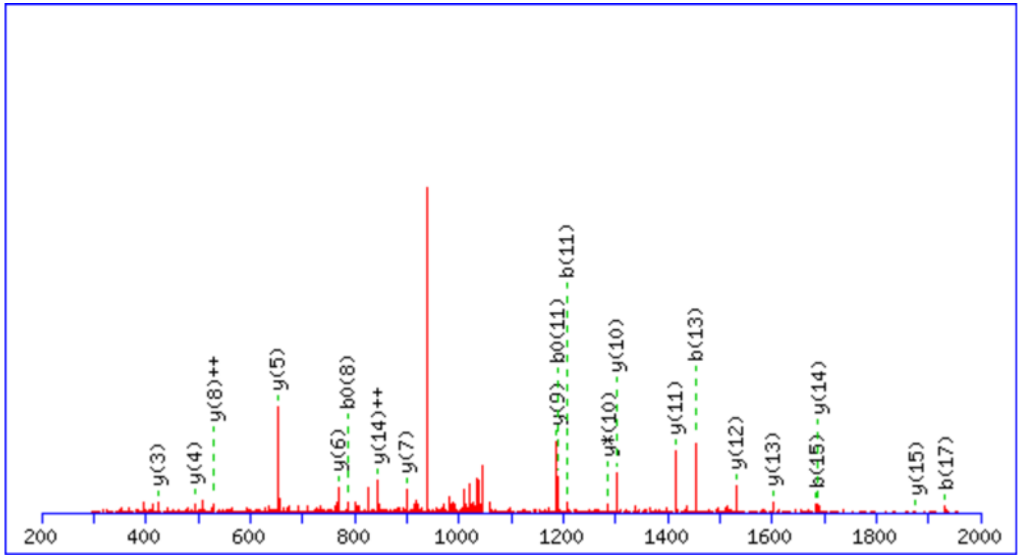


Peptide View

MS/MS Fragmentation of **GSSWSADLDKCMDCASCR**
Found in **IPI00010277**, Tax_Id=9606 Gene_Symbol=TNFRSF12A Isoform 1 of Tumor necrosis factor receptor superfamily member 12A
Experiment: 34 - OPB-1 **Fraction:** OPB-1

Match to Query 14582: 2104.807448 from(1053.411000,2+)
Title: OECHL100310_17.14416.14416.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 2104.807083**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59
Expect: 7.4e-006**Matches :** 21/180 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	58.028740	29.518008					**G**						
2	145.060768	73.034022			127.050203	64.028740	**S**	2048.792893	1024.900085	2031.766344	1016.386810	2030.782328	1015.894802
3	232.092796	116.550036			214.082231	107.544753	**S**	1961.760865	981.384071	1944.734316	972.870796	1943.750300	972.378788
4	418.172109	209.589693			400.161544	200.584410	**W**	***1874.728837***	937.868057	1857.702288	929.354782	1856.718272	928.862774
5	505.204137	253.105707			487.193572	244.100424	**S**	***1688.649524***	844.828400	1671.622975	836.315126	1670.638959	835.823118
6	576.241251	288.624264			558.230686	279.618981	**A**	***1601.617496***	801.312386	1584.590947	792.799112	1583.606931	792.307104
7	691.268194	346.137735			673.257629	337.132453	**D**	***1530.580382***	765.793829	1513.553833	757.280555	1512.569817	756.788547
8	804.352258	402.679767			786.341693	393.674485	**L**	***1415.553439***	708.280358	1398.526890	699.767083	1397.542874	699.275075
9	919.379201	460.193239			901.368636	451.187956	**D**	***1302.469375***	651.738326	1285.442826	643.225051	1284.458810	642.733043
10	1047.474164	524.240720	1030.447615	515.727446	1029.463599	515.235437	**K**	***1187.442432***	594.224854	1170.415883	585.711580	1169.431867	585.219572
11	**1207.504813**	604.256045	1190.478264	595.742770	1189.494248	595.250762	**C**	1059.347469	530.177373	1042.320920	521.664098	1041.336904	521.172090
12	1338.545298	669.776287	1321.518749	661.263013	1320.534733	660.771005	**M**	***899.316820***	450.162048	882.290271	441.648774	881.306255	441.156766
13	**1453.572241**	727.289759	1436.545692	718.776484	1435.561676	718.284476	**D**	***768.276335***	384.641806	751.249786	376.128531	750.265770	375.636523
14	1613.602890	807.305083	1596.576341	798.791809	1595.592325	798.299801	**C**	***653.249392***	327.128334	636.222843	318.615060	635.238827	318.123052
15	**1684.640004**	842.823640	1667.613455	834.310366	1666.629439	833.818358	**A**	***493.218743***	247.113010	476.192194	238.599735	475.208178	238.107727
16	1771.672032	886.339654	1754.645483	877.826380	1753.661467	877.334372	**S**	***422.181629***	211.594453	405.155080	203.081178	404.171064	202.589170
17	**1931.702681**	966.354979	1914.676132	957.841704	1913.692116	957.349696	**C**	335.149601	168.078439	318.123052	159.565164		
18							**R**	175.118952	88.063114	158.092403	79.549840		



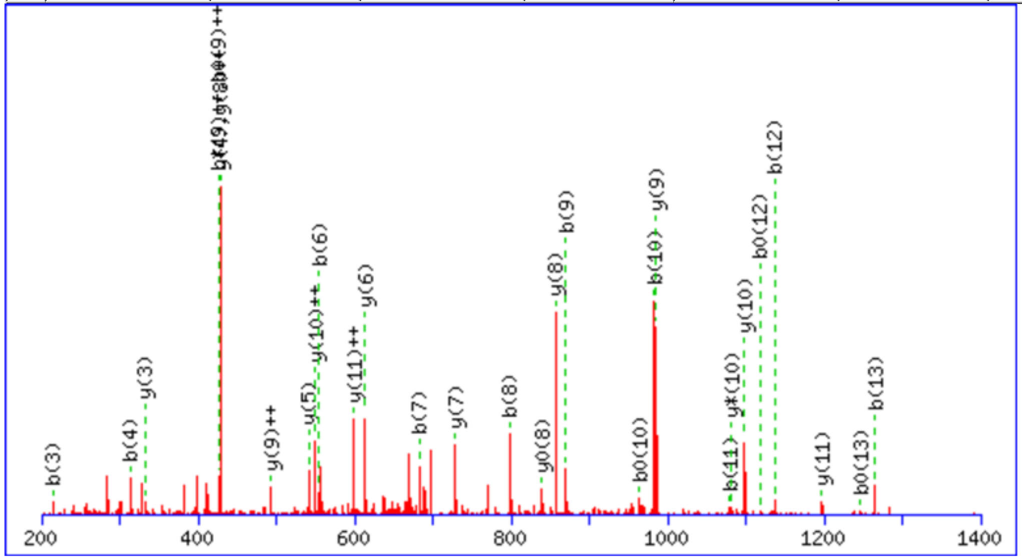
Peptide View

MS/MS Fragmentation of **GGVVLKEDALPGQK**
Found in **IPI00019906**, Tax_Id=9606 Gene_Symbol=BSG Isoform 2 of Basigin
Experiment: 34 - OPB-1 **Fraction:** OPB-1

Match to Query 8190: 1409.787848 from(705.901200,2+)
Title: OECHL100310_17.9813.9813.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1409.787827**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71
Expect: 3.3e-006**Matches :** 31/122 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.028740	29.518008					**G**							**14**
2	115.050204	58.028740					**G**	1353.773643	677.390460	1336.747094	668.877185	1335.763078	668.385177	**13**
3	***214.118618***	107.562947					**V**	1296.752179	648.879728	1279.725630	640.366453	1278.741614	639.874445	**12**
4	***313.187032***	157.097154					**V**	**1197.683765**	599.345521	1180.657216	590.832246	1179.673200	590.340238	**11**
5	***426.271096***	213.639186					**L**	**1098.615351**	549.811314	1081.588802	541.298039	1080.604786	540.806031	**10**
6	***554.366059***	277.686668	537.339510	269.173393			**K**	**985.531287**	493.269282	968.504738	484.756007	967.520722	484.263999	**9**

7	***683.408652***	342.207964	666.382103	333.694690	665.398087	333.202682	**E**	**857.436324**	429.221800	840.409775	420.708526	839.425759	420.216518	**8**
8	***798.435595***	399.721436	781.409046	391.208161	780.425030	390.716153	**D**	**728.393731**	364.700504	711.367182	356.187229	710.383166	355.695221	**7**
9	***869.472709***	435.239993	852.446160	426.726718	851.462144	426.234710	**A**	**613.366788**	307.187032	596.340239	298.673758			**6**
10	***982.556773***	491.782025	965.530224	483.268750	964.546208	482.776742	**L**	**542.329674**	271.668475	525.303125	263.155201			**5**
11	***1079.609537***	540.308407	1062.582988	531.795132	1061.598972	531.303124	**P**	**429.245610**	215.126443	412.219061	206.613169			**4**
12	***1136.631001***	568.819139	1119.604452	560.305864	1118.620436	559.813856	**G**	**332.192846**	166.600061	315.166297	158.086787			**3**
13	***1264.689579***	632.848428	1247.663030	624.335153	1246.679014	623.843145	**Q**	275.171382	138.089329	258.144833	129.576055			**2**
14							**K**	147.112804	74.060040	130.086255	65.546765			**1**



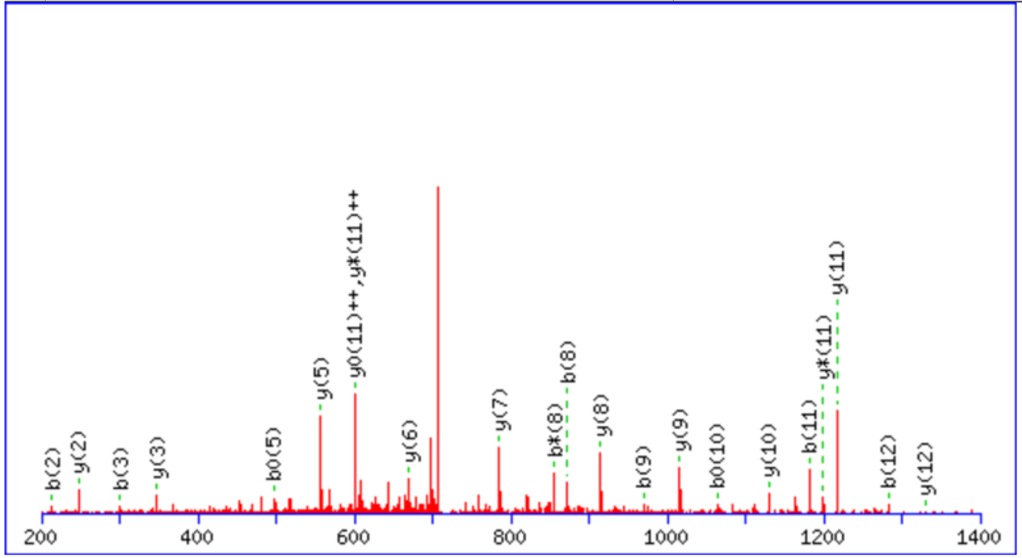
Peptide View

MS/MS Fragmentation of **VLSNTEDLPLVTK**
Found in **IPI00218851**, Tax_Id=9606 Gene_Symbol=LYNX1 Ly-6 neurotoxin-like protein 1 isoform a
Experiment: 34 - OPB-1 **Fraction:** OPB-1

Match to Query 8366: 1427.789448 from(714.902000,2+)
Title: OECHL100310_17.14286.14286.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1427.787155**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 79

Expect: 8.2e-007**Matches :** 22/132 fragment ions using 36 most intense peaks (help)

#	**b**	**b^{++}**	**b***	**b^{*++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	100.075690	50.541483					**V**							**13**
2	**213.159754**	107.083515					**L**	***1329.726023***	665.366650	1312.699474	656.853375	1311.715458	656.361367	**12**
3	**300.191782**	150.599529			282.181217	141.594247	**S**	***1216.641959***	608.824618	1199.615410	600.311343	1198.631394	599.819335	**11**
4	414.234709	207.620993	397.208160	199.107718	396.224144	198.615710	**N**	***1129.609931***	565.308604	1112.583382	556.795329	1111.599366	556.303321	**10**
5	515.282388	258.144832	498.255839	249.631558	497.271823	249.139550	**T**	***1015.567004***	508.287140	998.540455	499.773866	997.556439	499.281858	**9**
6	644.324981	322.666129	627.298432	314.152854	626.314416	313.660846	**E**	***914.519325***	457.763301	897.492776	449.250026	896.508760	448.758018	**8**
7	759.351924	380.179600	742.325375	371.666326	741.341359	371.174318	**D**	***785.476732***	393.242004	768.450183	384.728730	767.466167	384.236722	**7**
8	**872.435988**	436.721632	855.409439	428.208358	854.425423	427.716350	**L**	***670.449789***	335.728533	653.423240	327.215258	652.439224	326.723250	**6**
9	**969.488752**	485.248014	952.462203	476.734740	951.478187	476.242732	**P**	***557.365725***	279.186501	540.339176	270.673226	539.355160	270.181218	**5**
10	1082.572816	541.790046	1065.546267	533.276772	1064.562251	532.784764	**L**	460.312961	230.660119	443.286412	222.146844	442.302396	221.654836	**4**
11	**1181.641230**	591.324253	1164.614681	582.810979	1163.630665	582.318971	**V**	***347.228897***	174.118087	330.202348	165.604812	329.218332	165.112804	**3**
12	**1282.688909**	641.848093	1265.662360	633.334818	1264.678344	632.842810	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
13							**K**	147.112804	74.060040	130.086255	65.546765			**1**

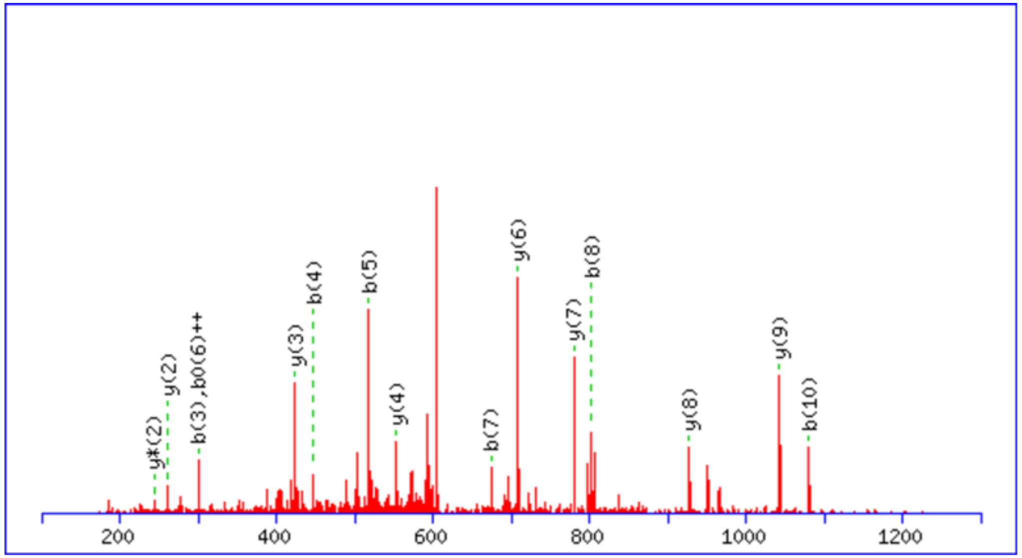


Peptide View

MS/MS Fragmentation of **ALDFAVGEYNK**
Found in **IPI00032293**, Tax_Id=9606 Gene_Symbol=CST3 Cystatin-C
Experiment: 34 - OPB-1 **Fraction:** OPB-1

Match to Query 6013: 1225.598048 from(613.806300,2+)
Title: OECHL100310_17.14766.14766.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1225.597885**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 0.00023**Matches :** 15/92 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	72.044390	36.525833					**A**							**11**
2	185.128454	93.067865					**L**	1155.568066	578.287671	1138.541517	569.774397	1137.557501	569.282389	**10**
3	***300.155397***	150.581336			282.144832	141.576054	**D**	***1042.484002***	521.745639	1025.457453	513.232365	1024.473437	512.740357	**9**
4	***447.223811***	224.115544			429.213246	215.110261	**F**	***927.457059***	464.232168	910.430510	455.718893	909.446494	455.226885	**8**
5	***518.260925***	259.634101			500.250360	250.628818	**A**	***780.388645***	390.697961	763.362096	382.184686	762.378080	381.692678	**7**
6	617.329339	309.168308			599.318774	300.163025	**V**	***709.351531***	355.179404	692.324982	346.666129	691.340966	346.174121	**6**
7	***674.350803***	337.679040			656.340238	328.673757	**G**	610.283117	305.645197	593.256568	297.131922	592.272552	296.639914	**5**
8	***803.393396***	402.200336			785.382831	393.195054	**E**	***553.261653***	277.134465	536.235104	268.621190	535.251088	268.129182	**4**
9	966.456725	483.732001			948.446160	474.726718	**Y**	***424.219060***	212.613168	407.192511	204.099893			**3**
10	***1080.499652***	540.753464	1063.473103	532.240190	1062.489087	531.748181	**N**	***261.155731***	131.081503	244.129182	122.568229			**2**
11							**K**	147.112804	74.060040	130.086255	65.546765			**1**



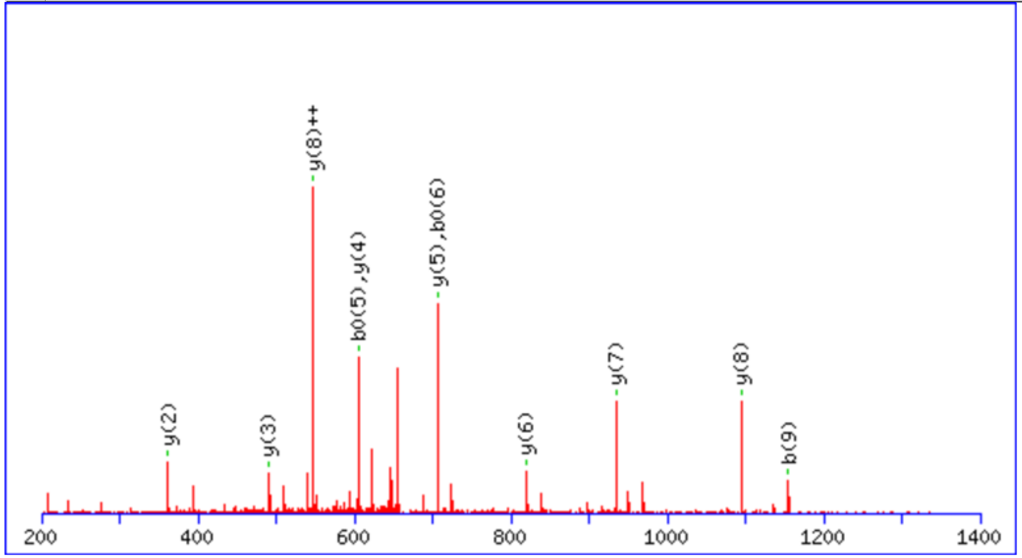
Peptide View

MS/MS Fragmentation of **SFCDLTDEWR**
Found in **IPI00010193**, Tax_Id=9606 Gene_Symbol=IFNAR2 Isoform 1 of Interferon-alpha/beta receptor beta chain
Experiment: 34 - OPB-1 **Fraction:** OPB-1

Match to Query 7493: 1327.551248 from(664.782900,2+)
Title: OECHL100310_17.16988.16988.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1327.550308**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00017**Matches :** 11/86 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**10**
2	235.107718	118.057497	217.097153	109.052214	**F**	1241.525550	621.266413	1224.499001	612.753138	1223.514985	612.261130	**9**
3	395.138367	198.072821	377.127802	189.067539	**C**	***1094.457136***	547.732206	1077.430587	539.218932	1076.446571	538.726924	**8**
4	510.165310	255.586293	492.154745	246.581010	**D**	***934.426487***	467.716882	917.399938	459.203607	916.415922	458.711599	**7**
5	623.249374	312.128325	605.238809	303.123043	**L**	***819.399544***	410.203410	802.372995	401.690135	801.388979	401.198127	**6**
6	724.297053	362.652165	706.286488	353.646882	**T**	***706.315480***	353.661378	689.288931	345.148103	688.304915	344.656095	**5**

7	839.323996	420.165636	821.313431	411.160353	**D**	***605.267801***	303.137539	588.241252	294.624264	587.257236	294.132256	**4**
8	968.366589	484.686933	950.356024	475.681650	**E**	***490.240858***	245.624067	473.214309	237.110792	472.230293	236.618784	**3**
9	1154.445902	577.726589	1136.435337	568.721306	**W**	***361.198265***	181.102770	344.171716	172.589496			**2**
10					**R**	175.118952	88.063114	158.092403	79.549839			**1**



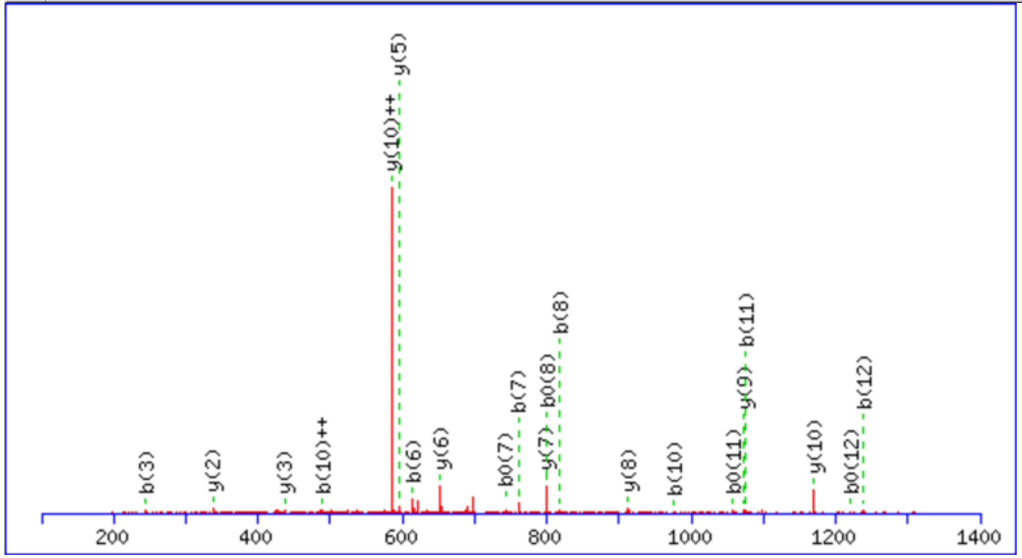
Peptide View

MS/MS Fragmentation of **DGAPCIFGGTVYR**
Found in **IPI00020977**, Tax_Id=9606 Gene_Symbol=CTGF Isoform 1 of Connective tissue growth factor
Experiment: 34 - OPB-1 **Fraction:** OPB-1

Match to Query 8210: 1411.655848 from(706.835200,2+)
Title: OECHL100310_17.15803.15803.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1411.655457**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00055**Matches :** 21/114 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	**D**							**13**
2	173.055683	87.031479	155.045118	78.026197	**G**	1297.635771	649.321524	1280.609222	640.808249	1279.625206	640.316241	**12**

3	***244.092797***	122.550036	226.082232	113.544754	**A**	1240.614307	620.810792	1223.587758	612.297517	1222.603742	611.805509	**11**
4	341.145561	171.076418	323.134996	162.071136	**P**	***1169.577193***	585.292235	1152.550644	576.778960	1151.566628	576.286952	**10**
5	501.176210	251.091743	483.165645	242.086461	**C**	***1072.524429***	536.765853	1055.497880	528.252578	1054.513864	527.760570	**9**
6	***614.260274***	307.633775	596.249709	298.628493	**I**	***912.493780***	456.750528	895.467231	448.237254	894.483215	447.745246	**8**
7	***761.328688***	381.167982	743.318123	372.162700	**F**	***799.409716***	400.208496	782.383167	391.695222	781.399151	391.203214	**7**
8	***818.350152***	409.678714	800.339587	400.673432	**G**	***652.341302***	326.674289	635.314753	318.161015	634.330737	317.669007	**6**
9	875.371616	438.189446	857.361051	429.184164	**G**	***595.319838***	298.163557	578.293289	289.650283	577.309273	289.158275	**5**
10	***976.419295***	488.713286	958.408730	479.708003	**T**	538.298374	269.652825	521.271825	261.139551	520.287809	260.647543	**4**
11	***1075.487709***	538.247493	1057.477144	529.242210	**V**	***437.250695***	219.128986	420.224146	210.615711			**3**
12	***1238.551038***	619.779157	1220.540473	610.773875	**Y**	***338.182281***	169.594778	321.155732	161.081504			**2**
13					**R**	175.118952	88.063114	158.092403	79.549839			**1**

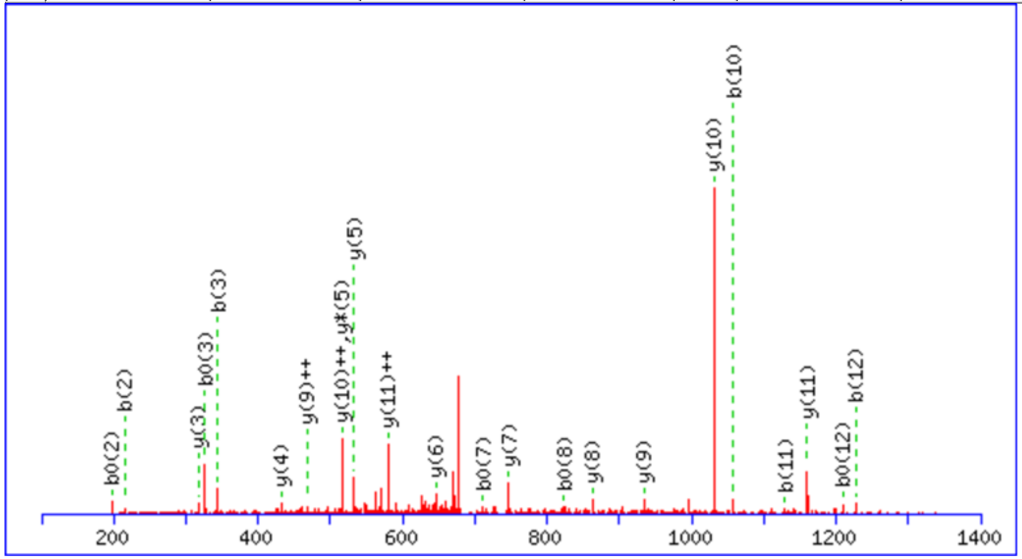


Peptide View

MS/MS Fragmentation of **LTEPADTITDAVK**
Found in **IPI00304808**, Tax_Id=9606 Gene_Symbol=KLK1 Isoform 1 of Kallikrein-1
Experiment: 34 - OPB-1 **Fraction:** OPB-1

Match to Query 7879: 1372.707648 from(687.361100,2+)
Title: OECHL100310_17.12658.12658.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1372.708572**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67
Expect: 3.1e-005**Matches :** 23/112 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							**13**
2	**215.139019**	108.073147	197.128454	99.067865	**T**	1260.631790	630.819533	1243.605241	622.306259	1242.621225	621.814251	**12**
3	**344.181612**	172.594444	326.171047	163.589162	**E**	***1159.584111***	580.295694	1142.557562	571.782419	1141.573546	571.290411	**11**
4	441.234376	221.120826	423.223811	212.115544	**P**	***1030.541518***	515.774397	1013.514969	507.261123	1012.530953	506.769115	**10**
5	512.271490	256.639383	494.260925	247.634101	**A**	***933.488754***	467.248015	916.462205	458.734741	915.478189	458.242733	**9**
6	627.298433	314.152855	609.287868	305.147572	**D**	***862.451640***	431.729458	845.425091	423.216184	844.441075	422.724176	**8**
7	728.346112	364.676694	710.335547	355.671412	**T**	***747.424697***	374.215987	730.398148	365.702712	729.414132	365.210704	**7**
8	841.430176	421.218726	823.419611	412.213444	**I**	***646.377018***	323.692147	629.350469	315.178873	628.366453	314.686865	**6**
9	942.477855	471.742566	924.467290	462.737283	**T**	***533.292954***	267.150115	516.266405	258.636841	515.282389	258.144833	**5**
10	**1057.504798**	529.256037	1039.494233	520.250755	**D**	***432.245275***	216.626276	415.218726	208.113001	414.234710	207.620993	**4**
11	**1128.541912**	564.774594	1110.531347	555.769312	**A**	***317.218332***	159.112804	300.191783	150.599530			**3**
12	**1227.610326**	614.308801	1209.599761	605.303519	**V**	246.181218	123.594247	229.154669	115.080973			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**

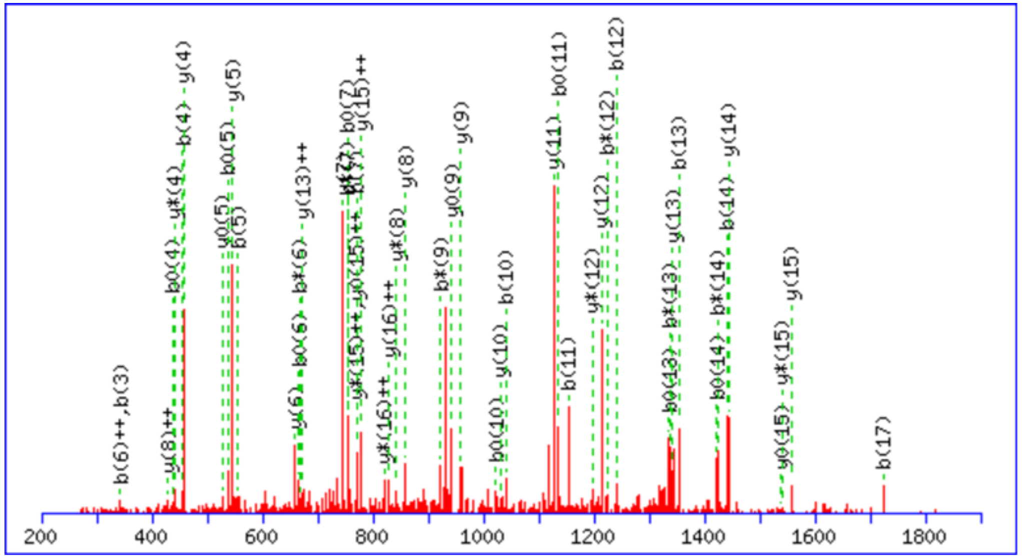


Peptide View

MS/MS Fragmentation of **EIVLTQSPATLSLSPGER**
Found in **IPI00816799**, Tax_Id=9606 Gene_Symbol=- Rheumatoid factor D5 light chain (Fragment)
Experiment: 34 - OPB-1 **Fraction:** OPB-1

Match to Query 13035: 1897.017648 from(949.516100,2+)
Title: OECHL100310_17.16775.16775.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1897.015640**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 0.00023**Matches :** 51/192 fragment ions using 106 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	**E**							**18**
2	243.133933	122.070605			225.123368	113.065322	**I**	1768.980341	884.993808	1751.953792	876.480534	1750.969776	875.988526	**17**
3	**342.202347**	171.604812			324.191782	162.599529	**V**	1655.896277	828.451776	1638.869728	819.938502	1637.885712	819.446494	**16**
4	**455.286411**	228.146844			437.275846	219.141561	**L**	***1556.827863***	778.917569	1539.801314	770.404295	1538.817298	769.912287	**15**
5	**556.334090**	278.670683			538.323525	269.665401	**T**	***1443.743799***	722.375537	1426.717250	713.862263	1425.733234	713.370255	**14**
6	684.392668	342.699972	667.366119	334.186698	666.382103	333.694690	**Q**	***1342.696120***	671.851698	1325.669571	663.338423	1324.685555	662.846415	**13**
7	**771.424696**	386.215986	754.398147	377.702712	753.414131	377.210704	**S**	***1214.637542***	607.822409	1197.610993	599.309134	1196.626977	598.817126	**12**
8	868.477460	434.742368	851.450911	426.229094	850.466895	425.737086	**P**	***1127.605514***	564.306395	1110.578965	555.793120	1109.594949	555.301112	**11**
9	939.514574	470.260925	922.488025	461.747651	921.504009	461.255643	**A**	***1030.552750***	515.780013	1013.526201	507.266738	1012.542185	506.774730	**10**
10	**1040.562253**	520.784765	1023.535704	512.271490	1022.551688	511.779482	**T**	***959.515636***	480.261456	942.489087	471.748181	941.505071	471.256173	**9**
11	**1153.646317**	577.326797	1136.619768	568.813522	1135.635752	568.321514	**L**	***858.467957***	429.737616	841.441408	421.224342	840.457392	420.732334	**8**
12	**1240.678345**	620.842811	1223.651796	612.329536	1222.667780	611.837528	**S**	***745.383893***	373.195585	728.357344	364.682310	727.373328	364.190302	**7**
13	**1353.762409**	677.384842	1336.735860	668.871568	1335.751844	668.379560	**L**	***658.351865***	329.679570	641.325316	321.166296	640.341300	320.674288	**6**
14	**1440.794437**	720.900857	1423.767888	712.387582	1422.783872	711.895574	**S**	***545.267801***	273.137539	528.241252	264.624264	527.257236	264.132256	**5**
15	1537.847201	769.427239	1520.820652	760.913964	1519.836636	760.421956	**P**	***458.235773***	229.621524	441.209224	221.108250	440.225208	220.616242	**4**
16	1594.868665	797.937971	1577.842116	789.424696	1576.858100	788.932688	**G**	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	**3**
17	**1723.911258**	862.459267	1706.884709	853.945992	1705.900693	853.453984	**E**	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**



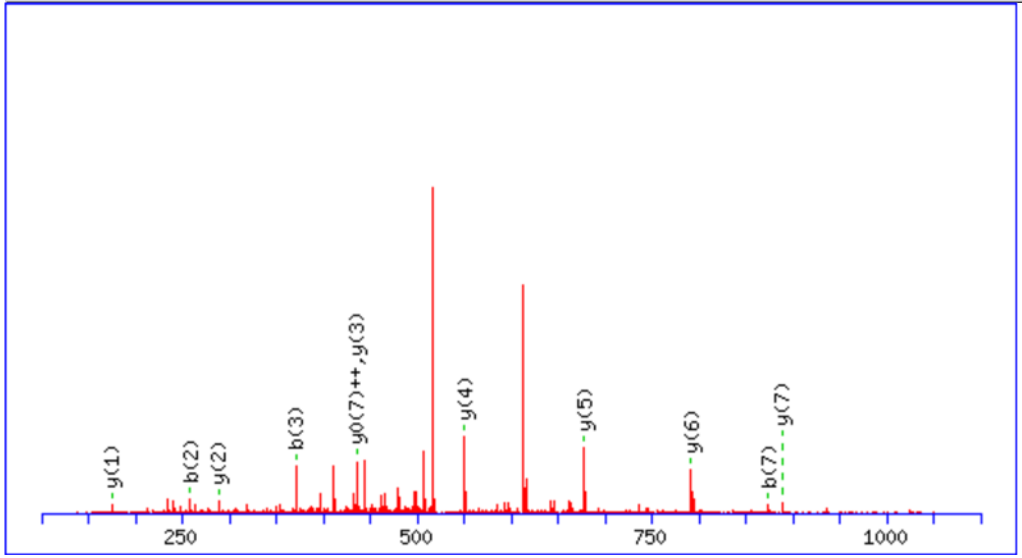
Peptide View

MS/MS Fragmentation of **CPLQDFLR**
Found in **IPI00003807**, Tax_Id=9606 Gene_Symbol=ACP2 Lysosomal acid phosphatase
Experiment: 34 - OPB-1 **Fraction:** OPB-1

Match to Query 3576: 1047.517248 from(524.765900,2+)
Title: OECHL100310_17.17068.17068.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1047.517151**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00026**Matches :** 11/64 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.037925	81.022600					**C**							**8**
2	**258.090689**	129.548982					**P**	***888.493779***	444.750528	871.467230	436.237253	870.483214	435.745245	**7**
3	**371.174753**	186.091015					**L**	***791.441015***	396.224146	774.414466	387.710871	773.430450	387.218863	**6**
4	499.233331	250.120304	482.206782	241.607029			**Q**	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	**5**
5	614.260274	307.633775	597.233725	299.120501	596.249709	298.628493	**D**	***550.298373***	275.652825	533.271824	267.139550	532.287808	266.647542	**4**
6	761.328688	381.167982	744.302139	372.654708	743.318123	372.162700	**F**	***435.271430***	218.139353	418.244881	209.626079			**3**

7	**874.412752**	437.710014	857.386203	429.196740	856.402187	428.704732	**L**	***288.203016***	144.605146	271.176467	136.091872			**2**
8							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



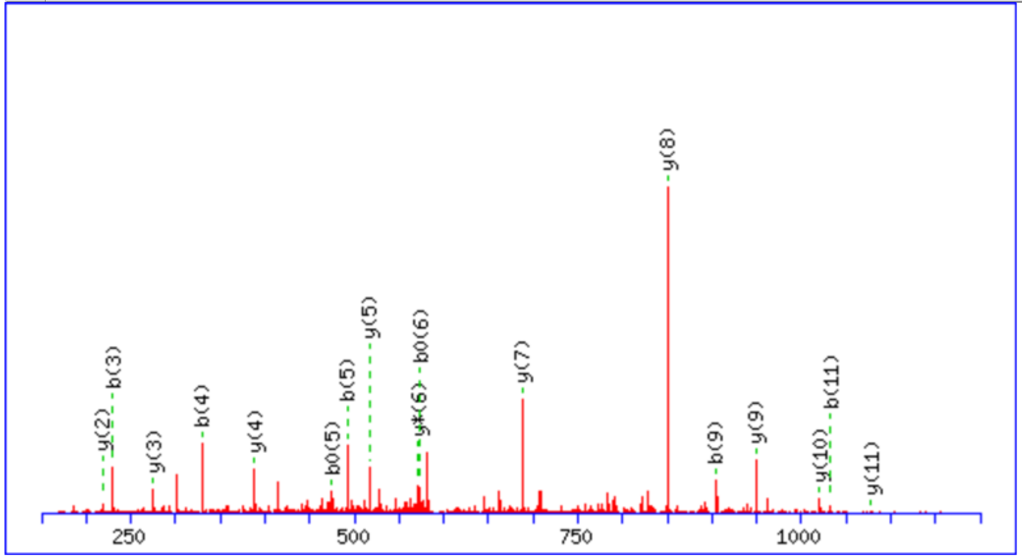
Peptide View

MS/MS Fragmentation of **TGAVYVAEIGAK**
Found in **IPI00552937**, Tax_Id=9606 Gene_Symbol=NHLRC3 NHL repeat-containing protein 3
Experiment: 34 - OPB-1 **Fraction:** OPB-1

Match to Query 5274: 1177.635648 from(589.825100,2+)
Title: OECHL100310_17.11474.11474.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1177.634277**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00021**Matches :** 17/102 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							**12**
2	159.076419	80.041847	141.065854	71.036565	**G**	***1077.593888***	539.300582	1060.567339	530.787308	1059.583323	530.295300	**11**
3	**230.113533**	115.560404	212.102968	106.555122	**A**	***1020.572424***	510.789850	1003.545875	502.276576	1002.561859	501.784568	**10**
4	**329.181947**	165.094611	311.171382	156.089329	**V**	***949.535310***	475.271293	932.508761	466.758019	931.524745	466.266011	**9**

5	**492.245276**	246.626276	474.234711	237.620994	**Y**	***850.466896***	425.737086	833.440347	417.223812	832.456331	416.731804	**8**
6	591.313690	296.160483	573.303125	287.155201	**V**	***687.403567***	344.205422	670.377018	335.692147	669.393002	335.200139	**7**
7	662.350804	331.679040	644.340239	322.673758	**A**	588.335153	294.671215	571.308604	286.157940	570.324588	285.665932	**6**
8	791.393397	396.200337	773.382832	387.195054	**E**	***517.298039***	259.152658	500.271490	250.639383	499.287474	250.147375	**5**
9	**904.477461**	452.742369	886.466896	443.737086	**I**	***388.255446***	194.631361	371.228897	186.118087			**4**
10	961.498925	481.253101	943.488360	472.247818	**G**	***275.171382***	138.089329	258.144833	129.576055			**3**
11	**1032.536039**	516.771658	1014.525474	507.766375	**A**	***218.149918***	109.578597	201.123369	101.065322			**2**
12					**K**	147.112804	74.060040	130.086255	65.546765			**1**



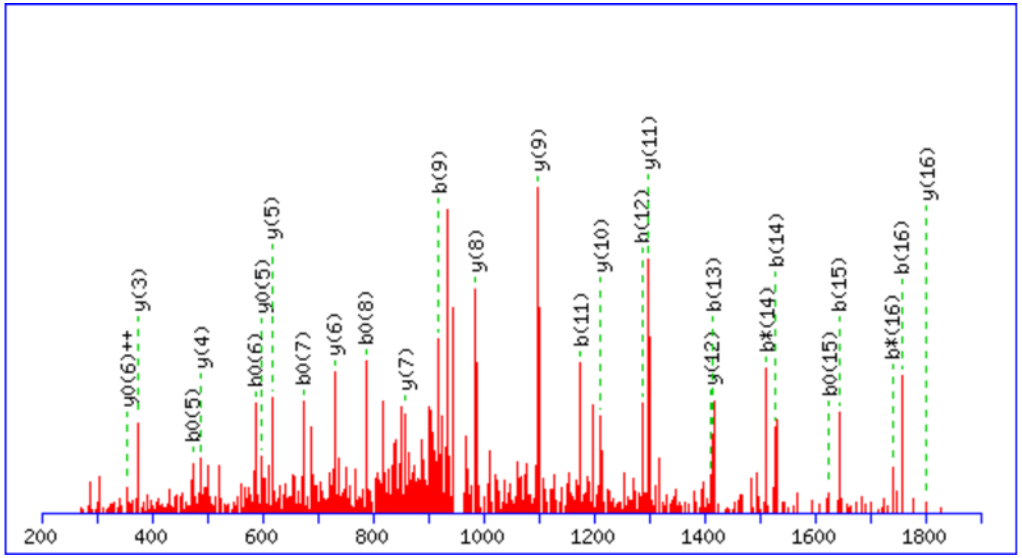
Peptide View

MS/MS Fragmentation of **TATFAISILQQIELDLK**
Found in **IPI00025491**, Tax_Id=9606 Gene_Symbol=EIF4A1;SNORA67 Eukaryotic initiation factor 4A-I
Experiment: 34 - OPB-1 **Fraction:** OPB-1

Match to Query 13106: 1903.067848 from(952.541200,2+)
Title: OECHL100310_17.23067.23067.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1903.066605**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53

Expect: 0.00011**Matches :** 27/170 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	**T**							**17**
2	173.092069	87.049672			155.081504	78.044390	**A**	***1803.026229***	902.016752	1785.999680	893.503478	1785.015664	893.011470	**16**
3	274.139748	137.573512			256.129183	128.568230	**T**	1731.989115	866.498195	1714.962566	857.984921	1713.978550	857.492913	**15**
4	421.208162	211.107719			403.197597	202.102436	**F**	1630.941436	815.974356	1613.914887	807.461081	1612.930871	806.969073	**14**
5	492.245276	246.626276			474.234711	237.620993	**A**	1483.873022	742.440149	1466.846473	733.926875	1465.862457	733.434867	**13**
6	605.329340	303.168308			587.318775	294.163026	**I**	***1412.835908***	706.921592	1395.809359	698.408317	1394.825343	697.916309	**12**
7	692.361368	346.684322			674.350803	337.679039	**S**	***1299.751844***	650.379560	1282.725295	641.866286	1281.741279	641.374277	**11**
8	805.445432	403.226354			787.434867	394.221071	**I**	***1212.719816***	606.863546	1195.693267	598.350272	1194.709251	597.858264	**10**
9	**918.529496**	459.768386			900.518931	450.763104	**L**	***1099.635752***	550.321514	1082.609203	541.808240	1081.625187	541.316231	**9**
10	1046.588074	523.797675	1029.561525	515.284401	1028.577509	514.792393	**Q**	***986.551688***	493.779482	969.525139	485.266207	968.541123	484.774199	**8**
11	**1174.646652**	587.826964	1157.620103	579.313690	1156.636087	578.821682	**Q**	***858.493110***	429.750193	841.466561	421.236918	840.482545	420.744910	**7**
12	**1287.730716**	644.368996	1270.704167	635.855722	1269.720151	635.363714	**I**	***730.434532***	365.720904	713.407983	357.207629	712.423967	356.715621	**6**
13	**1416.773309**	708.890292	1399.746760	700.377018	1398.762744	699.885010	**E**	***617.350468***	309.178872	600.323919	300.665597	599.339903	300.173589	**5**
14	**1529.857373**	765.432324	1512.830824	756.919050	1511.846808	756.427042	**L**	***488.307875***	244.657575	471.281326	236.144301	470.297310	235.652293	**4**
15	**1644.884316**	822.945796	1627.857767	814.432522	1626.873751	813.940513	**D**	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	**3**
16	**1757.968380**	879.487828	1740.941831	870.974553	1739.957815	870.482545	**L**	260.196868	130.602072	243.170319	122.088797			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**



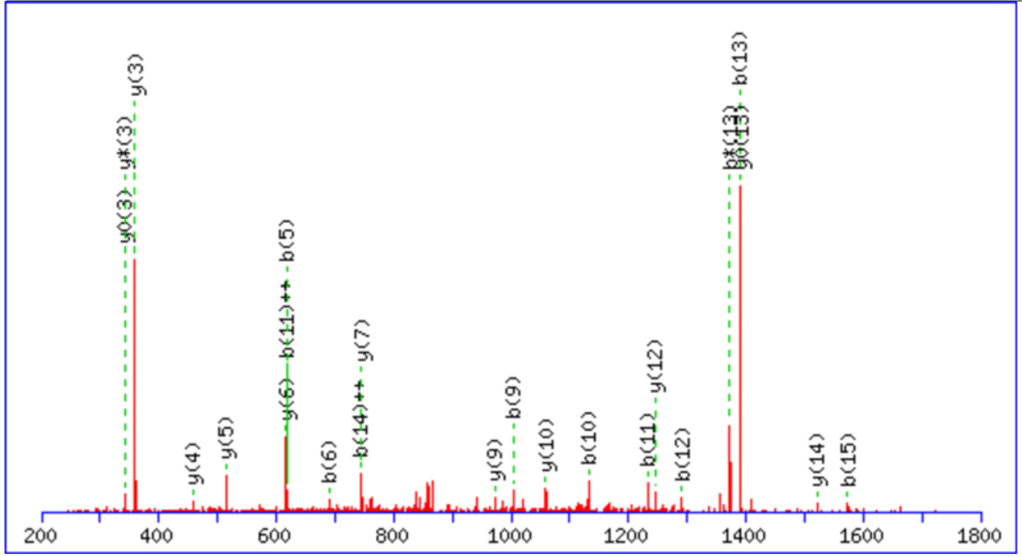
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 34 - OPB-1 **Fraction:** OPB-1

Match to Query 11754: 1746.916848 from(874.465700,2+)
Title: OECHL100310_17.17056.17056.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53
Expect: 0.00054**Matches :** 23/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	***618.349740***	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	***689.386854***	345.197065			671.376289	336.191782	**A**	1130.580027	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**

7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	858.467958	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



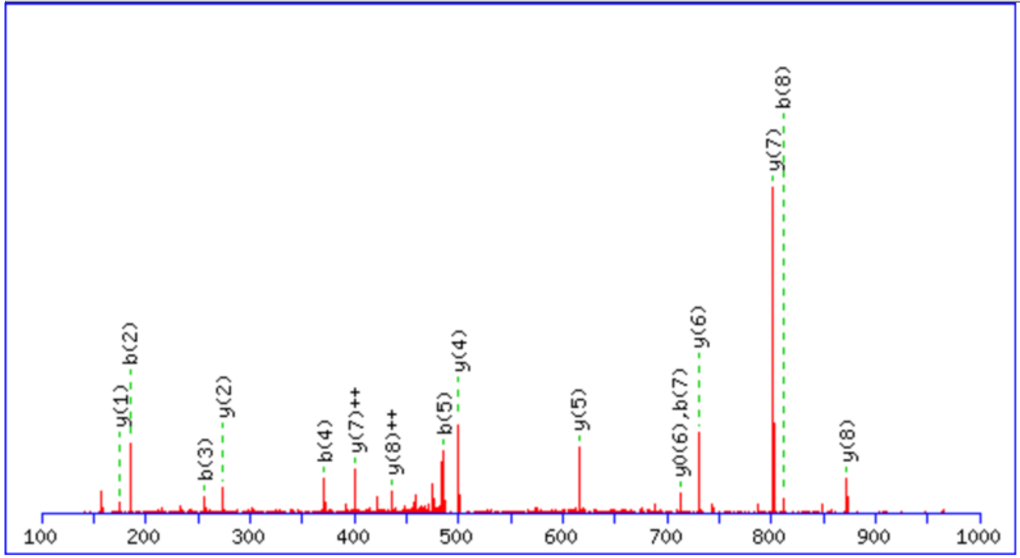
Peptide View

MS/MS Fragmentation of **LAADDPEVR**
Found in **IPI00025840**, Tax_Id=9606 Gene_Symbol=EFNA1 Isoform 1 of Ephrin-A1
Experiment: 34 - OPB-1 **Fraction:** OPB-1

Match to Query 2630: 984.487048 from(493.250800,2+)

Title: OECHL100310_17.5191.5191.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 984.487610**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00043**Matches :** 16/70 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							**9**
2	**185.128454**	93.067865			**A**	***872.410837***	436.709057	855.384288	428.195782	854.400272	427.703774	**8**
3	**256.165568**	128.586422			**A**	***801.373723***	401.190500	784.347174	392.677225	783.363158	392.185217	**7**
4	**371.192511**	186.099893	353.181946	177.094611	**D**	***730.336609***	365.671943	713.310060	357.158668	712.326044	356.666660	**6**
5	**486.219454**	243.613365	468.208889	234.608082	**D**	***615.309666***	308.158471	598.283117	299.645197	597.299101	299.153189	**5**
6	583.272218	292.139747	565.261653	283.134465	**P**	***500.282723***	250.644999	483.256174	242.131725	482.272158	241.639717	**4**
7	**712.314811**	356.661044	694.304246	347.655761	**E**	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	**3**
8	**811.383225**	406.195251	793.372660	397.189968	**V**	***274.187366***	137.597321	257.160817	129.084046			**2**
9					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



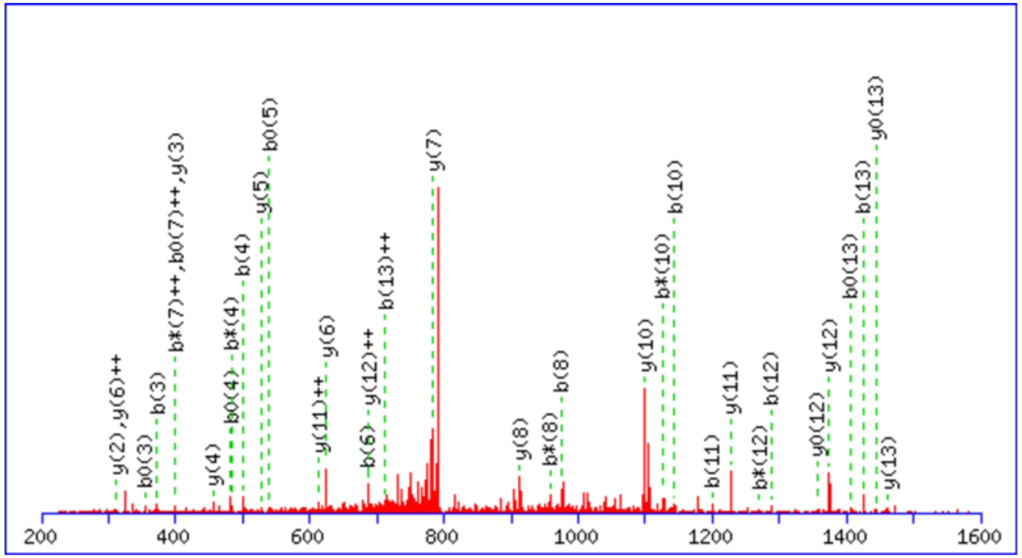
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**

Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 04 - S_B-1 **Fraction:** S_B-1

Match to Query 9745: 1597.706248 from(799.860400,2+)
Title: OECHL100310_15.2373.2373.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00041**Matches :** 35/144 fragment ions using 84 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					**H**							**14**
2	225.098216	113.052746			207.087651	104.047463	**S**	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.325325	**13**
3	**372.166630**	186.586953			354.156065	177.581671	**F**	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.809311	**12**
4	**500.261593**	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	**11**
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	**10**
6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	1042.437069	521.722173	1025.410520	513.208898	1024.426504	512.716890	**9**
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	***312.177864***	156.592570	295.151315	148.079295			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



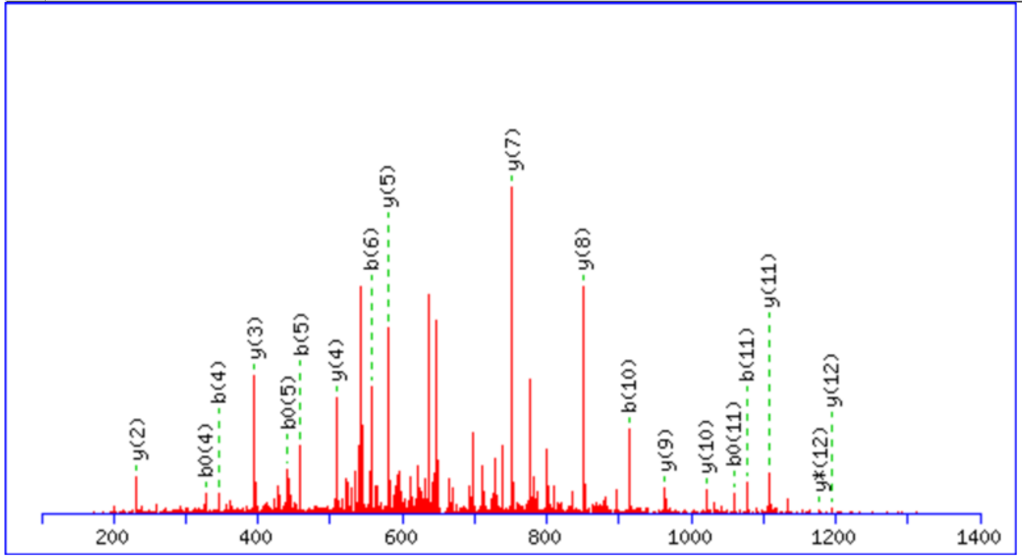
Peptide View

MS/MS Fragmentation of **LSSGLVTAALYGR**
Found in **IPI00218413**, Tax_Id=9606 Gene_Symbol=BTD Biotinidase
Experiment: 04 - S_B-1 **Fraction:** S_B-1

Match to Query 6811: 1306.726248 from(654.370400,2+)
Title: OECHL100310_15.17030.17030.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1306.724487**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 75
Expect: 1.3e-006**Matches :** 19/106 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							**13**
2	201.123368	101.065322	183.112803	92.060039	**S**	***1194.647714***	597.827495	1177.621165	589.314221	1176.637149	588.822212	**12**
3	288.155396	144.581336	270.144831	135.576053	**S**	***1107.615686***	554.311481	1090.589137	545.798206	1089.605121	545.306198	**11**
4	**345.176860**	173.092068	327.166295	164.086785	**G**	***1020.583658***	510.795467	1003.557109	502.282192	1002.573093	501.790184	**10**
5	**458.260924**	229.634100	440.250359	220.628817	**L**	***963.562194***	482.284735	946.535645	473.771460	945.551629	473.279452	**9**
6	**557.329338**	279.168307	539.318773	270.163025	**V**	***850.478130***	425.742703	833.451581	417.229428	832.467565	416.737420	**8**

7	658.377017	329.692147	640.366452	320.686864	**T**	***751.409716***	376.208496	734.383167	367.695221	733.399151	367.203213	**7**
8	729.414131	365.210704	711.403566	356.205421	**A**	650.362037	325.684656	633.335488	317.171382			**6**
9	800.451245	400.729261	782.440680	391.723978	**A**	***579.324923***	290.166099	562.298374	281.652825			**5**
10	**913.535309**	457.271293	895.524744	448.266010	**L**	***508.287809***	254.647542	491.261260	246.134268			**4**
11	**1076.598638**	538.802957	1058.588073	529.797674	**Y**	***395.203745***	198.105510	378.177196	189.592236			**3**
12	1133.620102	567.313689	1115.609537	558.308406	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
13					**R**	175.118952	88.063114	158.092403	79.549839			**1**

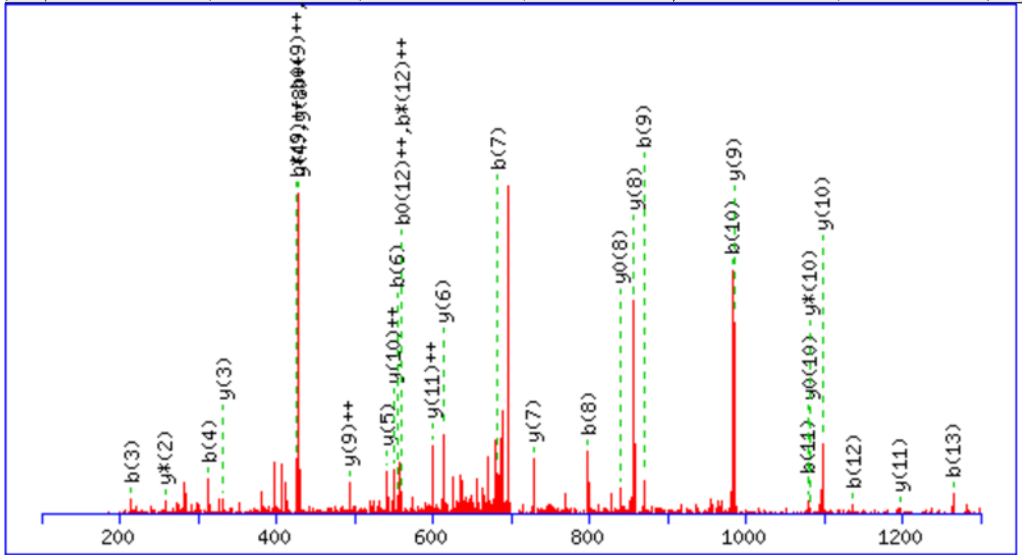


Peptide View

MS/MS Fragmentation of **GGVVLKEDALPGQK**
Found in **IPI00019906**, Tax_Id=9606 Gene_Symbol=BSG Isoform 2 of Basigin
Experiment: 04 - S_B-1 **Fraction:** S_B-1

Match to Query 7908: 1409.787448 from(705.901000,2+)
Title: OECHL100310_15.9534.9534.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1409.787827**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 3.3e-005**Matches :** 32/122 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	58.028740	29.518008					**G**							**14**
2	115.050204	58.028740					**G**	1353.773643	677.390460	1336.747094	668.877185	1335.763078	668.385177	**13**
3	***214.118618***	107.562947					**V**	1296.752179	648.879728	1279.725630	640.366453	1278.741614	639.874445	**12**
4	***313.187032***	157.097154					**V**	**1197.683765**	599.345521	1180.657216	590.832246	1179.673200	590.340238	**11**
5	***426.271096***	213.639186					**L**	**1098.615351**	549.811314	1081.588802	541.298039	1080.604786	540.806031	**10**
6	***554.366059***	277.686668	537.339510	269.173393			**K**	**985.531287**	493.269282	968.504738	484.756007	967.520722	484.263999	**9**
7	***683.408652***	342.207964	666.382103	333.694690	665.398087	333.202682	**E**	**857.436324**	429.221800	840.409775	420.708526	839.425759	420.216518	**8**
8	***798.435595***	399.721436	781.409046	391.208161	780.425030	390.716153	**D**	**728.393731**	364.700504	711.367182	356.187229	710.383166	355.695221	**7**
9	***869.472709***	435.239993	852.446160	426.726718	851.462144	426.234710	**A**	**613.366788**	307.187032	596.340239	298.673758			**6**
10	***982.556773***	491.782025	965.530224	483.268750	964.546208	482.776742	**L**	**542.329674**	271.668475	525.303125	263.155201			**5**
11	***1079.609537***	540.308407	1062.582988	531.795132	1061.598972	531.303124	**P**	**429.245610**	215.126443	412.219061	206.613169			**4**
12	***1136.631001***	568.819139	1119.604452	560.305864	1118.620436	559.813856	**G**	**332.192846**	166.600061	315.166297	158.086787			**3**
13	***1264.689579***	632.848428	1247.663030	624.335153	1246.679014	623.843145	**Q**	275.171382	138.089329	258.144833	129.576055			**2**
14							**K**	147.112804	74.060040	130.086255	65.546765			**1**

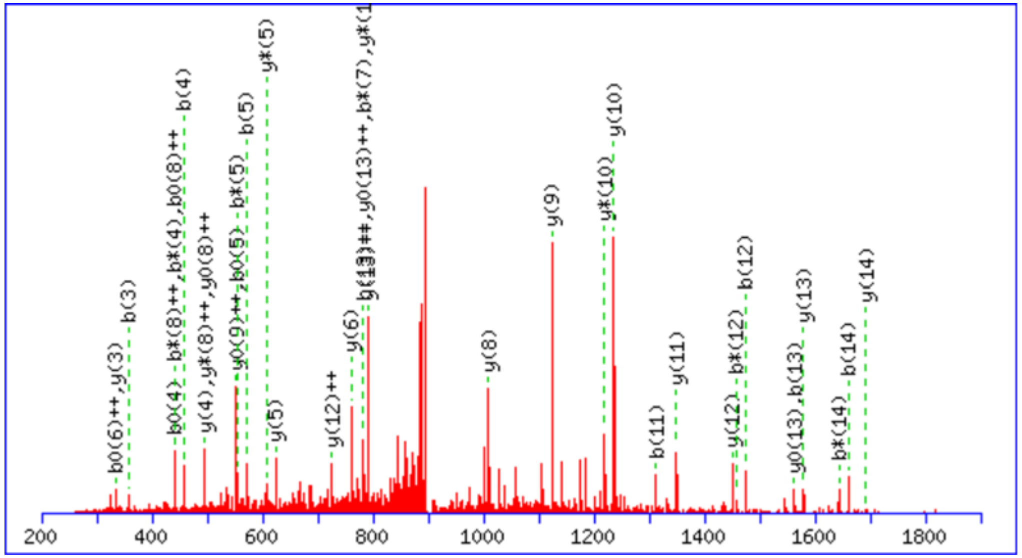


Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 04 - S_B-1 **Fraction:** S_B-1

Match to Query 11636: 1805.931848 from(903.973200,2+)
Title: OECHL100310_15.19344.19344.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 76
Expect: 3.1e-006**Matches :** 39/160 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**15**
2	228.134267	114.570771	211.107718	106.057497			**I**	***1692.895549***	846.951413	1675.869000	838.438138	1674.884984	837.946130	**14**
3	**357.176860**	179.092068	340.150311	170.578793	339.166295	170.086785	**E**	***1579.811485***	790.409381	1562.784936	781.896106	1561.800920	781.404098	**13**
4	**458.224539**	229.615907	441.197990	221.102633	440.213974	220.610625	**T**	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.882802	**12**
5	**571.308603**	286.157940	554.282054	277.644665	553.298038	277.152657	**I**	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.358962	**11**
6	684.392667	342.699972	667.366118	334.186697	666.382102	333.694689	**I**	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.816930	**10**
7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	**N**	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.274898	**9**
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	**T**	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.253435	**8**
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	**F**	908.462479	454.734878	891.435930	446.221603	890.451914	445.729595	**7**
10	1183.610599	592.308938	1166.584050	583.795663	1165.600034	583.303655	**H**	***761.394065***	381.200671	744.367516	372.687396	743.383500	372.195388	**6**
11	**1311.669177**	656.338227	1294.642628	647.824952	1293.658612	647.332944	**Q**	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.665932	**5**
12	**1474.732506**	737.869891	1457.705957	729.356617	1456.721941	728.864609	**Y**	***496.276575***	248.641926	479.250026	240.128651	478.266010	239.636643	**4**
13	**1561.764534**	781.385905	1544.737985	772.872631	1543.753969	772.380623	**S**	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.104979	**3**
14	**1660.832948**	830.920112	1643.806399	822.406838	1642.822383	821.914830	**V**	246.181218	123.594247	229.154669	115.080973			**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



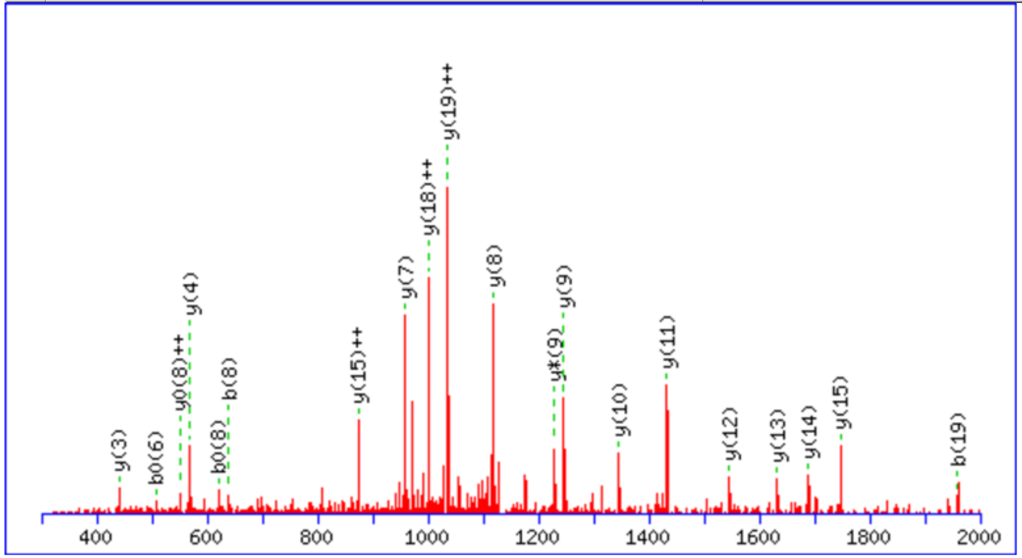
Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 04 - S_B-1 **Fraction:** S_B-1

Match to Query 14664: 2270.115448 from(1136.065000,2+)
Title: OECHL100310_15.10236.10236.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71
Expect: 1.7e-005**Matches :** 20/212 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	102.054955	51.531116			84.044390	42.525833	**T**						
2	201.123369	101.065322			183.112804	92.060040	**V**	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400	1076.5338
3	272.160483	136.583879			254.149918	127.578597	**A**	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986	1026.9996
4	329.181947	165.094611			311.171382	156.089329	**G**	1999.965437	1000.486357	1982.938888	991.973082	1981.954872	991.4810
5	426.234711	213.620994			408.224146	204.615711	**P**	1942.943973	971.975625	1925.917424	963.462350	1924.933408	962.9703
6	525.303125	263.155201			507.292560	254.149918	**V**	1845.891209	923.449243	1828.864660	914.935968	1827.880644	914.4439

7	582.324589	291.665933			564.314024	282.660650	**G**	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230	864.9097
8	**639.346053**	320.176665			621.335488	311.171382	**G**	***1689.801331***	845.404304	1672.774782	836.891029	1671.790766	836.3990
9	726.378081	363.692679			708.367516	354.687396	**S**	***1632.779867***	816.893572	1615.753318	808.380297	1614.769302	807.8882
10	839.462145	420.234711			821.451580	411.229428	**L**	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274	764.3722
11	926.494173	463.750725			908.483608	454.745442	**S**	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210	707.8302
12	1025.562587	513.284932			1007.552022	504.279649	**V**	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182	664.3142
13	1153.621165	577.314221	1136.594616	568.800946	1135.610600	568.308938	**Q**	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768	614.7800
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	**C**	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190	550.7507
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	**P**	***958.474106***	479.740691	941.447557	471.227417	940.463541	470.7354
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	**Y**	861.421342	431.214309	844.394793	422.701035	843.410777	422.2090
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	**E**	698.358013	349.682645	681.331464	341.169370	680.347448	340.6773
18	1830.905463	915.956370	1813.878914	907.443095	1812.894898	906.951087	**K**	***569.315420***	285.161348	552.288871	276.648074	551.304855	276.1560
19	**1959.948056**	980.477666	1942.921507	971.964392	1941.937491	971.472384	**E**	***441.220457***	221.113867	424.193908	212.600592	423.209892	212.1085
20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	**H**	312.177864	156.592570	295.151315	148.079295		
21							**R**	175.118952	88.063114	158.092403	79.549839		

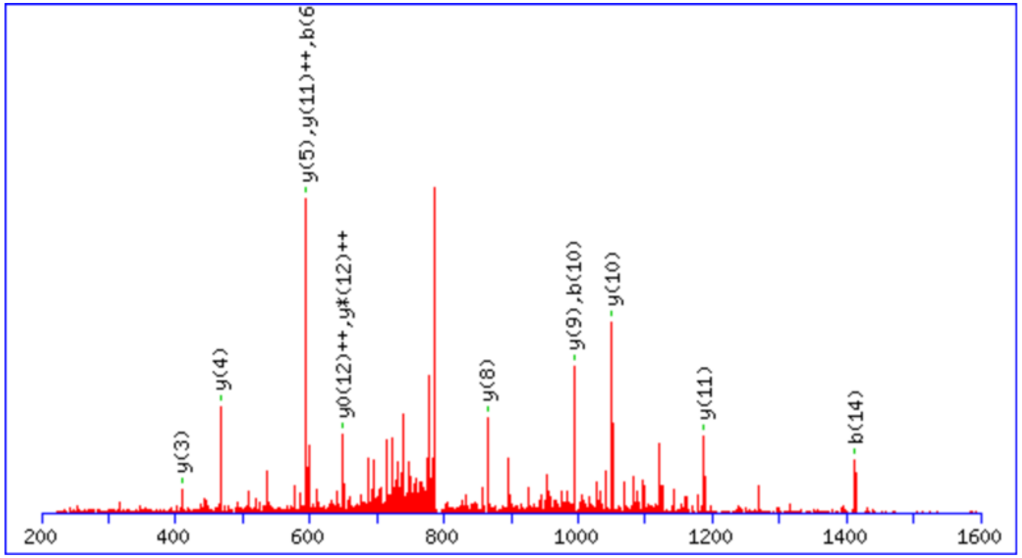


Peptide View

MS/MS Fragmentation of **ASLQHGQAAEKGPHR**
Found in **IPI00165044**, Tax_Id=9606 Gene_Symbol=FAM198B Isoform 2 of Protein ENED
Experiment: 04 - S_B-1 **Fraction:** S_B-1

Match to Query 9652: 1585.809248 from(793.911900,2+)
Title: OECHL100310_15.2005.2005.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1585.807312**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.0011**Matches :** 13/150 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	72.044390	36.525833					**A**							**15**
2	159.076418	80.041847			141.065853	71.036564	**S**	1515.777500	758.392388	1498.750951	749.879114	1497.766935	749.387106	**14**
3	272.160482	136.583879			254.149917	127.578597	**L**	1428.745472	714.876374	1411.718923	706.363100	1410.734907	705.871092	**13**
4	400.219060	200.613168	383.192511	192.099894	382.208495	191.607886	**Q**	1315.661408	658.334342	1298.634859	649.821068	1297.650843	649.329060	**12**
5	537.277972	269.142624	520.251423	260.629350	519.267407	260.137342	**H**	***1187.602830***	594.305053	1170.576281	585.791779	1169.592265	585.299771	**11**
6	**594.299436**	297.653356	577.272887	289.140082	576.288871	288.648074	**G**	***1050.543918***	525.775597	1033.517369	517.262323	1032.533353	516.770315	**10**
7	722.358014	361.682645	705.331465	353.169371	704.347449	352.677363	**Q**	***993.522454***	497.264865	976.495905	488.751591	975.511889	488.259583	**9**
8	793.395128	397.201202	776.368579	388.687928	775.384563	388.195920	**A**	***865.463876***	433.235576	848.437327	424.722302	847.453311	424.230294	**8**
9	864.432242	432.719759	847.405693	424.206485	846.421677	423.714477	**A**	794.426762	397.717019	777.400213	389.203745	776.416197	388.711737	**7**
10	**993.474835**	497.241056	976.448286	488.727781	975.464270	488.235773	**E**	723.389648	362.198462	706.363099	353.685188	705.379083	353.193180	**6**
11	1121.569798	561.288537	1104.543249	552.775263	1103.559233	552.283255	**K**	***594.347055***	297.677166	577.320506	289.163891			**5**
12	1178.591262	589.799269	1161.564713	581.285995	1160.580697	580.793987	**G**	***466.252092***	233.629684	449.225543	225.116409			**4**
13	1275.644026	638.325651	1258.617477	629.812377	1257.633461	629.320369	**P**	***409.230628***	205.118952	392.204079	196.605677			**3**
14	**1412.702938**	706.855107	1395.676389	698.341833	1394.692373	697.849825	**H**	312.177864	156.592570	295.151315	148.079295			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



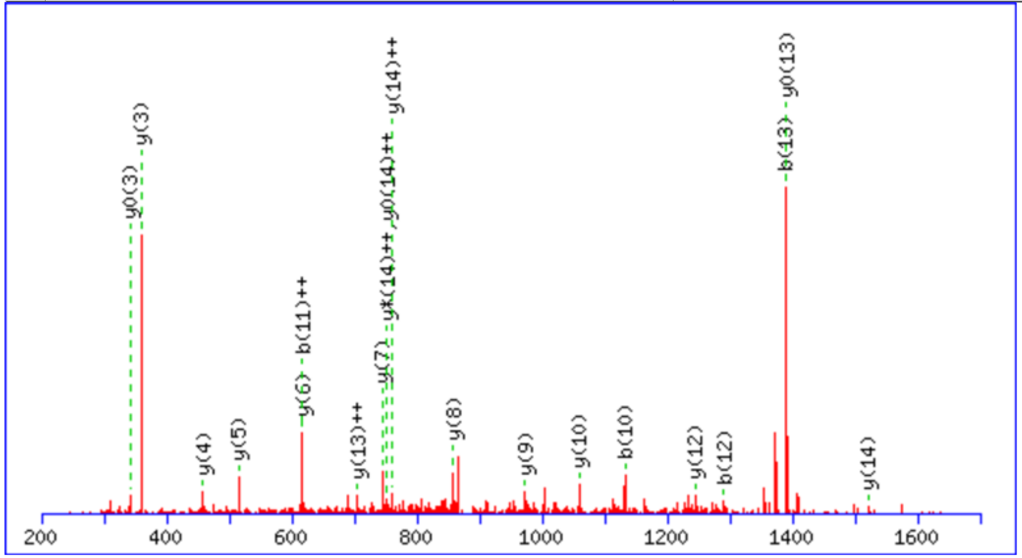
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 04 - S_B-1 **Fraction:** S_B-1

Match to Query 11131: 1746.917648 from(874.466100,2+)
Title: OECHL100310_15.16887.16887.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 76
Expect: 2.4e-006**Matches :** 20/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	618.349740	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	689.386854	345.197065			671.376289	336.191782	**A**	1130.580027	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**

7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	1003.545873	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	1233.636145	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	1573.810815	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



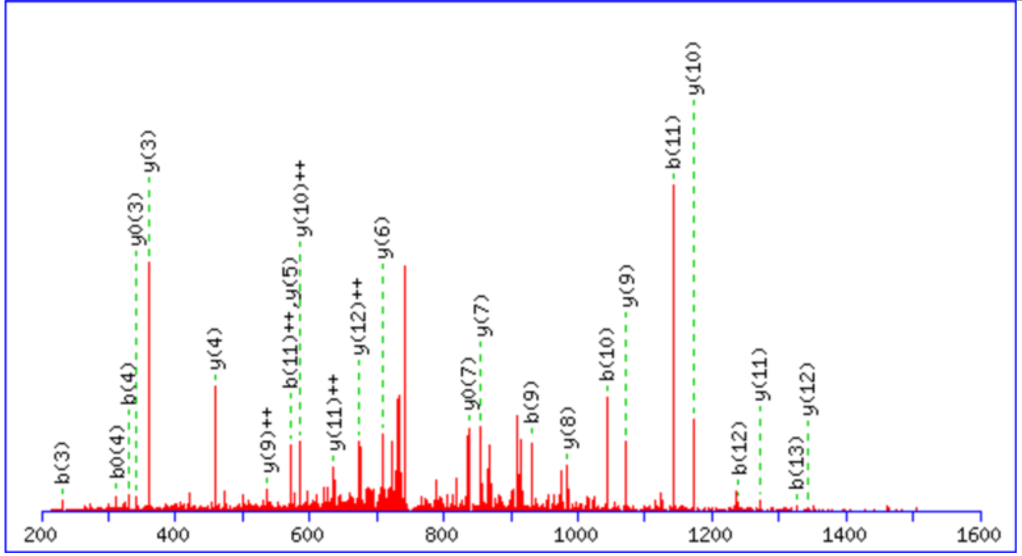
Peptide View

MS/MS Fragmentation of **SAAVTSEFHLVPSR**
Found in **IPI00043992**, Tax_Id=9606 Gene_Symbol=PVRL4 Poliovirus receptor-related protein 4
Experiment: 04 - S_B-1 **Fraction:** S_B-1

Match to Query 8837: 1499.775248 from(750.894900,2+)

Title: OECHL100310_15.13488.13488.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1499.773239**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 8.2e-005**Matches :** 25/128 fragment ions using 52 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**14**
2	159.076418	80.041847	141.065853	71.036564	**A**	1413.748490	707.377883	1396.721941	698.864609	1395.737925	698.372600	**13**
3	**230.113532**	115.560404	212.102967	106.555121	**A**	***1342.711376***	671.859326	1325.684827	663.346052	1324.700811	662.854043	**12**
4	**329.181946**	165.094611	311.171381	156.089328	**V**	***1271.674262***	636.340769	1254.647713	627.827495	1253.663697	627.335487	**11**
5	430.229625	215.618450	412.219060	206.613168	**T**	***1172.605848***	586.806562	1155.579299	578.293288	1154.595283	577.801279	**10**
6	517.261653	259.134465	499.251088	250.129182	**S**	***1071.558169***	536.282723	1054.531620	527.769448	1053.547604	527.277440	**9**
7	646.304246	323.655761	628.293681	314.650479	**E**	***984.526141***	492.766709	967.499592	484.253434	966.515576	483.761426	**8**
8	793.372660	397.189968	775.362095	388.184686	**F**	***855.483548***	428.245412	838.456999	419.732138	837.472983	419.240130	**7**
9	**930.431572**	465.719424	912.421007	456.714141	**H**	***708.415134***	354.711205	691.388585	346.197931	690.404569	345.705923	**6**
10	**1043.515636**	522.261456	1025.505071	513.256173	**L**	***571.356222***	286.181749	554.329673	277.668475	553.345657	277.176467	**5**
11	**1142.584050**	571.795663	1124.573485	562.790380	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
12	**1239.636814**	620.322045	1221.626249	611.316762	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
13	**1326.668842**	663.838059	1308.658277	654.832777	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
14					**R**	175.118952	88.063114	158.092403	79.549839			**1**



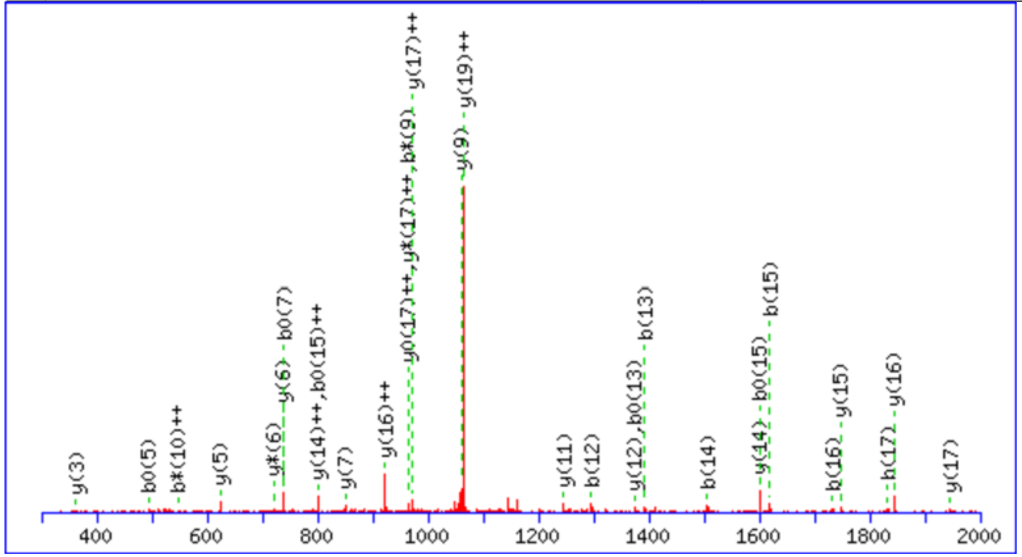
Peptide View

MS/MS Fragmentation of **IIPSTPFPQEGQPLILTCESK**
Found in **IPI00293836**, Tax_Id=9606 Gene_Symbol=CADM2 Isoform 3 of Cell adhesion molecule 2
Experiment: 04 - S_B-1 **Fraction:** S_B-1

Match to Query 15119: 2354.213448 from(1178.114000,2+)
Title: OECHL100310_15.18131.18131.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 2354.219177**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59
Expect: 0.00016**Matches :** 31/216 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	114.091340	57.549308					I						
2	227.175404	114.091340					I	2242.142399	1121.574837	2225.115850	1113.061563	2224.131834	1112.5695
3	324.228168	162.617722					P	2129.058335	1065.032805	2112.031786	1056.519531	2111.047770	1056.0275
4	411.260196	206.133736			393.249631	197.128454	S	2032.005571	1016.506423	2014.979022	1007.993149	2013.995006	1007.5011
5	512.307875	256.657576			494.297310	247.652293	T	***1944.973543***	972.990409	1927.946994	964.477135	1926.962978	963.9851
6	609.360639	305.183958			591.350074	296.178675	P	***1843.925864***	922.466570	1826.899315	913.953295	1825.915299	913.4612
7	756.429053	378.718165			738.418488	369.712882	F	***1746.873100***	873.940188	1729.846551	865.426913	1728.862535	864.9349
8	853.481817	427.244547			835.471252	418.239264	P	***1599.804686***	800.405981	1582.778137	791.892706	1581.794121	791.4006
9	981.540395	491.273836	964.513846	482.760561	963.529830	482.268553	Q	1502.751922	751.879599	1485.725373	743.366324	1484.741357	742.8743
10	1110.582988	555.795132	1093.556439	547.281858	1092.572423	546.789850	E	***1374.693344***	687.850310	1357.666795	679.337035	1356.682779	678.8450
11	1167.604452	584.305864	1150.577903	575.792590	1149.593887	575.300582	G	***1245.650751***	623.329013	1228.624202	614.815739	1227.640186	614.3237
12	**1295.663030**	648.335153	1278.636481	639.821879	1277.652465	639.329870	Q	1188.629287	594.818281	1171.602738	586.305007	1170.618722	585.8129
13	**1392.715794**	696.861535	1375.689245	688.348261	1374.705229	687.856252	P	***1060.570709***	530.788992	1043.544160	522.275718	1042.560144	521.7837
14	**1505.799858**	753.403567	1488.773309	744.890292	1487.789293	744.398284	L	963.517945	482.262610	946.491396	473.749336	945.507380	473.2573
15	**1618.883922**	809.945599	1601.857373	801.432324	1600.873357	800.940316	I	***850.433881***	425.720578	833.407332	417.207304	832.423316	416.7152
16	**1731.967986**	866.487631	1714.941437	857.974356	1713.957421	857.482348	L	***737.349817***	369.178547	720.323268	360.665272	719.339252	360.1732
17	**1833.015665**	917.011470	1815.989116	908.498196	1815.005100	908.006188	T	***624.265753***	312.636515	607.239204	304.123240	606.255188	303.6312
18	1993.046314	997.026795	1976.019765	988.513520	1975.035749	988.021512	C	523.218074	262.112675	506.191525	253.599401	505.207509	253.1073
19	2122.088907	1061.548091	2105.062358	1053.034817	2104.078342	1052.542809	E	***363.187425***	182.097350	346.160876	173.584076	345.176860	173.0920

20	2209.120935	1105.064105	2192.094386	1096.550831	2191.110370	1096.058823	**S**	234.144832	117.576054	217.118283	109.062780	216.134267	108.5707
21							**K**	147.112804	74.060040	130.086255	65.546765		



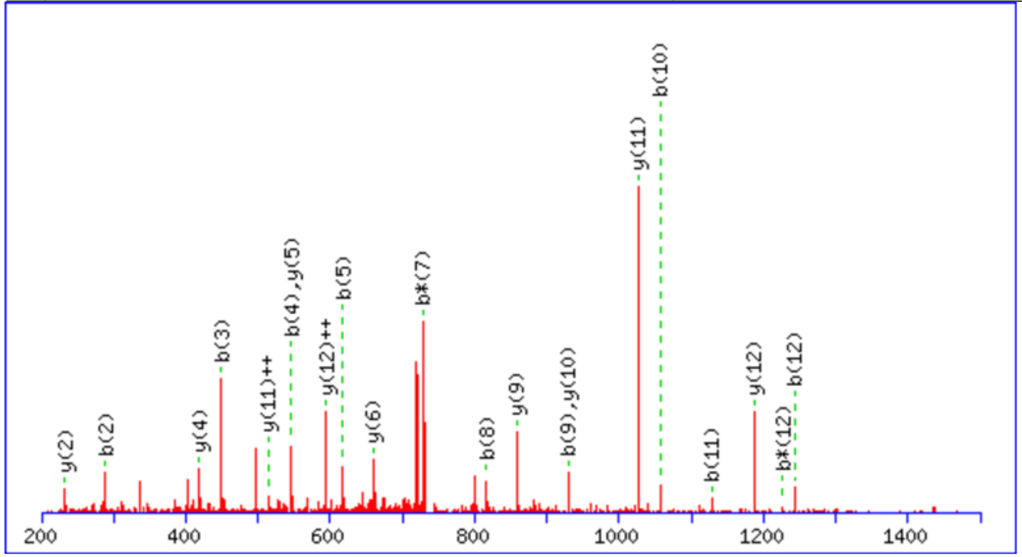
Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 04 - S_B-1 **Fraction:** S_B-1

Match to Query 8570: 1473.645448 from(737.830000,2+)
Title: OECHL100310_15.7378.7378.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00015**Matches :** 21/128 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	161.037925	81.022600					**C**							**14**
2	***289.096503***	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.809312	**13**
3	***449.127152***	225.067214	432.100603	216.553940			**C**	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.780023	**12**
4	***546.179916***	273.593596	529.153367	265.080322			**P**	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.764698	**11**

5	***617.217030***	309.112153	600.190481	300.598879			**A**	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.238316	**10**
6	674.238494	337.622885	657.211945	329.109611			**G**	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.719759	**9**
7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
8	***816.312722***	408.659999	799.286173	400.146725			**A**	730.384229	365.695753	713.357680	357.182478	712.373664	356.690470	**7**
9	***929.396786***	465.202031	912.370237	456.688757			**L**	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.171913	**6**
10	***1057.455364***	529.231320	1040.428815	520.718046			**Q**	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.629881	**5**
11	***1128.492478***	564.749877	1111.465929	556.236603			**A**	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.600592	**4**
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	347.167359	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
13	1300.540885	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	**232.140416**	116.573846	215.113867	108.060571			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



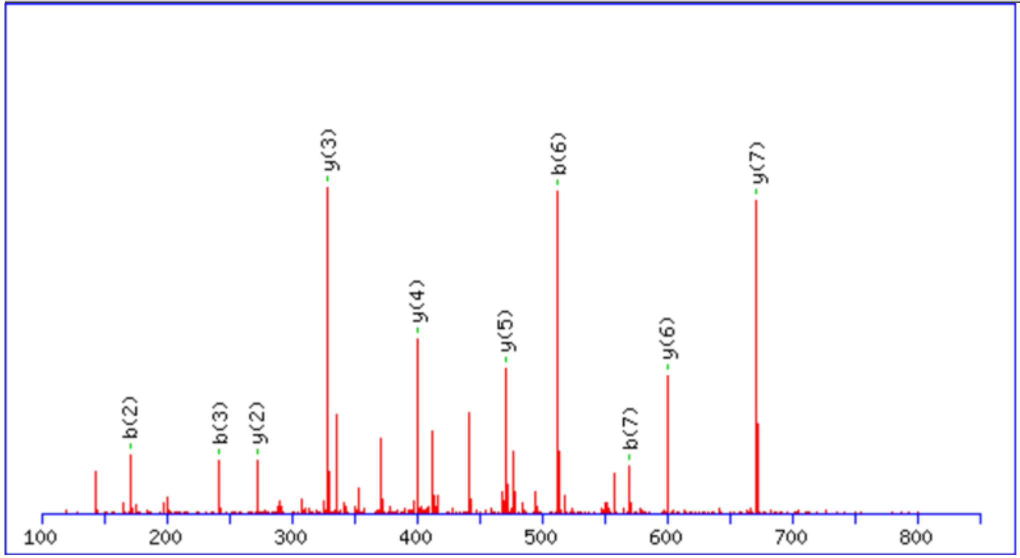
Peptide View

MS/MS Fragmentation of **GLAEAAGPR**
Found in **IPI00290826**, Tax_Id=9606 Gene_Symbol=FAM174A Membrane protein FAM174A
Experiment: 04 - S_B-1 **Fraction:** S_B-1

Match to Query 1156: 840.445448 from(421.230000,2+)

Title: OECHL100310_15.4353.4353.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 840.445343**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00056**Matches :** 10/64 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							9
2	**171.112804**	86.060040			L	784.431179	392.719228	767.404630	384.205953	766.420614	383.713945	8
3	**242.149918**	121.578597			A	***671.347115***	336.177196	654.320566	327.663921	653.336550	327.171913	7
4	371.192511	186.099894	353.181946	177.094611	E	***600.310001***	300.658639	583.283452	292.145364	582.299436	291.653356	6
5	442.229625	221.618450	424.219060	212.613168	A	***471.267408***	236.137342	454.240859	227.624067			5
6	**513.266739**	257.137008	495.256174	248.131725	A	***400.230294***	200.618785	383.203745	192.105510			4
7	**570.288203**	285.647740	552.277638	276.642457	G	***329.193180***	165.100228	312.166631	156.586953			3
8	667.340967	334.174122	649.330402	325.168839	P	***272.171716***	136.589496	255.145167	128.076221			2
9					R	175.118952	88.063114	158.092403	79.549839			1

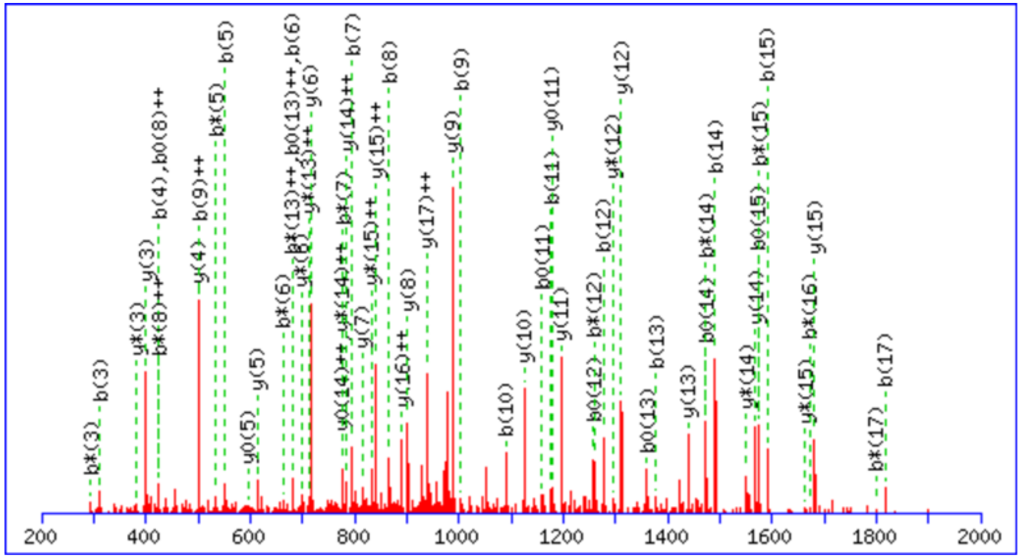


Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 26 - NOPD2 **Fraction:** NOPD2

Match to Query 14613: 1990.024248 from(996.019400,2+)
Title: OECHL100312_22.9987.9987.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_22.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 69
Expect: 1.7e-005**Matches :** 61/186 fragment ions using 128 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	***311.171381***	156.089328	294.144832	147.576054			**V**	1779.934789	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	***424.255445***	212.631361	407.228896	204.118086			**L**	**1680.866375**	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	***552.314023***	276.660650	535.287474	268.147375			**Q**	**1567.782311**	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	***680.372601***	340.689939	663.346052	332.176664			**Q**	**1439.723733**	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**
7	***795.399544***	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	**1311.665155**	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	***866.436658***	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	**1196.638212**	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	***1003.495570***	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	**1125.601098**	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	***1090.527598***	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	**988.542186**	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	***1177.559626***	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	**901.510158**	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	***1276.628040***	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	**814.478130**	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	***1377.675719***	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	**715.409716**	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	***1490.759783***	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	**614.362037**	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	***1591.807462***	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	**501.277973**	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	**400.230294**	200.618785	383.203745	192.105510			**3**
17	***1816.918804***	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**



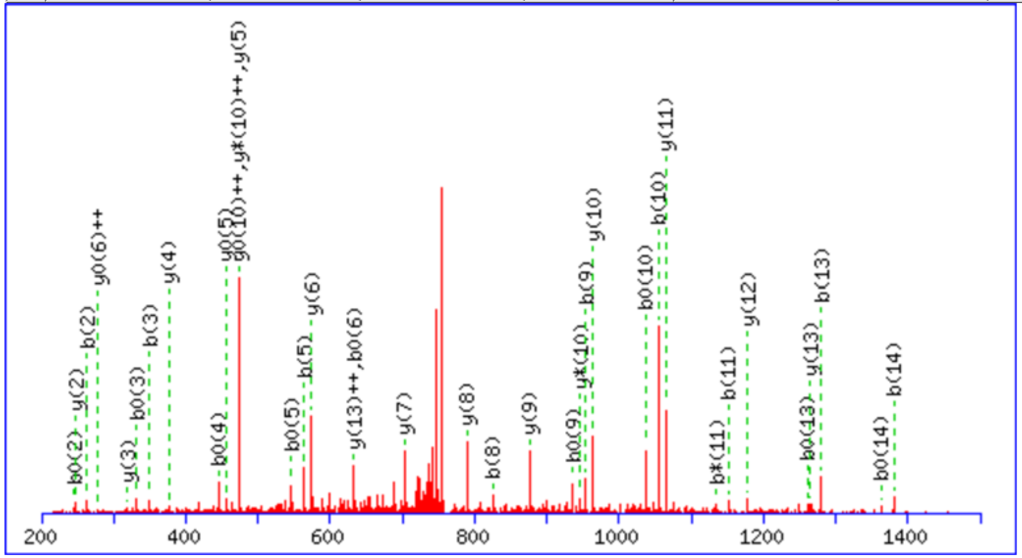
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 26 - NOPD2 **Fraction:** NOPD2

Match to Query 10836: 1525.726848 from(763.870700,2+)
Title: OECHL100312_22.10965.10965.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_22.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 84
Expect: 4.8e-007**Matches :** 37/150 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	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	**263.102633**	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	**350.134661**	175.570968			332.124096	166.565686	**S**	***1264.637937***	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	**564.266404**	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**

7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	**9**
8	**825.362488**	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.203410	**8**
9	**953.421066**	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	**7**
10	**1054.468745**	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	**6**
11	**1151.521509**	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	**5**
12	1208.542973	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	**4**
13	**1279.580087**	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	***319.197597***	160.102436	302.171048	151.589162	301.187032	151.097154	**3**
14	**1380.627766**	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



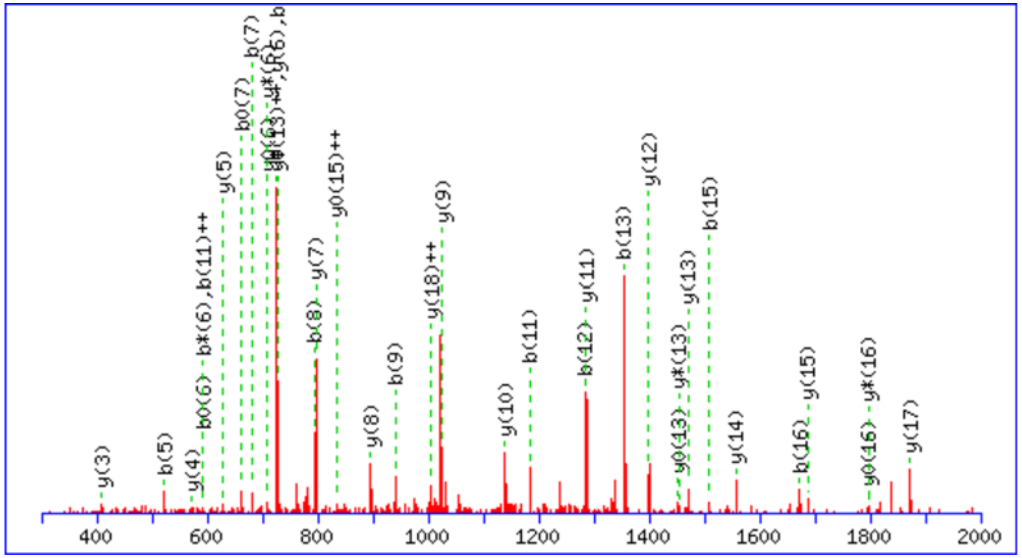
Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 26 - NOPD2 **Fraction:** NOPD2

Match to Query 15017: 2078.983448 from(1040.499000,2+)
Title: OECHL100312_22.17211.17211.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_22.raw

Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72
Expect: 1e-005**Matches :** 38/200 fragment ions using 84 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**19**
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973939	**18**
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444483	**17**
4	394.183344	197.595310	377.156795	189.082035			**Q**	1814.870790	907.939033	1797.844241	899.425759	1796.860225	898.933751	**16**
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904462	**15**
6	610.257965	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383165	**14**
7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867151	**13**
8	**794.379143**	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348594	**12**
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806562	**11**
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272355	**10**
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250892	**9**
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729595	**8**
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195388	**7**
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676831	**6**
15	**1508.712833**	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150449	**5**
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	***572.282723***	286.645000	555.256174	278.131725	554.272158	277.639717	**4**
17	1818.844576	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	**3**
18	1905.876604	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
19							**R**	175.118952	88.063114	158.092403	79.549840			**1**



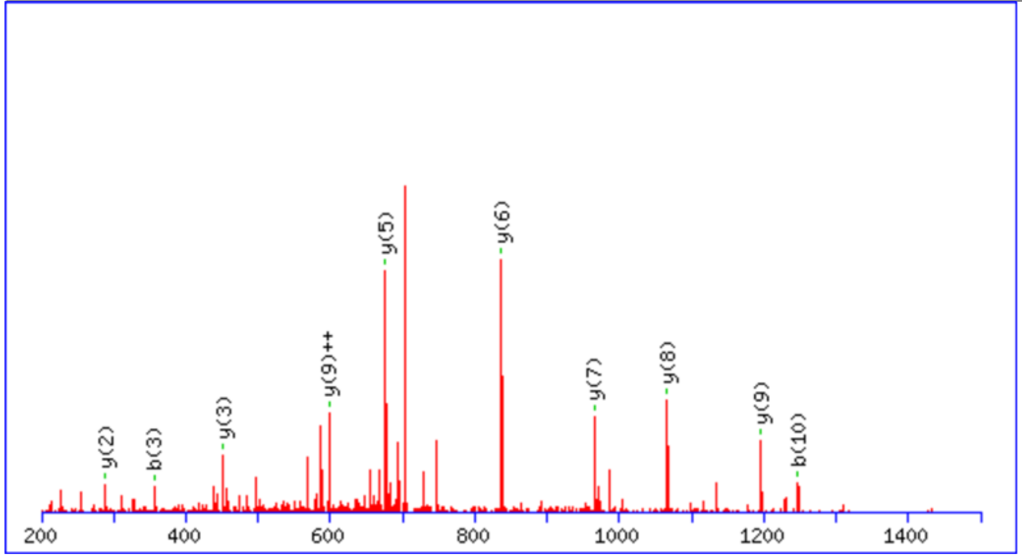
Peptide View

MS/MS Fragmentation of **LLETECPQYIR**
Found in **IPI00007047**, Tax_Id=9606 Gene_Symbol=S100A8 Protein S100-A8
Experiment: 26 - NOPD2 **Fraction:** NOPD2

Match to Query 9650: 1420.702048 from(711.358300,2+)
Title: OECHL100312_22.12622.12622.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_22.raw
Monoisotopic mass of neutral peptide Mr(calc): 1420.702026**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 9.3e-005**Matches :** 10/90 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	114.091340	57.549308					**L**							**11**
2	227.175404	114.091340					**L**	1308.625265	654.816271	1291.598716	646.302996	1290.614700	645.810988	**10**
3	**356.217997**	178.612637			338.207432	169.607354	**E**	***1195.541201***	598.274239	1178.514652	589.760964	1177.530636	589.268956	**9**
4	457.265676	229.136476			439.255111	220.131194	**T**	***1066.498608***	533.752942	1049.472059	525.239668	1048.488043	524.747660	**8**
5	586.308269	293.657773			568.297704	284.652490	**E**	***965.450929***	483.229103	948.424380	474.715828	947.440364	474.223820	**7**
6	746.338918	373.673097			728.328353	364.667815	**C**	***836.408336***	418.707806	819.381787	410.194531			**6**

7	843.391682	422.199479			825.381117	413.194197	**P**	***676.377687***	338.692481	659.351138	330.179207			**5**
8	971.450260	486.228768	954.423711	477.715494	953.439695	477.223486	**Q**	579.324923	290.166099	562.298374	281.652825			**4**
9	1134.513589	567.760433	1117.487040	559.247158	1116.503024	558.755150	**Y**	***451.266345***	226.136810	434.239796	217.623536			**3**
10	**1247.597653**	624.302465	1230.571104	615.789190	1229.587088	615.297182	**I**	***288.203016***	144.605146	271.176467	136.091871			**2**
11							**R**	175.118952	88.063114	158.092403	79.549839			**1**



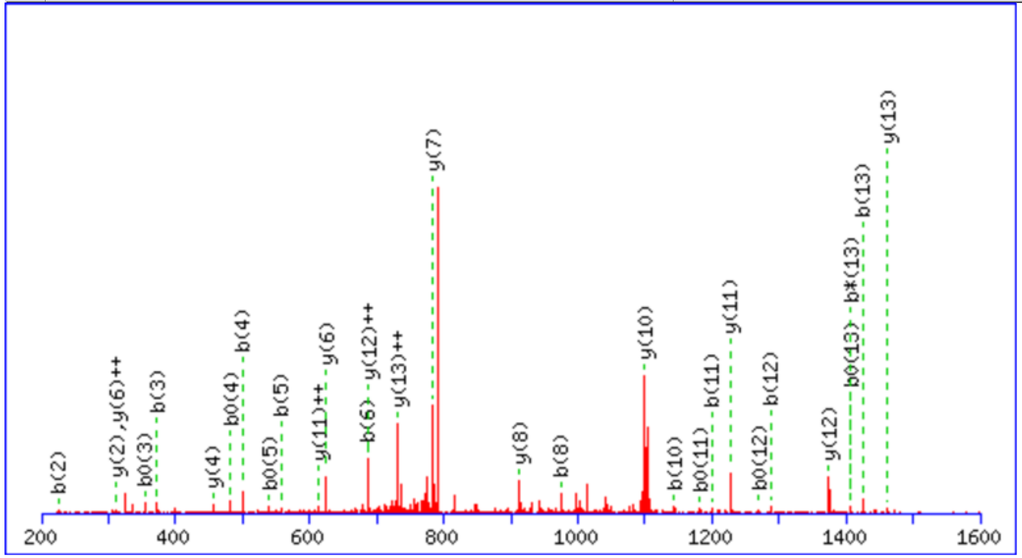
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 26 - NOPD2 **Fraction:** NOPD2

Match to Query 11608: 1597.705648 from(799.860100,2+)
Title: OECHL100312_22.2375.2375.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_22.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64
Expect: 2.5e-005**Matches :** 30/144 fragment ions using 55 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	138.066188	69.536732					**H**							**14**

2	***225.098216***	113.052746			207.087651	104.047463	**S**	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.325325	**13**
3	***372.166630***	186.586953			354.156065	177.581671	**F**	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.809311	**12**
4	***500.261593***	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	**11**
5	***557.283057***	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	**10**
6	***686.325650***	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	1042.437069	521.722173	1025.410520	513.208898	1024.426504	512.716890	**9**
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	***975.398892***	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	***1143.488770***	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	527.268470	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	***1200.510234***	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	***1287.542262***	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	399.209892	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	***1424.601174***	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	***312.177864***	156.592570	295.151315	148.079295			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



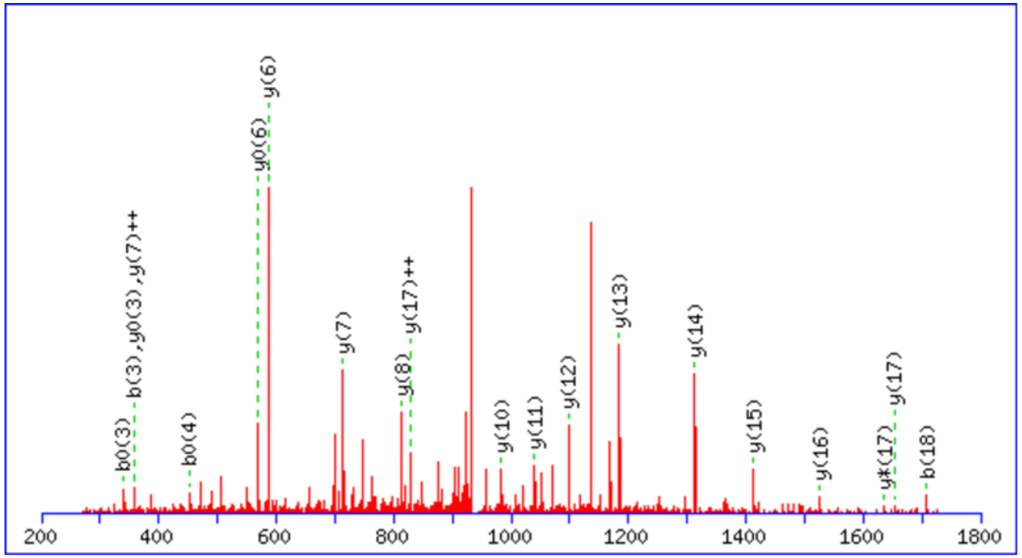
Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**

Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
Experiment: 26 - NOPD2 **Fraction:** NOPD2

Match to Query 14016: 1881.032648 from(941.523600,2+)
Title: OECHL100312_22.14159.14159.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_22.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 76
Expect: 1.3e-006**Matches :** 20/208 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	130.049869	65.528572			112.039304	56.523290	E							19
2	229.118283	115.062780			211.107718	106.057497	V	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.996686	18
3	**357.176861**	179.092069	340.150312	170.578794	339.166296	170.086786	Q	***1653.928246***	827.467761	1636.901697	818.954487	1635.917681	818.462479	17
4	470.260925	235.634101	453.234376	227.120826	452.250360	226.628818	L	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.433190	16
5	569.329339	285.168308	552.302790	276.655033	551.318774	276.163025	V	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.891158	15
6	698.371932	349.689604	681.345383	341.176330	680.361367	340.684322	E	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.356951	14
7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	S	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.835654	13
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	G	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.319640	12
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	G	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.808908	11
10	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	G	***983.599641***	492.303459	966.573092	483.790184	965.589076	483.298176	10
11	1069.552416	535.279846	1052.525867	526.766572	1051.541851	526.274564	L	926.578177	463.792727	909.551628	455.279452	908.567612	454.787444	9
12	1168.620830	584.814053	1151.594281	576.300779	1150.610265	575.808771	V	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.245412	8
13	1296.715793	648.861535	1279.689244	640.348260	1278.705228	639.856252	K	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.711205	7
14	1393.768557	697.387917	1376.742008	688.874642	1375.757992	688.382634	P	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.663723	6
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	G	489.277972	245.142624	472.251423	236.629349	471.267407	236.137341	5
16	1507.811485	754.409381	1490.784936	745.896106	1489.800920	745.404098	G	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	4
17	1594.843513	797.925395	1577.816964	789.412120	1576.832948	788.920112	S	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
18	**1707.927577**	854.467427	1690.901028	845.954152	1689.917012	845.462144	L	288.203016	144.605146	271.176467	136.091871			2
19							R	175.118952	88.063114	158.092403	79.549839			1



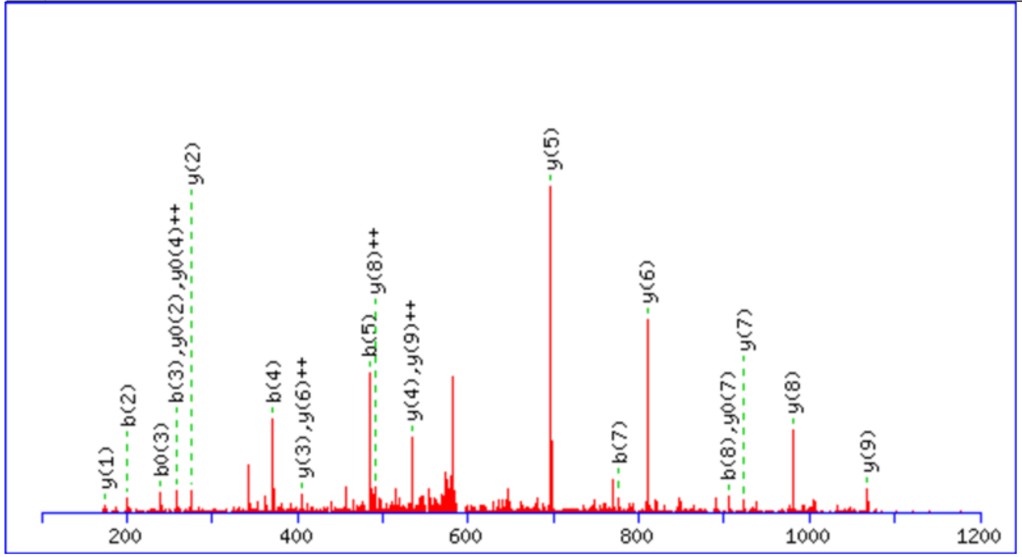
Peptide View

MS/MS Fragmentation of **ISGLIYEETR**
Found in **IPI00453473**, Tax_Id=9606 Gene_Symbol=HIST1H4K;HIST1H4D;HIST4H4;HIST1H4F;HIST1H4E;HIST1H4J;HIST2H4A;HIST1H4B;HIST1H4I;HIST1H4A;HIST1H4L;HIST1H4H;HIST1H4C;HIST2H4B Histone H4
Experiment: 26 - NOPD2 **Fraction:** NOPD2

Match to Query 6340: 1179.615248 from(590.814900,2+)
Title: OECHL100312_22.13004.13004.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_22.raw
Monoisotopic mass of neutral peptide Mr(calc): 1179.613525**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 5.1e-005**Matches :** 22/86 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**I**							**10**
2	**201.123368**	101.065322	183.112803	92.060039	**S**	***1067.536766***	534.272021	1050.510217	525.758747	1049.526201	525.266739	**9**
3	**258.144832**	129.576054	240.134267	120.570771	**G**	***980.504738***	490.756007	963.478189	482.242733	962.494173	481.750725	**8**
4	**371.228896**	186.118086	353.218331	177.112803	**L**	***923.483274***	462.245275	906.456725	453.732001	905.472709	453.239993	**7**
5	**484.312960**	242.660118	466.302395	233.654835	**I**	***810.399210***	405.703243	793.372661	397.189969	792.388645	396.697961	**6**

6	647.376289	324.191783	629.365724	315.186500	**Y**	***697.315146***	349.161211	680.288597	340.647937	679.304581	340.155929	**5**
7	**776.418882**	388.713079	758.408317	379.707797	**E**	***534.251817***	267.629547	517.225268	259.116272	516.241252	258.624264	**4**
8	**905.461475**	453.234376	887.450910	444.229093	**E**	***405.209224***	203.108250	388.182675	194.594975	387.198659	194.102967	**3**
9	1006.509154	503.758215	988.498589	494.752933	**T**	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	**2**
10					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



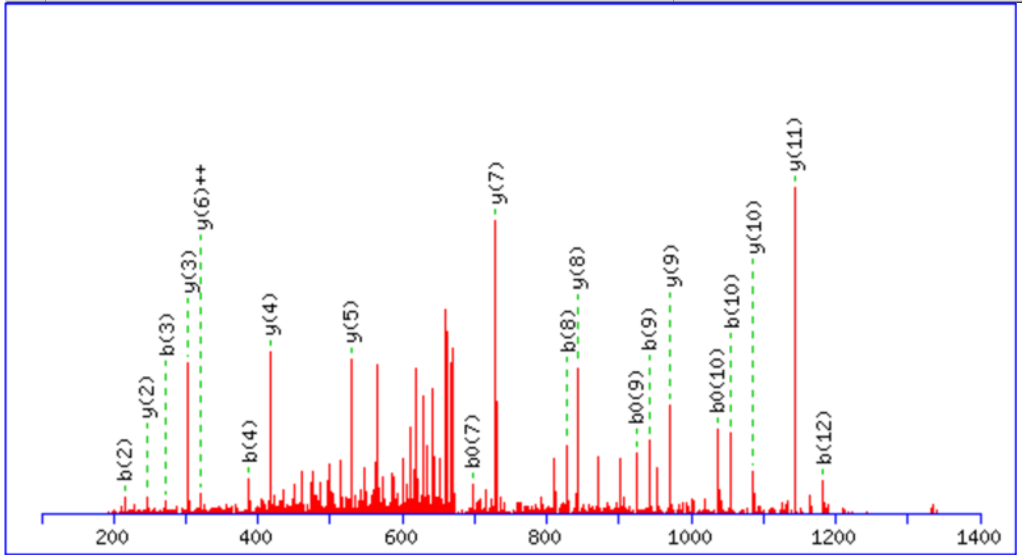
Peptide View

MS/MS Fragmentation of **TLGDQLSLLLGAR**
Found in **IPI00005707**, Tax_Id=9606 Gene_Symbol=MRC2 C-type mannose receptor 2
Experiment: 26 - NOPD2 **Fraction:** NOPD2

Match to Query 8956: 1355.778448 from(678.896500,2+)
Title: OECHL100312_22.20007.20007.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_22.raw
Monoisotopic mass of neutral peptide Mr(calc): 1355.777252**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64
Expect: 1.6e-005**Matches :** 20/124 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	**T**							**13**

2	**215.139019**	108.073147			197.128454	99.067865	**L**	1255.736863	628.372069	1238.710314	619.858795	1237.726298	619.366787	**12**
3	**272.160483**	136.583879			254.149918	127.578597	**G**	***1142.652799***	571.830038	1125.626250	563.316763	1124.642234	562.824755	**11**
4	**387.187426**	194.097351			369.176861	185.092069	**D**	***1085.631335***	543.319305	1068.604786	534.806031	1067.620770	534.314023	**10**
5	515.246004	258.126640	498.219455	249.613366	497.235439	249.121358	**Q**	***970.604392***	485.805834	953.577843	477.292559	952.593827	476.800551	**9**
6	628.330068	314.668672	611.303519	306.155398	610.319503	305.663390	**L**	***842.545814***	421.776545	825.519265	413.263270	824.535249	412.771262	**8**
7	715.362096	358.184686	698.335547	349.671412	697.351531	349.179404	**S**	***729.461750***	365.234513	712.435201	356.721238	711.451185	356.229230	**7**
8	**828.446160**	414.726718	811.419611	406.213444	810.435595	405.721436	**L**	642.429722	321.718499	625.403173	313.205224			**6**
9	**941.530224**	471.268750	924.503675	462.755476	923.519659	462.263468	**L**	***529.345658***	265.176467	512.319109	256.663192			**5**
10	**1054.614288**	527.810782	1037.587739	519.297508	1036.603723	518.805500	**L**	***416.261594***	208.634435	399.235045	200.121160			**4**
11	1111.635752	556.321514	1094.609203	547.808240	1093.625187	547.316231	**G**	***303.177530***	152.092403	286.150981	143.579128			**3**
12	**1182.672866**	591.840071	1165.646317	583.326797	1164.662301	582.834788	**A**	***246.156066***	123.581671	229.129517	115.068396			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

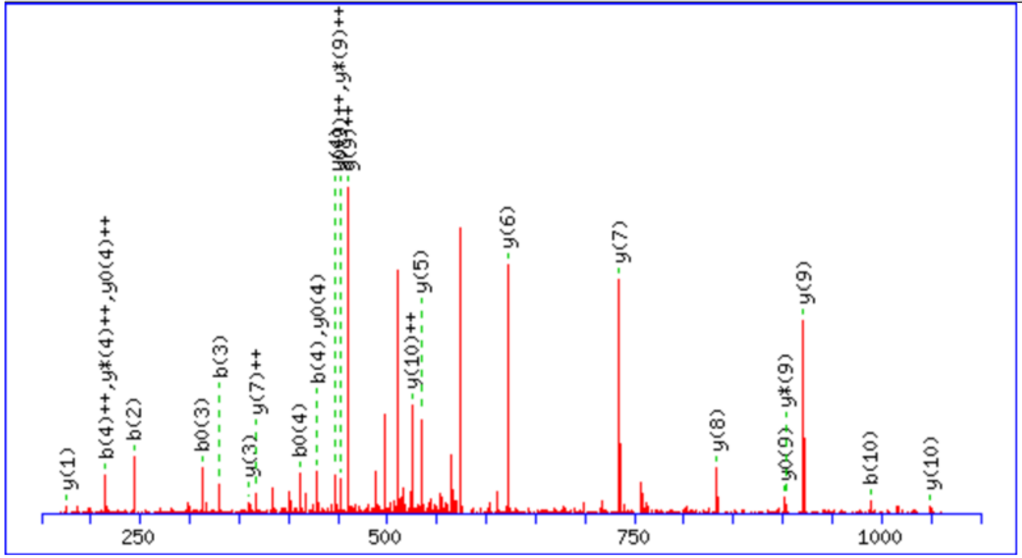


Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 26 - NOPD2 **Fraction:** NOPD2

Match to Query 6034: 1161.636648 from(581.825600,2+)
Title: OECHL100312_22.5587.5587.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_22.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62
Expect: 3.9e-005**Matches :** 26/94 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	114.091340	57.549308					**I**							**11**
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637	**10**
3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340	**9**
4	**429.234375**	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326	**8**
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119	**7**
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087	**6**
7	716.382495	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073	**5**
8	803.414523	402.210899			785.403958	393.205617	**S**	***447.267407***	224.137342	430.240858	215.624067	429.256842	215.132059	**4**
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053			**3**
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**

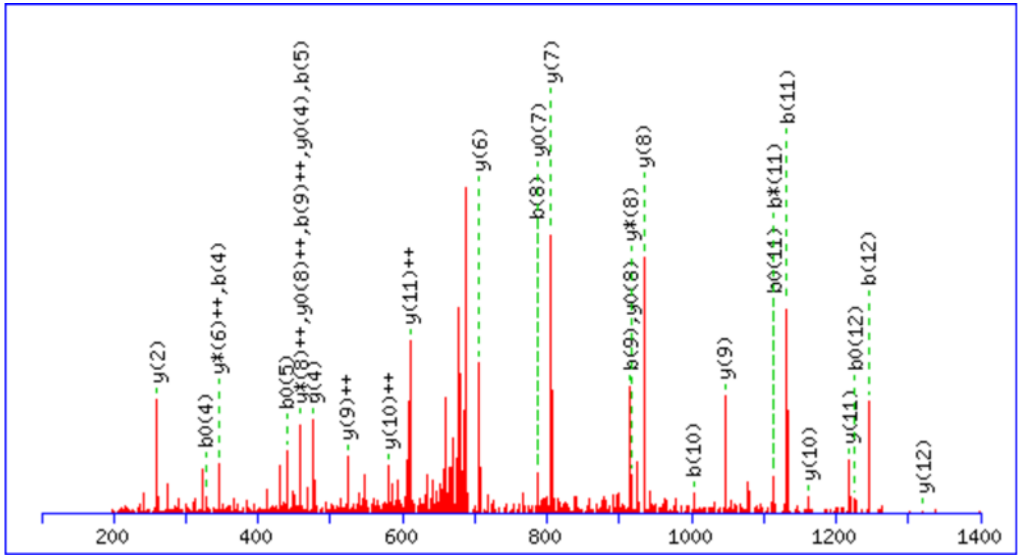


Peptide View

MS/MS Fragmentation of **ATGDIKVTESEIK**
Found in **IPI00302614**, Tax_Id=9606 Gene_Symbol=VTCN1 V-set domain containing T cell activation inhibitor 1
Experiment: 26 - NOPD2 **Fraction:** NOPD2

Match to Query 9353: 1389.735248 from(695.874900,2+)
Title: OECHL100312_22.8363.8363.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_22.raw
Monoisotopic mass of neutral peptide Mr(calc): 1389.735107**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57
Expect: 0.00024**Matches :** 32/128 fragment ions using 58 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					**A**							**13**
2	173.092069	87.049672			155.081504	78.044390	**T**	***1319.705288***	660.356282	1302.678739	651.843008	1301.694723	651.350999	**12**
3	230.113533	115.560404			212.102968	106.555122	**G**	***1218.657609***	609.832442	1201.631060	601.319168	1200.647044	600.827160	**11**
4	***345.140476***	173.073876			327.129911	164.068593	**D**	***1161.636145***	581.321710	1144.609596	572.808436	1143.625580	572.316428	**10**
5	***458.224540***	229.615908			440.213975	220.610626	**I**	***1046.609202***	523.808239	1029.582653	515.294964	1028.598637	514.802956	**9**
6	586.319503	293.663390	569.292954	285.150115	568.308938	284.658107	**K**	***933.525138***	467.266207	916.498589	458.752932	915.514573	458.260924	**8**
7	685.387917	343.197597	668.361368	334.684322	667.377352	334.192314	**V**	***805.430175***	403.218725	788.403626	394.705451	787.419610	394.213443	**7**
8	***786.435596***	393.721436	769.409047	385.208162	768.425031	384.716154	**T**	***706.361761***	353.684518	689.335212	345.171244	688.351196	344.679236	**6**
9	***915.478189***	458.242733	898.451640	449.729458	897.467624	449.237450	**E**	605.314082	303.160679	588.287533	294.647404	587.303517	294.155396	**5**
10	***1002.510217***	501.758747	985.483668	493.245472	984.499652	492.753464	**S**	***476.271489***	238.639382	459.244940	230.126108	458.260924	229.634100	**4**
11	***1131.552810***	566.280043	1114.526261	557.766769	1113.542245	557.274760	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
12	***1244.636874***	622.822075	1227.610325	614.308800	1226.626309	613.816792	**I**	***260.196868***	130.602072	243.170319	122.088797			**2**
13							**K**	147.112804	74.060040	130.086255	65.546765			**1**



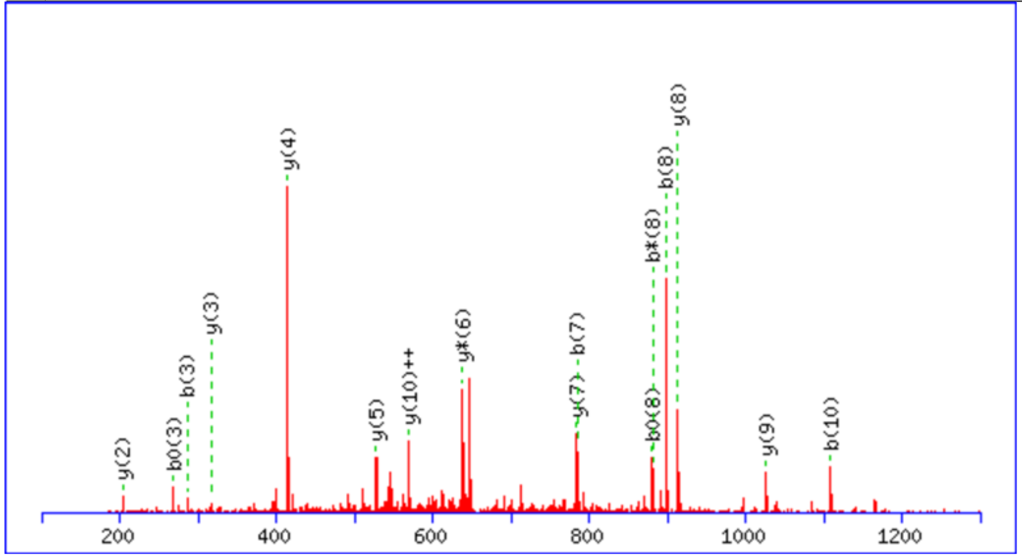
Peptide View

MS/MS Fragmentation of **ATLLEEQLPLGK**
Found in **IPI00414542**, Tax_Id=9606 Gene_Symbol=PDCD1LG2 Isoform 1 of Programmed cell death 1 ligand 2
Experiment: 26 - NOPD2 **Fraction:** NOPD2

Match to Query 8427: 1310.744648 from(656.379600,2+)
Title: OECHL100312_22.17080.17080.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_22.raw
Monoisotopic mass of neutral peptide Mr(calc): 1310.744537**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00028**Matches :** 16/106 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	72.044390	36.525833					**A**							**12**
2	173.092069	87.049672			155.081504	78.044390	**T**	1240.714731	620.861004	1223.688182	612.347729	1222.704166	611.855721	**11**
3	**286.176133**	143.591704			268.165568	134.586422	**L**	1139.667052	570.337164	1122.640503	561.823890	1121.656487	561.331882	**10**
4	399.260197	200.133737			381.249632	191.128454	**L**	***1026.582988***	513.795132	1009.556439	505.281858	1008.572423	504.789850	**9**
5	528.302790	264.655033			510.292225	255.649751	**E**	***913.498924***	457.253100	896.472375	448.739825	895.488359	448.247818	**8**
6	657.345383	329.176330			639.334818	320.171047	**E**	***784.456331***	392.731804	767.429782	384.218529	766.445766	383.726521	**7**

7	**785.403961**	393.205619	768.377412	384.692344	767.393396	384.200336	**Q**	655.413738	328.210507	638.387189	319.697232			**6**
8	**898.488025**	449.747651	881.461476	441.234376	880.477460	440.742368	**L**	***527.355160***	264.181218	510.328611	255.667943			**5**
9	995.540789	498.274033	978.514240	489.760758	977.530224	489.268750	**P**	***414.271096***	207.639186	397.244547	199.125911			**4**
10	**1108.624853**	554.816065	1091.598304	546.302790	1090.614288	545.810782	**L**	***317.218332***	159.112804	300.191783	150.599529			**3**
11	1165.646317	583.326797	1148.619768	574.813522	1147.635752	574.321514	**G**	***204.134268***	102.570772	187.107719	94.057497			**2**
12							**K**	147.112804	74.060040	130.086255	65.546765			**1**



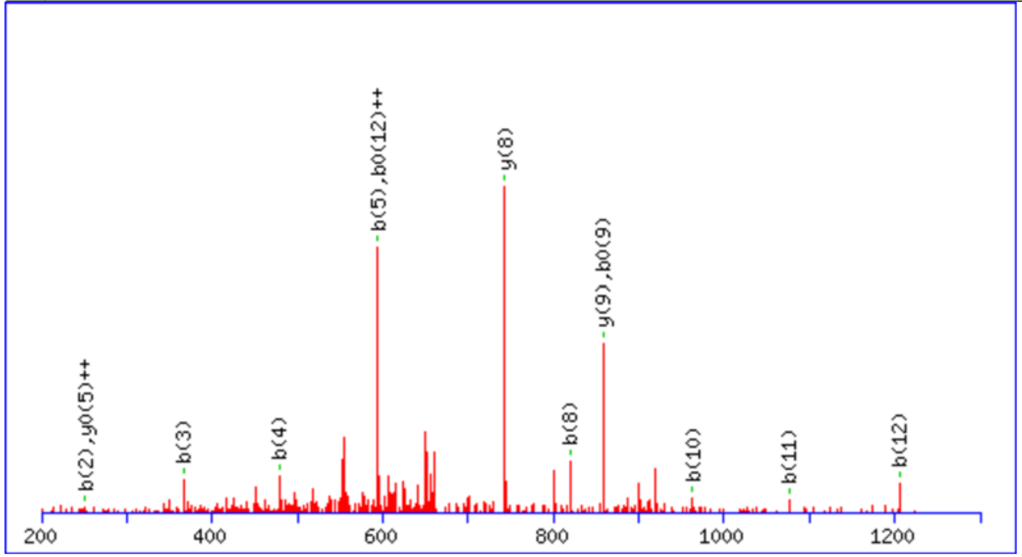
Peptide View

MS/MS Fragmentation of **SYDLDPGAGSLEI**
Found in **IPI00299435**, Tax_Id=9606 Gene_Symbol=APOF apolipoprotein F precursor
Experiment: 26 - NOPD2 **Fraction:** NOPD2

Match to Query 8717: 1335.620648 from(668.817600,2+)
Title: OECHL100312_22.18439.18439.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_22.raw
Monoisotopic mass of neutral peptide Mr(calc): 1335.619415**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00071**Matches :** 13/94 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#

1	88.039304	44.523290	70.028739	35.518008	**S**					**13**
2	***251.102633***	126.054954	233.092068	117.049672	**Y**	1249.594675	625.300975	1231.584110	616.295693	**12**
3	***366.129576***	183.568426	348.119011	174.563144	**D**	1086.531346	543.769311	1068.520781	534.764028	**11**
4	***479.213640***	240.110458	461.203075	231.105176	**L**	971.504403	486.255839	953.493838	477.250557	**10**
5	***594.240583***	297.623930	576.230018	288.618647	**D**	**858.420339**	429.713807	840.409774	420.708525	**9**
6	691.293347	346.150312	673.282782	337.145029	**P**	**743.393396**	372.200336	725.382831	363.195053	**8**
7	748.314811	374.661044	730.304246	365.655761	**G**	646.340632	323.673954	628.330067	314.668671	**7**
8	***819.351925***	410.179601	801.341360	401.174318	**A**	589.319168	295.163222	571.308603	286.157939	**6**
9	876.373389	438.690333	858.362824	429.685050	**G**	518.282054	259.644665	500.271489	250.639382	**5**
10	***963.405417***	482.206347	945.394852	473.201064	**S**	461.260590	231.133933	443.250025	222.128650	**4**
11	***1076.489481***	538.748379	1058.478916	529.743096	**L**	374.228562	187.617919	356.217997	178.612636	**3**
12	***1205.532074***	603.269675	1187.521509	594.264392	**E**	261.144498	131.075887	243.133933	122.070604	**2**
13					**I**	132.101905	66.554590			**1**



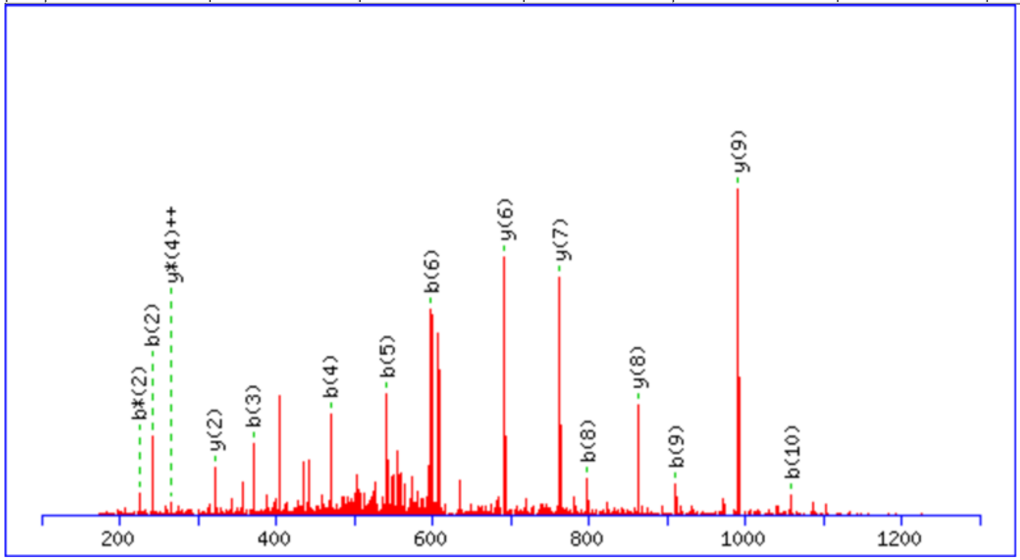
Peptide View

MS/MS Fragmentation of **IQEVAGSLIFR**

Found in **IPI00006988**, Tax_Id=9606 Gene_Symbol=RETN Resistin
Experiment: 26 - NOPD2 **Fraction:** NOPD2

Match to Query 7270: 1231.693448 from(616.854000,2+)
Title: OECHL100312_22.17087.17087.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_22.raw
Monoisotopic mass of neutral peptide Mr(calc): 1231.692459**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49
Expect: 0.00057**Matches :** 15/106 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	114.091340	57.549308					**I**							**11**
2	***242.149918***	121.578597	225.123369	113.065323			**Q**	1119.615685	560.311481	1102.589136	551.798206	1101.605120	551.306198	**10**
3	***371.192511***	186.099894	354.165962	177.586619	353.181946	177.094611	**E**	**991.557107**	496.282192	974.530558	487.768917	973.546542	487.276909	**9**
4	***470.260925***	235.634101	453.234376	227.120826	452.250360	226.628818	**V**	**862.514514**	431.760895	845.487965	423.247621	844.503949	422.755613	**8**
5	***541.298039***	271.152658	524.271490	262.639383	523.287474	262.147375	**A**	**763.446100**	382.226688	746.419551	373.713414	745.435535	373.221406	**7**
6	***598.319503***	299.663390	581.292954	291.150115	580.308938	290.658107	**G**	**692.408986**	346.708131	675.382437	338.194857	674.398421	337.702849	**6**
7	685.351531	343.179404	668.324982	334.666129	667.340966	334.174121	**S**	635.387522	318.197399	618.360973	309.684125	617.376957	309.192117	**5**
8	***798.435595***	399.721436	781.409046	391.208161	780.425030	390.716153	**L**	548.355494	274.681385	531.328945	266.168111			**4**
9	***911.519659***	456.263468	894.493110	447.750193	893.509094	447.258185	**I**	435.271430	218.139353	418.244881	209.626078			**3**
10	***1058.588073***	529.797675	1041.561524	521.284400	1040.577508	520.792392	**F**	**322.187366**	161.597321	305.160817	153.084046			**2**
11							**R**	175.118952	88.063114	158.092403	79.549839			**1**

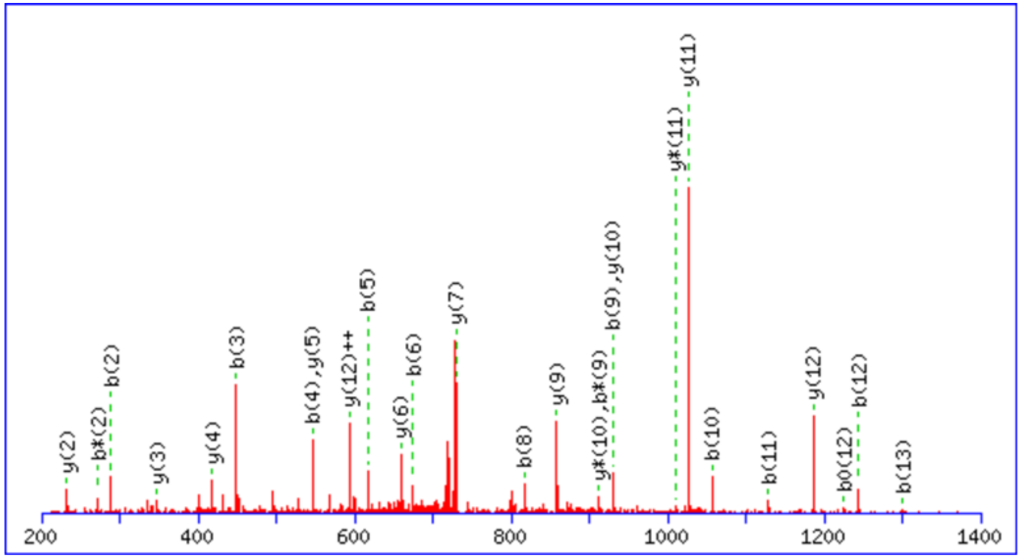


Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: S_B-2 **Fraction:** S_B-2

Match to Query 10302: 1473.645648 from(737.830100,2+)
Title: OECHL100312_19.9139.9139.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 76
Expect: 1.3e-006**Matches :** 27/128 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	161.037925	81.022600					**C**							**14**
2	***289.096503***	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.809312	**13**
3	***449.127152***	225.067214	432.100603	216.553940			**C**	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.780023	**12**
4	***546.179916***	273.593596	529.153367	265.080322			**P**	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.764698	**11**
5	***617.217030***	309.112153	600.190481	300.598879			**A**	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.238316	**10**
6	***674.238494***	337.622885	657.211945	329.109611			**G**	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.719759	**9**
7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
8	***816.312722***	408.659999	799.286173	400.146725			**A**	**730.384229**	365.695753	713.357680	357.182478	712.373664	356.690470	**7**
9	***929.396786***	465.202031	912.370237	456.688757			**L**	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.171913	**6**
10	***1057.455364***	529.231320	1040.428815	520.718046			**Q**	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.629881	**5**
11	***1128.492478***	564.749877	1111.465929	556.236603			**A**	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.600592	**4**
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	**347.167359**	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
13	***1300.540885***	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	**232.140416**	116.573846	215.113867	108.060571			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



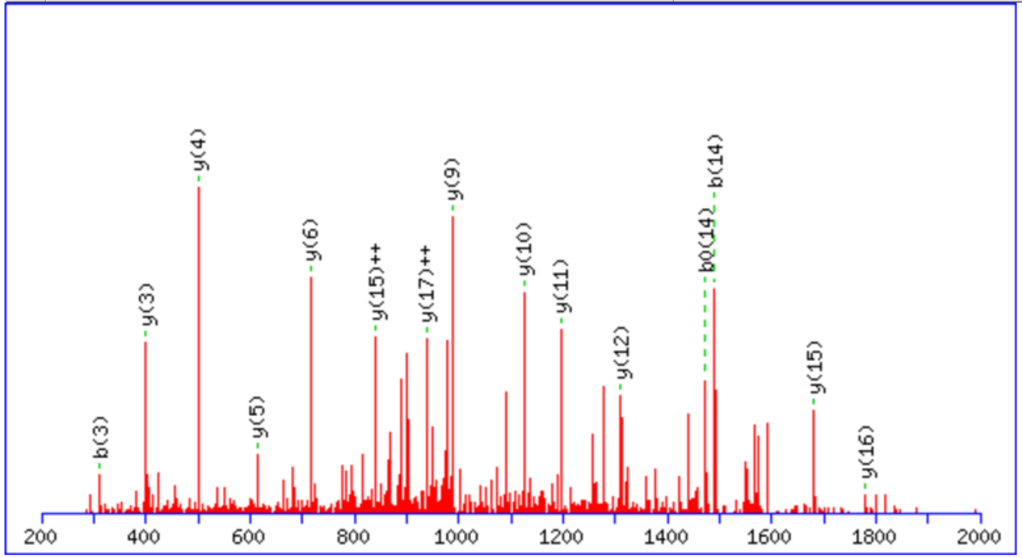
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: S_B-2 **Fraction:** S_B-2

Match to Query 14570: 1990.026048 from(996.020300,2+)
Title: OECHL100312_19.11409.11409.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 95
Expect: 3.7e-008**Matches :** 15/186 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	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	424.255445	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	552.314023	276.660650	535.287474	268.147375			**Q**	1567.782311	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	680.372601	340.689939	663.346052	332.176664			**Q**	1439.723733	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**

7	795.399544	398.203410	778.372995	389.690136	777.388979	389.198128	D	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	12
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	A	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	11
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	H	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	10
10	1090.527598	545.767437	1073.501049	537.254163	1072.517033	536.762155	S	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	9
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	S	901.510158	451.258717	884.483609	442.745443	883.499593	442.253435	8
12	1276.628040	638.817658	1259.601491	630.304384	1258.617475	629.812376	V	814.478130	407.742703	797.451581	399.229428	796.467565	398.737420	7
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	T	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	6
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	I	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	5
15	1591.807462	796.407369	1574.780913	787.894095	1573.796897	787.402087	T	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	4
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	P	***400.230294***	200.618785	383.203745	192.105510			3
17	1816.918804	908.963040	1799.892255	900.449766	1798.908239	899.957758	Q	303.177530	152.092403	286.150981	143.579128			2
18							R	175.118952	88.063114	158.092403	79.549839			1

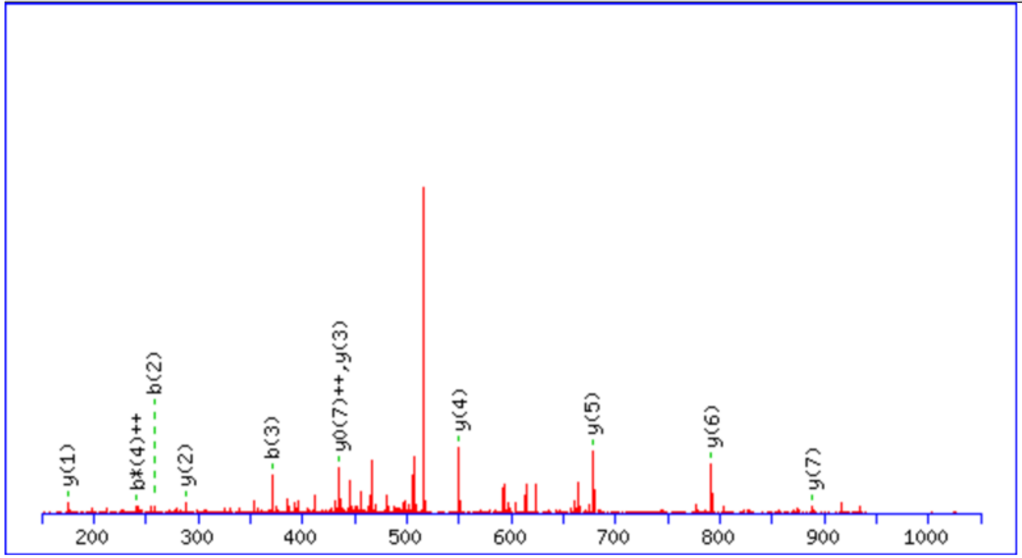


Peptide View

MS/MS Fragmentation of **CPLQDFLR**
Found in **IPI00003807**, Tax_Id=9606 Gene_Symbol=ACP2 Lysosomal acid phosphatase
Experiment: S_B-2 **Fraction:** S_B-2

Match to Query 4655: 1047.516848 from(524.765700,2+)
Title: OECHL100312_19.17455.17455.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1047.517151**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53
Expect: 0.00046**Matches :** 11/64 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	161.037925	81.022600					C							8
2	**258.090689**	129.548982					P	***888.493779***	444.750528	871.467230	436.237253	870.483214	435.745245	7
3	**371.174753**	186.091015					L	***791.441015***	396.224146	774.414466	387.710871	773.430450	387.218863	6
4	499.233331	250.120304	482.206782	241.607029			Q	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	5
5	614.260274	307.633775	597.233725	299.120501	596.249709	298.628493	D	***550.298373***	275.652825	533.271824	267.139550	532.287808	266.647542	4
6	761.328688	381.167982	744.302139	372.654708	743.318123	372.162700	F	***435.271430***	218.139353	418.244881	209.626079			3
7	874.412752	437.710014	857.386203	429.196740	856.402187	428.704732	L	***288.203016***	144.605146	271.176467	136.091872			2
8							R	***175.118952***	88.063114	158.092403	79.549840			1



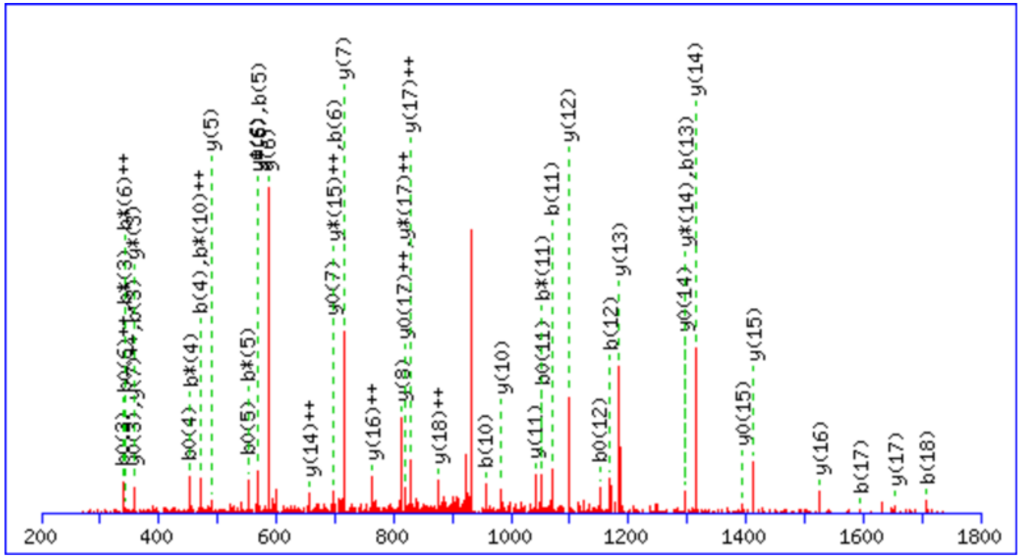
Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**

Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
Experiment: S_B-2 **Fraction:** S_B-2

Match to Query 13925: 1881.032048 from(941.523300,2+)
Title: OECHL100312_19.14400.14400.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 1.2e-006**Matches :** 50/208 fragment ions using 75 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	**E**							**19**
2	229.118283	115.062780			211.107718	106.057497	**V**	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.996686	**18**
3	***357.176861***	179.092069	340.150312	170.578794	339.166296	170.086786	**Q**	***1653.928246***	827.467761	1636.901697	818.954487	1635.917681	818.462479	**17**
4	***470.260925***	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.433190	**16**
5	***569.329339***	285.168308	552.302790	276.655033	551.318774	276.163025	**V**	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.891158	**15**
6	***698.371932***	349.689604	681.345383	341.176330	680.361367	340.684322	**E**	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.356951	**14**
7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	**S**	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.835654	**13**
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	**G**	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.319640	**12**
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	**G**	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.808908	**11**
10	***956.468352***	478.737814	939.441803	470.224540	938.457787	469.732532	**G**	***983.599641***	492.303459	966.573092	483.790184	965.589076	483.298176	**10**
11	***1069.552416***	535.279846	1052.525867	526.766572	1051.541851	526.274564	**L**	926.578177	463.792727	909.551628	455.279452	908.567612	454.787444	**9**
12	***1168.620830***	584.814053	1151.594281	576.300779	1150.610265	575.808771	**V**	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.245412	**8**
13	***1296.715793***	648.861535	1279.689244	640.348260	1278.705228	639.856252	**K**	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.711205	**7**
14	1393.768557	697.387917	1376.742008	688.874642	1375.757992	688.382634	**P**	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.663723	**6**
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	**G**	***489.277972***	245.142624	472.251423	236.629349	471.267407	236.137341	**5**
16	1507.811485	754.409381	1490.784936	745.896106	1489.800920	745.404098	**G**	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	**4**
17	***1594.843513***	797.925395	1577.816964	789.412120	1576.832948	788.920112	**S**	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	**3**
18	***1707.927577***	854.467427	1690.901028	845.954152	1689.917012	845.462144	**L**	288.203016	144.605146	271.176467	136.091871			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



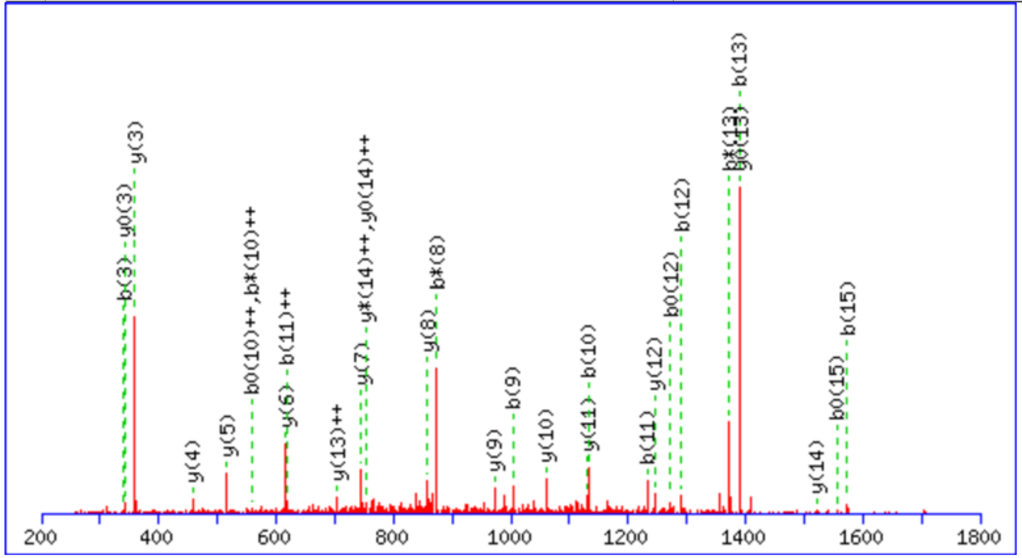
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: S_B-2 **Fraction:** S_B-2

Match to Query 12801: 1746.917048 from(874.465800,2+)
Title: OECHL100312_19.17548.17548.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 81
Expect: 9e-007**Matches :** 30/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	**340.259468**	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	618.349740	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	689.386854	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**

7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



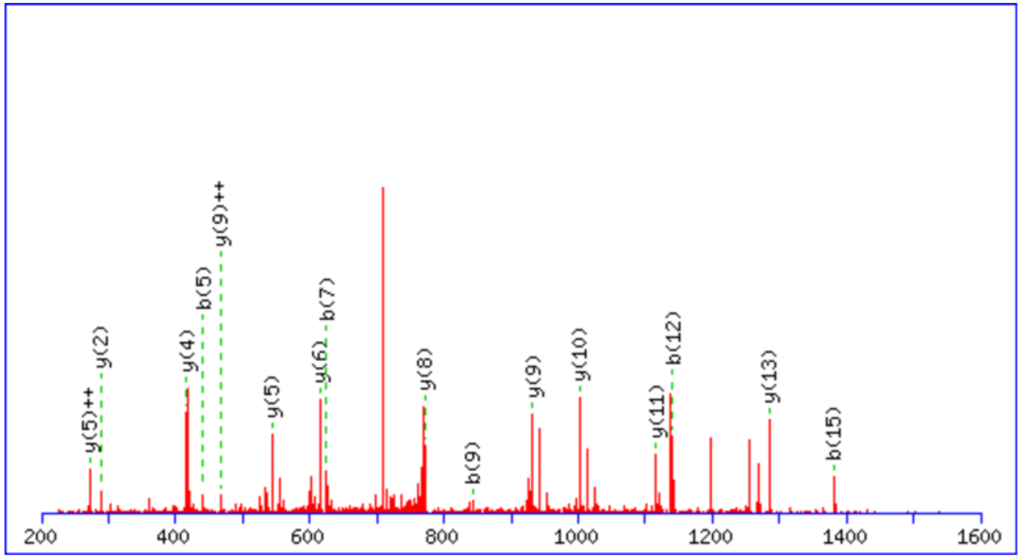
Peptide View

MS/MS Fragmentation of **AAQGLLACGVAQGALR**
Found in **IPI00021085**, Tax_Id=9606 Gene_Symbol=PGLYRP1 Peptidoglycan recognition protein
Experiment: S_B-2 **Fraction:** S_B-2

Match to Query 11169: 1554.830448 from(778.422500,2+)

Title: OECHL100312_19.15886.15886.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1554.830032**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60
Expect: 0.00012**Matches :** 16/116 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	72.044390	36.525833			A					16
2	143.081504	72.044390			A	1484.800211	742.903743	1467.773662	734.390469	15
3	271.140082	136.073679	254.113533	127.560405	Q	1413.763097	707.385186	1396.736548	698.871912	14
4	328.161546	164.584411	311.134997	156.071136	G	***1285.704519***	643.355897	1268.677970	634.842623	13
5	**441.245610**	221.126443	424.219061	212.613169	L	1228.683055	614.845165	1211.656506	606.331891	12
6	554.329674	277.668475	537.303125	269.155201	L	***1115.598991***	558.303133	1098.572442	549.789859	11
7	**625.366788**	313.187032	608.340239	304.673758	A	***1002.514927***	501.761101	985.488378	493.247827	10
8	785.397437	393.202357	768.370888	384.689082	C	***931.477813***	466.242544	914.451264	457.729270	9
9	**842.418901**	421.713089	825.392352	413.199814	G	***771.447164***	386.227220	754.420615	377.713945	8
10	941.487315	471.247296	924.460766	462.734021	V	714.425700	357.716488	697.399151	349.203213	7
11	1012.524429	506.765853	995.497880	498.252578	A	***615.357286***	308.182281	598.330737	299.669006	6
12	**1140.583007**	570.795142	1123.556458	562.281867	Q	***544.320172***	272.663724	527.293623	264.150449	5
13	1197.604471	599.305873	1180.577922	590.792599	G	***416.261594***	208.634435	399.235045	200.121160	4
14	1268.641585	634.824430	1251.615036	626.311156	A	359.240130	180.123703	342.213581	171.610428	3
15	**1381.725649**	691.366462	1364.699100	682.853188	L	***288.203016***	144.605146	271.176467	136.091871	2
16					R	175.118952	88.063114	158.092403	79.549839	1



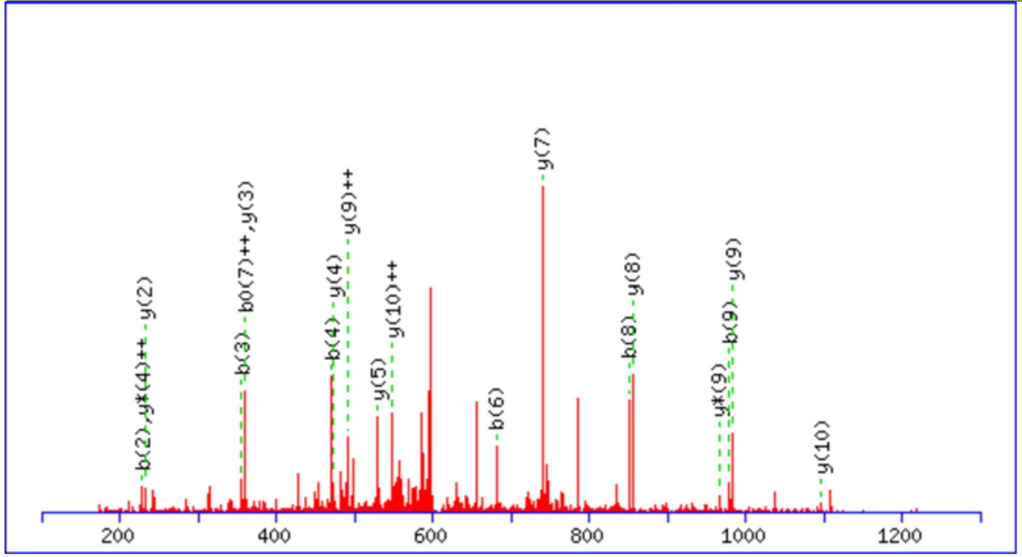
Peptide View

MS/MS Fragmentation of **INQDPLGIQGR**
Found in **IPI00414909**, Tax_Id=9606 Gene_Symbol=NAGA Alpha-N-acetylgalactosaminidase
Experiment: S_B-2 **Fraction:** S_B-2

Match to Query 7014: 1209.645248 from(605.829900,2+)
Title: OECHL100312_19.12329.12329.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1209.646576**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57
Expect: 0.00018**Matches :** 19/98 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	114.091340	57.549308					**I**							**11**
2	**228.134267**	114.570771	211.107718	106.057497			**N**	***1097.569798***	549.288537	1080.543249	540.775263	1079.559233	540.283255	**10**
3	**356.192845**	178.600060	339.166296	170.086786			**Q**	***983.526871***	492.267074	966.500322	483.753799	965.516306	483.261791	**9**
4	**471.219788**	236.113532	454.193239	227.600258	453.209223	227.108250	**D**	***855.468293***	428.237785	838.441744	419.724510	837.457728	419.232502	**8**
5	568.272552	284.639914	551.246003	276.126640	550.261987	275.634632	**P**	***740.441350***	370.724313	723.414801	362.211039			**7**
6	**681.356616**	341.181946	664.330067	332.668672	663.346051	332.176664	**L**	643.388586	322.197931	626.362037	313.684657			**6**

7	738.378080	369.692678	721.351531	361.179404	720.367515	360.687396	**G**	***530.304522***	265.655899	513.277973	257.142625			**5**
8	**851.462144**	426.234710	834.435595	417.721436	833.451579	417.229428	**I**	***473.283058***	237.145167	456.256509	228.631892			**4**
9	**979.520722**	490.263999	962.494173	481.750725	961.510157	481.258717	**Q**	***360.198994***	180.603135	343.172445	172.089860			**3**
10	1036.542186	518.774731	1019.515637	510.261457	1018.531621	509.769449	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
11							**R**	175.118952	88.063114	158.092403	79.549839			**1**



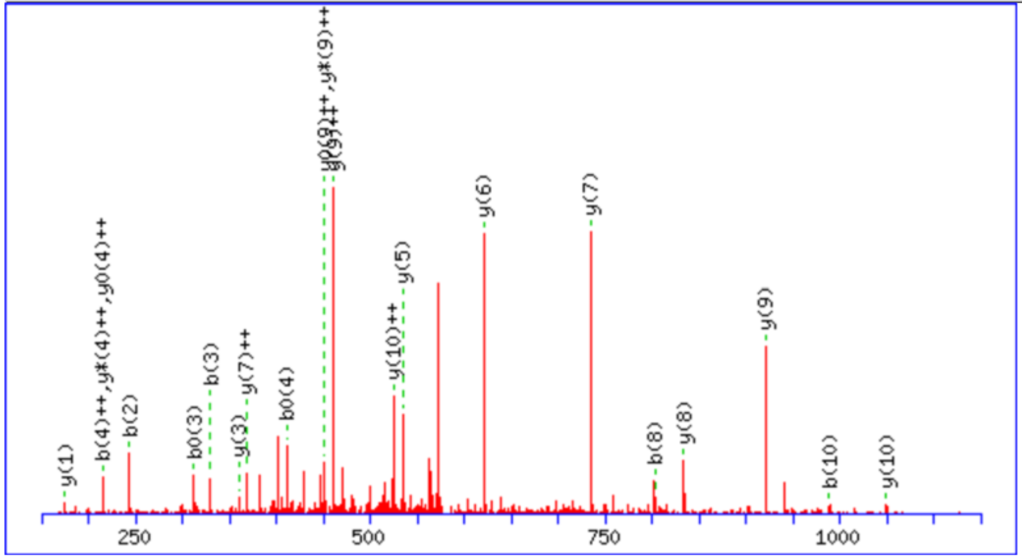
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: S_B-2 **Fraction:** S_B-2

Match to Query 6341: 1161.635648 from(581.825100,2+)
Title: OECHL100312_19.6624.6624.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00018**Matches :** 22/94 fragment ions using 37 most intense peaks (help)

#	**b**	**b^{++}**	**b***	**b^{*++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	114.091340	57.549308					**I**							**11**

2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637	**10**
3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340	**9**
4	429.234375	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326	**8**
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119	**7**
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087	**6**
7	716.382495	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073	**5**
8	**803.414523**	402.210899			785.403958	393.205617	**S**	447.267407	224.137342	430.240858	215.624067	429.256842	215.132059	**4**
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053			**3**
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



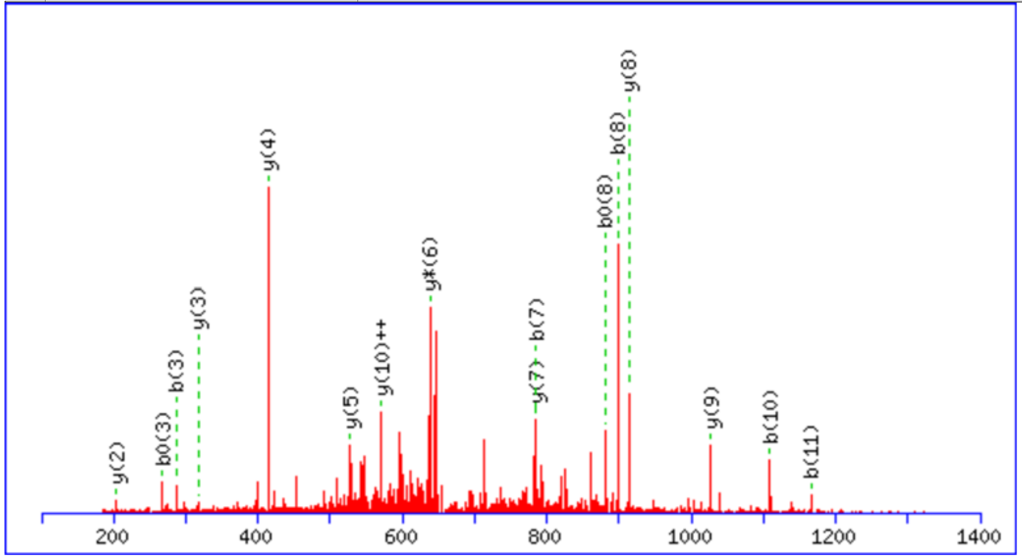
Peptide View

MS/MS Fragmentation of **ATLLEEQLPLGK**
Found in **IPI00414542**, Tax_Id=9606 Gene_Symbol=PDCD1LG2 Isoform 1 of Programmed cell death 1 ligand 2
Experiment: S_B-2 **Fraction:** S_B-2

Match to Query 8625: 1310.747248 from(656.380900,2+)

Title: OECHL100312_19.17470.17470.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1310.744537**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49
Expect: 0.00056**Matches :** 16/106 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	72.044390	36.525833					A							12
2	173.092069	87.049672			155.081504	78.044390	T	1240.714731	620.861004	1223.688182	612.347729	1222.704166	611.855721	11
3	**286.176133**	143.591704			268.165568	134.586422	L	1139.667052	570.337164	1122.640503	561.823890	1121.656487	561.331882	10
4	399.260197	200.133737			381.249632	191.128454	L	***1026.582988***	513.795132	1009.556439	505.281858	1008.572423	504.789850	9
5	528.302790	264.655033			510.292225	255.649751	E	***913.498924***	457.253100	896.472375	448.739825	895.488359	448.247818	8
6	657.345383	329.176330			639.334818	320.171047	E	***784.456331***	392.731804	767.429782	384.218529	766.445766	383.726521	7
7	**785.403961**	393.205619	768.377412	384.692344	767.393396	384.200336	Q	655.413738	328.210507	638.387189	319.697232			6
8	**898.488025**	449.747651	881.461476	441.234376	880.477460	440.742368	L	***527.355160***	264.181218	510.328611	255.667943			5
9	995.540789	498.274033	978.514240	489.760758	977.530224	489.268750	P	***414.271096***	207.639186	397.244547	199.125911			4
10	**1108.624853**	554.816065	1091.598304	546.302790	1090.614288	545.810782	L	***317.218332***	159.112804	300.191783	150.599529			3
11	**1165.646317**	583.326797	1148.619768	574.813522	1147.635752	574.321514	G	***204.134268***	102.570772	187.107719	94.057497			2
12							K	147.112804	74.060040	130.086255	65.546765			1

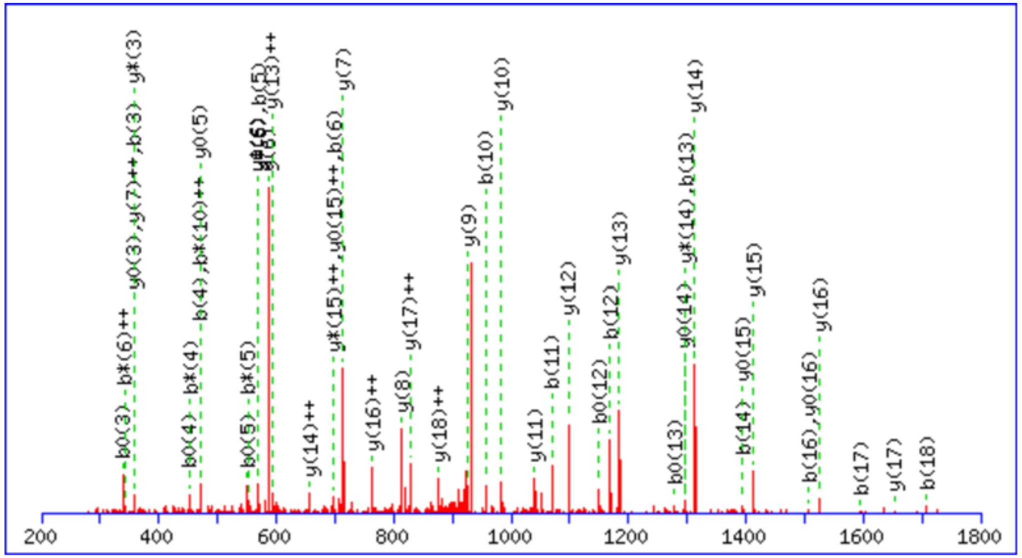


Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**
Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
Experiment: 53 - PyC-2 **Fraction:** PyC-2

Match to Query 14931: 1881.032648 from(941.523600,2+)
Title: OECHL100312_17.14043.14043.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 108
Expect: 7.6e-010**Matches :** 50/208 fragment ions using 59 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	**E**							**19**
2	229.118283	115.062780			211.107718	106.057497	**V**	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.996686	**18**
3	***357.176861***	179.092069	340.150312	170.578794	339.166296	170.086786	**Q**	***1653.928246***	827.467761	1636.901697	818.954487	1635.917681	818.462479	**17**
4	***470.260925***	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.433190	**16**
5	***569.329339***	285.168308	552.302790	276.655033	551.318774	276.163025	**V**	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.891158	**15**
6	***698.371932***	349.689604	681.345383	341.176330	680.361367	340.684322	**E**	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.356951	**14**
7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	**S**	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.835654	**13**
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	**G**	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.319640	**12**
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	**G**	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.808908	**11**
10	***956.468352***	478.737814	939.441803	470.224540	938.457787	469.732532	**G**	***983.599641***	492.303459	966.573092	483.790184	965.589076	483.298176	**10**
11	***1069.552416***	535.279846	1052.525867	526.766572	1051.541851	526.274564	**L**	***926.578177***	463.792727	909.551628	455.279452	908.567612	454.787444	**9**
12	***1168.620830***	584.814053	1151.594281	576.300779	1150.610265	575.808771	**V**	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.245412	**8**
13	***1296.715793***	648.861535	1279.689244	640.348260	1278.705228	639.856252	**K**	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.711205	**7**
14	***1393.768557***	697.387917	1376.742008	688.874642	1375.757992	688.382634	**P**	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.663723	**6**
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	**G**	489.277972	245.142624	472.251423	236.629349	471.267407	236.137341	**5**
16	***1507.811485***	754.409381	1490.784936	745.896106	1489.800920	745.404098	**G**	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	**4**
17	***1594.843513***	797.925395	1577.816964	789.412120	1576.832948	788.920112	**S**	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	**3**
18	***1707.927577***	854.467427	1690.901028	845.954152	1689.917012	845.462144	**L**	288.203016	144.605146	271.176467	136.091871			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



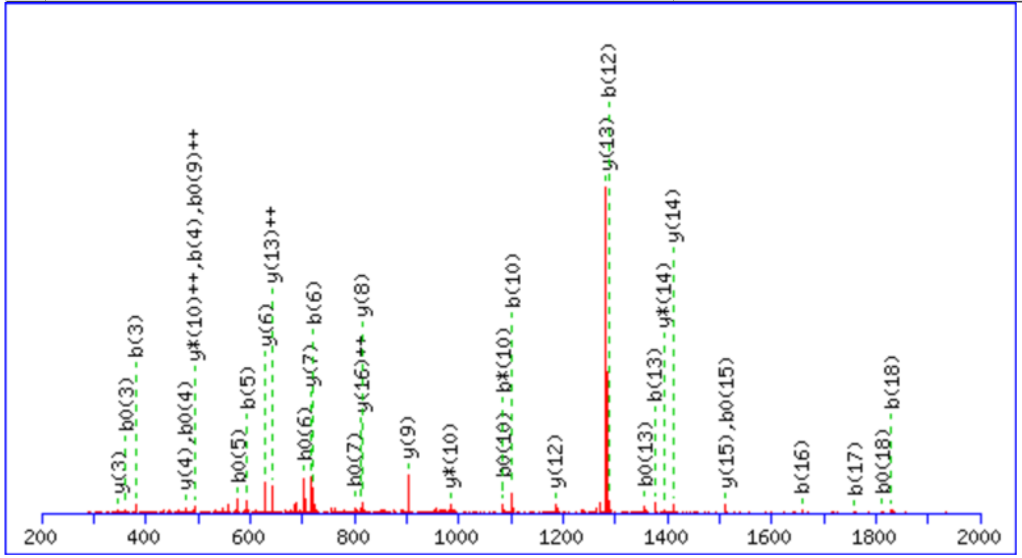
Peptide View

MS/MS Fragmentation of **SYELTQPPSVSVSPGQTAR**
Found in **IPI00382440**, Tax_Id=9606 Gene_Symbol=- Ig lambda chain V-IV region Hil
Experiment: 53 - PyC-2 **Fraction:** PyC-2

Match to Query 15603: 2002.997448 from(1002.506000,2+)
Title: OECHL100312_17.13507.13507.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 2002.995987**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70
Expect: 1.9e-005**Matches :** 36/202 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	**S**							**19**
2	251.102633	126.054954			233.092068	117.049672	**Y**	1916.971234	958.989255	1899.944685	950.475981	1898.960669	949.983973	**18**
3	***380.145226***	190.576251			362.134661	181.570969	**E**	1753.907905	877.457591	1736.881356	868.944316	1735.897340	868.452308	**17**
4	***493.229290***	247.118283			475.218725	238.113001	**L**	1624.865312	812.936294	1607.838763	804.423020	1606.854747	803.931012	**16**
5	***594.276969***	297.642123			576.266404	288.636840	**T**	***1511.781248***	756.394262	1494.754699	747.880988	1493.770683	747.388980	**15**
6	***722.335547***	361.671412	705.308998	353.158137	704.324982	352.666129	**Q**	***1410.733569***	705.870423	1393.707020	697.357148	1392.723004	696.865140	**14**

7	819.388311	410.197794	802.361762	401.684519	801.377746	401.192511	**P**	***1282.674991***	641.841134	1265.648442	633.327859	1264.664426	632.835851	**13**
8	916.441075	458.724176	899.414526	450.210901	898.430510	449.718893	**P**	***1185.622227***	593.314752	1168.595678	584.801477	1167.611662	584.309469	**12**
9	1003.473103	502.240190	986.446554	493.726915	985.462538	493.234907	**S**	1088.569463	544.788370	1071.542914	536.275095	1070.558898	535.783087	**11**
10	***1102.541517***	551.774397	1085.514968	543.261122	1084.530952	542.769114	**V**	1001.537435	501.272356	984.510886	492.759081	983.526870	492.267073	**10**
11	1189.573545	595.290411	1172.546996	586.777136	1171.562980	586.285128	**S**	***902.469021***	451.738149	885.442472	443.224874	884.458456	442.732866	**9**
12	***1288.641959***	644.824618	1271.615410	636.311343	1270.631394	635.819335	**V**	***815.436993***	408.222135	798.410444	399.708860	797.426428	399.216852	**8**
13	***1375.673987***	688.340632	1358.647438	679.827357	1357.663422	679.335349	**S**	***716.368579***	358.687928	699.342030	350.174653	698.358014	349.682645	**7**
14	1472.726751	736.867014	1455.700202	728.353739	1454.716186	727.861731	**P**	***629.336551***	315.171914	612.310002	306.658639	611.325986	306.166631	**6**
15	1529.748215	765.377746	1512.721666	756.864471	1511.737650	756.372463	**G**	532.283787	266.645532	515.257238	258.132257	514.273222	257.640249	**5**
16	***1657.806793***	829.407035	1640.780244	820.893760	1639.796228	820.401752	**Q**	***475.262323***	238.134800	458.235774	229.621525	457.251758	229.129517	**4**
17	***1758.854472***	879.930874	1741.827923	871.417600	1740.843907	870.925592	**T**	***347.203745***	174.105510	330.177196	165.592236	329.193180	165.100228	**3**
18	***1829.891586***	915.449431	1812.865037	906.936157	1811.881021	906.444149	**A**	246.156066	123.581671	229.129517	115.068396			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



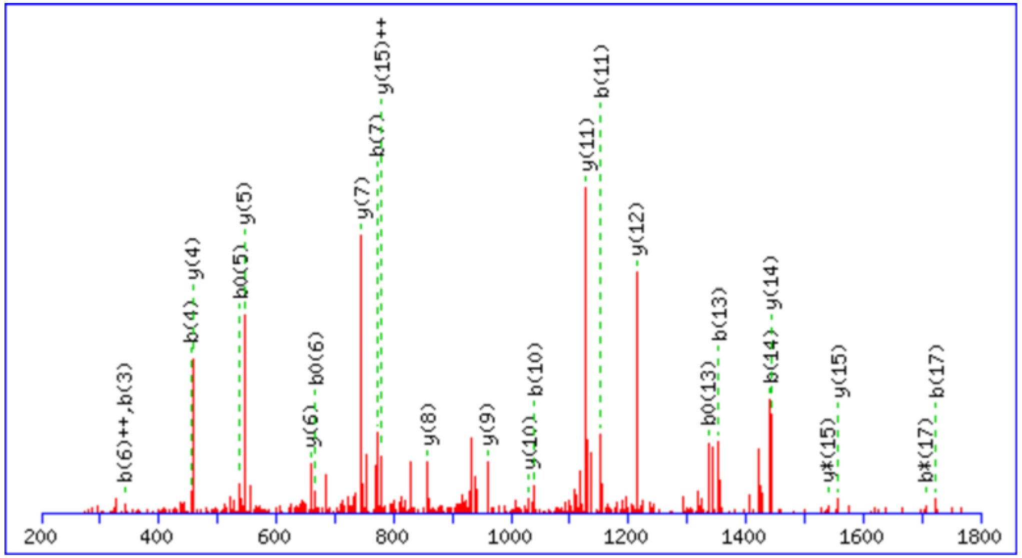
Peptide View

MS/MS Fragmentation of **EIVLTQSPATLSLSPGER**

Found in **IPI00816799**, Tax_Id=9606 Gene_Symbol=- Rheumatoid factor D5 light chain (Fragment)
Experiment: 53 - PyC-2 **Fraction:** PyC-2

Match to Query 15027: 1897.016448 from(949.515500,2+)
Title: OECHL100312_17.17260.17260.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1897.015640**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 96
Expect: 2.1e-008**Matches :** 26/192 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	130.049869	65.528572			112.039304	56.523290	**E**							**18**
2	243.133933	122.070605			225.123368	113.065322	**I**	1768.980341	884.993808	1751.953792	876.480534	1750.969776	875.988526	**17**
3	**342.202347**	171.604812			324.191782	162.599529	**V**	1655.896277	828.451776	1638.869728	819.938502	1637.885712	819.446494	**16**
4	**455.286411**	228.146844			437.275846	219.141561	**L**	***1556.827863***	778.917569	1539.801314	770.404295	1538.817298	769.912287	**15**
5	556.334090	278.670683			538.323525	269.665401	**T**	***1443.743799***	722.375537	1426.717250	713.862263	1425.733234	713.370255	**14**
6	684.392668	342.699972	667.366119	334.186698	666.382103	333.694690	**Q**	1342.696120	671.851698	1325.669571	663.338423	1324.685555	662.846415	**13**
7	**771.424696**	386.215986	754.398147	377.702712	753.414131	377.210704	**S**	***1214.637542***	607.822409	1197.610993	599.309134	1196.626977	598.817126	**12**
8	868.477460	434.742368	851.450911	426.229094	850.466895	425.737086	**P**	***1127.605514***	564.306395	1110.578965	555.793120	1109.594949	555.301112	**11**
9	939.514574	470.260925	922.488025	461.747651	921.504009	461.255643	**A**	***1030.552750***	515.780013	1013.526201	507.266738	1012.542185	506.774730	**10**
10	**1040.562253**	520.784765	1023.535704	512.271490	1022.551688	511.779482	**T**	***959.515636***	480.261456	942.489087	471.748181	941.505071	471.256173	**9**
11	**1153.646317**	577.326797	1136.619768	568.813522	1135.635752	568.321514	**L**	***858.467957***	429.737616	841.441408	421.224342	840.457392	420.732334	**8**
12	1240.678345	620.842811	1223.651796	612.329536	1222.667780	611.837528	**S**	***745.383893***	373.195585	728.357344	364.682310	727.373328	364.190302	**7**
13	**1353.762409**	677.384842	1336.735860	668.871568	1335.751844	668.379560	**L**	***658.351865***	329.679570	641.325316	321.166296	640.341300	320.674288	**6**
14	**1440.794437**	720.900857	1423.767888	712.387582	1422.783872	711.895574	**S**	***545.267801***	273.137539	528.241252	264.624264	527.257236	264.132256	**5**
15	1537.847201	769.427239	1520.820652	760.913964	1519.836636	760.421956	**P**	***458.235773***	229.621524	441.209224	221.108250	440.225208	220.616242	**4**
16	1594.868665	797.937971	1577.842116	789.424696	1576.858100	788.932688	**G**	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	**3**
17	**1723.911258**	862.459267	1706.884709	853.945992	1705.900693	853.453984	**E**	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**



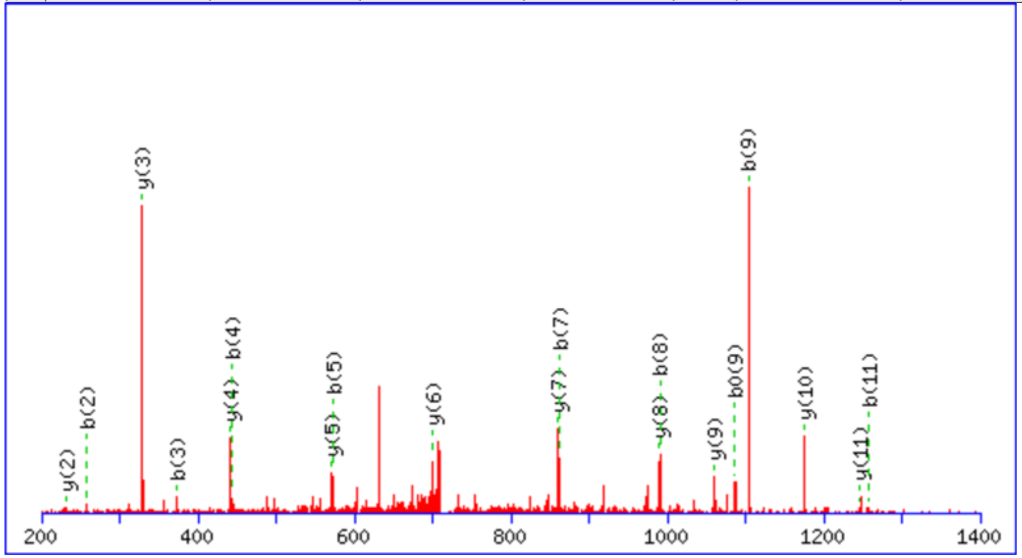
Peptide View

MS/MS Fragmentation of **WADAECEEIPGR**
Found in **IPI00027436**, Tax_Id=9606 Gene_Symbol=NGFR Tumor necrosis factor receptor superfamily member 16
Experiment: 53 - PyC-2 **Fraction:** PyC-2

Match to Query 10298: 1431.608848 from(716.811700,2+)
Title: OECHL100312_17.11280.11280.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1431.608856**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 74
Expect: 9.2e-007**Matches :** 19/98 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	187.086589	94.046932			**W**							**12**
2	**258.123703**	129.565490			**A**	***1246.536843***	623.772060	1229.510294	615.258785	1228.526278	614.766777	**11**
3	**373.150646**	187.078961	355.140081	178.073679	**D**	***1175.499729***	588.253502	1158.473180	579.740228	1157.489164	579.248220	**10**
4	**444.187760**	222.597518	426.177195	213.592236	**A**	***1060.472786***	530.740031	1043.446237	522.226757	1042.462221	521.734749	**9**
5	**573.230353**	287.118815	555.219788	278.113532	**E**	***989.435672***	495.221474	972.409123	486.708199	971.425107	486.216191	**8**
6	733.261002	367.134139	715.250437	358.128857	**C**	***860.393079***	430.700178	843.366530	422.186903	842.382514	421.694895	**7**

7	**862.303595**	431.655436	844.293030	422.650153	**E**	***700.362430***	350.684853	683.335881	342.171578	682.351865	341.679570	**6**
8	**991.346188**	496.176732	973.335623	487.171450	**E**	***571.319837***	286.163556	554.293288	277.650282	553.309272	277.158274	**5**
9	**1104.430252**	552.718764	1086.419687	543.713482	**I**	***442.277244***	221.642260	425.250695	213.128985			**4**
10	1201.483016	601.245146	1183.472451	592.239864	**P**	***329.193180***	165.100228	312.166631	156.586953			**3**
11	**1258.504480**	629.755878	1240.493915	620.750596	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**



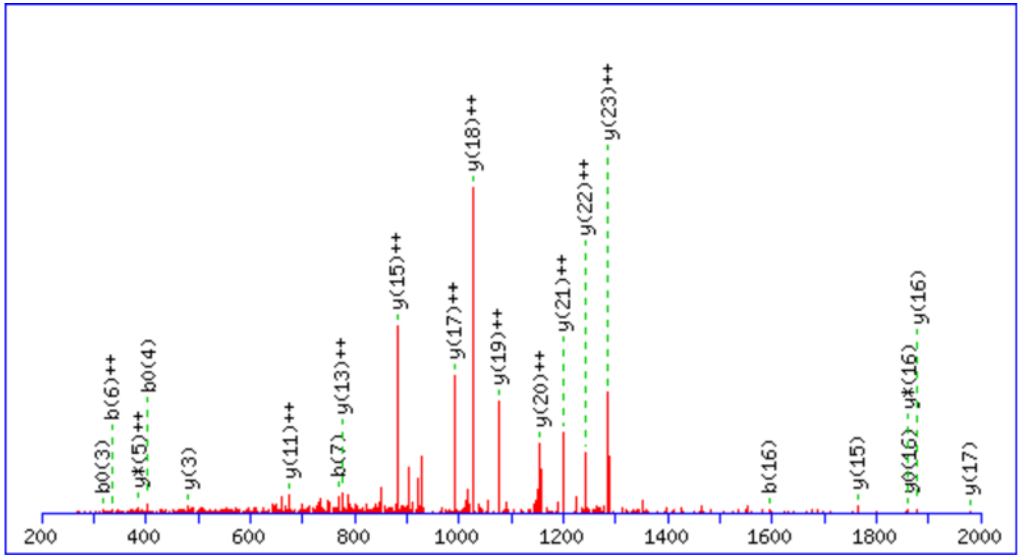
Peptide View

MS/MS Fragmentation of **SCSSSCVATDPDSIGAAHLIFCCFR**
Found in **IPI00022620**, Tax_Id=9606 Gene_Symbol=SLURP1 Secreted Ly-6/uPAR-related protein 1
Experiment: 53 - PyC-2 **Fraction:** PyC-2

Match to Query 18984: 2817.204372 from(940.075400,3+)
Title: OECHL100312_17.20065.20065.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 2817.197922**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 9.7e-005**Matches :** 23/216 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#

1	88.039304	44.523290	70.028739	35.518008	**S**							**25**
2	248.069953	124.538614	230.059388	115.533332	**C**	2731.173141	1366.090208	2714.146592	1357.576934	2713.162576	1357.084926	**24**
3	**335.101981**	168.054628	317.091416	159.049346	**S**	2571.142492	1286.074884	2554.115943	1277.561609	2553.131927	1277.069601	**23**
4	422.134009	211.570642	404.123444	202.565360	**S**	2484.110464	1242.558870	2467.083915	1234.045595	2466.099899	1233.553587	**22**
5	509.166037	255.086656	491.155472	246.081374	**S**	2397.078436	1199.042856	2380.051887	1190.529581	2379.067871	1190.037573	**21**
6	669.196686	335.101981	651.186121	326.096699	**C**	2310.046408	1155.526842	2293.019859	1147.013567	2292.035843	1146.521559	**20**
7	**768.265100**	384.636188	750.254535	375.630905	**V**	2150.015759	1075.511517	2132.989210	1066.998243	2132.005194	1066.506235	**19**
8	839.302214	420.154745	821.291649	411.149462	**A**	2050.947345	1025.977310	2033.920796	1017.464036	2032.936780	1016.972028	**18**
9	940.349893	470.678585	922.339328	461.673302	**T**	**1979.910231**	990.458753	1962.883682	981.945479	1961.899666	981.453471	**17**
10	1055.376836	528.192056	1037.366271	519.186773	**D**	**1878.862552**	939.934914	1861.836003	931.421639	1860.851987	930.929631	**16**
11	1152.429600	576.718438	1134.419035	567.713155	**P**	**1763.835609**	882.421442	1746.809060	873.908168	1745.825044	873.416160	**15**
12	1267.456543	634.231910	1249.445978	625.226627	**D**	1666.782845	833.895060	1649.756296	825.381786	1648.772280	824.889778	**14**
13	1354.488571	677.747924	1336.478006	668.742641	**S**	1551.755902	776.381589	1534.729353	767.868314	1533.745337	767.376306	**13**
14	1467.572635	734.289956	1449.562070	725.284673	**I**	1464.723874	732.865575	1447.697325	724.352300			**12**
15	1524.594099	762.800687	1506.583534	753.795405	**G**	1351.639810	676.323543	1334.613261	667.810268			**11**
16	**1595.631213**	798.319244	1577.620648	789.313962	**A**	1294.618346	647.812811	1277.591797	639.299536			**10**
17	1666.668327	833.837801	1648.657762	824.832519	**A**	1223.581232	612.294254	1206.554683	603.780979			**9**
18	1803.727239	902.367257	1785.716674	893.361975	**H**	1152.544118	576.775697	1135.517569	568.262422			**8**
19	1916.811303	958.909289	1898.800738	949.904007	**L**	1015.485206	508.246241	998.458657	499.732966			**7**
20	2029.895367	1015.451321	2011.884802	1006.446039	**I**	902.401142	451.704209	885.374593	443.190934			**6**
21	2176.963781	1088.985528	2158.953216	1079.980246	**F**	789.317078	395.162177	772.290529	386.648902			**5**
22	2336.994430	1169.000853	2318.983865	1159.995570	**C**	642.248664	321.627970	625.222115	313.114695			**4**
23	2497.025079	1249.016177	2479.014514	1240.010895	**C**	**482.218015**	241.612645	465.191466	233.099371			**3**
24	2644.093493	1322.550384	2626.082928	1313.545102	**F**	322.187366	161.597321	305.160817	153.084046			**2**
25					**R**	175.118952	88.063114	158.092403	79.549839			**1**



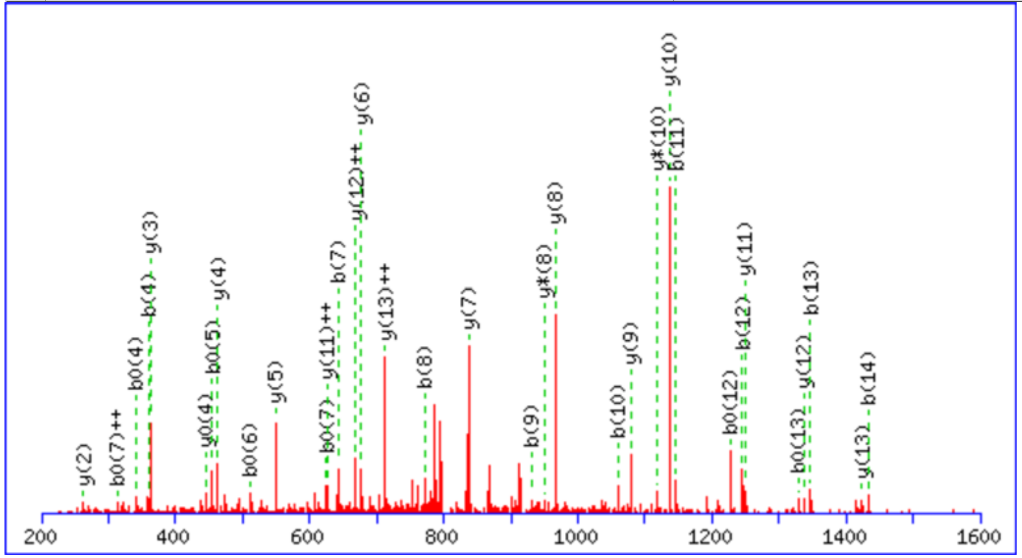
Peptide View

MS/MS Fragmentation of **AISSIGLECQSVTSR**
Found in **IPI00006988**, Tax_Id=9606 Gene_Symbol=RETN Resistin
Experiment: 53 - PyC-2 **Fraction:** PyC-2

Match to Query 12515: 1606.799448 from(804.407000,2+)
Title: OECHL100312_17.12166.12166.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1606.798462**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 96
Expect: 3.7e-008**Matches :** 34/144 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**15**
2	185.128454	93.067865					**I**	1536.768633	768.887955	1519.742084	760.374680	1518.758068	759.882672	**14**
3	272.160482	136.583879			254.149917	127.578596	**S**	***1423.684569***	712.345923	1406.658020	703.832648	1405.674004	703.340640	**13**
4	**359.192510**	180.099893			341.181945	171.094610	**S**	***1336.652541***	668.829909	1319.625992	660.316634	1318.641976	659.824626	**12**
5	472.276574	236.641925			454.266009	227.636642	**I**	***1249.620513***	625.313895	1232.593964	616.800620	1231.609948	616.308612	**11**
6	529.298038	265.152657			511.287473	256.147375	**G**	***1136.536449***	568.771863	1119.509900	560.258588	1118.525884	559.766580	**10**

7	642.382102	321.694689			624.371537	312.689407	L	1079.514985	540.261131	1062.488436	531.747856	1061.504420	531.255848	9
8	771.424695	386.215986			753.414130	377.210703	E	966.430921	483.719099	949.404372	475.205824	948.420356	474.713816	8
9	931.455344	466.231310			913.444779	457.226028	C	837.388328	419.197802	820.361779	410.684528	819.377763	410.192520	7
10	1059.513922	530.260599	1042.487373	521.747325	1041.503357	521.255317	Q	677.357679	339.182478	660.331130	330.669203	659.347114	330.177195	6
11	1146.545950	573.776613	1129.519401	565.263339	1128.535385	564.771331	S	549.299101	275.153189	532.272552	266.639914	531.288536	266.147906	5
12	1245.614364	623.310820	1228.587815	614.797546	1227.603799	614.305538	V	462.267073	231.637175	445.240524	223.123900	444.256508	222.631892	4
13	1346.662043	673.834660	1329.635494	665.321385	1328.651478	664.829377	T	363.198659	182.102968	346.172110	173.589693	345.188094	173.097685	3
14	1433.694071	717.350674	1416.667522	708.837399	1415.683506	708.345391	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
15							R	175.118952	88.063114	158.092403	79.549839			1



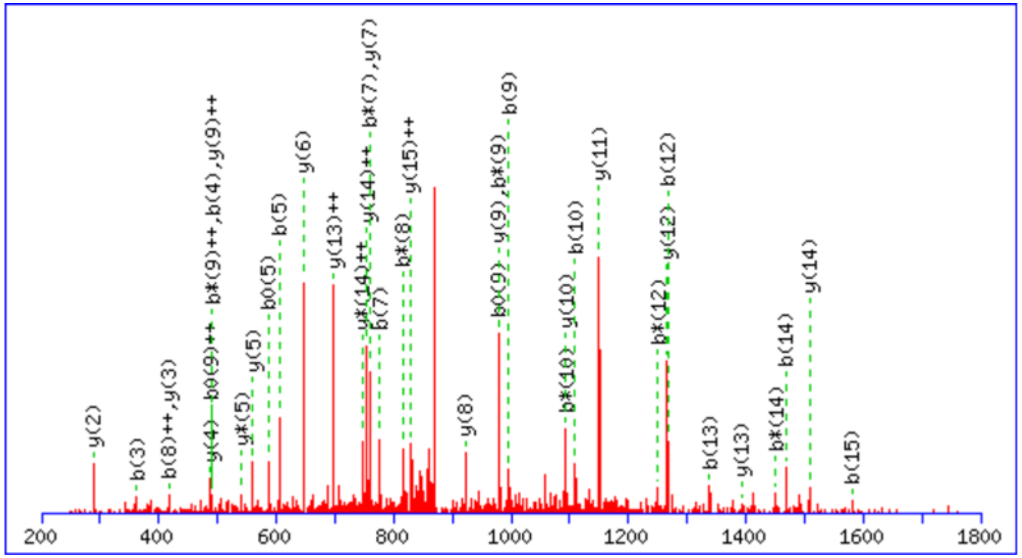
Peptide View

MS/MS Fragmentation of **VFDKDGNGYISAAELR**
Found in **IPI00075248**, Tax_Id=9606 Gene_Symbol=CALM3;CALM2;CALM1 Calmodulin
Experiment: 53 - PyC-2 **Fraction:** PyC-2

Match to Query 14160: 1753.864448 from(877.939500,2+)
Title: OECHL100312_17.13880.13880.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_17.raw

Monoisotopic mass of neutral peptide Mr(calc): 1753.863495**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 81
Expect: 1.1e-006**Matches :** 40/166 fragment ions using 73 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					**V**							**16**
2	247.144104	124.075690					**F**	1655.802376	828.404826	1638.775827	819.891551	1637.791811	819.399543	**15**
3	**362.171047**	181.589161			344.160482	172.583879	**D**	***1508.733962***	754.870619	1491.707413	746.357345	1490.723397	745.865337	**14**
4	**490.266010**	245.636643	473.239461	237.123369	472.255445	236.631361	**K**	***1393.707019***	697.357148	1376.680470	688.843873	1375.696454	688.351865	**13**
5	**605.292953**	303.150115	588.266404	294.636840	587.282388	294.144832	**D**	***1265.612056***	633.309666	1248.585507	624.796392	1247.601491	624.304383	**12**
6	662.314417	331.660847	645.287868	323.147572	644.303852	322.655564	**G**	***1150.585113***	575.796194	1133.558564	567.282920	1132.574548	566.790912	**11**
7	**776.357344**	388.682310	759.330795	380.169036	758.346779	379.677028	**N**	***1093.563649***	547.285462	1076.537100	538.772188	1075.553084	538.280180	**10**
8	833.378808	417.193042	816.352259	408.679768	815.368243	408.187760	**G**	***979.520722***	490.263999	962.494173	481.750724	961.510157	481.258716	**9**
9	**996.442137**	498.724707	979.415588	490.211432	978.431572	489.719424	**Y**	***922.499258***	461.753267	905.472709	453.239992	904.488693	452.747984	**8**
10	**1109.526201**	555.266738	1092.499652	546.753464	1091.515636	546.261456	**I**	***759.435929***	380.221603	742.409380	371.708328	741.425364	371.216320	**7**
11	1196.558229	598.782753	1179.531680	590.269478	1178.547664	589.777470	**S**	***646.351865***	323.679571	629.325316	315.166296	628.341300	314.674288	**6**
12	**1267.595343**	634.301310	1250.568794	625.788035	1249.584778	625.296027	**A**	***559.319837***	280.163557	542.293288	271.650282	541.309272	271.158274	**5**
13	**1338.632457**	669.819866	1321.605908	661.306592	1320.621892	660.814584	**A**	***488.282723***	244.644999	471.256174	236.131725	470.272158	235.639717	**4**
14	**1467.675050**	734.341163	1450.648501	725.827889	1449.664485	725.335881	**E**	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	**3**
15	**1580.759114**	790.883195	1563.732565	782.369921	1562.748549	781.877912	**L**	***288.203016***	144.605146	271.176467	136.091871			**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



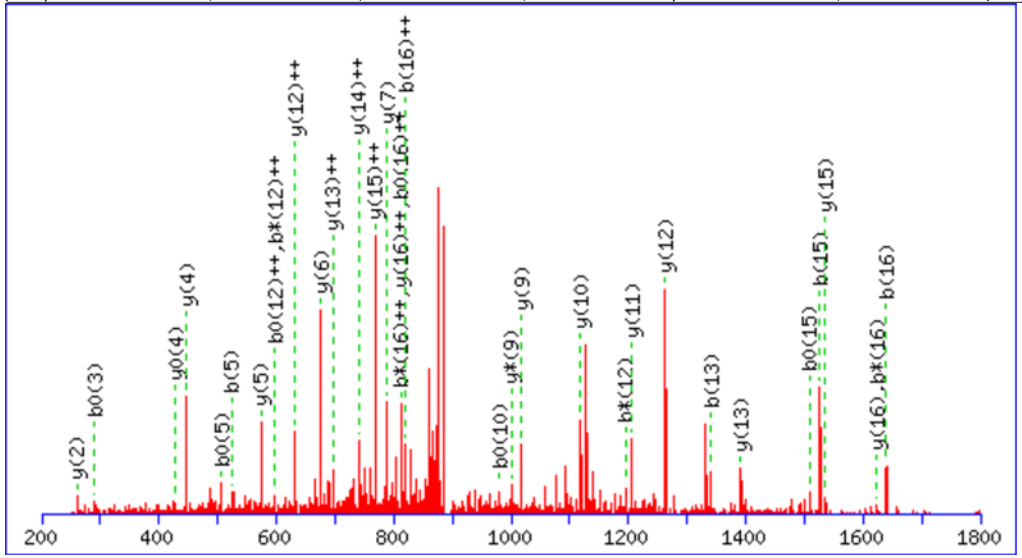
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 53 - PyC-2 **Fraction:** PyC-2

Match to Query 14318: 1784.879848 from(893.447200,2+)
Title: OECHL100312_17.7854.7854.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 73
Expect: 8.7e-006**Matches :** 34/170 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	164.070605	82.538940					**Y**							**17**
2	251.102633	126.054954			233.092068	117.049672	**S**	***1622.823172***	811.915224	1605.796623	803.401950	1604.812607	802.909941	**16**
3	308.124097	154.565687			290.113532	145.560404	**G**	***1535.791144***	768.399210	1518.764595	759.885936	1517.780579	759.393928	**15**
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.883195	**14**
5	**524.198718**	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.367182	**13**
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.845885	**12**

7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.335153	**11**
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.819139	**10**
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.295299	**9**
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.266010	**8**
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.742171	**7**
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.200139	**6**
13	**1340.632852**	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.676299	**5**
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	**4**
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**

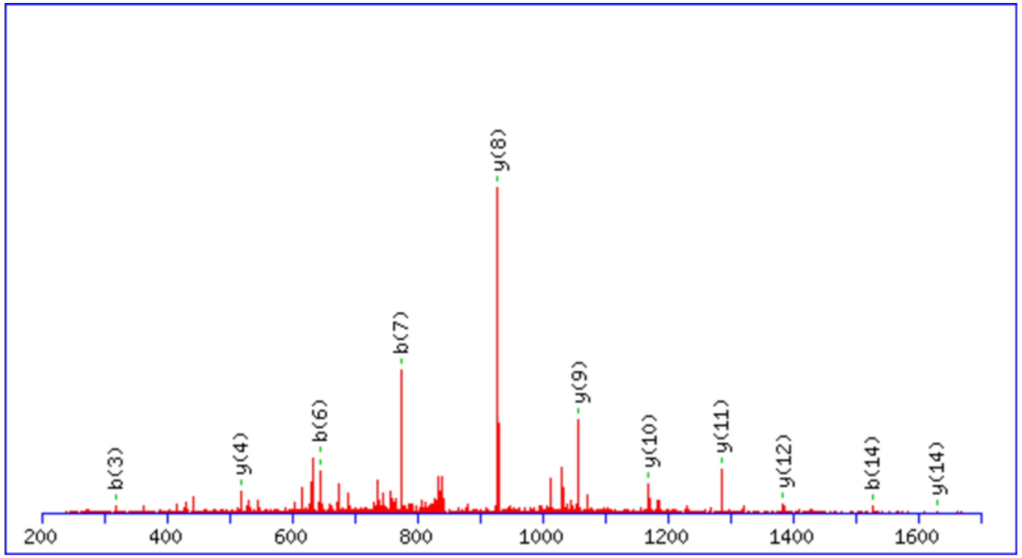


Peptide View

MS/MS Fragmentation of **AVFVDLEPTVIDEVR**
Found in **IPI00166768**, Tax_Id=9606 Gene_Symbol=TUBA1C TUBA1C protein
Experiment: 53 - PyC-2 **Fraction:** PyC-2

Match to Query 13751: 1700.900448 from(851.457500,2+)
Title: OECHL100312_17.20296.20296.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1700.898514**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.001**Matches :** 11/128 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**15**
2	171.112804	86.060040			**V**	***1630.868665***	815.937971	1613.842116	807.424696	1612.858100	806.932688	**14**
3	**318.181218**	159.594247			**F**	1531.800251	766.403764	1514.773702	757.890489	1513.789686	757.398481	**13**
4	417.249632	209.128454			**V**	***1384.731837***	692.869557	1367.705288	684.356282	1366.721272	683.864274	**12**
5	532.276575	266.641926	514.266010	257.636643	**D**	***1285.663423***	643.335350	1268.636874	634.822075	1267.652858	634.330067	**11**
6	**645.360639**	323.183958	627.350074	314.178675	**L**	***1170.636480***	585.821878	1153.609931	577.308604	1152.625915	576.816596	**10**
7	**774.403232**	387.705254	756.392667	378.699972	**E**	***1057.552416***	529.279846	1040.525867	520.766572	1039.541851	520.274564	**9**
8	871.455996	436.231636	853.445431	427.226354	**P**	***928.509823***	464.758550	911.483274	456.245275	910.499258	455.753267	**8**
9	972.503675	486.755476	954.493110	477.750193	**T**	831.457059	416.232168	814.430510	407.718893	813.446494	407.226885	**7**
10	1071.572089	536.289683	1053.561524	527.284400	**V**	730.409380	365.708328	713.382831	357.195054	712.398815	356.703046	**6**
11	1184.656153	592.831715	1166.645588	583.826432	**I**	631.340966	316.174121	614.314417	307.660846	613.330401	307.168838	**5**
12	1299.683096	650.345186	1281.672531	641.339904	**D**	***518.256902***	259.632089	501.230353	251.118815	500.246337	250.626807	**4**
13	1428.725689	714.866483	1410.715124	705.861200	**E**	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	**3**
14	**1527.794103**	764.400690	1509.783538	755.395407	**V**	274.187366	137.597321	257.160817	129.084047			**2**
15					**R**	175.118952	88.063114	158.092403	79.549839			**1**



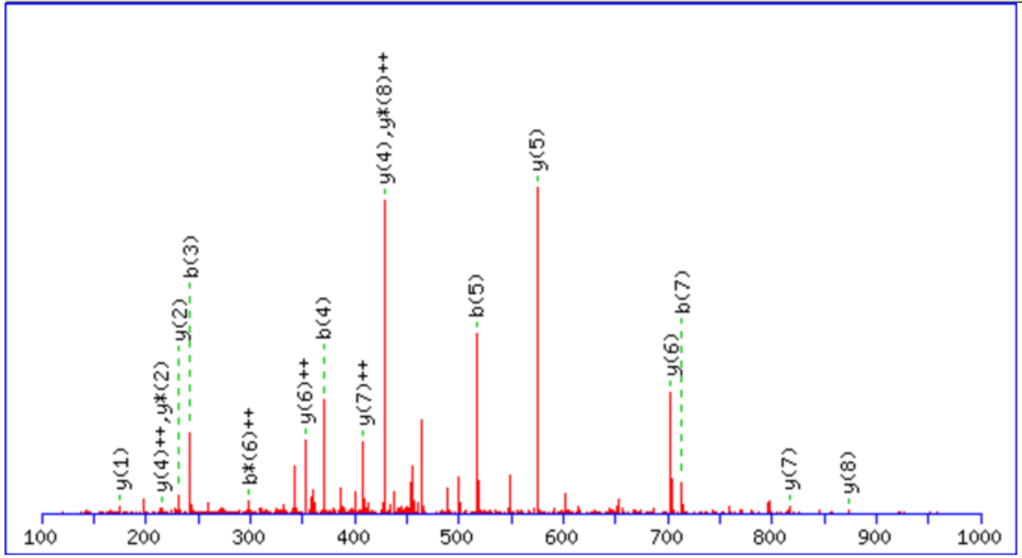
Peptide View

MS/MS Fragmentation of **AGLQFPVGR**
Found in **IPI00018278**, Tax_Id=9606 Gene_Symbol=H2AFV Histone H2A.V
Experiment: 53 - PyC-2 **Fraction:** PyC-2

Match to Query 2886: 943.523648 from(472.769100,2+)
Title: OECHL100312_17.13788.13788.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 943.523956**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00062**Matches :** 17/58 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			**A**					**9**
2	129.065854	65.036565			**G**	***873.494114***	437.250695	856.467565	428.737421	**8**
3	**242.149918**	121.578597			**L**	***816.472650***	408.739963	799.446101	400.226689	**7**
4	**370.208496**	185.607886	353.181947	177.094612	**Q**	***703.388586***	352.197931	686.362037	343.684657	**6**
5	**517.276910**	259.142093	500.250361	250.628819	**F**	***575.330008***	288.168642	558.303459	279.655368	**5**
6	614.329674	307.668475	597.303125	299.155201	**P**	***428.261594***	214.634435	411.235045	206.121160	**4**

7	**713.398088**	357.202682	696.371539	348.689408	**V**	331.208830	166.108053	314.182281	157.594778	**3**
8	770.419552	385.713414	753.393003	377.200140	**G**	***232.140416***	116.573846	215.113867	108.060571	**2**
9					**R**	***175.118952***	88.063114	158.092403	79.549839	**1**



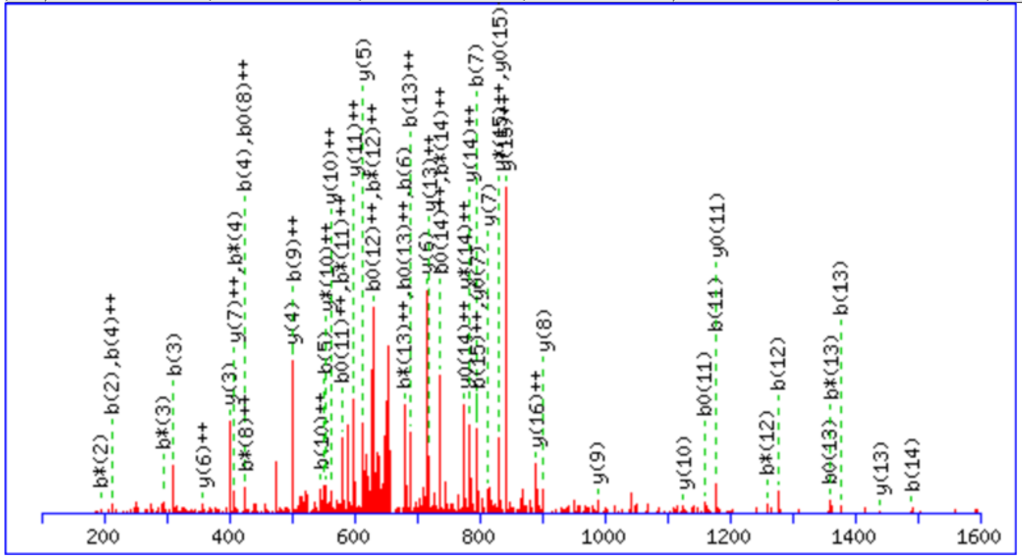
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 53 - PyC-2 **Fraction:** PyC-2

Match to Query 15557: 1990.020972 from(664.347600,3+)
Title: OECHL100312_17.9937.9937.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 0.0007**Matches :** 56/186 fragment ions using 92 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	***212.102967***	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	***311.171381***	156.089328	294.144832	147.576054			**V**	1779.934789	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**

4	***424.255445***	**212.631361**	407.228896	204.118086			L	1680.866375	840.936826	1663.839826	832.423551	1662.855810	831.931543	15
5	***552.314023***	276.660650	535.287474	268.147375			Q	1567.782311	784.394794	1550.755762	775.881519	1549.771746	775.389511	14
6	***680.372601***	340.689939	663.346052	332.176664			Q	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	13
7	***795.399544***	398.203410	778.372995	389.690136	777.388979	389.198128	D	1311.665155	656.336215	1294.638606	647.822941	1293.654590	647.330933	12
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	A	1196.638212	598.822744	1179.611663	590.309470	1178.627647	589.817462	11
9	1003.495570	**502.251423**	986.469021	493.738149	985.485005	493.246141	H	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	10
10	1090.527598	**545.767437**	1073.501049	537.254163	1072.517033	536.762155	S	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	9
11	***1177.559626***	589.283451	1160.533077	580.770177	1159.549061	580.278169	S	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	8
12	***1276.628040***	638.817658	1259.601491	630.304384	1258.617475	629.812376	V	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.737420	7
13	***1377.675719***	**689.341498**	1360.649170	680.828223	1359.665154	680.336215	T	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	6
14	***1490.759783***	745.883530	1473.733234	737.370255	1472.749218	736.878247	I	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	5
15	1591.807462	**796.407369**	1574.780913	787.894095	1573.796897	787.402087	T	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	4
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	P	***400.230294***	200.618785	383.203745	192.105510			3
17	1816.918804	908.963040	1799.892255	900.449766	1798.908239	899.957758	Q	303.177530	152.092403	286.150981	143.579128			2
18							R	175.118952	88.063114	158.092403	79.549839			1

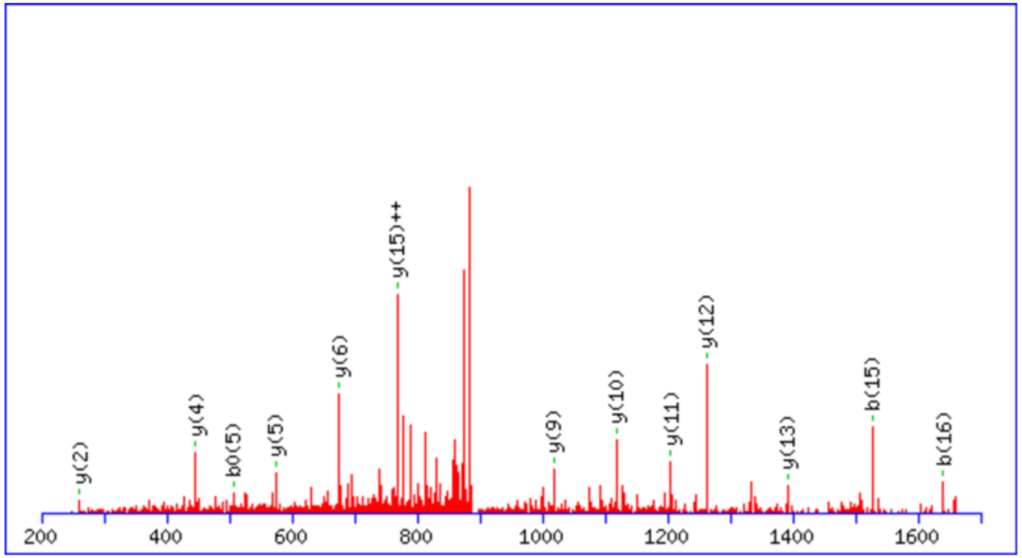


Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 20 - NOPB2 **Fraction:** NOPB2

Match to Query 10924: 1784.880648 from(893.447600,2+)
Title: OECHL100312_09.7129.7129.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 79
Expect: 1.8e-006**Matches :** 13/170 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	164.070605	82.538940					**Y**							**17**
2	251.102633	126.054954			233.092068	117.049672	**S**	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.909941	**16**
3	308.124097	154.565687			290.113532	145.560404	**G**	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.393928	**15**
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.883195	**14**
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.367182	**13**
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.845885	**12**
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.335153	**11**
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.819139	**10**
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.295299	**9**
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.266010	**8**
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	788.487631	394.747453	771.461082	386.234179	770.477066	385.742171	**7**
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.200139	**6**
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.676299	**5**
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	**4**
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**



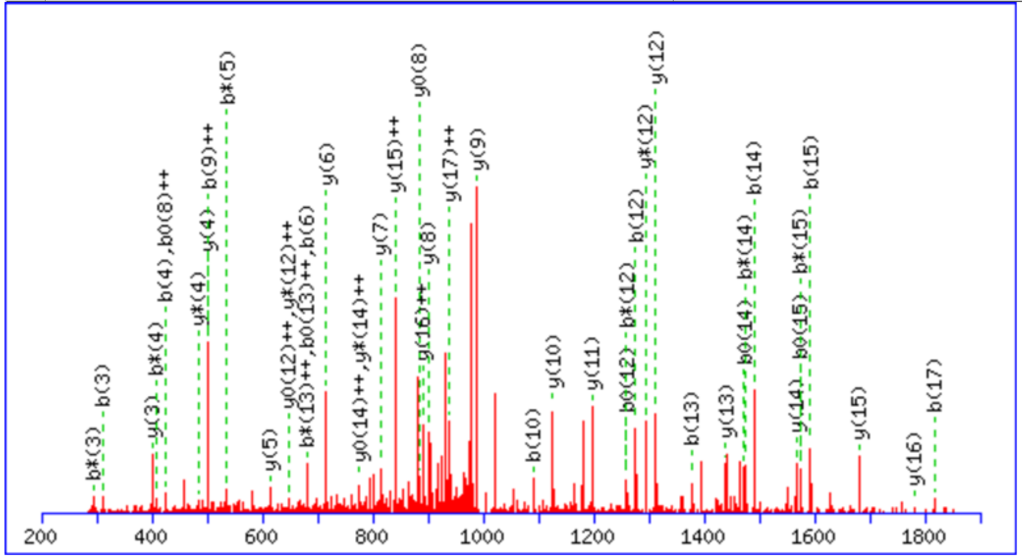
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 20 - NOPB2 **Fraction:** NOPB2

Match to Query 11930: 1990.025048 from(996.019800,2+)
Title: OECHL100312_09.9245.9245.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72
Expect: 8.2e-006**Matches :** 46/186 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	115.050203	58.028740	98.023654	49.515465			N							18
2	212.102967	106.555121	195.076418	98.041847			P	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	17
3	**311.171381**	156.089328	294.144832	147.576054			V	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	16
4	**424.255445**	212.631361	407.228896	204.118086			L	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	15
5	552.314023	276.660650	535.287474	268.147375			Q	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.389511	14
6	**680.372601**	340.689939	663.346052	332.176664			Q	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	13

7	795.399544	398.203410	778.372995	389.690136	777.388979	389.198128	D	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	12
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	A	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	11
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	H	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	10
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	S	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	9
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	S	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	8
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	V	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.737420	7
13	**1377.675719**	689.341498	1360.649170	680.828223	1359.665154	680.336215	T	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	6
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	I	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	5
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	T	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	4
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	P	***400.230294***	200.618785	383.203745	192.105510			3
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	Q	303.177530	152.092403	286.150981	143.579128			2
18							R	175.118952	88.063114	158.092403	79.549839			1

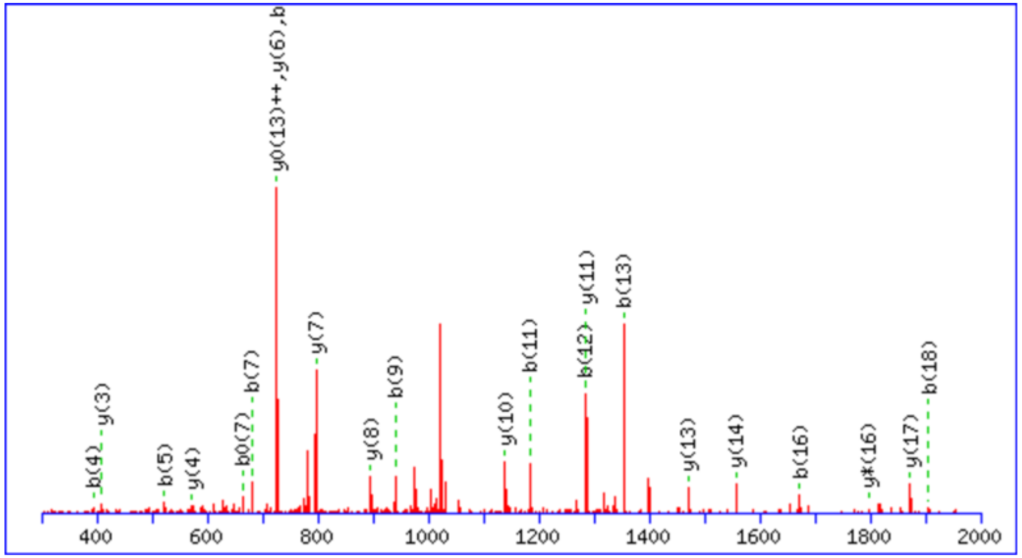


Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 20 - NOPB2 **Fraction:** NOPB2

Match to Query 12260: 2078.985448 from(1040.500000,2+)
Title: OECHL100312_09.15719.15719.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 3.9e-006**Matches :** 23/200 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	72.044390	36.525833					**A**							**19**
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973939	**18**
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444483	**17**
4	***394.183344***	197.595310	377.156795	189.082035			**Q**	1814.870790	907.939033	1797.844241	899.425759	1796.860225	898.933751	**16**
5	***523.225937***	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	1686.812212	843.909744	1669.785663	835.396470	1668.801647	834.904462	**15**
6	610.257965	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383165	**14**
7	***681.295079***	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867151	**13**
8	794.379143	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	1399.700477	700.353877	1382.673928	691.840602	1381.689912	691.348594	**12**
9	***941.447557***	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806562	**11**
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272355	**10**
11	***1184.533077***	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	1025.505072	513.256174	1008.478523	504.742900	1007.494507	504.250892	**9**
12	***1283.601491***	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729595	**8**
13	***1354.638605***	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195388	**7**
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676831	**6**
15	1508.712833	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	629.304187	315.155732	612.277638	306.642457	611.293622	306.150449	**5**
16	***1671.776162***	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	***572.282723***	286.645000	555.256174	278.131725	554.272158	277.639717	**4**
17	1818.844576	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	**3**
18	***1905.876604***	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
19							**R**	175.118952	88.063114	158.092403	79.549840			**1**



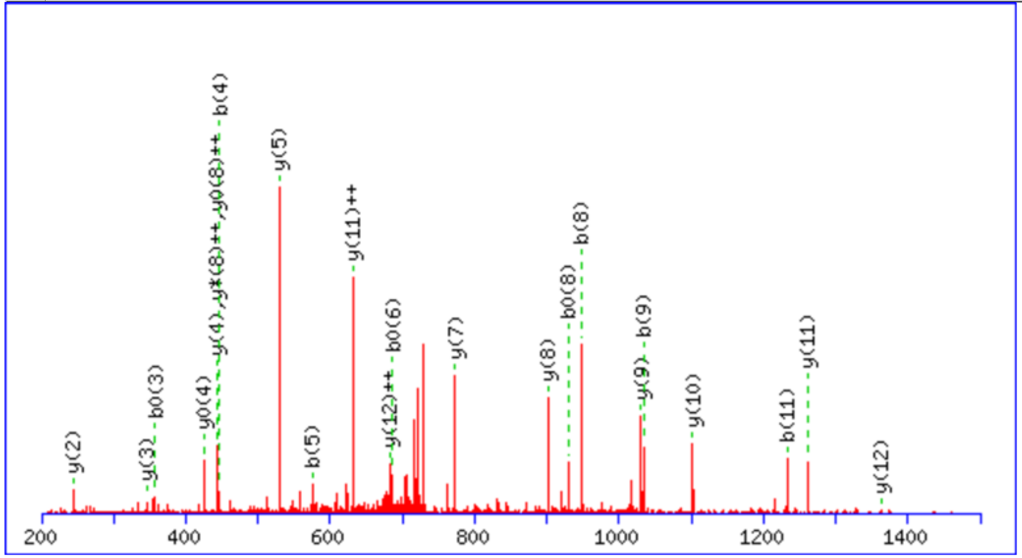
Peptide View

MS/MS Fragmentation of **ITCAEEGWSPTPK**
Found in **IPI00006154**, Tax_Id=9606 Gene_Symbol=CFHR2 Isoform Long of Complement factor H-related protein 2
Experiment: 20 - NOPB2 **Fraction:** NOPB2

Match to Query 8433: 1474.677248 from(738.345900,2+)
Title: OECHL100312_09.9707.9707.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1474.676224 **Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only) **Ions Score:** 70
Expect: 1.2e-005 **Matches :** 23/114 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**I**							**13**
2	215.139019	108.073147	197.128454	99.067865	**T**	***1362.599444***	681.803360	1345.572895	673.290086	1344.588879	672.798078	**12**
3	375.169668	188.088472	357.159103	179.083190	**C**	***1261.551765***	631.279521	1244.525216	622.766246	1243.541200	622.274238	**11**
4	**446.206782**	223.607029	428.196217	214.601747	**A**	***1101.521116***	551.264196	1084.494567	542.750922	1083.510551	542.258914	**10**
5	**575.249375**	288.128326	557.238810	279.123043	**E**	***1030.484002***	515.745639	1013.457453	507.232365	1012.473437	506.740357	**9**
6	704.291968	352.649622	686.281403	343.644340	**E**	***901.441409***	451.224343	884.414860	442.711068	883.430844	442.219060	**8**

7	761.313432	381.160354	743.302867	372.155072	**G**	***772.398816***	386.703046	755.372267	378.189772	754.388251	377.697764	**7**
8	**947.392745**	474.200011	929.382180	465.194728	**W**	715.377352	358.192314	698.350803	349.679040	697.366787	349.187032	**6**
9	**1034.424773**	517.716025	1016.414208	508.710742	**S**	***529.298039***	265.152658	512.271490	256.639383	511.287474	256.147375	**5**
10	1131.477537	566.242407	1113.466972	557.237124	**P**	***442.266011***	221.636644	425.239462	213.123369	424.255446	212.631361	**4**
11	**1232.525216**	616.766246	1214.514651	607.760964	**T**	***345.213247***	173.110262	328.186698	164.596987	327.202682	164.104979	**3**
12	1329.577980	665.292628	1311.567415	656.287346	**P**	***244.165568***	122.586422	227.139019	114.073148			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**

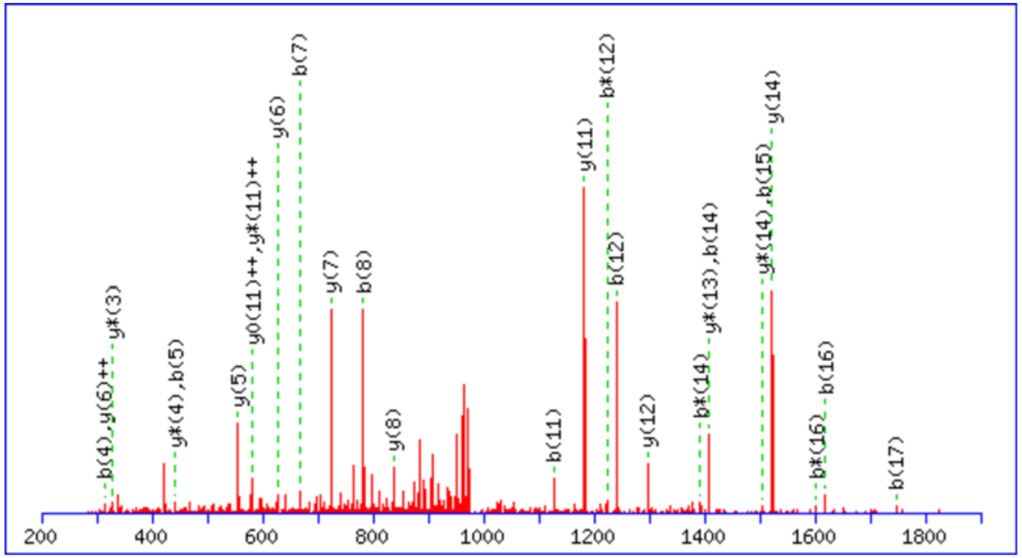


Peptide View

MS/MS Fragmentation of **ANAGKPKDPTFIPAPIQAK**
Found in **IPI00032220**, Tax_Id=9606 Gene_Symbol=AGT Angiotensinogen
Experiment: 20 - NOPB2 **Fraction:** NOPB2

Match to Query 11800: 1963.088448 from(982.551500,2+)
Title: OECHL100312_09.10861.10861.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1963.089066**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53
Expect: 0.00019**Matches :** 27/182 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**19**
2	186.087317	93.547296	169.060768	85.034022			**N**	1893.059261	947.033269	1876.032712	938.519994	1875.048696	938.027986	**18**
3	257.124431	129.065854	240.097882	120.552579			**A**	1779.016334	890.011805	1761.989785	881.498531	1761.005769	881.006523	**17**
4	***314.145895***	157.576585	297.119346	149.063311			**G**	1707.979220	854.493248	1690.952671	845.979974	1689.968655	845.487965	**16**
5	***442.240858***	221.624067	425.214309	213.110793			**K**	1650.957756	825.982516	1633.931207	817.469242	1632.947191	816.977234	**15**
6	539.293622	270.150449	522.267073	261.637175			**P**	**1522.862793**	761.935035	1505.836244	753.421760	1504.852228	752.929752	**14**
7	***667.388585***	334.197931	650.362036	325.684656			**K**	1425.810029	713.408653	1408.783480	704.895378	1407.799464	704.403370	**13**
8	***782.415528***	391.711402	765.388979	383.198128	764.404963	382.706120	**D**	**1297.715066**	649.361171	1280.688517	640.847897	1279.704501	640.355888	**12**
9	879.468292	440.237784	862.441743	431.724510	861.457727	431.232502	**P**	**1182.688123**	591.847700	1165.661574	583.334425	1164.677558	582.842417	**11**
10	980.515971	490.761624	963.489422	482.248349	962.505406	481.756341	**T**	1085.635359	543.321318	1068.608810	534.808043	1067.624794	534.316035	**10**
11	***1127.584385***	564.295831	1110.557836	555.782556	1109.573820	555.290548	**F**	984.587680	492.797478	967.561131	484.284204			**9**
12	***1240.668449***	620.837863	1223.641900	612.324588	1222.657884	611.832580	**I**	**837.519266**	419.263271	820.492717	410.749997			**8**
13	1337.721213	669.364245	1320.694664	660.850970	1319.710648	660.358962	**P**	**724.435202**	362.721239	707.408653	354.207965			**7**
14	***1408.758327***	704.882802	1391.731778	696.369527	1390.747762	695.877519	**A**	**627.382438**	314.194857	610.355889	305.681583			**6**
15	***1505.811091***	753.409184	1488.784542	744.895909	1487.800526	744.403901	**P**	**556.345324**	278.676300	539.318775	270.163026			**5**
16	***1618.895155***	809.951215	1601.868606	801.437941	1600.884590	800.945933	**I**	459.292560	230.149918	442.266011	221.636643			**4**
17	***1746.953733***	873.980505	1729.927184	865.467230	1728.943168	864.975222	**Q**	346.208496	173.607886	329.181947	165.094612			**3**
18	1817.990847	909.499062	1800.964298	900.985787	1799.980282	900.493779	**A**	218.149918	109.578597	201.123369	101.065322			**2**
19							**K**	147.112804	74.060040	130.086255	65.546765			**1**



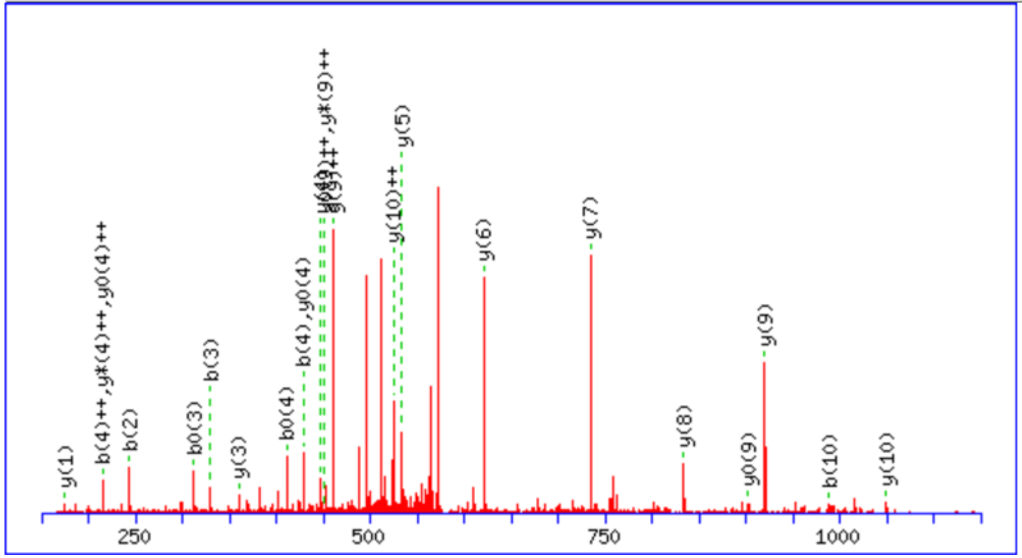
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 20 - NOPB2 **Fraction:** NOPB2

Match to Query 4715: 1161.635048 from(581.824800,2+)
Title: OECHL100312_09.5136.5136.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00049**Matches :** 24/94 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					**I**							**11**
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637	**10**
3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340	**9**
4	**429.234375**	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326	**8**
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119	**7**
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087	**6**

7	716.382495	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073	**5**
8	803.414523	402.210899			785.403958	393.205617	**S**	***447.267407***	224.137342	430.240858	215.624067	429.256842	215.132059	**4**
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053			**3**
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



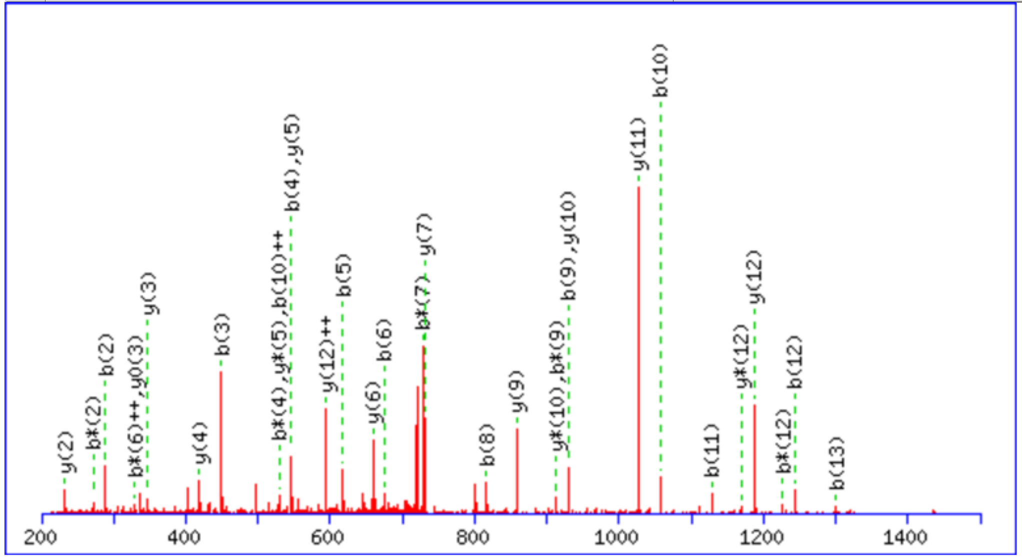
Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 20 - NOPB2 **Fraction:** NOPB2

Match to Query 8420: 1473.646048 from(737.830300,2+)
Title: OECHL100312_09.7040.7040.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 74
Expect: 1.8e-006**Matches :** 33/128 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	161.037925	81.022600					**C**							**14**

2	***289.096503***	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.809312	**13**
3	***449.127152***	225.067214	432.100603	216.553940			**C**	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.780023	**12**
4	***546.179916***	273.593596	529.153367	265.080322			**P**	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.764698	**11**
5	***617.217030***	309.112153	600.190481	300.598879			**A**	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.238316	**10**
6	***674.238494***	337.622885	657.211945	329.109611			**G**	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.719759	**9**
7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
8	***816.312722***	408.659999	799.286173	400.146725			**A**	**730.384229**	365.695753	713.357680	357.182478	712.373664	356.690470	**7**
9	***929.396786***	465.202031	912.370237	456.688757			**L**	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.171913	**6**
10	***1057.455364***	529.231320	1040.428815	520.718046			**Q**	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.629881	**5**
11	***1128.492478***	564.749877	1111.465929	556.236603			**A**	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.600592	**4**
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	**347.167359**	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
13	***1300.540885***	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	**232.140416**	116.573846	215.113867	108.060571			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



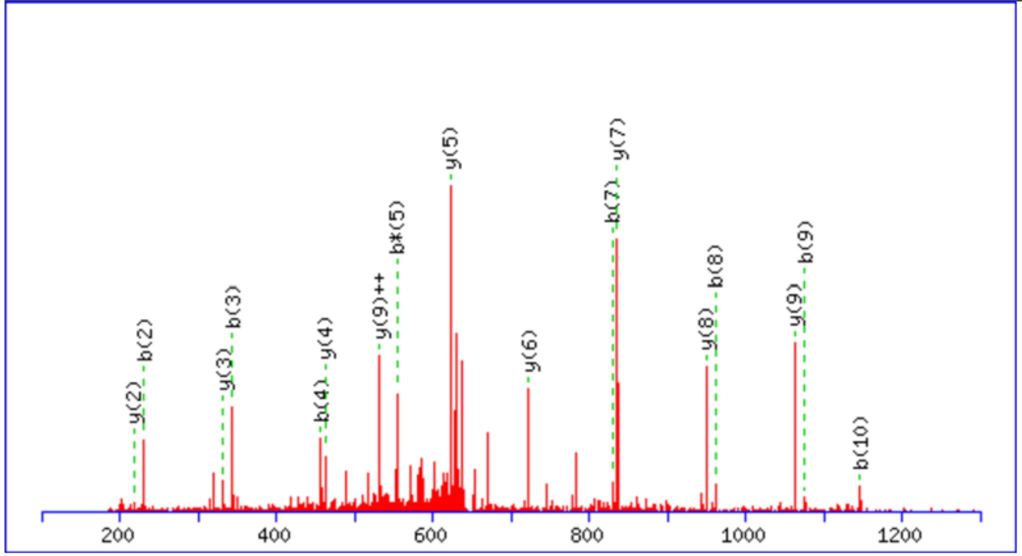
Peptide View

MS/MS Fragmentation of **TELLNVCMNAK**

Found in **IPI00441498**, Tax_Id=9606 Gene_Symbol=FOLR1 Folate receptor alpha
Experiment: 20 - NOPB2 **Fraction:** NOPB2

Match to Query 6597: 1291.627048 from(646.820800,2+)
Title: OECHL100312_09.13253.13253.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1291.626419**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.0011**Matches :** 17/94 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	102.054955	51.531116			84.044390	42.525833	T							11
2	***231.097548***	116.052412			213.086983	107.047130	E	1191.586041	596.296659	1174.559492	587.783384	1173.575476	587.291376	10
3	***344.181612***	172.594444			326.171047	163.589162	L	***1062.543448***	531.775362	1045.516899	523.262088			9
4	***457.265676***	229.136476			439.255111	220.131194	L	***949.459384***	475.233330	932.432835	466.720056			8
5	571.308603	286.157940	554.282054	277.644665	553.298038	277.152657	N	***836.375320***	418.691298	819.348771	410.178023			7
6	670.377017	335.692147	653.350468	327.178872	652.366452	326.686864	V	***722.332393***	361.669835	705.305844	353.156560			6
7	***830.407666***	415.707471	813.381117	407.194197	812.397101	406.702189	C	***623.263979***	312.135628	606.237430	303.622353			5
8	***961.448151***	481.227714	944.421602	472.714439	943.437586	472.222431	M	***463.233330***	232.120303	446.206781	223.607028			4
9	***1075.491078***	538.249177	1058.464529	529.735903	1057.480513	529.243895	N	***332.192845***	166.600060	315.166296	158.086786			3
10	***1146.528192***	573.767734	1129.501643	565.254460	1128.517627	564.762452	A	***218.149918***	109.578597	201.123369	101.065322			2
11							K	147.112804	74.060040	130.086255	65.546765			1

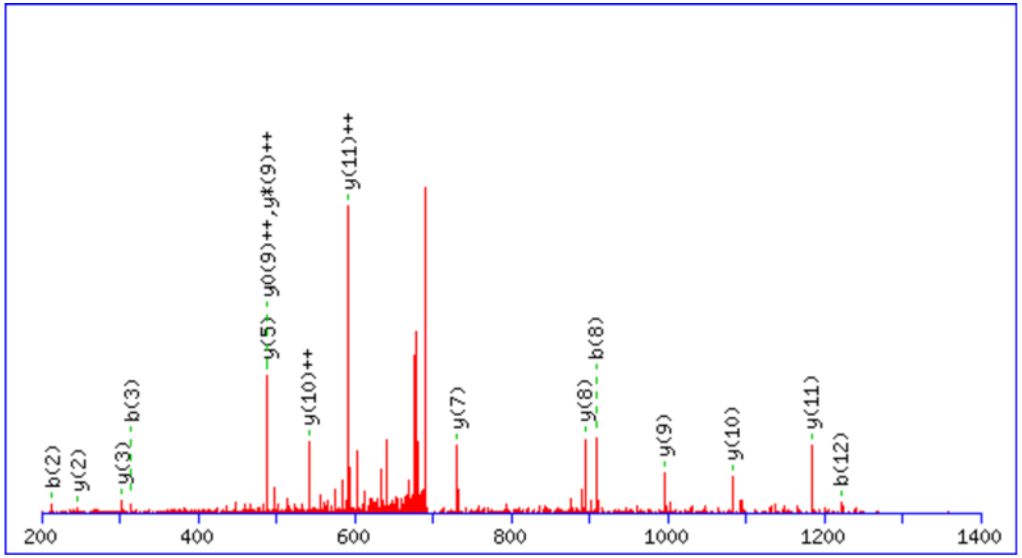


Peptide View

MS/MS Fragmentation of **IVTSTYKDGKGAR**
Found in **IPI00002745**, Tax_Id=9606 Gene_Symbol=CTSZ Cathepsin Z
Experiment: 20 - NOPB2 **Fraction:** NOPB2

Match to Query 7716: 1394.752448 from(698.383500,2+)
Title: OECHL100312_09.2294.2294.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1394.751770**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 5.4e-005**Matches :** 16/118 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	114.091340	57.549308					I							13
2	**213.159754**	107.083515					V	1282.674992	641.841134	1265.648443	633.327860	1264.664427	632.835851	12
3	**314.207433**	157.607354			296.196868	148.602072	T	***1183.606578***	592.306927	1166.580029	583.793653	1165.596013	583.301644	11
4	401.239461	201.123368			383.228896	192.118086	S	***1082.558899***	541.783087	1065.532350	533.269813	1064.548334	532.777805	10
5	502.287140	251.647208			484.276575	242.641925	T	***995.526871***	498.267073	978.500322	489.753799	977.516306	489.261791	9
6	665.350469	333.178873			647.339904	324.173590	Y	***894.479192***	447.743234	877.452643	439.229959	876.468627	438.737951	8
7	793.445432	397.226354	776.418883	388.713079	775.434867	388.221071	K	***731.415863***	366.211570	714.389314	357.698295	713.405298	357.206287	7
8	**908.472375**	454.739825	891.445826	446.226551	890.461810	445.734543	D	603.320900	302.164088	586.294351	293.650813	585.310335	293.158805	6
9	965.493839	483.250558	948.467290	474.737283	947.483274	474.245275	G	***488.293957***	244.650616	471.267408	236.137342			5
10	1093.588802	547.298039	1076.562253	538.784765	1075.578237	538.292757	K	431.272493	216.139884	414.245944	207.626610			4
11	1150.610266	575.808771	1133.583717	567.295497	1132.599701	566.803488	G	***303.177530***	152.092403	286.150981	143.579128			3
12	**1221.647380**	611.327328	1204.620831	602.814054	1203.636815	602.322045	A	***246.156066***	123.581671	229.129517	115.068396			2
13							R	175.118952	88.063114	158.092403	79.549839			1



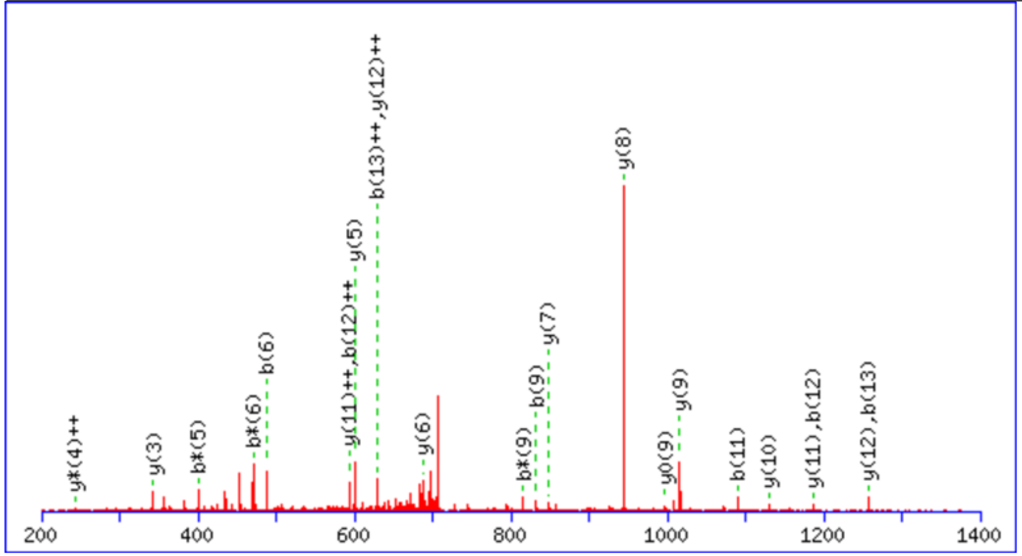
Peptide View

MS/MS Fragmentation of **SSAGNAPCSPCPAR**
Found in **IPI00005222**, Tax_Id=9606 Gene_Symbol=EPHB6 ephrin receptor EphB6 precursor
Experiment: 20 - NOPB2 **Fraction:** NOPB2

Match to Query 8033: 1430.604048 from(716.309300,2+)
Title: OECHL100312_09.2963.2963.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1430.603073**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 2.2e-005**Matches :** 23/138 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	**S**							**14**
2	175.071332	88.039304			157.060767	79.034021	**S**	1344.578331	672.792803	1327.551782	664.279529	1326.567766	663.787521	**13**
3	246.108446	123.557861			228.097881	114.552578	**A**	***1257.546303***	629.276790	1240.519754	620.763515	1239.535738	620.271507	**12**
4	303.129910	152.068593			285.119345	143.063311	**G**	***1186.509189***	593.758233	1169.482640	585.244958	1168.498624	584.752950	**11**
5	417.172837	209.090057	400.146288	200.576782	399.162272	200.084774	**N**	***1129.487725***	565.247501	1112.461176	556.734226	1111.477160	556.242218	**10**
6	**488.209951**	244.608613	471.183402	236.095339	470.199386	235.603331	**A**	***1015.444798***	508.226037	998.418249	499.712763	997.434233	499.220755	**9**

7	585.262715	293.134996	568.236166	284.621721	567.252150	284.129713	**P**	***944.407684***	472.707480	927.381135	464.194206	926.397119	463.702198	**8**
8	745.293364	373.150320	728.266815	364.637046	727.282799	364.145038	**C**	***847.354920***	424.181098	830.328371	415.667824	829.344355	415.175816	**7**
9	**832.325392**	416.666334	815.298843	408.153060	814.314827	407.661052	**S**	***687.324271***	344.165774	670.297722	335.652499	669.313706	335.160491	**6**
10	929.378156	465.192716	912.351607	456.679442	911.367591	456.187434	**P**	***600.292243***	300.649760	583.265694	292.136485			**5**
11	**1089.408805**	545.208041	1072.382256	536.694766	1071.398240	536.202758	**C**	503.239479	252.123377	486.212930	243.610103			**4**
12	**1186.461569**	**593.734423**	1169.435020	585.221148	1168.451004	584.729140	**P**	***343.208830***	172.108053	326.182281	163.594778			**3**
13	**1257.498683**	**629.252980**	1240.472134	620.739705	1239.488118	620.247697	**A**	246.156066	123.581671	229.129517	115.068396			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



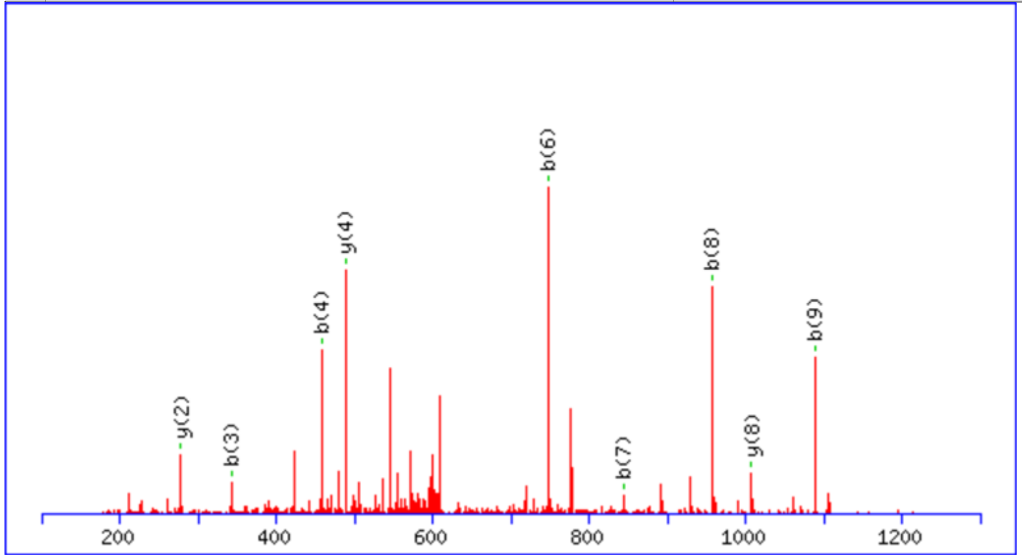
Peptide View

MS/MS Fragmentation of **ARDDCEPLMK**
Found in **IPI00017557**, Tax_Id=9606 Gene_Symbol=SFRP4 Secreted frizzled-related protein 4
Experiment: 20 - NOPB2 **Fraction:** NOPB2

Match to Query 5826: 1233.548848 from(617.781700,2+)
Title: OECHL100312_09.5001.5001.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1233.548172**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54

Expect: 0.00026**Matches :** 9/94 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	72.044390	36.525833					**A**							**10**
2	228.145501	114.576388	211.118952	106.063114			**R**	1163.518356	582.262816	1146.491807	573.749542	1145.507791	573.257534	**9**
3	***343.172444***	172.089860	326.145895	163.576585	325.161879	163.084577	**D**	**1007.417245**	504.212261	990.390696	495.698986	989.406680	495.206978	**8**
4	***458.199387***	229.603332	441.172838	221.090057	440.188822	220.598049	**D**	892.390302	446.698789	875.363753	438.185515	874.379737	437.693507	**7**
5	618.230036	309.618656	601.203487	301.105382	600.219471	300.613374	**C**	777.363359	389.185318	760.336810	380.672043	759.352794	380.180035	**6**
6	***747.272629***	374.139953	730.246080	365.626678	729.262064	365.134670	**E**	617.332710	309.169993	600.306161	300.656719	599.322145	300.164711	**5**
7	***844.325393***	422.666335	827.298844	414.153060	826.314828	413.661052	**P**	**488.290117**	244.648696	471.263568	236.135422			**4**
8	***957.409457***	479.208367	940.382908	470.695092	939.398892	470.203084	**L**	391.237353	196.122314	374.210804	187.609040			**3**
9	***1088.449942***	544.728609	1071.423393	536.215335	1070.439377	535.723326	**M**	**278.153289**	139.580282	261.126740	131.067008			**2**
10							**K**	147.112804	74.060040	130.086255	65.546765			**1**

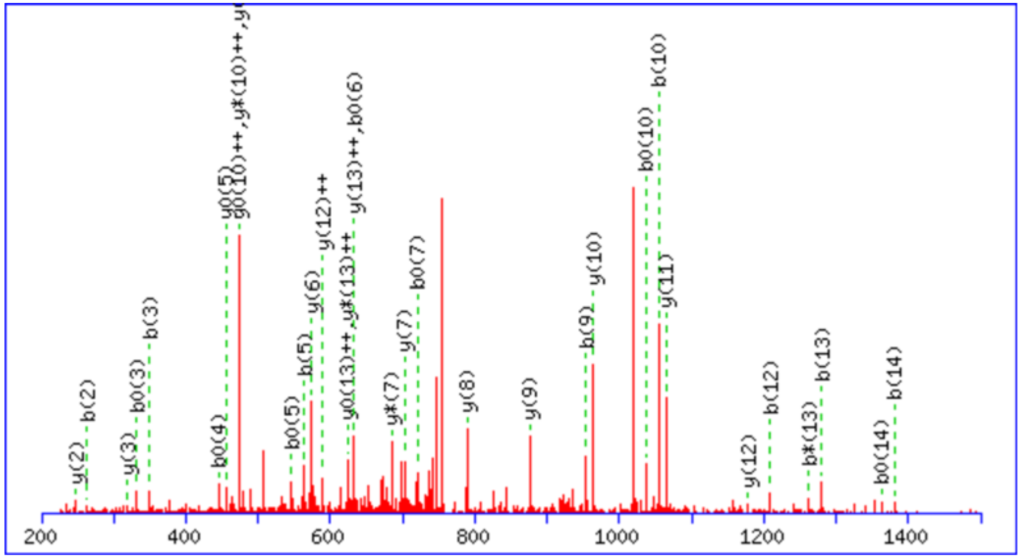


Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 20 - NOPB2 **Fraction:** NOPB2

Match to Query 8895: 1525.726448 from(763.870500,2+)
Title: OECHL100312_09.10382.10382.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57
Expect: 0.00025**Matches :** 34/150 fragment ions using 63 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	***350.134661***	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	**9**
8	825.362488	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.203410	**8**
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	**7**
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	**6**
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	**5**
12	***1208.542973***	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	376.219061	188.613168	359.192512	180.099894	358.208496	179.607886	**4**
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	***319.197597***	160.102436	302.171048	151.589162	301.187032	151.097154	**3**
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



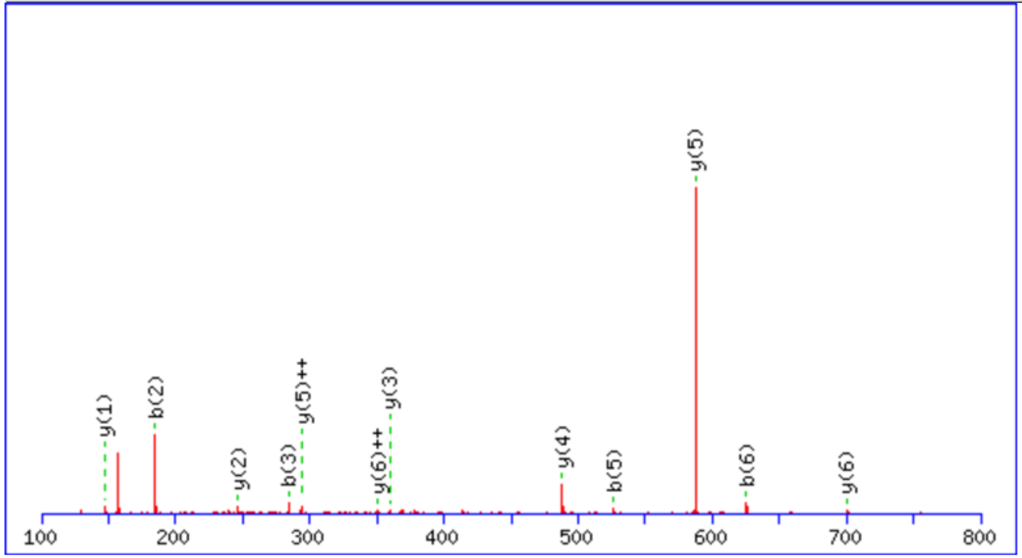
Peptide View

MS/MS Fragmentation of **ALVQIVK**
Found in **IPI00216569**, Tax_Id=9606 Gene_Symbol=CST7 Cystatin-F precursor
Experiment: 20 - NOPB2 **Fraction:** NOPB2

Match to Query 575: 770.489648 from(386.252100,2+)
Title: OECHL100312_09.11311.11311.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 770.490173**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: Q4 :** Deamidated (NQ)**Ions Score:** 53 **Expect:** 0.00021**Matches :** 12/42 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					7
2	**185.128454**	93.067865			L	***700.460354***	350.733815	683.433805	342.220541	6
3	**284.196868**	142.602072			V	***587.376290***	294.191783	570.349741	285.678509	5
4	413.239462	207.123369	396.212913	198.610095	Q	***488.307876***	244.657576	471.281327	236.144301	4
5	**526.323526**	263.665401	509.296977	255.152127	I	***359.265282***	180.136279	342.238733	171.623004	3
6	**625.391940**	313.199608	608.365391	304.686333	V	***246.181218***	123.594247	229.154669	115.080972	2

7					**K**	***147.112804***	74.060040	130.086255	65.546765	**1**



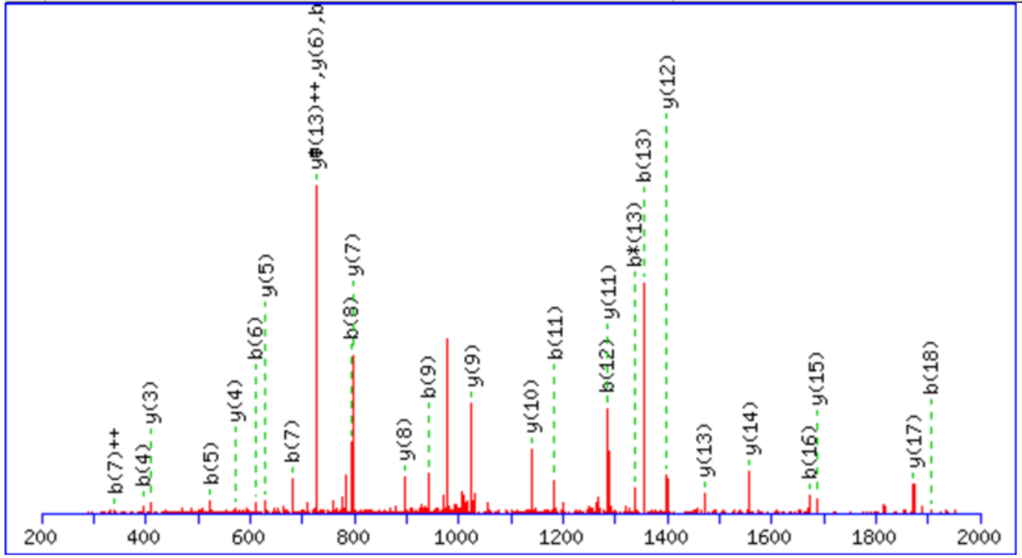
Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 08 - S_C-2 **Fraction:** S_C-2

Match to Query 12536: 2078.983448 from(1040.499000,2+)
Title: OECHL100312_05.15741.15741.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 95
Expect: 5.2e-008**Matches :** 30/200 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	72.044390	36.525833					**A**							**19**
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973939	**18**
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444483	**17**
4	**394.183344**	197.595310	377.156795	189.082035			**Q**	1814.870790	907.939033	1797.844241	899.425759	1796.860225	898.933751	**16**
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904462	**15**

6	**610.257965**	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383165	**14**
7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867151	**13**
8	**794.379143**	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348594	**12**
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806562	**11**
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272355	**10**
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250892	**9**
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729595	**8**
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195388	**7**
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676831	**6**
15	1508.712833	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150449	**5**
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	***572.282723***	286.645000	555.256174	278.131725	554.272158	277.639717	**4**
17	1818.844576	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	**3**
18	**1905.876604**	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
19							**R**	175.118952	88.063114	158.092403	79.549840			**1**

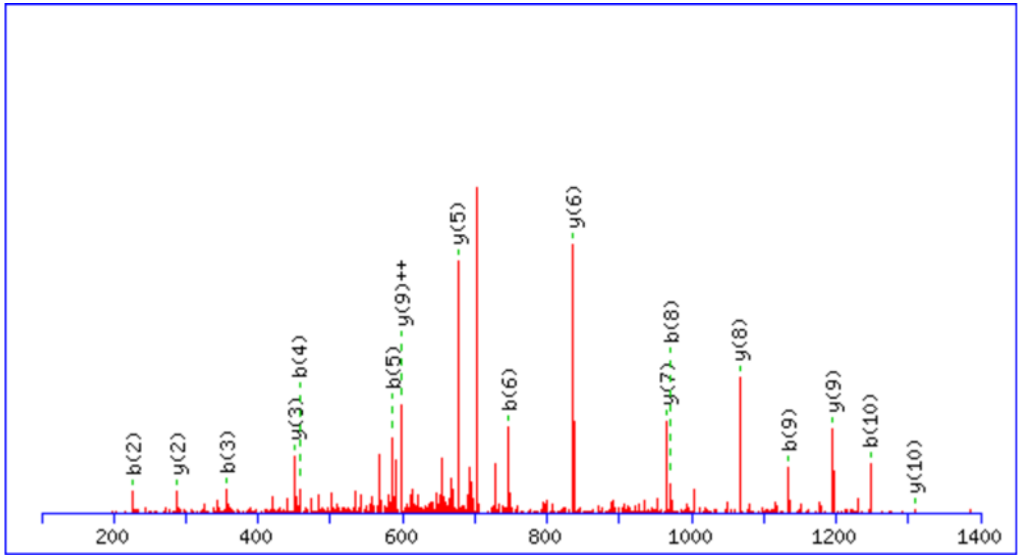


Peptide View

MS/MS Fragmentation of **LLETECPQYIR**
Found in **IPI00007047**, Tax_Id=9606 Gene_Symbol=S100A8 Protein S100-A8
Experiment: 08 - S_C-2 **Fraction:** S_C-2

Match to Query 8250: 1420.701448 from(711.358000,2+)
Title: OECHL100312_05.11194.11194.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1420.702026**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70
Expect: 1.4e-005**Matches :** 17/90 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	114.091340	57.549308					L							11
2	***227.175404***	114.091340					L	***1308.625265***	654.816271	1291.598716	646.302996	1290.614700	645.810988	10
3	***356.217997***	178.612637			338.207432	169.607354	E	***1195.541201***	598.274239	1178.514652	589.760964	1177.530636	589.268956	9
4	***457.265676***	229.136476			439.255111	220.131194	T	***1066.498608***	533.752942	1049.472059	525.239668	1048.488043	524.747660	8
5	***586.308269***	293.657773			568.297704	284.652490	E	***965.450929***	483.229103	948.424380	474.715828	947.440364	474.223820	7
6	***746.338918***	373.673097			728.328353	364.667815	C	***836.408336***	418.707806	819.381787	410.194531			6
7	843.391682	422.199479			825.381117	413.194197	P	***676.377687***	338.692481	659.351138	330.179207			5
8	***971.450260***	486.228768	954.423711	477.715494	953.439695	477.223486	Q	579.324923	290.166099	562.298374	281.652825			4
9	***1134.513589***	567.760433	1117.487040	559.247158	1116.503024	558.755150	Y	***451.266345***	226.136810	434.239796	217.623536			3
10	***1247.597653***	624.302465	1230.571104	615.789190	1229.587088	615.297182	I	***288.203016***	144.605146	271.176467	136.091871			2
11							R	175.118952	88.063114	158.092403	79.549839			1



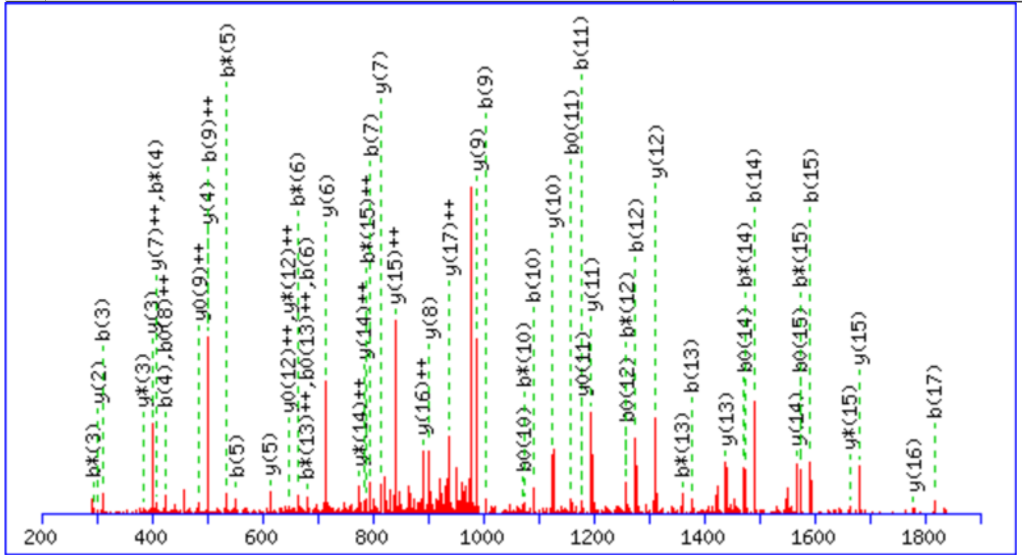
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 08 - S_C-2 **Fraction:** S_C-2

Match to Query 12196: 1990.024048 from(996.019300,2+)
Title: OECHL100312_05.8946.8946.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 86
Expect: 3.4e-007**Matches :** 59/186 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	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	**424.255445**	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	**552.314023**	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	**680.372601**	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**

7	**795.399544**	398.203410	778.372995	389.690136	777.388979	389.198128	D	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	12
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	A	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	11
9	**1003.495570**	502.251423	986.469021	493.738149	985.485005	493.246141	H	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	10
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	S	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	9
11	**1177.559626**	589.283451	1160.533077	580.770177	1159.549061	580.278169	S	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	8
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	V	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.737420	7
13	**1377.675719**	689.341498	1360.649170	680.828223	1359.665154	680.336215	T	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	6
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	I	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	5
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	T	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	4
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	P	***400.230294***	200.618785	383.203745	192.105510			3
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	Q	***303.177530***	152.092403	286.150981	143.579128			2
18							R	175.118952	88.063114	158.092403	79.549839			1

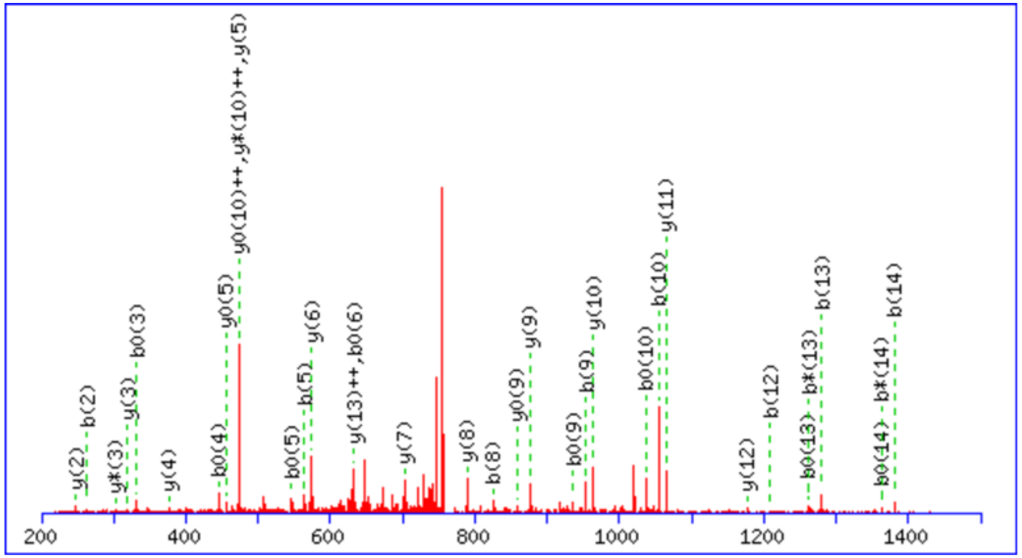


Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 08 - S_C-2 **Fraction:** S_C-2

Match to Query 9232: 1525.727448 from(763.871000,2+)
Title: OECHL100312_05.10003.10003.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 0.00016**Matches :** 35/150 fragment ions using 73 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	**263.102633**	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	350.134661	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	**564.266404**	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	**9**
8	**825.362488**	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.203410	**8**
9	**953.421066**	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	**7**
10	**1054.468745**	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	**6**
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	**5**
12	**1208.542973**	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	**4**
13	**1279.580087**	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	***319.197597***	160.102436	302.171048	151.589162	301.187032	151.097154	**3**
14	**1380.627766**	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



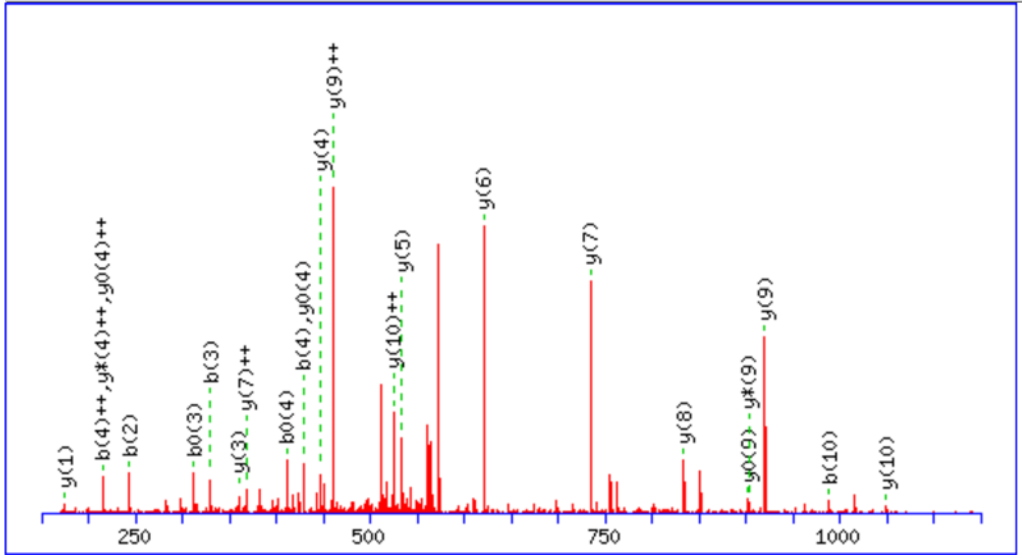
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 08 - S_C-2 **Fraction:** S_C-2

Match to Query 4941: 1161.635048 from(581.824800,2+)
Title: OECHL100312_05.4843.4843.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65
Expect: 2.3e-005**Matches :** 24/94 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					**I**							**11**
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637	**10**
3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340	**9**
4	**429.234375**	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326	**8**
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119	**7**
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087	**6**

7	716.382495	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073	**5**
8	803.414523	402.210899			785.403958	393.205617	**S**	***447.267407***	224.137342	430.240858	215.624067	429.256842	215.132059	**4**
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053			**3**
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



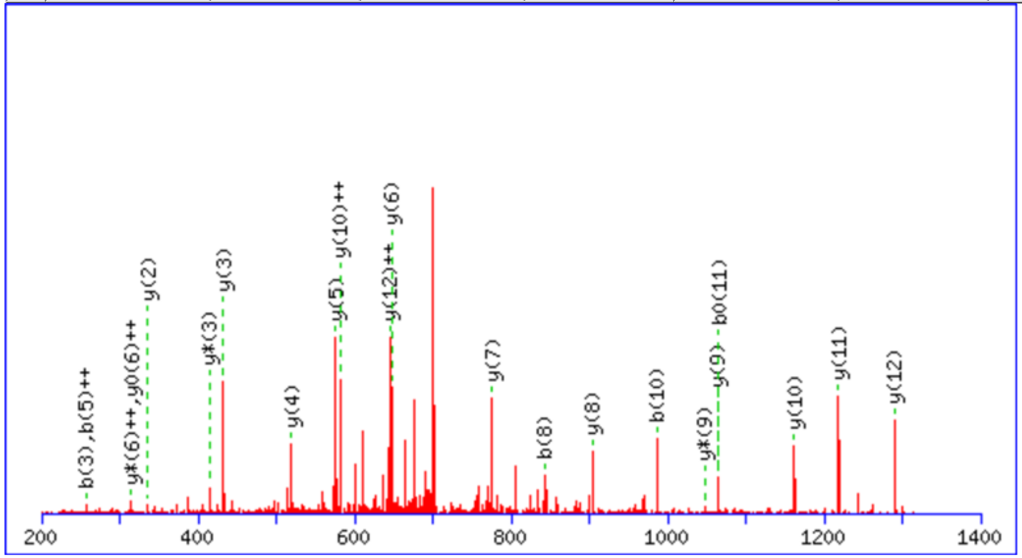
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 08 - S_C-2 **Fraction:** S_C-2

Match to Query 8209: 1416.624048 from(709.319300,2+)
Title: OECHL100312_05.1658.1658.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 87
Expect: 1.1e-007**Matches :** 22/128 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							**13**

2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	**12**
3	**257.160817**	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	**11**
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	**10**
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	**9**
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	**8**
7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	899.403979	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

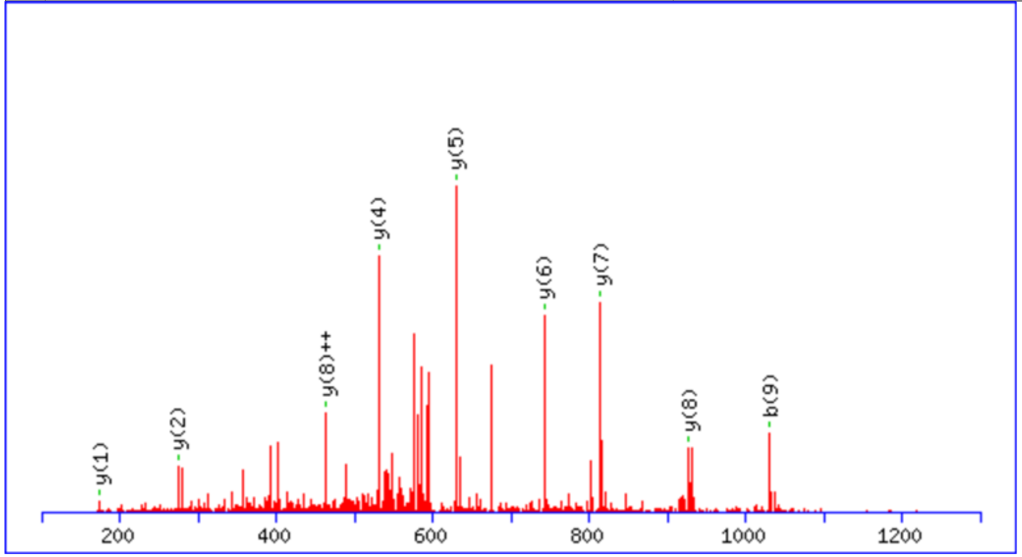


Peptide View

MS/MS Fragmentation of **YDIALVQEVR**
Found in **IPI00031065**, Tax_Id=9606 Gene_Symbol=DNASE1 Deoxyribonuclease-1
Experiment: 08 - S_C-2 **Fraction:** S_C-2

Match to Query 5583: 1204.645248 from(603.329900,2+)
Title: OECHL100312_05.14199.14199.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1204.645172**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00024**Matches :** 9/90 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	164.070605	82.538940					**Y**							**10**
2	279.097548	140.052412			261.086983	131.047130	**D**	1042.589136	521.798206	1025.562587	513.284932	1024.578571	512.792924	**9**
3	392.181612	196.594444			374.171047	187.589162	**I**	***927.562193***	464.284735	910.535644	455.771460	909.551628	455.279452	**8**
4	463.218726	232.113001			445.208161	223.107719	**A**	***814.478129***	407.742703	797.451580	399.229428	796.467564	398.737420	**7**
5	576.302790	288.655033			558.292225	279.649751	**L**	***743.441015***	372.224146	726.414466	363.710871	725.430450	363.218863	**6**
6	675.371204	338.189240			657.360639	329.183958	**V**	***630.356951***	315.682114	613.330402	307.168839	612.346386	306.676831	**5**
7	803.429782	402.218529	786.403233	393.705255	785.419217	393.213247	**Q**	***531.288537***	266.147907	514.261988	257.634632	513.277972	257.142624	**4**
8	932.472375	466.739826	915.445826	458.226551	914.461810	457.734543	**E**	403.229959	202.118618	386.203410	193.605343	385.219394	193.113335	**3**
9	1031.540789	516.274033	1014.514240	507.760758	1013.530224	507.268750	**V**	***274.187366***	137.597321	257.160817	129.084047			**2**
10							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**

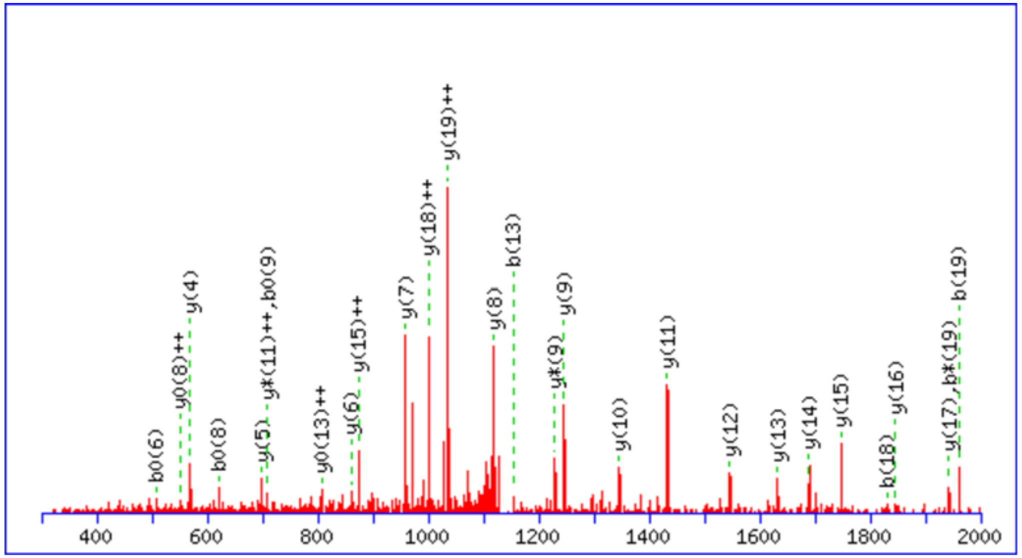


Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 08 - S_C-2 **Fraction:** S_C-2

Match to Query 13200: 2270.113448 from(1136.064000,2+)
Title: OECHL100312_05.9667.9667.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 87
Expect: 4.1e-007**Matches :** 28/212 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	102.054955	51.531116			84.044390	42.525833	T						
2	201.123369	101.065322			183.112804	92.060040	V	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400	1076.5338
3	272.160483	136.583879			254.149918	127.578597	A	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986	1026.9996
4	329.181947	165.094611			311.171382	156.089329	G	1999.965437	1000.486357	1982.938888	991.973082	1981.954872	991.4810
5	426.234711	213.620994			408.224146	204.615711	P	***1942.943973***	971.975625	1925.917424	963.462350	1924.933408	962.9703
6	525.303125	263.155201			507.292560	254.149918	V	***1845.891209***	923.449243	1828.864660	914.935968	1827.880644	914.4439
7	582.324589	291.665933			564.314024	282.660650	G	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230	864.9097
8	639.346053	320.176665			621.335488	311.171382	G	***1689.801331***	845.404304	1672.774782	836.891029	1671.790766	836.3990
9	726.378081	363.692679			708.367516	354.687396	S	***1632.779867***	816.893572	1615.753318	808.380297	1614.769302	807.8882
10	839.462145	420.234711			821.451580	411.229428	L	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274	764.3722
11	926.494173	463.750725			908.483608	454.745442	S	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210	707.8302
12	1025.562587	513.284932			1007.552022	504.279649	V	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182	664.3142
13	**1153.621165**	577.314221	1136.594616	568.800946	1135.610600	568.308938	Q	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768	614.7800
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	C	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190	550.7507
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	P	***958.474106***	479.740691	941.447557	471.227417	940.463541	470.7354
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	Y	***861.421342***	431.214309	844.394793	422.701035	843.410777	422.2090
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	E	***698.358013***	349.682645	681.331464	341.169370	680.347448	340.6773
18	**1830.905463**	915.956370	1813.878914	907.443095	1812.894898	906.951087	K	***569.315420***	285.161348	552.288871	276.648074	551.304855	276.1560
19	**1959.948056**	980.477666	1942.921507	971.964392	1941.937491	971.472384	E	441.220457	221.113867	424.193908	212.600592	423.209892	212.1085
20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	H	312.177864	156.592570	295.151315	148.079295		
21							R	175.118952	88.063114	158.092403	79.549839		



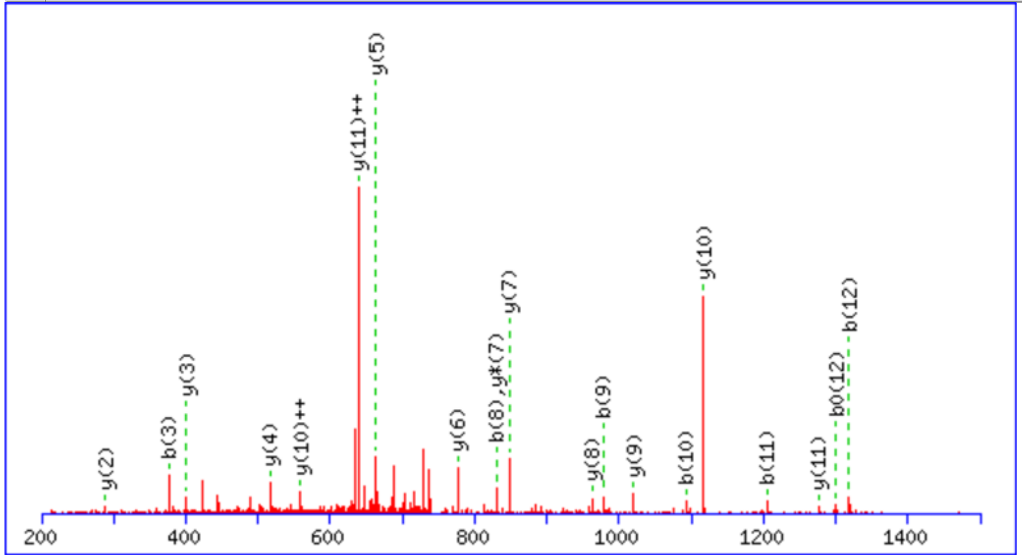
Peptide View

MS/MS Fragmentation of **TDCPGDALFDLLR**
Found in **IPI00163207**, Tax_Id=9606 Gene_Symbol=PGLYRP2 Isoform 1 of N-acetylmuramoyl-L-alanine amidase
Experiment: 08 - S_C-2 **Fraction:** S_C-2

Match to Query 8901: 1491.701448 from(746.858000,2+)
Title: OECHL100312_05.18109.18109.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1491.702789**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 68
Expect: 1.5e-005**Matches :** 20/114 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							**13**
2	217.081898	109.044587	199.071333	100.039304	**D**	1391.662378	696.334827	1374.635829	687.821552	1373.651813	687.329544	**12**
3	**377.112547**	189.059912	359.101982	180.054629	**C**	***1276.635435***	638.821355	1259.608886	630.308081	1258.624870	629.816073	**11**
4	474.165311	237.586294	456.154746	228.581011	**P**	***1116.604786***	558.806031	1099.578237	550.292756	1098.594221	549.800748	**10**
5	531.186775	266.097026	513.176210	257.091743	**G**	***1019.552022***	510.279649	1002.525473	501.766374	1001.541457	501.274366	**9**
6	646.213718	323.610497	628.203153	314.605215	**D**	***962.530558***	481.768917	945.504009	473.255642	944.519993	472.763634	**8**

7	717.250832	359.129054	699.240267	350.123772	**A**	***847.503615***	424.255445	830.477066	415.742171	829.493050	415.250163	**7**
8	**830.334896**	415.671086	812.324331	406.665804	**L**	***776.466501***	388.736888	759.439952	380.223614	758.455936	379.731606	**6**
9	**977.403310**	489.205293	959.392745	480.200011	**F**	***663.382437***	332.194856	646.355888	323.681582	645.371872	323.189574	**5**
10	**1092.430253**	546.718765	1074.419688	537.713482	**D**	***516.314023***	258.660649	499.287474	250.147375	498.303458	249.655367	**4**
11	**1205.514317**	603.260796	1187.503752	594.255514	**L**	***401.287080***	201.147178	384.260531	192.633903			**3**
12	**1318.598381**	659.802828	1300.587816	650.797546	**L**	***288.203016***	144.605146	271.176467	136.091871			**2**
13					**R**	175.118952	88.063114	158.092403	79.549839			**1**

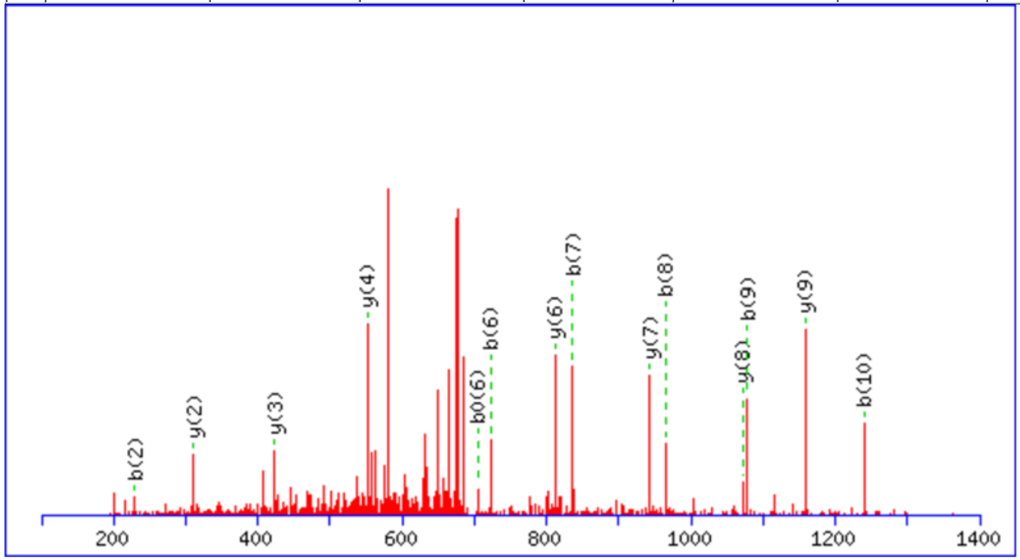


Peptide View

MS/MS Fragmentation of **DISEMFLQIYK**
Found in **IPI00385161**, Tax_Id=9606 Gene_Symbol=MUC1 Mucin short variant SV10
Experiment: 08 - S_C-2 **Fraction:** S_C-2

Match to Query 7940: 1385.689648 from(693.852100,2+)
Title: OECHL100312_05.17946.17946.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1385.690063**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 0.00045**Matches :** 14/92 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	116.034219	58.520748			98.023654	49.515465	**D**							**11**
2	***229.118283***	115.062779			211.107718	106.057497	**I**	1271.670423	636.338850	1254.643874	627.825575	1253.659858	627.333567	**10**
3	316.150311	158.578793			298.139746	149.573511	**S**	***1158.586359***	579.796818	1141.559810	571.283543	1140.575794	570.791535	**9**
4	445.192904	223.100090			427.182339	214.094808	**E**	***1071.554331***	536.280804	1054.527782	527.767529	1053.543766	527.275521	**8**
5	576.233389	288.620333			558.222824	279.615050	**M**	***942.511738***	471.759507	925.485189	463.246233			**7**
6	***723.301803***	362.154540			705.291238	353.149257	**F**	***811.471253***	406.239265	794.444704	397.725990			**6**
7	***836.385867***	418.696572			818.375302	409.691289	**L**	664.402839	332.705058	647.376290	324.191783			**5**
8	***964.444445***	482.725861	947.417896	474.212586	946.433880	473.720578	**Q**	***551.318775***	276.163026	534.292226	267.649751			**4**
9	***1077.528509***	539.267893	1060.501960	530.754618	1059.517944	530.262610	**I**	***423.260197***	212.133737	406.233648	203.620462			**3**
10	***1240.591838***	620.799557	1223.565289	612.286283	1222.581273	611.794275	**Y**	***310.176133***	155.591705	293.149584	147.078430			**2**
11							**K**	147.112804	74.060040	130.086255	65.546765			**1**



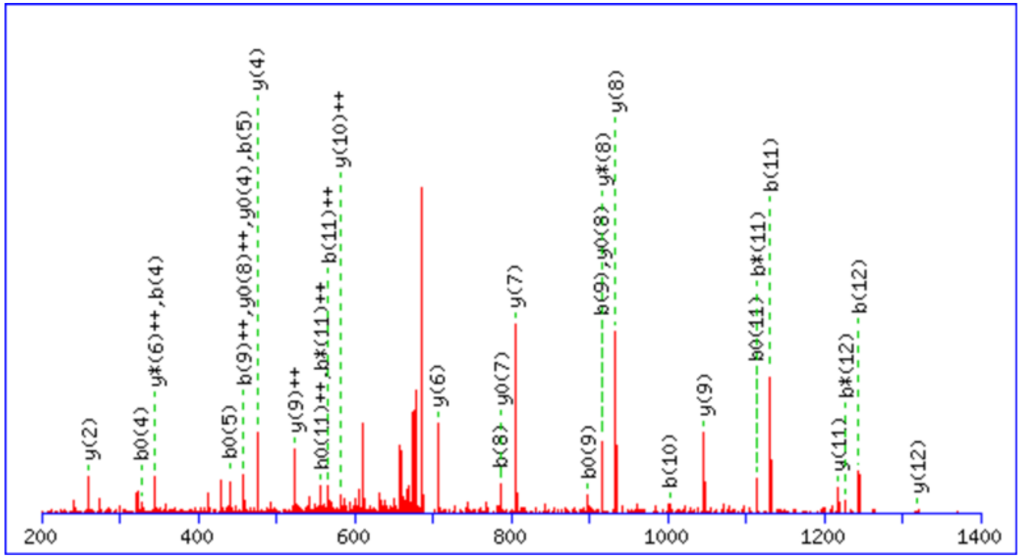
Peptide View

MS/MS Fragmentation of **ATGDIKVTESEIK**
Found in **IPI00302614**, Tax_Id=9606 Gene_Symbol=VTCN1 V-set domain containing T cell activation inhibitor 1

Experiment: 08 - S_C-2 **Fraction:** S_C-2

Match to Query 7980: 1389.735248 from(695.874900,2+)
Title: OECHL100312_05.7177.7177.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1389.735107**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 0.0003**Matches :** 33/128 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	72.044390	36.525833					**A**							**13**
2	173.092069	87.049672			155.081504	78.044390	**T**	***1319.705288***	660.356282	1302.678739	651.843008	1301.694723	651.350999	**12**
3	230.113533	115.560404			212.102968	106.555122	**G**	***1218.657609***	609.832442	1201.631060	601.319168	1200.647044	600.827160	**11**
4	***345.140476***	173.073876			327.129911	164.068593	**D**	1161.636145	581.321710	1144.609596	572.808436	1143.625580	572.316428	**10**
5	***458.224540***	229.615908			440.213975	220.610626	**I**	***1046.609202***	523.808239	1029.582653	515.294964	1028.598637	514.802956	**9**
6	586.319503	293.663390	569.292954	285.150115	568.308938	284.658107	**K**	***933.525138***	467.266207	916.498589	458.752932	915.514573	458.260924	**8**
7	685.387917	343.197597	668.361368	334.684322	667.377352	334.192314	**V**	***805.430175***	403.218725	788.403626	394.705451	787.419610	394.213443	**7**
8	***786.435596***	393.721436	769.409047	385.208162	768.425031	384.716154	**T**	***706.361761***	353.684518	689.335212	345.171244	688.351196	344.679236	**6**
9	***915.478189***	458.242733	898.451640	449.729458	897.467624	449.237450	**E**	605.314082	303.160679	588.287533	294.647404	587.303517	294.155396	**5**
10	***1002.510217***	501.758747	985.483668	493.245472	984.499652	492.753464	**S**	***476.271489***	238.639382	459.244940	230.126108	458.260924	229.634100	**4**
11	***1131.552810***	566.280043	1114.526261	557.766769	1113.542245	557.274760	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
12	***1244.636874***	622.822075	1227.610325	614.308800	1226.626309	613.816792	**I**	***260.196868***	130.602072	243.170319	122.088797			**2**
13							**K**	147.112804	74.060040	130.086255	65.546765			**1**



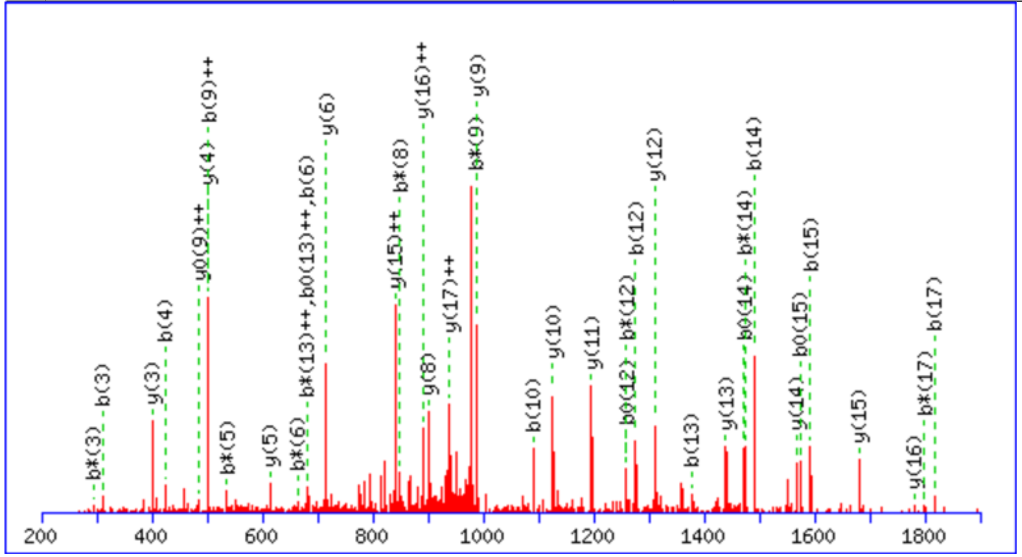
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 13354: 1990.027048 from(996.020800,2+)
Title: OECHL100312_03.9929.9929.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 86
Expect: 3.1e-007**Matches :** 40/186 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	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	**424.255445**	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	552.314023	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	**680.372601**	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**

7	795.399544	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	814.478130	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	**1377.675719**	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510			**3**
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**

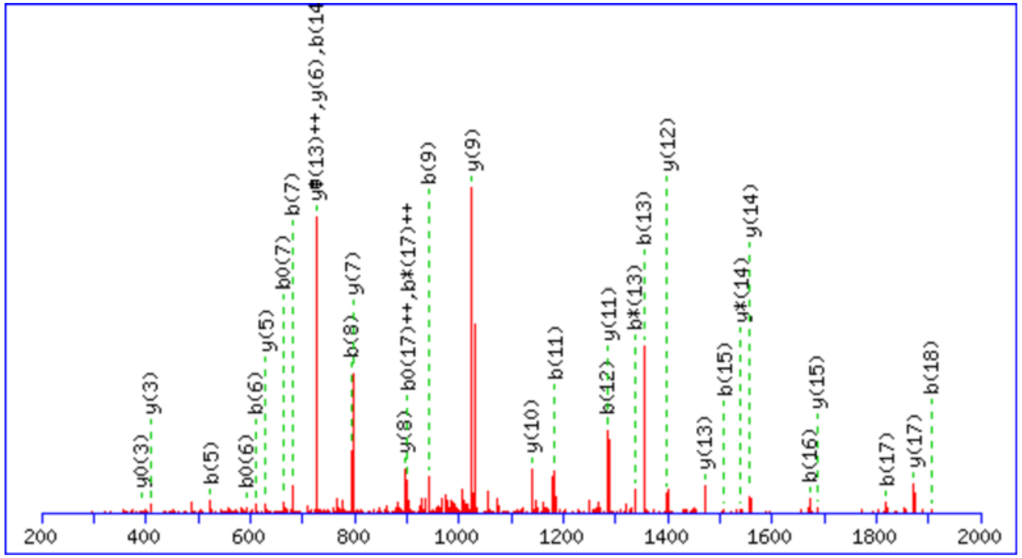


Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 13928: 2078.983448 from(1040.499000,2+)
Title: OECHL100312_03.17266.17266.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70
Expect: 1.5e-005**Matches :** 35/200 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	72.044390	36.525833					**A**							**19**
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973939	**18**
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444483	**17**
4	394.183344	197.595310	377.156795	189.082035			**Q**	1814.870790	907.939033	1797.844241	899.425759	1796.860225	898.933751	**16**
5	***523.225937***	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904462	**15**
6	***610.257965***	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383165	**14**
7	***681.295079***	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867151	**13**
8	***794.379143***	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348594	**12**
9	***941.447557***	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806562	**11**
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272355	**10**
11	***1184.533077***	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250892	**9**
12	***1283.601491***	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729595	**8**
13	***1354.638605***	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195388	**7**
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676831	**6**
15	***1508.712833***	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150449	**5**
16	***1671.776162***	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	572.282723	286.645000	555.256174	278.131725	554.272158	277.639717	**4**
17	***1818.844576***	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	**3**
18	***1905.876604***	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
19							**R**	175.118952	88.063114	158.092403	79.549840			**1**



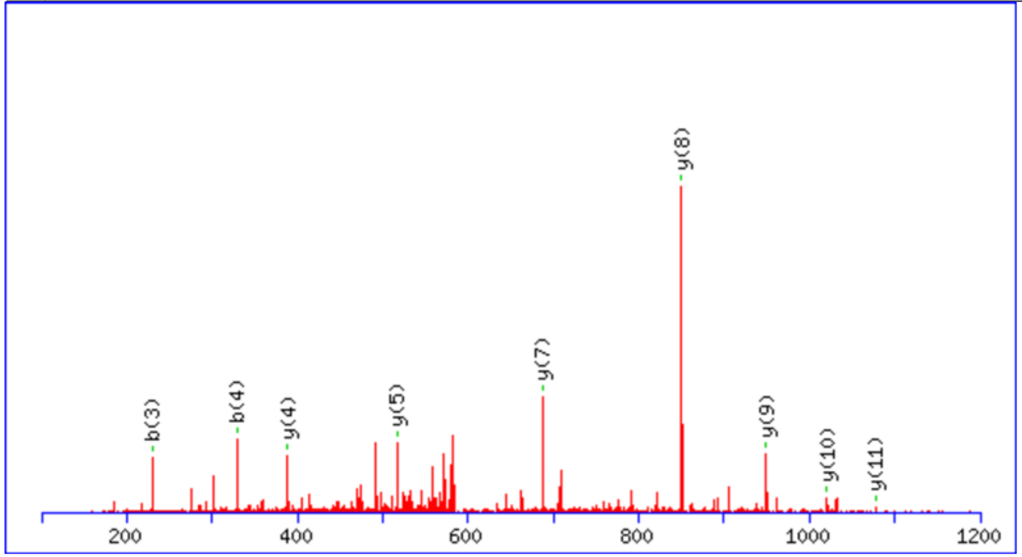
Peptide View

MS/MS Fragmentation of **TGAVYVAEIGAK**
Found in **IPI00552937**, Tax_Id=9606 Gene_Symbol=NHLRC3 NHL repeat-containing protein 3
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 5046: 1177.636048 from(589.825300,2+)
Title: OECHL100312_03.11508.11508.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1177.634277**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 73
Expect: 3.6e-006**Matches :** 9/102 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							**12**
2	159.076419	80.041847	141.065854	71.036565	**G**	***1077.593888***	539.300582	1060.567339	530.787308	1059.583323	530.295300	**11**
3	**230.113533**	115.560404	212.102968	106.555122	**A**	***1020.572424***	510.789850	1003.545875	502.276576	1002.561859	501.784568	**10**
4	**329.181947**	165.094611	311.171382	156.089329	**V**	***949.535310***	475.271293	932.508761	466.758019	931.524745	466.266011	**9**
5	492.245276	246.626276	474.234711	237.620994	**Y**	***850.466896***	425.737086	833.440347	417.223812	832.456331	416.731804	**8**
6	591.313690	296.160483	573.303125	287.155201	**V**	***687.403567***	344.205422	670.377018	335.692147	669.393002	335.200139	**7**

7	662.350804	331.679040	644.340239	322.673758	A	588.335153	294.671215	571.308604	286.157940	570.324588	285.665932	6
8	791.393397	396.200337	773.382832	387.195054	E	***517.298039***	259.152658	500.271490	250.639383	499.287474	250.147375	5
9	904.477461	452.742369	886.466896	443.737086	I	***388.255446***	194.631361	371.228897	186.118087			4
10	961.498925	481.253101	943.488360	472.247818	G	275.171382	138.089329	258.144833	129.576055			3
11	1032.536039	516.771658	1014.525474	507.766375	A	218.149918	109.578597	201.123369	101.065322			2
12					K	147.112804	74.060040	130.086255	65.546765			1



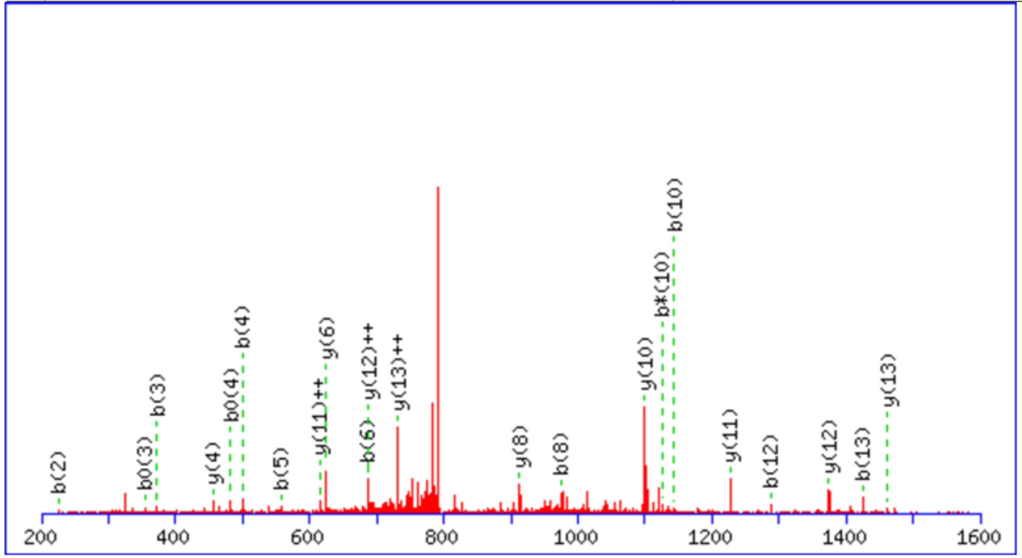
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 9882: 1597.706248 from(799.860400,2+)
Title: OECHL100312_03.2259.2259.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 0.00024**Matches :** 22/144 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	138.066188	69.536732					**H**							**14**
2	***225.098216***	113.052746			207.087651	104.047463	**S**	**1461.653938**	731.330607	1444.627389	722.817333	1443.643373	722.325325	**13**
3	***372.166630***	186.586953			354.156065	177.581671	**F**	**1374.621910**	687.814593	1357.595361	679.301319	1356.611345	678.809311	**12**
4	***500.261593***	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	**1227.553496**	614.280386	1210.526947	605.767112	1209.542931	605.275104	**11**
5	***557.283057***	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	**1099.458533**	550.232905	1082.431984	541.719630	1081.447968	541.227622	**10**
6	***686.325650***	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	1042.437069	521.722173	1025.410520	513.208898	1024.426504	512.716890	**9**
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	**913.394476**	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	***975.398892***	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	784.351883	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	**624.321234**	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	***1143.488770***	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	527.268470	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	1200.510234	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	**456.231356**	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	***1287.542262***	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	399.209892	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	***1424.601174***	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	312.177864	156.592570	295.151315	148.079295			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**

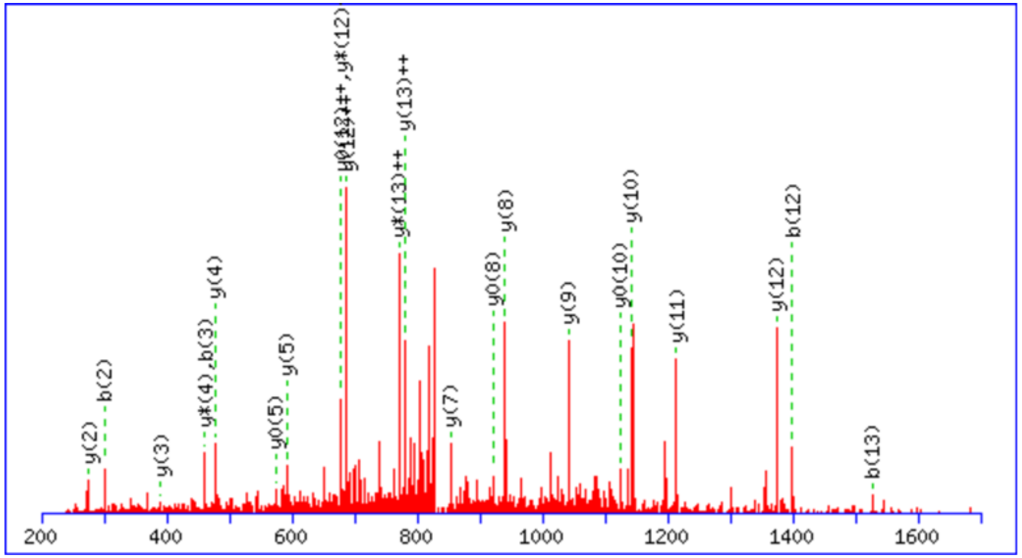


Peptide View

MS/MS Fragmentation of **LWCATTSNFDSDKK**
Found in **IPI00027509**, Tax_Id=9606 Gene_Symbol=MMP9 Matrix metalloproteinase-9
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 10686: 1671.757448 from(836.886000,2+)
Title: OECHL100312_03.10825.10825.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1671.756271**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 0.00011**Matches :** 23/130 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	114.091340	57.549308					L							14
2	**300.170653**	150.588965					W	1559.679484	780.343380	1542.652935	771.830106	1541.668919	771.338098	13
3	**460.201302**	230.604289					C	***1373.600171***	687.303724	1356.573622	678.790449	1355.589606	678.298441	12
4	531.238416	266.122846					A	***1213.569522***	607.288399	1196.542973	598.775125	1195.558957	598.283117	11
5	632.286095	316.646686			614.275530	307.641403	T	***1142.532408***	571.769842	1125.505859	563.256568	1124.521843	562.764560	10
6	733.333774	367.170525			715.323209	358.165243	T	***1041.484729***	521.246003	1024.458180	512.732728	1023.474164	512.240720	9
7	820.365802	410.686539			802.355237	401.681257	S	***940.437050***	470.722163	923.410501	462.208889	922.426485	461.716881	8
8	934.408729	467.708003	917.382180	459.194728	916.398164	458.702720	N	***853.405022***	427.206149	836.378473	418.692875	835.394457	418.200867	7
9	1081.477143	541.242210	1064.450594	532.728935	1063.466578	532.236927	F	739.362095	370.184686	722.335546	361.671411	721.351530	361.179403	6
10	1196.504086	598.755681	1179.477537	590.242407	1178.493521	589.750399	D	***592.293681***	296.650479	575.267132	288.137204	574.283116	287.645196	5
11	1283.536114	642.271695	1266.509565	633.758421	1265.525549	633.266413	S	***477.266738***	239.137007	460.240189	230.623733	459.256173	230.131725	4
12	**1398.563057**	699.785167	1381.536508	691.271892	1380.552492	690.779884	D	***390.234710***	195.620993	373.208161	187.107719	372.224145	186.615711	3
13	**1526.658020**	763.832648	1509.631471	755.319374	1508.647455	754.827366	K	***275.207767***	138.107521	258.181218	129.594247			2
14							K	147.112804	74.060040	130.086255	65.546765			1



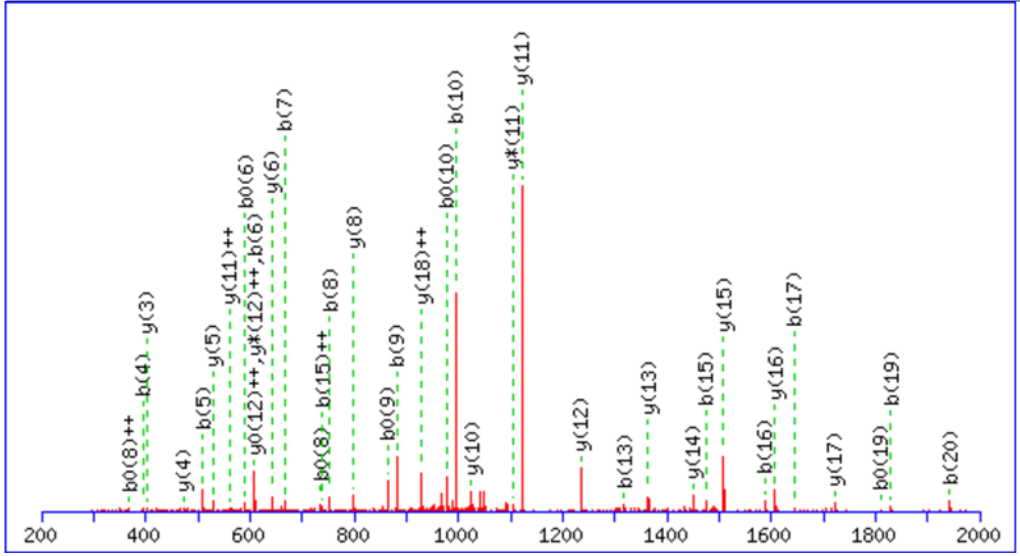
Peptide View

MS/MS Fragmentation of **AADHDVGSELPPEGVLGALLR**
Found in **IPI00002280**, Tax_Id=9606 Gene_Symbol=PCSK1N ProSAAS
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 14156: 2115.095448 from(1058.555000,2+)
Title: OECHL100312_03.20256.20256.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 2115.096024**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 2.8e-006**Matches :** 38/180 fragment ions using 68 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**21**
2	143.081504	72.044390			**A**	2045.066196	1023.036736	2028.039647	1014.523461	2027.055631	1014.031453	**20**
3	258.108447	129.557862	240.097882	120.552579	**D**	1974.029082	987.518179	1957.002533	979.004904	1956.018517	978.512896	**19**
4	***395.167359***	198.087317	377.156794	189.082035	**H**	1859.002139	930.004707	1841.975590	921.491433	1840.991574	920.999425	**18**
5	***510.194302***	255.600789	492.183737	246.595507	**D**	***1721.943227***	861.475251	1704.916678	852.961977	1703.932662	852.469969	**17**
6	***609.262716***	305.134996	591.252151	296.129714	**V**	***1606.916284***	803.961780	1589.889735	795.448505	1588.905719	794.956497	**16**

7	***666.284180***	333.645728	648.273615	324.640446	**G**	***1507.847870***	754.427573	1490.821321	745.914298	1489.837305	745.422290	**15**
8	***753.316208***	377.161742	735.305643	368.156460	**S**	***1450.826406***	725.916841	1433.799857	717.403566	1432.815841	716.911558	**14**
9	***882.358801***	441.683039	864.348236	432.677756	**E**	***1363.794378***	682.400827	1346.767829	673.887552	1345.783813	673.395544	**13**
10	***995.442865***	498.225071	977.432300	489.219788	**L**	***1234.751785***	617.879530	1217.725236	609.366256	1216.741220	608.874248	**12**
11	1092.495629	546.751453	1074.485064	537.746170	**P**	***1121.667721***	561.337498	1104.641172	552.824224	1103.657156	552.332216	**11**
12	1189.548393	595.277835	1171.537828	586.272552	**P**	***1024.614957***	512.811116	1007.588408	504.297842	1006.604392	503.805834	**10**
13	***1318.590986***	659.799131	1300.580421	650.793848	**E**	927.562193	464.284734	910.535644	455.771460	909.551628	455.279452	**9**
14	1375.612450	688.309863	1357.601885	679.304580	**G**	***798.519600***	399.763438	781.493051	391.250163			**8**
15	***1474.680864***	737.844070	1456.670299	728.838787	**V**	741.498136	371.252706	724.471587	362.739431			**7**
16	***1587.764928***	794.386102	1569.754363	785.380819	**L**	***642.429722***	321.718499	625.403173	313.205224			**6**
17	***1644.786392***	822.896834	1626.775827	813.891551	**G**	***529.345658***	265.176467	512.319109	256.663192			**5**
18	1715.823506	858.415391	1697.812941	849.410108	**A**	***472.324194***	236.665735	455.297645	228.152460			**4**
19	***1828.907570***	914.957423	1810.897005	905.952140	**L**	***401.287080***	201.147178	384.260531	192.633903			**3**
20	***1941.991634***	971.499455	1923.981069	962.494172	**L**	288.203016	144.605146	271.176467	136.091872			**2**
21					**R**	175.118952	88.063114	158.092403	79.549840			**1**

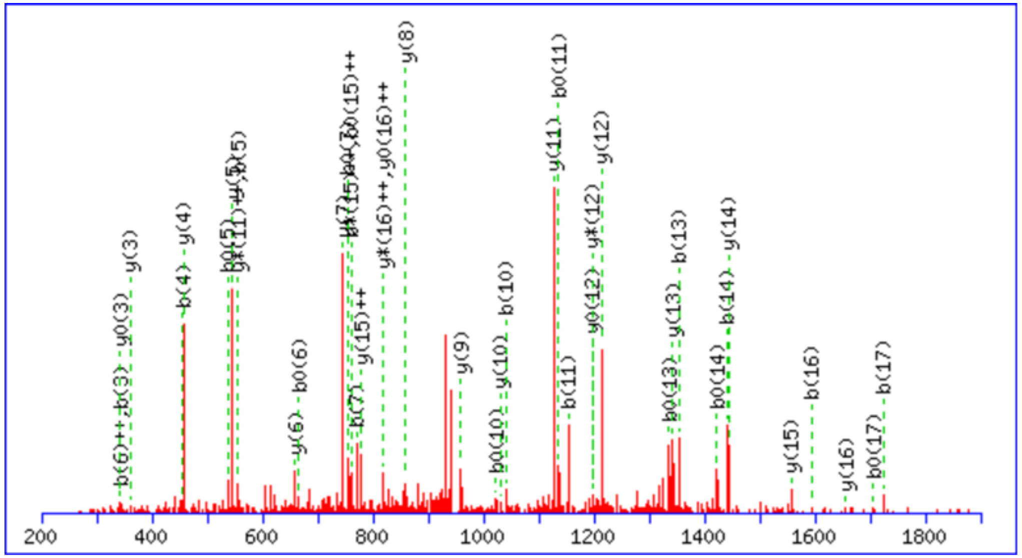


Peptide View

MS/MS Fragmentation of **EIVLTQSPATLSLSPGER**
Found in **IPI00816799**, Tax_Id=9606 Gene_Symbol=- Rheumatoid factor D5 light chain (Fragment)
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 12650: 1897.017848 from(949.516200,2+)
Title: OECHL100312_03.16697.16697.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1897.015640**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 82
Expect: 6.3e-007**Matches :** 42/192 fragment ions using 81 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	**E**							**18**
2	243.133933	122.070605			225.123368	113.065322	**I**	1768.980341	884.993808	1751.953792	876.480534	1750.969776	875.988526	**17**
3	**342.202347**	171.604812			324.191782	162.599529	**V**	***1655.896277***	828.451776	1638.869728	819.938502	1637.885712	819.446494	**16**
4	**455.286411**	228.146844			437.275846	219.141561	**L**	***1556.827863***	778.917569	1539.801314	770.404295	1538.817298	769.912287	**15**
5	**556.334090**	278.670683			538.323525	269.665401	**T**	***1443.743799***	722.375537	1426.717250	713.862263	1425.733234	713.370255	**14**
6	684.392668	342.699972	667.366119	334.186698	666.382103	333.694690	**Q**	***1342.696120***	671.851698	1325.669571	663.338423	1324.685555	662.846415	**13**
7	**771.424696**	386.215986	754.398147	377.702712	753.414131	377.210704	**S**	***1214.637542***	607.822409	1197.610993	599.309134	1196.626977	598.817126	**12**
8	868.477460	434.742368	851.450911	426.229094	850.466895	425.737086	**P**	***1127.605514***	564.306395	1110.578965	555.793120	1109.594949	555.301112	**11**
9	939.514574	470.260925	922.488025	461.747651	921.504009	461.255643	**A**	***1030.552750***	515.780013	1013.526201	507.266738	1012.542185	506.774730	**10**
10	**1040.562253**	520.784765	1023.535704	512.271490	1022.551688	511.779482	**T**	***959.515636***	480.261456	942.489087	471.748181	941.505071	471.256173	**9**
11	**1153.646317**	577.326797	1136.619768	568.813522	1135.635752	568.321514	**L**	***858.467957***	429.737616	841.441408	421.224342	840.457392	420.732334	**8**
12	1240.678345	620.842811	1223.651796	612.329536	1222.667780	611.837528	**S**	***745.383893***	373.195585	728.357344	364.682310	727.373328	364.190302	**7**
13	**1353.762409**	677.384842	1336.735860	668.871568	1335.751844	668.379560	**L**	***658.351865***	329.679570	641.325316	321.166296	640.341300	320.674288	**6**
14	**1440.794437**	720.900857	1423.767888	712.387582	1422.783872	711.895574	**S**	***545.267801***	273.137539	528.241252	264.624264	527.257236	264.132256	**5**
15	1537.847201	769.427239	1520.820652	760.913964	1519.836636	760.421956	**P**	***458.235773***	229.621524	441.209224	221.108250	440.225208	220.616242	**4**
16	**1594.868665**	797.937971	1577.842116	789.424696	1576.858100	788.932688	**G**	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	**3**
17	**1723.911258**	862.459267	1706.884709	853.945992	1705.900693	853.453984	**E**	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**



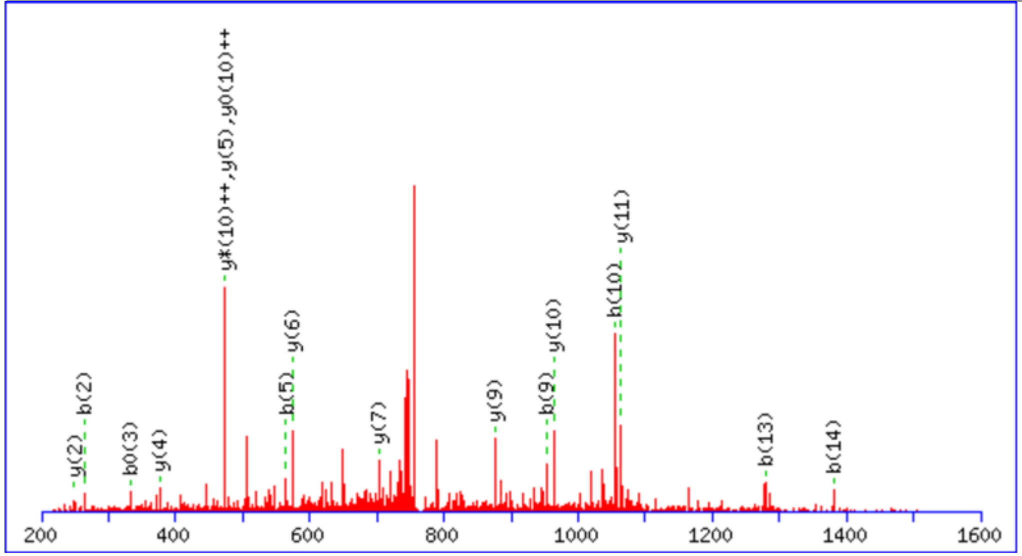
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 9188: 1525.727448 from(763.871000,2+)
Title: OECHL100312_03.11010.11010.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57
Expect: 0.00022**Matches :** 17/150 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	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	350.134661	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**
4	463.218725	232.113001			445.208160	223.107718	**L**	1177.605909	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**

7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	**9**
8	825.362488	413.184882			807.351923	404.179599	**S**	789.410110	395.208693	772.383561	386.695418	771.399545	386.203410	**8**
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	**7**
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	**6**
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	**5**
12	1208.542973	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	**4**
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	**3**
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



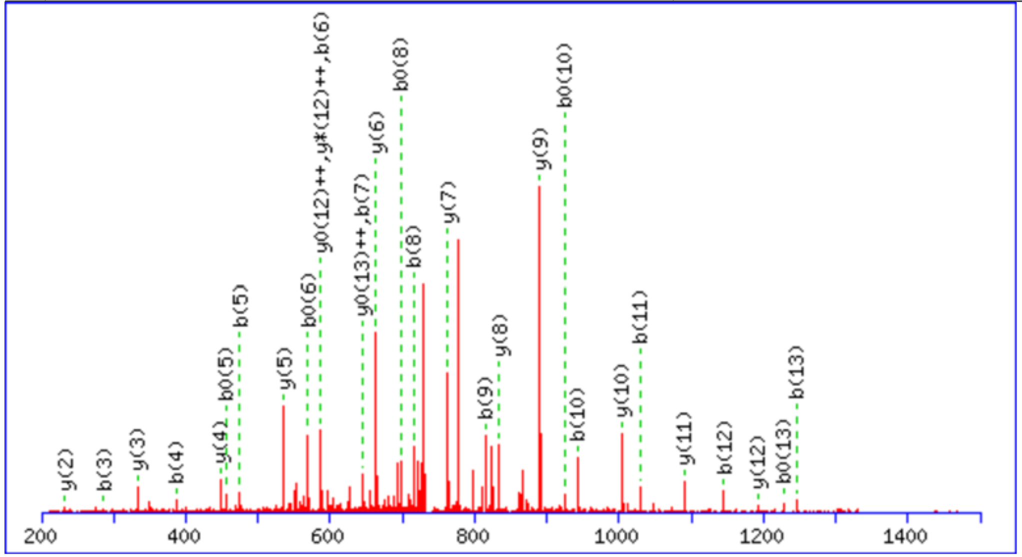
Peptide View

MS/MS Fragmentation of **GLDTSLGAVQSDTGR**
Found in **IPI00289931**, Tax_Id=9606 Gene_Symbol=MADCAM1 MADCAM1 protein
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 8684: 1475.721848 from(738.868200,2+)
Title: OECHL100312_03.11438.11438.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw

Monoisotopic mass of neutral peptide Mr(calc): 1475.721619**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71
Expect: 1.1e-005**Matches :** 30/142 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	58.028740	29.518008					**G**							**15**
2	171.112804	86.060040					**L**	1419.707414	710.357345	1402.680865	701.844071	1401.696849	701.352063	**14**
3	***286.139747***	143.573512			268.129182	134.568229	**D**	1306.623350	653.815313	1289.596801	645.302039	1288.612785	644.810031	**13**
4	***387.187426***	194.097351			369.176861	185.092069	**T**	**1191.596407**	596.301842	1174.569858	587.788567	1173.585842	587.296559	**12**
5	***474.219454***	237.613365			456.208889	228.608082	**S**	**1090.548728**	545.778002	1073.522179	537.264728	1072.538163	536.772719	**11**
6	***587.303518***	294.155397			569.292953	285.150115	**L**	**1003.516700**	502.261988	986.490151	493.748714	985.506135	493.256706	**10**
7	***644.324982***	322.666129			626.314417	313.660847	**G**	**890.432636**	445.719956	873.406087	437.206682	872.422071	436.714674	**9**
8	***715.362096***	358.184686			697.351531	349.179404	**A**	**833.411172**	417.209224	816.384623	408.695950	815.400607	408.203942	**8**
9	***814.430510***	407.718893			796.419945	398.713611	**V**	**762.374058**	381.690667	745.347509	373.177393	744.363493	372.685385	**7**
10	***942.489088***	471.748182	925.462539	463.234908	924.478523	462.742900	**Q**	**663.305644**	332.156460	646.279095	323.643186	645.295079	323.151178	**6**
11	***1029.521116***	515.264196	1012.494567	506.750922	1011.510551	506.258914	**S**	**535.247066**	268.127171	518.220517	259.613897	517.236501	259.121889	**5**
12	***1144.548059***	572.777668	1127.521510	564.264393	1126.537494	563.772385	**D**	**448.215038**	224.611157	431.188489	216.097882	430.204473	215.605874	**4**
13	***1245.595738***	623.301507	1228.569189	614.788233	1227.585173	614.296225	**T**	**333.188095**	167.097685	316.161546	158.584411	315.177530	158.092403	**3**
14	1302.617202	651.812239	1285.590653	643.298965	1284.606637	642.806957	**G**	**232.140416**	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**

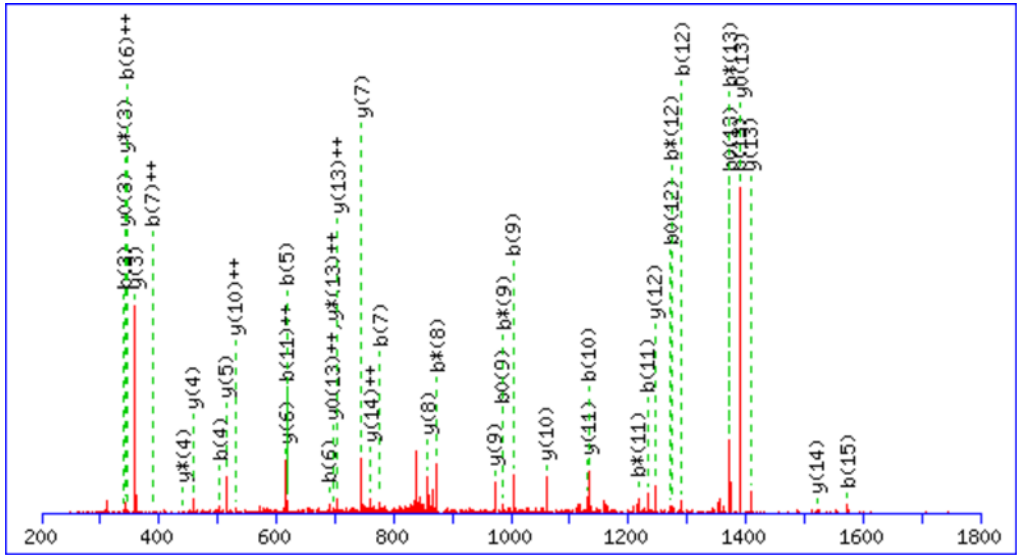


Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 11449: 1746.913848 from(874.464200,2+)
Title: OECHL100312_03.16952.16952.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 68
Expect: 1.8e-005**Matches :** 43/156 fragment ions using 86 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	**340.259468**	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	**503.322797**	252.165036					**Y**	***1408.670299***	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	**689.386854**	**345.197065**			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	**776.418882**	**388.713079**			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	**1233.636145**	**617.321710**	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



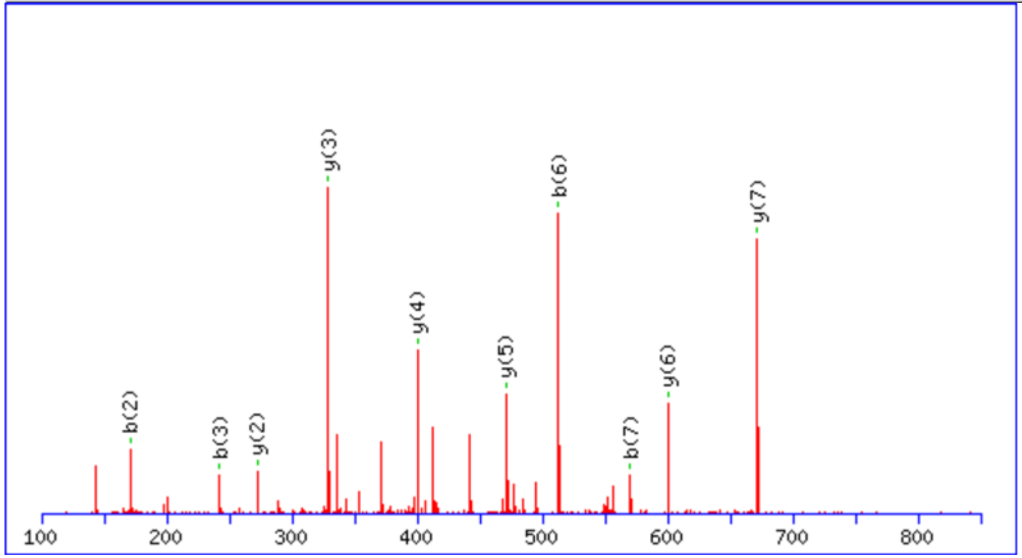
Peptide View

MS/MS Fragmentation of **GLAEAAGPR**
Found in **IPI00290826**, Tax_Id=9606 Gene_Symbol=FAM174A Membrane protein FAM174A
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 1086: 840.446648 from(421.230600,2+)
Title: OECHL100312_03.4180.4180.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 840.445343**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00053**Matches :** 10/64 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							9
2	**171.112804**	86.060040			L	784.431179	392.719228	767.404630	384.205953	766.420614	383.713945	8
3	**242.149918**	121.578597			A	***671.347115***	336.177196	654.320566	327.663921	653.336550	327.171913	7
4	371.192511	186.099894	353.181946	177.094611	E	***600.310001***	300.658639	583.283452	292.145364	582.299436	291.653356	6
5	442.229625	221.618450	424.219060	212.613168	A	***471.267408***	236.137342	454.240859	227.624067			5
6	**513.266739**	257.137008	495.256174	248.131725	A	***400.230294***	200.618785	383.203745	192.105510			4

7	**570.288203**	285.647740	552.277638	276.642457	**G**	***329.193180***	165.100228	312.166631	156.586953			**3**
8	667.340967	334.174122	649.330402	325.168839	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
9					**R**	175.118952	88.063114	158.092403	79.549839			**1**



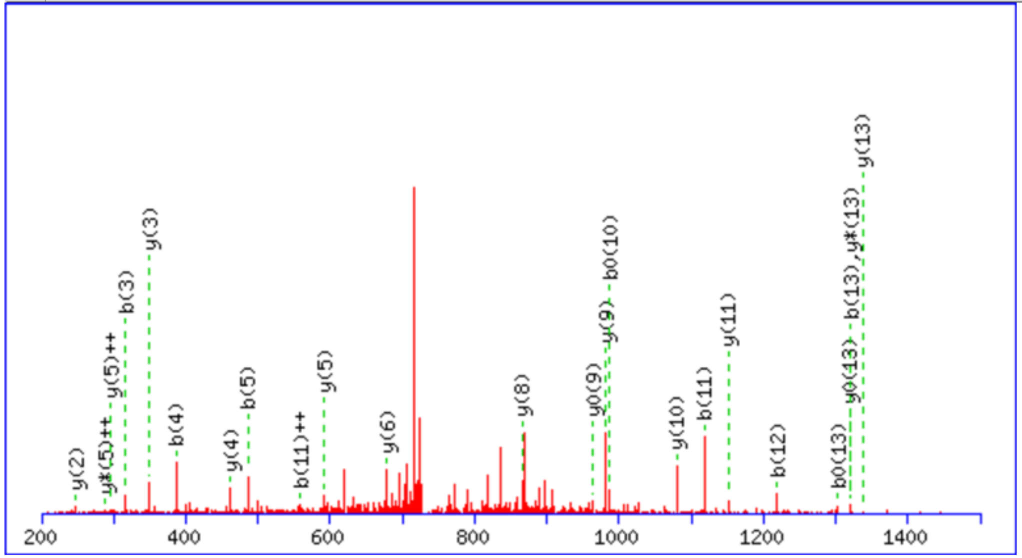
Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 8538: 1465.680448 from(733.847500,2+)
Title: OECHL100312_03.9908.9908.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 56 **Expect:** 0.00024**Matches :** 24/128 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	***1337.643082***	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	**316.113926**	158.560601	298.103361	149.555319	**A**	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**

4	**387.151040**	194.079158	369.140475	185.073875	**A**	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	**486.219454**	243.613365	468.208889	234.608082	**V**	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**
6	601.246397	301.126837	583.235832	292.121554	**D**	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	**9**
7	702.294076	351.650676	684.283511	342.645394	**T**	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	765.398875	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	876.358132	438.682704	858.347567	429.677421	**S**	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	1005.400725	503.204001	987.390160	494.198718	**E**	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	**1118.484789**	559.746033	1100.474224	550.740750	**I**	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	**1219.532468**	610.269872	1201.521903	601.264590	**T**	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	**1320.580147**	660.793712	1302.569582	651.788429	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**

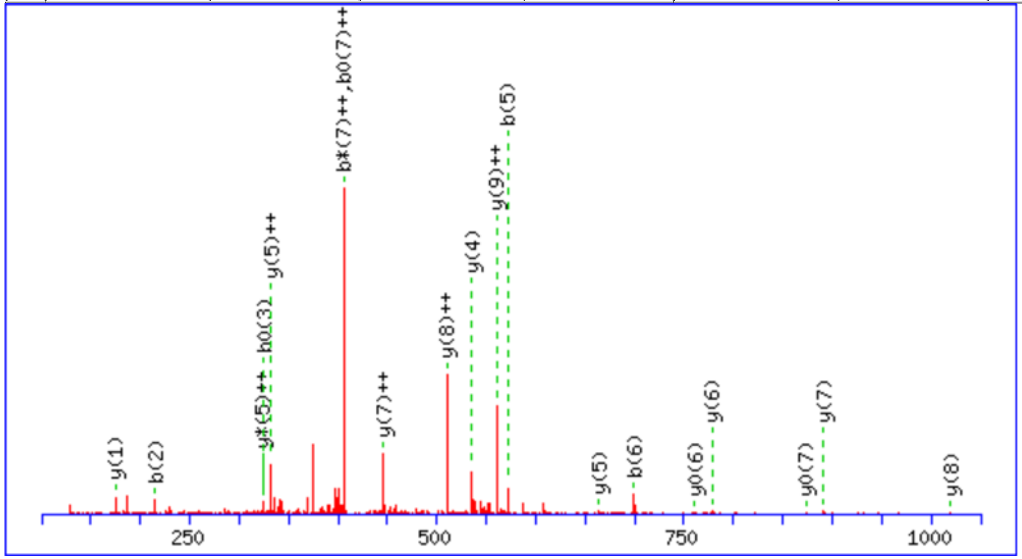


Peptide View

MS/MS Fragmentation of **ATKIDKEACR**
Found in **IPI00017704**, Tax_Id=9606 Gene_Symbol=COTL1 Coactosin-like protein
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 5881: 1232.618172 from(411.880000,3+)
Title: OECHL100312_03.3912.3912.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1232.618286**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 50 **Expect:** 0.0011**Matches :** 20/96 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	114.054955	57.531116					**A**							**10**
2	**215.102634**	108.054955			197.092069	99.049672	**T**	1120.577920	560.792598	1103.551371	552.279324	1102.567355	551.787316	**9**
3	343.197597	172.102436	326.171048	163.589162	325.187032	163.097154	**K**	***1019.530241***	510.268759	1002.503692	501.755484	1001.519676	501.263476	**8**
4	456.281661	228.644468	439.255112	220.131194	438.271096	219.639186	**I**	***891.435278***	446.221277	874.408729	437.708003	873.424713	437.215995	**7**
5	**571.308604**	286.157940	554.282055	277.644665	553.298039	277.152657	**D**	***778.351214***	389.679245	761.324665	381.165971	760.340649	380.673963	**6**
6	**699.403567**	350.205422	682.377018	341.692147	681.393002	341.200139	**K**	***663.324271***	332.165774	646.297722	323.652499	645.313706	323.160491	**5**
7	828.446160	414.726718	811.419611	406.213443	810.435595	405.721435	**E**	***535.229308***	268.118292	518.202759	259.605018	517.218743	259.113010	**4**
8	899.483274	450.245275	882.456725	441.732000	881.472709	441.239992	**A**	***406.186715***	203.596996	389.160166	195.083721			**3**
9	1059.513923	530.260600	1042.487374	521.747325	1041.503358	521.255317	**C**	335.149601	168.078439	318.123052	159.565164			**2**
10							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**

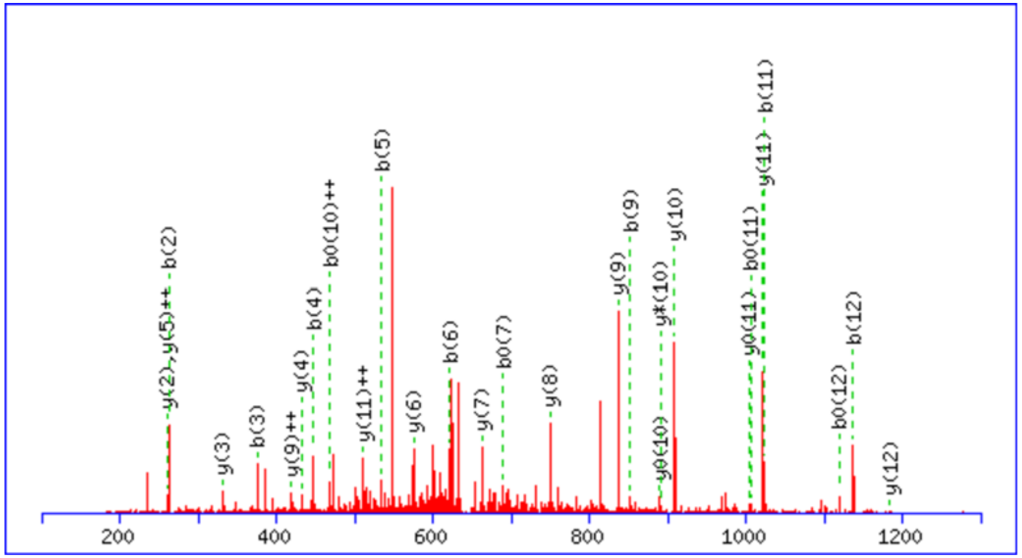


Peptide View

MS/MS Fragmentation of **VYIASSSGSTAIK**
Found in **IPI00025318**, Tax_Id=9606 Gene_Symbol=SH3BGRL SH3 domain-binding glutamic acid-rich-like protein
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 6718: 1282.676648 from(642.345600,2+)
Title: OECHL100312_03.8004.8004.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1282.676865**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00025**Matches :** 28/106 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			**V**							**13**
2	**263.139019**	132.073148			**Y**	***1184.615744***	592.811510	1167.589195	584.298236	1166.605179	583.806227	**12**
3	**376.223083**	188.615180			**I**	***1021.552415***	511.279846	1004.525866	502.766571	1003.541850	502.274563	**11**
4	**447.260197**	224.133737			**A**	***908.468351***	454.737814	891.441802	446.224539	890.457786	445.732531	**10**
5	**534.292225**	267.649751	516.281660	258.644468	**S**	***837.431237***	419.219257	820.404688	410.705982	819.420672	410.213974	**9**
6	**621.324253**	311.165765	603.313688	302.160482	**S**	***750.399209***	375.703243	733.372660	367.189968	732.388644	366.697960	**8**
7	708.356281	354.681779	690.345716	345.676496	**S**	***663.367181***	332.187229	646.340632	323.673954	645.356616	323.181946	**7**
8	765.377745	383.192511	747.367180	374.187228	**G**	***576.335153***	288.671215	559.308604	280.157940	558.324588	279.665932	**6**
9	**852.409773**	426.708525	834.399208	417.703242	**S**	519.313689	260.160483	502.287140	251.647208	501.303124	251.155200	**5**
10	953.457452	477.232364	935.446887	468.227082	**T**	***432.281661***	216.644468	415.255112	208.131194	414.271096	207.639186	**4**
11	**1024.494566**	512.750921	1006.484001	503.745638	**A**	***331.233982***	166.120629	314.207433	157.607354			**3**
12	**1137.578630**	569.292953	1119.568065	560.287670	**I**	***260.196868***	130.602072	243.170319	122.088798			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**



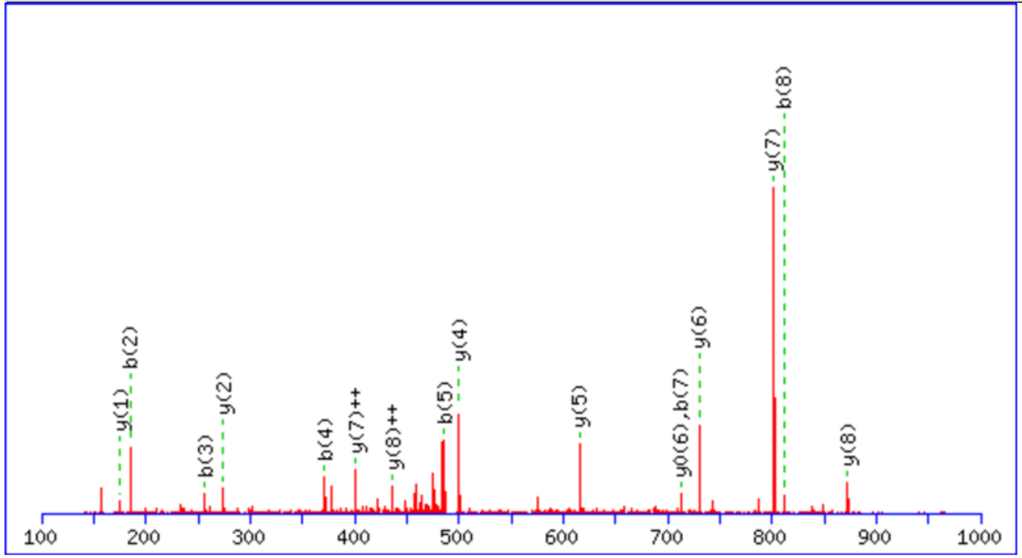
Peptide View

MS/MS Fragmentation of **LAADDPEVR**
Found in **IPI00025840**, Tax_Id=9606 Gene_Symbol=EFNA1 Isoform 1 of Ephrin-A1
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 2515: 984.488248 from(493.251400,2+)
Title: OECHL100312_03.5059.5059.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 984.487610**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00051**Matches :** 16/70 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	**185.128454**	93.067865			A	***872.410837***	436.709057	855.384288	428.195782	854.400272	427.703774	8
3	**256.165568**	128.586422			A	***801.373723***	401.190500	784.347174	392.677225	783.363158	392.185217	7
4	**371.192511**	186.099893	353.181946	177.094611	D	***730.336609***	365.671943	713.310060	357.158668	712.326044	356.666660	6
5	**486.219454**	243.613365	468.208889	234.608082	D	***615.309666***	308.158471	598.283117	299.645197	597.299101	299.153189	5
6	583.272218	292.139747	565.261653	283.134465	P	***500.282723***	250.644999	483.256174	242.131725	482.272158	241.639717	4

7	**712.314811**	356.661044	694.304246	347.655761	**E**	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	**3**
8	**811.383225**	406.195251	793.372660	397.189968	**V**	***274.187366***	137.597321	257.160817	129.084046			**2**
9					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



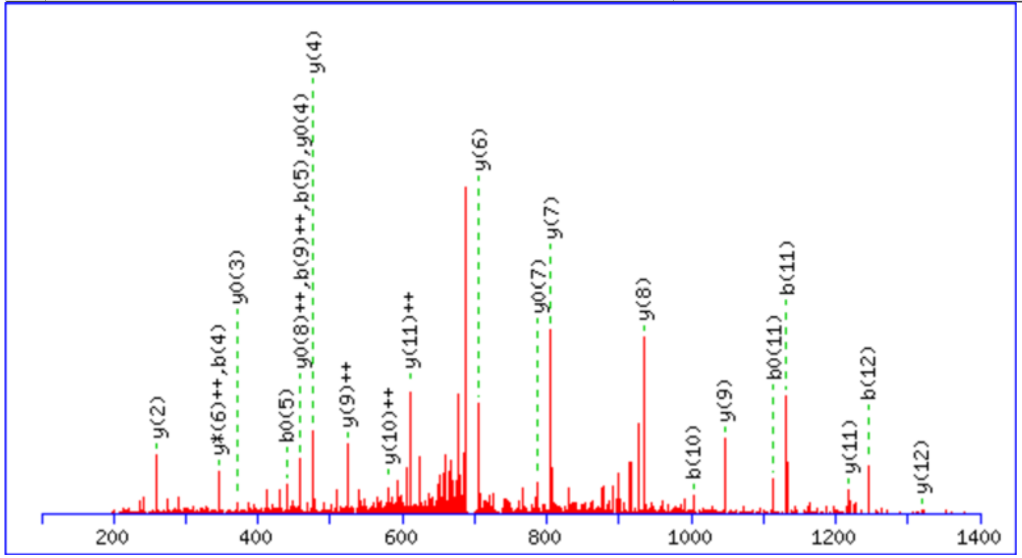
Peptide View

MS/MS Fragmentation of **ATGDIKVTESEIK**
Found in **IPI00302614**, Tax_Id=9606 Gene_Symbol=VTCN1 V-set domain containing T cell activation inhibitor 1
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 7845: 1389.736048 from(695.875300,2+)
Title: OECHL100312_03.8213.8213.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1389.735107**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00065**Matches :** 24/128 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**13**
2	173.092069	87.049672			155.081504	78.044390	**T**	***1319.705288***	660.356282	1302.678739	651.843008	1301.694723	651.350999	**12**
3	230.113533	115.560404			212.102968	106.555122	**G**	***1218.657609***	609.832442	1201.631060	601.319168	1200.647044	600.827160	**11**

4	***345.140476***	173.073876			327.129911	164.068593	**D**	1161.636145	581.321710	1144.609596	572.808436	1143.625580	572.316428	**10**
5	***458.224540***	229.615908			440.213975	220.610626	**I**	***1046.609202***	523.808239	1029.582653	515.294964	1028.598637	514.802956	**9**
6	586.319503	293.663390	569.292954	285.150115	568.308938	284.658107	**K**	***933.525138***	467.266207	916.498589	458.752932	915.514573	458.260924	**8**
7	685.387917	343.197597	668.361368	334.684322	667.377352	334.192314	**V**	***805.430175***	403.218725	788.403626	394.705451	787.419610	394.213443	**7**
8	786.435596	393.721436	769.409047	385.208162	768.425031	384.716154	**T**	***706.361761***	353.684518	689.335212	345.171244	688.351196	344.679236	**6**
9	915.478189	458.242733	898.451640	449.729458	897.467624	449.237450	**E**	605.314082	303.160679	588.287533	294.647404	587.303517	294.155396	**5**
10	***1002.510217***	501.758747	985.483668	493.245472	984.499652	492.753464	**S**	***476.271489***	238.639382	459.244940	230.126108	458.260924	229.634100	**4**
11	***1131.552810***	566.280043	1114.526261	557.766769	1113.542245	557.274760	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
12	***1244.636874***	622.822075	1227.610325	614.308800	1226.626309	613.816792	**I**	***260.196868***	130.602072	243.170319	122.088797			**2**
13							**K**	147.112804	74.060040	130.086255	65.546765			**1**



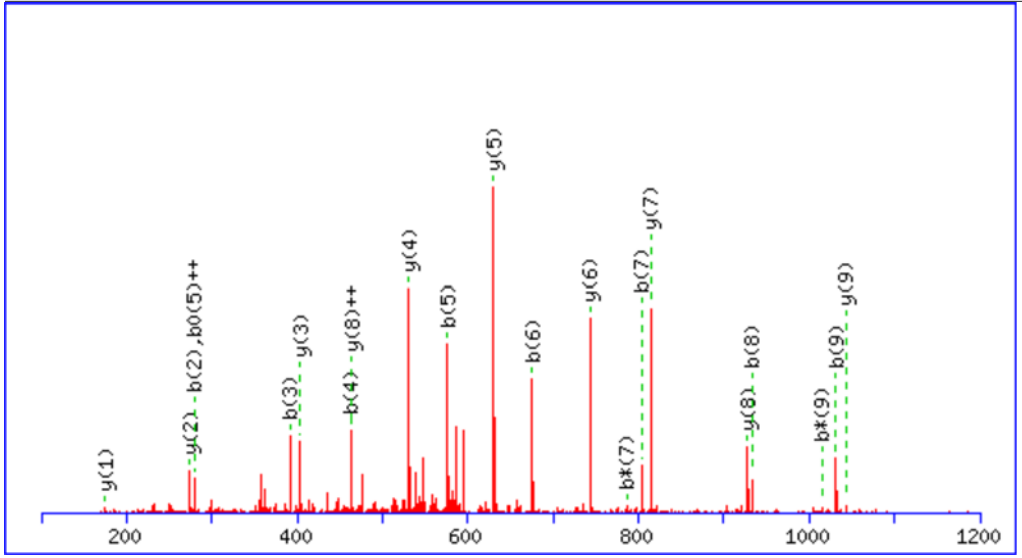
Peptide View

MS/MS Fragmentation of **YDIALVQEVR**
Found in **IPI00031065**, Tax_Id=9606 Gene_Symbol=DNASE1 Deoxyribonuclease-1
Experiment: 35 - OPB-2 **Fraction:** OPB-2

Match to Query 5397: 1204.646248 from(603.330400,2+)

Title: OECHL100312_03.15537.15537.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1204.645172**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.0006**Matches :** 21/90 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	164.070605	82.538940					Y							10
2	**279.097548**	140.052412			261.086983	131.047130	D	***1042.589136***	521.798206	1025.562587	513.284932	1024.578571	512.792924	9
3	**392.181612**	196.594444			374.171047	187.589162	I	***927.562193***	464.284735	910.535644	455.771460	909.551628	455.279452	8
4	**463.218726**	232.113001			445.208161	223.107719	A	***814.478129***	407.742703	797.451580	399.229428	796.467564	398.737420	7
5	**576.302790**	288.655033			558.292225	279.649751	L	***743.441015***	372.224146	726.414466	363.710871	725.430450	363.218863	6
6	**675.371204**	338.189240			657.360639	329.183958	V	***630.356951***	315.682114	613.330402	307.168839	612.346386	306.676831	5
7	**803.429782**	402.218529	786.403233	393.705255	785.419217	393.213247	Q	***531.288537***	266.147907	514.261988	257.634632	513.277972	257.142624	4
8	**932.472375**	466.739826	915.445826	458.226551	914.461810	457.734543	E	***403.229959***	202.118618	386.203410	193.605343	385.219394	193.113335	3
9	**1031.540789**	516.274033	1014.514240	507.760758	1013.530224	507.268750	V	***274.187366***	137.597321	257.160817	129.084047			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1

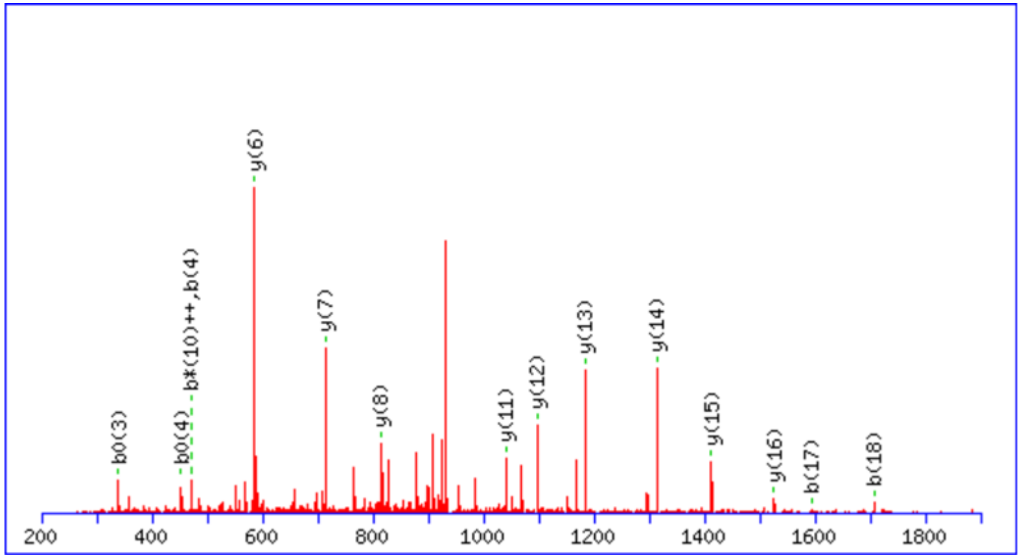


Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**
Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 13042: 1881.032048 from(941.523300,2+)
Title: OECHL100310_41.13600.13600.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 83
Expect: 2.6e-007**Matches :** 15/208 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	130.049869	65.528572			112.039304	56.523290	**E**							**19**
2	229.118283	115.062780			211.107718	106.057497	**V**	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.996686	**18**
3	357.176861	179.092069	340.150312	170.578794	339.166296	170.086786	**Q**	1653.928246	827.467761	1636.901697	818.954487	1635.917681	818.462479	**17**
4	**470.260925**	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.433190	**16**
5	569.329339	285.168308	552.302790	276.655033	551.318774	276.163025	**V**	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.891158	**15**
6	698.371932	349.689604	681.345383	341.176330	680.361367	340.684322	**E**	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.356951	**14**
7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	**S**	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.835654	**13**
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	**G**	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.319640	**12**
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	**G**	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.808908	**11**
10	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	**G**	983.599641	492.303459	966.573092	483.790184	965.589076	483.298176	**10**
11	1069.552416	535.279846	1052.525867	526.766572	1051.541851	526.274564	**L**	926.578177	463.792727	909.551628	455.279452	908.567612	454.787444	**9**
12	1168.620830	584.814053	1151.594281	576.300779	1150.610265	575.808771	**V**	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.245412	**8**
13	1296.715793	648.861535	1279.689244	640.348260	1278.705228	639.856252	**K**	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.711205	**7**
14	1393.768557	697.387917	1376.742008	688.874642	1375.757992	688.382634	**P**	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.663723	**6**
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	**G**	489.277972	245.142624	472.251423	236.629349	471.267407	236.137341	**5**
16	1507.811485	754.409381	1490.784936	745.896106	1489.800920	745.404098	**G**	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	**4**
17	**1594.843513**	797.925395	1577.816964	789.412120	1576.832948	788.920112	**S**	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	**3**
18	**1707.927577**	854.467427	1690.901028	845.954152	1689.917012	845.462144	**L**	288.203016	144.605146	271.176467	136.091871			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



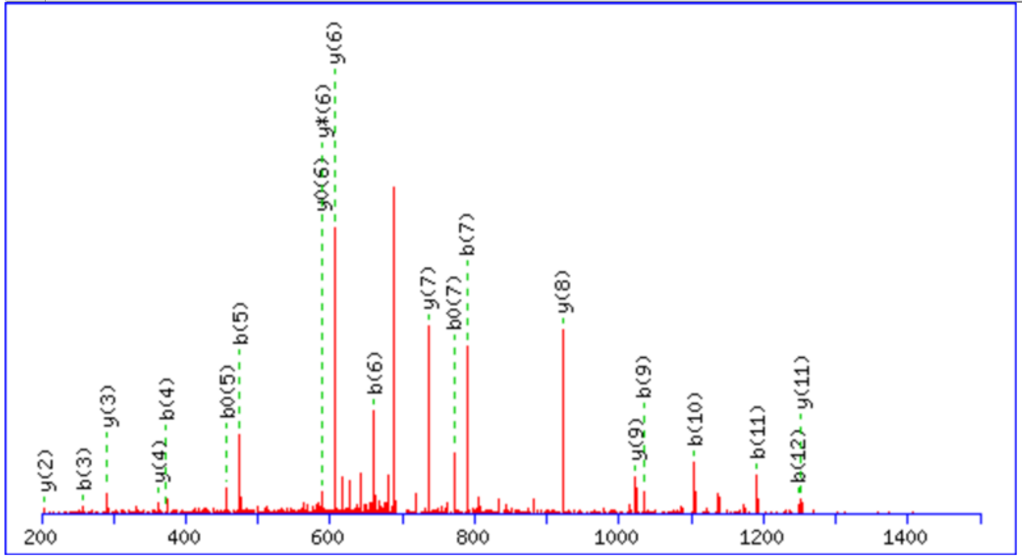
Peptide View

MS/MS Fragmentation of **AADDTWEPFASGK**
Found in **IPI00022432**, Tax_Id=9606 Gene_Symbol=TTR Transthyretin
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 8714: 1393.616048 from(697.815300,2+)
Title: OECHL100310_41.15146.15146.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1393.615005**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64
Expect: 2.5e-005**Matches :** 21/112 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							13
2	143.081504	72.044390			A	1323.585173	662.296225	1306.558624	653.782950	1305.574608	653.290942	12
3	***258.108447***	129.557862	240.097882	120.552579	D	***1252.548059***	626.777668	1235.521510	618.264393	1234.537494	617.772385	11
4	***373.135390***	187.071333	355.124825	178.066051	D	1137.521116	569.264196	1120.494567	560.750922	1119.510551	560.258914	10
5	***474.183069***	237.595173	456.172504	228.589890	T	***1022.494173***	511.750725	1005.467624	503.237450	1004.483608	502.745442	9
6	***660.262382***	330.634829	642.251817	321.629547	W	***921.446494***	461.226885	904.419945	452.713611	903.435929	452.221603	8

7	***789.304975***	395.156126	771.294410	386.150843	**E**	***735.367181***	368.187229	718.340632	359.673954	717.356616	359.181946	**7**
8	886.357739	443.682508	868.347174	434.677225	**P**	***606.324588***	303.665932	589.298039	295.152658	588.314023	294.660650	**6**
9	***1033.426153***	517.216715	1015.415588	508.211432	**F**	509.271824	255.139550	492.245275	246.626275	491.261259	246.134267	**5**
10	***1104.463267***	552.735272	1086.452702	543.729989	**A**	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	**4**
11	***1191.495295***	596.251286	1173.484730	587.246003	**S**	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	**3**
12	***1248.516759***	624.762018	1230.506194	615.756735	**G**	***204.134268***	102.570772	187.107719	94.057497			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**

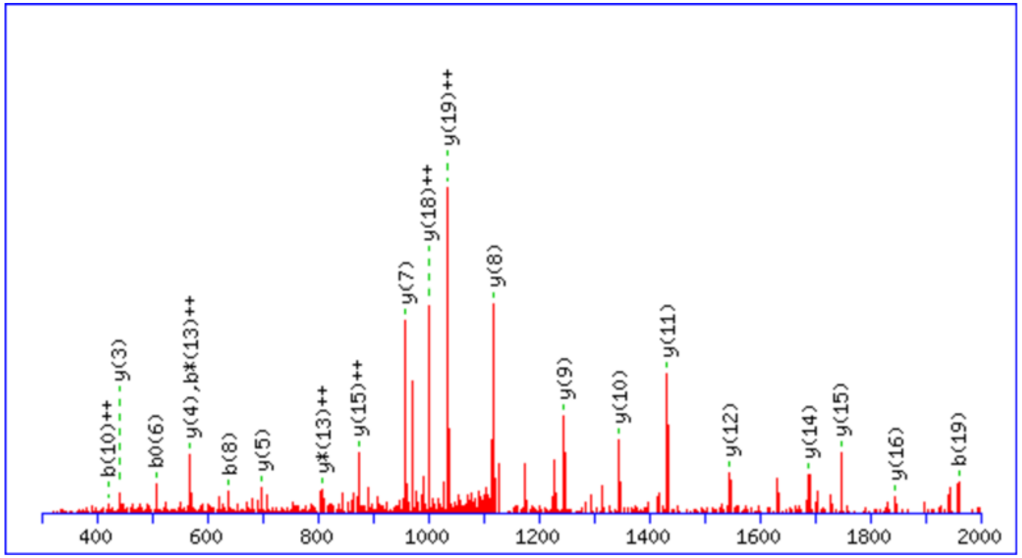


Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 14814: 2270.113448 from(1136.064000,2+)
Title: OECHL100310_41.10579.10579.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 78
Expect: 2.8e-006**Matches :** 21/212 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	102.054955	51.531116			84.044390	42.525833	**T**						
2	201.123369	101.065322			183.112804	92.060040	**V**	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400	1076.5338
3	272.160483	136.583879			254.149918	127.578597	**A**	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986	1026.9996
4	329.181947	165.094611			311.171382	156.089329	**G**	1999.965437	1000.486357	1982.938888	991.973082	1981.954872	991.4810
5	426.234711	213.620994			408.224146	204.615711	**P**	1942.943973	971.975625	1925.917424	963.462350	1924.933408	962.9703
6	525.303125	263.155201			507.292560	254.149918	**V**	***1845.891209***	923.449243	1828.864660	914.935968	1827.880644	914.4439
7	582.324589	291.665933			564.314024	282.660650	**G**	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230	864.9097
8	**639.346053**	320.176665			621.335488	311.171382	**G**	***1689.801331***	845.404304	1672.774782	836.891029	1671.790766	836.3990
9	726.378081	363.692679			708.367516	354.687396	**S**	1632.779867	816.893572	1615.753318	808.380297	1614.769302	807.8882
10	839.462145	420.234711			821.451580	411.229428	**L**	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274	764.3722
11	926.494173	463.750725			908.483608	454.745442	**S**	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210	707.8302
12	1025.562587	513.284932			1007.552022	504.279649	**V**	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182	664.3142
13	1153.621165	577.314221	1136.594616	568.800946	1135.610600	568.308938	**Q**	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768	614.7800
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	**C**	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190	550.7507
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	**P**	***958.474106***	479.740691	941.447557	471.227417	940.463541	470.7354
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	**Y**	861.421342	431.214309	844.394793	422.701035	843.410777	422.2090
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	**E**	***698.358013***	349.682645	681.331464	341.169370	680.347448	340.6773
18	1830.905463	915.956370	1813.878914	907.443095	1812.894898	906.951087	**K**	***569.315420***	285.161348	552.288871	276.648074	551.304855	276.1560
19	**1959.948056**	980.477666	1942.921507	971.964392	1941.937491	971.472384	**E**	***441.220457***	221.113867	424.193908	212.600592	423.209892	212.1085
20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	**H**	312.177864	156.592570	295.151315	148.079295		
21							**R**	175.118952	88.063114	158.092403	79.549839		



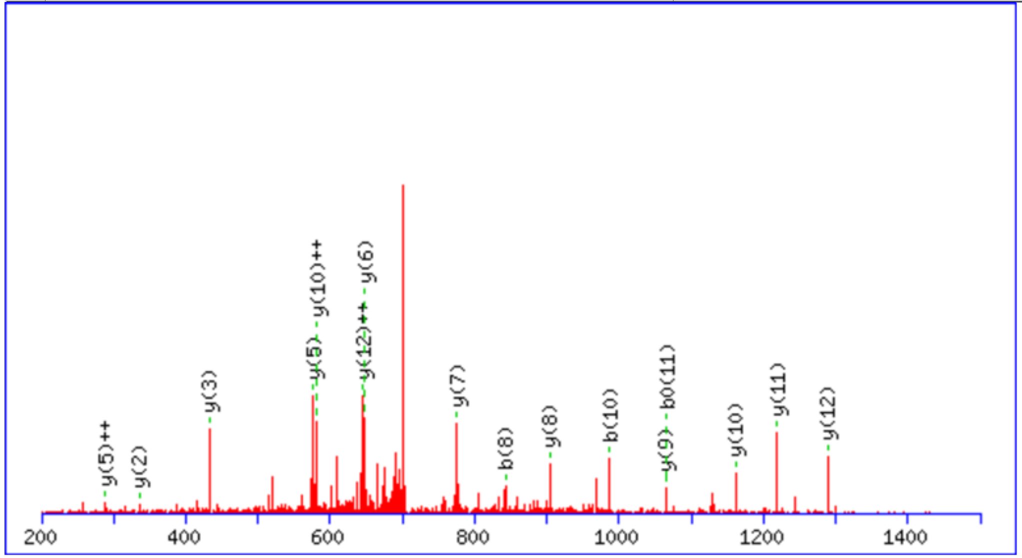
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 8909: 1416.624248 from(709.319400,2+)
Title: OECHL100310_41.1923.1923.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 86
Expect: 1.5e-007**Matches :** 16/128 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	129.102239	65.054757	112.075690	56.541483			**K**							**13**
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	**12**
3	257.160817	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	**11**
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	**10**
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	**9**
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	**8**

7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	899.403979	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	519.234393	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

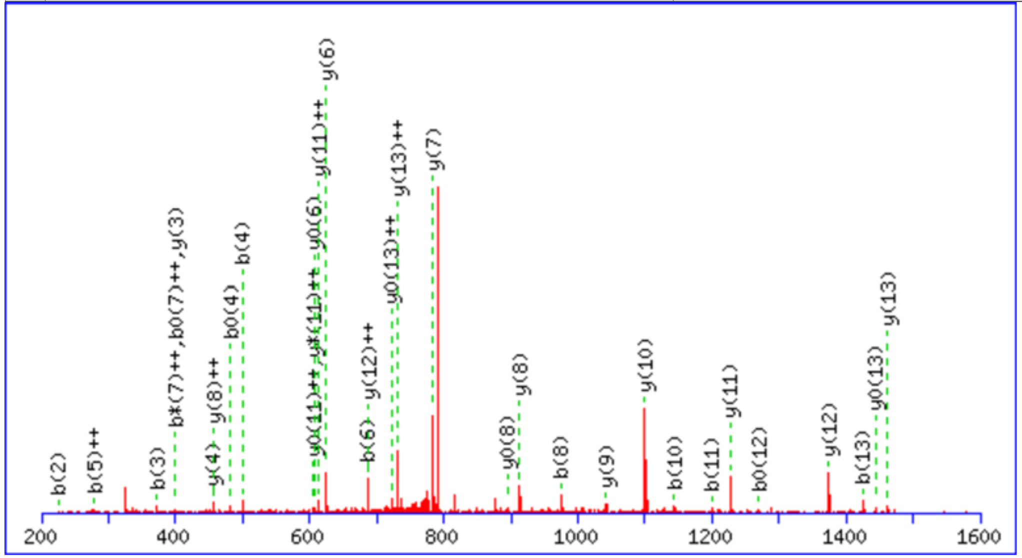


Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 10755: 1597.707648 from(799.861100,2+)
Title: OECHL100310_41.2182.2182.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62
Expect: 4.7e-005**Matches :** 33/144 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					H							14
2	**225.098216**	113.052746			207.087651	104.047463	S	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.325325	13
3	**372.166630**	186.586953			354.156065	177.581671	F	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.809311	12
4	**500.261593**	250.634435	483.235044	242.121160	482.251028	241.629152	K	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	11
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	G	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	10
6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	E	***1042.437069***	521.722173	1025.410520	513.208898	1024.426504	512.716890	9
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	E	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	8
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	C	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	7
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	P	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	6
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	A	527.268470	264.137873	510.241921	255.624598	509.257905	255.132590	5
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	G	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.614033	4
12	1287.542262	644.274769	1270.515713	635.761495	1269.531697	635.269487	S	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	3
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	H	312.177864	156.592570	295.151315	148.079295			2
14							R	175.118952	88.063114	158.092403	79.549839			1

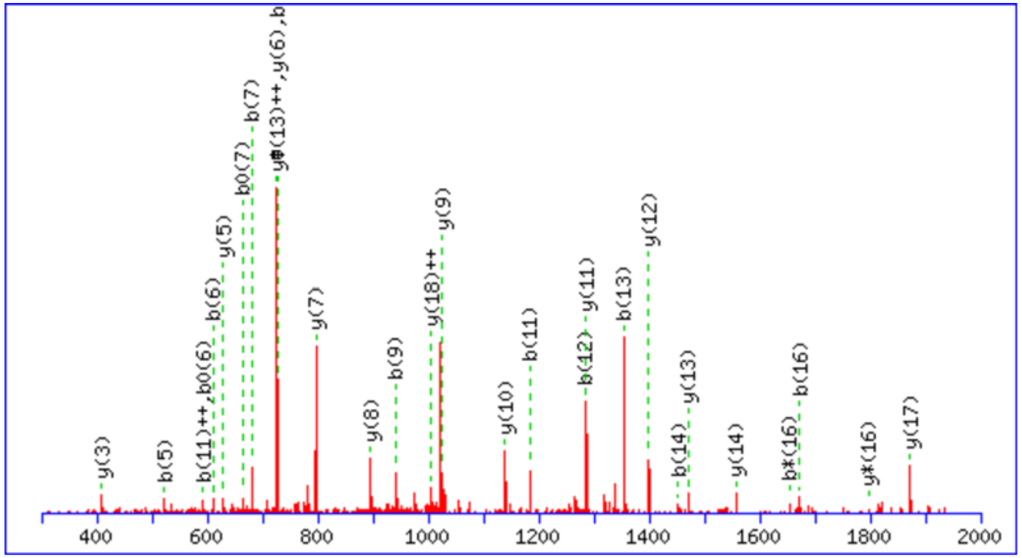


Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 14028: 2078.983448 from(1040.499000,2+)
Title: OECHL100310_41.16963.16963.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71
Expect: 1.2e-005**Matches :** 30/200 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	72.044390	36.525833					**A**							**19**
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973939	**18**
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444483	**17**
4	394.183344	197.595310	377.156795	189.082035			**Q**	1814.870790	907.939033	1797.844241	899.425759	1796.860225	898.933751	**16**
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	1686.812212	843.909744	1669.785663	835.396470	1668.801647	834.904462	**15**
6	**610.257965**	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383165	**14**
7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867151	**13**
8	794.379143	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348594	**12**
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806562	**11**
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272355	**10**
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250892	**9**
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729595	**8**
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195388	**7**
14	**1451.691369**	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676831	**6**
15	1508.712833	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150449	**5**
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	572.282723	286.645000	555.256174	278.131725	554.272158	277.639717	**4**
17	1818.844576	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	**3**
18	1905.876604	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
19							**R**	175.118952	88.063114	158.092403	79.549840			**1**



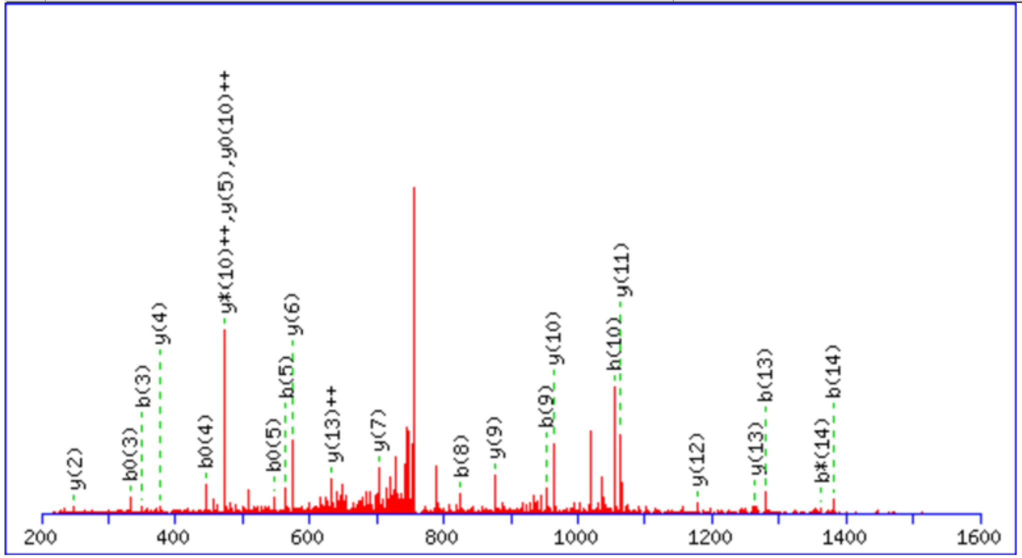
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 10031: 1525.728448 from(763.871500,2+)
Title: OECHL100310_41.10895.10895.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 69
Expect: 1.4e-005**Matches :** 24/150 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	263.102633	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	**350.134661**	175.570968			332.124096	166.565686	**S**	***1264.637937***	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	**564.266404**	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**

7	738.330460	369.668868			720.319895	360.663586	S	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	9
8	**825.362488**	413.184882			807.351923	404.179599	S	789.410110	395.208693	772.383561	386.695418	771.399545	386.203410	8
9	**953.421066**	477.214171	936.394517	468.700897	935.410501	468.208889	Q	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	7
10	**1054.468745**	527.738010	1037.442196	519.224736	1036.458180	518.732728	T	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	6
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	P	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	5
12	1208.542973	604.775124	1191.516424	596.261850	1190.532408	595.769842	G	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	4
13	**1279.580087**	640.293681	1262.553538	631.780407	1261.569522	631.288399	A	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	3
14	**1380.627766**	690.817521	1363.601217	682.304246	1362.617201	681.812238	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
15							K	147.112804	74.060040	130.086255	65.546765			1



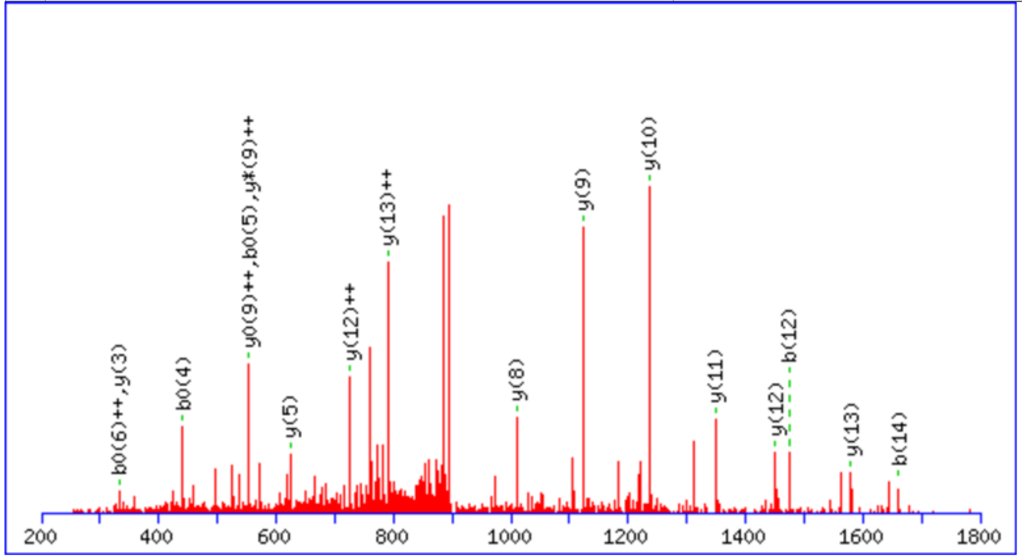
Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 12546: 1805.931848 from(903.973200,2+)
Title: OECHL100310_41.18853.18853.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw

Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72
Expect: 7.3e-006**Matches :** 17/160 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	115.050203	58.028740	98.023654	49.515465			N							15
2	228.134267	114.570771	211.107718	106.057497			I	1692.895549	846.951413	1675.869000	838.438138	1674.884984	837.946130	14
3	357.176860	179.092068	340.150311	170.578793	339.166295	170.086785	E	***1579.811485***	790.409381	1562.784936	781.896106	1561.800920	781.404098	13
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	T	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.882802	12
5	571.308603	286.157940	554.282054	277.644665	553.298038	277.152657	I	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.358962	11
6	684.392667	342.699972	667.366118	334.186697	666.382102	333.694689	I	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.816930	10
7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	N	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.274898	9
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	T	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.253435	8
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	F	908.462479	454.734878	891.435930	446.221603	890.451914	445.729595	7
10	1183.610599	592.308938	1166.584050	583.795663	1165.600034	583.303655	H	761.394065	381.200671	744.367516	372.687396	743.383500	372.195388	6
11	1311.669177	656.338227	1294.642628	647.824952	1293.658612	647.332944	Q	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.665932	5
12	**1474.732506**	737.869891	1457.705957	729.356617	1456.721941	728.864609	Y	496.276575	248.641926	479.250026	240.128651	478.266010	239.636643	4
13	1561.764534	781.385905	1544.737985	772.872631	1543.753969	772.380623	S	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.104979	3
14	**1660.832948**	830.920112	1643.806399	822.406838	1642.822383	821.914830	V	246.181218	123.594247	229.154669	115.080973			2
15							K	147.112804	74.060040	130.086255	65.546765			1

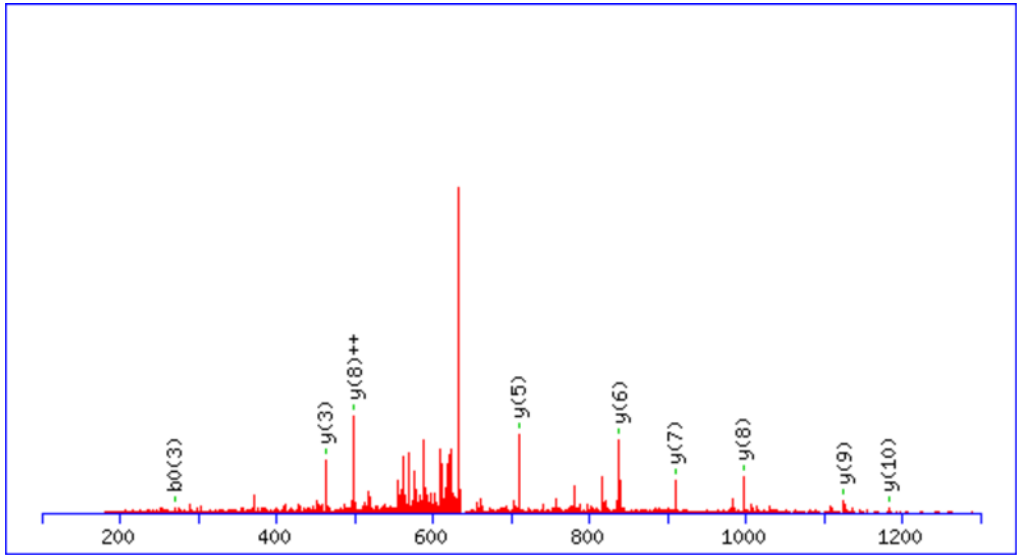


Peptide View

MS/MS Fragmentation of **TGESAEFVCKR**
Found in **IPI00011264**, Tax_Id=9606 Gene_Symbol=CFHR1;LOC100293069 Complement factor H-related protein 1
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 7355: 1282.599248 from(642.306900,2+)
Title: OECHL100310_41.5324.5324.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1282.597580**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00071**Matches :** 9/92 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	102.054955	51.531116			84.044390	42.525833	T							11
2	159.076419	80.041847			141.065854	71.036565	G	***1182.557184***	591.782230	1165.530635	583.268956	1164.546619	582.776948	10
3	288.119012	144.563144			270.108447	135.557862	E	***1125.535720***	563.271498	1108.509171	554.758224	1107.525155	554.266216	9
4	375.151040	188.079158			357.140475	179.073876	S	***996.493127***	498.750202	979.466578	490.236927	978.482562	489.744919	8
5	446.188154	223.597715			428.177589	214.592433	A	***909.461099***	455.234188	892.434550	446.720913	891.450534	446.228905	7
6	575.230747	288.119012			557.220182	279.113729	E	***838.423985***	419.715631	821.397436	411.202356	820.413420	410.710348	6
7	722.299161	361.653219			704.288596	352.647936	F	***709.381392***	355.194334	692.354843	346.681060			5
8	821.367575	411.187426			803.357010	402.182143	V	562.312978	281.660127	545.286429	273.146853			4
9	981.398224	491.202750			963.387659	482.197468	C	***463.244564***	232.125920	446.218015	223.612645			3
10	1109.493187	555.250232	1092.466638	546.736957	1091.482622	546.244949	K	303.213915	152.110595	286.187366	143.597321			2
11							R	175.118952	88.063114	158.092403	79.549839			1



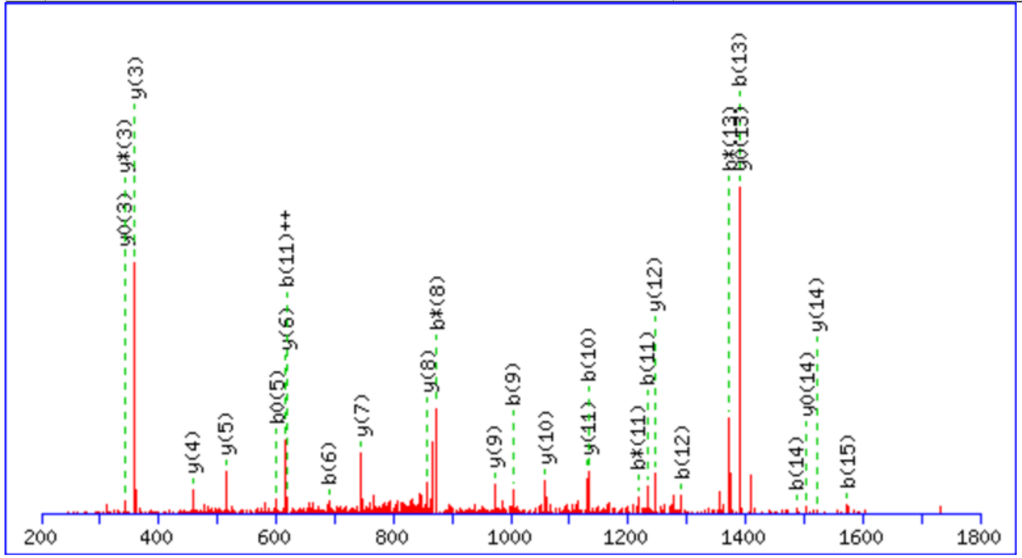
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 12120: 1746.916848 from(874.465700,2+)
Title: OECHL100310_41.16869.16869.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 82
Expect: 6.7e-007**Matches :** 28/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	618.349740	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	**689.386854**	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**

7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	**1486.778787**	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



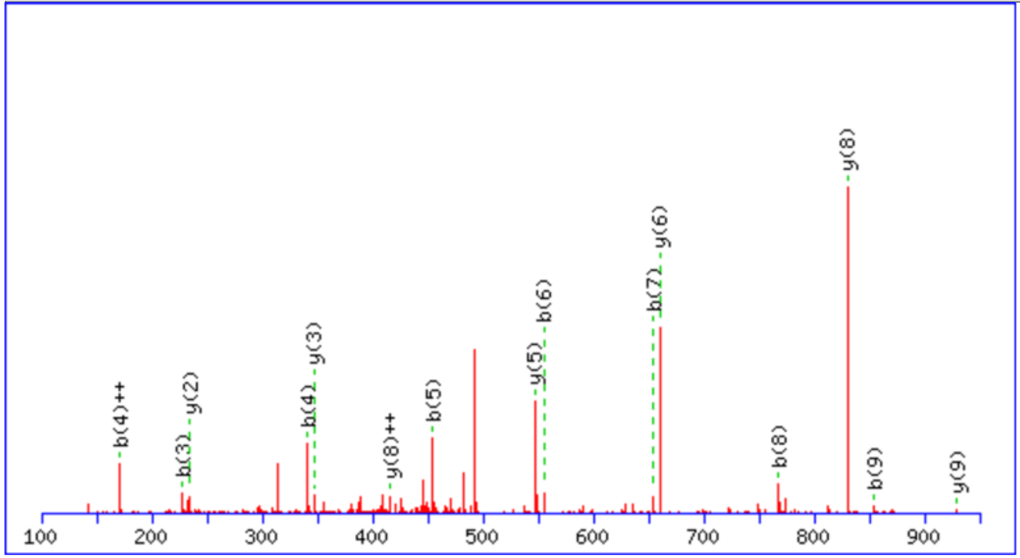
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 3026: 999.633048 from(500.823800,2+)

Title: OECHL100310_41.16988.16988.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828 **Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only) **Ions Score:** 67
Expect: 2.3e-006 **Matches :** 16/78 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	**929.602995**	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**

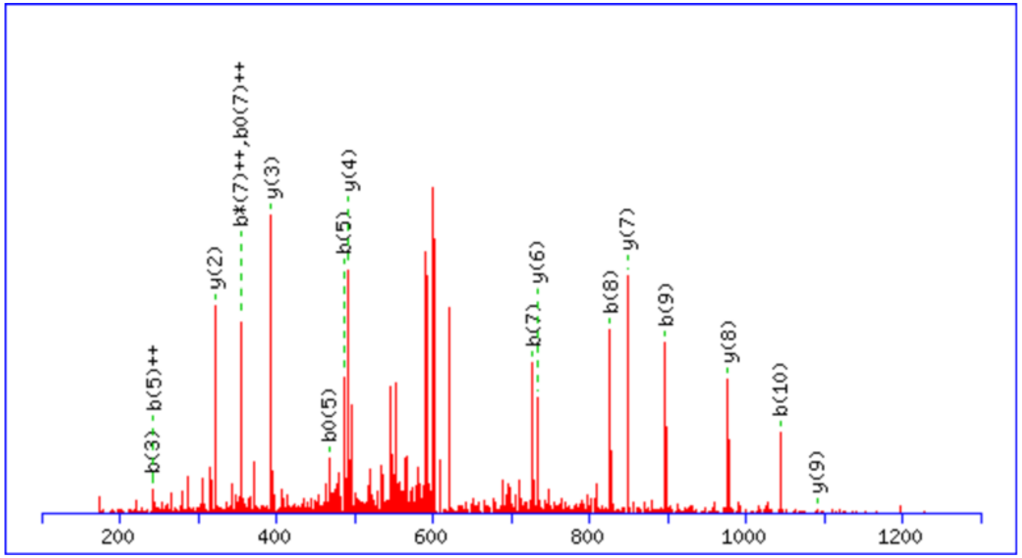


Peptide View

MS/MS Fragmentation of **AGLEDLQVAFR**
Found in **IPI00021536**, Tax_Id=9606 Gene_Symbol=CALML5 Calmodulin-like protein 5
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 6301: 1217.640648 from(609.827600,2+)
Title: OECHL100310_41.17471.17471.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1217.640427**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62
Expect: 5.5e-005**Matches :** 17/90 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							11
2	129.065854	65.036565					G	1147.610600	574.308938	1130.584051	565.795664	1129.600035	565.303655	10
3	***242.149918***	121.578597					L	***1090.589136***	545.798206	1073.562587	537.284931	1072.578571	536.792923	9
4	371.192511	186.099894			353.181946	177.094611	E	***977.505072***	489.256174	960.478523	480.742899	959.494507	480.250891	8
5	***486.219454***	243.613365			468.208889	234.608083	D	***848.462479***	424.734877	831.435930	416.221603	830.451914	415.729595	7
6	599.303518	300.155397			581.292953	291.150115	L	***733.435536***	367.221406	716.408987	358.708131			6
7	***727.362096***	364.184686	710.335547	355.671412	709.351531	355.179404	Q	620.351472	310.679374	603.324923	302.166099			5
8	***826.430510***	413.718893	809.403961	405.205619	808.419945	404.713611	V	***492.292894***	246.650085	475.266345	238.136810			4
9	***897.467624***	449.237450	880.441075	440.724176	879.457059	440.232168	A	***393.224480***	197.115878	376.197931	188.602603			3
10	***1044.536038***	522.771657	1027.509489	514.258383	1026.525473	513.766374	F	***322.187366***	161.597321	305.160817	153.084046			2
11							R	175.118952	88.063114	158.092403	79.549839			1



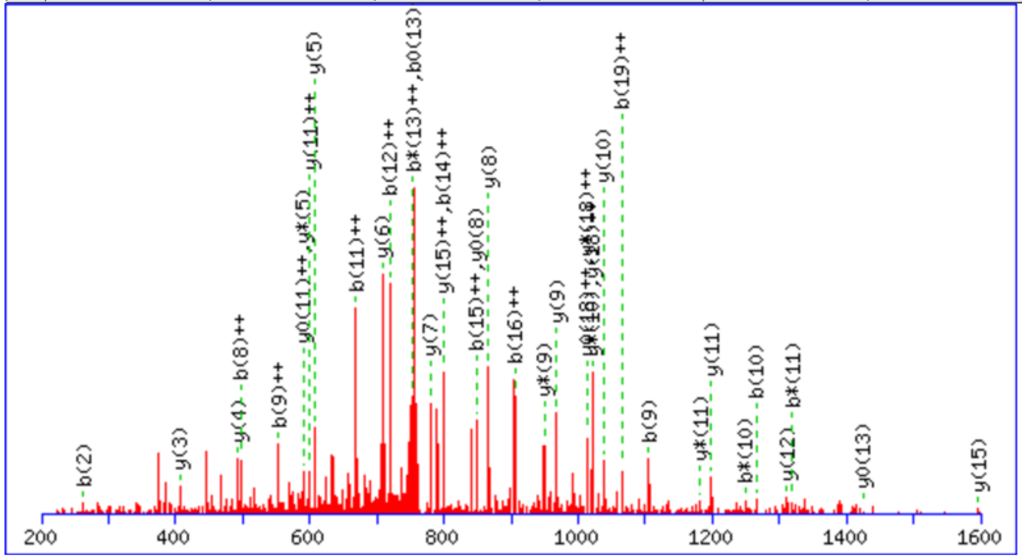
Peptide View

MS/MS Fragmentation of **TCECRPGMICATSATNSCAR**
Found in **IPI00006073**, Tax_Id=9606 Gene_Symbol=TNFRSF8 Isoform Long of Tumor necrosis factor receptor superfamily member 8
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 14955: 2301.937872 from(768.319900,3+)
Title: OECHL100310_41.7587.7587.3.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 2301.938110**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62
Expect: 1.5e-005**Matches :** 38/214 fragment ions using 55 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++
1	102.054955	51.531116			84.044390	42.525833	**T**						
2	**262.085604**	131.546440			244.075039	122.541158	**C**	2201.897712	1101.452494	2184.871163	1092.939219	2183.887147	1092.4472
3	391.128197	196.067737			373.117632	187.062454	**E**	2041.867063	1021.437170	2024.840514	1012.923895	2023.856498	1012.4318
4	551.158846	276.083061			533.148281	267.077779	**C**	1912.824470	956.915873	1895.797921	948.402599	1894.813905	947.9105
5	707.259957	354.133617	690.233408	345.620342	689.249392	345.128334	**R**	1752.793821	876.900549	1735.767272	868.387274	1734.783256	867.8952
6	804.312721	402.659999	787.286172	394.146724	786.302156	393.654716	**P**	***1596.692710***	798.849993	1579.666161	790.336719	1578.682145	789.8447

7	861.334185	431.170731	844.307636	422.657456	843.323620	422.165448	**G**	1499.639946	750.323611	1482.613397	741.810337	1481.629381	741.3183
8	992.374670	**496.690973**	975.348121	488.177699	974.364105	487.685691	**M**	1442.618482	721.812879	1425.591933	713.299605	1424.607917	712.8075
9	**1105.458734**	**553.233005**	1088.432185	544.719731	1087.448169	544.227723	**I**	***1311.577997***	656.292637	1294.551448	647.779362	1293.567432	647.2873
10	**1265.489383**	633.248330	1248.462834	624.735055	1247.478818	624.243047	**C**	***1198.493933***	599.750605	1181.467384	591.237330	1180.483368	590.7453
11	1336.526497	**668.766887**	1319.499948	660.253612	1318.515932	659.761604	**A**	***1038.463284***	519.735280	1021.436735	511.222006	1020.452719	510.7299
12	1437.574176	**719.290726**	1420.547627	710.777452	1419.563611	710.285444	**T**	***967.426170***	484.216723	950.399621	475.703449	949.415605	475.2114
13	1524.606204	762.806740	1507.579655	754.293466	1506.595639	753.801458	**S**	***866.378491***	433.692884	849.351942	425.179609	848.367926	424.6876
14	1595.643318	**798.325297**	1578.616769	789.812023	1577.632753	789.320015	**A**	***779.346463***	390.176870	762.319914	381.663595	761.335898	381.1715
15	1696.690997	**848.849137**	1679.664448	840.335862	1678.680432	839.843854	**T**	***708.309349***	354.658313	691.282800	346.145038	690.298784	345.6530
16	1810.733924	**905.870600**	1793.707375	897.357326	1792.723359	896.865318	**N**	***607.261670***	304.134473	590.235121	295.621199	589.251105	295.1291
17	1897.765952	949.386614	1880.739403	940.873340	1879.755387	940.381332	**S**	***493.218743***	247.113010	476.192194	238.599735	475.208178	238.1077
18	2057.796601	1029.401938	2040.770052	1020.888664	2039.786036	1020.396656	**C**	***406.186715***	203.596996	389.160166	195.083721		
19	2128.833715	**1064.920496**	2111.807166	1056.407221	2110.823150	1055.915213	**A**	246.156066	123.581671	229.129517	115.068397		
20							**R**	175.118952	88.063114	158.092403	79.549839		

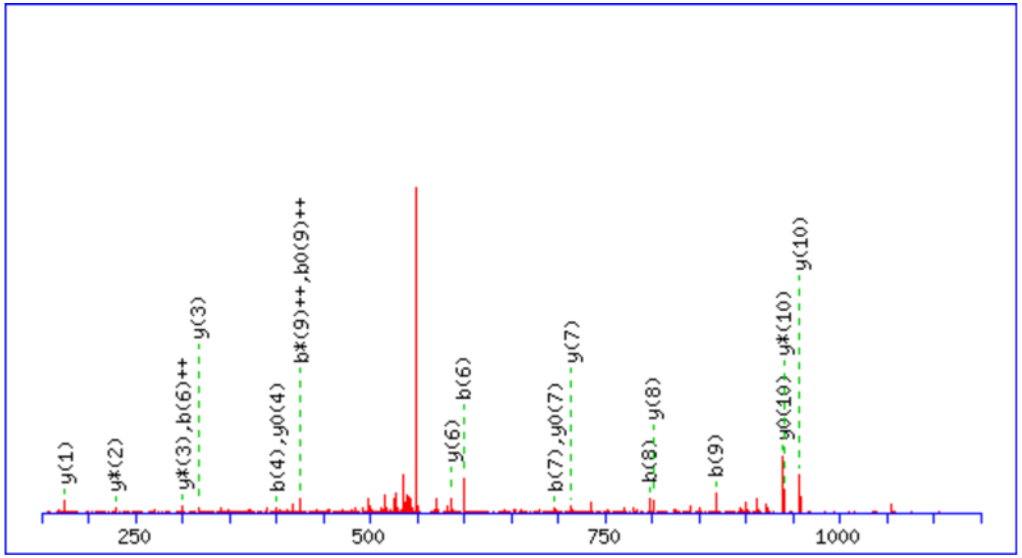


Peptide View

MS/MS Fragmentation of **RGVSQAPTAAR**
Found in **IPI00025365**, Tax_Id=9606 Gene_Symbol=EDN3 Isoform Long of Endothelin-3
Experiment: 13 - S_E-1 **Fraction:** S_E-1

Match to Query 4648: 1112.605448 from(557.310000,2+)
Title: OECHL100310_41.2024.2024.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1112.605042**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00086**Matches :** 21/108 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	157.108387	79.057831	140.081838	70.544557			**R**							**11**
2	214.129851	107.568564	197.103302	99.055289			**G**	***957.511221***	479.259249	940.484672	470.745974	939.500656	470.253966	**10**
3	313.198265	157.102770	296.171716	148.589496			**V**	900.489757	450.748517	883.463208	442.235242	882.479192	441.743234	**9**
4	***400.230293***	200.618785	383.203744	192.105510	382.219728	191.613502	**S**	***801.421343***	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
5	528.288871	264.648074	511.262322	256.134799	510.278306	255.642791	**Q**	***714.389315***	357.698296	697.362766	349.185021	696.378750	348.693013	**7**
6	***599.325985***	300.166631	582.299436	291.653356	581.315420	291.161348	**A**	***586.330737***	293.669007	569.304188	285.155732	568.320172	284.663724	**6**
7	***696.378749***	348.693013	679.352200	340.179738	678.368184	339.687730	**P**	515.293623	258.150450	498.267074	249.637175	497.283058	249.145167	**5**
8	***797.426428***	399.216852	780.399879	390.703578	779.415863	390.211570	**T**	418.240859	209.624068	401.214310	201.110793	400.230294	200.618785	**4**
9	***868.463542***	434.735409	851.436993	426.222135	850.452977	425.730127	**A**	***317.193180***	159.100228	300.166631	150.586953			**3**
10	***939.500656***	470.253966	922.474107	461.740692	921.490091	461.248684	**A**	246.156066	123.581671	229.129517	115.068397			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



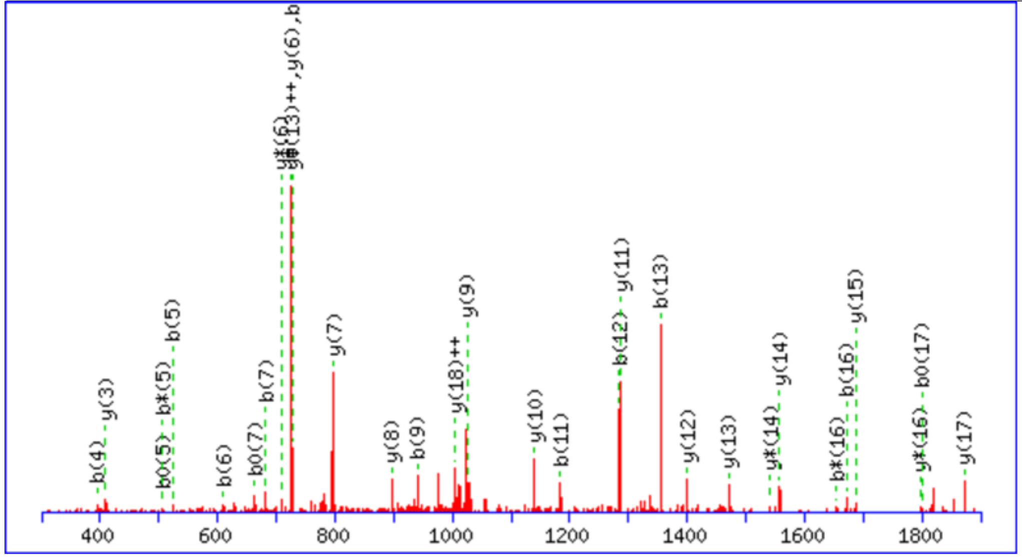
Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 14166: 2078.981448 from(1040.498000,2+)
Title: OECHL100310_39.16491.16491.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 82
Expect: 9.7e-007**Matches :** 33/200 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	72.044390	36.525833					**A**							**19**
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973939	**18**
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444483	**17**
4	**394.183344**	197.595310	377.156795	189.082035			**Q**	1814.870790	907.939033	1797.844241	899.425759	1796.860225	898.933751	**16**
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904462	**15**
6	**610.257965**	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383165	**14**

7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867151	**13**
8	794.379143	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348594	**12**
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806562	**11**
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272355	**10**
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250892	**9**
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729595	**8**
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195388	**7**
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676831	**6**
15	1508.712833	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	629.304187	315.155732	612.277638	306.642457	611.293622	306.150449	**5**
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	572.282723	286.645000	555.256174	278.131725	554.272158	277.639717	**4**
17	1818.844576	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	**3**
18	1905.876604	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
19							**R**	175.118952	88.063114	158.092403	79.549840			**1**



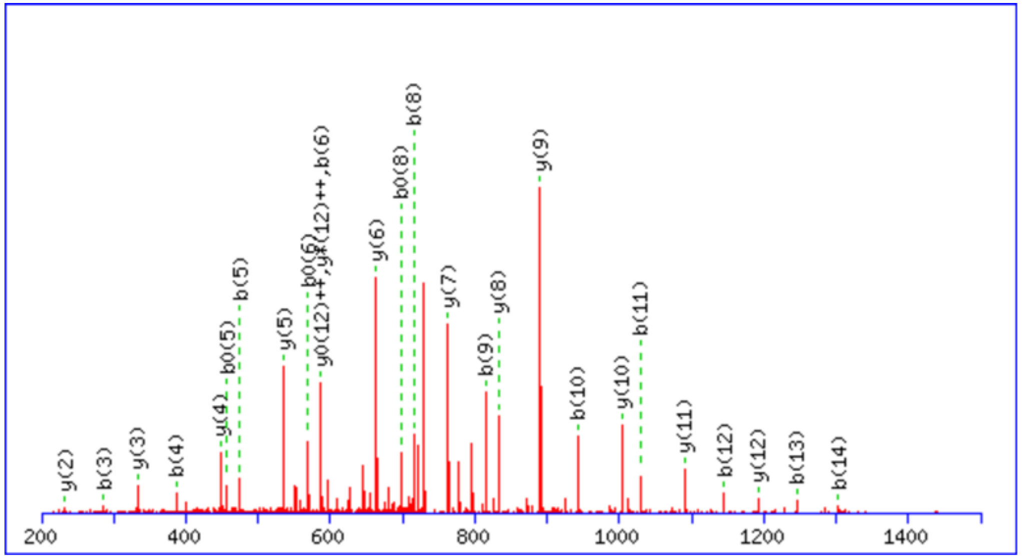
Peptide View

MS/MS Fragmentation of **GLDTSLGAVQSDTGR**

Found in **IPI00289931**, Tax_Id=9606 Gene_Symbol=MADCAM1 MADCAM1 protein
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 9341: 1475.721448 from(738.868000,2+)
Title: OECHL100310_39.10951.10951.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1475.721619**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 90
Expect: 1.2e-007**Matches :** 27/142 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					**G**							**15**
2	171.112804	86.060040					**L**	1419.707414	710.357345	1402.680865	701.844071	1401.696849	701.352063	**14**
3	***286.139747***	143.573512			268.129182	134.568229	**D**	1306.623350	653.815313	1289.596801	645.302039	1288.612785	644.810031	**13**
4	***387.187426***	194.097351			369.176861	185.092069	**T**	***1191.596407***	596.301842	1174.569858	587.788567	1173.585842	587.296559	**12**
5	***474.219454***	237.613365			456.208889	228.608082	**S**	***1090.548728***	545.778002	1073.522179	537.264728	1072.538163	536.772719	**11**
6	***587.303518***	294.155397			569.292953	285.150115	**L**	***1003.516700***	502.261988	986.490151	493.748714	985.506135	493.256706	**10**
7	644.324982	322.666129			626.314417	313.660847	**G**	***890.432636***	445.719956	873.406087	437.206682	872.422071	436.714674	**9**
8	***715.362096***	358.184686			697.351531	349.179404	**A**	***833.411172***	417.209224	816.384623	408.695950	815.400607	408.203942	**8**
9	***814.430510***	407.718893			796.419945	398.713611	**V**	***762.374058***	381.690667	745.347509	373.177393	744.363493	372.685385	**7**
10	***942.489088***	471.748182	925.462539	463.234908	924.478523	462.742900	**Q**	***663.305644***	332.156460	646.279095	323.643186	645.295079	323.151178	**6**
11	***1029.521116***	515.264196	1012.494567	506.750922	1011.510551	506.258914	**S**	***535.247066***	268.127171	518.220517	259.613897	517.236501	259.121889	**5**
12	***1144.548059***	572.777668	1127.521510	564.264393	1126.537494	563.772385	**D**	***448.215038***	224.611157	431.188489	216.097882	430.204473	215.605874	**4**
13	***1245.595738***	623.301507	1228.569189	614.788233	1227.585173	614.296225	**T**	***333.188095***	167.097685	316.161546	158.584411	315.177530	158.092403	**3**
14	***1302.617202***	651.812239	1285.590653	643.298965	1284.606637	642.806957	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



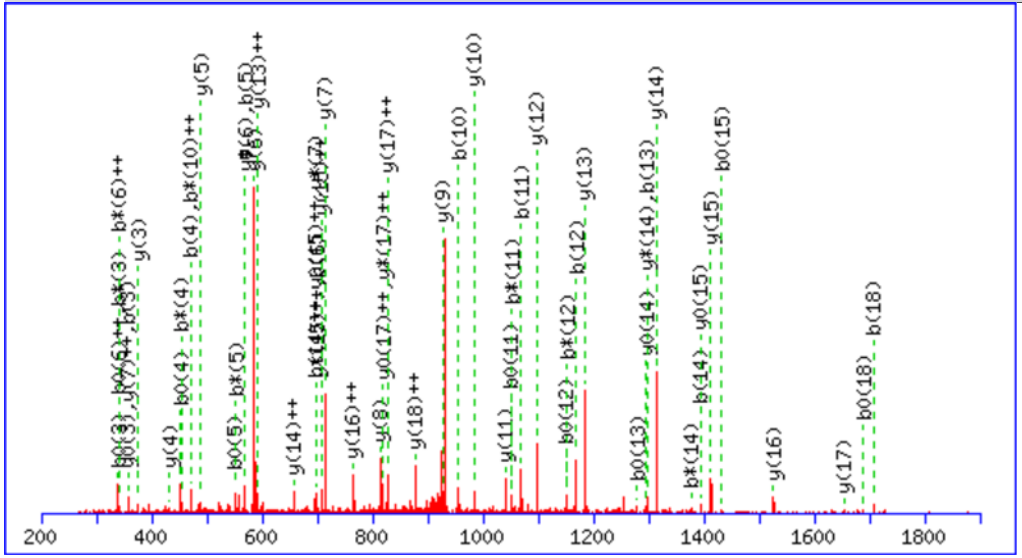
Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**
Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 13148: 1881.032648 from(941.523600,2+)
Title: OECHL100310_39.13360.13360.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 98
Expect: 7.6e-009**Matches :** 61/208 fragment ions using 92 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	**E**							**19**
2	229.118283	115.062780			211.107718	106.057497	**V**	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.996686	**18**
3	**357.176861**	179.092069	340.150312	170.578794	339.166296	170.086786	**Q**	***1653.928246***	827.467761	1636.901697	818.954487	1635.917681	818.462479	**17**
4	**470.260925**	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.433190	**16**
5	**569.329339**	285.168308	552.302790	276.655033	551.318774	276.163025	**V**	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.891158	**15**
6	**698.371932**	349.689604	681.345383	341.176330	680.361367	340.684322	**E**	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.356951	**14**

7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	**S**	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.835654	**13**
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	**G**	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.319640	**12**
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	**G**	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.808908	**11**
10	**956.468352**	478.737814	939.441803	470.224540	938.457787	469.732532	**G**	***983.599641***	492.303459	966.573092	483.790184	965.589076	483.298176	**10**
11	**1069.552416**	535.279846	1052.525867	526.766572	1051.541851	526.274564	**L**	***926.578177***	463.792727	909.551628	455.279452	908.567612	454.787444	**9**
12	**1168.620830**	584.814053	1151.594281	576.300779	1150.610265	575.808771	**V**	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.245412	**8**
13	**1296.715793**	648.861535	1279.689244	640.348260	1278.705228	639.856252	**K**	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.711205	**7**
14	**1393.768557**	697.387917	1376.742008	688.874642	1375.757992	688.382634	**P**	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.663723	**6**
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	**G**	***489.277972***	245.142624	472.251423	236.629349	471.267407	236.137341	**5**
16	1507.811485	754.409381	1490.784936	745.896106	1489.800920	745.404098	**G**	***432.256508***	216.631892	415.229959	208.118617	414.245943	207.626609	**4**
17	1594.843513	797.925395	1577.816964	789.412120	1576.832948	788.920112	**S**	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	**3**
18	**1707.927577**	854.467427	1690.901028	845.954152	1689.917012	845.462144	**L**	288.203016	144.605146	271.176467	136.091871			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



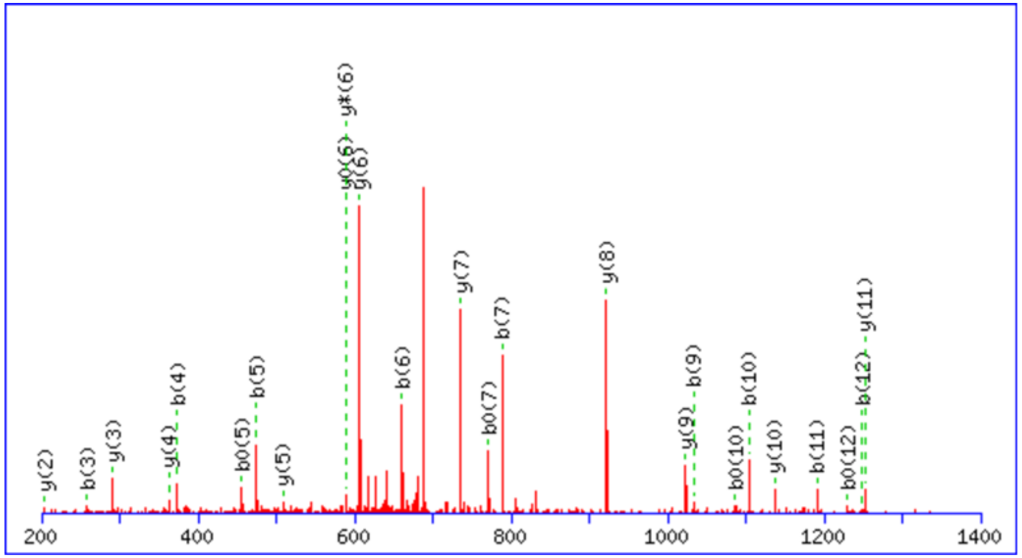
Peptide View

MS/MS Fragmentation of **AADDTWEPFASGK**

Found in **IPI00022432**, Tax_Id=9606 Gene_Symbol=TTR Transthyretin
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 8410: 1393.615048 from(697.814800,2+)
Title: OECHL100310_39.14738.14738.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1393.615005**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67
Expect: 1.1e-005**Matches :** 25/112 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**13**
2	143.081504	72.044390			**A**	1323.585173	662.296225	1306.558624	653.782950	1305.574608	653.290942	**12**
3	**258.108447**	129.557862	240.097882	120.552579	**D**	***1252.548059***	626.777668	1235.521510	618.264393	1234.537494	617.772385	**11**
4	**373.135390**	187.071333	355.124825	178.066051	**D**	***1137.521116***	569.264196	1120.494567	560.750922	1119.510551	560.258914	**10**
5	**474.183069**	237.595173	456.172504	228.589890	**T**	***1022.494173***	511.750725	1005.467624	503.237450	1004.483608	502.745442	**9**
6	**660.262382**	330.634829	642.251817	321.629547	**W**	***921.446494***	461.226885	904.419945	452.713611	903.435929	452.221603	**8**
7	**789.304975**	395.156126	771.294410	386.150843	**E**	***735.367181***	368.187229	718.340632	359.673954	717.356616	359.181946	**7**
8	886.357739	443.682508	868.347174	434.677225	**P**	***606.324588***	303.665932	589.298039	295.152658	588.314023	294.660650	**6**
9	**1033.426153**	517.216715	1015.415588	508.211432	**F**	***509.271824***	255.139550	492.245275	246.626275	491.261259	246.134267	**5**
10	**1104.463267**	552.735272	1086.452702	543.729989	**A**	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	**4**
11	**1191.495295**	596.251286	1173.484730	587.246003	**S**	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	**3**
12	**1248.516759**	624.762018	1230.506194	615.756735	**G**	***204.134268***	102.570772	187.107719	94.057497			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**



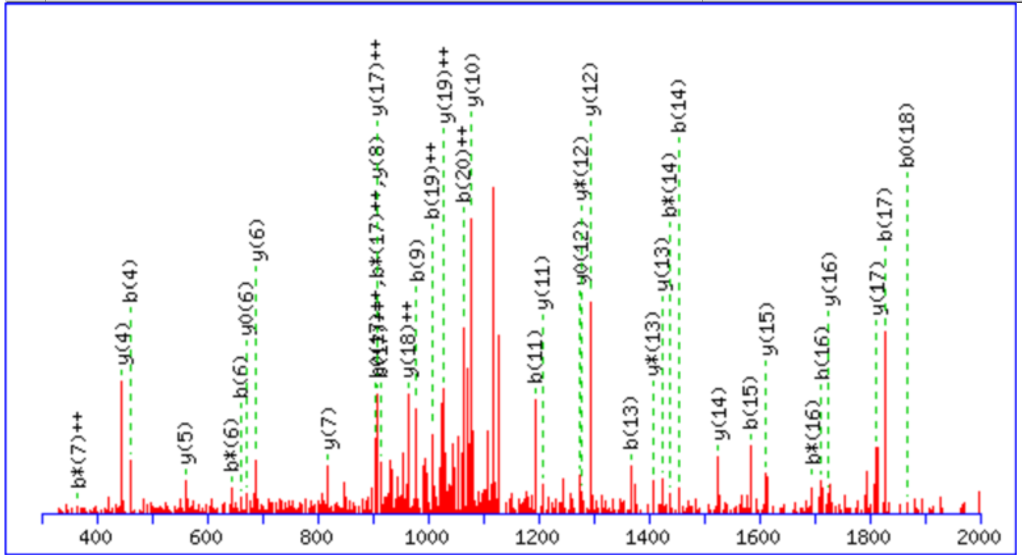
Peptide View

MS/MS Fragmentation of **SKEDSNSTESKSSSEEDGQLK**
Found in **IPI00012734**, Tax_Id=9606 Gene_Symbol=DMP1 Isoform 1 of Dentin matrix acidic phosphoprotein 1
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 14950: 2271.001448 from(1136.508000,2+)
Title: OECHL100310_39.2158.2158.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.998581**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60
Expect: 8e-005**Matches :** 39/230 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}
1	88.039304	44.523290			70.028739	35.518008	**S**						
2	216.134267	108.570771	199.107718	100.057497	198.123702	99.565489	**K**	2184.973868	1092.990572	2167.947319	1084.477297	2166.963303	1083.9852
3	345.176860	173.092068	328.150311	164.578793	327.166295	164.086785	**E**	2056.878905	1028.943090	2039.852356	1020.429816	2038.868340	1019.9378
4	**460.203803**	230.605539	443.177254	222.092265	442.193238	221.600257	**D**	1927.836312	964.421794	1910.809763	955.908520	1909.825747	955.4165
5	547.235831	274.121554	530.209282	265.608279	529.225266	265.116271	**S**	***1812.809369***	906.908323	1795.782820	898.395048	1794.798804	897.9030
6	**661.278758**	331.143017	644.252209	322.629743	643.268193	322.137735	**N**	***1725.777341***	863.392309	1708.750792	854.879034	1707.766776	854.3870

7	748.310786	374.659031	731.284237	366.145757	730.300221	365.653749	**S**	***1611.734414***	806.370845	1594.707865	797.857571	1593.723849	797.3655
8	849.358465	425.182871	832.331916	416.669596	831.347900	416.177588	**T**	***1524.702386***	762.854831	1507.675837	754.341557	1506.691821	753.8495
9	**978.401058**	489.704167	961.374509	481.190893	960.390493	480.698885	**E**	***1423.654707***	712.330992	1406.628158	703.817717	1405.644142	703.3257
10	1065.433086	533.220181	1048.406537	524.706907	1047.422521	524.214899	**S**	***1294.612114***	647.809695	1277.585565	639.296421	1276.601549	638.8044
11	**1193.528049**	597.267663	1176.501500	588.754388	1175.517484	588.262380	**K**	***1207.580086***	604.293681	1190.553537	595.780407	1189.569521	595.2883
12	1280.560077	640.783677	1263.533528	632.270402	1262.549512	631.778394	**S**	***1079.485123***	540.246200	1062.458574	531.732925	1061.474558	531.2409
13	**1367.592105**	684.299691	1350.565556	675.786416	1349.581540	675.294408	**S**	992.453095	496.730186	975.426546	488.216911	974.442530	487.7249
14	**1454.624133**	727.815705	1437.597584	719.302430	1436.613568	718.810422	**S**	***905.421067***	453.214172	888.394518	444.700897	887.410502	444.2088
15	**1583.666726**	792.337001	1566.640177	783.823727	1565.656161	783.331719	**E**	***818.389039***	409.698158	801.362490	401.184883	800.378474	400.6928
16	**1712.709319**	856.858298	1695.682770	848.345023	1694.698754	847.853015	**E**	***689.346446***	345.176861	672.319897	336.663587	671.335881	336.1715
17	**1827.736262**	**914.371769**	1810.709713	905.858495	1809.725697	905.366487	**D**	***560.303853***	280.655565	543.277304	272.142290	542.293288	271.6502
18	1884.757726	942.882501	1867.731177	934.369227	1866.747161	933.877219	**G**	***445.276910***	223.142093	428.250361	214.628818		
19	2012.816304	**1006.911790**	1995.789755	998.398516	1994.805739	997.906508	**Q**	388.255446	194.631361	371.228897	186.118087		
20	2125.900368	**1063.453822**	2108.873819	1054.940547	2107.889803	1054.448539	**L**	260.196868	130.602072	243.170319	122.088798		
21							**K**	147.112804	74.060040	130.086255	65.546765		

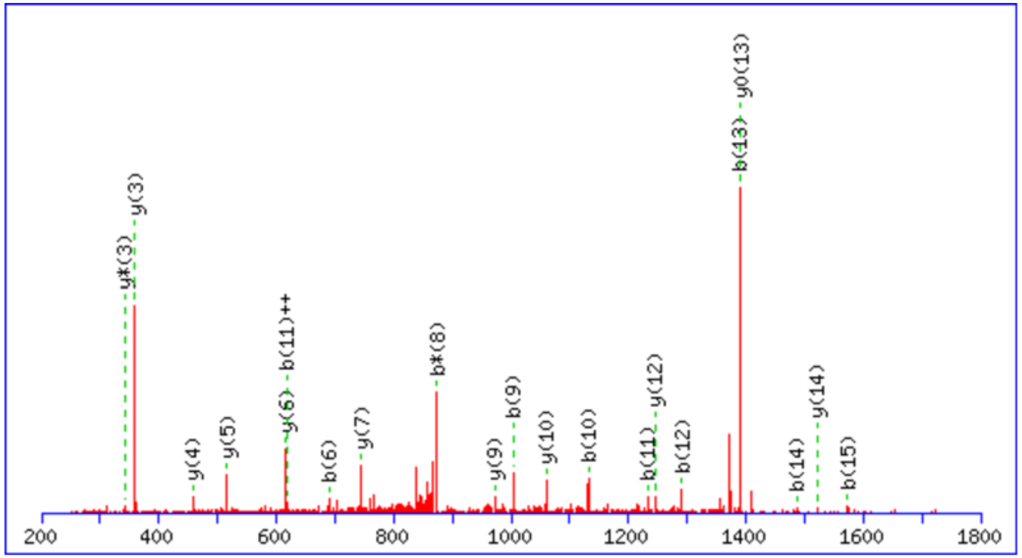


Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 12169: 1746.917648 from(874.466100,2+)
Title: OECHL100310_39.16395.16395.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72
Expect: 5.6e-006**Matches :** 21/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	618.349740	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	***689.386854***	345.197065			671.376289	336.191782	**A**	1130.580027	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	858.467958	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



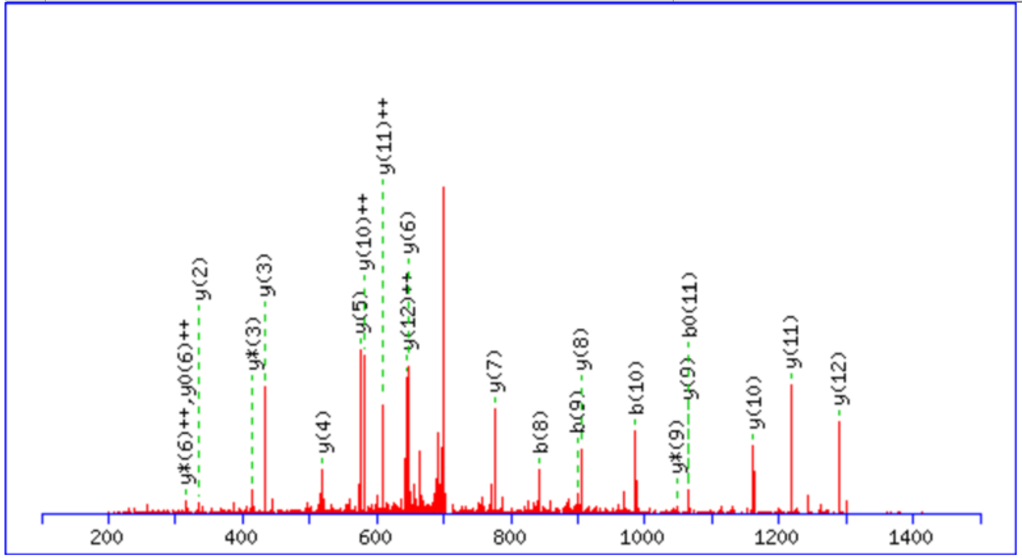
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 8600: 1416.624248 from(709.319400,2+)
Title: OECHL100310_39.1963.1963.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 88
Expect: 9.8e-008**Matches :** 22/128 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							**13**
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	**12**
3	257.160817	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	**11**
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	**10**
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	**9**
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	**8**

7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	**899.403979**	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

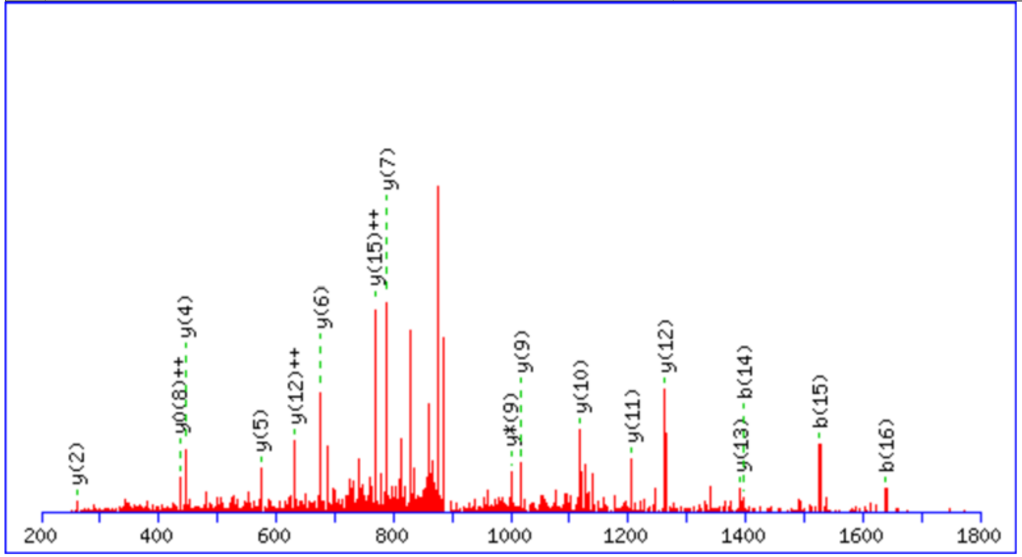


Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 12510: 1784.879448 from(893.447000,2+)
Title: OECHL100310_39.7441.7441.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67
Expect: 3.1e-005**Matches :** 17/170 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							17
2	251.102633	126.054954			233.092068	117.049672	S	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.909941	16
3	308.124097	154.565687			290.113532	145.560404	G	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.393928	15
4	395.156125	198.081701			377.145560	189.076418	S	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.883195	14
5	524.198718	262.602997			506.188153	253.597715	E	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.367182	13
6	581.220182	291.113729			563.209617	282.108447	G	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.845885	12
7	668.252210	334.629743			650.241645	325.624461	S	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.335153	11
8	769.299889	385.153583			751.289324	376.148300	T	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.819139	10
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	Q	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.295299	9
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	T	889.535310	445.271293	872.508761	436.758018	871.524745	436.266010	8
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	L	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.742171	7
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	T	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.200139	6
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	K	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.676299	5
14	**1397.654316**	699.330796	1380.627767	690.817522	1379.643751	690.325514	G	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	4
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	E	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	3
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	L	***260.196868***	130.602072	243.170319	122.088797			2
17							K	147.112804	74.060040	130.086255	65.546765			1

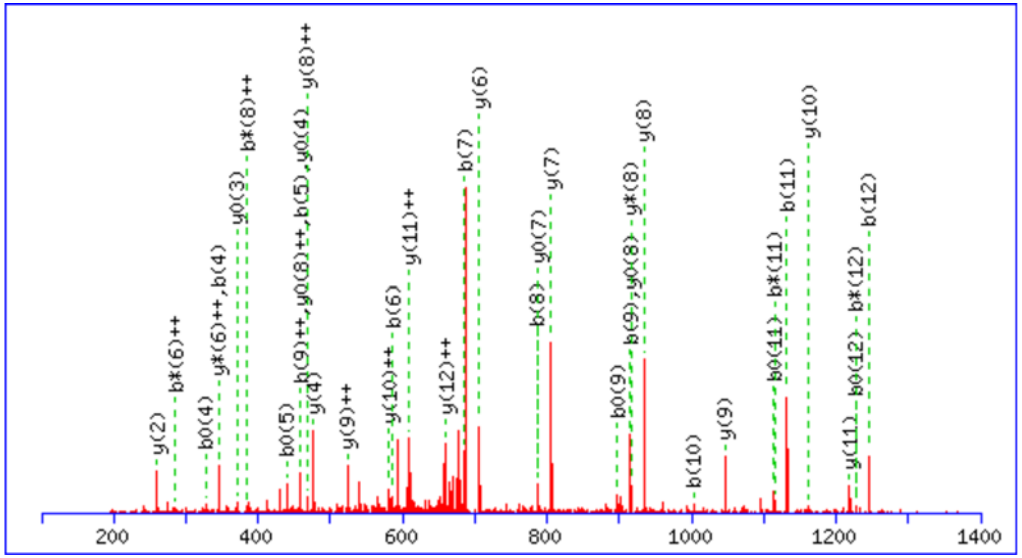


Peptide View

MS/MS Fragmentation of **ATGDIKVTESEIK**
Found in **IPI00302614**, Tax_Id=9606 Gene_Symbol=VTCN1 V-set domain containing T cell activation inhibitor 1
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 8385: 1389.735648 from(695.875100,2+)
Title: OECHL100310_39.8000.8000.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1389.735107**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 0.0004**Matches :** 39/128 fragment ions using 69 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**13**
2	173.092069	87.049672			155.081504	78.044390	**T**	1319.705288	660.356282	1302.678739	651.843008	1301.694723	651.350999	**12**
3	230.113533	115.560404			212.102968	106.555122	**G**	**1218.657609**	609.832442	1201.631060	601.319168	1200.647044	600.827160	**11**
4	***345.140476***	173.073876			327.129911	164.068593	**D**	**1161.636145**	581.321710	1144.609596	572.808436	1143.625580	572.316428	**10**
5	***458.224540***	229.615908			440.213975	220.610626	**I**	**1046.609202**	523.808239	1029.582653	515.294964	1028.598637	514.802956	**9**
6	***586.319503***	293.663390	569.292954	285.150115	568.308938	284.658107	**K**	**933.525138**	467.266207	916.498589	458.752932	915.514573	458.260924	**8**
7	***685.387917***	343.197597	668.361368	334.684322	667.377352	334.192314	**V**	**805.430175**	403.218725	788.403626	394.705451	787.419610	394.213443	**7**
8	***786.435596***	393.721436	769.409047	385.208162	768.425031	384.716154	**T**	**706.361761**	353.684518	689.335212	345.171244	688.351196	344.679236	**6**
9	***915.478189***	458.242733	898.451640	449.729458	897.467624	449.237450	**E**	605.314082	303.160679	588.287533	294.647404	587.303517	294.155396	**5**
10	***1002.510217***	501.758747	985.483668	493.245472	984.499652	492.753464	**S**	**476.271489**	238.639382	459.244940	230.126108	458.260924	229.634100	**4**
11	***1131.552810***	566.280043	1114.526261	557.766769	1113.542245	557.274760	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
12	***1244.636874***	622.822075	1227.610325	614.308800	1226.626309	613.816792	**I**	**260.196868**	130.602072	243.170319	122.088797			**2**
13							**K**	147.112804	74.060040	130.086255	65.546765			**1**



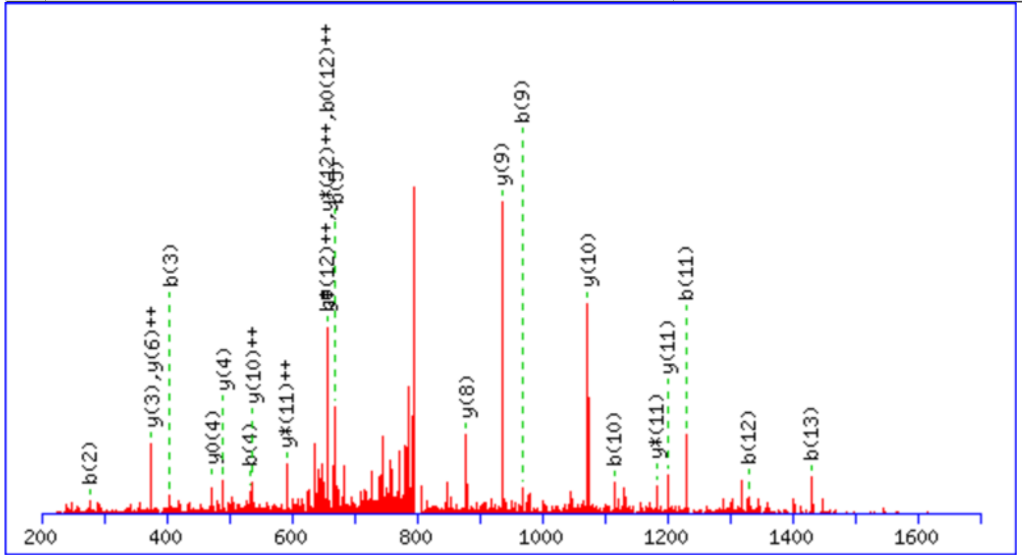
Peptide View

MS/MS Fragmentation of **LYQQHGAGLFDVTR**
Found in **IPI00554538**, Tax_Id=9606 Gene_Symbol=TPP1 Putative uncharacterized protein TPP1
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 10745: 1603.810648 from(802.912600,2+)
Title: OECHL100310_39.13413.13413.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1603.810699**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00093**Matches :** 24/130 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	114.091340	57.549308					**L**							**14**
2	***277.154669***	139.080973					**Y**	1491.733905	746.370591	1474.707356	737.857316	1473.723340	737.365308	**13**
3	***405.213247***	203.110262	388.186698	194.596987			**Q**	1328.670576	664.838926	1311.644027	656.325652	1310.660011	655.833644	**12**
4	***533.271825***	267.139551	516.245276	258.626276			**Q**	**1200.611998**	600.809637	1183.585449	592.296363	1182.601433	591.804355	**11**
5	***670.330737***	335.669007	653.304188	327.155732			**H**	**1072.553420**	536.780348	1055.526871	528.267074	1054.542855	527.775066	**10**
6	727.352201	364.179739	710.325652	355.666464			**G**	**935.494508**	468.250892	918.467959	459.737618	917.483943	459.245610	**9**

7	798.389315	399.698296	781.362766	391.185021			**A**	**878.473044**	439.740160	861.446495	431.226886	860.462479	430.734878	**8**
8	855.410779	428.209028	838.384230	419.695753			**G**	807.435930	404.221603	790.409381	395.708329	789.425365	395.216321	**7**
9	***968.494843***	484.751060	951.468294	476.237785			**L**	750.414466	375.710871	733.387917	367.197597	732.403901	366.705589	**6**
10	***1115.563257***	558.285267	1098.536708	549.771992			**F**	637.330402	319.168839	620.303853	310.655565	619.319837	310.163557	**5**
11	***1230.590200***	615.798738	1213.563651	607.285464	1212.579635	606.793456	**D**	**490.261988**	245.634632	473.235439	237.121358	472.251423	236.629350	**4**
12	***1329.658614***	665.332945	1312.632065	656.819671	1311.648049	656.327663	**V**	**375.235045**	188.121161	358.208496	179.607886	357.224480	179.115878	**3**
13	***1430.706293***	715.856785	1413.679744	707.343510	1412.695728	706.851502	**T**	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



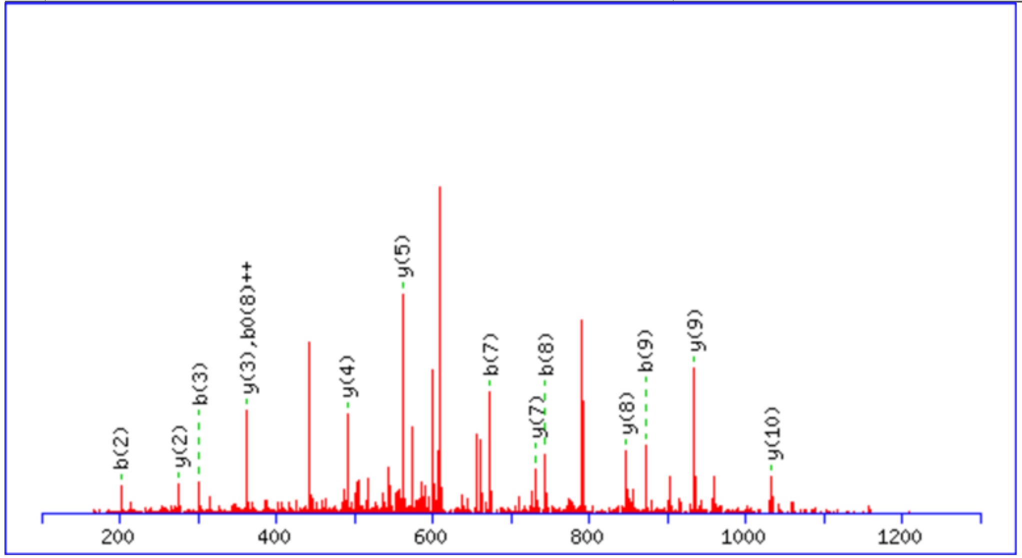
Peptide View

MS/MS Fragmentation of **SNVSDAVAQSTR**
Found in **IPI00465028**, Tax_Id=9606 Gene_Symbol=RCTPI1;TPI1 triosephosphate isomerase 1 isoform 2
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 6441: 1233.596048 from(617.805300,2+)
Title: OECHL100310_39.5646.5646.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1233.594940**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49

Expect: 0.0011**Matches :** 14/128 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							12
2	**202.082231**	101.544753	185.055682	93.031479	184.071666	92.539471	N	1147.570191	574.288733	1130.543642	565.775459	1129.559626	565.283451	11
3	**301.150645**	151.078960	284.124096	142.565686	283.140080	142.073678	V	***1033.527264***	517.267270	1016.500715	508.753995	1015.516699	508.261987	10
4	388.182673	194.594974	371.156124	186.081700	370.172108	185.589692	S	***934.458850***	467.733063	917.432301	459.219788	916.448285	458.727780	9
5	503.209616	252.108446	486.183067	243.595171	485.199051	243.103163	D	***847.426822***	424.217049	830.400273	415.703774	829.416257	415.211766	8
6	574.246730	287.627003	557.220181	279.113729	556.236165	278.621721	A	***732.399879***	366.703577	715.373330	358.190303	714.389314	357.698295	7
7	**673.315144**	337.161210	656.288595	328.647936	655.304579	328.155928	V	661.362765	331.185020	644.336216	322.671746	643.352200	322.179738	6
8	**744.352258**	372.679767	727.325709	364.166493	726.341693	363.674485	A	***562.294351***	281.650813	545.267802	273.137539	544.283786	272.645531	5
9	**872.410836**	436.709056	855.384287	428.195782	854.400271	427.703774	Q	***491.257237***	246.132256	474.230688	237.618982	473.246672	237.126974	4
10	959.442864	480.225070	942.416315	471.711795	941.432299	471.219788	S	***363.198659***	182.102967	346.172110	173.589693	345.188094	173.097685	3
11	1060.490543	530.748909	1043.463994	522.235635	1042.479978	521.743627	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
12							R	175.118952	88.063114	158.092403	79.549839			1

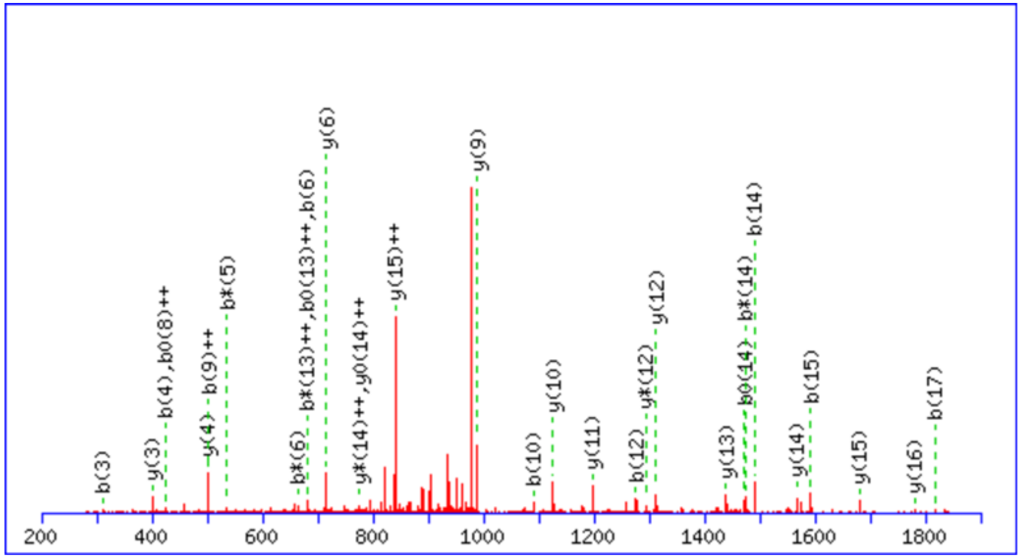


Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 13725: 1990.027848 from(996.021200,2+)
Title: OECHL100310_39.9430.9430.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67
Expect: 3e-005**Matches :** 31/186 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	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	**424.255445**	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	552.314023	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	**680.372601**	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**
7	795.399544	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	901.510158	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	814.478130	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	614.362037	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510			**3**
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**



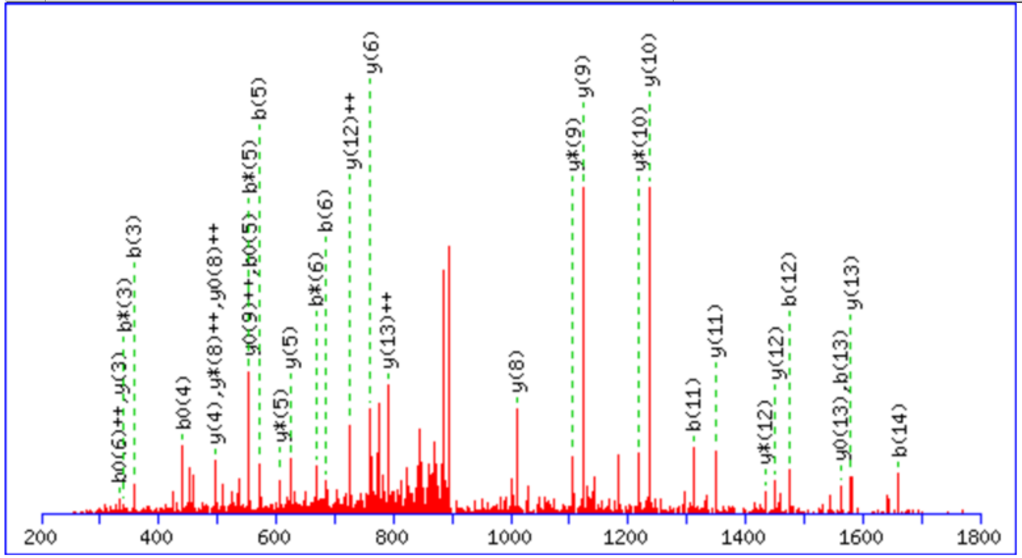
Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 12630: 1805.932448 from(903.973500,2+)
Title: OECHL100310_39.18847.18847.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63
Expect: 5.8e-005**Matches :** 33/160 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**15**
2	228.134267	114.570771	211.107718	106.057497			**I**	1692.895549	846.951413	1675.869000	838.438138	1674.884984	837.946130	**14**
3	**357.176860**	179.092068	340.150311	170.578793	339.166295	170.086785	**E**	***1579.811485***	790.409381	1562.784936	781.896106	1561.800920	781.404098	**13**
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	**T**	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.882802	**12**
5	**571.308603**	286.157940	554.282054	277.644665	553.298038	277.152657	**I**	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.358962	**11**
6	**684.392667**	342.699972	667.366118	334.186697	666.382102	333.694689	**I**	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.816930	**10**

7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	**N**	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.274898	**9**
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	**T**	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.253435	**8**
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	**F**	908.462479	454.734878	891.435930	446.221603	890.451914	445.729595	**7**
10	1183.610599	592.308938	1166.584050	583.795663	1165.600034	583.303655	**H**	***761.394065***	381.200671	744.367516	372.687396	743.383500	372.195388	**6**
11	**1311.669177**	656.338227	1294.642628	647.824952	1293.658612	647.332944	**Q**	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.665932	**5**
12	**1474.732506**	737.869891	1457.705957	729.356617	1456.721941	728.864609	**Y**	***496.276575***	248.641926	479.250026	240.128651	478.266010	239.636643	**4**
13	**1561.764534**	781.385905	1544.737985	772.872631	1543.753969	772.380623	**S**	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.104979	**3**
14	**1660.832948**	830.920112	1643.806399	822.406838	1642.822383	821.914830	**V**	246.181218	123.594247	229.154669	115.080973			**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



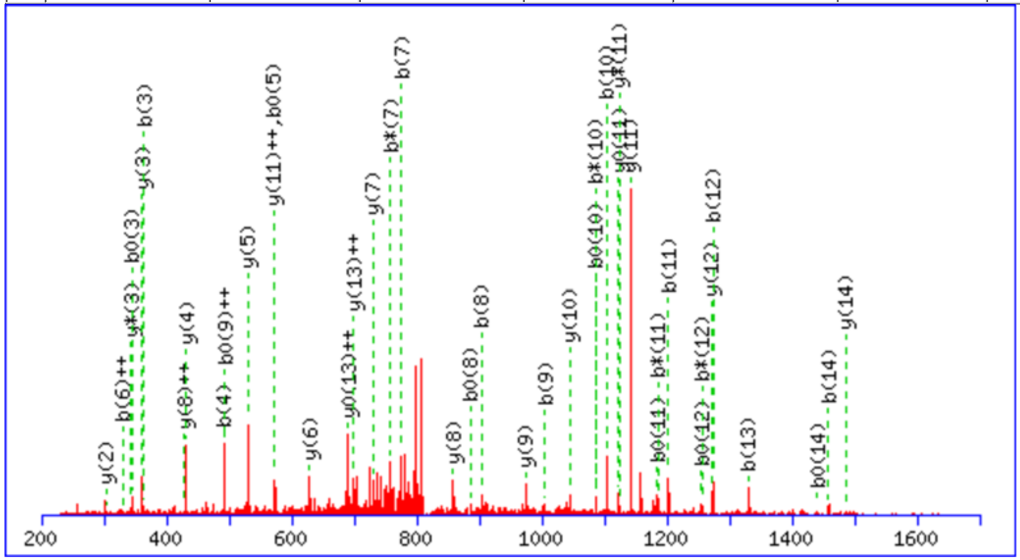
Peptide View

MS/MS Fragmentation of **FSQEPADQTVVAGQR**
Found in **IPI00470360**, Tax_Id=9606 Gene_Symbol=KIRREL Isoform 1 of Kin of IRRE-like protein 1
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 11001: 1631.789648 from(816.902100,2+)
Title: OECHL100310_39.7824.7824.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw

Monoisotopic mass of neutral peptide Mr(calc): 1631.790359**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00099**Matches :** 42/150 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	148.075690	74.541483					F							15
2	235.107718	118.057497			217.097153	109.052214	S	***1485.729213***	743.368245	1468.702664	734.854970	1467.718648	734.362962	14
3	**363.166296**	182.086786	346.139747	173.573512	345.155731	173.081504	Q	1398.697185	699.852231	1381.670636	691.338956	1380.686620	690.846948	13
4	**492.208889**	246.608082	475.182340	238.094808	474.198324	237.602800	E	***1270.638607***	635.822942	1253.612058	627.309667	1252.628042	626.817659	12
5	589.261653	295.134465	572.235104	286.621190	571.251088	286.129182	P	***1141.596014***	571.301645	1124.569465	562.788371	1123.585449	562.296363	11
6	660.298767	330.653022	643.272218	322.139747	642.288202	321.647739	A	***1044.543250***	522.775263	1027.516701	514.261989	1026.532685	513.769981	10
7	**775.325710**	388.166493	758.299161	379.653218	757.315145	379.161210	D	***973.506136***	487.256706	956.479587	478.743432	955.495571	478.251424	9
8	**903.384288**	452.195782	886.357739	443.682507	885.373723	443.190499	Q	***858.479193***	429.743235	841.452644	421.229960	840.468628	420.737952	8
9	**1004.431967**	502.719622	987.405418	494.206347	986.421402	493.714339	T	***730.420615***	365.713946	713.394066	357.200671	712.410050	356.708663	7
10	**1103.500381**	552.253829	1086.473832	543.740554	1085.489816	543.248546	V	***629.372936***	315.190106	612.346387	306.676832			6
11	**1202.568795**	601.788036	1185.542246	593.274761	1184.558230	592.782753	V	***530.304522***	265.655899	513.277973	257.142625			5
12	**1273.605909**	637.306593	1256.579360	628.793318	1255.595344	628.301310	A	***431.236108***	216.121692	414.209559	207.608417			4
13	**1330.627373**	665.817325	1313.600824	657.304050	1312.616808	656.812042	G	***360.198994***	180.603135	343.172445	172.089860			3
14	**1458.685951**	729.846614	1441.659402	721.333339	1440.675386	720.841331	Q	***303.177530***	152.092403	286.150981	143.579129			2
15							R	175.118952	88.063114	158.092403	79.549839			1

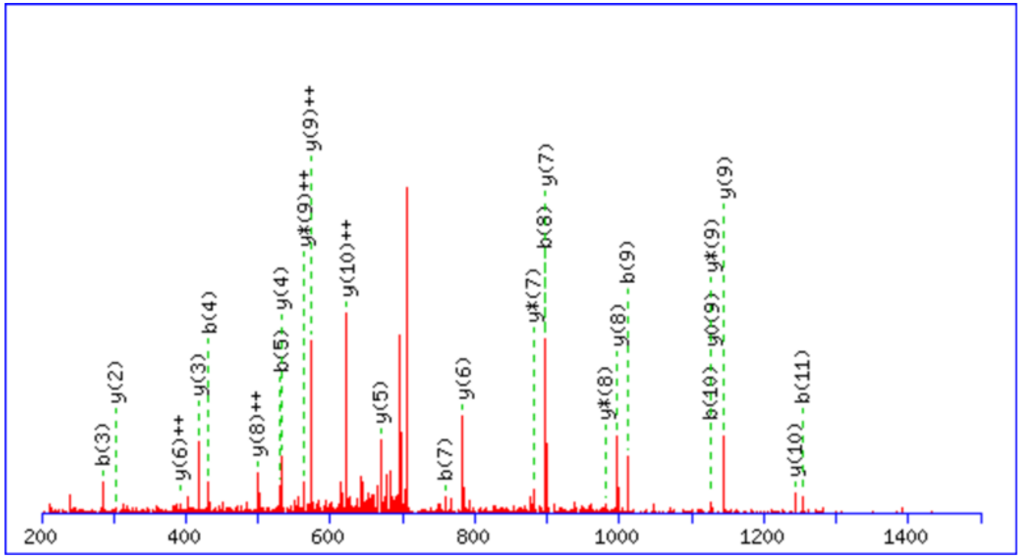


Peptide View

MS/MS Fragmentation of **ALVFVDNHDNQR**
Found in **IPI00021447**, Tax_Id=9606 Gene_Symbol=AMY2B Alpha-amylase 2B
Experiment: 43 - OPE-1 **Fraction:** OPE-1

Match to Query 8704: 1426.696848 from(714.355700,2+)
Title: OECHL100310_39.9138.9138.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1426.695328**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49
Expect: 0.0013**Matches :** 26/104 fragment ions using 59 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**12**
2	185.128454	93.067865					**L**	1356.665488	678.836382	1339.638939	670.323108	1338.654923	669.831100	**11**
3	**284.196868**	142.602072					**V**	***1243.581424***	622.294350	1226.554875	613.781076	1225.570859	613.289068	**10**
4	**431.265282**	216.136279					**F**	***1144.513010***	572.760143	1127.486461	564.246869	1126.502445	563.754861	**9**
5	**530.333696**	265.670486					**V**	***997.444596***	499.225936	980.418047	490.712662	979.434031	490.220654	**8**
6	645.360639	323.183958			627.350074	314.178675	**D**	***898.376182***	449.691729	881.349633	441.178455	880.365617	440.686447	**7**
7	**759.403566**	380.205421	742.377017	371.692146	741.393001	371.200138	**N**	***783.349239***	392.178258	766.322690	383.664983	765.338674	383.172975	**6**
8	**896.462478**	448.734877	879.435929	440.221602	878.451913	439.729594	**H**	***669.306312***	335.156794	652.279763	326.643520	651.295747	326.151512	**5**
9	**1011.489421**	506.248348	994.462872	497.735074	993.478856	497.243066	**D**	***532.247400***	266.627338	515.220851	258.114064	514.236835	257.622056	**4**
10	**1125.532348**	563.269812	1108.505799	554.756538	1107.521783	554.264529	**N**	***417.220457***	209.113867	400.193908	200.600592			**3**
11	**1253.590926**	627.299101	1236.564377	618.785827	1235.580361	618.293819	**Q**	***303.177530***	152.092403	286.150981	143.579129			**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**



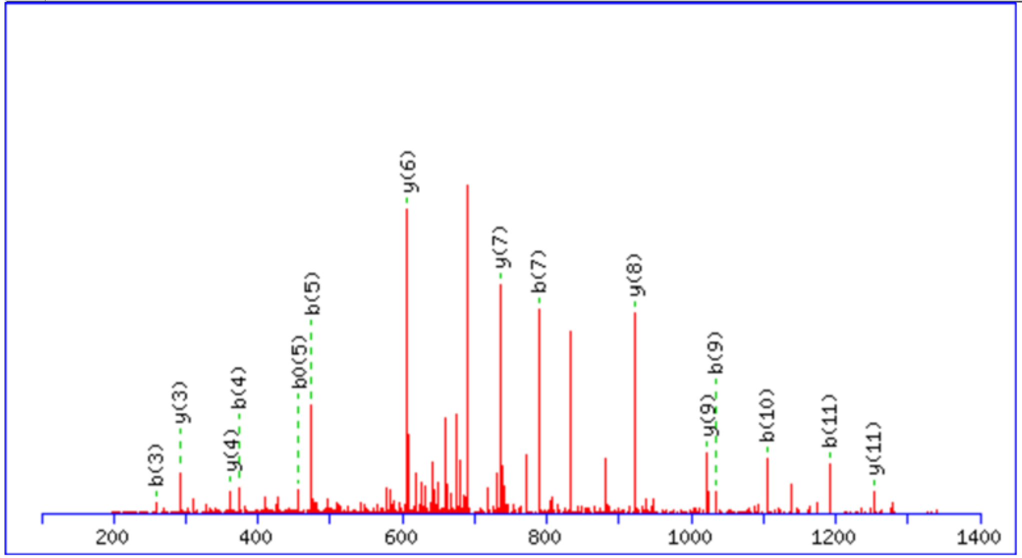
Peptide View

MS/MS Fragmentation of **AADDTWEPFASGK**
Found in **IPI00022432**, Tax_Id=9606 Gene_Symbol=TTR Transthyretin
Experiment: 28 - NOPE1 **Fraction:** NOPE1

Match to Query 8043: 1393.615248 from(697.814900,2+)
Title: OECHL100310_37.15266.15266.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1393.615005**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 0.0001**Matches :** 15/112 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**13**
2	143.081504	72.044390			**A**	1323.585173	662.296225	1306.558624	653.782950	1305.574608	653.290942	**12**
3	***258.108447***	129.557862	240.097882	120.552579	**D**	***1252.548059***	626.777668	1235.521510	618.264393	1234.537494	617.772385	**11**
4	***373.135390***	187.071333	355.124825	178.066051	**D**	1137.521116	569.264196	1120.494567	560.750922	1119.510551	560.258914	**10**
5	***474.183069***	237.595173	456.172504	228.589890	**T**	***1022.494173***	511.750725	1005.467624	503.237450	1004.483608	502.745442	**9**
6	660.262382	330.634829	642.251817	321.629547	**W**	***921.446494***	461.226885	904.419945	452.713611	903.435929	452.221603	**8**

7	***789.304975***	395.156126	771.294410	386.150843	**E**	***735.367181***	368.187229	718.340632	359.673954	717.356616	359.181946	**7**
8	886.357739	443.682508	868.347174	434.677225	**P**	***606.324588***	303.665932	589.298039	295.152658	588.314023	294.660650	**6**
9	***1033.426153***	517.216715	1015.415588	508.211432	**F**	509.271824	255.139550	492.245275	246.626275	491.261259	246.134267	**5**
10	***1104.463267***	552.735272	1086.452702	543.729989	**A**	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	**4**
11	***1191.495295***	596.251286	1173.484730	587.246003	**S**	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	**3**
12	1248.516759	624.762018	1230.506194	615.756735	**G**	204.134268	102.570772	187.107719	94.057497			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**

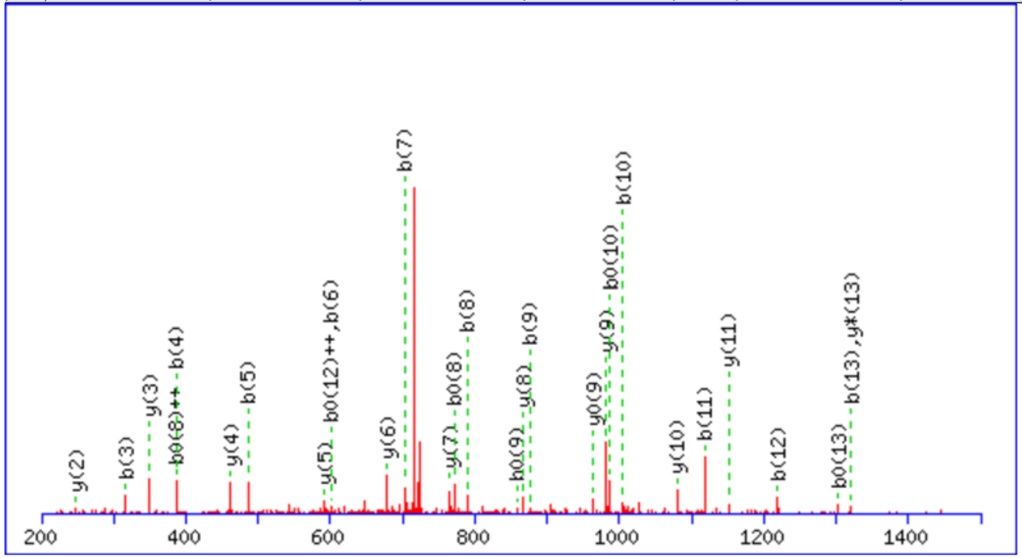


Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 28 - NOPE1 **Fraction:** NOPE1

Match to Query 8814: 1465.679248 from(733.846900,2+)
Title: OECHL100310_37.9995.9995.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 79 **Expect:** 1.1e-006**Matches :** 29/128 fragment ions using 48 most intense peaks (help)

#	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y^{*}**	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	1337.643082	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	***316.113926***	158.560601	298.103361	149.555319	**A**	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	***387.151040***	194.079158	369.140475	185.073875	**A**	**1151.579025**	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	***486.219454***	243.613365	468.208889	234.608082	**V**	**1080.541911**	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**
6	***601.246397***	301.126837	583.235832	292.121554	**D**	**981.473497**	491.240387	964.446948	482.727112	963.462932	482.235104	**9**
7	***702.294076***	351.650676	684.283511	342.645394	**T**	**866.446554**	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	***789.326104***	395.166690	771.315539	386.161408	**S**	**765.398875**	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	***876.358132***	438.682704	858.347567	429.677421	**S**	**678.366847**	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	***1005.400725***	503.204001	987.390160	494.198718	**E**	**591.334819**	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	***1118.484789***	559.746033	1100.474224	550.740750	**I**	**462.292226**	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	***1219.532468***	610.269872	1201.521903	601.264590	**T**	**349.208162**	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	***1320.580147***	660.793712	1302.569582	651.788429	**T**	**248.160483**	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**

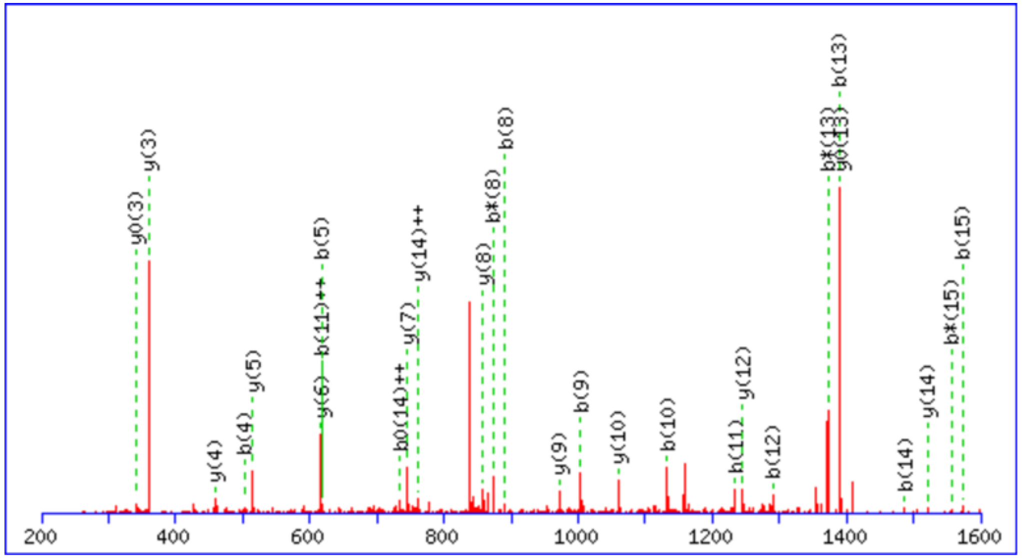


Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 28 - NOPE1 **Fraction:** NOPE1

Match to Query 11940: 1746.917248 from(874.465900,2+)
Title: OECHL100310_37.17246.17246.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 82
Expect: 7.2e-007**Matches :** 28/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	***503.322797***	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	***618.349740***	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	689.386854	345.197065			671.376289	336.191782	**A**	1130.580027	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	***890.461809***	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



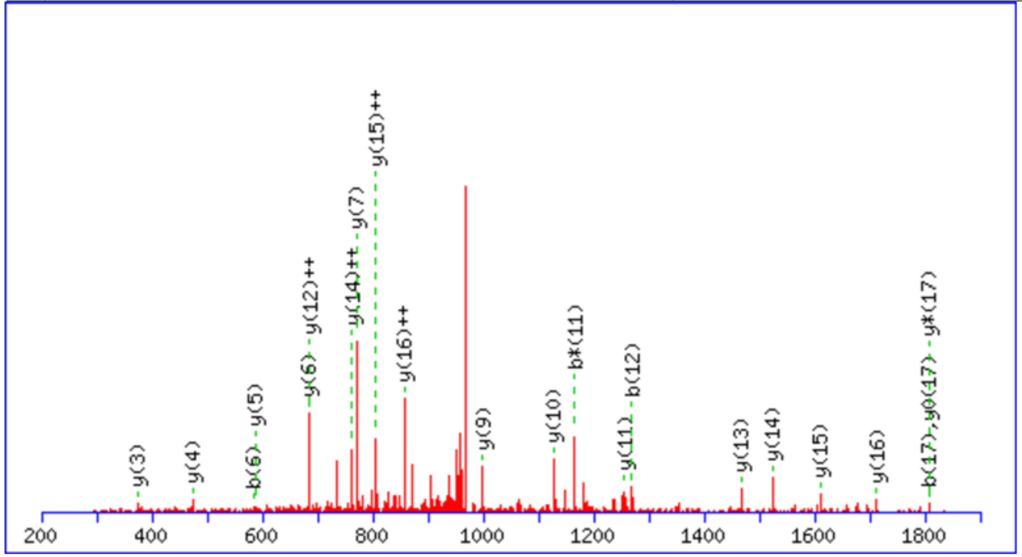
Peptide View

MS/MS Fragmentation of **QLTSGPNQEQVSPLTLLK**
Found in **IPI00029863**, Tax_Id=9606 Gene_Symbol=- 55 kDa protein
Experiment: 28 - NOPE1 **Fraction:** NOPE1

Match to Query 13717: 1952.058848 from(977.036700,2+)
Title: OECHL100310_37.18607.18607.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1952.057846**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 97
Expect: 1.1e-008**Matches :** 22/194 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							18
2	242.149918	121.578597	225.123369	113.065323			L	1825.006556	913.006916	1807.980007	904.493642	1806.995991	904.001634	17
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	T	***1711.922492***	856.464884	1694.895943	847.951610	1693.911927	847.459601	16
4	430.229625	215.618450	413.203076	207.105176	412.219060	206.613168	S	***1610.874813***	805.941044	1593.848264	797.427770	1592.864248	796.935762	15
5	487.251089	244.129182	470.224540	235.615908	469.240524	235.123900	G	***1523.842785***	762.425031	1506.816236	753.911756	1505.832220	753.419748	14
6	**584.303853**	292.655565	567.277304	284.142290	566.293288	283.650282	P	***1466.821321***	733.914298	1449.794772	725.401024	1448.810756	724.909016	13

7	698.346780	349.677028	681.320231	341.163753	680.336215	340.671745	**N**	1369.768557	685.387917	1352.742008	676.874642	1351.757992	676.382634	**12**
8	826.405358	413.706317	809.378809	405.193042	808.394793	404.701034	**Q**	***1255.725630***	628.366453	1238.699081	619.853179	1237.715065	619.361171	**11**
9	955.447951	478.227614	938.421402	469.714339	937.437386	469.222331	**E**	***1127.667052***	564.337164	1110.640503	555.823890	1109.656487	555.331882	**10**
10	1083.506529	542.256903	1066.479980	533.743628	1065.495964	533.251620	**Q**	***998.624459***	499.815868	981.597910	491.302593	980.613894	490.810585	**9**
11	1182.574943	591.791110	1165.548394	583.277835	1164.564378	582.785827	**V**	870.565881	435.786579	853.539332	427.273304	852.555316	426.781296	**8**
12	**1269.606971**	635.307124	1252.580422	626.793849	1251.596406	626.301841	**S**	***771.497467***	386.252371	754.470918	377.739097	753.486902	377.247089	**7**
13	1366.659735	683.833506	1349.633186	675.320231	1348.649170	674.828223	**P**	***684.465439***	342.736357	667.438890	334.223083	666.454874	333.731075	**6**
14	1479.743799	740.375538	1462.717250	731.862263	1461.733234	731.370255	**L**	***587.412675***	294.209975	570.386126	285.696701	569.402110	285.204693	**5**
15	1580.791478	790.899377	1563.764929	782.386103	1562.780913	781.894095	**T**	***474.328611***	237.667943	457.302062	229.154669	456.318046	228.662661	**4**
16	1693.875542	847.441409	1676.848993	838.928135	1675.864977	838.436127	**L**	***373.280932***	187.144104	356.254383	178.630829			**3**
17	**1806.959606**	903.983441	1789.933057	895.470167	1788.949041	894.978158	**L**	260.196868	130.602072	243.170319	122.088797			**2**
18							**K**	147.112804	74.060040	130.086255	65.546765			**1**

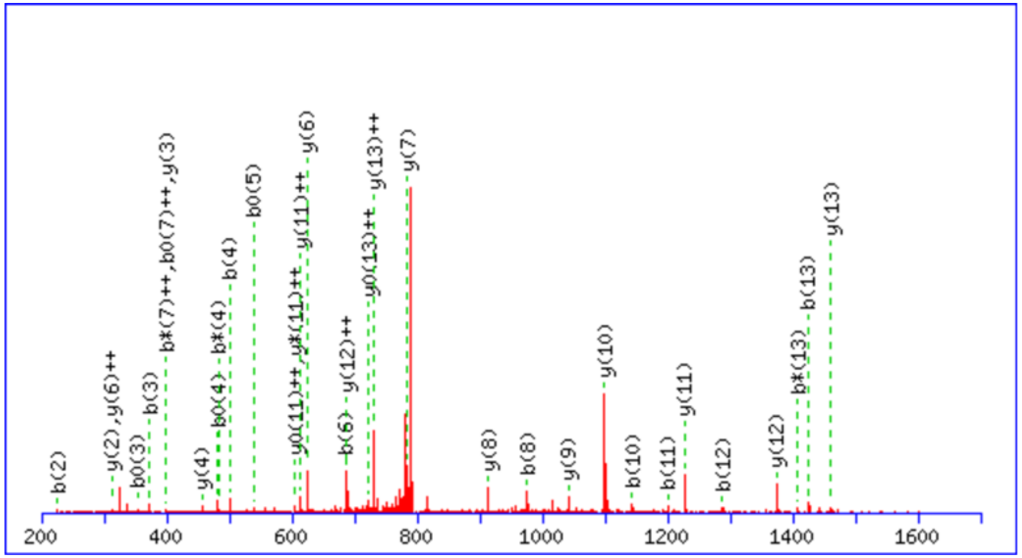


Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 28 - NOPE1 **Fraction:** NOPE1

Match to Query 10324: 1597.706848 from(799.860700,2+)
Title: OECHL100310_37.2251.2251.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 73
Expect: 3e-006**Matches :** 34/144 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	138.066188	69.536732					**H**							**14**
2	**225.098216**	113.052746			207.087651	104.047463	**S**	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.325325	**13**
3	**372.166630**	186.586953			354.156065	177.581671	**F**	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.809311	**12**
4	**500.261593**	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	**11**
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	**10**
6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	***1042.437069***	521.722173	1025.410520	513.208898	1024.426504	512.716890	**9**
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	527.268470	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	***312.177864***	156.592570	295.151315	148.079295			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



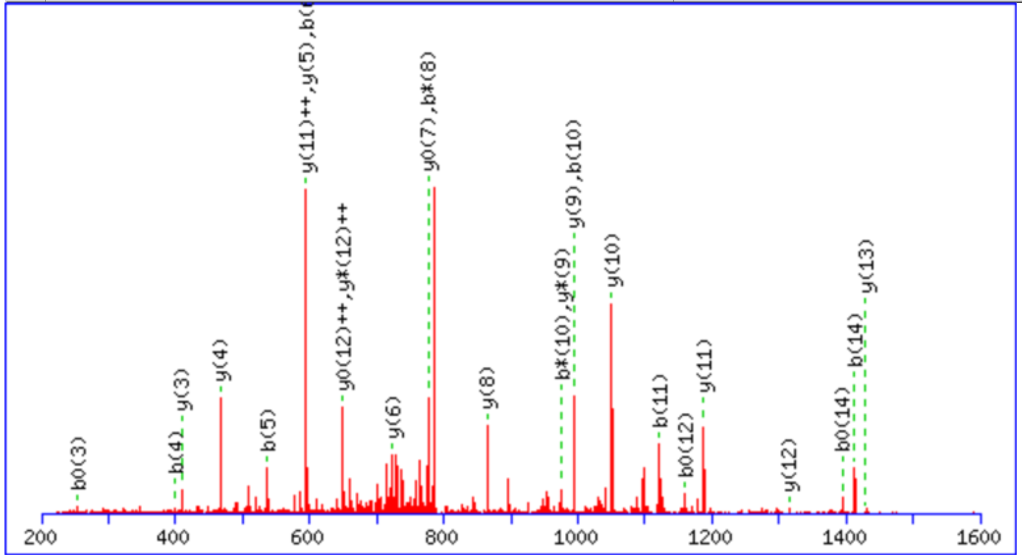
Peptide View

MS/MS Fragmentation of **ASLQHGQAAEKGPHR**
Found in **IPI00165044**, Tax_Id=9606 Gene_Symbol=FAM198B Isoform 2 of Protein ENED
Experiment: 28 - NOPE1 **Fraction:** NOPE1

Match to Query 10227: 1585.808048 from(793.911300,2+)
Title: OECHL100310_37.1804.1804.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1585.807312**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65
Expect: 4e-005**Matches :** 26/150 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**15**
2	159.076418	80.041847			141.065853	71.036564	**S**	1515.777500	758.392388	1498.750951	749.879114	1497.766935	749.387106	**14**
3	272.160482	136.583879			254.149917	127.578597	**L**	***1428.745472***	714.876374	1411.718923	706.363100	1410.734907	705.871092	**13**
4	**400.219060**	200.613168	383.192511	192.099894	382.208495	191.607886	**Q**	***1315.661408***	658.334342	1298.634859	649.821068	1297.650843	649.329060	**12**
5	**537.277972**	269.142624	520.251423	260.629350	519.267407	260.137342	**H**	***1187.602830***	594.305053	1170.576281	585.791779	1169.592265	585.299771	**11**
6	**594.299436**	297.653356	577.272887	289.140082	576.288871	288.648074	**G**	***1050.543918***	525.775597	1033.517369	517.262323	1032.533353	516.770315	**10**

7	722.358014	361.682645	705.331465	353.169371	704.347449	352.677363	**Q**	***993.522454***	497.264865	976.495905	488.751591	975.511889	488.259583	**9**
8	793.395128	397.201202	776.368579	388.687928	775.384563	388.195920	**A**	***865.463876***	433.235576	848.437327	424.722302	847.453311	424.230294	**8**
9	864.432242	432.719759	847.405693	424.206485	846.421677	423.714477	**A**	794.426762	397.717019	777.400213	389.203745	776.416197	388.711737	**7**
10	**993.474835**	497.241056	976.448286	488.727781	975.464270	488.235773	**E**	***723.389648***	362.198462	706.363099	353.685188	705.379083	353.193180	**6**
11	**1121.569798**	561.288537	1104.543249	552.775263	1103.559233	552.283255	**K**	***594.347055***	297.677166	577.320506	289.163891			**5**
12	1178.591262	589.799269	1161.564713	581.285995	1160.580697	580.793987	**G**	***466.252092***	233.629684	449.225543	225.116409			**4**
13	1275.644026	638.325651	1258.617477	629.812377	1257.633461	629.320369	**P**	***409.230628***	205.118952	392.204079	196.605677			**3**
14	**1412.702938**	706.855107	1395.676389	698.341833	1394.692373	697.849825	**H**	312.177864	156.592570	295.151315	148.079295			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



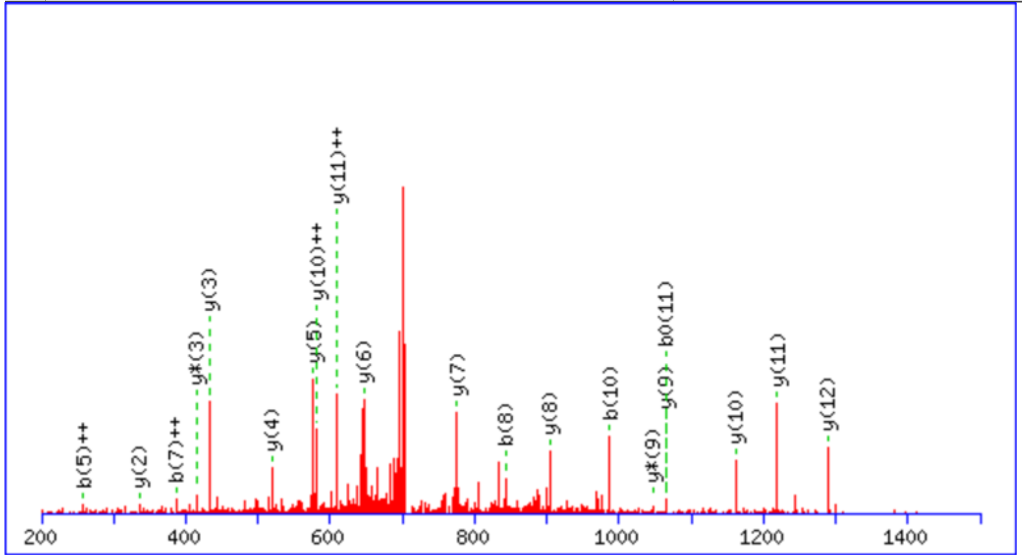
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 28 - NOPE1 **Fraction:** NOPE1

Match to Query 8267: 1416.624648 from(709.319600,2+)
Title: OECHL100310_37.2099.2099.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_37.raw

Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 85
Expect: 2.1e-007**Matches :** 20/128 fragment ions using 37 most intense peaks (help)

#	**b**	**b^{++}**	**b***	**b^{*++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	129.102239	65.054757	112.075690	56.541483			**K**							**13**
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	**12**
3	257.160817	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	**11**
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	**10**
5	514.244230	**257.625753**	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	**9**
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	**8**
7	771.345401	**386.176339**	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	899.403979	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

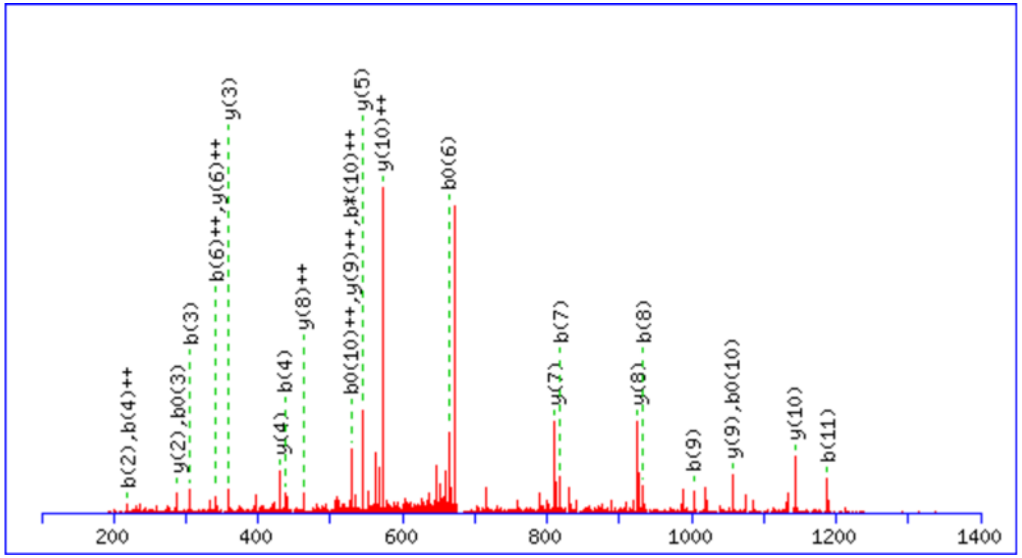


Peptide View

MS/MS Fragmentation of **AFSMDEHNAALR**
Found in **IPI00008239**, Tax_Id=9606 Gene_Symbol=GPRC5B cDNA FLJ55176, highly similar to G-protein coupled receptor family C group 5 member B
Experiment: 28 - NOPE1 **Fraction:** NOPE1

Match to Query 7729: 1360.618648 from(681.316600,2+)
Title: OECHL100310_37.9666.9666.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1360.619354**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.0004**Matches :** 26/102 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**12**
2	***219.112804***	110.060040					**F**	1290.589546	645.798411	1273.562997	637.285137	1272.578981	636.793128	**11**
3	***306.144832***	153.576054			288.134267	144.570772	**S**	***1143.521132***	572.264204	1126.494583	563.750929	1125.510567	563.258921	**10**
4	***437.185317***	**219.096296**			419.174752	210.091014	**M**	***1056.489104***	528.748190	1039.462555	520.234916	1038.478539	519.742908	**9**
5	552.212260	276.609768			534.201695	267.604486	**D**	***925.448619***	463.227947	908.422070	454.714673	907.438054	454.222665	**8**
6	681.254853	**341.131065**			663.244288	332.125782	**E**	***810.421676***	405.714476	793.395127	397.201201	792.411111	396.709193	**7**
7	***818.313765***	409.660521			800.303200	400.655238	**H**	681.379083	341.193179	664.352534	332.679905			**6**
8	***932.356692***	466.681984	915.330143	458.168709	914.346127	457.676701	**N**	***544.320171***	272.663724	527.293622	264.150449			**5**
9	***1003.393806***	502.200541	986.367257	493.687266	985.383241	493.195258	**A**	***430.277244***	215.642260	413.250695	207.128985			**4**
10	1074.430920	537.719098	1057.404371	529.205824	1056.420355	528.713816	**A**	***359.240130***	180.123703	342.213581	171.610428			**3**
11	***1187.514984***	594.261130	1170.488435	585.747856	1169.504419	585.255847	**L**	***288.203016***	144.605146	271.176467	136.091871			**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**



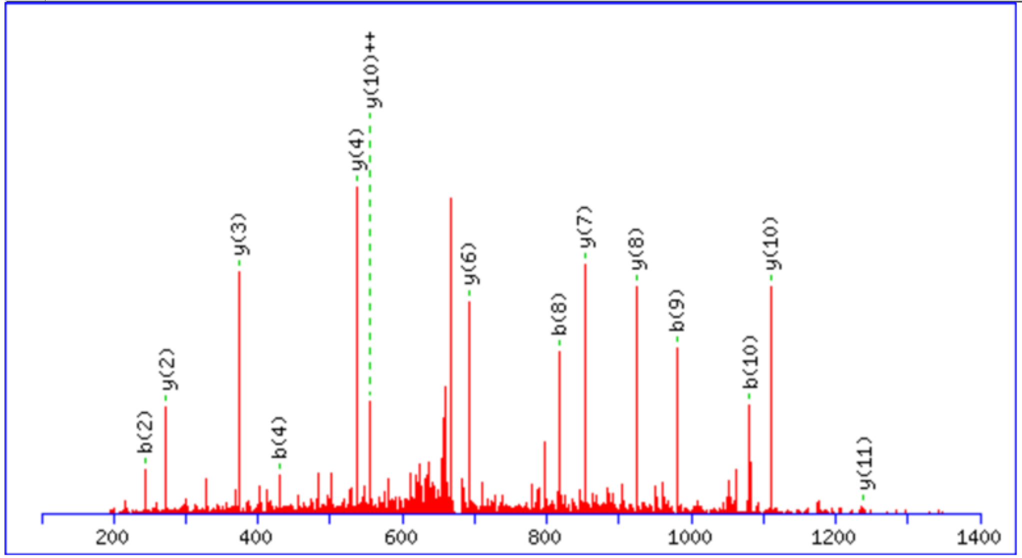
Peptide View

MS/MS Fragmentation of **LEGEACGVYTPR**
Found in **IPI00297284**, Tax_Id=9606 Gene_Symbol=IGFBP2 Insulin-like growth factor-binding protein 2
Experiment: 28 - NOPE1 **Fraction:** NOPE1

Match to Query 7627: 1350.626048 from(676.320300,2+)
Title: OECHL100310_37.8673.8673.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1350.623795**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00035**Matches :** 14/104 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							**12**
2	**243.133933**	122.070605	225.123368	113.065322	**E**	***1238.547015***	619.777146	1221.520466	611.263871	1220.536450	610.771863	**11**
3	300.155397	150.581336	282.144832	141.576054	**G**	***1109.504422***	555.255849	1092.477873	546.742575	1091.493857	546.250567	**10**
4	**429.197990**	215.102633	411.187425	206.097351	**E**	1052.482958	526.745117	1035.456409	518.231843	1034.472393	517.739835	**9**
5	500.235104	250.621190	482.224539	241.615908	**A**	***923.440365***	462.223821	906.413816	453.710546	905.429800	453.218538	**8**
6	660.265753	330.636515	642.255188	321.631232	**C**	***852.403251***	426.705264	835.376702	418.191989	834.392686	417.699981	**7**

7	717.287217	359.147247	699.276652	350.141964	**G**	***692.372602***	346.689939	675.346053	338.176665	674.362037	337.684657	**6**
8	**816.355631**	408.681454	798.345066	399.676171	**V**	635.351138	318.179207	618.324589	309.665933	617.340573	309.173925	**5**
9	**979.418960**	490.213118	961.408395	481.207836	**Y**	***536.282724***	268.645000	519.256175	260.131726	518.272159	259.639718	**4**
10	**1080.466639**	540.736958	1062.456074	531.731675	**T**	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	**3**
11	1177.519403	589.263340	1159.508838	580.258057	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**



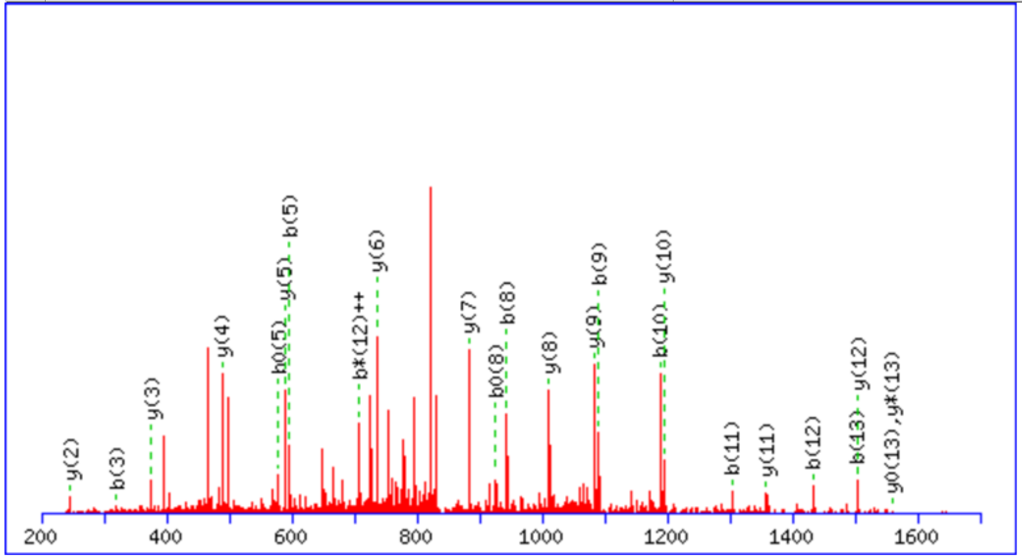
Peptide View

MS/MS Fragmentation of **TAFYLAEFFVNEAR**
Found in **IPI00023728**, Tax_Id=9606 Gene_Symbol=GGH Gamma-glutamyl hydrolase
Experiment: 28 - NOPE1 **Fraction:** NOPE1

Match to Query 11217: 1676.813848 from(839.414200,2+)
Title: OECHL100310_37.22010.22010.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1676.819839**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71
Expect: 9.6e-006**Matches :** 24/132 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	102.054955	51.531116			84.044390	42.525833	**T**							**14**
2	173.092069	87.049672			155.081504	78.044390	**A**	1576.779456	788.893366	1559.752907	780.380092	1558.768891	779.888083	**13**
3	**320.160483**	160.583879			302.149918	151.578597	**F**	***1505.742342***	753.374809	1488.715793	744.861535	1487.731777	744.369527	**12**
4	483.223812	242.115544			465.213247	233.110261	**Y**	***1358.673928***	679.840602	1341.647379	671.327328	1340.663363	670.835319	**11**
5	**596.307876**	298.657576			578.297311	289.652293	**L**	***1195.610599***	598.308938	1178.584050	589.795663	1177.600034	589.303655	**10**
6	667.344990	334.176133			649.334425	325.170850	**A**	***1082.526535***	541.766906	1065.499986	533.253631	1064.515970	532.761623	**9**
7	796.387583	398.697430			778.377018	389.692147	**E**	***1011.489421***	506.248349	994.462872	497.735074	993.478856	497.243066	**8**
8	**943.455997**	472.231636			925.445432	463.226354	**F**	***882.446828***	441.727052	865.420279	433.213778	864.436263	432.721770	**7**
9	**1090.524411**	545.765843			1072.513846	536.760561	**F**	***735.378414***	368.192845	718.351865	359.679571	717.367849	359.187563	**6**
10	**1189.592825**	595.300051			1171.582260	586.294768	**V**	***588.310000***	294.658638	571.283451	286.145364	570.299435	285.653356	**5**
11	**1303.635752**	652.321514	1286.609203	643.808240	1285.625187	643.316231	**N**	***489.241586***	245.124431	472.215037	236.611156	471.231021	236.119148	**4**
12	**1432.678345**	716.842811	1415.651796	708.329536	1414.667780	707.837528	**E**	***375.198659***	188.102968	358.172110	179.589693	357.188094	179.097685	**3**
13	**1503.715459**	752.361368	1486.688910	743.848093	1485.704894	743.356085	**A**	***246.156066***	123.581671	229.129517	115.068396			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**

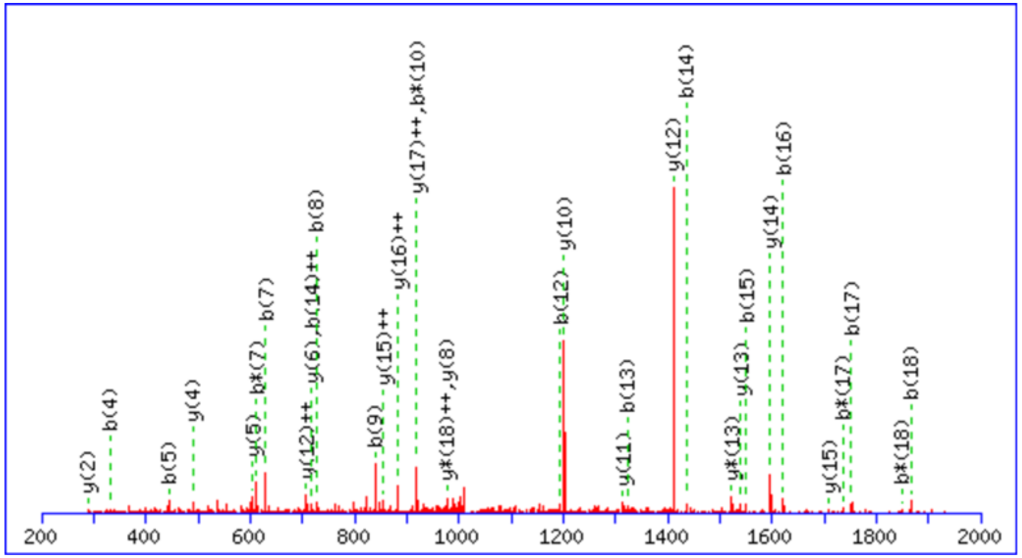


Peptide View

MS/MS Fragmentation of **AMAGLGQPLPQEELDAMIR**
Found in **IPI00021536**, Tax_Id=9606 Gene_Symbol=CALML5 Calmodulin-like protein 5
Experiment: 28 - NOPE1 **Fraction:** NOPE1

Match to Query 14313: 2039.019448 from(1020.517000,2+)
Title: OECHL100310_37.20138.20138.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 2039.017944**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66
Expect: 4.1e-005**Matches :** 34/174 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	72.044390	36.525833					**A**							**19**
2	203.084875	102.046075					**M**	1968.988147	984.997712	1951.961598	976.484437	1950.977582	975.992429	**18**
3	274.121989	137.564632					**A**	1837.947662	919.477469	1820.921113	910.964195	1819.937097	910.472187	**17**
4	***331.143453***	166.075364					**G**	1766.910548	883.958912	1749.883999	875.445638	1748.899983	874.953630	**16**
5	***444.227517***	222.617396					**L**	***1709.889084***	855.448180	1692.862535	846.934906	1691.878519	846.442898	**15**
6	501.248981	251.128128					**G**	***1596.805020***	798.906148	1579.778471	790.392874	1578.794455	789.900866	**14**
7	***629.307559***	315.157418	612.281010	306.644143			**Q**	***1539.783556***	770.395416	1522.757007	761.882142	1521.772991	761.390134	**13**
8	***726.360323***	363.683800	709.333774	355.170525			**P**	***1411.724978***	706.366127	1394.698429	697.852853	1393.714413	697.360844	**12**
9	***839.444387***	420.225832	822.417838	411.712557			**L**	***1314.672214***	657.839745	1297.645665	649.326471	1296.661649	648.834462	**11**
10	936.497151	468.752214	919.470602	460.238939			**P**	***1201.588150***	601.297713	1184.561601	592.784438	1183.577585	592.292430	**10**
11	1064.555729	532.781503	1047.529180	524.268228			**Q**	1104.535386	552.771331	1087.508837	544.258056	1086.524821	543.766048	**9**
12	***1193.598322***	597.302799	1176.571773	588.789525	1175.587757	588.297517	**E**	***976.476808***	488.742042	959.450259	480.228767	958.466243	479.736759	**8**
13	***1322.640915***	661.824096	1305.614366	653.310821	1304.630350	652.818813	**E**	847.434215	424.220746	830.407666	415.707471	829.423650	415.215463	**7**
14	***1435.724979***	718.366128	1418.698430	709.852853	1417.714414	709.360845	**L**	***718.391622***	359.699449	701.365073	351.186174	700.381057	350.694166	**6**
15	***1550.751922***	775.879599	1533.725373	767.366325	1532.741357	766.874317	**D**	***605.307558***	303.157417	588.281009	294.644142	587.296993	294.152134	**5**
16	***1621.789036***	811.398156	1604.762487	802.884882	1603.778471	802.392874	**A**	***490.280615***	245.643945	473.254066	237.130671			**4**
17	***1752.829521***	876.918399	1735.802972	868.405124	1734.818956	867.913116	**M**	419.243501	210.125388	402.216952	201.612114			**3**
18	***1865.913585***	933.460431	1848.887036	924.947156	1847.903020	924.455148	**I**	***288.203016***	144.605146	271.176467	136.091871			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



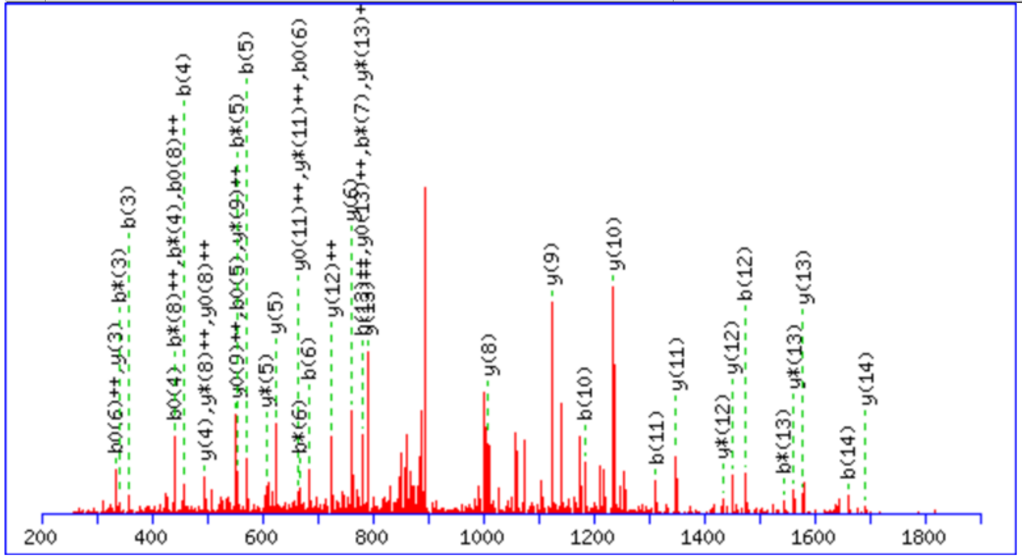
Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 28 - NOPE1 **Fraction:** NOPE1

Match to Query 12536: 1805.933048 from(903.973800,2+)
Title: OECHL100310_37.20230.20230.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60
Expect: 0.00012**Matches :** 45/160 fragment ions using 61 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**15**
2	228.134267	114.570771	211.107718	106.057497			**I**	***1692.895549***	846.951413	1675.869000	838.438138	1674.884984	837.946130	**14**
3	**357.176860**	179.092068	340.150311	170.578793	339.166295	170.086785	**E**	***1579.811485***	790.409381	1562.784936	781.896106	1561.800920	781.404098	**13**
4	**458.224539**	229.615907	441.197990	221.102633	440.213974	220.610625	**T**	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.882802	**12**
5	**571.308603**	286.157940	554.282054	277.644665	553.298038	277.152657	**I**	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.358962	**11**
6	**684.392667**	342.699972	667.366118	334.186697	666.382102	333.694689	**I**	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.816930	**10**

7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	**N**	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.274898	**9**
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	**T**	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.253435	**8**
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	**F**	908.462479	454.734878	891.435930	446.221603	890.451914	445.729595	**7**
10	**1183.610599**	592.308938	1166.584050	583.795663	1165.600034	583.303655	**H**	***761.394065***	381.200671	744.367516	372.687396	743.383500	372.195388	**6**
11	**1311.669177**	656.338227	1294.642628	647.824952	1293.658612	647.332944	**Q**	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.665932	**5**
12	**1474.732506**	737.869891	1457.705957	729.356617	1456.721941	728.864609	**Y**	***496.276575***	248.641926	479.250026	240.128651	478.266010	239.636643	**4**
13	1561.764534	781.385905	1544.737985	772.872631	1543.753969	772.380623	**S**	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.104979	**3**
14	**1660.832948**	830.920112	1643.806399	822.406838	1642.822383	821.914830	**V**	246.181218	123.594247	229.154669	115.080973			**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



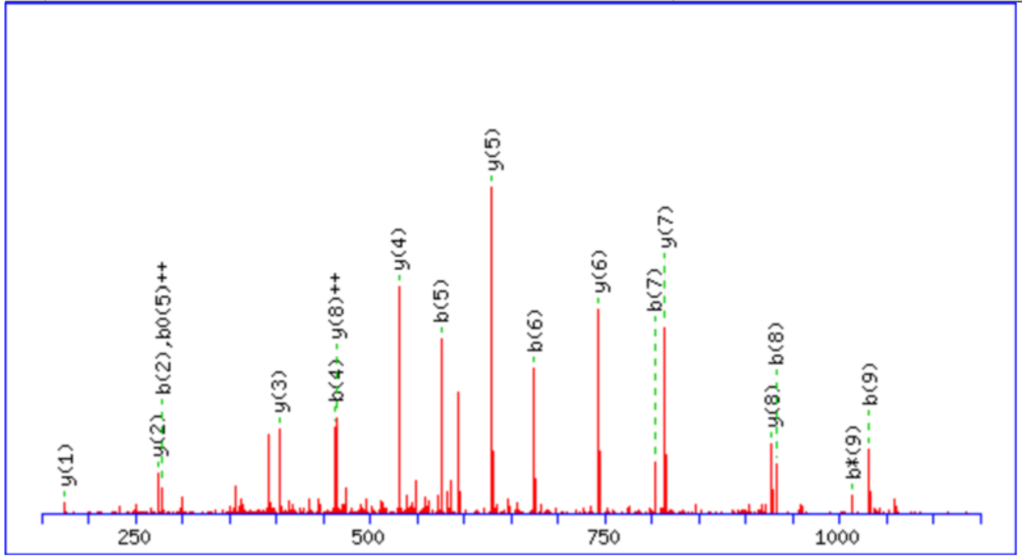
Peptide View

MS/MS Fragmentation of **YDIALVQEVR**
Found in **IPI00031065**, Tax_Id=9606 Gene_Symbol=DNASE1 Deoxyribonuclease-1
Experiment: 28 - NOPE1 **Fraction:** NOPE1

Match to Query 5550: 1204.646248 from(603.330400,2+)
Title: OECHL100310_37.15646.15646.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_37.raw

Monoisotopic mass of neutral peptide Mr(calc): 1204.645172**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 0.00018**Matches :** 18/90 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	164.070605	82.538940					**Y**							**10**
2	**279.097548**	140.052412			261.086983	131.047130	**D**	1042.589136	521.798206	1025.562587	513.284932	1024.578571	512.792924	**9**
3	392.181612	196.594444			374.171047	187.589162	**I**	***927.562193***	464.284735	910.535644	455.771460	909.551628	455.279452	**8**
4	**463.218726**	232.113001			445.208161	223.107719	**A**	***814.478129***	407.742703	797.451580	399.229428	796.467564	398.737420	**7**
5	**576.302790**	288.655033			558.292225	279.649751	**L**	***743.441015***	372.224146	726.414466	363.710871	725.430450	363.218863	**6**
6	**675.371204**	338.189240			657.360639	329.183958	**V**	***630.356951***	315.682114	613.330402	307.168839	612.346386	306.676831	**5**
7	**803.429782**	402.218529	786.403233	393.705255	785.419217	393.213247	**Q**	***531.288537***	266.147907	514.261988	257.634632	513.277972	257.142624	**4**
8	**932.472375**	466.739826	915.445826	458.226551	914.461810	457.734543	**E**	***403.229959***	202.118618	386.203410	193.605343	385.219394	193.113335	**3**
9	**1031.540789**	516.274033	1014.514240	507.760758	1013.530224	507.268750	**V**	***274.187366***	137.597321	257.160817	129.084047			**2**
10							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



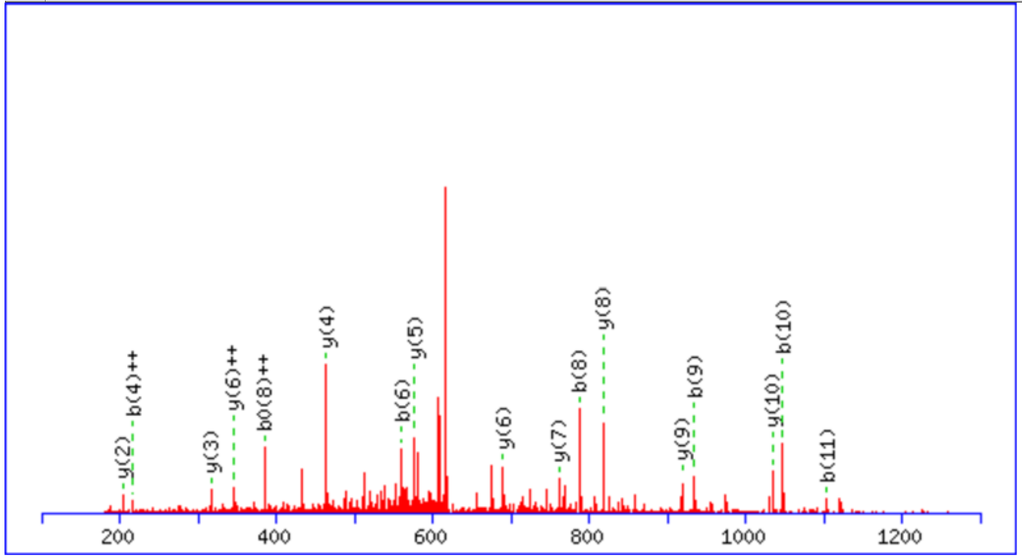
Peptide View

MS/MS Fragmentation of **DTDTGALLFIGK**
Found in **IPI00006114**, Tax_Id=9606 Gene_Symbol=SERPINF1 Pigment epithelium-derived factor

Experiment: 58 - PyE-1 **Fraction:** PyE-1

Match to Query 6965: 1249.656048 from(625.835300,2+)
Title: OECHL100310_35.17340.17340.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1249.655426**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 81
Expect: 6.5e-007**Matches :** 18/94 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	**D**							**12**
2	**217.081898**	109.044587	199.071333	100.039304	**T**	1135.635753	568.321514	1118.609204	559.808240	1117.625188	559.316232	**11**
3	332.108841	166.558058	314.098276	157.552776	**D**	***1034.588074***	517.797675	1017.561525	509.284401	1016.577509	508.792393	**10**
4	433.156520	217.081898	415.145955	208.076616	**T**	***919.561131***	460.284203	902.534582	451.770929	901.550566	451.278921	**9**
5	490.177984	245.592630	472.167419	236.587347	**G**	***818.513452***	409.760364	801.486903	401.247089			**8**
6	**561.215098**	281.111187	543.204533	272.105905	**A**	***761.491988***	381.249632	744.465439	372.736357			**7**
7	674.299162	337.653219	656.288597	328.647937	**L**	***690.454874***	345.731075	673.428325	337.217800			**6**
8	**787.383226**	394.195251	769.372661	385.189969	**L**	***577.370810***	289.189043	560.344261	280.675768			**5**
9	**934.451640**	467.729458	916.441075	458.724176	**F**	***464.286746***	232.647011	447.260197	224.133736			**4**
10	**1047.535704**	524.271490	1029.525139	515.266207	**I**	***317.218332***	159.112804	300.191783	150.599529			**3**
11	**1104.557168**	552.782222	1086.546603	543.776939	**G**	***204.134268***	102.570772	187.107719	94.057497			**2**
12					**K**	147.112804	74.060040	130.086255	65.546765			**1**

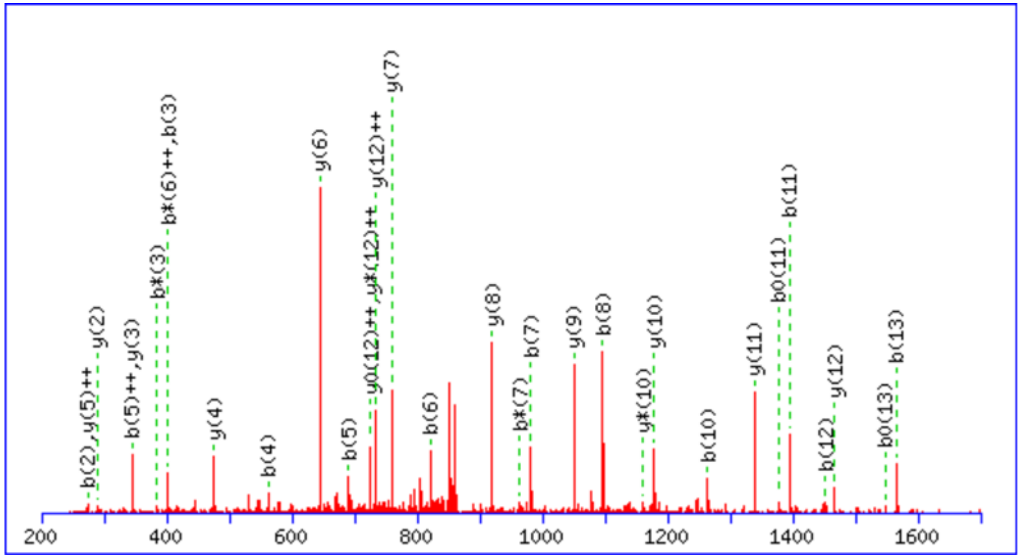


Peptide View

MS/MS Fragmentation of **CLQCQMCDPAMGLR**
Found in **IPI00024331**, Tax_Id=9606 Gene_Symbol=TNFRSF14 Tumor necrosis factor receptor superfamily member 14
Experiment: 58 - PyE-1 **Fraction:** PyE-1

Match to Query 12648: 1738.707448 from(870.361000,2+)
Title: OECHL100310_35.13645.13645.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1738.708160**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 80
Expect: 2.1e-007**Matches :** 32/126 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	161.037925	81.022600					**C**							**14**
2	***274.121989***	137.564632					**L**	1579.684789	790.346032	1562.658240	781.832758	1561.674224	781.340750	**13**
3	***402.180567***	201.593921	385.154018	193.080647			**Q**	**1466.600725**	733.804001	1449.574176	725.290726	1448.590160	724.798718	**12**
4	***562.211216***	281.609246	545.184667	273.095972			**C**	**1338.542147**	669.774711	1321.515598	661.261437	1320.531582	660.769429	**11**
5	***690.269794***	345.638535	673.243245	337.125261			**Q**	**1178.511498**	589.759387	1161.484949	581.246113	1160.500933	580.754105	**10**
6	***821.310279***	411.158778	804.283730	402.645503			**M**	**1050.452920**	525.730098	1033.426371	517.216824	1032.442355	516.724815	**9**
7	***981.340928***	491.174102	964.314379	482.660828			**C**	**919.412435**	460.209856	902.385886	451.696581	901.401870	451.204573	**8**
8	***1096.367871***	548.687574	1079.341322	540.174299	1078.357306	539.682291	**D**	**759.381786**	380.194531	742.355237	371.681256	741.371221	371.189248	**7**
9	1193.420635	597.213956	1176.394086	588.700681	1175.410070	588.208673	**P**	**644.354843**	322.681059	627.328294	314.167785			**6**
10	***1264.457749***	632.732513	1247.431200	624.219238	1246.447184	623.727230	**A**	547.302079	274.154677	530.275530	265.641403			**5**
11	***1395.498234***	698.252755	1378.471685	689.739481	1377.487669	689.247473	**M**	**476.264965**	238.636120	459.238416	230.122846			**4**
12	***1452.519698***	726.763487	1435.493149	718.250213	1434.509133	717.758205	**G**	**345.224480**	173.115878	328.197931	164.602603			**3**
13	***1565.603762***	783.305519	1548.577213	774.792245	1547.593197	774.300236	**L**	**288.203016**	144.605146	271.176467	136.091871			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



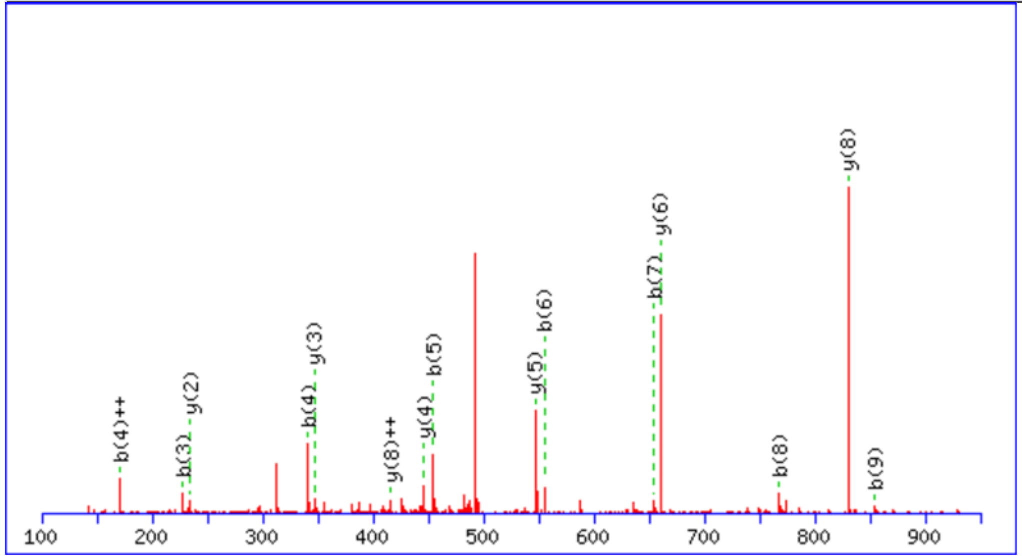
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 58 - PyE-1 **Fraction:** PyE-1

Match to Query 3194: 999.634048 from(500.824300,2+)
Title: OECHL100310_35.16575.16575.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65
Expect: 3.8e-006**Matches :** 16/78 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**

7	***654.418489***	327.712883	636.407924	318.707600	**V**	**446.297310**	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



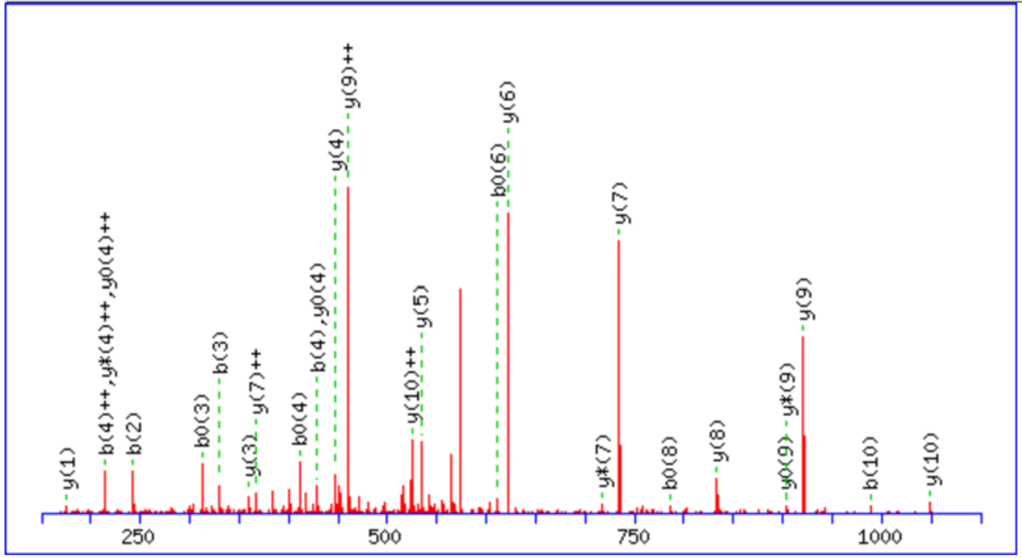
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 58 - PyE-1 **Fraction:** PyE-1

Match to Query 5561: 1161.636048 from(581.825300,2+)
Title: OECHL100310_35.4536.4536.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 1.3e-006**Matches :** 27/94 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					**I**							**11**
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637	**10**

3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340	**9**
4	**429.234375**	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326	**8**
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119	**7**
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087	**6**
7	716.382495	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073	**5**
8	803.414523	402.210899			785.403958	393.205617	**S**	***447.267407***	224.137342	430.240858	215.624067	429.256842	215.132059	**4**
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053			**3**
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



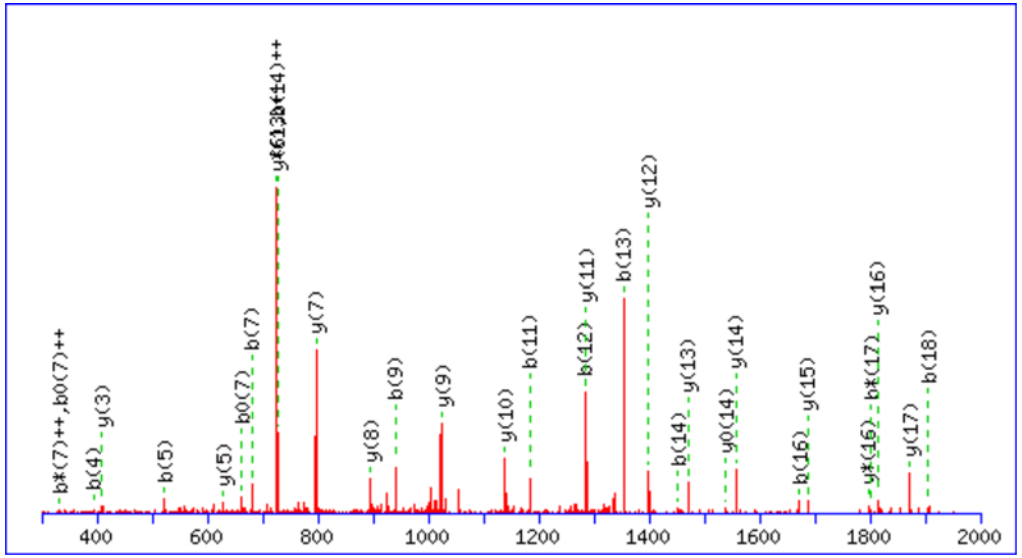
Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 58 - PyE-1 **Fraction:** PyE-1

Match to Query 15225: 2078.983448 from(1040.499000,2+)
Title: OECHL100310_35.16475.16475.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_35.raw

Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 101
Expect: 1.3e-008**Matches :** 32/200 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	72.044390	36.525833					A							19
2	209.103302	105.055289					H	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973939	18
3	266.124766	133.566021					G	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444483	17
4	**394.183344**	197.595310	377.156795	189.082035			Q	***1814.870790***	907.939033	1797.844241	899.425759	1796.860225	898.933751	16
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	E	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904462	15
6	610.257965	305.632621	593.231416	297.119346	592.247400	296.627338	S	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383165	14
7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	A	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867151	13
8	794.379143	397.693210	777.352594	389.179935	776.368578	388.687927	I	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348594	12
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	F	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806562	11
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	N	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272355	10
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	E	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250892	9
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	V	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729595	8
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	A	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195388	7
14	**1451.691369**	726.349322	1434.664820	717.836048	1433.680804	717.344040	P	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676831	6
15	1508.712833	754.860054	1491.686284	746.346780	1490.702268	745.854772	G	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150449	5
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	Y	572.282723	286.645000	555.256174	278.131725	554.272158	277.639717	4
17	1818.844576	909.925926	1801.818027	901.412652	1800.834011	900.920643	F	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	3
18	**1905.876604**	953.441940	1888.850055	944.928666	1887.866039	944.436658	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
19							R	175.118952	88.063114	158.092403	79.549840			1



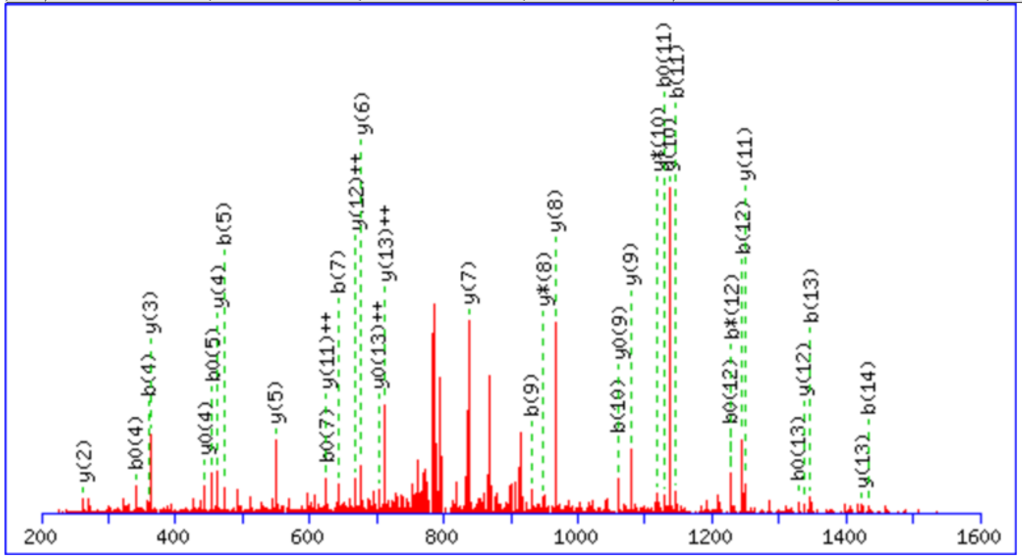
Peptide View

MS/MS Fragmentation of **AISSIGLECQSVTSR**
Found in **IPI00006988**, Tax_Id=9606 Gene_Symbol=RETN Resistin
Experiment: 58 - PyE-1 **Fraction:** PyE-1

Match to Query 11033: 1606.801448 from(804.408000,2+)
Title: OECHL100310_35.11799.11799.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1606.798462**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 80
Expect: 1.5e-006**Matches :** 36/144 fragment ions using 66 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					**A**							**15**
2	185.128454	93.067865					**I**	1536.768633	768.887955	1519.742084	760.374680	1518.758068	759.882672	**14**
3	272.160482	136.583879			254.149917	127.578596	**S**	***1423.684569***	712.345923	1406.658020	703.832648	1405.674004	703.340640	**13**
4	**359.192510**	180.099893			341.181945	171.094610	**S**	***1336.652541***	668.829909	1319.625992	660.316634	1318.641976	659.824626	**12**
5	**472.276574**	236.641925			454.266009	227.636642	**I**	***1249.620513***	625.313895	1232.593964	616.800620	1231.609948	616.308612	**11**
6	529.298038	265.152657			511.287473	256.147375	**G**	***1136.536449***	568.771863	1119.509900	560.258588	1118.525884	559.766580	**10**

7	**642.382102**	321.694689			624.371537	312.689407	**L**	***1079.514985***	540.261131	1062.488436	531.747856	1061.504420	531.255848	**9**
8	771.424695	386.215986			753.414130	377.210703	**E**	***966.430921***	483.719099	949.404372	475.205824	948.420356	474.713816	**8**
9	**931.455344**	466.231310			913.444779	457.226028	**C**	***837.388328***	419.197802	820.361779	410.684528	819.377763	410.192520	**7**
10	**1059.513922**	530.260599	1042.487373	521.747325	1041.503357	521.255317	**Q**	***677.357679***	339.182478	660.331130	330.669203	659.347114	330.177195	**6**
11	**1146.545950**	573.776613	1129.519401	565.263339	1128.535385	564.771331	**S**	***549.299101***	275.153189	532.272552	266.639914	531.288536	266.147906	**5**
12	**1245.614364**	623.310820	1228.587815	614.797546	1227.603799	614.305538	**V**	***462.267073***	231.637175	445.240524	223.123900	444.256508	222.631892	**4**
13	**1346.662043**	673.834660	1329.635494	665.321385	1328.651478	664.829377	**T**	***363.198659***	182.102968	346.172110	173.589693	345.188094	173.097685	**3**
14	**1433.694071**	717.350674	1416.667522	708.837399	1415.683506	708.345391	**S**	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



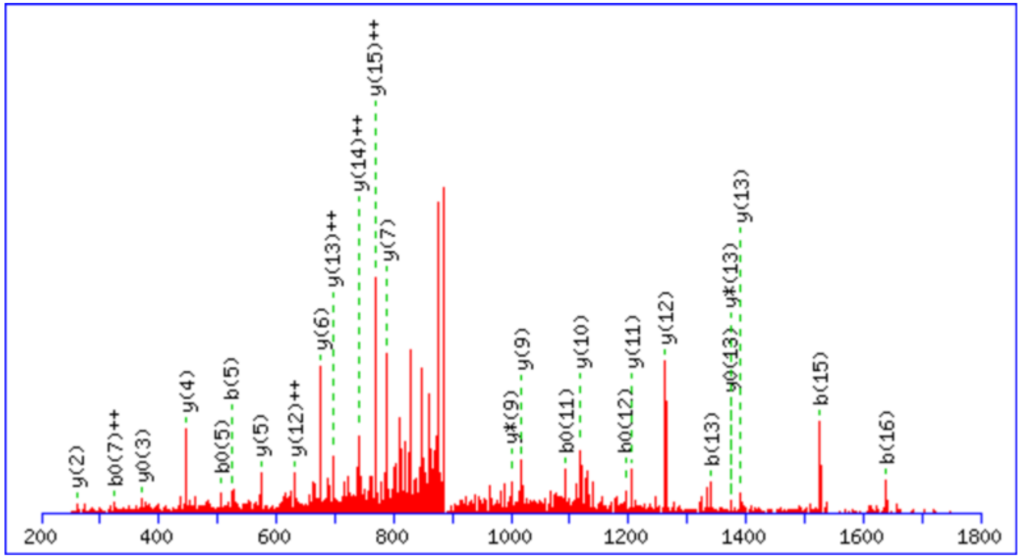
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 58 - PyE-1 **Fraction:** PyE-1

Match to Query 13010: 1784.880048 from(893.447300,2+)
Title: OECHL100310_35.7293.7293.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_35.raw

Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66
Expect: 3.9e-005**Matches :** 26/170 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	164.070605	82.538940					**Y**							**17**
2	251.102633	126.054954			233.092068	117.049672	**S**	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.909941	**16**
3	308.124097	154.565687			290.113532	145.560404	**G**	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.393928	**15**
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.883195	**14**
5	**524.198718**	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.367182	**13**
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.845885	**12**
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.335153	**11**
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.819139	**10**
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.295299	**9**
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.266010	**8**
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.742171	**7**
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.200139	**6**
13	**1340.632852**	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.676299	**5**
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	**4**
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**



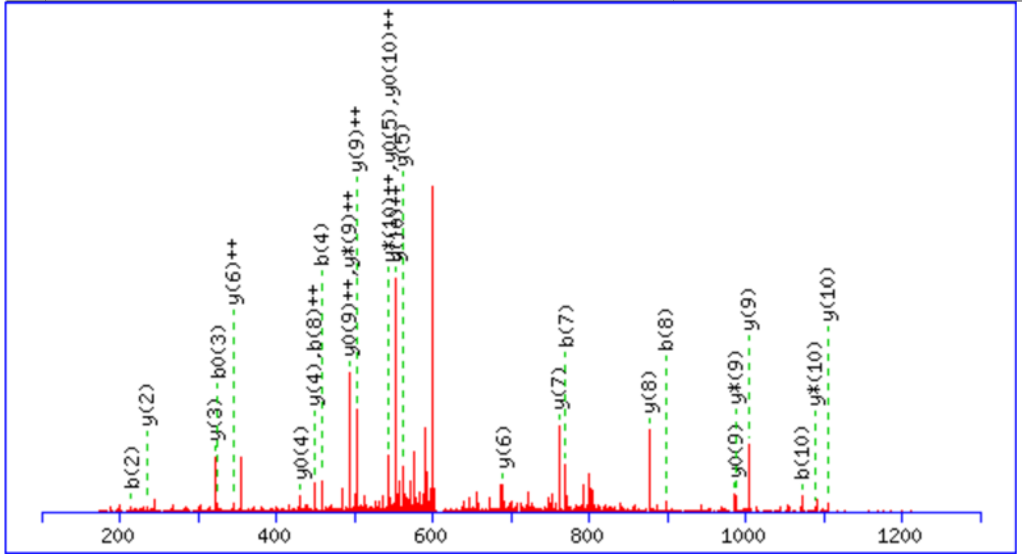
Peptide View

MS/MS Fragmentation of **ITQDAQLKSSK**
Found in **IPI00027482**, Tax_Id=9606 Gene_Symbol=SERPINA6 Corticosteroid-binding globulin
Experiment: 58 - PyE-1 **Fraction:** PyE-1

Match to Query 6283: 1217.662048 from(609.838300,2+)
Title: OECHL100310_35.2346.2346.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1217.661545**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 0.00025**Matches :** 28/112 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							11
2	**215.139019**	108.073147			197.128454	99.067865	T	***1105.584779***	553.296028	1088.558230	544.782753	1087.574214	544.290745	10
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	Q	***1004.537100***	502.772188	987.510551	494.258914	986.526535	493.766906	9
4	**458.224540**	229.615908	441.197991	221.102634	440.213975	220.610626	D	***876.478522***	438.742899	859.451973	430.229625	858.467957	429.737617	8
5	529.261654	265.134465	512.235105	256.621191	511.251089	256.129183	A	***761.451579***	381.229428	744.425030	372.716153	743.441014	372.224145	7
6	657.320232	329.163754	640.293683	320.650480	639.309667	320.158472	Q	***690.414465***	345.710871	673.387916	337.197596	672.403900	336.705588	6

7	**770.404296**	385.705786	753.377747	377.192512	752.393731	376.700504	**L**	***562.355887***	281.681582	545.329338	273.168307	544.345322	272.676299	**5**
8	**898.499259**	449.753268	881.472710	441.239993	880.488694	440.747985	**K**	***449.271823***	225.139549	432.245274	216.626275	431.261258	216.134267	**4**
9	985.531287	493.269282	968.504738	484.756007	967.520722	484.263999	**S**	***321.176860***	161.092068	304.150311	152.578793	303.166295	152.086785	**3**
10	**1072.563315**	536.785296	1055.536766	528.272021	1054.552750	527.780013	**S**	***234.144832***	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
11							**K**	147.112804	74.060040	130.086255	65.546765			**1**



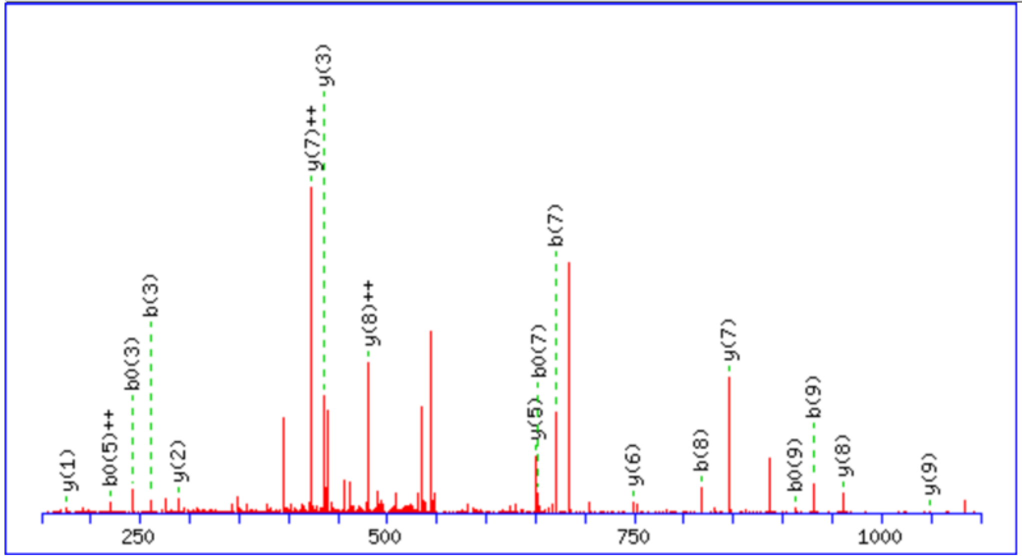
Peptide View

MS/MS Fragmentation of **GSDPVTIFLR**
Found in **IPI00027038**, Tax_Id=9606 Gene_Symbol=VSIG4 Isoform 1 of V-set and immunoglobulin domain-containing protein 4
Experiment: 58 - PyE-1 **Fraction:** PyE-1

Match to Query 4648: 1103.597248 from(552.805900,2+)
Title: OECHL100310_35.17678.17678.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1103.597519**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00053**Matches :** 18/80 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			**G**							**10**

2	145.060768	73.034022	127.050203	64.028740	**S**	***1047.583322***	524.295299	1030.556773	515.782025	1029.572757	515.290017	**9**
3	**260.087711**	130.547494	242.077146	121.542211	**D**	***960.551294***	480.779285	943.524745	472.266011	942.540729	471.774003	**8**
4	357.140475	179.073875	339.129910	170.068593	**P**	***845.524351***	423.265814	828.497802	414.752539	827.513786	414.260531	**7**
5	456.208889	228.608082	438.198324	219.602800	**V**	***748.471587***	374.739432	731.445038	366.226157	730.461022	365.734149	**6**
6	557.256568	279.131922	539.246003	270.126640	**T**	***649.403173***	325.205225	632.376624	316.691950	631.392608	316.199942	**5**
7	**670.340632**	335.673954	652.330067	326.668672	**I**	548.355494	274.681385	531.328945	266.168111			**4**
8	**817.409046**	409.208161	799.398481	400.202879	**F**	***435.271430***	218.139353	418.244881	209.626079			**3**
9	**930.493110**	465.750193	912.482545	456.744911	**L**	***288.203016***	144.605146	271.176467	136.091872			**2**
10					**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



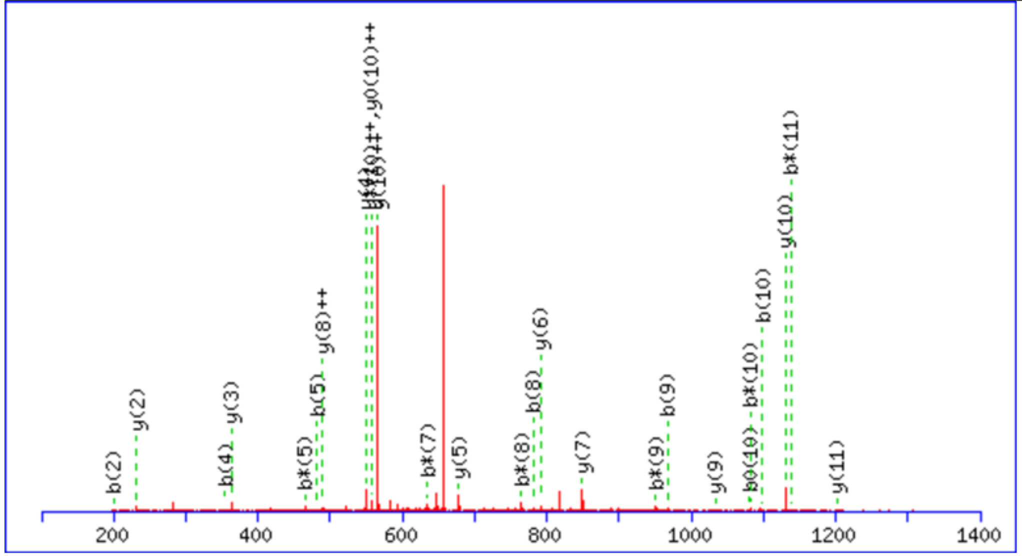
Peptide View

MS/MS Fragmentation of **QAPGQGLEWMGR**
Found in **IPI00009792**, Tax_Id=9606 Gene_Symbol=IGHV1OR15-1 Ig heavy chain V-I region V35
Experiment: 58 - PyE-1 **Fraction:** PyE-1

Match to Query 8084: 1328.630248 from(665.322400,2+)
Title: OECHL100310_35.14338.14338.2.dta
Data file \\BOROMIR\Masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100310_35.raw

Monoisotopic mass of neutral peptide Mr(calc): 1328.629547**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00095**Matches :** 26/110 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							12
2	**200.102968**	100.555122	183.076419	92.041848			A	***1201.578255***	601.292766	1184.551706	592.779491	1183.567690	592.287483	11
3	297.155732	149.081504	280.129183	140.568230			P	***1130.541141***	565.774208	1113.514592	557.260934	1112.530576	556.768926	10
4	**354.177196**	177.592236	337.150647	169.078961			G	***1033.488377***	517.247827	1016.461828	508.734552	1015.477812	508.242544	9
5	**482.235774**	241.621525	465.209225	233.108251			Q	976.466913	488.737095	959.440364	480.223820	958.456348	479.731812	8
6	539.257238	270.132257	522.230689	261.618983			G	***848.408335***	424.707806	831.381786	416.194531	830.397770	415.702523	7
7	652.341302	326.674289	635.314753	318.161015			L	***791.386871***	396.197074	774.360322	387.683799	773.376306	387.191791	6
8	**781.383895**	391.195586	764.357346	382.682311	763.373330	382.190303	E	***678.302807***	339.655042	661.276258	331.141767	660.292242	330.649759	5
9	**967.463208**	484.235242	950.436659	475.721968	949.452643	475.229960	W	***549.260214***	275.133745	532.233665	266.620471			4
10	**1098.503693**	549.755485	1081.477144	541.242210	1080.493128	540.750202	M	***363.180901***	182.094088	346.154352	173.580814			3
11	1155.525157	578.266217	1138.498608	569.752942	1137.514592	569.260934	G	***232.140416***	116.573846	215.113867	108.060571			2
12							R	175.118952	88.063114	158.092403	79.549839			1

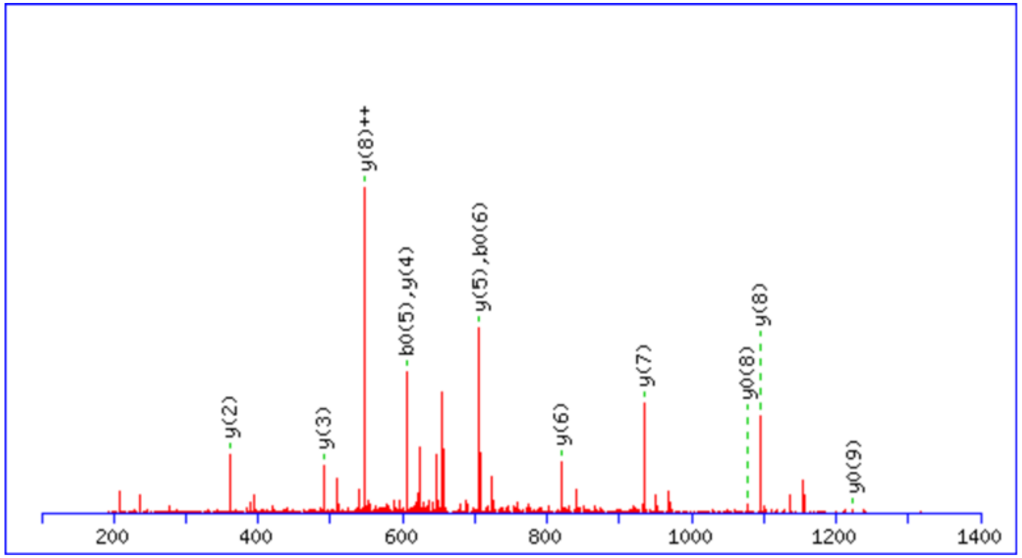


Peptide View

MS/MS Fragmentation of **SFCDLTDEWR**
Found in **IPI00010193**, Tax_Id=9606 Gene_Symbol=IFNAR2 Isoform 1 of Interferon-alpha/beta receptor beta chain
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 8055: 1327.552848 from(664.783700,2+)
Title: OECHL100312_44.17113.17113.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1327.550308**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59
Expect: 3e-005**Matches :** 12/86 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**10**
2	235.107718	118.057497	217.097153	109.052214	**F**	1241.525550	621.266413	1224.499001	612.753138	1223.514985	612.261130	**9**
3	395.138367	198.072821	377.127802	189.067539	**C**	***1094.457136***	547.732206	1077.430587	539.218932	1076.446571	538.726924	**8**
4	510.165310	255.586293	492.154745	246.581010	**D**	***934.426487***	467.716882	917.399938	459.203607	916.415922	458.711599	**7**
5	623.249374	312.128325	605.238809	303.123043	**L**	***819.399544***	410.203410	802.372995	401.690135	801.388979	401.198127	**6**
6	724.297053	362.652165	706.286488	353.646882	**T**	***706.315480***	353.661378	689.288931	345.148103	688.304915	344.656095	**5**
7	839.323996	420.165636	821.313431	411.160353	**D**	***605.267801***	303.137539	588.241252	294.624264	587.257236	294.132256	**4**
8	968.366589	484.686933	950.356024	475.681650	**E**	***490.240858***	245.624067	473.214309	237.110792	472.230293	236.618784	**3**
9	1154.445902	577.726589	1136.435337	568.721306	**W**	***361.198265***	181.102770	344.171716	172.589496			**2**
10					**R**	175.118952	88.063114	158.092403	79.549839			**1**



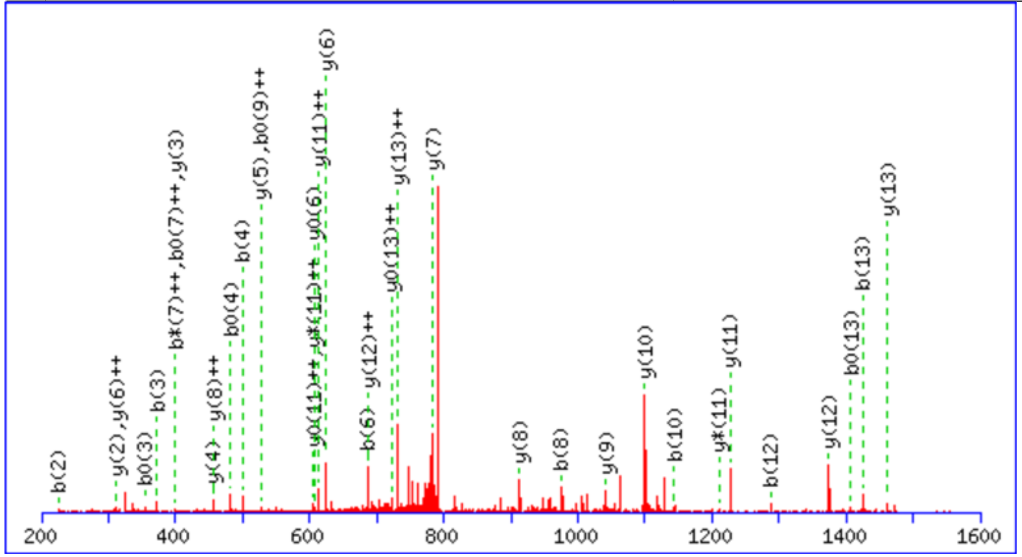
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 10725: 1597.706648 from(799.860600,2+)
Title: OECHL100312_44.2337.2337.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 73
Expect: 2.8e-006**Matches :** 36/144 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	138.066188	69.536732					**H**							**14**
2	**225.098216**	113.052746			207.087651	104.047463	**S**	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.325325	**13**
3	**372.166630**	186.586953			354.156065	177.581671	**F**	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.809311	**12**
4	**500.261593**	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	**11**
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	**10**
6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	***1042.437069***	521.722173	1025.410520	513.208898	1024.426504	512.716890	**9**

7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	1200.510234	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	***312.177864***	156.592570	295.151315	148.079295			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



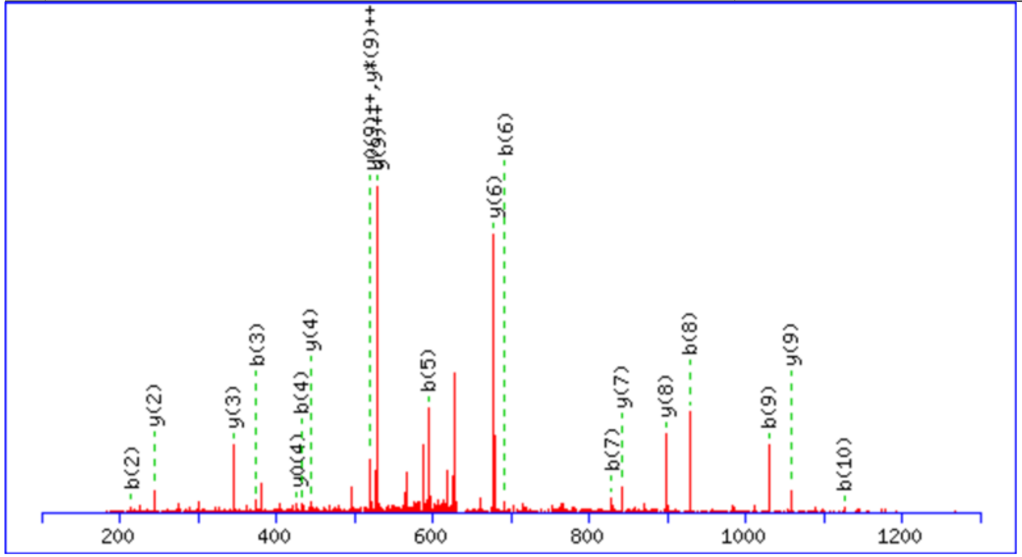
Peptide View

MS/MS Fragmentation of **VDCGYPHVTPK**
Found in **IPI00018909**, Tax_Id=9606 Gene_Symbol=TFF3 trefoil factor 3 precursor
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 7411: 1271.598048 from(636.806300,2+)
Title: OECHL100312_44.5703.5703.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1271.596878**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53

Expect: 0.00044**Matches :** 20/94 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			**V**							**11**
2	***215.102633***	108.054954	197.092068	99.049672	**D**	1173.535722	587.271499	1156.509173	578.758224	1155.525157	578.266216	**10**
3	***375.133282***	188.070279	357.122717	179.064997	**C**	**1058.508779**	529.758028	1041.482230	521.244753	1040.498214	520.752745	**9**
4	***432.154746***	216.581011	414.144181	207.575729	**G**	**898.478130**	449.742703	881.451581	441.229428	880.467565	440.737420	**8**
5	***595.218075***	298.112676	577.207510	289.107393	**Y**	**841.456666**	421.231971	824.430117	412.718696	823.446101	412.226688	**7**
6	***692.270839***	346.639058	674.260274	337.633775	**P**	**678.393337**	339.700307	661.366788	331.187032	660.382772	330.695024	**6**
7	***829.329751***	415.168514	811.319186	406.163231	**H**	581.340573	291.173925	564.314024	282.660650	563.330008	282.168642	**5**
8	***928.398165***	464.702721	910.387600	455.697438	**V**	**444.281661**	222.644468	427.255112	214.131194	426.271096	213.639186	**4**
9	***1029.445844***	515.226560	1011.435279	506.221277	**T**	**345.213247**	173.110261	328.186698	164.596987	327.202682	164.104979	**3**
10	***1126.498608***	563.752942	1108.488043	554.747659	**P**	**244.165568**	122.586422	227.139019	114.073148			**2**
11					**K**	147.112804	74.060040	130.086255	65.546765			**1**



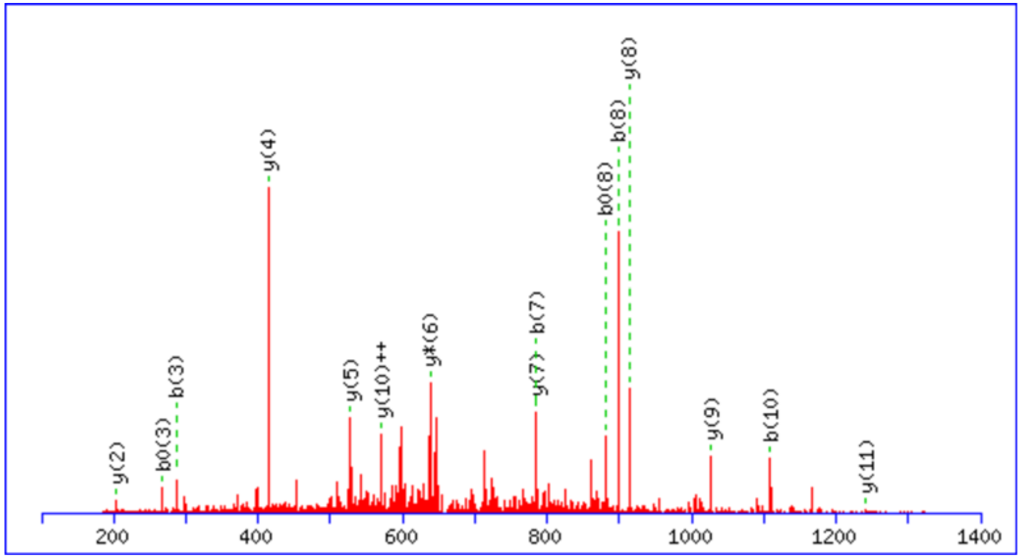
Peptide View

MS/MS Fragmentation of **ATLLEEQLPLGK**

Found in **IPI00414542**, Tax_Id=9606 Gene_Symbol=PDCD1LG2 Isoform 1 of Programmed cell death 1 ligand 2
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 7889: 1310.746848 from(656.380700,2+)
Title: OECHL100312_44.17062.17062.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1310.744537**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49
Expect: 0.00055**Matches :** 15/106 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	72.044390	36.525833					**A**							**12**
2	173.092069	87.049672			155.081504	78.044390	**T**	***1240.714731***	620.861004	1223.688182	612.347729	1222.704166	611.855721	**11**
3	**286.176133**	143.591704			268.165568	134.586422	**L**	1139.667052	570.337164	1122.640503	561.823890	1121.656487	561.331882	**10**
4	399.260197	200.133737			381.249632	191.128454	**L**	***1026.582988***	513.795132	1009.556439	505.281858	1008.572423	504.789850	**9**
5	528.302790	264.655033			510.292225	255.649751	**E**	***913.498924***	457.253100	896.472375	448.739825	895.488359	448.247818	**8**
6	657.345383	329.176330			639.334818	320.171047	**E**	***784.456331***	392.731804	767.429782	384.218529	766.445766	383.726521	**7**
7	**785.403961**	393.205619	768.377412	384.692344	767.393396	384.200336	**Q**	655.413738	328.210507	638.387189	319.697232			**6**
8	**898.488025**	449.747651	881.461476	441.234376	880.477460	440.742368	**L**	***527.355160***	264.181218	510.328611	255.667943			**5**
9	995.540789	498.274033	978.514240	489.760758	977.530224	489.268750	**P**	***414.271096***	207.639186	397.244547	199.125911			**4**
10	**1108.624853**	554.816065	1091.598304	546.302790	1090.614288	545.810782	**L**	317.218332	159.112804	300.191783	150.599529			**3**
11	1165.646317	583.326797	1148.619768	574.813522	1147.635752	574.321514	**G**	***204.134268***	102.570772	187.107719	94.057497			**2**
12							**K**	147.112804	74.060040	130.086255	65.546765			**1**



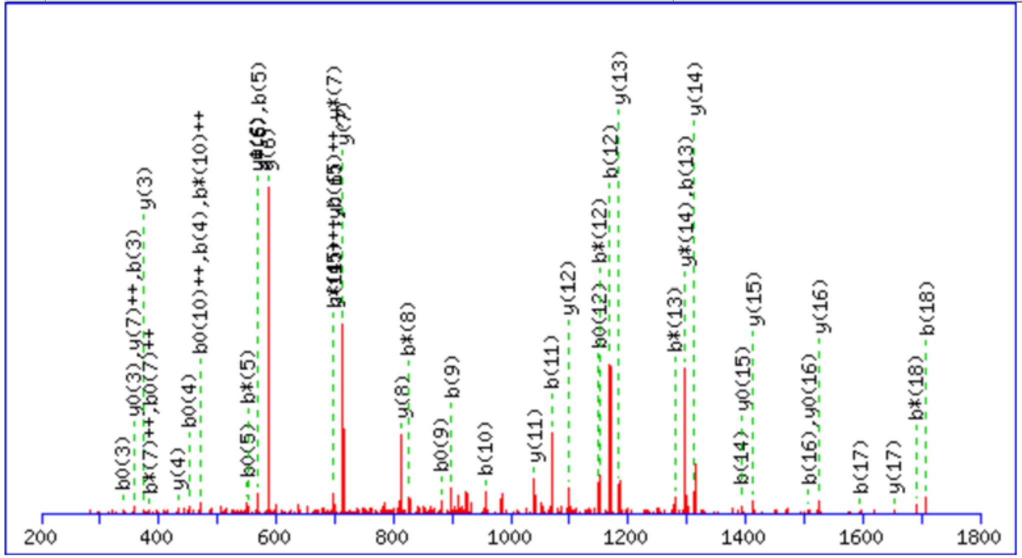
Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVQPGGSLR**
Found in **IPI00382494**, Tax_Id=9606 Gene_Symbol=- Ig heavy chain V-III region TEI
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 13578: 1880.999448 from(941.507000,2+)
Title: OECHL100312_44.15571.15571.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1880.995605**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 91
Expect: 6.6e-008**Matches :** 50/208 fragment ions using 72 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	**E**							**19**
2	229.118283	115.062780			211.107718	106.057497	**V**	1752.960275	876.983776	1735.933726	868.470501	1734.949710	867.978493	**18**
3	***357.176861***	179.092069	340.150312	170.578794	339.166296	170.086786	**Q**	***1653.891861***	827.449569	1636.865312	818.936294	1635.881296	818.444286	**17**
4	***470.260925***	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	***1525.833283***	763.420279	1508.806734	754.907005	1507.822718	754.414997	**16**
5	***569.329339***	285.168308	552.302790	276.655033	551.318774	276.163025	**V**	***1412.749219***	706.878248	1395.722670	698.364973	1394.738654	697.872965	**15**
6	***698.371932***	349.689604	681.345383	341.176330	680.361367	340.684322	**E**	***1313.680805***	657.344041	1296.654256	648.830766	1295.670240	648.338758	**14**

7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	**S**	***1184.638212***	592.822744	1167.611663	584.309470	1166.627647	583.817462	**13**
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	**G**	***1097.606184***	549.306730	1080.579635	540.793456	1079.595619	540.301447	**12**
9	***899.446888***	450.227082	882.420339	441.713808	881.436323	441.221800	**G**	***1040.584720***	520.795998	1023.558171	512.282723	1022.574155	511.790716	**11**
10	***956.468352***	478.737814	939.441803	470.224540	938.457787	469.732532	**G**	983.563256	492.285266	966.536707	483.771991	965.552691	483.279983	**10**
11	***1069.552416***	535.279846	1052.525867	526.766572	1051.541851	526.274564	**L**	926.541792	463.774534	909.515243	455.261259	908.531227	454.769251	**9**
12	***1168.620830***	584.814053	1151.594281	576.300779	1150.610265	575.808771	**V**	***813.457728***	407.232502	796.431179	398.719227	795.447163	398.227219	**8**
13	***1296.679408***	648.843342	1279.652859	640.330068	1278.668843	639.838060	**Q**	***714.389314***	357.698295	697.362765	349.185020	696.378749	348.693012	**7**
14	***1393.732172***	697.369724	1376.705623	688.856450	1375.721607	688.364442	**P**	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.663723	**6**
15	1450.753636	725.880456	1433.727087	717.367182	1432.743071	716.875174	**G**	489.277972	245.142624	472.251423	236.629349	471.267407	236.137341	**5**
16	***1507.775100***	754.391188	1490.748551	745.877914	1489.764535	745.385906	**G**	***432.256508***	216.631892	415.229959	208.118617	414.245943	207.626609	**4**
17	***1594.807128***	797.907202	1577.780579	789.393928	1576.796563	788.901920	**S**	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	**3**
18	***1707.891192***	854.449234	1690.864643	845.935960	1689.880627	845.443952	**L**	288.203016	144.605146	271.176467	136.091871			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



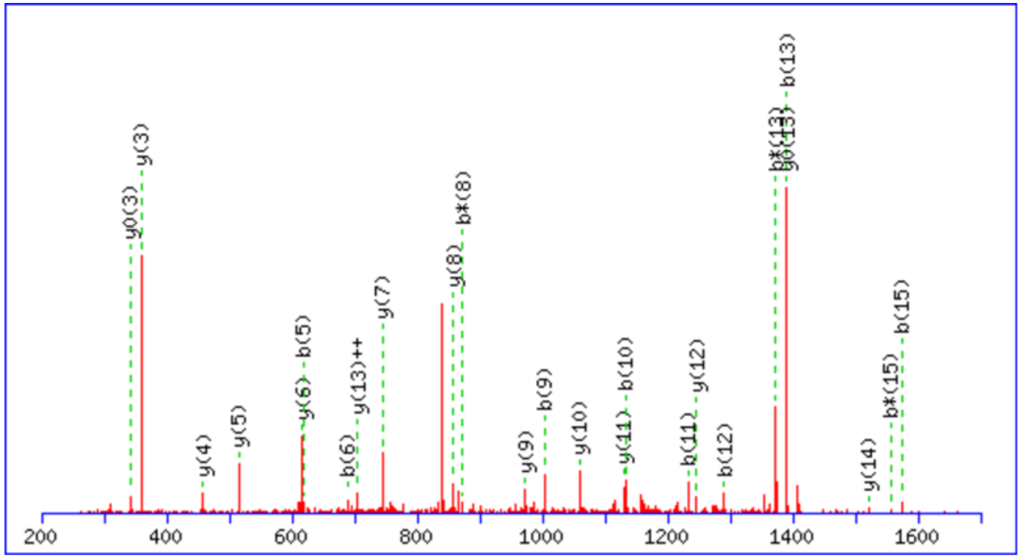
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**

Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 12397: 1746.919448 from(874.467000,2+)
Title: OECHL100312_44.17248.17248.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 78
Expect: 1.8e-006**Matches :** 25/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	**689.386854**	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



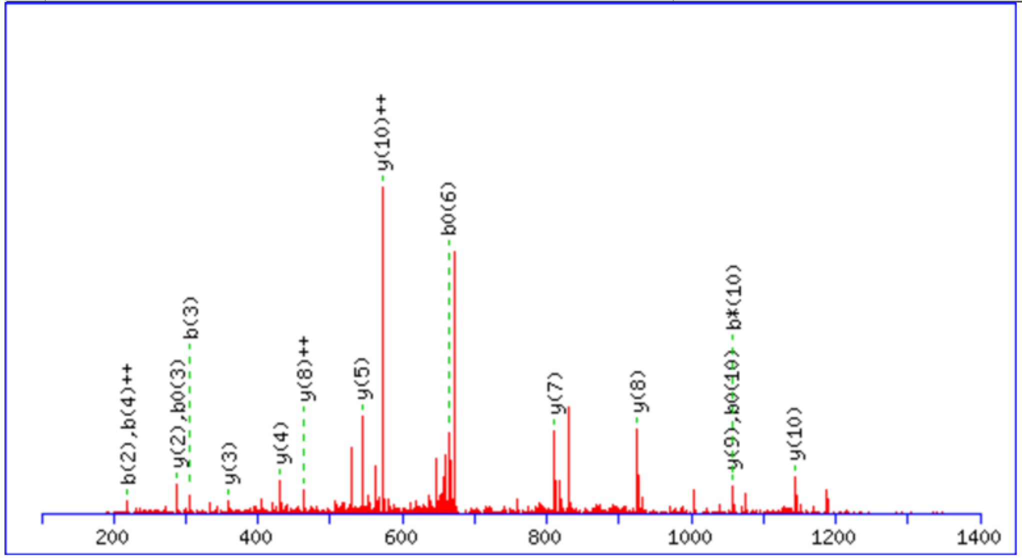
Peptide View

MS/MS Fragmentation of **AFSMDEHNAALR**
Found in **IPI00008239**, Tax_Id=9606 Gene_Symbol=GPRC5B cDNA FLJ55176, highly similar to G-protein coupled receptor family C group 5 member B
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 8361: 1360.618448 from(681.316500,2+)
Title: OECHL100312_44.9703.9703.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1360.619354**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 0.00014**Matches :** 17/102 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	72.044390	36.525833					**A**							**12**
2	**219.112804**	110.060040					**F**	1290.589546	645.798411	1273.562997	637.285137	1272.578981	636.793128	**11**
3	**306.144832**	153.576054			288.134267	144.570772	**S**	***1143.521132***	572.264204	1126.494583	563.750929	1125.510567	563.258921	**10**
4	437.185317	219.096296			419.174752	210.091014	**M**	***1056.489104***	528.748190	1039.462555	520.234916	1038.478539	519.742908	**9**
5	552.212260	276.609768			534.201695	267.604486	**D**	***925.448619***	463.227947	908.422070	454.714673	907.438054	454.222665	**8**
6	681.254853	341.131065			663.244288	332.125782	**E**	***810.421676***	405.714476	793.395127	397.201201	792.411111	396.709193	**7**

7	818.313765	409.660521			800.303200	400.655238	**H**	681.379083	341.193179	664.352534	332.679905			**6**
8	932.356692	466.681984	915.330143	458.168709	914.346127	457.676701	**N**	***544.320171***	272.663724	527.293622	264.150449			**5**
9	1003.393806	502.200541	986.367257	493.687266	985.383241	493.195258	**A**	***430.277244***	215.642260	413.250695	207.128985			**4**
10	1074.430920	537.719098	1057.404371	529.205824	1056.420355	528.713816	**A**	***359.240130***	180.123703	342.213581	171.610428			**3**
11	1187.514984	594.261130	1170.488435	585.747856	1169.504419	585.255847	**L**	***288.203016***	144.605146	271.176467	136.091871			**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**



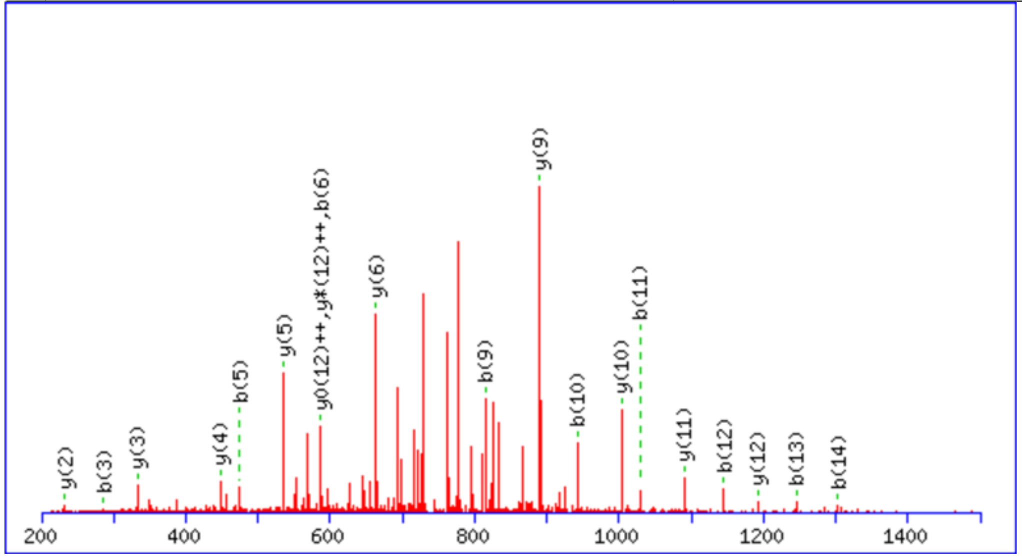
Peptide View

MS/MS Fragmentation of **GLDTSLGAVQSDTGR**
Found in **IPI00289931**, Tax_Id=9606 Gene_Symbol=MADCAM1 MADCAM1 protein
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 9512: 1475.721448 from(738.868000,2+)
Title: OECHL100312_44.11494.11494.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1475.721619**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 78
Expect: 2.2e-006**Matches :** 20/142 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#

1	58.028740	29.518008					**G**							**15**
2	171.112804	86.060040					**L**	1419.707414	710.357345	1402.680865	701.844071	1401.696849	701.352063	**14**
3	***286.139747***	143.573512			268.129182	134.568229	**D**	1306.623350	653.815313	1289.596801	645.302039	1288.612785	644.810031	**13**
4	387.187426	194.097351			369.176861	185.092069	**T**	***1191.596407***	596.301842	1174.569858	587.788567	1173.585842	587.296559	**12**
5	***474.219454***	237.613365			456.208889	228.608082	**S**	***1090.548728***	545.778002	1073.522179	537.264728	1072.538163	536.772719	**11**
6	***587.303518***	294.155397			569.292953	285.150115	**L**	***1003.516700***	502.261988	986.490151	493.748714	985.506135	493.256706	**10**
7	644.324982	322.666129			626.314417	313.660847	**G**	***890.432636***	445.719956	873.406087	437.206682	872.422071	436.714674	**9**
8	715.362096	358.184686			697.351531	349.179404	**A**	833.411172	417.209224	816.384623	408.695950	815.400607	408.203942	**8**
9	***814.430510***	407.718893			796.419945	398.713611	**V**	762.374058	381.690667	745.347509	373.177393	744.363493	372.685385	**7**
10	***942.489088***	471.748182	925.462539	463.234908	924.478523	462.742900	**Q**	***663.305644***	332.156460	646.279095	323.643186	645.295079	323.151178	**6**
11	***1029.521116***	515.264196	1012.494567	506.750922	1011.510551	506.258914	**S**	***535.247066***	268.127171	518.220517	259.613897	517.236501	259.121889	**5**
12	***1144.548059***	572.777668	1127.521510	564.264393	1126.537494	563.772385	**D**	***448.215038***	224.611157	431.188489	216.097882	430.204473	215.605874	**4**
13	***1245.595738***	623.301507	1228.569189	614.788233	1227.585173	614.296225	**T**	***333.188095***	167.097685	316.161546	158.584411	315.177530	158.092403	**3**
14	***1302.617202***	651.812239	1285.590653	643.298965	1284.606637	642.806957	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**

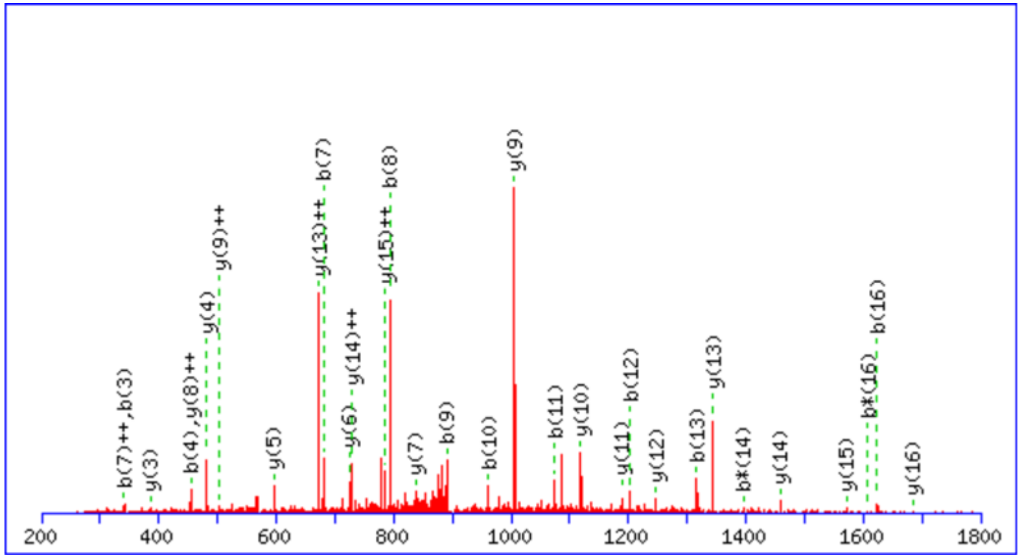


Peptide View

MS/MS Fragmentation of **ILLDPGALPALQNPPIR**
Found in **IPI00304865**, Tax_Id=9606 Gene_Symbol=TGFBR3 transforming growth factor, beta receptor III
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 12900: 1797.053448 from(899.534000,2+)
Title: OECHL100312_44.20189.20189.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1797.051224**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65
Expect: 3.1e-006**Matches :** 31/138 fragment ions using 77 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					**I**							**17**
2	227.175404	114.091340					**L**	***1684.974468***	842.990872	1667.947919	834.477598	1666.963903	833.985590	**16**
3	**340.259468**	170.633372					**L**	***1571.890404***	786.448840	1554.863855	777.935566	1553.879839	777.443558	**15**
4	**455.286411**	228.146843			437.275846	219.141561	**D**	***1458.806340***	729.906808	1441.779791	721.393534	1440.795775	720.901526	**14**
5	552.339175	276.673226			534.328610	267.667943	**P**	***1343.779397***	672.393337	1326.752848	663.880062			**13**
6	609.360639	305.183958			591.350074	296.178675	**G**	***1246.726633***	623.866955	1229.700084	615.353680			**12**
7	**680.397753**	340.702515			662.387188	331.697232	**A**	***1189.705169***	595.356223	1172.678620	586.842948			**11**
8	**793.481817**	397.244547			775.471252	388.239264	**L**	***1118.668055***	559.837665	1101.641506	551.324391			**10**
9	**890.534581**	445.770929			872.524016	436.765646	**P**	***1005.583991***	503.295634	988.557442	494.782359			**9**
10	**961.571695**	481.289486			943.561130	472.284203	**A**	908.531227	454.769252	891.504678	446.255977			**8**
11	**1074.655759**	537.831518			1056.645194	528.826235	**L**	***837.494113***	419.250695	820.467564	410.737420			**7**
12	**1202.714337**	601.860807	1185.687788	593.347532	1184.703772	592.855524	**Q**	***724.410049***	362.708663	707.383500	354.195388			**6**
13	**1316.757264**	658.882270	1299.730715	650.368996	1298.746699	649.876988	**N**	***596.351471***	298.679374	579.324922	290.166099			**5**
14	1413.810028	707.408652	1396.783479	698.895378	1395.799463	698.403370	**P**	***482.308544***	241.657910	465.281995	233.144635			**4**
15	1510.862792	755.935034	1493.836243	747.421760	1492.852227	746.929752	**P**	***385.255780***	193.131528	368.229231	184.618253			**3**
16	**1623.946856**	812.477066	1606.920307	803.963792	1605.936291	803.471784	**I**	288.203016	144.605146	271.176467	136.091871			**2**
17							**R**	175.118952	88.063114	158.092403	79.549839			**1**



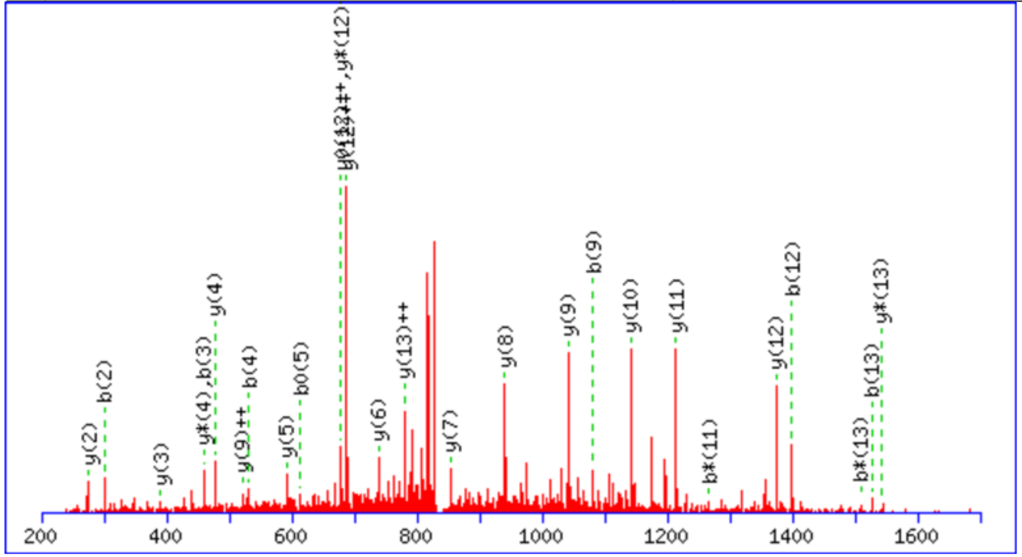
Peptide View

MS/MS Fragmentation of **LWCATTSNFDSDKK**
Found in **IPI00027509**, Tax_Id=9606 Gene_Symbol=MMP9 Matrix metalloproteinase-9
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 11610: 1671.759648 from(836.887100,2+)
Title: OECHL100312_44.10883.10883.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1671.756271**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 7e-005**Matches :** 27/130 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					**L**							**14**
2	**300.170653**	150.588965					**W**	1559.679484	780.343380	1542.652935	771.830106	1541.668919	771.338098	**13**
3	**460.201302**	230.604289					**C**	***1373.600171***	687.303724	1356.573622	678.790449	1355.589606	678.298441	**12**
4	**531.238416**	266.122846					**A**	***1213.569522***	607.288399	1196.542973	598.775125	1195.558957	598.283117	**11**
5	632.286095	316.646686			614.275530	307.641403	**T**	***1142.532408***	571.769842	1125.505859	563.256568	1124.521843	562.764560	**10**
6	733.333774	367.170525			715.323209	358.165243	**T**	***1041.484729***	521.246003	1024.458180	512.732728	1023.474164	512.240720	**9**

7	820.365802	410.686539			802.355237	401.681257	**S**	***940.437050***	470.722163	923.410501	462.208889	922.426485	461.716881	**8**
8	934.408729	467.708003	917.382180	459.194728	916.398164	458.702720	**N**	***853.405022***	427.206149	836.378473	418.692875	835.394457	418.200867	**7**
9	**1081.477143**	541.242210	1064.450594	532.728935	1063.466578	532.236927	**F**	***739.362095***	370.184686	722.335546	361.671411	721.351530	361.179403	**6**
10	1196.504086	598.755681	1179.477537	590.242407	1178.493521	589.750399	**D**	***592.293681***	296.650479	575.267132	288.137204	574.283116	287.645196	**5**
11	1283.536114	642.271695	1266.509565	633.758421	1265.525549	633.266413	**S**	***477.266738***	239.137007	460.240189	230.623733	459.256173	230.131725	**4**
12	**1398.563057**	699.785167	1381.536508	691.271892	1380.552492	690.779884	**D**	***390.234710***	195.620993	373.208161	187.107719	372.224145	186.615711	**3**
13	**1526.658020**	763.832648	1509.631471	755.319374	1508.647455	754.827366	**K**	***275.207767***	138.107521	258.181218	129.594247			**2**
14							**K**	147.112804	74.060040	130.086255	65.546765			**1**



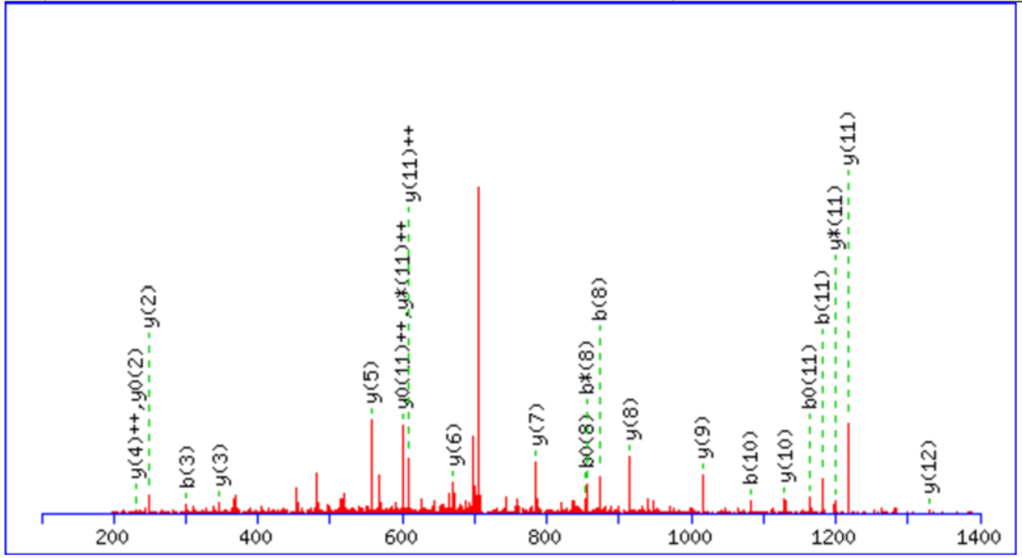
Peptide View

MS/MS Fragmentation of **VLSNTEDLPLVTK**
Found in **IPI00218851**, Tax_Id=9606 Gene_Symbol=LYNX1 Ly-6 neurotoxin-like protein 1 isoform a
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 9022: 1427.786448 from(714.900500,2+)
Title: OECHL100312_44.14445.14445.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1427.787155**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61

Expect: 6.4e-005**Matches :** 23/132 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	100.075690	50.541483					V							13
2	213.159754	107.083515					L	***1329.726023***	665.366650	1312.699474	656.853375	1311.715458	656.361367	12
3	**300.191782**	150.599529			282.181217	141.594247	S	***1216.641959***	608.824618	1199.615410	600.311343	1198.631394	599.819335	11
4	414.234709	207.620993	397.208160	199.107718	396.224144	198.615710	N	***1129.609931***	565.308604	1112.583382	556.795329	1111.599366	556.303321	10
5	515.282388	258.144832	498.255839	249.631558	497.271823	249.139550	T	***1015.567004***	508.287140	998.540455	499.773866	997.556439	499.281858	9
6	644.324981	322.666129	627.298432	314.152854	626.314416	313.660846	E	***914.519325***	457.763301	897.492776	449.250026	896.508760	448.758018	8
7	759.351924	380.179600	742.325375	371.666326	741.341359	371.174318	D	***785.476732***	393.242004	768.450183	384.728730	767.466167	384.236722	7
8	**872.435988**	436.721632	855.409439	428.208358	854.425423	427.716350	L	***670.449789***	335.728533	653.423240	327.215258	652.439224	326.723250	6
9	969.488752	485.248014	952.462203	476.734740	951.478187	476.242732	P	***557.365725***	279.186501	540.339176	270.673226	539.355160	270.181218	5
10	**1082.572816**	541.790046	1065.546267	533.276772	1064.562251	532.784764	L	460.312961	230.660119	443.286412	222.146844	442.302396	221.654836	4
11	**1181.641230**	591.324253	1164.614681	582.810979	1163.630665	582.318971	V	***347.228897***	174.118087	330.202348	165.604812	329.218332	165.112804	3
12	1282.688909	641.848093	1265.662360	633.334818	1264.678344	632.842810	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
13							K	147.112804	74.060040	130.086255	65.546765			1

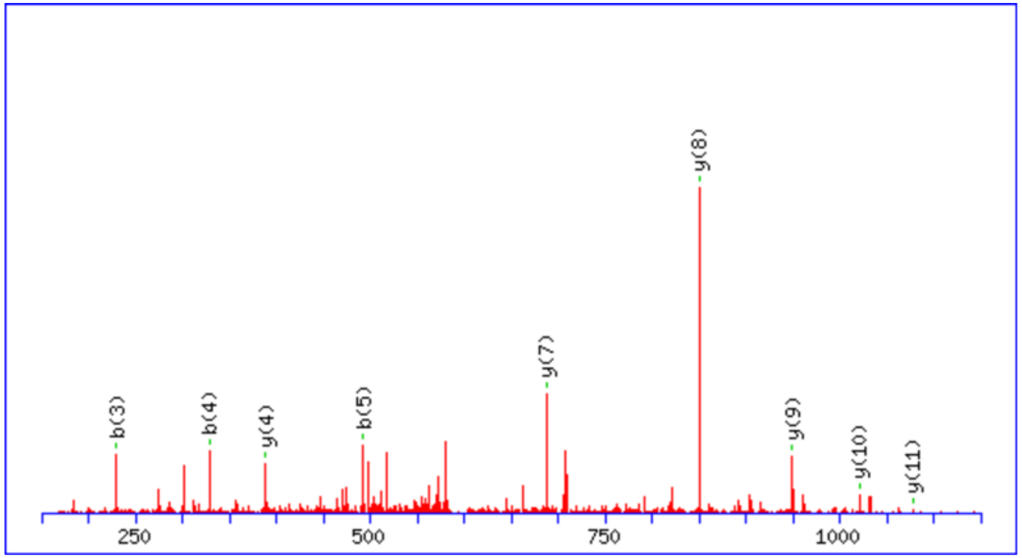


Peptide View

MS/MS Fragmentation of **TGAVYVAEIGAK**
Found in **IPI00552937**, Tax_Id=9606 Gene_Symbol=NHLRC3 NHL repeat-containing protein 3
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 5951: 1177.633448 from(589.824000,2+)
Title: OECHL100312_44.11514.11514.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1177.634277**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59
Expect: 8.8e-005**Matches :** 9/102 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							**12**
2	159.076419	80.041847	141.065854	71.036565	**G**	***1077.593888***	539.300582	1060.567339	530.787308	1059.583323	530.295300	**11**
3	**230.113533**	115.560404	212.102968	106.555122	**A**	***1020.572424***	510.789850	1003.545875	502.276576	1002.561859	501.784568	**10**
4	**329.181947**	165.094611	311.171382	156.089329	**V**	***949.535310***	475.271293	932.508761	466.758019	931.524745	466.266011	**9**
5	**492.245276**	246.626276	474.234711	237.620994	**Y**	***850.466896***	425.737086	833.440347	417.223812	832.456331	416.731804	**8**
6	591.313690	296.160483	573.303125	287.155201	**V**	***687.403567***	344.205422	670.377018	335.692147	669.393002	335.200139	**7**
7	662.350804	331.679040	644.340239	322.673758	**A**	588.335153	294.671215	571.308604	286.157940	570.324588	285.665932	**6**
8	791.393397	396.200337	773.382832	387.195054	**E**	517.298039	259.152658	500.271490	250.639383	499.287474	250.147375	**5**
9	904.477461	452.742369	886.466896	443.737086	**I**	***388.255446***	194.631361	371.228897	186.118087			**4**
10	961.498925	481.253101	943.488360	472.247818	**G**	275.171382	138.089329	258.144833	129.576055			**3**
11	1032.536039	516.771658	1014.525474	507.766375	**A**	218.149918	109.578597	201.123369	101.065322			**2**
12					**K**	147.112804	74.060040	130.086255	65.546765			**1**



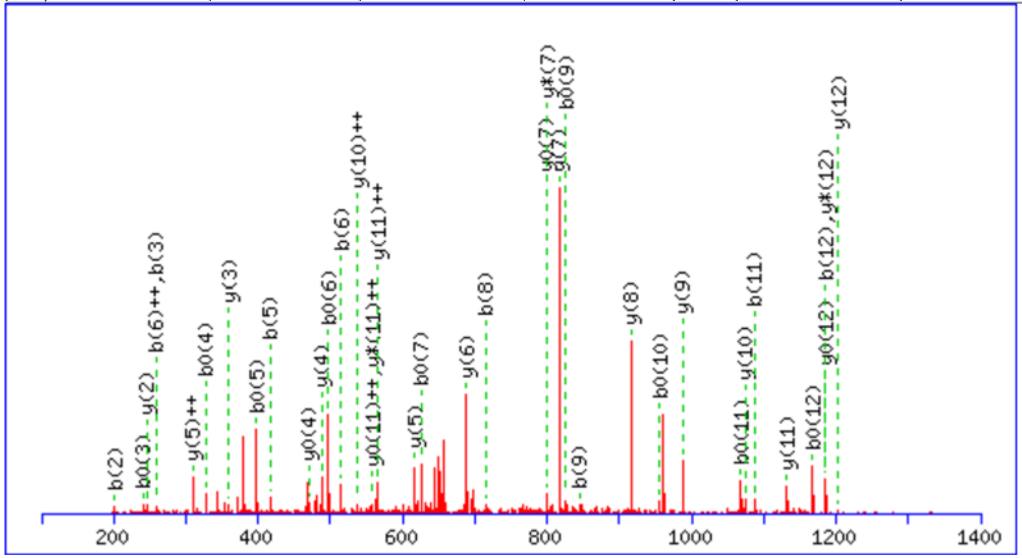
Peptide View

MS/MS Fragmentation of **EAGSAVEAEELVK**
Found in **IPI00008586**, Tax_Id=9606 Gene_Symbol=CSPG5 Isoform 1 of Chondroitin sulfate proteoglycan 5
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 8069: 1330.661448 from(666.338000,2+)
Title: OECHL100312_44.11549.11549.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1330.661591**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59
Expect: 0.00017**Matches :** 39/114 fragment ions using 89 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**E**							**13**
2	**201.086983**	101.047130	183.076418	92.041847	**A**	***1202.626309***	601.816793	1185.599760	593.303518	1184.615744	592.811510	**12**
3	**258.108447**	129.557862	240.097882	120.552579	**G**	***1131.589195***	566.298236	1114.562646	557.784961	1113.578630	557.292953	**11**
4	345.140475	173.073875	327.129910	164.068593	**S**	***1074.567731***	537.787504	1057.541182	529.274229	1056.557166	528.782221	**10**
5	**416.177589**	208.592432	398.167024	199.587150	**A**	***987.535703***	494.271490	970.509154	485.758215	969.525138	485.266207	**9**
6	**515.246003**	258.126640	497.235438	249.121357	**V**	***916.498589***	458.752933	899.472040	450.239658	898.488024	449.747650	**8**

7	644.288596	322.647936	626.278031	313.642653	**E**	***817.430175***	409.218726	800.403626	400.705451	799.419610	400.213443	**7**
8	**715.325710**	358.166493	697.315145	349.161210	**A**	***688.387582***	344.697429	671.361033	336.184155	670.377017	335.692147	**6**
9	**844.368303**	422.687790	826.357738	413.682507	**E**	***617.350468***	309.178872	600.323919	300.665598	599.339903	300.173590	**5**
10	973.410896	487.209086	955.400331	478.203803	**E**	***488.307875***	244.657576	471.281326	236.144301	470.297310	235.652293	**4**
11	**1086.494960**	543.751118	1068.484395	534.745836	**L**	***359.265282***	180.136279	342.238733	171.623005			**3**
12	**1185.563374**	593.285325	1167.552809	584.280043	**V**	***246.181218***	123.594247	229.154669	115.080973			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**

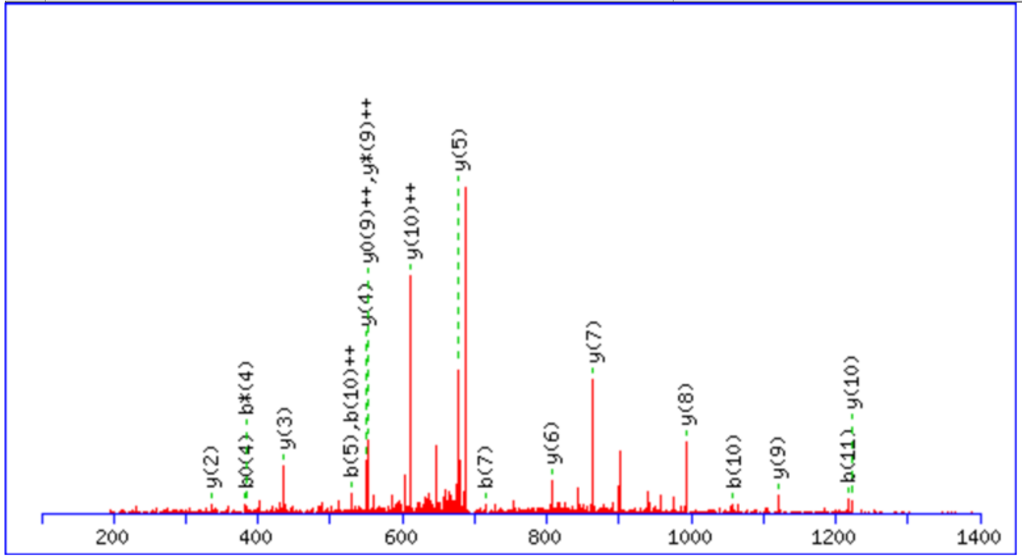


Peptide View

MS/MS Fragmentation of **VATQEGKEITCR**
Found in **IPI00031564**, Tax_Id=9606 Gene_Symbol=GGCT Isoform 1 of Gamma-glutamylcyclotransferase
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 8636: 1390.688448 from(696.351500,2+)
Title: OECHL100312_44.3666.3666.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1390.687454**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 0.00059**Matches :** 19/118 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					**V**							**12**
2	171.112804	86.060040					**A**	1292.626328	646.816802	1275.599779	638.303528	1274.615763	637.811520	**11**
3	272.160483	136.583879			254.149918	127.578597	**T**	***1221.589214***	611.298245	1204.562665	602.784971	1203.578649	602.292963	**10**
4	400.219061	200.613169	383.192512	192.099894	382.208496	191.607886	**Q**	***1120.541535***	560.774406	1103.514986	552.261131	1102.530970	551.769123	**9**
5	**529.261654**	265.134465	512.235105	256.621191	511.251089	256.129183	**E**	***992.482957***	496.745117	975.456408	488.231842	974.472392	487.739834	**8**
6	586.283118	293.645197	569.256569	285.131923	568.272553	284.639915	**G**	***863.440364***	432.223820	846.413815	423.710546	845.429799	423.218538	**7**
7	**714.378081**	357.692679	697.351532	349.179404	696.367516	348.687396	**K**	***806.418900***	403.713088	789.392351	395.199814	788.408335	394.707806	**6**
8	843.420674	422.213975	826.394125	413.700701	825.410109	413.208693	**E**	***678.323937***	339.665607	661.297388	331.152332	660.313372	330.660324	**5**
9	956.504738	478.756007	939.478189	470.242733	938.494173	469.750725	**I**	***549.281344***	275.144310	532.254795	266.631036	531.270779	266.139028	**4**
10	**1057.552417**	529.279847	1040.525868	520.766572	1039.541852	520.274564	**T**	***436.197280***	218.602278	419.170731	210.089003	418.186715	209.596995	**3**
11	**1217.583066**	609.295171	1200.556517	600.781897	1199.572501	600.289889	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**



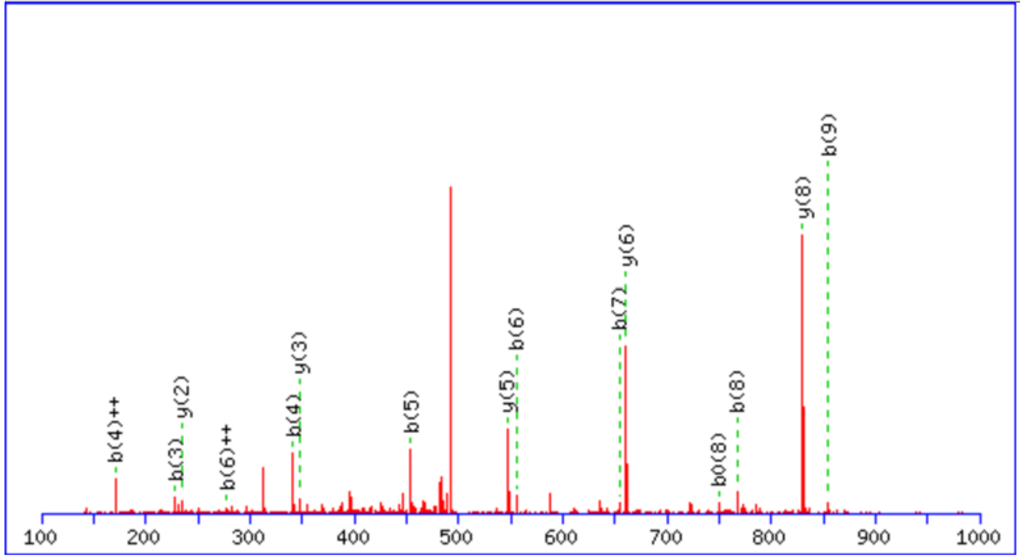
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**

Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 3489: 999.633248 from(500.823900,2+)
Title: OECHL100312_44.17419.17419.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 3.1e-005**Matches :** 16/78 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							10
2	***171.112804***	86.060040			V	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	9
3	***228.134268***	114.570772			G	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	8
4	***341.218332***	**171.112804**			L	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	7
5	***454.302396***	227.654836			L	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	6
6	***555.350075***	**278.178676**	537.339510	269.173393	T	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	5
7	***654.418489***	327.712883	636.407924	318.707600	V	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	4
8	***767.502553***	384.254915	749.491988	375.249632	I	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	3
9	***854.534581***	427.770929	836.524016	418.765646	S	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	2
10					K	147.112804	74.060040	130.086255	65.546765			1

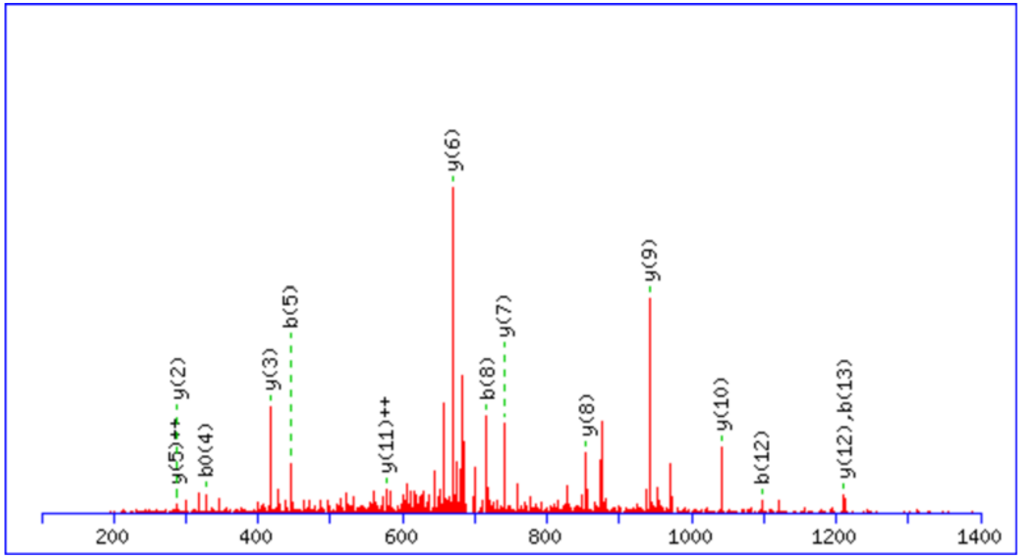


Peptide View

MS/MS Fragmentation of **SSGLVSNAPGVQIR**
Found in **IPI00022331**, Tax_Id=9606 Gene_Symbol=LCAT Phosphatidylcholine-sterol acyltransferase
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 8588: 1383.747048 from(692.880800,2+)
Title: OECHL100312_44.11620.11620.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1383.747025**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00029**Matches :** 15/128 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	88.039304	44.523290			70.028739	35.518008	**S**							**14**
2	175.071332	88.039304			157.060767	79.034021	**S**	1297.722275	649.364775	1280.695726	640.851501	1279.711710	640.359493	**13**
3	232.092796	116.550036			214.082231	107.544753	**G**	***1210.690247***	605.848762	1193.663698	597.335487	1192.679682	596.843479	**12**
4	345.176860	173.092068			327.166295	164.086785	**L**	1153.668783	577.338029	1136.642234	568.824755	1135.658218	568.332747	**11**
5	**444.245274**	222.626275			426.234709	213.620993	**V**	***1040.584719***	520.795998	1023.558170	512.282723	1022.574154	511.790715	**10**
6	531.277302	266.142289			513.266737	257.137007	**S**	***941.516305***	471.261790	924.489756	462.748516	923.505740	462.256508	**9**
7	645.320229	323.163753	628.293680	314.650478	627.309664	314.158470	**N**	***854.484277***	427.745776	837.457728	419.232502			**8**
8	**716.357343**	358.682310	699.330794	350.169035	698.346778	349.677027	**A**	***740.441350***	370.724313	723.414801	362.211038			**7**
9	813.410107	407.208692	796.383558	398.695417	795.399542	398.203409	**P**	***669.404236***	335.205756	652.377687	326.692481			**6**
10	870.431571	435.719424	853.405022	427.206149	852.421006	426.714141	**G**	572.351472	286.679374	555.324923	278.166099			**5**
11	969.499985	485.253631	952.473436	476.740356	951.489420	476.248348	**V**	515.330008	258.168642	498.303459	249.655367			**4**
12	**1097.558563**	549.282920	1080.532014	540.769645	1079.547998	540.277637	**Q**	***416.261594***	208.634435	399.235045	200.121160			**3**
13	**1210.642627**	605.824952	1193.616078	597.311677	1192.632062	596.819669	**I**	***288.203016***	144.605146	271.176467	136.091871			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



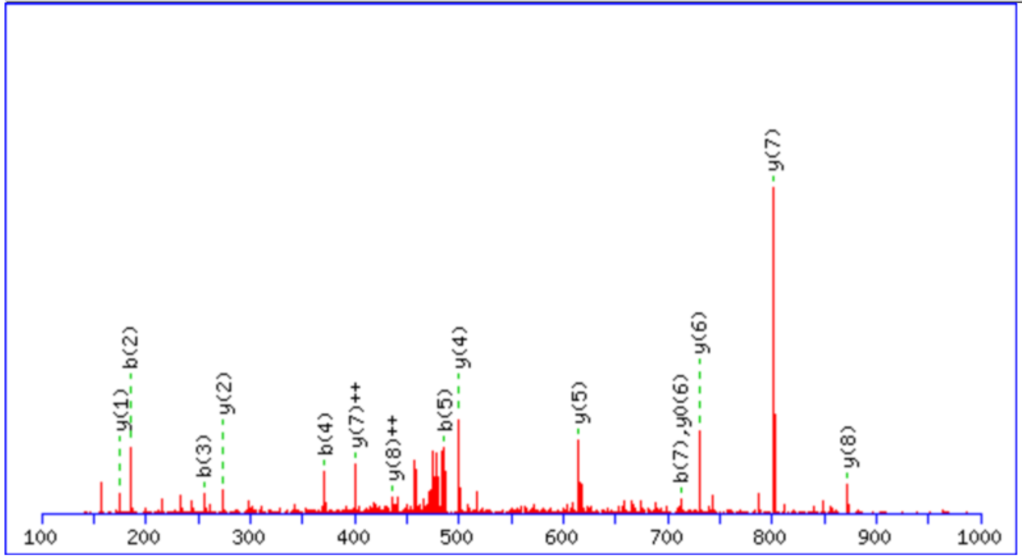
Peptide View

MS/MS Fragmentation of **LAADDPEVR**
Found in **IPI00025840**, Tax_Id=9606 Gene_Symbol=EFNA1 Isoform 1 of Ephrin-A1
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 3251: 984.488648 from(493.251600,2+)
Title: OECHL100312_44.5107.5107.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 984.487610**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53
Expect: 0.0004**Matches :** 15/70 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	**185.128454**	93.067865			A	***872.410837***	436.709057	855.384288	428.195782	854.400272	427.703774	8
3	**256.165568**	128.586422			A	***801.373723***	401.190500	784.347174	392.677225	783.363158	392.185217	7
4	**371.192511**	186.099893	353.181946	177.094611	D	***730.336609***	365.671943	713.310060	357.158668	712.326044	356.666660	6
5	**486.219454**	243.613365	468.208889	234.608082	D	***615.309666***	308.158471	598.283117	299.645197	597.299101	299.153189	5
6	583.272218	292.139747	565.261653	283.134465	P	***500.282723***	250.644999	483.256174	242.131725	482.272158	241.639717	4

7	**712.314811**	356.661044	694.304246	347.655761	**E**	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	**3**
8	811.383225	406.195251	793.372660	397.189968	**V**	***274.187366***	137.597321	257.160817	129.084046			**2**
9					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



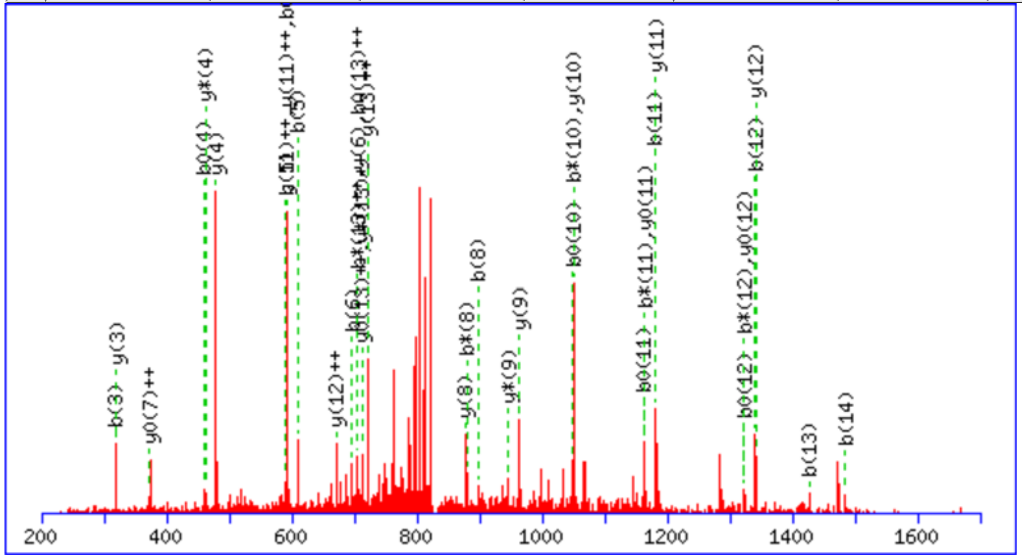
Peptide View

MS/MS Fragmentation of **TDTCMSSNGLLCSGR**
Found in **IPI00220350**, Tax_Id=9606 Gene_Symbol=ITGB3 Isoform Beta-3B of Integrin beta-3
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 11328: 1657.686248 from(829.850400,2+)
Title: OECHL100312_44.11034.11034.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1657.685837**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00018**Matches :** 39/150 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	102.054955	51.531116			84.044390	42.525833	**T**							**15**
2	217.081898	109.044587			199.071333	100.039304	**D**	1557.645424	779.326350	1540.618875	770.813075	1539.634859	770.321067	**14**
3	***318.129577***	159.568426			300.119012	150.563144	**T**	1442.618481	721.812878	1425.591932	713.299604	1424.607916	712.807596	**13**

4	478.160226	239.583751			460.149661	230.578469	**C**	***1341.570802***	671.289039	1324.544253	662.775765	1323.560237	662.283756	**12**
5	***609.200711***	305.103994			591.190146	296.098711	**M**	***1181.540153***	591.273714	1164.513604	582.760440	1163.529588	582.268432	**11**
6	***696.232739***	348.620008			678.222174	339.614725	**S**	***1050.499668***	525.753472	1033.473119	517.240197	1032.489103	516.748189	**10**
7	783.264767	392.136022			765.254202	383.130739	**S**	***963.467640***	482.237458	946.441091	473.724183	945.457075	473.232175	**9**
8	***897.307694***	449.157485	880.281145	440.644210	879.297129	440.152202	**N**	***876.435612***	438.721444	859.409063	430.208169	858.425047	429.716161	**8**
9	954.329158	477.668217	937.302609	469.154943	936.318593	468.662935	**G**	762.392685	381.699980	745.366136	373.186706	744.382120	372.694698	**7**
10	1067.413222	534.210249	1050.386673	525.696975	1049.402657	525.204966	**L**	***705.371221***	353.189248	688.344672	344.675974	687.360656	344.183966	**6**
11	***1180.497286***	590.752281	1163.470737	582.239006	1162.486721	581.746998	**L**	***592.287157***	296.647217	575.260608	288.133942	574.276592	287.641934	**5**
12	***1340.527935***	670.767605	1323.501386	662.254331	1322.517370	661.762323	**C**	***479.203093***	240.105184	462.176544	231.591910	461.192528	231.099902	**4**
13	***1427.559963***	714.283619	1410.533414	705.770345	1409.549398	705.278337	**S**	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	**3**
14	***1484.581427***	742.794351	1467.554878	734.281077	1466.570862	733.789069	**G**	232.140416	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**

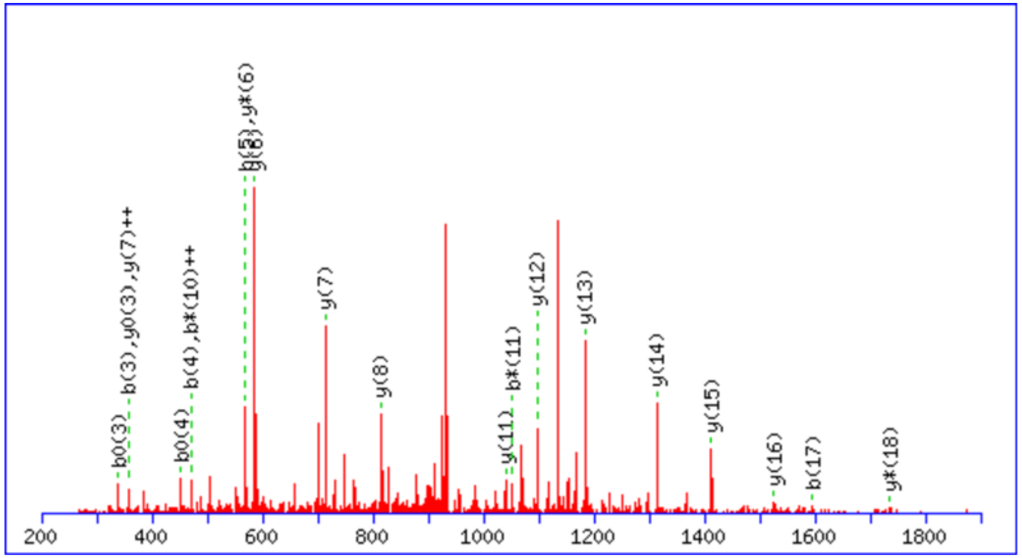


Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**
Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
Experiment: 29 - NOPE2 **Fraction:** NOPE2

Match to Query 13579: 1881.031248 from(941.522900,2+)
Title: OECHL100312_44.13733.13733.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_44.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00061**Matches :** 21/208 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							19
2	229.118283	115.062780			211.107718	106.057497	V	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.996686	18
3	**357.176861**	179.092069	340.150312	170.578794	339.166296	170.086786	Q	1653.928246	827.467761	1636.901697	818.954487	1635.917681	818.462479	17
4	**470.260925**	235.634101	453.234376	227.120826	452.250360	226.628818	L	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.433190	16
5	**569.329339**	285.168308	552.302790	276.655033	551.318774	276.163025	V	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.891158	15
6	698.371932	349.689604	681.345383	341.176330	680.361367	340.684322	E	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.356951	14
7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	S	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.835654	13
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	G	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.319640	12
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	G	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.808908	11
10	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	G	983.599641	492.303459	966.573092	483.790184	965.589076	483.298176	10
11	1069.552416	535.279846	1052.525867	526.766572	1051.541851	526.274564	L	926.578177	463.792727	909.551628	455.279452	908.567612	454.787444	9
12	1168.620830	584.814053	1151.594281	576.300779	1150.610265	575.808771	V	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.245412	8
13	1296.715793	648.861535	1279.689244	640.348260	1278.705228	639.856252	K	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.711205	7
14	1393.768557	697.387917	1376.742008	688.874642	1375.757992	688.382634	P	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.663723	6
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	G	489.277972	245.142624	472.251423	236.629349	471.267407	236.137341	5
16	1507.811485	754.409381	1490.784936	745.896106	1489.800920	745.404098	G	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	4
17	**1594.843513**	797.925395	1577.816964	789.412120	1576.832948	788.920112	S	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
18	1707.927577	854.467427	1690.901028	845.954152	1689.917012	845.462144	L	288.203016	144.605146	271.176467	136.091871			2
19							R	175.118952	88.063114	158.092403	79.549839			1



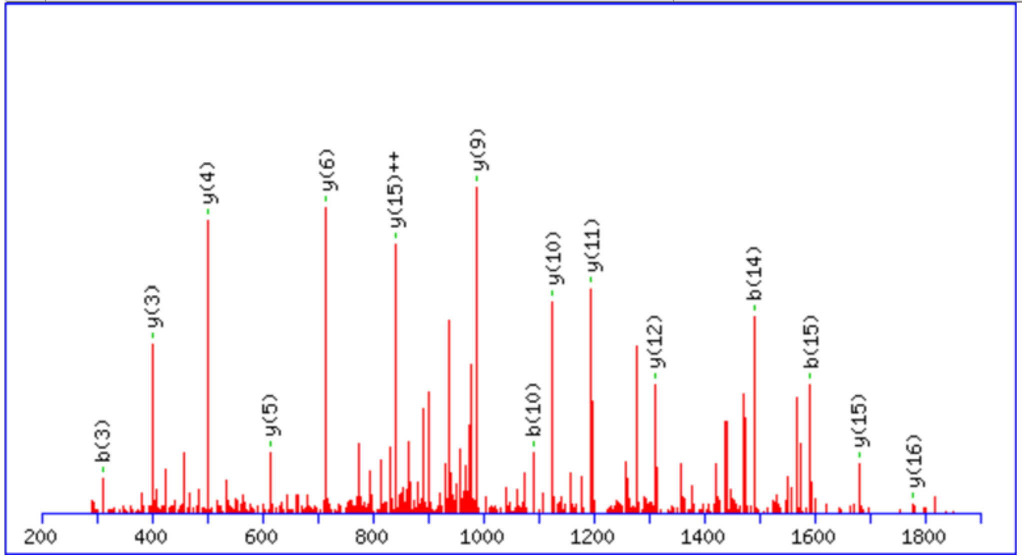
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 11 - S_D-2 **Fraction:** S_D-2

Match to Query 16309: 1990.024048 from(996.019300,2+)
Title: OECHL100312_42.10195.10195.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_42.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 90
Expect: 1.2e-007**Matches :** 15/186 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	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	424.255445	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	552.314023	276.660650	535.287474	268.147375			**Q**	1567.782311	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	680.372601	340.689939	663.346052	332.176664			**Q**	1439.723733	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**

7	795.399544	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	901.510158	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	1276.628040	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	814.478130	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510			**3**
17	1816.918804	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**

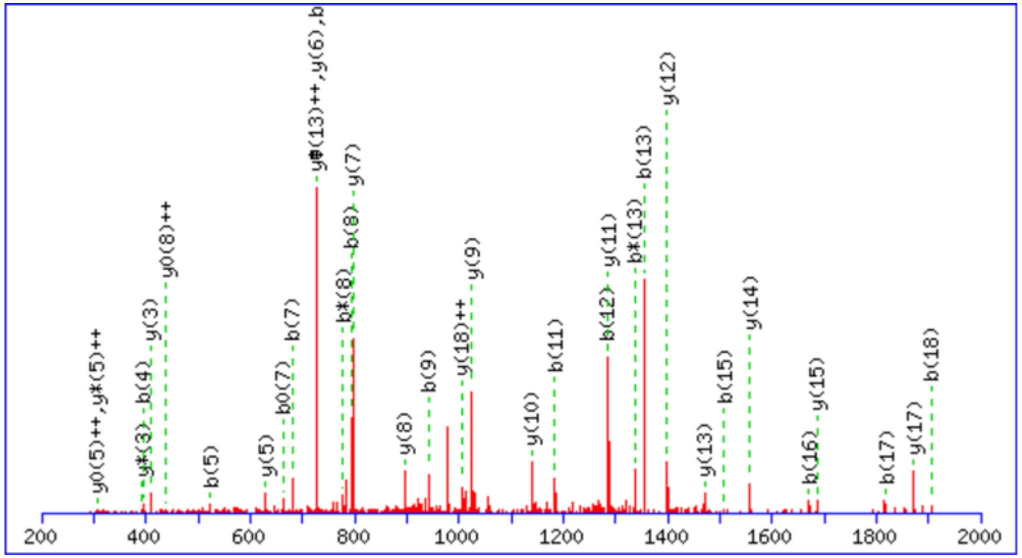


Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 11 - S_D-2 **Fraction:** S_D-2

Match to Query 16860: 2078.983448 from(1040.499000,2+)
Title: OECHL100312_42.17986.17986.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_42.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 87
Expect: 3.1e-007**Matches :** 36/200 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	72.044390	36.525833					**A**							**19**
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973939	**18**
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444483	**17**
4	***394.183344***	197.595310	377.156795	189.082035			**Q**	1814.870790	907.939033	1797.844241	899.425759	1796.860225	898.933751	**16**
5	***523.225937***	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904462	**15**
6	610.257965	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383165	**14**
7	***681.295079***	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867151	**13**
8	***794.379143***	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348594	**12**
9	***941.447557***	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806562	**11**
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272355	**10**
11	***1184.533077***	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250892	**9**
12	***1283.601491***	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729595	**8**
13	***1354.638605***	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195388	**7**
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676831	**6**
15	***1508.712833***	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150449	**5**
16	***1671.776162***	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	572.282723	286.645000	555.256174	278.131725	554.272158	277.639717	**4**
17	***1818.844576***	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	**3**
18	***1905.876604***	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
19							**R**	175.118952	88.063114	158.092403	79.549840			**1**



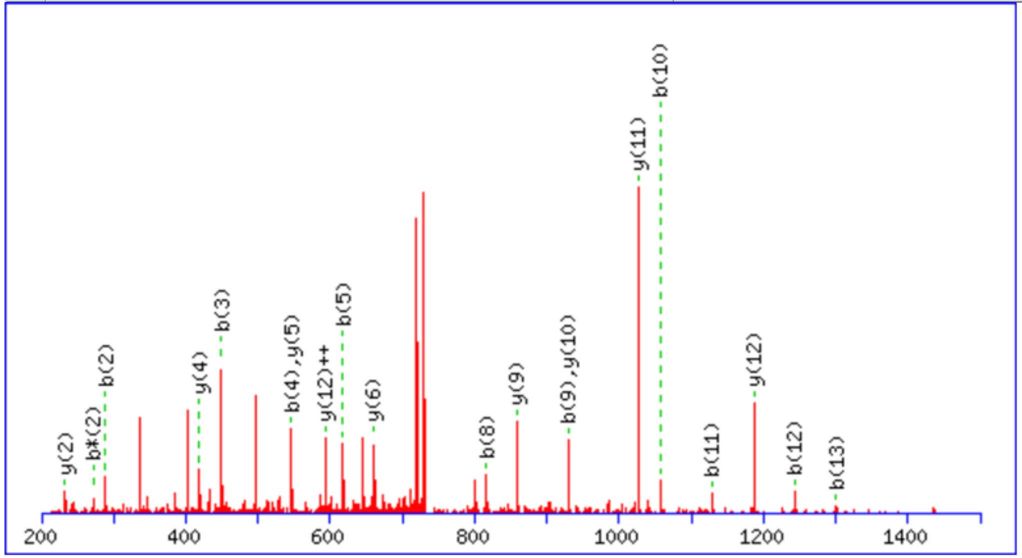
Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 11 - S_D-2 **Fraction:** S_D-2

Match to Query 11464: 1473.646248 from(737.830400,2+)
Title: OECHL100312_42.7775.7775.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_42.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65
Expect: 1.5e-005**Matches :** 20/128 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.037925	81.022600					**C**							**14**
2	***289.096503***	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.809312	**13**
3	***449.127152***	225.067214	432.100603	216.553940			**C**	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.780023	**12**
4	***546.179916***	273.593596	529.153367	265.080322			**P**	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.764698	**11**
5	***617.217030***	309.112153	600.190481	300.598879			**A**	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.238316	**10**
6	674.238494	337.622885	657.211945	329.109611			**G**	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.719759	**9**

7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
8	***816.312722***	408.659999	799.286173	400.146725			**A**	730.384229	365.695753	713.357680	357.182478	712.373664	356.690470	**7**
9	***929.396786***	465.202031	912.370237	456.688757			**L**	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.171913	**6**
10	***1057.455364***	529.231320	1040.428815	520.718046			**Q**	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.629881	**5**
11	***1128.492478***	564.749877	1111.465929	556.236603			**A**	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.600592	**4**
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	347.167359	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
13	***1300.540885***	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	**232.140416**	116.573846	215.113867	108.060571			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



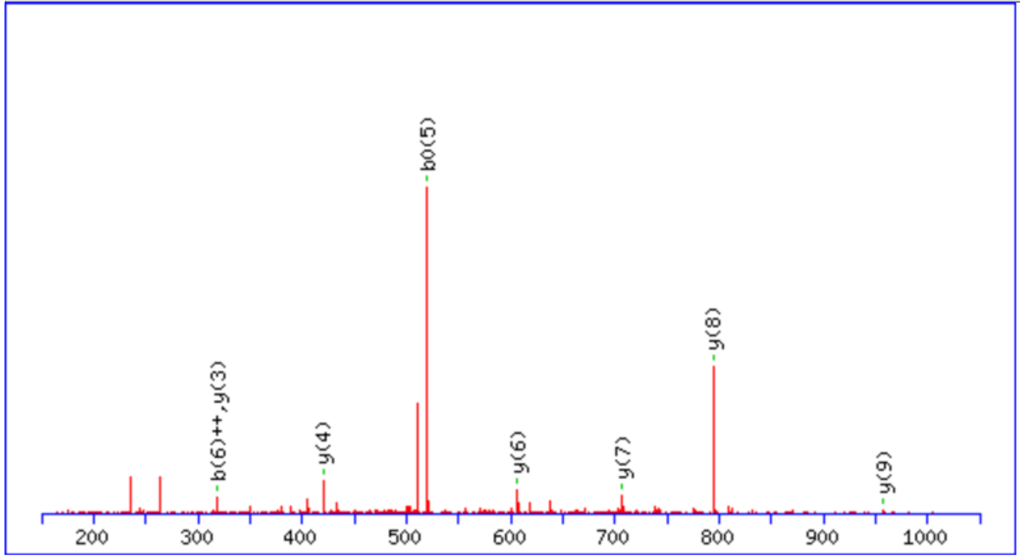
Peptide View

MS/MS Fragmentation of **VYSTSVTGSR**
Found in **IPI00010402**, Tax_Id=9606 Gene_Symbol=SH3BGRL3 Putative uncharacterized protein
Experiment: 11 - S_D-2 **Fraction:** S_D-2

Match to Query 5394: 1055.524048 from(528.769300,2+)
Title: OECHL100312_42.4711.4711.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_42.raw
Monoisotopic mass of neutral peptide Mr(calc): 1055.524750**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54

Expect: 0.00031**Matches :** 8/84 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			**V**							**10**
2	263.139019	132.073148			**Y**	***957.463601***	479.235439	940.437052	470.722164	939.453036	470.230156	**9**
3	350.171047	175.589161	332.160482	166.583879	**S**	***794.400272***	397.703774	777.373723	389.190499	776.389707	388.698491	**8**
4	451.218726	226.113001	433.208161	217.107719	**T**	***707.368244***	354.187760	690.341695	345.674486	689.357679	345.182478	**7**
5	538.250754	269.629015	520.240189	260.623733	**S**	***606.320565***	303.663921	589.294016	295.150646	588.310000	294.658638	**6**
6	637.319168	319.163222	619.308603	310.157940	**V**	519.288537	260.147907	502.261988	251.634632	501.277972	251.142624	**5**
7	738.366847	369.687062	720.356282	360.681779	**T**	***420.220123***	210.613699	403.193574	202.100425	402.209558	201.608417	**4**
8	795.388311	398.197794	777.377746	389.192511	**G**	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	**3**
9	882.420339	441.713808	864.409774	432.708525	**S**	262.150980	131.579128	245.124431	123.065853	244.140415	122.573845	**2**
10					**R**	175.118952	88.063114	158.092403	79.549839			**1**

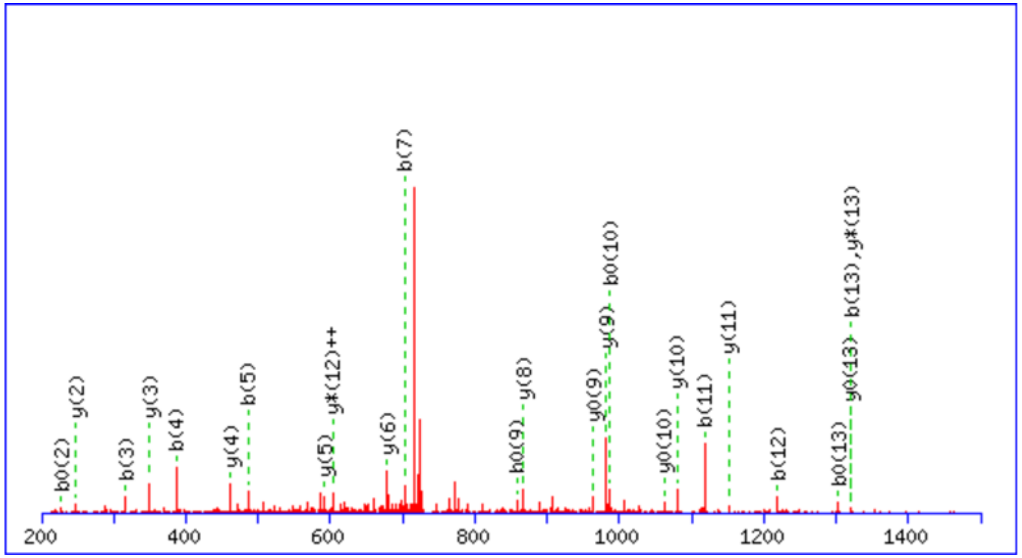


Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 11 - S_D-2 **Fraction:** S_D-2

Match to Query 11385: 1465.679448 from(733.847000,2+)
Title: OECHL100312_42.10230.10230.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_42.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 65 **Expect:** 2.6e-005**Matches :** 25/128 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	1337.643082	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	***316.113926***	158.560601	298.103361	149.555319	**A**	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	***387.151040***	194.079158	369.140475	185.073875	**A**	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	***486.219454***	243.613365	468.208889	234.608082	**V**	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**
6	601.246397	301.126837	583.235832	292.121554	**D**	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	**9**
7	***702.294076***	351.650676	684.283511	342.645394	**T**	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	765.398875	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	876.358132	438.682704	858.347567	429.677421	**S**	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	1005.400725	503.204001	987.390160	494.198718	**E**	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	***1118.484789***	559.746033	1100.474224	550.740750	**I**	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	***1219.532468***	610.269872	1201.521903	601.264590	**T**	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	***1320.580147***	660.793712	1302.569582	651.788429	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**



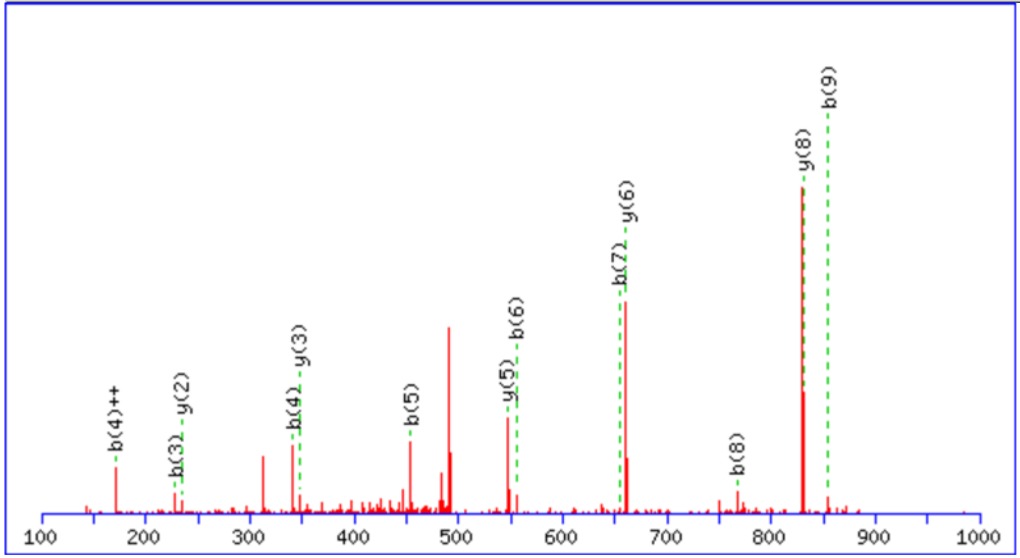
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 11 - S_D-2 **Fraction:** S_D-2

Match to Query 4276: 999.633448 from(500.824000,2+)
Title: OECHL100312_42.17905.17905.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_42.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63
Expect: 6.1e-006**Matches :** 14/78 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**

7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



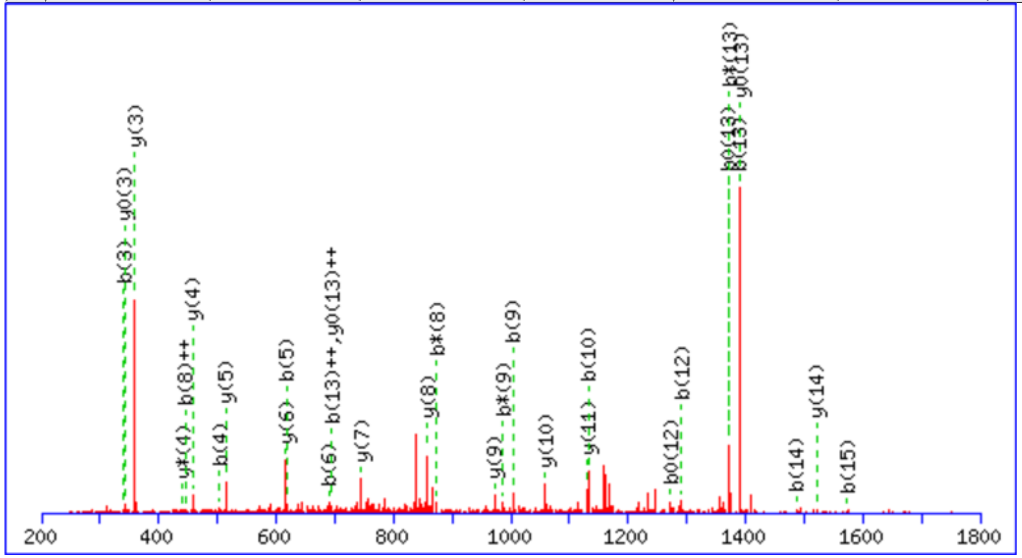
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 11 - S_D-2 **Fraction:** S_D-2

Match to Query 14399: 1746.916448 from(874.465500,2+)
Title: OECHL100312_42.17754.17754.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_42.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70
Expect: 1e-005**Matches :** 31/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**

3	***340.259468***	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	***503.322797***	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	***618.349740***	309.678508			600.339175	300.673226	**D**	1245.606970	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	***689.386854***	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	1233.636145	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**

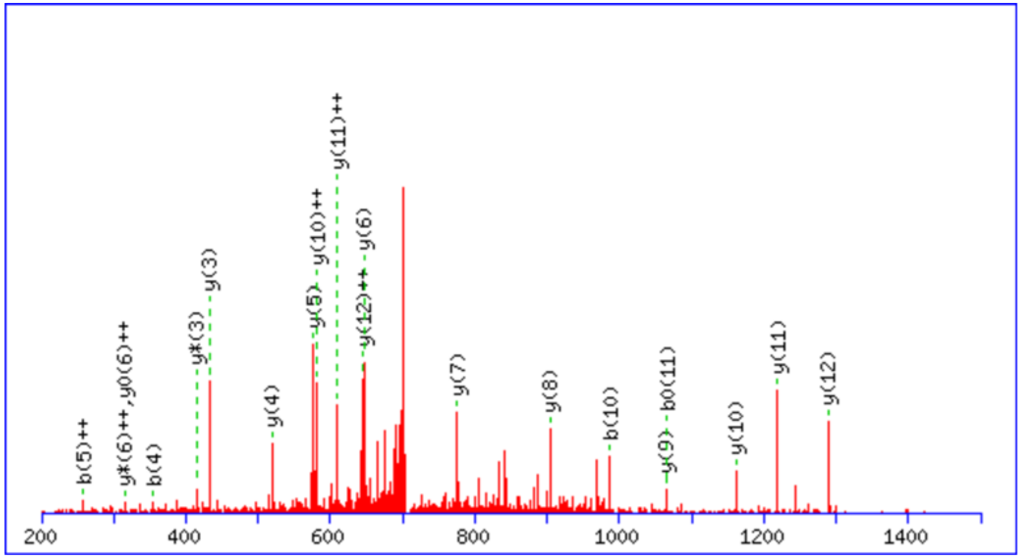


Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 11 - S_D-2 **Fraction:** S_D-2

Match to Query 10949: 1416.625248 from(709.319900,2+)
Title: OECHL100312_42.2294.2294.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_42.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 68
Expect: 9e-006**Matches :** 20/128 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							**13**
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	**12**
3	257.160817	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	**11**
4	**354.213581**	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	**10**
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	**9**
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	**8**
7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	842.382515	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	899.403979	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	335.149601	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**



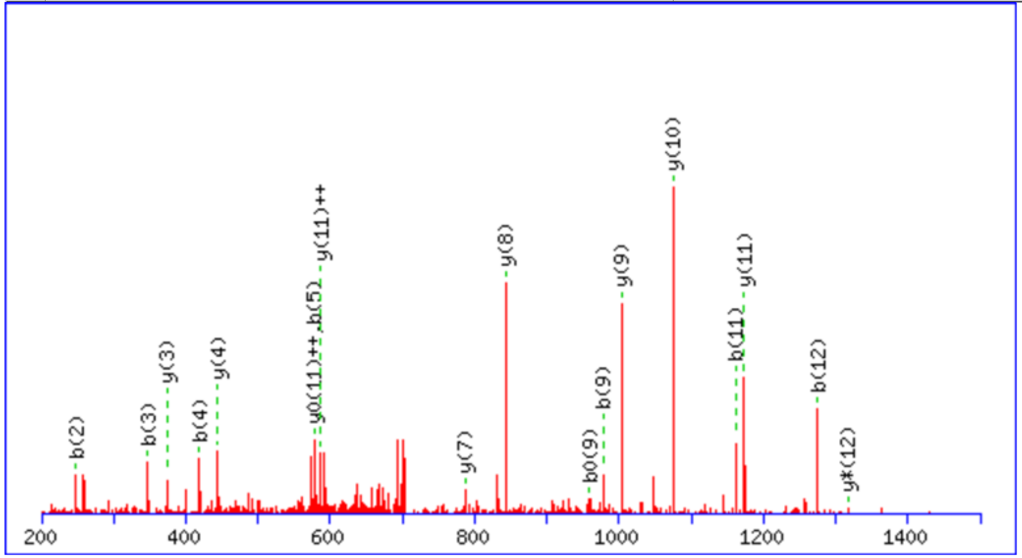
Peptide View

MS/MS Fragmentation of **SCVACGNDIALIK**
Found in **IPI00295663**, Tax_Id=9606 Gene_Symbol=CELA3A Chymotrypsin-like elastase family member 3A
Experiment: 11 - S_D-2 **Fraction:** S_D-2

Match to Query 10970: 1419.685848 from(710.850200,2+)
Title: OECHL100312_42.13479.13479.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_42.raw
Monoisotopic mass of neutral peptide Mr(calc): 1419.685013**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66
Expect: 3.6e-005**Matches :** 18/122 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	88.039304	44.523290			70.028739	35.518008	**S**							**13**
2	***248.069953***	124.538614			230.059388	115.533332	**C**	1333.660270	667.333773	1316.633721	658.820498	1315.649705	658.328490	**12**
3	***347.138367***	174.072822			329.127802	165.067539	**V**	***1173.629621***	587.318448	1156.603072	578.805174	1155.619056	578.313166	**11**
4	***418.175481***	209.591379			400.164916	200.586096	**A**	***1074.561207***	537.784242	1057.534658	529.270967	1056.550642	528.778959	**10**
5	***578.206130***	289.606703			560.195565	280.601421	**C**	***1003.524093***	502.265684	986.497544	493.752410	985.513528	493.260402	**9**
6	635.227594	318.117435			617.217029	309.112153	**G**	***843.493444***	422.250360	826.466895	413.737085	825.482879	413.245077	**8**

7	749.270521	375.138899	732.243972	366.625624	731.259956	366.133616	**N**	***786.471980***	393.739628	769.445431	385.226353	768.461415	384.734345	**7**
8	864.297464	432.652370	847.270915	424.139096	846.286899	423.647088	**D**	672.429053	336.718164	655.402504	328.204890	654.418488	327.712882	**6**
9	***977.381528***	489.194402	960.354979	480.681128	959.370963	480.189120	**I**	557.402110	279.204693	540.375561	270.691418			**5**
10	1048.418642	524.712959	1031.392093	516.199685	1030.408077	515.707677	**A**	***444.318046***	222.662661	427.291497	214.149386			**4**
11	***1161.502706***	581.254991	1144.476157	572.741717	1143.492141	572.249709	**L**	***373.280932***	187.144104	356.254383	178.630829			**3**
12	***1274.586770***	637.797023	1257.560221	629.283749	1256.576205	628.791740	**I**	260.196868	130.602072	243.170319	122.088797			**2**
13							**K**	147.112804	74.060040	130.086255	65.546765			**1**

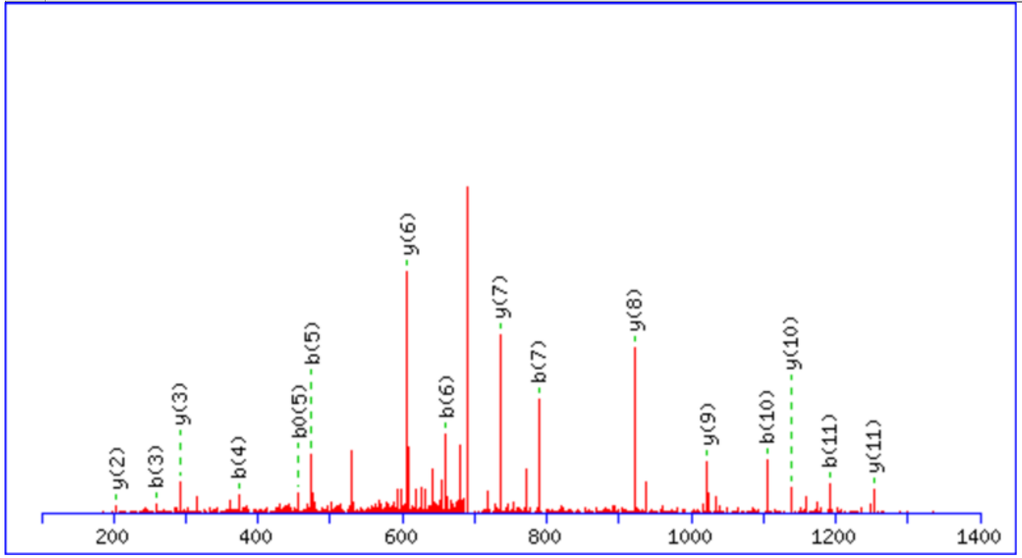


Peptide View

MS/MS Fragmentation of **AADDTWEPFASGK**
Found in **IPI00022432**, Tax_Id=9606 Gene_Symbol=TTR Transthyretin
Experiment: 11 - S_D-2 **Fraction:** S_D-2

Match to Query 10704: 1393.614248 from(697.814400,2+)
Title: OECHL100312_42.15702.15702.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_42.raw
Monoisotopic mass of neutral peptide Mr(calc): 1393.615005**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62
Expect: 3.5e-005**Matches :** 16/112 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833			A							13
2	143.081504	72.044390			A	1323.585173	662.296225	1306.558624	653.782950	1305.574608	653.290942	12
3	**258.108447**	129.557862	240.097882	120.552579	D	***1252.548059***	626.777668	1235.521510	618.264393	1234.537494	617.772385	11
4	**373.135390**	187.071333	355.124825	178.066051	D	***1137.521116***	569.264196	1120.494567	560.750922	1119.510551	560.258914	10
5	**474.183069**	237.595173	456.172504	228.589890	T	***1022.494173***	511.750725	1005.467624	503.237450	1004.483608	502.745442	9
6	**660.262382**	330.634829	642.251817	321.629547	W	***921.446494***	461.226885	904.419945	452.713611	903.435929	452.221603	8
7	**789.304975**	395.156126	771.294410	386.150843	E	***735.367181***	368.187229	718.340632	359.673954	717.356616	359.181946	7
8	886.357739	443.682508	868.347174	434.677225	P	***606.324588***	303.665932	589.298039	295.152658	588.314023	294.660650	6
9	1033.426153	517.216715	1015.415588	508.211432	F	509.271824	255.139550	492.245275	246.626275	491.261259	246.134267	5
10	**1104.463267**	552.735272	1086.452702	543.729989	A	362.203410	181.605343	345.176861	173.092068	344.192845	172.600060	4
11	**1191.495295**	596.251286	1173.484730	587.246003	S	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
12	1248.516759	624.762018	1230.506194	615.756735	G	***204.134268***	102.570772	187.107719	94.057497			2
13					K	147.112804	74.060040	130.086255	65.546765			1

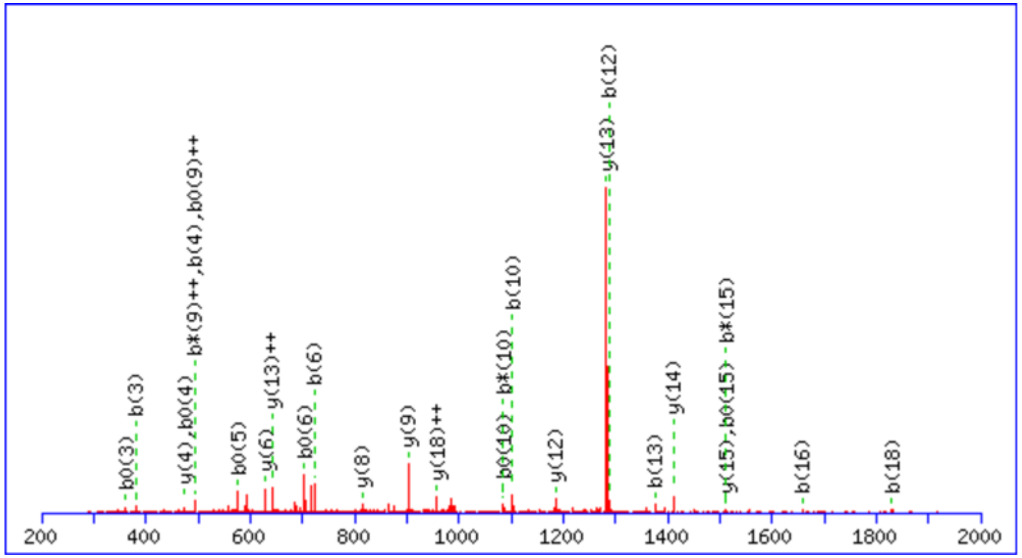


Peptide View

MS/MS Fragmentation of **SYELTQPPSVSVSPGQTAR**
Found in **IPI00382440**, Tax_Id=9606 Gene_Symbol=- Ig lambda chain V-IV region Hil
Experiment: 56 - PyD-2 **Fraction:** PyD-2

Match to Query 15372: 2002.997448 from(1002.506000,2+)
Title: OECHL100312_40.13555.13555.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_40.raw
Monoisotopic mass of neutral peptide Mr(calc): 2002.995987**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70
Expect: 1.9e-005**Matches :** 28/202 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	88.039304	44.523290			70.028739	35.518008	**S**							**19**
2	251.102633	126.054954			233.092068	117.049672	**Y**	1916.971234	958.989255	1899.944685	950.475981	1898.960669	949.983973	**18**
3	***380.145226***	190.576251			362.134661	181.570969	**E**	1753.907905	877.457591	1736.881356	868.944316	1735.897340	868.452308	**17**
4	***493.229290***	247.118283			475.218725	238.113001	**L**	1624.865312	812.936294	1607.838763	804.423020	1606.854747	803.931012	**16**
5	594.276969	297.642123			576.266404	288.636840	**T**	***1511.781248***	756.394262	1494.754699	747.880988	1493.770683	747.388980	**15**
6	***722.335547***	361.671412	705.308998	353.158137	704.324982	352.666129	**Q**	***1410.733569***	705.870423	1393.707020	697.357148	1392.723004	696.865140	**14**
7	819.388311	410.197794	802.361762	401.684519	801.377746	401.192511	**P**	***1282.674991***	641.841134	1265.648442	633.327859	1264.664426	632.835851	**13**
8	916.441075	458.724176	899.414526	450.210901	898.430510	449.718893	**P**	***1185.622227***	593.314752	1168.595678	584.801477	1167.611662	584.309469	**12**
9	1003.473103	502.240190	986.446554	493.726915	985.462538	493.234907	**S**	1088.569463	544.788370	1071.542914	536.275095	1070.558898	535.783087	**11**
10	***1102.541517***	551.774397	1085.514968	543.261122	1084.530952	542.769114	**V**	1001.537435	501.272356	984.510886	492.759081	983.526870	492.267073	**10**
11	1189.573545	595.290411	1172.546996	586.777136	1171.562980	586.285128	**S**	***902.469021***	451.738149	885.442472	443.224874	884.458456	442.732866	**9**
12	***1288.641959***	644.824618	1271.615410	636.311343	1270.631394	635.819335	**V**	***815.436993***	408.222135	798.410444	399.708860	797.426428	399.216852	**8**
13	***1375.673987***	688.340632	1358.647438	679.827357	1357.663422	679.335349	**S**	716.368579	358.687928	699.342030	350.174653	698.358014	349.682645	**7**
14	1472.726751	736.867014	1455.700202	728.353739	1454.716186	727.861731	**P**	***629.336551***	315.171914	612.310002	306.658639	611.325986	306.166631	**6**
15	1529.748215	765.377746	1512.721666	756.864471	1511.737650	756.372463	**G**	532.283787	266.645532	515.257238	258.132257	514.273222	257.640249	**5**
16	***1657.806793***	829.407035	1640.780244	820.893760	1639.796228	820.401752	**Q**	***475.262323***	238.134800	458.235774	229.621525	457.251758	229.129517	**4**
17	1758.854472	879.930874	1741.827923	871.417600	1740.843907	870.925592	**T**	347.203745	174.105510	330.177196	165.592236	329.193180	165.100228	**3**
18	***1829.891586***	915.449431	1812.865037	906.936157	1811.881021	906.444149	**A**	246.156066	123.581671	229.129517	115.068396			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



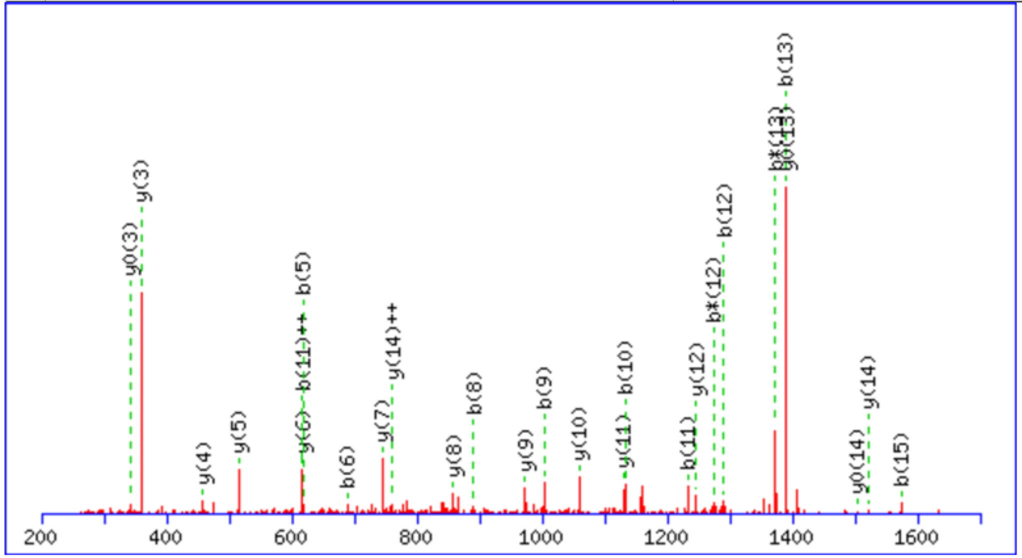
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 56 - PyD-2 **Fraction:** PyD-2

Match to Query 13450: 1746.919848 from(874.467200,2+)
Title: OECHL100312_40.17406.17406.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_40.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 80
Expect: 1.2e-006**Matches :** 27/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	**689.386854**	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**

7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	**890.461809**	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



Peptide View

MS/MS Fragmentation of **AIYKGPGSEAGP**
Found in **IPI00011284**, Tax_Id=9606 Gene_Symbol=COMT Isoform Membrane-bound of Catechol O-methyltransferase
Experiment: 56 - PyD-2 **Fraction:** PyD-2

Match to Query 6285: 1145.574248 from(573.794400,2+)

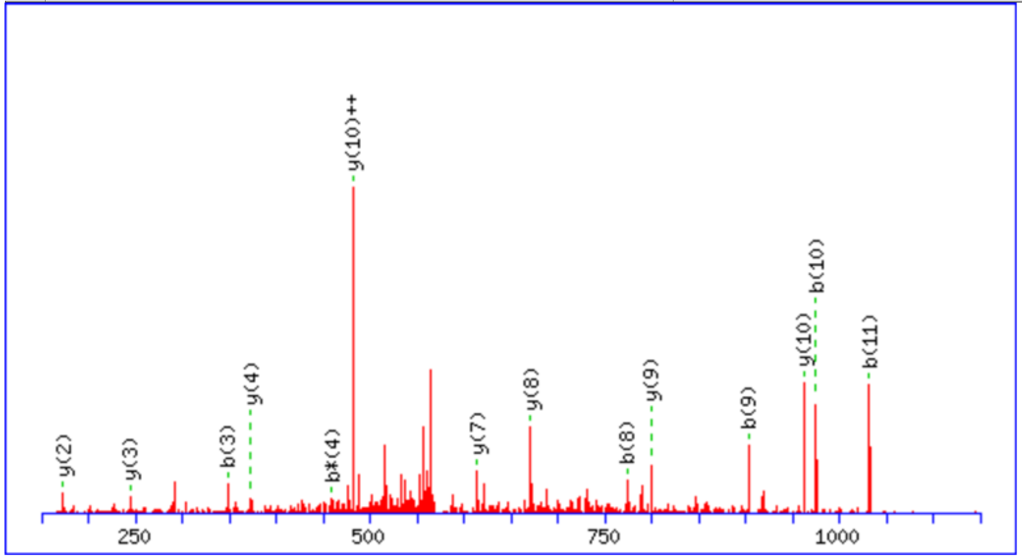
Title: OECHL100312_40.7986.7986.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_40.raw

Monoisotopic mass of neutral peptide Mr(calc): 1145.571671**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53

Expect: 0.00062**Matches :** 14/90 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	72.044390	36.525833					**A**							**12**
2	185.128454	93.067865					**I**	1075.541852	538.274564	1058.515303	529.761290	1057.531287	529.269282	**11**
3	**348.191783**	174.599529					**Y**	***962.457788***	481.732532	945.431239	473.219258	944.447223	472.727250	**10**
4	476.286746	238.647011	459.260197	230.133737			**K**	***799.394459***	400.200868	782.367910	391.687593	781.383894	391.195585	**9**
5	533.308210	267.157743	516.281661	258.644469			**G**	***671.299496***	336.153386			653.288931	327.148104	**8**
6	630.360974	315.684125	613.334425	307.170851			**P**	***614.278032***	307.642654			596.267467	298.637372	**7**
7	687.382438	344.194857	670.355889	335.681583			**G**	517.225268	259.116272			499.214703	250.110990	**6**
8	**774.414466**	387.710871	757.387917	379.197597	756.403901	378.705589	**S**	460.203804	230.605540			442.193239	221.600257	**5**
9	**903.457059**	452.232168	886.430510	443.718893	885.446494	443.226885	**E**	***373.171776***	187.089526			355.161211	178.084243	**4**
10	**974.494173**	487.750725	957.467624	479.237450	956.483608	478.745442	**A**	***244.129183***	122.568229					**3**
11	**1031.515637**	516.261457	1014.489088	507.748182	1013.505072	507.256174	**G**	***173.092069***	87.049672					**2**
12							**P**	116.070605	58.538941					**1**

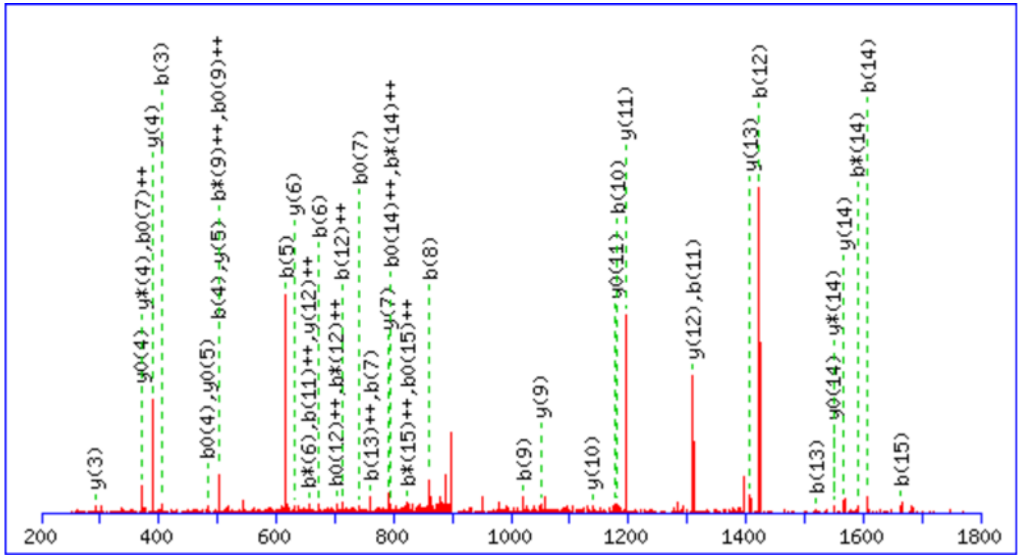


Peptide View

MS/MS Fragmentation of **SRCPDGSTCCELPSGK**
Found in **IPI00182138**, Tax_Id=9606 Gene_Symbol=GRN Isoform 2 of Granulins
Experiment: 56 - PyD-2 **Fraction:** PyD-2

Match to Query 13888: 1809.745248 from(905.879900,2+)
Title: OECHL100312_40.4749.4749.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_40.raw
Monoisotopic mass of neutral peptide Mr(calc): 1809.744415**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 5.3e-007**Matches :** 47/174 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	88.039304	44.523290			70.028739	35.518008	**S**							**16**
2	244.140415	122.573845	227.113866	114.060571	226.129850	113.568563	**R**	1723.719653	862.363465	1706.693104	853.850190	1705.709088	853.358182	**15**
3	***404.171064***	202.589170	387.144515	194.075896	386.160499	193.583888	**C**	**1567.618542**	784.312909	1550.591993	775.799635	1549.607977	775.307627	**14**
4	***501.223828***	251.115552	484.197279	242.602277	483.213263	242.110269	**P**	**1407.587893**	704.297585	1390.561344	695.784310	1389.577328	695.292302	**13**
5	***616.250771***	308.629024	599.224222	300.115749	598.240206	299.623741	**D**	**1310.535129**	655.771203	1293.508580	647.257928	1292.524564	646.765920	**12**
6	***673.272235***	337.139756	656.245686	328.626481	655.261670	328.134473	**G**	**1195.508186**	598.257731	1178.481637	589.744457	1177.497621	589.252449	**11**
7	***760.304263***	380.655770	743.277714	372.142495	742.293698	371.650487	**S**	**1138.486722**	569.746999	1121.460173	561.233725	1120.476157	560.741717	**10**
8	***861.351942***	431.179609	844.325393	422.666335	843.341377	422.174327	**T**	**1051.454694**	526.230985	1034.428145	517.717711	1033.444129	517.225703	**9**
9	***1021.382591***	511.194934	1004.356042	502.681659	1003.372026	502.189651	**C**	950.407015	475.707146	933.380466	467.193871	932.396450	466.701863	**8**
10	***1181.413240***	591.210258	1164.386691	582.696984	1163.402675	582.204976	**C**	**790.376366**	395.691821	773.349817	387.178547	772.365801	386.686539	**7**
11	***1310.455833***	**655.731555**	1293.429284	647.218280	1292.445268	646.726272	**E**	**630.345717**	315.676497	613.319168	307.163222	612.335152	306.671214	**6**
12	***1423.539897***	**712.273587**	1406.513348	703.760312	1405.529332	703.268304	**L**	**501.303124**	251.155200	484.276575	242.641925	483.292559	242.149917	**5**
13	***1520.592661***	**760.799969**	1503.566112	752.286694	1502.582096	751.794686	**P**	**388.219060**	194.613168	371.192511	186.099894	370.208495	185.607886	**4**
14	***1607.624689***	804.315983	1590.598140	795.802708	1589.614124	795.310700	**S**	**291.166296**	146.086786	274.139747	137.573512	273.155731	137.081504	**3**
15	***1664.646153***	832.826715	1647.619604	824.313440	1646.635588	823.821432	**G**	204.134268	102.570772	187.107719	94.057497			**2**
16							**K**	147.112804	74.060040	130.086255	65.546765			**1**



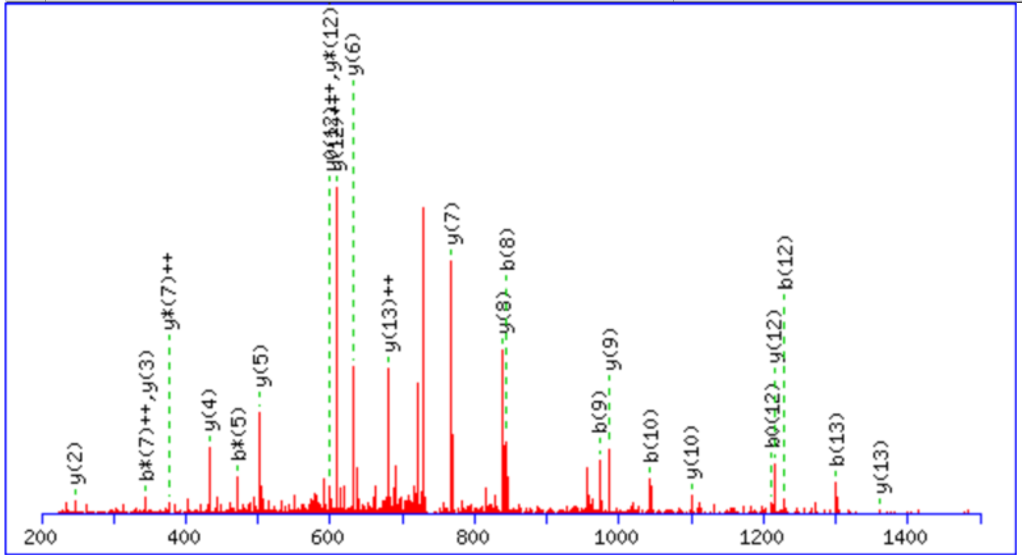
Peptide View

MS/MS Fragmentation of **LFGGNFAHQASVAR**
Found in **IPI00298237**, Tax_Id=9606 Gene_Symbol=TPP1 cDNA FLJ56402, highly similar to Tripeptidyl-peptidase 1
Experiment: 56 - PyD-2 **Fraction:** PyD-2

Match to Query 10367: 1473.747248 from(737.880900,2+)
Title: OECHL100312_40.12205.12205.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_40.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.747696**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 91
Expect: 9.4e-008**Matches :** 24/122 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					**L**							**14**
2	261.159754	131.083515					**F**	***1361.670909***	681.339093	1344.644360	672.825818	1343.660344	672.333810	**13**
3	318.181218	159.594247					**G**	***1214.602495***	607.804886	1197.575946	599.291611	1196.591930	598.799603	**12**
4	375.202682	188.104979					**G**	1157.581031	579.294154	1140.554482	570.780879	1139.570466	570.288871	**11**
5	489.245609	245.126442	472.219060	236.613168			**N**	***1100.559567***	550.783422	1083.533018	542.270147	1082.549002	541.778139	**10**
6	636.314023	318.660650	619.287474	310.147375			**F**	***986.516640***	493.761958	969.490091	485.248684	968.506075	484.756676	**9**

7	707.351137	354.179207	690.324588	345.665932			**A**	***839.448226***	420.227751	822.421677	411.714477	821.437661	411.222469	**8**
8	**844.410049**	422.708663	827.383500	414.195388			**H**	***768.411112***	384.709194	751.384563	376.195920	750.400547	375.703912	**7**
9	**972.468627**	486.737952	955.442078	478.224677			**Q**	***631.352200***	316.179738	614.325651	307.666464	613.341635	307.174456	**6**
10	**1043.505741**	522.256509	1026.479192	513.743234			**A**	***503.293622***	252.150449	486.267073	243.637175	485.283057	243.145167	**5**
11	1130.537769	565.772523	1113.511220	557.259248	1112.527204	556.767240	**S**	***432.256508***	216.631892	415.229959	208.118618	414.245943	207.626610	**4**
12	**1229.606183**	615.306730	1212.579634	606.793455	1211.595618	606.301447	**V**	***345.224480***	173.115878	328.197931	164.602603			**3**
13	**1300.643297**	650.825287	1283.616748	642.312012	1282.632732	641.820004	**A**	***246.156066***	123.581671	229.129517	115.068396			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



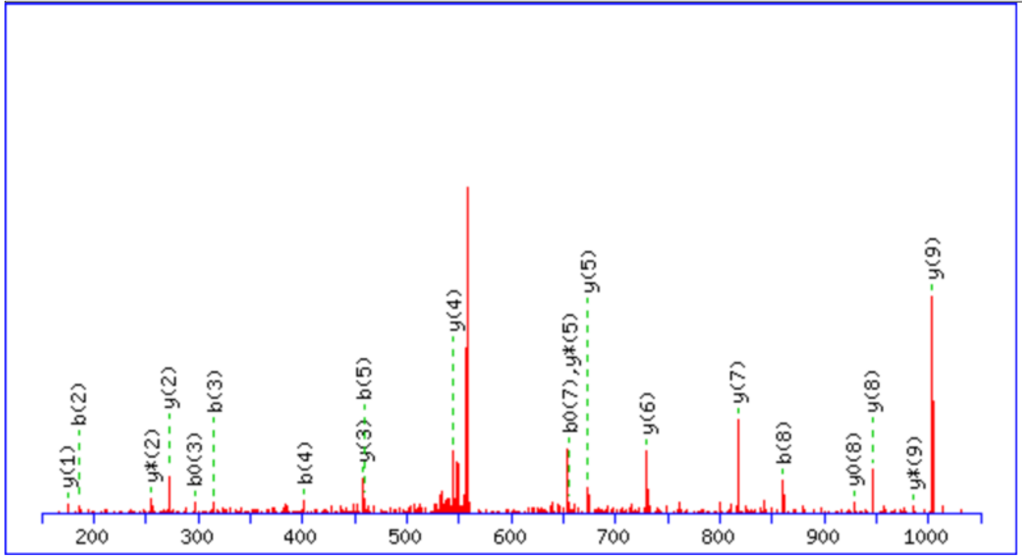
Peptide View

MS/MS Fragmentation of **KGESGQSWPR**
Found in **IPI00015029**, Tax_Id=9606 Gene_Symbol=PTGES3 Prostaglandin E synthase 3
Experiment: 56 - PyD-2 **Fraction:** PyD-2

Match to Query 6064: 1130.545048 from(566.279800,2+)
Title: OECHL100312_40.4156.4156.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_40.raw
Monoisotopic mass of neutral peptide Mr(calc): 1130.546860**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 83

Expect: 5.2e-007**Matches :** 20/98 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	129.102239	65.054757	112.075690	56.541483			**K**							**10**
2	**186.123703**	93.565489	169.097154	85.052215			**G**	***1003.459184***	502.233230	986.432635	493.719956	985.448619	493.227948	**9**
3	**315.166296**	158.086786	298.139747	149.573512	297.155731	149.081504	**E**	***946.437720***	473.722498	929.411171	465.209224	928.427155	464.717216	**8**
4	**402.198324**	201.602800	385.171775	193.089526	384.187759	192.597518	**S**	***817.395127***	409.201202	800.368578	400.687927	799.384562	400.195919	**7**
5	**459.219788**	230.113532	442.193239	221.600258	441.209223	221.108250	**G**	***730.363099***	365.685188	713.336550	357.171913	712.352534	356.679905	**6**
6	587.278366	294.142821	570.251817	285.629547	569.267801	285.137539	**Q**	***673.341635***	337.174456	656.315086	328.661181	655.331070	328.169173	**5**
7	674.310394	337.658835	657.283845	329.145560	656.299829	328.653552	**S**	***545.283057***	273.145167	528.256508	264.631892	527.272492	264.139884	**4**
8	**860.389707**	430.698492	843.363158	422.185217	842.379142	421.693209	**W**	***458.251029***	229.629153	441.224480	221.115878			**3**
9	957.442471	479.224874	940.415922	470.711599	939.431906	470.219591	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
10							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**

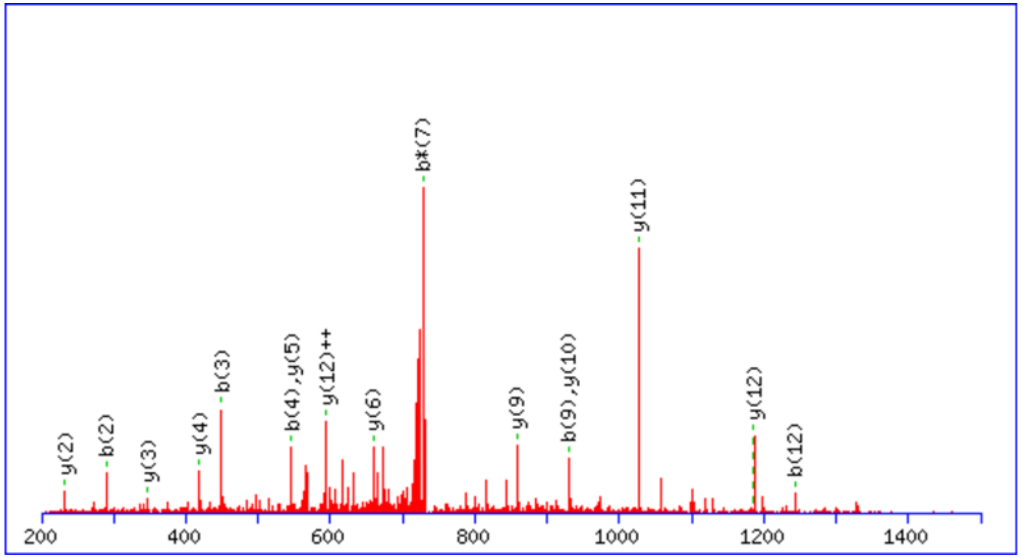


Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 56 - PyD-2 **Fraction:** PyD-2

Match to Query 10350: 1473.646248 from(737.830400,2+)
Title: OECHL100312_40.7511.7511.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_40.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 0.00012**Matches :** 16/128 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	161.037925	81.022600					**C**							**14**
2	**289.096503**	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.809312	**13**
3	**449.127152**	225.067214	432.100603	216.553940			**C**	***1186.563334***	593.785305	1169.536785	585.272031	1168.552769	584.780023	**12**
4	**546.179916**	273.593596	529.153367	265.080322			**P**	***1026.532685***	513.769981	1009.506136	505.256706	1008.522120	504.764698	**11**
5	617.217030	309.112153	600.190481	300.598879			**A**	***929.479921***	465.243599	912.453372	456.730324	911.469356	456.238316	**10**
6	674.238494	337.622885	657.211945	329.109611			**G**	***858.442807***	429.725042	841.416258	421.211767	840.432242	420.719759	**9**
7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
8	816.312722	408.659999	799.286173	400.146725			**A**	730.384229	365.695753	713.357680	357.182478	712.373664	356.690470	**7**
9	**929.396786**	465.202031	912.370237	456.688757			**L**	***659.347115***	330.177196	642.320566	321.663921	641.336550	321.171913	**6**
10	1057.455364	529.231320	1040.428815	520.718046			**Q**	***546.263051***	273.635164	529.236502	265.121889	528.252486	264.629881	**5**
11	1128.492478	564.749877	1111.465929	556.236603			**A**	***418.204473***	209.605874	401.177924	201.092600	400.193908	200.600592	**4**
12	**1243.519421**	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
13	1300.540885	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



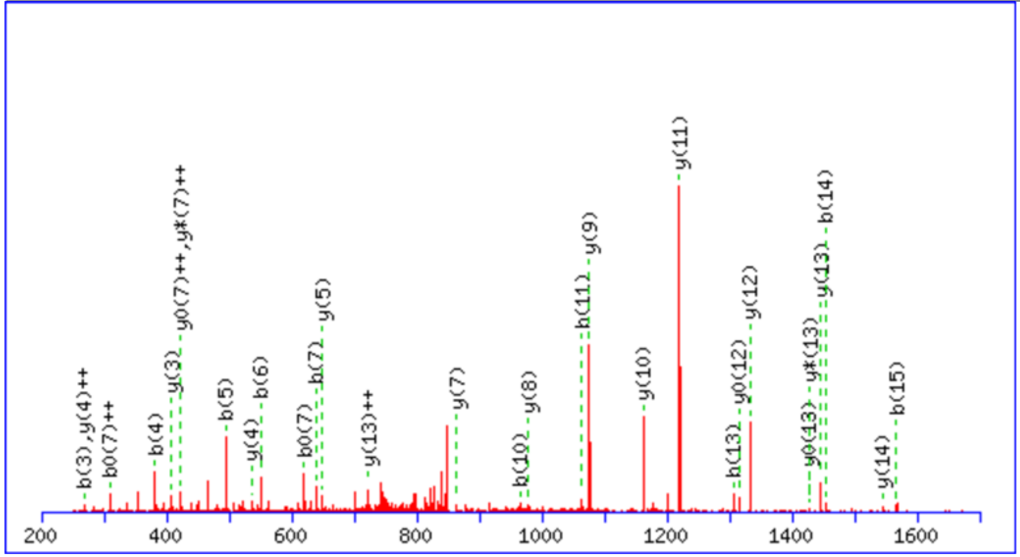
Peptide View

MS/MS Fragmentation of **APVILGSPDDVLEFLK**
Found in **IPI00073772**, Tax_Id=9606 Gene_Symbol=FBP1 Fructose-1,6-bisphosphatase 1
Experiment: 56 - PyD-2 **Fraction:** PyD-2

Match to Query 13215: 1711.939648 from(856.977100,2+)
Title: OECHL100312_40.22529.22529.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_40.raw
Monoisotopic mass of neutral peptide Mr(calc): 1711.939636**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 73
Expect: 3.4e-006**Matches :** 30/132 fragment ions using 58 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**16**
2	169.097154	85.052215			**P**	1641.909801	821.458538	1624.883252	812.945264	1623.899236	812.453256	**15**
3	***268.165568***	134.586422			**V**	***1544.857037***	772.932156	1527.830488	764.418882	1526.846472	763.926874	**14**
4	***381.249632***	191.128454			**I**	***1445.788623***	723.397949	1428.762074	714.884675	1427.778058	714.392667	**13**
5	***494.333696***	247.670486			**L**	***1332.704559***	666.855917	1315.678010	658.342643	1314.693994	657.850635	**12**
6	***551.355160***	276.181218			**G**	***1219.620495***	610.313885	1202.593946	601.800611	1201.609930	601.308603	**11**

7	***638.387188***	319.697232	620.376623	310.691950	**S**	***1162.599031***	581.803153	1145.572482	573.289879	1144.588466	572.797871	**10**
8	735.439952	368.223614	717.429387	359.218332	**P**	***1075.567003***	538.287139	1058.540454	529.773865	1057.556438	529.281857	**9**
9	850.466895	425.737086	832.456330	416.731803	**D**	***978.514239***	489.760757	961.487690	481.247483	960.503674	480.755475	**8**
10	***965.493838***	483.250557	947.483273	474.245274	**D**	***863.487296***	432.247286	846.460747	423.734011	845.476731	423.242003	**7**
11	***1064.562252***	532.784764	1046.551687	523.779481	**V**	748.460353	374.733814	731.433804	366.220540	730.449788	365.728532	**6**
12	1177.646316	589.326796	1159.635751	580.321513	**L**	***649.391939***	325.199607	632.365390	316.686333	631.381374	316.194325	**5**
13	***1306.688909***	653.848092	1288.678344	644.842810	**E**	***536.307875***	268.657576	519.281326	260.144301	518.297310	259.652293	**4**
14	***1453.757323***	727.382299	1435.746758	718.377017	**F**	***407.265282***	204.136279	390.238733	195.623004			**3**
15	***1566.841387***	783.924331	1548.830822	774.919049	**L**	260.196868	130.602072	243.170319	122.088797			**2**
16					**K**	147.112804	74.060040	130.086255	65.546765			**1**



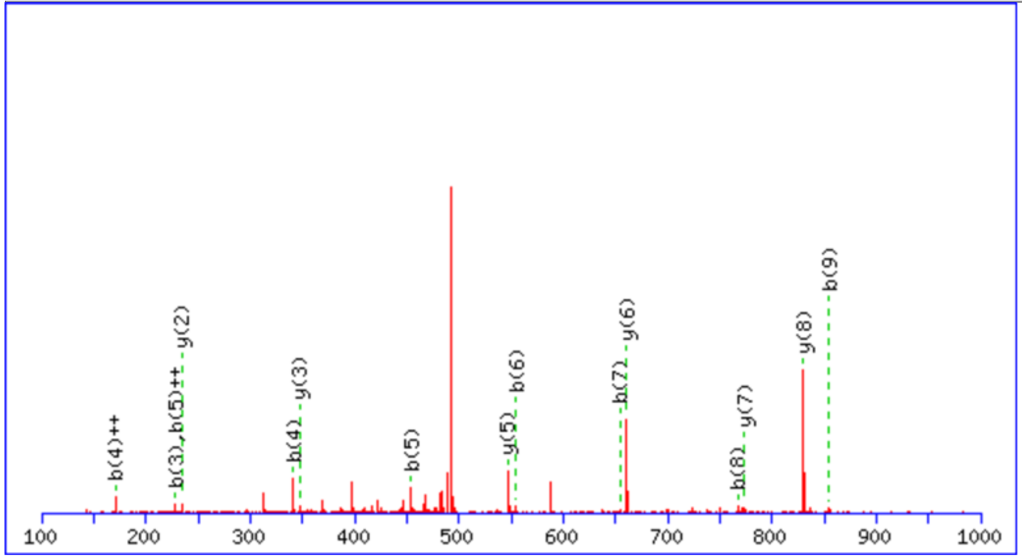
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 56 - PyD-2 **Fraction:** PyD-2

Match to Query 4208: 999.633048 from(500.823800,2+)

Title: OECHL100312_40.17372.17372.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_40.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 5.2e-005**Matches :** 16/78 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	**171.112804**			**L**	**773.513117**	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	**227.654836**			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**

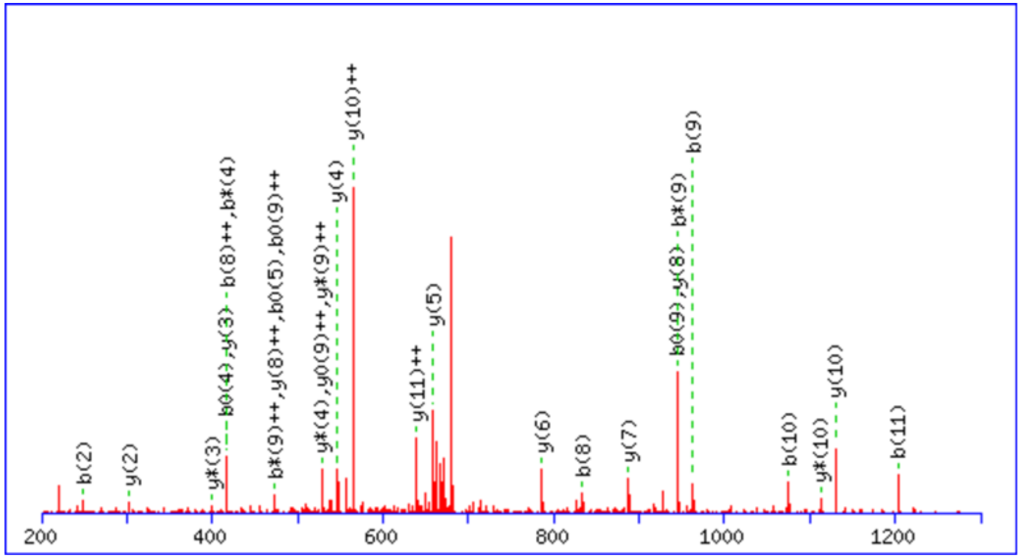


Peptide View

MS/MS Fragmentation of **TFGQGTKLEIKR**
Found in **IPI00827643**, Tax_Id=9606 Gene_Symbol=- HRV Fab 027-VL (Fragment)
Experiment: 56 - PyD-2 **Fraction:** PyD-2

Match to Query 9455: 1376.781048 from(689.397800,2+)
Title: OECHL100312_40.7976.7976.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_40.raw
Monoisotopic mass of neutral peptide Mr(calc): 1376.777588**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57
Expect: 6.9e-005**Matches :** 29/120 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	102.054955	51.531116			84.044390	42.525833	**T**							**12**
2	**249.123369**	125.065322			231.112804	116.060040	**F**	1276.737198	638.872237	1259.710649	630.358963	1258.726633	629.866955	**11**
3	306.144833	153.576054			288.134268	144.570772	**G**	***1129.668784***	565.338030	1112.642235	556.824756	1111.658219	556.332748	**10**
4	434.203411	217.605343	417.176862	209.092069	416.192846	208.600061	**Q**	1072.647320	536.827298	1055.620771	528.314024	1054.636755	527.822016	**9**
5	491.224875	246.116075	474.198326	237.602801	473.214310	237.110793	**G**	***944.588742***	472.798009	927.562193	464.284735	926.578177	463.792727	**8**
6	592.272554	296.639915	575.246005	288.126641	574.261989	287.634633	**T**	***887.567278***	444.287277	870.540729	435.774003	869.556713	435.281995	**7**
7	720.367517	360.687397	703.340968	352.174122	702.356952	351.682114	**K**	***786.519599***	393.763438	769.493050	385.250163	768.509034	384.758155	**6**
8	**833.451581**	417.229429	816.425032	408.716154	815.441016	408.224146	**L**	***658.424636***	329.715956	641.398087	321.202682	640.414071	320.710674	**5**
9	**962.494174**	481.750725	945.467625	473.237451	944.483609	472.745443	**E**	***545.340572***	273.173924	528.314023	264.660650	527.330007	264.168642	**4**
10	**1075.578238**	538.292757	1058.551689	529.779483	1057.567673	529.287475	**I**	***416.297979***	208.652627	399.271430	200.139353			**3**
11	**1203.673201**	602.340239	1186.646652	593.826964	1185.662636	593.334956	**K**	***303.213915***	152.110595	286.187366	143.597321			**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**



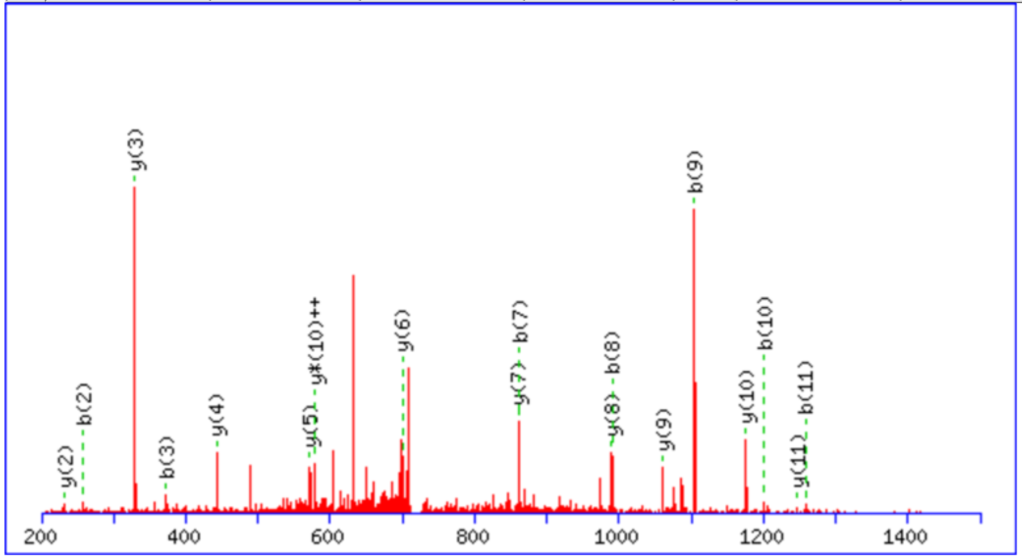
Peptide View

MS/MS Fragmentation of **WADAECEEIPGR**
Found in **IPI00027436**, Tax_Id=9606 Gene_Symbol=NGFR Tumor necrosis factor receptor superfamily member 16
Experiment: 56 - PyD-2 **Fraction:** PyD-2

Match to Query 9819: 1431.611848 from(716.813200,2+)
Title: OECHL100312_40.11208.11208.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_40.raw
Monoisotopic mass of neutral peptide Mr(calc): 1431.608856**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67
Expect: 7.2e-006**Matches :** 18/98 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	187.086589	94.046932			**W**							**12**
2	**258.123703**	129.565490			**A**	***1246.536843***	623.772060	1229.510294	615.258785	1228.526278	614.766777	**11**
3	**373.150646**	187.078961	355.140081	178.073679	**D**	***1175.499729***	588.253502	1158.473180	579.740228	1157.489164	579.248220	**10**
4	444.187760	222.597518	426.177195	213.592236	**A**	***1060.472786***	530.740031	1043.446237	522.226757	1042.462221	521.734749	**9**
5	573.230353	287.118815	555.219788	278.113532	**E**	***989.435672***	495.221474	972.409123	486.708199	971.425107	486.216191	**8**
6	733.261002	367.134139	715.250437	358.128857	**C**	***860.393079***	430.700178	843.366530	422.186903	842.382514	421.694895	**7**

7	**862.303595**	431.655436	844.293030	422.650153	**E**	***700.362430***	350.684853	683.335881	342.171578	682.351865	341.679570	**6**
8	**991.346188**	496.176732	973.335623	487.171450	**E**	***571.319837***	286.163556	554.293288	277.650282	553.309272	277.158274	**5**
9	**1104.430252**	552.718764	1086.419687	543.713482	**I**	***442.277244***	221.642260	425.250695	213.128985			**4**
10	**1201.483016**	601.245146	1183.472451	592.239864	**P**	***329.193180***	165.100228	312.166631	156.586953			**3**
11	**1258.504480**	629.755878	1240.493915	620.750596	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**



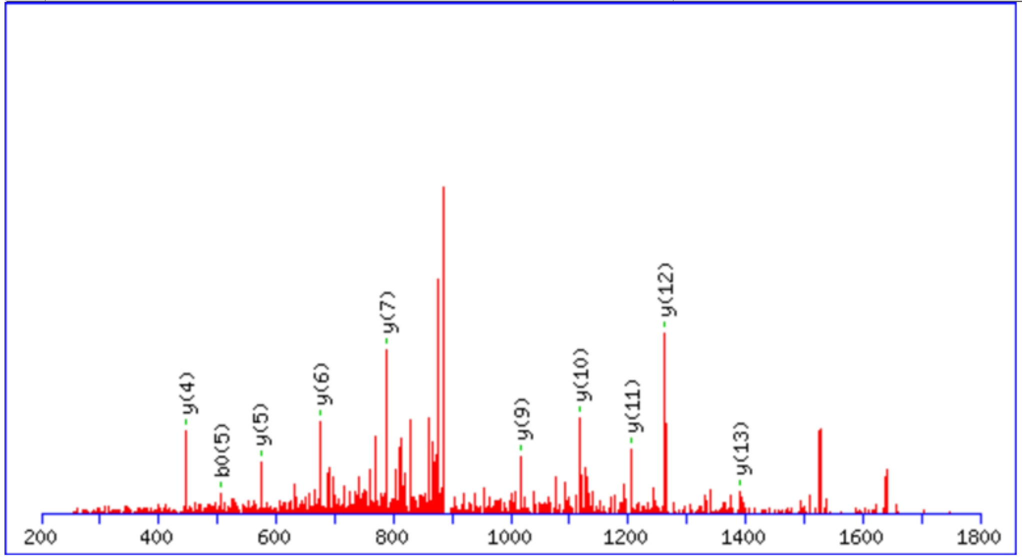
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 56 - PyD-2 **Fraction:** PyD-2

Match to Query 13723: 1784.880048 from(893.447300,2+)
Title: OECHL100312_40.7612.7612.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_40.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66
Expect: 3.5e-005**Matches :** 10/170 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	164.070605	82.538940					**Y**							**17**
2	251.102633	126.054954			233.092068	117.049672	**S**	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.909941	**16**
3	308.124097	154.565687			290.113532	145.560404	**G**	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.393928	**15**
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.883195	**14**
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.367182	**13**
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.845885	**12**
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.335153	**11**
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.819139	**10**
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.295299	**9**
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.266010	**8**
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.742171	**7**
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.200139	**6**
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.676299	**5**
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	**4**
15	1526.696909	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
16	1639.780973	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	260.196868	130.602072	243.170319	122.088797			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**

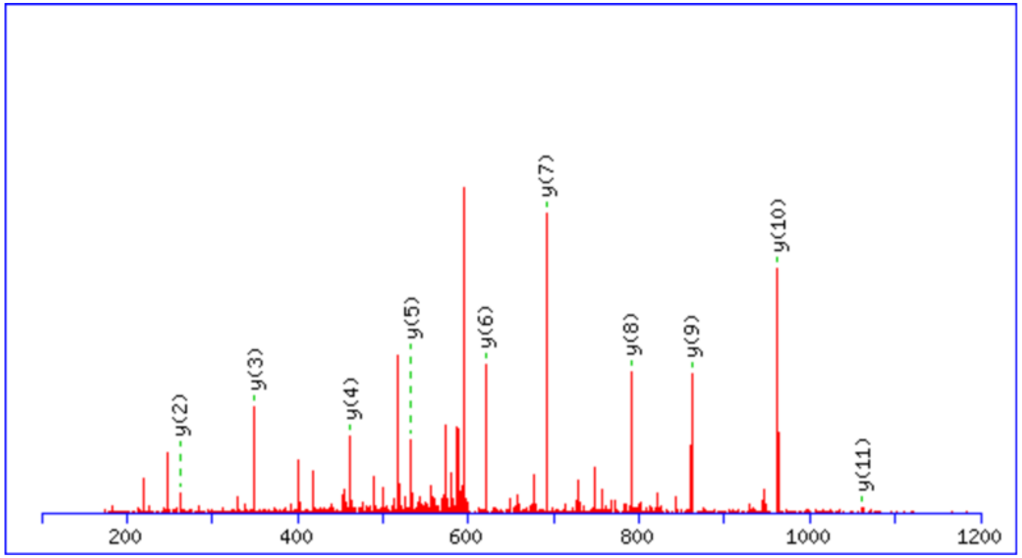


Peptide View

MS/MS Fragmentation of **MVTAVASALSSR**
Found in **IPI00220706**, Tax_Id=9606 Gene_Symbol=HBG2;HBG1 Hemoglobin subunit gamma-1
Experiment: 56 - PyD-2 **Fraction:** PyD-2

Match to Query 7196: 1207.623248 from(604.818900,2+)
Title: OECHL100312_40.10286.10286.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_40.raw
Monoisotopic mass of neutral peptide Mr(calc): 1207.623062**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: M1 :** Oxidation (M), with neutral loss 63.998285**Ions Score:** 57 **Expect:** 0.00019**Matches :** 10/104 fragment ions using 31 most intense peaks (help)

#	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y^{*}**	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	84.044391	42.525833			**M**							**12**
2	183.112805	92.060040			**V**	***1061.594949***	531.301113	1044.568400	522.787838	1043.584384	522.295830	**11**
3	284.160484	142.583880	266.149919	133.578598	**T**	***962.526535***	481.766906	945.499986	473.253631	944.515970	472.761623	**10**
4	355.197598	178.102437	337.187033	169.097155	**A**	***861.478856***	431.243066	844.452307	422.729791	843.468291	422.237783	**9**
5	454.266012	227.636644	436.255447	218.631362	**V**	***790.441742***	395.724509	773.415193	387.211234	772.431177	386.719226	**8**
6	525.303126	263.155201	507.292561	254.149919	**A**	***691.373328***	346.190302	674.346779	337.677028	673.362763	337.185020	**7**
7	612.335154	306.671215	594.324589	297.665933	**S**	***620.336214***	310.671745	603.309665	302.158471	602.325649	301.666463	**6**
8	683.372268	342.189772	665.361703	333.184489	**A**	***533.304186***	267.155731	516.277637	258.642457	515.293621	258.150449	**5**
9	796.456332	398.731804	778.445767	389.726521	**L**	***462.267072***	231.637174	445.240523	223.123899	444.256507	222.631891	**4**
10	883.488360	442.247818	865.477795	433.242535	**S**	***349.183008***	175.095142	332.156459	166.581867	331.172443	166.089859	**3**
11	970.520388	485.763832	952.509823	476.758549	**S**	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**



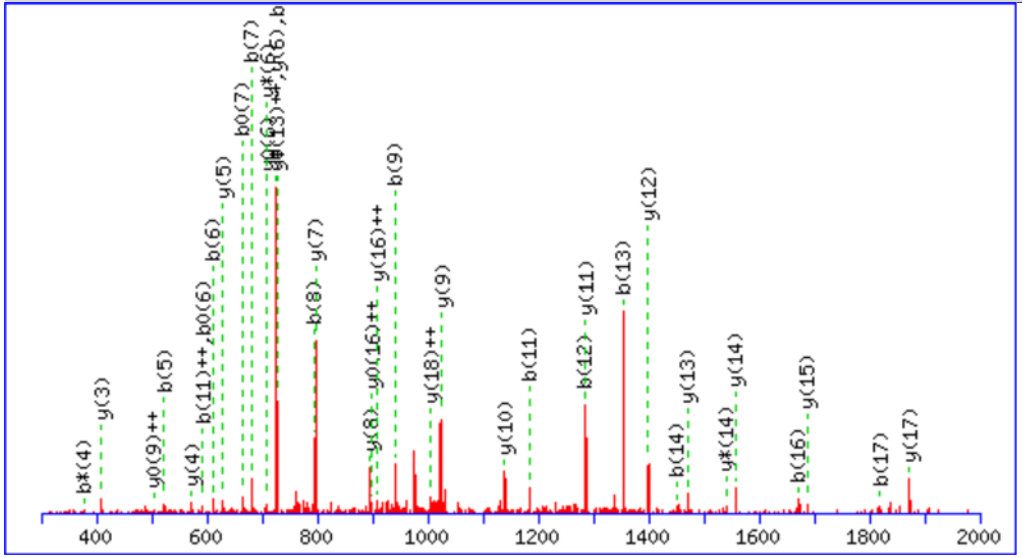
Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 15511: 2078.987448 from(1040.501000,2+)
Title: OECHL100312_38.17308.17308.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 73
Expect: 7.2e-006**Matches :** 39/200 fragment ions using 82 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							19
2	209.103302	105.055289					H	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973939	18
3	266.124766	133.566021					G	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444483	17
4	394.183344	197.595310	377.156795	189.082035			Q	1814.870790	907.939033	1797.844241	899.425759	1796.860225	898.933751	16
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	E	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904462	15
6	**610.257965**	305.632621	593.231416	297.119346	592.247400	296.627338	S	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383165	14

7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867151	**13**
8	**794.379143**	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348594	**12**
9	**941.447557**	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806562	**11**
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272355	**10**
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250892	**9**
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729595	**8**
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195388	**7**
14	**1451.691369**	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676831	**6**
15	1508.712833	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150449	**5**
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	***572.282723***	286.645000	555.256174	278.131725	554.272158	277.639717	**4**
17	**1818.844576**	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	**3**
18	1905.876604	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
19							**R**	175.118952	88.063114	158.092403	79.549840			**1**



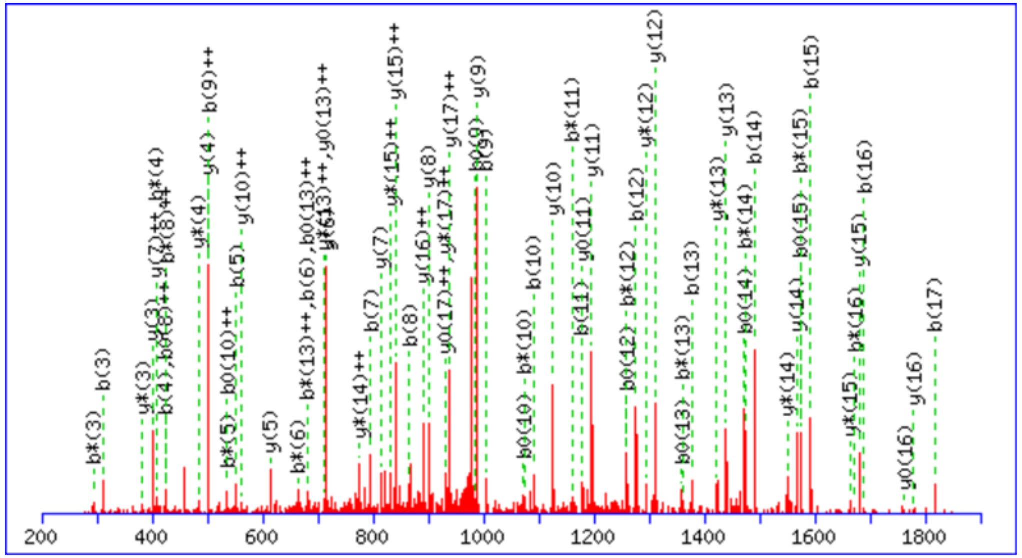
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**

Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 15050: 1990.024248 from(996.019400,2+)
Title: OECHL100312_38.10225.10225.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 2.5e-006**Matches :** 71/186 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	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	***311.171381***	156.089328	294.144832	147.576054			**V**	**1779.934789**	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	***424.255445***	212.631361	407.228896	204.118086			**L**	**1680.866375**	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	***552.314023***	276.660650	535.287474	268.147375			**Q**	**1567.782311**	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	***680.372601***	340.689939	663.346052	332.176664			**Q**	**1439.723733**	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**
7	***795.399544***	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	**1311.665155**	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	***866.436658***	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	**1196.638212**	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	***1003.495570***	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	**1125.601098**	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	***1090.527598***	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	**988.542186**	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	***1177.559626***	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	**901.510158**	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	***1276.628040***	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	**814.478130**	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	***1377.675719***	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	**715.409716**	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	***1490.759783***	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	**614.362037**	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	***1591.807462***	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	**501.277973**	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	***1688.860226***	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	**400.230294**	200.618785	383.203745	192.105510			**3**
17	***1816.918804***	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**



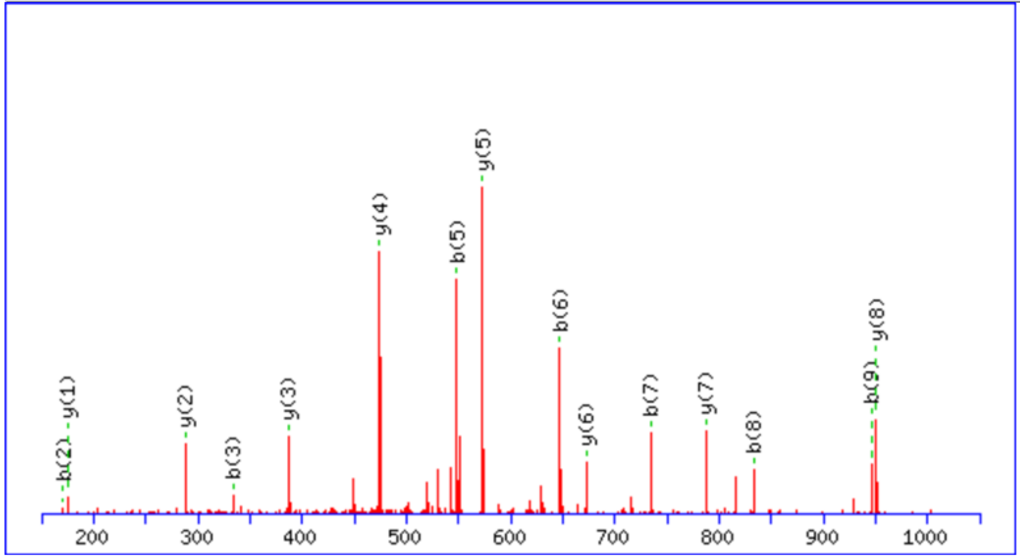
Peptide View

MS/MS Fragmentation of **GLYDVVSVLR**
Found in **IPI00796189**, Tax_Id=9606 Gene_Symbol=ICOSLG Putative uncharacterized protein ICOSLG
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 5770: 1119.628848 from(560.821700,2+)
Title: OECHL100312_38.18856.18856.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1119.628815**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 1e-006**Matches :** 15/78 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			**G**							**10**
2	**171.112804**	86.060040			**L**	1063.614622	532.310949	1046.588073	523.797675	1045.604057	523.305667	**9**
3	**334.176133**	167.591704			**Y**	***950.530558***	475.768917	933.504009	467.255642	932.519993	466.763634	**8**
4	449.203076	225.105176	431.192511	216.099894	**D**	***787.467229***	394.237253	770.440680	385.723978	769.456664	385.231970	**7**
5	**548.271490**	274.639383	530.260925	265.634101	**V**	***672.440286***	336.723781	655.413737	328.210507	654.429721	327.718499	**6**
6	**647.339904**	324.173590	629.329339	315.168308	**V**	***573.371872***	287.189574	556.345323	278.676299	555.361307	278.184291	**5**

7	**734.371932**	367.689604	716.361367	358.684322	**S**	***474.303458***	237.655367	457.276909	229.142092	456.292893	228.650084	**4**
8	**833.440346**	417.223811	815.429781	408.218528	**V**	***387.271430***	194.139353	370.244881	185.626078			**3**
9	**946.524410**	473.765843	928.513845	464.760561	**L**	***288.203016***	144.605146	271.176467	136.091871			**2**
10					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



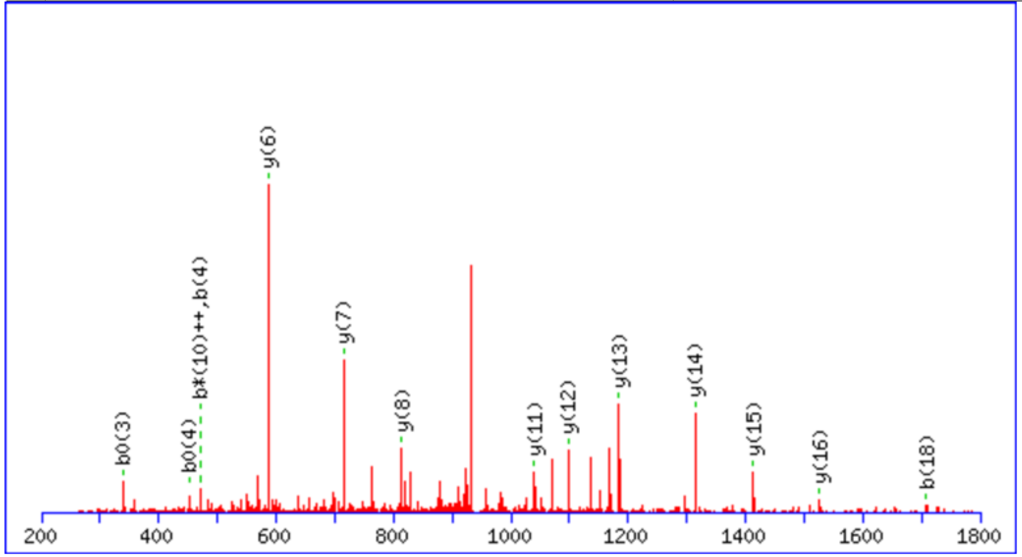
Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**
Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 14490: 1881.033848 from(941.524200,2+)
Title: OECHL100312_38.13957.13957.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 78
Expect: 9.3e-007**Matches :** 14/208 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	130.049869	65.528572			112.039304	56.523290	**E**							**19**
2	229.118283	115.062780			211.107718	106.057497	**V**	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.996686	**18**

3	357.176861	179.092069	340.150312	170.578794	339.166296	170.086786	**Q**	1653.928246	827.467761	1636.901697	818.954487	1635.917681	818.462479	**17**
4	**470.260925**	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.433190	**16**
5	569.329339	285.168308	552.302790	276.655033	551.318774	276.163025	**V**	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.891158	**15**
6	698.371932	349.689604	681.345383	341.176330	680.361367	340.684322	**E**	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.356951	**14**
7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	**S**	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.835654	**13**
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	**G**	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.319640	**12**
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	**G**	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.808908	**11**
10	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	**G**	983.599641	492.303459	966.573092	483.790184	965.589076	483.298176	**10**
11	1069.552416	535.279846	1052.525867	526.766572	1051.541851	526.274564	**L**	926.578177	463.792727	909.551628	455.279452	908.567612	454.787444	**9**
12	1168.620830	584.814053	1151.594281	576.300779	1150.610265	575.808771	**V**	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.245412	**8**
13	1296.715793	648.861535	1279.689244	640.348260	1278.705228	639.856252	**K**	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.711205	**7**
14	1393.768557	697.387917	1376.742008	688.874642	1375.757992	688.382634	**P**	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.663723	**6**
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	**G**	489.277972	245.142624	472.251423	236.629349	471.267407	236.137341	**5**
16	1507.811485	754.409381	1490.784936	745.896106	1489.800920	745.404098	**G**	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	**4**
17	1594.843513	797.925395	1577.816964	789.412120	1576.832948	788.920112	**S**	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	**3**
18	**1707.927577**	854.467427	1690.901028	845.954152	1689.917012	845.462144	**L**	288.203016	144.605146	271.176467	136.091871			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



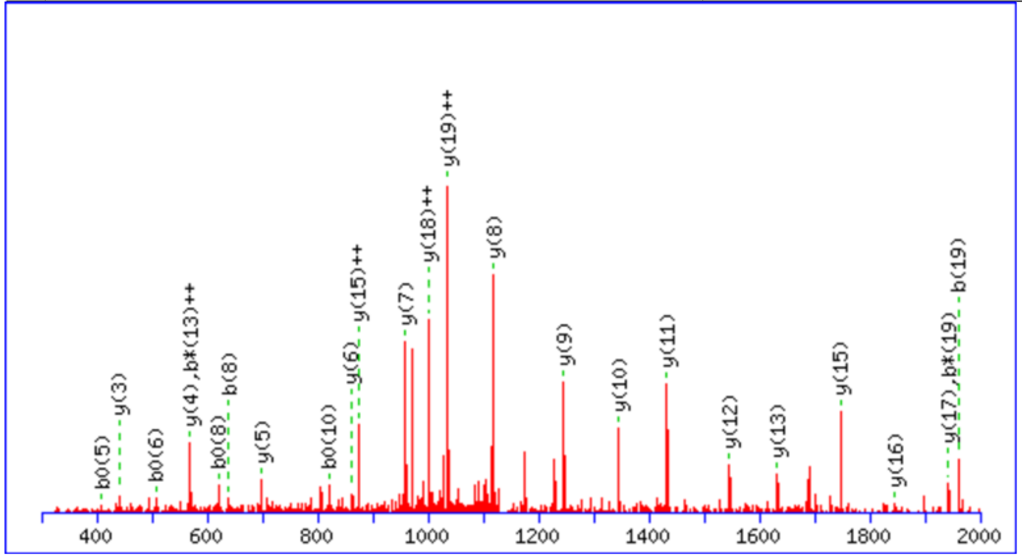
Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 16280: 2270.111448 from(1136.063000,2+)
Title: OECHL100312_38.10845.10845.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 112
Expect: 1.2e-009**Matches :** 25/212 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	102.054955	51.531116			84.044390	42.525833	**T**						
2	201.123369	101.065322			183.112804	92.060040	**V**	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400	1076.5338
3	272.160483	136.583879			254.149918	127.578597	**A**	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986	1026.9996
4	329.181947	165.094611			311.171382	156.089329	**G**	1999.965437	1000.486357	1982.938888	991.973082	1981.954872	991.4810
5	426.234711	213.620994			408.224146	204.615711	**P**	***1942.943973***	971.975625	1925.917424	963.462350	1924.933408	962.9703
6	525.303125	263.155201			507.292560	254.149918	**V**	***1845.891209***	923.449243	1828.864660	914.935968	1827.880644	914.4439
7	582.324589	291.665933			564.314024	282.660650	**G**	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230	864.9097
8	**639.346053**	320.176665			621.335488	311.171382	**G**	1689.801331	845.404304	1672.774782	836.891029	1671.790766	836.3990
9	726.378081	363.692679			708.367516	354.687396	**S**	***1632.779867***	816.893572	1615.753318	808.380297	1614.769302	807.8882
10	839.462145	420.234711			821.451580	411.229428	**L**	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274	764.3722
11	926.494173	463.750725			908.483608	454.745442	**S**	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210	707.8302
12	1025.562587	513.284932			1007.552022	504.279649	**V**	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182	664.3142
13	1153.621165	577.314221	1136.594616	568.800946	1135.610600	568.308938	**Q**	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768	614.7800
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	**C**	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190	550.7507
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	**P**	***958.474106***	479.740691	941.447557	471.227417	940.463541	470.7354
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	**Y**	***861.421342***	431.214309	844.394793	422.701035	843.410777	422.2090
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	**E**	***698.358013***	349.682645	681.331464	341.169370	680.347448	340.6773
18	1830.905463	915.956370	1813.878914	907.443095	1812.894898	906.951087	**K**	***569.315420***	285.161348	552.288871	276.648074	551.304855	276.1560
19	**1959.948056**	980.477666	1942.921507	971.964392	1941.937491	971.472384	**E**	***441.220457***	221.113867	424.193908	212.600592	423.209892	212.1085

20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	**H**	312.177864	156.592570	295.151315	148.079295		
21							**R**	175.118952	88.063114	158.092403	79.549839		



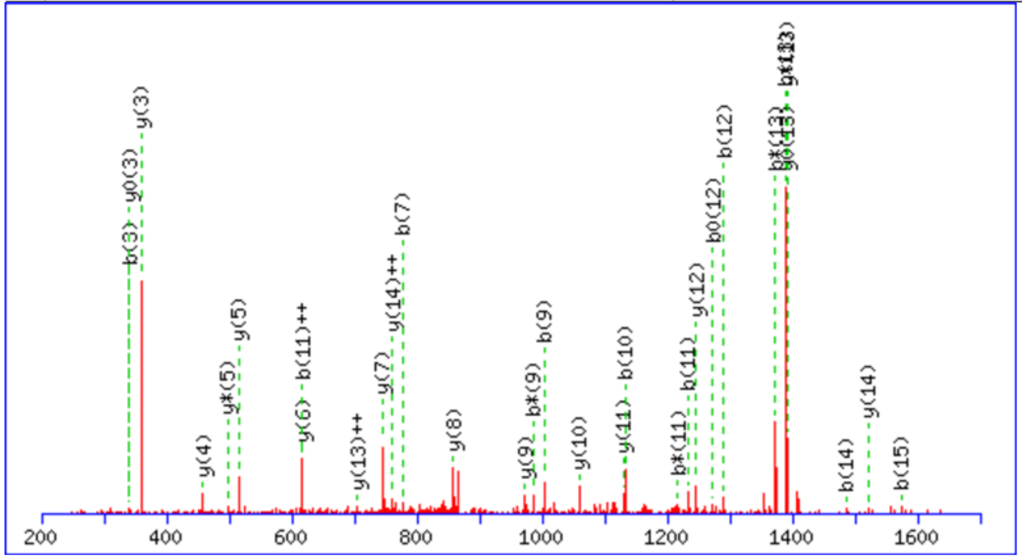
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 13534: 1746.916848 from(874.465700,2+)
Title: OECHL100312_38.17241.17241.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 74
Expect: 4.4e-006**Matches :** 31/156 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	***340.259468***	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**

5	618.349740	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	689.386854	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	***776.418882***	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**

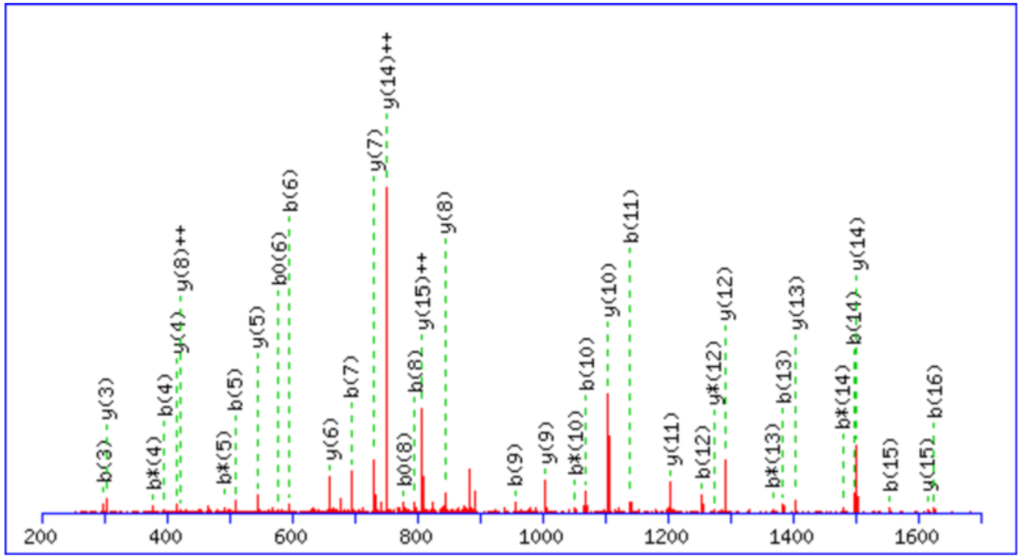


Peptide View

MS/MS Fragmentation of **GQLPISVTCIADEIGAR**
Found in **IPI00240345**, Tax_Id=9606 Gene_Symbol=CLEC14A C-type lectin domain family 14 member A
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 13931: 1798.926048 from(900.470300,2+)
Title: OECHL100312_38.20003.20003.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1798.924728**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 82
Expect: 8.5e-007**Matches :** 38/172 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					**G**							**17**
2	186.087318	93.547297	169.060769	85.034023			**Q**	1742.910548	871.958912	1725.883999	863.445638	1724.899983	862.953630	**16**
3	***299.171382***	150.089329	282.144833	141.576055			**L**	**1614.851970**	807.929623	1597.825421	799.416349	1596.841405	798.924340	**15**
4	***396.224146***	198.615711	379.197597	190.102436			**P**	**1501.767906**	751.387591	1484.741357	742.874317	1483.757341	742.382309	**14**
5	***509.308210***	255.157743	492.281661	246.644468			**I**	**1404.715142**	702.861209	1387.688593	694.347935	1386.704577	693.855927	**13**
6	***596.340238***	298.673757	579.313689	290.160483	578.329673	289.668475	**S**	**1291.631078**	646.319177	1274.604529	637.805903	1273.620513	637.313895	**12**
7	***695.408652***	348.207964	678.382103	339.694689	677.398087	339.202681	**V**	**1204.599050**	602.803163	1187.572501	594.289889	1186.588485	593.797881	**11**
8	***796.456331***	398.731804	779.429782	390.218529	778.445766	389.726521	**T**	**1105.530636**	553.268956	1088.504087	544.755682	1087.520071	544.263674	**10**
9	***956.486980***	478.747128	939.460431	470.233854	938.476415	469.741846	**C**	**1004.482957**	502.745117	987.456408	494.231842	986.472392	493.739834	**9**
10	***1069.571044***	535.289160	1052.544495	526.775886	1051.560479	526.283878	**I**	**844.452308**	422.729792	827.425759	414.216518	826.441743	413.724510	**8**
11	***1140.608158***	570.807717	1123.581609	562.294443	1122.597593	561.802435	**A**	**731.368244**	366.187760	714.341695	357.674486	713.357679	357.182478	**7**
12	***1255.635101***	628.321189	1238.608552	619.807914	1237.624536	619.315906	**D**	**660.331130**	330.669203	643.304581	322.155929	642.320565	321.663921	**6**
13	***1384.677694***	692.842485	1367.651145	684.329211	1366.667129	683.837203	**E**	**545.304187**	273.155732	528.277638	264.642457	527.293622	264.150449	**5**
14	***1497.761758***	749.384517	1480.735209	740.871243	1479.751193	740.379235	**I**	**416.261594**	208.634435	399.235045	200.121160			**4**
15	***1554.783222***	777.895249	1537.756673	769.381975	1536.772657	768.889967	**G**	**303.177530**	152.092403	286.150981	143.579128			**3**
16	***1625.820336***	813.413806	1608.793787	804.900532	1607.809771	804.408524	**A**	246.156066	123.581671	229.129517	115.068396			**2**
17							**R**	175.118952	88.063114	158.092403	79.549839			**1**



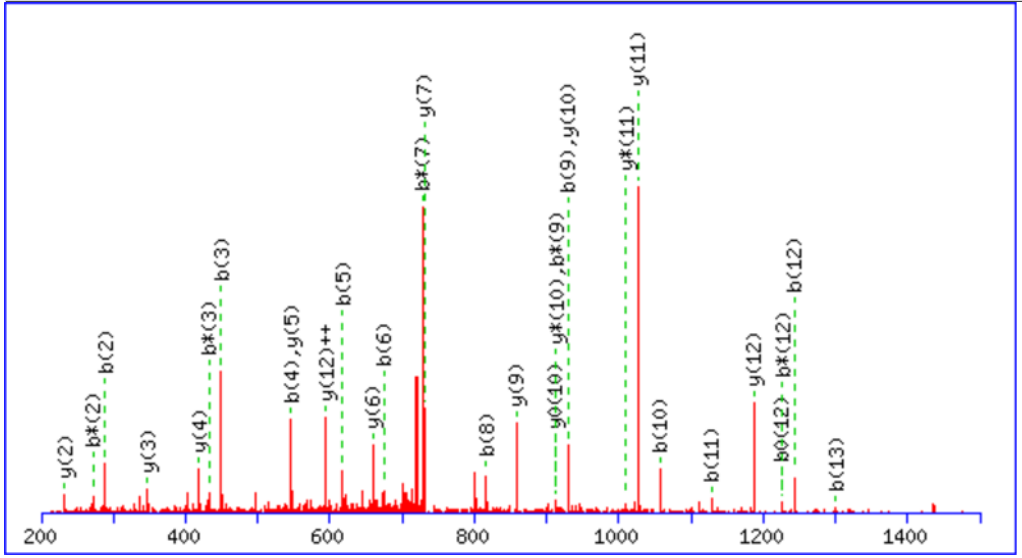
Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 10785: 1473.645648 from(737.830100,2+)
Title: OECHL100312_38.7858.7858.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63
Expect: 2.2e-005**Matches :** 31/128 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	161.037925	81.022600					**C**							**14**
2	***289.096503***	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.809312	**13**
3	***449.127152***	225.067214	432.100603	216.553940			**C**	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.780023	**12**
4	***546.179916***	273.593596	529.153367	265.080322			**P**	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.764698	**11**
5	***617.217030***	309.112153	600.190481	300.598879			**A**	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.238316	**10**
6	***674.238494***	337.622885	657.211945	329.109611			**G**	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.719759	**9**

7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
8	***816.312722***	408.659999	799.286173	400.146725			**A**	**730.384229**	365.695753	713.357680	357.182478	712.373664	356.690470	**7**
9	***929.396786***	465.202031	912.370237	456.688757			**L**	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.171913	**6**
10	***1057.455364***	529.231320	1040.428815	520.718046			**Q**	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.629881	**5**
11	***1128.492478***	564.749877	1111.465929	556.236603			**A**	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.600592	**4**
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	**347.167359**	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
13	***1300.540885***	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	**232.140416**	116.573846	215.113867	108.060571			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



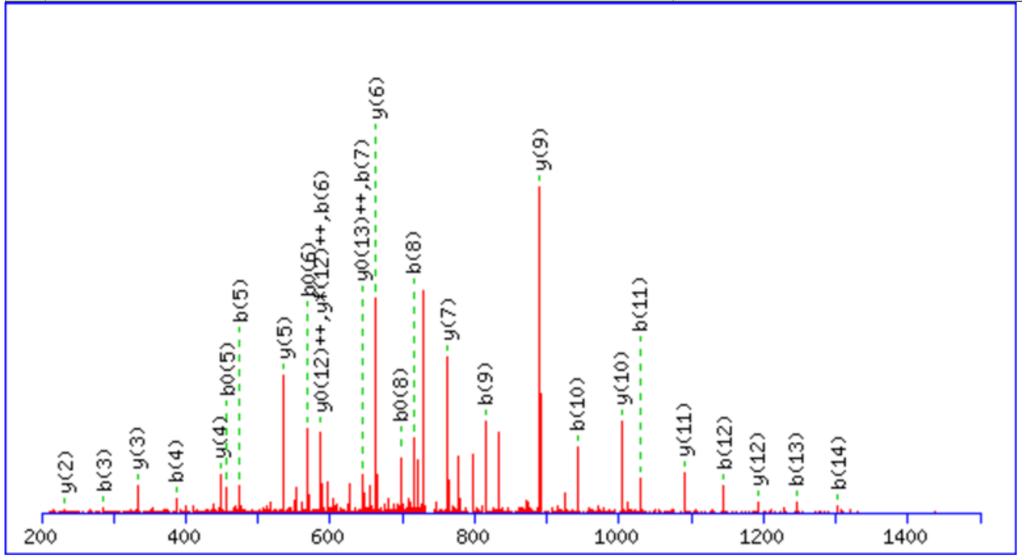
Peptide View

MS/MS Fragmentation of **GLDTSLGAVQSDTGR**
Found in **IPI00289931**, Tax_Id=9606 Gene_Symbol=MADCAM1 MADCAM1 protein
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 10814: 1475.722848 from(738.868700,2+)
Title: OECHL100312_38.11659.11659.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1475.721619**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 102

Expect: 9.8e-009**Matches :** 28/142 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							15
2	171.112804	86.060040					L	1419.707414	710.357345	1402.680865	701.844071	1401.696849	701.352063	14
3	***286.139747***	143.573512			268.129182	134.568229	D	1306.623350	653.815313	1289.596801	645.302039	1288.612785	644.810031	13
4	***387.187426***	194.097351			369.176861	185.092069	T	**1191.596407**	596.301842	1174.569858	587.788567	1173.585842	587.296559	12
5	***474.219454***	237.613365			456.208889	228.608082	S	**1090.548728**	545.778002	1073.522179	537.264728	1072.538163	536.772719	11
6	***587.303518***	294.155397			569.292953	285.150115	L	**1003.516700**	502.261988	986.490151	493.748714	985.506135	493.256706	10
7	***644.324982***	322.666129			626.314417	313.660847	G	**890.432636**	445.719956	873.406087	437.206682	872.422071	436.714674	9
8	***715.362096***	358.184686			697.351531	349.179404	A	833.411172	417.209224	816.384623	408.695950	815.400607	408.203942	8
9	***814.430510***	407.718893			796.419945	398.713611	V	**762.374058**	381.690667	745.347509	373.177393	744.363493	372.685385	7
10	***942.489088***	471.748182	925.462539	463.234908	924.478523	462.742900	Q	**663.305644**	332.156460	646.279095	323.643186	645.295079	323.151178	6
11	***1029.521116***	515.264196	1012.494567	506.750922	1011.510551	506.258914	S	**535.247066**	268.127171	518.220517	259.613897	517.236501	259.121889	5
12	***1144.548059***	572.777668	1127.521510	564.264393	1126.537494	563.772385	D	**448.215038**	224.611157	431.188489	216.097882	430.204473	215.605874	4
13	***1245.595738***	623.301507	1228.569189	614.788233	1227.585173	614.296225	T	**333.188095**	167.097685	316.161546	158.584411	315.177530	158.092403	3
14	***1302.617202***	651.812239	1285.590653	643.298965	1284.606637	642.806957	G	**232.140416**	116.573846	215.113867	108.060571			2
15							R	175.118952	88.063114	158.092403	79.549839			1

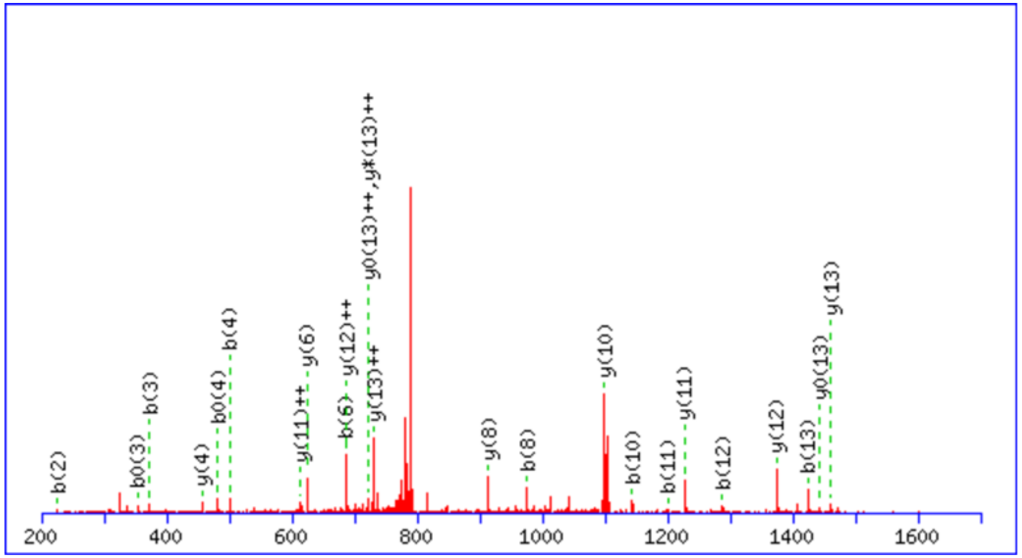


Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 12079: 1597.708248 from(799.861400,2+)
Title: OECHL100312_38.2397.2397.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 0.0001**Matches :** 24/144 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					**H**							**14**
2	***225.098216***	113.052746			207.087651	104.047463	**S**	**1461.653938**	731.330607	1444.627389	722.817333	1443.643373	722.325325	**13**
3	***372.166630***	186.586953			354.156065	177.581671	**F**	**1374.621910**	687.814593	1357.595361	679.301319	1356.611345	678.809311	**12**
4	***500.261593***	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	**1227.553496**	614.280386	1210.526947	605.767112	1209.542931	605.275104	**11**
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	**1099.458533**	550.232905	1082.431984	541.719630	1081.447968	541.227622	**10**
6	***686.325650***	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	1042.437069	521.722173	1025.410520	513.208898	1024.426504	512.716890	**9**
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	**913.394476**	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	***975.398892***	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	784.351883	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	**624.321234**	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	***1143.488770***	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	527.268470	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	***1200.510234***	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	**456.231356**	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	***1287.542262***	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	399.209892	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	***1424.601174***	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	312.177864	156.592570	295.151315	148.079295			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



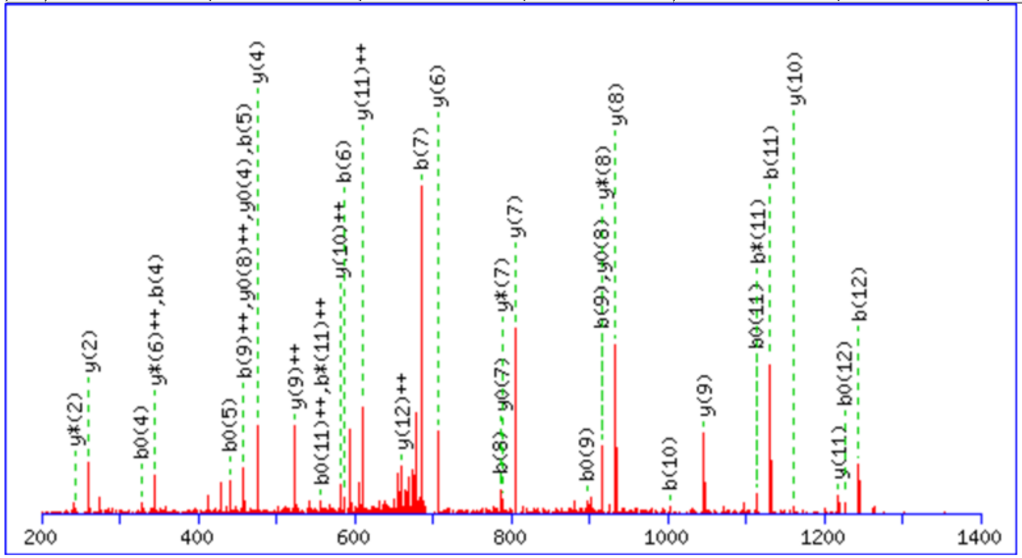
Peptide View

MS/MS Fragmentation of **ATGDIKVTESEIK**
Found in **IPI00302614**, Tax_Id=9606 Gene_Symbol=VTCN1 V-set domain containing T cell activation inhibitor 1
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 9928: 1389.735048 from(695.874800,2+)
Title: OECHL100312_38.8572.8572.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1389.735107**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 7.7e-005**Matches :** 38/128 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**13**
2	173.092069	87.049672			155.081504	78.044390	**T**	1319.705288	660.356282	1302.678739	651.843008	1301.694723	651.350999	**12**
3	230.113533	115.560404			212.102968	106.555122	**G**	***1218.657609***	609.832442	1201.631060	601.319168	1200.647044	600.827160	**11**
4	***345.140476***	173.073876			327.129911	164.068593	**D**	***1161.636145***	581.321710	1144.609596	572.808436	1143.625580	572.316428	**10**
5	***458.224540***	229.615908			440.213975	220.610626	**I**	***1046.609202***	523.808239	1029.582653	515.294964	1028.598637	514.802956	**9**
6	***586.319503***	293.663390	569.292954	285.150115	568.308938	284.658107	**K**	***933.525138***	467.266207	916.498589	458.752932	915.514573	458.260924	**8**

7	***685.387917***	343.197597	668.361368	334.684322	667.377352	334.192314	**V**	***805.430175***	403.218725	788.403626	394.705451	787.419610	394.213443	**7**
8	***786.435596***	393.721436	769.409047	385.208162	768.425031	384.716154	**T**	***706.361761***	353.684518	689.335212	345.171244	688.351196	344.679236	**6**
9	***915.478189***	458.242733	898.451640	449.729458	897.467624	449.237450	**E**	605.314082	303.160679	588.287533	294.647404	587.303517	294.155396	**5**
10	***1002.510217***	501.758747	985.483668	493.245472	984.499652	492.753464	**S**	***476.271489***	238.639382	459.244940	230.126108	458.260924	229.634100	**4**
11	***1131.552810***	566.280043	1114.526261	557.766769	1113.542245	557.274760	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
12	***1244.636874***	622.822075	1227.610325	614.308800	1226.626309	613.816792	**I**	***260.196868***	130.602072	243.170319	122.088797			**2**
13							**K**	147.112804	74.060040	130.086255	65.546765			**1**

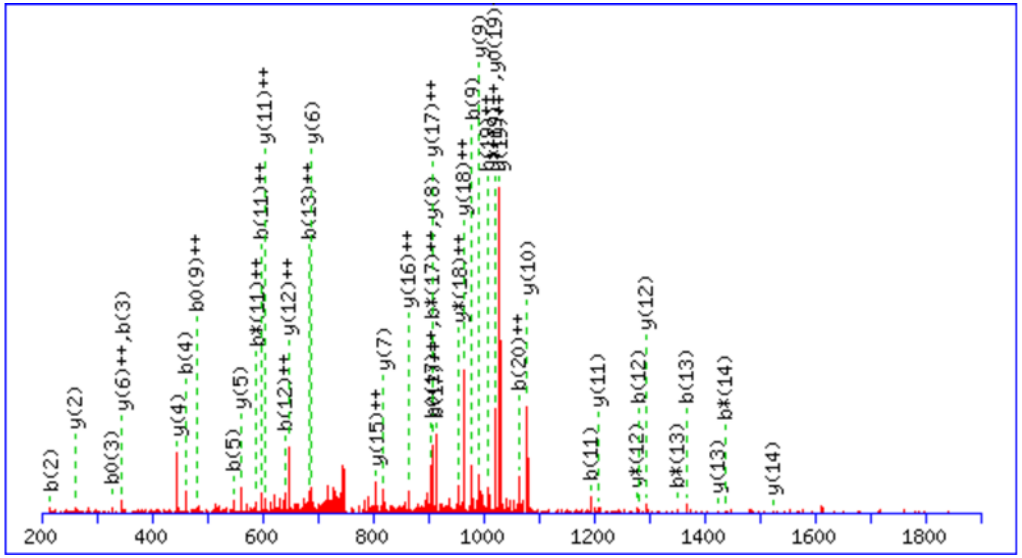


Peptide View

MS/MS Fragmentation of **SKEDSNSTESKSSSEEDGQLK**
Found in **IPI00012734**, Tax_Id=9606 Gene_Symbol=DMP1 Isoform 1 of Dentin matrix acidic phosphoprotein 1
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 16287: 2271.000672 from(758.007500,3+)
Title: OECHL100312_38.2390.2390.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.998581**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00074**Matches :** 45/230 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	88.039304	44.523290			70.028739	35.518008	**S**						
2	**216.134267**	108.570771	199.107718	100.057497	198.123702	99.565489	**K**	2184.973868	1092.990572	2167.947319	1084.477297	2166.963303	1083.9852
3	**345.176860**	173.092068	328.150311	164.578793	327.166295	164.086785	**E**	2056.878905	1028.943090	2039.852356	1020.429816	2038.868340	1019.9378
4	**460.203803**	230.605539	443.177254	222.092265	442.193238	221.600257	**D**	1927.836312	964.421794	1910.809763	955.908520	1909.825747	955.4165
5	**547.235831**	274.121554	530.209282	265.608279	529.225266	265.116271	**S**	1812.809369	906.908323	1795.782820	898.395048	1794.798804	897.9030
6	661.278758	331.143017	644.252209	322.629743	643.268193	322.137735	**N**	1725.777341	863.392309	1708.750792	854.879034	1707.766776	854.3870
7	748.310786	374.659031	731.284237	366.145757	730.300221	365.653749	**S**	1611.734414	806.370845	1594.707865	797.857571	1593.723849	797.3655
8	849.358465	425.182871	832.331916	416.669596	831.347900	416.177588	**T**	***1524.702386***	762.854831	1507.675837	754.341557	1506.691821	753.8495
9	**978.401058**	489.704167	961.374509	481.190893	960.390493	480.698885	**E**	***1423.654707***	712.330992	1406.628158	703.817717	1405.644142	703.3257
10	1065.433086	533.220181	1048.406537	524.706907	1047.422521	524.214899	**S**	***1294.612114***	647.809695	1277.585565	639.296421	1276.601549	638.8044
11	**1193.528049**	**597.267663**	1176.501500	588.754388	1175.517484	588.262380	**K**	***1207.580086***	604.293681	1190.553537	595.780407	1189.569521	595.2883
12	**1280.560077**	**640.783677**	1263.533528	632.270402	1262.549512	631.778394	**S**	***1079.485123***	540.246200	1062.458574	531.732925	1061.474558	531.2409
13	**1367.592105**	**684.299691**	1350.565556	675.786416	1349.581540	675.294408	**S**	***992.453095***	496.730186	975.426546	488.216911	974.442530	487.7249
14	1454.624133	727.815705	1437.597584	719.302430	1436.613568	718.810422	**S**	***905.421067***	453.214172	888.394518	444.700897	887.410502	444.2088
15	1583.666726	792.337001	1566.640177	783.823727	1565.656161	783.331719	**E**	***818.389039***	409.698158	801.362490	401.184883	800.378474	400.6928
16	1712.709319	856.858298	1695.682770	848.345023	1694.698754	847.853015	**E**	***689.346446***	345.176861	672.319897	336.663587	671.335881	336.1715
17	1827.736262	**914.371769**	1810.709713	905.858495	1809.725697	905.366487	**D**	***560.303853***	280.655565	543.277304	272.142290	542.293288	271.6502
18	1884.757726	942.882501	1867.731177	934.369227	1866.747161	933.877219	**G**	***445.276910***	223.142093	428.250361	214.628818		
19	2012.816304	**1006.911790**	1995.789755	998.398516	1994.805739	997.906508	**Q**	388.255446	194.631361	371.228897	186.118087		
20	2125.900368	**1063.453822**	2108.873819	1054.940547	2107.889803	1054.448539	**L**	***260.196868***	130.602072	243.170319	122.088798		
21							**K**	147.112804	74.060040	130.086255	65.546765		



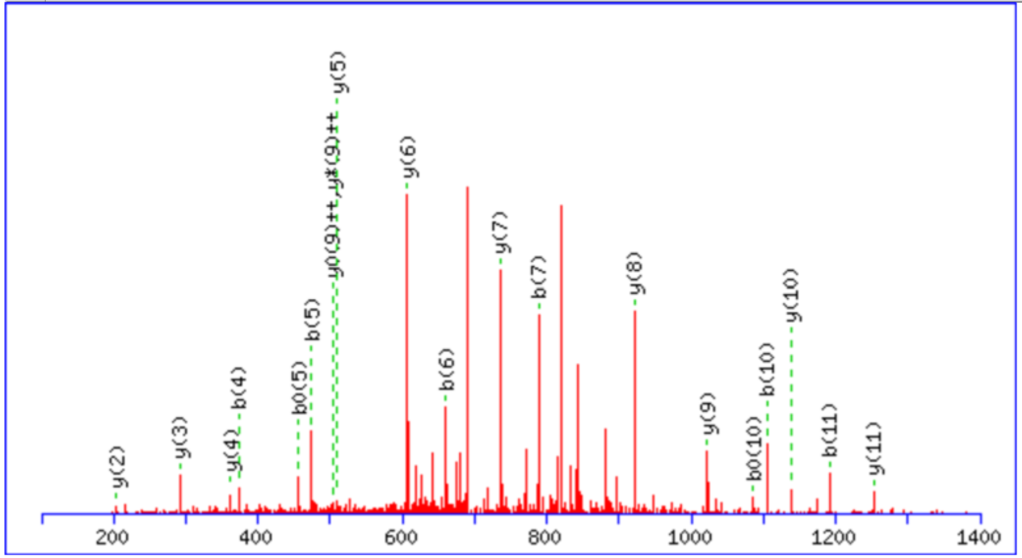
Peptide View

MS/MS Fragmentation of **AADDTWEPFASGK**
Found in **IPI00022432**, Tax_Id=9606 Gene_Symbol=TTR Transthyretin
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 9952: 1393.616248 from(697.815400,2+)
Title: OECHL100312_38.15347.15347.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1393.615005**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70
Expect: 6e-006**Matches :** 20/112 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**13**
2	143.081504	72.044390			**A**	1323.585173	662.296225	1306.558624	653.782950	1305.574608	653.290942	**12**
3	258.108447	129.557862	240.097882	120.552579	**D**	***1252.548059***	626.777668	1235.521510	618.264393	1234.537494	617.772385	**11**
4	**373.135390**	187.071333	355.124825	178.066051	**D**	***1137.521116***	569.264196	1120.494567	560.750922	1119.510551	560.258914	**10**
5	**474.183069**	237.595173	456.172504	228.589890	**T**	***1022.494173***	511.750725	1005.467624	503.237450	1004.483608	502.745442	**9**
6	**660.262382**	330.634829	642.251817	321.629547	**W**	***921.446494***	461.226885	904.419945	452.713611	903.435929	452.221603	**8**

7	**789.304975**	395.156126	771.294410	386.150843	**E**	***735.367181***	368.187229	718.340632	359.673954	717.356616	359.181946	**7**
8	886.357739	443.682508	868.347174	434.677225	**P**	***606.324588***	303.665932	589.298039	295.152658	588.314023	294.660650	**6**
9	1033.426153	517.216715	1015.415588	508.211432	**F**	***509.271824***	255.139550	492.245275	246.626275	491.261259	246.134267	**5**
10	**1104.463267**	552.735272	1086.452702	543.729989	**A**	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	**4**
11	**1191.495295**	596.251286	1173.484730	587.246003	**S**	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	**3**
12	1248.516759	624.762018	1230.506194	615.756735	**G**	***204.134268***	102.570772	187.107719	94.057497			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**

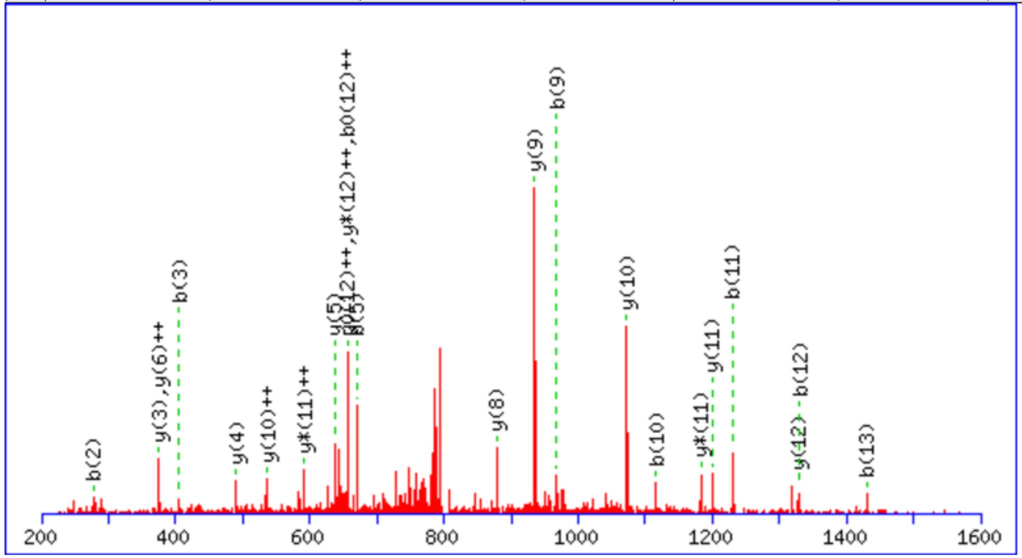


Peptide View

MS/MS Fragmentation of **LYQQHGAGLFDVTR**
Found in **IPI00554538**, Tax_Id=9606 Gene_Symbol=TPP1 Putative uncharacterized protein TPP1
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 12136: 1603.810848 from(802.912700,2+)
Title: OECHL100312_38.14002.14002.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1603.810699**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.0013**Matches :** 23/130 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	114.091340	57.549308					**L**							**14**
2	***277.154669***	139.080973					**Y**	1491.733905	746.370591	1474.707356	737.857316	1473.723340	737.365308	**13**
3	***405.213247***	203.110262	388.186698	194.596987			**Q**	***1328.670576***	664.838926	1311.644027	656.325652	1310.660011	655.833644	**12**
4	533.271825	267.139551	516.245276	258.626276			**Q**	***1200.611998***	600.809637	1183.585449	592.296363	1182.601433	591.804355	**11**
5	***670.330737***	335.669007	653.304188	327.155732			**H**	***1072.553420***	536.780348	1055.526871	528.267074	1054.542855	527.775066	**10**
6	727.352201	364.179739	710.325652	355.666464			**G**	***935.494508***	468.250892	918.467959	459.737618	917.483943	459.245610	**9**
7	798.389315	399.698296	781.362766	391.185021			**A**	***878.473044***	439.740160	861.446495	431.226886	860.462479	430.734878	**8**
8	855.410779	428.209028	838.384230	419.695753			**G**	807.435930	404.221603	790.409381	395.708329	789.425365	395.216321	**7**
9	***968.494843***	484.751060	951.468294	476.237785			**L**	750.414466	375.710871	733.387917	367.197597	732.403901	366.705589	**6**
10	***1115.563257***	558.285267	1098.536708	549.771992			**F**	***637.330402***	319.168839	620.303853	310.655565	619.319837	310.163557	**5**
11	***1230.590200***	615.798738	1213.563651	607.285464	1212.579635	606.793456	**D**	***490.261988***	245.634632	473.235439	237.121358	472.251423	236.629350	**4**
12	***1329.658614***	665.332945	1312.632065	656.819671	1311.648049	656.327663	**V**	***375.235045***	188.121161	358.208496	179.607886	357.224480	179.115878	**3**
13	***1430.706293***	715.856785	1413.679744	707.343510	1412.695728	706.851502	**T**	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**

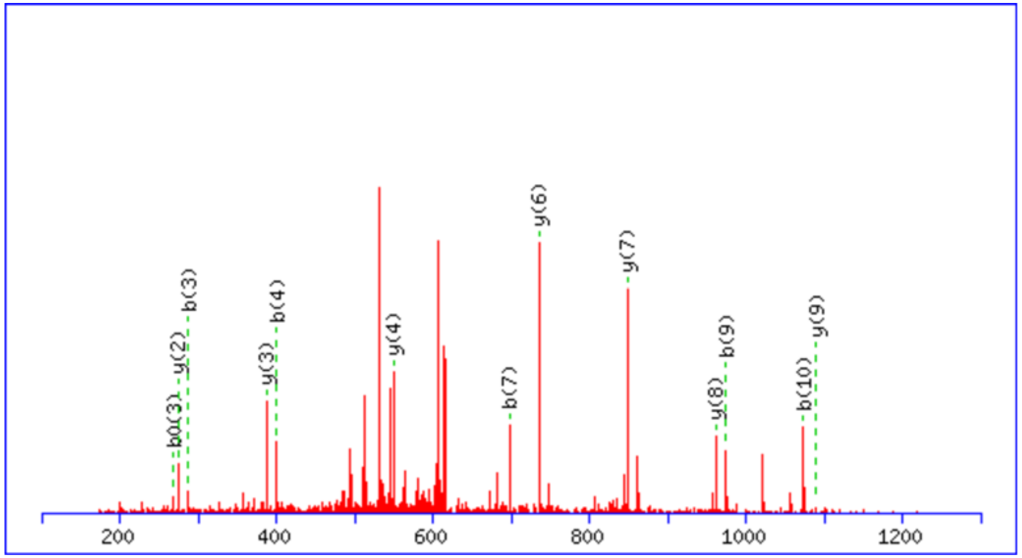


Peptide View

MS/MS Fragmentation of **ASQILNAYLVR**
Found in **IPI00289920**, Tax_Id=9606 Gene_Symbol=UPK3A Isoform 1 of Uroplakin-3a
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 8252: 1246.702848 from(624.358700,2+)
Title: OECHL100312_38.16268.16268.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1246.703339**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00036**Matches :** 13/96 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	72.044390	36.525833					**A**							**11**
2	159.076418	80.041847			141.065853	71.036564	**S**	1176.673534	588.840405	1159.646985	580.327131	1158.662969	579.835123	**10**
3	**287.134996**	144.071136	270.108447	135.557862	269.124431	135.065854	**Q**	***1089.641506***	545.324391	1072.614957	536.811117			**9**
4	**400.219060**	200.613168	383.192511	192.099894	382.208495	191.607886	**I**	***961.582928***	481.295102	944.556379	472.781828			**8**
5	513.303124	257.155200	496.276575	248.641926	495.292559	248.149918	**L**	***848.498864***	424.753070	831.472315	416.239795			**7**
6	627.346051	314.176664	610.319502	305.663389	609.335486	305.171381	**N**	***735.414800***	368.211038	718.388251	359.697764			**6**
7	**698.383165**	349.695221	681.356616	341.181946	680.372600	340.689938	**A**	621.371873	311.189575	604.345324	302.676300			**5**
8	861.446494	431.226885	844.419945	422.713611	843.435929	422.221603	**Y**	***550.334759***	275.671018	533.308210	267.157743			**4**
9	**974.530558**	487.768917	957.504009	479.255643	956.519993	478.763635	**L**	***387.271430***	194.139353	370.244881	185.626078			**3**
10	**1073.598972**	537.303124	1056.572423	528.789850	1055.588407	528.297842	**V**	***274.187366***	137.597321	257.160817	129.084046			**2**
11							**R**	175.118952	88.063114	158.092403	79.549839			**1**



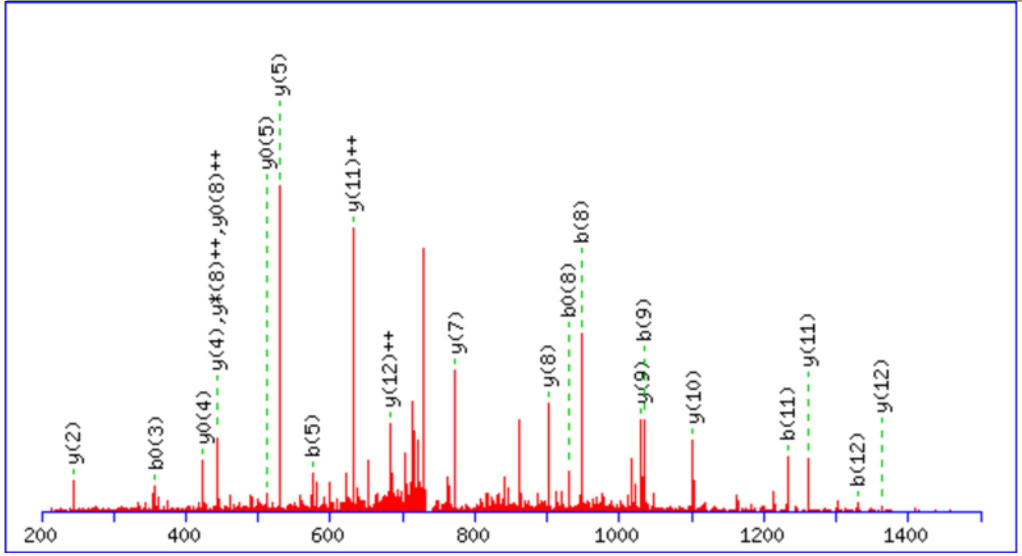
Peptide View

MS/MS Fragmentation of **ITCAEEGWSPTPK**
Found in **IPI00006154**, Tax_Id=9606 Gene_Symbol=CFHR2 Isoform Long of Complement factor H-related protein 2
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 10803: 1474.676648 from(738.345600,2+)
Title: OECHL100312_38.10602.10602.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1474.676224**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 0.00024**Matches :** 22/114 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							13
2	215.139019	108.073147	197.128454	99.067865	T	***1362.599444***	681.803360	1345.572895	673.290086	1344.588879	672.798078	12
3	375.169668	188.088472	357.159103	179.083190	C	***1261.551765***	631.279521	1244.525216	622.766246	1243.541200	622.274238	11
4	446.206782	223.607029	428.196217	214.601747	A	***1101.521116***	551.264196	1084.494567	542.750922	1083.510551	542.258914	10
5	**575.249375**	288.128326	557.238810	279.123043	E	***1030.484002***	515.745639	1013.457453	507.232365	1012.473437	506.740357	9
6	704.291968	352.649622	686.281403	343.644340	E	***901.441409***	451.224343	884.414860	442.711068	883.430844	442.219060	8

7	761.313432	381.160354	743.302867	372.155072	**G**	***772.398816***	386.703046	755.372267	378.189772	754.388251	377.697764	**7**
8	**947.392745**	474.200011	929.382180	465.194728	**W**	715.377352	358.192314	698.350803	349.679040	697.366787	349.187032	**6**
9	**1034.424773**	517.716025	1016.414208	508.710742	**S**	***529.298039***	265.152658	512.271490	256.639383	511.287474	256.147375	**5**
10	1131.477537	566.242407	1113.466972	557.237124	**P**	***442.266011***	221.636644	425.239462	213.123369	424.255446	212.631361	**4**
11	**1232.525216**	616.766246	1214.514651	607.760964	**T**	345.213247	173.110262	328.186698	164.596987	327.202682	164.104979	**3**
12	**1329.577980**	665.292628	1311.567415	656.287346	**P**	***244.165568***	122.586422	227.139019	114.073148			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**

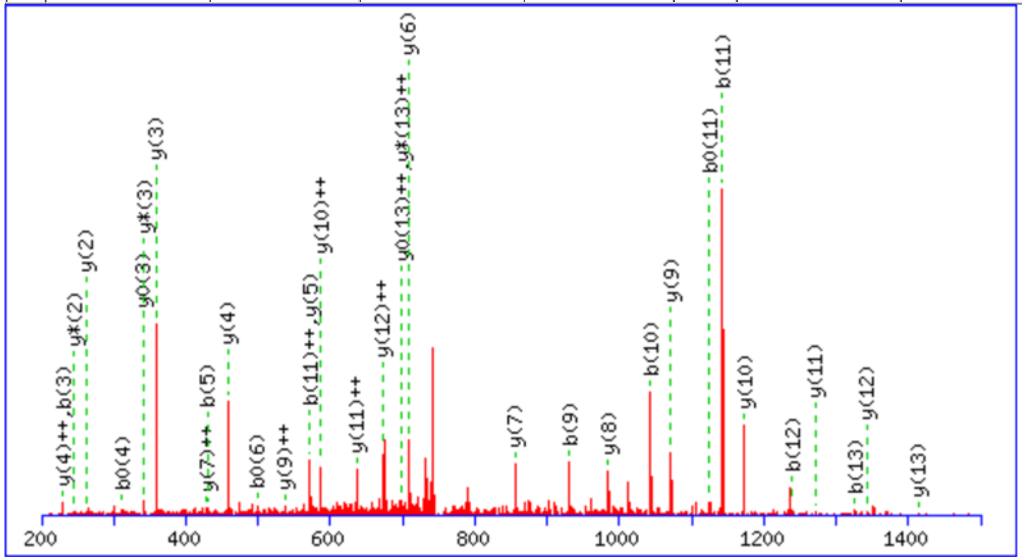


Peptide View

MS/MS Fragmentation of **SAAVTSEFHLVPSR**
Found in **IPI00043992**, Tax_Id=9606 Gene_Symbol=PVRL4 Poliovirus receptor-related protein 4
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 11036: 1499.774048 from(750.894300,2+)
Title: OECHL100312_38.14040.14040.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1499.773239**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 0.00029**Matches :** 34/128 fragment ions using 100 most intense peaks (help)

#	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y^{*}**	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	88.039304	44.523290	70.028739	35.518008	**S**							**14**
2	159.076418	80.041847	141.065853	71.036564	**A**	***1413.748490***	707.377883	1396.721941	698.864609	1395.737925	698.372600	**13**
3	**230.113532**	115.560404	212.102967	106.555121	**A**	***1342.711376***	671.859326	1325.684827	663.346052	1324.700811	662.854043	**12**
4	329.181946	165.094611	311.171381	156.089328	**V**	***1271.674262***	636.340769	1254.647713	627.827495	1253.663697	627.335487	**11**
5	**430.229625**	215.618450	412.219060	206.613168	**T**	***1172.605848***	586.806562	1155.579299	578.293288	1154.595283	577.801279	**10**
6	517.261653	259.134465	499.251088	250.129182	**S**	***1071.558169***	536.282723	1054.531620	527.769448	1053.547604	527.277440	**9**
7	646.304246	323.655761	628.293681	314.650479	**E**	***984.526141***	492.766709	967.499592	484.253434	966.515576	483.761426	**8**
8	793.372660	397.189968	775.362095	388.184686	**F**	***855.483548***	428.245412	838.456999	419.732138	837.472983	419.240130	**7**
9	**930.431572**	465.719424	912.421007	456.714141	**H**	***708.415134***	354.711205	691.388585	346.197931	690.404569	345.705923	**6**
10	**1043.515636**	522.261456	1025.505071	513.256173	**L**	***571.356222***	286.181749	554.329673	277.668475	553.345657	277.176467	**5**
11	**1142.584050**	571.795663	1124.573485	562.790380	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
12	**1239.636814**	620.322045	1221.626249	611.316762	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
13	**1326.668842**	663.838059	1308.658277	654.832777	**S**	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
14					**R**	175.118952	88.063114	158.092403	79.549839			**1**

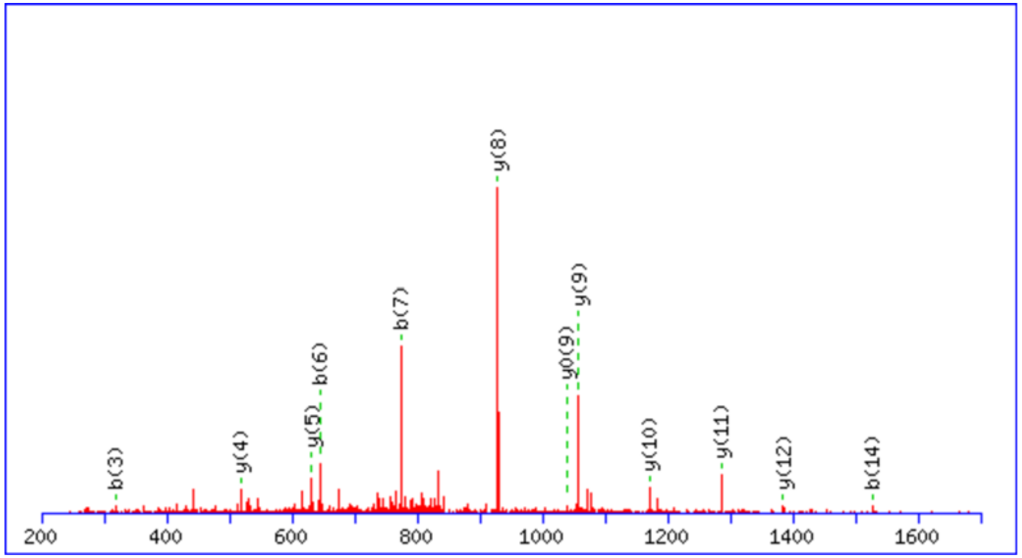


Peptide View

MS/MS Fragmentation of **AVFVDLEPTVIDEVR**
Found in **IPI00166768**, Tax_Id=9606 Gene_Symbol=TUBA1C TUBA1C protein
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 13142: 1700.901248 from(851.457900,2+)
Title: OECHL100312_38.19741.19741.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1700.898514**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00043**Matches :** 12/128 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**15**
2	171.112804	86.060040			**V**	1630.868665	815.937971	1613.842116	807.424696	1612.858100	806.932688	**14**
3	**318.181218**	159.594247			**F**	1531.800251	766.403764	1514.773702	757.890489	1513.789686	757.398481	**13**
4	417.249632	209.128454			**V**	***1384.731837***	692.869557	1367.705288	684.356282	1366.721272	683.864274	**12**
5	532.276575	266.641926	514.266010	257.636643	**D**	***1285.663423***	643.335350	1268.636874	634.822075	1267.652858	634.330067	**11**
6	**645.360639**	323.183958	627.350074	314.178675	**L**	***1170.636480***	585.821878	1153.609931	577.308604	1152.625915	576.816596	**10**
7	**774.403232**	387.705254	756.392667	378.699972	**E**	***1057.552416***	529.279846	1040.525867	520.766572	1039.541851	520.274564	**9**
8	871.455996	436.231636	853.445431	427.226354	**P**	***928.509823***	464.758550	911.483274	456.245275	910.499258	455.753267	**8**
9	972.503675	486.755476	954.493110	477.750193	**T**	831.457059	416.232168	814.430510	407.718893	813.446494	407.226885	**7**
10	1071.572089	536.289683	1053.561524	527.284400	**V**	730.409380	365.708328	713.382831	357.195054	712.398815	356.703046	**6**
11	1184.656153	592.831715	1166.645588	583.826432	**I**	***631.340966***	316.174121	614.314417	307.660846	613.330401	307.168838	**5**
12	1299.683096	650.345186	1281.672531	641.339904	**D**	***518.256902***	259.632089	501.230353	251.118815	500.246337	250.626807	**4**
13	1428.725689	714.866483	1410.715124	705.861200	**E**	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	**3**
14	**1527.794103**	764.400690	1509.783538	755.395407	**V**	274.187366	137.597321	257.160817	129.084047			**2**
15					**R**	175.118952	88.063114	158.092403	79.549839			**1**



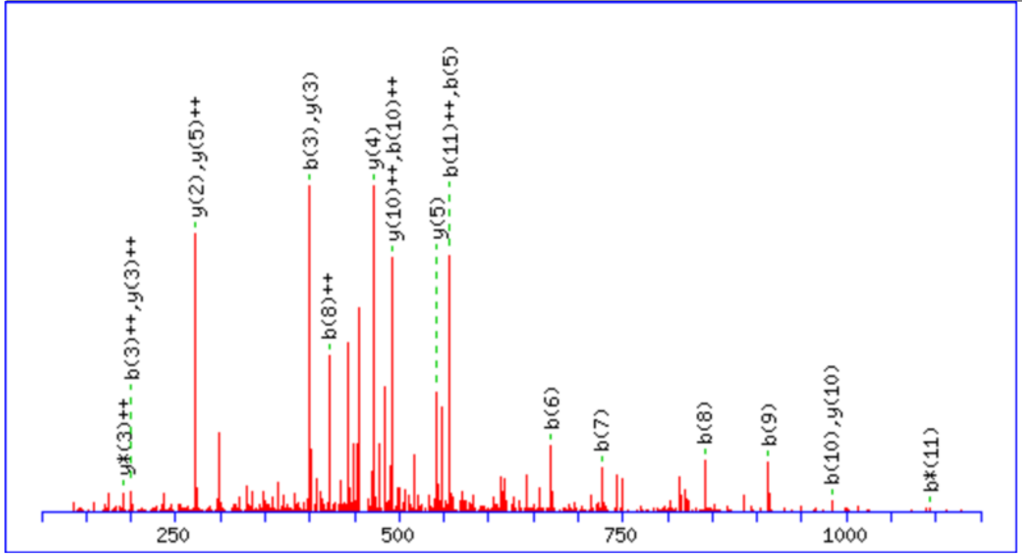
Peptide View

MS/MS Fragmentation of **VYHVGLGDAAQPR**
Found in **IPI00297252**, Tax_Id=9606 Gene_Symbol=SULF2 Isoform 1 of Extracellular sulfatase Sulf-2
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 9862: 1381.711872 from(461.577900,3+)
Title: OECHL100312_38.9264.9264.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1381.710251**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 0.00035**Matches :** 21/100 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	100.075690	50.541483					**V**							**13**
2	263.139019	132.073148					**Y**	1283.649112	642.328194	1266.622563	633.814920	1265.638547	633.322912	**12**
3	***400.197931***	**200.602603**					**H**	1120.585783	560.796530	1103.559234	552.283255	1102.575218	551.791247	**11**
4	499.266345	250.136811					**V**	**983.526871**	492.267074	966.500322	483.753799	965.516306	483.261791	**10**
5	***556.287809***	278.647543					**G**	884.458457	442.732867	867.431908	434.219592	866.447892	433.727584	**9**
6	***669.371873***	335.189575					**L**	827.436993	414.222135	810.410444	405.708860	809.426428	405.216852	**8**

7	***726.393337***	363.700307					**G**	714.352929	357.680103	697.326380	349.166828	696.342364	348.674820	**7**
8	***841.420280***	**421.213778**			823.409715	412.208496	**D**	657.331465	329.169371	640.304916	320.656096	639.320900	320.164088	**6**
9	***912.457394***	456.732335			894.446829	447.727053	**A**	**542.304522**	271.655899	525.277973	263.142625			**5**
10	***983.494508***	**492.250892**			965.483943	483.245610	**A**	**471.267408**	236.137342	454.240859	227.624068			**4**
11	1111.553086	**556.280181**	1094.526537	547.766907	1093.542521	547.274899	**Q**	**400.230294**	200.618785	383.203745	192.105511			**3**
12	1208.605850	604.806563	1191.579301	596.293289	1190.595285	595.801281	**P**	**272.171716**	136.589496	255.145167	128.076221			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

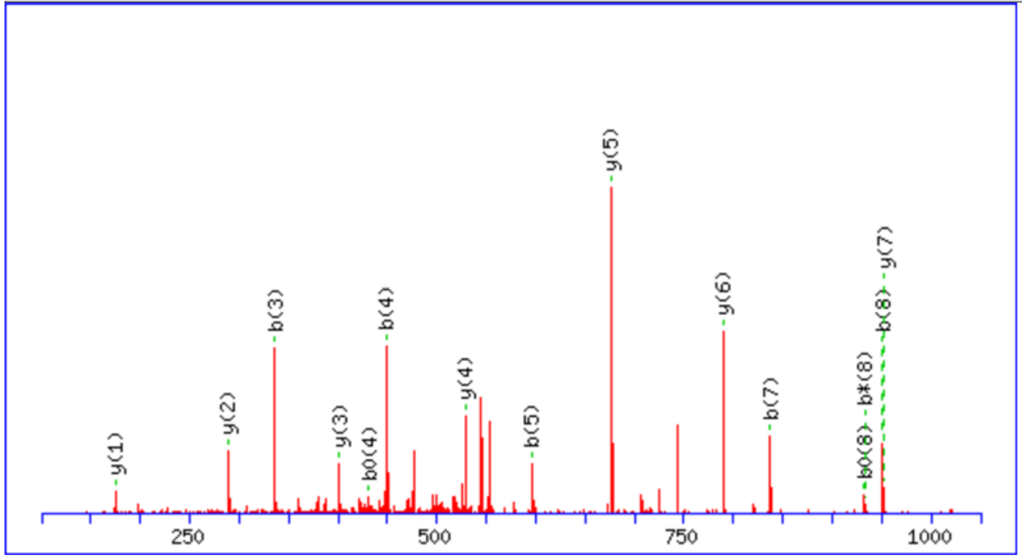


Peptide View

MS/MS Fragmentation of **DGYLFQLLR**
Found in **IPI00022371**, Tax_Id=9606 Gene_Symbol=HRG Histidine-rich glycoprotein
Experiment: 44 - OPE-2 **Fraction:** OPE-2

Match to Query 5805: 1123.602448 from(562.808500,2+)
Title: OECHL100312_38.20519.20519.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_38.raw
Monoisotopic mass of neutral peptide Mr(calc): 1123.602585**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49
Expect: 0.00082**Matches :** 15/70 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	116.034219	58.520748			98.023654	49.515465	**D**					**9**
2	173.055683	87.031479			155.045118	78.026197	**G**	1009.582929	505.295103	992.556380	496.781828	**8**
3	**336.119012**	168.563144			318.108447	159.557862	**Y**	***952.561465***	476.784371	935.534916	468.271096	**7**
4	**449.203076**	225.105176			431.192511	216.099894	**L**	***789.498136***	395.252706	772.471587	386.739432	**6**
5	**596.271490**	298.639383			578.260925	289.634101	**F**	***676.414072***	338.710674	659.387523	330.197400	**5**
6	724.330068	362.668672	707.303519	354.155398	706.319503	353.663390	**Q**	***529.345658***	265.176467	512.319109	256.663193	**4**
7	**837.414132**	419.210704	820.387583	410.697430	819.403567	410.205422	**L**	***401.287080***	201.147178	384.260531	192.633904	**3**
8	**950.498196**	475.752736	933.471647	467.239462	932.487631	466.747454	**L**	***288.203016***	144.605146	271.176467	136.091872	**2**
9							**R**	***175.118952***	88.063114	158.092403	79.549840	**1**



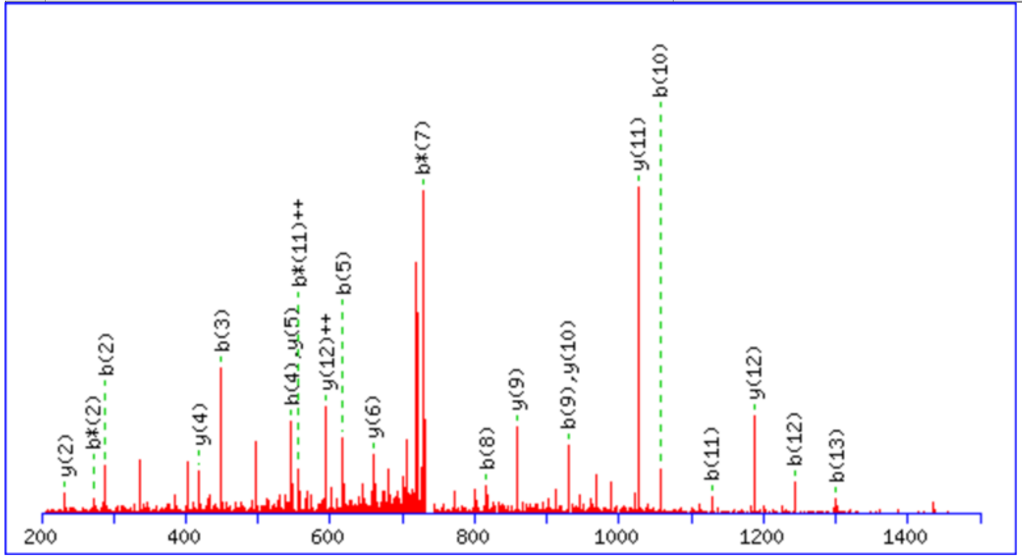
Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 14 - S_E-2 **Fraction:** S_E-2

Match to Query 10089: 1473.645048 from(737.829800,2+)

Title: OECHL100312_36.7469.7469.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_36.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66
Expect: 1.4e-005**Matches :** 22/128 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.037925	81.022600					**C**							**14**
2	***289.096503***	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.809312	**13**
3	***449.127152***	225.067214	432.100603	216.553940			**C**	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.780023	**12**
4	***546.179916***	273.593596	529.153367	265.080322			**P**	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.764698	**11**
5	***617.217030***	309.112153	600.190481	300.598879			**A**	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.238316	**10**
6	674.238494	337.622885	657.211945	329.109611			**G**	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.719759	**9**
7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
8	***816.312722***	408.659999	799.286173	400.146725			**A**	730.384229	365.695753	713.357680	357.182478	712.373664	356.690470	**7**
9	***929.396786***	465.202031	912.370237	456.688757			**L**	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.171913	**6**
10	***1057.455364***	529.231320	1040.428815	520.718046			**Q**	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.629881	**5**
11	***1128.492478***	564.749877	1111.465929	556.236603			**A**	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.600592	**4**
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	347.167359	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
13	***1300.540885***	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	**232.140416**	116.573846	215.113867	108.060571			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**

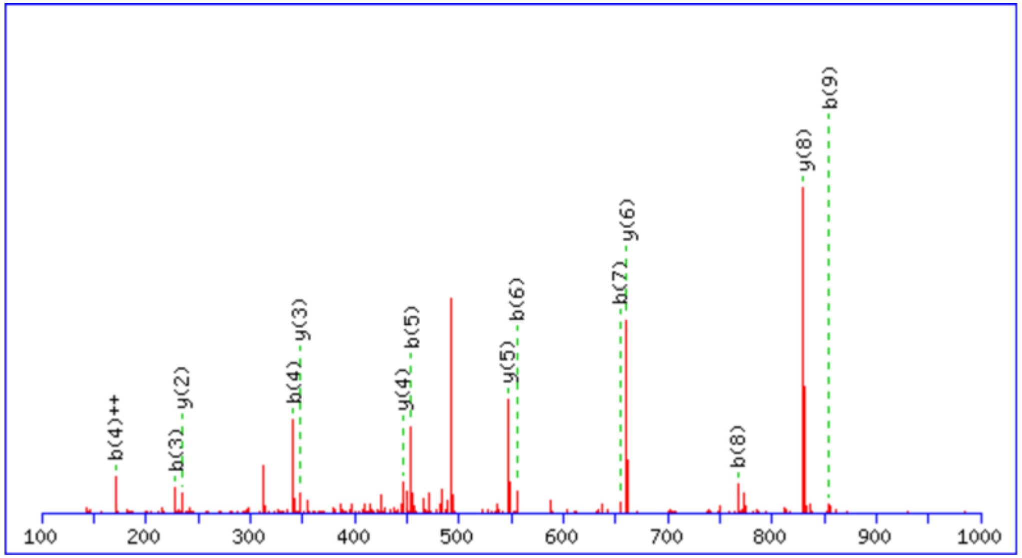


Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 14 - S_E-2 **Fraction:** S_E-2

Match to Query 3675: 999.635448 from(500.825000,2+)
Title: OECHL100312_36.17303.17303.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_36.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63
Expect: 5.5e-006**Matches :** 15/78 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	**446.297310**	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



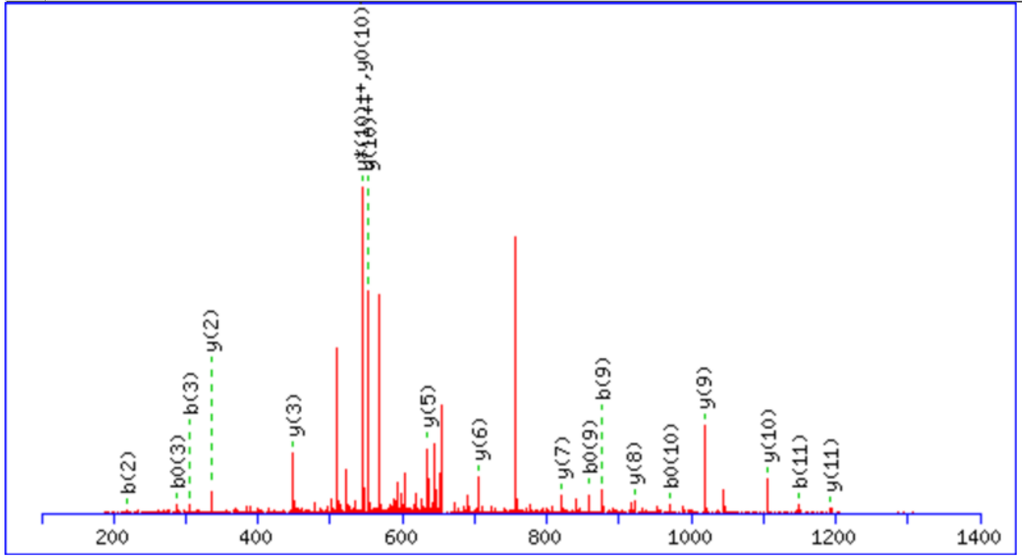
Peptide View

MS/MS Fragmentation of **MSSPTDASVICR**
Found in **IPI00021302**, Tax_Id=9606 Gene_Symbol=SUSD2 Sushi domain-containing protein 2
Experiment: 14 - S_E-2 **Fraction:** S_E-2

Match to Query 8684: 1322.594248 from(662.304400,2+)
Title: OECHL100312_36.9159.9159.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_36.raw
Monoisotopic mass of neutral peptide Mr(calc): 1322.595871**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62
Expect: 4.2e-005**Matches :** 19/100 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518			**M**							**12**
2	**219.079789**	110.043532	201.069224	101.038250	**S**	***1192.562663***	596.784969	1175.536114	588.271695	1174.552098	587.779687	**11**
3	**306.111817**	153.559546	288.101252	144.554264	**S**	***1105.530635***	553.268955	1088.504086	544.755681	1087.520070	544.263673	**10**
4	403.164581	202.085928	385.154016	193.080646	**P**	***1018.498607***	509.752942	1001.472058	501.239667	1000.488042	500.747659	**9**
5	504.212260	252.609768	486.201695	243.604485	**T**	***921.445843***	461.226560	904.419294	452.713285	903.435278	452.221277	**8**
6	619.239203	310.123240	601.228638	301.117957	**D**	***820.398164***	410.702720	803.371615	402.189445	802.387599	401.697437	**7**

7	690.276317	345.641797	672.265752	336.636514	**A**	***705.371221***	353.189249	688.344672	344.675974	687.360656	344.183966	**6**
8	777.308345	389.157810	759.297780	380.152528	**S**	***634.334107***	317.670692	617.307558	309.157417	616.323542	308.665409	**5**
9	**876.376759**	438.692017	858.366194	429.686735	**V**	547.302079	274.154678	530.275530	265.641403			**4**
10	989.460823	495.234049	971.450258	486.228767	**I**	***448.233665***	224.620470	431.207116	216.107196			**3**
11	**1149.491472**	575.249374	1131.480907	566.244091	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**



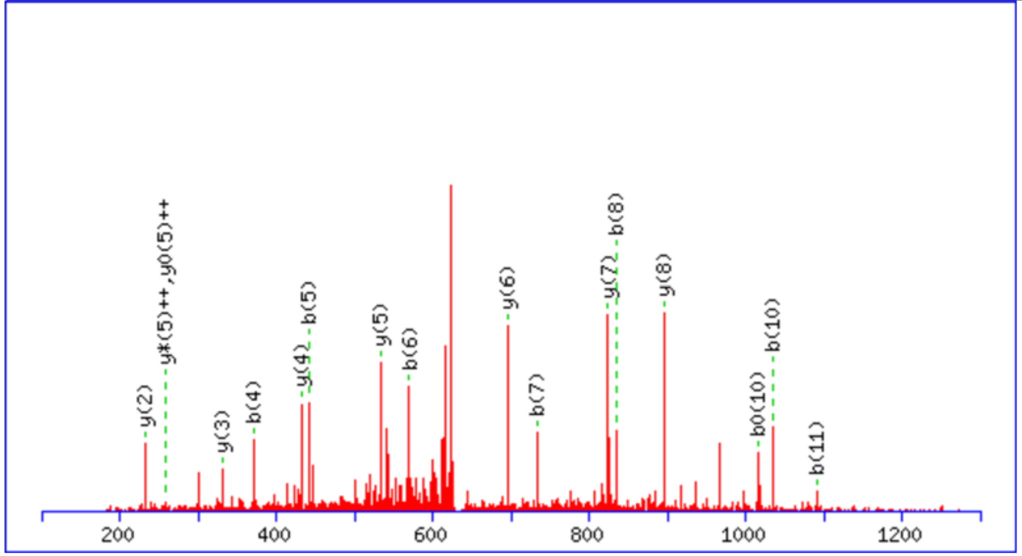
Peptide View

MS/MS Fragmentation of **ADLAAQYTTVGR**
Found in **IPI00019988**, Tax_Id=9606 Gene_Symbol=SGSH N-sulphoglucosamine sulphohydrolase
Experiment: 14 - S_E-2 **Fraction:** S_E-2

Match to Query 7840: 1264.641848 from(633.328200,2+)
Title: OECHL100312_36.10733.10733.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_36.raw
Monoisotopic mass of neutral peptide Mr(calc): 1264.641159**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65
Expect: 2.6e-005**Matches :** 17/114 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	72.044390	36.525833					**A**							**12**
2	187.071333	94.039304			169.060768	85.034022	**D**	1194.611330	597.809303	1177.584781	589.296029	1176.600765	588.804021	**11**
3	300.155397	150.581336			282.144832	141.576054	**L**	1079.584387	540.295832	1062.557838	531.782557	1061.573822	531.290549	**10**
4	***371.192511***	186.099894			353.181946	177.094611	**A**	966.500323	483.753800	949.473774	475.240525	948.489758	474.748517	**9**
5	***442.229625***	221.618450			424.219060	212.613168	**A**	***895.463209***	448.235243	878.436660	439.721968	877.452644	439.229960	**8**
6	***570.288203***	285.647740	553.261654	277.134465	552.277638	276.642457	**Q**	***824.426095***	412.716686	807.399546	404.203411	806.415530	403.711403	**7**
7	***733.351532***	367.179404	716.324983	358.666130	715.340967	358.174122	**Y**	***696.367517***	348.687397	679.340968	340.174122	678.356952	339.682114	**6**
8	***834.399211***	417.703244	817.372662	409.189969	816.388646	408.697961	**T**	***533.304188***	267.155732	516.277639	258.642458	515.293623	258.150450	**5**
9	935.446890	468.227083	918.420341	459.713809	917.436325	459.221801	**T**	***432.256509***	216.631892	415.229960	208.118618	414.245944	207.626610	**4**
10	***1034.515304***	517.761290	1017.488755	509.248016	1016.504739	508.756008	**V**	***331.208830***	166.108053	314.182281	157.594778			**3**
11	***1091.536768***	546.272022	1074.510219	537.758748	1073.526203	537.266740	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**

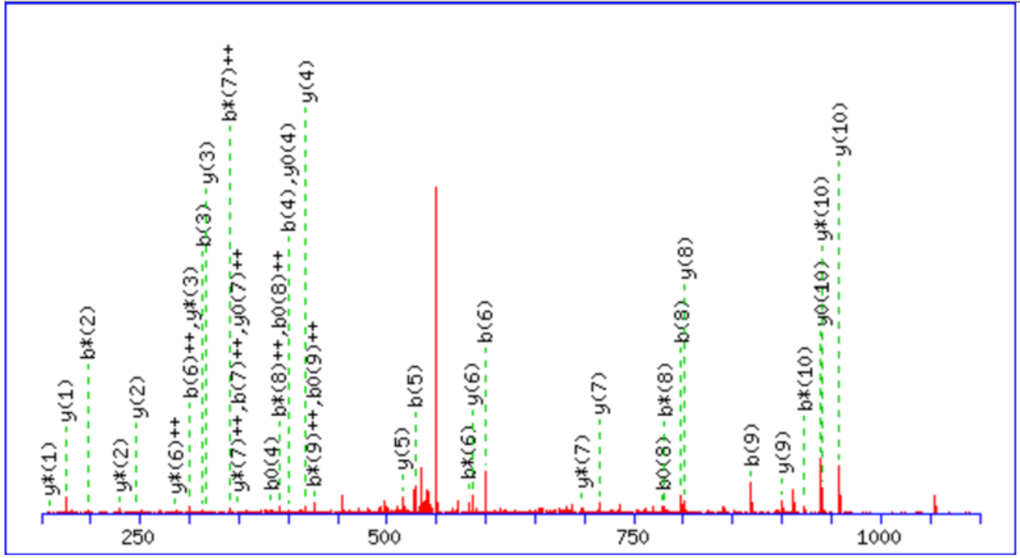


Peptide View

MS/MS Fragmentation of **RGVSQAPTAAR**
Found in **IPI00025365**, Tax_Id=9606 Gene_Symbol=EDN3 Isoform Long of Endothelin-3
Experiment: 14 - S_E-2 **Fraction:** S_E-2

Match to Query 5348: 1112.605848 from(557.310200,2+)
Title: OECHL100312_36.2297.2297.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_36.raw
Monoisotopic mass of neutral peptide Mr(calc): 1112.605042**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00027**Matches :** 40/108 fragment ions using 84 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			**R**							**11**
2	214.129851	107.568564	197.103302	99.055289			**G**	***957.511221***	479.259249	940.484672	470.745974	939.500656	470.253966	**10**
3	**313.198265**	157.102770	296.171716	148.589496			**V**	***900.489757***	450.748517	883.463208	442.235242	882.479192	441.743234	**9**
4	**400.230293**	200.618785	383.203744	192.105510	382.219728	191.613502	**S**	***801.421343***	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
5	**528.288871**	264.648074	511.262322	256.134799	510.278306	255.642791	**Q**	***714.389315***	357.698296	697.362766	349.185021	696.378750	348.693013	**7**
6	**599.325985**	300.166631	582.299436	291.653356	581.315420	291.161348	**A**	***586.330737***	293.669007	569.304188	285.155732	568.320172	284.663724	**6**
7	696.378749	348.693013	679.352200	340.179738	678.368184	339.687730	**P**	***515.293623***	258.150450	498.267074	249.637175	497.283058	249.145167	**5**
8	**797.426428**	399.216852	780.399879	390.703578	779.415863	390.211570	**T**	***418.240859***	209.624068	401.214310	201.110793	400.230294	200.618785	**4**
9	**868.463542**	434.735409	851.436993	426.222135	850.452977	425.730127	**A**	***317.193180***	159.100228	300.166631	150.586953			**3**
10	**939.500656**	470.253966	922.474107	461.740692	921.490091	461.248684	**A**	***246.156066***	123.581671	229.129517	115.068397			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**

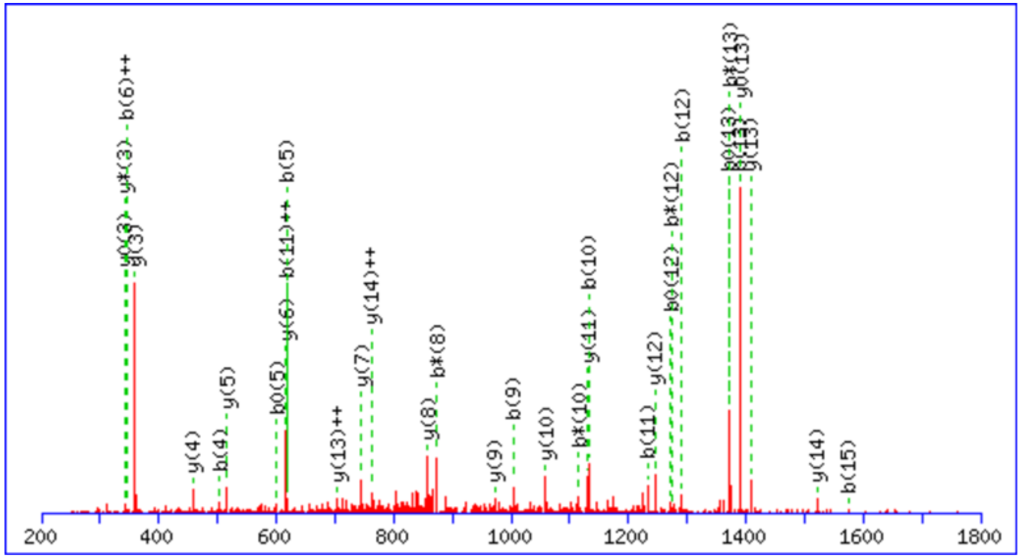


Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 14 - S_E-2 **Fraction:** S_E-2

Match to Query 12835: 1746.916848 from(874.465700,2+)
Title: OECHL100312_36.17047.17047.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_36.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63
Expect: 5.5e-005**Matches :** 34/156 fragment ions using 75 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	**503.322797**	252.165036					**Y**	***1408.670299***	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	689.386854	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



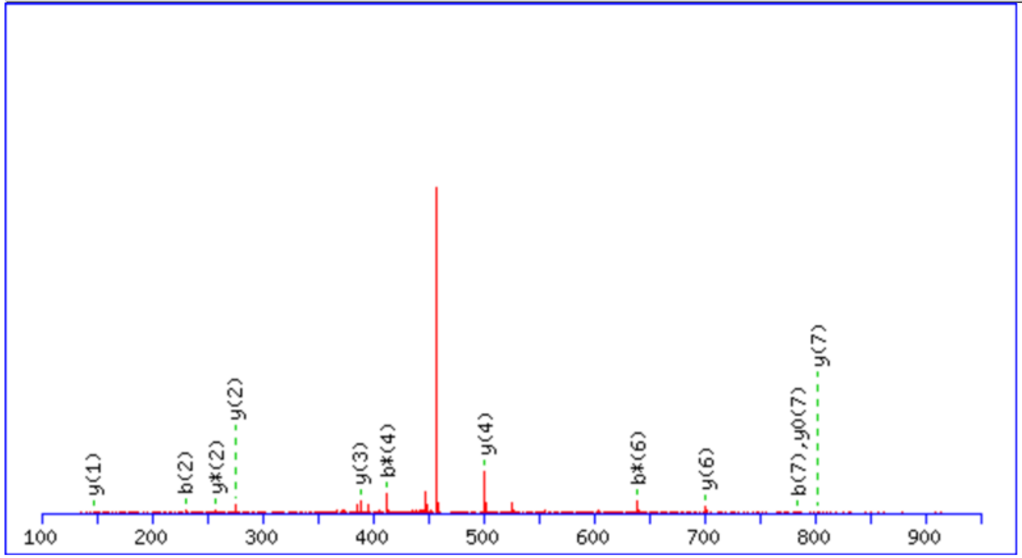
Peptide View

MS/MS Fragmentation of **QTSILIQK**
Found in **IPI00020687**, Tax_Id=9606 Gene_Symbol=SPINK1 Pancreatic secretory trypsin inhibitor
Experiment: 14 - S_E-2 **Fraction:** S_E-2

Match to Query 2456: 929.555048 from(465.784800,2+)
Title: OECHL100312_36.8243.8243.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_36.raw
Monoisotopic mass of neutral peptide Mr(calc): 929.554565**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00012**Matches :** 12/72 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	129.065854	65.036565	112.039305	56.523291			Q							8
2	**230.113533**	115.560405	213.086984	107.047130	212.102968	106.555122	T	***802.503281***	401.755279	785.476732	393.242004	784.492716	392.749996	7
3	317.145561	159.076418	300.119012	150.563144	299.134996	150.071136	S	***701.455602***	351.231439	684.429053	342.718165	683.445037	342.226157	6
4	430.229625	215.618450	413.203076	207.105176	412.219060	206.613168	I	614.423574	307.715425	597.397025	299.202151			5
5	543.313689	272.160483	526.287140	263.647208	525.303124	263.155200	L	***501.339510***	251.173393	484.312961	242.660119			4
6	656.397753	328.702515	639.371204	320.189240	638.387188	319.697232	I	***388.255446***	194.631361	371.228897	186.118087			3

7	**784.456331**	392.731804	767.429782	384.218529	766.445766	383.726521	**Q**	***275.171382***	138.089329	258.144833	129.576055			**2**
8							**K**	***147.112804***	74.060040	130.086255	65.546765			**1**



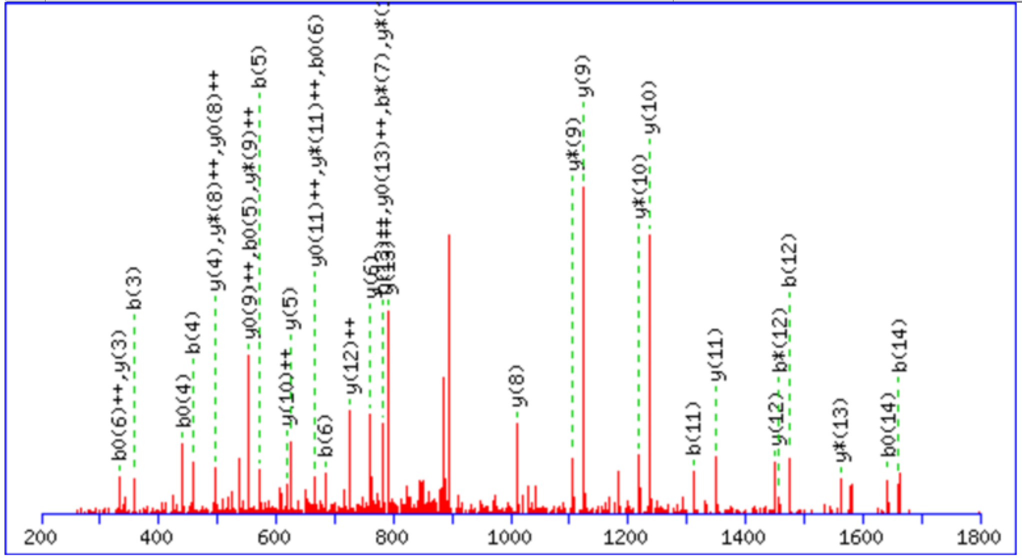
Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 14 - S_E-2 **Fraction:** S_E-2

Match to Query 13272: 1805.931848 from(903.973200,2+)
Title: OECHL100312_36.19507.19507.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_36.raw
Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00038**Matches :** 38/160 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**15**
2	228.134267	114.570771	211.107718	106.057497			**I**	1692.895549	846.951413	1675.869000	838.438138	1674.884984	837.946130	**14**
3	**357.176860**	179.092068	340.150311	170.578793	339.166295	170.086785	**E**	1579.811485	790.409381	1562.784936	781.896106	1561.800920	781.404098	**13**
4	**458.224539**	229.615907	441.197990	221.102633	440.213974	220.610625	**T**	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.882802	**12**

5	**571.308603**	286.157940	554.282054	277.644665	553.298038	277.152657	**I**	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.358962	**11**
6	**684.392667**	342.699972	667.366118	334.186697	666.382102	333.694689	**I**	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.816930	**10**
7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	**N**	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.274898	**9**
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	**T**	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.253435	**8**
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	**F**	908.462479	454.734878	891.435930	446.221603	890.451914	445.729595	**7**
10	1183.610599	592.308938	1166.584050	583.795663	1165.600034	583.303655	**H**	***761.394065***	381.200671	744.367516	372.687396	743.383500	372.195388	**6**
11	**1311.669177**	656.338227	1294.642628	647.824952	1293.658612	647.332944	**Q**	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.665932	**5**
12	**1474.732506**	737.869891	1457.705957	729.356617	1456.721941	728.864609	**Y**	***496.276575***	248.641926	479.250026	240.128651	478.266010	239.636643	**4**
13	1561.764534	781.385905	1544.737985	772.872631	1543.753969	772.380623	**S**	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.104979	**3**
14	**1660.832948**	830.920112	1643.806399	822.406838	1642.822383	821.914830	**V**	246.181218	123.594247	229.154669	115.080973			**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**

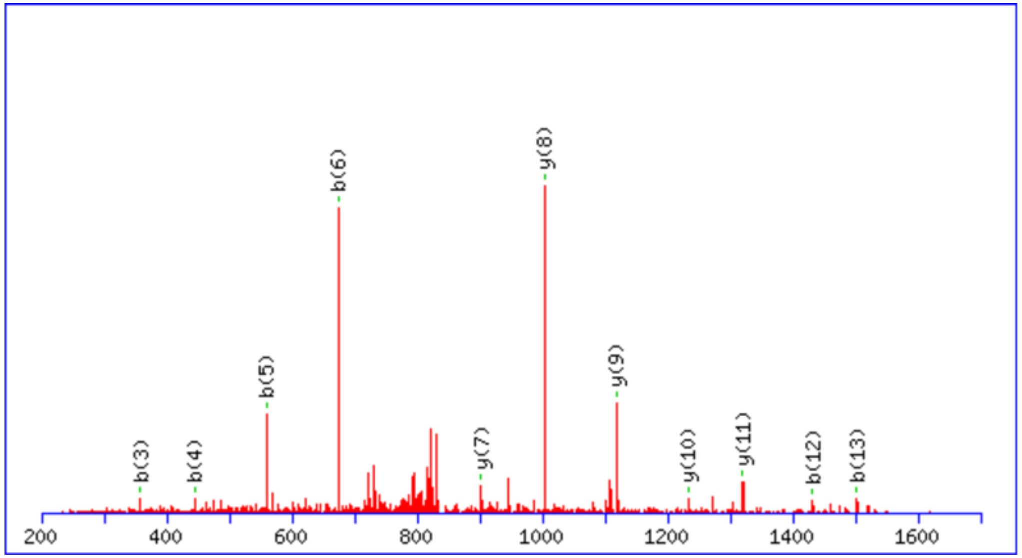


Peptide View

MS/MS Fragmentation of **SLRSDDTAVYYCAR**
Found in **IPI00829701**, Tax_Id=9606 Gene_Symbol=LOC100292483;LOC100290448 similar to pre-B lymphocyte gene 2
Experiment: 14 - S_E-2 **Fraction:** S_E-2

Match to Query 12124: 1675.763248 from(838.888900,2+)
Title: OECHL100312_36.9105.9105.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_36.raw
Monoisotopic mass of neutral peptide Mr(calc): 1675.762405**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00087**Matches :** 11/138 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	88.039304	44.523290			70.028739	35.518008	**S**							**14**
2	201.123368	101.065322			183.112803	92.060039	**L**	1589.737669	795.372472	1572.711120	786.859198	1571.727104	786.367190	**13**
3	***357.224479***	179.115877	340.197930	170.602603	339.213914	170.110595	**R**	1476.653605	738.830441	1459.627056	730.317166	1458.643040	729.825158	**12**
4	***444.256507***	222.631891	427.229958	214.118617	426.245942	213.626609	**S**	***1320.552494***	660.779885	1303.525945	652.266611	1302.541929	651.774603	**11**
5	***559.283450***	280.145363	542.256901	271.632089	541.272885	271.140081	**D**	***1233.520466***	617.263871	1216.493917	608.750597	1215.509901	608.258588	**10**
6	***674.310393***	337.658835	657.283844	329.145560	656.299828	328.653552	**D**	***1118.493523***	559.750399	1101.466974	551.237125	1100.482958	550.745117	**9**
7	775.358072	388.182674	758.331523	379.669400	757.347507	379.177392	**T**	***1003.466580***	502.236928	986.440031	493.723654	985.456015	493.231646	**8**
8	846.395186	423.701231	829.368637	415.187956	828.384621	414.695948	**A**	***902.418901***	451.713089	885.392352	443.199814			**7**
9	945.463600	473.235438	928.437051	464.722163	927.453035	464.230155	**V**	831.381787	416.194532	814.355238	407.681257			**6**
10	1108.526929	554.767102	1091.500380	546.253828	1090.516364	545.761820	**Y**	732.313373	366.660325	715.286824	358.147050			**5**
11	1271.590258	636.298767	1254.563709	627.785493	1253.579693	627.293484	**Y**	569.250044	285.128660	552.223495	276.615386			**4**
12	***1431.620907***	716.314092	1414.594358	707.800817	1413.610342	707.308809	**C**	406.186715	203.596995	389.160166	195.083721			**3**
13	***1502.658021***	751.832649	1485.631472	743.319374	1484.647456	742.827366	**A**	246.156066	123.581671	229.129517	115.068396			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



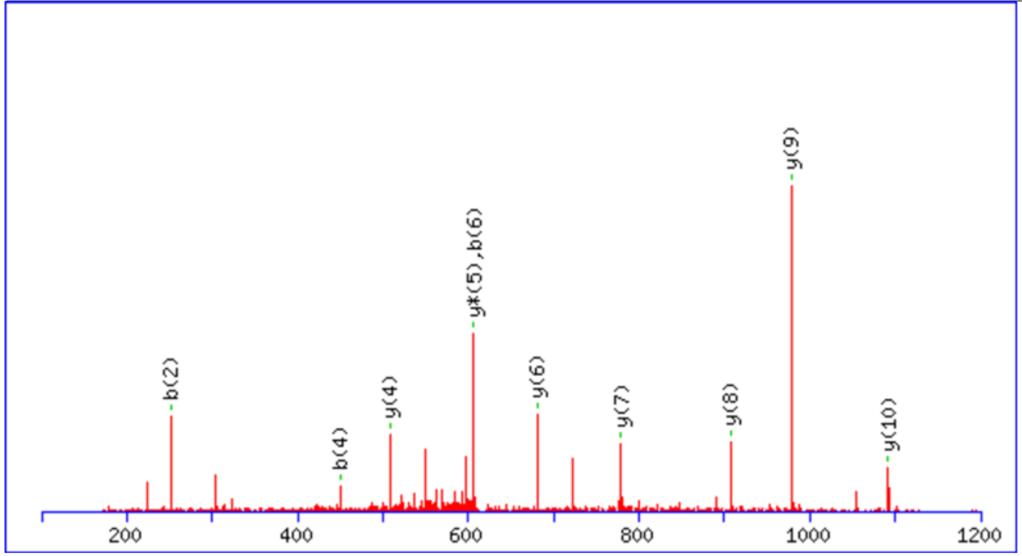
Peptide View

MS/MS Fragmentation of **HLAQVGDSMDR**
Found in **IPI00413587**, Tax_Id=9606 Gene_Symbol=BID Isoform 1 of BH3-interacting domain death agonist
Experiment: 14 - S_E-2 **Fraction:** S_E-2

Match to Query 7318: 1227.567448 from(614.791000,2+)
Title: OECHL100312_36.5548.5548.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_36.raw
Monoisotopic mass of neutral peptide Mr(calc): 1227.566620**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00024**Matches :** 10/100 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	138.066188	69.536732					**H**							**11**
2	**251.150252**	126.078764					**L**	***1091.514985***	546.261131	1074.488436	537.747856	1073.504420	537.255848	**10**
3	322.187366	161.597321					**A**	***978.430921***	489.719099	961.404372	481.205824	960.420356	480.713816	**9**
4	**450.245944**	225.626610	433.219395	217.113335			**Q**	***907.393807***	454.200542	890.367258	445.687267	889.383242	445.195259	**8**
5	549.314358	275.160817	532.287809	266.647542			**V**	***779.335229***	390.171253	762.308680	381.657978	761.324664	381.165970	**7**
6	**606.335822**	303.671549	589.309273	295.158275			**G**	***680.266815***	340.637046	663.240266	332.123771	662.256250	331.631763	**6**

7	721.362765	361.185021	704.336216	352.671746	703.352200	352.179738	**D**	623.245351	312.126314	606.218802	303.613039	605.234786	303.121031	**5**
8	808.394793	404.701034	791.368244	396.187760	790.384228	395.695752	**S**	***508.218408***	254.612842	491.191859	246.099567	490.207843	245.607559	**4**
9	939.435278	470.221277	922.408729	461.708002	921.424713	461.215994	**M**	421.186380	211.096828	404.159831	202.583553	403.175815	202.091546	**3**
10	1054.462221	527.734749	1037.435672	519.221474	1036.451656	518.729466	**D**	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	**2**
11							**R**	175.118952	88.063114	158.092403	79.549839			**1**



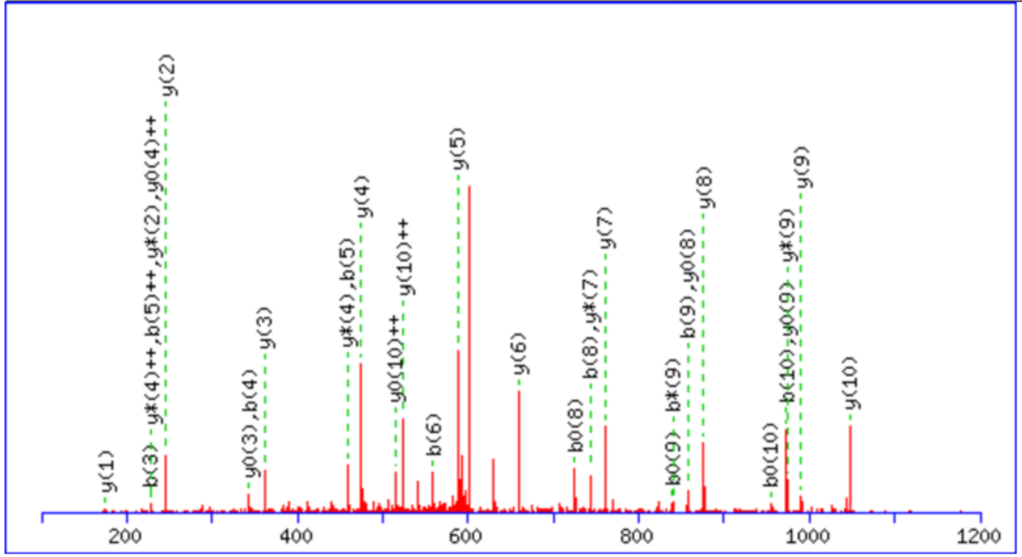
Peptide View

MS/MS Fragmentation of **GLGDDTALNDAR**
Found in **IPI00216914**, Tax_Id=9606 Gene_Symbol=VMO1 Vitelline membrane outer layer protein 1 homolog
Experiment: 59 - PyE-2 **Fraction:** PyE-2

Match to Query 7716: 1216.568048 from(609.291300,2+)
Title: OECHL100312_34.8866.8866.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_34.raw
Monoisotopic mass of neutral peptide Mr(calc): 1216.568390**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 78
Expect: 1.1e-006**Matches :** 33/106 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					**G**							**12**

2	171.112804	86.060040					**L**	1160.554207	580.780742	1143.527658	572.267467	1142.543642	571.775459	**11**
3	**228.134268**	114.570772					**G**	***1047.470143***	524.238710	1030.443594	515.725435	1029.459578	515.233427	**10**
4	**343.161211**	172.084243			325.150646	163.078961	**D**	***990.448679***	495.727978	973.422130	487.214703	972.438114	486.722695	**9**
5	**458.188154**	229.597715			440.177589	220.592433	**D**	***875.421736***	438.214506	858.395187	429.701232	857.411171	429.209224	**8**
6	**559.235833**	280.121555			541.225268	271.116272	**T**	***760.394793***	380.701035	743.368244	372.187760	742.384228	371.695752	**7**
7	630.272947	315.640112			612.262382	306.634829	**A**	***659.347114***	330.177195	642.320565	321.663921	641.336549	321.171913	**6**
8	**743.357011**	372.182144			725.346446	363.176861	**L**	***588.310000***	294.658638	571.283451	286.145364	570.299435	285.653356	**5**
9	**857.399938**	429.203607	840.373389	420.690333	839.389373	420.198325	**N**	***475.225936***	238.116606	458.199387	229.603331	457.215371	229.111323	**4**
10	**972.426881**	486.717079	955.400332	478.203804	954.416316	477.711796	**D**	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	**3**
11	1043.463995	522.235636	1026.437446	513.722361	1025.453430	513.230353	**A**	***246.156066***	123.581671	229.129517	115.068397			**2**
12							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**

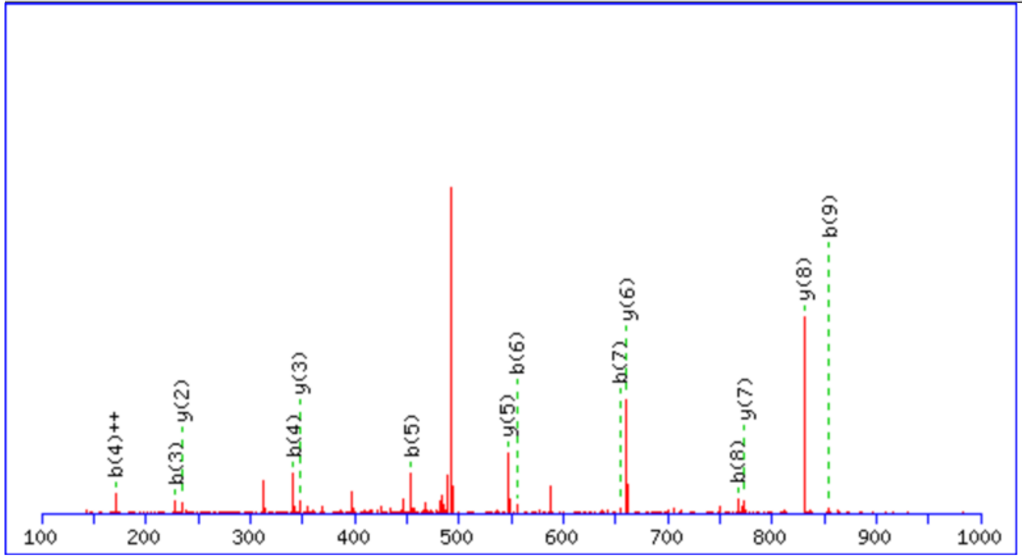


Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 59 - PyE-2 **Fraction:** PyE-2

Match to Query 4311: 999.633048 from(500.823800,2+)
Title: OECHL100312_34.17458.17458.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_34.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53
Expect: 5.7e-005**Matches :** 15/78 fragment ions using 33 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	**773.513117**	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**

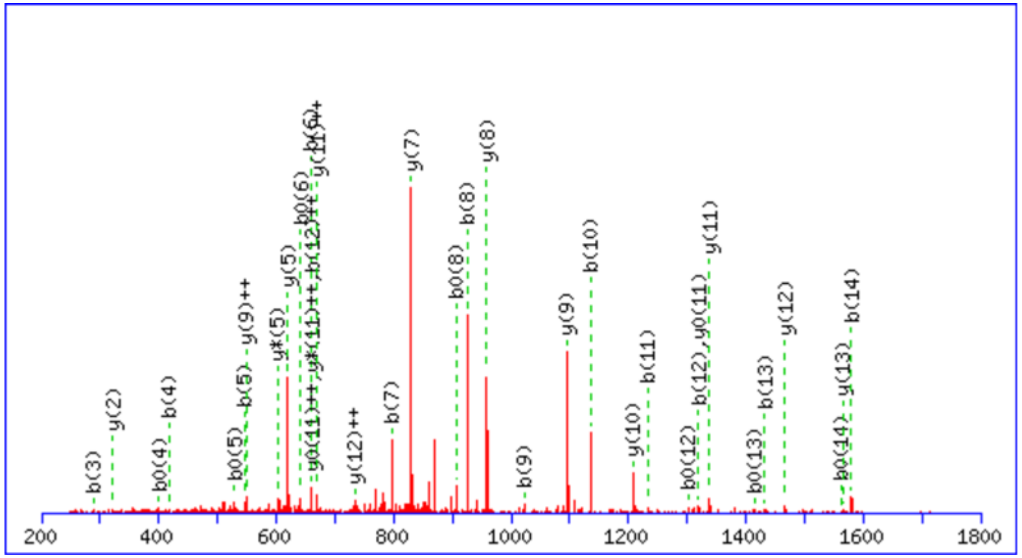


Peptide View

MS/MS Fragmentation of **STVEELHEPIPSLFR**
Found in **IPI00410487**, Tax_Id=9606 Gene_Symbol=TWSG1 Isoform 1 of Twisted gastrulation protein homolog 1
Experiment: 59 - PyE-2 **Fraction:** PyE-2

Match to Query 13829: 1752.907048 from(877.460800,2+)
Title: OECHL100312_34.17772.17772.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_34.raw
Monoisotopic mass of neutral peptide Mr(calc): 1752.904633**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 68
Expect: 1.6e-005**Matches :** 36/134 fragment ions using 72 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**15**
2	189.086983	95.047129	171.076418	86.041847	**T**	1666.879898	833.943587	1649.853349	825.430313	1648.869333	824.938304	**14**
3	***288.155397***	144.581336	270.144832	135.576054	**V**	**1565.832219**	783.419748	1548.805670	774.906473	1547.821654	774.414465	**13**
4	***417.197990***	209.102633	399.187425	200.097351	**E**	**1466.763805**	733.885541	1449.737256	725.372266	1448.753240	724.880258	**12**
5	***546.240583***	273.623930	528.230018	264.618647	**E**	**1337.721212**	669.364244	1320.694663	660.850970	1319.710647	660.358961	**11**
6	***659.324647***	330.165962	641.314082	321.160679	**L**	**1208.678619**	604.842948	1191.652070	596.329673	1190.668054	595.837665	**10**
7	***796.383559***	398.695418	778.372994	389.690135	**H**	**1095.594555**	548.300915	1078.568006	539.787641	1077.583990	539.295633	**9**
8	***925.426152***	463.216714	907.415587	454.211432	**E**	**958.535643**	479.771460	941.509094	471.258185	940.525078	470.766177	**8**
9	***1022.478916***	511.743096	1004.468351	502.737814	**P**	**829.493050**	415.250163	812.466501	406.736889	811.482485	406.244881	**7**
10	***1135.562980***	568.285128	1117.552415	559.279845	**I**	732.440286	366.723781	715.413737	358.210507	714.429721	357.718499	**6**
11	***1232.615744***	616.811510	1214.605179	607.806227	**P**	**619.356222**	310.181749	602.329673	301.668475	601.345657	301.176467	**5**
12	***1319.647772***	660.327524	1301.637207	651.322242	**S**	522.303458	261.655367	505.276909	253.142093	504.292893	252.650085	**4**
13	***1432.731836***	716.869556	1414.721271	707.864273	**L**	435.271430	218.139353	418.244881	209.626078			**3**
14	***1579.800250***	790.403763	1561.789685	781.398481	**F**	**322.187366**	161.597321	305.160817	153.084047			**2**
15					**R**	175.118952	88.063114	158.092403	79.549839			**1**



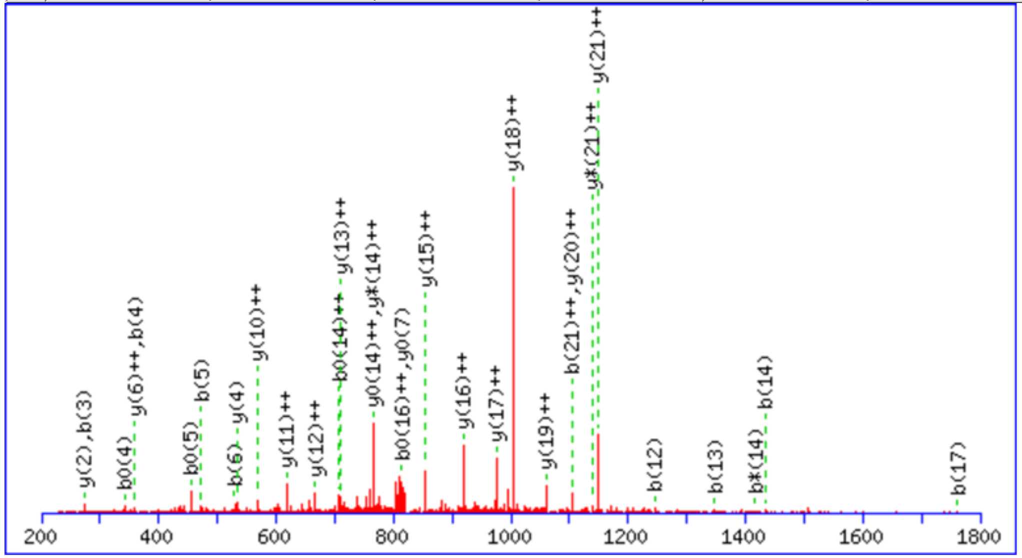
Peptide View

MS/MS Fragmentation of **AISSIGLECQSVTSRGDLATCPR**
Found in **IPI00006988**, Tax_Id=9606 Gene_Symbol=RETN Resistin
Experiment: 59 - PyE-2 **Fraction:** PyE-2

Match to Query 17580: 2477.199372 from(826.740400,3+)
Title: OECHL100312_34.13936.13936.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_34.raw
Monoisotopic mass of neutral peptide Mr(calc): 2477.200256**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66
Expect: 5.3e-005**Matches :** 32/236 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	72.044390	36.525833					**A**						
2	185.128454	93.067865					**I**	2407.170421	1204.088848	2390.143872	1195.575574	2389.159856	1195.0835
3	**272.160482**	136.583879			254.149917	127.578596	**S**	2294.086357	1147.546816	2277.059808	1139.033542	2276.075792	1138.5415
4	**359.192510**	180.099893			341.181945	171.094610	**S**	2207.054329	1104.030802	2190.027780	1095.517528	2189.043764	1095.0255
5	**472.276574**	236.641925			454.266009	227.636642	**I**	2120.022301	1060.514788	2102.995752	1052.001514	2102.011736	1051.5095
6	**529.298038**	265.152657			511.287473	256.147375	**G**	2006.938237	1003.972757	1989.911688	995.459482	1988.927672	994.9674

7	642.382102	321.694689			624.371537	312.689407	**L**	1949.916773	975.462025	1932.890224	966.948750	1931.906208	966.4567
8	771.424695	386.215986			753.414130	377.210703	**E**	1836.832709	918.919993	1819.806160	910.406718	1818.822144	909.9147
9	931.455344	466.231310			913.444779	457.226028	**C**	1707.790116	854.398696	1690.763567	845.885422	1689.779551	845.3934
10	1059.513922	530.260599	1042.487373	521.747325	1041.503357	521.255317	**Q**	1547.759467	774.383372	1530.732918	765.870097	1529.748902	765.3780
11	1146.545950	573.776613	1129.519401	565.263339	1128.535385	564.771331	**S**	1419.700889	710.354083	1402.674340	701.840808	1401.690324	701.3488
12	**1245.614364**	623.310820	1228.587815	614.797546	1227.603799	614.305538	**V**	1332.668861	666.838069	1315.642312	658.324794	1314.658296	657.8327
13	**1346.662043**	673.834660	1329.635494	665.321385	1328.651478	664.829377	**T**	1233.600447	617.303862	1216.573898	608.790587	1215.589882	608.2985
14	**1433.694071**	717.350674	1416.667522	708.837399	1415.683506	708.345391	**S**	1132.552768	566.780022	1115.526219	558.266748	1114.542203	557.7747
15	1589.795182	795.401229	1572.768633	786.887955	1571.784617	786.395947	**R**	1045.520740	523.264008	1028.494191	514.750734	1027.510175	514.2587
16	1646.816646	823.911961	1629.790097	815.398687	1628.806081	814.906679	**G**	889.419629	445.213453	872.393080	436.700178	871.409064	436.2081
17	**1761.843589**	881.425433	1744.817040	872.912158	1743.833024	872.420150	**D**	832.398165	416.702721	815.371616	408.189446	814.387600	407.6974
18	1874.927653	937.967465	1857.901104	929.454190	1856.917088	928.962182	**L**	717.371222	359.189249	700.344673	350.675975	699.360657	350.1839
19	1945.964767	973.486022	1928.938218	964.972747	1927.954202	964.480739	**A**	604.287158	302.647217	587.260609	294.133943	586.276593	293.6419
20	2047.012446	1024.009861	2029.985897	1015.496587	2029.001881	1015.004579	**T**	533.250044	267.128660	516.223495	258.615386	515.239479	258.1233
21	2207.043095	1104.025185	2190.016546	1095.511911	2189.032530	1095.019903	**C**	432.202365	216.604820	415.175816	208.091546		
22	2304.095859	1152.551567	2287.069310	1144.038293	2286.085294	1143.546285	**P**	272.171716	136.589496	255.145167	128.076221		
23							**R**	175.118952	88.063114	158.092403	79.549839		

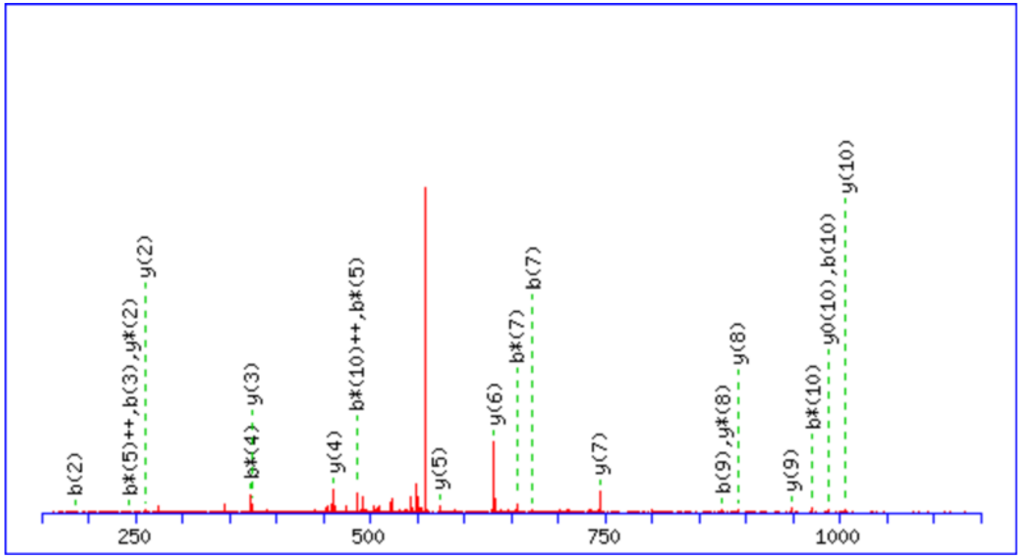


Peptide View

MS/MS Fragmentation of **QGGFLGLSNIK**
Found in **IPI00013955**, Tax_Id=9606 Gene_Symbol=MUC1 Isoform 1 of Mucin-1
Experiment: 59 - PyE-2 **Fraction:** PyE-2

Match to Query 6518: 1132.623848 from(567.319200,2+)
Title: OECHL100312_34.17051.17051.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_34.raw
Monoisotopic mass of neutral peptide Mr(calc): 1132.624054**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62
Expect: 4.2e-005**Matches :** 23/100 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			**Q**							**11**
2	**186.087318**	93.547297	169.060769	85.034023			**G**	***1005.572757***	503.290017	988.546208	494.776742	987.562192	494.284734	**10**
3	**243.108782**	122.058029	226.082233	113.544755			**G**	***948.551293***	474.779285	931.524744	466.266010	930.540728	465.774002	**9**
4	390.177196	195.592236	373.150647	187.078962			**F**	***891.529829***	446.268553	874.503280	437.755278	873.519264	437.263270	**8**
5	503.261260	252.134268	486.234711	243.620994			**L**	***744.461415***	372.734346	727.434866	364.221071	726.450850	363.729063	**7**
6	560.282724	280.645000	543.256175	272.131726			**G**	***631.377351***	316.192314	614.350802	307.679039	613.366786	307.187031	**6**
7	**673.366788**	337.187032	656.340239	328.673758			**L**	***574.355887***	287.681582	557.329338	279.168307	556.345322	278.676299	**5**
8	760.398816	380.703046	743.372267	372.189772	742.388251	371.697764	**S**	***461.271823***	231.139550	444.245274	222.626275	443.261258	222.134267	**4**
9	**874.441743**	437.724510	857.415194	429.211235	856.431178	428.719227	**N**	***374.239795***	187.623536	357.213246	179.110261			**3**
10	**987.525807**	494.266542	970.499258	485.753267	969.515242	485.261259	**I**	***260.196868***	130.602072	243.170319	122.088798			**2**
11							**K**	147.112804	74.060040	130.086255	65.546766			**1**



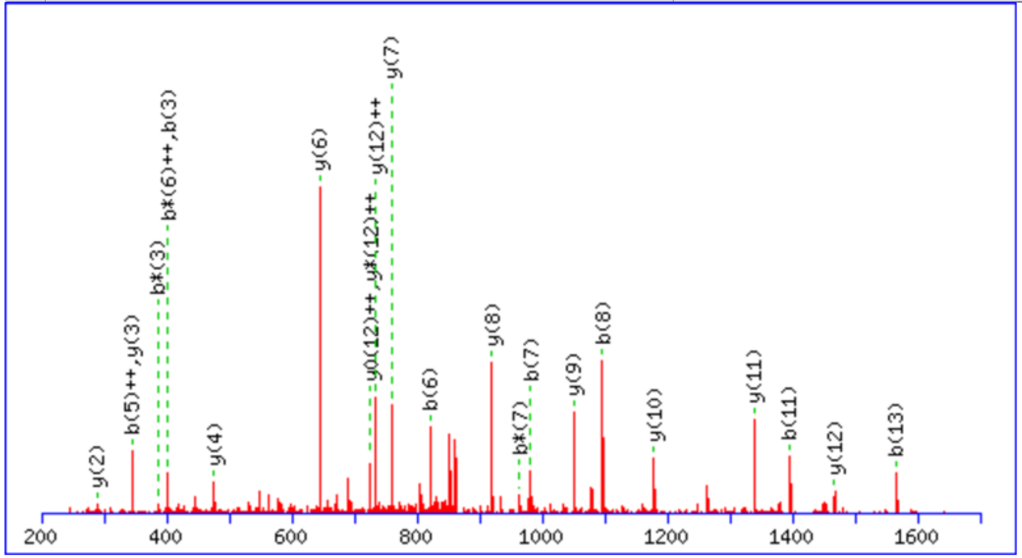
Peptide View

MS/MS Fragmentation of **CLQCQMCDPAMGLR**
Found in **IPI00024331**, Tax_Id=9606 Gene_Symbol=TNFRSF14 Tumor necrosis factor receptor superfamily member 14
Experiment: 59 - PyE-2 **Fraction:** PyE-2

Match to Query 13750: 1738.709048 from(870.361800,2+)
Title: OECHL100312_34.14252.14252.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_34.raw
Monoisotopic mass of neutral peptide Mr(calc): 1738.708160**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 78
Expect: 3.2e-007**Matches :** 23/126 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	161.037925	81.022600					**C**							**14**
2	274.121989	137.564632					**L**	1579.684789	790.346032	1562.658240	781.832758	1561.674224	781.340750	**13**
3	**402.180567**	201.593921	385.154018	193.080647			**Q**	***1466.600725***	733.804001	1449.574176	725.290726	1448.590160	724.798718	**12**
4	562.211216	281.609246	545.184667	273.095972			**C**	***1338.542147***	669.774711	1321.515598	661.261437	1320.531582	660.769429	**11**
5	690.269794	345.638535	673.243245	337.125261			**Q**	***1178.511498***	589.759387	1161.484949	581.246113	1160.500933	580.754105	**10**
6	**821.310279**	411.158778	804.283730	402.645503			**M**	***1050.452920***	525.730098	1033.426371	517.216824	1032.442355	516.724815	**9**

7	**981.340928**	491.174102	964.314379	482.660828			**C**	***919.412435***	460.209856	902.385886	451.696581	901.401870	451.204573	**8**
8	**1096.367871**	548.687574	1079.341322	540.174299	1078.357306	539.682291	**D**	***759.381786***	380.194531	742.355237	371.681256	741.371221	371.189248	**7**
9	1193.420635	597.213956	1176.394086	588.700681	1175.410070	588.208673	**P**	***644.354843***	322.681059	627.328294	314.167785			**6**
10	1264.457749	632.732513	1247.431200	624.219238	1246.447184	623.727230	**A**	547.302079	274.154677	530.275530	265.641403			**5**
11	**1395.498234**	698.252755	1378.471685	689.739481	1377.487669	689.247473	**M**	***476.264965***	238.636120	459.238416	230.122846			**4**
12	1452.519698	726.763487	1435.493149	718.250213	1434.509133	717.758205	**G**	***345.224480***	173.115878	328.197931	164.602603			**3**
13	**1565.603762**	783.305519	1548.577213	774.792245	1547.593197	774.300236	**L**	***288.203016***	144.605146	271.176467	136.091871			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



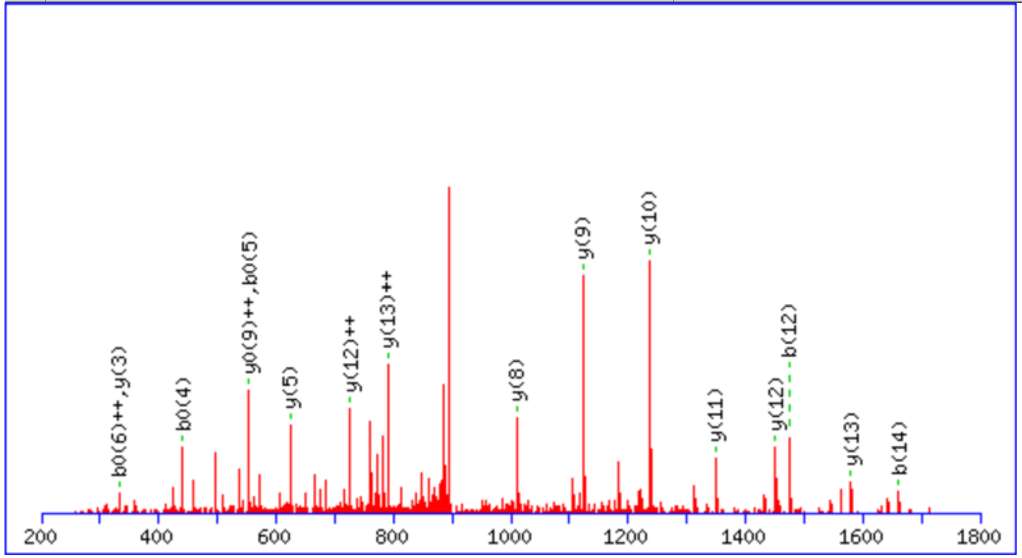
Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 59 - PyE-2 **Fraction:** PyE-2

Match to Query 14137: 1805.932848 from(903.973700,2+)
Title: OECHL100312_34.20229.20229.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_34.raw
Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 78

Expect: 2e-006**Matches :** 16/160 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	115.050203	58.028740	98.023654	49.515465			N							15
2	228.134267	114.570771	211.107718	106.057497			I	1692.895549	846.951413	1675.869000	838.438138	1674.884984	837.946130	14
3	357.176860	179.092068	340.150311	170.578793	339.166295	170.086785	E	***1579.811485***	790.409381	1562.784936	781.896106	1561.800920	781.404098	13
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	T	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.882802	12
5	571.308603	286.157940	554.282054	277.644665	553.298038	277.152657	I	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.358962	11
6	684.392667	342.699972	667.366118	334.186697	666.382102	333.694689	I	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.816930	10
7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	N	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.274898	9
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	T	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.253435	8
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	F	908.462479	454.734878	891.435930	446.221603	890.451914	445.729595	7
10	1183.610599	592.308938	1166.584050	583.795663	1165.600034	583.303655	H	761.394065	381.200671	744.367516	372.687396	743.383500	372.195388	6
11	1311.669177	656.338227	1294.642628	647.824952	1293.658612	647.332944	Q	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.665932	5
12	**1474.732506**	737.869891	1457.705957	729.356617	1456.721941	728.864609	Y	496.276575	248.641926	479.250026	240.128651	478.266010	239.636643	4
13	1561.764534	781.385905	1544.737985	772.872631	1543.753969	772.380623	S	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.104979	3
14	**1660.832948**	830.920112	1643.806399	822.406838	1642.822383	821.914830	V	246.181218	123.594247	229.154669	115.080973			2
15							K	147.112804	74.060040	130.086255	65.546765			1

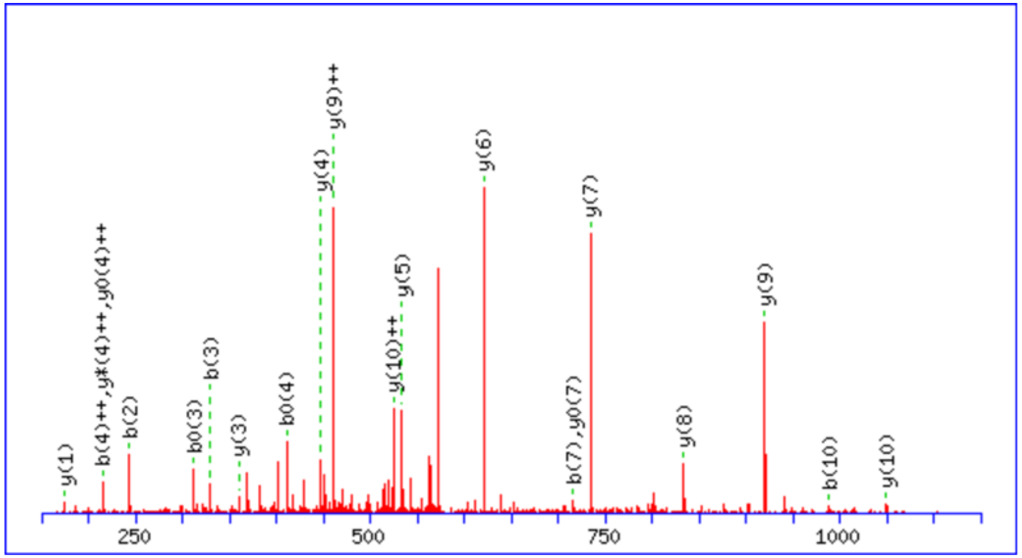


Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 59 - PyE-2 **Fraction:** PyE-2

Match to Query 7018: 1161.635048 from(581.824800,2+)
Title: OECHL100312_34.5225.5225.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_34.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 1.4e-006**Matches :** 21/94 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					**I**							**11**
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637	**10**
3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340	**9**
4	429.234375	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326	**8**
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119	**7**
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087	**6**
7	**716.382495**	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073	**5**
8	803.414523	402.210899			785.403958	393.205617	**S**	***447.267407***	224.137342	430.240858	215.624067	429.256842	215.132059	**4**
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053			**3**
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



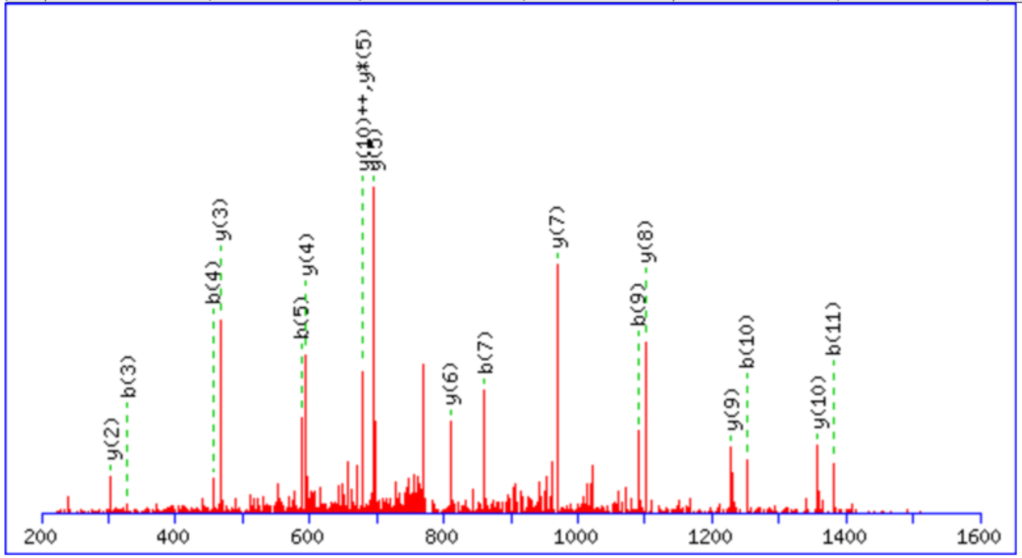
Peptide View

MS/MS Fragmentation of **VVEQMCITQYER**
Found in **IPI00022284**, Tax_Id=9606 Gene_Symbol=PRNP Major prion protein
Experiment: 59 - PyE-2 **Fraction:** PyE-2

Match to Query 11841: 1554.718448 from(778.366500,2+)
Title: OECHL100312_34.13386.13386.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_34.raw
Monoisotopic mass of neutral peptide Mr(calc): 1554.717041**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 68
Expect: 1.6e-005**Matches :** 18/120 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	100.075690	50.541483					**V**							**12**
2	199.144104	100.075690					**V**	1456.655914	728.831595	1439.629365	720.318321	1438.645349	719.826313	**11**
3	**328.186697**	164.596987			310.176132	155.591704	**E**	***1357.587500***	679.297388	1340.560951	670.784114	1339.576935	670.292106	**10**
4	**456.245275**	228.626276	439.218726	220.113001	438.234710	219.620993	**Q**	***1228.544907***	614.776092	1211.518358	606.262817	1210.534342	605.770809	**9**
5	**587.285760**	294.146518	570.259211	285.633244	569.275195	285.141236	**M**	***1100.486329***	550.746803	1083.459780	542.233528	1082.475764	541.741520	**8**
6	747.316409	374.161843	730.289860	365.648568	729.305844	365.156560	**C**	***969.445844***	485.226560	952.419295	476.713286	951.435279	476.221278	**7**

7	**860.400473**	430.703875	843.373924	422.190600	842.389908	421.698592	**I**	***809.415195***	405.211236	792.388646	396.697961	791.404630	396.205953	**6**
8	961.448152	481.227714	944.421603	472.714440	943.437587	472.222432	**T**	***696.331131***	348.669204	679.304582	340.155929	678.320566	339.663921	**5**
9	**1089.506730**	545.257003	1072.480181	536.743729	1071.496165	536.251721	**Q**	***595.283452***	298.145364	578.256903	289.632090	577.272887	289.140082	**4**
10	**1252.570059**	626.788668	1235.543510	618.275393	1234.559494	617.783385	**Y**	***467.224874***	234.116075	450.198325	225.602801	449.214309	225.110793	**3**
11	**1381.612652**	691.309964	1364.586103	682.796690	1363.602087	682.304682	**E**	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**



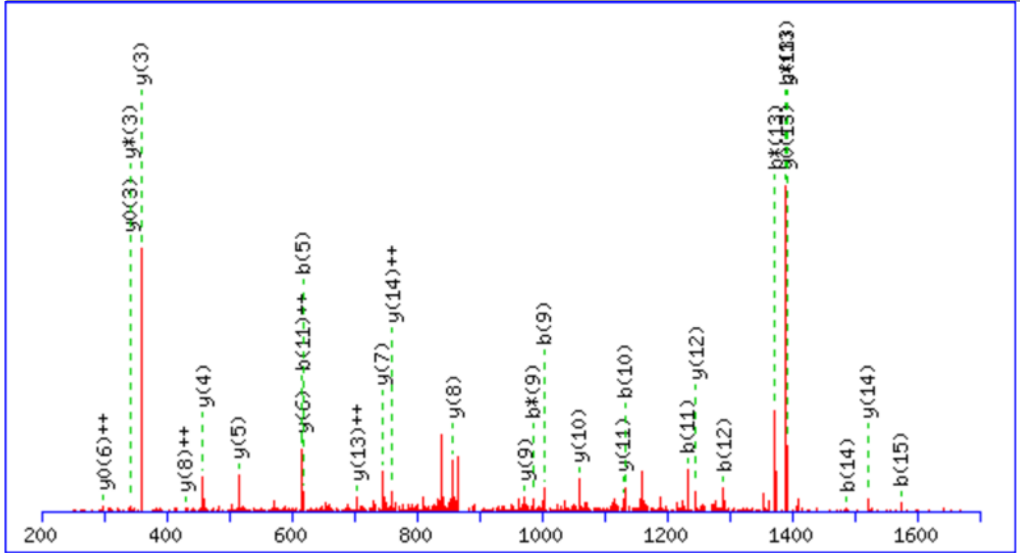
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 59 - PyE-2 **Fraction:** PyE-2

Match to Query 13793: 1746.916848 from(874.465700,2+)
Title: OECHL100312_34.17246.17246.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_34.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66
Expect: 2.7e-005**Matches :** 30/156 fragment ions using 58 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#

1	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	689.386854	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	**1486.778787**	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**

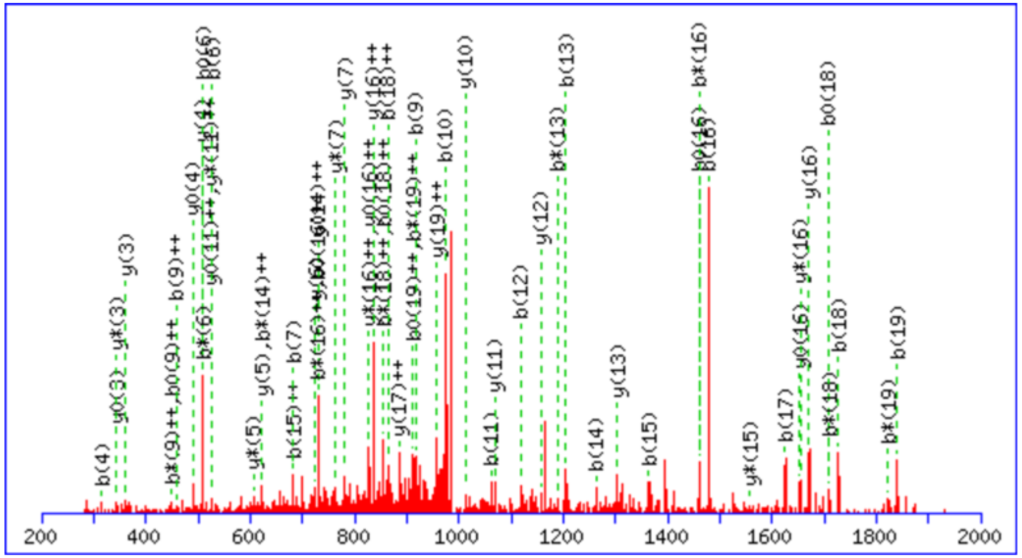


Peptide View

MS/MS Fragmentation of **ASGVPNRFSGSGSGTDFTLK**
Found in **IPI00387110**, Tax_Id=9606 Gene_Symbol=- Ig kappa chain V-II region MIL
Experiment: 59 - PyE-2 **Fraction:** PyE-2

Match to Query 15263: 1984.950448 from(993.482500,2+)
Title: OECHL100312_34.13780.13780.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_34.raw
Monoisotopic mass of neutral peptide Mr(calc): 1984.949051**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N6 :** Deamidated (NQ)**Ions Score:** 51 **Expect:** 0.0013**Matches :** 60/212 fragment ions using 145 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					**A**							**20**
2	159.076418	80.041847			141.065853	71.036564	**S**	1914.919197	957.963236	1897.892648	949.449962	1896.908632	948.957954	**19**
3	216.097882	108.552579			198.087317	99.547296	**G**	1827.887169	914.447222	1810.860620	905.933948	1809.876604	905.441940	**18**
4	***315.166296***	158.086786			297.155731	149.081504	**V**	1770.865705	885.936490	1753.839156	877.423216	1752.855140	876.931208	**17**
5	412.219060	206.613168			394.208495	197.607885	**P**	**1671.797291**	836.402283	1654.770742	827.889009	1653.786726	827.397001	**16**
6	***527.246003***	264.126640	510.219454	255.613365	509.235438	255.121357	**N**	1574.744527	787.875902	1557.717978	779.362627	1556.733962	778.870619	**15**
7	***683.347114***	342.177195	666.320565	333.663920	665.336549	333.171912	**R**	1459.717584	730.362430	1442.691035	721.849156	1441.707019	721.357148	**14**
8	830.415528	415.711402	813.388979	407.198127	812.404963	406.706119	**F**	**1303.616473**	652.311875	1286.589924	643.798600	1285.605908	643.306592	**13**
9	***917.447556***	459.227416	900.421007	450.714141	899.436991	450.222133	**S**	**1156.548059**	578.777668	1139.521510	570.264393	1138.537494	569.772385	**12**
10	***974.469020***	487.738148	957.442471	479.224873	956.458455	478.732865	**G**	**1069.516031**	535.261654	1052.489482	526.748379	1051.505466	526.256371	**11**
11	***1061.501048***	531.254162	1044.474499	522.740887	1043.490483	522.248879	**S**	**1012.494567**	506.750922	995.468018	498.237647	994.484002	497.745639	**10**
12	***1118.522512***	559.764894	1101.495963	551.251619	1100.511947	550.759611	**G**	925.462539	463.234908	908.435990	454.721633	907.451974	454.229625	**9**
13	***1205.554540***	603.280908	1188.527991	594.767633	1187.543975	594.275625	**S**	868.441075	434.724176	851.414526	426.210901	850.430510	425.718893	**8**
14	***1262.576004***	631.791640	1245.549455	623.278365	1244.565439	622.786357	**G**	**781.409047**	391.208162	764.382498	382.694887	763.398482	382.202879	**7**
15	***1363.623683***	682.315479	1346.597134	673.802205	1345.613118	673.310197	**T**	**724.387583**	362.697430	707.361034	354.184155	706.377018	353.692147	**6**
16	***1478.650626***	739.828951	1461.624077	731.315677	1460.640061	730.823668	**D**	**623.339904**	312.173590	606.313355	303.660316	605.329339	303.168308	**5**
17	***1625.719040***	813.363158	1608.692491	804.849884	1607.708475	804.357875	**F**	**508.312961**	254.660118	491.286412	246.146844	490.302396	245.654836	**4**
18	***1726.766719***	863.886998	1709.740170	855.373723	1708.756154	854.881715	**T**	**361.244547**	181.125911	344.217998	172.612637	343.233982	172.120629	**3**
19	***1839.850783***	920.429029	1822.824234	911.915755	1821.840218	911.423747	**L**	260.196868	130.602072	243.170319	122.088797			**2**
20							**K**	147.112804	74.060040	130.086255	65.546765			**1**



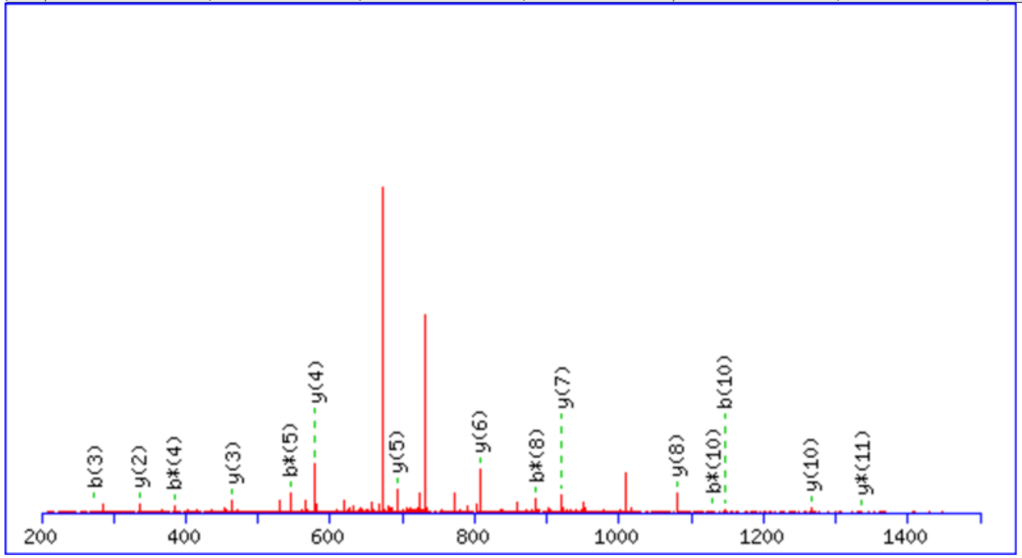
Peptide View

MS/MS Fragmentation of **QSGQCLDIDECR**
Found in **IPI00294615**, Tax_Id=9606 Gene_Symbol=FBLN5 Fibulin-5
Experiment: 59 - PyE-2 **Fraction:** PyE-2

Match to Query 10825: 1479.610248 from(740.812400,2+)
Title: OECHL100312_34.8594.8594.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_34.raw
Monoisotopic mass of neutral peptide Mr(calc): 1479.608231**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00015**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	129.065854	65.036565	112.039305	56.523291			**Q**							**12**
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	**S**	1352.556927	676.782102	1335.530378	668.268827	1334.546362	667.776819	**11**
3	**273.119346**	137.063311	256.092797	128.550037	255.108781	128.058029	**G**	***1265.524899***	633.266088	1248.498350	624.752813	1247.514334	624.260805	**10**
4	401.177924	201.092600	384.151375	192.579326	383.167359	192.087318	**Q**	1208.503435	604.755356	1191.476886	596.242081	1190.492870	595.750073	**9**
5	561.208573	281.107925	544.182024	272.594650	543.198008	272.102642	**C**	***1080.444857***	540.726067	1063.418308	532.212792	1062.434292	531.720784	**8**
6	674.292637	337.649957	657.266088	329.136682	656.282072	328.644674	**L**	***920.414208***	460.710742	903.387659	452.197468	902.403643	451.705460	**7**

7	789.319580	395.163428	772.293031	386.650154	771.309015	386.158146	**D**	***807.330144***	404.168710	790.303595	395.655436	789.319579	395.163428	**6**
8	902.403644	451.705460	885.377095	443.192186	884.393079	442.700178	**I**	***692.303201***	346.655239	675.276652	338.141964	674.292636	337.649956	**5**
9	1017.430587	509.218932	1000.404038	500.705657	999.420022	500.213649	**D**	***579.219137***	290.113207	562.192588	281.599932	561.208572	281.107924	**4**
10	**1146.473180**	573.740228	1129.446631	565.226954	1128.462615	564.734946	**E**	***464.192194***	232.599735	447.165645	224.086461	446.181629	223.594453	**3**
11	1306.503829	653.755553	1289.477280	645.242278	1288.493264	644.750270	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**



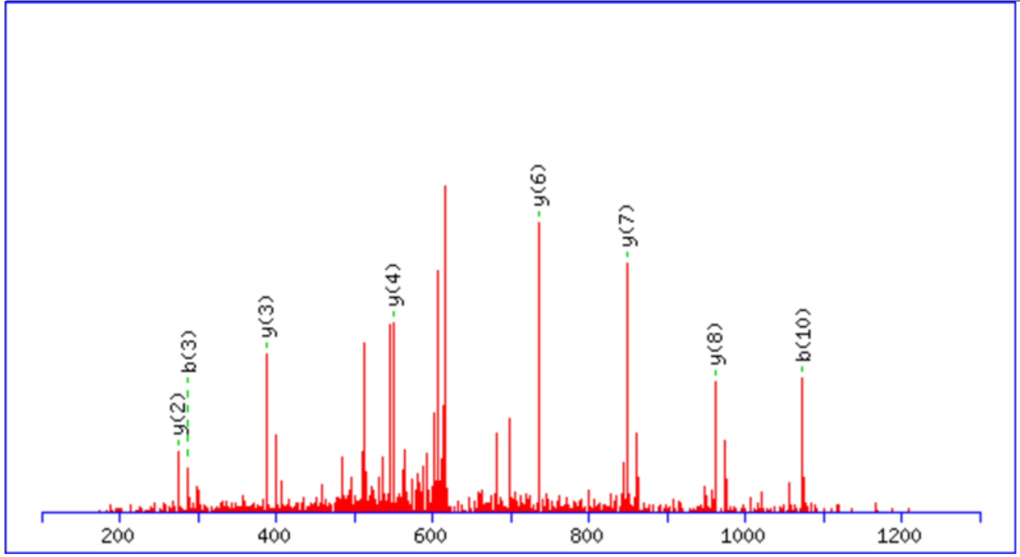
Peptide View

MS/MS Fragmentation of **ASQILNAYLVR**
Found in **IPI00289920**, Tax_Id=9606 Gene_Symbol=UPK3A Isoform 1 of Uroplakin-3a
Experiment: 59 - PyE-2 **Fraction:** PyE-2

Match to Query 8387: 1246.702848 from(624.358700,2+)
Title: OECHL100312_34.16112.16112.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_34.raw
Monoisotopic mass of neutral peptide Mr(calc): 1246.703339**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49
Expect: 0.00049**Matches :** 8/96 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	72.044390	36.525833					**A**							**11**
2	159.076418	80.041847			141.065853	71.036564	**S**	1176.673534	588.840405	1159.646985	580.327131	1158.662969	579.835123	**10**
3	**287.134996**	144.071136	270.108447	135.557862	269.124431	135.065854	**Q**	1089.641506	545.324391	1072.614957	536.811117			**9**
4	400.219060	200.613168	383.192511	192.099894	382.208495	191.607886	**I**	***961.582928***	481.295102	944.556379	472.781828			**8**
5	513.303124	257.155200	496.276575	248.641926	495.292559	248.149918	**L**	***848.498864***	424.753070	831.472315	416.239795			**7**
6	627.346051	314.176664	610.319502	305.663389	609.335486	305.171381	**N**	***735.414800***	368.211038	718.388251	359.697764			**6**
7	698.383165	349.695221	681.356616	341.181946	680.372600	340.689938	**A**	621.371873	311.189575	604.345324	302.676300			**5**
8	861.446494	431.226885	844.419945	422.713611	843.435929	422.221603	**Y**	***550.334759***	275.671018	533.308210	267.157743			**4**
9	974.530558	487.768917	957.504009	479.255643	956.519993	478.763635	**L**	***387.271430***	194.139353	370.244881	185.626078			**3**
10	**1073.598972**	537.303124	1056.572423	528.789850	1055.588407	528.297842	**V**	***274.187366***	137.597321	257.160817	129.084046			**2**
11							**R**	175.118952	88.063114	158.092403	79.549839			**1**

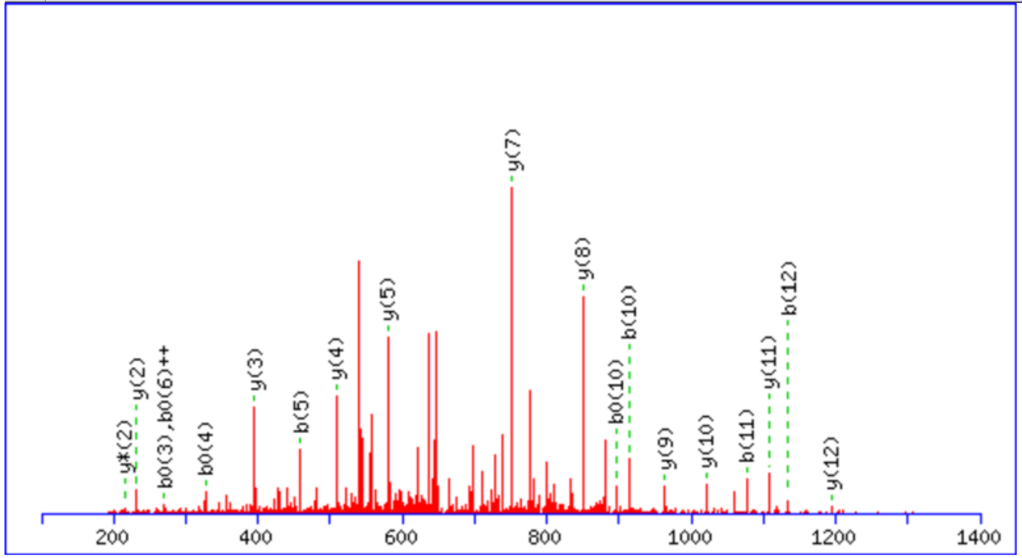


Peptide View

MS/MS Fragmentation of **LSSGLVTAALYGR**
Found in **IPI00218413**, Tax_Id=9606 Gene_Symbol=BTD Biotinidase
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 7853: 1306.724848 from(654.369700,2+)
Title: OECHL100312_32.17307.17307.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 1306.724487**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72
Expect: 2.2e-006**Matches :** 19/106 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							**13**
2	201.123368	101.065322	183.112803	92.060039	**S**	***1194.647714***	597.827495	1177.621165	589.314221	1176.637149	588.822212	**12**
3	288.155396	144.581336	270.144831	135.576053	**S**	***1107.615686***	554.311481	1090.589137	545.798206	1089.605121	545.306198	**11**
4	345.176860	173.092068	327.166295	164.086785	**G**	***1020.583658***	510.795467	1003.557109	502.282192	1002.573093	501.790184	**10**
5	**458.260924**	229.634100	440.250359	220.628817	**L**	***963.562194***	482.284735	946.535645	473.771460	945.551629	473.279452	**9**
6	557.329338	279.168307	539.318773	270.163025	**V**	***850.478130***	425.742703	833.451581	417.229428	832.467565	416.737420	**8**
7	658.377017	329.692147	640.366452	320.686864	**T**	***751.409716***	376.208496	734.383167	367.695221	733.399151	367.203213	**7**
8	729.414131	365.210704	711.403566	356.205421	**A**	650.362037	325.684656	633.335488	317.171382			**6**
9	800.451245	400.729261	782.440680	391.723978	**A**	***579.324923***	290.166099	562.298374	281.652825			**5**
10	**913.535309**	457.271293	895.524744	448.266010	**L**	***508.287809***	254.647542	491.261260	246.134268			**4**
11	**1076.598638**	538.802957	1058.588073	529.797674	**Y**	***395.203745***	198.105510	378.177196	189.592236			**3**
12	**1133.620102**	567.313689	1115.609537	558.308406	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
13					**R**	175.118952	88.063114	158.092403	79.549839			**1**

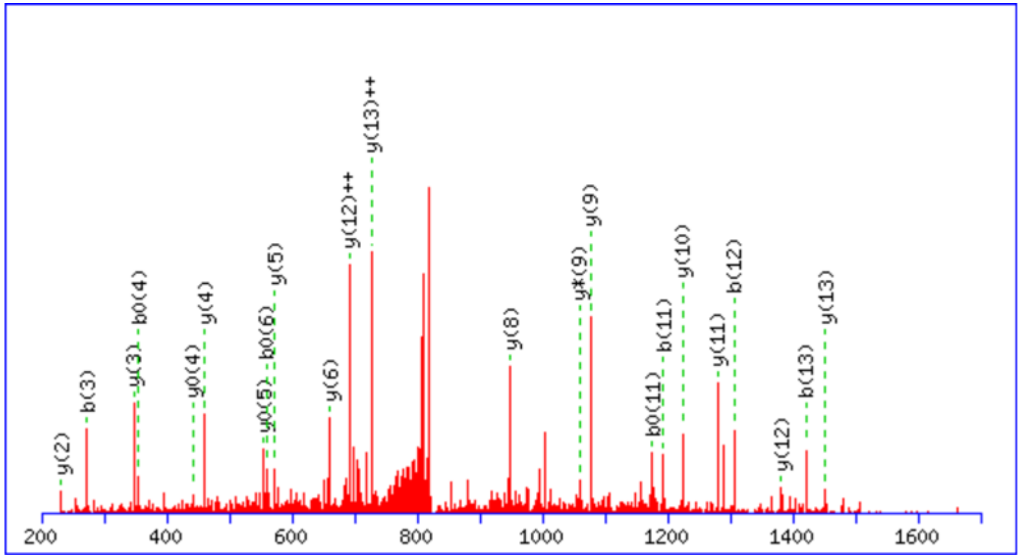


Peptide View

MS/MS Fragmentation of **VTATGFQQCSLIDGR**
Found in **IPI00333140**, Tax_Id=9606 Gene_Symbol=DNER Delta and Notch-like epidermal growth factor-related receptor
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 11071: 1651.800048 from(826.907300,2+)
Title: OECHL100312_32.14068.14068.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 1651.798828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 79
Expect: 1.5e-006**Matches :** 23/150 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	100.075690	50.541483					**V**							**15**
2	201.123369	101.065322			183.112804	92.060040	**T**	1553.737670	777.372473	1536.711121	768.859198	1535.727105	768.367190	**14**
3	**272.160483**	136.583879			254.149918	127.578597	**A**	***1452.689991***	726.848633	1435.663442	718.335359	1434.679426	717.843351	**13**
4	373.208162	187.107719			355.197597	178.102437	**T**	***1381.652877***	691.330076	1364.626328	682.816802	1363.642312	682.324794	**12**
5	430.229626	215.618451			412.219061	206.613169	**G**	***1280.605198***	640.806237	1263.578649	632.292962	1262.594633	631.800954	**11**
6	577.298040	289.152658			559.287475	280.147376	**F**	***1223.583734***	612.295505	1206.557185	603.782230	1205.573169	603.290222	**10**
7	705.356618	353.181947	688.330069	344.668673	687.346053	344.176665	**Q**	***1076.515320***	538.761298	1059.488771	530.248023	1058.504755	529.756015	**9**
8	833.415196	417.211236	816.388647	408.697962	815.404631	408.205954	**Q**	***948.456742***	474.732009	931.430193	466.218734	930.446177	465.726726	**8**
9	993.445845	497.226561	976.419296	488.713286	975.435280	488.221278	**C**	820.398164	410.702720	803.371615	402.189445	802.387599	401.697437	**7**
10	1080.477873	540.742575	1063.451324	532.229300	1062.467308	531.737292	**S**	***660.367515***	330.687395	643.340966	322.174121	642.356950	321.682113	**6**
11	**1193.561937**	597.284607	1176.535388	588.771332	1175.551372	588.279324	**L**	***573.335487***	287.171381	556.308938	278.658107	555.324922	278.166099	**5**
12	**1306.646001**	653.826638	1289.619452	645.313364	1288.635436	644.821356	**I**	***460.251423***	230.629349	443.224874	222.116075	442.240858	221.624067	**4**
13	**1421.672944**	711.340110	1404.646395	702.826836	1403.662379	702.334827	**D**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
14	1478.694408	739.850842	1461.667859	731.337567	1460.683843	730.845559	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



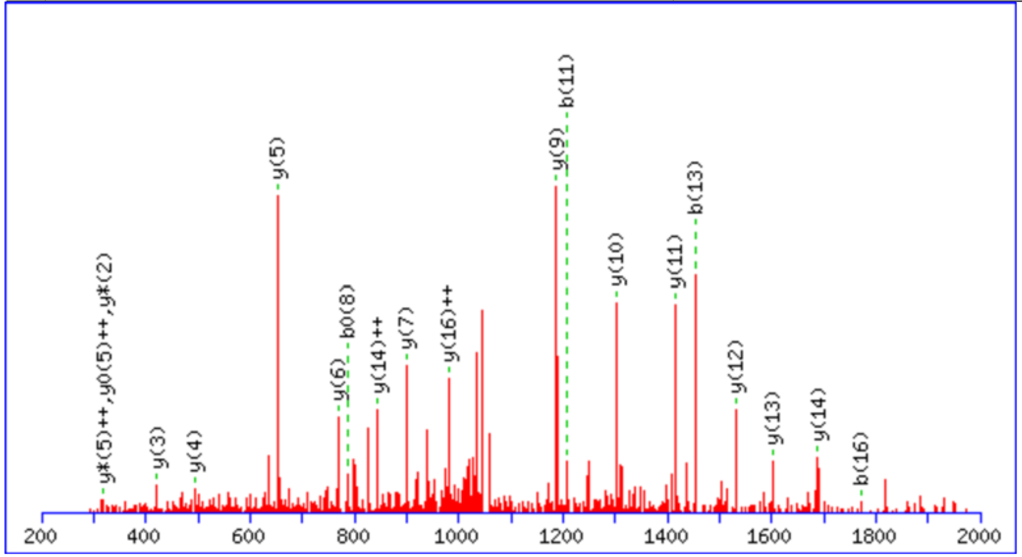
Peptide View

MS/MS Fragmentation of **GSSWSADLDKCMDCASCR**
Found in **IPI00010277**, Tax_Id=9606 Gene_Symbol=TNFRSF12A Isoform 1 of Tumor necrosis factor receptor superfamily member 12A
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 14721: 2104.807448 from(1053.411000,2+)
Title: OECHL100312_32.14613.14613.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 2104.807083**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71
Expect: 4.2e-007**Matches :** 20/180 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	58.028740	29.518008					G						
2	145.060768	73.034022			127.050203	64.028740	S	2048.792893	1024.900085	2031.766344	1016.386810	2030.782328	1015.894802
3	232.092796	116.550036			214.082231	107.544753	S	1961.760865	981.384071	1944.734316	972.870796	1943.750300	972.378788
4	418.172109	209.589693			400.161544	200.584410	W	1874.728837	937.868057	1857.702288	929.354782	1856.718272	928.862774
5	505.204137	253.105707			487.193572	244.100424	S	***1688.649524***	844.828400	1671.622975	836.315126	1670.638959	835.823118
6	576.241251	288.624264			558.230686	279.618981	A	***1601.617496***	801.312386	1584.590947	792.799112	1583.606931	792.307104

7	691.268194	346.137735			673.257629	337.132453	**D**	***1530.580382***	765.793829	1513.553833	757.280555	1512.569817	756.788547
8	804.352258	402.679767			786.341693	393.674485	**L**	***1415.553439***	708.280358	1398.526890	699.767083	1397.542874	699.275075
9	919.379201	460.193239			901.368636	451.187956	**D**	***1302.469375***	651.738326	1285.442826	643.225051	1284.458810	642.733043
10	1047.474164	524.240720	1030.447615	515.727446	1029.463599	515.235437	**K**	***1187.442432***	594.224854	1170.415883	585.711580	1169.431867	585.219572
11	**1207.504813**	604.256045	1190.478264	595.742770	1189.494248	595.250762	**C**	1059.347469	530.177373	1042.320920	521.664098	1041.336904	521.172090
12	1338.545298	669.776287	1321.518749	661.263013	1320.534733	660.771005	**M**	***899.316820***	450.162048	882.290271	441.648774	881.306255	441.156766
13	**1453.572241**	727.289759	1436.545692	718.776484	1435.561676	718.284476	**D**	***768.276335***	384.641806	751.249786	376.128531	750.265770	375.636523
14	1613.602890	807.305083	1596.576341	798.791809	1595.592325	798.299801	**C**	***653.249392***	327.128334	636.222843	318.615060	635.238827	318.123052
15	1684.640004	842.823640	1667.613455	834.310366	1666.629439	833.818358	**A**	***493.218743***	247.113010	476.192194	238.599735	475.208178	238.107727
16	**1771.672032**	886.339654	1754.645483	877.826380	1753.661467	877.334372	**S**	***422.181629***	211.594453	405.155080	203.081178	404.171064	202.589170
17	1931.702681	966.354979	1914.676132	957.841704	1913.692116	957.349696	**C**	335.149601	168.078439	318.123052	159.565164		
18							**R**	175.118952	88.063114	158.092403	79.549840		

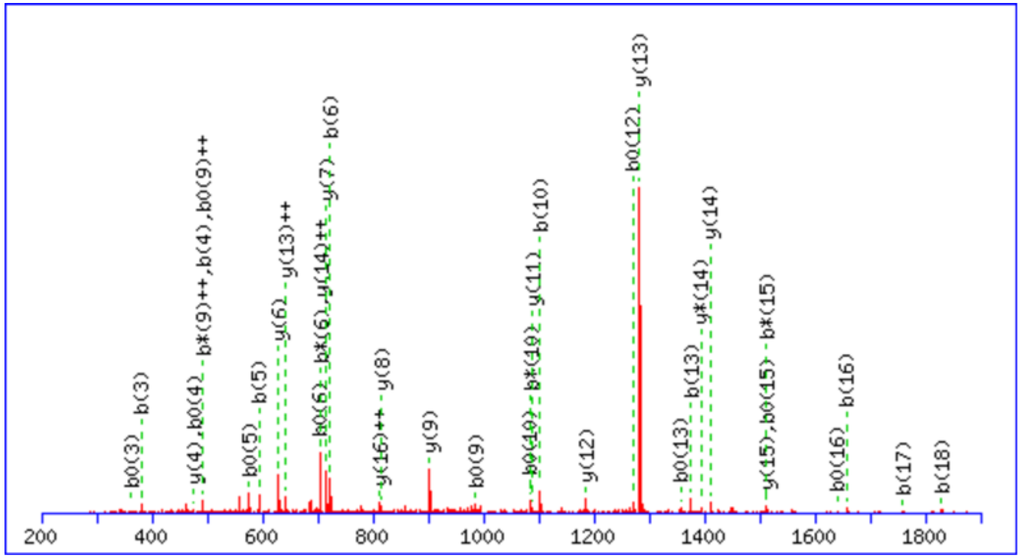


Peptide View

MS/MS Fragmentation of **SYELTQPPSVSVSPGQTAR**
Found in **IPI00382440**, Tax_Id=9606 Gene_Symbol=- Ig lambda chain V-IV region Hil
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 14039: 2002.995448 from(1002.505000,2+)
Title: OECHL100312_32.13438.13438.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 2002.995987**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 0.00013**Matches :** 38/202 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	**S**							**19**
2	251.102633	126.054954			233.092068	117.049672	**Y**	1916.971234	958.989255	1899.944685	950.475981	1898.960669	949.983973	**18**
3	***380.145226***	190.576251			362.134661	181.570969	**E**	1753.907905	877.457591	1736.881356	868.944316	1735.897340	868.452308	**17**
4	***493.229290***	247.118283			475.218725	238.113001	**L**	1624.865312	812.936294	1607.838763	804.423020	1606.854747	803.931012	**16**
5	***594.276969***	297.642123			576.266404	288.636840	**T**	***1511.781248***	756.394262	1494.754699	747.880988	1493.770683	747.388980	**15**
6	***722.335547***	361.671412	705.308998	353.158137	704.324982	352.666129	**Q**	***1410.733569***	705.870423	1393.707020	697.357148	1392.723004	696.865140	**14**
7	819.388311	410.197794	802.361762	401.684519	801.377746	401.192511	**P**	***1282.674991***	641.841134	1265.648442	633.327859	1264.664426	632.835851	**13**
8	916.441075	458.724176	899.414526	450.210901	898.430510	449.718893	**P**	***1185.622227***	593.314752	1168.595678	584.801477	1167.611662	584.309469	**12**
9	1003.473103	502.240190	986.446554	493.726915	985.462538	493.234907	**S**	***1088.569463***	544.788370	1071.542914	536.275095	1070.558898	535.783087	**11**
10	***1102.541517***	551.774397	1085.514968	543.261122	1084.530952	542.769114	**V**	1001.537435	501.272356	984.510886	492.759081	983.526870	492.267073	**10**
11	1189.573545	595.290411	1172.546996	586.777136	1171.562980	586.285128	**S**	***902.469021***	451.738149	885.442472	443.224874	884.458456	442.732866	**9**
12	1288.641959	644.824618	1271.615410	636.311343	1270.631394	635.819335	**V**	***815.436993***	408.222135	798.410444	399.708860	797.426428	399.216852	**8**
13	***1375.673987***	688.340632	1358.647438	679.827357	1357.663422	679.335349	**S**	***716.368579***	358.687928	699.342030	350.174653	698.358014	349.682645	**7**
14	1472.726751	736.867014	1455.700202	728.353739	1454.716186	727.861731	**P**	***629.336551***	315.171914	612.310002	306.658639	611.325986	306.166631	**6**
15	1529.748215	765.377746	1512.721666	756.864471	1511.737650	756.372463	**G**	532.283787	266.645532	515.257238	258.132257	514.273222	257.640249	**5**
16	***1657.806793***	829.407035	1640.780244	820.893760	1639.796228	820.401752	**Q**	***475.262323***	238.134800	458.235774	229.621525	457.251758	229.129517	**4**
17	***1758.854472***	879.930874	1741.827923	871.417600	1740.843907	870.925592	**T**	347.203745	174.105510	330.177196	165.592236	329.193180	165.100228	**3**
18	***1829.891586***	915.449431	1812.865037	906.936157	1811.881021	906.444149	**A**	246.156066	123.581671	229.129517	115.068396			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



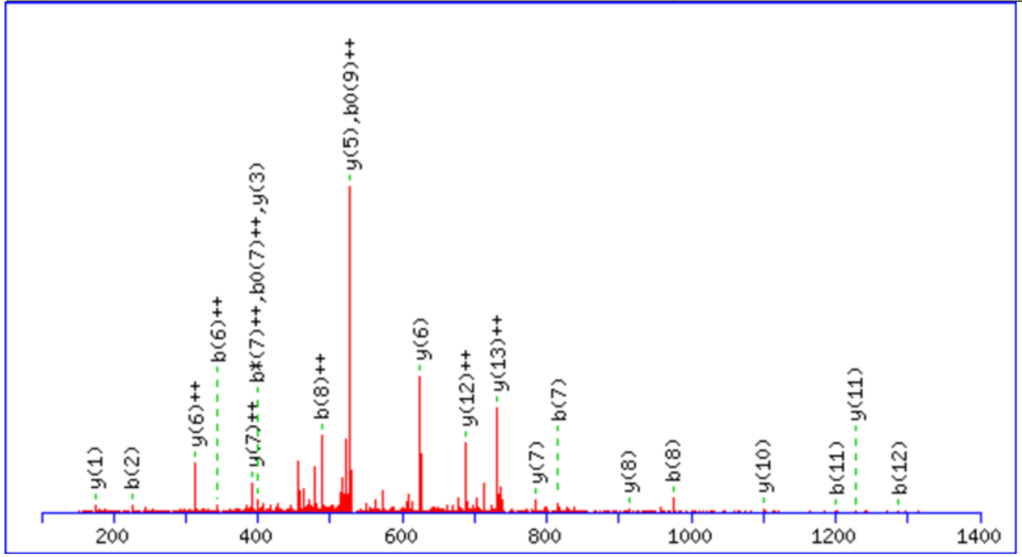
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 10452: 1597.705872 from(533.575900,3+)
Title: OECHL100312_32.2471.2471.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64
Expect: 2.2e-005**Matches :** 22/144 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	138.066188	69.536732					**H**							**14**
2	***225.098216***	113.052746			207.087651	104.047463	**S**	1461.653938	731.330607	1444.627389	722.817333	1443.643373	722.325325	**13**
3	372.166630	186.586953			354.156065	177.581671	**F**	1374.621910	687.814593	1357.595361	679.301319	1356.611345	678.809311	**12**
4	500.261593	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	**11**
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	**10**
6	686.325650	**343.666463**	669.299101	335.153189	668.315085	334.661181	**E**	1042.437069	521.722173	1025.410520	513.208898	1024.426504	512.716890	**9**

7	***815.368243***	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	***975.398892***	**488.203084**	958.372343	479.689810	957.388327	479.197802	**C**	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	1143.488770	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	***1200.510234***	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	456.231356	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	***1287.542262***	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	1424.601174	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	312.177864	156.592570	295.151315	148.079295			**2**
14							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



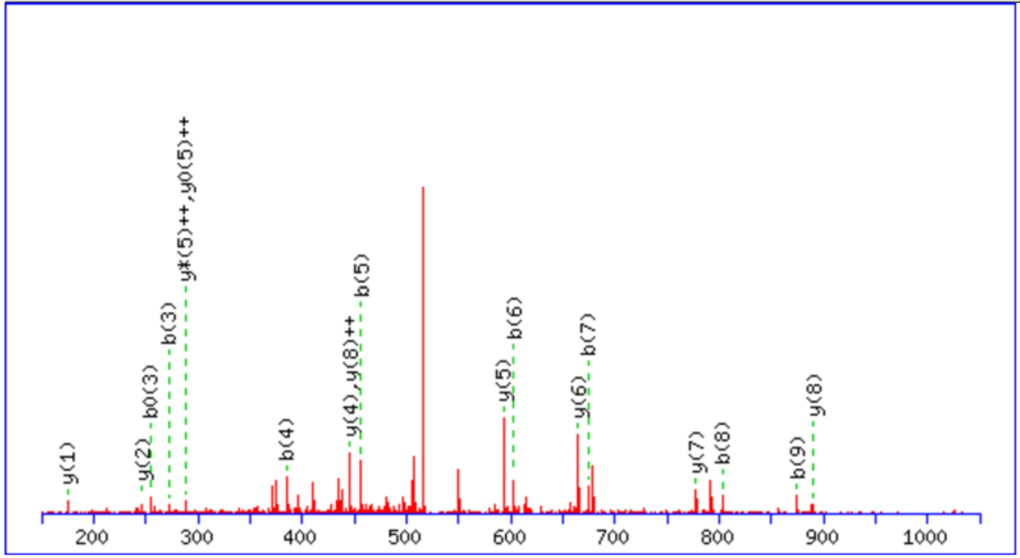
Peptide View

MS/MS Fragmentation of **GTLLAFAEAR**
Found in **IPI00029817**, Tax_Id=9606 Gene_Symbol=NEU1 Sialidase-1
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 4163: 1047.571048 from(524.792800,2+)
Title: OECHL100312_32.17074.17074.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 1047.571274**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57

Expect: 0.00016**Matches :** 18/84 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.028740	29.518008			**G**							**10**
2	159.076419	80.041847	141.065854	71.036565	**T**	991.557108	496.282192	974.530559	487.768918	973.546543	487.276910	**9**
3	***272.160483***	136.583879	254.149918	127.578597	**L**	***890.509429***	445.758353	873.482880	437.245078	872.498864	436.753070	**8**
4	***385.244547***	193.125912	367.233982	184.120629	**L**	***777.425365***	389.216321	760.398816	380.703046	759.414800	380.211038	**7**
5	***456.281661***	228.644469	438.271096	219.639186	**A**	***664.341301***	332.674289	647.314752	324.161014	646.330736	323.669006	**6**
6	***603.350075***	302.178676	585.339510	293.173393	**F**	***593.304187***	297.155732	576.277638	288.642457	575.293622	288.150449	**5**
7	***674.387189***	337.697233	656.376624	328.691950	**A**	***446.235773***	223.621524	429.209224	215.108250	428.225208	214.616242	**4**
8	***803.429782***	402.218529	785.419217	393.213247	**E**	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	**3**
9	***874.466896***	437.737086	856.456331	428.731804	**A**	***246.156066***	123.581671	229.129517	115.068397			**2**
10					**R**	***175.118952***	88.063114	158.092403	79.549840			**1**

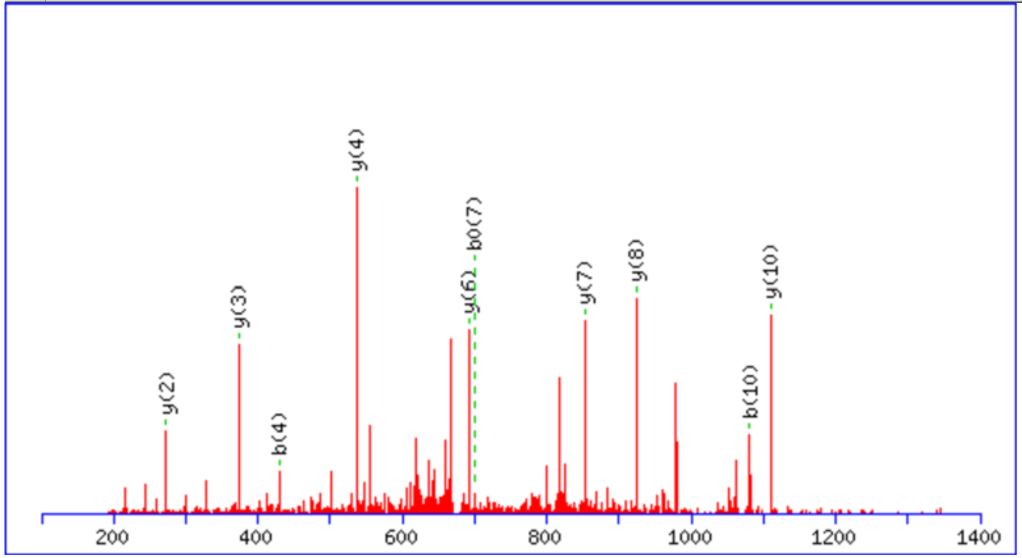


Peptide View

MS/MS Fragmentation of **LEGEACGVYTPR**
Found in **IPI00297284**, Tax_Id=9606 Gene_Symbol=IGFBP2 Insulin-like growth factor-binding protein 2
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 8237: 1350.627048 from(676.320800,2+)
Title: OECHL100312_32.8612.8612.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 1350.623795**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 9e-005**Matches :** 10/104 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							**12**
2	243.133933	122.070605	225.123368	113.065322	**E**	1238.547015	619.777146	1221.520466	611.263871	1220.536450	610.771863	**11**
3	300.155397	150.581336	282.144832	141.576054	**G**	***1109.504422***	555.255849	1092.477873	546.742575	1091.493857	546.250567	**10**
4	**429.197990**	215.102633	411.187425	206.097351	**E**	1052.482958	526.745117	1035.456409	518.231843	1034.472393	517.739835	**9**
5	500.235104	250.621190	482.224539	241.615908	**A**	***923.440365***	462.223821	906.413816	453.710546	905.429800	453.218538	**8**
6	660.265753	330.636515	642.255188	321.631232	**C**	***852.403251***	426.705264	835.376702	418.191989	834.392686	417.699981	**7**
7	717.287217	359.147247	699.276652	350.141964	**G**	***692.372602***	346.689939	675.346053	338.176665	674.362037	337.684657	**6**
8	816.355631	408.681454	798.345066	399.676171	**V**	635.351138	318.179207	618.324589	309.665933	617.340573	309.173925	**5**
9	979.418960	490.213118	961.408395	481.207836	**Y**	***536.282724***	268.645000	519.256175	260.131726	518.272159	259.639718	**4**
10	**1080.466639**	540.736958	1062.456074	531.731675	**T**	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	**3**
11	1177.519403	589.263340	1159.508838	580.258057	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**

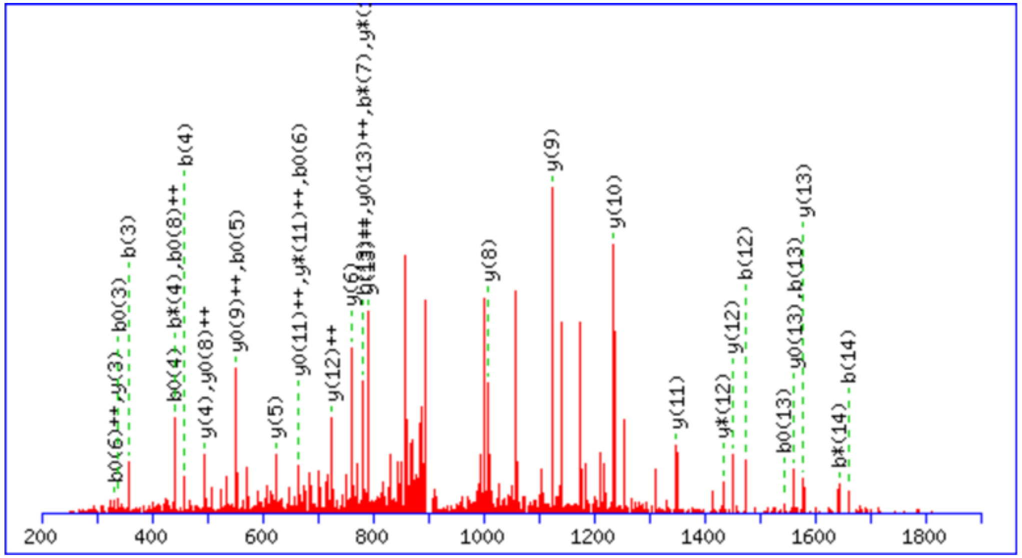


Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 12703: 1805.933248 from(903.973900,2+)
Title: OECHL100312_32.20085.20085.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57
Expect: 0.00027**Matches :** 36/160 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	115.050203	58.028740	98.023654	49.515465			**N**							**15**
2	228.134267	114.570771	211.107718	106.057497			**I**	1692.895549	846.951413	1675.869000	838.438138	1674.884984	837.946130	**14**
3	**357.176860**	179.092068	340.150311	170.578793	339.166295	170.086785	**E**	***1579.811485***	790.409381	1562.784936	781.896106	1561.800920	781.404098	**13**
4	**458.224539**	229.615907	441.197990	221.102633	440.213974	220.610625	**T**	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.882802	**12**
5	571.308603	286.157940	554.282054	277.644665	553.298038	277.152657	**I**	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.358962	**11**
6	684.392667	342.699972	667.366118	334.186697	666.382102	333.694689	**I**	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.816930	**10**
7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	**N**	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.274898	**9**
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	**T**	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.253435	**8**
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	**F**	908.462479	454.734878	891.435930	446.221603	890.451914	445.729595	**7**
10	1183.610599	592.308938	1166.584050	583.795663	1165.600034	583.303655	**H**	***761.394065***	381.200671	744.367516	372.687396	743.383500	372.195388	**6**
11	1311.669177	656.338227	1294.642628	647.824952	1293.658612	647.332944	**Q**	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.665932	**5**
12	**1474.732506**	737.869891	1457.705957	729.356617	1456.721941	728.864609	**Y**	***496.276575***	248.641926	479.250026	240.128651	478.266010	239.636643	**4**
13	**1561.764534**	781.385905	1544.737985	772.872631	1543.753969	772.380623	**S**	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.104979	**3**
14	**1660.832948**	830.920112	1643.806399	822.406838	1642.822383	821.914830	**V**	246.181218	123.594247	229.154669	115.080973			**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



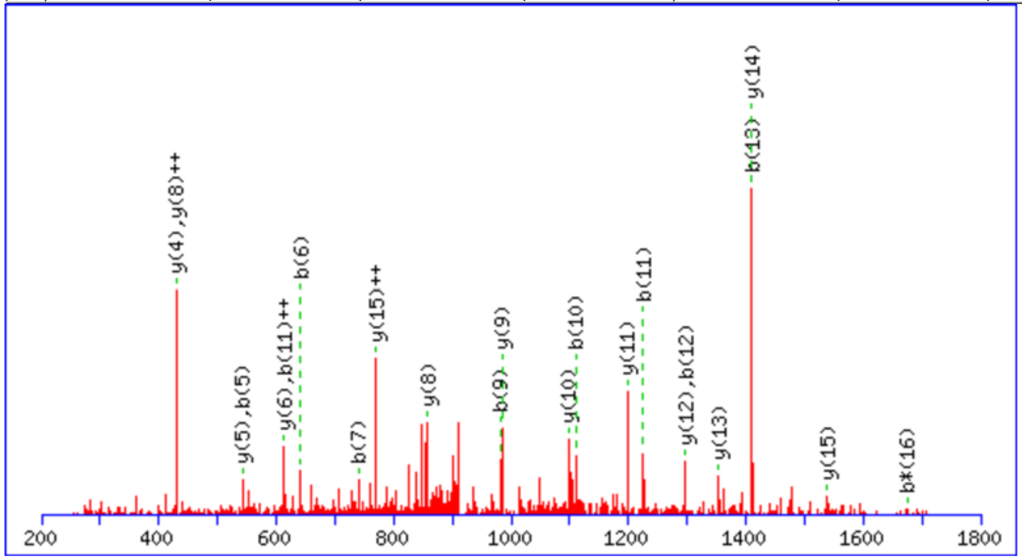
Peptide View

MS/MS Fragmentation of **WLKGGVVLKEDALPGQK**
Found in **IPI00019906**, Tax_Id=9606 Gene_Symbol=BSG Isoform 2 of Basigin
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 12919: 1837.047448 from(919.531000,2+)
Title: OECHL100312_32.13954.13954.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 1837.046158**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 83
Expect: 1.2e-007**Matches :** 23/158 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	187.086589	94.046932					**W**							**17**
2	300.170653	150.588965					**L**	1651.974134	826.490705	1634.947585	817.977431	1633.963569	817.485423	**16**
3	428.265616	214.636446	411.239067	206.123172			**K**	***1538.890070***	769.948673	1521.863521	761.435399	1520.879505	760.943390	**15**
4	485.287080	243.147178	468.260531	234.633904			**G**	***1410.795107***	705.901191	1393.768558	697.387917	1392.784542	696.895909	**14**
5	**542.308544**	271.657910	525.281995	263.144636			**G**	***1353.773643***	677.390460	1336.747094	668.877185	1335.763078	668.385177	**13**
6	**641.376958**	321.192117	624.350409	312.678843			**V**	***1296.752179***	648.879727	1279.725630	640.366453	1278.741614	639.874445	**12**

7	**740.445372**	370.726324	723.418823	362.213050			**V**	***1197.683765***	599.345521	1180.657216	590.832246	1179.673200	590.340238	**11**
8	853.529436	427.268356	836.502887	418.755082			**L**	***1098.615351***	549.811314	1081.588802	541.298039	1080.604786	540.806031	**10**
9	**981.624399**	491.315838	964.597850	482.802563			**K**	***985.531287***	493.269282	968.504738	484.756007	967.520722	484.263999	**9**
10	**1110.666992**	555.837134	1093.640443	547.323860	1092.656427	546.831852	**E**	***857.436324***	429.221800	840.409775	420.708526	839.425759	420.216518	**8**
11	**1225.693935**	613.350606	1208.667386	604.837331	1207.683370	604.345323	**D**	728.393731	364.700503	711.367182	356.187229	710.383166	355.695221	**7**
12	**1296.731049**	648.869163	1279.704500	640.355888	1278.720484	639.863880	**A**	***613.366788***	307.187032	596.340239	298.673757			**6**
13	**1409.815113**	705.411195	1392.788564	696.897920	1391.804548	696.405912	**L**	***542.329674***	271.668475	525.303125	263.155200			**5**
14	1506.867877	753.937577	1489.841328	745.424302	1488.857312	744.932294	**P**	***429.245610***	215.126443	412.219061	206.613168			**4**
15	1563.889341	782.448309	1546.862792	773.935034	1545.878776	773.443026	**G**	332.192846	166.600061	315.166297	158.086786			**3**
16	1691.947919	846.477598	1674.921370	837.964323	1673.937354	837.472315	**Q**	275.171382	138.089329	258.144833	129.576054			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**

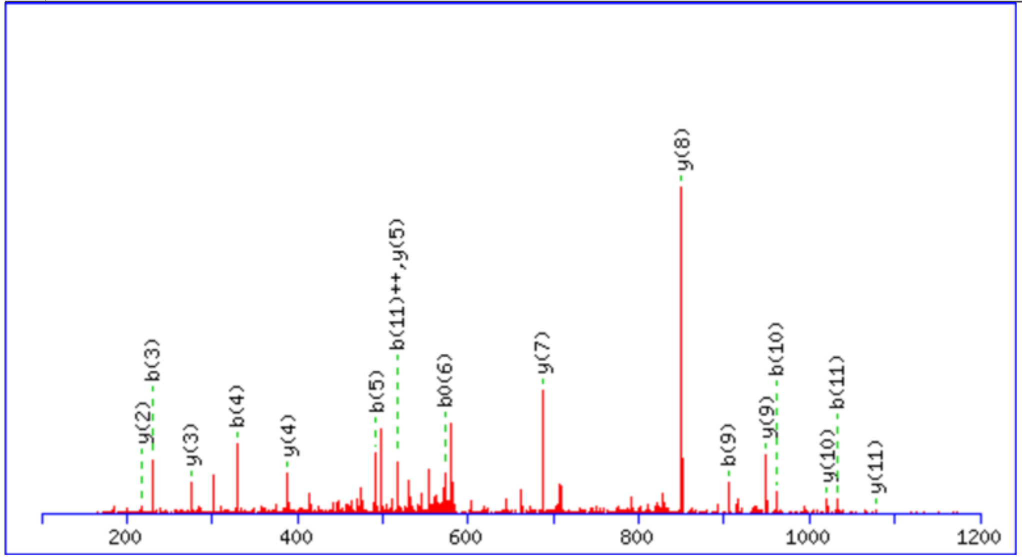


Peptide View

MS/MS Fragmentation of **TGAVYVAEIGAK**
Found in **IPI00552937**, Tax_Id=9606 Gene_Symbol=NHLRC3 NHL repeat-containing protein 3
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 5814: 1177.632048 from(589.823300,2+)
Title: OECHL100312_32.11299.11299.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 1177.634277**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63
Expect: 3.3e-005**Matches :** 17/102 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							12
2	159.076419	80.041847	141.065854	71.036565	G	***1077.593888***	539.300582	1060.567339	530.787308	1059.583323	530.295300	11
3	**230.113533**	115.560404	212.102968	106.555122	A	***1020.572424***	510.789850	1003.545875	502.276576	1002.561859	501.784568	10
4	**329.181947**	165.094611	311.171382	156.089329	V	***949.535310***	475.271293	932.508761	466.758019	931.524745	466.266011	9
5	**492.245276**	246.626276	474.234711	237.620994	Y	***850.466896***	425.737086	833.440347	417.223812	832.456331	416.731804	8
6	591.313690	296.160483	573.303125	287.155201	V	***687.403567***	344.205422	670.377018	335.692147	669.393002	335.200139	7
7	662.350804	331.679040	644.340239	322.673758	A	588.335153	294.671215	571.308604	286.157940	570.324588	285.665932	6
8	791.393397	396.200337	773.382832	387.195054	E	***517.298039***	259.152658	500.271490	250.639383	499.287474	250.147375	5
9	**904.477461**	452.742369	886.466896	443.737086	I	***388.255446***	194.631361	371.228897	186.118087			4
10	**961.498925**	481.253101	943.488360	472.247818	G	***275.171382***	138.089329	258.144833	129.576055			3
11	**1032.536039**	516.771658	1014.525474	507.766375	A	***218.149918***	109.578597	201.123369	101.065322			2
12					K	147.112804	74.060040	130.086255	65.546765			1

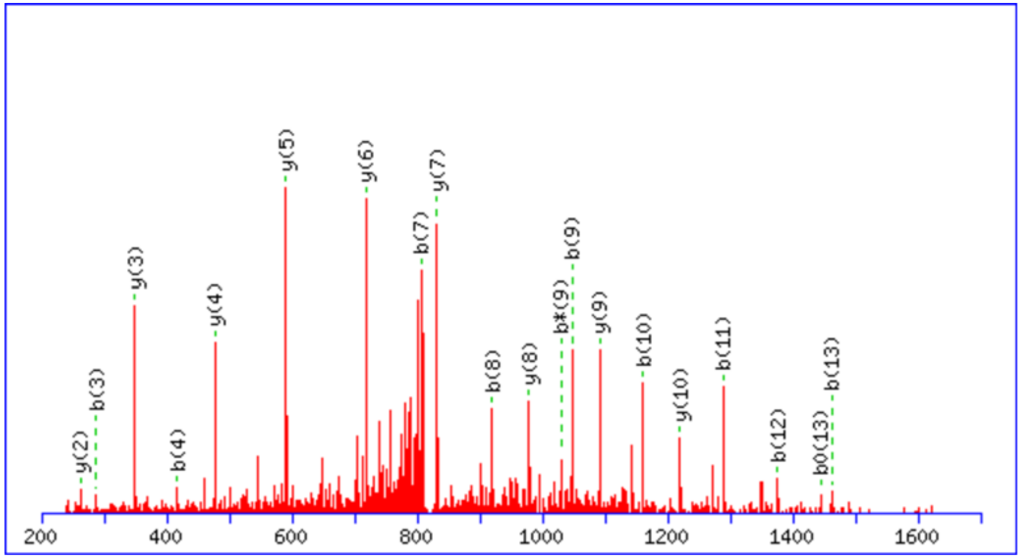


Peptide View

MS/MS Fragmentation of **SAEEQNFLQLQSSR**
Found in **IPI00045033**, Tax_Id=9606 Gene_Symbol=CD209 Isoform 6 of CD209 antigen
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 10738: 1635.785248 from(818.899900,2+)
Title: OECHL100312_32.14278.14278.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 1635.785233**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 78
Expect: 2.5e-006**Matches :** 20/146 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	88.039304	44.523290			70.028739	35.518008	S							14
2	159.076418	80.041847			141.065853	71.036564	A	1549.760511	775.383893	1532.733962	766.870619	1531.749946	766.378611	13
3	***288.119011***	144.563144			270.108446	135.557861	E	1478.723397	739.865336	1461.696848	731.352062	1460.712832	730.860054	12
4	***417.161604***	209.084440			399.151039	200.079158	E	1349.680804	675.344040	1332.654255	666.830765	1331.670239	666.338757	11
5	545.220182	273.113729	528.193633	264.600455	527.209617	264.108447	Q	***1220.638211***	610.822743	1203.611662	602.309469	1202.627646	601.817461	10
6	659.263109	330.135193	642.236560	321.621918	641.252544	321.129910	N	***1092.579633***	546.793454	1075.553084	538.280180	1074.569068	537.788172	9
7	***806.331523***	403.669400	789.304974	395.156125	788.320958	394.664117	F	***978.536706***	489.771991	961.510157	481.258716	960.526141	480.766708	8
8	***919.415587***	460.211432	902.389038	451.698157	901.405022	451.206149	L	***831.468292***	416.237784	814.441743	407.724509	813.457727	407.232501	7
9	***1047.474165***	524.240720	1030.447616	515.727446	1029.463600	515.235438	Q	***718.384228***	359.695752	701.357679	351.182477	700.373663	350.690469	6
10	***1160.558229***	580.782752	1143.531680	572.269478	1142.547664	571.777470	L	***590.325650***	295.666463	573.299101	287.153189	572.315085	286.661181	5
11	***1288.616807***	644.812041	1271.590258	636.298767	1270.606242	635.806759	Q	***477.241586***	239.124431	460.215037	230.611156	459.231021	230.119148	4
12	***1375.648835***	688.328055	1358.622286	679.814781	1357.638270	679.322773	S	***349.183008***	175.095142	332.156459	166.581868	331.172443	166.089860	3
13	***1462.680863***	731.844069	1445.654314	723.330795	1444.670298	722.838787	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
14							R	175.118952	88.063114	158.092403	79.549839			1



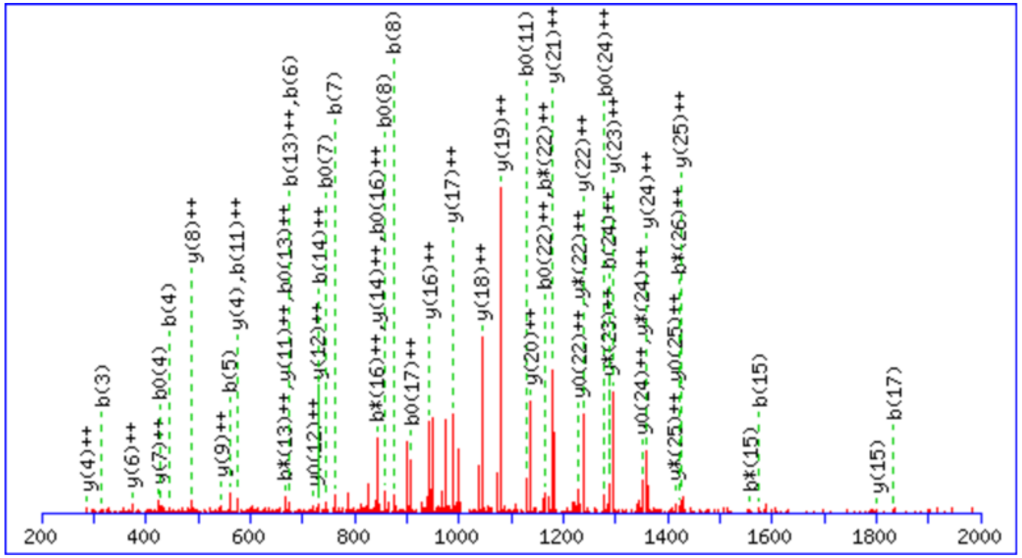
Peptide View

MS/MS Fragmentation of **DAEEDDSLANSSDLLKELLETGDNRER**
Found in **IPI00000828**, Tax_Id=9606 Gene_Symbol=PENK Proenkephalin-A
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 17645: 3033.407172 from(1012.143000,3+)
Title: OECHL100312_32.20692.20692.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 3033.401001**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 3.8e-006**Matches :** 54/292 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	116.034219	58.520748			98.023654	49.515465	D						
2	187.071333	94.039304			169.060768	85.034022	A	2919.381392	1460.194334	2902.354843	1451.681059	2901.370827	1451.1890
3	**316.113926**	158.560601			298.103361	149.555319	E	2848.344278	1424.675777	2831.317729	1416.162502	2830.333713	1415.6704
4	**445.156519**	223.081898			427.145954	214.076615	E	2719.301685	1360.154480	2702.275136	1351.641206	2701.291120	1351.1491
5	**560.183462**	280.595369			542.172897	271.590087	D	2590.259092	1295.633184	2573.232543	1287.119909	2572.248527	1286.6279
6	**675.210405**	338.108841			657.199840	329.103558	D	2475.232149	1238.119712	2458.205600	1229.606438	2457.221584	1229.1144

7	**762.242433**	381.624855			744.231868	372.619572	**S**	2360.205206	1180.606241	2343.178657	1172.092966	2342.194641	1171.6009
8	**875.326497**	438.166887			857.315932	429.161604	**L**	2273.173178	1137.090227	2256.146629	1128.576952	2255.162613	1128.0849
9	946.363611	473.685444			928.353046	464.680161	**A**	2160.089114	1080.548195	2143.062565	1072.034920	2142.078549	1071.5429
10	1060.406538	530.706907	1043.379989	522.193633	1042.395973	521.701624	**N**	2089.052000	1045.029638	2072.025451	1036.516363	2071.041435	1036.0243
11	1147.438566	**574.222921**	1130.412017	565.709647	1129.428001	565.217639	**S**	1975.009073	988.008174	1957.982524	979.494900	1956.998508	979.0028
12	1234.470594	617.738935	1217.444045	609.225661	1216.460029	608.733653	**S**	1887.977045	944.492160	1870.950496	935.978886	1869.966480	935.4868
13	1349.497537	**675.252407**	1332.470988	666.739132	1331.486972	666.247124	**D**	1800.945017	900.976146	1783.918468	892.462872	1782.934452	891.9708
14	1462.581601	**731.794439**	1445.555052	723.281164	1444.571036	722.789156	**L**	1685.918074	843.462675	1668.891525	834.949400	1667.907509	834.4573
15	**1575.665665**	788.336471	1558.639116	779.823196	1557.655100	779.331188	**L**	1572.834010	786.920643	1555.807461	778.407368	1554.823445	777.9153
16	1703.760628	852.383952	1686.734079	843.870678	1685.750063	843.378670	**K**	1459.749946	730.378611	1442.723397	721.865336	1441.739381	721.3733
17	**1832.803221**	916.905248	1815.776672	908.391974	1814.792656	907.899966	**E**	1331.654983	666.331129	1314.628434	657.817855	1313.644418	657.3258
18	1945.887285	973.447280	1928.860736	964.934006	1927.876720	964.441998	**L**	1202.612390	601.809833	1185.585841	593.296558	1184.601825	592.8045
19	2058.971349	1029.989312	2041.944800	1021.476038	2040.960784	1020.984030	**L**	1089.528326	545.267801	1072.501777	536.754526	1071.517761	536.2625
20	2188.013942	1094.510609	2170.987393	1085.997334	2170.003377	1085.505326	**E**	976.444262	488.725769	959.417713	480.212494	958.433697	479.7204
21	2289.061621	1145.034448	2272.035072	1136.521174	2271.051056	1136.029166	**T**	847.401669	424.204472	830.375120	415.691198	829.391104	415.1991
22	2346.083085	1173.545180	2329.056536	1165.031906	2328.072520	1164.539898	**G**	746.353990	373.680633	729.327441	365.167358	728.343425	364.6753
23	2461.110028	1231.058652	2444.083479	1222.545377	2443.099463	1222.053369	**D**	689.332526	345.169901	672.305977	336.656626	671.321961	336.1646
24	2575.152955	**1288.080115**	2558.126406	1279.566841	2557.142390	1279.074833	**N**	574.305583	287.656430	557.279034	279.143155	556.295018	278.6511
25	2731.254066	1366.130671	2714.227517	1357.617396	2713.243501	1357.125388	**R**	460.262656	230.634966	443.236107	222.121692	442.252091	221.6296
26	2860.296659	1430.651967	2843.270110	1422.138693	2842.286094	1421.646685	**E**	304.161545	152.584411	287.134996	144.071136	286.150980	143.5791
27							**R**	175.118952	88.063114	158.092403	79.549839		



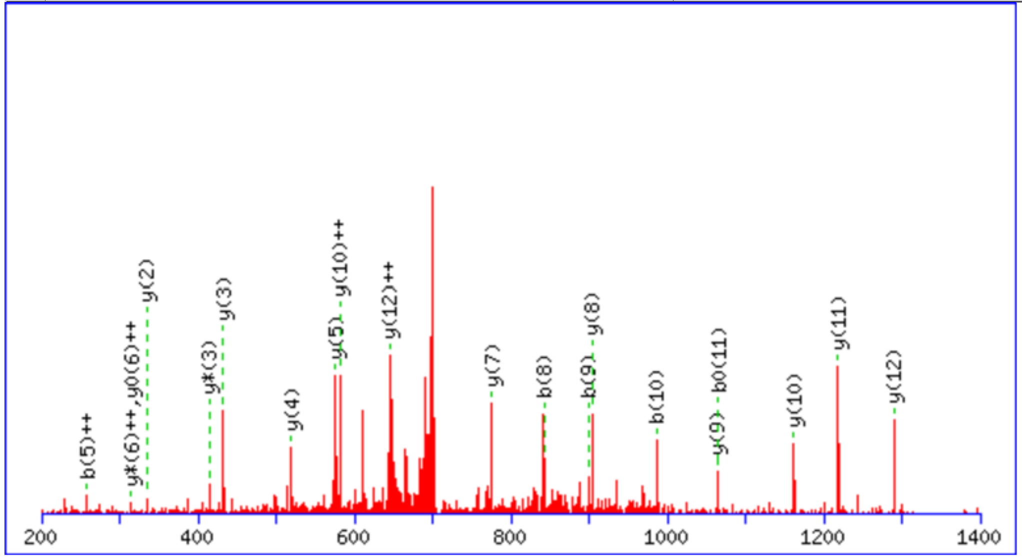
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 8792: 1416.624448 from(709.319500,2+)
Title: OECHL100312_32.2328.2328.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67
Expect: 1.1e-005**Matches :** 20/128 fragment ions using 36 most intense peaks   (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							**13**
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	**12**
3	257.160817	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	**11**
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	**10**
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	**9**
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	**8**

7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	647.292971	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	**899.403979**	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

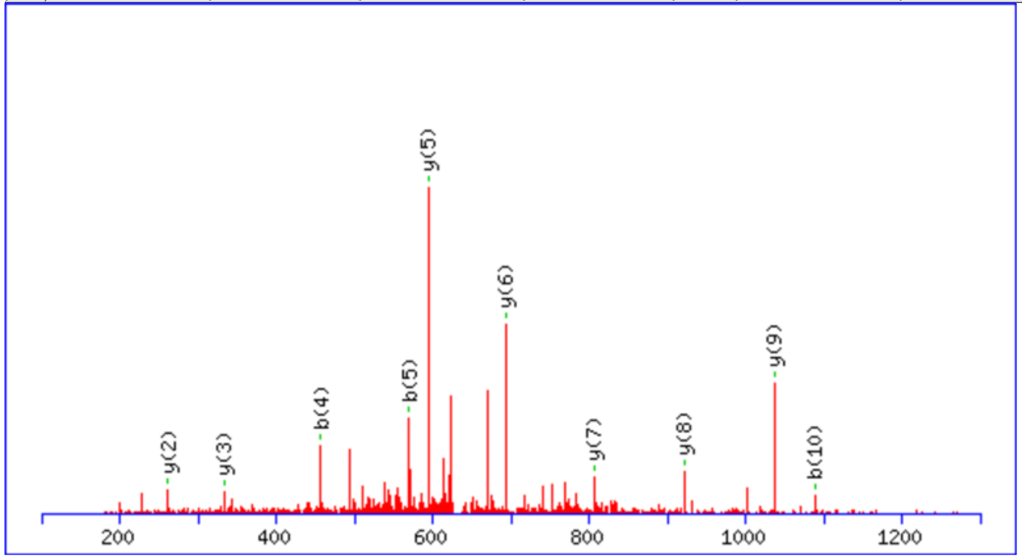


Peptide View

MS/MS Fragmentation of **LLDDLVTCASR**
Found in **IPI00299485**, Tax_Id=9606 Gene_Symbol=CD93 Complement component C1q receptor
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 7251: 1261.633848 from(631.824200,2+)
Title: OECHL100312_32.15071.15071.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 1261.633636**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67
Expect: 2.6e-005**Matches :** 10/94 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							**11**
2	227.175404	114.091340			**L**	1149.556850	575.282063	1132.530301	566.768789	1131.546285	566.276781	**10**
3	342.202347	171.604811	324.191782	162.599529	**D**	***1036.472786***	518.740031	1019.446237	510.226757	1018.462221	509.734749	**9**
4	**457.229290**	229.118283	439.218725	220.113001	**D**	***921.445843***	461.226560	904.419294	452.713285	903.435278	452.221277	**8**
5	**570.313354**	285.660315	552.302789	276.655033	**L**	***806.418900***	403.713088	789.392351	395.199814	788.408335	394.707806	**7**
6	669.381768	335.194522	651.371203	326.189239	**V**	***693.334836***	347.171056	676.308287	338.657782	675.324271	338.165774	**6**
7	770.429447	385.718362	752.418882	376.713079	**T**	***594.266422***	297.636849	577.239873	289.123575	576.255857	288.631567	**5**
8	930.460096	465.733686	912.449531	456.728404	**C**	493.218743	247.113010	476.192194	238.599735	475.208178	238.107727	**4**
9	1001.497210	501.252243	983.486645	492.246961	**A**	***333.188094***	167.097685	316.161545	158.584410	315.177529	158.092402	**3**
10	**1088.529238**	544.768257	1070.518673	535.762975	**S**	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
11					**R**	175.118952	88.063114	158.092403	79.549839			**1**



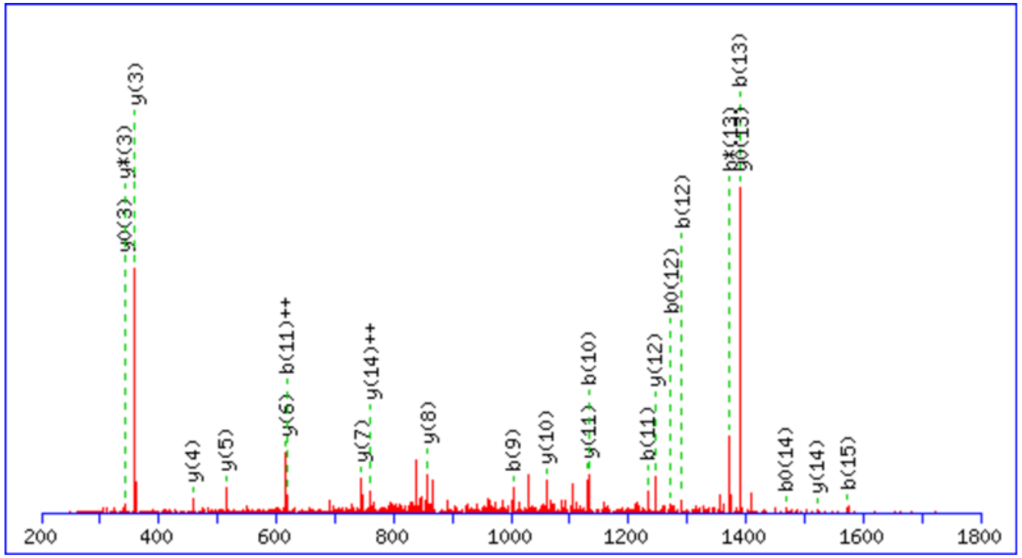
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU

Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 12275: 1746.917048 from(874.465800,2+)
Title: OECHL100312_32.17167.17167.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59
Expect: 0.00012**Matches :** 24/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	618.349740	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	689.386854	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	972.510885	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



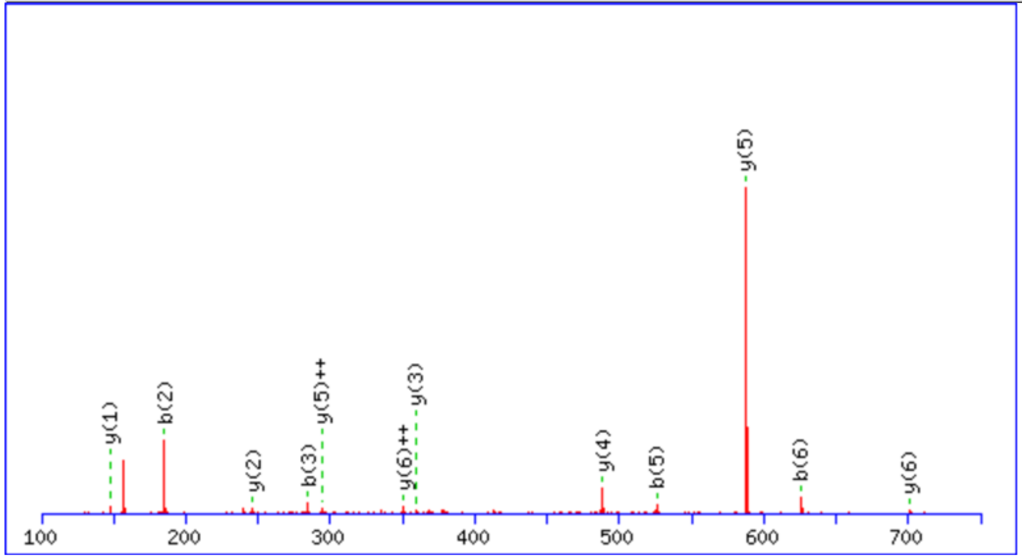
Peptide View

MS/MS Fragmentation of **ALVQIVK**
Found in **IPI00216569**, Tax_Id=9606 Gene_Symbol=CST7 Cystatin-F precursor
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 887: 770.490648 from(386.252600,2+)
Title: OECHL100312_32.11799.11799.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 770.490173**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: Q4 :** Deamidated (NQ)**Ions Score:** 55 **Expect:** 0.00012**Matches :** 12/42 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					7
2	**185.128454**	93.067865			L	***700.460354***	350.733815	683.433805	342.220541	6
3	**284.196868**	142.602072			V	***587.376290***	294.191783	570.349741	285.678509	5
4	413.239462	207.123369	396.212913	198.610095	Q	***488.307876***	244.657576	471.281327	236.144301	4
5	**526.323526**	263.665401	509.296977	255.152127	I	***359.265282***	180.136279	342.238733	171.623004	3
6	**625.391940**	313.199608	608.365391	304.686333	V	***246.181218***	123.594247	229.154669	115.080972	2

7					**K**	***147.112804***	74.060040	130.086255	65.546765	**1**



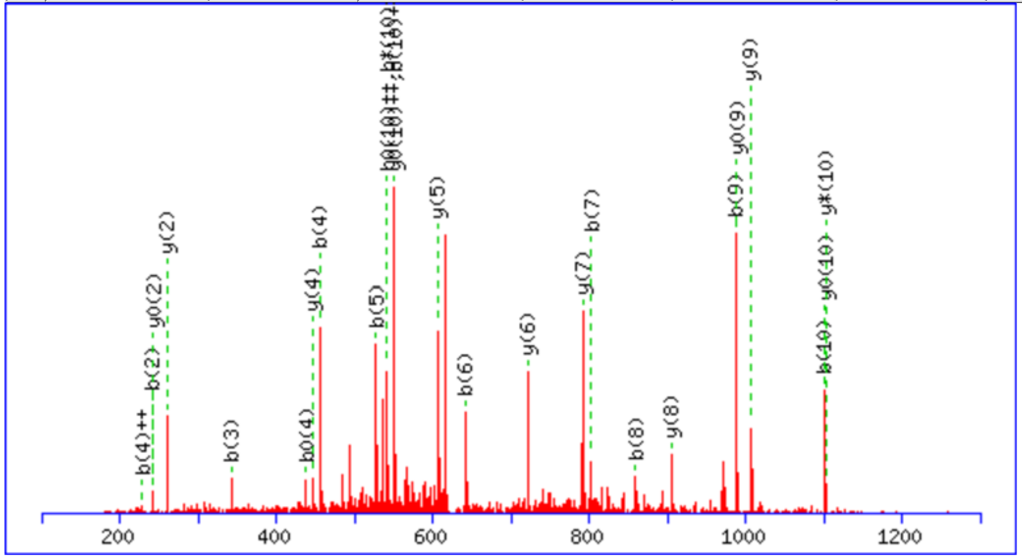
Peptide View

MS/MS Fragmentation of **KITIADCGQLE**
Found in **IPI00419585**, Tax_Id=9606 Gene_Symbol=PPIA Peptidyl-prolyl cis-trans isomerase A
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 7073: 1246.626048 from(624.320300,2+)
Title: OECHL100312_32.11241.11241.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 1246.622726**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00088**Matches :** 26/112 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	129.102239	65.054757	112.075690	56.541483			**K**							**11**
2	***242.186303***	121.596790	225.159754	113.083515			**I**	1119.535053	560.271165	1102.508504	551.757890	1101.524488	551.265882	**10**
3	***343.233982***	172.120629	326.207433	163.607355	325.223417	163.115347	**T**	**1006.450989**	503.729133	989.424440	495.215858	988.440424	494.723850	**9**
4	***456.318046***	228.662661	439.291497	220.149387	438.307481	219.657379	**I**	**905.403310**	453.205293	888.376761	444.692019	887.392745	444.200011	**8**
5	***527.355160***	264.181218	510.328611	255.667944	509.344595	255.175936	**A**	**792.319246**	396.663261	775.292697	388.149987	774.308681	387.657979	**7**

6	***642.382103***	321.694690	625.355554	313.181415	624.371538	312.689407	**D**	**721.282132**	361.144704	704.255583	352.631430	703.271567	352.139422	**6**
7	***802.412752***	401.710014	785.386203	393.196740	784.402187	392.704732	**C**	**606.255189**	303.631233	589.228640	295.117958	588.244624	294.625950	**5**
8	***859.434216***	430.220746	842.407667	421.707472	841.423651	421.215464	**G**	**446.224540**	223.615908	429.197991	215.102634	428.213975	214.610626	**4**
9	***987.492794***	494.250035	970.466245	485.736761	969.482229	485.244753	**Q**	389.203076	195.105176	372.176527	186.591902	371.192511	186.099894	**3**
10	***1100.576858***	550.792067	1083.550309	542.278793	1082.566293	541.786785	**L**	**261.144498**	131.075887			243.133933	122.070605	**2**
11							**E**	148.060434	74.533855			130.049869	65.528573	**1**



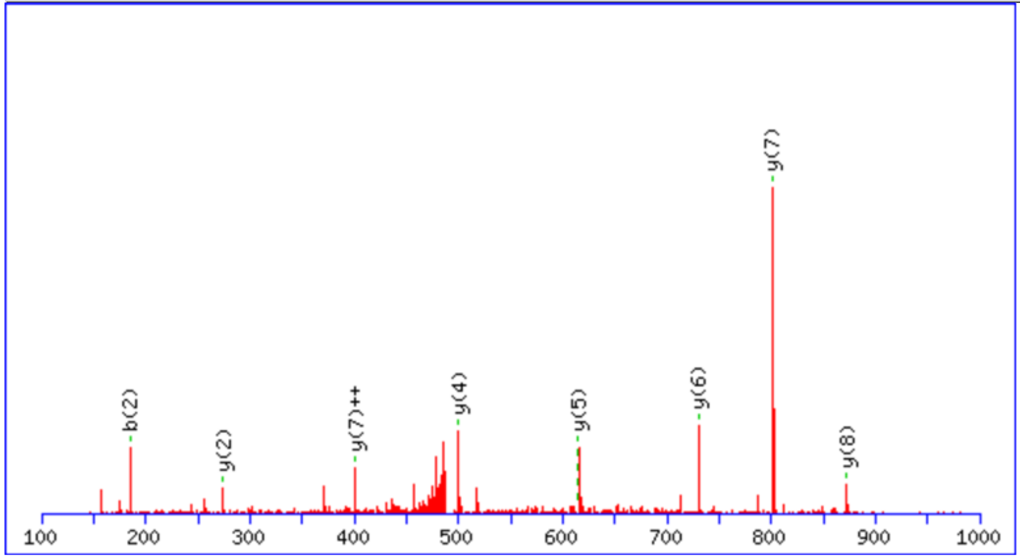
Peptide View

MS/MS Fragmentation of **LAADDPEVR**
Found in **IPI00025840**, Tax_Id=9606 Gene_Symbol=EFNA1 Isoform 1 of Ephrin-A1
Experiment: 23 - NOPC2 **Fraction:** NOPC2

Match to Query 3217: 984.487448 from(493.251000,2+)
Title: OECHL100312_32.5390.5390.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_32.raw
Monoisotopic mass of neutral peptide Mr(calc): 984.487610**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00068**Matches :** 8/70 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#

1	114.091340	57.549308			**L**							**9**
2	185.128454	93.067865			**A**	***872.410837***	436.709057	855.384288	428.195782	854.400272	427.703774	**8**
3	256.165568	128.586422			**A**	***801.373723***	401.190500	784.347174	392.677225	783.363158	392.185217	**7**
4	371.192511	186.099893	353.181946	177.094611	**D**	***730.336609***	365.671943	713.310060	357.158668	712.326044	356.666660	**6**
5	486.219454	243.613365	468.208889	234.608082	**D**	***615.309666***	308.158471	598.283117	299.645197	597.299101	299.153189	**5**
6	583.272218	292.139747	565.261653	283.134465	**P**	***500.282723***	250.644999	483.256174	242.131725	482.272158	241.639717	**4**
7	712.314811	356.661044	694.304246	347.655761	**E**	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	**3**
8	811.383225	406.195251	793.372660	397.189968	**V**	***274.187366***	137.597321	257.160817	129.084046			**2**
9					**R**	175.118952	88.063114	158.092403	79.549839			**1**



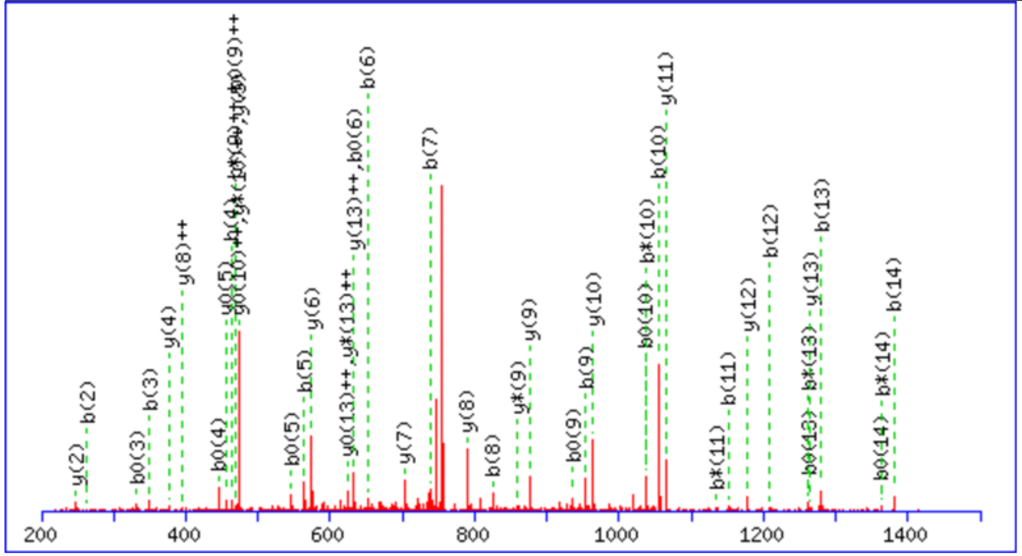
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 41 - OPD-2 **Fraction:** OPD-2

Match to Query 10118: 1525.727048 from(763.870800,2+)
Title: OECHL100312_30.10984.10984.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_30.raw

Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 81
Expect: 8.7e-007**Matches :** 46/150 fragment ions using 84 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.034219	58.520748			98.023654	49.515465	D							15
2	***263.102633***	132.054954			245.092068	123.049672	F	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	14
3	***350.134661***	175.570968			332.124096	166.565686	S	**1264.637937**	632.822607	1247.611388	624.309332	1246.627372	623.817324	13
4	***463.218725***	232.113001			445.208160	223.107718	L	**1177.605909**	589.306592	1160.579360	580.793318	1159.595344	580.301310	12
5	***564.266404***	282.636840			546.255839	273.631558	T	**1064.521845**	532.764561	1047.495296	524.251286	1046.511280	523.759278	11
6	***651.298432***	326.152854			633.287867	317.147572	S	**963.474166**	482.240721	946.447617	473.727446	945.463601	473.235438	10
7	***738.330460***	369.668868			720.319895	360.663586	S	**876.442138**	438.724707	859.415589	430.211432	858.431573	429.719424	9
8	***825.362488***	413.184882			807.351923	404.179599	S	**789.410110**	395.208693	772.383561	386.695418	771.399545	386.203410	8
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	Q	**702.378082**	351.692679	685.351533	343.179404	684.367517	342.687396	7
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	T	**574.319504**	287.663390	557.292955	279.150115	556.308939	278.658107	6
11	***1151.521509***	576.264392	1134.494960	567.751118	1133.510944	567.259110	P	**473.271825**	237.139550	456.245276	228.626276	455.261260	228.134268	5
12	***1208.542973***	604.775124	1191.516424	596.261850	1190.532408	595.769842	G	**376.219061**	188.613168	359.192512	180.099894	358.208496	179.607886	4
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	A	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	3
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	T	**248.160483**	124.583879	231.133934	116.070605	230.149918	115.578597	2
15							K	147.112804	74.060040	130.086255	65.546765			1

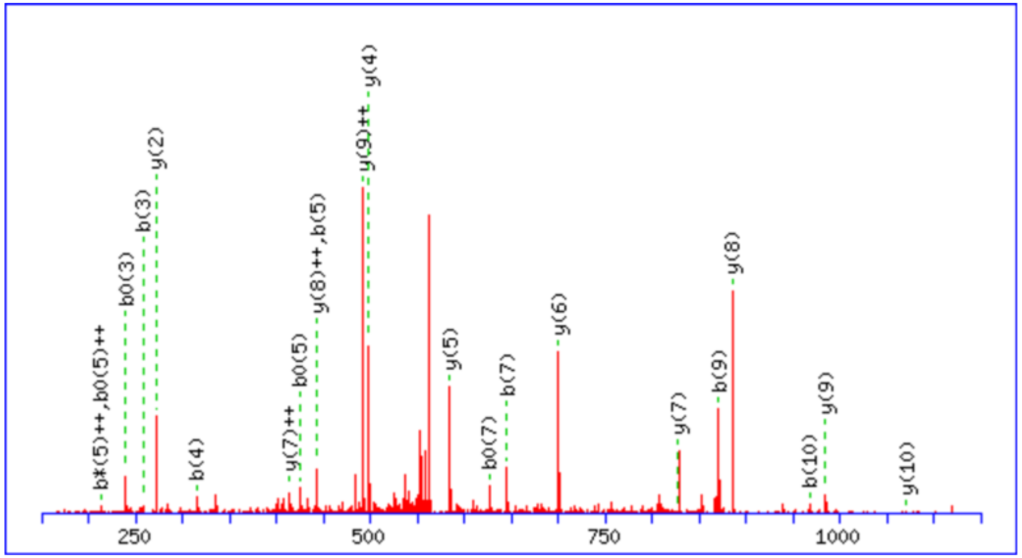


Peptide View

MS/MS Fragmentation of **ASVGQDSPEPR**
Found in **IPI00044369**, Tax_Id=9606 Gene_Symbol=PLXDC2 Isoform 1 of Plexin domain-containing protein 2
Experiment: 41 - OPD-2 **Fraction:** OPD-2

Match to Query 5462: 1141.536048 from(571.775300,2+)
Title: OECHL100312_30.3287.3287.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_30.raw
Monoisotopic mass of neutral peptide Mr(calc): 1141.536362**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64
Expect: 2.6e-005**Matches :** 22/106 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	72.044390	36.525833					**A**							**11**
2	159.076418	80.041847			141.065853	71.036564	**S**	***1071.506528***	536.256902	1054.479979	527.743628	1053.495963	527.251620	**10**
3	**258.144832**	129.576054			240.134267	120.570772	**V**	***984.474500***	492.740888	967.447951	484.227614	966.463935	483.735606	**9**
4	**315.166296**	158.086786			297.155731	149.081504	**G**	***885.406086***	443.206681	868.379537	434.693407	867.395521	434.201399	**8**
5	**443.224874**	222.116075	426.198325	213.602801	425.214309	213.110793	**Q**	***828.384622***	414.695949	811.358073	406.182675	810.374057	405.690667	**7**
6	558.251817	279.629547	541.225268	271.116272	540.241252	270.624264	**D**	***700.326044***	350.666660	683.299495	342.153386	682.315479	341.661378	**6**
7	**645.283845**	323.145561	628.257296	314.632286	627.273280	314.140278	**S**	***585.299101***	293.153189	568.272552	284.639914	567.288536	284.147906	**5**
8	742.336609	371.671943	725.310060	363.158668	724.326044	362.666660	**P**	***498.267073***	249.637174	481.240524	241.123900	480.256508	240.631892	**4**
9	**871.379202**	436.193239	854.352653	427.679965	853.368637	427.187957	**E**	401.214309	201.110792	384.187760	192.597518	383.203744	192.105510	**3**
10	**968.431966**	484.719621	951.405417	476.206347	950.421401	475.714339	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
11							**R**	175.118952	88.063114	158.092403	79.549839			**1**



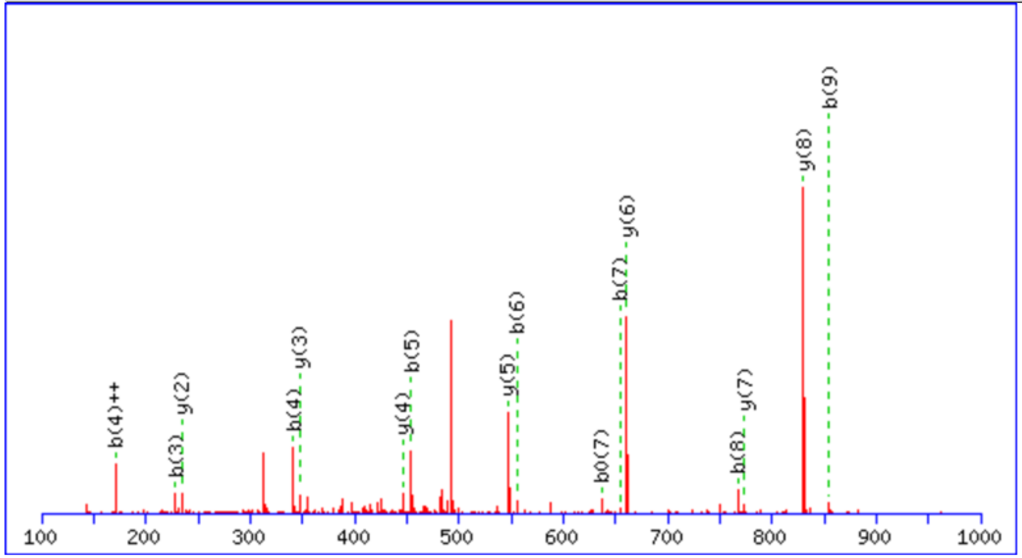
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 41 - OPD-2 **Fraction:** OPD-2

Match to Query 3391: 999.635048 from(500.824800,2+)
Title: OECHL100312_30.16809.16809.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_30.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57
Expect: 2.5e-005**Matches :** 17/78 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	**773.513117**	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**

7	***654.418489***	327.712883	636.407924	318.707600	**V**	**446.297310**	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



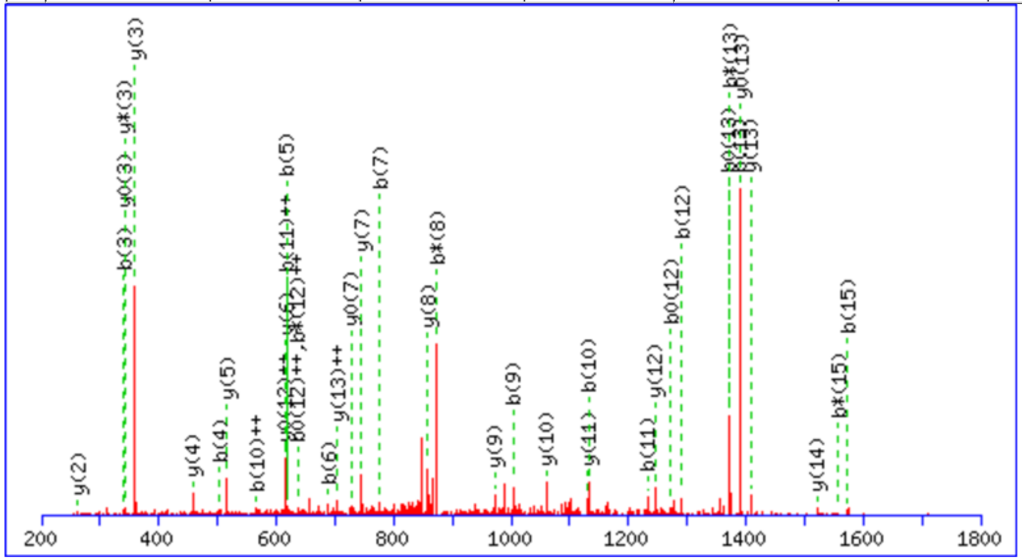
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 41 - OPD-2 **Fraction:** OPD-2

Match to Query 11928: 1746.917648 from(874.466100,2+)
Title: OECHL100312_30.16592.16592.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_30.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 73
Expect: 5e-006**Matches :** 39/156 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**

3	**340.259468**	170.633372					I	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	14
4	**503.322797**	252.165036					Y	***1408.670299***	704.838788	1391.643750	696.325513	1390.659734	695.833505	13
5	**618.349740**	309.678508			600.339175	300.673226	D	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	12
6	**689.386854**	345.197065			671.376289	336.191782	A	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	11
7	**776.418882**	388.713079			758.408317	379.707796	S	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	10
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	9
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	L	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	8
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	E	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	7
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	T	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	6
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	G	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	5
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	V	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	4
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
16							R	175.118952	88.063114	158.092403	79.549839			1

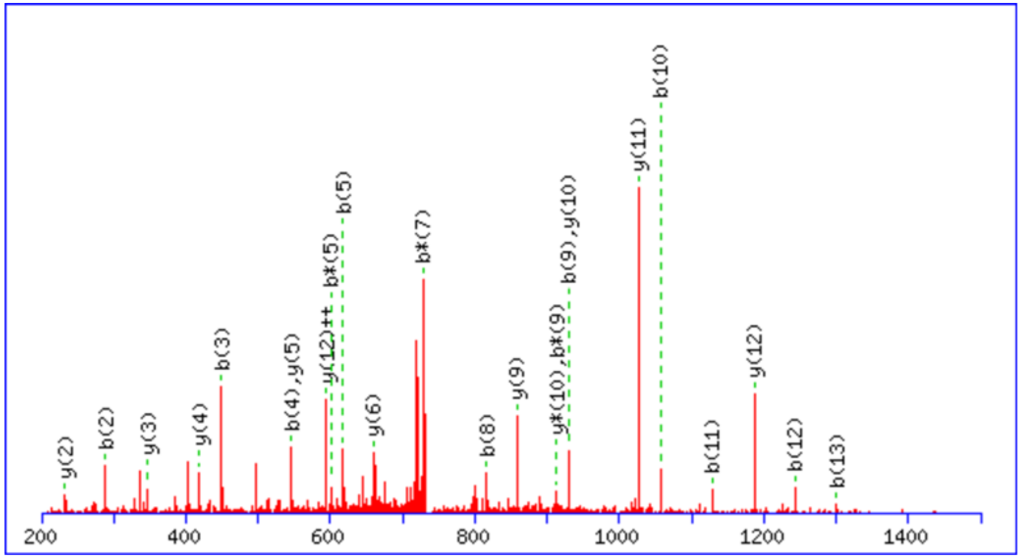


Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 41 - OPD-2 **Fraction:** OPD-2

Match to Query 9619: 1473.646248 from(737.830400,2+)
Title: OECHL100312_30.7758.7758.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_30.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 69
Expect: 6.4e-006**Matches :** 24/128 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.037925	81.022600					**C**							**14**
2	***289.096503***	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.809312	**13**
3	***449.127152***	225.067214	432.100603	216.553940			**C**	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.780023	**12**
4	***546.179916***	273.593596	529.153367	265.080322			**P**	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.764698	**11**
5	***617.217030***	309.112153	600.190481	300.598879			**A**	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.238316	**10**
6	674.238494	337.622885	657.211945	329.109611			**G**	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.719759	**9**
7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
8	***816.312722***	408.659999	799.286173	400.146725			**A**	730.384229	365.695753	713.357680	357.182478	712.373664	356.690470	**7**
9	***929.396786***	465.202031	912.370237	456.688757			**L**	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.171913	**6**
10	***1057.455364***	529.231320	1040.428815	520.718046			**Q**	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.629881	**5**
11	***1128.492478***	564.749877	1111.465929	556.236603			**A**	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.600592	**4**
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	**347.167359**	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
13	***1300.540885***	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	**232.140416**	116.573846	215.113867	108.060571			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



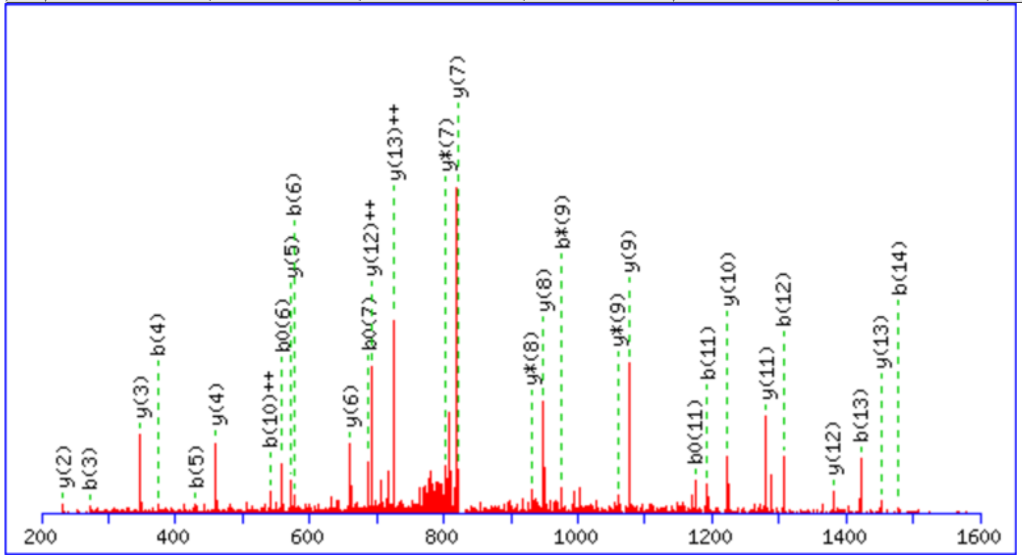
Peptide View

MS/MS Fragmentation of **VTATGFQQCSLIDGR**
Found in **IPI00333140**, Tax_Id=9606 Gene_Symbol=DNER Delta and Notch-like epidermal growth factor-related receptor
Experiment: 41 - OPD-2 **Fraction:** OPD-2

Match to Query 11182: 1651.798848 from(826.906700,2+)
Title: OECHL100312_30.13821.13821.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_30.raw
Monoisotopic mass of neutral peptide Mr(calc): 1651.798828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 80
Expect: 1.6e-006**Matches :** 30/150 fragment ions using 55 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					**V**							**15**
2	201.123369	101.065322			183.112804	92.060040	**T**	1553.737670	777.372473	1536.711121	768.859198	1535.727105	768.367190	**14**
3	**272.160483**	136.583879			254.149918	127.578597	**A**	***1452.689991***	726.848633	1435.663442	718.335359	1434.679426	717.843351	**13**
4	**373.208162**	187.107719			355.197597	178.102437	**T**	***1381.652877***	691.330076	1364.626328	682.816802	1363.642312	682.324794	**12**
5	**430.229626**	215.618451			412.219061	206.613169	**G**	***1280.605198***	640.806237	1263.578649	632.292962	1262.594633	631.800954	**11**
6	**577.298040**	289.152658			559.287475	280.147376	**F**	***1223.583734***	612.295505	1206.557185	603.782230	1205.573169	603.290222	**10**

7	705.356618	353.181947	688.330069	344.668673	687.346053	344.176665	**Q**	***1076.515320***	538.761298	1059.488771	530.248023	1058.504755	529.756015	**9**
8	833.415196	417.211236	816.388647	408.697962	815.404631	408.205954	**Q**	***948.456742***	474.732009	931.430193	466.218734	930.446177	465.726726	**8**
9	993.445845	497.226561	976.419296	488.713286	975.435280	488.221278	**C**	***820.398164***	410.702720	803.371615	402.189445	802.387599	401.697437	**7**
10	1080.477873	540.742575	1063.451324	532.229300	1062.467308	531.737292	**S**	***660.367515***	330.687395	643.340966	322.174121	642.356950	321.682113	**6**
11	**1193.561937**	597.284607	1176.535388	588.771332	1175.551372	588.279324	**L**	***573.335487***	287.171381	556.308938	278.658107	555.324922	278.166099	**5**
12	**1306.646001**	653.826638	1289.619452	645.313364	1288.635436	644.821356	**I**	***460.251423***	230.629349	443.224874	222.116075	442.240858	221.624067	**4**
13	**1421.672944**	711.340110	1404.646395	702.826836	1403.662379	702.334827	**D**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
14	**1478.694408**	739.850842	1461.667859	731.337567	1460.683843	730.845559	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



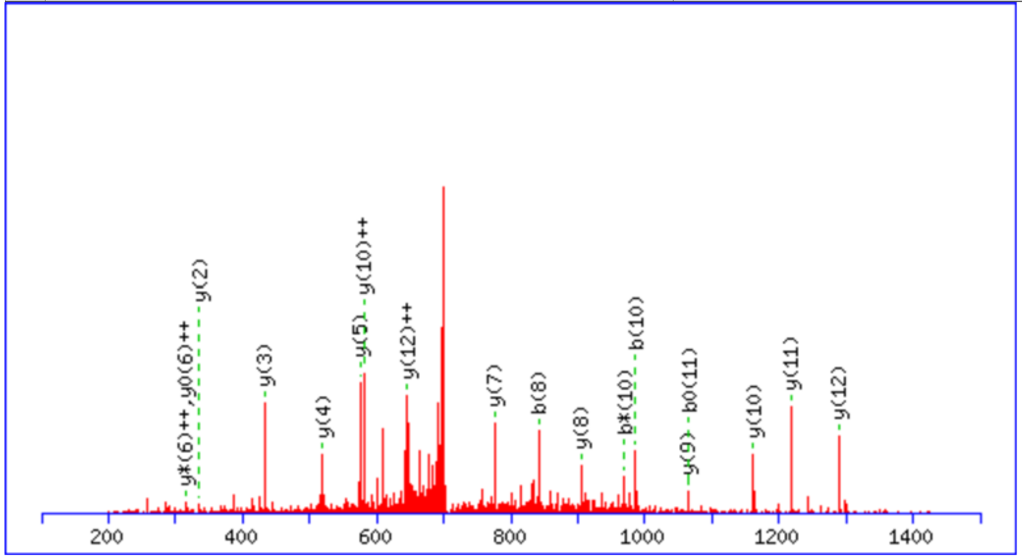
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 41 - OPD-2 **Fraction:** OPD-2

Match to Query 9065: 1416.624648 from(709.319600,2+)
Title: OECHL100312_30.2218.2218.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_30.raw

Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66
Expect: 1.5e-005**Matches :** 18/128 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							**13**
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	**12**
3	257.160817	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	**11**
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	**10**
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	**9**
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	**8**
7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	647.292971	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	899.403979	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

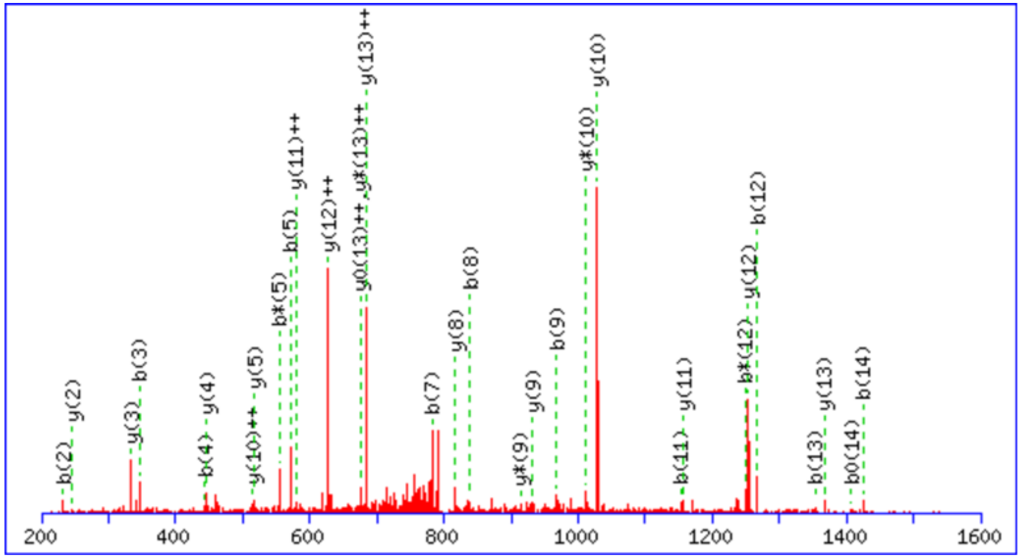


Peptide View

MS/MS Fragmentation of **ACNPQPNGENAISAR**
Found in **IPI00169285**, Tax_Id=9606 Gene_Symbol=PLBD2 Putative phospholipase B-like 2
Experiment: 41 - OPD-2 **Fraction:** OPD-2

Match to Query 10750: 1597.727848 from(799.871200,2+)
Title: OECHL100312_30.5854.5854.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_30.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.726669**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64
Expect: 3.2e-005**Matches :** 32/144 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	72.044390	36.525833					**A**							**15**
2	***232.075039***	116.541158					**C**	1527.696865	764.352071	1510.670316	755.838796	1509.686300	755.346788	**14**
3	***346.117966***	173.562621	329.091417	165.049347			**N**	***1367.666216***	684.336746	1350.639667	675.823472	1349.655651	675.331464	**13**
4	***443.170730***	222.089003	426.144181	213.575729			**P**	***1253.623289***	627.315283	1236.596740	618.802008	1235.612724	618.310000	**12**
5	***571.229308***	286.118292	554.202759	277.605018			**Q**	***1156.570525***	578.788901	1139.543976	570.275626	1138.559960	569.783618	**11**
6	668.282072	334.644674	651.255523	326.131400			**P**	***1028.511947***	514.759612	1011.485398	506.246337	1010.501382	505.754329	**10**
7	***782.324999***	391.666138	765.298450	383.152863			**N**	***931.459183***	466.233230	914.432634	457.719955	913.448618	457.227947	**9**
8	***839.346463***	420.176870	822.319914	411.663595			**G**	***817.416256***	409.211766	800.389707	400.698492	799.405691	400.206484	**8**
9	***968.389056***	484.698166	951.362507	476.184892	950.378491	475.692884	**E**	760.394792	380.701034	743.368243	372.187760	742.384227	371.695752	**7**
10	1082.431983	541.719630	1065.405434	533.206355	1064.421418	532.714347	**N**	631.352199	316.179738	614.325650	307.666463	613.341634	307.174455	**6**
11	***1153.469097***	577.238187	1136.442548	568.724912	1135.458532	568.232904	**A**	***517.309272***	259.158274	500.282723	250.644999	499.298707	250.152991	**5**
12	***1266.553161***	633.780219	1249.526612	625.266944	1248.542596	624.774936	**I**	***446.272158***	223.639717	429.245609	215.126442	428.261593	214.634434	**4**
13	***1353.585189***	677.296233	1336.558640	668.782958	1335.574624	668.290950	**S**	***333.188094***	167.097685	316.161545	158.584410	315.177529	158.092402	**3**
14	***1424.622303***	712.814790	1407.595754	704.301515	1406.611738	703.809507	**A**	***246.156066***	123.581671	229.129517	115.068396			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



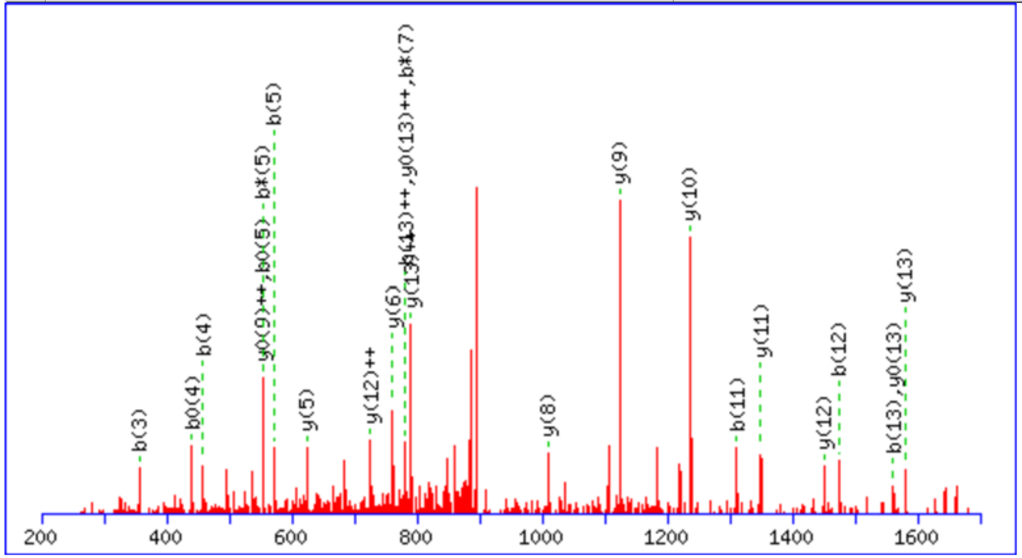
Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 41 - OPD-2 **Fraction:** OPD-2

Match to Query 12342: 1805.932048 from(903.973300,2+)
Title: OECHL100312_30.18507.18507.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_30.raw
Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64
Expect: 5e-005**Matches :** 24/160 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**15**
2	228.134267	114.570771	211.107718	106.057497			**I**	1692.895549	846.951413	1675.869000	838.438138	1674.884984	837.946130	**14**
3	***357.176860***	179.092068	340.150311	170.578793	339.166295	170.086785	**E**	***1579.811485***	790.409381	1562.784936	781.896106	1561.800920	781.404098	**13**
4	***458.224539***	229.615907	441.197990	221.102633	440.213974	220.610625	**T**	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.882802	**12**
5	***571.308603***	286.157940	554.282054	277.644665	553.298038	277.152657	**I**	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.358962	**11**
6	684.392667	342.699972	667.366118	334.186697	666.382102	333.694689	**I**	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.816930	**10**

7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	N	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.274898	9
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	T	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.253435	8
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	F	908.462479	454.734878	891.435930	446.221603	890.451914	445.729595	7
10	1183.610599	592.308938	1166.584050	583.795663	1165.600034	583.303655	H	***761.394065***	381.200671	744.367516	372.687396	743.383500	372.195388	6
11	***1311.669177***	656.338227	1294.642628	647.824952	1293.658612	647.332944	Q	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.665932	5
12	***1474.732506***	737.869891	1457.705957	729.356617	1456.721941	728.864609	Y	496.276575	248.641926	479.250026	240.128651	478.266010	239.636643	4
13	***1561.764534***	781.385905	1544.737985	772.872631	1543.753969	772.380623	S	333.213246	167.110261	316.186697	158.596987	315.202681	158.104979	3
14	1660.832948	830.920112	1643.806399	822.406838	1642.822383	821.914830	V	246.181218	123.594247	229.154669	115.080973			2
15							K	147.112804	74.060040	130.086255	65.546765			1



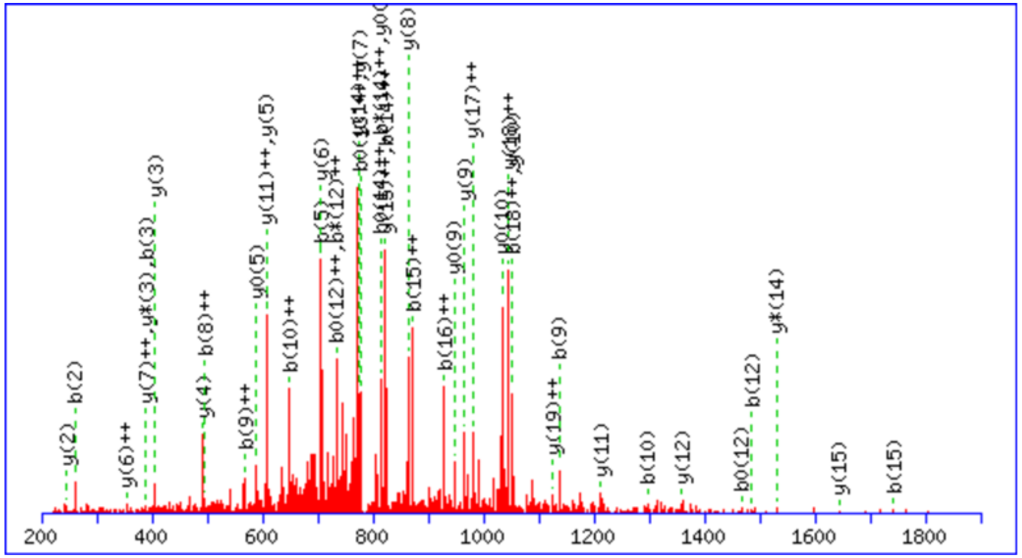
Peptide View

MS/MS Fragmentation of **VCECRPGMFCSTSAVNSCAR**
Found in **IPI00006073**, Tax_Id=9606 Gene_Symbol=TNFRSF8 Isoform Long of Tumor necrosis factor receptor superfamily member 8
Experiment: 41 - OPD-2 **Fraction:** OPD-2

Match to Query 14590: 2347.956972 from(783.659600,3+)
Title: OECHL100312_30.10138.10138.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_30.raw

Monoisotopic mass of neutral peptide Mr(calc): 2347.958862**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 4.2e-005**Matches :** 46/210 fragment ions using 73 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}
1	100.075690	50.541483					V						
2	**260.106339**	130.556807					C	2249.897711	1125.452493	2232.871162	1116.939219	2231.887146	1116.4472
3	**389.148932**	195.078104			371.138367	186.072822	E	2089.867062	1045.437169	2072.840513	1036.923894	2071.856497	1036.4318
4	549.179581	275.093429			531.169016	266.088146	C	1960.824469	980.915873	1943.797920	972.402598	1942.813904	971.9105
5	**705.280692**	353.143984	688.254143	344.630710	687.270127	344.138702	R	1800.793820	900.900548	1783.767271	892.387274	1782.783255	891.8952
6	802.333456	401.670366	785.306907	393.157092	784.322891	392.665084	P	***1644.692709***	822.849993	1627.666160	814.336718	1626.682144	813.8447
7	859.354920	430.181098	842.328371	421.667824	841.344355	421.175816	G	1547.639945	774.323611	1530.613396	765.810336	1529.629380	765.3183
8	990.395405	**495.701341**	973.368856	487.188066	972.384840	486.696058	M	1490.618481	745.812879	1473.591932	737.299604	1472.607916	736.8075
9	**1137.463819**	**569.235548**	1120.437270	560.722273	1119.453254	560.230265	F	***1359.577996***	680.292636	1342.551447	671.779362	1341.567431	671.2873
10	**1297.494468**	**649.250872**	1280.467919	640.737598	1279.483903	640.245590	C	***1212.509582***	606.758429	1195.483033	598.245155	1194.499017	597.7531
11	1384.526496	692.766886	1367.499947	684.253612	1366.515931	683.761604	S	***1052.478933***	526.743105	1035.452384	518.229830	1034.468368	517.7378
12	**1485.574175**	743.290726	1468.547626	734.777451	1467.563610	734.285443	T	***965.446905***	483.227091	948.420356	474.713816	947.436340	474.2218
13	1572.606203	786.806740	1555.579654	778.293465	1554.595638	777.801457	S	***864.399226***	432.703251	847.372677	424.189977	846.388661	423.6979
14	1643.643317	**822.325297**	1626.616768	813.812022	1625.632752	813.320014	A	***777.367198***	389.187237	760.340649	380.673963	759.356633	380.1819
15	**1742.711731**	**871.859504**	1725.685182	863.346229	1724.701166	862.854221	V	***706.330084***	353.668680	689.303535	345.155406	688.319519	344.6633
16	1856.754658	**928.880967**	1839.728109	920.367693	1838.744093	919.875685	N	***607.261670***	304.134473	590.235121	295.621199	589.251105	295.1291
17	1943.786686	972.396981	1926.760137	963.883707	1925.776121	963.391699	S	***493.218743***	247.113010	476.192194	238.599735	475.208178	238.1077
18	2103.817335	**1052.412306**	2086.790786	1043.899031	2085.806770	1043.407023	C	***406.186715***	203.596996	389.160166	195.083721		
19	2174.854449	1087.930863	2157.827900	1079.417588	2156.843884	1078.925580	A	***246.156066***	123.581671	229.129517	115.068397		
20							R	175.118952	88.063114	158.092403	79.549839		



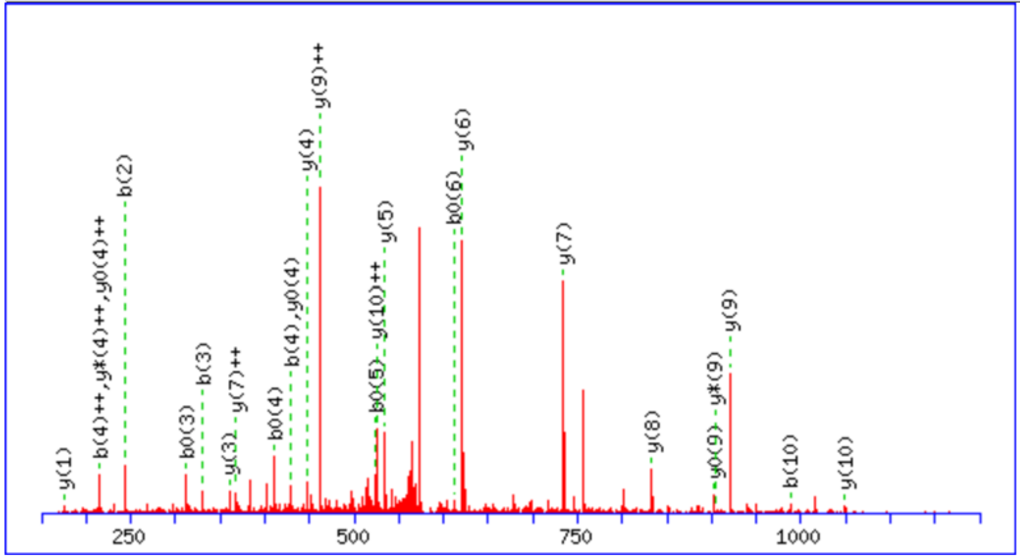
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 41 - OPD-2 **Fraction:** OPD-2

Match to Query 5756: 1161.636648 from(581.825600,2+)
Title: OECHL100312_30.5848.5848.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_30.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00035**Matches :** 26/94 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	114.091340	57.549308					**I**							**11**
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637	**10**
3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340	**9**
4	**429.234375**	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326	**8**
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119	**7**
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087	**6**

7	716.382495	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073	**5**
8	803.414523	402.210899			785.403958	393.205617	**S**	***447.267407***	224.137342	430.240858	215.624067	429.256842	215.132059	**4**
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053			**3**
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



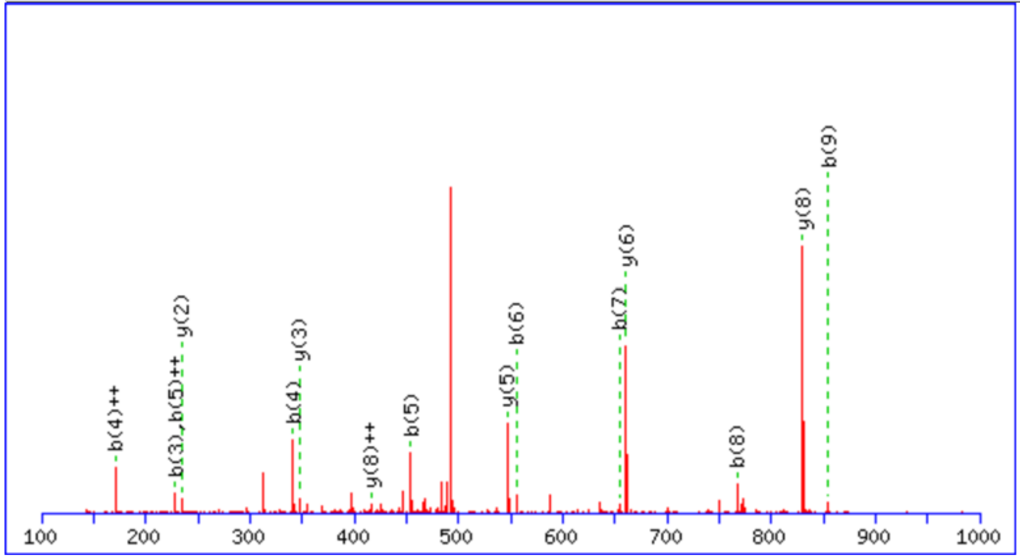
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 3844: 999.633248 from(500.823900,2+)
Title: OECHL100312_28.17170.17170.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65
Expect: 3.4e-006**Matches :** 16/78 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**

2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	**171.112804**			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	**227.654836**			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



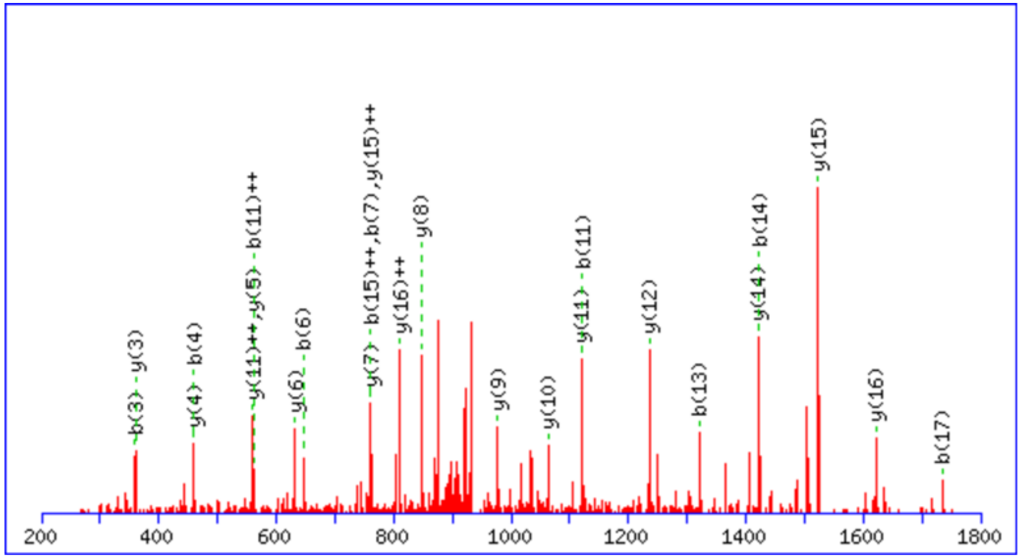
Peptide View

MS/MS Fragmentation of **CVVTGEDGSESEATVNVK**
Found in **IPI00385035**, Tax_Id=9606 Gene_Symbol=NCAM1 Neural cell adhesion molecule (Fragment)
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 14194: 1879.851448 from(940.933000,2+)
Title: OECHL100312_28.8481.8481.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw

Monoisotopic mass of neutral peptide Mr(calc): 1879.846954**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 118
Expect: 1.9e-010**Matches :** 26/160 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	161.037925	81.022600					C							18
2	260.106339	130.556807					V	1720.823565	860.915421	1703.797016	852.402146	1702.813000	851.910138	17
3	**359.174753**	180.091015					V	***1621.755151***	811.381214	1604.728602	802.867939	1603.744586	802.375931	16
4	**460.222432**	230.614854			442.211867	221.609572	T	***1522.686737***	761.847007	1505.660188	753.333732	1504.676172	752.841724	15
5	517.243896	259.125586			499.233331	250.120304	G	***1421.639058***	711.323167	1404.612509	702.809893	1403.628493	702.317885	14
6	**646.286489**	323.646883			628.275924	314.641600	E	1364.617594	682.812435	1347.591045	674.299161	1346.607029	673.807153	13
7	**761.313432**	381.160354			743.302867	372.155072	D	***1235.575001***	618.291139	1218.548452	609.777864	1217.564436	609.285856	12
8	818.334896	409.671086			800.324331	400.665804	G	***1120.548058***	560.777667	1103.521509	552.264393	1102.537493	551.772385	11
9	905.366924	453.187100			887.356359	444.181818	S	***1063.526594***	532.266935	1046.500045	523.753661	1045.516029	523.261653	10
10	1034.409517	517.708397			1016.398952	508.703114	E	***976.494566***	488.750921	959.468017	480.237647	958.484001	479.745639	9
11	**1121.441545**	**561.224411**			1103.430980	552.219128	S	***847.451973***	424.229625	830.425424	415.716350	829.441408	415.224342	8
12	1250.484138	625.745707			1232.473573	616.740425	E	***760.419945***	380.713611	743.393396	372.200336	742.409380	371.708328	7
13	**1321.521252**	661.264264			1303.510687	652.258982	A	***631.377352***	316.192314	614.350803	307.679040	613.366787	307.187032	6
14	**1422.568931**	711.788104			1404.558366	702.782821	T	***560.340238***	280.673757	543.313689	272.160483	542.329673	271.668475	5
15	1521.637345	**761.322311**			1503.626780	752.317028	V	***459.292559***	230.149918	442.266010	221.636643			4
16	1635.680272	818.343774	1618.653723	809.830500	1617.669707	809.338492	N	***360.224145***	180.615711	343.197596	172.102436			3
17	**1734.748686**	867.877981	1717.722137	859.364707	1716.738121	858.872699	V	246.181218	123.594247	229.154669	115.080973			2
18							K	147.112804	74.060040	130.086255	65.546765			1



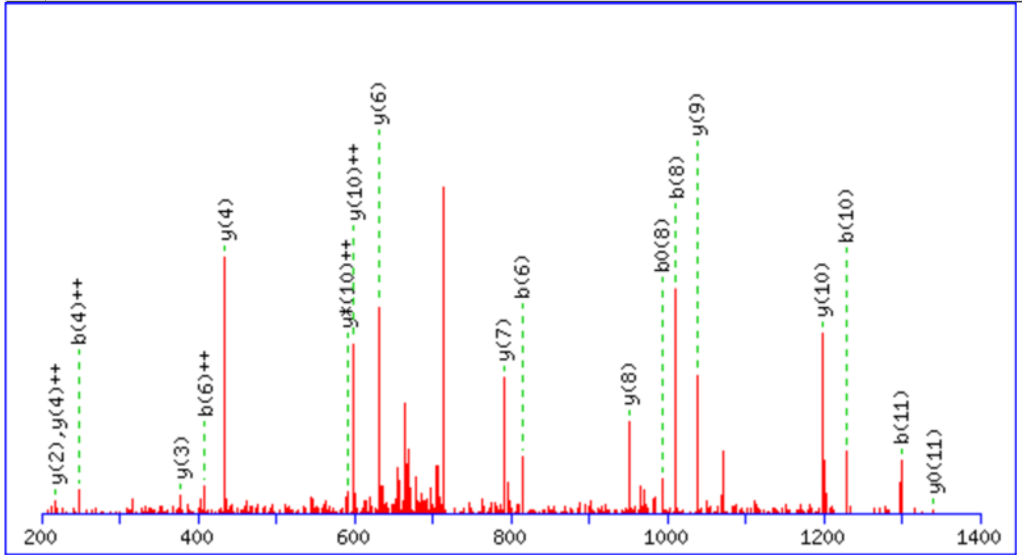
Peptide View

MS/MS Fragmentation of **SCCSCCPVGCAK**
Found in **IPI00008752**, Tax_Id=9606 Gene_Symbol=MT1L;MT1G;MT1JP;MT1E Isoform 1 of Metallothionein-1G
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 9925: 1444.501848 from(723.258200,2+)
Title: OECHL100312_28.3532.3532.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw
Monoisotopic mass of neutral peptide Mr(calc): 1444.502609**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65
Expect: 3.5e-007**Matches :** 21/94 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**12**
2	**248.069953**	124.538614	230.059388	115.533332	**C**	1358.477833	679.742555	1341.451284	671.229280	1340.467268	670.737272	**11**
3	**408.100602**	204.553939	390.090037	195.548657	**C**	***1198.447184***	599.727230	1181.420635	591.213956	1180.436619	590.721948	**10**
4	495.132630	**248.069953**	477.122065	239.064671	**S**	***1038.416535***	519.711906	1021.389986	511.198631	1020.405970	510.706623	**9**
5	655.163279	328.085278	637.152714	319.079995	**C**	***951.384507***	476.195892	934.357958	467.682617			**8**
6	**815.193928**	**408.100602**	797.183363	399.095320	**C**	***791.353858***	396.180567	774.327309	387.667293			**7**

7	912.246692	456.626984	894.236127	447.621702	P	***631.323209***	316.165243	614.296660	307.651968			6
8	**1011.315106**	506.161191	993.304541	497.155909	V	534.270445	267.638861	517.243896	259.125586			5
9	1068.336570	534.671923	1050.326005	525.666641	G	***435.202031***	218.104654	418.175482	209.591379			4
10	**1228.367219**	614.687248	1210.356654	605.681965	C	***378.180567***	189.593921	361.154018	181.080647			3
11	**1299.404333**	650.205805	1281.393768	641.200522	A	***218.149918***	109.578597	201.123369	101.065322			2
12					K	147.112804	74.060040	130.086255	65.546765			1



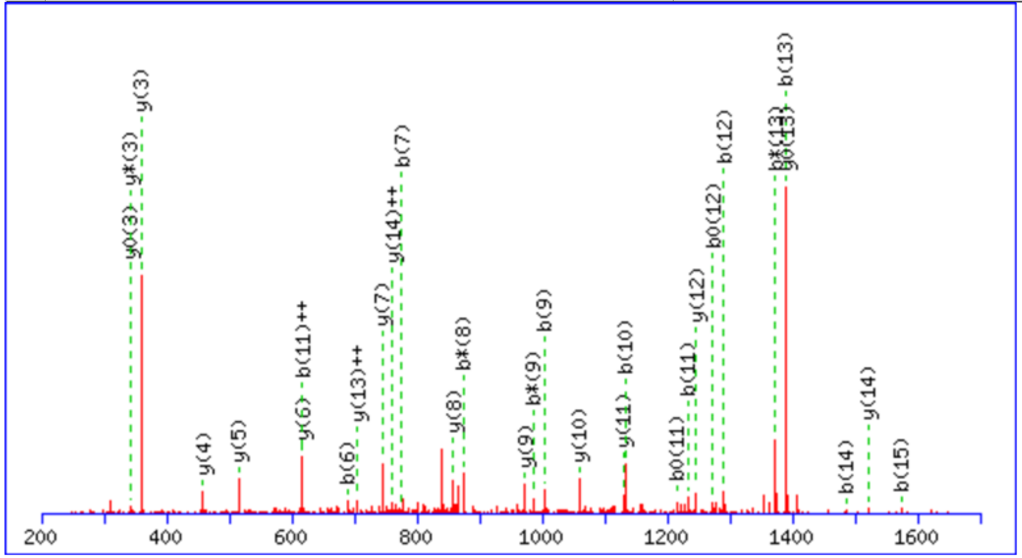
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 13232: 1746.918848 from(874.466700,2+)
Title: OECHL100312_28.16895.16895.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 85
Expect: 4e-007**Matches :** 31/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	618.349740	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	***689.386854***	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	***776.418882***	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**

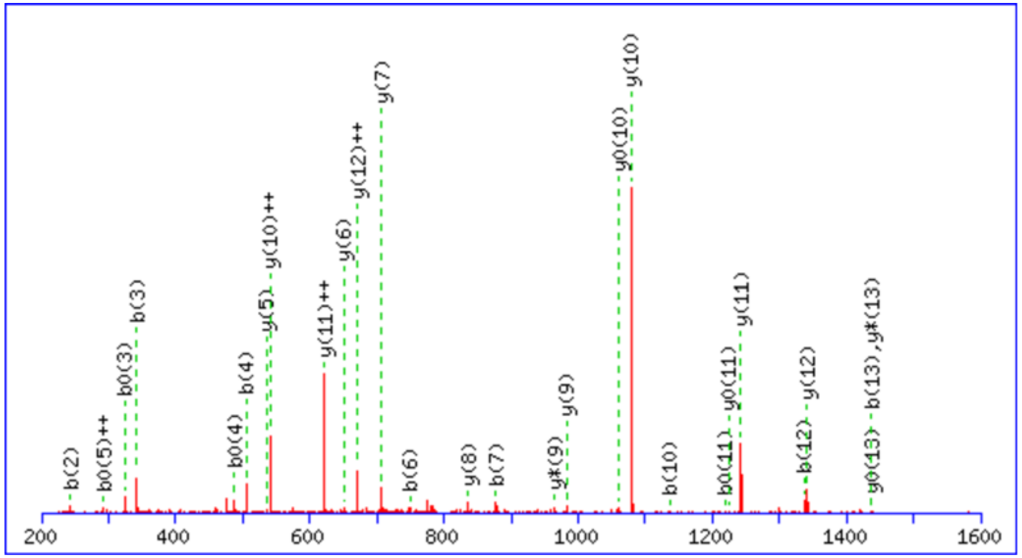


Peptide View

MS/MS Fragmentation of **EIVYPFQGDSTVTK**
Found in **IPI00066856**, Tax_Id=9606 Gene_Symbol=LYPD2 Ly6/PLAUR domain-containing protein 2
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 11361: 1582.789448 from(792.402000,2+)
Title: OECHL100312_28.15084.15084.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw
Monoisotopic mass of neutral peptide Mr(calc): 1582.787903**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53
Expect: 0.00063**Matches :** 28/142 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	130.049869	65.528572			112.039304	56.523290	**E**							**14**
2	***243.133933***	122.070605			225.123368	113.065322	**I**	1454.752574	727.879925	1437.726025	719.366651	1436.742009	718.874643	**13**
3	***342.202347***	171.604812			324.191782	162.599529	**V**	***1341.668510***	671.337893	1324.641961	662.824619	1323.657945	662.332611	**12**
4	***505.265676***	253.136476			487.255111	244.131194	**Y**	***1242.600096***	621.803686	1225.573547	613.290412	1224.589531	612.798404	**11**
5	602.318440	301.662858			584.307875	292.657576	**P**	***1079.536767***	540.272022	1062.510218	531.758747	1061.526202	531.266739	**10**
6	***749.386854***	375.197065			731.376289	366.191783	**F**	***982.484003***	491.745640	965.457454	483.232365	964.473438	482.740357	**9**
7	***877.445432***	439.226354	860.418883	430.713080	859.434867	430.221072	**Q**	***835.415589***	418.211433	818.389040	409.698158	817.405024	409.206150	**8**
8	934.466896	467.737086	917.440347	459.223812	916.456331	458.731804	**G**	***707.357011***	354.182144	690.330462	345.668869	689.346446	345.176861	**7**
9	1049.493839	525.250558	1032.467290	516.737283	1031.483274	516.245275	**D**	***650.335547***	325.671412	633.308998	317.158137	632.324982	316.666129	**6**
10	***1136.525867***	568.766572	1119.499318	560.253297	1118.515302	559.761289	**S**	***535.308604***	268.157940	518.282055	259.644666	517.298039	259.152658	**5**
11	1237.573546	619.290411	1220.546997	610.777137	1219.562981	610.285129	**T**	448.276576	224.641926	431.250027	216.128652	430.266011	215.636644	**4**
12	***1336.641960***	668.824618	1319.615411	660.311344	1318.631395	659.819336	**V**	347.228897	174.118087	330.202348	165.604812	329.218332	165.112804	**3**
13	***1437.689639***	719.348458	1420.663090	710.835183	1419.679074	710.343175	**T**	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14							**K**	147.112804	74.060040	130.086255	65.546765			**1**



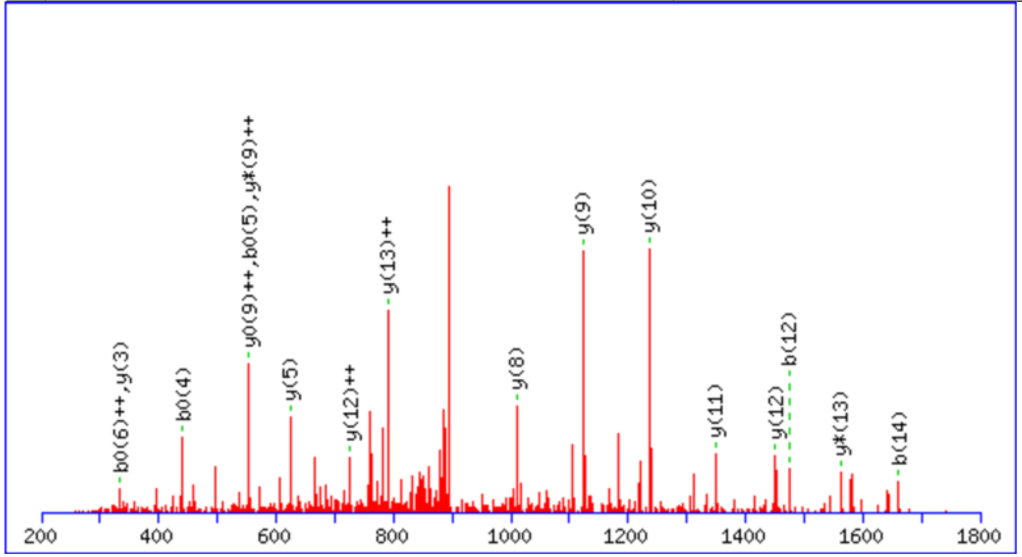
Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 13677: 1805.934448 from(903.974500,2+)
Title: OECHL100312_28.19690.19690.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw
Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65
Expect: 3.7e-005**Matches :** 17/160 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	115.050203	58.028740	98.023654	49.515465			**N**							**15**
2	228.134267	114.570771	211.107718	106.057497			**I**	1692.895549	846.951413	1675.869000	838.438138	1674.884984	837.946130	**14**
3	357.176860	179.092068	340.150311	170.578793	339.166295	170.086785	**E**	1579.811485	790.409381	1562.784936	781.896106	1561.800920	781.404098	**13**
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	**T**	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.882802	**12**
5	571.308603	286.157940	554.282054	277.644665	553.298038	277.152657	**I**	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.358962	**11**
6	684.392667	342.699972	667.366118	334.186697	666.382102	333.694689	**I**	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.816930	**10**

7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	**N**	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.274898	**9**
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	**T**	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.253435	**8**
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	**F**	908.462479	454.734878	891.435930	446.221603	890.451914	445.729595	**7**
10	1183.610599	592.308938	1166.584050	583.795663	1165.600034	583.303655	**H**	761.394065	381.200671	744.367516	372.687396	743.383500	372.195388	**6**
11	1311.669177	656.338227	1294.642628	647.824952	1293.658612	647.332944	**Q**	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.665932	**5**
12	**1474.732506**	737.869891	1457.705957	729.356617	1456.721941	728.864609	**Y**	496.276575	248.641926	479.250026	240.128651	478.266010	239.636643	**4**
13	1561.764534	781.385905	1544.737985	772.872631	1543.753969	772.380623	**S**	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.104979	**3**
14	**1660.832948**	830.920112	1643.806399	822.406838	1642.822383	821.914830	**V**	246.181218	123.594247	229.154669	115.080973			**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



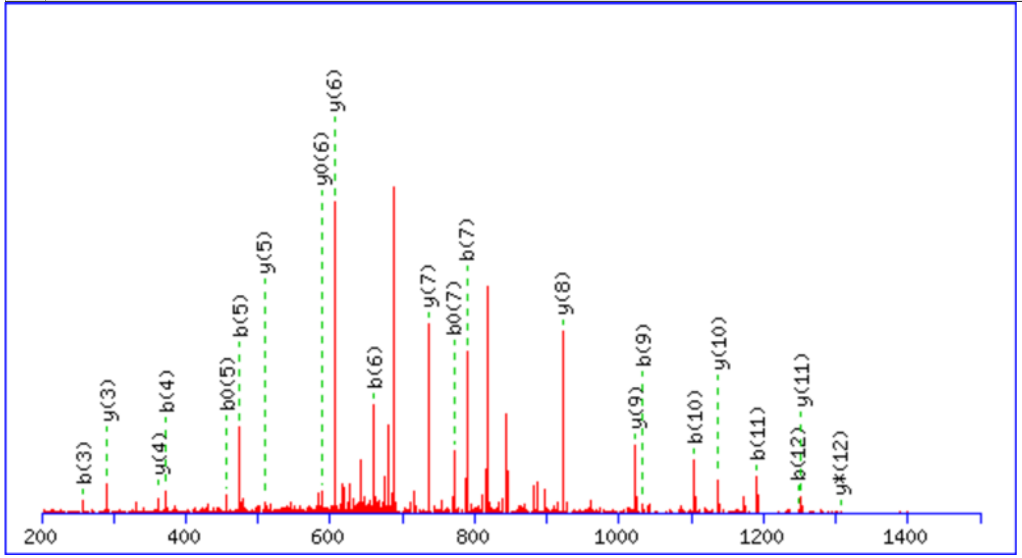
Peptide View

MS/MS Fragmentation of **AADDTWEPFASGK**
Found in **IPI00022432**, Tax_Id=9606 Gene_Symbol=TTR Transthyretin
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 9388: 1393.615048 from(697.814800,2+)
Title: OECHL100312_28.15078.15078.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw

Monoisotopic mass of neutral peptide Mr(calc): 1393.615005**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 4.7e-005**Matches :** 22/112 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**13**
2	143.081504	72.044390			**A**	1323.585173	662.296225	1306.558624	653.782950	1305.574608	653.290942	**12**
3	***258.108447***	129.557862	240.097882	120.552579	**D**	***1252.548059***	626.777668	1235.521510	618.264393	1234.537494	617.772385	**11**
4	***373.135390***	187.071333	355.124825	178.066051	**D**	***1137.521116***	569.264196	1120.494567	560.750922	1119.510551	560.258914	**10**
5	***474.183069***	237.595173	456.172504	228.589890	**T**	***1022.494173***	511.750725	1005.467624	503.237450	1004.483608	502.745442	**9**
6	***660.262382***	330.634829	642.251817	321.629547	**W**	***921.446494***	461.226885	904.419945	452.713611	903.435929	452.221603	**8**
7	***789.304975***	395.156126	771.294410	386.150843	**E**	***735.367181***	368.187229	718.340632	359.673954	717.356616	359.181946	**7**
8	886.357739	443.682508	868.347174	434.677225	**P**	***606.324588***	303.665932	589.298039	295.152658	588.314023	294.660650	**6**
9	***1033.426153***	517.216715	1015.415588	508.211432	**F**	***509.271824***	255.139550	492.245275	246.626275	491.261259	246.134267	**5**
10	***1104.463267***	552.735272	1086.452702	543.729989	**A**	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	**4**
11	***1191.495295***	596.251286	1173.484730	587.246003	**S**	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	**3**
12	***1248.516759***	624.762018	1230.506194	615.756735	**G**	204.134268	102.570772	187.107719	94.057497			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**

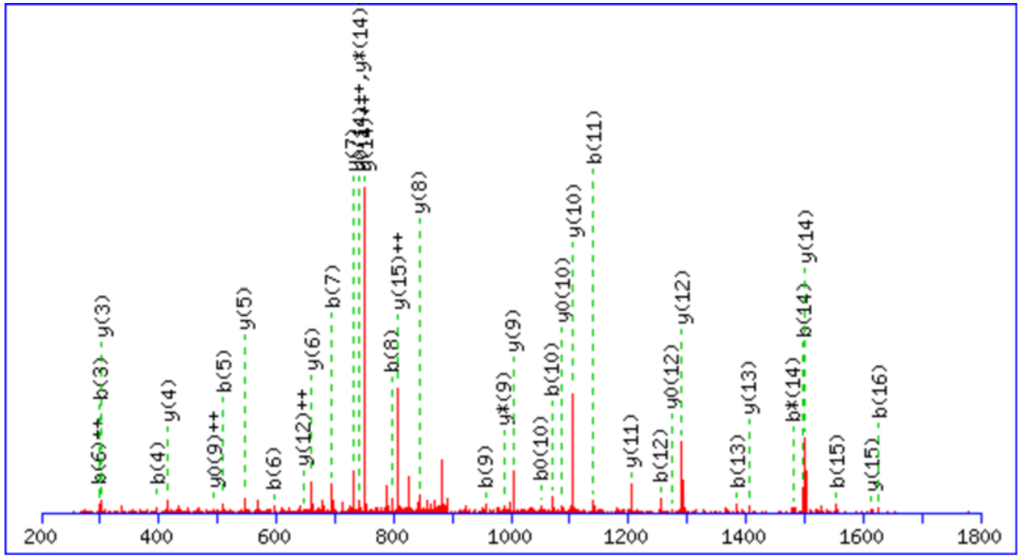


Peptide View

MS/MS Fragmentation of **GQLPISVTCIADEIGAR**
Found in **IPI00240345**, Tax_Id=9606 Gene_Symbol=CLEC14A C-type lectin domain family 14 member A
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 13630: 1798.926648 from(900.470600,2+)
Title: OECHL100312_28.19855.19855.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw
Monoisotopic mass of neutral peptide Mr(calc): 1798.924728**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 80
Expect: 1.2e-006**Matches :** 39/172 fragment ions using 86 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					**G**							**17**
2	186.087318	93.547297	169.060769	85.034023			**Q**	1742.910548	871.958912	1725.883999	863.445638	1724.899983	862.953630	**16**
3	***299.171382***	150.089329	282.144833	141.576055			**L**	**1614.851970**	807.929623	1597.825421	799.416349	1596.841405	798.924340	**15**
4	***396.224146***	198.615711	379.197597	190.102436			**P**	**1501.767906**	751.387591	1484.741357	742.874317	1483.757341	742.382309	**14**
5	***509.308210***	255.157743	492.281661	246.644468			**I**	**1404.715142**	702.861209	1387.688593	694.347935	1386.704577	693.855927	**13**
6	***596.340238***	298.673757	579.313689	290.160483	578.329673	289.668475	**S**	**1291.631078**	646.319177	1274.604529	637.805903	1273.620513	637.313895	**12**
7	***695.408652***	348.207964	678.382103	339.694689	677.398087	339.202681	**V**	**1204.599050**	602.803163	1187.572501	594.289889	1186.588485	593.797881	**11**
8	***796.456331***	398.731804	779.429782	390.218529	778.445766	389.726521	**T**	**1105.530636**	553.268956	1088.504087	544.755682	1087.520071	544.263674	**10**
9	***956.486980***	478.747128	939.460431	470.233854	938.476415	469.741846	**C**	**1004.482957**	502.745117	987.456408	494.231842	986.472392	493.739834	**9**
10	***1069.571044***	535.289160	1052.544495	526.775886	1051.560479	526.283878	**I**	**844.452308**	422.729792	827.425759	414.216518	826.441743	413.724510	**8**
11	***1140.608158***	570.807717	1123.581609	562.294443	1122.597593	561.802435	**A**	**731.368244**	366.187760	714.341695	357.674486	713.357679	357.182478	**7**
12	***1255.635101***	628.321189	1238.608552	619.807914	1237.624536	619.315906	**D**	**660.331130**	330.669203	643.304581	322.155929	642.320565	321.663921	**6**
13	***1384.677694***	692.842485	1367.651145	684.329211	1366.667129	683.837203	**E**	**545.304187**	273.155732	528.277638	264.642457	527.293622	264.150449	**5**
14	***1497.761758***	749.384517	1480.735209	740.871243	1479.751193	740.379235	**I**	**416.261594**	208.634435	399.235045	200.121160			**4**
15	***1554.783222***	777.895249	1537.756673	769.381975	1536.772657	768.889967	**G**	**303.177530**	152.092403	286.150981	143.579128			**3**
16	***1625.820336***	813.413806	1608.793787	804.900532	1607.809771	804.408524	**A**	246.156066	123.581671	229.129517	115.068396			**2**
17							**R**	175.118952	88.063114	158.092403	79.549839			**1**



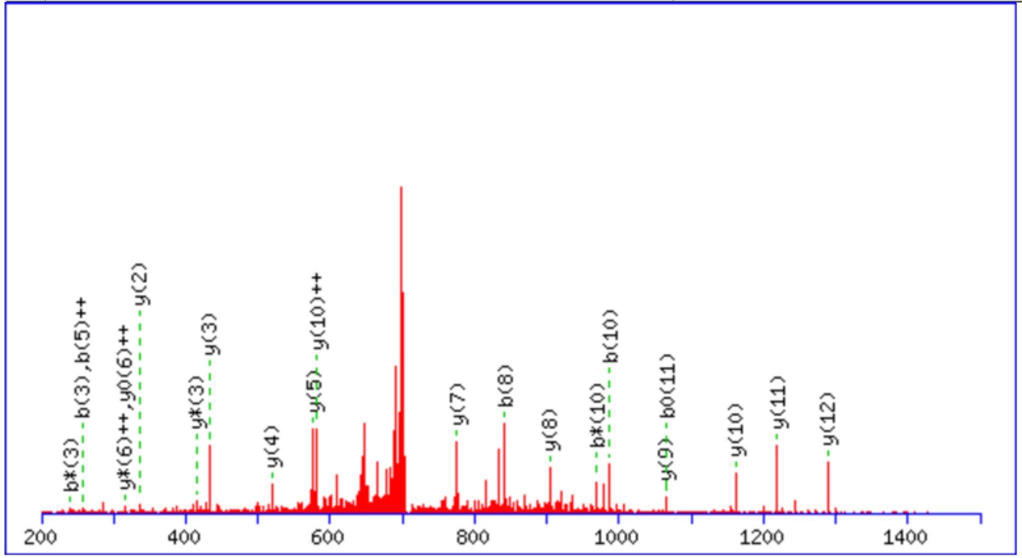
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 9607: 1416.624648 from(709.319600,2+)
Title: OECHL100312_28.2324.2324.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 69
Expect: 7.4e-006**Matches :** 21/128 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							**13**
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	**12**
3	**257.160817**	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	**11**
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	**10**
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	**9**
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	**8**

7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	647.292971	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	899.403979	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

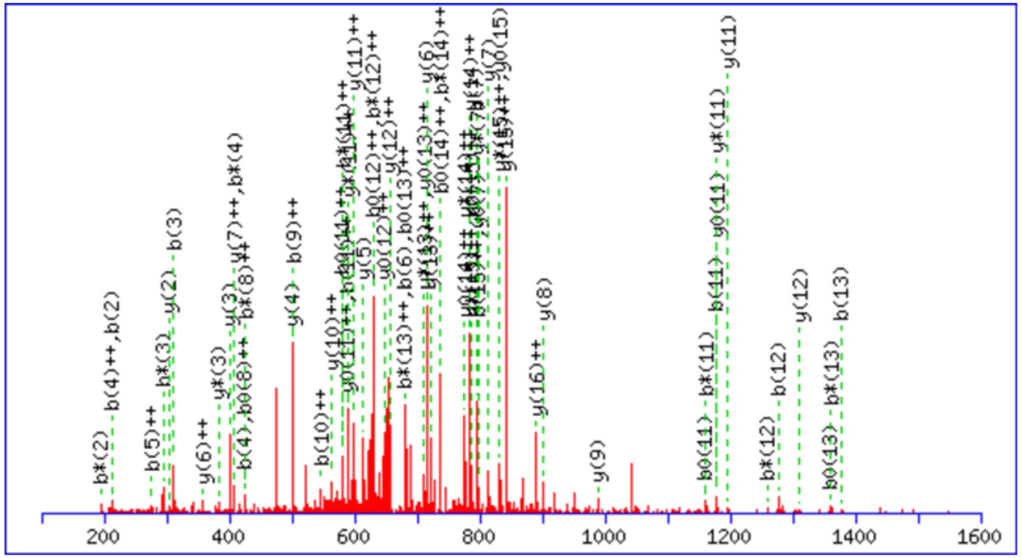


Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 14840: 1990.018872 from(664.346900,3+)
Title: OECHL100312_28.9590.9590.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.0016**Matches :** 67/186 fragment ions using 125 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	**212.102967**	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	1779.934789	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	**424.255445**	**212.631361**	407.228896	204.118086			**L**	1680.866375	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	552.314023	**276.660650**	535.287474	268.147375			**Q**	1567.782311	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	**680.372601**	340.689939	663.346052	332.176664			**Q**	1439.723733	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**
7	**795.399544**	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	1003.495570	**502.251423**	986.469021	493.738149	985.485005	493.246141	**H**	1125.601098	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	1090.527598	**545.767437**	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	**1177.559626**	**589.283451**	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	**1377.675719**	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	1490.759783	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	1591.807462	**796.407369**	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510			**3**
17	1816.918804	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	***303.177530***	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**



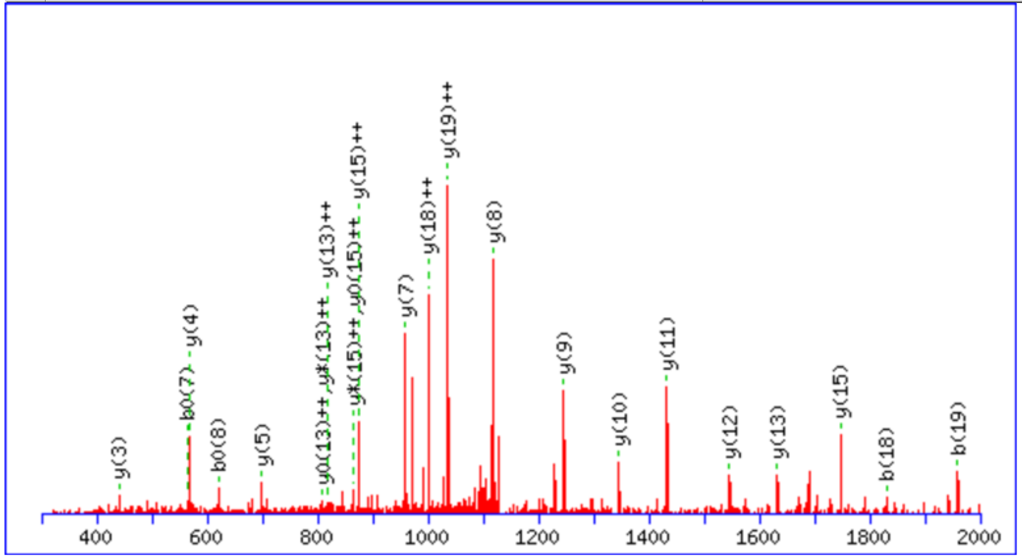
Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 16202: 2270.113448 from(1136.064000,2+)
Title: OECHL100312_28.10107.10107.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 73
Expect: 1e-005**Matches :** 23/212 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	102.054955	51.531116			84.044390	42.525833	T						
2	201.123369	101.065322			183.112804	92.060040	V	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400	1076.5338
3	272.160483	136.583879			254.149918	127.578597	A	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986	1026.9996
4	329.181947	165.094611			311.171382	156.089329	G	1999.965437	1000.486357	1982.938888	991.973082	1981.954872	991.4810
5	426.234711	213.620994			408.224146	204.615711	P	1942.943973	971.975625	1925.917424	963.462350	1924.933408	962.9703
6	525.303125	263.155201			507.292560	254.149918	V	1845.891209	923.449243	1828.864660	914.935968	1827.880644	914.4439

7	582.324589	291.665933			564.314024	282.660650	**G**	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230	864.9097
8	639.346053	320.176665			621.335488	311.171382	**G**	1689.801331	845.404304	1672.774782	836.891029	1671.790766	836.3990
9	726.378081	363.692679			708.367516	354.687396	**S**	***1632.779867***	816.893572	1615.753318	808.380297	1614.769302	807.8882
10	839.462145	420.234711			821.451580	411.229428	**L**	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274	764.3722
11	926.494173	463.750725			908.483608	454.745442	**S**	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210	707.8302
12	1025.562587	513.284932			1007.552022	504.279649	**V**	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182	664.3142
13	1153.621165	577.314221	1136.594616	568.800946	1135.610600	568.308938	**Q**	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768	614.7800
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	**C**	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190	550.7507
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	**P**	***958.474106***	479.740691	941.447557	471.227417	940.463541	470.7354
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	**Y**	861.421342	431.214309	844.394793	422.701035	843.410777	422.2090
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	**E**	***698.358013***	349.682645	681.331464	341.169370	680.347448	340.6773
18	**1830.905463**	915.956370	1813.878914	907.443095	1812.894898	906.951087	**K**	***569.315420***	285.161348	552.288871	276.648074	551.304855	276.1560
19	**1959.948056**	980.477666	1942.921507	971.964392	1941.937491	971.472384	**E**	***441.220457***	221.113867	424.193908	212.600592	423.209892	212.1085
20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	**H**	312.177864	156.592570	295.151315	148.079295		
21							**R**	175.118952	88.063114	158.092403	79.549839		

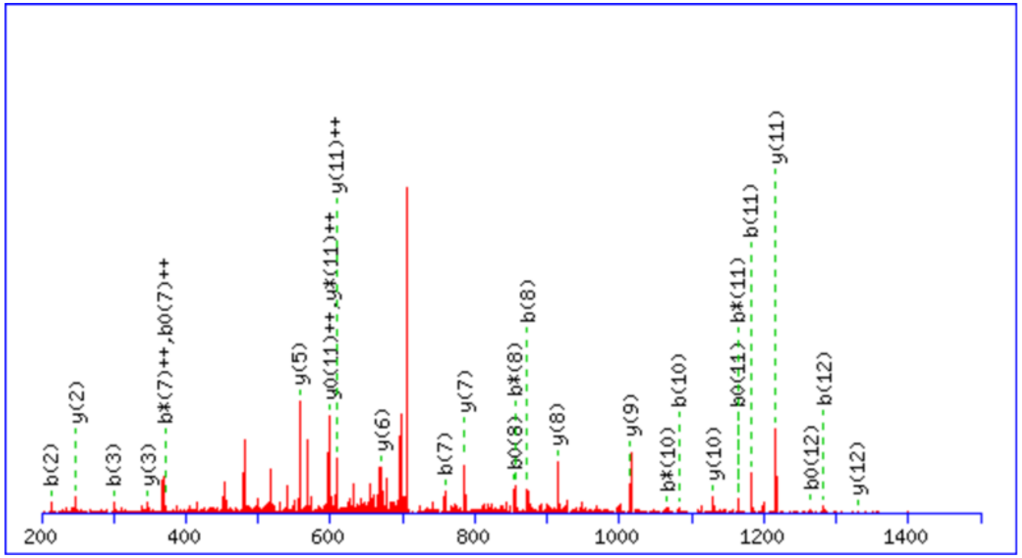


Peptide View

MS/MS Fragmentation of **VLSNTEDLPLVTK**
Found in **IPI00218851**, Tax_Id=9606 Gene_Symbol=LYNX1 Ly-6 neurotoxin-like protein 1 isoform a
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 9678: 1427.787248 from(714.900900,2+)
Title: OECHL100312_28.14351.14351.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw
Monoisotopic mass of neutral peptide Mr(calc): 1427.787155**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 0.00019**Matches :** 28/132 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	100.075690	50.541483					**V**							**13**
2	**213.159754**	107.083515					**L**	***1329.726023***	665.366650	1312.699474	656.853375	1311.715458	656.361367	**12**
3	**300.191782**	150.599529			282.181217	141.594247	**S**	***1216.641959***	608.824618	1199.615410	600.311343	1198.631394	599.819335	**11**
4	414.234709	207.620993	397.208160	199.107718	396.224144	198.615710	**N**	***1129.609931***	565.308604	1112.583382	556.795329	1111.599366	556.303321	**10**
5	515.282388	258.144832	498.255839	249.631558	497.271823	249.139550	**T**	***1015.567004***	508.287140	998.540455	499.773866	997.556439	499.281858	**9**
6	644.324981	322.666129	627.298432	314.152854	626.314416	313.660846	**E**	***914.519325***	457.763301	897.492776	449.250026	896.508760	448.758018	**8**
7	**759.351924**	380.179600	742.325375	371.666326	741.341359	371.174318	**D**	***785.476732***	393.242004	768.450183	384.728730	767.466167	384.236722	**7**
8	**872.435988**	436.721632	855.409439	428.208358	854.425423	427.716350	**L**	***670.449789***	335.728533	653.423240	327.215258	652.439224	326.723250	**6**
9	969.488752	485.248014	952.462203	476.734740	951.478187	476.242732	**P**	***557.365725***	279.186501	540.339176	270.673226	539.355160	270.181218	**5**
10	**1082.572816**	541.790046	1065.546267	533.276772	1064.562251	532.784764	**L**	460.312961	230.660119	443.286412	222.146844	442.302396	221.654836	**4**
11	**1181.641230**	591.324253	1164.614681	582.810979	1163.630665	582.318971	**V**	***347.228897***	174.118087	330.202348	165.604812	329.218332	165.112804	**3**
12	**1282.688909**	641.848093	1265.662360	633.334818	1264.678344	632.842810	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
13							**K**	147.112804	74.060040	130.086255	65.546765			**1**



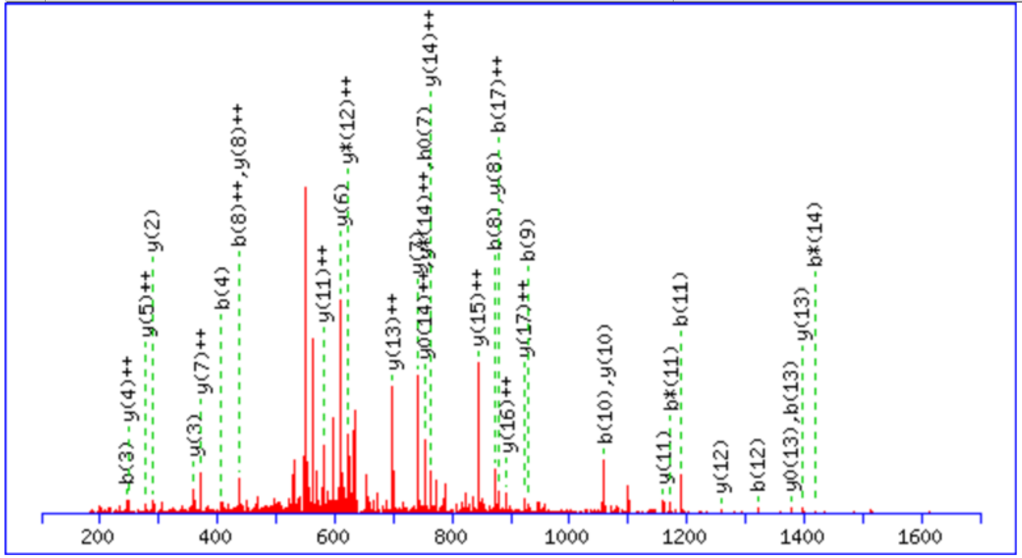
Peptide View

MS/MS Fragmentation of **SGVYQHVTGEMMGGHAIR**
Found in **IPI00295741**, Tax_Id=9606 Gene_Symbol=CTSB Cathepsin B
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 14523: 1928.898972 from(643.973600,3+)
Title: OECHL100312_28.11727.11727.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw
Monoisotopic mass of neutral peptide Mr(calc): 1928.898544**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57
Expect: 0.00033**Matches :** 36/180 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	88.039304	44.523290			70.028739	35.518008	S							18
2	145.060768	73.034022			127.050203	64.028740	G	1842.873787	921.940531	1825.847238	913.427257	1824.863222	912.935249	17
3	**244.129182**	122.568229			226.118617	113.562947	V	1785.852323	893.429799	1768.825774	884.916525	1767.841758	884.424517	16
4	**407.192511**	204.099894			389.181946	195.094611	Y	1686.783909	843.895592	1669.757360	835.382318	1668.773344	834.890310	15
5	535.251089	268.129183	518.224540	259.615908	517.240524	259.123900	Q	1523.720580	762.363928	1506.694031	753.850654	1505.710015	753.358645	14
6	672.310001	336.658639	655.283452	328.145364	654.299436	327.653356	H	***1395.662002***	698.334639	1378.635453	689.821364	1377.651437	689.329356	13

7	771.378415	386.192846	754.351866	377.679571	753.367850	377.187563	**V**	***1258.603090***	629.805183	1241.576541	621.291908	1240.592525	620.799900	**12**
8	**872.426094**	436.716685	855.399545	428.203411	854.415529	427.711403	**T**	***1159.534676***	580.270976	1142.508127	571.757702	1141.524111	571.265694	**11**
9	**929.447558**	465.227417	912.421009	456.714143	911.436993	456.222135	**G**	***1058.486997***	529.747136	1041.460448	521.233862	1040.476432	520.741854	**10**
10	**1058.490151**	529.748714	1041.463602	521.235439	1040.479586	520.743431	**E**	1001.465533	501.236404	984.438984	492.723130	983.454968	492.231122	**9**
11	**1189.530636**	595.268956	1172.504087	586.755682	1171.520071	586.263674	**M**	***872.422940***	436.715108	855.396391	428.201833			**8**
12	**1320.571121**	660.789199	1303.544572	652.275924	1302.560556	651.783916	**M**	***741.382455***	371.194865	724.355906	362.681591			**7**
13	**1377.592585**	689.299931	1360.566036	680.786656	1359.582020	680.294648	**G**	***610.341970***	305.674623	593.315421	297.161348			**6**
14	1434.614049	717.810663	1417.587500	709.297388	1416.603484	708.805380	**G**	553.320506	277.163891	536.293957	268.650616			**5**
15	1571.672961	786.340119	1554.646412	777.826844	1553.662396	777.334836	**H**	496.299042	248.653159	479.272493	240.139884			**4**
16	1642.710075	821.858676	1625.683526	813.345401	1624.699510	812.853393	**A**	***359.240130***	180.123703	342.213581	171.610428			**3**
17	1755.794139	878.400707	1738.767590	869.887433	1737.783574	869.395425	**I**	***288.203016***	144.605146	271.176467	136.091871			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**

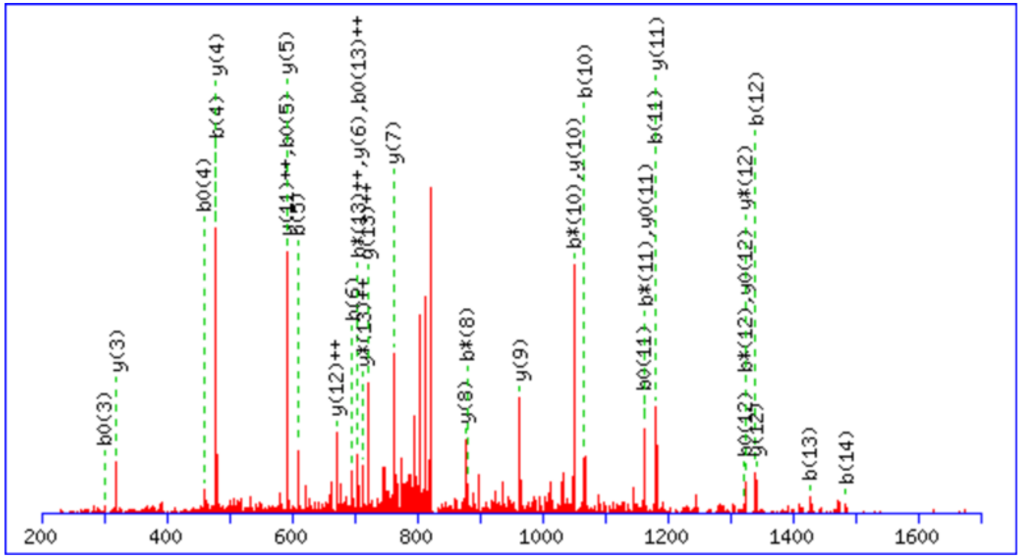


Peptide View

MS/MS Fragmentation of **TDTCMSSNGLLCSGR**
Found in **IPI00220350**, Tax_Id=9606 Gene_Symbol=ITGB3 Isoform Beta-3B of Integrin beta-3
Experiment: 38 - OPC-2 **Fraction:** OPC-2

Match to Query 12206: 1657.686848 from(829.850700,2+)
Title: OECHL100312_28.10528.10528.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_28.raw
Monoisotopic mass of neutral peptide Mr(calc): 1657.685837**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 8.3e-005**Matches :** 36/150 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	102.054955	51.531116			84.044390	42.525833	**T**							**15**
2	217.081898	109.044587			199.071333	100.039304	**D**	1557.645424	779.326350	1540.618875	770.813075	1539.634859	770.321067	**14**
3	318.129577	159.568426			300.119012	150.563144	**T**	1442.618481	721.812878	1425.591932	713.299604	1424.607916	712.807596	**13**
4	***478.160226***	239.583751			460.149661	230.578469	**C**	***1341.570802***	671.289039	1324.544253	662.775765	1323.560237	662.283756	**12**
5	***609.200711***	305.103994			591.190146	296.098711	**M**	***1181.540153***	591.273714	1164.513604	582.760440	1163.529588	582.268432	**11**
6	***696.232739***	348.620008			678.222174	339.614725	**S**	***1050.499668***	525.753472	1033.473119	517.240197	1032.489103	516.748189	**10**
7	783.264767	392.136022			765.254202	383.130739	**S**	***963.467640***	482.237458	946.441091	473.724183	945.457075	473.232175	**9**
8	897.307694	449.157485	880.281145	440.644210	879.297129	440.152202	**N**	***876.435612***	438.721444	859.409063	430.208169	858.425047	429.716161	**8**
9	954.329158	477.668217	937.302609	469.154943	936.318593	468.662935	**G**	***762.392685***	381.699980	745.366136	373.186706	744.382120	372.694698	**7**
10	***1067.413222***	534.210249	1050.386673	525.696975	1049.402657	525.204966	**L**	***705.371221***	353.189248	688.344672	344.675974	687.360656	344.183966	**6**
11	***1180.497286***	590.752281	1163.470737	582.239006	1162.486721	581.746998	**L**	***592.287157***	296.647217	575.260608	288.133942	574.276592	287.641934	**5**
12	***1340.527935***	670.767605	1323.501386	662.254331	1322.517370	661.762323	**C**	***479.203093***	240.105184	462.176544	231.591910	461.192528	231.099902	**4**
13	***1427.559963***	714.283619	1410.533414	705.770345	1409.549398	705.278337	**S**	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	**3**
14	***1484.581427***	742.794351	1467.554878	734.281077	1466.570862	733.789069	**G**	232.140416	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



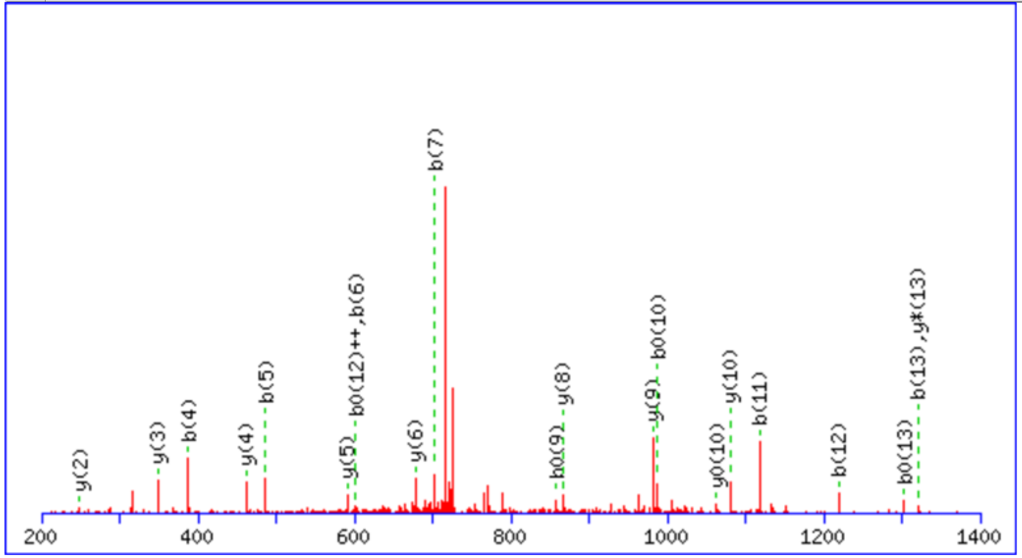
Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 02 - S_A-2 **Fraction:** S_A-2

Match to Query 9337: 1465.682648 from(733.848600,2+)
Title: OECHL100312_26.9169.9169.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_26.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 77 **Expect:** 1.9e-006**Matches :** 21/128 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	1337.643082	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	316.113926	158.560601	298.103361	149.555319	**A**	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	***387.151040***	194.079158	369.140475	185.073875	**A**	1151.579025	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	***486.219454***	243.613365	468.208889	234.608082	**V**	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**
6	***601.246397***	301.126837	583.235832	292.121554	**D**	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	**9**

7	***702.294076***	351.650676	684.283511	342.645394	**T**	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	765.398875	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	876.358132	438.682704	858.347567	429.677421	**S**	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	1005.400725	503.204001	987.390160	494.198718	**E**	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	***1118.484789***	559.746033	1100.474224	550.740750	**I**	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	***1219.532468***	610.269872	1201.521903	601.264590	**T**	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	***1320.580147***	660.793712	1302.569582	651.788429	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**



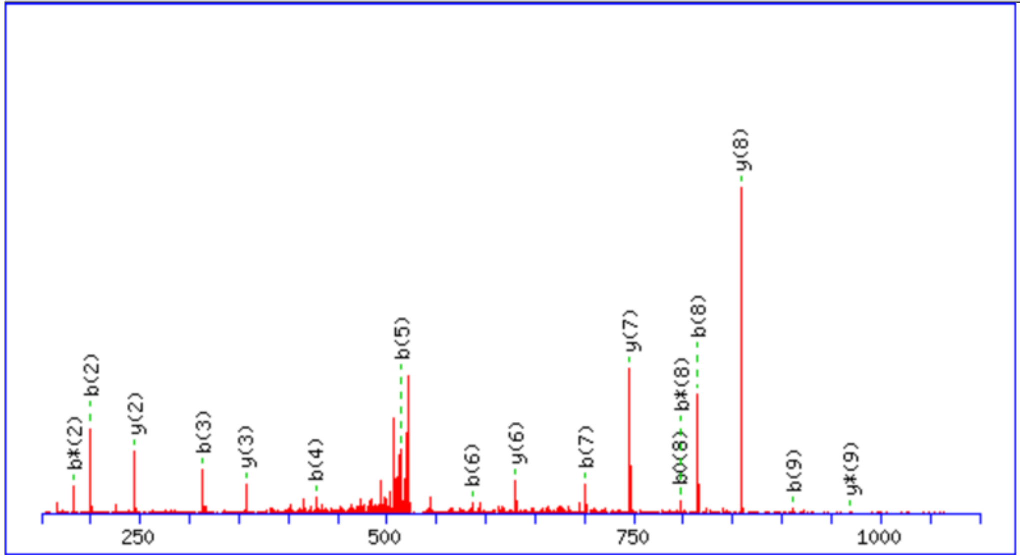
Peptide View

MS/MS Fragmentation of **AQLDSADIPK**
Found in **IPI00026303**, Tax_Id=9606 Gene_Symbol=PI15 Peptidase inhibitor 15
Experiment: 02 - S_A-2 **Fraction:** S_A-2

Match to Query 4043: 1056.545048 from(529.279800,2+)
Title: OECHL100312_26.8885.8885.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_26.raw
Monoisotopic mass of neutral peptide Mr(calc): 1056.545120**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54

Expect: 0.00041**Matches :** 17/94 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							10
2	***200.102968***	100.555122	183.076419	92.041848			Q	986.515302	493.761289	969.488753	485.248015	968.504737	484.756007	9
3	***313.187032***	157.097154	296.160483	148.583879			L	**858.456724**	429.732000	841.430175	421.218726	840.446159	420.726718	8
4	***428.213975***	214.610626	411.187426	206.097351	410.203410	205.605343	D	**745.372660**	373.189968	728.346111	364.676694	727.362095	364.184686	7
5	***515.246003***	258.126640	498.219454	249.613365	497.235438	249.121357	S	**630.345717**	315.676497	613.319168	307.163222	612.335152	306.671214	6
6	***586.283117***	293.645197	569.256568	285.131922	568.272552	284.639914	A	543.313689	272.160483	526.287140	263.647208	525.303124	263.155200	5
7	***701.310060***	351.158668	684.283511	342.645394	683.299495	342.153386	D	472.276575	236.641926	455.250026	228.128651	454.266010	227.636643	4
8	***814.394124***	407.700700	797.367575	399.187426	796.383559	398.695418	I	**357.249632**	179.128454	340.223083	170.615180			3
9	***911.446888***	456.227082	894.420339	447.713808	893.436323	447.221800	P	**244.165568**	122.586422	227.139019	114.073148			2
10							K	147.112804	74.060040	130.086255	65.546766			1

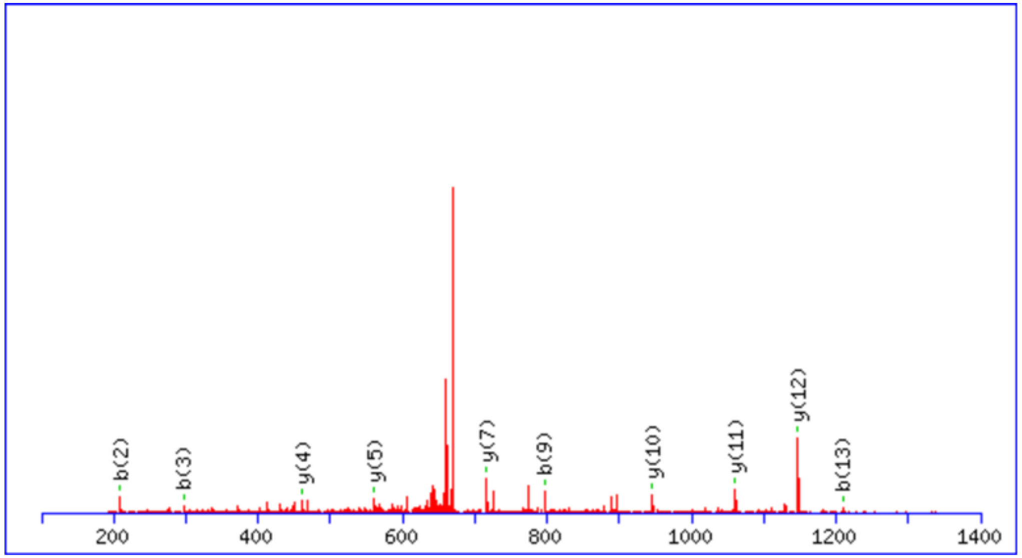


Peptide View

MS/MS Fragmentation of **AHSDGGDGVVSQVK**
Found in **IPI00029751**, Tax_Id=9606 Gene_Symbol=CNTN1 Isoform 1 of Contactin-1
Experiment: 02 - S_A-2 **Fraction:** S_A-2

Match to Query 8310: 1354.650048 from(678.332300,2+)
Title: OECHL100312_26.3922.3922.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100312_26.raw
Monoisotopic mass of neutral peptide Mr(calc): 1354.647736**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00057**Matches :** 10/124 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	72.044390	36.525833					**A**							**14**
2	***209.103302***	105.055289					**H**	1284.617870	642.812573	1267.591321	634.299299	1266.607305	633.807291	**13**
3	***296.135330***	148.571303			278.124765	139.566021	**S**	***1147.558958***	574.283117	1130.532409	565.769843	1129.548393	565.277835	**12**
4	411.162273	206.084775			393.151708	197.079492	**D**	***1060.526930***	530.767103	1043.500381	522.253829	1042.516365	521.761821	**11**
5	468.183737	234.595507			450.173172	225.590224	**G**	***945.499987***	473.253632	928.473438	464.740357	927.489422	464.248349	**10**
6	525.205201	263.106239			507.194636	254.100956	**G**	888.478523	444.742900	871.451974	436.229625	870.467958	435.737617	**9**
7	640.232144	320.619710			622.221579	311.614428	**D**	831.457059	416.232168	814.430510	407.718893	813.446494	407.226885	**8**
8	697.253608	349.130442			679.243043	340.125160	**G**	***716.430116***	358.718696	699.403567	350.205422	698.419551	349.713414	**7**
9	***796.322022***	398.664649			778.311457	389.659367	**V**	659.408652	330.207964	642.382103	321.694690	641.398087	321.202682	**6**
10	895.390436	448.198856			877.379871	439.193574	**V**	***560.340238***	280.673757	543.313689	272.160483	542.329673	271.668475	**5**
11	982.422464	491.714870			964.411899	482.709588	**S**	***461.271824***	231.139550	444.245275	222.626276	443.261259	222.134268	**4**
12	1110.481042	555.744159	1093.454493	547.230885	1092.470477	546.738877	**Q**	374.239796	187.623536	357.213247	179.110262			**3**
13	***1209.549456***	605.278366	1192.522907	596.765092	1191.538891	596.273084	**V**	246.181218	123.594247	229.154669	115.080973			**2**
14							**K**	147.112804	74.060040	130.086255	65.546765			**1**

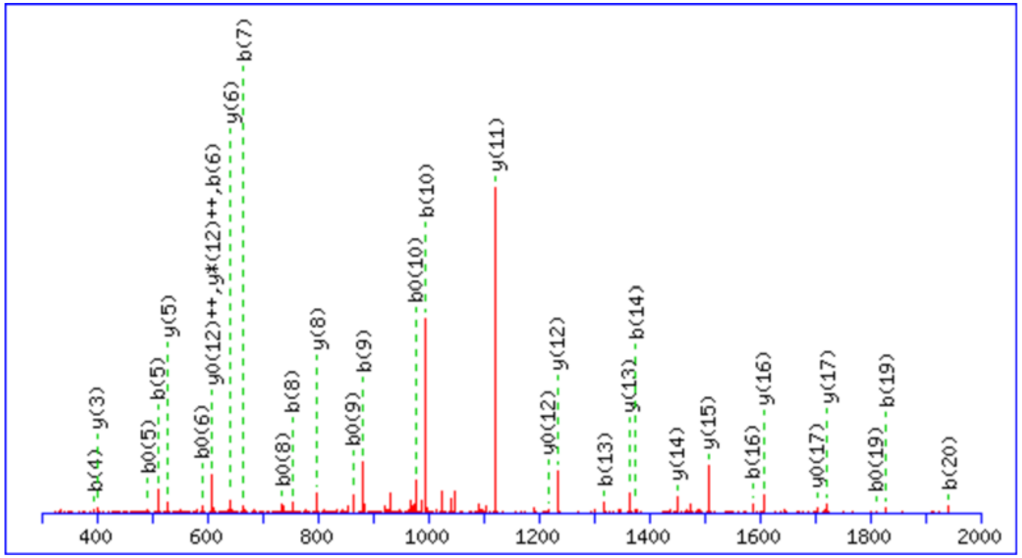

b(2)
b(3)
y(4)
y(5)
y(7)
b(9)
y(10)
y(11)
y(12)
b(13)
200
400
600
800
1000
1200
1400

Peptide View

MS/MS Fragmentation of **AADHDVGSELPPEGVLGALLR**
Found in **IPI00002280**, Tax_Id=9606 Gene_Symbol=PCSK1N ProSAAS
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 16025: 2115.095448 from(1058.555000,2+)
Title: OECHL100317_19.21876.21876.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 2115.096024**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 83
Expect: 5.9e-007**Matches :** 33/180 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**21**
2	143.081504	72.044390			**A**	2045.066196	1023.036736	2028.039647	1014.523461	2027.055631	1014.031453	**20**
3	258.108447	129.557862	240.097882	120.552579	**D**	1974.029082	987.518179	1957.002533	979.004904	1956.018517	978.512896	**19**
4	***395.167359***	198.087317	377.156794	189.082035	**H**	1859.002139	930.004707	1841.975590	921.491433	1840.991574	920.999425	**18**
5	***510.194302***	255.600789	492.183737	246.595507	**D**	***1721.943227***	861.475251	1704.916678	852.961977	1703.932662	852.469969	**17**
6	***609.262716***	305.134996	591.252151	296.129714	**V**	***1606.916284***	803.961780	1589.889735	795.448505	1588.905719	794.956497	**16**
7	***666.284180***	333.645728	648.273615	324.640446	**G**	***1507.847870***	754.427573	1490.821321	745.914298	1489.837305	745.422290	**15**
8	***753.316208***	377.161742	735.305643	368.156460	**S**	***1450.826406***	725.916841	1433.799857	717.403566	1432.815841	716.911558	**14**
9	***882.358801***	441.683039	864.348236	432.677756	**E**	***1363.794378***	682.400827	1346.767829	673.887552	1345.783813	673.395544	**13**
10	***995.442865***	498.225071	977.432300	489.219788	**L**	***1234.751785***	617.879530	1217.725236	609.366256	1216.741220	608.874248	**12**
11	1092.495629	546.751453	1074.485064	537.746170	**P**	***1121.667721***	561.337498	1104.641172	552.824224	1103.657156	552.332216	**11**
12	1189.548393	595.277835	1171.537828	586.272552	**P**	1024.614957	512.811116	1007.588408	504.297842	1006.604392	503.805834	**10**
13	***1318.590986***	659.799131	1300.580421	650.793848	**E**	927.562193	464.284734	910.535644	455.771460	909.551628	455.279452	**9**
14	***1375.612450***	688.309863	1357.601885	679.304580	**G**	***798.519600***	399.763438	781.493051	391.250163			**8**
15	1474.680864	737.844070	1456.670299	728.838787	**V**	741.498136	371.252706	724.471587	362.739431			**7**
16	***1587.764928***	794.386102	1569.754363	785.380819	**L**	***642.429722***	321.718499	625.403173	313.205224			**6**
17	1644.786392	822.896834	1626.775827	813.891551	**G**	***529.345658***	265.176467	512.319109	256.663192			**5**
18	1715.823506	858.415391	1697.812941	849.410108	**A**	472.324194	236.665735	455.297645	228.152460			**4**
19	***1828.907570***	914.957423	1810.897005	905.952140	**L**	***401.287080***	201.147178	384.260531	192.633903			**3**
20	***1941.991634***	971.499455	1923.981069	962.494172	**L**	288.203016	144.605146	271.176467	136.091872			**2**
21					**R**	175.118952	88.063114	158.092403	79.549840			**1**



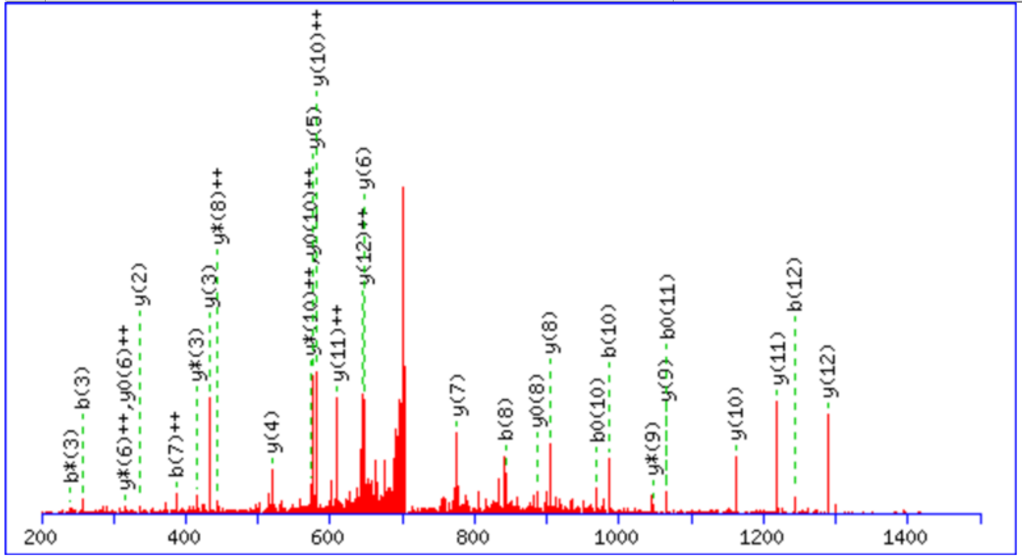
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 9453: 1416.625048 from(709.319800,2+)
Title: OECHL100317_19.2437.2437.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67
Expect: 1.4e-005**Matches :** 30/128 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	129.102239	65.054757	112.075690	56.541483			**K**							**13**
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	**12**
3	**257.160817**	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	**11**
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	**10**
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	**9**
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	**8**

7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	899.403979	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	**1243.519420**	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

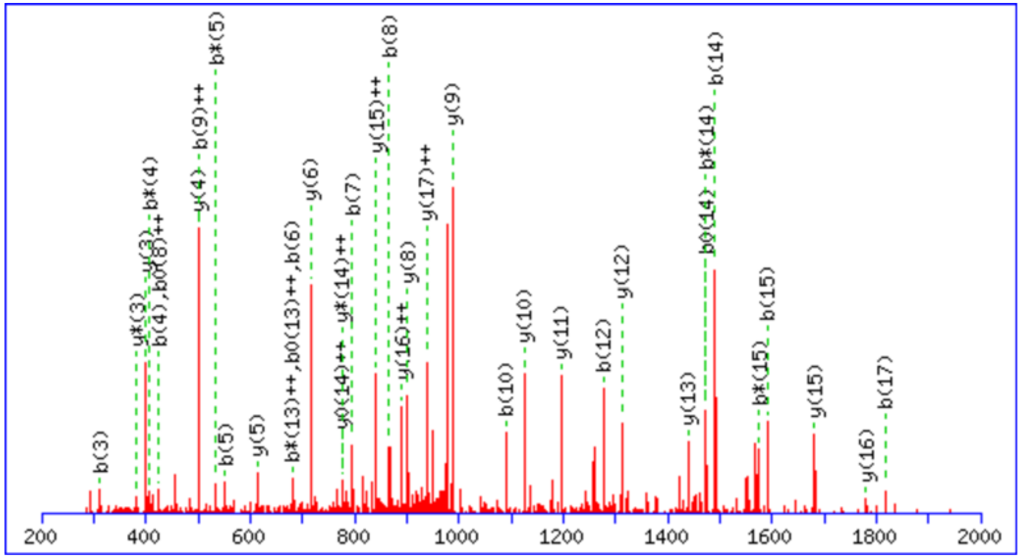


Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 15157: 1990.025448 from(996.020000,2+)
Title: OECHL100317_19.10615.10615.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 75
Expect: 3.9e-006**Matches :** 38/186 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	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	***311.171381***	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	***424.255445***	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	***552.314023***	276.660650	535.287474	268.147375			**Q**	1567.782311	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	***680.372601***	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**
7	***795.399544***	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	***866.436658***	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	***1090.527598***	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	***1276.628040***	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	814.478130	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	***1490.759783***	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	***1591.807462***	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510			**3**
17	***1816.918804***	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**



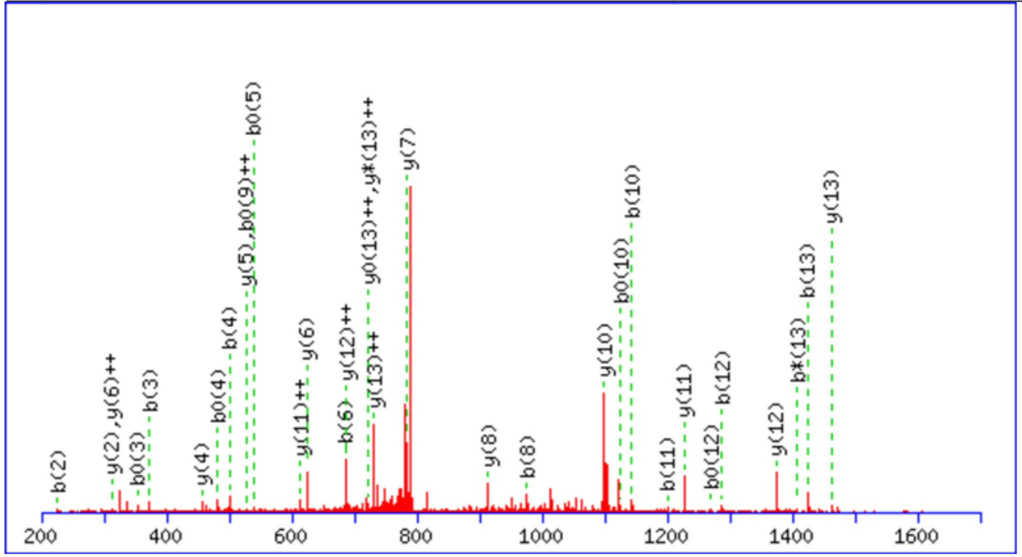
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 11261: 1597.705448 from(799.860000,2+)
Title: OECHL100317_19.2599.2599.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64
Expect: 2.3e-005**Matches :** 32/144 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	138.066188	69.536732					H							14
2	***225.098216***	113.052746			207.087651	104.047463	S	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.325325	13
3	***372.166630***	186.586953			354.156065	177.581671	F	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.809311	12
4	***500.261593***	250.634435	483.235044	242.121160	482.251028	241.629152	K	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	11
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	G	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	10
6	***686.325650***	343.666463	669.299101	335.153189	668.315085	334.661181	E	1042.437069	521.722173	1025.410520	513.208898	1024.426504	512.716890	9

7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	***975.398892***	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	***1143.488770***	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	***1200.510234***	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	***1287.542262***	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	399.209892	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	***1424.601174***	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	***312.177864***	156.592570	295.151315	148.079295			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



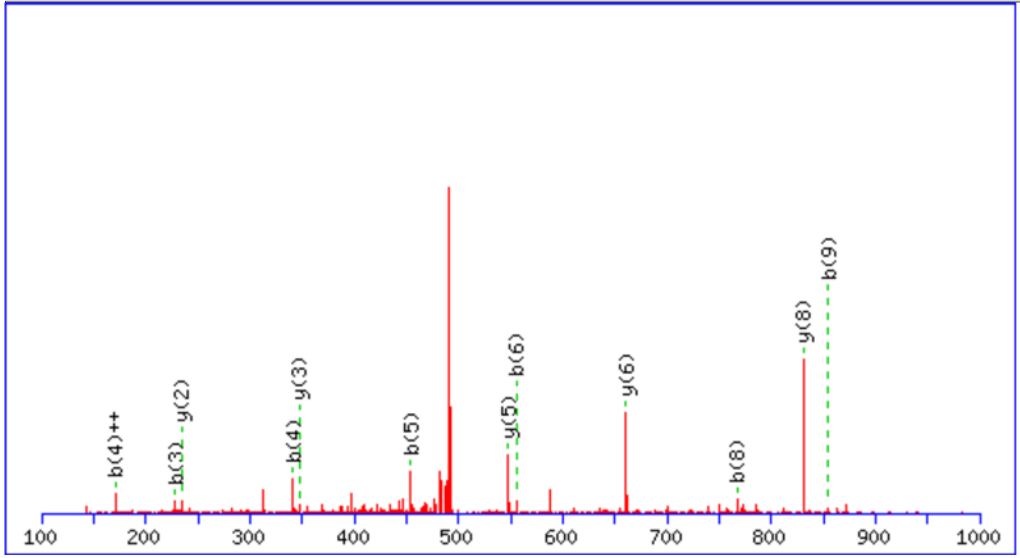
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 4027: 999.633048 from(500.823800,2+)
Title: OECHL100317_19.18069.18069.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51

Expect: 0.0001**Matches :** 13/78 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	654.418489	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**

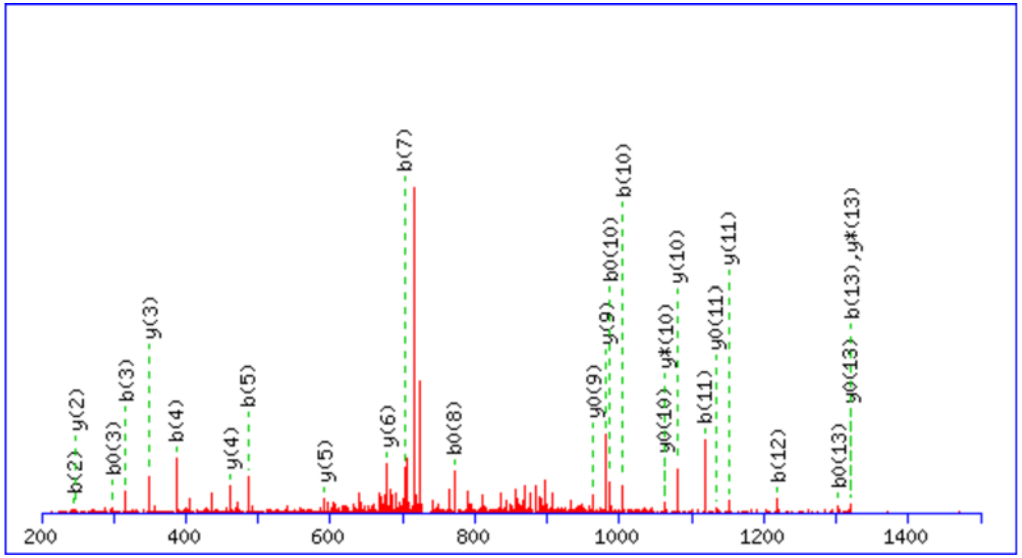


Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 9967: 1465.677848 from(733.846200,2+)
Title: OECHL100317_19.10576.10576.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 61 **Expect:** 5.9e-005**Matches :** 27/128 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	***245.076812***	123.042044	227.066247	114.036761	**D**	1337.643082	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	***316.113926***	158.560601	298.103361	149.555319	**A**	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	***387.151040***	194.079158	369.140475	185.073875	**A**	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	***486.219454***	243.613365	468.208889	234.608082	**V**	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**
6	601.246397	301.126837	583.235832	292.121554	**D**	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	**9**
7	***702.294076***	351.650676	684.283511	342.645394	**T**	866.446554	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	765.398875	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	876.358132	438.682704	858.347567	429.677421	**S**	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	***1005.400725***	503.204001	987.390160	494.198718	**E**	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	***1118.484789***	559.746033	1100.474224	550.740750	**I**	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	***1219.532468***	610.269872	1201.521903	601.264590	**T**	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	***1320.580147***	660.793712	1302.569582	651.788429	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**



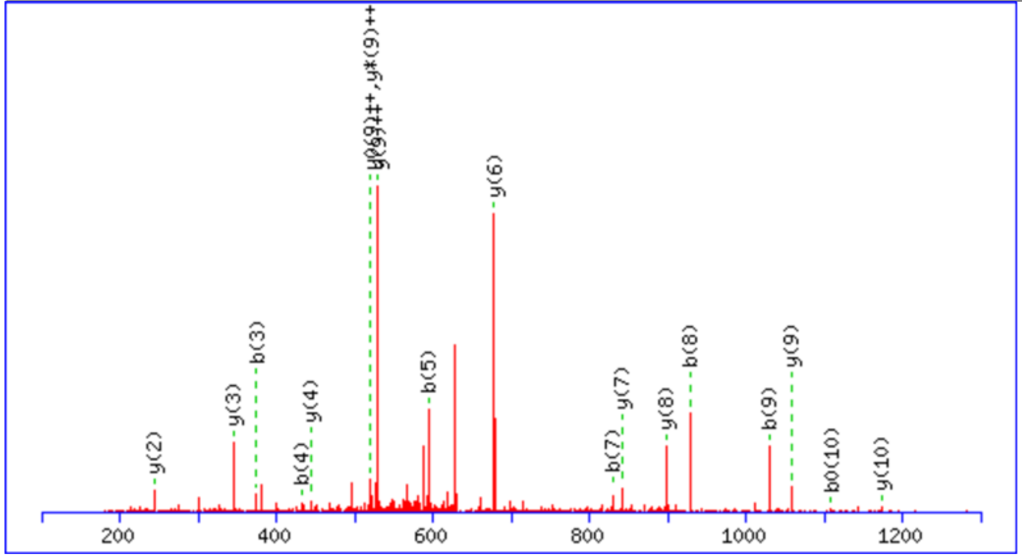
Peptide View

MS/MS Fragmentation of **VDCGYPHVTPK**
Found in **IPI00018909**, Tax_Id=9606 Gene_Symbol=TFF3 trefoil factor 3 precursor
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 8155: 1271.598048 from(636.806300,2+)
Title: OECHL100317_19.6268.6268.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1271.596878**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00096**Matches :** 18/94 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			**V**							**11**
2	215.102633	108.054954	197.092068	99.049672	**D**	***1173.535722***	587.271499	1156.509173	578.758224	1155.525157	578.266216	**10**
3	**375.133282**	188.070279	357.122717	179.064997	**C**	***1058.508779***	529.758028	1041.482230	521.244753	1040.498214	520.752745	**9**
4	**432.154746**	216.581011	414.144181	207.575729	**G**	***898.478130***	449.742703	881.451581	441.229428	880.467565	440.737420	**8**
5	**595.218075**	298.112676	577.207510	289.107393	**Y**	***841.456666***	421.231971	824.430117	412.718696	823.446101	412.226688	**7**
6	692.270839	346.639058	674.260274	337.633775	**P**	***678.393337***	339.700307	661.366788	331.187032	660.382772	330.695024	**6**

7	**829.329751**	415.168514	811.319186	406.163231	**H**	581.340573	291.173925	564.314024	282.660650	563.330008	282.168642	**5**
8	**928.398165**	464.702721	910.387600	455.697438	**V**	***444.281661***	222.644468	427.255112	214.131194	426.271096	213.639186	**4**
9	**1029.445844**	515.226560	1011.435279	506.221277	**T**	***345.213247***	173.110261	328.186698	164.596987	327.202682	164.104979	**3**
10	1126.498608	563.752942	1108.488043	554.747659	**P**	***244.165568***	122.586422	227.139019	114.073148			**2**
11					**K**	147.112804	74.060040	130.086255	65.546765			**1**



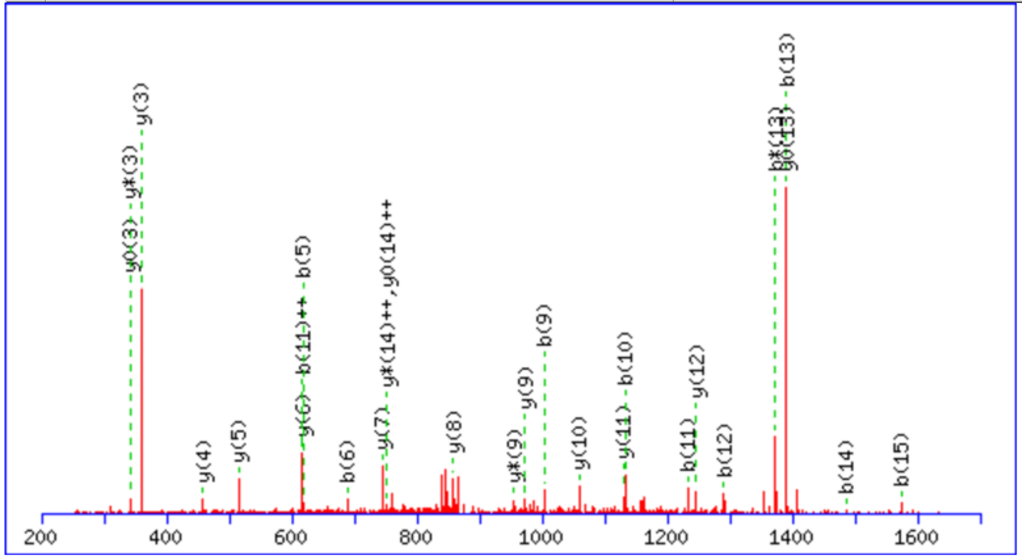
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 13192: 1746.917848 from(874.466200,2+)
Title: OECHL100317_19.17817.17817.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 74
Expect: 4.9e-006**Matches :** 27/156 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	114.091340	57.549308					**L**							**16**

2	227.175404	114.091340					L	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	15
3	340.259468	170.633372					I	1521.754363	761.380820	1504.727814	752.867545	1503.743798	752.375537	14
4	503.322797	252.165036					Y	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	13
5	***618.349740***	309.678508			600.339175	300.673226	D	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	12
6	***689.386854***	345.197065			671.376289	336.191782	A	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	11
7	776.418882	388.713079			758.408317	379.707796	S	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	10
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	9
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	L	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	8
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	E	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	7
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	T	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	6
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	G	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	5
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	V	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	4
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
16							R	175.118952	88.063114	158.092403	79.549839			1

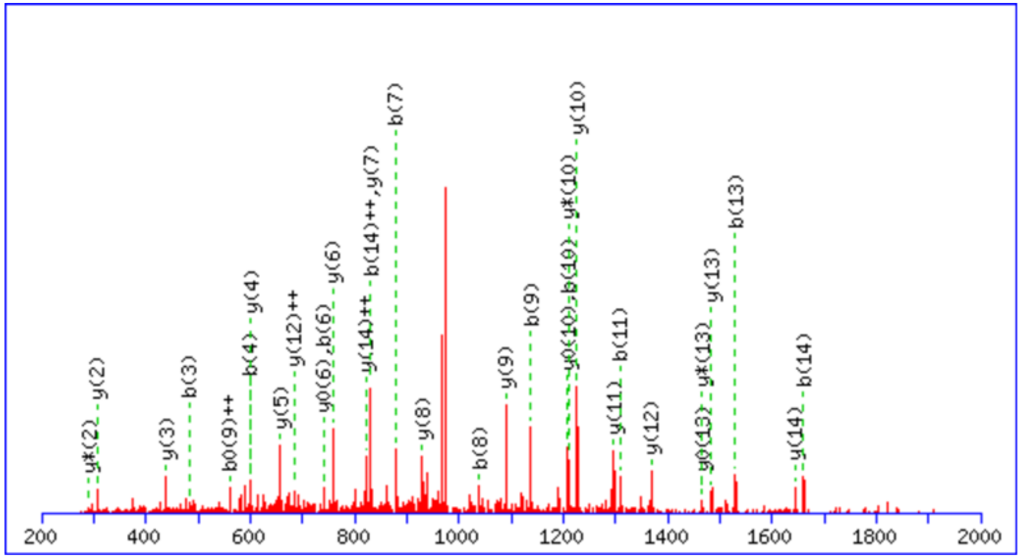


Peptide View

MS/MS Fragmentation of **CYCDAAHCVATGYMCK**
Found in **IPI00011899**, Tax_Id=9606 Gene_Symbol=BAMBI BMP and activin membrane-bound inhibitor homolog
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 14961: 1965.731248 from(983.872900,2+)
Title: OECHL100317_19.11543.11543.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1965.730026**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72
Expect: 1.6e-007**Matches :** 33/134 fragment ions using 66 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	161.037925	81.022600			**C**							**16**
2	324.101254	162.554265			**Y**	1806.706648	903.856962	1789.680099	895.343688	1788.696083	894.851680	**15**
3	**484.131903**	242.569590			**C**	***1643.643319***	822.325298	1626.616770	813.812023	1625.632754	813.320015	**14**
4	**599.158846**	300.083061	581.148281	291.077779	**D**	***1483.612670***	742.309973	1466.586121	733.796699	1465.602105	733.304691	**13**
5	670.195960	335.601618	652.185395	326.596336	**A**	***1368.585727***	684.796502	1351.559178	676.283227	1350.575162	675.791219	**12**
6	**741.233074**	371.120175	723.222509	362.114893	**A**	***1297.548613***	649.277945	1280.522064	640.764670	1279.538048	640.272662	**11**
7	**878.291986**	439.649631	860.281421	430.644348	**H**	***1226.511499***	613.759388	1209.484950	605.246113	1208.500934	604.754105	**10**
8	**1038.322635**	519.664956	1020.312070	510.659673	**C**	***1089.452587***	545.229932	1072.426038	536.716657	1071.442022	536.224649	**9**
9	**1137.391049**	569.199163	1119.380484	560.193880	**V**	***929.421938***	465.214607	912.395389	456.701333	911.411373	456.209325	**8**
10	**1208.428163**	604.717720	1190.417598	595.712437	**A**	***830.353524***	415.680400	813.326975	407.167126	812.342959	406.675118	**7**
11	**1309.475842**	655.241559	1291.465277	646.236277	**T**	***759.316410***	380.161843	742.289861	371.648569	741.305845	371.156561	**6**
12	1366.497306	683.752291	1348.486741	674.747008	**G**	***658.268731***	329.638004	641.242182	321.124729			**5**
13	**1529.560635**	765.283956	1511.550070	756.278673	**Y**	***601.247267***	301.127272	584.220718	292.613997			**4**
14	**1660.601120**	830.804198	1642.590555	821.798916	**M**	***438.183938***	219.595607	421.157389	211.082333			**3**
15	1820.631769	910.819523	1802.621204	901.814240	**C**	***307.143453***	154.075365	290.116904	145.562090			**2**
16					**K**	147.112804	74.060040	130.086255	65.546765			**1**



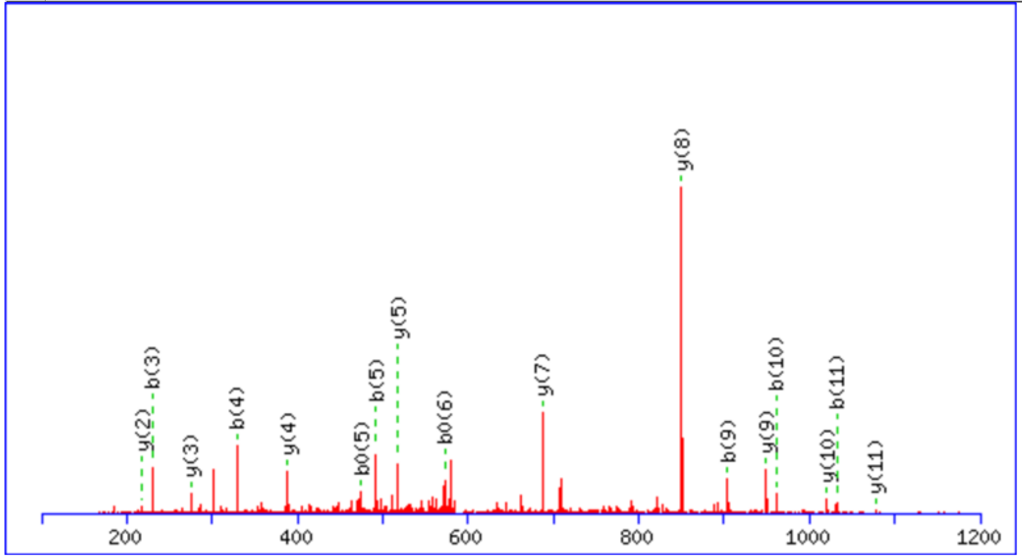
Peptide View

MS/MS Fragmentation of **TGAVYVAEIGAK**
Found in **IPI00552937**, Tax_Id=9606 Gene_Symbol=NHLRC3 NHL repeat-containing protein 3
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 6633: 1177.633048 from(589.823800,2+)
Title: OECHL100317_19.12173.12173.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1177.634277**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65
Expect: 2.3e-005**Matches :** 17/102 fragment ions using 31 most intense peaks (help)

#	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	102.054955	51.531116	84.044390	42.525833	**T**							**12**
2	159.076419	80.041847	141.065854	71.036565	**G**	***1077.593888***	539.300582	1060.567339	530.787308	1059.583323	530.295300	**11**
3	**230.113533**	115.560404	212.102968	106.555122	**A**	***1020.572424***	510.789850	1003.545875	502.276576	1002.561859	501.784568	**10**
4	**329.181947**	165.094611	311.171382	156.089329	**V**	***949.535310***	475.271293	932.508761	466.758019	931.524745	466.266011	**9**
5	**492.245276**	246.626276	474.234711	237.620994	**Y**	***850.466896***	425.737086	833.440347	417.223812	832.456331	416.731804	**8**
6	591.313690	296.160483	573.303125	287.155201	**V**	***687.403567***	344.205422	670.377018	335.692147	669.393002	335.200139	**7**

7	662.350804	331.679040	644.340239	322.673758	A	588.335153	294.671215	571.308604	286.157940	570.324588	285.665932	6
8	791.393397	396.200337	773.382832	387.195054	E	***517.298039***	259.152658	500.271490	250.639383	499.287474	250.147375	5
9	**904.477461**	452.742369	886.466896	443.737086	I	***388.255446***	194.631361	371.228897	186.118087			4
10	**961.498925**	481.253101	943.488360	472.247818	G	***275.171382***	138.089329	258.144833	129.576055			3
11	**1032.536039**	516.771658	1014.525474	507.766375	A	***218.149918***	109.578597	201.123369	101.065322			2
12					K	147.112804	74.060040	130.086255	65.546765			1



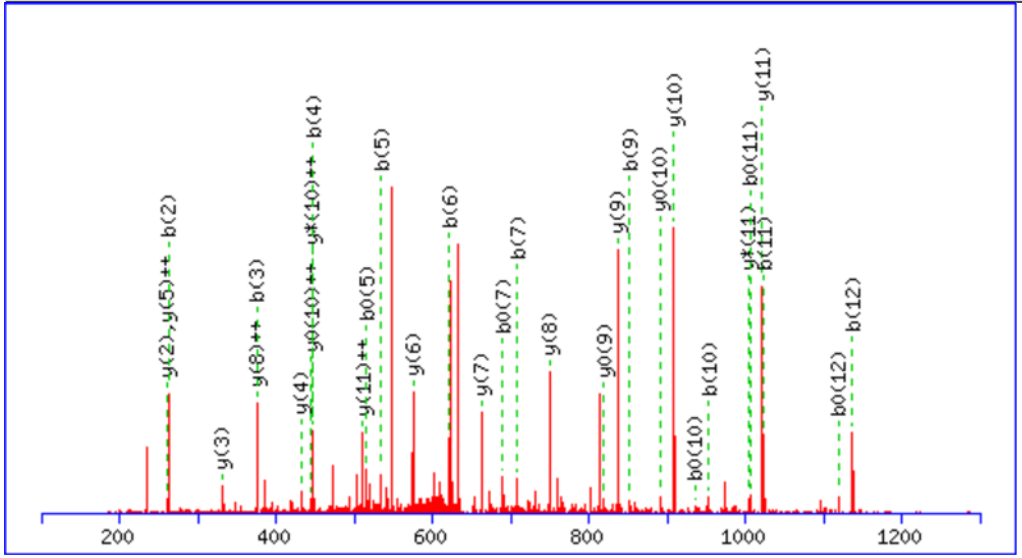
Peptide View

MS/MS Fragmentation of **VYIASSSGSTAIK**
Found in **IPI00025318**, Tax_Id=9606 Gene_Symbol=SH3BGRL SH3 domain-binding glutamic acid-rich-like protein
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 8249: 1282.676848 from(642.345700,2+)
Title: OECHL100317_19.8607.8607.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1282.676865**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60
Expect: 7e-005**Matches :** 32/106 fragment ions using 63 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#

1	100.075690	50.541483			**V**							**13**
2	***263.139019***	132.073148			**Y**	1184.615744	592.811510	1167.589195	584.298236	1166.605179	583.806227	**12**
3	***376.223083***	188.615180			**I**	**1021.552415**	511.279846	1004.525866	502.766571	1003.541850	502.274563	**11**
4	***447.260197***	224.133737			**A**	**908.468351**	454.737814	891.441802	446.224539	890.457786	445.732531	**10**
5	***534.292225***	267.649751	516.281660	258.644468	**S**	**837.431237**	419.219257	820.404688	410.705982	819.420672	410.213974	**9**
6	***621.324253***	311.165765	603.313688	302.160482	**S**	**750.399209**	375.703243	733.372660	367.189968	732.388644	366.697960	**8**
7	***708.356281***	354.681779	690.345716	345.676496	**S**	**663.367181**	332.187229	646.340632	323.673954	645.356616	323.181946	**7**
8	765.377745	383.192511	747.367180	374.187228	**G**	**576.335153**	288.671215	559.308604	280.157940	558.324588	279.665932	**6**
9	***852.409773***	426.708525	834.399208	417.703242	**S**	519.313689	260.160483	502.287140	251.647208	501.303124	251.155200	**5**
10	***953.457452***	477.232364	935.446887	468.227082	**T**	**432.281661**	216.644468	415.255112	208.131194	414.271096	207.639186	**4**
11	***1024.494566***	512.750921	1006.484001	503.745638	**A**	**331.233982**	166.120629	314.207433	157.607354			**3**
12	***1137.578630***	569.292953	1119.568065	560.287670	**I**	**260.196868**	130.602072	243.170319	122.088798			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**



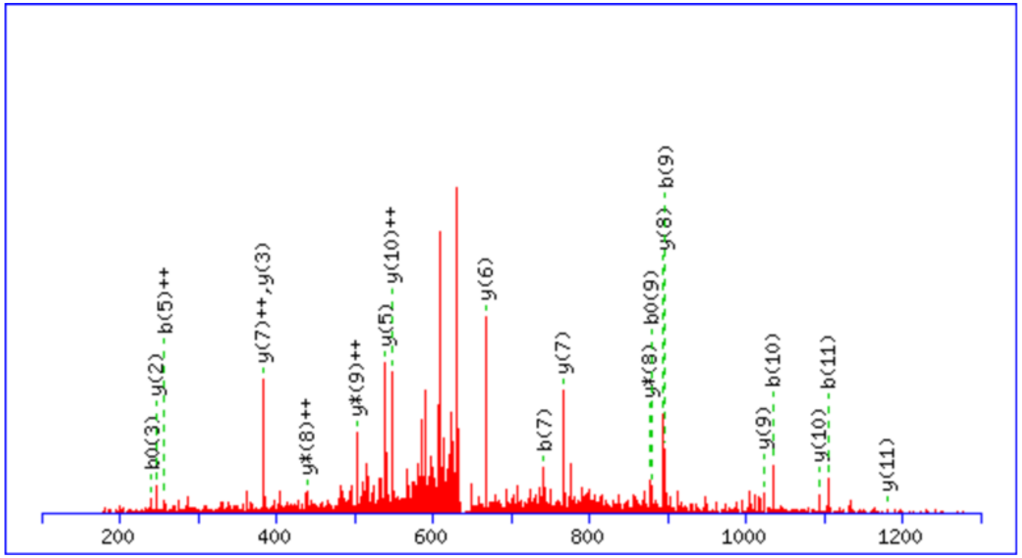
Peptide View

MS/MS Fragmentation of **VSAQQVQGVHAR**

Found in **IPI00011832**, Tax_Id=9606 Gene_Symbol=SPP2 Secreted phosphoprotein 24
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 8218: 1278.680248 from(640.347400,2+)
Title: OECHL100317_19.4481.4481.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1278.679291**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49
Expect: 0.00086**Matches :** 21/104 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	100.075690	50.541483					**V**							**12**
2	187.107718	94.057497			169.097153	85.052214	**S**	***1180.618146***	590.812711	1163.591597	582.299437	1162.607581	581.807429	**11**
3	258.144832	129.576054			240.134267	120.570772	**A**	***1093.586118***	547.296697	1076.559569	538.783423			**10**
4	386.203410	193.605343	369.176861	185.092069	368.192845	184.600061	**Q**	***1022.549004***	511.778140	1005.522455	503.264866			**9**
5	514.261988	257.634632	497.235439	249.121358	496.251423	248.629350	**Q**	***894.490426***	447.748851	877.463877	439.235577			**8**
6	613.330402	307.168839	596.303853	298.655565	595.319837	298.163557	**V**	***766.431848***	383.719562	749.405299	375.206288			**7**
7	**741.388980**	371.198128	724.362431	362.684854	723.378415	362.192846	**Q**	***667.363434***	334.185355	650.336885	325.672081			**6**
8	798.410444	399.708860	781.383895	391.195586	780.399879	390.703578	**G**	***539.304856***	270.156066	522.278307	261.642792			**5**
9	**897.478858**	449.243067	880.452309	440.729793	879.468293	440.237785	**V**	482.283392	241.645334	465.256843	233.132059			**4**
10	**1034.537770**	517.772523	1017.511221	509.259249	1016.527205	508.767241	**H**	***383.214978***	192.111127	366.188429	183.597852			**3**
11	**1105.574884**	553.291080	1088.548335	544.777806	1087.564319	544.285798	**A**	***246.156066***	123.581671	229.129517	115.068396			**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**



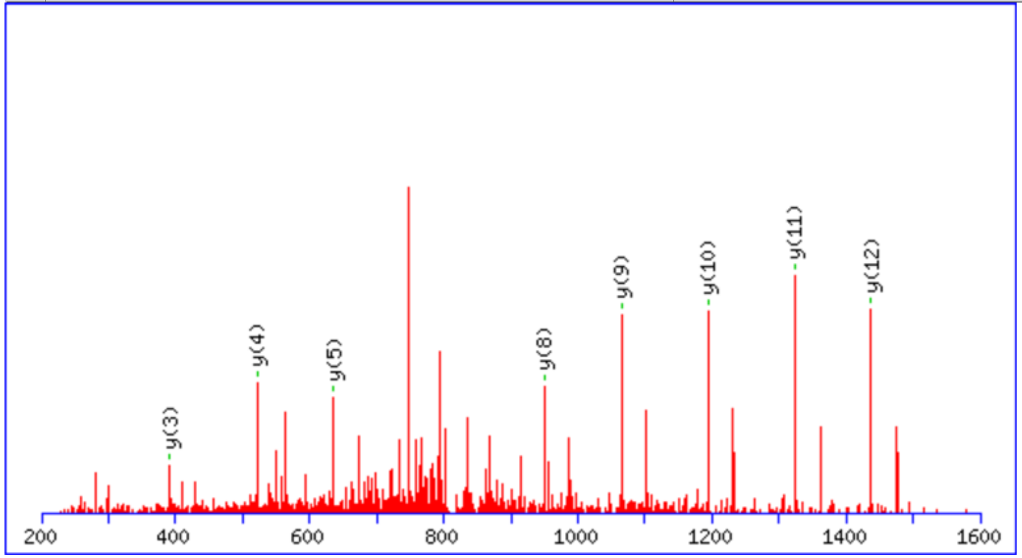
Peptide View

MS/MS Fragmentation of **GKIEEDSEVLMMIK**
Found in **IPI00034319**, Tax_Id=9606 Gene_Symbol=CUTA Isoform A of Protein CutA
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 11430: 1620.810448 from(811.412500,2+)
Title: OECHL100317_19.17952.17952.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1620.810242**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53
Expect: 0.00074**Matches :** 8/136 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	58.028740	29.518008					G							14
2	186.123703	93.565489	169.097154	85.052215			K	1564.796093	782.901684	1547.769544	774.388410	1546.785528	773.896402	13
3	299.207767	150.107521	282.181218	141.594247			I	***1436.701130***	718.854203	1419.674581	710.340929	1418.690565	709.848920	12
4	428.250360	214.628818	411.223811	206.115544	410.239795	205.623536	E	***1323.617066***	662.312171	1306.590517	653.798896	1305.606501	653.306888	11
5	557.292953	279.150115	540.266404	270.636840	539.282388	270.144832	E	***1194.574473***	597.790874	1177.547924	589.277600	1176.563908	588.785592	10
6	672.319896	336.663586	655.293347	328.150312	654.309331	327.658304	D	***1065.531880***	533.269578	1048.505331	524.756303	1047.521315	524.264295	9

7	759.351924	380.179600	742.325375	371.666326	741.341359	371.174318	**S**	***950.504937***	475.756106	933.478388	467.242832	932.494372	466.750824	**8**
8	888.394517	444.700897	871.367968	436.187622	870.383952	435.695614	**E**	863.472909	432.240092	846.446360	423.726818	845.462344	423.234810	**7**
9	987.462931	494.235104	970.436382	485.721829	969.452366	485.229821	**V**	734.430316	367.718796	717.403767	359.205521			**6**
10	1100.546995	550.777135	1083.520446	542.263861	1082.536430	541.771853	**L**	***635.361902***	318.184589	618.335353	309.671314			**5**
11	1231.587480	616.297378	1214.560931	607.784104	1213.576915	607.292095	**M**	***522.277838***	261.642557	505.251289	253.129282			**4**
12	1362.627965	681.817620	1345.601416	673.304346	1344.617400	672.812338	**M**	***391.237353***	196.122314	374.210804	187.609040			**3**
13	1475.712029	738.359652	1458.685480	729.846378	1457.701464	729.354370	**I**	260.196868	130.602072	243.170319	122.088797			**2**
14							**K**	147.112804	74.060040	130.086255	65.546765			**1**



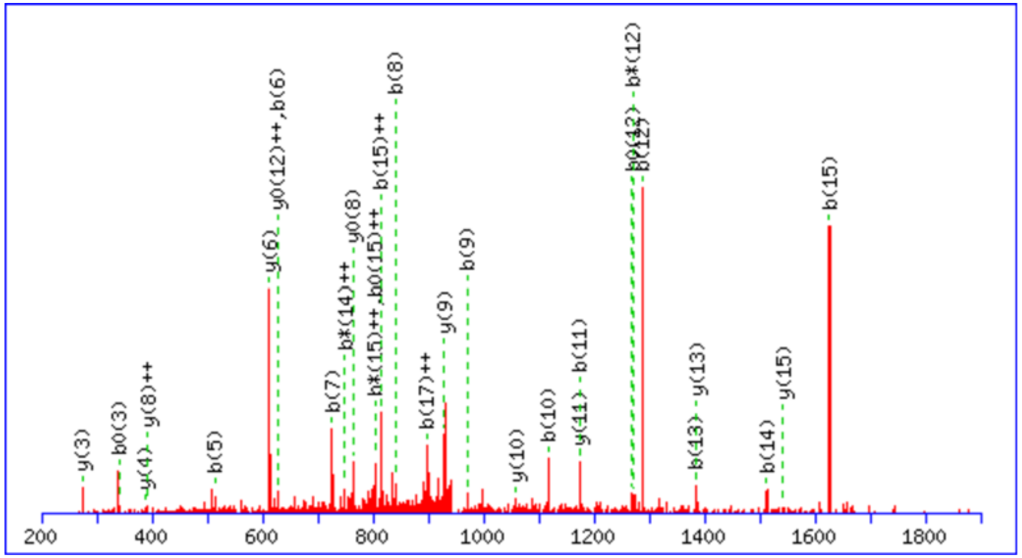
Peptide View

MS/MS Fragmentation of **NKDGVLVDEFGLPQIPAS**
Found in **IPI00100796**, Tax_Id=9606 Gene_Symbol=CHMP5 Charged multivesicular body protein 5
Experiment: 36 - OPB-3 **Fraction:** OPB-3

Match to Query 14415: 1897.980248 from(949.997400,2+)
Title: OECHL100317_19.21039.21039.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_19.raw
Monoisotopic mass of neutral peptide Mr(calc): 1897.978546**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50

Expect: 0.0013**Matches :** 30/192 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	243.145166	122.076221	226.118617	113.562947			**K**	1784.942893	892.975085	1767.916344	884.461810	1766.932328	883.969802	**17**
3	358.172109	179.589693	341.145560	171.076418	340.161544	170.584410	**D**	1656.847930	828.927603	1639.821381	820.414329	1638.837365	819.922321	**16**
4	415.193573	208.100425	398.167024	199.587150	397.183008	199.095142	**G**	**1541.820987**	771.414132	1524.794438	762.900857	1523.810422	762.408849	**15**
5	***514.261987***	257.634632	497.235438	249.121357	496.251422	248.629349	**V**	1484.799523	742.903400	1467.772974	734.390125	1466.788958	733.898117	**14**
6	***627.346051***	314.176664	610.319502	305.663389	609.335486	305.171381	**L**	**1385.731109**	693.369193	1368.704560	684.855918	1367.720544	684.363910	**13**
7	***726.414465***	363.710871	709.387916	355.197596	708.403900	354.705588	**V**	1272.647045	636.827160	1255.620496	628.313886	1254.636480	627.821878	**12**
8	***841.441408***	421.224342	824.414859	412.711068	823.430843	412.219060	**D**	**1173.578631**	587.292954	1156.552082	578.779679	1155.568066	578.287671	**11**
9	***970.484001***	485.745639	953.457452	477.232364	952.473436	476.740356	**E**	**1058.551688**	529.779482	1041.525139	521.266208	1040.541123	520.774200	**10**
10	***1117.552415***	559.279846	1100.525866	550.766571	1099.541850	550.274563	**F**	**929.509095**	465.258186	912.482546	456.744911	911.498530	456.252903	**9**
11	***1174.573879***	587.790578	1157.547330	579.277303	1156.563314	578.785295	**G**	782.440681	391.723979	765.414132	383.210704	764.430116	382.718696	**8**
12	***1287.657943***	644.332609	1270.631394	635.819335	1269.647378	635.327327	**L**	725.419217	363.213247	708.392668	354.699972	707.408652	354.207964	**7**
13	***1384.710707***	692.858992	1367.684158	684.345717	1366.700142	683.853709	**P**	**612.335153**	306.671215	595.308604	298.157940	594.324588	297.665932	**6**
14	***1512.769285***	756.888281	1495.742736	748.375006	1494.758720	747.882998	**Q**	515.282389	258.144833	498.255840	249.631558	497.271824	249.139550	**5**
15	***1625.853349***	813.430313	1608.826800	804.917038	1607.842784	804.425030	**I**	**387.223811**	194.115543			369.213246	185.110261	**4**
16	1722.906113	861.956695	1705.879564	853.443420	1704.895548	852.951412	**P**	**274.139747**	137.573512			256.129182	128.568229	**3**
17	1793.943227	897.475252	1776.916678	888.961977	1775.932662	888.469969	**A**	177.086983	89.047130			159.076418	80.041847	**2**
18							**S**	106.049869	53.528573			88.039304	44.523290	**1**



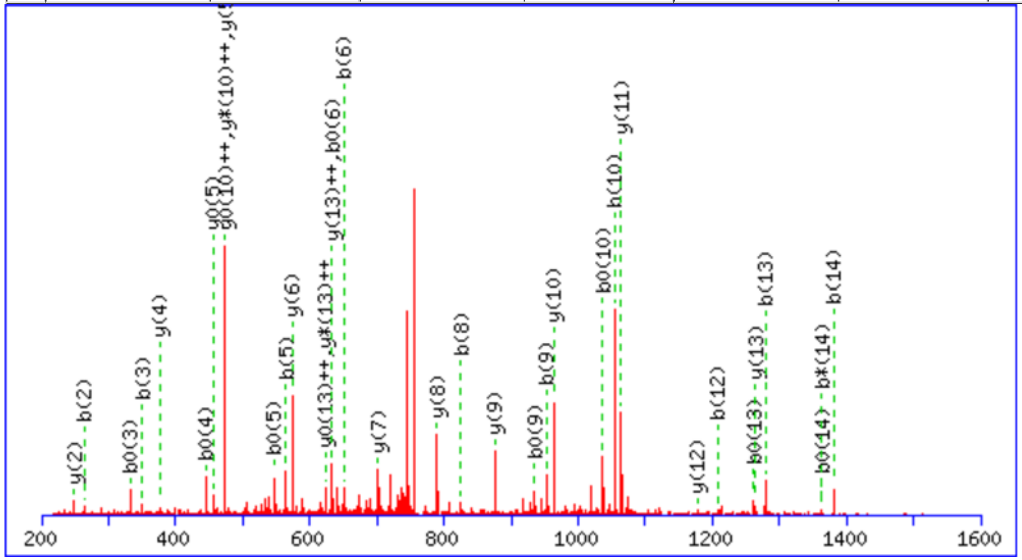
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 11269: 1525.727048 from(763.870800,2+)
Title: OECHL100317_17.10967.10967.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 86
Expect: 2.8e-007**Matches :** 36/150 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	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	***350.134661***	175.570968			332.124096	166.565686	**S**	***1264.637937***	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	***651.298432***	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**

7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	**9**
8	***825.362488***	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.203410	**8**
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	**7**
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	**6**
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	**5**
12	***1208.542973***	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	**4**
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	**3**
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



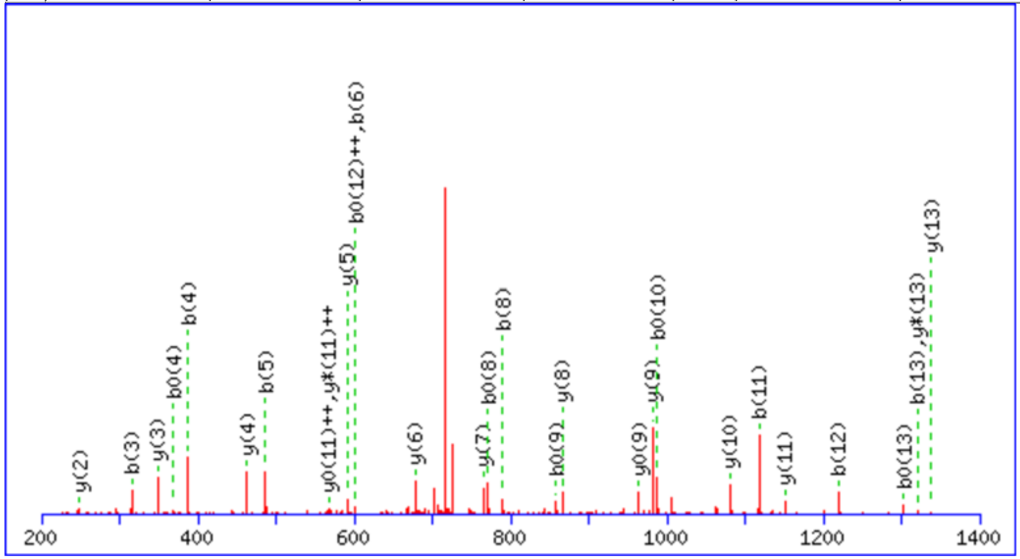
Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 10657: 1465.679248 from(733.846900,2+)
Title: OECHL100317_17.10113.10113.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw

Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 102 **Expect:** 5.2e-009**Matches :** 29/128 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	S							14
2	245.076812	123.042044	227.066247	114.036761	D	***1337.643082***	669.325179	1320.616533	660.811905	1319.632517	660.319897	13
3	**316.113926**	158.560601	298.103361	149.555319	A	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	12
4	**387.151040**	194.079158	369.140475	185.073875	A	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	11
5	**486.219454**	243.613365	468.208889	234.608082	V	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	10
6	**601.246397**	301.126837	583.235832	292.121554	D	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	9
7	702.294076	351.650676	684.283511	342.645394	T	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	8
8	**789.326104**	395.166690	771.315539	386.161408	S	***765.398875***	383.203076	748.372326	374.689801	747.388310	374.197793	7
9	876.358132	438.682704	858.347567	429.677421	S	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	6
10	1005.400725	503.204001	987.390160	494.198718	E	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	5
11	**1118.484789**	559.746033	1100.474224	550.740750	I	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	4
12	**1219.532468**	610.269872	1201.521903	601.264590	T	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	3
13	**1320.580147**	660.793712	1302.569582	651.788429	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
14					K	147.112804	74.060040	130.086255	65.546765			1

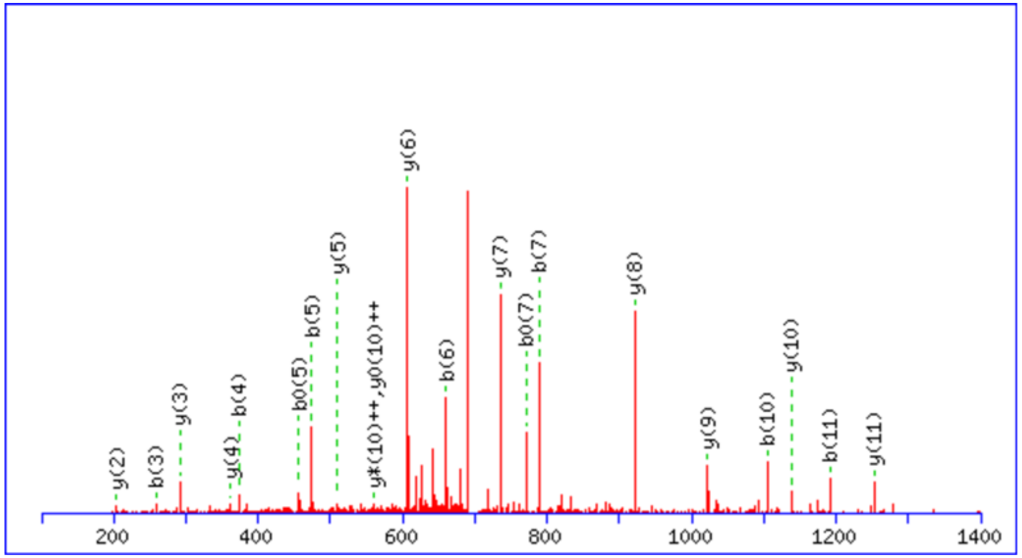


Peptide View

MS/MS Fragmentation of **AADDTWEPFASGK**
Found in **IPI00022432**, Tax_Id=9606 Gene_Symbol=TTR Transthyretin
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 9782: 1393.616248 from(697.815400,2+)
Title: OECHL100317_17.15538.15538.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1393.615005**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 75
Expect: 2e-006**Matches :** 21/112 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**13**
2	143.081504	72.044390			**A**	1323.585173	662.296225	1306.558624	653.782950	1305.574608	653.290942	**12**
3	**258.108447**	129.557862	240.097882	120.552579	**D**	***1252.548059***	626.777668	1235.521510	618.264393	1234.537494	617.772385	**11**
4	**373.135390**	187.071333	355.124825	178.066051	**D**	***1137.521116***	569.264196	1120.494567	560.750922	1119.510551	560.258914	**10**
5	**474.183069**	237.595173	456.172504	228.589890	**T**	***1022.494173***	511.750725	1005.467624	503.237450	1004.483608	502.745442	**9**
6	**660.262382**	330.634829	642.251817	321.629547	**W**	***921.446494***	461.226885	904.419945	452.713611	903.435929	452.221603	**8**
7	**789.304975**	395.156126	771.294410	386.150843	**E**	***735.367181***	368.187229	718.340632	359.673954	717.356616	359.181946	**7**
8	886.357739	443.682508	868.347174	434.677225	**P**	***606.324588***	303.665932	589.298039	295.152658	588.314023	294.660650	**6**
9	1033.426153	517.216715	1015.415588	508.211432	**F**	***509.271824***	255.139550	492.245275	246.626275	491.261259	246.134267	**5**
10	**1104.463267**	552.735272	1086.452702	543.729989	**A**	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	**4**
11	**1191.495295**	596.251286	1173.484730	587.246003	**S**	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	**3**
12	1248.516759	624.762018	1230.506194	615.756735	**G**	***204.134268***	102.570772	187.107719	94.057497			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**



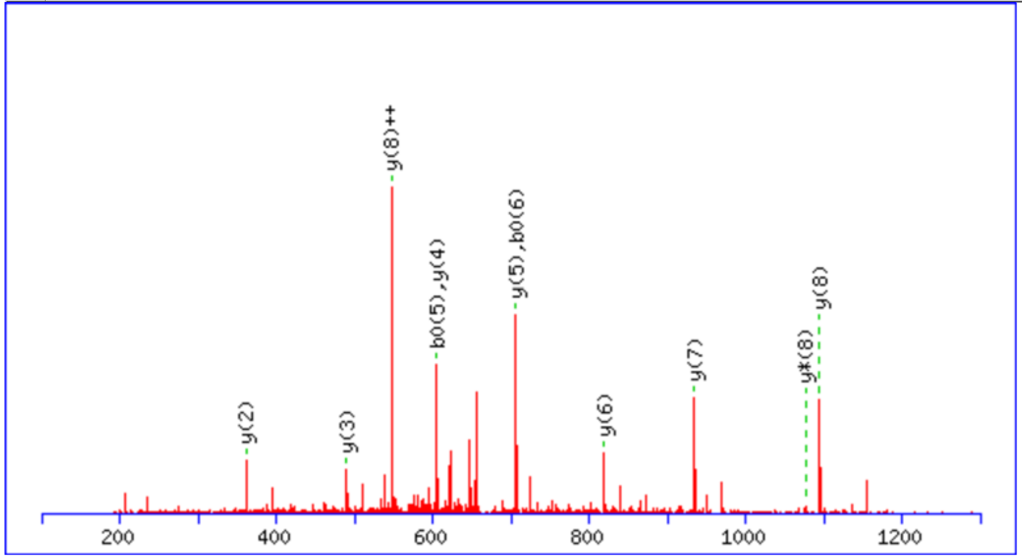
Peptide View

MS/MS Fragmentation of **SFCDLTDEWR**
Found in **IPI00010193**, Tax_Id=9606 Gene_Symbol=IFNAR2 Isoform 1 of Interferon-alpha/beta receptor beta chain
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 9167: 1327.549248 from(664.781900,2+)
Title: OECHL100317_17.17344.17344.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1327.550308**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 3.3e-005**Matches :** 11/86 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**10**
2	235.107718	118.057497	217.097153	109.052214	**F**	1241.525550	621.266413	1224.499001	612.753138	1223.514985	612.261130	**9**
3	395.138367	198.072821	377.127802	189.067539	**C**	***1094.457136***	547.732206	1077.430587	539.218932	1076.446571	538.726924	**8**
4	510.165310	255.586293	492.154745	246.581010	**D**	***934.426487***	467.716882	917.399938	459.203607	916.415922	458.711599	**7**
5	623.249374	312.128325	605.238809	303.123043	**L**	***819.399544***	410.203410	802.372995	401.690135	801.388979	401.198127	**6**
6	724.297053	362.652165	706.286488	353.646882	**T**	***706.315480***	353.661378	689.288931	345.148103	688.304915	344.656095	**5**

7	839.323996	420.165636	821.313431	411.160353	**D**	***605.267801***	303.137539	588.241252	294.624264	587.257236	294.132256	**4**
8	968.366589	484.686933	950.356024	475.681650	**E**	***490.240858***	245.624067	473.214309	237.110792	472.230293	236.618784	**3**
9	1154.445902	577.726589	1136.435337	568.721306	**W**	***361.198265***	181.102770	344.171716	172.589496			**2**
10					**R**	175.118952	88.063114	158.092403	79.549839			**1**



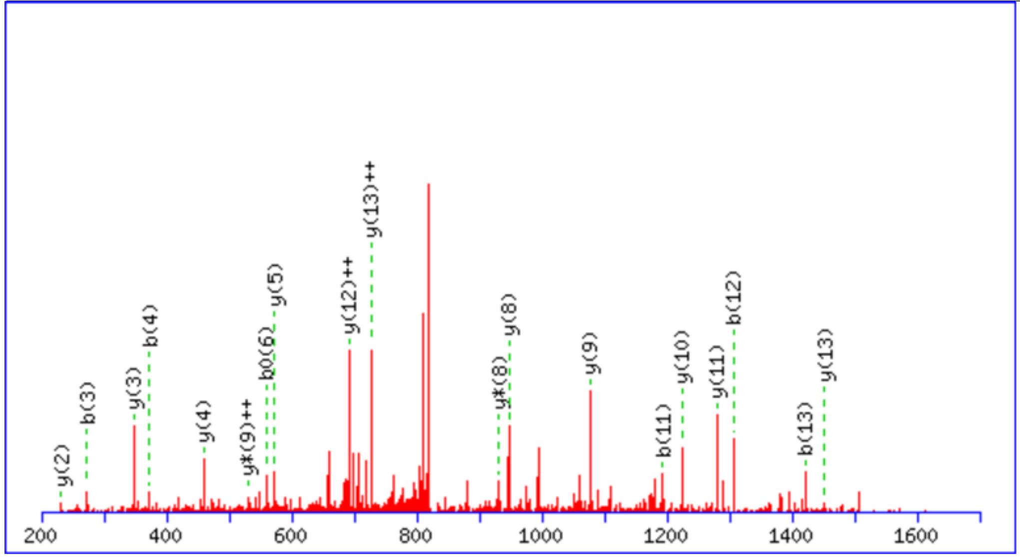
Peptide View

MS/MS Fragmentation of **VTATGFQQCSLIDGR**
Found in **IPI00333140**, Tax_Id=9606 Gene_Symbol=DNER Delta and Notch-like epidermal growth factor-related receptor
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 12705: 1651.800448 from(826.907500,2+)
Title: OECHL100317_17.14059.14059.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1651.798828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70
Expect: 1.2e-005**Matches :** 19/150 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	100.075690	50.541483					**V**							**15**
2	201.123369	101.065322			183.112804	92.060040	**T**	1553.737670	777.372473	1536.711121	768.859198	1535.727105	768.367190	**14**

3	**272.160483**	136.583879			254.149918	127.578597	**A**	***1452.689991***	726.848633	1435.663442	718.335359	1434.679426	717.843351	**13**
4	**373.208162**	187.107719			355.197597	178.102437	**T**	1381.652877	691.330076	1364.626328	682.816802	1363.642312	682.324794	**12**
5	430.229626	215.618451			412.219061	206.613169	**G**	***1280.605198***	640.806237	1263.578649	632.292962	1262.594633	631.800954	**11**
6	577.298040	289.152658			559.287475	280.147376	**F**	***1223.583734***	612.295505	1206.557185	603.782230	1205.573169	603.290222	**10**
7	705.356618	353.181947	688.330069	344.668673	687.346053	344.176665	**Q**	***1076.515320***	538.761298	1059.488771	530.248023	1058.504755	529.756015	**9**
8	833.415196	417.211236	816.388647	408.697962	815.404631	408.205954	**Q**	***948.456742***	474.732009	931.430193	466.218734	930.446177	465.726726	**8**
9	993.445845	497.226561	976.419296	488.713286	975.435280	488.221278	**C**	820.398164	410.702720	803.371615	402.189445	802.387599	401.697437	**7**
10	1080.477873	540.742575	1063.451324	532.229300	1062.467308	531.737292	**S**	660.367515	330.687395	643.340966	322.174121	642.356950	321.682113	**6**
11	**1193.561937**	597.284607	1176.535388	588.771332	1175.551372	588.279324	**L**	***573.335487***	287.171381	556.308938	278.658107	555.324922	278.166099	**5**
12	**1306.646001**	653.826638	1289.619452	645.313364	1288.635436	644.821356	**I**	***460.251423***	230.629349	443.224874	222.116075	442.240858	221.624067	**4**
13	**1421.672944**	711.340110	1404.646395	702.826836	1403.662379	702.334827	**D**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
14	1478.694408	739.850842	1461.667859	731.337567	1460.683843	730.845559	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



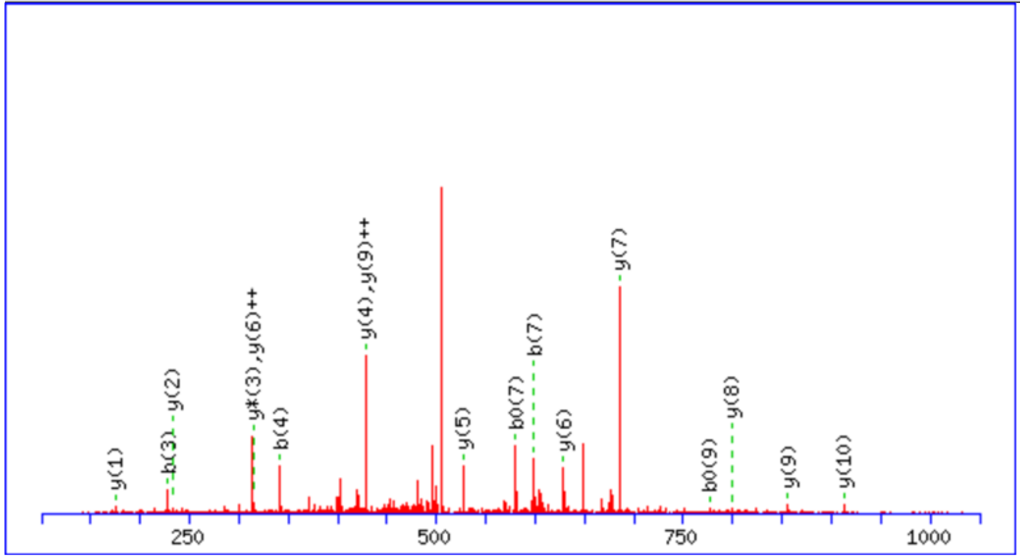
Peptide View

MS/MS Fragmentation of **IGGIGTVPVGR**

Found in **IPI00014424**, Tax_Id=9606 Gene_Symbol=EEF1A2 Elongation factor 1-alpha 2
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 4412: 1024.602448 from(513.308500,2+)
Title: OECHL100317_17.11138.11138.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1024.602951**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 75
Expect: 8.6e-007**Matches :** 17/80 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							11
2	171.112804	86.060040			G	***912.526143***	456.766710	895.499594	448.253435	894.515578	447.761427	10
3	**228.134268**	114.570772			G	***855.504679***	428.255978	838.478130	419.742703	837.494114	419.250695	9
4	**341.218332**	171.112804			I	***798.483215***	399.745246	781.456666	391.231971	780.472650	390.739963	8
5	398.239796	199.623536			G	***685.399151***	343.203214	668.372602	334.689939	667.388586	334.197931	7
6	499.287475	250.147375	481.276910	241.142093	T	***628.377687***	314.692482	611.351138	306.179207	610.367122	305.687199	6
7	**598.355889**	299.681583	580.345324	290.676300	V	***527.330008***	264.168642	510.303459	255.655368			5
8	695.408653	348.207965	677.398088	339.202682	P	***428.261594***	214.634435	411.235045	206.121161			4
9	794.477067	397.742172	776.466502	388.736889	V	331.208830	166.108053	314.182281	157.594779			3
10	851.498531	426.252904	833.487966	417.247621	G	***232.140416***	116.573846	215.113867	108.060572			2
11					R	***175.118952***	88.063114	158.092403	79.549840			1

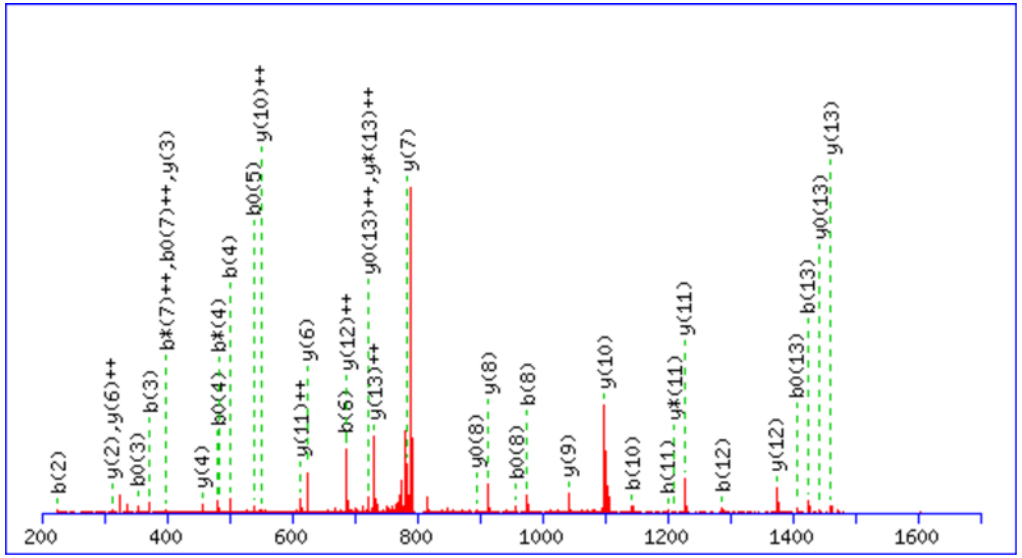


Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 12009: 1597.704648 from(799.859600,2+)
Title: OECHL100317_17.2203.2203.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 68
Expect: 1.1e-005**Matches :** 38/144 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	138.066188	69.536732					**H**							**14**
2	**225.098216**	113.052746			207.087651	104.047463	**S**	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.325325	**13**
3	**372.166630**	186.586953			354.156065	177.581671	**F**	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.809311	**12**
4	**500.261593**	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	**11**
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	**10**
6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	***1042.437069***	521.722173	1025.410520	513.208898	1024.426504	512.716890	**9**
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	527.268470	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	***312.177864***	156.592570	295.151315	148.079295			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



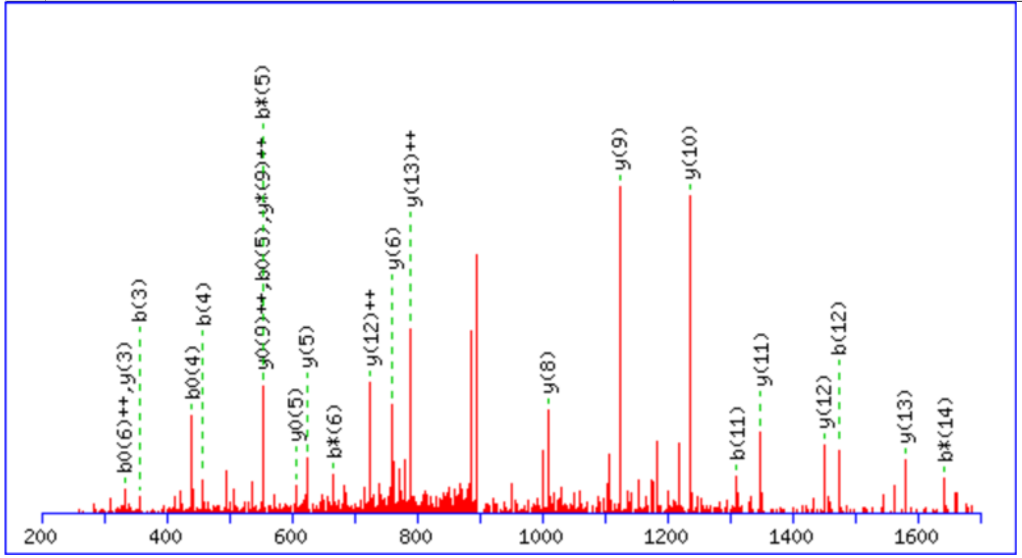
Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 14091: 1805.932648 from(903.973600,2+)
Title: OECHL100317_17.20309.20309.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 68
Expect: 2.1e-005**Matches :** 24/160 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	115.050203	58.028740	98.023654	49.515465			**N**							**15**
2	228.134267	114.570771	211.107718	106.057497			**I**	1692.895549	846.951413	1675.869000	838.438138	1674.884984	837.946130	**14**
3	**357.176860**	179.092068	340.150311	170.578793	339.166295	170.086785	**E**	***1579.811485***	790.409381	1562.784936	781.896106	1561.800920	781.404098	**13**
4	**458.224539**	229.615907	441.197990	221.102633	440.213974	220.610625	**T**	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.882802	**12**
5	571.308603	286.157940	554.282054	277.644665	553.298038	277.152657	**I**	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.358962	**11**
6	684.392667	342.699972	667.366118	334.186697	666.382102	333.694689	**I**	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.816930	**10**

7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	**N**	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.274898	**9**
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	**T**	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.253435	**8**
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	**F**	908.462479	454.734878	891.435930	446.221603	890.451914	445.729595	**7**
10	1183.610599	592.308938	1166.584050	583.795663	1165.600034	583.303655	**H**	***761.394065***	381.200671	744.367516	372.687396	743.383500	372.195388	**6**
11	**1311.669177**	656.338227	1294.642628	647.824952	1293.658612	647.332944	**Q**	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.665932	**5**
12	**1474.732506**	737.869891	1457.705957	729.356617	1456.721941	728.864609	**Y**	496.276575	248.641926	479.250026	240.128651	478.266010	239.636643	**4**
13	1561.764534	781.385905	1544.737985	772.872631	1543.753969	772.380623	**S**	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.104979	**3**
14	1660.832948	830.920112	1643.806399	822.406838	1642.822383	821.914830	**V**	246.181218	123.594247	229.154669	115.080973			**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



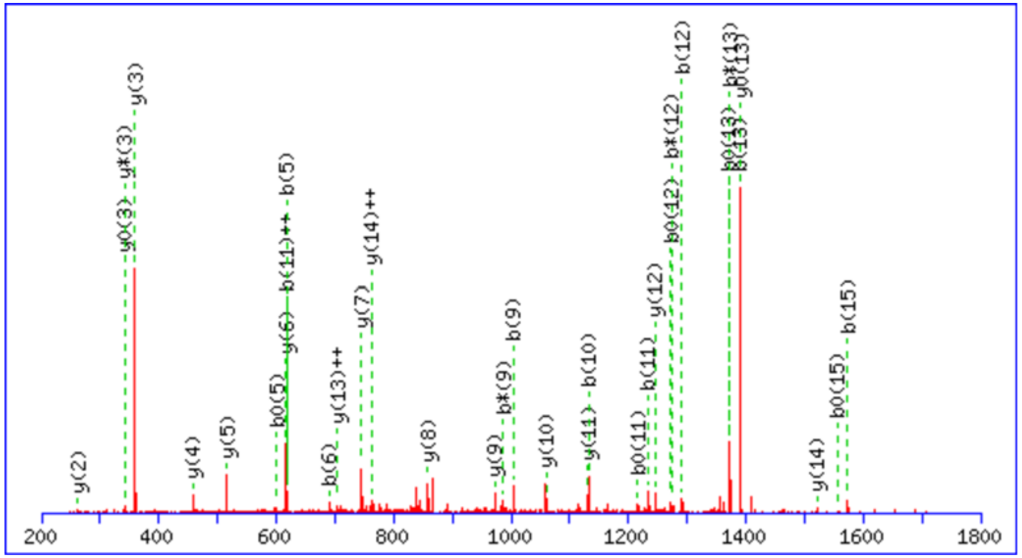
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 13658: 1746.917648 from(874.466100,2+)
Title: OECHL100317_17.17469.17469.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw

Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 79
Expect: 1.2e-006**Matches :** 34/156 fragment ions using 59 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							16
2	227.175404	114.091340					L	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	15
3	340.259468	170.633372					I	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	14
4	503.322797	252.165036					Y	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	13
5	**618.349740**	309.678508			600.339175	300.673226	D	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	12
6	**689.386854**	345.197065			671.376289	336.191782	A	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	11
7	776.418882	388.713079			758.408317	379.707796	S	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	10
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	9
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	L	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	8
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	E	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	7
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	T	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	6
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	G	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	5
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	V	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	4
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
16							R	175.118952	88.063114	158.092403	79.549839			1



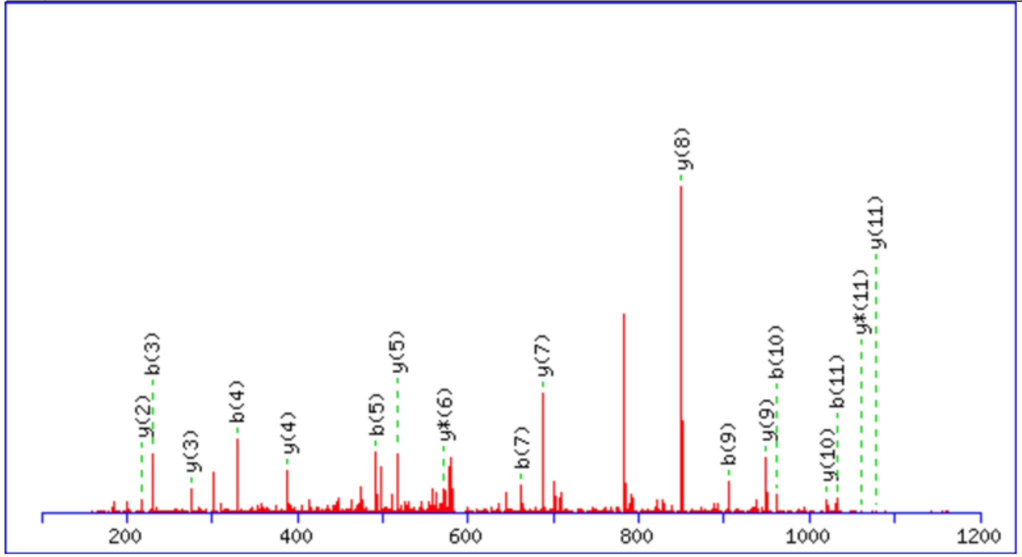
Peptide View

MS/MS Fragmentation of **TGAVYVAEIGAK**
Found in **IPI00552937**, Tax_Id=9606 Gene_Symbol=NHLRC3 NHL repeat-containing protein 3
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 6942: 1177.634048 from(589.824300,2+)
Title: OECHL100317_17.11674.11674.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1177.634277**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67
Expect: 1.2e-005**Matches :** 18/102 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	**T**							**12**
2	159.076419	80.041847	141.065854	71.036565	**G**	***1077.593888***	539.300582	1060.567339	530.787308	1059.583323	530.295300	**11**
3	**230.113533**	115.560404	212.102968	106.555122	**A**	***1020.572424***	510.789850	1003.545875	502.276576	1002.561859	501.784568	**10**
4	**329.181947**	165.094611	311.171382	156.089329	**V**	***949.535310***	475.271293	932.508761	466.758019	931.524745	466.266011	**9**
5	**492.245276**	246.626276	474.234711	237.620994	**Y**	***850.466896***	425.737086	833.440347	417.223812	832.456331	416.731804	**8**
6	591.313690	296.160483	573.303125	287.155201	**V**	***687.403567***	344.205422	670.377018	335.692147	669.393002	335.200139	**7**

7	**662.350804**	331.679040	644.340239	322.673758	**A**	588.335153	294.671215	571.308604	286.157940	570.324588	285.665932	**6**
8	791.393397	396.200337	773.382832	387.195054	**E**	***517.298039***	259.152658	500.271490	250.639383	499.287474	250.147375	**5**
9	**904.477461**	452.742369	886.466896	443.737086	**I**	***388.255446***	194.631361	371.228897	186.118087			**4**
10	**961.498925**	481.253101	943.488360	472.247818	**G**	***275.171382***	138.089329	258.144833	129.576055			**3**
11	**1032.536039**	516.771658	1014.525474	507.766375	**A**	***218.149918***	109.578597	201.123369	101.065322			**2**
12					**K**	147.112804	74.060040	130.086255	65.546765			**1**



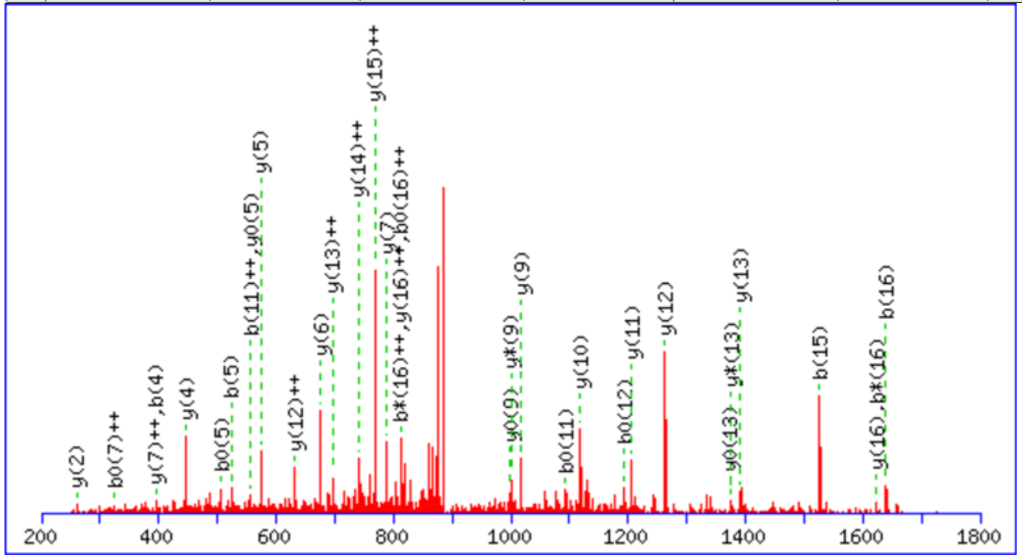
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 13938: 1784.878448 from(893.446500,2+)
Title: OECHL100317_17.7792.7792.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 0.00012**Matches :** 34/170 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	164.070605	82.538940					**Y**							**17**
2	251.102633	126.054954			233.092068	117.049672	**S**	***1622.823172***	811.915224	1605.796623	803.401950	1604.812607	802.909941	**16**
3	308.124097	154.565687			290.113532	145.560404	**G**	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.393928	**15**
4	**395.156125**	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.883195	**14**
5	**524.198718**	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.367182	**13**
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.845885	**12**
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.335153	**11**
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.819139	**10**
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.295299	**9**
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.266010	**8**
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.742171	**7**
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.200139	**6**
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.676299	**5**
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	**4**
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**

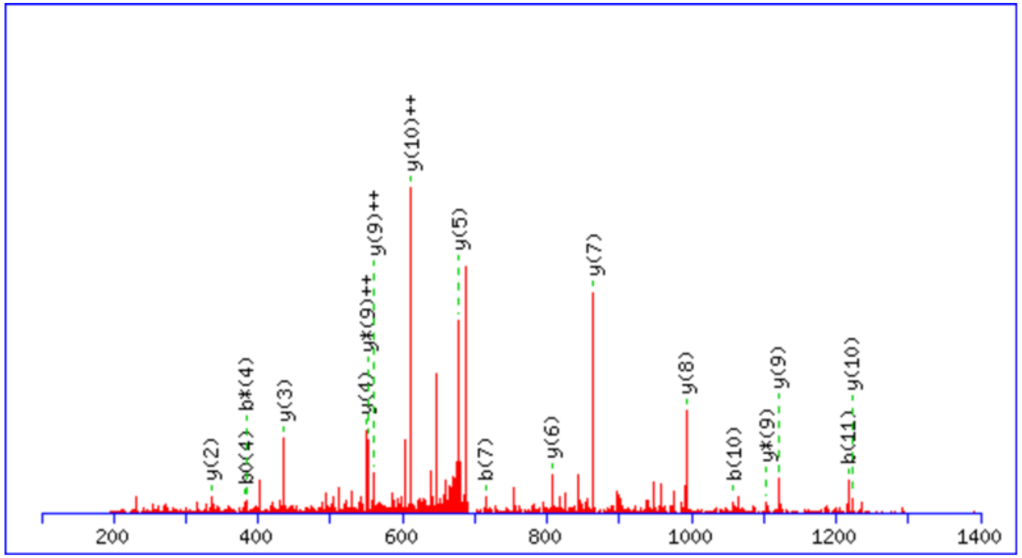


Peptide View

MS/MS Fragmentation of **VATQEGKEITCR**
Found in **IPI00031564**, Tax_Id=9606 Gene_Symbol=GGCT Isoform 1 of Gamma-glutamylcyclotransferase
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 9763: 1390.687048 from(696.350800,2+)
Title: OECHL100317_17.3603.3603.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1390.687454**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 0.0001**Matches :** 18/118 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	100.075690	50.541483					**V**							**12**
2	171.112804	86.060040					**A**	1292.626328	646.816802	1275.599779	638.303528	1274.615763	637.811520	**11**
3	272.160483	136.583879			254.149918	127.578597	**T**	***1221.589214***	611.298245	1204.562665	602.784971	1203.578649	602.292963	**10**
4	400.219061	200.613169	383.192512	192.099894	382.208496	191.607886	**Q**	***1120.541535***	560.774406	1103.514986	552.261131	1102.530970	551.769123	**9**
5	529.261654	265.134465	512.235105	256.621191	511.251089	256.129183	**E**	***992.482957***	496.745117	975.456408	488.231842	974.472392	487.739834	**8**
6	586.283118	293.645197	569.256569	285.131923	568.272553	284.639915	**G**	***863.440364***	432.223820	846.413815	423.710546	845.429799	423.218538	**7**
7	**714.378081**	357.692679	697.351532	349.179404	696.367516	348.687396	**K**	***806.418900***	403.713088	789.392351	395.199814	788.408335	394.707806	**6**
8	843.420674	422.213975	826.394125	413.700701	825.410109	413.208693	**E**	***678.323937***	339.665607	661.297388	331.152332	660.313372	330.660324	**5**
9	956.504738	478.756007	939.478189	470.242733	938.494173	469.750725	**I**	***549.281344***	275.144310	532.254795	266.631036	531.270779	266.139028	**4**
10	**1057.552417**	529.279847	1040.525868	520.766572	1039.541852	520.274564	**T**	***436.197280***	218.602278	419.170731	210.089003	418.186715	209.596995	**3**
11	**1217.583066**	609.295171	1200.556517	600.781897	1199.572501	600.289889	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**



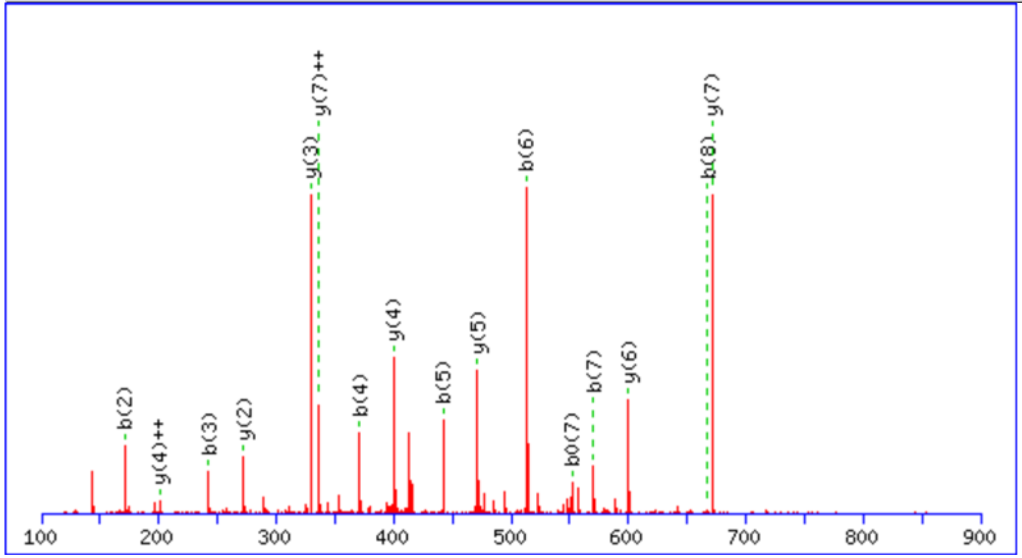
Peptide View

MS/MS Fragmentation of **GLAEAAGPR**
Found in **IPI00290826**, Tax_Id=9606 Gene_Symbol=FAM174A Membrane protein FAM174A
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 1499: 840.445648 from(421.230100,2+)
Title: OECHL100317_17.4131.4131.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 840.445343**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00051**Matches :** 16/64 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			**G**							**9**
2	***171.112804***	86.060040			**L**	784.431179	392.719228	767.404630	384.205953	766.420614	383.713945	**8**
3	***242.149918***	121.578597			**A**	**671.347115**	336.177196	654.320566	327.663921	653.336550	327.171913	**7**
4	***371.192511***	186.099894	353.181946	177.094611	**E**	**600.310001**	300.658639	583.283452	292.145364	582.299436	291.653356	**6**
5	***442.229625***	221.618450	424.219060	212.613168	**A**	**471.267408**	236.137342	454.240859	227.624067			**5**
6	***513.266739***	257.137008	495.256174	248.131725	**A**	**400.230294**	200.618785	383.203745	192.105510			**4**

7	***570.288203***	285.647740	552.277638	276.642457	**G**	**329.193180**	165.100228	312.166631	156.586953			**3**
8	***667.340967***	334.174122	649.330402	325.168839	**P**	**272.171716**	136.589496	255.145167	128.076221			**2**
9					**R**	175.118952	88.063114	158.092403	79.549839			**1**



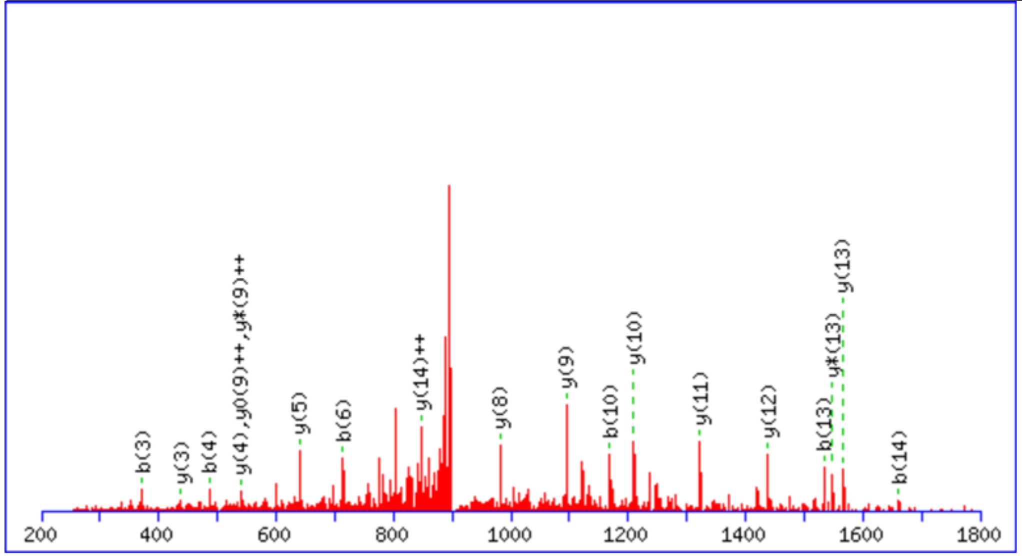
Peptide View

MS/MS Fragmentation of **NKQDLDINNITTYKK**
Found in **IPI00220361**, Tax_Id=9606 Gene_Symbol=CALB1 Calbindin
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 14098: 1806.948048 from(904.481300,2+)
Title: OECHL100317_17.10434.10434.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1806.947540**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 0.00037**Matches :** 19/156 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**15**
2	243.145166	122.076221	226.118617	113.562947			**K**	1693.911927	847.459602	1676.885378	838.946327	1675.901362	838.454319	**14**
3	***371.203744***	186.105510	354.177195	177.592236			**Q**	***1565.816964***	783.412120	1548.790415	774.898846	1547.806399	774.406838	**13**

4	***486.230687***	243.618982	469.204138	235.105707	468.220122	234.613699	**D**	***1437.758386***	719.382831	1420.731837	710.869557	1419.747821	710.377548	**12**
5	599.314751	300.161014	582.288202	291.647739	581.304186	291.155731	**L**	***1322.731443***	661.869359	1305.704894	653.356085	1304.720878	652.864077	**11**
6	***714.341694***	357.674485	697.315145	349.161211	696.331129	348.669203	**D**	***1209.647379***	605.327328	1192.620830	596.814053	1191.636814	596.322045	**10**
7	827.425758	414.216517	810.399209	405.703243	809.415193	405.211235	**I**	***1094.620436***	547.813856	1077.593887	539.300582	1076.609871	538.808573	**9**
8	941.468685	471.237981	924.442136	462.724706	923.458120	462.232698	**N**	***981.536372***	491.271824	964.509823	482.758550	963.525807	482.266542	**8**
9	1055.511612	528.259444	1038.485063	519.746170	1037.501047	519.254162	**N**	867.493445	434.250361	850.466896	425.737086	849.482880	425.245078	**7**
10	***1168.595676***	584.801476	1151.569127	576.288202	1150.585111	575.796193	**I**	753.450518	377.228897	736.423969	368.715623	735.439953	368.223615	**6**
11	1269.643355	635.325315	1252.616806	626.812041	1251.632790	626.320033	**T**	***640.366454***	320.686865	623.339905	312.173591	622.355889	311.681583	**5**
12	1370.691034	685.849155	1353.664485	677.335881	1352.680469	676.843872	**T**	***539.318775***	270.163026	522.292226	261.649751	521.308210	261.157743	**4**
13	***1533.754363***	767.380820	1516.727814	758.867545	1515.743798	758.375537	**Y**	***438.271096***	219.639186	421.244547	211.125912			**3**
14	***1661.849326***	831.428301	1644.822777	822.915027	1643.838761	822.423019	**K**	275.207767	138.107521	258.181218	129.594247			**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**

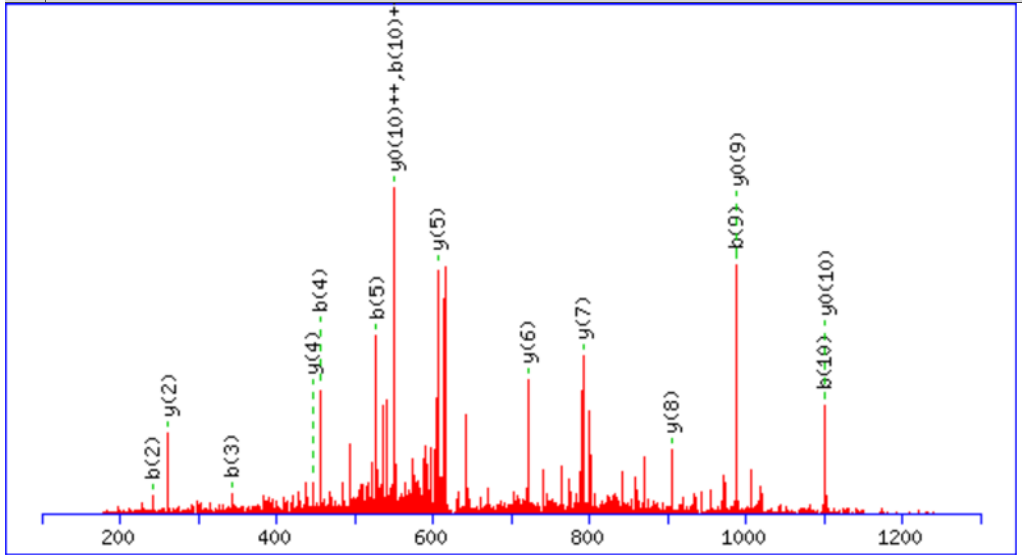


Peptide View

MS/MS Fragmentation of **KITIADCGQLE**
Found in **IPI00419585**, Tax_Id=9606 Gene_Symbol=PPIA Peptidyl-prolyl cis-trans isomerase A
Experiment: 18 - NOPA3 **Fraction:** NOPA3

Match to Query 8181: 1246.622048 from(624.318300,2+)
Title: OECHL100317_17.11607.11607.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_17.raw
Monoisotopic mass of neutral peptide Mr(calc): 1246.622726**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00093**Matches :** 16/112 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	129.102239	65.054757	112.075690	56.541483			K							11
2	***242.186303***	121.596790	225.159754	113.083515			I	1119.535053	560.271165	1102.508504	551.757890	1101.524488	551.265882	10
3	***343.233982***	172.120629	326.207433	163.607355	325.223417	163.115347	T	1006.450989	503.729133	989.424440	495.215858	988.440424	494.723850	9
4	***456.318046***	228.662661	439.291497	220.149387	438.307481	219.657379	I	***905.403310***	453.205293	888.376761	444.692019	887.392745	444.200011	8
5	***527.355160***	264.181218	510.328611	255.667944	509.344595	255.175936	A	***792.319246***	396.663261	775.292697	388.149987	774.308681	387.657979	7
6	642.382103	321.694690	625.355554	313.181415	624.371538	312.689407	D	***721.282132***	361.144704	704.255583	352.631430	703.271567	352.139422	6
7	802.412752	401.710014	785.386203	393.196740	784.402187	392.704732	C	***606.255189***	303.631233	589.228640	295.117958	588.244624	294.625950	5
8	859.434216	430.220746	842.407667	421.707472	841.423651	421.215464	G	***446.224540***	223.615908	429.197991	215.102634	428.213975	214.610626	4
9	***987.492794***	494.250035	970.466245	485.736761	969.482229	485.244753	Q	389.203076	195.105176	372.176527	186.591902	371.192511	186.099894	3
10	***1100.576858***	550.792067	1083.550309	542.278793	1082.566293	541.786785	L	***261.144498***	131.075887			243.133933	122.070605	2
11							E	148.060434	74.533855			130.049869	65.528573	1

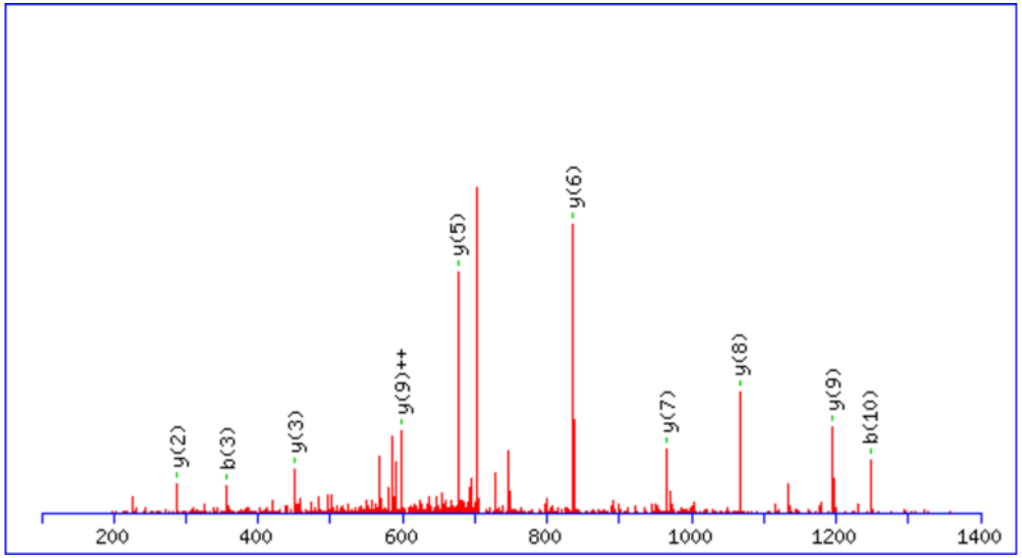


Peptide View

MS/MS Fragmentation of **LLETECPQYIR**
Found in **IPI00007047**, Tax_Id=9606 Gene_Symbol=S100A8 Protein S100-A8
Experiment: 27 - NOPD3 **Fraction:** NOPD3

Match to Query 9235: 1420.702448 from(711.358500,2+)
Title: OECHL100317_15.12578.12578.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1420.702026**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62
Expect: 7.6e-005**Matches :** 10/90 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	114.091340	57.549308					**L**							**11**
2	227.175404	114.091340					**L**	1308.625265	654.816271	1291.598716	646.302996	1290.614700	645.810988	**10**
3	**356.217997**	178.612637			338.207432	169.607354	**E**	***1195.541201***	598.274239	1178.514652	589.760964	1177.530636	589.268956	**9**
4	457.265676	229.136476			439.255111	220.131194	**T**	***1066.498608***	533.752942	1049.472059	525.239668	1048.488043	524.747660	**8**
5	586.308269	293.657773			568.297704	284.652490	**E**	***965.450929***	483.229103	948.424380	474.715828	947.440364	474.223820	**7**
6	746.338918	373.673097			728.328353	364.667815	**C**	***836.408336***	418.707806	819.381787	410.194531			**6**
7	843.391682	422.199479			825.381117	413.194197	**P**	***676.377687***	338.692481	659.351138	330.179207			**5**
8	971.450260	486.228768	954.423711	477.715494	953.439695	477.223486	**Q**	579.324923	290.166099	562.298374	281.652825			**4**
9	1134.513589	567.760433	1117.487040	559.247158	1116.503024	558.755150	**Y**	***451.266345***	226.136810	434.239796	217.623536			**3**
10	**1247.597653**	624.302465	1230.571104	615.789190	1229.587088	615.297182	**I**	***288.203016***	144.605146	271.176467	136.091871			**2**
11							**R**	175.118952	88.063114	158.092403	79.549839			**1**



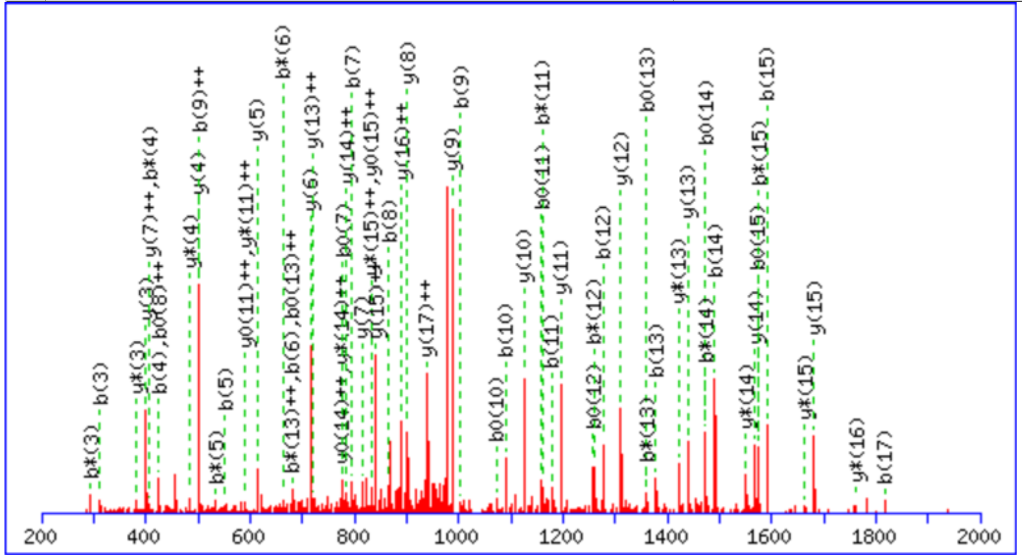
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 27 - NOPD3 **Fraction:** NOPD3

Match to Query 14039: 1990.025648 from(996.020100,2+)
Title: OECHL100317_15.10128.10128.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72
Expect: 9.6e-006**Matches :** 65/186 fragment ions using 125 most intense peaks (help)

#	b	$\mathbf{b}^{++}$	b*	$\mathbf{b*}^{++}$	$\mathbf{b}^{0}$	$\mathbf{b}^{0++}$	Seq.	y	$\mathbf{y}^{++}$	y*	$\mathbf{y*}^{++}$	$\mathbf{y}^{0}$	$\mathbf{y}^{0++}$	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	***311.171381***	156.089328	294.144832	147.576054			**V**	1779.934789	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	***424.255445***	212.631361	407.228896	204.118086			**L**	**1680.866375**	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	***552.314023***	276.660650	535.287474	268.147375			**Q**	**1567.782311**	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	***680.372601***	340.689939	663.346052	332.176664			**Q**	**1439.723733**	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**

7	795.399544	398.203410	778.372995	389.690136	777.388979	389.198128	D	1311.665155	656.336215	1294.638606	647.822941	1293.654590	647.330933	12
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	A	1196.638212	598.822744	1179.611663	590.309470	1178.627647	589.817462	11
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	H	1125.601098	563.304187	1108.574549	554.790913	1107.590533	554.298905	10
10	1090.527598	545.767437	1073.501049	537.254163	1072.517033	536.762155	S	988.542186	494.774731	971.515637	486.261457	970.531621	485.769449	9
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	S	901.510158	451.258717	884.483609	442.745443	883.499593	442.253435	8
12	1276.628040	638.817658	1259.601491	630.304384	1258.617475	629.812376	V	814.478130	407.742703	797.451581	399.229428	796.467565	398.737420	7
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	T	715.409716	358.208496	698.383167	349.695221	697.399151	349.203213	6
14	1490.759783	745.883530	1473.733234	737.370255	1472.749218	736.878247	I	614.362037	307.684656	597.335488	299.171382	596.351472	298.679374	5
15	1591.807462	796.407369	1574.780913	787.894095	1573.796897	787.402087	T	501.277973	251.142624	484.251424	242.629350	483.267408	242.137342	4
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	P	400.230294	200.618785	383.203745	192.105510			3
17	1816.918804	908.963040	1799.892255	900.449766	1798.908239	899.957758	Q	303.177530	152.092403	286.150981	143.579128			2
18							R	175.118952	88.063114	158.092403	79.549839			1

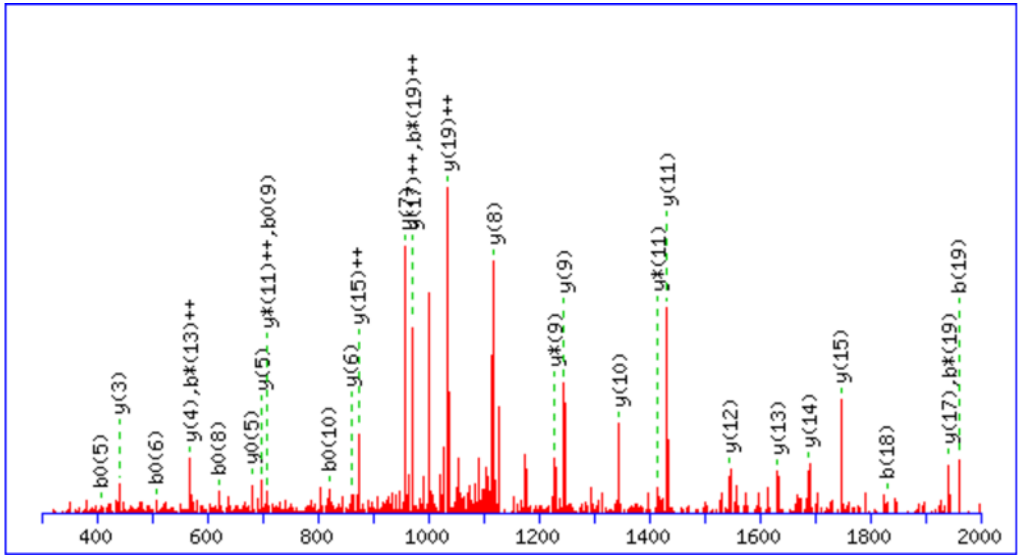


Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 27 - NOPD3 **Fraction:** NOPD3

Match to Query 15214: 2270.113448 from(1136.064000,2+)
Title: OECHL100317_15.10837.10837.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 3.9e-006**Matches :** 31/212 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	102.054955	51.531116			84.044390	42.525833	**T**						
2	201.123369	101.065322			183.112804	92.060040	**V**	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400	1076.5338
3	272.160483	136.583879			254.149918	127.578597	**A**	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986	1026.9996
4	329.181947	165.094611			311.171382	156.089329	**G**	1999.965437	1000.486357	1982.938888	991.973082	1981.954872	991.4810
5	426.234711	213.620994			408.224146	204.615711	**P**	***1942.943973***	971.975625	1925.917424	963.462350	1924.933408	962.9703
6	525.303125	263.155201			507.292560	254.149918	**V**	1845.891209	923.449243	1828.864660	914.935968	1827.880644	914.4439
7	582.324589	291.665933			564.314024	282.660650	**G**	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230	864.9097
8	639.346053	320.176665			621.335488	311.171382	**G**	***1689.801331***	845.404304	1672.774782	836.891029	1671.790766	836.3990
9	726.378081	363.692679			708.367516	354.687396	**S**	***1632.779867***	816.893572	1615.753318	808.380297	1614.769302	807.8882
10	839.462145	420.234711			821.451580	411.229428	**L**	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274	764.3722
11	926.494173	463.750725			908.483608	454.745442	**S**	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210	707.8302
12	1025.562587	513.284932			1007.552022	504.279649	**V**	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182	664.3142
13	1153.621165	577.314221	1136.594616	568.800946	1135.610600	568.308938	**Q**	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768	614.7800
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	**C**	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190	550.7507
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	**P**	***958.474106***	479.740691	941.447557	471.227417	940.463541	470.7354
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	**Y**	***861.421342***	431.214309	844.394793	422.701035	843.410777	422.2090
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	**E**	***698.358013***	349.682645	681.331464	341.169370	680.347448	340.6773
18	1830.905463	915.956370	1813.878914	907.443095	1812.894898	906.951087	**K**	***569.315420***	285.161348	552.288871	276.648074	551.304855	276.1560
19	1959.948056	980.477666	1942.921507	971.964392	1941.937491	971.472384	**E**	***441.220457***	221.113867	424.193908	212.600592	423.209892	212.1085
20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	**H**	312.177864	156.592570	295.151315	148.079295		
21							**R**	175.118952	88.063114	158.092403	79.549839		



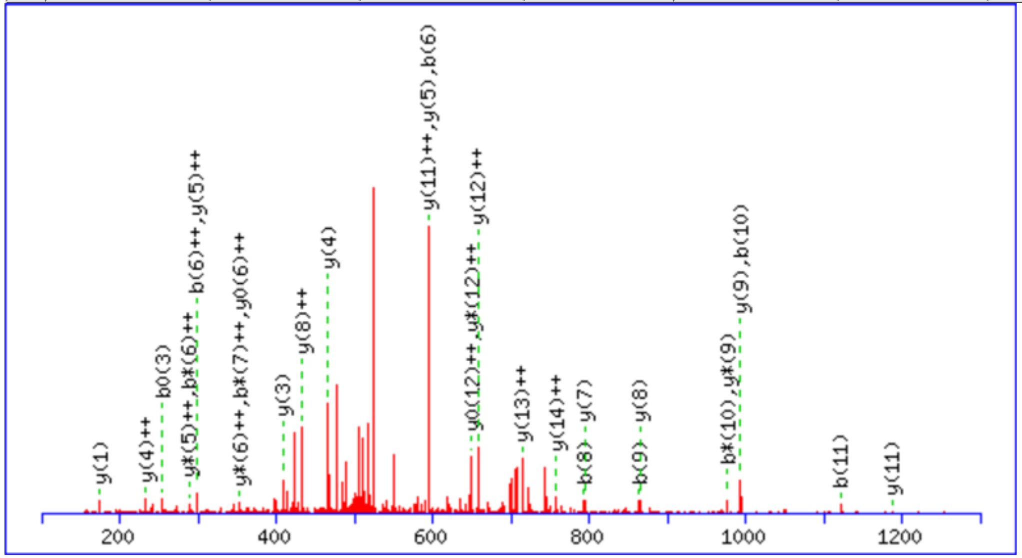
Peptide View

MS/MS Fragmentation of **ASLQHGQAAEKGPHR**
Found in **IPI00165044**, Tax_Id=9606 Gene_Symbol=FAM198B Isoform 2 of Protein ENED
Experiment: 27 - NOPD3 **Fraction:** NOPD3

Match to Query 10994: 1585.807272 from(529.609700,3+)
Title: OECHL100317_15.1843.1843.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1585.807312**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57
Expect: 0.00032**Matches :** 31/150 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	72.044390	36.525833					**A**							**15**
2	159.076418	80.041847			141.065853	71.036564	**S**	1515.777500	758.392388	1498.750951	749.879114	1497.766935	749.387106	**14**
3	272.160482	136.583879			254.149917	127.578597	**L**	1428.745472	714.876374	1411.718923	706.363100	1410.734907	705.871092	**13**
4	400.219060	200.613168	383.192511	192.099894	382.208495	191.607886	**Q**	1315.661408	658.334342	1298.634859	649.821068	1297.650843	649.329060	**12**
5	537.277972	269.142624	520.251423	260.629350	519.267407	260.137342	**H**	***1187.602830***	594.305053	1170.576281	585.791779	1169.592265	585.299771	**11**
6	***594.299436***	297.653356	577.272887	289.140082	576.288871	288.648074	**G**	1050.543918	525.775597	1033.517369	517.262323	1032.533353	516.770315	**10**

7	722.358014	361.682645	705.331465	353.169371	704.347449	352.677363	**Q**	***993.522454***	497.264865	976.495905	488.751591	975.511889	488.259583	**9**
8	***793.395128***	397.201202	776.368579	388.687928	775.384563	388.195920	**A**	***865.463876***	433.235576	848.437327	424.722302	847.453311	424.230294	**8**
9	***864.432242***	432.719759	847.405693	424.206485	846.421677	423.714477	**A**	***794.426762***	397.717019	777.400213	389.203745	776.416197	388.711737	**7**
10	***993.474835***	497.241056	976.448286	488.727781	975.464270	488.235773	**E**	723.389648	362.198462	706.363099	353.685188	705.379083	353.193180	**6**
11	***1121.569798***	561.288537	1104.543249	552.775263	1103.559233	552.283255	**K**	***594.347055***	297.677166	577.320506	289.163891			**5**
12	1178.591262	589.799269	1161.564713	581.285995	1160.580697	580.793987	**G**	***466.252092***	233.629684	449.225543	225.116409			**4**
13	1275.644026	638.325651	1258.617477	629.812377	1257.633461	629.320369	**P**	***409.230628***	205.118952	392.204079	196.605677			**3**
14	1412.702938	706.855107	1395.676389	698.341833	1394.692373	697.849825	**H**	312.177864	156.592570	295.151315	148.079295			**2**
15							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



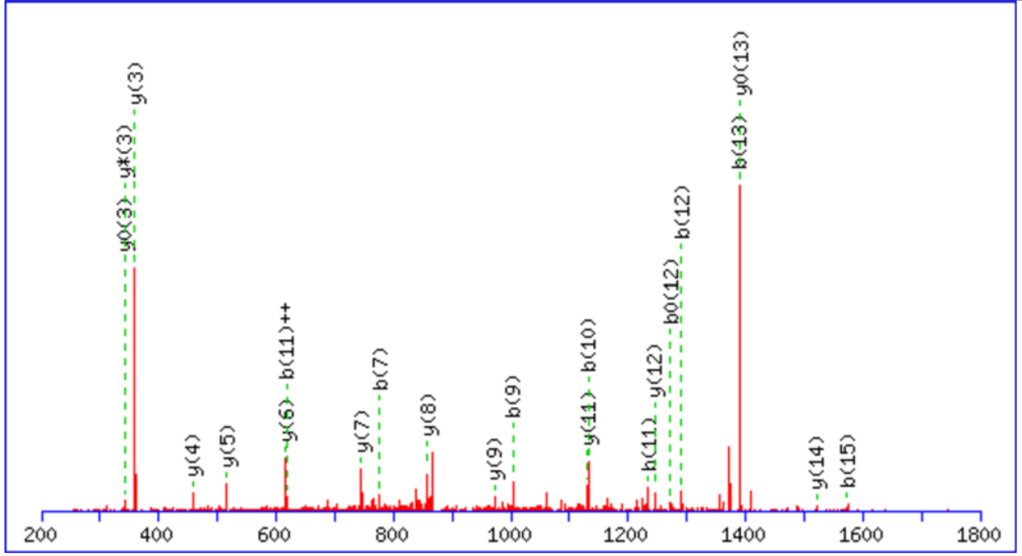
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 27 - NOPD3 **Fraction:** NOPD3

Match to Query 12494: 1746.915648 from(874.465100,2+)
Title: OECHL100317_15.17015.17015.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_15.raw

Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 82
Expect: 7.2e-007**Matches :** 22/156 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							16
2	227.175404	114.091340					L	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	15
3	340.259468	170.633372					I	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	14
4	503.322797	252.165036					Y	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	13
5	618.349740	309.678508			600.339175	300.673226	D	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	12
6	689.386854	345.197065			671.376289	336.191782	A	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	11
7	**776.418882**	388.713079			758.408317	379.707796	S	1059.542913	530.275095	1042.516364	521.761820	1041.532348	521.269812	10
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	9
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	L	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	8
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	E	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	7
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	T	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	6
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	G	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	5
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	V	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	4
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
16							R	175.118952	88.063114	158.092403	79.549839			1

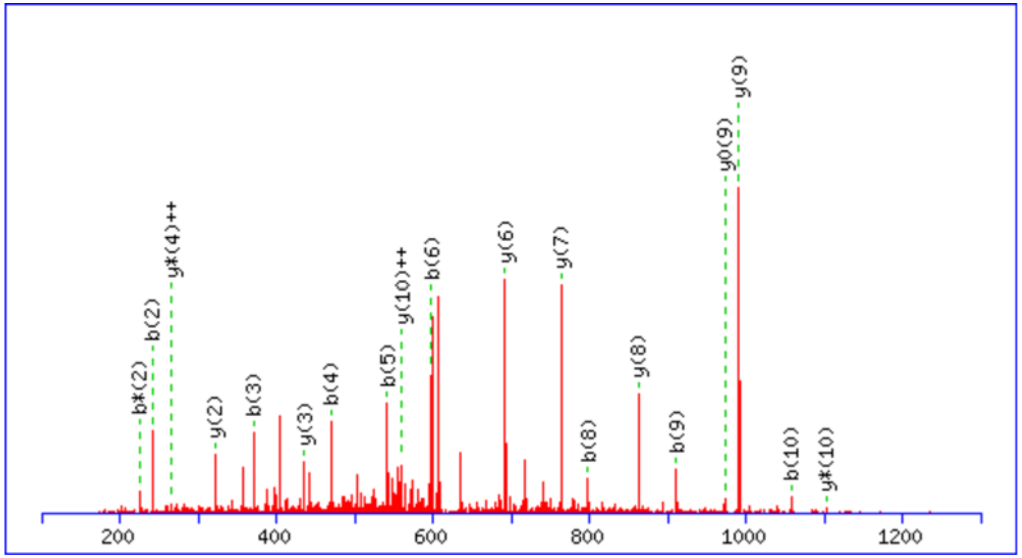


Peptide View

MS/MS Fragmentation of **IQEVAGSLIFR**
Found in **IPI00006988**, Tax_Id=9606 Gene_Symbol=RETN Resistin
Experiment: 27 - NOPD3 **Fraction:** NOPD3

Match to Query 6983: 1231.692448 from(616.853500,2+)
Title: OECHL100317_15.16886.16886.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1231.692459**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59
Expect: 5.4e-005**Matches :** 19/106 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	114.091340	57.549308					**I**							**11**
2	***242.149918***	121.578597	225.123369	113.065323			**Q**	1119.615685	560.311481	1102.589136	551.798206	1101.605120	551.306198	**10**
3	***371.192511***	186.099894	354.165962	177.586619	353.181946	177.094611	**E**	**991.557107**	496.282192	974.530558	487.768917	973.546542	487.276909	**9**
4	***470.260925***	235.634101	453.234376	227.120826	452.250360	226.628818	**V**	**862.514514**	431.760895	845.487965	423.247621	844.503949	422.755613	**8**
5	***541.298039***	271.152658	524.271490	262.639383	523.287474	262.147375	**A**	**763.446100**	382.226688	746.419551	373.713414	745.435535	373.221406	**7**
6	***598.319503***	299.663390	581.292954	291.150115	580.308938	290.658107	**G**	**692.408986**	346.708131	675.382437	338.194857	674.398421	337.702849	**6**
7	685.351531	343.179404	668.324982	334.666129	667.340966	334.174121	**S**	635.387522	318.197399	618.360973	309.684125	617.376957	309.192117	**5**
8	***798.435595***	399.721436	781.409046	391.208161	780.425030	390.716153	**L**	548.355494	274.681385	531.328945	266.168111			**4**
9	***911.519659***	456.263468	894.493110	447.750193	893.509094	447.258185	**I**	**435.271430**	218.139353	418.244881	209.626078			**3**
10	***1058.588073***	529.797675	1041.561524	521.284400	1040.577508	520.792392	**F**	**322.187366**	161.597321	305.160817	153.084046			**2**
11							**R**	175.118952	88.063114	158.092403	79.549839			**1**



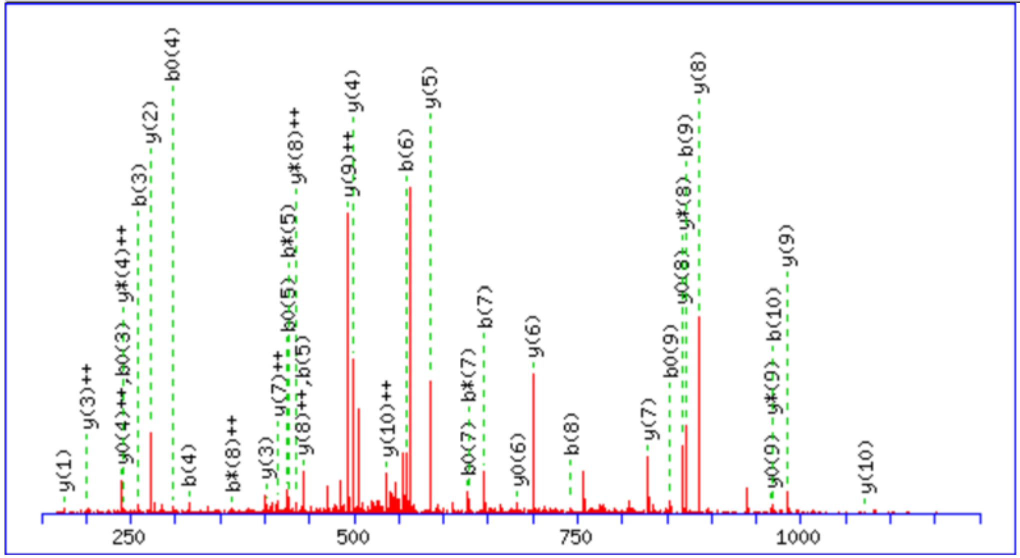
Peptide View

MS/MS Fragmentation of **ASVGQDSPEPR**
Found in **IPI00044369**, Tax_Id=9606 Gene_Symbol=PLXDC2 Isoform 1 of Plexin domain-containing protein 2
Experiment: 27 - NOPD3 **Fraction:** NOPD3

Match to Query 5394: 1141.536248 from(571.775400,2+)
Title: OECHL100317_15.3274.3274.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1141.536362**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 0.0001**Matches :** 39/106 fragment ions using 90 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					**A**							**11**
2	159.076418	80.041847			141.065853	71.036564	**S**	***1071.506528***	536.256902	1054.479979	527.743628	1053.495963	527.251620	**10**
3	**258.144832**	129.576054			240.134267	120.570772	**V**	***984.474500***	492.740888	967.447951	484.227614	966.463935	483.735606	**9**
4	**315.166296**	158.086786			297.155731	149.081504	**G**	***885.406086***	443.206681	868.379537	434.693407	867.395521	434.201399	**8**
5	**443.224874**	222.116075	426.198325	213.602801	425.214309	213.110793	**Q**	***828.384622***	414.695949	811.358073	406.182675	810.374057	405.690667	**7**
6	**558.251817**	279.629547	541.225268	271.116272	540.241252	270.624264	**D**	***700.326044***	350.666660	683.299495	342.153386	682.315479	341.661378	**6**

7	**645.283845**	323.145561	628.257296	314.632286	627.273280	314.140278	**S**	***585.299101***	293.153189	568.272552	284.639914	567.288536	284.147906	**5**
8	**742.336609**	371.671943	725.310060	363.158668	724.326044	362.666660	**P**	***498.267073***	249.637174	481.240524	241.123900	480.256508	240.631892	**4**
9	**871.379202**	436.193239	854.352653	427.679965	853.368637	427.187957	**E**	***401.214309***	201.110792	384.187760	192.597518	383.203744	192.105510	**3**
10	**968.431966**	484.719621	951.405417	476.206347	950.421401	475.714339	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



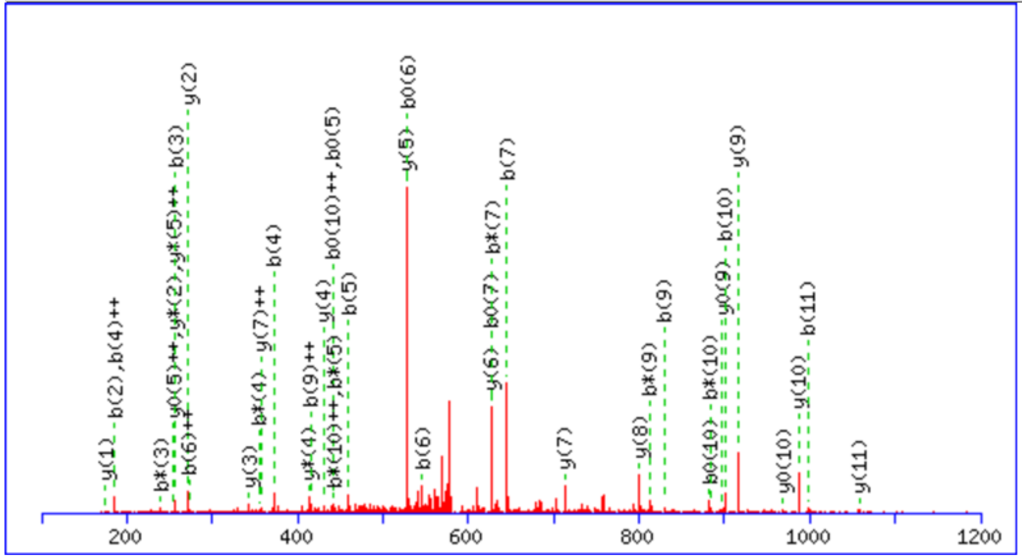
Peptide View

MS/MS Fragmentation of **NAADSSVPSAPR**
Found in **IPI00909783**, Tax_Id=9606 Gene_Symbol=SPINT2 serine protease inhibitor, Kunitz type, 2 isoform b precursor
Experiment: 27 - NOPD3 **Fraction:** NOPD3

Match to Query 5823: 1170.562448 from(586.288500,2+)
Title: OECHL100317_15.5113.5113.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1170.562897**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 5e-005**Matches :** 42/120 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	115.050203	58.028740	98.023654	49.515465			**N**							**12**

2	**186.087317**	93.547296	169.060768	85.034022			**A**	***1057.527263***	529.267270	1040.500714	520.753995	1039.516698	520.261987	**11**
3	**257.124431**	129.065854	240.097882	120.552579			**A**	***986.490149***	493.748713	969.463600	485.235438	968.479584	484.743430	**10**
4	**372.151374**	**186.579325**	355.124825	178.066051	354.140809	177.574043	**D**	***915.453035***	458.230156	898.426486	449.716881	897.442470	449.224873	**9**
5	**459.183402**	230.095339	442.156853	221.582065	441.172837	221.090057	**S**	***800.426092***	400.716684	783.399543	392.203410	782.415527	391.711402	**8**
6	**546.215430**	**273.611353**	529.188881	265.098079	528.204865	264.606071	**S**	***713.394064***	357.200670	696.367515	348.687396	695.383499	348.195388	**7**
7	**645.283844**	323.145560	628.257295	314.632286	627.273279	314.140278	**V**	***626.362036***	313.684656	609.335487	305.171382	608.351471	304.679374	**6**
8	742.336608	371.671942	725.310059	363.158668	724.326043	362.666660	**P**	***527.293622***	264.150449	510.267073	255.637175	509.283057	255.145167	**5**
9	**829.368636**	**415.187956**	812.342087	406.674682	811.358071	406.182674	**S**	***430.240858***	215.624067	413.214309	207.110793	412.230293	206.618785	**4**
10	**900.405750**	450.706513	883.379201	442.193239	882.395185	441.701231	**A**	***343.208830***	172.108053	326.182281	163.594779			**3**
11	**997.458514**	499.232895	980.431965	490.719621	979.447949	490.227613	**P**	***272.171716***	136.589496	255.145167	128.076222			**2**
12							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**

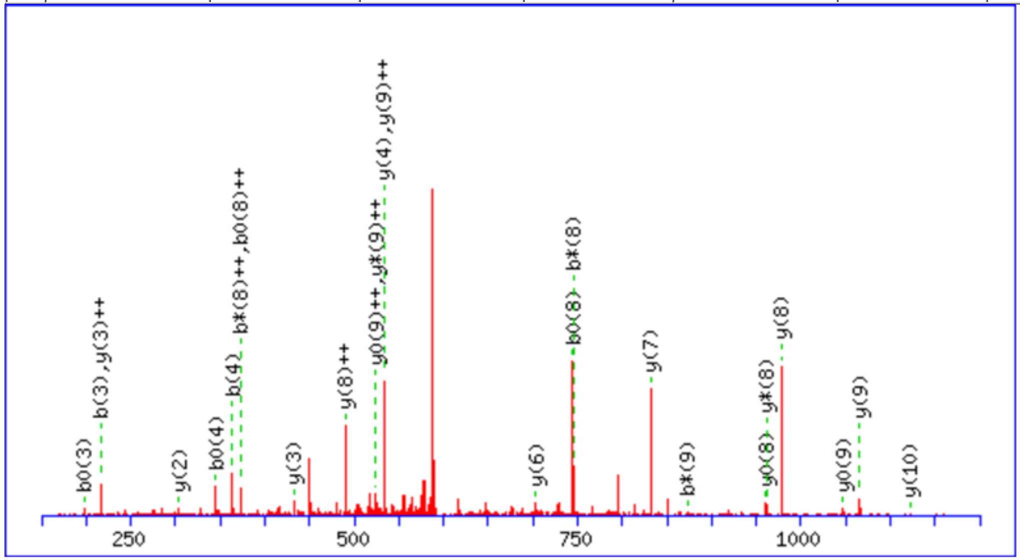


Peptide View

MS/MS Fragmentation of **AGSFKVATQER**
Found in **IPI00643388**, Tax_Id=9606 Gene_Symbol=RGL4 RGL4 protein
Experiment: 27 - NOPD3 **Fraction:** NOPD3

Match to Query 6211: 1192.623048 from(597.318800,2+)
Title: OECHL100317_15.2345.2345.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_15.raw
Monoisotopic mass of neutral peptide Mr(calc): 1192.620026**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53
Expect: 0.00038**Matches :** 25/106 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							11
2	129.065854	65.036565					G	***1122.590199***	561.798738	1105.563650	553.285463	1104.579634	552.793455	10
3	**216.097882**	108.552579			198.087317	99.547296	S	***1065.568735***	533.288006	1048.542186	524.774731	1047.558170	524.282723	9
4	**363.166296**	182.086786			345.155731	173.081504	F	***978.536707***	489.771992	961.510158	481.258717	960.526142	480.766709	8
5	491.261259	246.134267	474.234710	237.620993	473.250694	237.128985	K	***831.468293***	416.237785	814.441744	407.724510	813.457728	407.232502	7
6	590.329673	295.668475	573.303124	287.155200	572.319108	286.663192	V	***703.373330***	352.190303	686.346781	343.677029	685.362765	343.185021	6
7	661.366787	331.187032	644.340238	322.673757	643.356222	322.181749	A	604.304916	302.656096	587.278367	294.142822	586.294351	293.650814	5
8	762.414466	381.710871	745.387917	373.197597	744.403901	372.705589	T	***533.267802***	267.137539	516.241253	258.624265	515.257237	258.132257	4
9	890.473044	445.740160	873.446495	437.226886	872.462479	436.734878	Q	***432.220123***	216.613700	415.193574	208.100425	414.209558	207.608417	3
10	1019.515637	510.261457	1002.489088	501.748182	1001.505072	501.256174	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
11							R	175.118952	88.063114	158.092403	79.549840			1

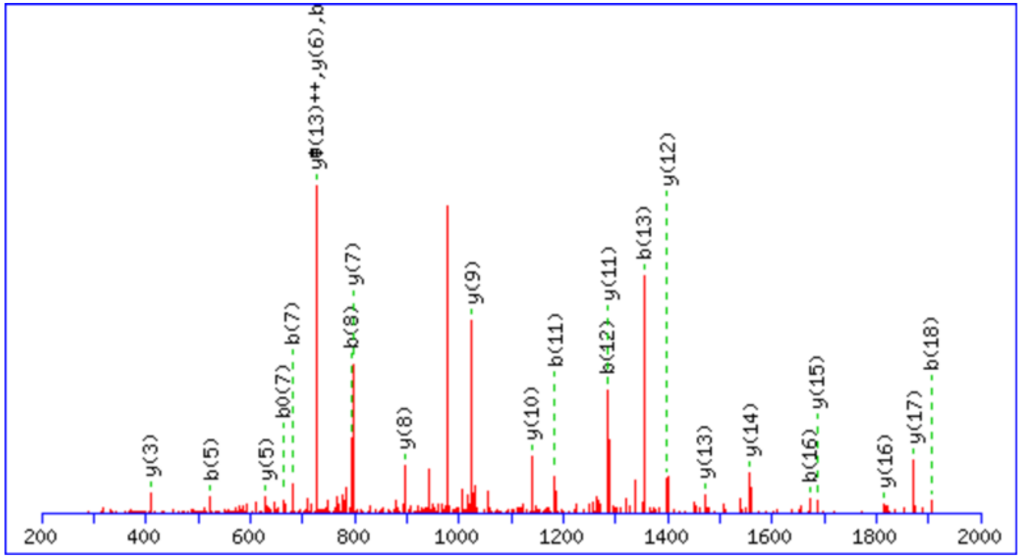


Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 09 - S_C-3 **Fraction:** S_C-3

Match to Query 13488: 2078.983448 from(1040.499000,2+)
Title: OECHL100317_13.16098.16098.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 90
Expect: 1.8e-007**Matches :** 26/200 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**19**
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973939	**18**
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444483	**17**
4	394.183344	197.595310	377.156795	189.082035			**Q**	***1814.870790***	907.939033	1797.844241	899.425759	1796.860225	898.933751	**16**
5	**523.225937**	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904462	**15**
6	610.257965	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383165	**14**
7	**681.295079**	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867151	**13**
8	**794.379143**	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348594	**12**
9	941.447557	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806562	**11**
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272355	**10**
11	**1184.533077**	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250892	**9**
12	**1283.601491**	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729595	**8**
13	**1354.638605**	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195388	**7**
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676831	**6**
15	1508.712833	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150449	**5**
16	**1671.776162**	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	572.282723	286.645000	555.256174	278.131725	554.272158	277.639717	**4**
17	1818.844576	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	**3**
18	**1905.876604**	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
19							**R**	175.118952	88.063114	158.092403	79.549840			**1**



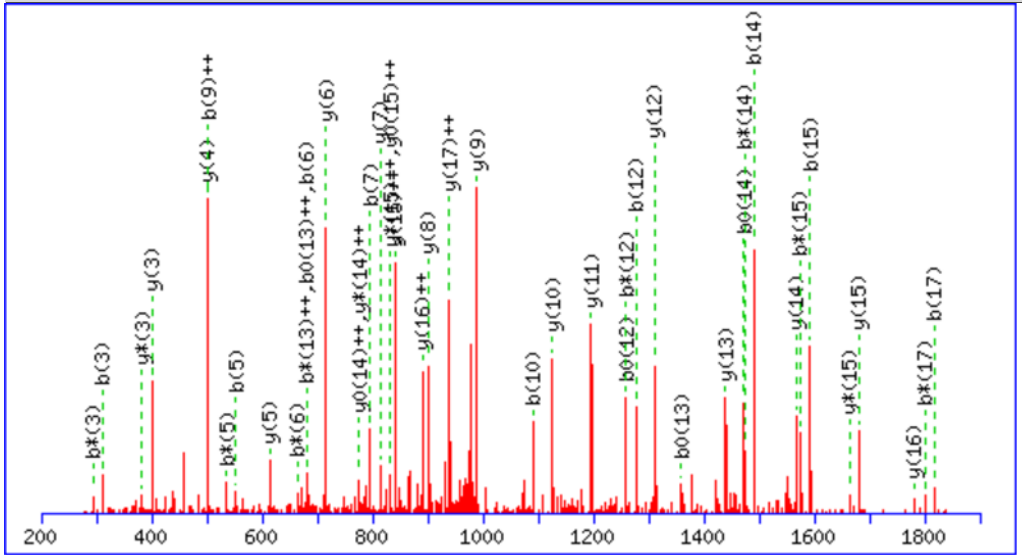
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 09 - S_C-3 **Fraction:** S_C-3

Match to Query 13113: 1990.023848 from(996.019200,2+)
Title: OECHL100317_13.9052.9052.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 86
Expect: 3.5e-007**Matches :** 45/186 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	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	424.255445	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	**552.314023**	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	**680.372601**	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**

7	**795.399544**	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510			**3**
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**

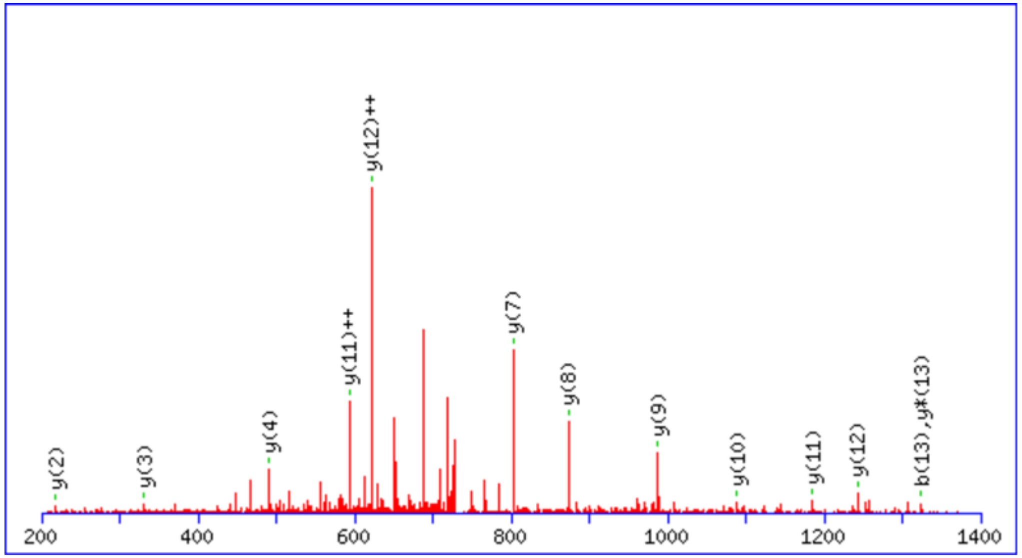


Peptide View

MS/MS Fragmentation of **EVGPTNADPVCLAK**
Found in **IPI00017601**, Tax_Id=9606 Gene_Symbol=CP Ceruloplasmin
Experiment: 09 - S_C-3 **Fraction:** S_C-3

Match to Query 9447: 1469.718448 from(735.866500,2+)
Title: OECHL100317_13.10352.10352.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1469.718430**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 96
Expect: 2.7e-008**Matches :** 13/134 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	130.049869	65.528572			112.039304	56.523290	**E**							**14**
2	229.118283	115.062780			211.107718	106.057497	**V**	1341.683114	671.345195	1324.656565	662.831920	1323.672549	662.339912	**13**
3	286.139747	143.573512			268.129182	134.568229	**G**	***1242.614700***	621.810988	1225.588151	613.297713	1224.604135	612.805705	**12**
4	383.192511	192.099894			365.181946	183.094611	**P**	***1185.593236***	593.300256	1168.566687	584.786982	1167.582671	584.294973	**11**
5	484.240190	242.623733			466.229625	233.618451	**T**	***1088.540472***	544.773874	1071.513923	536.260600	1070.529907	535.768591	**10**
6	598.283117	299.645197	581.256568	291.131922	580.272552	290.639914	**N**	***987.492793***	494.250034	970.466244	485.736760	969.482228	485.244752	**9**
7	669.320231	335.163754	652.293682	326.650479	651.309666	326.158471	**A**	***873.449866***	437.228571	856.423317	428.715296	855.439301	428.223288	**8**
8	784.347174	392.677225	767.320625	384.163951	766.336609	383.671943	**D**	***802.412752***	401.710014	785.386203	393.196739	784.402187	392.704731	**7**
9	881.399938	441.203607	864.373389	432.690333	863.389373	432.198325	**P**	687.385809	344.196542	670.359260	335.683268			**6**
10	980.468352	490.737814	963.441803	482.224539	962.457787	481.732531	**V**	590.333045	295.670160	573.306496	287.156886			**5**
11	1140.499001	570.753138	1123.472452	562.239864	1122.488436	561.747856	**C**	***491.264631***	246.135953	474.238082	237.622679			**4**
12	1253.583065	627.295170	1236.556516	618.781896	1235.572500	618.289888	**L**	***331.233982***	166.120629	314.207433	157.607354			**3**
13	1324.620179	662.813727	1307.593630	654.300453	1306.609614	653.808445	**A**	***218.149918***	109.578597	201.123369	101.065322			**2**
14							**K**	147.112804	74.060040	130.086255	65.546765			**1**



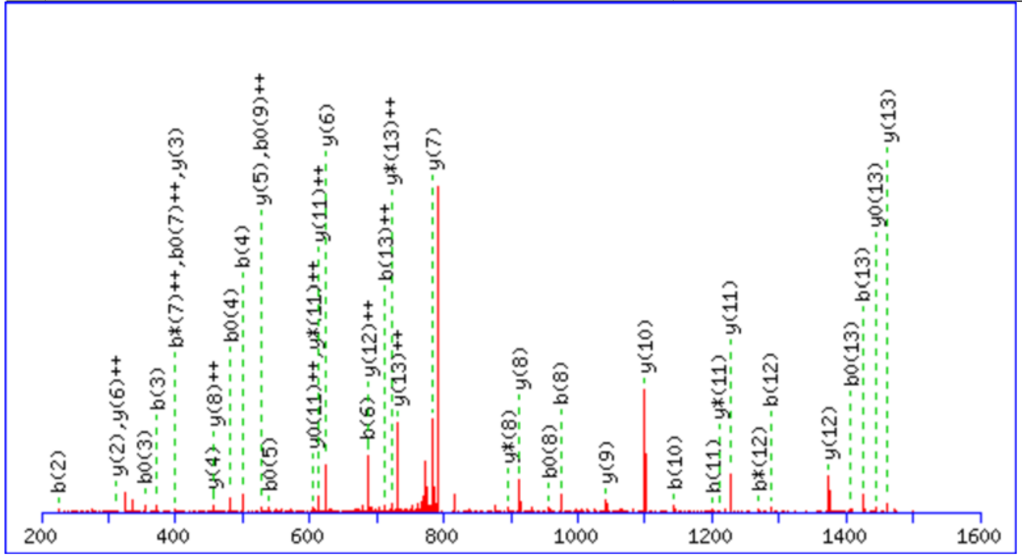
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00922148**, Tax_Id=9606 Gene_Symbol=- cDNA FLJ53081, highly similar to Tumor necrosis factor receptor superfamily member 10C
Experiment: 09 - S_C-3 **Fraction:** S_C-3

Match to Query 10453: 1597.707848 from(799.861200,2+)
Title: OECHL100317_13.2215.2215.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 82
Expect: 4.3e-007**Matches :** 42/144 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	138.066188	69.536732					H							14
2	**225.098216**	113.052746			207.087651	104.047463	S	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.325325	13
3	**372.166630**	186.586953			354.156065	177.581671	F	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.809311	12
4	**500.261593**	250.634435	483.235044	242.121160	482.251028	241.629152	K	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	11
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	G	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	10
6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	E	***1042.437069***	521.722173	1025.410520	513.208898	1024.426504	512.716890	9

7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	***312.177864***	156.592570	295.151315	148.079295			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



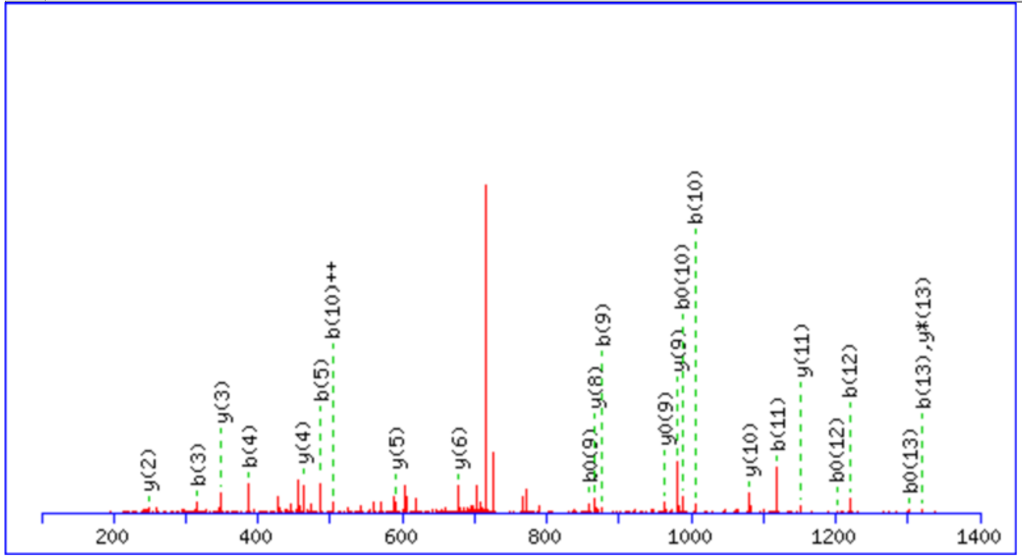
Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 09 - S_C-3 **Fraction:** S_C-3

Match to Query 9393: 1465.679648 from(733.847100,2+)
Title: OECHL100317_13.8912.8912.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable**

modifications: N-term : Acetyl (N-term)**Ions Score:** 66 **Expect:** 2e-005**Matches :** 24/128 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	1337.643082	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	***316.113926***	158.560601	298.103361	149.555319	**A**	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	***387.151040***	194.079158	369.140475	185.073875	**A**	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	***486.219454***	243.613365	468.208889	234.608082	**V**	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**
6	601.246397	301.126837	583.235832	292.121554	**D**	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	**9**
7	702.294076	351.650676	684.283511	342.645394	**T**	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	765.398875	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	***876.358132***	438.682704	858.347567	429.677421	**S**	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	***1005.400725***	503.204001	987.390160	494.198718	**E**	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	***1118.484789***	559.746033	1100.474224	550.740750	**I**	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	***1219.532468***	610.269872	1201.521903	601.264590	**T**	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	***1320.580147***	660.793712	1302.569582	651.788429	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**

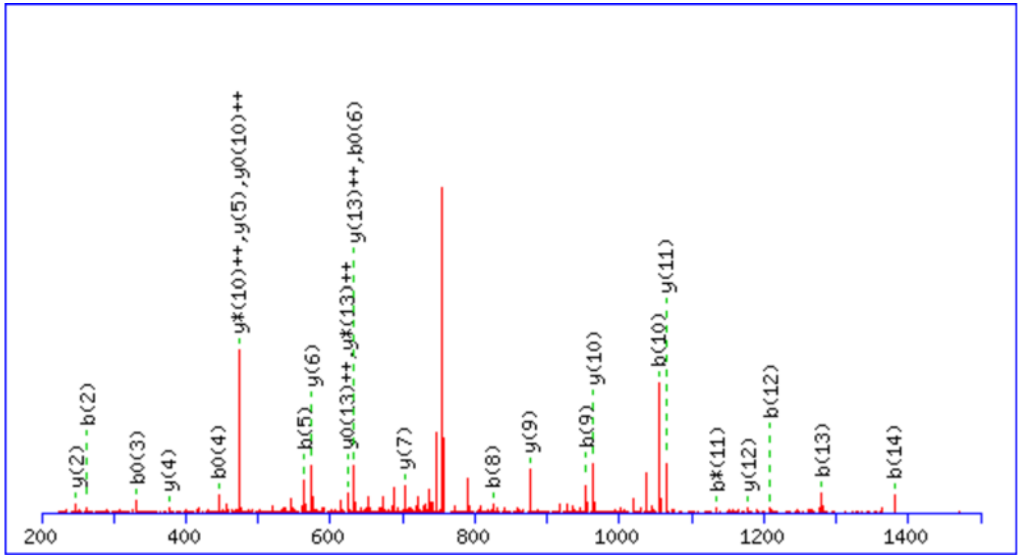


Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 09 - S_C-3 **Fraction:** S_C-3

Match to Query 9938: 1525.723048 from(763.868800,2+)
Title: OECHL100317_13.9935.9935.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72
Expect: 7.4e-006**Matches :** 26/150 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	350.134661	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	**9**
8	***825.362488***	413.184882			807.351923	404.179599	**S**	789.410110	395.208693	772.383561	386.695418	771.399545	386.203410	**8**
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	**7**
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	**6**
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	**5**
12	***1208.542973***	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	**4**
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	**3**
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



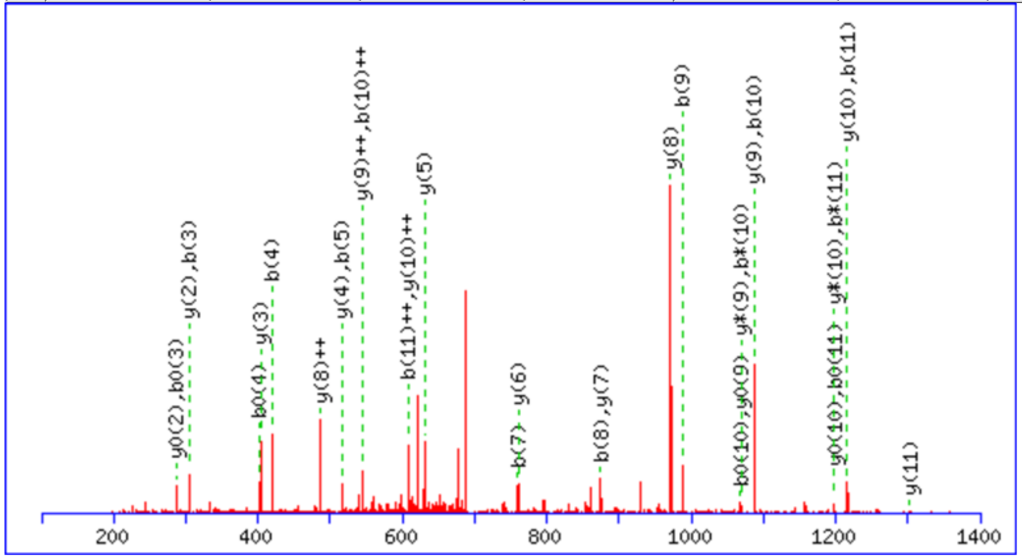
Peptide View

MS/MS Fragmentation of **SSEDPNEDIVER**
Found in **IPI00178926**, Tax_Id=9606 Gene_Symbol=IGJ Immunoglobulin J chain
Experiment: 09 - S_C-3 **Fraction:** S_C-3

Match to Query 8612: 1388.606648 from(695.310600,2+)
Title: OECHL100317_13.6542.6542.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1388.605545**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 3.4e-005**Matches :** 34/120 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	88.039304	44.523290			70.028739	35.518008	**S**							**12**
2	175.071332	88.039304			157.060767	79.034021	**S**	***1302.580814***	651.794045	1285.554265	643.280771	1284.570249	642.788763	**11**
3	**304.113925**	152.560600			286.103360	143.555318	**E**	***1215.548786***	608.278031	1198.522237	599.764757	1197.538221	599.272749	**10**
4	**419.140868**	210.074072			401.130303	201.068790	**D**	***1086.506193***	543.756735	1069.479644	535.243460	1068.495628	534.751452	**9**
5	**516.193632**	258.600454			498.183067	249.595172	**P**	***971.479250***	486.243263	954.452701	477.729989	953.468685	477.237981	**8**
6	630.236559	315.621918	613.210010	307.108643	612.225994	306.616635	**N**	***874.426486***	437.716881	857.399937	429.203607	856.415921	428.711599	**7**

7	**759.279152**	380.143214	742.252603	371.629940	741.268587	371.137932	**E**	***760.383559***	380.695418	743.357010	372.182143	742.372994	371.690135	**6**
8	**874.306095**	437.656686	857.279546	429.143411	856.295530	428.651403	**D**	***631.340966***	316.174121	614.314417	307.660847	613.330401	307.168839	**5**
9	**987.390159**	494.198718	970.363610	485.685443	969.379594	485.193435	**I**	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.655367	**4**
10	**1086.458573**	543.732925	1069.432024	535.219650	1068.448008	534.727642	**V**	***403.229959***	202.118618	386.203410	193.605343	385.219394	193.113335	**3**
11	**1215.501166**	608.254221	1198.474617	599.740947	1197.490601	599.248939	**E**	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**



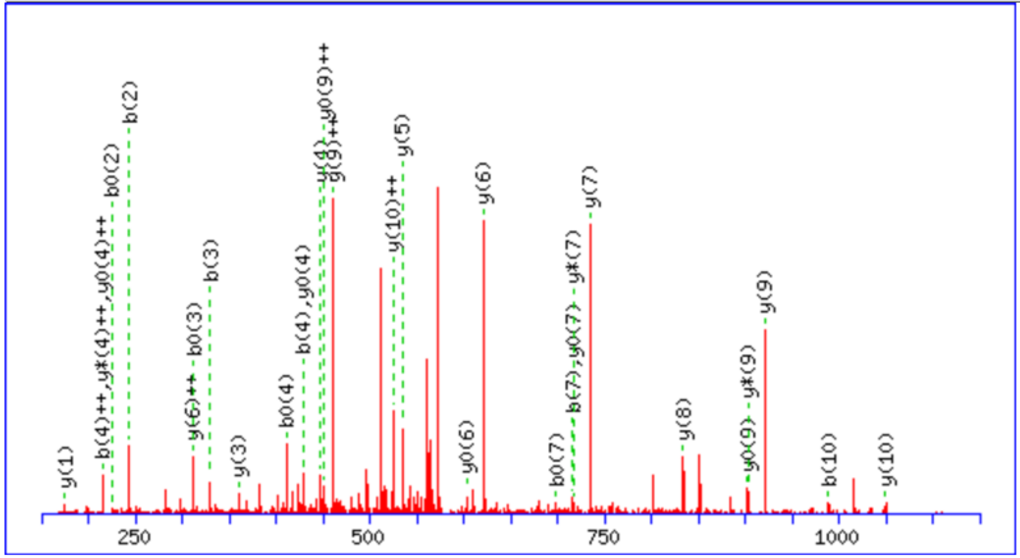
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 09 - S_C-3 **Fraction:** S_C-3

Match to Query 5670: 1161.635648 from(581.825100,2+)
Title: OECHL100317_13.5425.5425.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51
Expect: 0.00046**Matches :** 31/94 fragment ions using 66 most intense peaks (help)

#	**b**	**b^{++}**	**b^{*}**	**b^{*++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y^{*}**	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**

1	114.091340	57.549308					**I**							**11**
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637	**10**
3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340	**9**
4	**429.234375**	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326	**8**
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119	**7**
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087	**6**
7	**716.382495**	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073	**5**
8	803.414523	402.210899			785.403958	393.205617	**S**	***447.267407***	224.137342	430.240858	215.624067	429.256842	215.132059	**4**
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053			**3**
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**

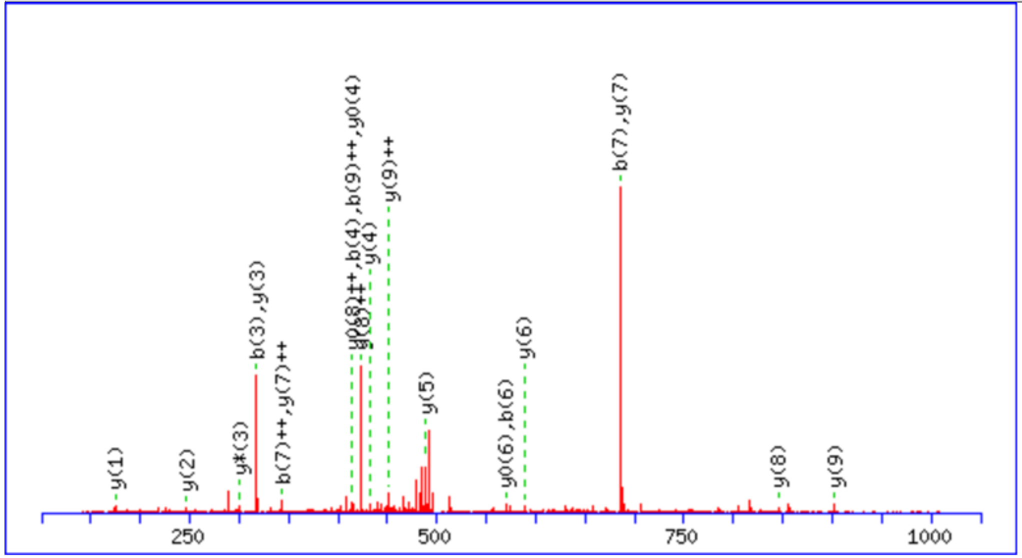


Peptide View

MS/MS Fragmentation of **VGCPVGDAAR**
Found in **IPI00099670**, Tax_Id=9606 Gene_Symbol=CEL carboxyl ester lipase precursor
Experiment: 09 - S_C-3 **Fraction:** S_C-3

Match to Query 3103: 1000.475448 from(501.245000,2+)
Title: OECHL100317_13.3671.3671.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1000.476028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49
Expect: 0.00071**Matches :** 22/72 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			**V**							**10**
2	157.097154	79.052215			**G**	***902.414878***	451.711077	885.388329	443.197803	884.404313	442.705795	**9**
3	**317.127803**	159.067540			**C**	***845.393414***	423.200345	828.366865	414.687071	827.382849	414.195063	**8**
4	**414.180567**	207.593922			**P**	***685.362765***	343.185021	668.336216	334.671746	667.352200	334.179738	**7**
5	513.248981	257.128129			**V**	***588.310001***	294.658639	571.283452	286.145364	570.299436	285.653356	**6**
6	**570.270445**	285.638861			**G**	***489.241587***	245.124431	472.215038	236.611157	471.231022	236.119149	**5**
7	**685.297388**	343.152332	667.286823	334.147050	**D**	***432.220123***	216.613699	415.193574	208.100425	414.209558	207.608417	**4**
8	756.334502	378.670889	738.323937	369.665607	**A**	***317.193180***	159.100228	300.166631	150.586953			**3**
9	827.371616	414.189446	809.361051	405.184164	**A**	***246.156066***	123.581671	229.129517	115.068397			**2**
10					**R**	***175.118952***	88.063114	158.092403	79.549840			**1**

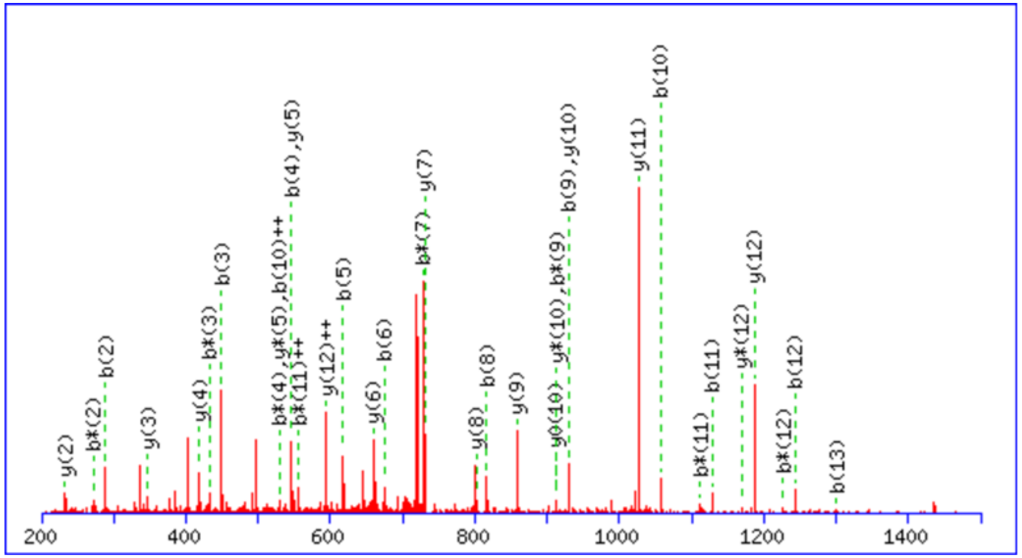


Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 09 - S_C-3 **Fraction:** S_C-3

Match to Query 9476: 1473.646048 from(737.830300,2+)
Title: OECHL100317_13.6994.6994.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57
Expect: 9.4e-005**Matches :** 36/128 fragment ions using 78 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.037925	81.022600					**C**							**14**
2	***289.096503***	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.809312	**13**
3	***449.127152***	225.067214	432.100603	216.553940			**C**	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.780023	**12**
4	***546.179916***	273.593596	529.153367	265.080322			**P**	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.764698	**11**
5	***617.217030***	309.112153	600.190481	300.598879			**A**	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.238316	**10**
6	***674.238494***	337.622885	657.211945	329.109611			**G**	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.719759	**9**
7	745.275608	373.141442	728.249059	364.628168			**A**	**801.421343**	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
8	***816.312722***	408.659999	799.286173	400.146725			**A**	**730.384229**	365.695753	713.357680	357.182478	712.373664	356.690470	**7**
9	***929.396786***	465.202031	912.370237	456.688757			**L**	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.171913	**6**
10	***1057.455364***	529.231320	1040.428815	520.718046			**Q**	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.629881	**5**
11	***1128.492478***	564.749877	1111.465929	556.236603			**A**	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.600592	**4**
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	**347.167359**	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
13	***1300.540885***	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	**232.140416**	116.573846	215.113867	108.060571			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



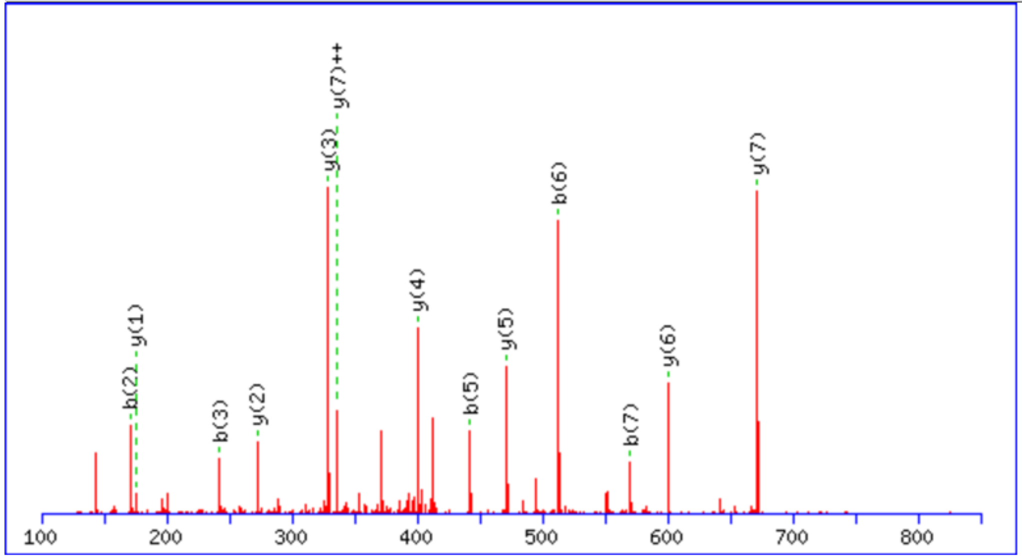
Peptide View

MS/MS Fragmentation of **GLAEAAGPR**
Found in **IPI00290826**, Tax_Id=9606 Gene_Symbol=FAM174A Membrane protein FAM174A
Experiment: 09 - S_C-3 **Fraction:** S_C-3

Match to Query 1336: 840.445448 from(421.230000,2+)
Title: OECHL100317_13.4166.4166.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_13.raw
Monoisotopic mass of neutral peptide Mr(calc): 840.445343**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 0.00028**Matches :** 13/64 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			**G**							**9**
2	**171.112804**	86.060040			**L**	784.431179	392.719228	767.404630	384.205953	766.420614	383.713945	**8**
3	**242.149918**	121.578597			**A**	***671.347115***	336.177196	654.320566	327.663921	653.336550	327.171913	**7**
4	371.192511	186.099894	353.181946	177.094611	**E**	***600.310001***	300.658639	583.283452	292.145364	582.299436	291.653356	**6**
5	**442.229625**	221.618450	424.219060	212.613168	**A**	***471.267408***	236.137342	454.240859	227.624067			**5**
6	**513.266739**	257.137008	495.256174	248.131725	**A**	***400.230294***	200.618785	383.203745	192.105510			**4**

7	**570.288203**	285.647740	552.277638	276.642457	**G**	***329.193180***	165.100228	312.166631	156.586953			**3**
8	667.340967	334.174122	649.330402	325.168839	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
9					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



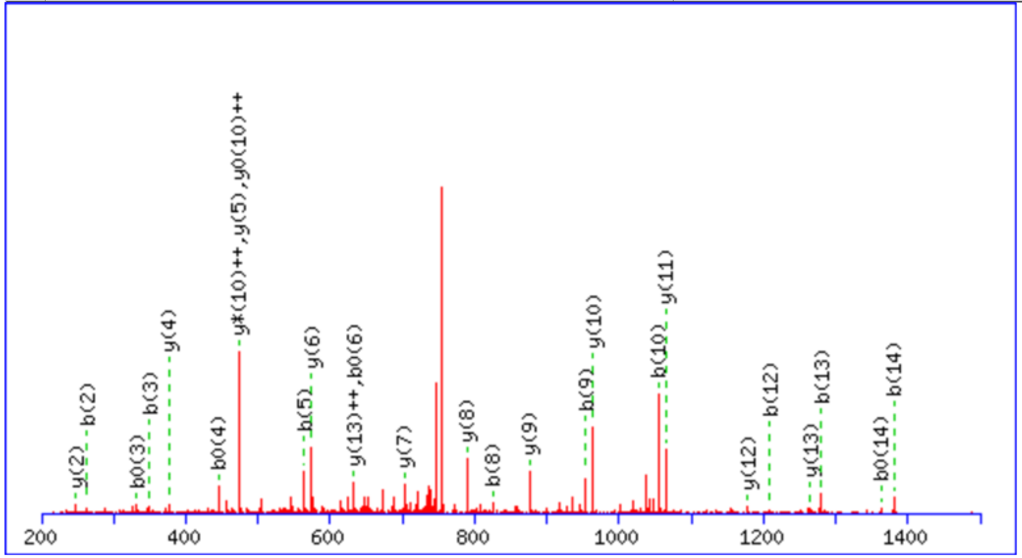
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 33 - OPA-3 **Fraction:** OPA-3

Match to Query 10998: 1525.726448 from(763.870500,2+)
Title: OECHL100317_11.11317.11317.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 92
Expect: 7.6e-008**Matches :** 27/150 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	***350.134661***	175.570968			332.124096	166.565686	**S**	***1264.637937***	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**

4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	**9**
8	***825.362488***	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.203410	**8**
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	**7**
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	**6**
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	**5**
12	***1208.542973***	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	**4**
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	**3**
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**

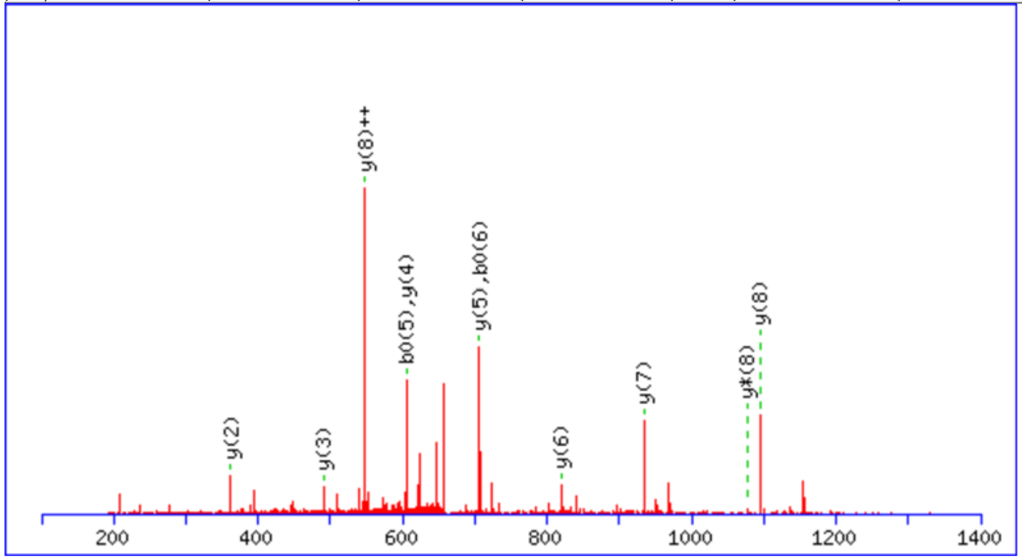


Peptide View

MS/MS Fragmentation of **SFCDLTDEWR**
Found in **IPI00010193**, Tax_Id=9606 Gene_Symbol=IFNAR2 Isoform 1 of Interferon-alpha/beta receptor beta chain
Experiment: 33 - OPA-3 **Fraction:** OPA-3

Match to Query 8986: 1327.550848 from(664.782700,2+)
Title: OECHL100317_11.17385.17385.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1327.550308**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 3.6e-005**Matches :** 11/86 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**10**
2	235.107718	118.057497	217.097153	109.052214	**F**	1241.525550	621.266413	1224.499001	612.753138	1223.514985	612.261130	**9**
3	395.138367	198.072821	377.127802	189.067539	**C**	***1094.457136***	547.732206	1077.430587	539.218932	1076.446571	538.726924	**8**
4	510.165310	255.586293	492.154745	246.581010	**D**	***934.426487***	467.716882	917.399938	459.203607	916.415922	458.711599	**7**
5	623.249374	312.128325	605.238809	303.123043	**L**	***819.399544***	410.203410	802.372995	401.690135	801.388979	401.198127	**6**
6	724.297053	362.652165	706.286488	353.646882	**T**	***706.315480***	353.661378	689.288931	345.148103	688.304915	344.656095	**5**
7	839.323996	420.165636	821.313431	411.160353	**D**	***605.267801***	303.137539	588.241252	294.624264	587.257236	294.132256	**4**
8	968.366589	484.686933	950.356024	475.681650	**E**	***490.240858***	245.624067	473.214309	237.110792	472.230293	236.618784	**3**
9	1154.445902	577.726589	1136.435337	568.721306	**W**	***361.198265***	181.102770	344.171716	172.589496			**2**
10					**R**	175.118952	88.063114	158.092403	79.549839			**1**

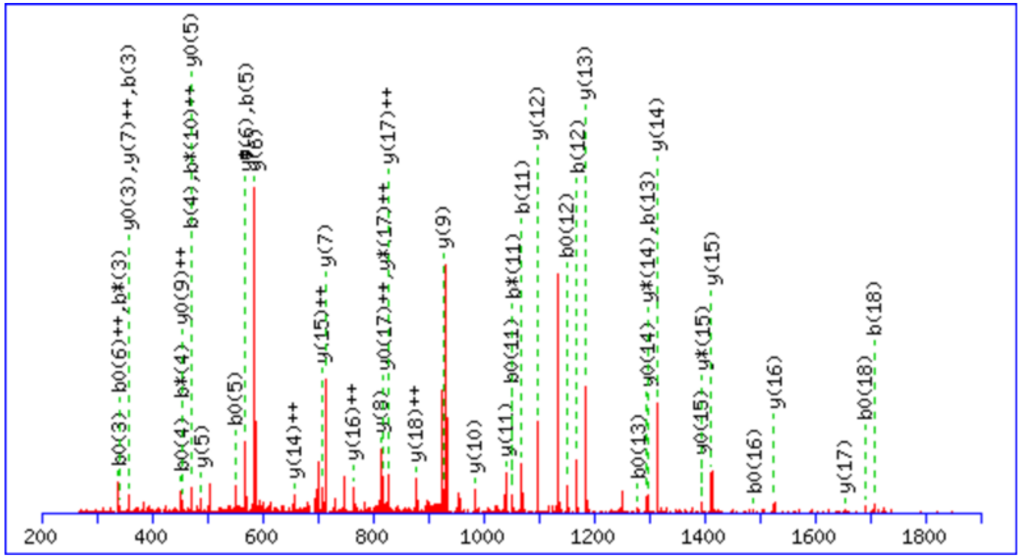


Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**
Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
Experiment: 33 - OPA-3 **Fraction:** OPA-3

Match to Query 14304: 1881.031248 from(941.522900,2+)
Title: OECHL100317_11.14136.14136.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66
Expect: 1.6e-005**Matches :** 50/208 fragment ions using 93 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	**E**							**19**
2	229.118283	115.062780			211.107718	106.057497	**V**	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.996686	**18**
3	**357.176861**	179.092069	340.150312	170.578794	339.166296	170.086786	**Q**	***1653.928246***	827.467761	1636.901697	818.954487	1635.917681	818.462479	**17**
4	**470.260925**	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.433190	**16**
5	**569.329339**	285.168308	552.302790	276.655033	551.318774	276.163025	**V**	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.891158	**15**
6	698.371932	349.689604	681.345383	341.176330	680.361367	340.684322	**E**	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.356951	**14**
7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	**S**	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.835654	**13**
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	**G**	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.319640	**12**
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	**G**	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.808908	**11**
10	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	**G**	***983.599641***	492.303459	966.573092	483.790184	965.589076	483.298176	**10**
11	**1069.552416**	535.279846	1052.525867	526.766572	1051.541851	526.274564	**L**	***926.578177***	463.792727	909.551628	455.279452	908.567612	454.787444	**9**
12	**1168.620830**	584.814053	1151.594281	576.300779	1150.610265	575.808771	**V**	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.245412	**8**
13	**1296.715793**	648.861535	1279.689244	640.348260	1278.705228	639.856252	**K**	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.711205	**7**
14	1393.768557	697.387917	1376.742008	688.874642	1375.757992	688.382634	**P**	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.663723	**6**
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	**G**	***489.277972***	245.142624	472.251423	236.629349	471.267407	236.137341	**5**
16	1507.811485	754.409381	1490.784936	745.896106	1489.800920	745.404098	**G**	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	**4**
17	1594.843513	797.925395	1577.816964	789.412120	1576.832948	788.920112	**S**	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	**3**
18	**1707.927577**	854.467427	1690.901028	845.954152	1689.917012	845.462144	**L**	288.203016	144.605146	271.176467	136.091871			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



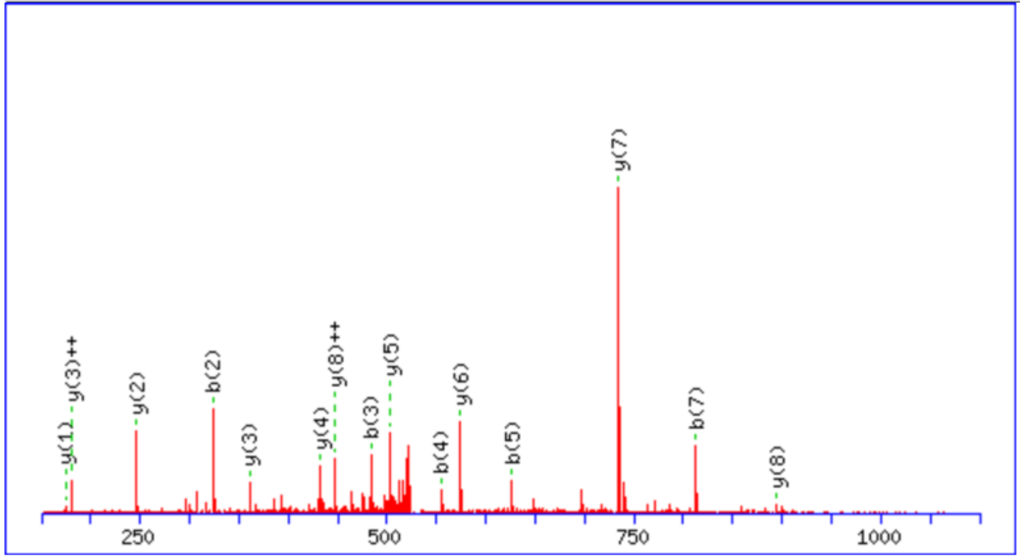
Peptide View

MS/MS Fragmentation of **YCCAAADAR**
Found in **IPI00455600**, Tax_Id=9606 Gene_Symbol=SHISA3 Protein shisa-3 homolog
Experiment: 33 - OPA-3 **Fraction:** OPA-3

Match to Query 4752: 1056.413048 from(529.213800,2+)
Title: OECHL100317_11.3574.3574.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1056.411682**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 5e-006**Matches :** 15/64 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			**Y**							**9**
2	**324.101254**	162.554265			**C**	***894.355649***	447.681462	877.329100	439.168188	876.345084	438.676180	**8**
3	**484.131903**	242.569590			**C**	***734.325000***	367.666138	717.298451	359.152863	716.314435	358.660855	**7**
4	**555.169017**	278.088147			**A**	***574.294351***	287.650813	557.267802	279.137539	556.283786	278.645531	**6**
5	**626.206131**	313.606704			**A**	***503.257237***	252.132256	486.230688	243.618982	485.246672	243.126974	**5**
6	697.243245	349.125261			**A**	***432.220123***	216.613699	415.193574	208.100425	414.209558	207.608417	**4**

7	**812.270188**	406.638732	794.259623	397.633449	**D**	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	**3**
8	883.307302	442.157289	865.296737	433.152006	**A**	***246.156066***	123.581671	229.129517	115.068396			**2**
9					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



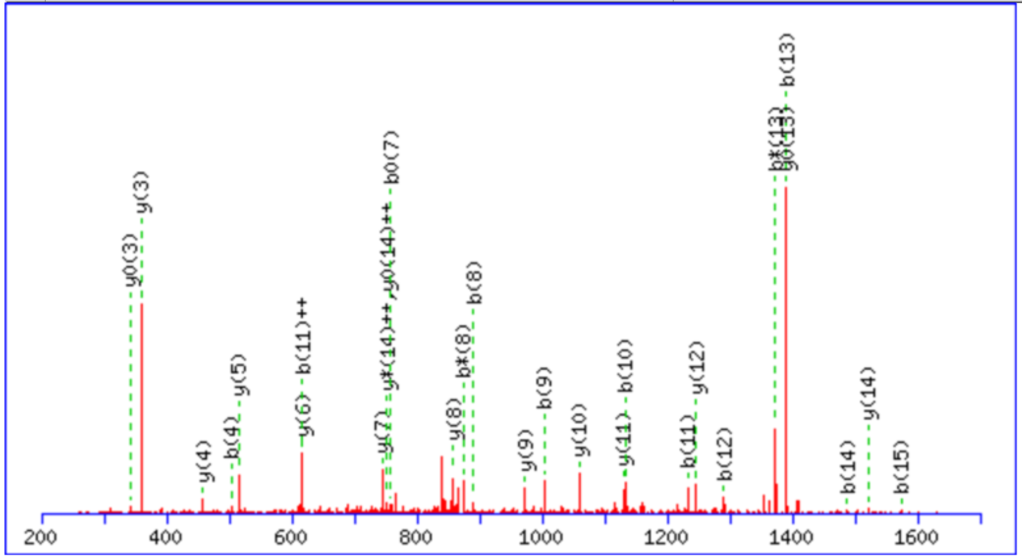
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 33 - OPA-3 **Fraction:** OPA-3

Match to Query 13240: 1746.915648 from(874.465100,2+)
Title: OECHL100317_11.17504.17504.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 84
Expect: 4e-007**Matches :** 28/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**

4	***503.322797***	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	618.349740	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	689.386854	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	***890.461809***	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



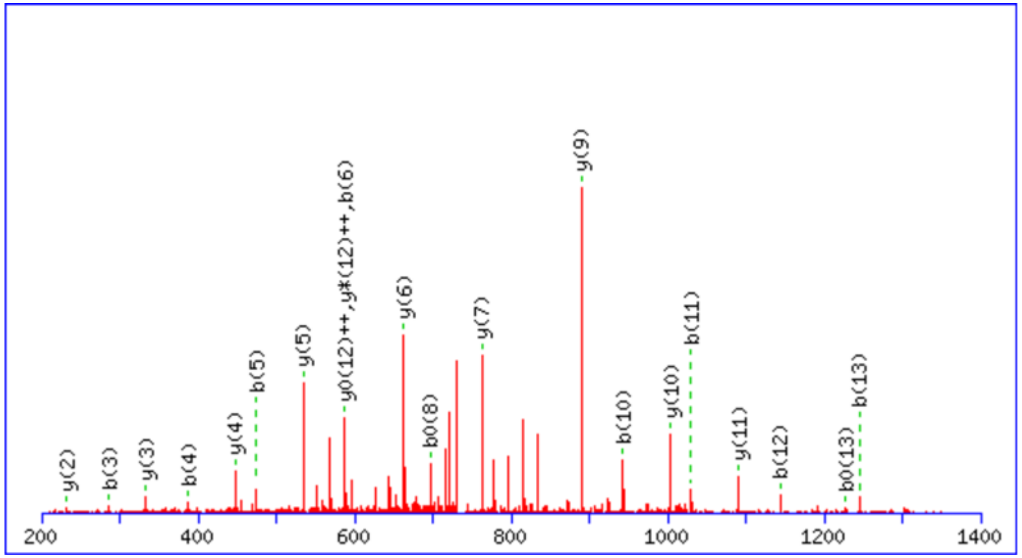
Peptide View

MS/MS Fragmentation of **GLDTSLGAVQSDTGR**

Found in **IPI00289931**, Tax_Id=9606 Gene_Symbol=MADCAM1 MADCAM1 protein
Experiment: 33 - OPA-3 **Fraction:** OPA-3

Match to Query 10502: 1475.720848 from(738.867700,2+)
Title: OECHL100317_11.11812.11812.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1475.721619**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 82
Expect: 9.2e-007**Matches :** 21/142 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	58.028740	29.518008					**G**							**15**
2	171.112804	86.060040					**L**	1419.707414	710.357345	1402.680865	701.844071	1401.696849	701.352063	**14**
3	***286.139747***	143.573512			268.129182	134.568229	**D**	1306.623350	653.815313	1289.596801	645.302039	1288.612785	644.810031	**13**
4	***387.187426***	194.097351			369.176861	185.092069	**T**	1191.596407	596.301842	1174.569858	587.788567	1173.585842	587.296559	**12**
5	***474.219454***	237.613365			456.208889	228.608082	**S**	***1090.548728***	545.778002	1073.522179	537.264728	1072.538163	536.772719	**11**
6	***587.303518***	294.155397			569.292953	285.150115	**L**	***1003.516700***	502.261988	986.490151	493.748714	985.506135	493.256706	**10**
7	644.324982	322.666129			626.314417	313.660847	**G**	***890.432636***	445.719956	873.406087	437.206682	872.422071	436.714674	**9**
8	715.362096	358.184686			697.351531	349.179404	**A**	833.411172	417.209224	816.384623	408.695950	815.400607	408.203942	**8**
9	814.430510	407.718893			796.419945	398.713611	**V**	***762.374058***	381.690667	745.347509	373.177393	744.363493	372.685385	**7**
10	***942.489088***	471.748182	925.462539	463.234908	924.478523	462.742900	**Q**	***663.305644***	332.156460	646.279095	323.643186	645.295079	323.151178	**6**
11	***1029.521116***	515.264196	1012.494567	506.750922	1011.510551	506.258914	**S**	***535.247066***	268.127171	518.220517	259.613897	517.236501	259.121889	**5**
12	***1144.548059***	572.777668	1127.521510	564.264393	1126.537494	563.772385	**D**	***448.215038***	224.611157	431.188489	216.097882	430.204473	215.605874	**4**
13	***1245.595738***	623.301507	1228.569189	614.788233	1227.585173	614.296225	**T**	***333.188095***	167.097685	316.161546	158.584411	315.177530	158.092403	**3**
14	1302.617202	651.812239	1285.590653	643.298965	1284.606637	642.806957	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



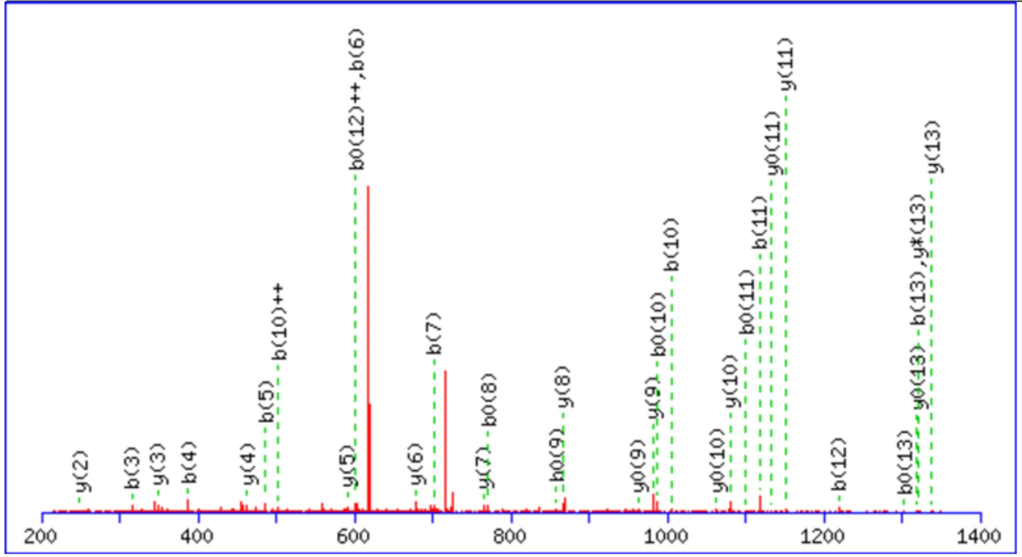
Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 33 - OPA-3 **Fraction:** OPA-3

Match to Query 10388: 1465.678048 from(733.846300,2+)
Title: OECHL100317_11.10246.10246.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 49 **Expect:** 0.001**Matches :** 32/128 fragment ions using 84 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	S							14
2	245.076812	123.042044	227.066247	114.036761	D	***1337.643082***	669.325179	1320.616533	660.811905	1319.632517	660.319897	13
3	**316.113926**	158.560601	298.103361	149.555319	A	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	12
4	**387.151040**	194.079158	369.140475	185.073875	A	***1151.579025***	576.293151	1134.552476	567.779876	1133.568460	567.287868	11
5	**486.219454**	243.613365	468.208889	234.608082	V	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	10
6	**601.246397**	301.126837	583.235832	292.121554	D	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	9

7	**702.294076**	351.650676	684.283511	342.645394	**T**	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	***765.398875***	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	876.358132	438.682704	858.347567	429.677421	**S**	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	**1005.400725**	503.204001	987.390160	494.198718	**E**	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	**1118.484789**	559.746033	1100.474224	550.740750	**I**	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	**1219.532468**	610.269872	1201.521903	601.264590	**T**	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	**1320.580147**	660.793712	1302.569582	651.788429	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**



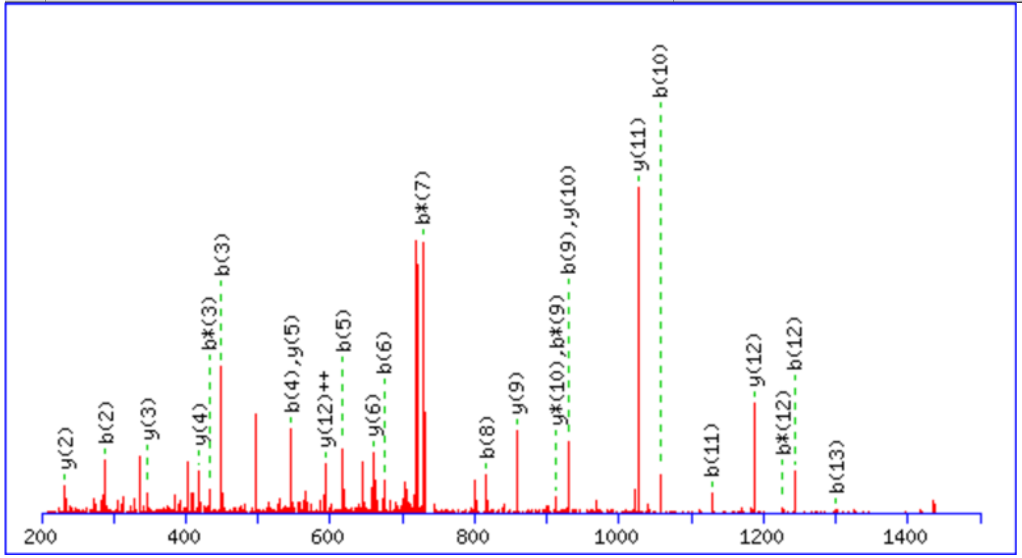
Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 33 - OPA-3 **Fraction:** OPA-3

Match to Query 10473: 1473.645448 from(737.830000,2+)
Title: OECHL100317_11.8060.8060.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 68

Expect: 7.6e-006**Matches :** 26/128 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	161.037925	81.022600					C							14
2	***289.096503***	145.051890	272.069954	136.538615			Q	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.809312	13
3	***449.127152***	225.067214	432.100603	216.553940			C	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.780023	12
4	***546.179916***	273.593596	529.153367	265.080322			P	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.764698	11
5	***617.217030***	309.112153	600.190481	300.598879			A	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.238316	10
6	***674.238494***	337.622885	657.211945	329.109611			G	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.719759	9
7	745.275608	373.141442	728.249059	364.628168			A	801.421343	401.214310	784.394794	392.701035	783.410778	392.209027	8
8	***816.312722***	408.659999	799.286173	400.146725			A	730.384229	365.695753	713.357680	357.182478	712.373664	356.690470	7
9	***929.396786***	465.202031	912.370237	456.688757			L	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.171913	6
10	***1057.455364***	529.231320	1040.428815	520.718046			Q	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.629881	5
11	***1128.492478***	564.749877	1111.465929	556.236603			A	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.600592	4
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	D	**347.167359**	174.087317	330.140810	165.574043	329.156794	165.082035	3
13	***1300.540885***	650.774081	1283.514336	642.260806	1282.530320	641.768798	G	**232.140416**	116.573846	215.113867	108.060571			2
14							R	175.118952	88.063114	158.092403	79.549839			1

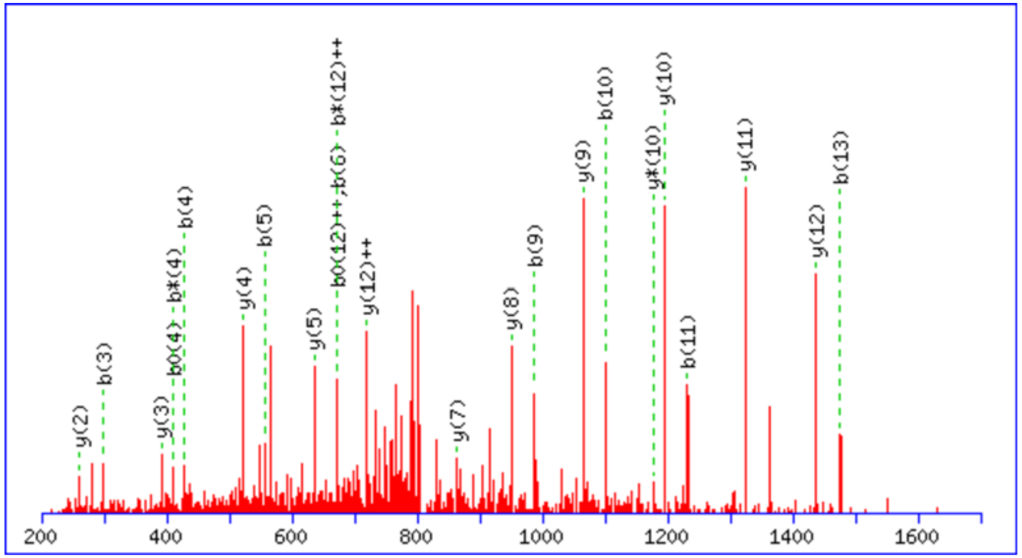


Peptide View

MS/MS Fragmentation of **GKIEEDSEVLMMIK**
Found in **IPI00034319**, Tax_Id=9606 Gene_Symbol=CUTA Isoform A of Protein CutA
Experiment: 33 - OPA-3 **Fraction:** OPA-3

Match to Query 11854: 1620.811848 from(811.413200,2+)
Title: OECHL100317_11.17578.17578.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1620.810242**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65
Expect: 4.2e-005**Matches :** 24/136 fragment ions using 41 most intense peaks (help)

#	**b**	**b^{++}**	**b***	**b^{*++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	58.028740	29.518008					**G**							**14**
2	186.123703	93.565489	169.097154	85.052215			**K**	1564.796093	782.901684	1547.769544	774.388410	1546.785528	773.896402	**13**
3	**299.207767**	150.107521	282.181218	141.594247			**I**	***1436.701130***	718.854203	1419.674581	710.340929	1418.690565	709.848920	**12**
4	**428.250360**	214.628818	411.223811	206.115544	410.239795	205.623536	**E**	***1323.617066***	662.312171	1306.590517	653.798896	1305.606501	653.306888	**11**
5	**557.292953**	279.150115	540.266404	270.636840	539.282388	270.144832	**E**	***1194.574473***	597.790874	1177.547924	589.277600	1176.563908	588.785592	**10**
6	**672.319896**	336.663586	655.293347	328.150312	654.309331	327.658304	**D**	***1065.531880***	533.269578	1048.505331	524.756303	1047.521315	524.264295	**9**
7	759.351924	380.179600	742.325375	371.666326	741.341359	371.174318	**S**	***950.504937***	475.756106	933.478388	467.242832	932.494372	466.750824	**8**
8	888.394517	444.700897	871.367968	436.187622	870.383952	435.695614	**E**	***863.472909***	432.240092	846.446360	423.726818	845.462344	423.234810	**7**
9	**987.462931**	494.235104	970.436382	485.721829	969.452366	485.229821	**V**	734.430316	367.718796	717.403767	359.205521			**6**
10	**1100.546995**	550.777135	1083.520446	542.263861	1082.536430	541.771853	**L**	***635.361902***	318.184589	618.335353	309.671314			**5**
11	**1231.587480**	616.297378	1214.560931	607.784104	1213.576915	607.292095	**M**	***522.277838***	261.642557	505.251289	253.129282			**4**
12	1362.627965	681.817620	1345.601416	673.304346	1344.617400	672.812338	**M**	***391.237353***	196.122314	374.210804	187.609040			**3**
13	**1475.712029**	738.359652	1458.685480	729.846378	1457.701464	729.354370	**I**	***260.196868***	130.602072	243.170319	122.088797			**2**
14							**K**	147.112804	74.060040	130.086255	65.546765			**1**



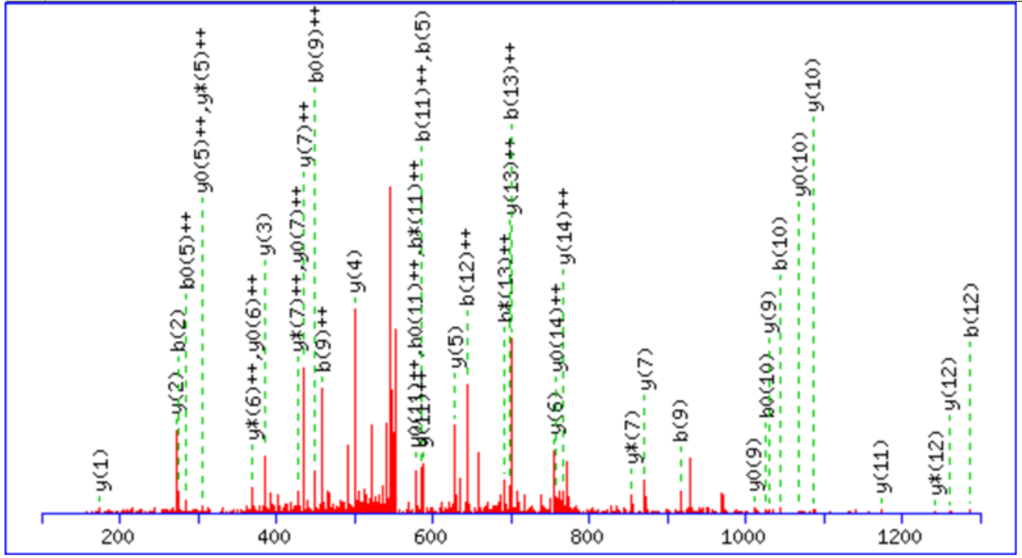
Peptide View

MS/MS Fragmentation of **HHHSSGGTDQQDIPR**
Found in **IPI00790100**, Tax_Id=9606 Gene_Symbol=PRH1;PRR4;PRH2 cDNA FLJ54977, weakly similar to Proline-rich protein 4
Experiment: 33 - OPA-3 **Fraction:** OPA-3

Match to Query 12451: 1670.749572 from(557.923800,3+)
Title: OECHL100317_11.2959.2959.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_11.raw
Monoisotopic mass of neutral peptide Mr(calc): 1670.750961**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 6.1e-005**Matches :** 42/138 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	138.066188	69.536732					**H**							**15**
2	**275.125100**	138.066188					**H**	1534.699309	767.853293	1517.672760	759.340018	1516.688744	758.848010	**14**
3	412.184012	206.595644					**H**	1397.640397	699.323837	1380.613848	690.810562	1379.629832	690.318554	**13**
4	499.216040	250.111658			481.205475	241.106375	**S**	***1260.581485***	630.794381	1243.554936	622.281106	1242.570920	621.789098	**12**
5	**586.248068**	293.627672			568.237503	284.622390	**S**	***1173.549457***	587.278367	1156.522908	578.765092	1155.538892	578.273084	**11**
6	643.269532	322.138404			625.258967	313.133122	**G**	***1086.517429***	543.762353	1069.490880	535.249078	1068.506864	534.757070	**10**

7	700.290996	350.649136			682.280431	341.643854	**G**	***1029.495965***	515.251621	1012.469416	506.738346	1011.485400	506.246338	**9**
8	801.338675	401.172976			783.328110	392.167693	**T**	972.474501	486.740889	955.447952	478.227614	954.463936	477.735606	**8**
9	**916.365618**	**458.686447**			898.355053	449.681165	**D**	***871.426822***	436.217049	854.400273	427.703775	853.416257	427.211767	**7**
10	**1044.424196**	522.715736	1027.397647	514.202462	1026.413631	513.710454	**Q**	***756.399879***	378.703578	739.373330	370.190303	738.389314	369.698295	**6**
11	1172.482774	**586.745025**	1155.456225	578.231751	1154.472209	577.739743	**Q**	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	**5**
12	**1287.509717**	**644.258497**	1270.483168	635.745222	1269.499152	635.253214	**D**	***500.282723***	250.644999	483.256174	242.131725	482.272158	241.639717	**4**
13	1400.593781	**700.800529**	1383.567232	692.287254	1382.583216	691.795246	**I**	***385.255780***	193.131528	368.229231	184.618253			**3**
14	1497.646545	749.326911	1480.619996	740.813636	1479.635980	740.321628	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
15							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



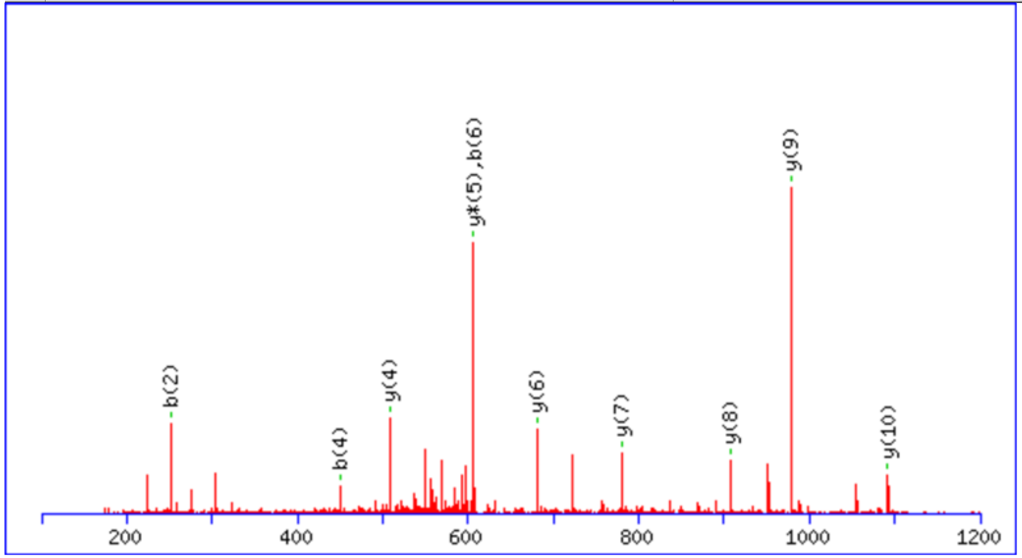
Peptide View

MS/MS Fragmentation of **HLAQVGDSMDR**
Found in **IPI00413587**, Tax_Id=9606 Gene_Symbol=BID Isoform 1 of BH3-interacting domain death agonist
Experiment: 33 - OPA-3 **Fraction:** OPA-3

Match to Query 7639: 1227.567048 from(614.790800,2+)
Title: OECHL100317_11.5842.5842.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_11.raw

Monoisotopic mass of neutral peptide Mr(calc): 1227.566620**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00071**Matches :** 10/100 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	138.066188	69.536732					H							11
2	**251.150252**	126.078764					L	***1091.514985***	546.261131	1074.488436	537.747856	1073.504420	537.255848	10
3	322.187366	161.597321					A	***978.430921***	489.719099	961.404372	481.205824	960.420356	480.713816	9
4	**450.245944**	225.626610	433.219395	217.113335			Q	***907.393807***	454.200542	890.367258	445.687267	889.383242	445.195259	8
5	549.314358	275.160817	532.287809	266.647542			V	***779.335229***	390.171253	762.308680	381.657978	761.324664	381.165970	7
6	**606.335822**	303.671549	589.309273	295.158275			G	***680.266815***	340.637046	663.240266	332.123771	662.256250	331.631763	6
7	721.362765	361.185021	704.336216	352.671746	703.352200	352.179738	D	623.245351	312.126314	606.218802	303.613039	605.234786	303.121031	5
8	808.394793	404.701034	791.368244	396.187760	790.384228	395.695752	S	***508.218408***	254.612842	491.191859	246.099567	490.207843	245.607559	4
9	939.435278	470.221277	922.408729	461.708002	921.424713	461.215994	M	421.186380	211.096828	404.159831	202.583553	403.175815	202.091546	3
10	1054.462221	527.734749	1037.435672	519.221474	1036.451656	518.729466	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
11							R	175.118952	88.063114	158.092403	79.549839			1



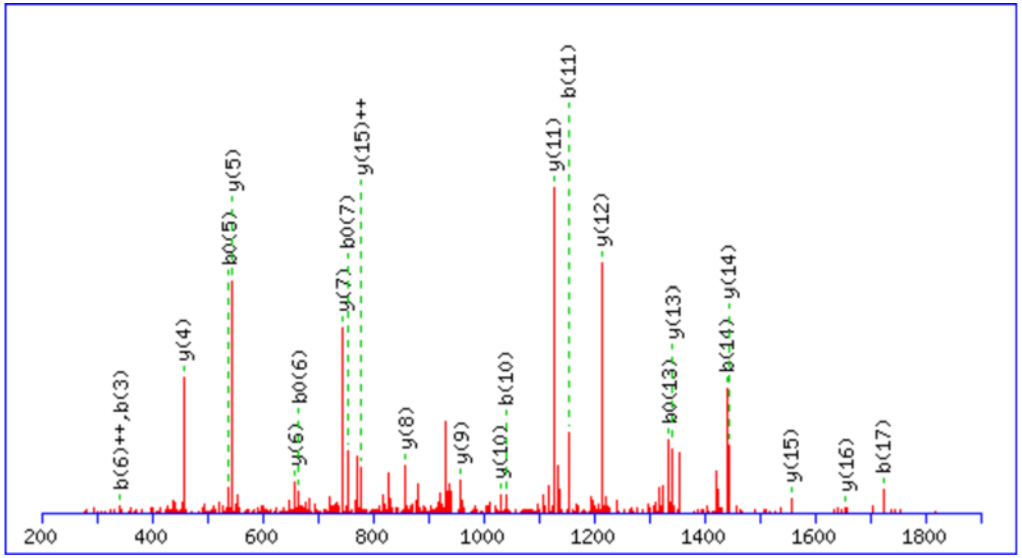
Peptide View

MS/MS Fragmentation of **EIVLTQSPATLSLSPGER**

Found in **IPI00816799**, Tax_Id=9606 Gene_Symbol=- Rheumatoid factor D5 light chain (Fragment)
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 14798: 1897.017248 from(949.515900,2+)
Title: OECHL100317_09.16384.16384.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1897.015640**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 113
Expect: 4.5e-010**Matches :** 24/192 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	**E**							**18**
2	243.133933	122.070605			225.123368	113.065322	**I**	1768.980341	884.993808	1751.953792	876.480534	1750.969776	875.988526	**17**
3	**342.202347**	171.604812			324.191782	162.599529	**V**	***1655.896277***	828.451776	1638.869728	819.938502	1637.885712	819.446494	**16**
4	455.286411	228.146844			437.275846	219.141561	**L**	***1556.827863***	778.917569	1539.801314	770.404295	1538.817298	769.912287	**15**
5	556.334090	278.670683			538.323525	269.665401	**T**	***1443.743799***	722.375537	1426.717250	713.862263	1425.733234	713.370255	**14**
6	684.392668	342.699972	667.366119	334.186698	666.382103	333.694690	**Q**	***1342.696120***	671.851698	1325.669571	663.338423	1324.685555	662.846415	**13**
7	771.424696	386.215986	754.398147	377.702712	753.414131	377.210704	**S**	***1214.637542***	607.822409	1197.610993	599.309134	1196.626977	598.817126	**12**
8	868.477460	434.742368	851.450911	426.229094	850.466895	425.737086	**P**	***1127.605514***	564.306395	1110.578965	555.793120	1109.594949	555.301112	**11**
9	939.514574	470.260925	922.488025	461.747651	921.504009	461.255643	**A**	***1030.552750***	515.780013	1013.526201	507.266738	1012.542185	506.774730	**10**
10	**1040.562253**	520.784765	1023.535704	512.271490	1022.551688	511.779482	**T**	***959.515636***	480.261456	942.489087	471.748181	941.505071	471.256173	**9**
11	**1153.646317**	577.326797	1136.619768	568.813522	1135.635752	568.321514	**L**	***858.467957***	429.737616	841.441408	421.224342	840.457392	420.732334	**8**
12	1240.678345	620.842811	1223.651796	612.329536	1222.667780	611.837528	**S**	***745.383893***	373.195585	728.357344	364.682310	727.373328	364.190302	**7**
13	1353.762409	677.384842	1336.735860	668.871568	1335.751844	668.379560	**L**	***658.351865***	329.679570	641.325316	321.166296	640.341300	320.674288	**6**
14	**1440.794437**	720.900857	1423.767888	712.387582	1422.783872	711.895574	**S**	***545.267801***	273.137539	528.241252	264.624264	527.257236	264.132256	**5**
15	1537.847201	769.427239	1520.820652	760.913964	1519.836636	760.421956	**P**	***458.235773***	229.621524	441.209224	221.108250	440.225208	220.616242	**4**
16	1594.868665	797.937971	1577.842116	789.424696	1576.858100	788.932688	**G**	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	**3**
17	**1723.911258**	862.459267	1706.884709	853.945992	1705.900693	853.453984	**E**	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**



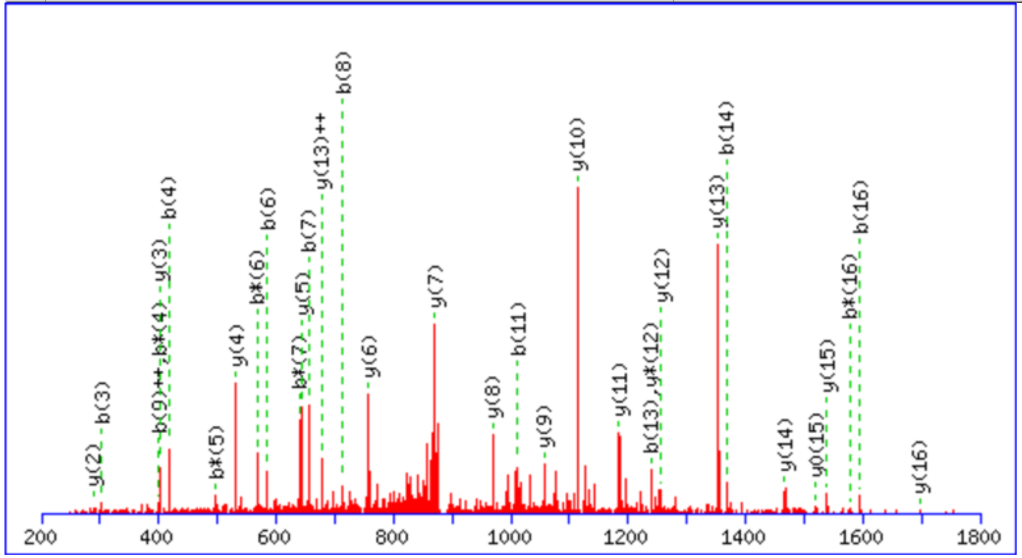
Peptide View

MS/MS Fragmentation of **ACANPAAGSVILLENLR**
Found in **IPI00169383**, Tax_Id=9606 Gene_Symbol=PGK1 Phosphoglycerate kinase 1
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 13940: 1767.931448 from(884.973000,2+)
Title: OECHL100317_09.19797.19797.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1767.930115**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 107
Expect: 2.1e-009**Matches :** 33/164 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	72.044390	36.525833					**A**							**17**
2	232.075039	116.541158					**C**	***1697.900316***	849.453796	1680.873767	840.940521	1679.889751	840.448513	**16**
3	**303.112153**	152.059714					**A**	***1537.869667***	769.438471	1520.843118	760.925197	1519.859102	760.433189	**15**
4	**417.155080**	209.081178	400.128531	200.567904			**N**	***1466.832553***	733.919914	1449.806004	725.406640	1448.821988	724.914632	**14**
5	514.207844	257.607560	497.181295	249.094286			**P**	***1352.789626***	676.898451	1335.763077	668.385176	1334.779061	667.893168	**13**
6	**585.244958**	293.126117	568.218409	284.612843			**A**	***1255.736862***	628.372069	1238.710313	619.858794	1237.726297	619.366786	**12**

7	**656.282072**	328.644674	639.255523	320.131399			A	***1184.699748***	592.853512	1167.673199	584.340237	1166.689183	583.848229	11
8	**713.303536**	357.155406	696.276987	348.642132			G	***1113.662634***	557.334955	1096.636085	548.821680	1095.652069	548.329672	10
9	800.335564	400.671420	783.309015	392.158145	782.324999	391.666137	S	***1056.641170***	528.824223	1039.614621	520.310948	1038.630605	519.818940	9
10	899.403978	450.205627	882.377429	441.692352	881.393413	441.200344	V	***969.609142***	485.308209	952.582593	476.794934	951.598577	476.302926	8
11	**1012.488042**	506.747659	995.461493	498.234384	994.477477	497.742376	I	***870.540728***	435.774002	853.514179	427.260727	852.530163	426.768719	7
12	1125.572106	563.289691	1108.545557	554.776416	1107.561541	554.284408	L	***757.456664***	379.231970	740.430115	370.718695	739.446099	370.226687	6
13	**1238.656170**	619.831723	1221.629621	611.318448	1220.645605	610.826440	L	***644.372600***	322.689938	627.346051	314.176663	626.362035	313.684655	5
14	**1367.698763**	684.353019	1350.672214	675.839745	1349.688198	675.347737	E	***531.288536***	266.147906	514.261987	257.634631	513.277971	257.142623	4
15	1481.741690	741.374483	1464.715141	732.861208	1463.731125	732.369200	N	***402.245943***	201.626609	385.219394	193.113335			3
16	**1594.825754**	797.916515	1577.799205	789.403240	1576.815189	788.911232	L	***288.203016***	144.605146	271.176467	136.091871			2
17							R	175.118952	88.063114	158.092403	79.549839			1

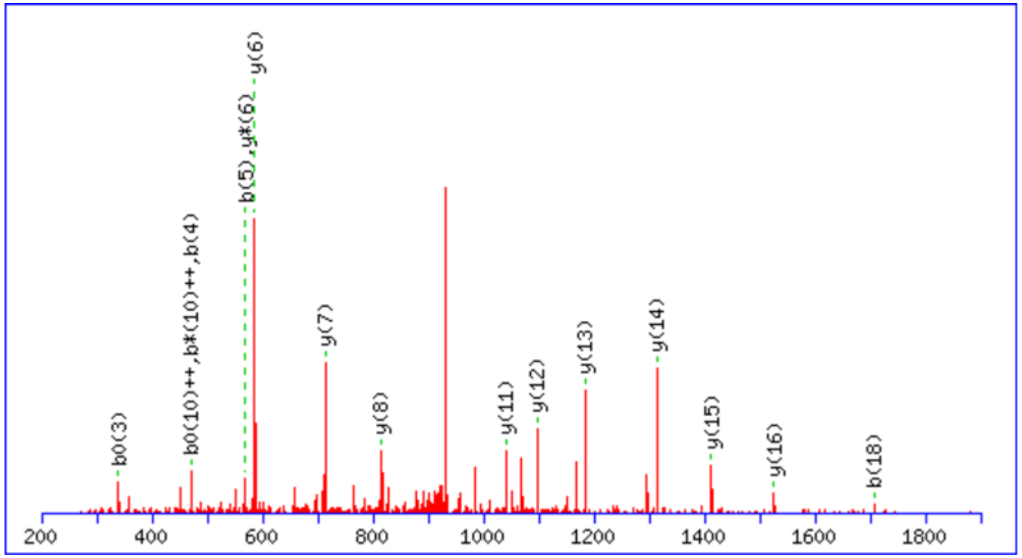


Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**
Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 14687: 1881.030048 from(941.522300,2+)
Title: OECHL100317_09.13780.13780.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 78
Expect: 1e-006**Matches :** 16/208 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	130.049869	65.528572			112.039304	56.523290	**E**							**19**
2	229.118283	115.062780			211.107718	106.057497	**V**	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.996686	**18**
3	357.176861	179.092069	340.150312	170.578794	339.166296	170.086786	**Q**	1653.928246	827.467761	1636.901697	818.954487	1635.917681	818.462479	**17**
4	**470.260925**	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.433190	**16**
5	**569.329339**	285.168308	552.302790	276.655033	551.318774	276.163025	**V**	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.891158	**15**
6	698.371932	349.689604	681.345383	341.176330	680.361367	340.684322	**E**	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.356951	**14**
7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	**S**	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.835654	**13**
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	**G**	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.319640	**12**
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	**G**	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.808908	**11**
10	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	**G**	983.599641	492.303459	966.573092	483.790184	965.589076	483.298176	**10**
11	1069.552416	535.279846	1052.525867	526.766572	1051.541851	526.274564	**L**	926.578177	463.792727	909.551628	455.279452	908.567612	454.787444	**9**
12	1168.620830	584.814053	1151.594281	576.300779	1150.610265	575.808771	**V**	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.245412	**8**
13	1296.715793	648.861535	1279.689244	640.348260	1278.705228	639.856252	**K**	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.711205	**7**
14	1393.768557	697.387917	1376.742008	688.874642	1375.757992	688.382634	**P**	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.663723	**6**
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	**G**	489.277972	245.142624	472.251423	236.629349	471.267407	236.137341	**5**
16	1507.811485	754.409381	1490.784936	745.896106	1489.800920	745.404098	**G**	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	**4**
17	1594.843513	797.925395	1577.816964	789.412120	1576.832948	788.920112	**S**	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	**3**
18	**1707.927577**	854.467427	1690.901028	845.954152	1689.917012	845.462144	**L**	288.203016	144.605146	271.176467	136.091871			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



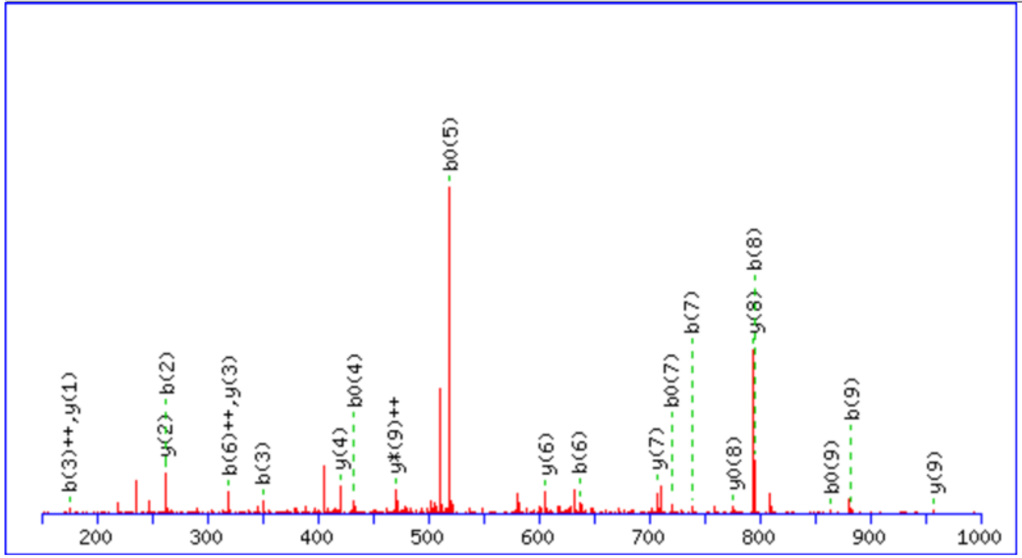
Peptide View

MS/MS Fragmentation of **VYSTSVTGSR**
Found in **IPI00010402**, Tax_Id=9606 Gene_Symbol=SH3BGRL3 Putative uncharacterized protein
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 4919: 1055.523448 from(528.769000,2+)
Title: OECHL100317_09.4489.4489.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1055.524750**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52
Expect: 0.00057**Matches :** 22/84 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.075690	50.541483			**V**							**10**
2	**263.139019**	132.073148			**Y**	***957.463601***	479.235439	940.437052	470.722164	939.453036	470.230156	**9**
3	**350.171047**	175.589161	332.160482	166.583879	**S**	***794.400272***	397.703774	777.373723	389.190499	776.389707	388.698491	**8**
4	451.218726	226.113001	433.208161	217.107719	**T**	***707.368244***	354.187760	690.341695	345.674486	689.357679	345.182478	**7**
5	538.250754	269.629015	520.240189	260.623733	**S**	***606.320565***	303.663921	589.294016	295.150646	588.310000	294.658638	**6**
6	**637.319168**	319.163222	619.308603	310.157940	**V**	519.288537	260.147907	502.261988	251.634632	501.277972	251.142624	**5**

7	**738.366847**	369.687062	720.356282	360.681779	**T**	***420.220123***	210.613699	403.193574	202.100425	402.209558	201.608417	**4**
8	**795.388311**	398.197794	777.377746	389.192511	**G**	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	**3**
9	**882.420339**	441.713808	864.409774	432.708525	**S**	***262.150980***	131.579128	245.124431	123.065853	244.140415	122.573845	**2**
10					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



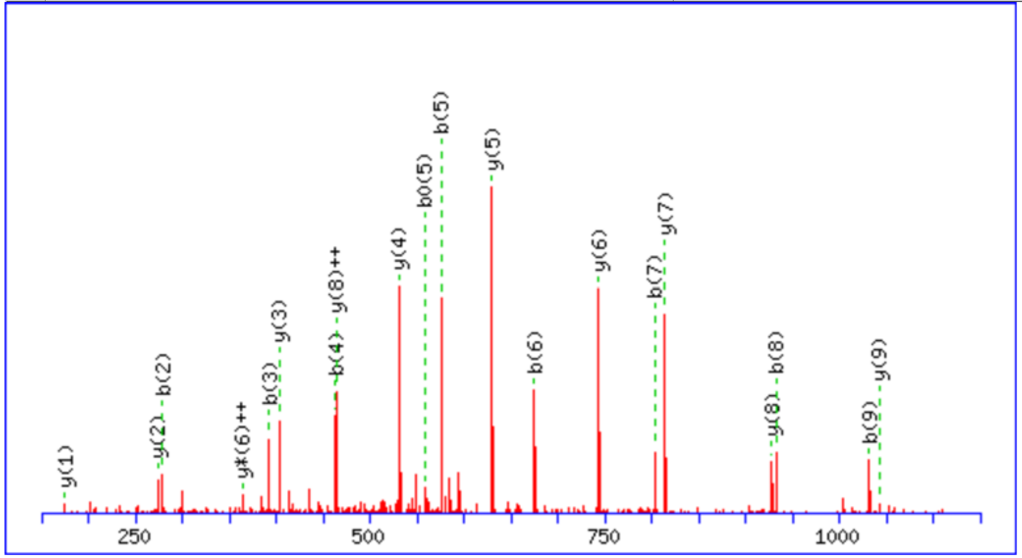
Peptide View

MS/MS Fragmentation of **YDIALVQEVR**
Found in **IPI00031065**, Tax_Id=9606 Gene_Symbol=DNASE1 Deoxyribonuclease-1
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 7283: 1204.648448 from(603.331500,2+)
Title: OECHL100317_09.15357.15357.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1204.645172**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60
Expect: 6.9e-005**Matches :** 20/90 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					**Y**							**10**
2	**279.097548**	140.052412			261.086983	131.047130	**D**	***1042.589136***	521.798206	1025.562587	513.284932	1024.578571	512.792924	**9**

3	**392.181612**	196.594444			374.171047	187.589162	**I**	***927.562193***	464.284735	910.535644	455.771460	909.551628	455.279452	**8**
4	**463.218726**	232.113001			445.208161	223.107719	**A**	***814.478129***	407.742703	797.451580	399.229428	796.467564	398.737420	**7**
5	**576.302790**	288.655033			558.292225	279.649751	**L**	***743.441015***	372.224146	726.414466	363.710871	725.430450	363.218863	**6**
6	**675.371204**	338.189240			657.360639	329.183958	**V**	***630.356951***	315.682114	613.330402	307.168839	612.346386	306.676831	**5**
7	**803.429782**	402.218529	786.403233	393.705255	785.419217	393.213247	**Q**	***531.288537***	266.147907	514.261988	257.634632	513.277972	257.142624	**4**
8	**932.472375**	466.739826	915.445826	458.226551	914.461810	457.734543	**E**	***403.229959***	202.118618	386.203410	193.605343	385.219394	193.113335	**3**
9	**1031.540789**	516.274033	1014.514240	507.760758	1013.530224	507.268750	**V**	***274.187366***	137.597321	257.160817	129.084047			**2**
10							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



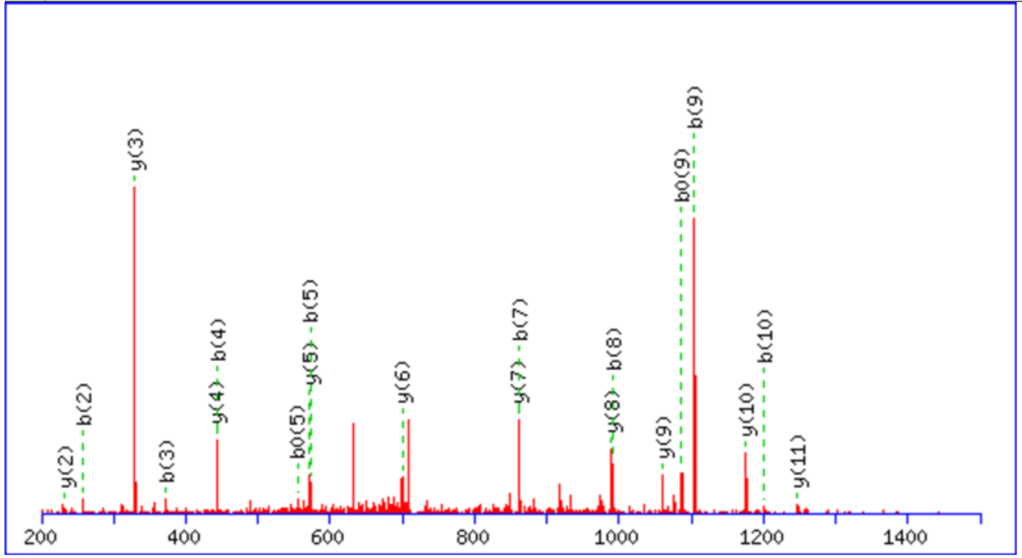
Peptide View

MS/MS Fragmentation of **WADAECEEIPGR**
Found in **IPI00027436**, Tax_Id=9606 Gene_Symbol=NGFR Tumor necrosis factor receptor superfamily member 16
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 9738: 1431.608048 from(716.811300,2+)
Title: OECHL100317_09.11262.11262.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1431.608856**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 75

Expect: 9e-007**Matches :** 20/98 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.086589	94.046932			**W**							**12**
2	**258.123703**	129.565490			**A**	***1246.536843***	623.772060	1229.510294	615.258785	1228.526278	614.766777	**11**
3	**373.150646**	187.078961	355.140081	178.073679	**D**	***1175.499729***	588.253502	1158.473180	579.740228	1157.489164	579.248220	**10**
4	**444.187760**	222.597518	426.177195	213.592236	**A**	***1060.472786***	530.740031	1043.446237	522.226757	1042.462221	521.734749	**9**
5	**573.230353**	287.118815	555.219788	278.113532	**E**	***989.435672***	495.221474	972.409123	486.708199	971.425107	486.216191	**8**
6	733.261002	367.134139	715.250437	358.128857	**C**	***860.393079***	430.700178	843.366530	422.186903	842.382514	421.694895	**7**
7	**862.303595**	431.655436	844.293030	422.650153	**E**	***700.362430***	350.684853	683.335881	342.171578	682.351865	341.679570	**6**
8	**991.346188**	496.176732	973.335623	487.171450	**E**	***571.319837***	286.163556	554.293288	277.650282	553.309272	277.158274	**5**
9	**1104.430252**	552.718764	1086.419687	543.713482	**I**	***442.277244***	221.642260	425.250695	213.128985			**4**
10	**1201.483016**	601.245146	1183.472451	592.239864	**P**	***329.193180***	165.100228	312.166631	156.586953			**3**
11	1258.504480	629.755878	1240.493915	620.750596	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**

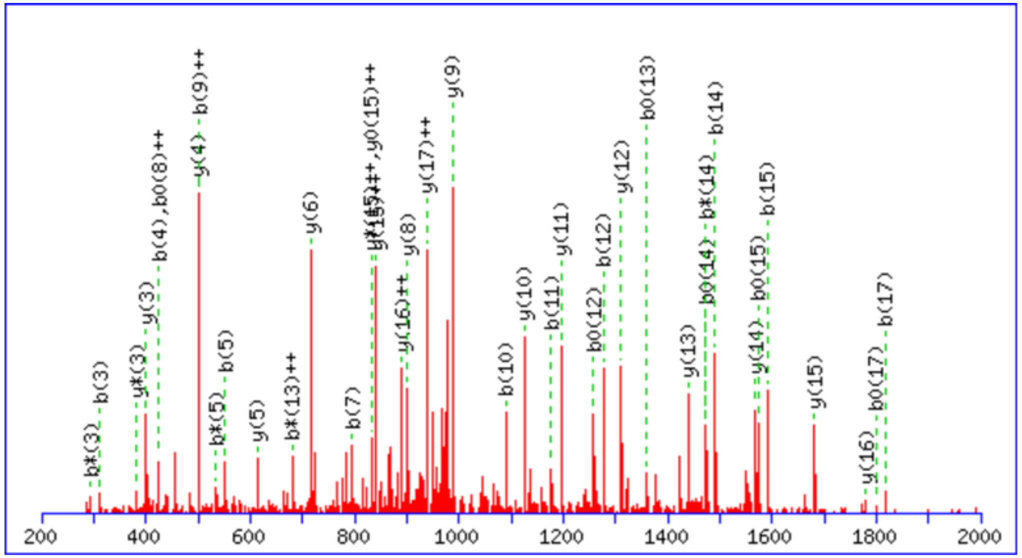


Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 15353: 1990.022248 from(996.018400,2+)
Title: OECHL100317_09.10055.10055.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 84
Expect: 5.9e-007**Matches :** 40/186 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	115.050203	58.028740	98.023654	49.515465			N							18
2	212.102967	106.555121	195.076418	98.041847			P	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	17
3	**311.171381**	156.089328	294.144832	147.576054			V	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	16
4	**424.255445**	212.631361	407.228896	204.118086			L	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	15
5	**552.314023**	276.660650	535.287474	268.147375			Q	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.389511	14
6	680.372601	340.689939	663.346052	332.176664			Q	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	13
7	**795.399544**	398.203410	778.372995	389.690136	777.388979	389.198128	D	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	12
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	A	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	11
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	H	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	10
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	S	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	9
11	**1177.559626**	589.283451	1160.533077	580.770177	1159.549061	580.278169	S	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	8
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	V	814.478130	407.742703	797.451581	399.229428	796.467565	398.737420	7
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	T	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	6
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	I	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	5
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	T	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	4
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	P	***400.230294***	200.618785	383.203745	192.105510			3
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	Q	303.177530	152.092403	286.150981	143.579128			2
18							R	175.118952	88.063114	158.092403	79.549839			1



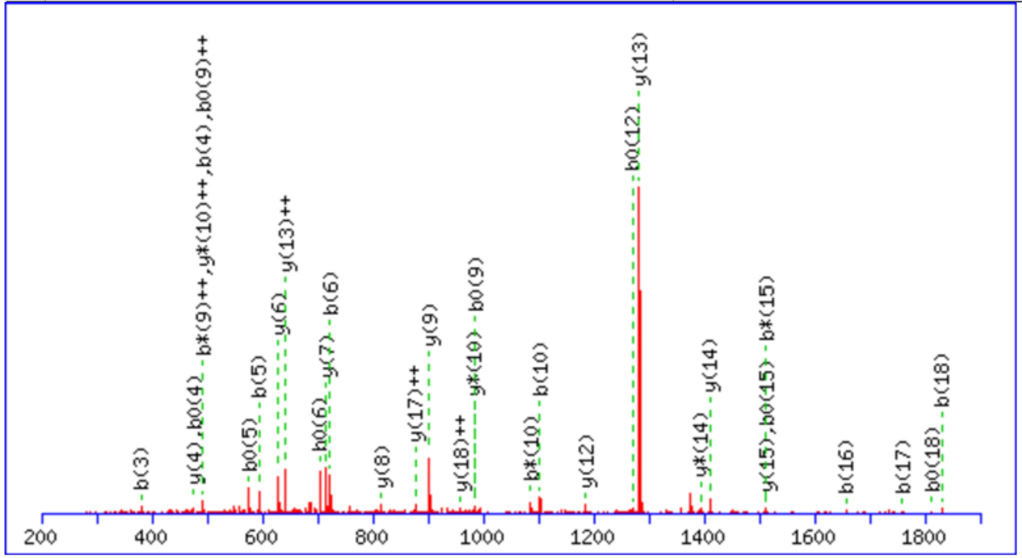
Peptide View

MS/MS Fragmentation of **SYELTQPPSVSVSPGQTAR**
Found in **IPI00382440**, Tax_Id=9606 Gene_Symbol=- Ig lambda chain V-IV region Hil
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 15401: 2002.995448 from(1002.505000,2+)
Title: OECHL100317_09.13369.13369.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 2002.995987**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64
Expect: 7.5e-005**Matches :** 34/202 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	88.039304	44.523290			70.028739	35.518008	**S**							**19**
2	251.102633	126.054954			233.092068	117.049672	**Y**	1916.971234	958.989255	1899.944685	950.475981	1898.960669	949.983973	**18**
3	***380.145226***	190.576251			362.134661	181.570969	**E**	1753.907905	877.457591	1736.881356	868.944316	1735.897340	868.452308	**17**
4	***493.229290***	247.118283			475.218725	238.113001	**L**	1624.865312	812.936294	1607.838763	804.423020	1606.854747	803.931012	**16**
5	***594.276969***	297.642123			576.266404	288.636840	**T**	***1511.781248***	756.394262	1494.754699	747.880988	1493.770683	747.388980	**15**
6	***722.335547***	361.671412	705.308998	353.158137	704.324982	352.666129	**Q**	***1410.733569***	705.870423	1393.707020	697.357148	1392.723004	696.865140	**14**

7	819.388311	410.197794	802.361762	401.684519	801.377746	401.192511	**P**	***1282.674991***	641.841134	1265.648442	633.327859	1264.664426	632.835851	**13**
8	916.441075	458.724176	899.414526	450.210901	898.430510	449.718893	**P**	***1185.622227***	593.314752	1168.595678	584.801477	1167.611662	584.309469	**12**
9	1003.473103	502.240190	986.446554	493.726915	985.462538	493.234907	**S**	1088.569463	544.788370	1071.542914	536.275095	1070.558898	535.783087	**11**
10	***1102.541517***	551.774397	1085.514968	543.261122	1084.530952	542.769114	**V**	1001.537435	501.272356	984.510886	492.759081	983.526870	492.267073	**10**
11	1189.573545	595.290411	1172.546996	586.777136	1171.562980	586.285128	**S**	***902.469021***	451.738149	885.442472	443.224874	884.458456	442.732866	**9**
12	1288.641959	644.824618	1271.615410	636.311343	1270.631394	635.819335	**V**	***815.436993***	408.222135	798.410444	399.708860	797.426428	399.216852	**8**
13	1375.673987	688.340632	1358.647438	679.827357	1357.663422	679.335349	**S**	***716.368579***	358.687928	699.342030	350.174653	698.358014	349.682645	**7**
14	1472.726751	736.867014	1455.700202	728.353739	1454.716186	727.861731	**P**	***629.336551***	315.171914	612.310002	306.658639	611.325986	306.166631	**6**
15	1529.748215	765.377746	1512.721666	756.864471	1511.737650	756.372463	**G**	532.283787	266.645532	515.257238	258.132257	514.273222	257.640249	**5**
16	***1657.806793***	829.407035	1640.780244	820.893760	1639.796228	820.401752	**Q**	***475.262323***	238.134800	458.235774	229.621525	457.251758	229.129517	**4**
17	***1758.854472***	879.930874	1741.827923	871.417600	1740.843907	870.925592	**T**	347.203745	174.105510	330.177196	165.592236	329.193180	165.100228	**3**
18	***1829.891586***	915.449431	1812.865037	906.936157	1811.881021	906.444149	**A**	246.156066	123.581671	229.129517	115.068396			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**



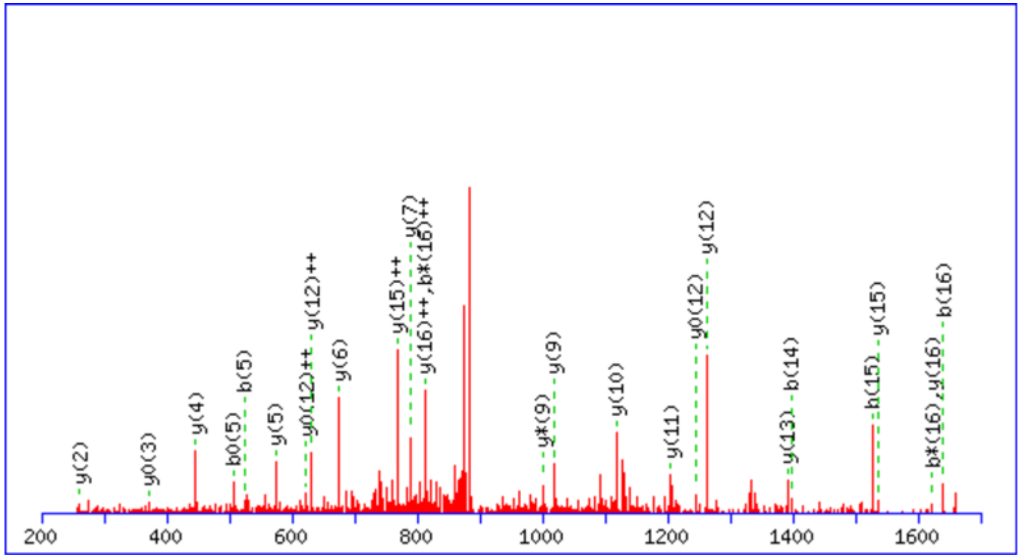
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**

Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 14027: 1784.879848 from(893.447200,2+)
Title: OECHL100317_09.8083.8083.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 83
Expect: 8.1e-007**Matches :** 26/170 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	164.070605	82.538940					Y							17
2	251.102633	126.054954			233.092068	117.049672	S	***1622.823172***	811.915224	1605.796623	803.401950	1604.812607	802.909941	16
3	308.124097	154.565687			290.113532	145.560404	G	***1535.791144***	768.399210	1518.764595	759.885936	1517.780579	759.393928	15
4	395.156125	198.081701			377.145560	189.076418	S	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.883195	14
5	**524.198718**	262.602997			506.188153	253.597715	E	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.367182	13
6	581.220182	291.113729			563.209617	282.108447	G	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.845885	12
7	668.252210	334.629743			650.241645	325.624461	S	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.335153	11
8	769.299889	385.153583			751.289324	376.148300	T	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.819139	10
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	Q	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.295299	9
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	T	889.535310	445.271293	872.508761	436.758018	871.524745	436.266010	8
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	L	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.742171	7
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	T	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.200139	6
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	K	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.676299	5
14	**1397.654316**	699.330796	1380.627767	690.817522	1379.643751	690.325514	G	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	4
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	E	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	3
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	L	***260.196868***	130.602072	243.170319	122.088797			2
17							K	147.112804	74.060040	130.086255	65.546765			1



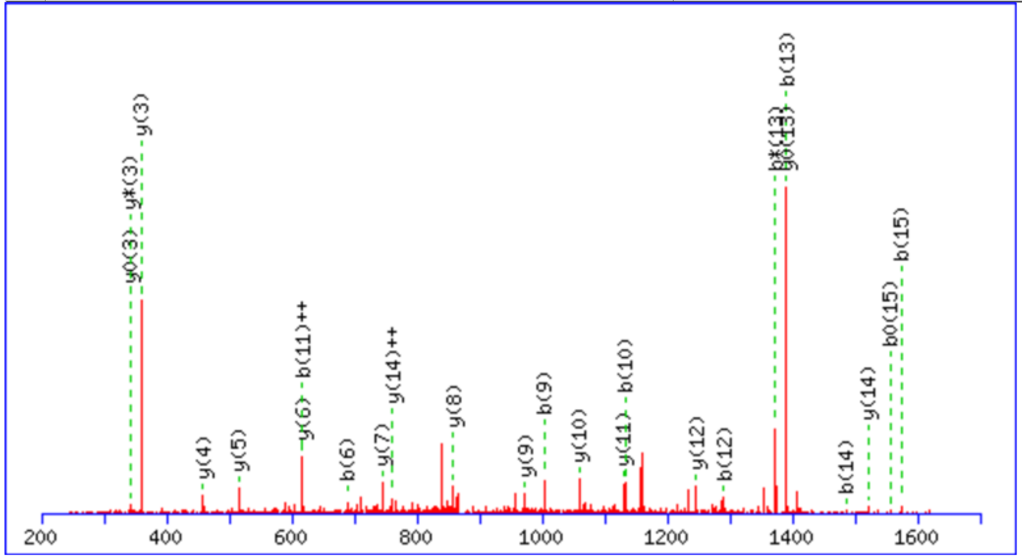
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 13812: 1746.917048 from(874.465800,2+)
Title: OECHL100317_09.16604.16604.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 75
Expect: 3e-006**Matches :** 25/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	618.349740	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	**689.386854**	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**

7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	1233.636145	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	**1486.778787**	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



Peptide View

MS/MS Fragmentation of **GAVSQTYPSGTCAYIQR**
Found in **IPI00001759**, Tax_Id=9606 Gene_Symbol=OLR1 Oxidized low-density lipoprotein receptor 1
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 14502: 1857.869448 from(929.942000,2+)

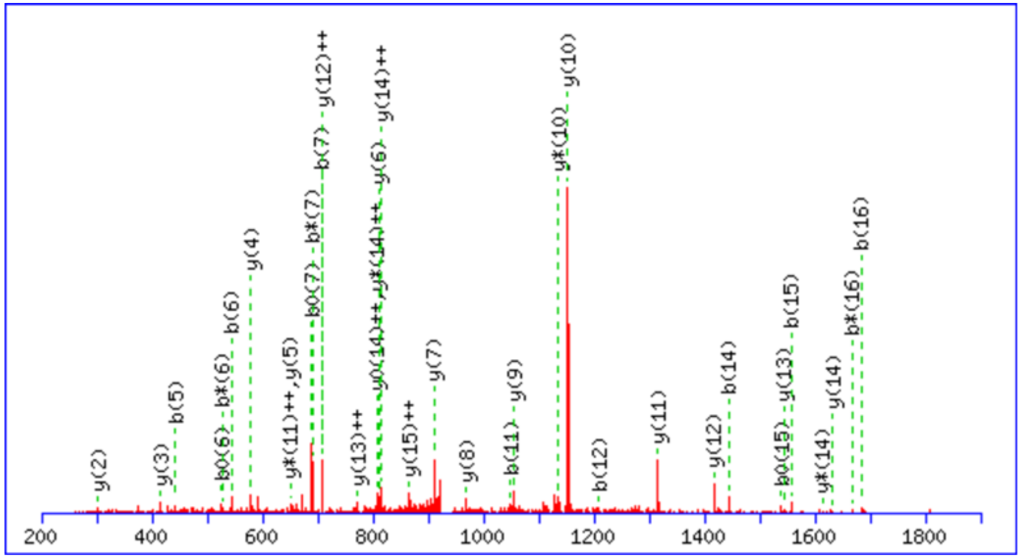
Title: OECHL100317_09.11160.11160.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw

Monoisotopic mass of neutral peptide Mr(calc): 1857.867950**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 73

Expect: 6e-006**Matches :** 36/166 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	58.028740	29.518008					G							17
2	129.065854	65.036565					A	1801.853763	901.430520	1784.827214	892.917245	1783.843198	892.425237	16
3	228.134268	114.570772					V	1730.816649	865.911963	1713.790100	857.398688	1712.806084	856.906680	15
4	315.166296	158.086786			297.155731	149.081504	S	***1631.748235***	816.377756	1614.721686	807.864481	1613.737670	807.372473	14
5	**443.224874**	222.116075	426.198325	213.602801	425.214309	213.110793	Q	***1544.716207***	772.861742	1527.689658	764.348467	1526.705642	763.856459	13
6	**544.272553**	272.639915	527.246004	264.126640	526.261988	263.634632	T	***1416.657629***	708.832453	1399.631080	700.319178	1398.647064	699.827170	12
7	**707.335882**	354.171579	690.309333	345.658305	689.325317	345.166297	Y	***1315.609950***	658.308613	1298.583401	649.795339	1297.599385	649.303331	11
8	804.388646	402.697961	787.362097	394.184687	786.378081	393.692679	P	***1152.546621***	576.776949	1135.520072	568.263674	1134.536056	567.771666	10
9	891.420674	446.213975	874.394125	437.700701	873.410109	437.208693	S	***1055.493857***	528.250567	1038.467308	519.737292	1037.483292	519.245284	9
10	948.442138	474.724707	931.415589	466.211433	930.431573	465.719425	G	***968.461829***	484.734553	951.435280	476.221278	950.451264	475.729270	8
11	**1049.489817**	525.248547	1032.463268	516.735272	1031.479252	516.243264	T	***911.440365***	456.223821	894.413816	447.710546	893.429800	447.218538	7
12	**1209.520466**	605.263871	1192.493917	596.750597	1191.509901	596.258589	C	***810.392686***	405.699981	793.366137	397.186707			6
13	1280.557580	640.782428	1263.531031	632.269154	1262.547015	631.777146	A	***650.362037***	325.684657	633.335488	317.171382			5
14	**1443.620909**	722.314093	1426.594360	713.800818	1425.610344	713.308810	Y	***579.324923***	290.166100	562.298374	281.652825			4
15	**1556.704973**	778.856125	1539.678424	770.342850	1538.694408	769.850842	I	***416.261594***	208.634435	399.235045	200.121160			3
16	**1684.763551**	842.885414	1667.737002	834.372139	1666.752986	833.880131	Q	***303.177530***	152.092403	286.150981	143.579129			2
17							R	175.118952	88.063114	158.092403	79.549839			1



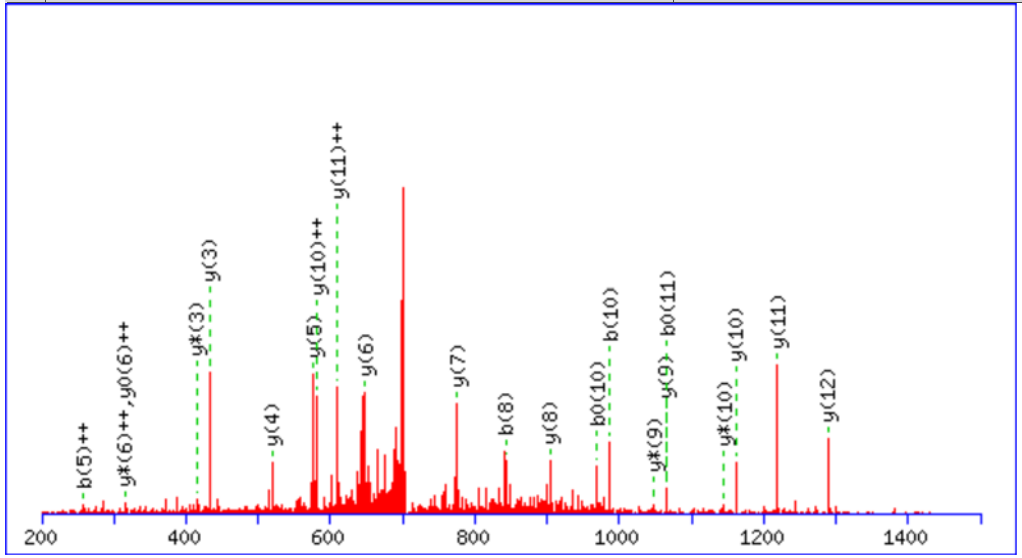
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 9641: 1416.625048 from(709.319800,2+)
Title: OECHL100317_09.2298.2298.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 69
Expect: 7.6e-006**Matches :** 22/128 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							**13**
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	**12**
3	257.160817	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	**11**
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	**10**
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	**9**
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	**8**

7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	899.403979	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	335.149601	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

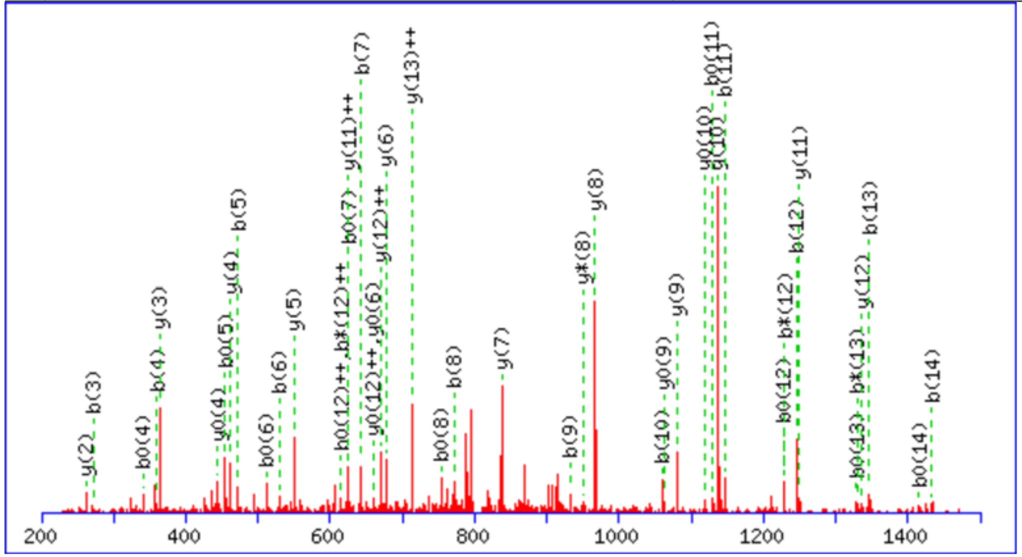


Peptide View

MS/MS Fragmentation of **AISSIGLECQSVTSR**
Found in **IPI00006988**, Tax_Id=9606 Gene_Symbol=RETN Resistin
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 12060: 1606.799248 from(804.406900,2+)
Title: OECHL100317_09.12112.12112.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1606.798462**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 69
Expect: 2e-005**Matches :** 45/144 fragment ions using 91 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					**A**							**15**
2	185.128454	93.067865					**I**	1536.768633	768.887955	1519.742084	760.374680	1518.758068	759.882672	**14**
3	***272.160482***	136.583879			254.149917	127.578596	**S**	1423.684569	712.345923	1406.658020	703.832648	1405.674004	703.340640	**13**
4	***359.192510***	180.099893			341.181945	171.094610	**S**	**1336.652541**	668.829909	1319.625992	660.316634	1318.641976	659.824626	**12**
5	***472.276574***	236.641925			454.266009	227.636642	**I**	**1249.620513**	625.313895	1232.593964	616.800620	1231.609948	616.308612	**11**
6	***529.298038***	265.152657			511.287473	256.147375	**G**	**1136.536449**	568.771863	1119.509900	560.258588	1118.525884	559.766580	**10**
7	***642.382102***	321.694689			624.371537	312.689407	**L**	**1079.514985**	540.261131	1062.488436	531.747856	1061.504420	531.255848	**9**
8	***771.424695***	386.215986			753.414130	377.210703	**E**	**966.430921**	483.719099	949.404372	475.205824	948.420356	474.713816	**8**
9	***931.455344***	466.231310			913.444779	457.226028	**C**	**837.388328**	419.197802	820.361779	410.684528	819.377763	410.192520	**7**
10	***1059.513922***	530.260599	1042.487373	521.747325	1041.503357	521.255317	**Q**	**677.357679**	339.182478	660.331130	330.669203	659.347114	330.177195	**6**
11	***1146.545950***	573.776613	1129.519401	565.263339	1128.535385	564.771331	**S**	**549.299101**	275.153189	532.272552	266.639914	531.288536	266.147906	**5**
12	***1245.614364***	623.310820	1228.587815	614.797546	1227.603799	614.305538	**V**	**462.267073**	231.637175	445.240524	223.123900	444.256508	222.631892	**4**
13	***1346.662043***	673.834660	1329.635494	665.321385	1328.651478	664.829377	**T**	**363.198659**	182.102968	346.172110	173.589693	345.188094	173.097685	**3**
14	***1433.694071***	717.350674	1416.667522	708.837399	1415.683506	708.345391	**S**	**262.150980**	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**

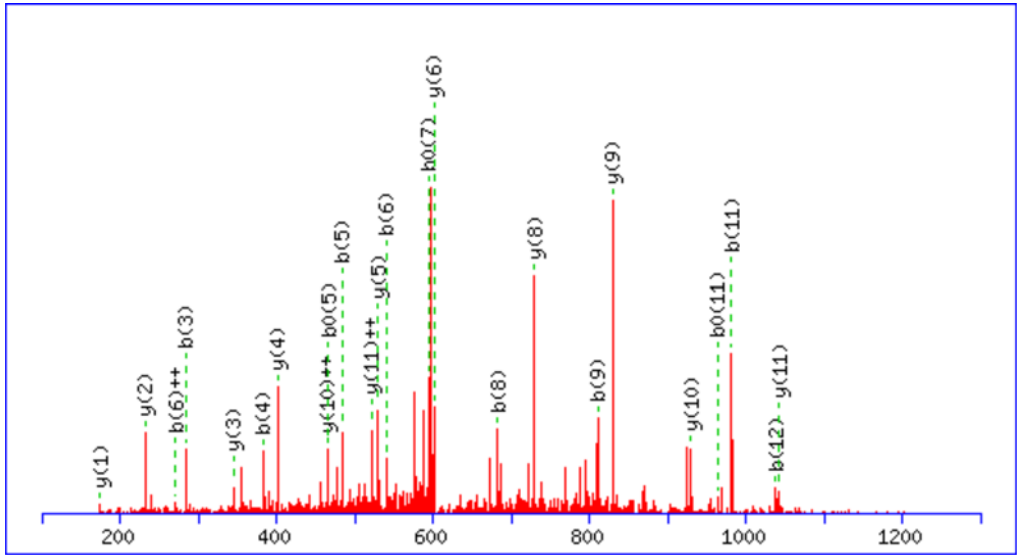


Peptide View

MS/MS Fragmentation of **VALVTGAAQGIGR**
Found in **IPI00290420**, Tax_Id=9606 Gene_Symbol=HPGD hydroxyprostaglandin dehydrogenase 15-(NAD) isoform 2
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 7361: 1211.698648 from(606.856600,2+)
Title: OECHL100317_09.11594.11594.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 1211.698624**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66
Expect: 1e-005**Matches :** 24/104 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	100.075690	50.541483					**V**							**13**
2	171.112804	86.060040					**A**	1113.637485	557.322381	1096.610936	548.809106	1095.626920	548.317098	**12**
3	**284.196868**	142.602072					**L**	***1042.600371***	521.803824	1025.573822	513.290549	1024.589806	512.798541	**11**
4	**383.265282**	192.136279					**V**	***929.516307***	465.261792	912.489758	456.748517	911.505742	456.256509	**10**
5	**484.312961**	242.660119			466.302396	233.654836	**T**	***830.447893***	415.727585	813.421344	407.214310	812.437328	406.722302	**9**
6	**541.334425**	271.170851			523.323860	262.165568	**G**	***729.400214***	365.203745	712.373665	356.690471			**8**
7	612.371539	306.689408			594.360974	297.684125	**A**	672.378750	336.693013	655.352201	328.179738			**7**
8	**683.408653**	342.207965			665.398088	333.202682	**A**	***601.341636***	301.174456	584.315087	292.661182			**6**
9	**811.467231**	406.237254	794.440682	397.723979	793.456666	397.231971	**Q**	***530.304522***	265.655899	513.277973	257.142625			**5**
10	868.488695	434.747986	851.462146	426.234711	850.478130	425.742703	**G**	***402.245944***	201.626610	385.219395	193.113335			**4**
11	**981.572759**	491.290018	964.546210	482.776743	963.562194	482.284735	**I**	***345.224480***	173.115878	328.197931	164.602603			**3**
12	**1038.594223**	519.800750	1021.567674	511.287475	1020.583658	510.795467	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
13							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



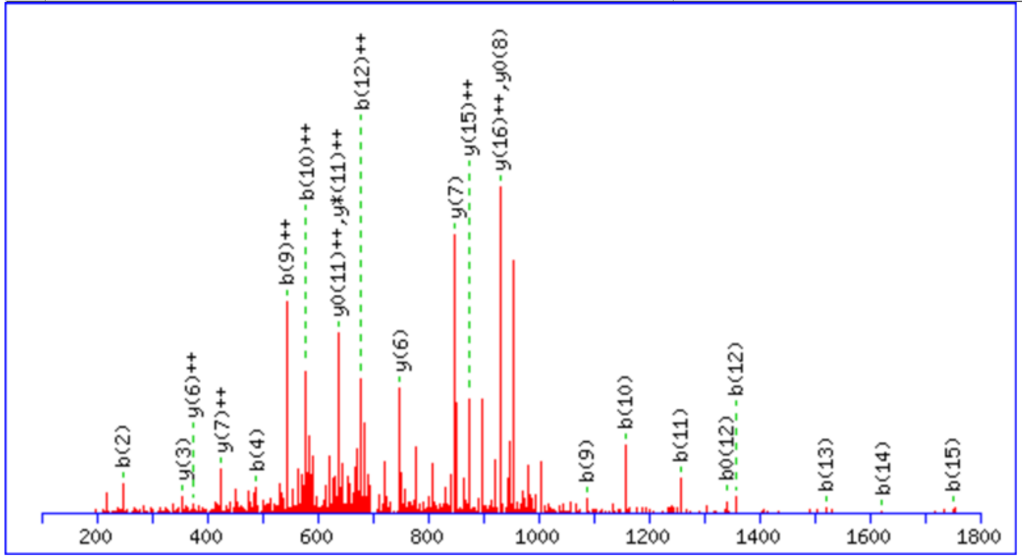
Peptide View

MS/MS Fragmentation of **VFLENVIRDAVTYTEHAK**
Found in **IPI00453473**, Tax_Id=9606 Gene_Symbol=HIST1H4K;HIST1H4D;HIST4H4;HIST1H4F;HIST1H4E;HIST1H4J;HIST2H4A;HIST1H4B;HIST1H4I;HIST1H4A;HIST1H4L;HIST1H4H;HIST1H4C;HIST2H4B Histone H4
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 16145: 2104.094772 from(702.372200,3+)
Title: OECHL100317_09.21757.21757.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 2104.095291**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 0.00021**Matches :** 23/184 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					**V**							**18**
2	***247.144104***	124.075690					**F**	2006.034168	1003.520722	1989.007619	995.007448	1988.023603	994.515440	**17**
3	360.228168	180.617722					**L**	1858.965754	929.986515	1841.939205	921.473241	1840.955189	920.981233	**16**
4	***489.270761***	245.139018			471.260196	236.133736	**E**	1745.881690	873.444483	1728.855141	864.931209	1727.871125	864.439201	**15**
5	603.313688	302.160482	586.287139	293.647208	585.303123	293.155200	**N**	1616.839097	808.923187	1599.812548	800.409912	1598.828532	799.917904	**14**

6	702.382102	351.694689	685.355553	343.181415	684.371537	342.689407	**V**	1502.796170	751.901723	1485.769621	743.388449	1484.785605	742.896441	**13**
7	815.466166	408.236721	798.439617	399.723447	797.455601	399.231439	**I**	1403.727756	702.367516	1386.701207	693.854242	1385.717191	693.362234	**12**
8	971.567277	486.287277	954.540728	477.774002	953.556712	477.281994	**R**	1290.643692	645.825484	1273.617143	637.312210	1272.633127	636.820202	**11**
9	***1086.594220***	**543.800748**	1069.567671	535.287474	1068.583655	534.795466	**D**	1134.542581	567.774929	1117.516032	559.261654	1116.532016	558.769646	**10**
10	***1157.631334***	**579.319305**	1140.604785	570.806031	1139.620769	570.314023	**A**	1019.515638	510.261457	1002.489089	501.748183	1001.505073	501.256175	**9**
11	***1256.699748***	628.853512	1239.673199	620.340238	1238.689183	619.848230	**V**	948.478524	474.742900	931.451975	466.229626	930.467959	465.737618	**8**
12	***1357.747427***	**679.377352**	1340.720878	670.864077	1339.736862	670.372069	**T**	**849.410110**	425.208693	832.383561	416.695419	831.399545	416.203411	**7**
13	***1520.810756***	760.909016	1503.784207	752.395742	1502.800191	751.903734	**Y**	**748.362431**	374.684854	731.335882	366.171579	730.351866	365.679571	**6**
14	***1621.858435***	811.432856	1604.831886	802.919581	1603.847870	802.427573	**T**	585.299102	293.153189	568.272553	284.639915	567.288537	284.147907	**5**
15	***1750.901028***	875.954152	1733.874479	867.440878	1732.890463	866.948870	**E**	484.251423	242.629350	467.224874	234.116075	466.240858	233.624067	**4**
16	1887.959940	944.483608	1870.933391	935.970334	1869.949375	935.478326	**H**	**355.208830**	178.108053	338.182281	169.594779			**3**
17	1958.997054	980.002165	1941.970505	971.488891	1940.986489	970.996883	**A**	218.149918	109.578597	201.123369	101.065323			**2**
18							**K**	147.112804	74.060040	130.086255	65.546766			**1**



Peptide View

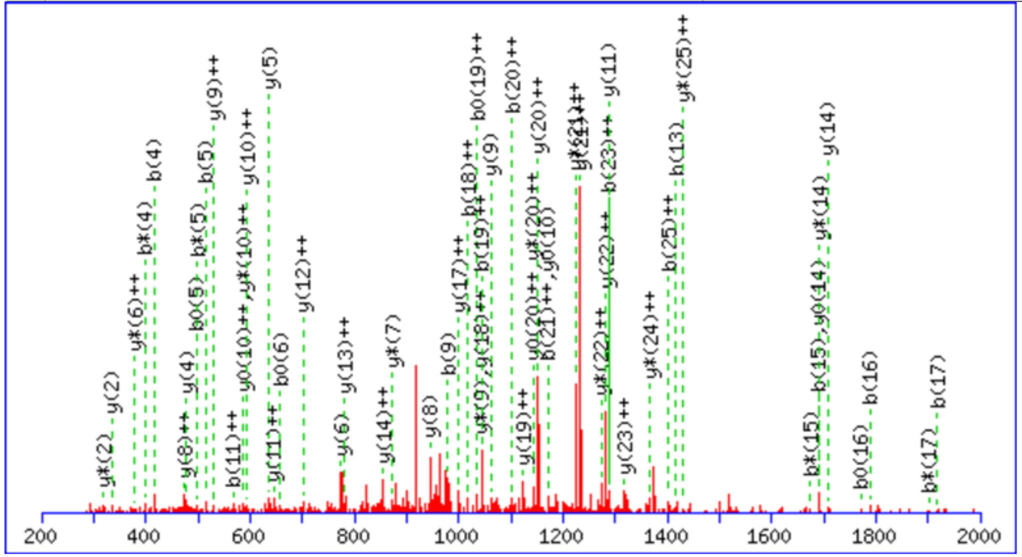
MS/MS Fragmentation of **TENAVCGCSPGHFCIVQDGDHCAACR**

Found in **IPI00024331**, Tax_Id=9606 Gene_Symbol=TNFRSF14 Tumor necrosis factor receptor superfamily member 14
Experiment: 54 - PyC-3 **Fraction:** PyC-3

Match to Query 19249: 2977.185972 from(993.402600,3+)
Title: OECHL100317_09.11272.11272.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_09.raw
Monoisotopic mass of neutral peptide Mr(calc): 2977.178284**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53
Expect: 6.8e-005**Matches :** 59/284 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	102.054955	51.531116			84.044390	42.525833	**T**						
2	231.097548	116.052412			213.086983	107.047130	**E**	2877.137837	1439.072556	2860.111288	1430.559282	2859.127272	1430.0672
3	345.140475	173.073876	328.113926	164.560601	327.129910	164.068593	**N**	2748.095244	1374.551260	2731.068695	1366.037985	2730.084679	1365.5459
4	**416.177589**	208.592433	399.151040	200.079158	398.167024	199.587150	**A**	2634.052317	1317.529796	2617.025768	1309.016522	2616.041752	1308.5245
5	**515.246003**	258.126640	498.219454	249.613365	497.235438	249.121357	**V**	2563.015203	1282.011239	2545.988654	1273.497965	2545.004638	1273.0059
6	675.276652	338.141964	658.250103	329.628690	657.266087	329.136682	**C**	2463.946789	1232.477032	2446.920240	1223.963758	2445.936224	1223.4717
7	732.298116	366.652696	715.271567	358.139422	714.287551	357.647414	**G**	2303.916140	1152.461708	2286.889591	1143.948433	2285.905575	1143.4564
8	892.328765	446.668021	875.302216	438.154746	874.318200	437.662738	**C**	2246.894676	1123.950976	2229.868127	1115.437701	2228.884111	1114.9456
9	**979.360793**	490.184035	962.334244	481.670760	961.350228	481.178752	**S**	2086.864027	1043.935651	2069.837478	1035.422377	2068.853462	1034.9303
10	1076.413557	538.710417	1059.387008	530.197142	1058.402992	529.705134	**P**	1999.831999	1000.419638	1982.805450	991.906363	1981.821434	991.4143
11	1133.435021	***567.221149***	1116.408472	558.707874	1115.424456	558.215866	**G**	1902.779235	951.893256	1885.752686	943.379981	1884.768670	942.8879
12	1270.493933	635.750605	1253.467384	627.237330	1252.483368	626.745322	**H**	1845.757771	923.382524	1828.731222	914.869249	1827.747206	914.3772
13	**1417.562347**	709.284812	1400.535798	700.771537	1399.551782	700.279529	**F**	**1708.698859**	854.853068	1691.672310	846.339793	1690.688294	845.8477
14	1577.592996	789.300136	1560.566447	780.786862	1559.582431	780.294854	**C**	1561.630445	781.318861	1544.603896	772.805586	1543.619880	772.3135
15	**1690.677060**	845.842168	1673.650511	837.328894	1672.666495	836.836885	**I**	1401.599796	701.303536	1384.573247	692.790262	1383.589231	692.2982
16	**1789.745474**	895.376375	1772.718925	886.863101	1771.734909	886.371093	**V**	**1288.515732**	644.761504	1271.489183	636.248230	1270.505167	635.7562
17	**1917.804052**	959.405664	1900.777503	950.892390	1899.793487	950.400382	**Q**	1189.447318	595.227297	1172.420769	586.714023	1171.436753	586.2220
18	2032.830995	***1016.919136***	2015.804446	1008.405861	2014.820430	1007.913853	**D**	**1061.388740**	531.198008	1044.362191	522.684734	1043.378175	522.1927
19	2089.852459	***1045.429868***	2072.825910	1036.916593	2071.841894	1036.424585	**G**	**946.361797**	473.684537	929.335248	465.171262	928.351232	464.6792
20	2204.879402	***1102.943339***	2187.852853	1094.430064	2186.868837	1093.938056	**D**	889.340333	445.173804	872.313784	436.660530	871.329768	436.1685
21	2341.938314	***1171.472795***	2324.911765	1162.959520	2323.927749	1162.467512	**H**	**774.313390**	387.660333	757.286841	379.147059		
22	2501.968963	1251.488119	2484.942414	1242.974845	2483.958398	1242.482837	**C**	**637.254478**	319.130877	620.227929	310.617603		
23	2573.006077	***1287.006676***	2555.979528	1278.493402	2554.995512	1278.001394	**A**	**477.223829**	239.115553	460.197280	230.602278		
24	2644.043191	1322.525234	2627.016642	1314.011959	2626.032626	1313.519951	**A**	406.186715	203.596995	389.160166	195.083721		

25	2804.073840	***1402.540558***	2787.047291	1394.027283	2786.063275	1393.535275	**C**	**335.149601**	168.078438	318.123052	159.565164		
26							**R**	175.118952	88.063114	158.092403	79.549839		



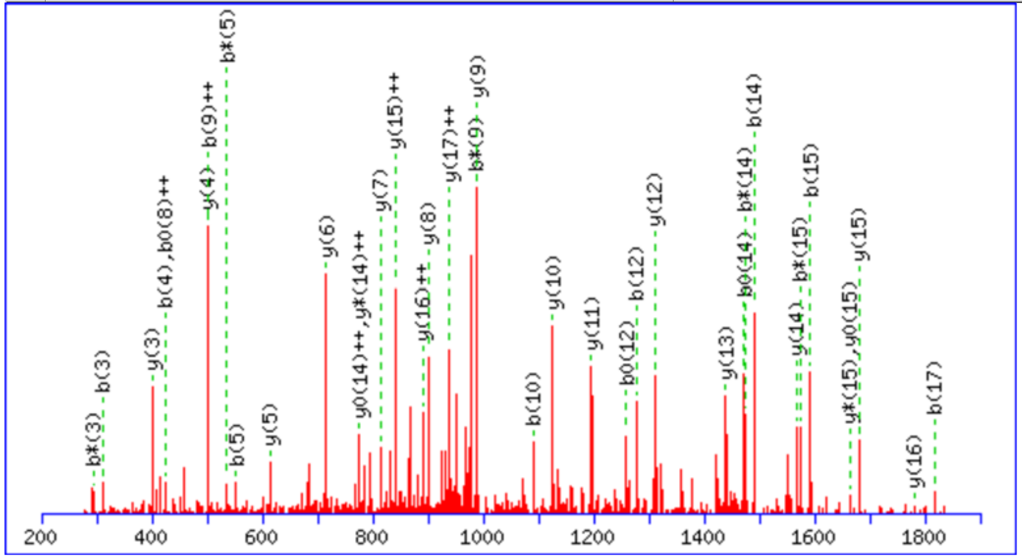
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 05 - S_B-3 **Fraction:** S_B-3

Match to Query 14287: 1990.024648 from(996.019600,2+)
Title: OECHL100317_07.10158.10158.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 94
Expect: 6e-008**Matches :** 38/186 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	**424.255445**	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**

5	**552.314023**	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	680.372601	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**
7	795.399544	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510			**3**
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**

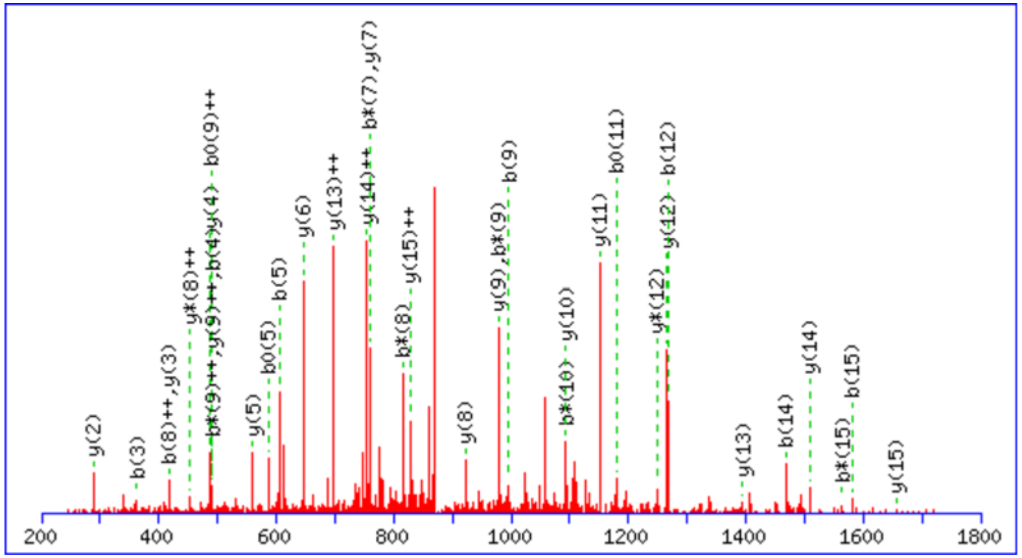


Peptide View

MS/MS Fragmentation of **VFDKDGNGYISAAELR**
Found in **IPI00075248**, Tax_Id=9606 Gene_Symbol=CALM3;CALM2;CALM1 Calmodulin
Experiment: 05 - S_B-3 **Fraction:** S_B-3

Match to Query 12462: 1753.863648 from(877.939100,2+)
Title: OECHL100317_07.14110.14110.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1753.863495**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 104
Expect: 5.6e-009**Matches :** 37/166 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	100.075690	50.541483					**V**							**16**
2	247.144104	124.075690					**F**	***1655.802376***	828.404826	1638.775827	819.891551	1637.791811	819.399543	**15**
3	**362.171047**	181.589161			344.160482	172.583879	**D**	***1508.733962***	754.870619	1491.707413	746.357345	1490.723397	745.865337	**14**
4	**490.266010**	245.636643	473.239461	237.123369	472.255445	236.631361	**K**	***1393.707019***	697.357148	1376.680470	688.843873	1375.696454	688.351865	**13**
5	**605.292953**	303.150115	588.266404	294.636840	587.282388	294.144832	**D**	***1265.612056***	633.309666	1248.585507	624.796392	1247.601491	624.304383	**12**
6	662.314417	331.660847	645.287868	323.147572	644.303852	322.655564	**G**	***1150.585113***	575.796194	1133.558564	567.282920	1132.574548	566.790912	**11**
7	776.357344	388.682310	759.330795	380.169036	758.346779	379.677028	**N**	***1093.563649***	547.285462	1076.537100	538.772188	1075.553084	538.280180	**10**
8	833.378808	417.193042	816.352259	408.679768	815.368243	408.187760	**G**	***979.520722***	490.263999	962.494173	481.750724	961.510157	481.258716	**9**
9	**996.442137**	498.724707	979.415588	490.211432	978.431572	489.719424	**Y**	***922.499258***	461.753267	905.472709	453.239992	904.488693	452.747984	**8**
10	1109.526201	555.266738	1092.499652	546.753464	1091.515636	546.261456	**I**	***759.435929***	380.221603	742.409380	371.708328	741.425364	371.216320	**7**
11	1196.558229	598.782753	1179.531680	590.269478	1178.547664	589.777470	**S**	***646.351865***	323.679571	629.325316	315.166296	628.341300	314.674288	**6**
12	**1267.595343**	634.301310	1250.568794	625.788035	1249.584778	625.296027	**A**	***559.319837***	280.163557	542.293288	271.650282	541.309272	271.158274	**5**
13	1338.632457	669.819866	1321.605908	661.306592	1320.621892	660.814584	**A**	***488.282723***	244.644999	471.256174	236.131725	470.272158	235.639717	**4**
14	**1467.675050**	734.341163	1450.648501	725.827889	1449.664485	725.335881	**E**	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	**3**
15	**1580.759114**	790.883195	1563.732565	782.369921	1562.748549	781.877912	**L**	***288.203016***	144.605146	271.176467	136.091871			**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**



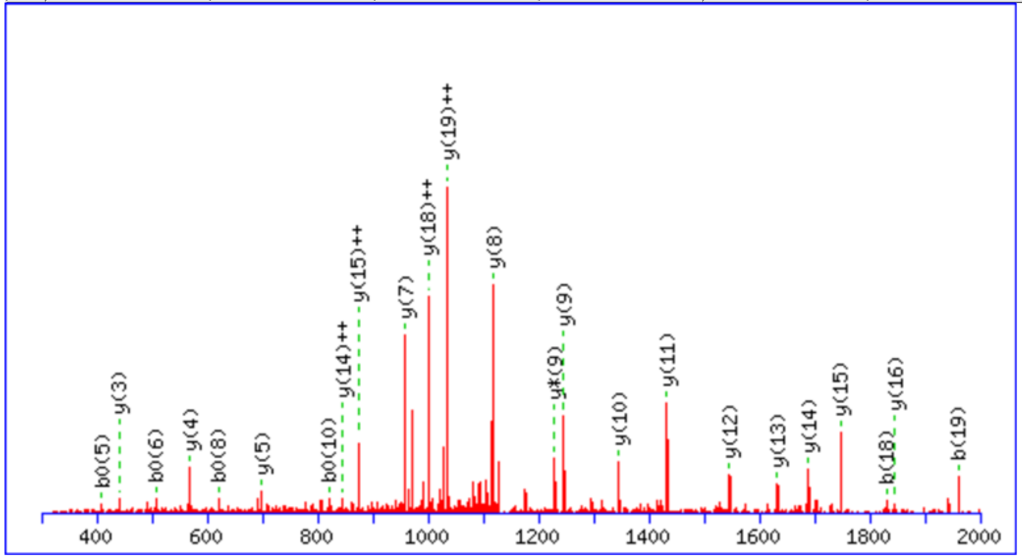
Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 05 - S_B-3 **Fraction:** S_B-3

Match to Query 15830: 2270.115448 from(1136.065000,2+)
Title: OECHL100317_07.10824.10824.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 104
Expect: 8.5e-009**Matches :** 24/212 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	102.054955	51.531116			84.044390	42.525833	**T**						
2	201.123369	101.065322			183.112804	92.060040	**V**	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400	1076.5338
3	272.160483	136.583879			254.149918	127.578597	**A**	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986	1026.9996
4	329.181947	165.094611			311.171382	156.089329	**G**	1999.965437	1000.486357	1982.938888	991.973082	1981.954872	991.4810
5	426.234711	213.620994			408.224146	204.615711	**P**	1942.943973	971.975625	1925.917424	963.462350	1924.933408	962.9703
6	525.303125	263.155201			507.292560	254.149918	**V**	***1845.891209***	923.449243	1828.864660	914.935968	1827.880644	914.4439

7	582.324589	291.665933			564.314024	282.660650	**G**	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230	864.9097
8	639.346053	320.176665			621.335488	311.171382	**G**	***1689.801331***	845.404304	1672.774782	836.891029	1671.790766	836.3990
9	726.378081	363.692679			708.367516	354.687396	**S**	***1632.779867***	816.893572	1615.753318	808.380297	1614.769302	807.8882
10	839.462145	420.234711			821.451580	411.229428	**L**	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274	764.3722
11	926.494173	463.750725			908.483608	454.745442	**S**	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210	707.8302
12	1025.562587	513.284932			1007.552022	504.279649	**V**	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182	664.3142
13	1153.621165	577.314221	1136.594616	568.800946	1135.610600	568.308938	**Q**	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768	614.7800
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	**C**	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190	550.7507
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	**P**	***958.474106***	479.740691	941.447557	471.227417	940.463541	470.7354
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	**Y**	861.421342	431.214309	844.394793	422.701035	843.410777	422.2090
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	**E**	***698.358013***	349.682645	681.331464	341.169370	680.347448	340.6773
18	**1830.905463**	915.956370	1813.878914	907.443095	1812.894898	906.951087	**K**	***569.315420***	285.161348	552.288871	276.648074	551.304855	276.1560
19	**1959.948056**	980.477666	1942.921507	971.964392	1941.937491	971.472384	**E**	***441.220457***	221.113867	424.193908	212.600592	423.209892	212.1085
20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	**H**	312.177864	156.592570	295.151315	148.079295		
21							**R**	175.118952	88.063114	158.092403	79.549839		

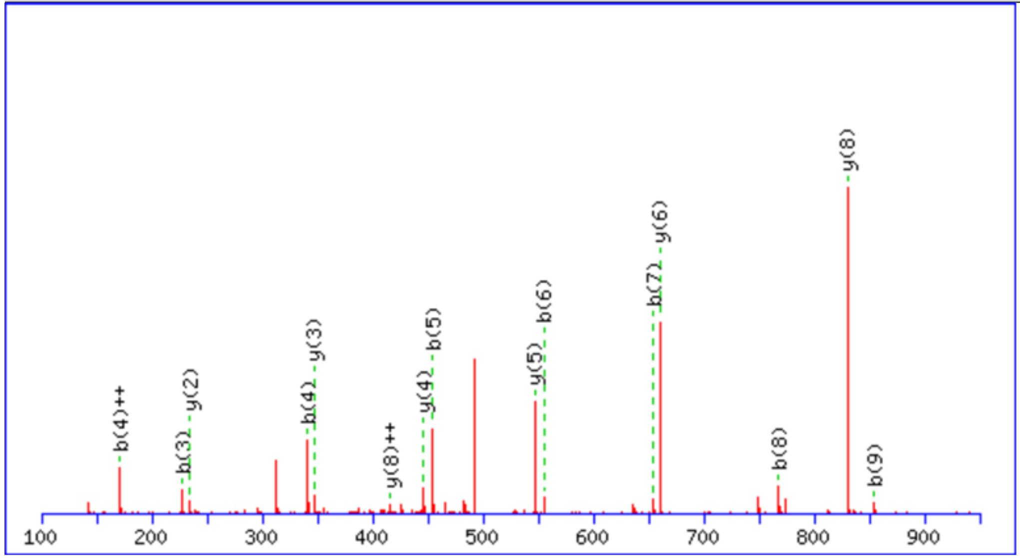


Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 05 - S_B-3 **Fraction:** S_B-3

Match to Query 3371: 999.634848 from(500.824700,2+)
Title: OECHL100317_07.18066.18066.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65
Expect: 3.7e-006**Matches :** 16/78 fragment ions using 24 most intense peaks (help)

#	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	**446.297310**	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



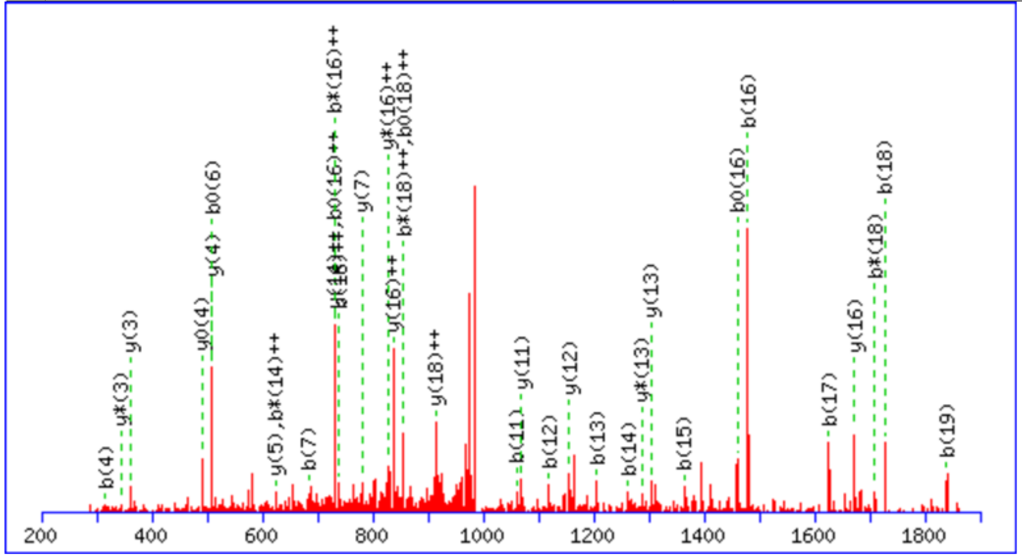
Peptide View

MS/MS Fragmentation of **ASGVPDRFSGSGSGTDFTLK**
Found in **IPI00387107**, Tax_Id=9606 Gene_Symbol=IGKV2-40 Ig kappa chain V-II region Cum
Experiment: 05 - S_B-3 **Fraction:** S_B-3

Match to Query 14259: 1984.948448 from(993.481500,2+)
Title: OECHL100317_07.14020.14020.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1984.949066**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00054**Matches :** 35/210 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**20**
2	159.076418	80.041847			141.065853	71.036564	**S**	1914.919197	957.963236	1897.892648	949.449962	1896.908632	948.957954	**19**
3	216.097882	108.552579			198.087317	99.547296	**G**	1827.887169	914.447222	1810.860620	905.933948	1809.876604	905.441940	**18**
4	***315.166296***	158.086786			297.155731	149.081504	**V**	1770.865705	885.936490	1753.839156	877.423216	1752.855140	876.931208	**17**
5	412.219060	206.613168			394.208495	197.607885	**P**	**1671.797291**	836.402283	1654.770742	827.889009	1653.786726	827.397001	**16**
6	527.246003	264.126640			509.235438	255.121357	**D**	1574.744527	787.875902	1557.717978	779.362627	1556.733962	778.870619	**15**
7	***683.347114***	342.177195	666.320565	333.663920	665.336549	333.171912	**R**	1459.717584	730.362430	1442.691035	721.849156	1441.707019	721.357148	**14**
8	830.415528	415.711402	813.388979	407.198127	812.404963	406.706119	**F**	**1303.616473**	652.311875	1286.589924	643.798600	1285.605908	643.306592	**13**
9	917.447556	459.227416	900.421007	450.714141	899.436991	450.222133	**S**	**1156.548059**	578.777668	1139.521510	570.264393	1138.537494	569.772385	**12**
10	974.469020	487.738148	957.442471	479.224873	956.458455	478.732865	**G**	**1069.516031**	535.261654	1052.489482	526.748379	1051.505466	526.256371	**11**
11	***1061.501048***	531.254162	1044.474499	522.740887	1043.490483	522.248879	**S**	1012.494567	506.750922	995.468018	498.237647	994.484002	497.745639	**10**
12	***1118.522512***	559.764894	1101.495963	551.251619	1100.511947	550.759611	**G**	925.462539	463.234908	908.435990	454.721633	907.451974	454.229625	**9**
13	***1205.554540***	603.280908	1188.527991	594.767633	1187.543975	594.275625	**S**	868.441075	434.724176	851.414526	426.210901	850.430510	425.718893	**8**
14	***1262.576004***	631.791640	1245.549455	623.278365	1244.565439	622.786357	**G**	**781.409047**	391.208162	764.382498	382.694887	763.398482	382.202879	**7**
15	***1363.623683***	682.315479	1346.597134	673.802205	1345.613118	673.310197	**T**	724.387583	362.697430	707.361034	354.184155	706.377018	353.692147	**6**
16	***1478.650626***	739.828951	1461.624077	731.315677	1460.640061	730.823668	**D**	**623.339904**	312.173590	606.313355	303.660316	605.329339	303.168308	**5**
17	***1625.719040***	813.363158	1608.692491	804.849884	1607.708475	804.357875	**F**	**508.312961**	254.660118	491.286412	246.146844	490.302396	245.654836	**4**
18	***1726.766719***	863.886998	1709.740170	855.373723	1708.756154	854.881715	**T**	**361.244547**	181.125911	344.217998	172.612637	343.233982	172.120629	**3**
19	***1839.850783***	920.429029	1822.824234	911.915755	1821.840218	911.423747	**L**	260.196868	130.602072	243.170319	122.088797			**2**

20							**K**	147.112804	74.060040	130.086255	65.546765			**1**



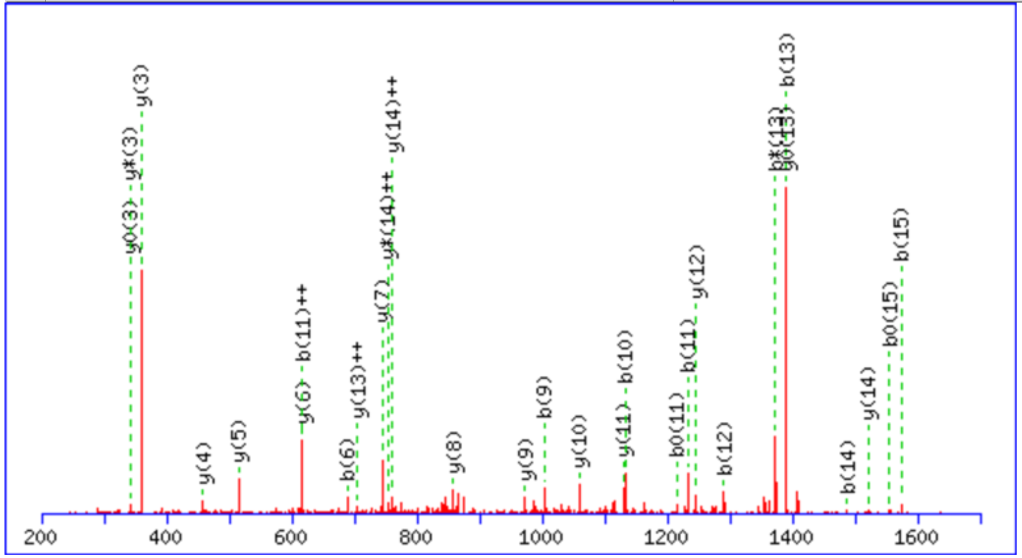
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 05 - S_B-3 **Fraction:** S_B-3

Match to Query 12390: 1746.919048 from(874.466800,2+)
Title: OECHL100317_07.17875.17875.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 86
Expect: 3e-007**Matches :** 29/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	618.349740	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**

6	**689.386854**	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	**1486.778787**	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**

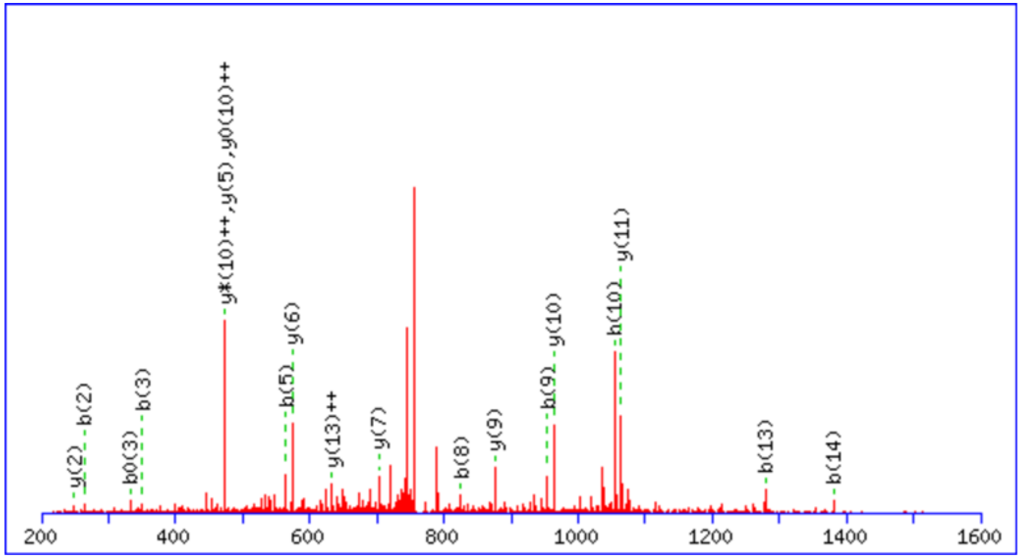


Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 05 - S_B-3 **Fraction:** S_B-3

Match to Query 10149: 1525.727048 from(763.870800,2+)
Title: OECHL100317_07.11159.11159.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64
Expect: 5.1e-005**Matches :** 19/150 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	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	***350.134661***	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**
4	463.218725	232.113001			445.208160	223.107718	**L**	1177.605909	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	**9**
8	***825.362488***	413.184882			807.351923	404.179599	**S**	789.410110	395.208693	772.383561	386.695418	771.399545	386.203410	**8**
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	**7**
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	**6**
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	**5**
12	1208.542973	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	376.219061	188.613168	359.192512	180.099894	358.208496	179.607886	**4**
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	**3**
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



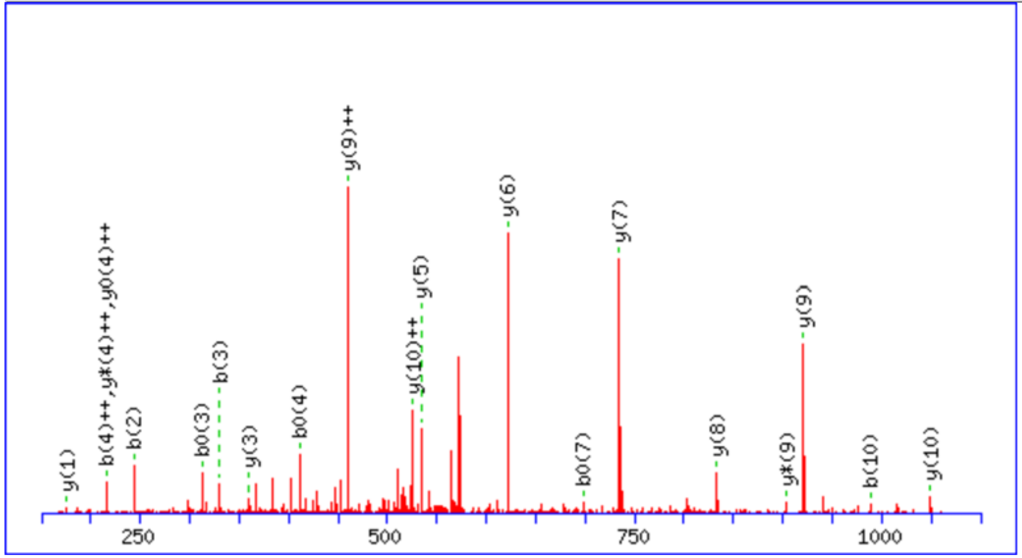
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 05 - S_B-3 **Fraction:** S_B-3

Match to Query 5746: 1161.634848 from(581.824700,2+)
Title: OECHL100317_07.5602.5602.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_07.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00019**Matches :** 20/94 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					**I**							**11**
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637	**10**
3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340	**9**
4	429.234375	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326	**8**
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119	**7**
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087	**6**

7	716.382495	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073	**5**
8	803.414523	402.210899			785.403958	393.205617	**S**	447.267407	224.137342	430.240858	215.624067	429.256842	215.132059	**4**
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053			**3**
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



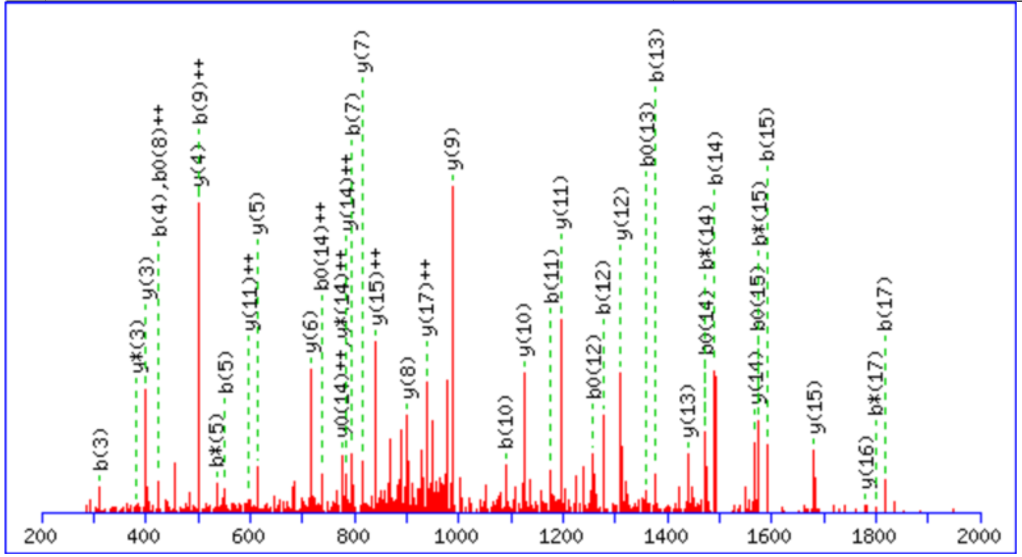
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 39 - OPC-3 **Fraction:** OPC-3

Match to Query 14965: 1990.026448 from(996.020500,2+)
Title: OECHL100317_05.10073.10073.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 84
Expect: 4.5e-007**Matches :** 43/186 fragment ions using 81 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**18**

2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	**424.255445**	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	**552.314023**	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	680.372601	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**
7	**795.399544**	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	**1177.559626**	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	**1377.675719**	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510			**3**
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**

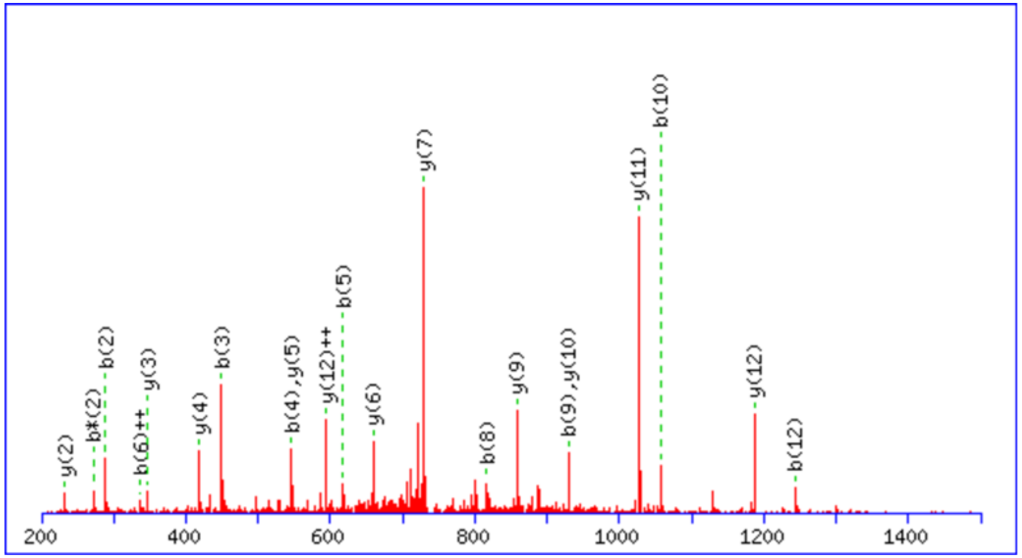


Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 39 - OPC-3 **Fraction:** OPC-3

Match to Query 10374: 1473.646048 from(737.830300,2+)
Title: OECHL100317_05.7977.7977.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62
Expect: 3.1e-005**Matches :** 21/128 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	161.037925	81.022600					**C**							**14**
2	**289.096503**	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.809312	**13**
3	**449.127152**	225.067214	432.100603	216.553940			**C**	***1186.563334***	593.785305	1169.536785	585.272031	1168.552769	584.780023	**12**
4	**546.179916**	273.593596	529.153367	265.080322			**P**	***1026.532685***	513.769981	1009.506136	505.256706	1008.522120	504.764698	**11**
5	**617.217030**	309.112153	600.190481	300.598879			**A**	***929.479921***	465.243599	912.453372	456.730324	911.469356	456.238316	**10**
6	674.238494	337.622885	657.211945	329.109611			**G**	***858.442807***	429.725042	841.416258	421.211767	840.432242	420.719759	**9**
7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
8	**816.312722**	408.659999	799.286173	400.146725			**A**	***730.384229***	365.695753	713.357680	357.182478	712.373664	356.690470	**7**
9	**929.396786**	465.202031	912.370237	456.688757			**L**	***659.347115***	330.177196	642.320566	321.663921	641.336550	321.171913	**6**
10	**1057.455364**	529.231320	1040.428815	520.718046			**Q**	***546.263051***	273.635164	529.236502	265.121889	528.252486	264.629881	**5**
11	1128.492478	564.749877	1111.465929	556.236603			**A**	***418.204473***	209.605874	401.177924	201.092600	400.193908	200.600592	**4**
12	**1243.519421**	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
13	1300.540885	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



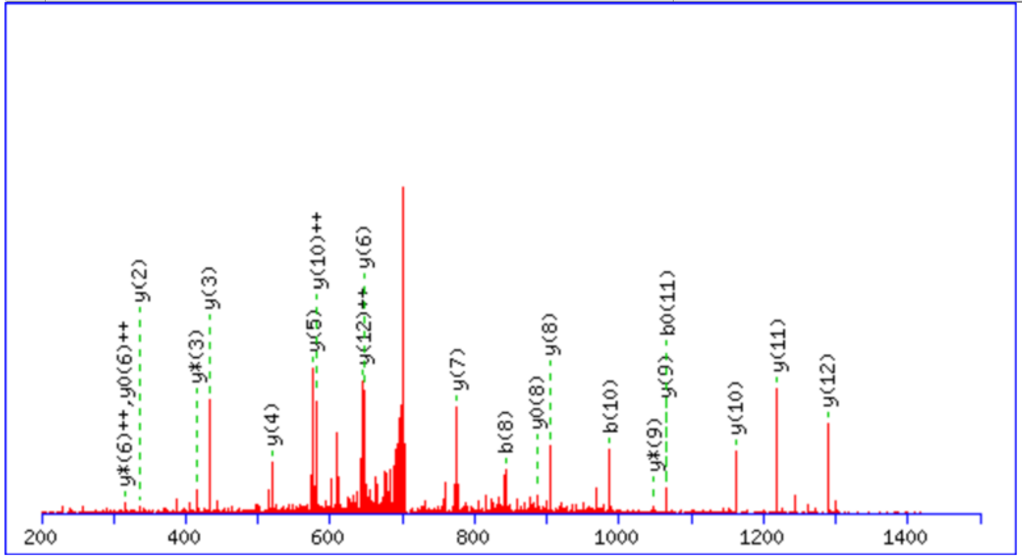
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 39 - OPC-3 **Fraction:** OPC-3

Match to Query 9691: 1416.624048 from(709.319300,2+)
Title: OECHL100317_05.2329.2329.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 84
Expect: 2.4e-007**Matches :** 21/128 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			K							13
2	200.139353	100.573315	183.112804	92.060040			A	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.266422	12
3	257.160817	129.084047	240.134268	120.570772			G	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.747865	11
4	354.213581	177.610429	337.187032	169.097154			P	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.237133	10
5	514.244230	257.625753	497.217681	249.112479			C	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.710751	9
6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	E	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.695427	8

7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.174130	**7**
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.144841	**6**
9	899.403979	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.626284	**5**
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.115552	**4**
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546			**3**
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

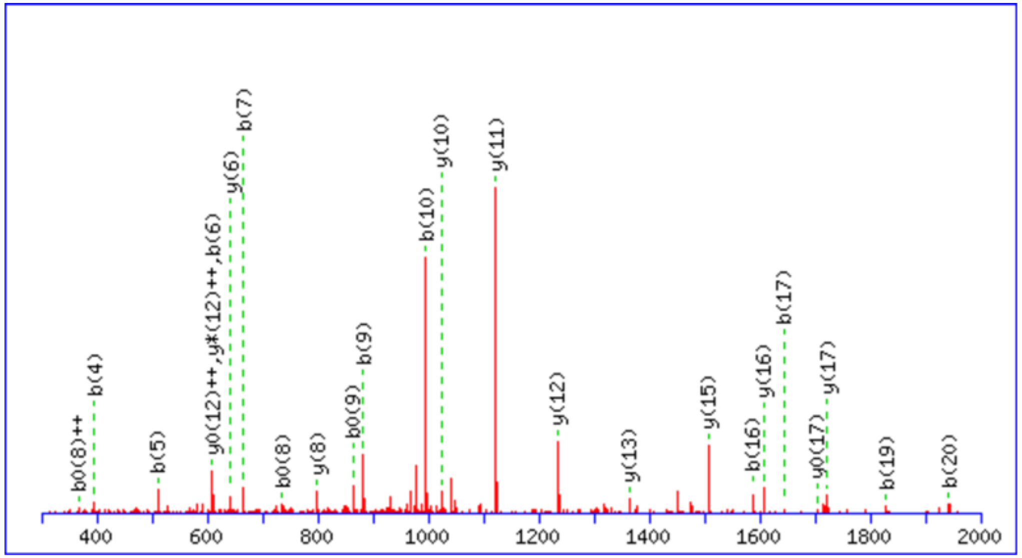


Peptide View

MS/MS Fragmentation of **AADHDVGSELPPEGVLGALLR**
Found in **IPI00002280**, Tax_Id=9606 Gene_Symbol=PCSK1N ProSAAS
Experiment: 39 - OPC-3 **Fraction:** OPC-3

Match to Query 15717: 2115.097448 from(1058.556000,2+)
Title: OECHL100317_05.20857.20857.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 2115.096024**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 83
Expect: 6.2e-007**Matches :** 25/180 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833			A							21
2	143.081504	72.044390			A	2045.066196	1023.036736	2028.039647	1014.523461	2027.055631	1014.031453	20
3	258.108447	129.557862	240.097882	120.552579	D	1974.029082	987.518179	1957.002533	979.004904	1956.018517	978.512896	19
4	***395.167359***	198.087317	377.156794	189.082035	H	1859.002139	930.004707	1841.975590	921.491433	1840.991574	920.999425	18
5	***510.194302***	255.600789	492.183737	246.595507	D	***1721.943227***	861.475251	1704.916678	852.961977	1703.932662	852.469969	17
6	***609.262716***	305.134996	591.252151	296.129714	V	***1606.916284***	803.961780	1589.889735	795.448505	1588.905719	794.956497	16
7	***666.284180***	333.645728	648.273615	324.640446	G	***1507.847870***	754.427573	1490.821321	745.914298	1489.837305	745.422290	15
8	753.316208	377.161742	735.305643	368.156460	S	1450.826406	725.916841	1433.799857	717.403566	1432.815841	716.911558	14
9	***882.358801***	441.683039	864.348236	432.677756	E	***1363.794378***	682.400827	1346.767829	673.887552	1345.783813	673.395544	13
10	***995.442865***	498.225071	977.432300	489.219788	L	***1234.751785***	617.879530	1217.725236	609.366256	1216.741220	608.874248	12
11	1092.495629	546.751453	1074.485064	537.746170	P	***1121.667721***	561.337498	1104.641172	552.824224	1103.657156	552.332216	11
12	1189.548393	595.277835	1171.537828	586.272552	P	***1024.614957***	512.811116	1007.588408	504.297842	1006.604392	503.805834	10
13	1318.590986	659.799131	1300.580421	650.793848	E	927.562193	464.284734	910.535644	455.771460	909.551628	455.279452	9
14	1375.612450	688.309863	1357.601885	679.304580	G	***798.519600***	399.763438	781.493051	391.250163			8
15	1474.680864	737.844070	1456.670299	728.838787	V	741.498136	371.252706	724.471587	362.739431			7
16	***1587.764928***	794.386102	1569.754363	785.380819	L	***642.429722***	321.718499	625.403173	313.205224			6
17	***1644.786392***	822.896834	1626.775827	813.891551	G	529.345658	265.176467	512.319109	256.663192			5
18	1715.823506	858.415391	1697.812941	849.410108	A	472.324194	236.665735	455.297645	228.152460			4
19	***1828.907570***	914.957423	1810.897005	905.952140	L	401.287080	201.147178	384.260531	192.633903			3
20	***1941.991634***	971.499455	1923.981069	962.494172	L	288.203016	144.605146	271.176467	136.091872			2
21					R	175.118952	88.063114	158.092403	79.549840			1



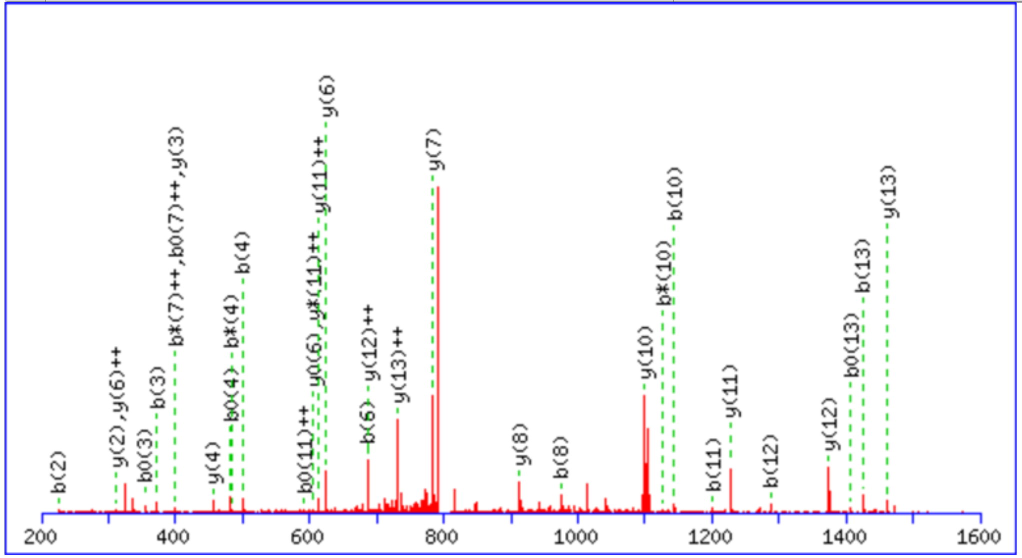
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 39 - OPC-3 **Fraction:** OPC-3

Match to Query 11625: 1597.706048 from(799.860300,2+)
Title: OECHL100317_05.2480.2480.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62
Expect: 3.4e-005**Matches :** 33/144 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	138.066188	69.536732					**H**							**14**
2	**225.098216**	113.052746			207.087651	104.047463	**S**	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.325325	**13**
3	**372.166630**	186.586953			354.156065	177.581671	**F**	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.809311	**12**
4	**500.261593**	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	**11**
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	**10**
6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	1042.437069	521.722173	1025.410520	513.208898	1024.426504	512.716890	**9**

7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	E	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	8
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	C	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	7
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	P	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	6
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	A	527.268470	264.137873	510.241921	255.624598	509.257905	255.132590	5
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	G	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.614033	4
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	S	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	3
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	H	***312.177864***	156.592570	295.151315	148.079295			2
14							R	175.118952	88.063114	158.092403	79.549839			1



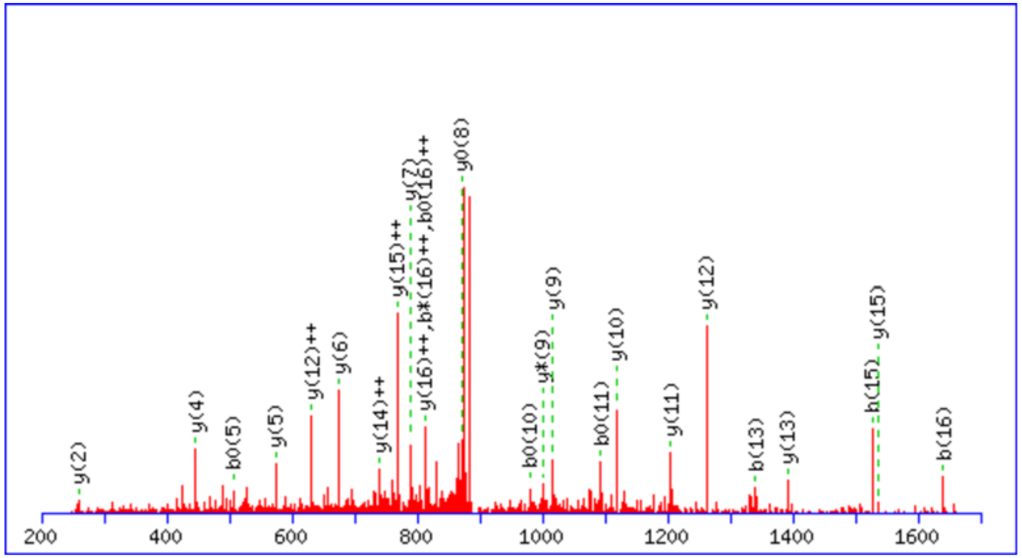
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 39 - OPC-3 **Fraction:** OPC-3

Match to Query 13743: 1784.880448 from(893.447500,2+)
Title: OECHL100317_05.8067.8067.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 69

Expect: 2e-005**Matches :** 25/170 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	164.070605	82.538940					**Y**							**17**
2	251.102633	126.054954			233.092068	117.049672	**S**	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.909941	**16**
3	308.124097	154.565687			290.113532	145.560404	**G**	***1535.791144***	768.399210	1518.764595	759.885936	1517.780579	759.393928	**15**
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.883195	**14**
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.367182	**13**
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.845885	**12**
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.335153	**11**
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.819139	**10**
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.295299	**9**
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.266010	**8**
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.742171	**7**
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.200139	**6**
13	**1340.632852**	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.676299	**5**
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	**4**
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**



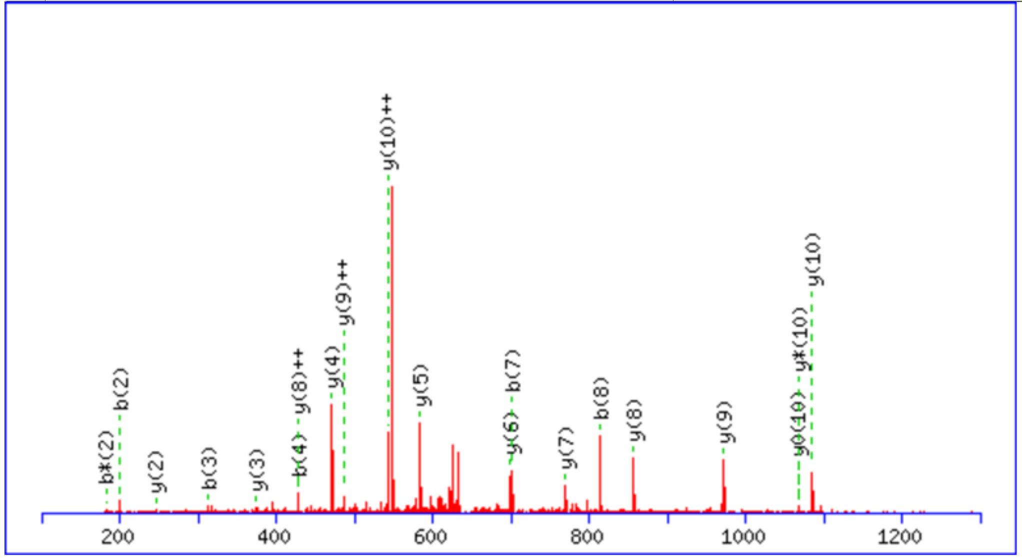
Peptide View

MS/MS Fragmentation of **AQLDSADIPKAR**
Found in **IPI00026303**, Tax_Id=9606 Gene_Symbol=PI15 Peptidase inhibitor 15
Experiment: 39 - OPC-3 **Fraction:** OPC-3

Match to Query 8493: 1283.683848 from(642.849200,2+)
Title: OECHL100317_05.8301.8301.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1283.683334**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54
Expect: 0.00031**Matches :** 20/114 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	72.044390	36.525833					**A**							**12**
2	**200.102968**	100.555122	183.076419	92.041848			**Q**	1213.653527	607.330402	1196.626978	598.817127	1195.642962	598.325119	**11**
3	**313.187032**	157.097154	296.160483	148.583879			**L**	***1085.594949***	543.301113	1068.568400	534.787838	1067.584384	534.295830	**10**
4	**428.213975**	214.610626	411.187426	206.097351	410.203410	205.605343	**D**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
5	515.246003	258.126640	498.219454	249.613365	497.235438	249.121357	**S**	***857.483942***	429.245609	840.457393	420.732335	839.473377	420.240327	**8**
6	586.283117	293.645197	569.256568	285.131922	568.272552	284.639914	**A**	***770.451914***	385.729595	753.425365	377.216321	752.441349	376.724313	**7**

7	**701.310060**	351.158668	684.283511	342.645394	683.299495	342.153386	**D**	***699.414800***	350.211038	682.388251	341.697764	681.404235	341.205756	**6**
8	**814.394124**	407.700700	797.367575	399.187426	796.383559	398.695418	**I**	***584.387857***	292.697567	567.361308	284.184292			**5**
9	911.446888	456.227082	894.420339	447.713808	893.436323	447.221800	**P**	***471.303793***	236.155535	454.277244	227.642260			**4**
10	1039.541851	520.274564	1022.515302	511.761289	1021.531286	511.269281	**K**	***374.251029***	187.629153	357.224480	179.115878			**3**
11	1110.578965	555.793121	1093.552416	547.279846	1092.568400	546.787838	**A**	***246.156066***	123.581671	229.129517	115.068396			**2**
12							**R**	175.118952	88.063114	158.092403	79.549839			**1**



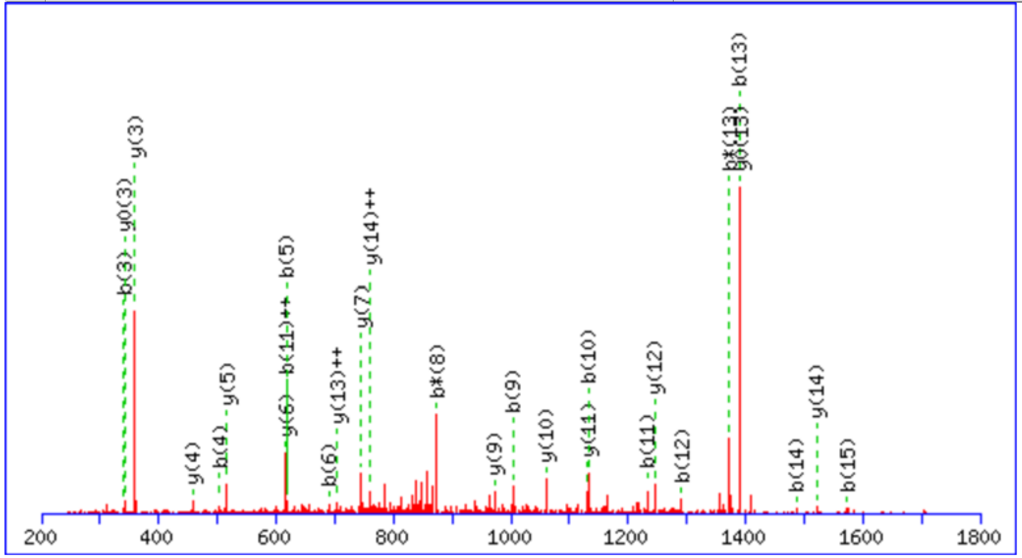
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 39 - OPC-3 **Fraction:** OPC-3

Match to Query 13459: 1746.917248 from(874.465900,2+)
Title: OECHL100317_05.17438.17438.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 80
Expect: 1e-006**Matches :** 28/156 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	114.091340	57.549308					**L**							**16**
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	**15**
3	***340.259468***	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	**14**
4	***503.322797***	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	**13**
5	***618.349740***	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	**12**
6	***689.386854***	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	**11**
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	**10**
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	**9**
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	858.467958	429.737617	841.441409	421.224343	840.457393	420.732335	**8**
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	**7**
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	**6**
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	**5**
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	**4**
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	**3**
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	**2**
16							**R**	175.118952	88.063114	158.092403	79.549839			**1**

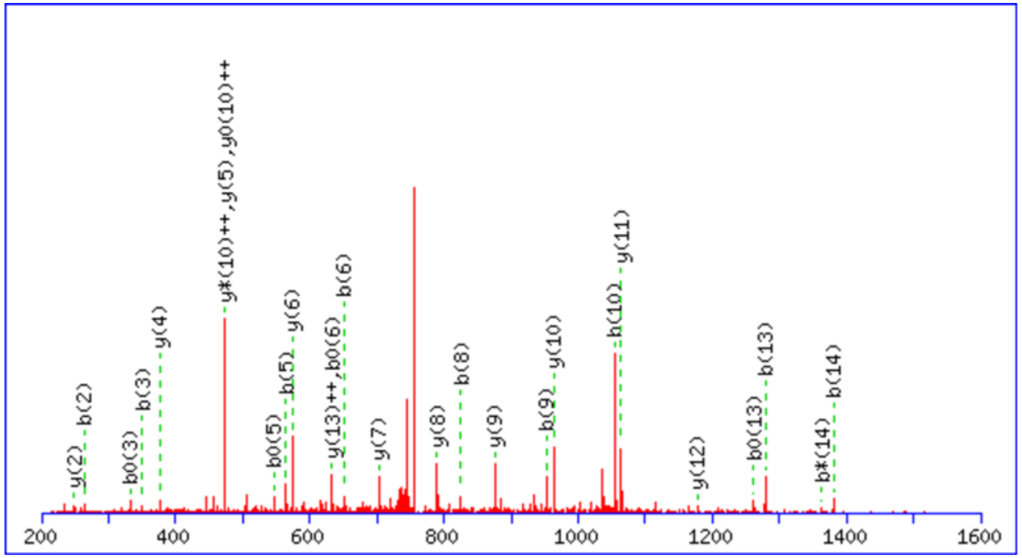


Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 39 - OPC-3 **Fraction:** OPC-3

Match to Query 10814: 1525.726448 from(763.870500,2+)
Title: OECHL100317_05.10929.10929.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 2.2e-006**Matches :** 27/150 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	***350.134661***	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	***651.298432***	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	**9**
8	***825.362488***	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.203410	**8**
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	**7**
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	**6**
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	**5**
12	1208.542973	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	**4**
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	**3**
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



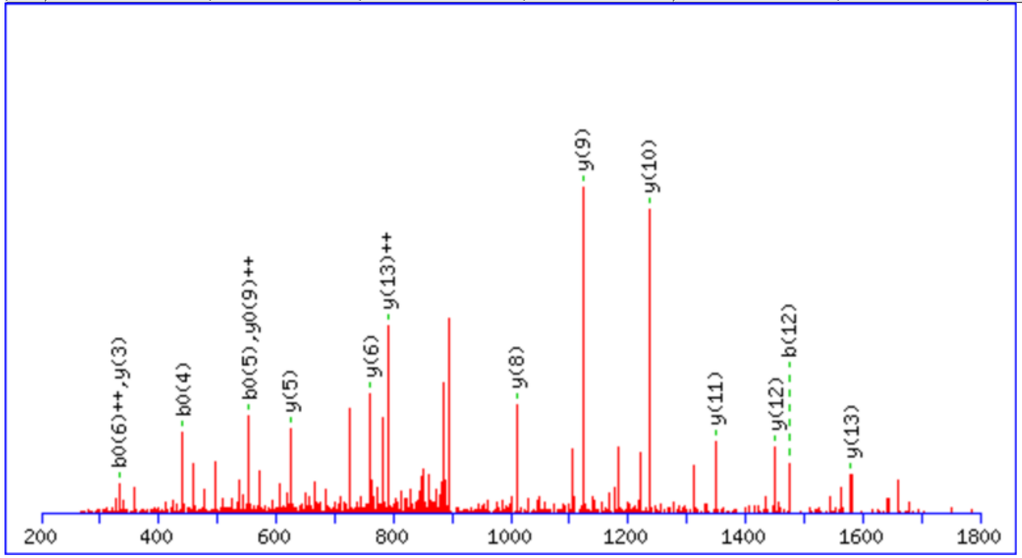
Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 39 - OPC-3 **Fraction:** OPC-3

Match to Query 13866: 1805.932248 from(903.973400,2+)
Title: OECHL100317_05.20313.20313.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 68
Expect: 2.1e-005**Matches :** 15/160 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	115.050203	58.028740	98.023654	49.515465			**N**							**15**
2	228.134267	114.570771	211.107718	106.057497			**I**	1692.895549	846.951413	1675.869000	838.438138	1674.884984	837.946130	**14**
3	357.176860	179.092068	340.150311	170.578793	339.166295	170.086785	**E**	***1579.811485***	790.409381	1562.784936	781.896106	1561.800920	781.404098	**13**
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	**T**	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.882802	**12**
5	571.308603	286.157940	554.282054	277.644665	553.298038	277.152657	**I**	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.358962	**11**
6	684.392667	342.699972	667.366118	334.186697	666.382102	333.694689	**I**	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.816930	**10**

7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	**N**	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.274898	**9**
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	**T**	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.253435	**8**
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	**F**	908.462479	454.734878	891.435930	446.221603	890.451914	445.729595	**7**
10	1183.610599	592.308938	1166.584050	583.795663	1165.600034	583.303655	**H**	***761.394065***	381.200671	744.367516	372.687396	743.383500	372.195388	**6**
11	1311.669177	656.338227	1294.642628	647.824952	1293.658612	647.332944	**Q**	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.665932	**5**
12	1474.732506	737.869891	1457.705957	729.356617	1456.721941	728.864609	**Y**	496.276575	248.641926	479.250026	240.128651	478.266010	239.636643	**4**
13	1561.764534	781.385905	1544.737985	772.872631	1543.753969	772.380623	**S**	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.104979	**3**
14	1660.832948	830.920112	1643.806399	822.406838	1642.822383	821.914830	**V**	246.181218	123.594247	229.154669	115.080973			**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



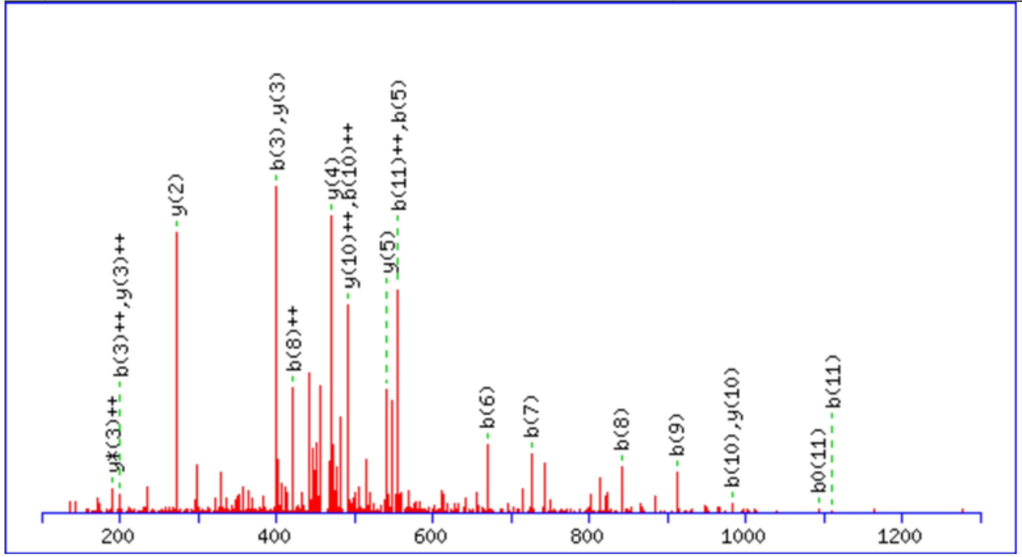
Peptide View

MS/MS Fragmentation of **VYHVGLGDAAQPR**
Found in **IPI00297252**, Tax_Id=9606 Gene_Symbol=SULF2 Isoform 1 of Extracellular sulfatase Sulf-2
Experiment: 39 - OPC-3 **Fraction:** OPC-3

Match to Query 9449: 1381.711272 from(461.577700,3+)
Title: OECHL100317_05.9232.9232.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_05.raw

Monoisotopic mass of neutral peptide Mr(calc): 1381.710251**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64
Expect: 3.7e-005**Matches :** 21/100 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	100.075690	50.541483					**V**							**13**
2	263.139019	132.073148					**Y**	1283.649112	642.328194	1266.622563	633.814920	1265.638547	633.322912	**12**
3	***400.197931***	**200.602603**					**H**	1120.585783	560.796530	1103.559234	552.283255	1102.575218	551.791247	**11**
4	499.266345	250.136811					**V**	**983.526871**	492.267074	966.500322	483.753799	965.516306	483.261791	**10**
5	***556.287809***	278.647543					**G**	884.458457	442.732867	867.431908	434.219592	866.447892	433.727584	**9**
6	***669.371873***	335.189575					**L**	827.436993	414.222135	810.410444	405.708860	809.426428	405.216852	**8**
7	***726.393337***	363.700307					**G**	714.352929	357.680103	697.326380	349.166828	696.342364	348.674820	**7**
8	***841.420280***	**421.213778**			823.409715	412.208496	**D**	657.331465	329.169371	640.304916	320.656096	639.320900	320.164088	**6**
9	***912.457394***	456.732335			894.446829	447.727053	**A**	**542.304522**	271.655899	525.277973	263.142625			**5**
10	***983.494508***	**492.250892**			965.483943	483.245610	**A**	**471.267408**	236.137342	454.240859	227.624068			**4**
11	***1111.553086***	**556.280181**	1094.526537	547.766907	1093.542521	547.274899	**Q**	**400.230294**	200.618785	383.203745	192.105511			**3**
12	1208.605850	604.806563	1191.579301	596.293289	1190.595285	595.801281	**P**	**272.171716**	136.589496	255.145167	128.076221			**2**
13							**R**	175.118952	88.063114	158.092403	79.549839			**1**

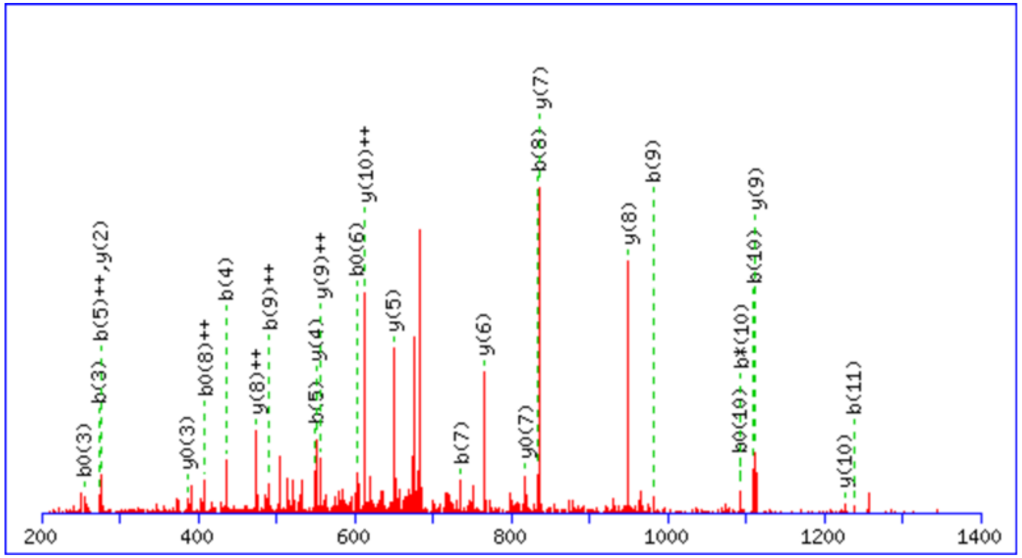


Peptide View

MS/MS Fragmentation of **GTNYLADVFEKK**
Found in **IPI00219806**, Tax_Id=9606 Gene_Symbol=S100A7 Protein S100-A7
Experiment: 39 - OPC-3 **Fraction:** OPC-3

Match to Query 9466: 1383.704848 from(692.859700,2+)
Title: OECHL100317_05.16680.16680.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1383.703415**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 0.00028**Matches :** 28/122 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					**G**							**12**
2	159.076419	80.041847			141.065854	71.036565	**T**	1327.689244	664.348260	1310.662695	655.834986	1309.678679	655.342977	**11**
3	***273.119346***	137.063311	256.092797	128.550037	255.108781	128.058029	**N**	***1226.641565***	613.824420	1209.615016	605.311146	1208.631000	604.819138	**10**
4	***436.182675***	218.594976	419.156126	210.081701	418.172110	209.589693	**Y**	***1112.598638***	556.802957	1095.572089	548.289682	1094.588073	547.797674	**9**
5	***549.266739***	275.137008	532.240190	266.623733	531.256174	266.131725	**L**	***949.535309***	475.271292	932.508760	466.758018	931.524744	466.266010	**8**
6	620.303853	310.655565	603.277304	302.142290	602.293288	301.650282	**A**	***836.451245***	418.729260	819.424696	410.215986	818.440680	409.723978	**7**
7	***735.330796***	368.169036	718.304247	359.655761	717.320231	359.163753	**D**	***765.414131***	383.210703	748.387582	374.697429	747.403566	374.205421	**6**
8	***834.399210***	417.703243	817.372661	409.189968	816.388645	408.697960	**V**	***650.387188***	325.697232	633.360639	317.183957	632.376623	316.691949	**5**
9	***981.467624***	491.237450	964.441075	482.724175	963.457059	482.232167	**F**	***551.318774***	276.163025	534.292225	267.649750	533.308209	267.157742	**4**
10	***1110.510217***	555.758746	1093.483668	547.245472	1092.499652	546.753464	**E**	404.250360	202.628818	387.223811	194.115543	386.239795	193.623535	**3**
11	***1238.605180***	619.806228	1221.578631	611.292953	1220.594615	610.800945	**K**	***275.207767***	138.107521	258.181218	129.594247			**2**
12							**K**	147.112804	74.060040	130.086255	65.546765			**1**



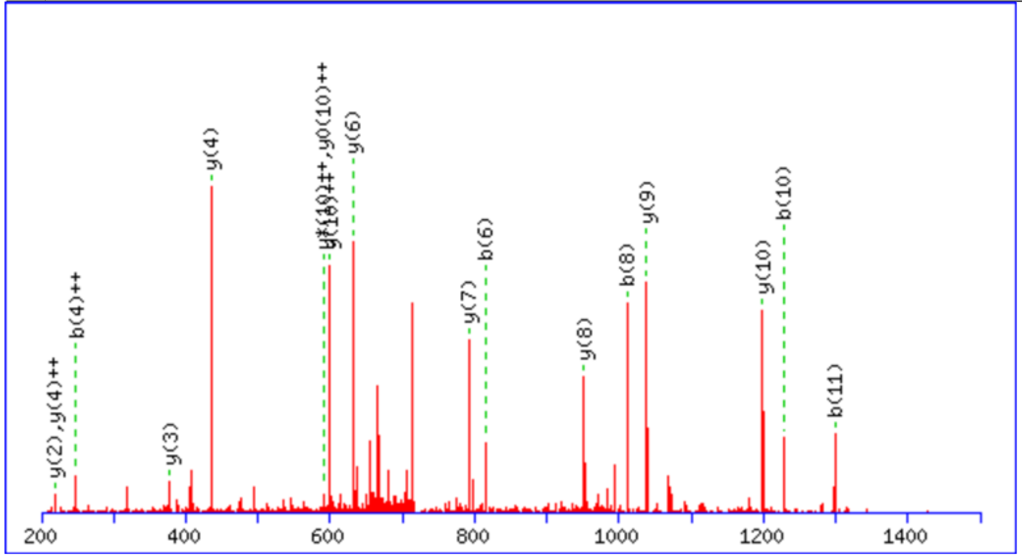
Peptide View

MS/MS Fragmentation of **SCCSCCPVGCAK**
Found in **IPI00008752**, Tax_Id=9606 Gene_Symbol=MT1L;MT1G;MT1JP;MT1E Isoform 1 of Metallothionein-1G
Experiment: 39 - OPC-3 **Fraction:** OPC-3

Match to Query 10055: 1444.504448 from(723.259500,2+)
Title: OECHL100317_05.3477.3477.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_05.raw
Monoisotopic mass of neutral peptide Mr(calc): 1444.502609**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 3.4e-006**Matches :** 18/94 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**12**
2	**248.069953**	124.538614	230.059388	115.533332	**C**	1358.477833	679.742555	1341.451284	671.229280	1340.467268	670.737272	**11**
3	408.100602	204.553939	390.090037	195.548657	**C**	***1198.447184***	599.727230	1181.420635	591.213956	1180.436619	590.721948	**10**
4	495.132630	248.069953	477.122065	239.064671	**S**	***1038.416535***	519.711906	1021.389986	511.198631	1020.405970	510.706623	**9**
5	655.163279	328.085278	637.152714	319.079995	**C**	***951.384507***	476.195892	934.357958	467.682617			**8**
6	**815.193928**	408.100602	797.183363	399.095320	**C**	***791.353858***	396.180567	774.327309	387.667293			**7**

7	912.246692	456.626984	894.236127	447.621702	**P**	***631.323209***	316.165243	614.296660	307.651968			**6**
8	**1011.315106**	506.161191	993.304541	497.155909	**V**	534.270445	267.638861	517.243896	259.125586			**5**
9	1068.336570	534.671923	1050.326005	525.666641	**G**	***435.202031***	218.104654	418.175482	209.591379			**4**
10	**1228.367219**	614.687248	1210.356654	605.681965	**C**	***378.180567***	189.593921	361.154018	181.080647			**3**
11	**1299.404333**	650.205805	1281.393768	641.200522	**A**	***218.149918***	109.578597	201.123369	101.065322			**2**
12					**K**	147.112804	74.060040	130.086255	65.546765			**1**



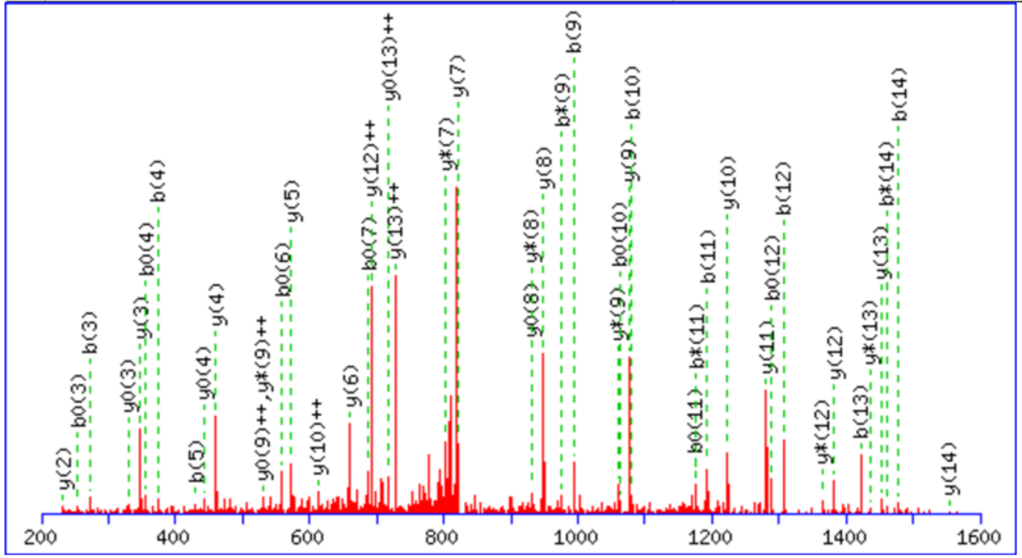
Peptide View

MS/MS Fragmentation of **VTATGFQQCSLIDGR**
Found in **IPI00333140**, Tax_Id=9606 Gene_Symbol=DNER Delta and Notch-like epidermal growth factor-related receptor
Experiment: 21 - NOPB3 **Fraction:** NOPB3

Match to Query 10898: 1651.799248 from(826.906900,2+)
Title: OECHL100317_03.13303.13303.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1651.798828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 107
Expect: 3e-009**Matches :** 46/150 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	100.075690	50.541483					**V**							**15**
2	201.123369	101.065322			183.112804	92.060040	**T**	***1553.737670***	777.372473	1536.711121	768.859198	1535.727105	768.367190	**14**
3	**272.160483**	136.583879			254.149918	127.578597	**A**	***1452.689991***	726.848633	1435.663442	718.335359	1434.679426	717.843351	**13**
4	**373.208162**	187.107719			355.197597	178.102437	**T**	***1381.652877***	691.330076	1364.626328	682.816802	1363.642312	682.324794	**12**
5	**430.229626**	215.618451			412.219061	206.613169	**G**	***1280.605198***	640.806237	1263.578649	632.292962	1262.594633	631.800954	**11**
6	577.298040	289.152658			559.287475	280.147376	**F**	***1223.583734***	612.295505	1206.557185	603.782230	1205.573169	603.290222	**10**
7	705.356618	353.181947	688.330069	344.668673	687.346053	344.176665	**Q**	***1076.515320***	538.761298	1059.488771	530.248023	1058.504755	529.756015	**9**
8	833.415196	417.211236	816.388647	408.697962	815.404631	408.205954	**Q**	***948.456742***	474.732009	931.430193	466.218734	930.446177	465.726726	**8**
9	**993.445845**	497.226561	976.419296	488.713286	975.435280	488.221278	**C**	***820.398164***	410.702720	803.371615	402.189445	802.387599	401.697437	**7**
10	**1080.477873**	540.742575	1063.451324	532.229300	1062.467308	531.737292	**S**	***660.367515***	330.687395	643.340966	322.174121	642.356950	321.682113	**6**
11	**1193.561937**	597.284607	1176.535388	588.771332	1175.551372	588.279324	**L**	***573.335487***	287.171381	556.308938	278.658107	555.324922	278.166099	**5**
12	**1306.646001**	653.826638	1289.619452	645.313364	1288.635436	644.821356	**I**	***460.251423***	230.629349	443.224874	222.116075	442.240858	221.624067	**4**
13	**1421.672944**	711.340110	1404.646395	702.826836	1403.662379	702.334827	**D**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
14	**1478.694408**	739.850842	1461.667859	731.337567	1460.683843	730.845559	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**

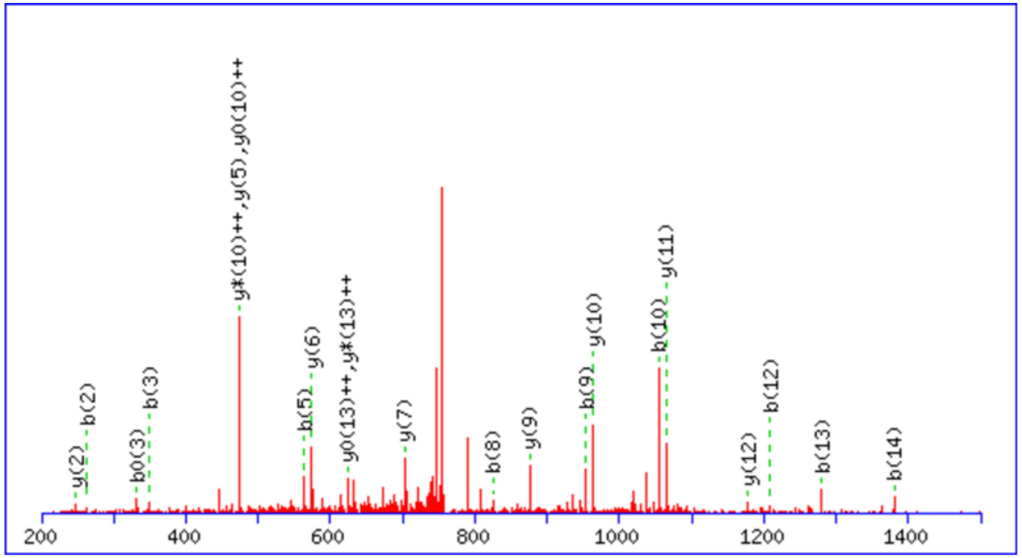


Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 21 - NOPB3 **Fraction:** NOPB3

Match to Query 9813: 1525.725648 from(763.870100,2+)
Title: OECHL100317_03.10767.10767.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 88
Expect: 1.8e-007**Matches :** 22/150 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	116.034219	58.520748			98.023654	49.515465	**D**							**15**
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.351531	**14**
3	***350.134661***	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.817324	**13**
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.301310	**12**
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.759278	**11**
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.235438	**10**
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.719424	**9**
8	***825.362488***	413.184882			807.351923	404.179599	**S**	789.410110	395.208693	772.383561	386.695418	771.399545	386.203410	**8**
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.687396	**7**
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.658107	**6**
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.134268	**5**
12	***1208.542973***	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	376.219061	188.613168	359.192512	180.099894	358.208496	179.607886	**4**
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	**3**
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
15							**K**	147.112804	74.060040	130.086255	65.546765			**1**



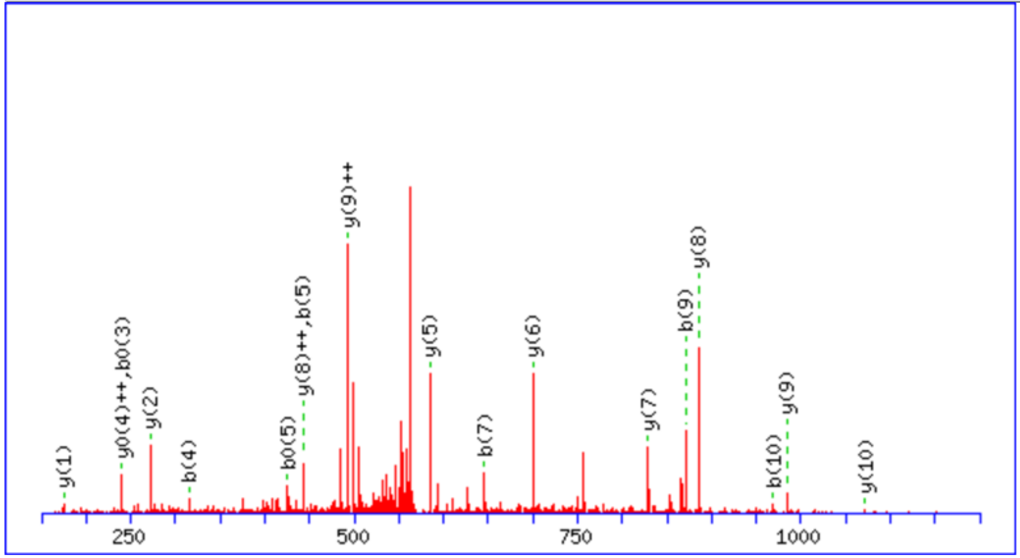
Peptide View

MS/MS Fragmentation of **ASVGQDSPEPR**
Found in **IPI00044369**, Tax_Id=9606 Gene_Symbol=PLXDC2 Isoform 1 of Plexin domain-containing protein 2
Experiment: 21 - NOPB3 **Fraction:** NOPB3

Match to Query 5159: 1141.536248 from(571.775400,2+)
Title: OECHL100317_03.3279.3279.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1141.536362**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 76
Expect: 1.5e-006**Matches :** 18/106 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	72.044390	36.525833					**A**							**11**
2	159.076418	80.041847			141.065853	71.036564	**S**	***1071.506528***	536.256902	1054.479979	527.743628	1053.495963	527.251620	**10**
3	258.144832	129.576054			240.134267	120.570772	**V**	***984.474500***	492.740888	967.447951	484.227614	966.463935	483.735606	**9**
4	**315.166296**	158.086786			297.155731	149.081504	**G**	***885.406086***	443.206681	868.379537	434.693407	867.395521	434.201399	**8**
5	**443.224874**	222.116075	426.198325	213.602801	425.214309	213.110793	**Q**	***828.384622***	414.695949	811.358073	406.182675	810.374057	405.690667	**7**
6	558.251817	279.629547	541.225268	271.116272	540.241252	270.624264	**D**	***700.326044***	350.666660	683.299495	342.153386	682.315479	341.661378	**6**

7	**645.283845**	323.145561	628.257296	314.632286	627.273280	314.140278	**S**	***585.299101***	293.153189	568.272552	284.639914	567.288536	284.147906	**5**
8	742.336609	371.671943	725.310060	363.158668	724.326044	362.666660	**P**	498.267073	249.637174	481.240524	241.123900	480.256508	240.631892	**4**
9	**871.379202**	436.193239	854.352653	427.679965	853.368637	427.187957	**E**	401.214309	201.110792	384.187760	192.597518	383.203744	192.105510	**3**
10	**968.431966**	484.719621	951.405417	476.206347	950.421401	475.714339	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



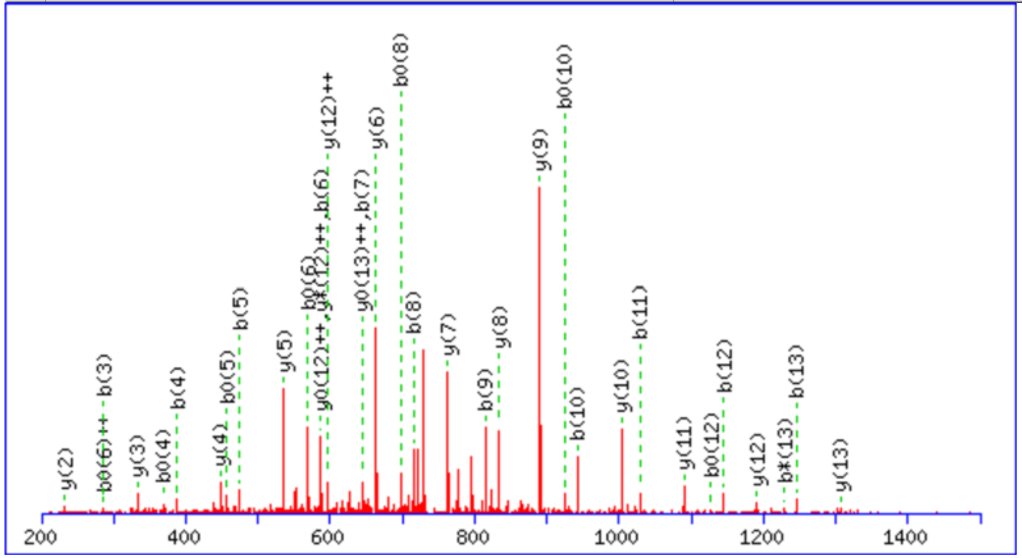
Peptide View

MS/MS Fragmentation of **GLDTSLGAVQSDTGR**
Found in **IPI00289931**, Tax_Id=9606 Gene_Symbol=MADCAM1 MADCAM1 protein
Experiment: 21 - NOPB3 **Fraction:** NOPB3

Match to Query 9345: 1475.722448 from(738.868500,2+)
Title: OECHL100317_03.11053.11053.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1475.721619**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 95
Expect: 4.9e-008**Matches :** 35/142 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	58.028740	29.518008					**G**							**15**

2	171.112804	86.060040					**L**	1419.707414	710.357345	1402.680865	701.844071	1401.696849	701.352063	**14**
3	**286.139747**	143.573512			268.129182	134.568229	**D**	***1306.623350***	653.815313	1289.596801	645.302039	1288.612785	644.810031	**13**
4	**387.187426**	194.097351			369.176861	185.092069	**T**	***1191.596407***	596.301842	1174.569858	587.788567	1173.585842	587.296559	**12**
5	**474.219454**	237.613365			456.208889	228.608082	**S**	***1090.548728***	545.778002	1073.522179	537.264728	1072.538163	536.772719	**11**
6	**587.303518**	294.155397			569.292953	285.150115	**L**	***1003.516700***	502.261988	986.490151	493.748714	985.506135	493.256706	**10**
7	**644.324982**	322.666129			626.314417	313.660847	**G**	***890.432636***	445.719956	873.406087	437.206682	872.422071	436.714674	**9**
8	**715.362096**	358.184686			697.351531	349.179404	**A**	***833.411172***	417.209224	816.384623	408.695950	815.400607	408.203942	**8**
9	**814.430510**	407.718893			796.419945	398.713611	**V**	***762.374058***	381.690667	745.347509	373.177393	744.363493	372.685385	**7**
10	**942.489088**	471.748182	925.462539	463.234908	924.478523	462.742900	**Q**	***663.305644***	332.156460	646.279095	323.643186	645.295079	323.151178	**6**
11	**1029.521116**	515.264196	1012.494567	506.750922	1011.510551	506.258914	**S**	***535.247066***	268.127171	518.220517	259.613897	517.236501	259.121889	**5**
12	**1144.548059**	572.777668	1127.521510	564.264393	1126.537494	563.772385	**D**	***448.215038***	224.611157	431.188489	216.097882	430.204473	215.605874	**4**
13	**1245.595738**	623.301507	1228.569189	614.788233	1227.585173	614.296225	**T**	***333.188095***	167.097685	316.161546	158.584411	315.177530	158.092403	**3**
14	1302.617202	651.812239	1285.590653	643.298965	1284.606637	642.806957	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**

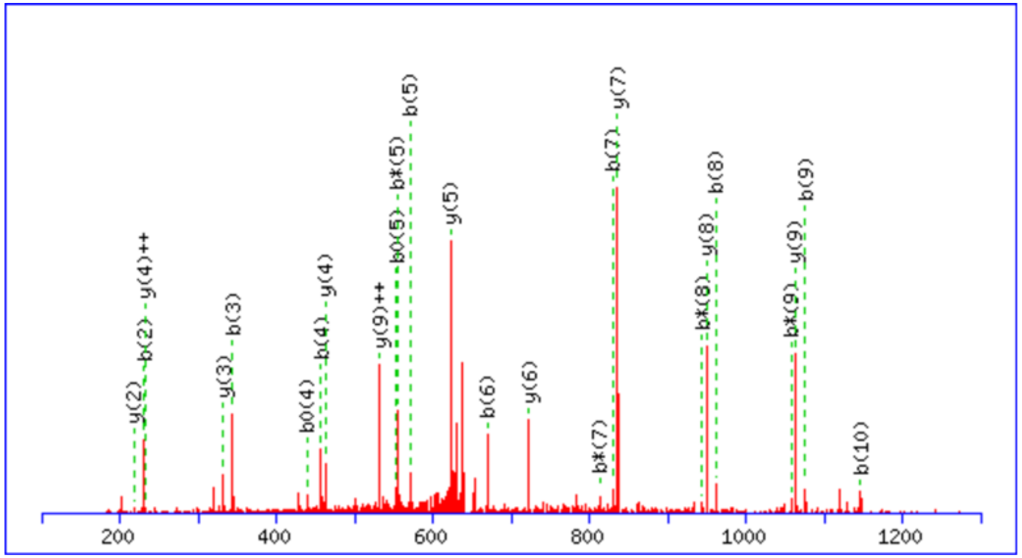


Peptide View

MS/MS Fragmentation of **TELLNVCMNAK**
Found in **IPI00441498**, Tax_Id=9606 Gene_Symbol=FOLR1 Folate receptor alpha
Experiment: 21 - NOPB3 **Fraction:** NOPB3

Match to Query 7592: 1291.626448 from(646.820500,2+)
Title: OECHL100317_03.13353.13353.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1291.626419**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60
Expect: 8.4e-005**Matches :** 25/94 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	102.054955	51.531116			84.044390	42.525833	**T**							**11**
2	***231.097548***	116.052412			213.086983	107.047130	**E**	1191.586041	596.296659	1174.559492	587.783384	1173.575476	587.291376	**10**
3	***344.181612***	172.594444			326.171047	163.589162	**L**	**1062.543448**	531.775362	1045.516899	523.262088			**9**
4	***457.265676***	229.136476			439.255111	220.131194	**L**	**949.459384**	475.233330	932.432835	466.720056			**8**
5	***571.308603***	286.157940	554.282054	277.644665	553.298038	277.152657	**N**	**836.375320**	418.691298	819.348771	410.178023			**7**
6	***670.377017***	335.692147	653.350468	327.178872	652.366452	326.686864	**V**	**722.332393**	361.669835	705.305844	353.156560			**6**
7	***830.407666***	415.707471	813.381117	407.194197	812.397101	406.702189	**C**	**623.263979**	312.135628	606.237430	303.622353			**5**
8	***961.448151***	481.227714	944.421602	472.714439	943.437586	472.222431	**M**	**463.233330**	232.120303	446.206781	223.607028			**4**
9	***1075.491078***	538.249177	1058.464529	529.735903	1057.480513	529.243895	**N**	**332.192845**	166.600060	315.166296	158.086786			**3**
10	***1146.528192***	573.767734	1129.501643	565.254460	1128.517627	564.762452	**A**	**218.149918**	109.578597	201.123369	101.065322			**2**
11							**K**	147.112804	74.060040	130.086255	65.546765			**1**



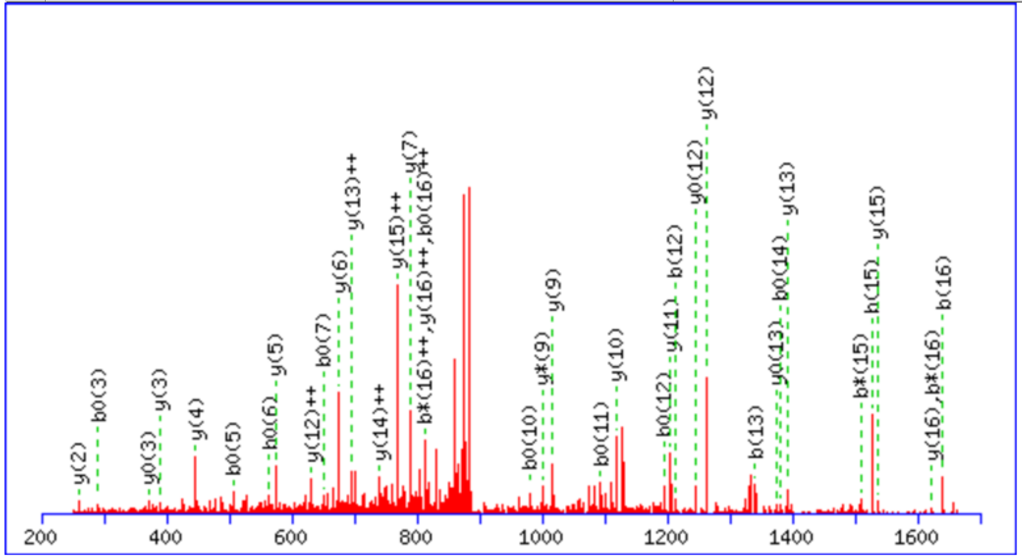
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 21 - NOPB3 **Fraction:** NOPB3

Match to Query 11849: 1784.880048 from(893.447300,2+)
Title: OECHL100317_03.7643.7643.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77
Expect: 2.8e-006**Matches :** 38/170 fragment ions using 74 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					**Y**							**17**
2	251.102633	126.054954			233.092068	117.049672	**S**	***1622.823172***	811.915224	1605.796623	803.401950	1604.812607	802.909941	**16**
3	308.124097	154.565687			290.113532	145.560404	**G**	***1535.791144***	768.399210	1518.764595	759.885936	1517.780579	759.393928	**15**
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.883195	**14**
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.367182	**13**
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.845885	**12**

7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.335153	**11**
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.819139	**10**
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.295299	**9**
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.266010	**8**
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.742171	**7**
12	**1212.537889**	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.200139	**6**
13	**1340.632852**	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.676299	**5**
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	**4**
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	***389.239461***	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**

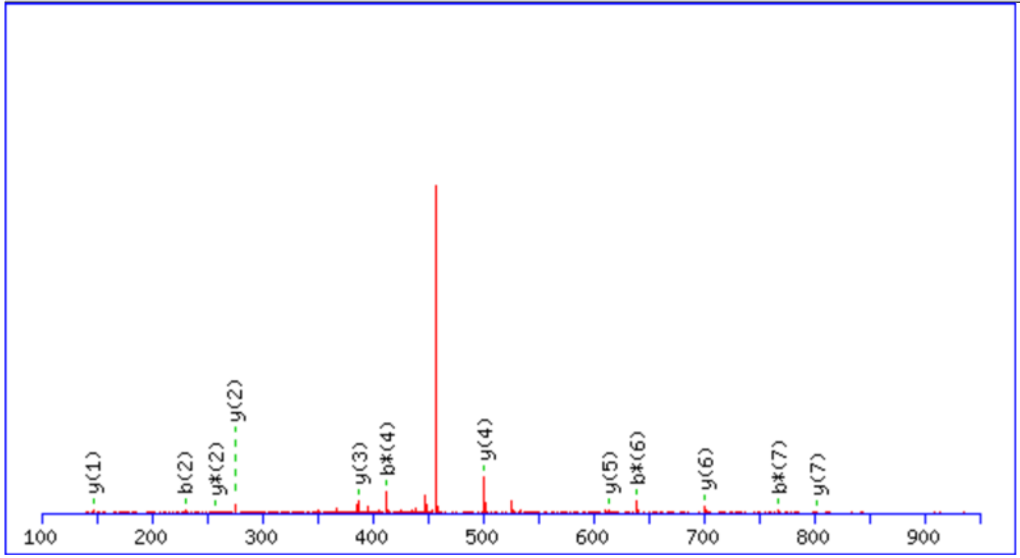


Peptide View

MS/MS Fragmentation of **QTSILIQK**
Found in **IPI00020687**, Tax_Id=9606 Gene_Symbol=SPINK1 Pancreatic secretory trypsin inhibitor
Experiment: 21 - NOPB3 **Fraction:** NOPB3

Match to Query 2085: 929.554648 from(465.784600,2+)
Title: OECHL100317_03.8180.8180.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 929.554565**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59
Expect: 4.7e-005**Matches :** 12/72 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	129.065854	65.036565	112.039305	56.523291			**Q**							**8**
2	230.113533	115.560405	213.086984	107.047130	212.102968	106.555122	**T**	***802.503281***	401.755279	785.476732	393.242004	784.492716	392.749996	**7**
3	317.145561	159.076418	300.119012	150.563144	299.134996	150.071136	**S**	***701.455602***	351.231439	684.429053	342.718165	683.445037	342.226157	**6**
4	430.229625	215.618450	413.203076	207.105176	412.219060	206.613168	**I**	***614.423574***	307.715425	597.397025	299.202151			**5**
5	543.313689	272.160483	526.287140	263.647208	525.303124	263.155200	**L**	***501.339510***	251.173393	484.312961	242.660119			**4**
6	656.397753	328.702515	639.371204	320.189240	638.387188	319.697232	**I**	***388.255446***	194.631361	371.228897	186.118087			**3**
7	784.456331	392.731804	767.429782	384.218529	766.445766	383.726521	**Q**	***275.171382***	138.089329	258.144833	129.576055			**2**
8							**K**	***147.112804***	74.060040	130.086255	65.546765			**1**



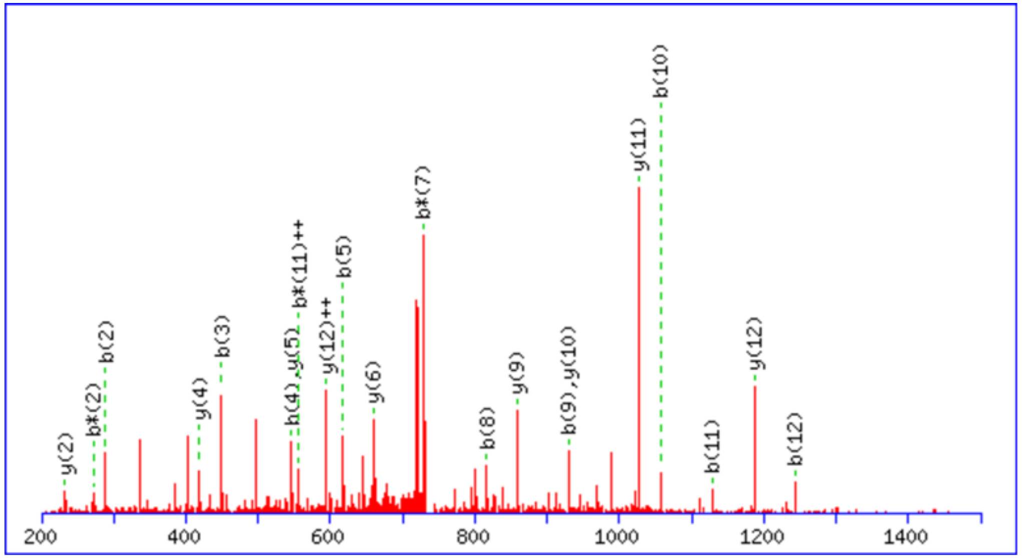
Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**

Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 21 - NOPB3 **Fraction:** NOPB3

Match to Query 9320: 1473.646648 from(737.830600,2+)
Title: OECHL100317_03.7415.7415.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_03.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53
Expect: 0.00025**Matches :** 21/128 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.037925	81.022600					**C**							**14**
2	***289.096503***	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.809312	**13**
3	***449.127152***	225.067214	432.100603	216.553940			**C**	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.780023	**12**
4	***546.179916***	273.593596	529.153367	265.080322			**P**	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.764698	**11**
5	***617.217030***	309.112153	600.190481	300.598879			**A**	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.238316	**10**
6	674.238494	337.622885	657.211945	329.109611			**G**	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.719759	**9**
7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
8	***816.312722***	408.659999	799.286173	400.146725			**A**	730.384229	365.695753	713.357680	357.182478	712.373664	356.690470	**7**
9	***929.396786***	465.202031	912.370237	456.688757			**L**	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.171913	**6**
10	***1057.455364***	529.231320	1040.428815	520.718046			**Q**	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.629881	**5**
11	***1128.492478***	564.749877	1111.465929	556.236603			**A**	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.600592	**4**
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	347.167359	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
13	1300.540885	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	**232.140416**	116.573846	215.113867	108.060571			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**



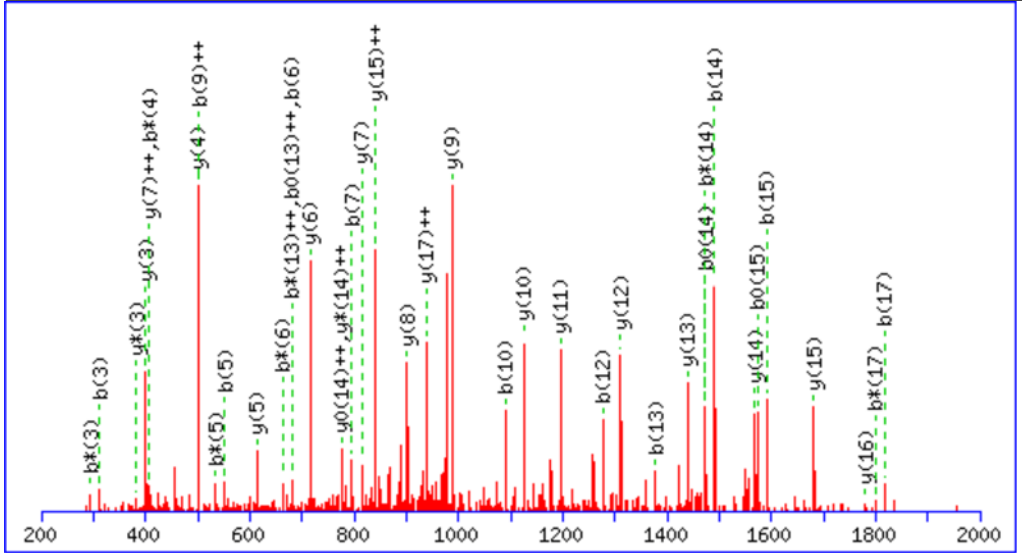
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 15882: 1990.022448 from(996.018500,2+)
Title: OECHL100317_01.10231.10231.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 99
Expect: 1.8e-008**Matches :** 41/186 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	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.992132	**17**
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.465750	**16**
4	424.255445	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.931543	**15**
5	**552.314023**	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.389511	**14**
6	**680.372601**	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.360222	**13**

7	**795.399544**	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.330933	**12**
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.817462	**11**
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.298905	**10**
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.769449	**9**
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	**8**
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.737420	**7**
13	**1377.675719**	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.203213	**6**
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	**5**
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	**4**
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510			**3**
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128			**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**

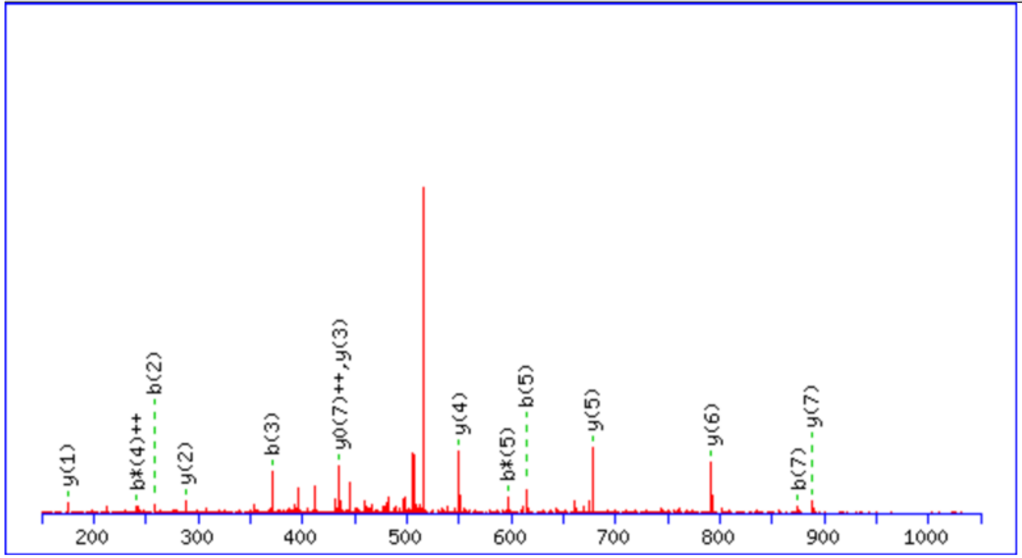


Peptide View

MS/MS Fragmentation of **CPLQDFLR**
Found in **IPI00003807**, Tax_Id=9606 Gene_Symbol=ACP2 Lysosomal acid phosphatase
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 5211: 1047.516648 from(524.765600,2+)
Title: OECHL100317_01.17340.17340.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1047.517151**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62
Expect: 5.5e-005**Matches :** 14/64 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.037925	81.022600					C							8
2	**258.090689**	129.548982					P	***888.493779***	444.750528	871.467230	436.237253	870.483214	435.745245	7
3	**371.174753**	186.091015					L	***791.441015***	396.224146	774.414466	387.710871	773.430450	387.218863	6
4	499.233331	250.120304	482.206782	241.607029			Q	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	5
5	**614.260274**	307.633775	597.233725	299.120501	596.249709	298.628493	D	***550.298373***	275.652825	533.271824	267.139550	532.287808	266.647542	4
6	761.328688	381.167982	744.302139	372.654708	743.318123	372.162700	F	***435.271430***	218.139353	418.244881	209.626079			3
7	**874.412752**	437.710014	857.386203	429.196740	856.402187	428.704732	L	***288.203016***	144.605146	271.176467	136.091872			2
8							R	***175.118952***	88.063114	158.092403	79.549840			1



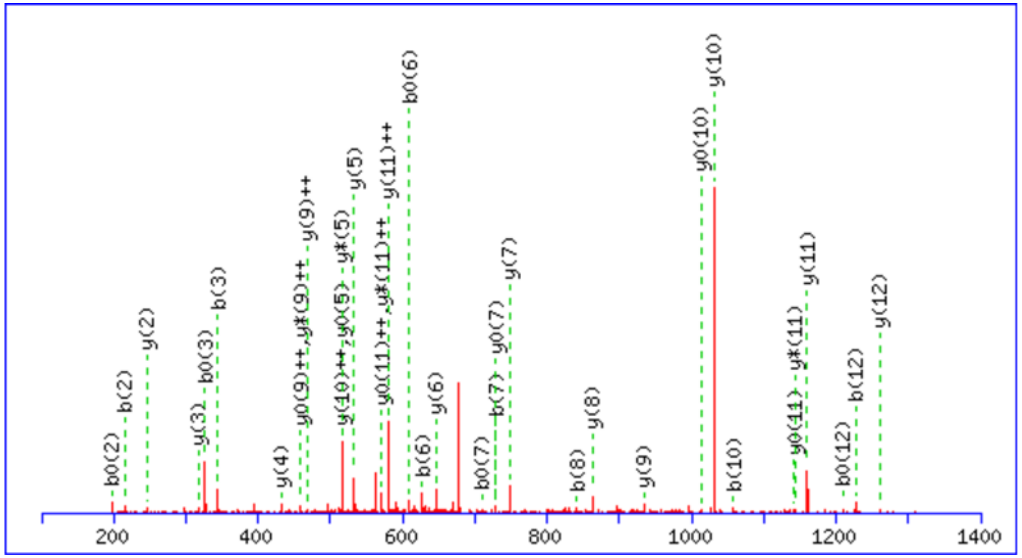
Peptide View

MS/MS Fragmentation of **LTEPADTITDAVK**

Found in **IPI00304808**, Tax_Id=9606 Gene_Symbol=KLK1 Isoform 1 of Kallikrein-1
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 9843: 1372.708648 from(687.361600,2+)
Title: OECHL100317_01.12873.12873.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1372.708572**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71
Expect: 1.2e-005**Matches :** 36/112 fragment ions using 67 most intense peaks (help)

#	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	114.091340	57.549308			**L**							**13**
2	**215.139019**	108.073147	197.128454	99.067865	**T**	***1260.631790***	630.819533	1243.605241	622.306259	1242.621225	621.814251	**12**
3	**344.181612**	172.594444	326.171047	163.589162	**E**	***1159.584111***	580.295694	1142.557562	571.782419	1141.573546	571.290411	**11**
4	441.234376	221.120826	423.223811	212.115544	**P**	***1030.541518***	515.774397	1013.514969	507.261123	1012.530953	506.769115	**10**
5	512.271490	256.639383	494.260925	247.634101	**A**	***933.488754***	467.248015	916.462205	458.734741	915.478189	458.242733	**9**
6	**627.298433**	314.152855	609.287868	305.147572	**D**	***862.451640***	431.729458	845.425091	423.216184	844.441075	422.724176	**8**
7	**728.346112**	364.676694	710.335547	355.671412	**T**	***747.424697***	374.215987	730.398148	365.702712	729.414132	365.210704	**7**
8	**841.430176**	421.218726	823.419611	412.213444	**I**	***646.377018***	323.692147	629.350469	315.178873	628.366453	314.686865	**6**
9	942.477855	471.742566	924.467290	462.737283	**T**	***533.292954***	267.150115	516.266405	258.636841	515.282389	258.144833	**5**
10	**1057.504798**	529.256037	1039.494233	520.250755	**D**	***432.245275***	216.626276	415.218726	208.113001	414.234710	207.620993	**4**
11	1128.541912	564.774594	1110.531347	555.769312	**A**	***317.218332***	159.112804	300.191783	150.599530			**3**
12	**1227.610326**	614.308801	1209.599761	605.303519	**V**	***246.181218***	123.594247	229.154669	115.080973			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**



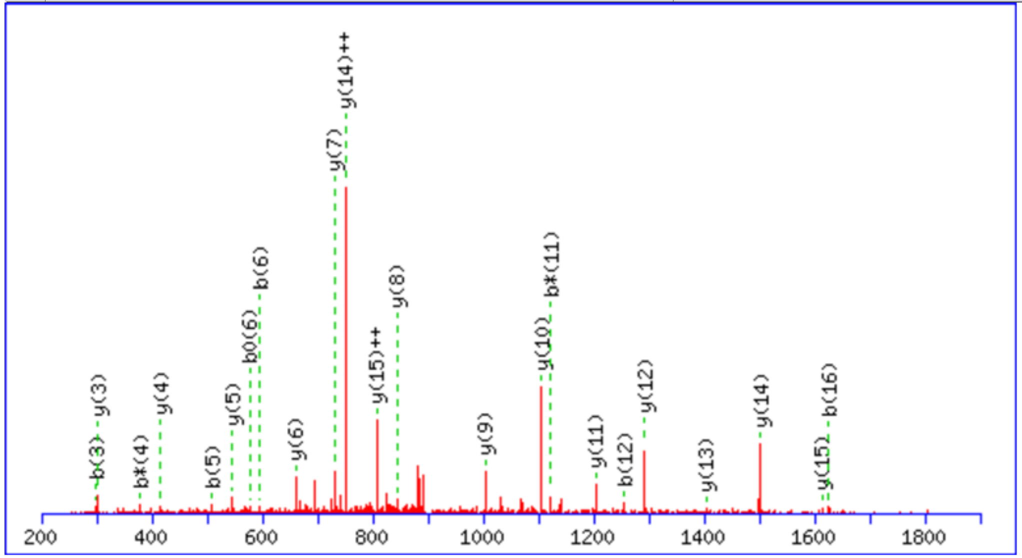
Peptide View

MS/MS Fragmentation of **GQLPISVTCIADEIGAR**
Found in **IPI00240345**, Tax_Id=9606 Gene_Symbol=CLEC14A C-type lectin domain family 14 member A
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 14570: 1798.925448 from(900.470000,2+)
Title: OECHL100317_01.21247.21247.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1798.924728**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 82
Expect: 8.1e-007**Matches :** 23/172 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	58.028740	29.518008					G							17
2	186.087318	93.547297	169.060769	85.034023			Q	1742.910548	871.958912	1725.883999	863.445638	1724.899983	862.953630	16
3	**299.171382**	150.089329	282.144833	141.576055			L	***1614.851970***	807.929623	1597.825421	799.416349	1596.841405	798.924340	15
4	396.224146	198.615711	379.197597	190.102436			P	***1501.767906***	751.387591	1484.741357	742.874317	1483.757341	742.382309	14
5	**509.308210**	255.157743	492.281661	246.644468			I	***1404.715142***	702.861209	1387.688593	694.347935	1386.704577	693.855927	13
6	**596.340238**	298.673757	579.313689	290.160483	578.329673	289.668475	S	***1291.631078***	646.319177	1274.604529	637.805903	1273.620513	637.313895	12

7	695.408652	348.207964	678.382103	339.694689	677.398087	339.202681	**V**	***1204.599050***	602.803163	1187.572501	594.289889	1186.588485	593.797881	**11**
8	796.456331	398.731804	779.429782	390.218529	778.445766	389.726521	**T**	***1105.530636***	553.268956	1088.504087	544.755682	1087.520071	544.263674	**10**
9	956.486980	478.747128	939.460431	470.233854	938.476415	469.741846	**C**	***1004.482957***	502.745117	987.456408	494.231842	986.472392	493.739834	**9**
10	1069.571044	535.289160	1052.544495	526.775886	1051.560479	526.283878	**I**	***844.452308***	422.729792	827.425759	414.216518	826.441743	413.724510	**8**
11	1140.608158	570.807717	1123.581609	562.294443	1122.597593	561.802435	**A**	***731.368244***	366.187760	714.341695	357.674486	713.357679	357.182478	**7**
12	**1255.635101**	628.321189	1238.608552	619.807914	1237.624536	619.315906	**D**	***660.331130***	330.669203	643.304581	322.155929	642.320565	321.663921	**6**
13	1384.677694	692.842485	1367.651145	684.329211	1366.667129	683.837203	**E**	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.150449	**5**
14	1497.761758	749.384517	1480.735209	740.871243	1479.751193	740.379235	**I**	***416.261594***	208.634435	399.235045	200.121160			**4**
15	1554.783222	777.895249	1537.756673	769.381975	1536.772657	768.889967	**G**	***303.177530***	152.092403	286.150981	143.579128			**3**
16	**1625.820336**	813.413806	1608.793787	804.900532	1607.809771	804.408524	**A**	246.156066	123.581671	229.129517	115.068396			**2**
17							**R**	175.118952	88.063114	158.092403	79.549839			**1**

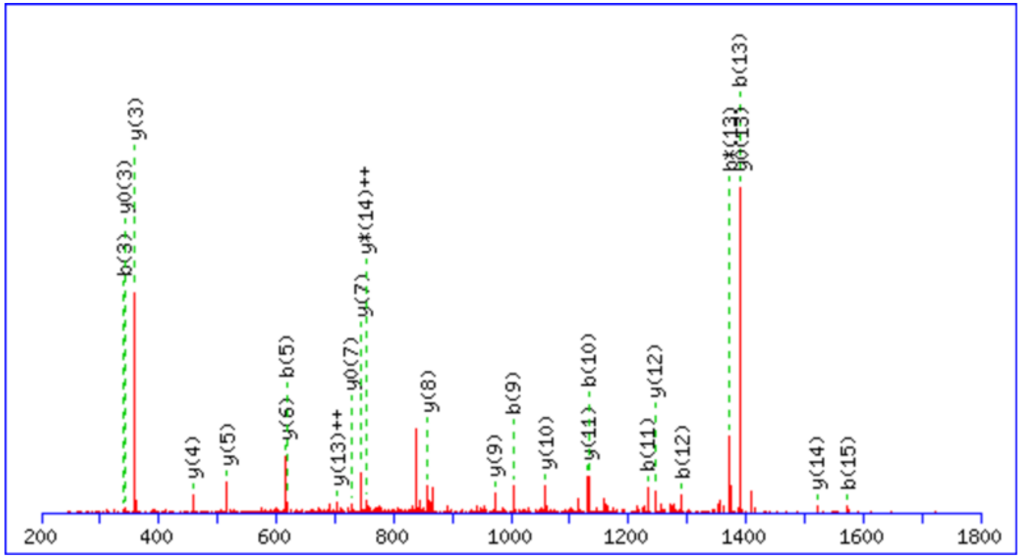


Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 14180: 1746.916648 from(874.465600,2+)
Title: OECHL100317_01.17307.17307.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 75
Expect: 3.3e-006**Matches :** 25/156 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	114.091340	57.549308					L							16
2	227.175404	114.091340					L	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.917569	15
3	**340.259468**	170.633372					I	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.375537	14
4	503.322797	252.165036					Y	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.833505	13
5	**618.349740**	309.678508			600.339175	300.673226	D	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.301841	12
6	689.386854	345.197065			671.376289	336.191782	A	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.788369	11
7	776.418882	388.713079			758.408317	379.707796	S	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.269812	10
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.753798	9
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	L	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	8
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	E	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	7
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	T	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	6
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	G	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	5
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	V	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	4
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
16							R	175.118952	88.063114	158.092403	79.549839			1



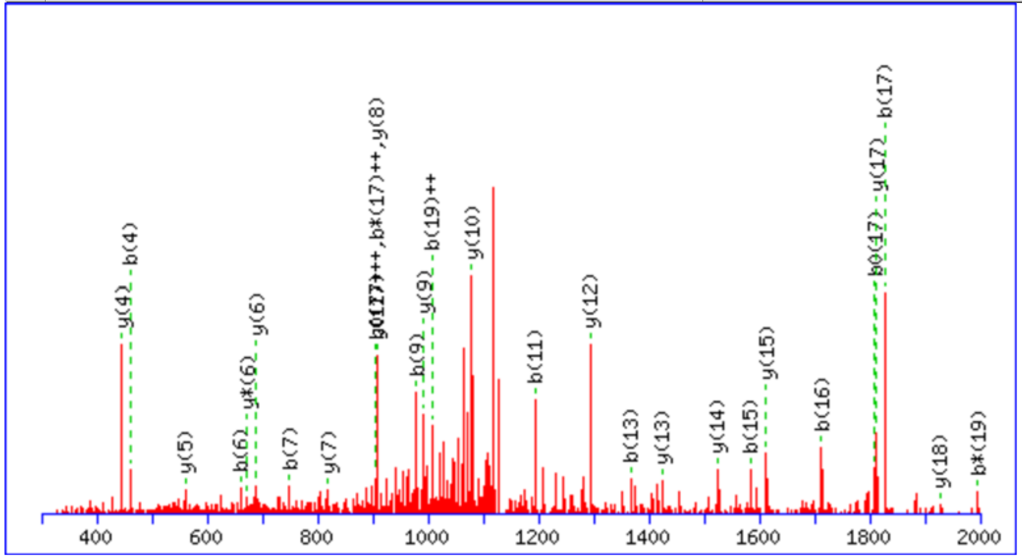
Peptide View

MS/MS Fragmentation of **SKEDSNSTESKSSSEEDGQLK**
Found in **IPI00012734**, Tax_Id=9606 Gene_Symbol=DMP1 Isoform 1 of Dentin matrix acidic phosphoprotein 1
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 17617: 2270.999448 from(1136.507000,2+)
Title: OECHL100317_01.2376.2376.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.998581**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 76
Expect: 2.1e-006**Matches :** 29/230 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	88.039304	44.523290			70.028739	35.518008	**S**						
2	216.134267	108.570771	199.107718	100.057497	198.123702	99.565489	**K**	2184.973868	1092.990572	2167.947319	1084.477297	2166.963303	1083.9852
3	345.176860	173.092068	328.150311	164.578793	327.166295	164.086785	**E**	2056.878905	1028.943090	2039.852356	1020.429816	2038.868340	1019.9378
4	**460.203803**	230.605539	443.177254	222.092265	442.193238	221.600257	**D**	***1927.836312***	964.421794	1910.809763	955.908520	1909.825747	955.4165
5	547.235831	274.121554	530.209282	265.608279	529.225266	265.116271	**S**	***1812.809369***	906.908323	1795.782820	898.395048	1794.798804	897.9030
6	**661.278758**	331.143017	644.252209	322.629743	643.268193	322.137735	**N**	1725.777341	863.392309	1708.750792	854.879034	1707.766776	854.3870

7	**748.310786**	374.659031	731.284237	366.145757	730.300221	365.653749	**S**	***1611.734414***	806.370845	1594.707865	797.857571	1593.723849	797.3655
8	849.358465	425.182871	832.331916	416.669596	831.347900	416.177588	**T**	***1524.702386***	762.854831	1507.675837	754.341557	1506.691821	753.8495
9	**978.401058**	489.704167	961.374509	481.190893	960.390493	480.698885	**E**	***1423.654707***	712.330992	1406.628158	703.817717	1405.644142	703.3257
10	1065.433086	533.220181	1048.406537	524.706907	1047.422521	524.214899	**S**	***1294.612114***	647.809695	1277.585565	639.296421	1276.601549	638.8044
11	**1193.528049**	597.267663	1176.501500	588.754388	1175.517484	588.262380	**K**	1207.580086	604.293681	1190.553537	595.780407	1189.569521	595.2883
12	1280.560077	640.783677	1263.533528	632.270402	1262.549512	631.778394	**S**	***1079.485123***	540.246200	1062.458574	531.732925	1061.474558	531.2409
13	**1367.592105**	684.299691	1350.565556	675.786416	1349.581540	675.294408	**S**	***992.453095***	496.730186	975.426546	488.216911	974.442530	487.7249
14	1454.624133	727.815705	1437.597584	719.302430	1436.613568	718.810422	**S**	***905.421067***	453.214172	888.394518	444.700897	887.410502	444.2088
15	**1583.666726**	792.337001	1566.640177	783.823727	1565.656161	783.331719	**E**	***818.389039***	409.698158	801.362490	401.184883	800.378474	400.6928
16	**1712.709319**	856.858298	1695.682770	848.345023	1694.698754	847.853015	**E**	***689.346446***	345.176861	672.319897	336.663587	671.335881	336.1715
17	**1827.736262**	914.371769	1810.709713	905.858495	1809.725697	905.366487	**D**	***560.303853***	280.655565	543.277304	272.142290	542.293288	271.6502
18	1884.757726	942.882501	1867.731177	934.369227	1866.747161	933.877219	**G**	***445.276910***	223.142093	428.250361	214.628818		
19	2012.816304	1006.911790	1995.789755	998.398516	1994.805739	997.906508	**Q**	388.255446	194.631361	371.228897	186.118087		
20	2125.900368	1063.453822	2108.873819	1054.940547	2107.889803	1054.448539	**L**	260.196868	130.602072	243.170319	122.088798		
21							**K**	147.112804	74.060040	130.086255	65.546765		

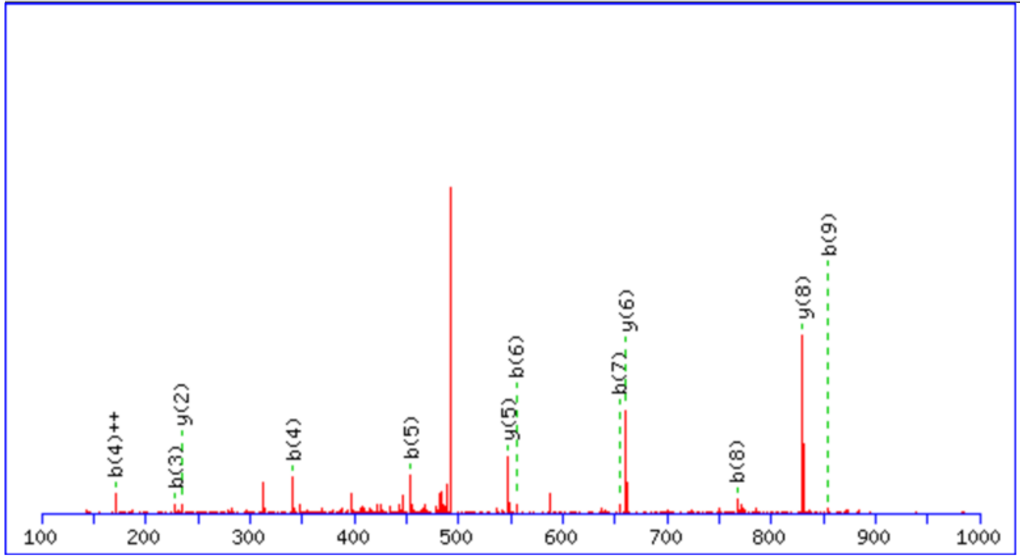


Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 4467: 999.633848 from(500.824200,2+)
Title: OECHL100317_01.17502.17502.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.00011**Matches :** 13/78 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**

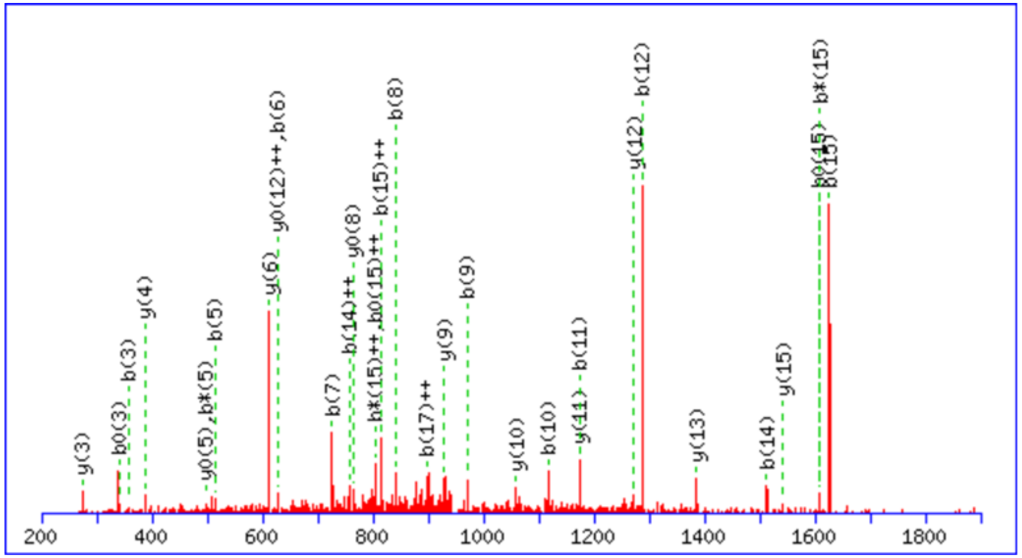


Peptide View

MS/MS Fragmentation of **NKDGVLVDEFGLPQIPAS**
Found in **IPI00100796**, Tax_Id=9606 Gene_Symbol=CHMP5 Charged multivesicular body protein 5
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 15280: 1897.980848 from(949.997700,2+)
Title: OECHL100317_01.20671.20671.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1897.978546**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56
Expect: 0.00041**Matches :** 32/192 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			**N**							**18**
2	243.145166	122.076221	226.118617	113.562947			**K**	1784.942893	892.975085	1767.916344	884.461810	1766.932328	883.969802	**17**
3	***358.172109***	179.589693	341.145560	171.076418	340.161544	170.584410	**D**	1656.847930	828.927603	1639.821381	820.414329	1638.837365	819.922321	**16**
4	415.193573	208.100425	398.167024	199.587150	397.183008	199.095142	**G**	**1541.820987**	771.414132	1524.794438	762.900857	1523.810422	762.408849	**15**
5	***514.261987***	257.634632	497.235438	249.121357	496.251422	248.629349	**V**	1484.799523	742.903400	1467.772974	734.390125	1466.788958	733.898117	**14**
6	***627.346051***	314.176664	610.319502	305.663389	609.335486	305.171381	**L**	**1385.731109**	693.369193	1368.704560	684.855918	1367.720544	684.363910	**13**
7	***726.414465***	363.710871	709.387916	355.197596	708.403900	354.705588	**V**	**1272.647045**	636.827160	1255.620496	628.313886	1254.636480	627.821878	**12**
8	***841.441408***	421.224342	824.414859	412.711068	823.430843	412.219060	**D**	**1173.578631**	587.292954	1156.552082	578.779679	1155.568066	578.287671	**11**
9	***970.484001***	485.745639	953.457452	477.232364	952.473436	476.740356	**E**	**1058.551688**	529.779482	1041.525139	521.266208	1040.541123	520.774200	**10**
10	***1117.552415***	559.279846	1100.525866	550.766571	1099.541850	550.274563	**F**	**929.509095**	465.258186	912.482546	456.744911	911.498530	456.252903	**9**
11	***1174.573879***	587.790578	1157.547330	579.277303	1156.563314	578.785295	**G**	782.440681	391.723979	765.414132	383.210704	764.430116	382.718696	**8**
12	***1287.657943***	644.332609	1270.631394	635.819335	1269.647378	635.327327	**L**	725.419217	363.213247	708.392668	354.699972	707.408652	354.207964	**7**
13	1384.710707	692.858992	1367.684158	684.345717	1366.700142	683.853709	**P**	**612.335153**	306.671215	595.308604	298.157940	594.324588	297.665932	**6**
14	***1512.769285***	**756.888281**	1495.742736	748.375006	1494.758720	747.882998	**Q**	515.282389	258.144833	498.255840	249.631558	497.271824	249.139550	**5**
15	***1625.853349***	**813.430313**	1608.826800	804.917038	1607.842784	804.425030	**I**	**387.223811**	194.115543			369.213246	185.110261	**4**
16	1722.906113	861.956695	1705.879564	853.443420	1704.895548	852.951412	**P**	**274.139747**	137.573512			256.129182	128.568229	**3**
17	1793.943227	**897.475252**	1776.916678	888.961977	1775.932662	888.469969	**A**	177.086983	89.047130			159.076418	80.041847	**2**
18							**S**	106.049869	53.528573			88.039304	44.523290	**1**



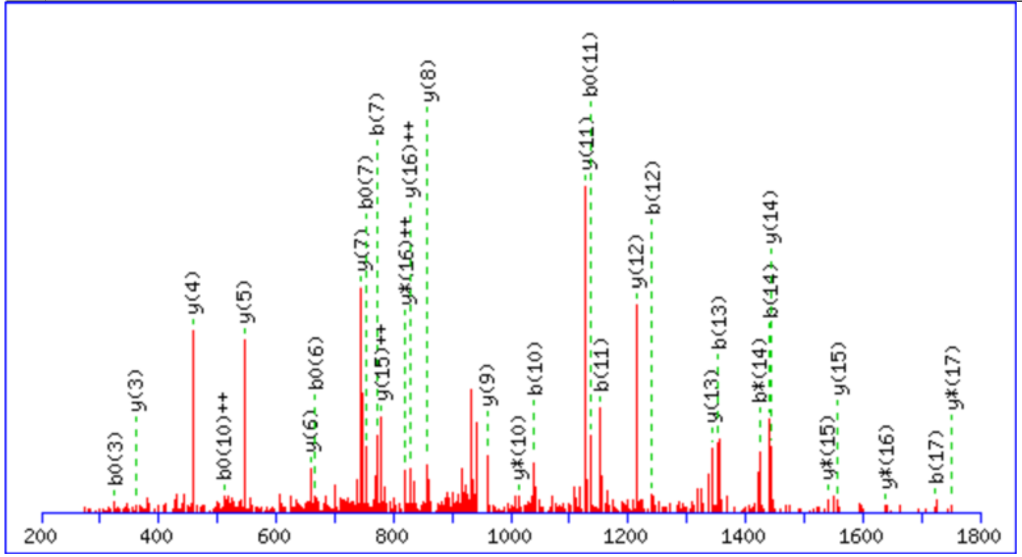
Peptide View

MS/MS Fragmentation of **EIVLTQSPATLSLSPGER**
Found in **IPI00816799**, Tax_Id=9606 Gene_Symbol=- Rheumatoid factor D5 light chain (Fragment)
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 15273: 1897.016448 from(949.515500,2+)
Title: OECHL100317_01.17055.17055.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1897.015640**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72
Expect: 5.6e-006**Matches :** 32/192 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	130.049869	65.528572			112.039304	56.523290	**E**							**18**
2	243.133933	122.070605			225.123368	113.065322	**I**	1768.980341	884.993808	1751.953792	876.480534	1750.969776	875.988526	**17**
3	342.202347	171.604812			324.191782	162.599529	**V**	1655.896277	828.451776	1638.869728	819.938502	1637.885712	819.446494	**16**
4	455.286411	228.146844			437.275846	219.141561	**L**	***1556.827863***	778.917569	1539.801314	770.404295	1538.817298	769.912287	**15**
5	556.334090	278.670683			538.323525	269.665401	**T**	***1443.743799***	722.375537	1426.717250	713.862263	1425.733234	713.370255	**14**
6	684.392668	342.699972	667.366119	334.186698	666.382103	333.694690	**Q**	***1342.696120***	671.851698	1325.669571	663.338423	1324.685555	662.846415	**13**

7	**771.424696**	386.215986	754.398147	377.702712	753.414131	377.210704	**S**	***1214.637542***	607.822409	1197.610993	599.309134	1196.626977	598.817126	**12**
8	868.477460	434.742368	851.450911	426.229094	850.466895	425.737086	**P**	***1127.605514***	564.306395	1110.578965	555.793120	1109.594949	555.301112	**11**
9	939.514574	470.260925	922.488025	461.747651	921.504009	461.255643	**A**	1030.552750	515.780013	1013.526201	507.266738	1012.542185	506.774730	**10**
10	**1040.562253**	520.784765	1023.535704	512.271490	1022.551688	511.779482	**T**	***959.515636***	480.261456	942.489087	471.748181	941.505071	471.256173	**9**
11	**1153.646317**	577.326797	1136.619768	568.813522	1135.635752	568.321514	**L**	***858.467957***	429.737616	841.441408	421.224342	840.457392	420.732334	**8**
12	**1240.678345**	620.842811	1223.651796	612.329536	1222.667780	611.837528	**S**	***745.383893***	373.195585	728.357344	364.682310	727.373328	364.190302	**7**
13	**1353.762409**	677.384842	1336.735860	668.871568	1335.751844	668.379560	**L**	***658.351865***	329.679570	641.325316	321.166296	640.341300	320.674288	**6**
14	**1440.794437**	720.900857	1423.767888	712.387582	1422.783872	711.895574	**S**	***545.267801***	273.137539	528.241252	264.624264	527.257236	264.132256	**5**
15	1537.847201	769.427239	1520.820652	760.913964	1519.836636	760.421956	**P**	***458.235773***	229.621524	441.209224	221.108250	440.225208	220.616242	**4**
16	1594.868665	797.937971	1577.842116	789.424696	1576.858100	788.932688	**G**	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	**3**
17	**1723.911258**	862.459267	1706.884709	853.945992	1705.900693	853.453984	**E**	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	**2**
18							**R**	175.118952	88.063114	158.092403	79.549839			**1**

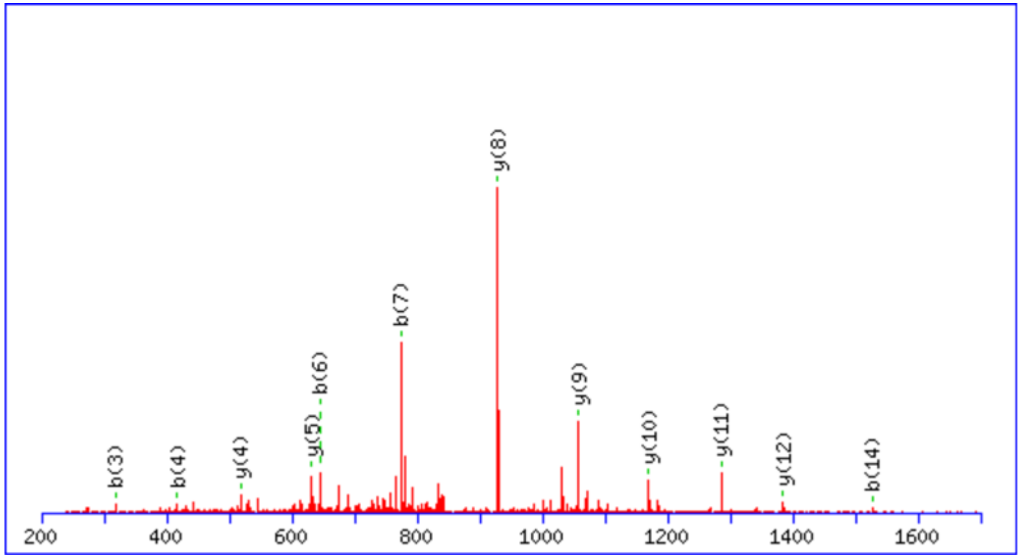


Peptide View

MS/MS Fragmentation of **AVFVDLEPTVIDEVR**
Found in **IPI00166768**, Tax_Id=9606 Gene_Symbol=TUBA1C TUBA1C protein
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 13668: 1700.900448 from(851.457500,2+)
Title: OECHL100317_01.20605.20605.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1700.898514**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55
Expect: 0.00041**Matches :** 12/128 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**15**
2	171.112804	86.060040			**V**	1630.868665	815.937971	1613.842116	807.424696	1612.858100	806.932688	**14**
3	***318.181218***	159.594247			**F**	1531.800251	766.403764	1514.773702	757.890489	1513.789686	757.398481	**13**
4	***417.249632***	209.128454			**V**	***1384.731837***	692.869557	1367.705288	684.356282	1366.721272	683.864274	**12**
5	532.276575	266.641926	514.266010	257.636643	**D**	***1285.663423***	643.335350	1268.636874	634.822075	1267.652858	634.330067	**11**
6	***645.360639***	323.183958	627.350074	314.178675	**L**	***1170.636480***	585.821878	1153.609931	577.308604	1152.625915	576.816596	**10**
7	***774.403232***	387.705254	756.392667	378.699972	**E**	***1057.552416***	529.279846	1040.525867	520.766572	1039.541851	520.274564	**9**
8	871.455996	436.231636	853.445431	427.226354	**P**	***928.509823***	464.758550	911.483274	456.245275	910.499258	455.753267	**8**
9	972.503675	486.755476	954.493110	477.750193	**T**	831.457059	416.232168	814.430510	407.718893	813.446494	407.226885	**7**
10	1071.572089	536.289683	1053.561524	527.284400	**V**	730.409380	365.708328	713.382831	357.195054	712.398815	356.703046	**6**
11	1184.656153	592.831715	1166.645588	583.826432	**I**	***631.340966***	316.174121	614.314417	307.660846	613.330401	307.168838	**5**
12	1299.683096	650.345186	1281.672531	641.339904	**D**	***518.256902***	259.632089	501.230353	251.118815	500.246337	250.626807	**4**
13	1428.725689	714.866483	1410.715124	705.861200	**E**	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	**3**
14	***1527.794103***	764.400690	1509.783538	755.395407	**V**	274.187366	137.597321	257.160817	129.084047			**2**
15					**R**	175.118952	88.063114	158.092403	79.549839			**1**



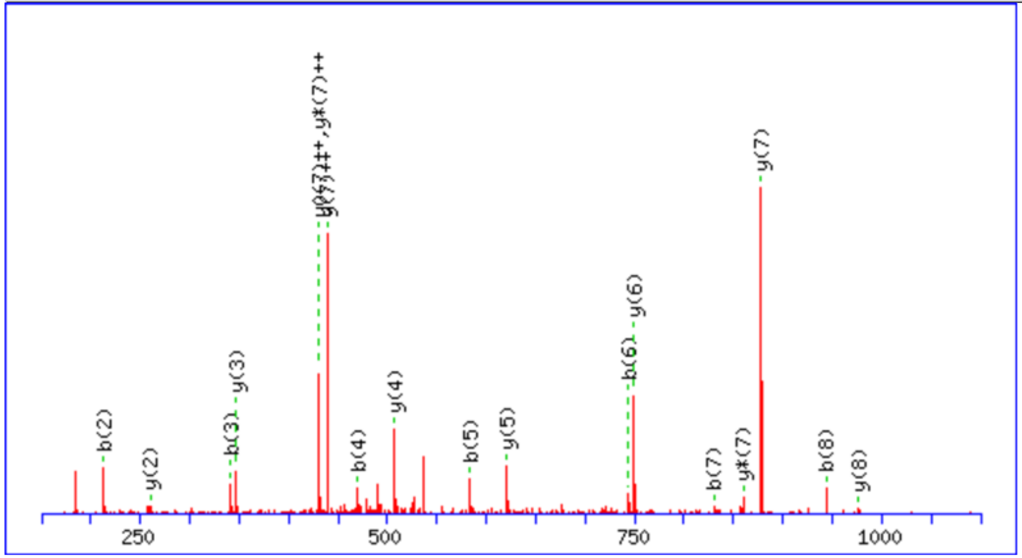
Peptide View

MS/MS Fragmentation of **LVQELCSLK**
Found in **IPI00018275**, Tax_Id=9606 Gene_Symbol=PRND Prion-like protein doppel
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 5710: 1088.589248 from(545.301900,2+)
Title: OECHL100317_01.12065.12065.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1088.589966**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 0.00012**Matches :** 18/82 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	114.091340	57.549308					L							9
2	***213.159754***	107.083515					V	***976.513194***	488.760235	959.486645	480.246961	958.502629	479.754953	8
3	***341.218332***	171.112804	324.191783	162.599529			Q	***877.444780***	439.226028	860.418231	430.712754	859.434215	430.220746	7
4	***470.260925***	235.634100	453.234376	227.120826	452.250360	226.628818	E	***749.386202***	375.196739	732.359653	366.683465	731.375637	366.191457	6
5	***583.344989***	292.176133	566.318440	283.662858	565.334424	283.170850	L	***620.343609***	310.675443	603.317060	302.162168	602.333044	301.670160	5
6	***743.375638***	372.191457	726.349089	363.678183	725.365073	363.186175	C	***507.259545***	254.133410	490.232996	245.620136	489.248980	245.128128	4

7	***830.407666***	415.707471	813.381117	407.194197	812.397101	406.702189	**S**	***347.228896***	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
8	***943.491730***	472.249503	926.465181	463.736229	925.481165	463.244221	**L**	***260.196868***	130.602072	243.170319	122.088797			**2**
9							**K**	147.112804	74.060040	130.086255	65.546765			**1**



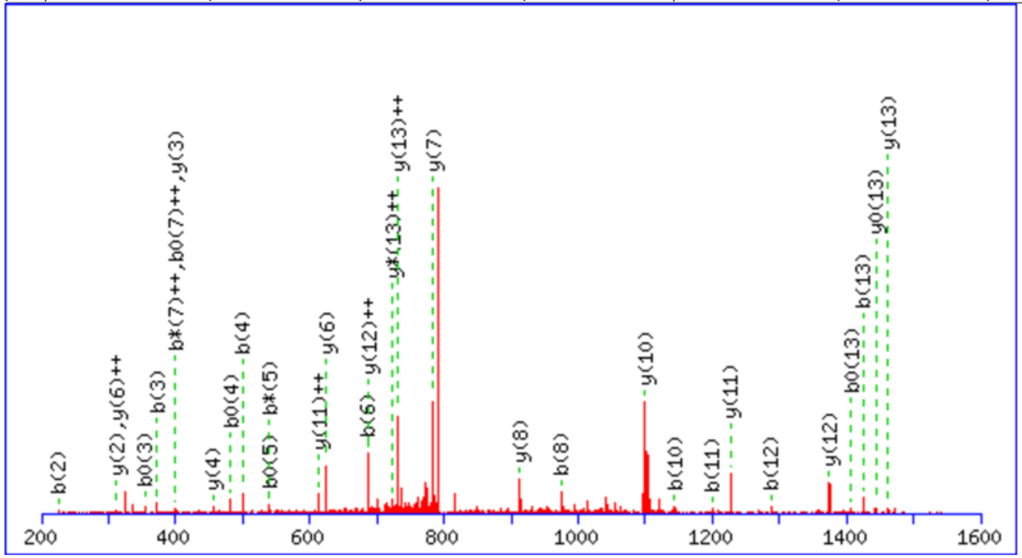
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 12300: 1597.706848 from(799.860700,2+)
Title: OECHL100317_01.2380.2380.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61
Expect: 4.4e-005**Matches :** 32/144 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	138.066188	69.536732					**H**							**14**
2	**225.098216**	113.052746			207.087651	104.047463	**S**	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.325325	**13**
3	**372.166630**	186.586953			354.156065	177.581671	**F**	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.809311	**12**

4	**500.261593**	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.275104	**11**
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.227622	**10**
6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	1042.437069	521.722173	1025.410520	513.208898	1024.426504	512.716890	**9**
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.195594	**8**
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.674297	**7**
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.658973	**6**
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	527.268470	264.137873	510.241921	255.624598	509.257905	255.132590	**5**
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.614033	**4**
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	**3**
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	***312.177864***	156.592570	295.151315	148.079295			**2**
14							**R**	175.118952	88.063114	158.092403	79.549839			**1**

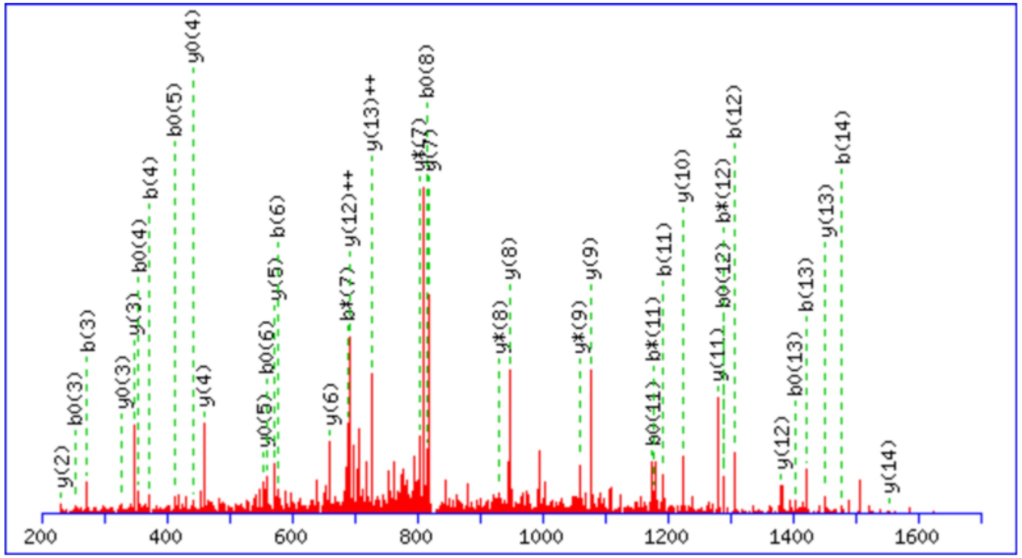


Peptide View

MS/MS Fragmentation of **VTATGFQQCSLIDGR**
Found in **IPI00333140**, Tax_Id=9606 Gene_Symbol=DNER Delta and Notch-like epidermal growth factor-related receptor
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 13090: 1651.802048 from(826.908300,2+)
Title: OECHL100317_01.14147.14147.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1651.798828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 78
Expect: 2.2e-006**Matches :** 39/150 fragment ions using 84 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					**V**							**15**
2	201.123369	101.065322			183.112804	92.060040	**T**	***1553.737670***	777.372473	1536.711121	768.859198	1535.727105	768.367190	**14**
3	**272.160483**	136.583879			254.149918	127.578597	**A**	***1452.689991***	726.848633	1435.663442	718.335359	1434.679426	717.843351	**13**
4	**373.208162**	187.107719			355.197597	178.102437	**T**	***1381.652877***	691.330076	1364.626328	682.816802	1363.642312	682.324794	**12**
5	430.229626	215.618451			412.219061	206.613169	**G**	***1280.605198***	640.806237	1263.578649	632.292962	1262.594633	631.800954	**11**
6	**577.298040**	289.152658			559.287475	280.147376	**F**	***1223.583734***	612.295505	1206.557185	603.782230	1205.573169	603.290222	**10**
7	705.356618	353.181947	688.330069	344.668673	687.346053	344.176665	**Q**	***1076.515320***	538.761298	1059.488771	530.248023	1058.504755	529.756015	**9**
8	833.415196	417.211236	816.388647	408.697962	815.404631	408.205954	**Q**	***948.456742***	474.732009	931.430193	466.218734	930.446177	465.726726	**8**
9	993.445845	497.226561	976.419296	488.713286	975.435280	488.221278	**C**	***820.398164***	410.702720	803.371615	402.189445	802.387599	401.697437	**7**
10	1080.477873	540.742575	1063.451324	532.229300	1062.467308	531.737292	**S**	***660.367515***	330.687395	643.340966	322.174121	642.356950	321.682113	**6**
11	**1193.561937**	597.284607	1176.535388	588.771332	1175.551372	588.279324	**L**	***573.335487***	287.171381	556.308938	278.658107	555.324922	278.166099	**5**
12	**1306.646001**	653.826638	1289.619452	645.313364	1288.635436	644.821356	**I**	***460.251423***	230.629349	443.224874	222.116075	442.240858	221.624067	**4**
13	**1421.672944**	711.340110	1404.646395	702.826836	1403.662379	702.334827	**D**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	**3**
14	**1478.694408**	739.850842	1461.667859	731.337567	1460.683843	730.845559	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
15							**R**	175.118952	88.063114	158.092403	79.549839			**1**



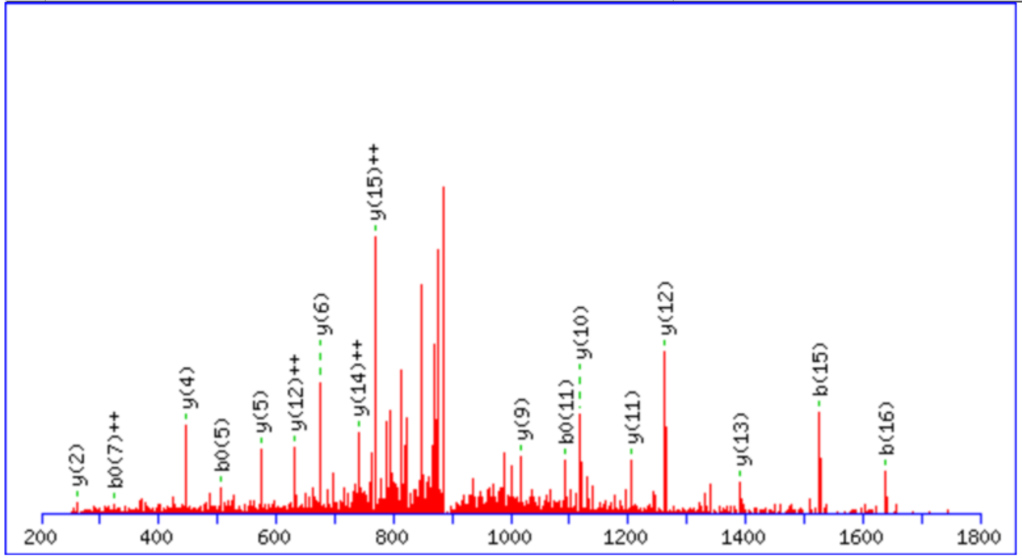
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 14451: 1784.881048 from(893.447800,2+)
Title: OECHL100317_01.7949.7949.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58
Expect: 0.00025**Matches :** 17/170 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	164.070605	82.538940					**Y**							**17**
2	251.102633	126.054954			233.092068	117.049672	**S**	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.909941	**16**
3	308.124097	154.565687			290.113532	145.560404	**G**	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.393928	**15**
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.883195	**14**
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.367182	**13**
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.845885	**12**

7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.335153	**11**
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.819139	**10**
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.295299	**9**
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.266010	**8**
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	788.487631	394.747453	771.461082	386.234179	770.477066	385.742171	**7**
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.200139	**6**
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.676299	**5**
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.628818	**4**
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	**3**
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**

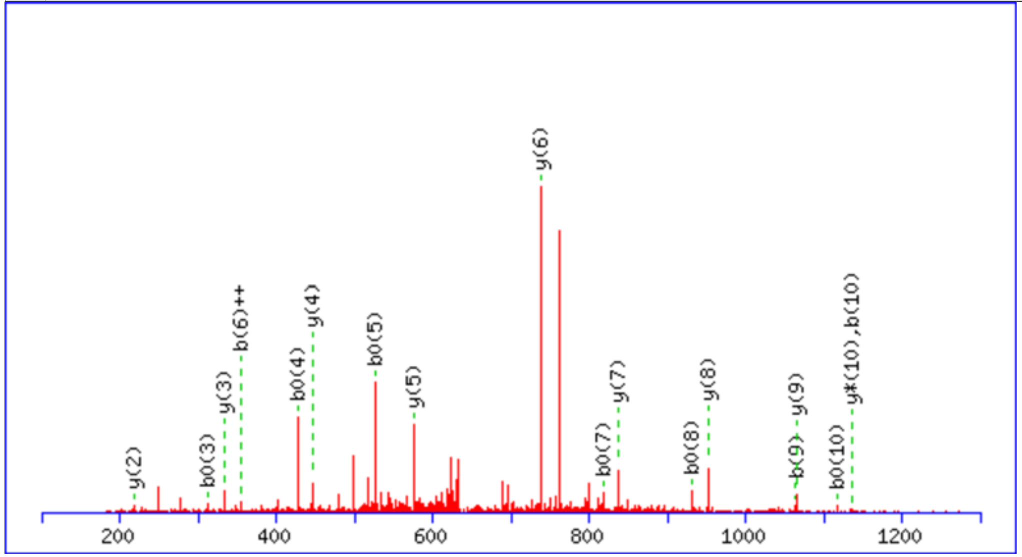


Peptide View

MS/MS Fragmentation of **ESLDVYELDAK**
Found in **IPI00013698**, Tax_Id=9606 Gene_Symbol=ASAH1 Isoform 1 of Acid ceramidase
Experiment: 48 - PyA-3 **Fraction:** PyA-3

Match to Query 8852: 1280.615848 from(641.315200,2+)
Title: OECHL100317_01.14725.14725.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_01.raw
Monoisotopic mass of neutral peptide Mr(calc): 1280.613586**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50
Expect: 0.001**Matches :** 18/96 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**E**							**11**
2	217.081897	109.044586	199.071332	100.039304	**S**	1152.578296	576.792786	1135.551747	568.279512	1134.567731	567.787504	**10**
3	330.165961	165.586618	312.155396	156.581336	**L**	***1065.546268***	533.276772	1048.519719	524.763498	1047.535703	524.271490	**9**
4	445.192904	223.100090	427.182339	214.094808	**D**	***952.462204***	476.734740	935.435655	468.221466	934.451639	467.729458	**8**
5	544.261318	272.634297	526.250753	263.629015	**V**	***837.435261***	419.221269	820.408712	410.707994	819.424696	410.215986	**7**
6	707.324647	354.165962	689.314082	345.160679	**Y**	***738.366847***	369.687062	721.340298	361.173787	720.356282	360.681779	**6**
7	836.367240	418.687258	818.356675	409.681976	**E**	***575.303518***	288.155397	558.276969	279.642123	557.292953	279.150115	**5**
8	949.451304	475.229290	931.440739	466.224008	**L**	***446.260925***	223.634101	429.234376	215.120826	428.250360	214.628818	**4**
9	**1064.478247**	532.742762	1046.467682	523.737479	**D**	***333.176861***	167.092069	316.150312	158.578794	315.166296	158.086786	**3**
10	**1135.515361**	568.261319	1117.504796	559.256036	**A**	***218.149918***	109.578597	201.123369	101.065322			**2**
11					**K**	147.112804	74.060040	130.086255	65.546765			**1**

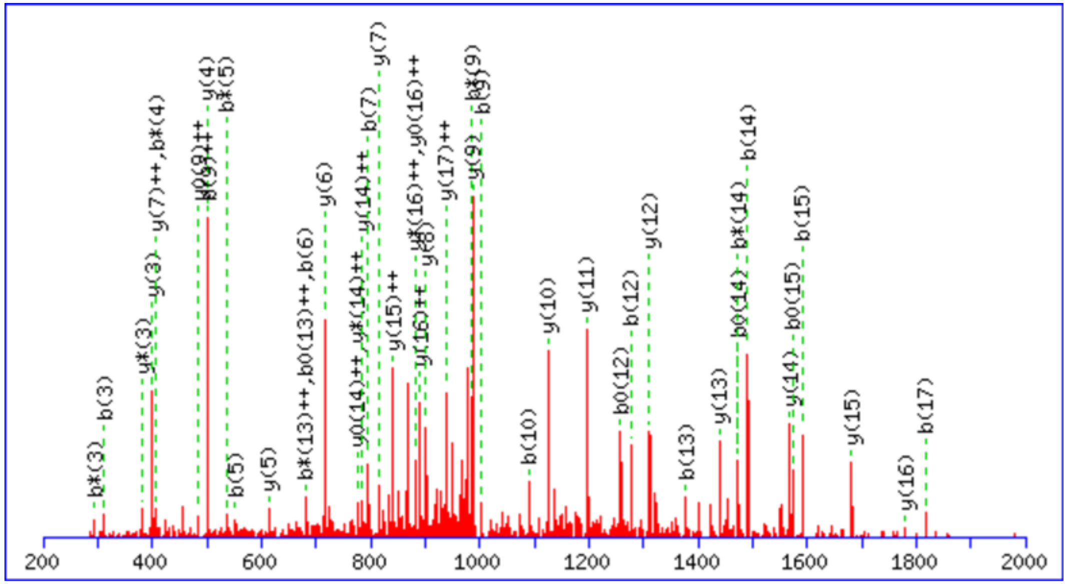


Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 06 - S_B-4 **Fraction:** S_B-4

Match to Query 14203: 1990.025648 from(996.020100,2+)
Title: OECHL100317_41.10310.10310.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 86 **Expect:** 3.6e-007**Matches :** 47/186 fragment ions using 81 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}
1	115.050203	58.028740	98.023654	49.515465			**N**						
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.9921
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.4657
4	424.255445	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.9315
5	**552.314023**	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.3895
6	**680.372601**	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.3602
7	**795.399544**	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.3309
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.8174
9	**1003.495570**	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.2989
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.7694
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.2534
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.7374
13	**1377.675719**	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.2032
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.6793
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.1373
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510		
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128		
18							**R**	175.118952	88.063114	158.092403	79.549839		



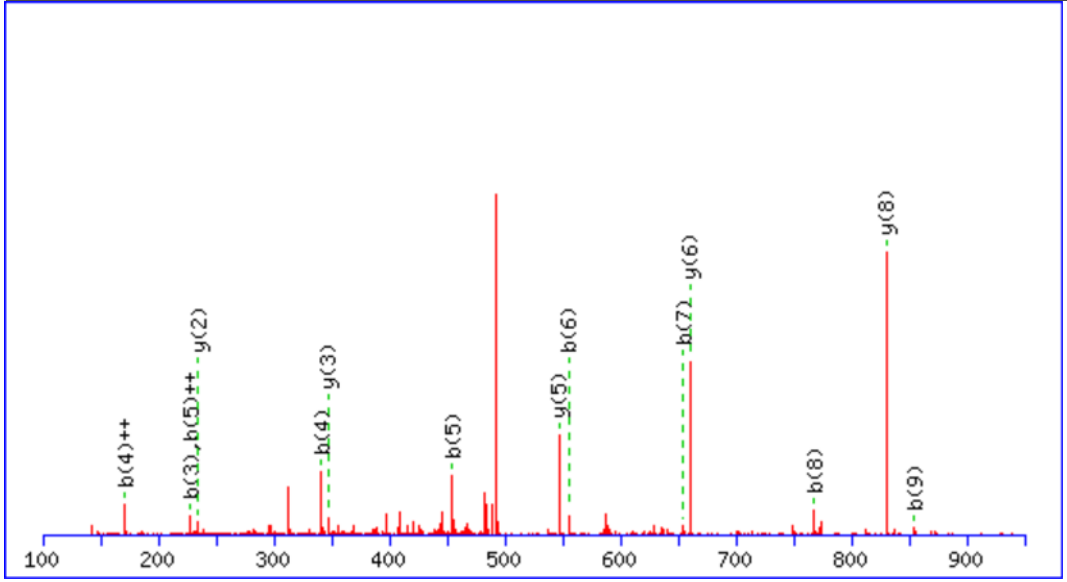
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 06 - S_B-4 **Fraction:** S_B-4

Match to Query 3258: 999.632848 from(500.823700,2+)
Title: OECHL100317_41.16955.16955.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65 **Expect:** 4e-006**Matches :** 15/78 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	**171.112804**			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	**227.654836**			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**

6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



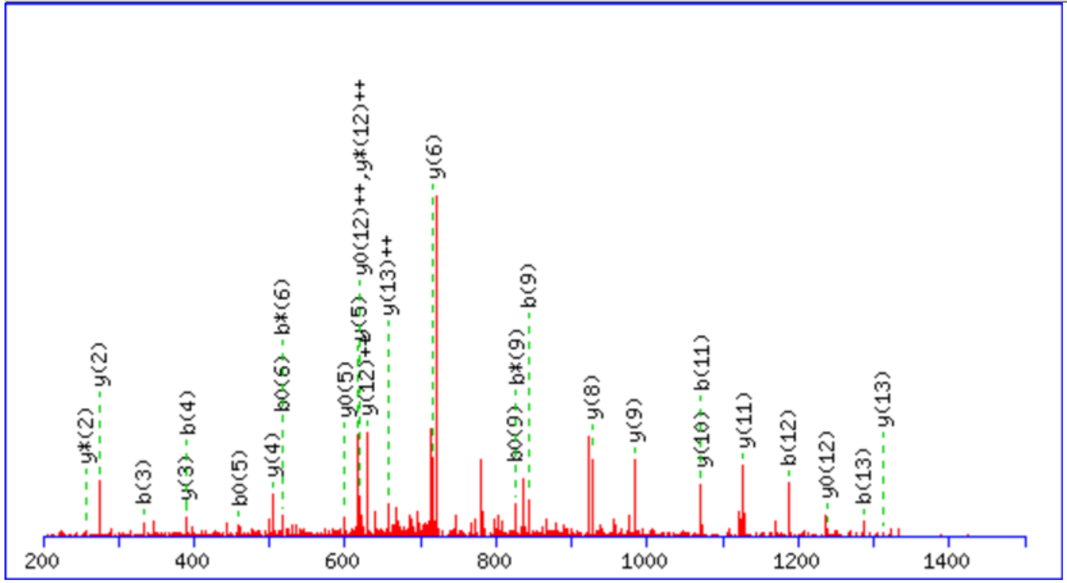
Peptide View

MS/MS Fragmentation of **FGQGSGPIVLDDVR**
Found in **IPI00418512**, Tax_Id=9606 Gene_Symbol=DMBT1 Isoform 4 of Deleted in malignant brain tumors 1 protein
Experiment: 06 - S_B-4 **Fraction:** S_B-4

Match to Query 9283: 1458.751248 from(730.382900,2+)
Title: OECHL100317_41.15380.15380.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1458.746719**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65 **Expect:** 4.8e-005**Matches :** 28/140 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	148.075690	74.541483					F						
2	205.097154	103.052215					G	***1312.685556***	656.846416	1295.659007	648.333142	1294.674991	647.8411
3	**333.155732**	167.081504	316.129183	158.568230			Q	1255.664092	628.335684	1238.637543	619.822410	1237.653527	619.3304
4	**390.177196**	195.592236	373.150647	187.078961			G	***1127.605514***	564.306395	1110.578965	555.793121	1109.594949	555.3011
5	477.209224	239.108250	460.182675	230.594976	459.198659	230.102968	S	***1070.584050***	535.795663	1053.557501	527.282389	1052.573485	526.7903
6	534.230688	267.618982	517.204139	259.105708	516.220123	258.613700	G	***983.552022***	492.279649	966.525473	483.766375	965.541457	483.2743
7	631.283452	316.145364	614.256903	307.632090	613.272887	307.140082	P	***926.530558***	463.768917	909.504009	455.255643	908.519993	454.7636
8	744.367516	372.687396	727.340967	364.174122	726.356951	363.682114	I	829.477794	415.242535	812.451245	406.729261	811.467229	406.2372
9	**843.435930**	422.221603	826.409381	413.708329	825.425365	413.216321	V	***716.393730***	358.700503	699.367181	350.187229	698.383165	349.6952
10	956.519994	478.763635	939.493445	470.250361	938.509429	469.758353	L	***617.325316***	309.166296	600.298767	300.653022	599.314751	300.1610
11	**1071.546937**	536.277107	1054.520388	527.763832	1053.536372	527.271824	D	***504.241252***	252.624264	487.214703	244.110990	486.230687	243.6189
12	**1186.573880**	593.790578	1169.547331	585.277304	1168.563315	584.785296	D	***389.214309***	195.110793	372.187760	186.597518	371.203744	186.1055
13	**1285.642294**	643.324785	1268.615745	634.811511	1267.631729	634.319503	V	***274.187366***	137.597321	257.160817	129.084047		
14							R	175.118952	88.063114	158.092403	79.549839		

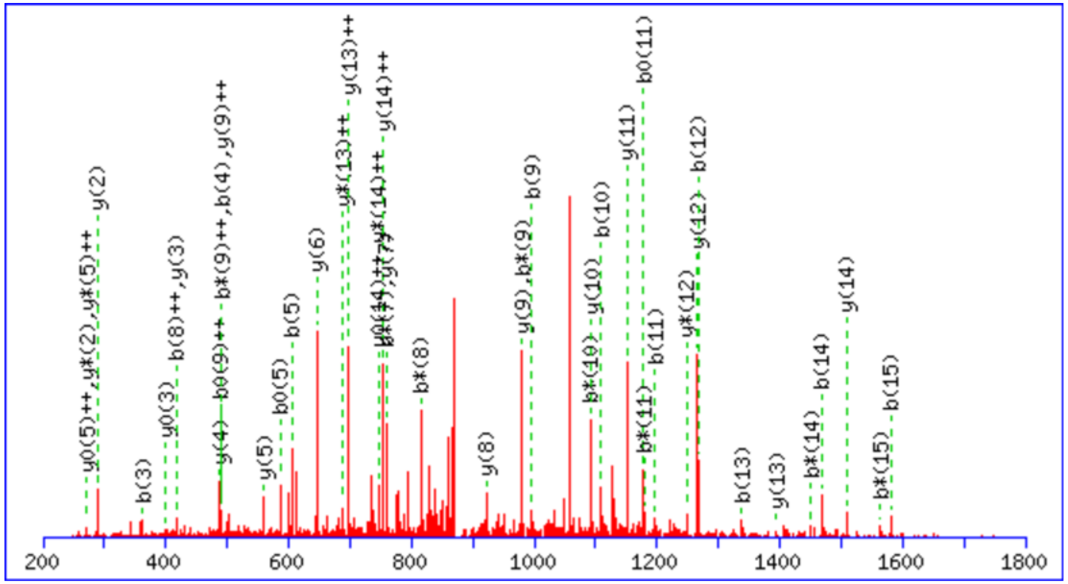


Peptide View

MS/MS Fragmentation of **VFDKDGNGYISAAELR**
Found in **IPI00075248**, Tax_Id=9606 Gene_Symbol=CALM3;CALM2;CALM1 Calmodulin
Experiment: 06 - S_B-4 **Fraction:** S_B-4

Match to Query 12239: 1753.866648 from(877.940600,2+)
Title: OECHL100317_41.13664.13664.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1753.863495**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72 **Expect:** 9.5e-006**Matches :** 46/166 fragment ions using 89 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}
1	100.075690	50.541483					**V**						
2	247.144104	124.075690					**F**	1655.802376	828.404826	1638.775827	819.891551	1637.791811	819.3995
3	**362.171047**	181.589161			344.160482	172.583879	**D**	***1508.733962***	754.870619	1491.707413	746.357345	1490.723397	745.8653
4	**490.266010**	245.636643	473.239461	237.123369	472.255445	236.631361	**K**	***1393.707019***	697.357148	1376.680470	688.843873	1375.696454	688.3518
5	**605.292953**	303.150115	588.266404	294.636840	587.282388	294.144832	**D**	***1265.612056***	633.309666	1248.585507	624.796392	1247.601491	624.3043
6	662.314417	331.660847	645.287868	323.147572	644.303852	322.655564	**G**	***1150.585113***	575.796194	1133.558564	567.282920	1132.574548	566.7909
7	776.357344	388.682310	759.330795	380.169036	758.346779	379.677028	**N**	***1093.563649***	547.285462	1076.537100	538.772188	1075.553084	538.2801
8	833.378808	417.193042	816.352259	408.679768	815.368243	408.187760	**G**	***979.520722***	490.263999	962.494173	481.750724	961.510157	481.2587
9	**996.442137**	498.724707	979.415588	490.211432	978.431572	489.719424	**Y**	***922.499258***	461.753267	905.472709	453.239992	904.488693	452.7479
10	**1109.526201**	555.266738	1092.499652	546.753464	1091.515636	546.261456	**I**	***759.435929***	380.221603	742.409380	371.708328	741.425364	371.2163
11	**1196.558229**	598.782753	1179.531680	590.269478	1178.547664	589.777470	**S**	***646.351865***	323.679571	629.325316	315.166296	628.341300	314.6742
12	**1267.595343**	634.301310	1250.568794	625.788035	1249.584778	625.296027	**A**	***559.319837***	280.163557	542.293288	271.650282	541.309272	271.1582
13	**1338.632457**	669.819866	1321.605908	661.306592	1320.621892	660.814584	**A**	***488.282723***	244.644999	471.256174	236.131725	470.272158	235.6397
14	**1467.675050**	734.341163	1450.648501	725.827889	1449.664485	725.335881	**E**	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.1211
15	**1580.759114**	790.883195	1563.732565	782.369921	1562.748549	781.877912	**L**	***288.203016***	144.605146	271.176467	136.091871		
16							**R**	175.118952	88.063114	158.092403	79.549839		



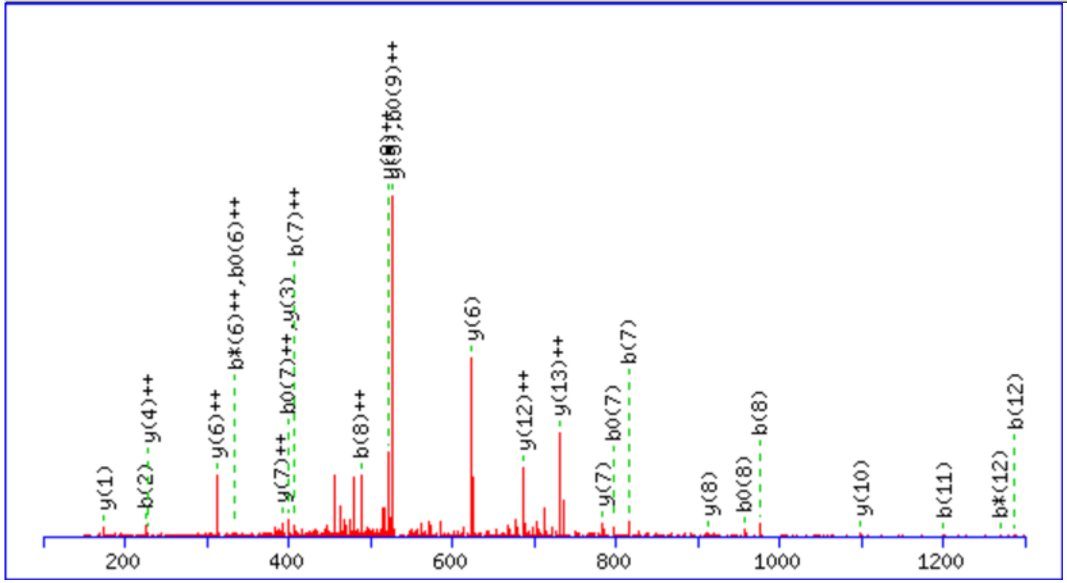
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 06 - S_B-4 **Fraction:** S_B-4

Match to Query 10630: 1597.706172 from(533.576000,3+)
Title: OECHL100317_41.2407.2407.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 57 **Expect:** 0.00013**Matches :** 27/144 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	138.066188	69.536732					**H**						
2	**225.098216**	113.052746			207.087651	104.047463	**S**	1461.653938	731.330607	1444.627389	722.817333	1443.643373	722.3253
3	372.166630	186.586953			354.156065	177.581671	**F**	1374.621910	687.814593	1357.595361	679.301319	1356.611345	678.8093
4	500.261593	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	1227.553496	614.280386	1210.526947	605.767112	1209.542931	605.2751
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.2276

6	686.325650	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	1042.437069	521.722173	1025.410520	513.208898	1024.426504	512.7168
7	**815.368243**	**408.187760**	798.341694	399.674485	797.357678	399.182477	**E**	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.1955
8	**975.398892**	**488.203084**	958.372343	479.689810	957.388327	479.197802	**C**	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.6742
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.6589
10	1143.488770	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.1325
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	456.231356	228.619316	439.204807	220.106041	438.220791	219.6140
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.1033
13	1424.601174	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	312.177864	156.592570	295.151315	148.079295		
14							**R**	***175.118952***	88.063114	158.092403	79.549839		



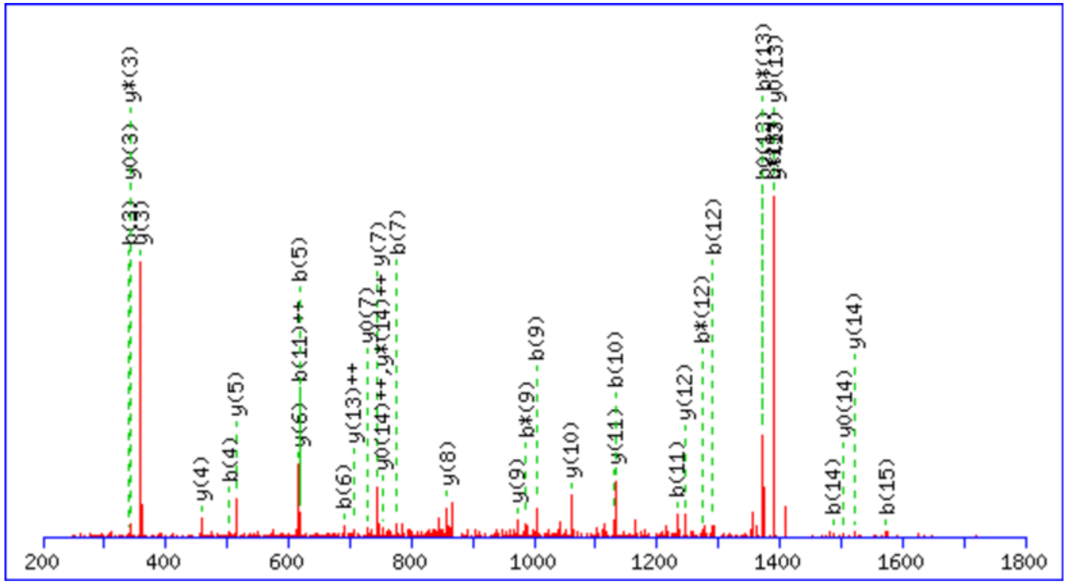
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 06 - S_B-4 **Fraction:** S_B-4

Match to Query 12173: 1746.916448 from(874.465500,2+)

Title: OECHL100317_41.16827.16827.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 73 **Expect:** 4.7e-006**Matches :** 37/156 fragment ions using 71 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	***340.259468***	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	***503.322797***	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	***618.349740***	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018
6	***689.386854***	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	***776.418882***	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							**R**	175.118952	88.063114	158.092403	79.549839		



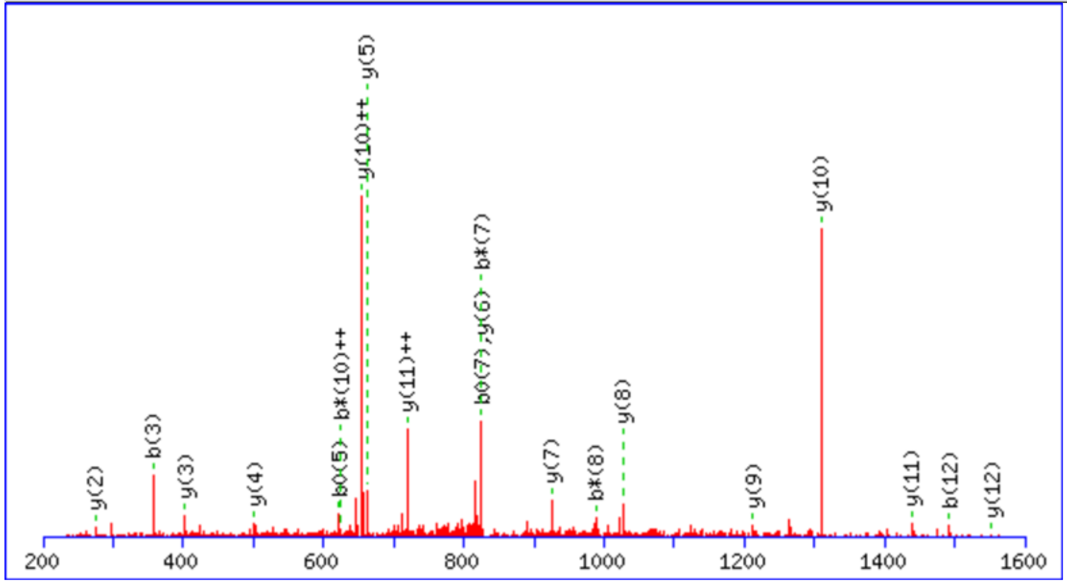
Peptide View

MS/MS Fragmentation of **NLEPWTTYCVQVR**
Found in **IPI00646217**, Tax_Id=9606 Gene_Symbol=IL10RB cDNA FLJ42063 fis, clone SYNOV2005817, highly similar to CYTOKINE RECEPTOR CLASS-II CRF2-4
Experiment: 06 - S_B-4 **Fraction:** S_B-4

Match to Query 11392: 1664.804448 from(833.409500,2+)
Title: OECHL100317_41.17352.17352.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1664.798080**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 68 **Expect:** 2.1e-005**Matches :** 20/128 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	115.050203	58.028740	98.023654	49.515465			**N**						
2	228.134267	114.570771	211.107718	106.057497			**L**	***1551.762428***	776.384852	1534.735879	767.871578	1533.751863	767.3795
3	**357.176860**	179.092068	340.150311	170.578793	339.166295	170.086785	**E**	***1438.678364***	719.842820	1421.651815	711.329546	1420.667799	710.8375
4	454.229624	227.618450	437.203075	219.105176	436.219059	218.613168	**P**	***1309.635771***	655.321524	1292.609222	646.808249	1291.625206	646.3162

5	640.308937	320.658107	623.282388	312.144832	622.298372	311.652824	**W**	***1212.583007***	606.795142	1195.556458	598.281867	1194.572442	597.7898
6	741.356616	371.181946	724.330067	362.668672	723.346051	362.176664	**T**	***1026.503694***	513.755485	1009.477145	505.242211	1008.493129	504.7502
7	842.404295	421.705786	825.377746	413.192511	824.393730	412.700503	**T**	***925.456015***	463.231646	908.429466	454.718371	907.445450	454.2263
8	1005.467624	503.237450	988.441075	494.724176	987.457059	494.232168	**Y**	***824.408336***	412.707806	807.381787	404.194532		
9	1165.498273	583.252775	1148.471724	574.739500	1147.487708	574.247492	**C**	***661.345007***	331.176142	644.318458	322.662867		
10	1264.566687	632.786982	1247.540138	624.273707	1246.556122	623.781699	**V**	***501.314358***	251.160817	484.287809	242.647543		
11	1392.625265	696.816271	1375.598716	688.302996	1374.614700	687.810988	**Q**	***402.245944***	201.626610	385.219395	193.113336		
12	**1491.693679**	746.350478	1474.667130	737.837203	1473.683114	737.345195	**V**	***274.187366***	137.597321	257.160817	129.084047		
13							**R**	175.118952	88.063114	158.092403	79.549839		



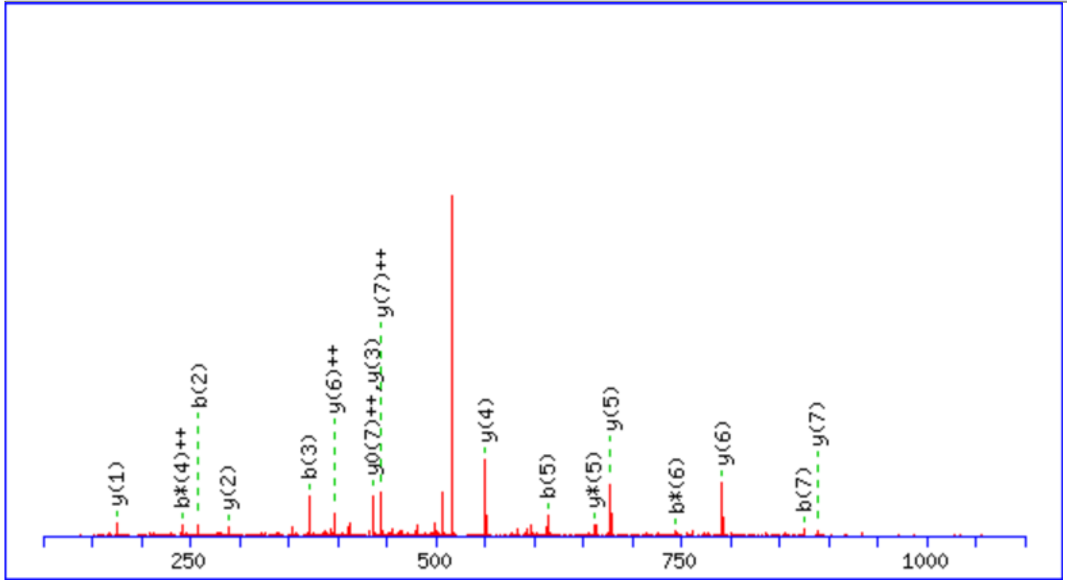
Peptide View

MS/MS Fragmentation of **CPLQDFLR**
Found in **IPI00003807**, Tax_Id=9606 Gene_Symbol=ACP2 Lysosomal acid phosphatase
Experiment: 06 - S_B-4 **Fraction:** S_B-4

Match to Query 4051: 1047.518448 from(524.766500,2+)

Title: OECHL100317_41.16775.16775.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1047.517151**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54 **Expect:** 0.00037**Matches :** 17/64 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	161.037925	81.022600					C							8
2	**258.090689**	129.548982					P	***888.493779***	444.750528	871.467230	436.237253	870.483214	435.745245	7
3	**371.174753**	186.091015					L	***791.441015***	396.224146	774.414466	387.710871	773.430450	387.218863	6
4	499.233331	250.120304	482.206782	241.607029			Q	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	5
5	**614.260274**	307.633775	597.233725	299.120501	596.249709	298.628493	D	***550.298373***	275.652825	533.271824	267.139550	532.287808	266.647542	4
6	761.328688	381.167982	744.302139	372.654708	743.318123	372.162700	F	***435.271430***	218.139353	418.244881	209.626079			3
7	**874.412752**	437.710014	857.386203	429.196740	856.402187	428.704732	L	***288.203016***	144.605146	271.176467	136.091872			2
8							R	***175.118952***	88.063114	158.092403	79.549840			1



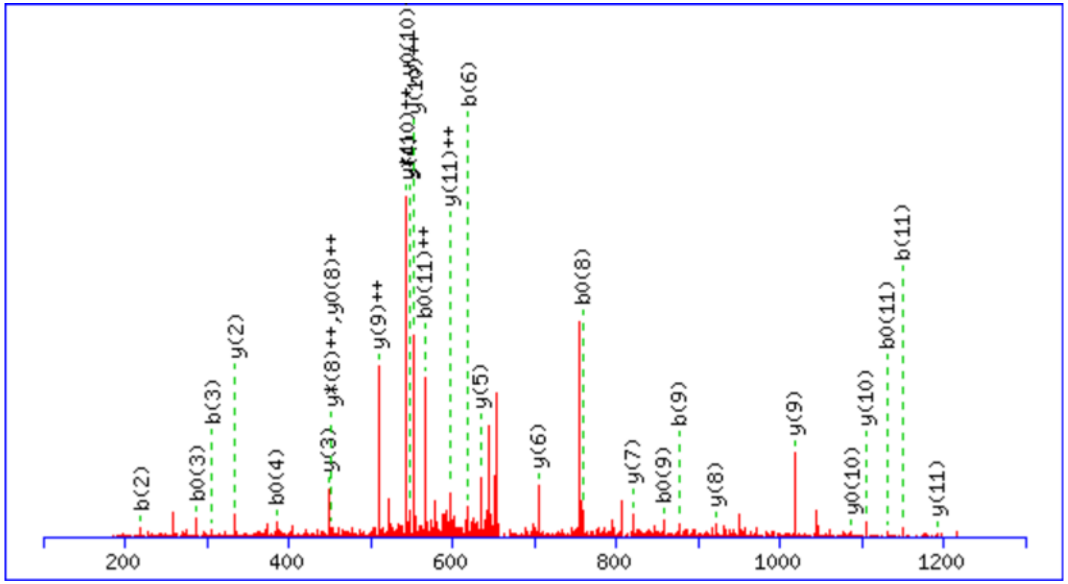
Peptide View

MS/MS Fragmentation of **MSSPTDASVICR**

Found in **IPI00021302**, Tax_Id=9606 Gene_Symbol=SUSD2 Sushi domain-containing protein 2
Experiment: 06 - S_B-4 **Fraction:** S_B-4

Match to Query 7838: 1322.595648 from(662.305100,2+)
Title: OECHL100317_41.9821.9821.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1322.595871**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 50 **Expect:** 0.00056**Matches :** 29/100 fragment ions using 75 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518			**M**							**12**
2	**219.079789**	110.043532	201.069224	101.038250	**S**	***1192.562663***	596.784969	1175.536114	588.271695	1174.552098	587.779687	**11**
3	**306.111817**	153.559546	288.101252	144.554264	**S**	***1105.530635***	553.268955	1088.504086	544.755681	1087.520070	544.263673	**10**
4	403.164581	202.085928	385.154016	193.080646	**P**	***1018.498607***	509.752942	1001.472058	501.239667	1000.488042	500.747659	**9**
5	504.212260	252.609768	486.201695	243.604485	**T**	***921.445843***	461.226560	904.419294	452.713285	903.435278	452.221277	**8**
6	**619.239203**	310.123240	601.228638	301.117957	**D**	***820.398164***	410.702720	803.371615	402.189445	802.387599	401.697437	**7**
7	690.276317	345.641797	672.265752	336.636514	**A**	***705.371221***	353.189249	688.344672	344.675974	687.360656	344.183966	**6**
8	777.308345	389.157810	759.297780	380.152528	**S**	***634.334107***	317.670692	617.307558	309.157417	616.323542	308.665409	**5**
9	**876.376759**	438.692017	858.366194	429.686735	**V**	***547.302079***	274.154678	530.275530	265.641403			**4**
10	989.460823	495.234049	971.450258	486.228767	**I**	***448.233665***	224.620470	431.207116	216.107196			**3**
11	**1149.491472**	575.249374	1131.480907	566.244091	**C**	***335.149601***	168.078438	318.123052	159.565164			**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**



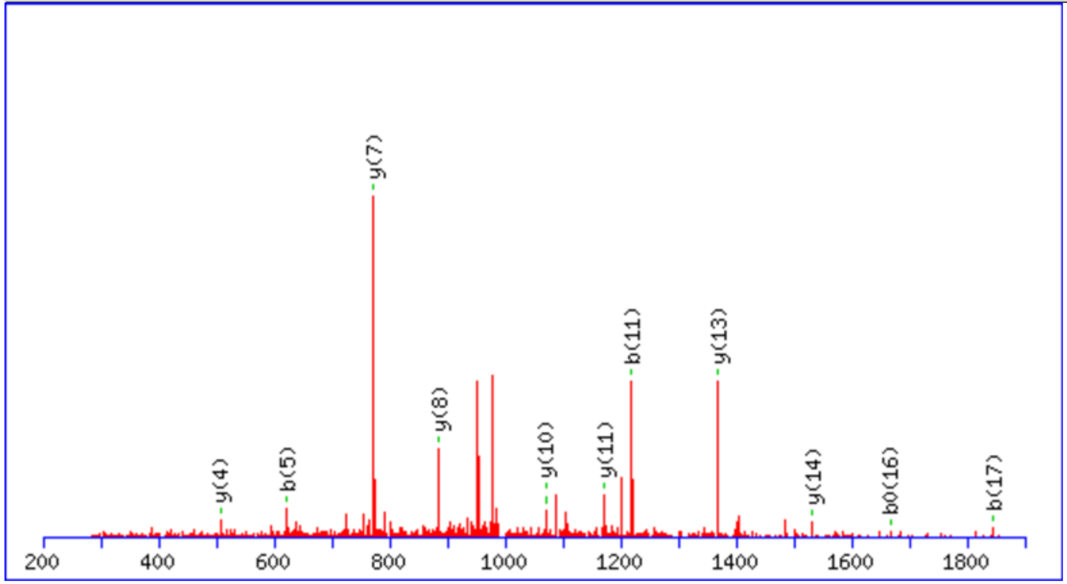
Peptide View

MS/MS Fragmentation of **ACLDYPVTSVLPPASLCK**
Found in **IPI00023974**, Tax_Id=9606 Gene_Symbol=PTTG1IP Pituitary tumor-transforming gene 1 protein-interacting protein
Experiment: 06 - S_B-4 **Fraction:** S_B-4

Match to Query 14198: 1989.989048 from(996.001800,2+)
Title: OECHL100317_41.18278.18278.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_41.raw
Monoisotopic mass of neutral peptide Mr(calc): 1989.990372**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49 **Expect:** 0.0021**Matches :** 11/158 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**18**
2	232.075039	116.541158			**C**	1919.960535	960.483906	1902.933986	951.970631	1901.949970	951.478623	**17**
3	345.159103	173.083190			**L**	1759.929886	880.468581	1742.903337	871.955307	1741.919321	871.463299	**16**
4	460.186046	230.596661	442.175481	221.591379	**D**	1646.845822	823.926549	1629.819273	815.413275	1628.835257	814.921267	**15**
5	**623.249375**	312.128326	605.238810	303.123043	**Y**	***1531.818879***	766.413078	1514.792330	757.899803	1513.808314	757.407795	**14**

6	720.302139	360.654708	702.291574	351.649425	**P**	***1368.755550***	684.881413	1351.729001	676.368139	1350.744985	675.876131	**13**
7	819.370553	410.188915	801.359988	401.183632	**V**	1271.702786	636.355031	1254.676237	627.841757	1253.692221	627.349749	**12**
8	920.418232	460.712754	902.407667	451.707472	**T**	***1172.634372***	586.820824	1155.607823	578.307550	1154.623807	577.815542	**11**
9	1007.450260	504.228768	989.439695	495.223486	**S**	***1071.586693***	536.296985	1054.560144	527.783710	1053.576128	527.291702	**10**
10	1106.518674	553.762975	1088.508109	544.757693	**V**	984.554665	492.780971	967.528116	484.267696	966.544100	483.775688	**9**
11	**1219.602738**	610.305007	1201.592173	601.299725	**L**	***885.486251***	443.246764	868.459702	434.733489	867.475686	434.241481	**8**
12	1316.655502	658.831389	1298.644937	649.826107	**P**	***772.402187***	386.704732	755.375638	378.191457	754.391622	377.699449	**7**
13	1413.708266	707.357771	1395.697701	698.352489	**P**	675.349423	338.178350	658.322874	329.665075	657.338858	329.173067	**6**
14	1484.745380	742.876328	1466.734815	733.871046	**A**	578.296659	289.651968	561.270110	281.138693	560.286094	280.646685	**5**
15	1571.777408	786.392342	1553.766843	777.387060	**S**	***507.259545***	254.133411	490.232996	245.620136	489.248980	245.128128	**4**
16	1684.861472	842.934374	1666.850907	833.929092	**L**	420.227517	210.617396	403.200968	202.104122			**3**
17	**1844.892121**	922.949699	1826.881556	913.944416	**C**	307.143453	154.075365	290.116904	145.562090			**2**
18					**K**	147.112804	74.060040	130.086255	65.546765			**1**

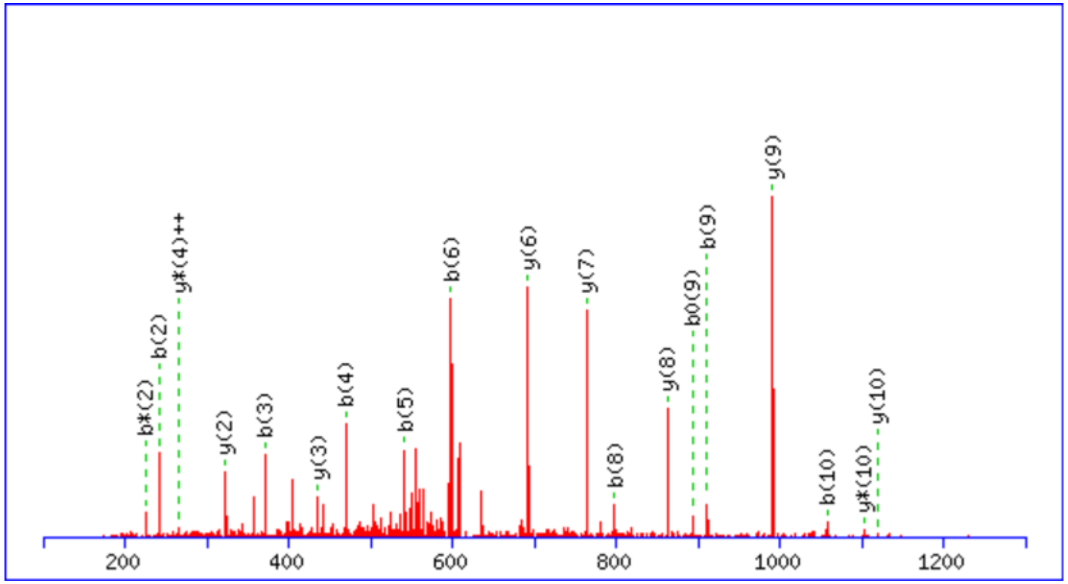


Peptide View

MS/MS Fragmentation of **IQEVAGSLIFR**
Found in **IPI00006988**, Tax_Id=9606 Gene_Symbol=RETN Resistin
Experiment: 03 - S_A-3 **Fraction:** S_A-3

Match to Query 7017: 1231.692448 from(616.853500,2+)
Title: OECHL100317_39.16377.16377.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1231.692459**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 60 **Expect:** 4.2e-005**Matches :** 19/106 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}
1	114.091340	57.549308					**I**						
2	***242.149918***	121.578597	225.123369	113.065323			**Q**	***1119.615685***	560.311481	1102.589136	551.798206	1101.605120	551.3061
3	***371.192511***	186.099894	354.165962	177.586619	353.181946	177.094611	**E**	***991.557107***	496.282192	974.530558	487.768917	973.546542	487.2769
4	***470.260925***	235.634101	453.234376	227.120826	452.250360	226.628818	**V**	***862.514514***	431.760895	845.487965	423.247621	844.503949	422.7556
5	***541.298039***	271.152658	524.271490	262.639383	523.287474	262.147375	**A**	***763.446100***	382.226688	746.419551	373.713414	745.435535	373.2214
6	***598.319503***	299.663390	581.292954	291.150115	580.308938	290.658107	**G**	***692.408986***	346.708131	675.382437	338.194857	674.398421	337.7028
7	685.351531	343.179404	668.324982	334.666129	667.340966	334.174121	**S**	635.387522	318.197399	618.360973	309.684125	617.376957	309.1921
8	***798.435595***	399.721436	781.409046	391.208161	780.425030	390.716153	**L**	548.355494	274.681385	531.328945	266.168111		
9	***911.519659***	456.263468	894.493110	447.750193	893.509094	447.258185	**I**	***435.271430***	218.139353	418.244881	209.626078		
10	***1058.588073***	529.797675	1041.561524	521.284400	1040.577508	520.792392	**F**	***322.187366***	161.597321	305.160817	153.084046		
11							**R**	175.118952	88.063114	158.092403	79.549839		



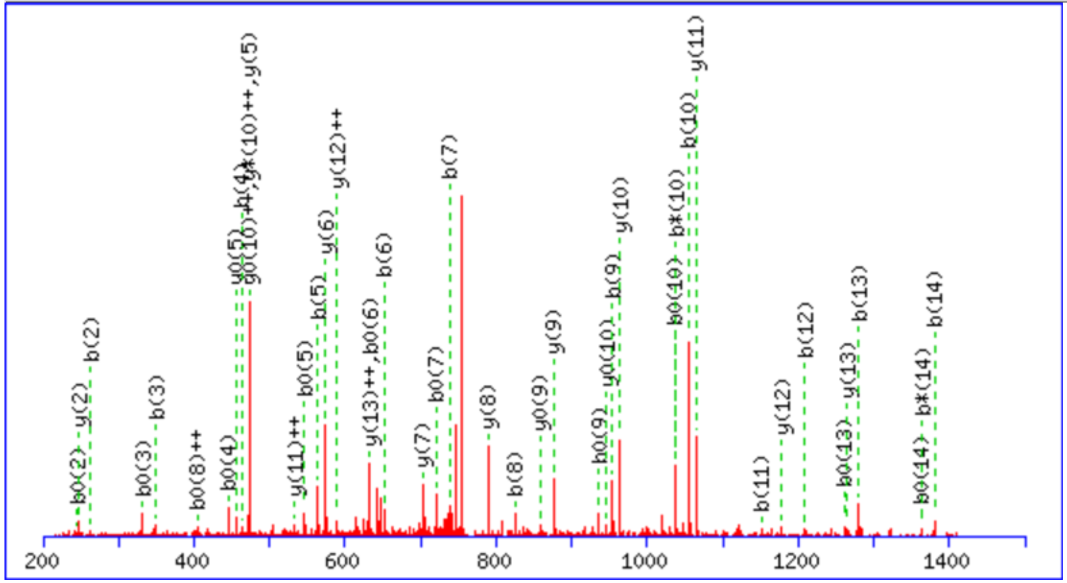
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 03 - S_A-3 **Fraction:** S_A-3

Match to Query 10192: 1525.725448 from(763.870000,2+)
Title: OECHL100317_39.10807.10807.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 85 **Expect:** 3.5e-007**Matches :** 44/150 fragment ions using 84 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	116.034219	58.520748			98.023654	49.515465	**D**						
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.3515
3	***350.134661***	175.570968			332.124096	166.565686	**S**	**1264.637937**	632.822607	1247.611388	624.309332	1246.627372	623.8173
4	***463.218725***	232.113001			445.208160	223.107718	**L**	**1177.605909**	589.306592	1160.579360	580.793318	1159.595344	580.3013
5	***564.266404***	282.636840			546.255839	273.631558	**T**	**1064.521845**	532.764561	1047.495296	524.251286	1046.511280	523.7592

6	***651.298432***	326.152854			633.287867	317.147572	**S**	**963.474166**	482.240721	946.447617	473.727446	945.463601	473.2354
7	***738.330460***	369.668868			720.319895	360.663586	**S**	**876.442138**	438.724707	859.415589	430.211432	858.431573	429.7194
8	***825.362488***	413.184882			807.351923	404.179599	**S**	**789.410110**	395.208693	772.383561	386.695418	771.399545	386.2034
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	**702.378082**	351.692679	685.351533	343.179404	684.367517	342.6873
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	**574.319504**	287.663390	557.292955	279.150115	556.308939	278.6581
11	***1151.521509***	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	**473.271825**	237.139550	456.245276	228.626276	455.261260	228.1342
12	***1208.542973***	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	376.219061	188.613168	359.192512	180.099894	358.208496	179.6078
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.0971
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	**248.160483**	124.583879	231.133934	116.070605	230.149918	115.5785
15							**K**	147.112804	74.060040	130.086255	65.546765		

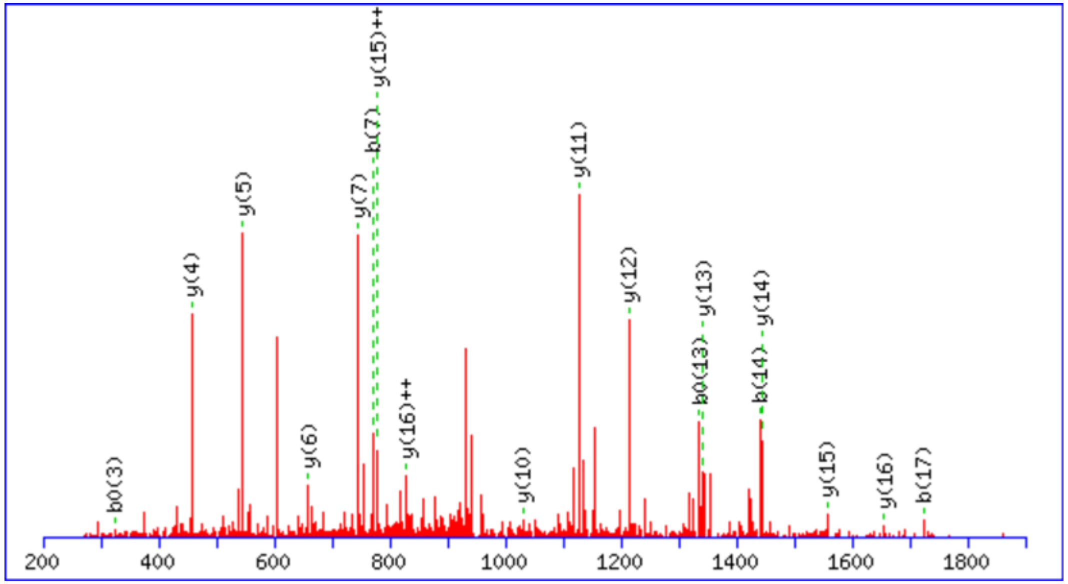


Peptide View

MS/MS Fragmentation of **EIVLTQSPATLSLSPGER**
Found in **IPI00816799**, Tax_Id=9606 Gene_Symbol=- Rheumatoid factor D5 light chain (Fragment)
Experiment: 03 - S_A-3 **Fraction:** S_A-3

Match to Query 13179: 1897.018048 from(949.516300,2+)
Title: OECHL100317_39.16247.16247.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1897.015640**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 79 **Expect:** 1.3e-006**Matches :** 18/192 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	130.049869	65.528572			112.039304	56.523290	**E**						
2	243.133933	122.070605			225.123368	113.065322	**I**	1768.980341	884.993808	1751.953792	876.480534	1750.969776	875.9885
3	342.202347	171.604812			324.191782	162.599529	**V**	***1655.896277***	828.451776	1638.869728	819.938502	1637.885712	819.4464
4	455.286411	228.146844			437.275846	219.141561	**L**	***1556.827863***	778.917569	1539.801314	770.404295	1538.817298	769.9122
5	556.334090	278.670683			538.323525	269.665401	**T**	***1443.743799***	722.375537	1426.717250	713.862263	1425.733234	713.3702
6	684.392668	342.699972	667.366119	334.186698	666.382103	333.694690	**Q**	***1342.696120***	671.851698	1325.669571	663.338423	1324.685555	662.8464
7	**771.424696**	386.215986	754.398147	377.702712	753.414131	377.210704	**S**	***1214.637542***	607.822409	1197.610993	599.309134	1196.626977	598.8171
8	868.477460	434.742368	851.450911	426.229094	850.466895	425.737086	**P**	***1127.605514***	564.306395	1110.578965	555.793120	1109.594949	555.3011
9	939.514574	470.260925	922.488025	461.747651	921.504009	461.255643	**A**	***1030.552750***	515.780013	1013.526201	507.266738	1012.542185	506.7747
10	1040.562253	520.784765	1023.535704	512.271490	1022.551688	511.779482	**T**	959.515636	480.261456	942.489087	471.748181	941.505071	471.2561
11	1153.646317	577.326797	1136.619768	568.813522	1135.635752	568.321514	**L**	858.467957	429.737616	841.441408	421.224342	840.457392	420.7323
12	1240.678345	620.842811	1223.651796	612.329536	1222.667780	611.837528	**S**	***745.383893***	373.195585	728.357344	364.682310	727.373328	364.1903
13	1353.762409	677.384842	1336.735860	668.871568	1335.751844	668.379560	**L**	***658.351865***	329.679570	641.325316	321.166296	640.341300	320.6742
14	**1440.794437**	720.900857	1423.767888	712.387582	1422.783872	711.895574	**S**	***545.267801***	273.137539	528.241252	264.624264	527.257236	264.1322
15	1537.847201	769.427239	1520.820652	760.913964	1519.836636	760.421956	**P**	***458.235773***	229.621524	441.209224	221.108250	440.225208	220.6162
16	1594.868665	797.937971	1577.842116	789.424696	1576.858100	788.932688	**G**	361.183009	181.095142	344.156460	172.581868	343.172444	172.0898
17	**1723.911258**	862.459267	1706.884709	853.945992	1705.900693	853.453984	**E**	304.161545	152.584410	287.134996	144.071136	286.150980	143.5791
18							**R**	175.118952	88.063114	158.092403	79.549839		



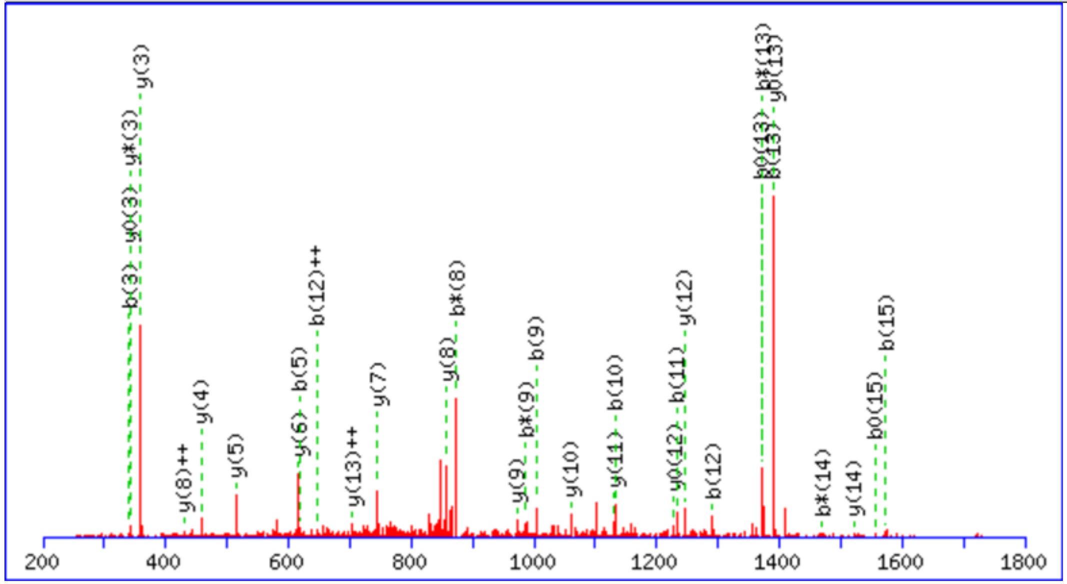
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 03 - S_A-3 **Fraction:** S_A-3

Match to Query 12073: 1746.916448 from(874.465500,2+)
Title: OECHL100317_39.16441.16441.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65 **Expect:** 3.4e-005**Matches :** 32/156 fragment ions using 59 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	**340.259468**	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018

6	689.386854	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							**R**	175.118952	88.063114	158.092403	79.549839		



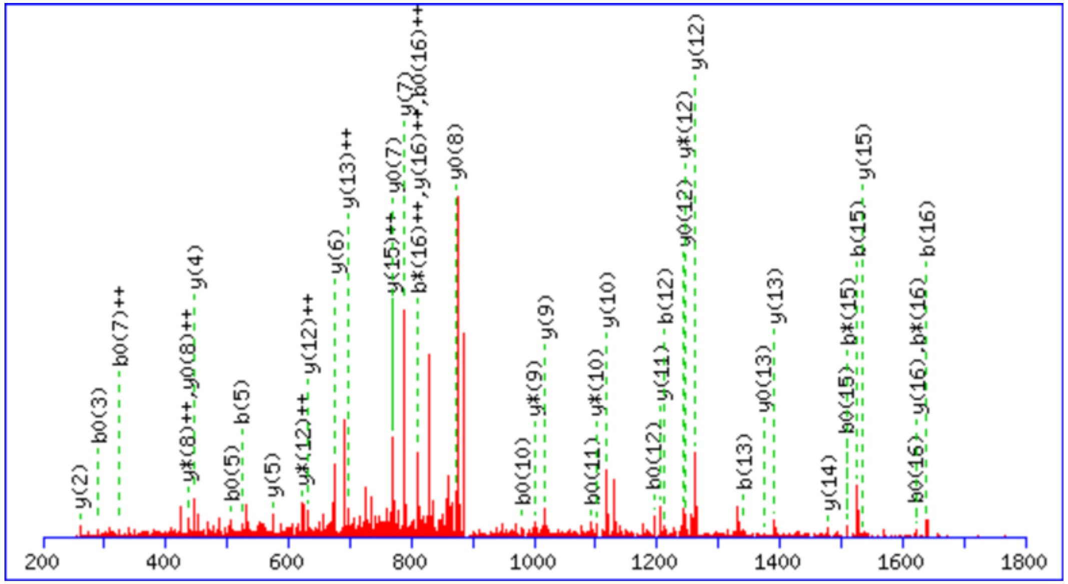
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P

Experiment: 03 - S_A-3 **Fraction:** S_A-3

Match to Query 12432: 1784.878848 from(893.446700,2+)
Title: OECHL100317_39.7461.7461.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56 **Expect:** 0.0004**Matches :** 44/170 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	164.070605	82.538940					**Y**						
2	251.102633	126.054954			233.092068	117.049672	**S**	***1622.823172***	811.915224	1605.796623	803.401950	1604.812607	802.9099
3	308.124097	154.565687			290.113532	145.560404	**G**	***1535.791144***	768.399210	1518.764595	759.885936	1517.780579	759.3939
4	395.156125	198.081701			377.145560	189.076418	**S**	***1478.769680***	739.888478	1461.743131	731.375204	1460.759115	730.8831
5	**524.198718**	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.3671
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.8458
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.3351
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.8191
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.2952
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.2660
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.7421
12	**1212.537889**	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.2001
13	**1340.632852**	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.6762
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.6288
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.1180
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		



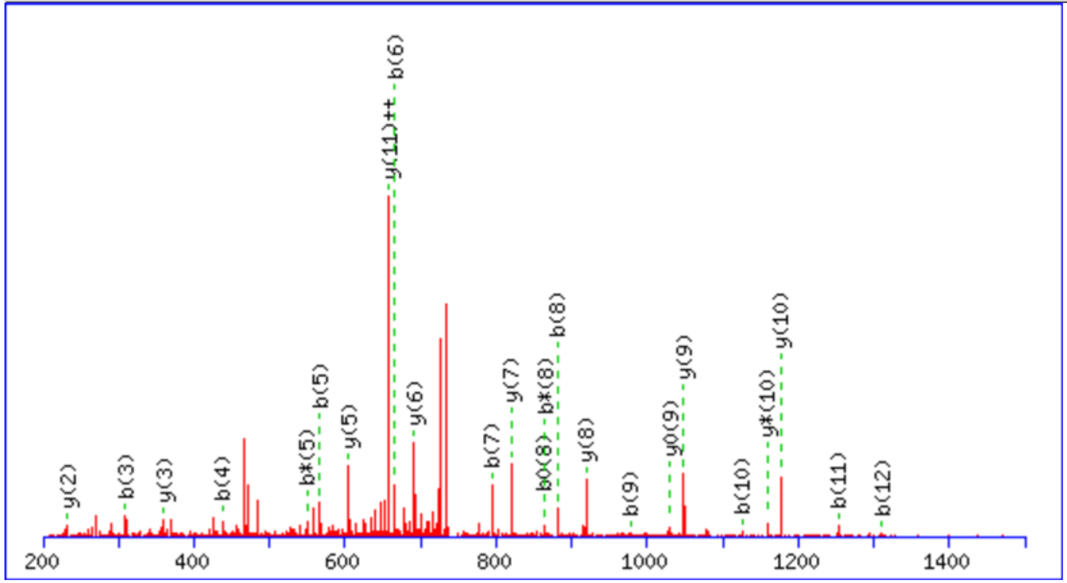
Peptide View

MS/MS Fragmentation of **NGHQEVESPFQGR**
Found in **IPI00020747**, Tax_Id=9606 Gene_Symbol=SCN3B Sodium channel subunit beta-3
Experiment: 03 - S_A-3 **Fraction:** S_A-3

Match to Query 9762: 1483.681048 from(742.847800,2+)
Title: OECHL100317_39.7647.7647.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 1483.680405**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50 **Expect:** 0.00093**Matches :** 24/126 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	115.050203	58.028740	98.023654	49.515465			**N**						
2	172.071667	86.539471	155.045118	78.026197			**G**	1370.644754	685.826015	1353.618205	677.312741	1352.634189	676.8207
3	***309.130579***	155.068927	292.104030	146.555653			**H**	1313.623290	657.315283	1296.596741	648.802009	1295.612725	648.3100
4	***437.189157***	219.098216	420.162608	210.584942			**Q**	**1176.564378**	588.785827	1159.537829	580.272553	1158.553813	579.7805
5	***566.231750***	283.619513	549.205201	275.106239	548.221185	274.614231	**E**	**1048.505800**	524.756538	1031.479251	516.243264	1030.495235	515.7512

6	***665.300164***	333.153720	648.273615	324.640446	647.289599	324.148438	**V**	**919.463207**	460.235242	902.436658	451.721967	901.452642	451.2299
7	***794.342757***	397.675017	777.316208	389.161742	776.332192	388.669734	**E**	**820.394793**	410.701035	803.368244	402.187760	802.384228	401.6957
8	***881.374785***	441.191031	864.348236	432.677756	863.364220	432.185748	**S**	**691.352200**	346.179738	674.325651	337.666464	673.341635	337.1744
9	***978.427549***	489.717413	961.401000	481.204138	960.416984	480.712130	**P**	**604.320172**	302.663724	587.293623	294.150450		
10	***1125.495963***	563.251620	1108.469414	554.738345	1107.485398	554.246337	**F**	507.267408	254.137342	490.240859	245.624068		
11	***1253.554541***	627.280909	1236.527992	618.767634	1235.543976	618.275626	**Q**	**360.198994**	180.603135	343.172445	172.089860		
12	***1310.576005***	655.791641	1293.549456	647.278366	1292.565440	646.786358	**G**	**232.140416**	116.573846	215.113867	108.060571		
13							**R**	175.118952	88.063114	158.092403	79.549839		



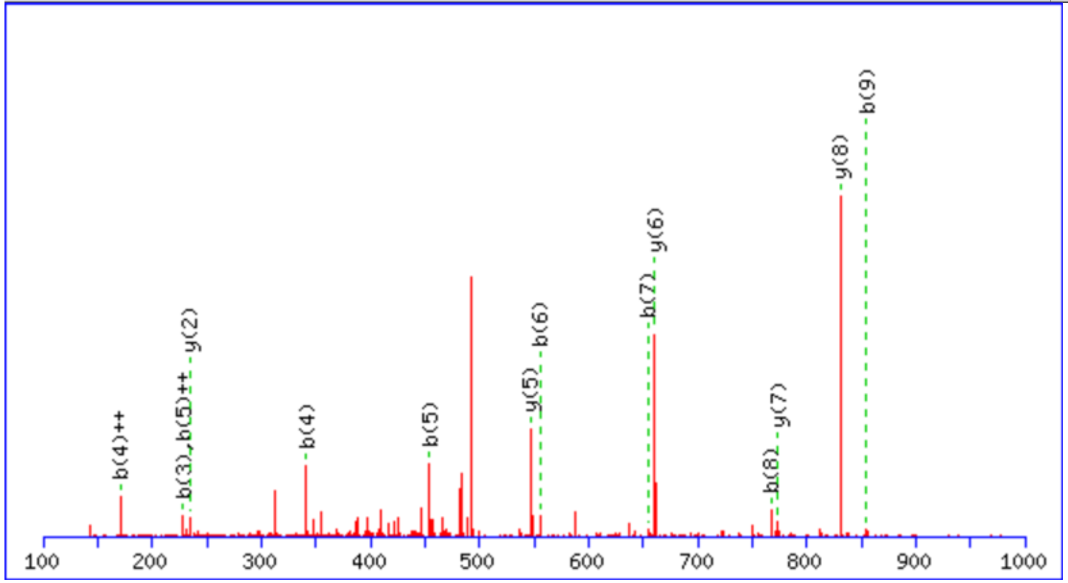
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 03 - S_A-3 **Fraction:** S_A-3

Match to Query 3212: 999.634648 from(500.824600,2+)
Title: OECHL100317_39.16660.16660.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_39.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50 **Expect:** 0.00012**Matches :** 15/78 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	**171.112804**			**L**	**773.513117**	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	**227.654836**			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**

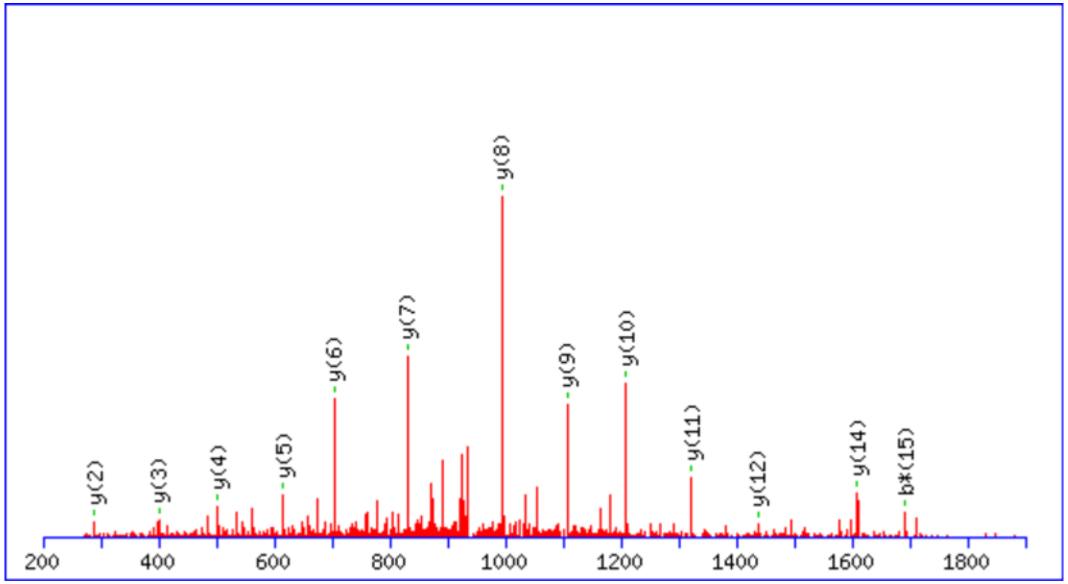


Peptide View

MS/MS Fragmentation of **FQDGDLTLYQSNTILR**
Found in **IPI00219757**, Tax_Id=9606 Gene_Symbol=GSTP1 Glutathione S-transferase P
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 14061: 1882.943248 from(942.478900,2+)
Title: OECHL100317_37.18015.18015.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1882.942490**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 110 **Expect:** 1.7e-009**Matches :** 13/168 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	148.075690	74.541483					F						
2	276.134268	138.570772	259.107719	130.057497			Q	1736.881356	868.944316	1719.854807	860.431041	1718.870791	859.9390
3	391.161211	196.084243	374.134662	187.570969	373.150646	187.078961	D	***1608.822778***	804.915027	1591.796229	796.401752	1590.812213	795.9097
4	448.182675	224.594975	431.156126	216.081701	430.172110	215.589693	G	1493.795835	747.401555	1476.769286	738.888281	1475.785270	738.3962
5	563.209618	282.108447	546.183069	273.595172	545.199053	273.103164	D	***1436.774371***	718.890823	1419.747822	710.377549	1418.763806	709.8855
6	676.293682	338.650479	659.267133	330.137205	658.283117	329.645197	L	***1321.747428***	661.377352	1304.720879	652.864078	1303.736863	652.3720
7	777.341361	389.174319	760.314812	380.661044	759.330796	380.169036	T	***1208.663364***	604.835320	1191.636815	596.322045	1190.652799	595.8300
8	890.425425	445.716351	873.398876	437.203076	872.414860	436.711068	L	***1107.615685***	554.311480	1090.589136	545.798206	1089.605120	545.3061
9	1053.488754	527.248015	1036.462205	518.734741	1035.478189	518.242732	Y	***994.531621***	497.769448	977.505072	489.256174	976.521056	488.7641
10	1181.547332	591.277304	1164.520783	582.764029	1163.536767	582.272021	Q	***831.468292***	416.237784	814.441743	407.724509	813.457727	407.2325
11	1268.579360	634.793318	1251.552811	626.280044	1250.568795	625.788035	S	***703.409714***	352.208495	686.383165	343.695220	685.399149	343.2032
12	1382.622287	691.814781	1365.595738	683.301507	1364.611722	682.809499	N	***616.377686***	308.692481	599.351137	300.179206	598.367121	299.6871
13	1483.669966	742.338621	1466.643417	733.825347	1465.659401	733.333338	T	***502.334759***	251.671017	485.308210	243.157743	484.324194	242.6657
14	1596.754030	798.880653	1579.727481	790.367378	1578.743465	789.875370	I	***401.287080***	201.147178	384.260531	192.633903		
15	1709.838094	855.422685	1692.811545	846.909410	1691.827529	846.417402	L	***288.203016***	144.605146	271.176467	136.091871		
16							R	175.118952	88.063114	158.092403	79.549839		



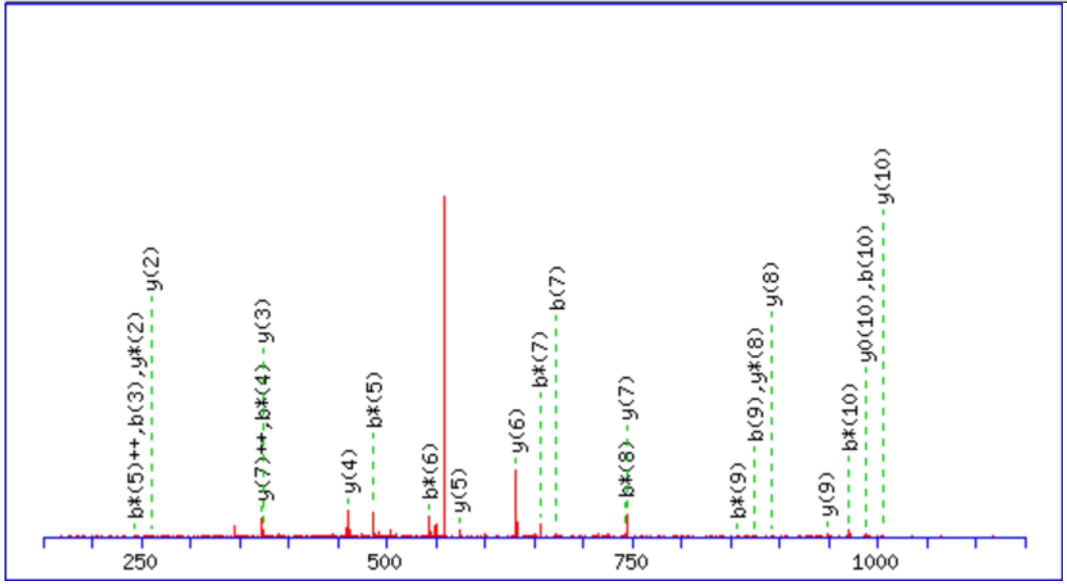
Peptide View

MS/MS Fragmentation of **QGGFLGLSNIK**
Found in **IPI00013955**, Tax_Id=9606 Gene_Symbol=MUC1 Isoform 1 of Mucin-1
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 5694: 1132.624448 from(567.319500,2+)
Title: OECHL100317_37.17125.17125.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1132.624054**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 69 **Expect:** 9.6e-006**Matches :** 25/100 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			**Q**							**11**
2	186.087318	93.547297	169.060769	85.034023			**G**	***1005.572757***	503.290017	988.546208	494.776742	987.562192	494.284734	**10**
3	**243.108782**	122.058029	226.082233	113.544755			**G**	***948.551293***	474.779285	931.524744	466.266010	930.540728	465.774002	**9**
4	390.177196	195.592236	373.150647	187.078962			**F**	***891.529829***	446.268553	874.503280	437.755278	873.519264	437.263270	**8**
5	503.261260	252.134268	486.234711	243.620994			**L**	***744.461415***	372.734346	727.434866	364.221071	726.450850	363.729063	**7**

6	560.282724	280.645000	543.256175	272.131726			**G**	***631.377351***	316.192314	614.350802	307.679039	613.366786	307.187031	**6**
7	**673.366788**	337.187032	656.340239	328.673758			**L**	***574.355887***	287.681582	557.329338	279.168307	556.345322	278.676299	**5**
8	760.398816	380.703046	743.372267	372.189772	742.388251	371.697764	**S**	***461.271823***	231.139550	444.245274	222.626275	443.261258	222.134267	**4**
9	**874.441743**	437.724510	857.415194	429.211235	856.431178	428.719227	**N**	***374.239795***	187.623536	357.213246	179.110261			**3**
10	**987.525807**	494.266542	970.499258	485.753267	969.515242	485.261259	**I**	***260.196868***	130.602072	243.170319	122.088798			**2**
11							**K**	147.112804	74.060040	130.086255	65.546766			**1**

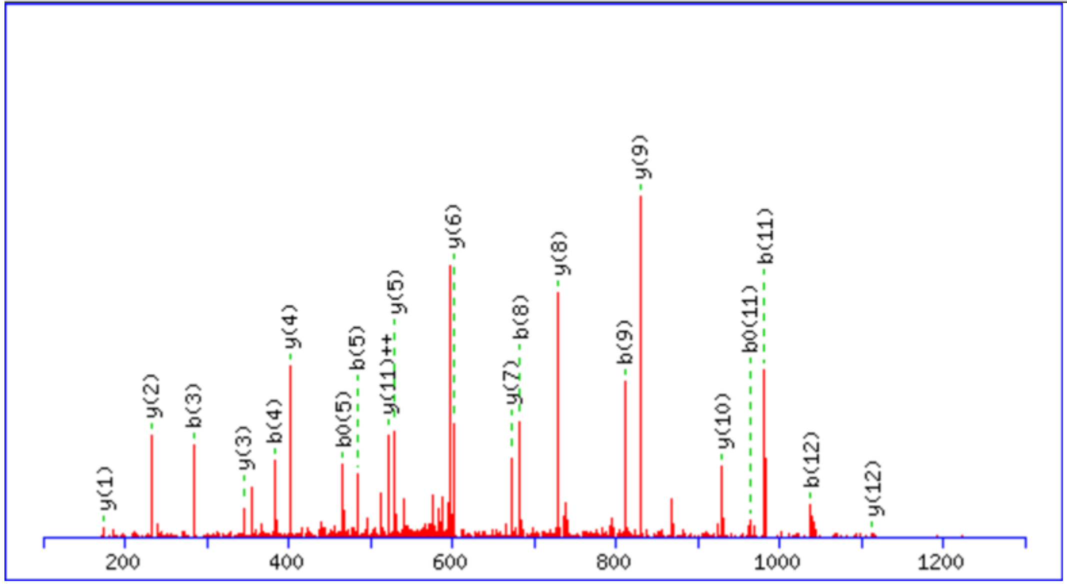


Peptide View

MS/MS Fragmentation of **VALVTGAAQGIGR**
Found in **IPI00290420**, Tax_Id=9606 Gene_Symbol=HPGD hydroxyprostaglandin dehydrogenase 15-(NAD) isoform 2
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 6826: 1211.698648 from(606.856600,2+)
Title: OECHL100317_37.11501.11501.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1211.698624**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 95 **Expect:** 1.3e-008**Matches :** 21/104 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	100.075690	50.541483					**V**						
2	171.112804	86.060040					**A**	***1113.637485***	557.322381	1096.610936	548.809106	1095.626920	548.3170
3	**284.196868**	142.602072					**L**	1042.600371	521.803824	1025.573822	513.290549	1024.589806	512.7985
4	**383.265282**	192.136279					**V**	***929.516307***	465.261792	912.489758	456.748517	911.505742	456.2565
5	**484.312961**	242.660119			466.302396	233.654836	**T**	***830.447893***	415.727585	813.421344	407.214310	812.437328	406.7223
6	541.334425	271.170851			523.323860	262.165568	**G**	***729.400214***	365.203745	712.373665	356.690471		
7	612.371539	306.689408			594.360974	297.684125	**A**	***672.378750***	336.693013	655.352201	328.179738		
8	**683.408653**	342.207965			665.398088	333.202682	**A**	***601.341636***	301.174456	584.315087	292.661182		
9	**811.467231**	406.237254	794.440682	397.723979	793.456666	397.231971	**Q**	***530.304522***	265.655899	513.277973	257.142625		
10	868.488695	434.747986	851.462146	426.234711	850.478130	425.742703	**G**	***402.245944***	201.626610	385.219395	193.113335		
11	**981.572759**	491.290018	964.546210	482.776743	963.562194	482.284735	**I**	***345.224480***	173.115878	328.197931	164.602603		
12	**1038.594223**	519.800750	1021.567674	511.287475	1020.583658	510.795467	**G**	***232.140416***	116.573846	215.113867	108.060571		
13							**R**	***175.118952***	88.063114	158.092403	79.549839		

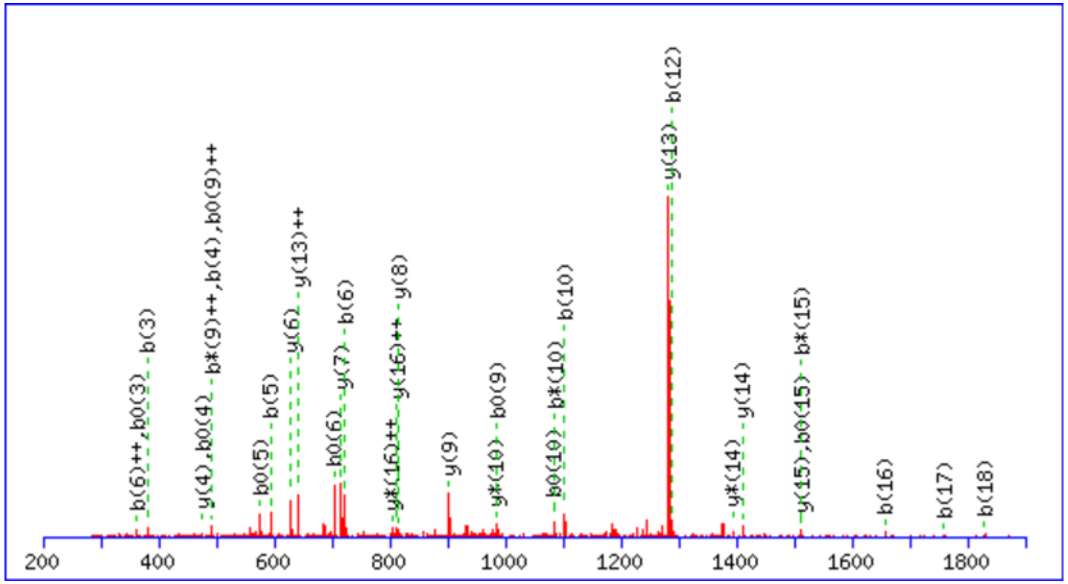


Peptide View

MS/MS Fragmentation of **SYELTQPPSVSVSPGQTAR**
Found in **IPI00382440**, Tax_Id=9606 Gene_Symbol=- Ig lambda chain V-IV region Hil
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 14823: 2002.995448 from(1002.505000,2+)
Title: OECHL100317_37.13335.13335.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 2002.995987**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 55 **Expect:** 0.00058**Matches :** 34/202 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	88.039304	44.523290			70.028739	35.518008	S						
2	251.102633	126.054954			233.092068	117.049672	Y	1916.971234	958.989255	1899.944685	950.475981	1898.960669	949.9839
3	***380.145226***	190.576251			362.134661	181.570969	E	1753.907905	877.457591	1736.881356	868.944316	1735.897340	868.4523
4	***493.229290***	247.118283			475.218725	238.113001	L	1624.865312	812.936294	1607.838763	804.423020	1606.854747	803.9310
5	***594.276969***	297.642123			576.266404	288.636840	T	***1511.781248***	756.394262	1494.754699	747.880988	1493.770683	747.3889
6	***722.335547***	361.671412	705.308998	353.158137	704.324982	352.666129	Q	***1410.733569***	705.870423	1393.707020	697.357148	1392.723004	696.8651
7	819.388311	410.197794	802.361762	401.684519	801.377746	401.192511	P	***1282.674991***	641.841134	1265.648442	633.327859	1264.664426	632.8358
8	916.441075	458.724176	899.414526	450.210901	898.430510	449.718893	P	1185.622227	593.314752	1168.595678	584.801477	1167.611662	584.3094
9	1003.473103	502.240190	986.446554	493.726915	985.462538	493.234907	S	1088.569463	544.788370	1071.542914	536.275095	1070.558898	535.7830
10	***1102.541517***	551.774397	1085.514968	543.261122	1084.530952	542.769114	V	1001.537435	501.272356	984.510886	492.759081	983.526870	492.2670
11	1189.573545	595.290411	1172.546996	586.777136	1171.562980	586.285128	S	***902.469021***	451.738149	885.442472	443.224874	884.458456	442.7328
12	***1288.641959***	644.824618	1271.615410	636.311343	1270.631394	635.819335	V	***815.436993***	408.222135	798.410444	399.708860	797.426428	399.2168
13	1375.673987	688.340632	1358.647438	679.827357	1357.663422	679.335349	S	***716.368579***	358.687928	699.342030	350.174653	698.358014	349.6826
14	1472.726751	736.867014	1455.700202	728.353739	1454.716186	727.861731	P	***629.336551***	315.171914	612.310002	306.658639	611.325986	306.1666
15	1529.748215	765.377746	1512.721666	756.864471	1511.737650	756.372463	G	532.283787	266.645532	515.257238	258.132257	514.273222	257.6402
16	***1657.806793***	829.407035	1640.780244	820.893760	1639.796228	820.401752	Q	***475.262323***	238.134800	458.235774	229.621525	457.251758	229.1295
17	***1758.854472***	879.930874	1741.827923	871.417600	1740.843907	870.925592	T	347.203745	174.105510	330.177196	165.592236	329.193180	165.1002
18	***1829.891586***	915.449431	1812.865037	906.936157	1811.881021	906.444149	A	246.156066	123.581671	229.129517	115.068396		
19							R	175.118952	88.063114	158.092403	79.549839		



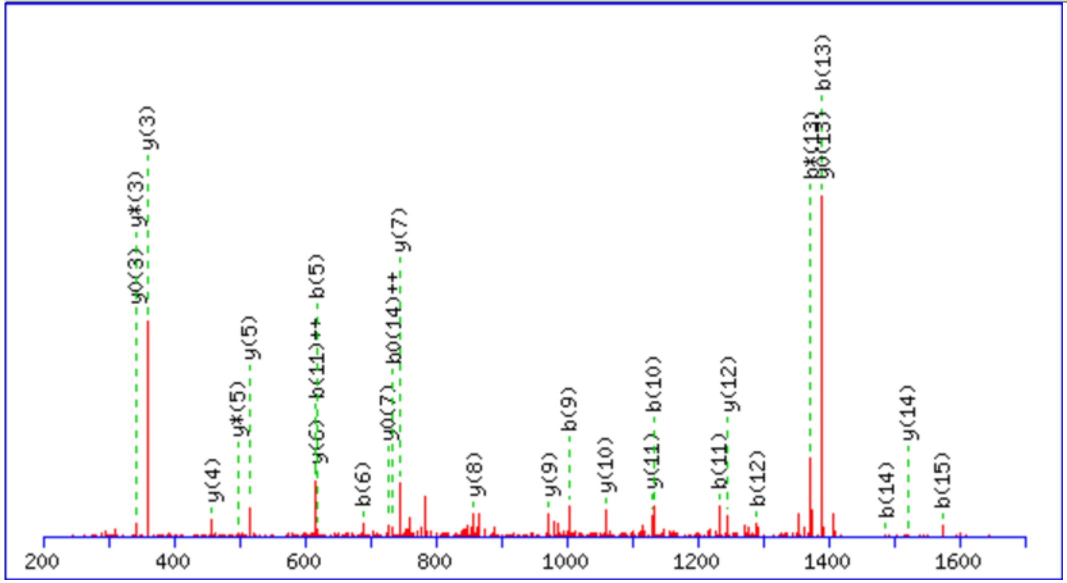
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 12999: 1746.915448 from(874.465000,2+)
Title: OECHL100317_37.17334.17334.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 86 **Expect:** 2.5e-007**Matches :** 28/156 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	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	***618.349740***	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018

6	***689.386854***	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							**R**	175.118952	88.063114	158.092403	79.549839		



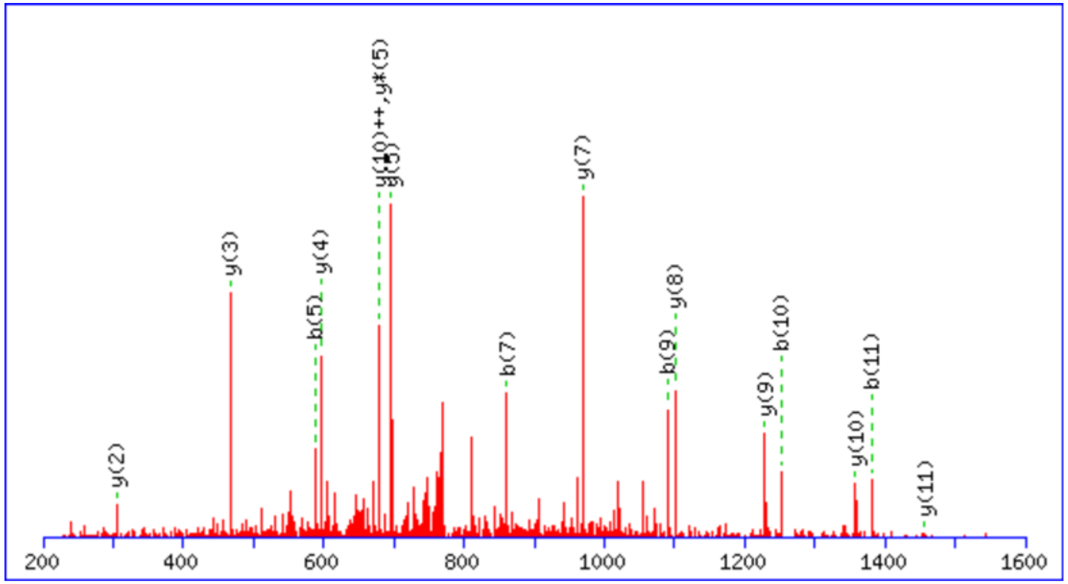
Peptide View

MS/MS Fragmentation of **VVEQMCITQYER**
Found in **IPI00022284**, Tax_Id=9606 Gene_Symbol=PRNP Major prion protein

Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 10954: 1554.720448 from(778.367500,2+)
Title: OECHL100317_37.13249.13249.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1554.717041**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63 **Expect:** 5.1e-005**Matches :** 16/120 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	100.075690	50.541483					**V**						
2	199.144104	100.075690					**V**	***1456.655914***	728.831595	1439.629365	720.318321	1438.645349	719.8263
3	328.186697	164.596987			310.176132	155.591704	**E**	***1357.587500***	679.297388	1340.560951	670.784114	1339.576935	670.2921
4	456.245275	228.626276	439.218726	220.113001	438.234710	219.620993	**Q**	***1228.544907***	614.776092	1211.518358	606.262817	1210.534342	605.7708
5	**587.285760**	294.146518	570.259211	285.633244	569.275195	285.141236	**M**	***1100.486329***	550.746803	1083.459780	542.233528	1082.475764	541.7415
6	747.316409	374.161843	730.289860	365.648568	729.305844	365.156560	**C**	***969.445844***	485.226560	952.419295	476.713286	951.435279	476.2212
7	**860.400473**	430.703875	843.373924	422.190600	842.389908	421.698592	**I**	809.415195	405.211236	792.388646	396.697961	791.404630	396.2059
8	961.448152	481.227714	944.421603	472.714440	943.437587	472.222432	**T**	***696.331131***	348.669204	679.304582	340.155929	678.320566	339.6639
9	**1089.506730**	545.257003	1072.480181	536.743729	1071.496165	536.251721	**Q**	***595.283452***	298.145364	578.256903	289.632090	577.272887	289.1400
10	**1252.570059**	626.788668	1235.543510	618.275393	1234.559494	617.783385	**Y**	***467.224874***	234.116075	450.198325	225.602801	449.214309	225.1107
11	**1381.612652**	691.309964	1364.586103	682.796690	1363.602087	682.304682	**E**	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.5791
12							**R**	175.118952	88.063114	158.092403	79.549839		



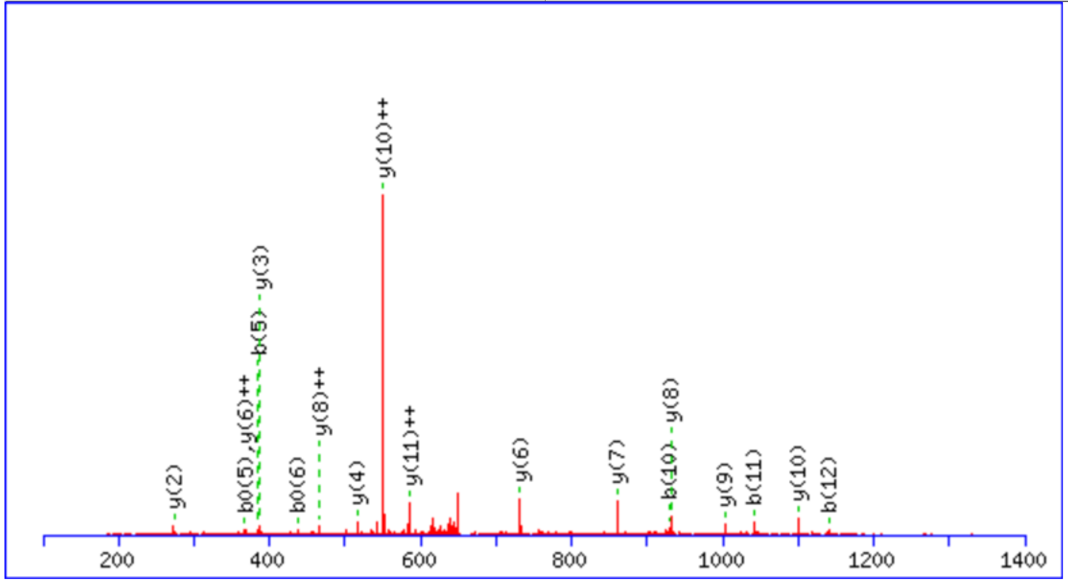
Peptide View

MS/MS Fragmentation of **SGAPAAESKEIVR**
Found in **IPI00299977**, Tax_Id=9606 Gene_Symbol=PHPT1 14 kDa phosphohistidine phosphatase
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 8420: 1313.695848 from(657.855200,2+)
Title: OECHL100317_37.4815.4815.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1313.693893**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 50 **Expect:** 0.0013**Matches :** 18/122 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	88.039304	44.523290			70.028739	35.518008	S						
2	145.060768	73.034022			127.050203	64.028740	G	1227.669177	614.338227	1210.642628	605.824952	1209.658612	605.3329
3	216.097882	108.552579			198.087317	99.547296	A	1170.647713	585.827495	1153.621164	577.314220	1152.637148	576.8222
4	313.150646	157.078961			295.140081	148.073679	P	***1099.610599***	550.308938	1082.584050	541.795663	1081.600034	541.3036
5	**384.187760**	192.597518			366.177195	183.592235	A	***1002.557835***	501.782556	985.531286	493.269281	984.547270	492.7772

6	455.224874	228.116075			437.214309	219.110792	**A**	***931.520721***	466.263999	914.494172	457.750724	913.510156	457.2587
7	584.267467	292.637372			566.256902	283.632089	**E**	***860.483607***	430.745442	843.457058	422.232167	842.473042	421.7401
8	671.299495	336.153386			653.288930	327.148103	**S**	***731.441014***	366.224145	714.414465	357.710871	713.430449	357.2188
9	799.394458	400.200867	782.367909	391.687592	781.383893	391.195585	**K**	644.408986	322.708131	627.382437	314.194857	626.398421	313.7028
10	**928.437051**	464.722164	911.410502	456.208889	910.426486	455.716881	**E**	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.6553
11	**1041.521115**	521.264196	1024.494566	512.750921	1023.510550	512.258913	**I**	***387.271430***	194.139353	370.244881	185.626079		
12	**1140.589529**	570.798403	1123.562980	562.285128	1122.578964	561.793120	**V**	***274.187366***	137.597321	257.160817	129.084047		
13							**R**	175.118952	88.063114	158.092403	79.549839		



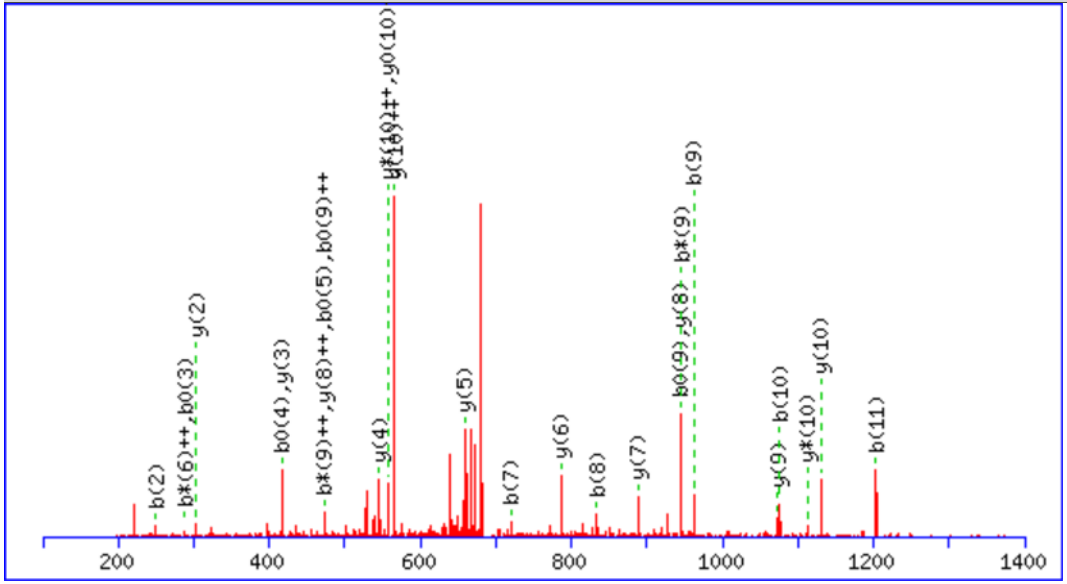
Peptide View

MS/MS Fragmentation of **TFGQGTKLEIKR**
Found in **IPI00827643**, Tax_Id=9606 Gene_Symbol=- HRV Fab 027-VL (Fragment)
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 9007: 1376.778448 from(689.396500,2+)
Title: OECHL100317_37.8370.8370.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1376.777588**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63 **Expect:** 1.8e-005**Matches :** 28/120 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	102.054955	51.531116			84.044390	42.525833	T						
2	**249.123369**	125.065322			231.112804	116.060040	F	1276.737198	638.872237	1259.710649	630.358963	1258.726633	629.8669
3	306.144833	153.576054			288.134268	144.570772	G	***1129.668784***	565.338030	1112.642235	556.824756	1111.658219	556.3327
4	434.203411	217.605343	417.176862	209.092069	416.192846	208.600061	Q	***1072.647320***	536.827298	1055.620771	528.314024	1054.636755	527.8220
5	491.224875	246.116075	474.198326	237.602801	473.214310	237.110793	G	***944.588742***	472.798009	927.562193	464.284735	926.578177	463.7927
6	592.272554	296.639915	575.246005	288.126641	574.261989	287.634633	T	***887.567278***	444.287277	870.540729	435.774003	869.556713	435.2819
7	**720.367517**	360.687397	703.340968	352.174122	702.356952	351.682114	K	***786.519599***	393.763438	769.493050	385.250163	768.509034	384.7581
8	**833.451581**	417.229429	816.425032	408.716154	815.441016	408.224146	L	***658.424636***	329.715956	641.398087	321.202682	640.414071	320.7106
9	**962.494174**	481.750725	945.467625	473.237451	944.483609	472.745443	E	***545.340572***	273.173924	528.314023	264.660650	527.330007	264.1686
10	**1075.578238**	538.292757	1058.551689	529.779483	1057.567673	529.287475	I	***416.297979***	208.652627	399.271430	200.139353		
11	**1203.673201**	602.340239	1186.646652	593.826964	1185.662636	593.334956	K	***303.213915***	152.110595	286.187366	143.597321		
12							R	175.118952	88.063114	158.092403	79.549839		

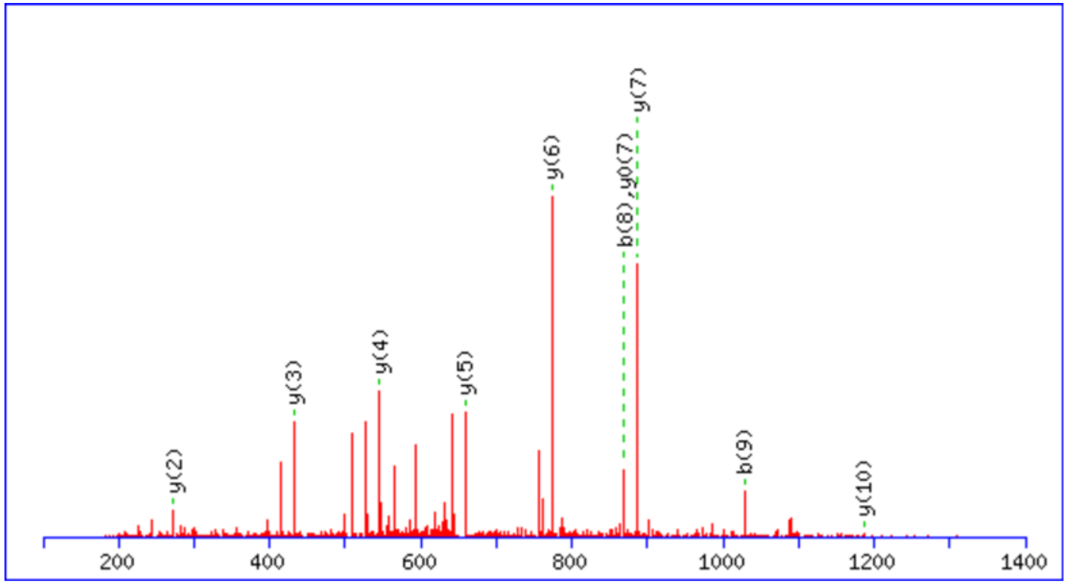


Peptide View

MS/MS Fragmentation of **IGDKLDIICPR**
Found in **IPI00024307**, Tax_Id=9606 Gene_Symbol=EFNB1 Ephrin-B1
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 8200: 1298.700648 from(650.357600,2+)
Title: OECHL100317_37.12246.12246.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1298.701645**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 62 **Expect:** 7.1e-005**Matches :** 10/100 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	114.091340	57.549308					**I**						
2	171.112804	86.060040					**G**	***1186.624870***	593.816073	1169.598321	585.302799	1168.614305	584.8107
3	286.139747	143.573512			268.129182	134.568229	**D**	1129.603406	565.305341	1112.576857	556.792067	1111.592841	556.3000
4	414.234710	207.620993	397.208161	199.107719	396.224145	198.615711	**K**	1014.576463	507.791870	997.549914	499.278595	996.565898	498.7865
5	527.318774	264.163025	510.292225	255.649751	509.308209	255.157743	**L**	***886.481500***	443.744388	869.454951	435.231113	868.470935	434.7391
6	642.345717	321.676497	625.319168	313.163222	624.335152	312.671214	**D**	***773.397436***	387.202356	756.370887	378.689081	755.386871	378.1970
7	755.429781	378.218529	738.403232	369.705254	737.419216	369.213246	**I**	***658.370493***	329.688885	641.343944	321.175610		
8	**868.513845**	434.760561	851.487296	426.247286	850.503280	425.755278	**I**	***545.286429***	273.146853	528.259880	264.633578		
9	**1028.544494**	514.775885	1011.517945	506.262610	1010.533929	505.770603	**C**	***432.202365***	216.604820	415.175816	208.091546		
10	1125.597258	563.302267	1108.570709	554.788993	1107.586693	554.296985	**P**	***272.171716***	136.589496	255.145167	128.076221		
11							**R**	175.118952	88.063114	158.092403	79.549839		



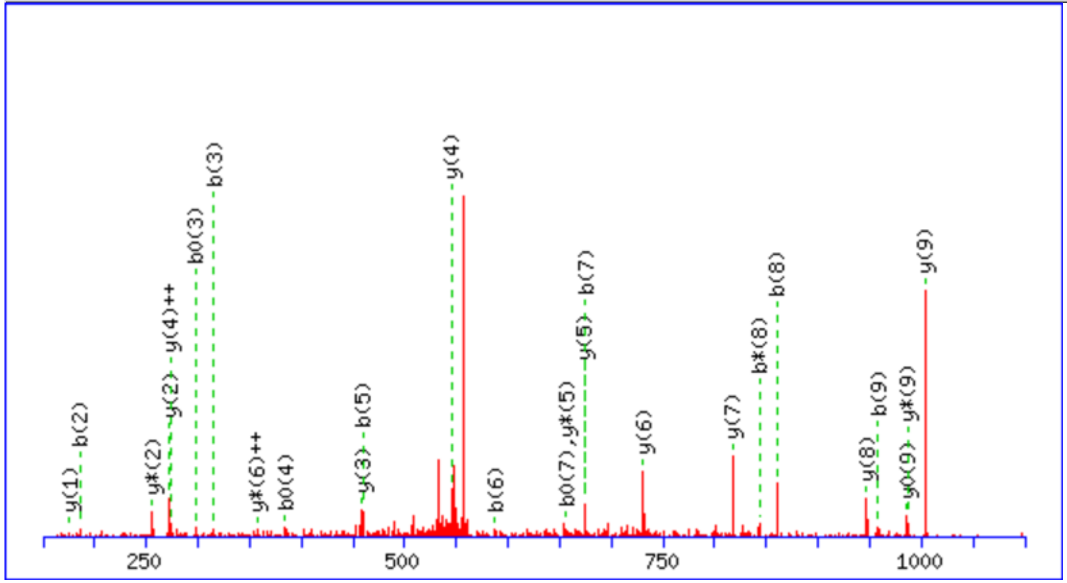
Peptide View

MS/MS Fragmentation of **KGESGQSWPR**
Found in **IPI00015029**, Tax_Id=9606 Gene_Symbol=PTGES3 Prostaglandin E synthase 3
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 5659: 1130.545848 from(566.280200,2+)
Title: OECHL100317_37.4223.4223.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1130.546860**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65 **Expect:** 3.2e-005**Matches :** 26/98 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			**K**							**10**
2	**186.123703**	93.565489	169.097154	85.052215			**G**	***1003.459184***	502.233230	986.432635	493.719956	985.448619	493.227948	**9**
3	**315.166296**	158.086786	298.139747	149.573512	297.155731	149.081504	**E**	***946.437720***	473.722498	929.411171	465.209224	928.427155	464.717216	**8**
4	402.198324	201.602800	385.171775	193.089526	384.187759	192.597518	**S**	***817.395127***	409.201202	800.368578	400.687927	799.384562	400.195919	**7**
5	**459.219788**	230.113532	442.193239	221.600258	441.209223	221.108250	**G**	***730.363099***	365.685188	713.336550	357.171913	712.352534	356.679905	**6**

6	**587.278366**	294.142821	570.251817	285.629547	569.267801	285.137539	**Q**	***673.341635***	337.174456	656.315086	328.661181	655.331070	328.169173	**5**
7	**674.310394**	337.658835	657.283845	329.145560	656.299829	328.653552	**S**	***545.283057***	273.145167	528.256508	264.631892	527.272492	264.139884	**4**
8	**860.389707**	430.698492	843.363158	422.185217	842.379142	421.693209	**W**	***458.251029***	229.629153	441.224480	221.115878			**3**
9	**957.442471**	479.224874	940.415922	470.711599	939.431906	470.219591	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
10							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



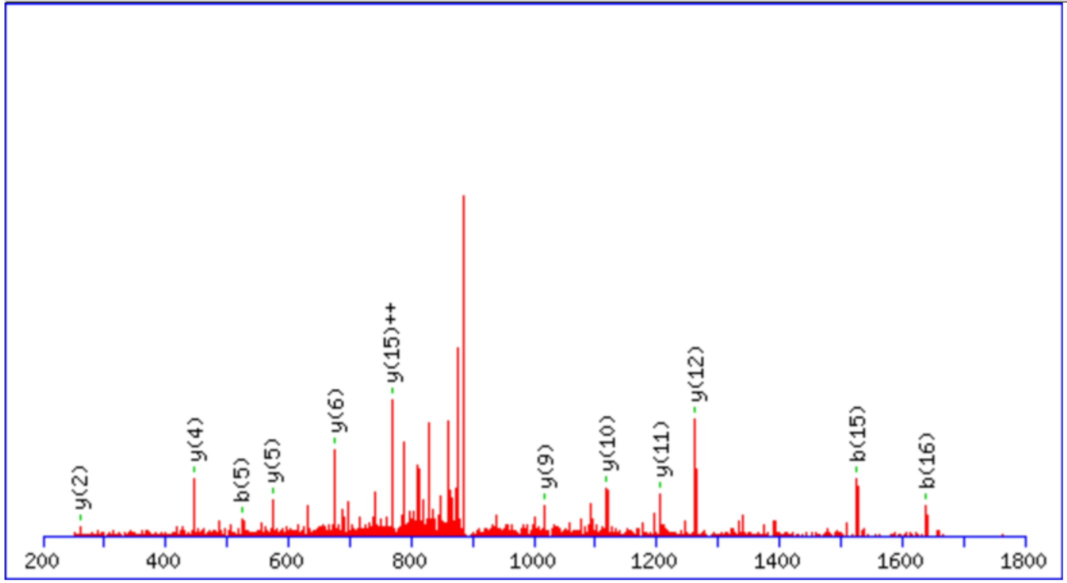
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 13263: 1784.879648 from(893.447100,2+)
Title: OECHL100317_37.7902.7902.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60 **Expect:** 0.00017**Matches :** 12/170 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	164.070605	82.538940					**Y**						
2	251.102633	126.054954			233.092068	117.049672	**S**	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.9099
3	308.124097	154.565687			290.113532	145.560404	**G**	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.3939
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.8831
5	**524.198718**	262.602997			506.188153	253.597715	**E**	1391.737652	696.372464	1374.711103	687.859190	1373.727087	687.3671
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.8458
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.3351
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.8191
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.2952
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.2660
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	788.487631	394.747453	771.461082	386.234179	770.477066	385.7421
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.2001
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.6762
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.6288
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.1180
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		

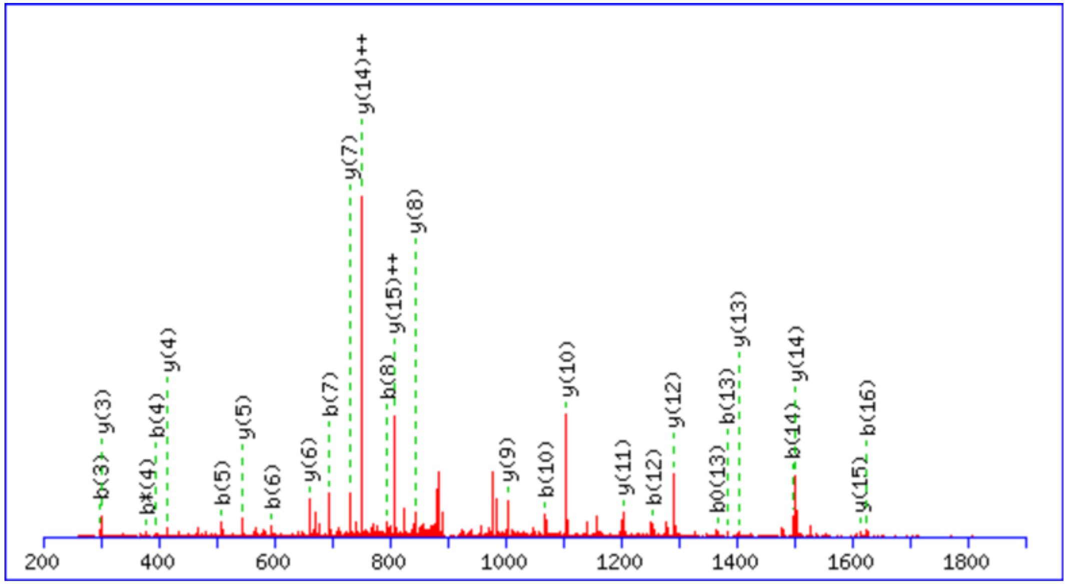


Peptide View

MS/MS Fragmentation of **GQLPISVTCIADEIGAR**
Found in **IPI00240345**, Tax_Id=9606 Gene_Symbol=CLEC14A C-type lectin domain family 14 member A
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 13380: 1798.925848 from(900.470200,2+)
Title: OECHL100317_37.20367.20367.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1798.924728**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 63 **Expect:** 7.4e-005**Matches :** 28/172 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	58.028740	29.518008					**G**						
2	186.087318	93.547297	169.060769	85.034023			**Q**	1742.910548	871.958912	1725.883999	863.445638	1724.899983	862.9536
3	**299.171382**	150.089329	282.144833	141.576055			**L**	***1614.851970***	807.929623	1597.825421	799.416349	1596.841405	798.9243
4	**396.224146**	198.615711	379.197597	190.102436			**P**	***1501.767906***	751.387591	1484.741357	742.874317	1483.757341	742.3823
5	**509.308210**	255.157743	492.281661	246.644468			**I**	***1404.715142***	702.861209	1387.688593	694.347935	1386.704577	693.8559
6	**596.340238**	298.673757	579.313689	290.160483	578.329673	289.668475	**S**	***1291.631078***	646.319177	1274.604529	637.805903	1273.620513	637.3138
7	**695.408652**	348.207964	678.382103	339.694689	677.398087	339.202681	**V**	***1204.599050***	602.803163	1187.572501	594.289889	1186.588485	593.7978
8	**796.456331**	398.731804	779.429782	390.218529	778.445766	389.726521	**T**	***1105.530636***	553.268956	1088.504087	544.755682	1087.520071	544.2636
9	956.486980	478.747128	939.460431	470.233854	938.476415	469.741846	**C**	***1004.482957***	502.745117	987.456408	494.231842	986.472392	493.7398
10	**1069.571044**	535.289160	1052.544495	526.775886	1051.560479	526.283878	**I**	***844.452308***	422.729792	827.425759	414.216518	826.441743	413.7245
11	1140.608158	570.807717	1123.581609	562.294443	1122.597593	561.802435	**A**	***731.368244***	366.187760	714.341695	357.674486	713.357679	357.1824
12	**1255.635101**	628.321189	1238.608552	619.807914	1237.624536	619.315906	**D**	***660.331130***	330.669203	643.304581	322.155929	642.320565	321.6639
13	**1384.677694**	692.842485	1367.651145	684.329211	1366.667129	683.837203	**E**	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.1504
14	**1497.761758**	749.384517	1480.735209	740.871243	1479.751193	740.379235	**I**	***416.261594***	208.634435	399.235045	200.121160		
15	1554.783222	777.895249	1537.756673	769.381975	1536.772657	768.889967	**G**	***303.177530***	152.092403	286.150981	143.579128		
16	**1625.820336**	813.413806	1608.793787	804.900532	1607.809771	804.408524	**A**	246.156066	123.581671	229.129517	115.068396		
17							**R**	175.118952	88.063114	158.092403	79.549839		



Peptide View

MS/MS Fragmentation of **ASHPEDPASVVEAR**

Found in **IPI00296141**, Tax_Id=9606 Gene_Symbol=DPP7 Dipeptidyl-peptidase 2

Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 9698: 1463.700448 from(732.857500,2+)

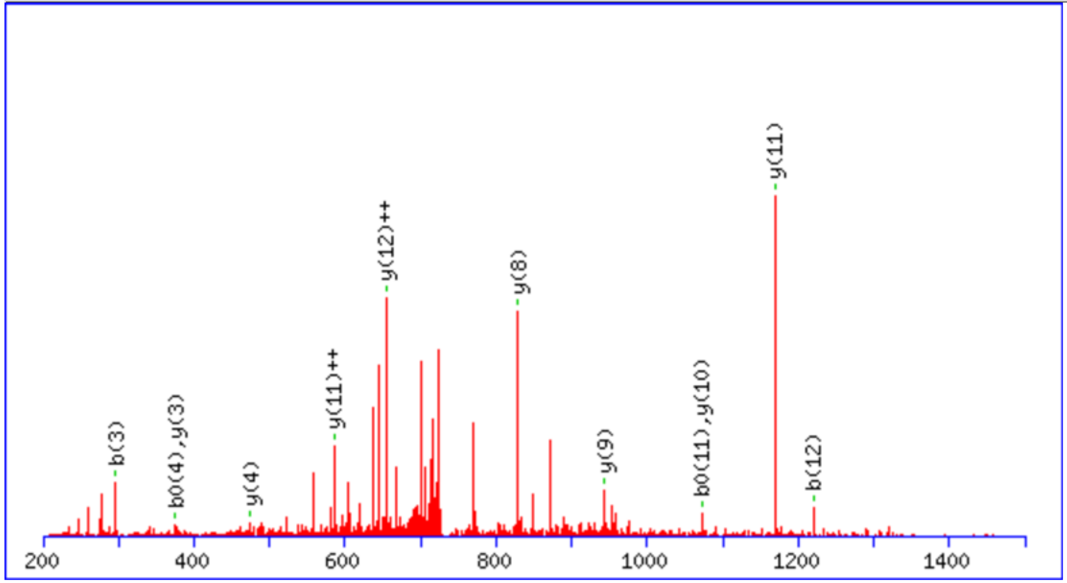
Title: OECHL100317_37.8269.8269.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw

Monoisotopic mass of neutral peptide Mr(calc): 1463.700455**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51 **Expect:** 0.00076**Matches :** 12/124 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**14**
2	159.076418	80.041847	141.065853	71.036564	**S**	1393.670633	697.338955	1376.644084	688.825680	1375.660068	688.333672	**13**
3	**296.135330**	148.571303	278.124765	139.566021	**H**	1306.638605	653.822940	1289.612056	645.309666	1288.628040	644.817658	**12**
4	393.188094	197.097685	375.177529	188.092403	**P**	***1169.579693***	585.293484	1152.553144	576.780210	1151.569128	576.288202	**11**
5	522.230687	261.618982	504.220122	252.613699	**E**	***1072.526929***	536.767102	1055.500380	528.253828	1054.516364	527.761820	**10**

6	637.257630	319.132453	619.247065	310.127171	**D**	***943.484336***	472.245806	926.457787	463.732531	925.473771	463.240523	**9**
7	734.310394	367.658835	716.299829	358.653553	**P**	***828.457393***	414.732334	811.430844	406.219060	810.446828	405.727052	**8**
8	805.347508	403.177392	787.336943	394.172110	**A**	731.404629	366.205952	714.378080	357.692678	713.394064	357.200670	**7**
9	892.379536	446.693406	874.368971	437.688124	**S**	660.367515	330.687395	643.340966	322.174121	642.356950	321.682113	**6**
10	991.447950	496.227613	973.437385	487.222331	**V**	573.335487	287.171382	556.308938	278.658107	555.324922	278.166099	**5**
11	1090.516364	545.761820	1072.505799	536.756538	**V**	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.631892	**4**
12	**1219.558957**	610.283117	1201.548392	601.277834	**E**	***375.198659***	188.102967	358.172110	179.589693	357.188094	179.097685	**3**
13	1290.596071	645.801673	1272.585506	636.796391	**A**	246.156066	123.581671	229.129517	115.068396			**2**
14					**R**	175.118952	88.063114	158.092403	79.549839			**1**



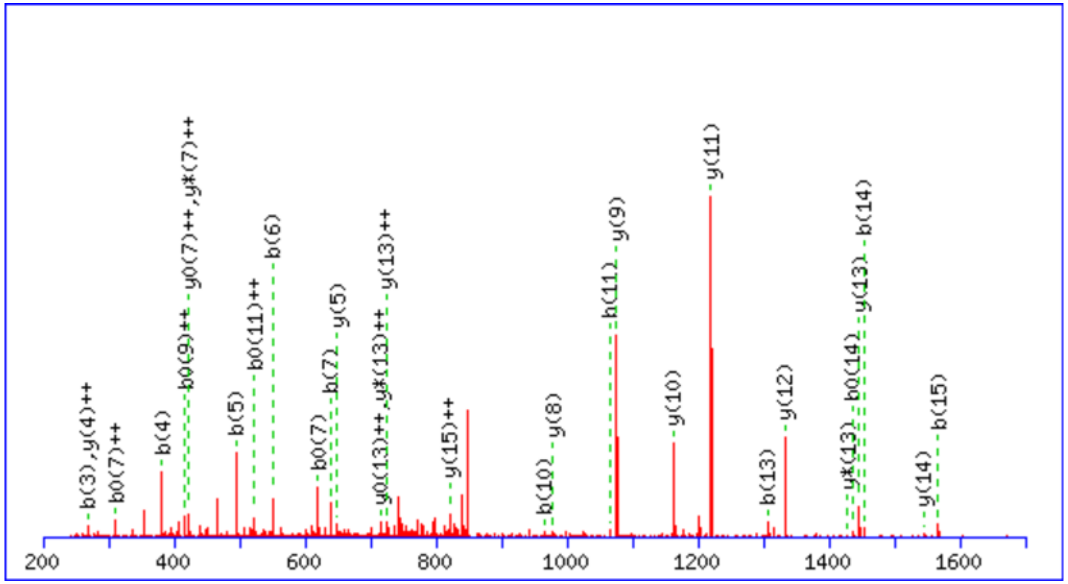
Peptide View

MS/MS Fragmentation of **APVILGSPDDVLEFLK**
Found in **IPI00073772**, Tax_Id=9606 Gene_Symbol=FBP1 Fructose-1,6-bisphosphatase 1
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 12781: 1711.939448 from(856.977000,2+)

Title: OECHL100317_37.22359.22359.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1711.939636**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58 **Expect:** 0.00011**Matches :** 31/132 fragment ions using 57 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**16**
2	169.097154	85.052215			**P**	1641.909801	821.458538	1624.883252	812.945264	1623.899236	812.453256	**15**
3	***268.165568***	134.586422			**V**	***1544.857037***	772.932156	1527.830488	764.418882	1526.846472	763.926874	**14**
4	***381.249632***	191.128454			**I**	***1445.788623***	723.397949	1428.762074	714.884675	1427.778058	714.392667	**13**
5	***494.333696***	247.670486			**L**	***1332.704559***	666.855917	1315.678010	658.342643	1314.693994	657.850635	**12**
6	***551.355160***	276.181218			**G**	***1219.620495***	610.313885	1202.593946	601.800611	1201.609930	601.308603	**11**
7	***638.387188***	319.697232	620.376623	310.691950	**S**	***1162.599031***	581.803153	1145.572482	573.289879	1144.588466	572.797871	**10**
8	735.439952	368.223614	717.429387	359.218332	**P**	***1075.567003***	538.287139	1058.540454	529.773865	1057.556438	529.281857	**9**
9	850.466895	425.737086	832.456330	416.731803	**D**	***978.514239***	489.760757	961.487690	481.247483	960.503674	480.755475	**8**
10	***965.493838***	483.250557	947.483273	474.245274	**D**	863.487296	432.247286	846.460747	423.734011	845.476731	423.242003	**7**
11	***1064.562252***	532.784764	1046.551687	523.779481	**V**	748.460353	374.733814	731.433804	366.220540	730.449788	365.728532	**6**
12	1177.646316	589.326796	1159.635751	580.321513	**L**	***649.391939***	325.199607	632.365390	316.686333	631.381374	316.194325	**5**
13	***1306.688909***	653.848092	1288.678344	644.842810	**E**	536.307875	268.657576	519.281326	260.144301	518.297310	259.652293	**4**
14	***1453.757323***	727.382299	1435.746758	718.377017	**F**	407.265282	204.136279	390.238733	195.623004			**3**
15	***1566.841387***	783.924331	1548.830822	774.919049	**L**	260.196868	130.602072	243.170319	122.088797			**2**
16					**K**	147.112804	74.060040	130.086255	65.546765			**1**



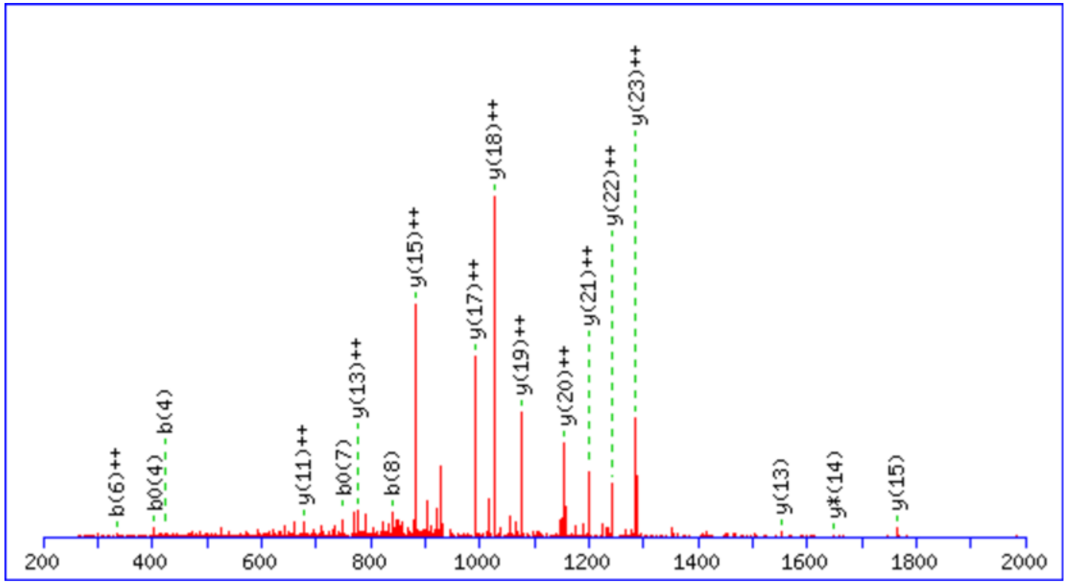
Peptide View

MS/MS Fragmentation of **SCSSSCVATDPDSIGAAHLIFCCFR**
Found in **IPI00022620**, Tax_Id=9606 Gene_Symbol=SLURP1 Secreted Ly-6/uPAR-related protein 1
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 18343: 2817.198072 from(940.073300,3+)
Title: OECHL100317_37.19816.19816.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 2817.197922**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52 **Expect:** 0.00035**Matches :** 19/216 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							25
2	248.069953	124.538614	230.059388	115.533332	C	2731.173141	1366.090208	2714.146592	1357.576934	2713.162576	1357.084926	24
3	**335.101981**	168.054628	317.091416	159.049346	S	2571.142492	1286.074884	2554.115943	1277.561609	2553.131927	1277.069601	23
4	**422.134009**	211.570642	404.123444	202.565360	S	2484.110464	1242.558870	2467.083915	1234.045595	2466.099899	1233.553587	22
5	509.166037	255.086656	491.155472	246.081374	S	2397.078436	1199.042856	2380.051887	1190.529581	2379.067871	1190.037573	21

6	669.196686	335.101981	651.186121	326.096699	**C**	2310.046408	1155.526842	2293.019859	1147.013567	2292.035843	1146.521559	**20**
7	768.265100	384.636188	750.254535	375.630905	**V**	2150.015759	1075.511517	2132.989210	1066.998243	2132.005194	1066.506235	**19**
8	**839.302214**	420.154745	821.291649	411.149462	**A**	2050.947345	1025.977310	2033.920796	1017.464036	2032.936780	1016.972028	**18**
9	940.349893	470.678585	922.339328	461.673302	**T**	1979.910231	990.458753	1962.883682	981.945479	1961.899666	981.453471	**17**
10	1055.376836	528.192056	1037.366271	519.186773	**D**	1878.862552	939.934914	1861.836003	931.421639	1860.851987	930.929631	**16**
11	1152.429600	576.718438	1134.419035	567.713155	**P**	**1763.835609**	882.421442	1746.809060	873.908168	1745.825044	873.416160	**15**
12	1267.456543	634.231910	1249.445978	625.226627	**D**	1666.782845	833.895060	1649.756296	825.381786	1648.772280	824.889778	**14**
13	1354.488571	677.747924	1336.478006	668.742641	**S**	**1551.755902**	776.381589	1534.729353	767.868314	1533.745337	767.376306	**13**
14	1467.572635	734.289956	1449.562070	725.284673	**I**	1464.723874	732.865575	1447.697325	724.352300			**12**
15	1524.594099	762.800687	1506.583534	753.795405	**G**	1351.639810	676.323543	1334.613261	667.810268			**11**
16	1595.631213	798.319244	1577.620648	789.313962	**A**	1294.618346	647.812811	1277.591797	639.299536			**10**
17	1666.668327	833.837801	1648.657762	824.832519	**A**	1223.581232	612.294254	1206.554683	603.780979			**9**
18	1803.727239	902.367257	1785.716674	893.361975	**H**	1152.544118	576.775697	1135.517569	568.262422			**8**
19	1916.811303	958.909289	1898.800738	949.904007	**L**	1015.485206	508.246241	998.458657	499.732966			**7**
20	2029.895367	1015.451321	2011.884802	1006.446039	**I**	902.401142	451.704209	885.374593	443.190934			**6**
21	2176.963781	1088.985528	2158.953216	1079.980246	**F**	789.317078	395.162177	772.290529	386.648902			**5**
22	2336.994430	1169.000853	2318.983865	1159.995570	**C**	642.248664	321.627970	625.222115	313.114695			**4**
23	2497.025079	1249.016177	2479.014514	1240.010895	**C**	482.218015	241.612645	465.191466	233.099371			**3**
24	2644.093493	1322.550384	2626.082928	1313.545102	**F**	322.187366	161.597321	305.160817	153.084046			**2**
25					**R**	175.118952	88.063114	158.092403	79.549839			**1**



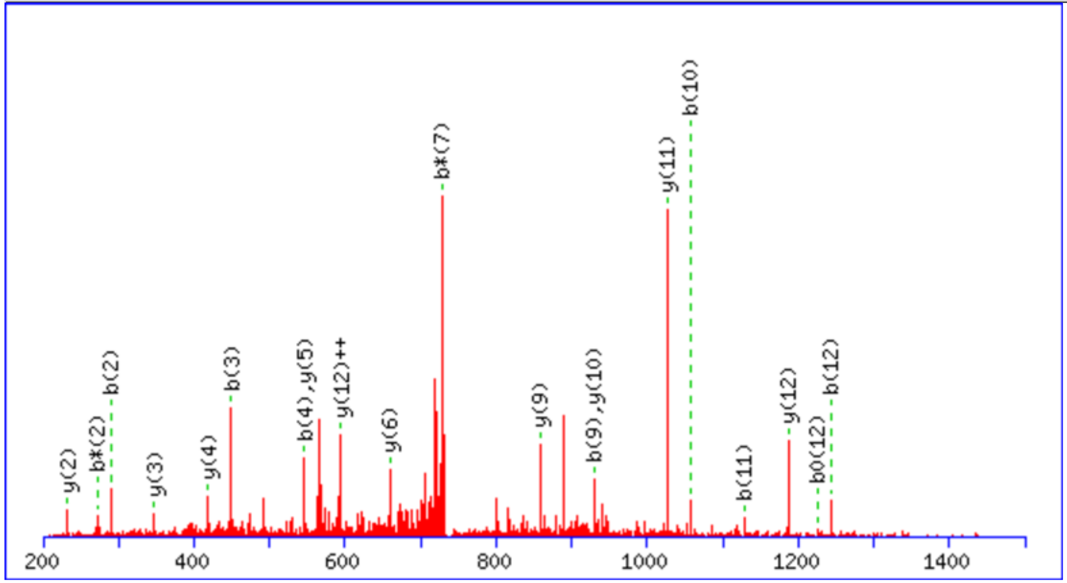
Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 57 - PyD-3 **Fraction:** PyD-3

Match to Query 9904: 1473.646648 from(737.830600,2+)
Title: OECHL100317_37.7833.7833.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_37.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 51 **Expect:** 0.00041**Matches :** 20/128 fragment ions using 39 most intense peaks   (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	161.037925	81.022600					C						
2	**289.096503**	145.051890	272.069954	136.538615			Q	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.8093
3	**449.127152**	225.067214	432.100603	216.553940			C	***1186.563334***	593.785305	1169.536785	585.272031	1168.552769	584.7800
4	**546.179916**	273.593596	529.153367	265.080322			P	***1026.532685***	513.769981	1009.506136	505.256706	1008.522120	504.7646
5	617.217030	309.112153	600.190481	300.598879			A	***929.479921***	465.243599	912.453372	456.730324	911.469356	456.2383

6	674.238494	337.622885	657.211945	329.109611			**G**	***858.442807***	429.725042	841.416258	421.211767	840.432242	420.7197
7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.2090
8	816.312722	408.659999	799.286173	400.146725			**A**	730.384229	365.695753	713.357680	357.182478	712.373664	356.6904
9	**929.396786**	465.202031	912.370237	456.688757			**L**	***659.347115***	330.177196	642.320566	321.663921	641.336550	321.1719
10	**1057.455364**	529.231320	1040.428815	520.718046			**Q**	***546.263051***	273.635164	529.236502	265.121889	528.252486	264.6298
11	**1128.492478**	564.749877	1111.465929	556.236603			**A**	***418.204473***	209.605874	401.177924	201.092600	400.193908	200.6005
12	**1243.519421**	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.0820
13	1300.540885	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	***232.140416***	116.573846	215.113867	108.060571		
14							**R**	175.118952	88.063114	158.092403	79.549839		



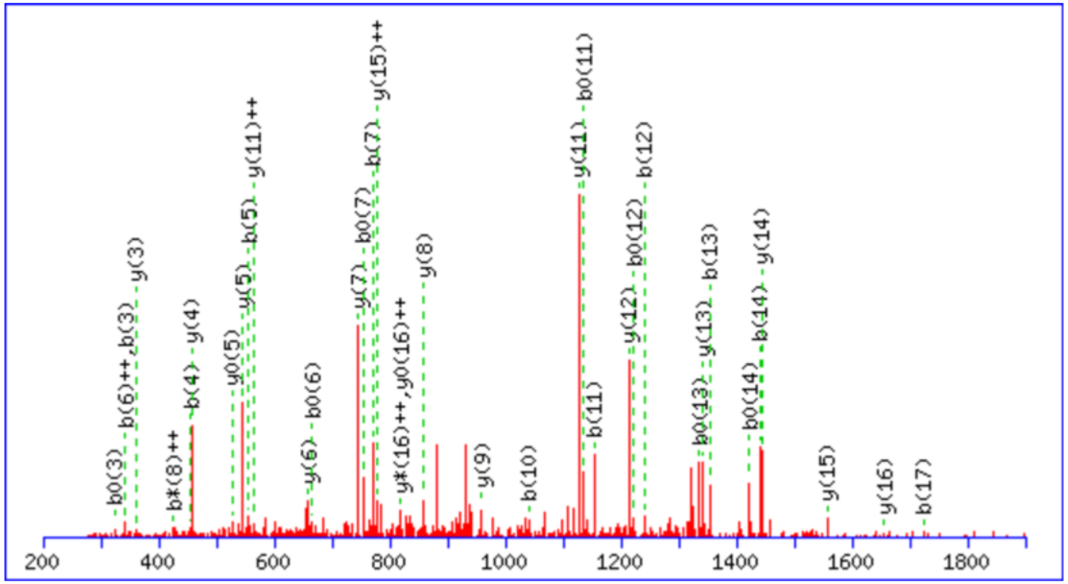
Peptide View

MS/MS Fragmentation of **EIVLTQSPATLSLSPGER**
Found in **IPI00816799**, Tax_Id=9606 Gene_Symbol=- Rheumatoid factor D5 light chain (Fragment)
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 13470: 1897.019648 from(949.517100,2+)

Title: OECHL100317_35.16820.16820.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1897.015640**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 80 **Expect:** 8.7e-007**Matches :** 37/192 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	130.049869	65.528572			112.039304	56.523290	**E**						
2	243.133933	122.070605			225.123368	113.065322	**I**	1768.980341	884.993808	1751.953792	876.480534	1750.969776	875.9885
3	**342.202347**	171.604812			324.191782	162.599529	**V**	***1655.896277***	828.451776	1638.869728	819.938502	1637.885712	819.4464
4	**455.286411**	228.146844			437.275846	219.141561	**L**	***1556.827863***	778.917569	1539.801314	770.404295	1538.817298	769.9122
5	**556.334090**	278.670683			538.323525	269.665401	**T**	***1443.743799***	722.375537	1426.717250	713.862263	1425.733234	713.3702
6	684.392668	342.699972	667.366119	334.186698	666.382103	333.694690	**Q**	***1342.696120***	671.851698	1325.669571	663.338423	1324.685555	662.8464
7	**771.424696**	386.215986	754.398147	377.702712	753.414131	377.210704	**S**	***1214.637542***	607.822409	1197.610993	599.309134	1196.626977	598.8171
8	868.477460	434.742368	851.450911	426.229094	850.466895	425.737086	**P**	***1127.605514***	564.306395	1110.578965	555.793120	1109.594949	555.3011
9	939.514574	470.260925	922.488025	461.747651	921.504009	461.255643	**A**	1030.552750	515.780013	1013.526201	507.266738	1012.542185	506.7747
10	**1040.562253**	520.784765	1023.535704	512.271490	1022.551688	511.779482	**T**	***959.515636***	480.261456	942.489087	471.748181	941.505071	471.2561
11	**1153.646317**	577.326797	1136.619768	568.813522	1135.635752	568.321514	**L**	***858.467957***	429.737616	841.441408	421.224342	840.457392	420.7323
12	**1240.678345**	620.842811	1223.651796	612.329536	1222.667780	611.837528	**S**	***745.383893***	373.195585	728.357344	364.682310	727.373328	364.1903
13	**1353.762409**	677.384842	1336.735860	668.871568	1335.751844	668.379560	**L**	***658.351865***	329.679570	641.325316	321.166296	640.341300	320.6742
14	**1440.794437**	720.900857	1423.767888	712.387582	1422.783872	711.895574	**S**	***545.267801***	273.137539	528.241252	264.624264	527.257236	264.1322
15	1537.847201	769.427239	1520.820652	760.913964	1519.836636	760.421956	**P**	***458.235773***	229.621524	441.209224	221.108250	440.225208	220.6162
16	1594.868665	797.937971	1577.842116	789.424696	1576.858100	788.932688	**G**	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.0898
17	**1723.911258**	862.459267	1706.884709	853.945992	1705.900693	853.453984	**E**	304.161545	152.584410	287.134996	144.071136	286.150980	143.5791
18							**R**	175.118952	88.063114	158.092403	79.549839		



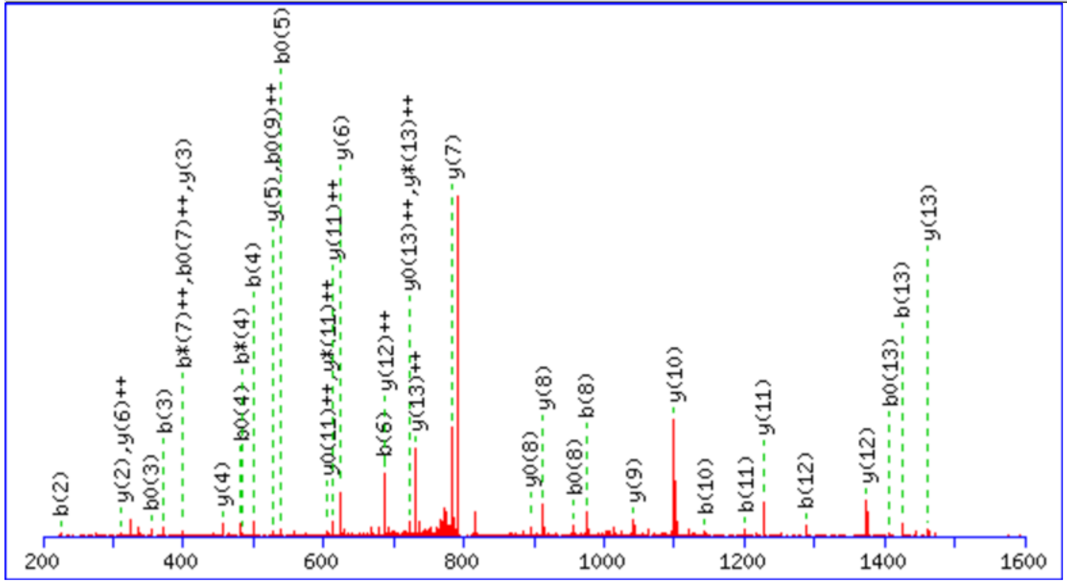
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 10578: 1597.705648 from(799.860100,2+)
Title: OECHL100317_35.2223.2223.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 91 **Expect:** 5e-008**Matches :** 39/144 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	138.066188	69.536732					H						
2	**225.098216**	113.052746			207.087651	104.047463	S	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.3253
3	**372.166630**	186.586953			354.156065	177.581671	F	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.8093
4	**500.261593**	250.634435	483.235044	242.121160	482.251028	241.629152	K	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.2751
5	557.283057	279.145167	540.256508	270.631892	539.272492	270.139884	G	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.2276

6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	E	***1042.437069***	521.722173	1025.410520	513.208898	1024.426504	512.7168
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	E	***913.394476***	457.200876	896.367927	448.687602	895.383911	448.1955
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	C	***784.351883***	392.679580	767.325334	384.166305	766.341318	383.6742
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	P	***624.321234***	312.664255	607.294685	304.150981	606.310669	303.6589
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	A	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.1325
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	G	***456.231356***	228.619316	439.204807	220.106041	438.220791	219.6140
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	S	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.1033
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	H	***312.177864***	156.592570	295.151315	148.079295		
14							R	175.118952	88.063114	158.092403	79.549839		



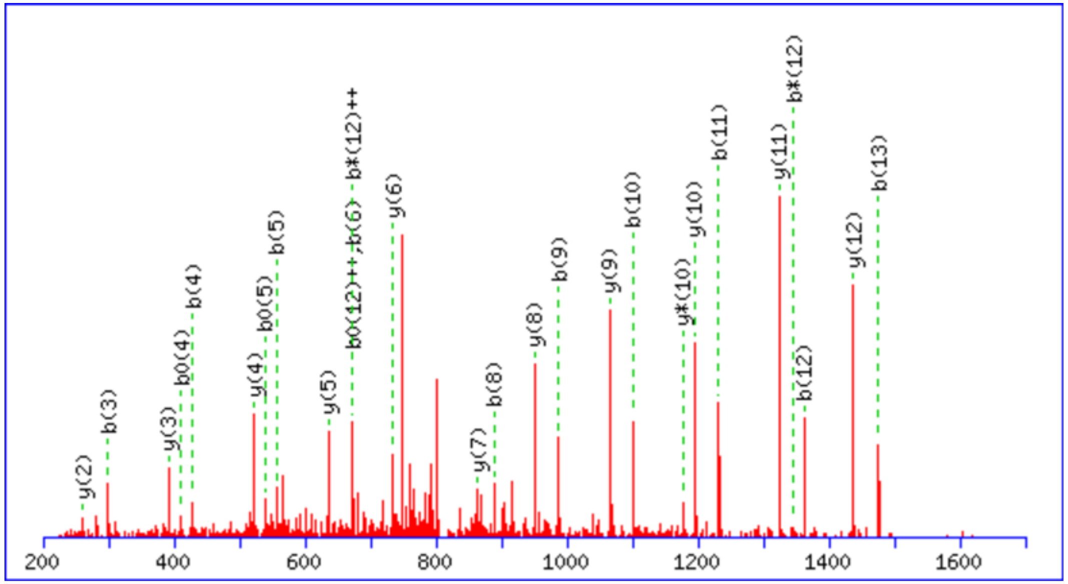
Peptide View

MS/MS Fragmentation of **GKIEEDSEVLMMIK**
Found in **IPI00034319**, Tax_Id=9606 Gene_Symbol=CUTA Isoform A of Protein CutA
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 10755: 1620.811848 from(811.413200,2+)

Title: OECHL100317_35.17095.17095.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1620.810242**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 83 **Expect:** 7e-007**Matches :** 27/136 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	58.028740	29.518008					**G**						
2	186.123703	93.565489	169.097154	85.052215			**K**	1564.796093	782.901684	1547.769544	774.388410	1546.785528	773.8964
3	**299.207767**	150.107521	282.181218	141.594247			**I**	***1436.701130***	718.854203	1419.674581	710.340929	1418.690565	709.8489
4	**428.250360**	214.628818	411.223811	206.115544	410.239795	205.623536	**E**	***1323.617066***	662.312171	1306.590517	653.798896	1305.606501	653.3068
5	**557.292953**	279.150115	540.266404	270.636840	539.282388	270.144832	**E**	***1194.574473***	597.790874	1177.547924	589.277600	1176.563908	588.7855
6	**672.319896**	336.663586	655.293347	328.150312	654.309331	327.658304	**D**	***1065.531880***	533.269578	1048.505331	524.756303	1047.521315	524.2642
7	759.351924	380.179600	742.325375	371.666326	741.341359	371.174318	**S**	***950.504937***	475.756106	933.478388	467.242832	932.494372	466.7508
8	**888.394517**	444.700897	871.367968	436.187622	870.383952	435.695614	**E**	***863.472909***	432.240092	846.446360	423.726818	845.462344	423.2348
9	**987.462931**	494.235104	970.436382	485.721829	969.452366	485.229821	**V**	***734.430316***	367.718796	717.403767	359.205521		
10	**1100.546995**	550.777135	1083.520446	542.263861	1082.536430	541.771853	**L**	***635.361902***	318.184589	618.335353	309.671314		
11	**1231.587480**	616.297378	1214.560931	607.784104	1213.576915	607.292095	**M**	***522.277838***	261.642557	505.251289	253.129282		
12	**1362.627965**	681.817620	1345.601416	673.304346	1344.617400	672.812338	**M**	***391.237353***	196.122314	374.210804	187.609040		
13	**1475.712029**	738.359652	1458.685480	729.846378	1457.701464	729.354370	**I**	***260.196868***	130.602072	243.170319	122.088797		
14							**K**	147.112804	74.060040	130.086255	65.546765		



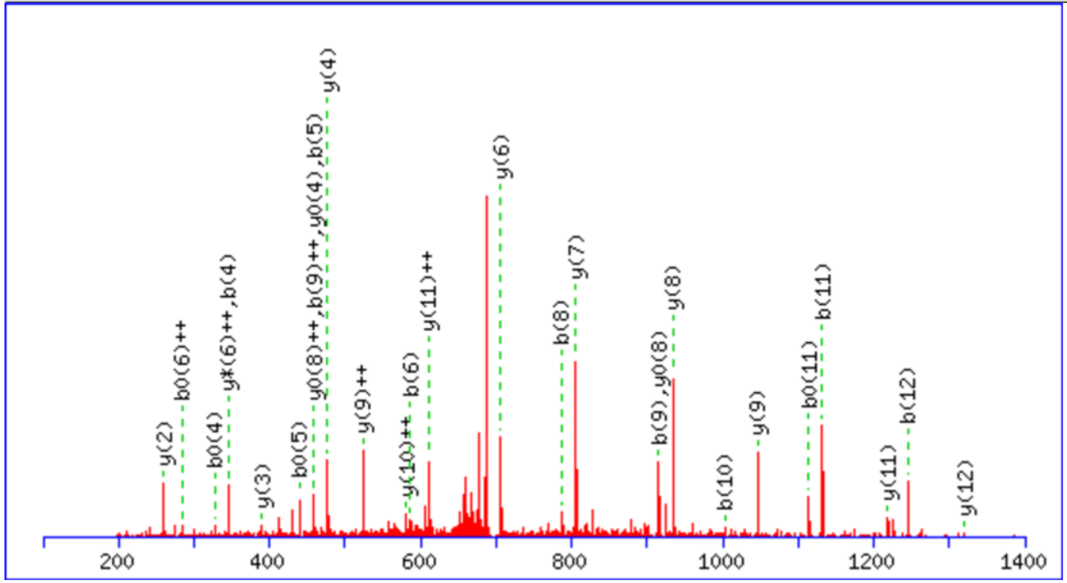
Peptide View

MS/MS Fragmentation of **ATGDIKVTESEIK**
Found in **IPI00302614**, Tax_Id=9606 Gene_Symbol=VTCN1 V-set domain containing T cell activation inhibitor 1
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 8508: 1389.734648 from(695.874600,2+)
Title: OECHL100317_35.8190.8190.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1389.735107**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 77 **Expect:** 2.3e-006**Matches :** 29/128 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	72.044390	36.525833					**A**						
2	173.092069	87.049672			155.081504	78.044390	**T**	***1319.705288***	660.356282	1302.678739	651.843008	1301.694723	651.3509
3	230.113533	115.560404			212.102968	106.555122	**G**	***1218.657609***	609.832442	1201.631060	601.319168	1200.647044	600.8271
4	***345.140476***	173.073876			327.129911	164.068593	**D**	1161.636145	581.321710	1144.609596	572.808436	1143.625580	572.3164
5	***458.224540***	229.615908			440.213975	220.610626	**I**	***1046.609202***	523.808239	1029.582653	515.294964	1028.598637	514.8029

6	***586.319503***	293.663390	569.292954	285.150115	568.308938	284.658107	**K**	***933.525138***	467.266207	916.498589	458.752932	915.514573	458.2609
7	685.387917	343.197597	668.361368	334.684322	667.377352	334.192314	**V**	***805.430175***	403.218725	788.403626	394.705451	787.419610	394.2134
8	***786.435596***	393.721436	769.409047	385.208162	768.425031	384.716154	**T**	***706.361761***	353.684518	689.335212	345.171244	688.351196	344.6792
9	***915.478189***	458.242733	898.451640	449.729458	897.467624	449.237450	**E**	605.314082	303.160679	588.287533	294.647404	587.303517	294.1553
10	***1002.510217***	501.758747	985.483668	493.245472	984.499652	492.753464	**S**	***476.271489***	238.639382	459.244940	230.126108	458.260924	229.6341
11	***1131.552810***	566.280043	1114.526261	557.766769	1113.542245	557.274760	**E**	***389.239461***	195.123368	372.212912	186.610094	371.228896	186.1180
12	***1244.636874***	622.822075	1227.610325	614.308800	1226.626309	613.816792	**I**	***260.196868***	130.602072	243.170319	122.088797		
13							**K**	147.112804	74.060040	130.086255	65.546765		



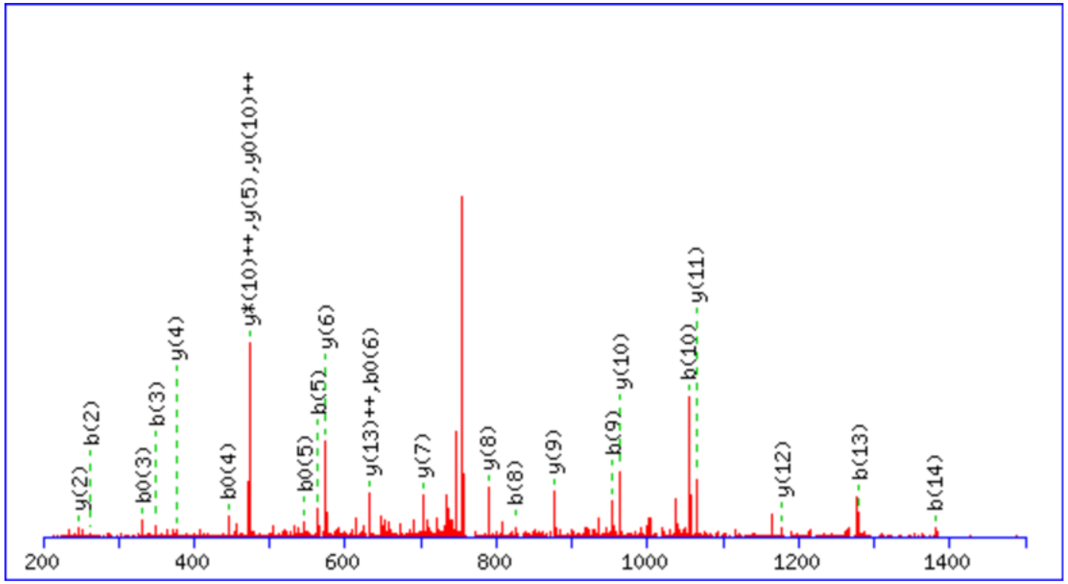
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 9954: 1525.729048 from(763.871800,2+)
Title: OECHL100317_35.10816.10816.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 57 **Expect:** 0.0002**Matches :** 25/150 fragment ions using 50 most intense peaks (help)

#	**b**	**b^{++}**	**b***	**b^{*++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**
1	116.034219	58.520748			98.023654	49.515465	**D**						
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.3515
3	***350.134661***	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.8173
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.3013
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.7592
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.2354
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.7194
8	***825.362488***	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.2034
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.6873
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.6581
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.1342
12	1208.542973	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.6078
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.0971
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.5785
15							**K**	147.112804	74.060040	130.086255	65.546765		



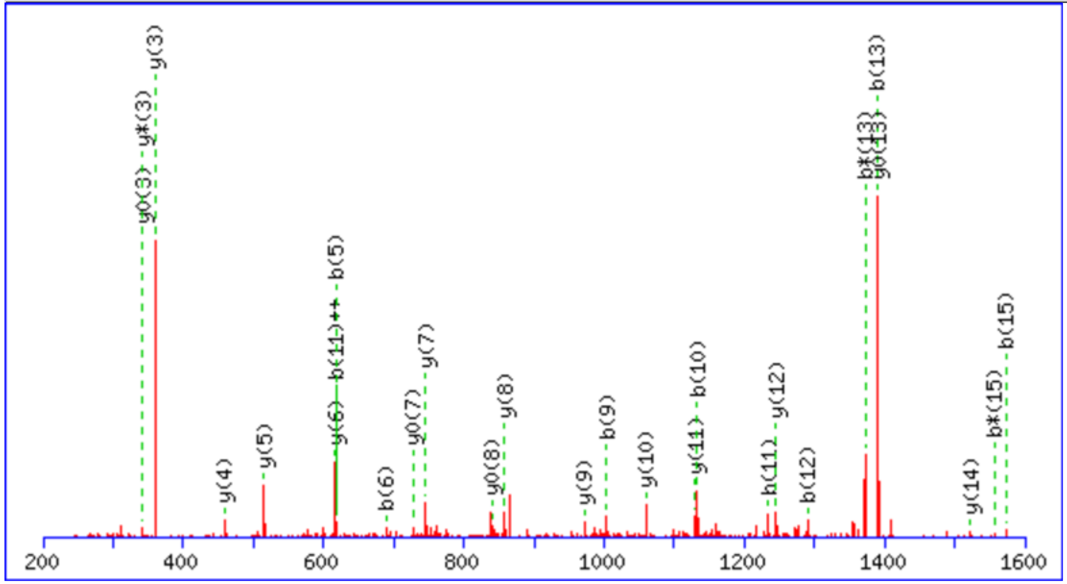
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 12255: 1746.917648 from(874.466100,2+)
Title: OECHL100317_35.17062.17062.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 82 **Expect:** 6e-007**Matches :** 27/156 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	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018

6	**689.386854**	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							**R**	175.118952	88.063114	158.092403	79.549839		



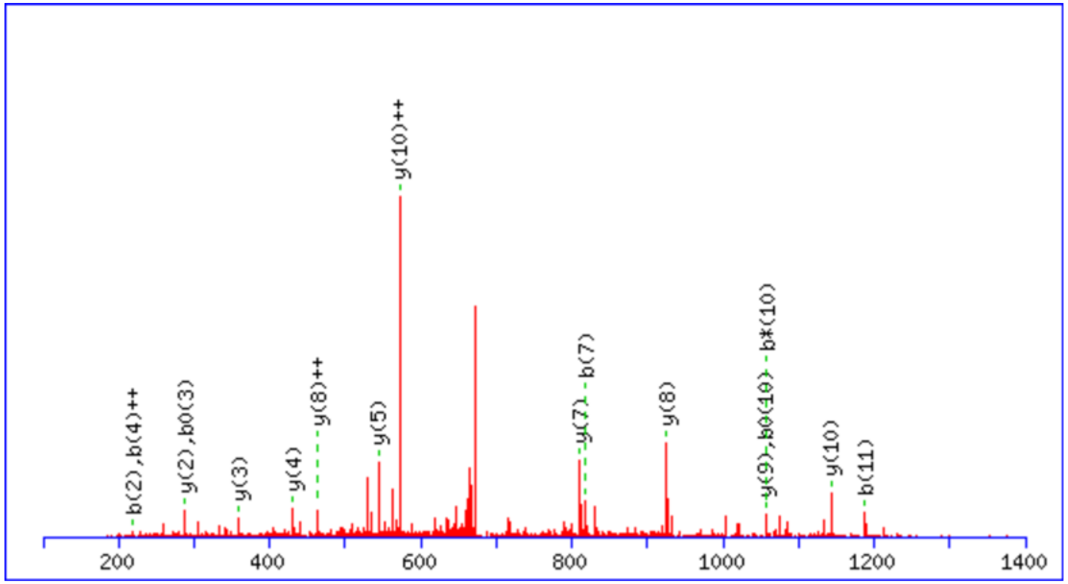
Peptide View

MS/MS Fragmentation of **AFSMDEHNAALR**
Found in **IPI00008239**, Tax_Id=9606 Gene_Symbol=GPRC5B cDNA FLJ55176, highly similar to G-protein coupled receptor family C group 5 member B

Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 8249: 1360.621248 from(681.317900,2+)
Title: OECHL100317_35.9683.9683.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1360.619354**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56 **Expect:** 0.00018**Matches :** 17/102 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	72.044390	36.525833					**A**						
2	**219.112804**	110.060040					**F**	1290.589546	645.798411	1273.562997	637.285137	1272.578981	636.7931
3	306.144832	153.576054			288.134267	144.570772	**S**	***1143.521132***	572.264204	1126.494583	563.750929	1125.510567	563.2589
4	437.185317	219.096296			419.174752	210.091014	**M**	***1056.489104***	528.748190	1039.462555	520.234916	1038.478539	519.7429
5	552.212260	276.609768			534.201695	267.604486	**D**	***925.448619***	463.227947	908.422070	454.714673	907.438054	454.2226
6	681.254853	341.131065			663.244288	332.125782	**E**	***810.421676***	405.714476	793.395127	397.201201	792.411111	396.7091
7	**818.313765**	409.660521			800.303200	400.655238	**H**	681.379083	341.193179	664.352534	332.679905		
8	932.356692	466.681984	915.330143	458.168709	914.346127	457.676701	**N**	***544.320171***	272.663724	527.293622	264.150449		
9	1003.393806	502.200541	986.367257	493.687266	985.383241	493.195258	**A**	***430.277244***	215.642260	413.250695	207.128985		
10	1074.430920	537.719098	1057.404371	529.205824	1056.420355	528.713816	**A**	***359.240130***	180.123703	342.213581	171.610428		
11	**1187.514984**	594.261130	1170.488435	585.747856	1169.504419	585.255847	**L**	***288.203016***	144.605146	271.176467	136.091871		
12							**R**	175.118952	88.063114	158.092403	79.549839		



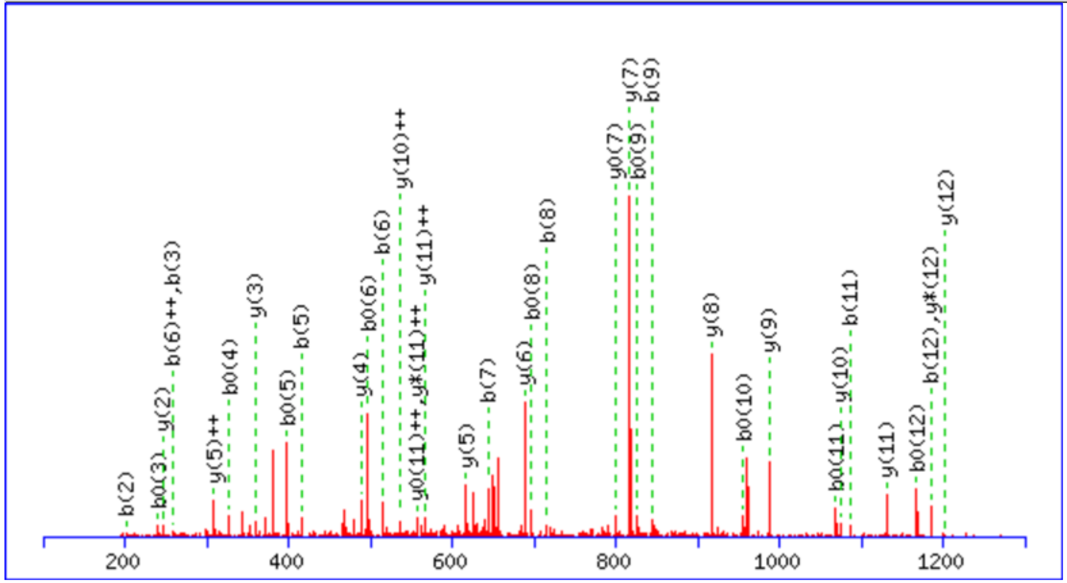
Peptide View

MS/MS Fragmentation of **EAGSAVEAEELVK**
Found in **IPI00008586**, Tax_Id=9606 Gene_Symbol=CSPG5 Isoform 1 of Chondroitin sulfate proteoglycan 5
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 7963: 1330.660248 from(666.337400,2+)
Title: OECHL100317_35.11369.11369.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1330.661591**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 65 **Expect:** 4.8e-005**Matches :** 37/114 fragment ions using 76 most intense peaks   (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**E**							**13**
2	**201.086983**	101.047130	183.076418	92.041847	**A**	***1202.626309***	601.816793	1185.599760	593.303518	1184.615744	592.811510	**12**
3	**258.108447**	129.557862	240.097882	120.552579	**G**	***1131.589195***	566.298236	1114.562646	557.784961	1113.578630	557.292953	**11**
4	345.140475	173.073875	327.129910	164.068593	**S**	***1074.567731***	537.787504	1057.541182	529.274229	1056.557166	528.782221	**10**
5	**416.177589**	208.592432	398.167024	199.587150	**A**	***987.535703***	494.271490	970.509154	485.758215	969.525138	485.266207	**9**

6	**515.246003**	258.126640	497.235438	249.121357	**V**	***916.498589***	458.752933	899.472040	450.239658	898.488024	449.747650	**8**
7	**644.288596**	322.647936	626.278031	313.642653	**E**	***817.430175***	409.218726	800.403626	400.705451	799.419610	400.213443	**7**
8	**715.325710**	358.166493	697.315145	349.161210	**A**	***688.387582***	344.697429	671.361033	336.184155	670.377017	335.692147	**6**
9	**844.368303**	422.687790	826.357738	413.682507	**E**	***617.350468***	309.178872	600.323919	300.665598	599.339903	300.173590	**5**
10	973.410896	487.209086	955.400331	478.203803	**E**	***488.307875***	244.657576	471.281326	236.144301	470.297310	235.652293	**4**
11	**1086.494960**	543.751118	1068.484395	534.745836	**L**	***359.265282***	180.136279	342.238733	171.623005			**3**
12	**1185.563374**	593.285325	1167.552809	584.280043	**V**	***246.181218***	123.594247	229.154669	115.080973			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**



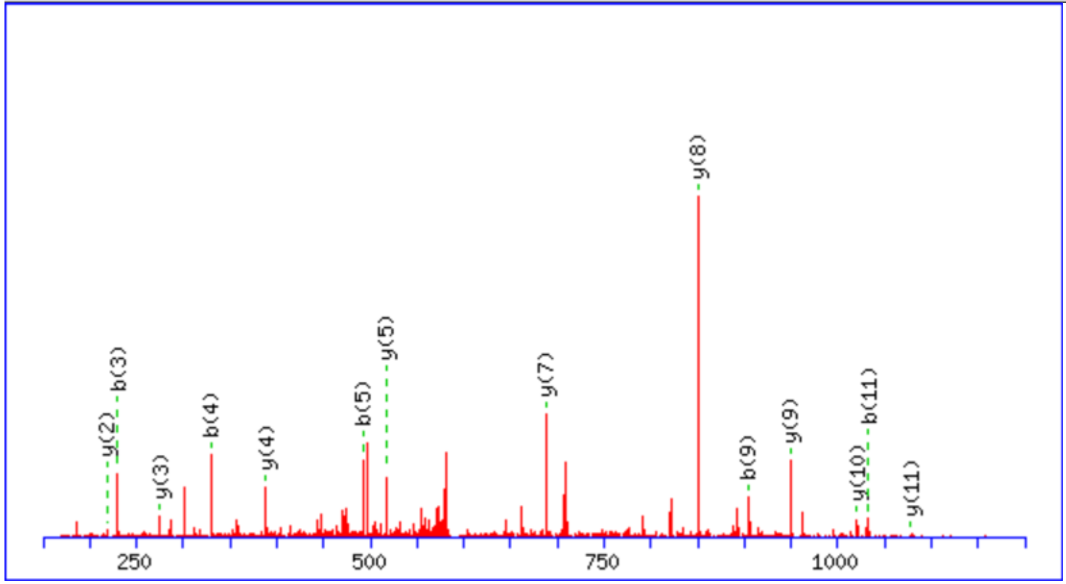
Peptide View

MS/MS Fragmentation of **TGAVYYVAEIGAK**
Found in **IPI00552937**, Tax_Id=9606 Gene_Symbol=NHLRC3 NHL repeat-containing protein 3
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 5904: 1177.634848 from(589.824700,2+)
Title: OECHL100317_35.11336.11336.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1177.634277**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 62 **Expect:** 4.4e-005**Matches :** 14/102 fragment ions using 30 most intense peaks (help)

#	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y^{*}**	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	102.054955	51.531116	84.044390	42.525833	**T**							**12**
2	159.076419	80.041847	141.065854	71.036565	**G**	***1077.593888***	539.300582	1060.567339	530.787308	1059.583323	530.295300	**11**
3	**230.113533**	115.560404	212.102968	106.555122	**A**	***1020.572424***	510.789850	1003.545875	502.276576	1002.561859	501.784568	**10**
4	**329.181947**	165.094611	311.171382	156.089329	**V**	***949.535310***	475.271293	932.508761	466.758019	931.524745	466.266011	**9**
5	**492.245276**	246.626276	474.234711	237.620994	**Y**	***850.466896***	425.737086	833.440347	417.223812	832.456331	416.731804	**8**
6	591.313690	296.160483	573.303125	287.155201	**V**	***687.403567***	344.205422	670.377018	335.692147	669.393002	335.200139	**7**
7	662.350804	331.679040	644.340239	322.673758	**A**	588.335153	294.671215	571.308604	286.157940	570.324588	285.665932	**6**
8	791.393397	396.200337	773.382832	387.195054	**E**	***517.298039***	259.152658	500.271490	250.639383	499.287474	250.147375	**5**
9	**904.477461**	452.742369	886.466896	443.737086	**I**	***388.255446***	194.631361	371.228897	186.118087			**4**
10	961.498925	481.253101	943.488360	472.247818	**G**	***275.171382***	138.089329	258.144833	129.576055			**3**
11	**1032.536039**	516.771658	1014.525474	507.766375	**A**	***218.149918***	109.578597	201.123369	101.065322			**2**
12					**K**	147.112804	74.060040	130.086255	65.546765			**1**

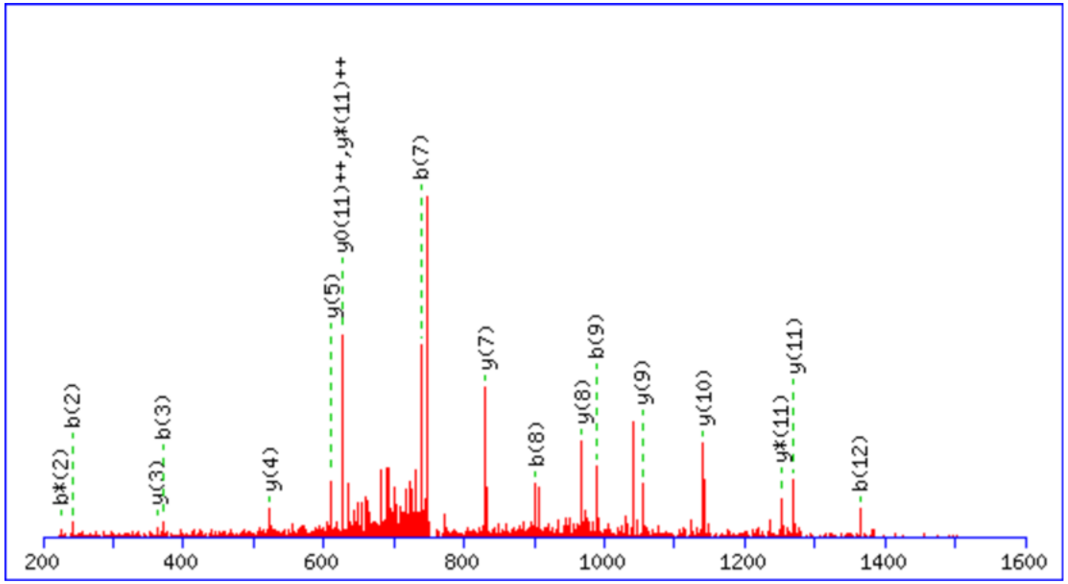


Peptide View

MS/MS Fragmentation of **LQQSSHGYSCSEK**
Found in **IPI00646291**, Tax_Id=9606 Gene_Symbol=GPR180 Integral membrane protein GPR180
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 9793: 1509.654648 from(755.834600,2+)
Title: OECHL100317_35.2400.2400.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1509.651794**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 60 **Expect:** 4.6e-005**Matches :** 18/134 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	114.091340	57.549308					**L**						
2	***242.149918***	121.578597	225.123369	113.065323			**Q**	1397.575019	699.291148	1380.548470	690.777873	1379.564454	690.2858
3	***370.208496***	185.607886	353.181947	177.094612			**Q**	***1269.516441***	635.261859	1252.489892	626.748584	1251.505876	626.2565
4	457.240524	229.123900	440.213975	220.610626	439.229959	220.118618	**S**	***1141.457863***	571.232570	1124.431314	562.719295	1123.447298	562.2272
5	544.272552	272.639914	527.246003	264.126640	526.261987	263.634632	**S**	***1054.425835***	527.716556	1037.399286	519.203281	1036.415270	518.7112
6	681.331464	341.169370	664.304915	332.656095	663.320899	332.164087	**H**	***967.393807***	484.200542	950.367258	475.687267	949.383242	475.1952
7	***738.352928***	369.680102	721.326379	361.166828	720.342363	360.674820	**G**	***830.334895***	415.671086	813.308346	407.157811	812.324330	406.6658
8	***901.416257***	451.211767	884.389708	442.698492	883.405692	442.206484	**Y**	773.313431	387.160354	756.286882	378.647079	755.302866	378.1550
9	***988.448285***	494.727781	971.421736	486.214506	970.437720	485.722498	**S**	***610.250102***	305.628689	593.223553	297.115415	592.239537	296.6234
10	1148.478934	574.743105	1131.452385	566.229831	1130.468369	565.737822	**C**	***523.218074***	262.112675	506.191525	253.599401	505.207509	253.1073
11	1235.510962	618.259119	1218.484413	609.745845	1217.500397	609.253837	**S**	***363.187425***	182.097351	346.160876	173.584076	345.176860	173.0920
12	***1364.553555***	682.780416	1347.527006	674.267141	1346.542990	673.775133	**E**	276.155397	138.581337	259.128848	130.068062	258.144832	129.5760
13							**K**	147.112804	74.060040	130.086255	65.546765		



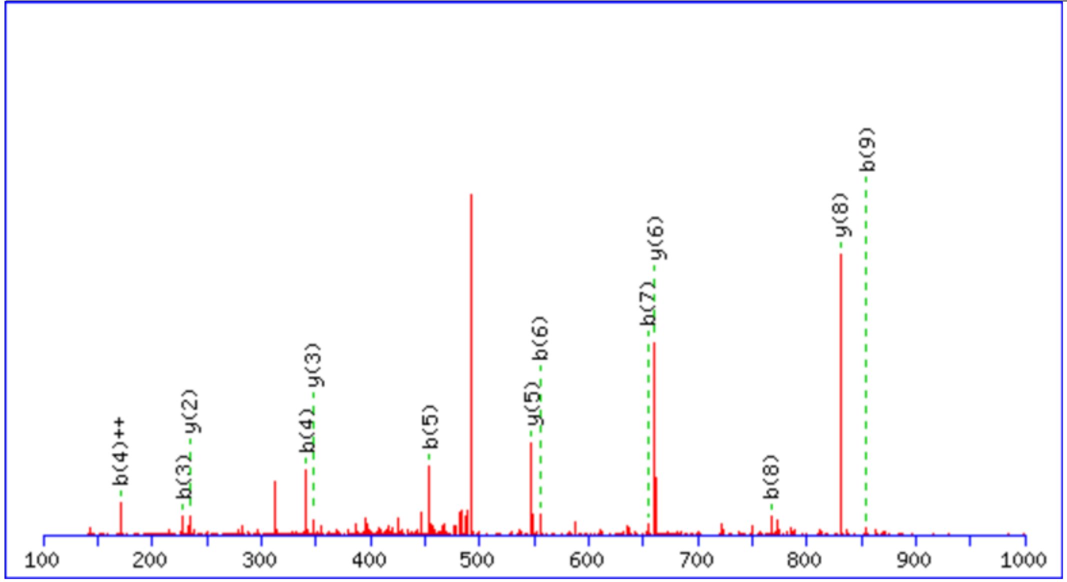
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 3413: 999.633448 from(500.824000,2+)
Title: OECHL100317_35.17226.17226.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59 **Expect:** 1.5e-005**Matches :** 14/78 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**

6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



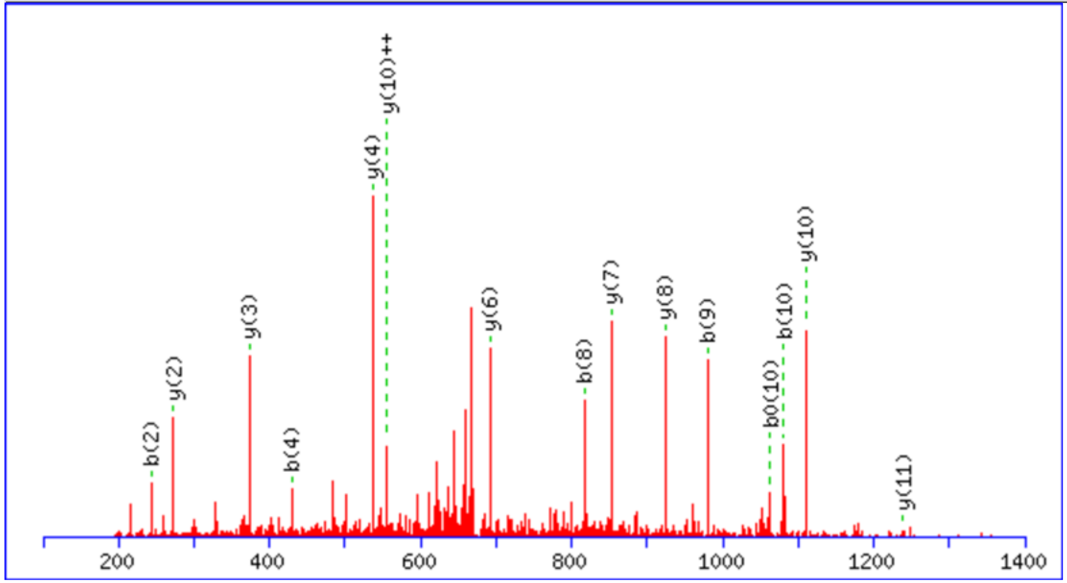
Peptide View

MS/MS Fragmentation of **LEGEACGVYTPR**
Found in **IPI00297284**, Tax_Id=9606 Gene_Symbol=IGFBP2 Insulin-like growth factor-binding protein 2
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 8135: 1350.624848 from(676.319700,2+)
Title: OECHL100317_35.8693.8693.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1350.623795**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 57 **Expect:** 0.0002**Matches :** 15/104 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#

1	114.091340	57.549308			**L**							**12**
2	**243.133933**	122.070605	225.123368	113.065322	**E**	***1238.547015***	619.777146	1221.520466	611.263871	1220.536450	610.771863	**11**
3	300.155397	150.581336	282.144832	141.576054	**G**	***1109.504422***	555.255849	1092.477873	546.742575	1091.493857	546.250567	**10**
4	**429.197990**	215.102633	411.187425	206.097351	**E**	1052.482958	526.745117	1035.456409	518.231843	1034.472393	517.739835	**9**
5	500.235104	250.621190	482.224539	241.615908	**A**	***923.440365***	462.223821	906.413816	453.710546	905.429800	453.218538	**8**
6	660.265753	330.636515	642.255188	321.631232	**C**	***852.403251***	426.705264	835.376702	418.191989	834.392686	417.699981	**7**
7	717.287217	359.147247	699.276652	350.141964	**G**	***692.372602***	346.689939	675.346053	338.176665	674.362037	337.684657	**6**
8	**816.355631**	408.681454	798.345066	399.676171	**V**	635.351138	318.179207	618.324589	309.665933	617.340573	309.173925	**5**
9	**979.418960**	490.213118	961.408395	481.207836	**Y**	***536.282724***	268.645000	519.256175	260.131726	518.272159	259.639718	**4**
10	**1080.466639**	540.736958	1062.456074	531.731675	**T**	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	**3**
11	1177.519403	589.263340	1159.508838	580.258057	**P**	***272.171716***	136.589496	255.145167	128.076221			**2**
12					**R**	175.118952	88.063114	158.092403	79.549839			**1**



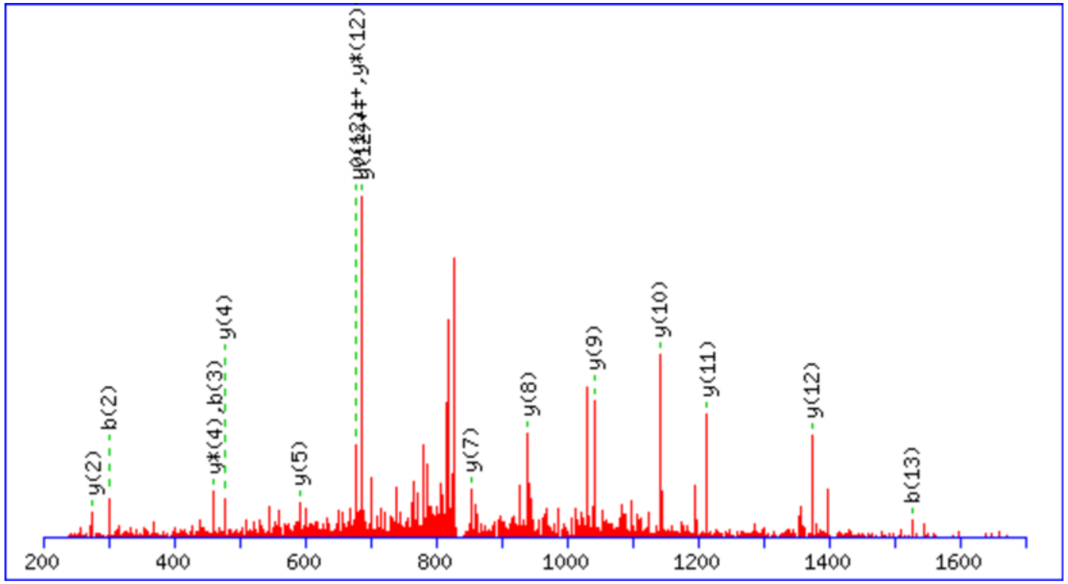
Peptide View

MS/MS Fragmentation of **LWCATTSNFDSDKK**

Found in **IPI00027509**, Tax_Id=9606 Gene_Symbol=MMP9 Matrix metalloproteinase-9
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 11466: 1671.757248 from(836.885900,2+)
Title: OECHL100317_35.10710.10710.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1671.756271**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 51 **Expect:** 0.0006**Matches :** 16/130 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	114.091340	57.549308					**L**						
2	**300.170653**	150.588965					**W**	1559.679484	780.343380	1542.652935	771.830106	1541.668919	771.3380
3	**460.201302**	230.604289					**C**	***1373.600171***	687.303724	1356.573622	678.790449	1355.589606	678.2984
4	531.238416	266.122846					**A**	***1213.569522***	607.288399	1196.542973	598.775125	1195.558957	598.2831
5	632.286095	316.646686			614.275530	307.641403	**T**	***1142.532408***	571.769842	1125.505859	563.256568	1124.521843	562.7645
6	733.333774	367.170525			715.323209	358.165243	**T**	***1041.484729***	521.246003	1024.458180	512.732728	1023.474164	512.2407
7	820.365802	410.686539			802.355237	401.681257	**S**	***940.437050***	470.722163	923.410501	462.208889	922.426485	461.7168
8	934.408729	467.708003	917.382180	459.194728	916.398164	458.702720	**N**	***853.405022***	427.206149	836.378473	418.692875	835.394457	418.2008
9	1081.477143	541.242210	1064.450594	532.728935	1063.466578	532.236927	**F**	739.362095	370.184686	722.335546	361.671411	721.351530	361.1794
10	1196.504086	598.755681	1179.477537	590.242407	1178.493521	589.750399	**D**	***592.293681***	296.650479	575.267132	288.137204	574.283116	287.6451
11	1283.536114	642.271695	1266.509565	633.758421	1265.525549	633.266413	**S**	***477.266738***	239.137007	460.240189	230.623733	459.256173	230.1317
12	1398.563057	699.785167	1381.536508	691.271892	1380.552492	690.779884	**D**	390.234710	195.620993	373.208161	187.107719	372.224145	186.6157
13	**1526.658020**	763.832648	1509.631471	755.319374	1508.647455	754.827366	**K**	***275.207767***	138.107521	258.181218	129.594247		
14							**K**	147.112804	74.060040	130.086255	65.546765		



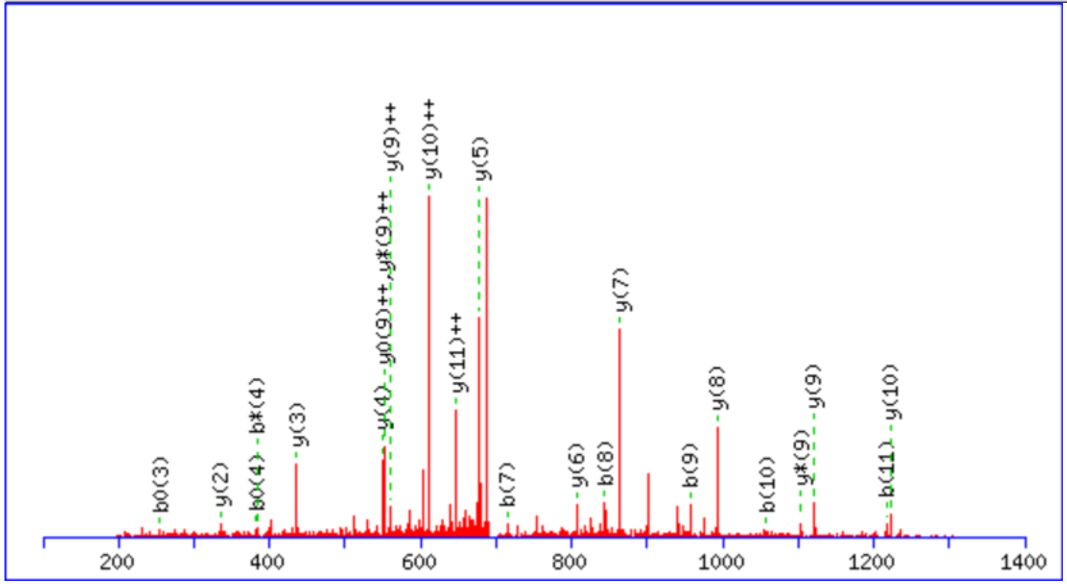
Peptide View

MS/MS Fragmentation of **VATQEGKEITCR**
Found in **IPI00031564**, Tax_Id=9606 Gene_Symbol=GGCT Isoform 1 of Gamma-glutamylcyclotransferase
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 8515: 1390.686448 from(696.350500,2+)
Title: OECHL100317_35.3605.3605.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1390.687454**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54 **Expect:** 0.00051**Matches :** 23/118 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	100.075690	50.541483					V						
2	171.112804	86.060040					A	1292.626328	646.816802	1275.599779	638.303528	1274.615763	637.8115
3	272.160483	136.583879			254.149918	127.578597	T	***1221.589214***	611.298245	1204.562665	602.784971	1203.578649	602.2929
4	400.219061	200.613169	383.192512	192.099894	382.208496	191.607886	Q	***1120.541535***	560.774406	1103.514986	552.261131	1102.530970	551.7691
5	529.261654	265.134465	512.235105	256.621191	511.251089	256.129183	E	***992.482957***	496.745117	975.456408	488.231842	974.472392	487.7398

6	586.283118	293.645197	569.256569	285.131923	568.272553	284.639915	**G**	***863.440364***	432.223820	846.413815	423.710546	845.429799	423.2185
7	**714.378081**	357.692679	697.351532	349.179404	696.367516	348.687396	**K**	***806.418900***	403.713088	789.392351	395.199814	788.408335	394.7078
8	**843.420674**	422.213975	826.394125	413.700701	825.410109	413.208693	**E**	***678.323937***	339.665607	661.297388	331.152332	660.313372	330.6603
9	**956.504738**	478.756007	939.478189	470.242733	938.494173	469.750725	**I**	***549.281344***	275.144310	532.254795	266.631036	531.270779	266.1390
10	**1057.552417**	529.279847	1040.525868	520.766572	1039.541852	520.274564	**T**	***436.197280***	218.602278	419.170731	210.089003	418.186715	209.5969
11	**1217.583066**	609.295171	1200.556517	600.781897	1199.572501	600.289889	**C**	***335.149601***	168.078438	318.123052	159.565164		
12							**R**	175.118952	88.063114	158.092403	79.549839		



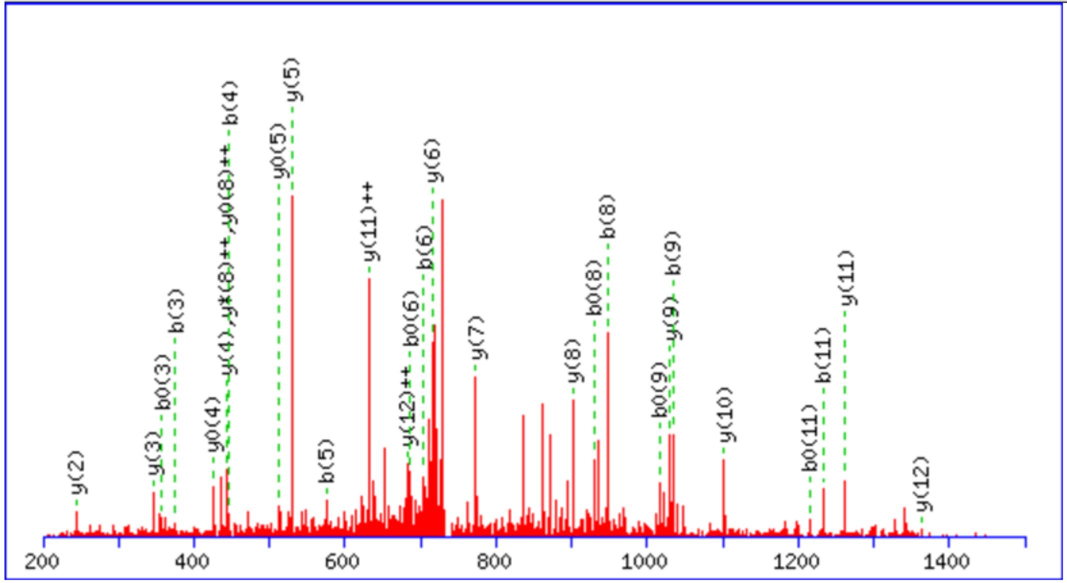
Peptide View

MS/MS Fragmentation of **ITCAEEGWSPTPK**
Found in **IPI00006154**, Tax_Id=9606 Gene_Symbol=CFHR2 Isoform Long of Complement factor H-related protein 2
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 9383: 1474.682048 from(738.348300,2+)
Title: OECHL100317_35.10220.10220.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1474.676224**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**

Score: 50 **Expect:** 0.001**Matches :** 29/114 fragment ions using 75 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**I**							**13**
2	215.139019	108.073147	197.128454	99.067865	**T**	***1362.599444***	681.803360	1345.572895	673.290086	1344.588879	672.798078	**12**
3	**375.169668**	188.088472	357.159103	179.083190	**C**	***1261.551765***	631.279521	1244.525216	622.766246	1243.541200	622.274238	**11**
4	**446.206782**	223.607029	428.196217	214.601747	**A**	***1101.521116***	551.264196	1084.494567	542.750922	1083.510551	542.258914	**10**
5	**575.249375**	288.128326	557.238810	279.123043	**E**	***1030.484002***	515.745639	1013.457453	507.232365	1012.473437	506.740357	**9**
6	**704.291968**	352.649622	686.281403	343.644340	**E**	***901.441409***	451.224343	884.414860	442.711068	883.430844	442.219060	**8**
7	761.313432	381.160354	743.302867	372.155072	**G**	***772.398816***	386.703046	755.372267	378.189772	754.388251	377.697764	**7**
8	**947.392745**	474.200011	929.382180	465.194728	**W**	***715.377352***	358.192314	698.350803	349.679040	697.366787	349.187032	**6**
9	**1034.424773**	517.716025	1016.414208	508.710742	**S**	***529.298039***	265.152658	512.271490	256.639383	511.287474	256.147375	**5**
10	1131.477537	566.242407	1113.466972	557.237124	**P**	***442.266011***	221.636644	425.239462	213.123369	424.255446	212.631361	**4**
11	**1232.525216**	616.766246	1214.514651	607.760964	**T**	***345.213247***	173.110262	328.186698	164.596987	327.202682	164.104979	**3**
12	1329.577980	665.292628	1311.567415	656.287346	**P**	***244.165568***	122.586422	227.139019	114.073148			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**

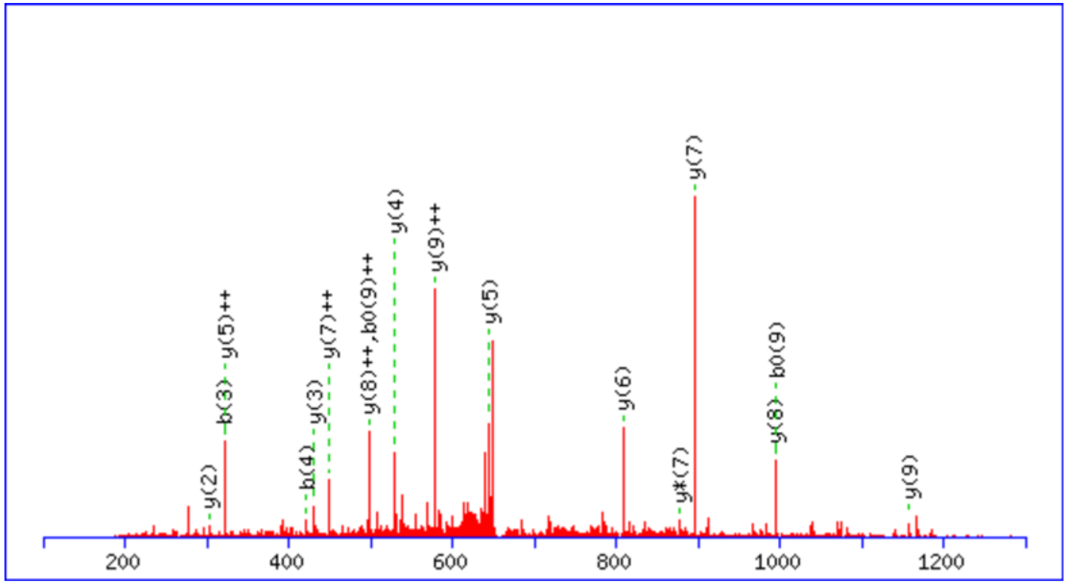


Peptide View

MS/MS Fragmentation of **SAYVSYDVQKR**
Found in **IPI00395903**, Tax_Id=9606 Gene_Symbol=TMEM106B Transmembrane protein 106B
Experiment: 30 - NOPE3 **Fraction:** NOPE3

Match to Query 7820: 1314.658848 from(658.336700,2+)
Title: OECHL100317_35.6668.6668.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_35.raw
Monoisotopic mass of neutral peptide Mr(calc): 1314.656799**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 49 **Expect:** 0.0015**Matches :** 17/96 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	88.039304	44.523290			70.028739	35.518008	**S**						
2	159.076418	80.041847			141.065853	71.036564	**A**	1228.632064	614.819670	1211.605515	606.306396	1210.621499	605.8143
3	**322.139747**	161.573512			304.129182	152.568229	**Y**	***1157.594950***	579.301113	1140.568401	570.787839	1139.584385	570.2958
4	**421.208161**	211.107719			403.197596	202.102436	**V**	***994.531621***	497.769449	977.505072	489.256174	976.521056	488.7641
5	508.240189	254.623733			490.229624	245.618450	**S**	***895.463207***	448.235242	878.436658	439.721967	877.452642	439.2299
6	671.303518	336.155397			653.292953	327.150115	**Y**	***808.431179***	404.719228	791.404630	396.205953	790.420614	395.7139
7	786.330461	393.668869			768.319896	384.663586	**D**	***645.367850***	323.187563	628.341301	314.674289	627.357285	314.1822
8	885.398875	443.203076			867.388310	434.197793	**V**	***530.340907***	265.674092	513.314358	257.160817		
9	1013.457453	507.232365	996.430904	498.719090	995.446888	498.227082	**Q**	***431.272493***	216.139885	414.245944	207.626610		
10	1141.552416	571.279846	1124.525867	562.766572	1123.541851	562.274564	**K**	***303.213915***	152.110596	286.187366	143.597321		
11							**R**	175.118952	88.063114	158.092403	79.549839		



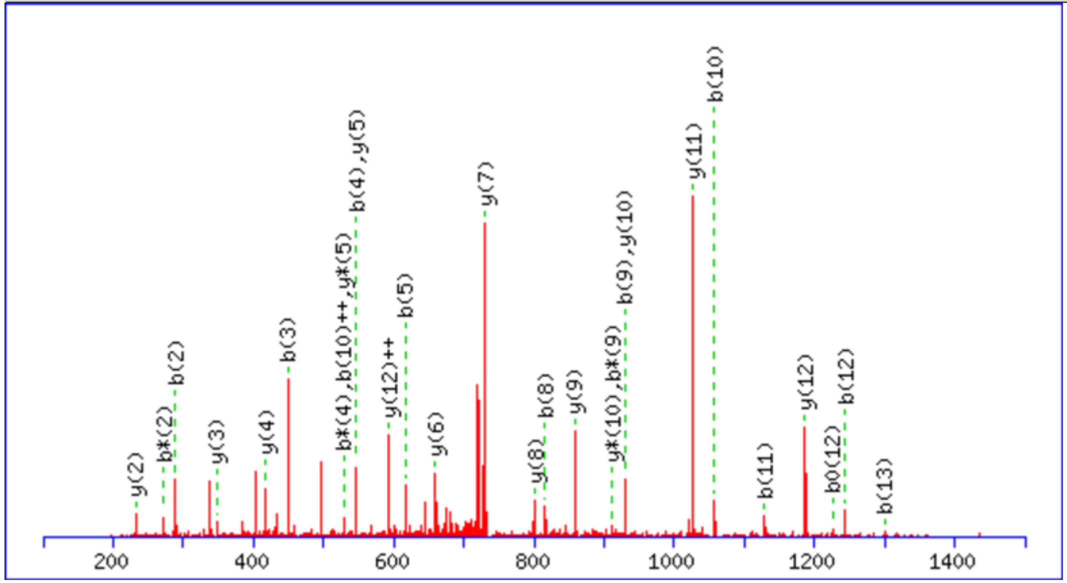
Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 42 - OPD-3 **Fraction:** OPD-3

Match to Query 8920: 1473.645448 from(737.830000,2+)
Title: OECHL100317_33.7665.7665.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 72 **Expect:** 3.1e-006**Matches :** 29/128 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	161.037925	81.022600					C						
2	**289.096503**	145.051890	272.069954	136.538615			Q	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.8093
3	**449.127152**	225.067214	432.100603	216.553940			C	***1186.563334***	593.785305	1169.536785	585.272031	1168.552769	584.7800
4	**546.179916**	273.593596	529.153367	265.080322			P	***1026.532685***	513.769981	1009.506136	505.256706	1008.522120	504.7646
5	**617.217030**	309.112153	600.190481	300.598879			A	***929.479921***	465.243599	912.453372	456.730324	911.469356	456.2383

6	674.238494	337.622885	657.211945	329.109611			**G**	***858.442807***	429.725042	841.416258	421.211767	840.432242	420.7197
7	745.275608	373.141442	728.249059	364.628168			**A**	***801.421343***	401.214310	784.394794	392.701035	783.410778	392.2090
8	**816.312722**	408.659999	799.286173	400.146725			**A**	***730.384229***	365.695753	713.357680	357.182478	712.373664	356.6904
9	**929.396786**	465.202031	912.370237	456.688757			**L**	***659.347115***	330.177196	642.320566	321.663921	641.336550	321.1719
10	**1057.455364**	529.231320	1040.428815	520.718046			**Q**	***546.263051***	273.635164	529.236502	265.121889	528.252486	264.6298
11	**1128.492478**	564.749877	1111.465929	556.236603			**A**	***418.204473***	209.605874	401.177924	201.092600	400.193908	200.6005
12	**1243.519421**	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.0820
13	**1300.540885**	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	***232.140416***	116.573846	215.113867	108.060571		
14							**R**	175.118952	88.063114	158.092403	79.549839		



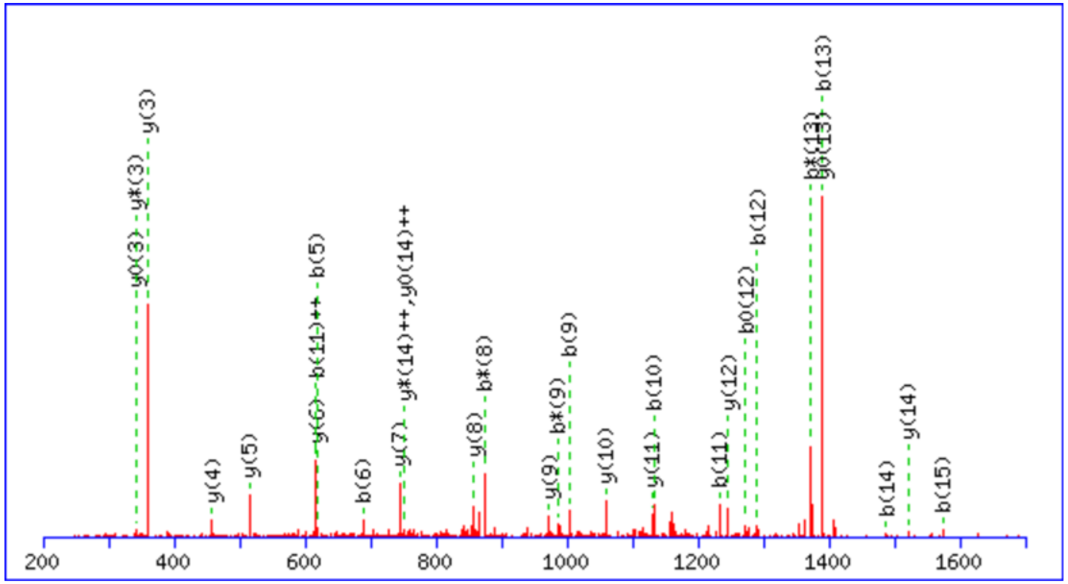
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 42 - OPD-3 **Fraction:** OPD-3

Match to Query 11399: 1746.915648 from(874.465100,2+)

Title: OECHL100317_33.16649.16649.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 83 **Expect:** 5.5e-007**Matches :** 30/156 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	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	***618.349740***	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018
6	***689.386854***	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							**R**	175.118952	88.063114	158.092403	79.549839		



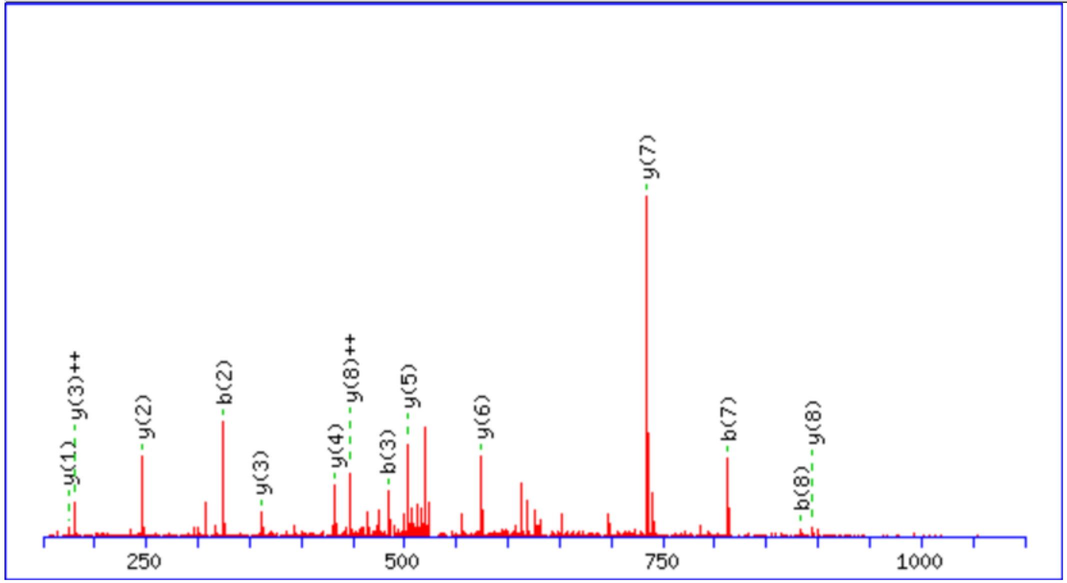
Peptide View

MS/MS Fragmentation of **YCCAAADAR**
Found in **IPI00455600**, Tax_Id=9606 Gene_Symbol=SHISA3 Protein shisa-3 homolog
Experiment: 42 - OPD-3 **Fraction:** OPD-3

Match to Query 3846: 1056.411248 from(529.212900,2+)
Title: OECHL100317_33.3257.3257.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1056.411682**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 59 **Expect:** 8.8e-006**Matches :** 14/64 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							9
2	**324.101254**	162.554265			C	***894.355649***	447.681462	877.329100	439.168188	876.345084	438.676180	8
3	**484.131903**	242.569590			C	***734.325000***	367.666138	717.298451	359.152863	716.314435	358.660855	7
4	555.169017	278.088147			A	***574.294351***	287.650813	557.267802	279.137539	556.283786	278.645531	6
5	626.206131	313.606704			A	***503.257237***	252.132256	486.230688	243.618982	485.246672	243.126974	5

6	697.243245	349.125261			**A**	***432.220123***	216.613699	415.193574	208.100425	414.209558	207.608417	**4**
7	**812.270188**	406.638732	794.259623	397.633449	**D**	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	**3**
8	**883.307302**	442.157289	865.296737	433.152006	**A**	***246.156066***	123.581671	229.129517	115.068396			**2**
9					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



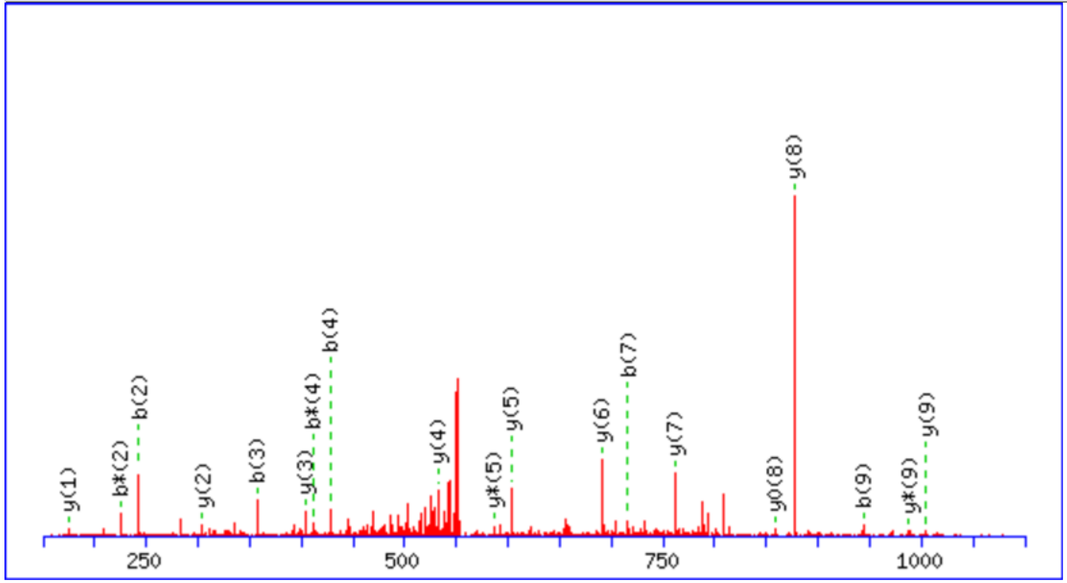
Peptide View

MS/MS Fragmentation of **LQDASAEVER**
Found in **IPI00026241**, Tax_Id=9606 Gene_Symbol=BST2 Bone marrow stromal antigen 2
Experiment: 42 - OPD-3 **Fraction:** OPD-3

Match to Query 4616: 1116.543048 from(559.278800,2+)
Title: OECHL100317_33.4897.4897.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1116.541092**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55 **Expect:** 0.00034**Matches :** 20/100 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	114.091340	57.549308					**L**							**10**

2	**242.149918**	121.578597	225.123369	113.065323			**Q**	***1004.464329***	502.735803	987.437780	494.222528	986.453764	493.730520	**9**
3	**357.176861**	179.092069	340.150312	170.578794	339.166296	170.086786	**D**	***876.405751***	438.706514	859.379202	430.193239	858.395186	429.701231	**8**
4	**428.213975**	214.610626	411.187426	206.097351	410.203410	205.605343	**A**	***761.378808***	381.193042	744.352259	372.679767	743.368243	372.187759	**7**
5	515.246003	258.126640	498.219454	249.613365	497.235438	249.121357	**S**	***690.341694***	345.674485	673.315145	337.161210	672.331129	336.669202	**6**
6	**586.283117**	293.645197	569.256568	285.131922	568.272552	284.639914	**A**	***603.309666***	302.158471	586.283117	293.645197	585.299101	293.153189	**5**
7	**715.325710**	358.166493	698.299161	349.653219	697.315145	349.161211	**E**	***532.272552***	266.639914	515.246003	258.126640	514.261987	257.634632	**4**
8	814.394124	407.700700	797.367575	399.187426	796.383559	398.695418	**V**	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	**3**
9	**943.436717**	472.221997	926.410168	463.708722	925.426152	463.216714	**E**	***304.161545***	152.584410	287.134996	144.071136	286.150980	143.579128	**2**
10							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



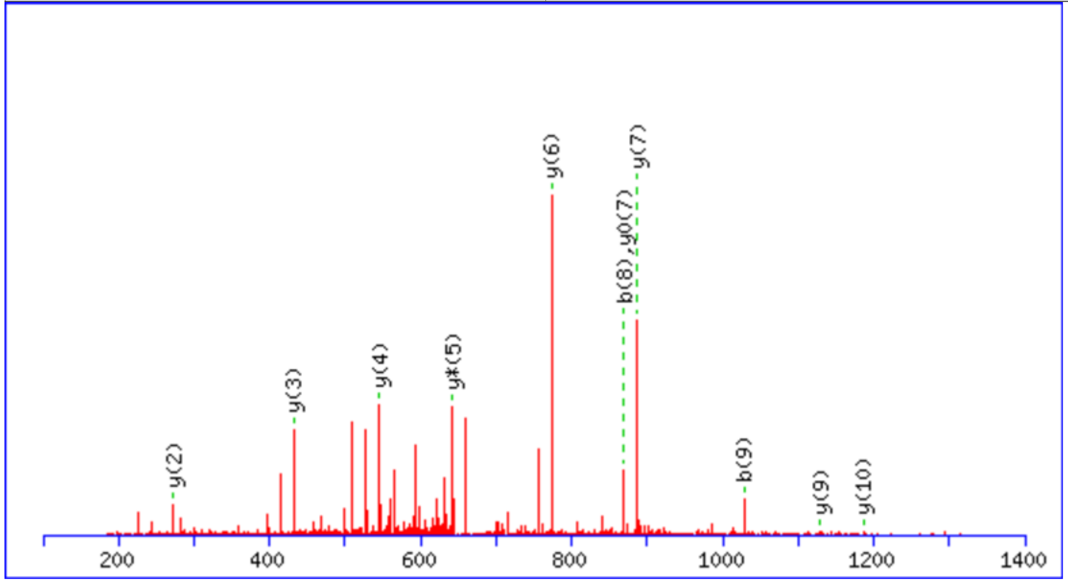
Peptide View

MS/MS Fragmentation of **IGDKLDIICPR**
Found in **IPI00024307**, Tax_Id=9606 Gene_Symbol=EFNB1 Ephrin-B1
Experiment: 42 - OPD-3 **Fraction:** OPD-3

Match to Query 7433: 1298.701848 from(650.358200,2+)

Title: OECHL100317_33.12507.12507.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1298.701645**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 62 **Expect:** 6.3e-005**Matches :** 11/100 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	114.091340	57.549308					**I**						
2	171.112804	86.060040					**G**	***1186.624870***	593.816073	1169.598321	585.302799	1168.614305	584.8107
3	286.139747	143.573512			268.129182	134.568229	**D**	***1129.603406***	565.305341	1112.576857	556.792067	1111.592841	556.3000
4	414.234710	207.620993	397.208161	199.107719	396.224145	198.615711	**K**	1014.576463	507.791870	997.549914	499.278595	996.565898	498.7865
5	527.318774	264.163025	510.292225	255.649751	509.308209	255.157743	**L**	***886.481500***	443.744388	869.454951	435.231113	868.470935	434.7391
6	642.345717	321.676497	625.319168	313.163222	624.335152	312.671214	**D**	***773.397436***	387.202356	756.370887	378.689081	755.386871	378.1970
7	755.429781	378.218529	738.403232	369.705254	737.419216	369.213246	**I**	658.370493	329.688885	641.343944	321.175610		
8	**868.513845**	434.760561	851.487296	426.247286	850.503280	425.755278	**I**	***545.286429***	273.146853	528.259880	264.633578		
9	**1028.544494**	514.775885	1011.517945	506.262610	1010.533929	505.770603	**C**	***432.202365***	216.604820	415.175816	208.091546		
10	1125.597258	563.302267	1108.570709	554.788993	1107.586693	554.296985	**P**	***272.171716***	136.589496	255.145167	128.076221		
11							**R**	175.118952	88.063114	158.092403	79.549839		

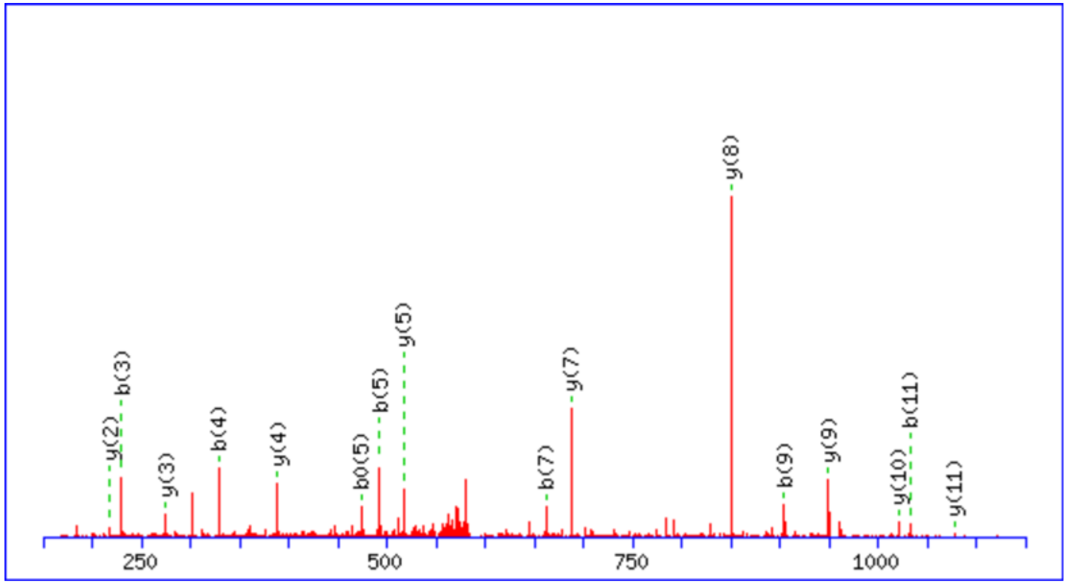


Peptide View

MS/MS Fragmentation of **TGAVYVAEIGAK**
Found in **IPI00552937**, Tax_Id=9606 Gene_Symbol=NHLRC3 NHL repeat-containing protein 3
Experiment: 42 - OPD-3 **Fraction:** OPD-3

Match to Query 5495: 1177.634048 from(589.824300,2+)
Title: OECHL100317_33.11513.11513.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1177.634277**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65 **Expect:** 2.2e-005**Matches :** 16/102 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							12
2	159.076419	80.041847	141.065854	71.036565	G	***1077.593888***	539.300582	1060.567339	530.787308	1059.583323	530.295300	11
3	**230.113533**	115.560404	212.102968	106.555122	A	***1020.572424***	510.789850	1003.545875	502.276576	1002.561859	501.784568	10
4	**329.181947**	165.094611	311.171382	156.089329	V	***949.535310***	475.271293	932.508761	466.758019	931.524745	466.266011	9
5	**492.245276**	246.626276	474.234711	237.620994	Y	***850.466896***	425.737086	833.440347	417.223812	832.456331	416.731804	8
6	591.313690	296.160483	573.303125	287.155201	V	***687.403567***	344.205422	670.377018	335.692147	669.393002	335.200139	7
7	**662.350804**	331.679040	644.340239	322.673758	A	588.335153	294.671215	571.308604	286.157940	570.324588	285.665932	6
8	791.393397	396.200337	773.382832	387.195054	E	***517.298039***	259.152658	500.271490	250.639383	499.287474	250.147375	5
9	**904.477461**	452.742369	886.466896	443.737086	I	***388.255446***	194.631361	371.228897	186.118087			4
10	961.498925	481.253101	943.488360	472.247818	G	***275.171382***	138.089329	258.144833	129.576055			3
11	**1032.536039**	516.771658	1014.525474	507.766375	A	***218.149918***	109.578597	201.123369	101.065322			2
12					K	147.112804	74.060040	130.086255	65.546765			1



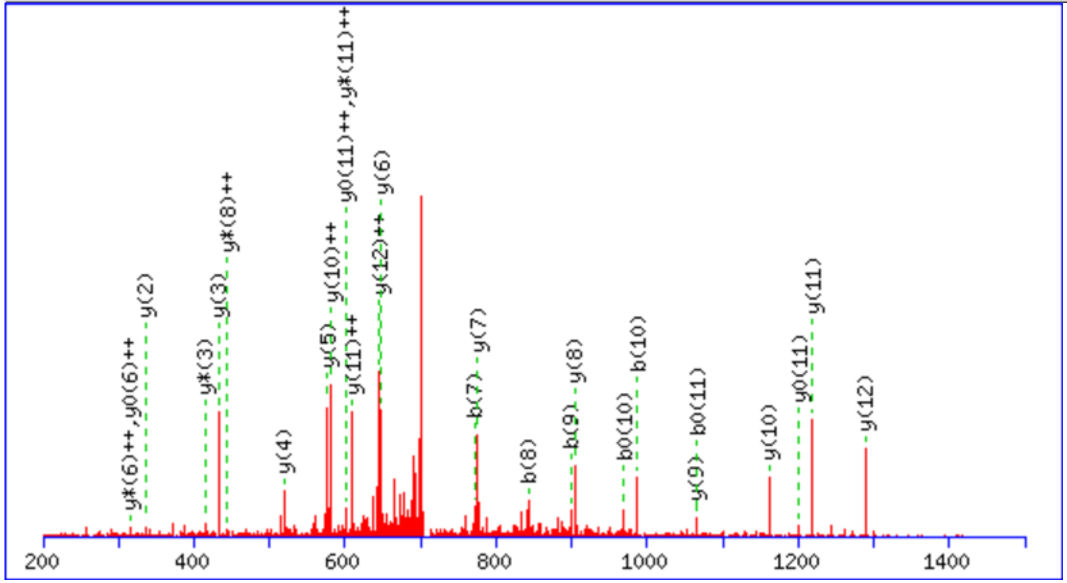
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 42 - OPD-3 **Fraction:** OPD-3

Match to Query 8365: 1416.625048 from(709.319800,2+)
Title: OECHL100317_33.2088.2088.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 75 **Expect:** 2e-006**Matches :** 27/128 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	129.102239	65.054757	112.075690	56.541483			**K**						
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.2664
3	257.160817	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.7478
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.2371
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.7107

6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.6954
7	**771.345401**	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.1741
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.1448
9	**899.403979**	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.6262
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.1155
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546		
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164		
13							**R**	175.118952	88.063114	158.092403	79.549839		



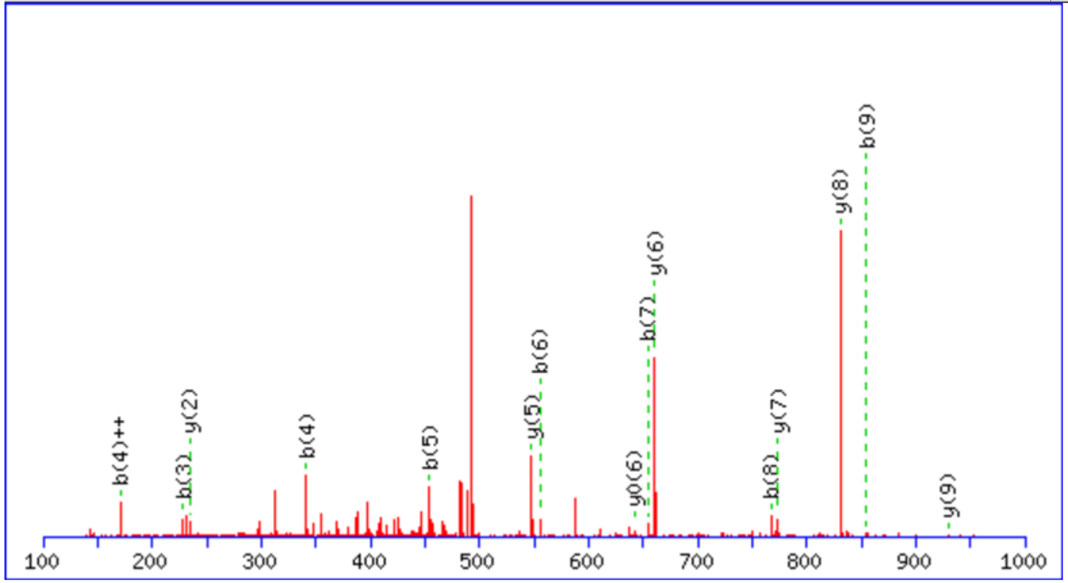
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 42 - OPD-3 **Fraction:** OPD-3

Match to Query 3054: 999.635048 from(500.824800,2+)
Title: OECHL100317_33.16797.16797.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55 **Expect:** 3.6e-005**Matches :** 16/78 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	**929.602995**	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	**773.513117**	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**

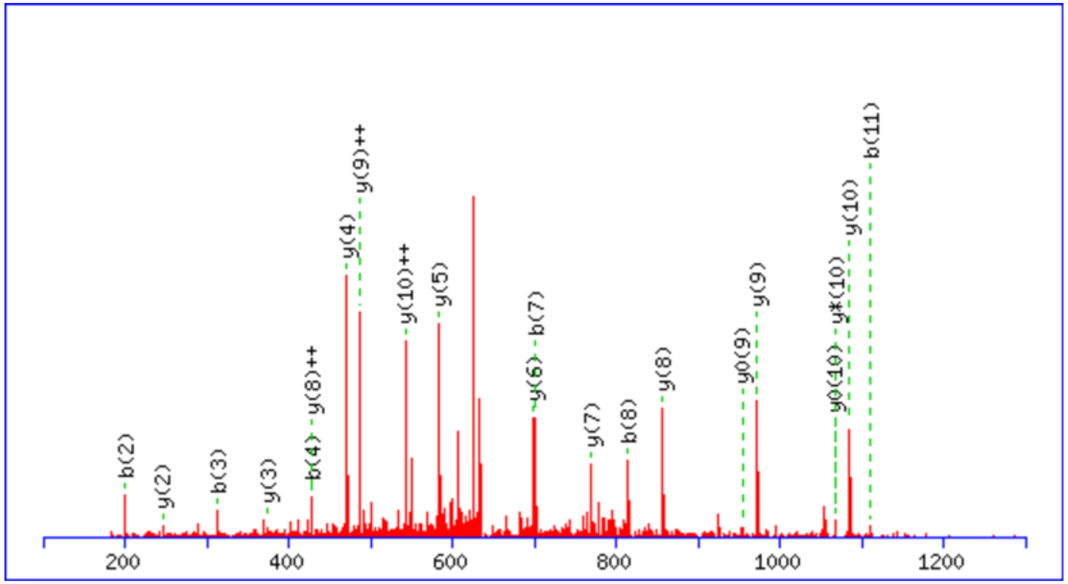


Peptide View

MS/MS Fragmentation of **AQLDSADIPKAR**
Found in **IPI00026303**, Tax_Id=9606 Gene_Symbol=PI15 Peptidase inhibitor 15
Experiment: 42 - OPD-3 **Fraction:** OPD-3

Match to Query 7217: 1283.683248 from(642.848900,2+)
Title: OECHL100317_33.7945.7945.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1283.683334**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 59 **Expect:** 0.0001**Matches :** 21/114 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	72.044390	36.525833					**A**						
2	**200.102968**	100.555122	183.076419	92.041848			**Q**	1213.653527	607.330402	1196.626978	598.817127	1195.642962	598.3251
3	**313.187032**	157.097154	296.160483	148.583879			**L**	***1085.594949***	543.301113	1068.568400	534.787838	1067.584384	534.2958
4	**428.213975**	214.610626	411.187426	206.097351	410.203410	205.605343	**D**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
5	515.246003	258.126640	498.219454	249.613365	497.235438	249.121357	**S**	***857.483942***	429.245609	840.457393	420.732335	839.473377	420.2403
6	586.283117	293.645197	569.256568	285.131922	568.272552	284.639914	**A**	***770.451914***	385.729595	753.425365	377.216321	752.441349	376.7243
7	**701.310060**	351.158668	684.283511	342.645394	683.299495	342.153386	**D**	***699.414800***	350.211038	682.388251	341.697764	681.404235	341.2057
8	**814.394124**	407.700700	797.367575	399.187426	796.383559	398.695418	**I**	***584.387857***	292.697567	567.361308	284.184292		
9	911.446888	456.227082	894.420339	447.713808	893.436323	447.221800	**P**	***471.303793***	236.155535	454.277244	227.642260		
10	1039.541851	520.274564	1022.515302	511.761289	1021.531286	511.269281	**K**	***374.251029***	187.629153	357.224480	179.115878		
11	**1110.578965**	555.793121	1093.552416	547.279846	1092.568400	546.787838	**A**	***246.156066***	123.581671	229.129517	115.068396		
12							**R**	175.118952	88.063114	158.092403	79.549839		



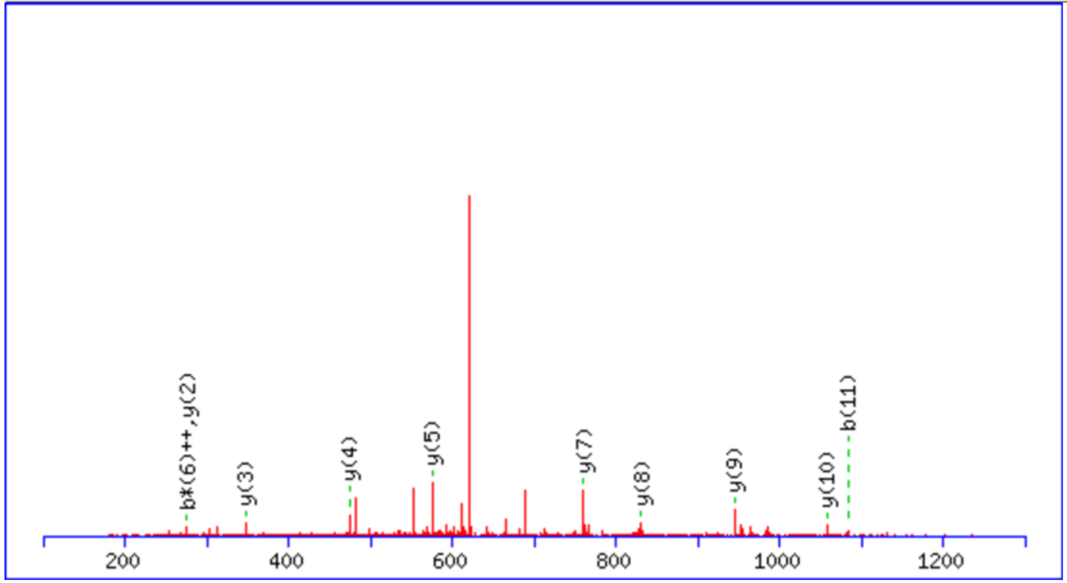
Peptide View

MS/MS Fragmentation of **QAINAALTQATR**
Found in **IPI00307446**, Tax_Id=9606 Gene_Symbol=PCDH24 Protocadherin-24
Experiment: 42 - OPD-3 **Fraction:** OPD-3

Match to Query 6940: 1256.683248 from(629.348900,2+)
Title: OECHL100317_33.10487.10487.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1256.683670**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 76 **Expect:** 2e-006**Matches :** 10/116 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	129.065854	65.036565	112.039305	56.523291			**Q**						
2	200.102968	100.555122	183.076419	92.041848			**A**	1129.632399	565.319837	1112.605850	556.806563	1111.621834	556.3145
3	313.187032	157.097154	296.160483	148.583879			**I**	***1058.595285***	529.801280	1041.568736	521.288006	1040.584720	520.7959
4	427.229959	214.118618	410.203410	205.605343			**N**	***945.511221***	473.259249	928.484672	464.745974	927.500656	464.2539
5	498.267073	249.637175	481.240524	241.123900			**A**	***831.468294***	416.237785	814.441745	407.724511	813.457729	407.2325

6	569.304187	285.155732	552.277638	276.642457			**A**	***760.431180***	380.719228	743.404631	372.205953	742.420615	371.7139
7	682.388251	341.697764	665.361702	333.184489			**L**	689.394066	345.200671	672.367517	336.687396	671.383501	336.1953
8	783.435930	392.221603	766.409381	383.708329	765.425365	383.216321	**T**	***576.310002***	288.658639	559.283453	280.145364	558.299437	279.6533
9	911.494508	456.250892	894.467959	447.737618	893.483943	447.245610	**Q**	***475.262323***	238.134799	458.235774	229.621525	457.251758	229.1295
10	982.531622	491.769449	965.505073	483.256175	964.521057	482.764167	**A**	***347.203745***	174.105510	330.177196	165.592236	329.193180	165.1002
11	1083.579301	542.293289	1066.552752	533.780014	1065.568736	533.288006	**T**	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.5816
12							**R**	175.118952	88.063114	158.092403	79.549839		



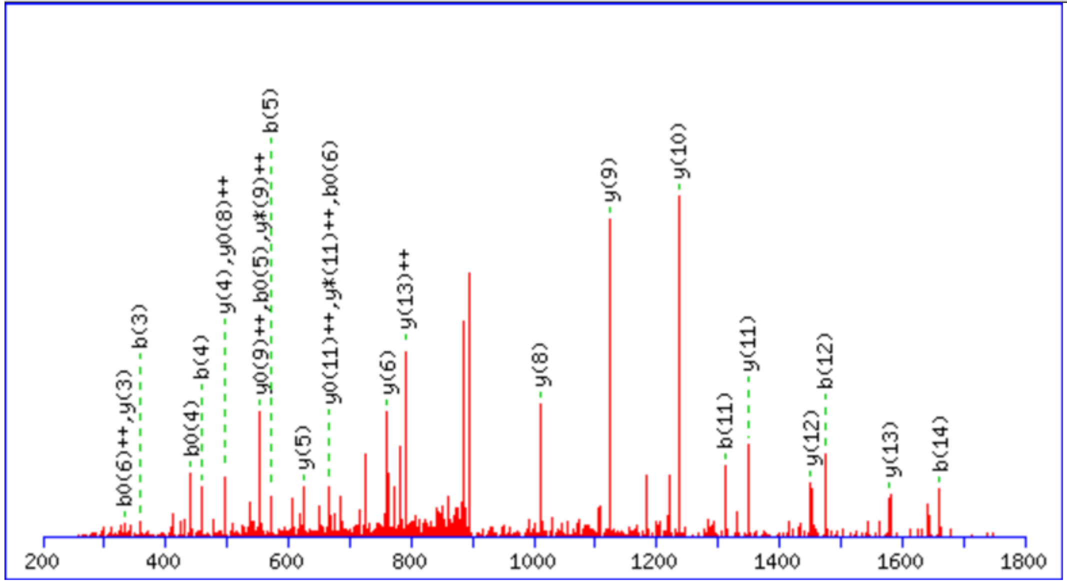
Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 42 - OPD-3 **Fraction:** OPD-3

Match to Query 11785: 1805.932648 from(903.973600,2+)
Title: OECHL100317_33.18425.18425.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**

Score: 74 **Expect:** 4.8e-006**Matches :** 26/160 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	115.050203	58.028740	98.023654	49.515465			N						
2	228.134267	114.570771	211.107718	106.057497			I	1692.895549	846.951413	1675.869000	838.438138	1674.884984	837.9461
3	**357.176860**	179.092068	340.150311	170.578793	339.166295	170.086785	E	***1579.811485***	790.409381	1562.784936	781.896106	1561.800920	781.4040
4	**458.224539**	229.615907	441.197990	221.102633	440.213974	220.610625	T	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.8828
5	**571.308603**	286.157940	554.282054	277.644665	553.298038	277.152657	I	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.3589
6	684.392667	342.699972	667.366118	334.186697	666.382102	333.694689	I	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.8169
7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	N	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.2748
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	T	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.2534
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	F	908.462479	454.734878	891.435930	446.221603	890.451914	445.7295
10	1183.610599	592.308938	1166.584050	583.795663	1165.600034	583.303655	H	***761.394065***	381.200671	744.367516	372.687396	743.383500	372.1953
11	**1311.669177**	656.338227	1294.642628	647.824952	1293.658612	647.332944	Q	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.6659
12	**1474.732506**	737.869891	1457.705957	729.356617	1456.721941	728.864609	Y	***496.276575***	248.641926	479.250026	240.128651	478.266010	239.6366
13	1561.764534	781.385905	1544.737985	772.872631	1543.753969	772.380623	S	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.1049
14	**1660.832948**	830.920112	1643.806399	822.406838	1642.822383	821.914830	V	246.181218	123.594247	229.154669	115.080973		
15							K	147.112804	74.060040	130.086255	65.546765		



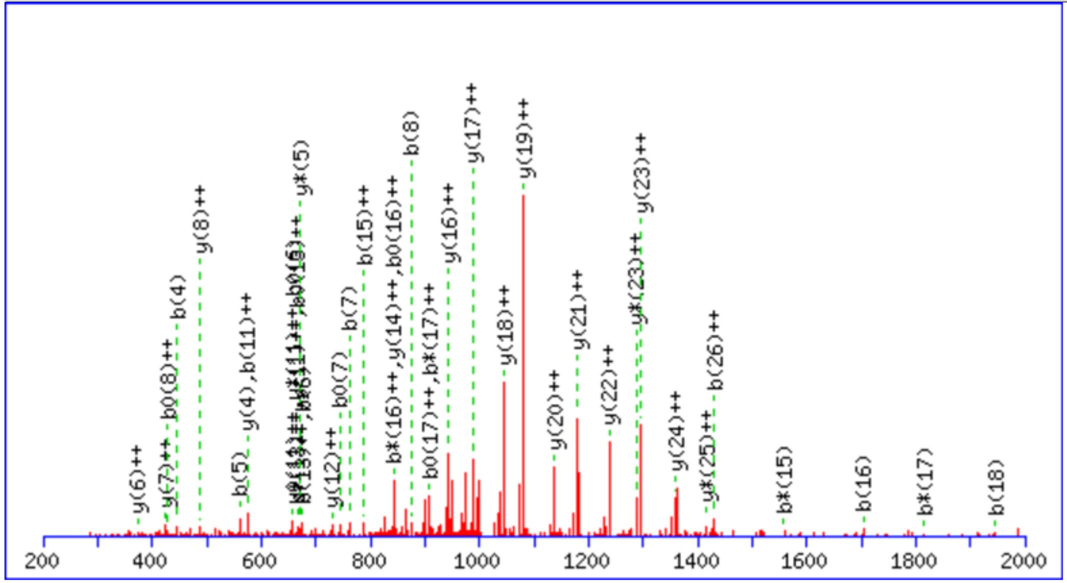
Peptide View

MS/MS Fragmentation of **DAEEDDSLANSSDLLKELLETGDNRER**
Found in **IPI00000828**, Tax_Id=9606 Gene_Symbol=PENK Proenkephalin-A
Experiment: 42 - OPD-3 **Fraction:** OPD-3

Match to Query 15570: 3033.407172 from(1012.143000,3+)
Title: OECHL100317_33.18872.18872.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 3033.401001**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 73 **Expect:** 9.3e-006**Matches :** 43/292 fragment ions using 68 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	
1	116.034219	58.520748			98.023654	49.515465	**D**						
2	187.071333	94.039304			169.060768	85.034022	**A**	2919.381392	1460.194334	2902.354843	1451.681059	2901.370827	14
3	316.113926	158.560601			298.103361	149.555319	**E**	2848.344278	1424.675777	2831.317729	1416.162502	2830.333713	14
4	**445.156519**	223.081898			427.145954	214.076615	**E**	2719.301685	1360.154480	2702.275136	1351.641206	2701.291120	13
5	**560.183462**	280.595369			542.172897	271.590087	**D**	2590.259092	1295.633184	2573.232543	1287.119909	2572.248527	12
6	**675.210405**	338.108841			657.199840	329.103558	**D**	2475.232149	1238.119712	2458.205600	1229.606438	2457.221584	12
7	**762.242433**	381.624855			744.231868	372.619572	**S**	2360.205206	1180.606241	2343.178657	1172.092966	2342.194641	11
8	**875.326497**	438.166887			857.315932	429.161604	**L**	2273.173178	1137.090227	2256.146629	1128.576952	2255.162613	11
9	946.363611	473.685444			928.353046	464.680161	**A**	2160.089114	1080.548195	2143.062565	1072.034920	2142.078549	10
10	1060.406538	530.706907	1043.379989	522.193633	1042.395973	521.701624	**N**	2089.052000	1045.029638	2072.025451	1036.516363	2071.041435	10
11	1147.438566	**574.222921**	1130.412017	565.709647	1129.428001	565.217639	**S**	1975.009073	988.008174	1957.982524	979.494900	1956.998508	9
12	1234.470594	617.738935	1217.444045	609.225661	1216.460029	608.733653	**S**	1887.977045	944.492160	1870.950496	935.978886	1869.966480	9
13	1349.497537	**675.252407**	1332.470988	666.739132	1331.486972	666.247124	**D**	1800.945017	900.976146	1783.918468	892.462872	1782.934452	8
14	1462.581601	731.794439	1445.555052	723.281164	1444.571036	722.789156	**L**	1685.918074	843.462675	1668.891525	834.949400	1667.907509	8
15	1575.665665	**788.336471**	1558.639116	779.823196	1557.655100	779.331188	**L**	1572.834010	786.920643	1555.807461	778.407368	1554.823445	7
16	**1703.760628**	852.383952	1686.734079	843.870678	1685.750063	843.378670	**K**	1459.749946	730.378611	1442.723397	721.865336	1441.739381	7
17	1832.803221	916.905248	1815.776672	908.391974	1814.792656	907.899966	**E**	1331.654983	666.331129	1314.628434	657.817855	1313.644418	6
18	**1945.887285**	973.447280	1928.860736	964.934006	1927.876720	964.441998	**L**	1202.612390	601.809833	1185.585841	593.296558	1184.601825	5

19	2058.971349	1029.989312	2041.944800	1021.476038	2040.960784	1020.984030	**L**	1089.528326	545.267801	1072.501777	536.754526	1071.517761	5
20	2188.013942	1094.510609	2170.987393	1085.997334	2170.003377	1085.505326	**E**	976.444262	488.725769	959.417713	480.212494	958.433697	4
21	2289.061621	1145.034448	2272.035072	1136.521174	2271.051056	1136.029166	**T**	847.401669	424.204472	830.375120	415.691198	829.391104	4
22	2346.083085	1173.545180	2329.056536	1165.031906	2328.072520	1164.539898	**G**	746.353990	373.680633	729.327441	365.167358	728.343425	3
23	2461.110028	1231.058652	2444.083479	1222.545377	2443.099463	1222.053369	**D**	689.332526	345.169901	672.305977	336.656626	671.321961	3
24	2575.152955	1288.080115	2558.126406	1279.566841	2557.142390	1279.074833	**N**	574.305583	287.656430	557.279034	279.143155	556.295018	2
25	2731.254066	1366.130671	2714.227517	1357.617396	2713.243501	1357.125388	**R**	460.262656	230.634966	443.236107	222.121692	442.252091	2
26	2860.296659	**1430.651967**	2843.270110	1422.138693	2842.286094	1421.646685	**E**	304.161545	152.584411	287.134996	144.071136	286.150980	1
27							**R**	175.118952	88.063114	158.092403	79.549839		



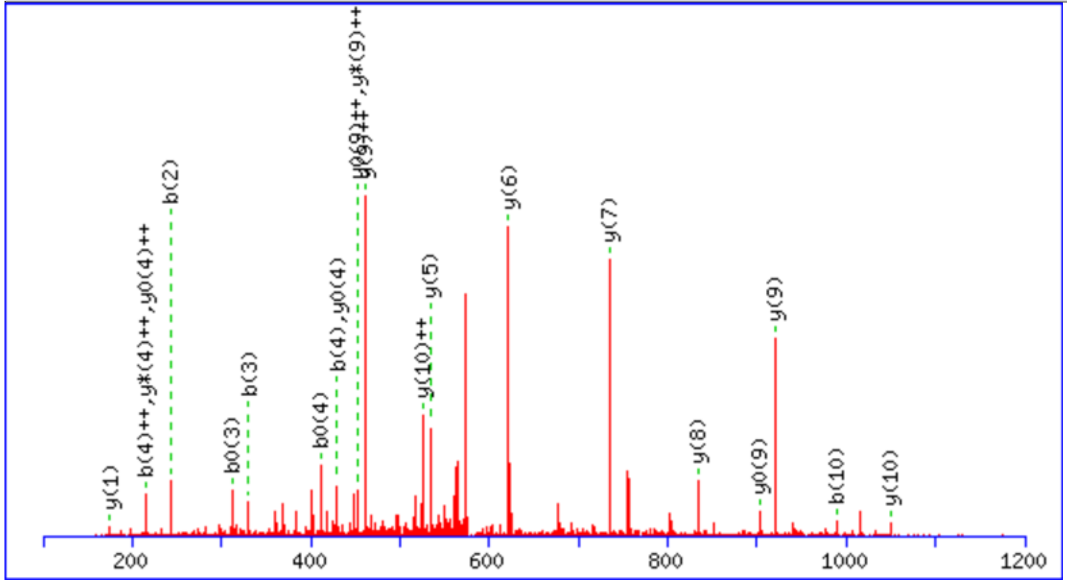
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 42 - OPD-3 **Fraction:** OPD-3

Match to Query 5239: 1161.635248 from(581.824900,2+)

Title: OECHL100317_33.5675.5675.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_33.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 50 **Expect:** 0.00067**Matches :** 22/94 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	114.091340	57.549308					**I**						
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637
3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340
4	**429.234375**	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087
7	716.382495	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073
8	803.414523	402.210899			785.403958	393.205617	**S**	447.267407	224.137342	430.240858	215.624067	429.256842	215.132059
9	860.435987	430.721632			842.425422	421.716349	**G**	360.235379	180.621328	343.208830	172.108053		
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321		
11							**R**	***175.118952***	88.063114	158.092403	79.549840		

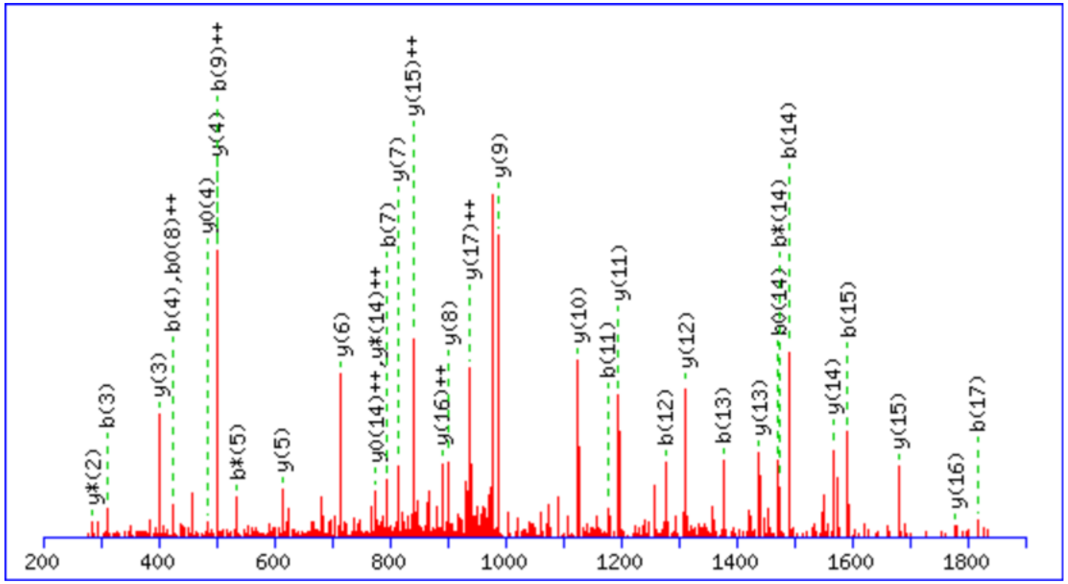


Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 14441: 1990.024248 from(996.019400,2+)
Title: OECHL100317_31.9739.9739.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 92 **Expect:** 8e-008**Matches :** 35/186 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}
1	115.050203	58.028740	98.023654	49.515465			N						
2	212.102967	106.555121	195.076418	98.041847			P	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.9921
3	**311.171381**	156.089328	294.144832	147.576054			V	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.4657
4	**424.255445**	212.631361	407.228896	204.118086			L	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.9315
5	552.314023	276.660650	535.287474	268.147375			Q	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.3895
6	680.372601	340.689939	663.346052	332.176664			Q	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.3602
7	**795.399544**	398.203410	778.372995	389.690136	777.388979	389.198128	D	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.3309
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	A	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.8174
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	H	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.2989
10	1090.527598	545.767437	1073.501049	537.254163	1072.517033	536.762155	S	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.7694
11	**1177.559626**	589.283451	1160.533077	580.770177	1159.549061	580.278169	S	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.2534
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	V	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.7374
13	**1377.675719**	689.341498	1360.649170	680.828223	1359.665154	680.336215	T	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.2032
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	I	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.6793
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	T	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.1373
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	P	***400.230294***	200.618785	383.203745	192.105510		
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	Q	303.177530	152.092403	286.150981	143.579128		
18							R	175.118952	88.063114	158.092403	79.549839		



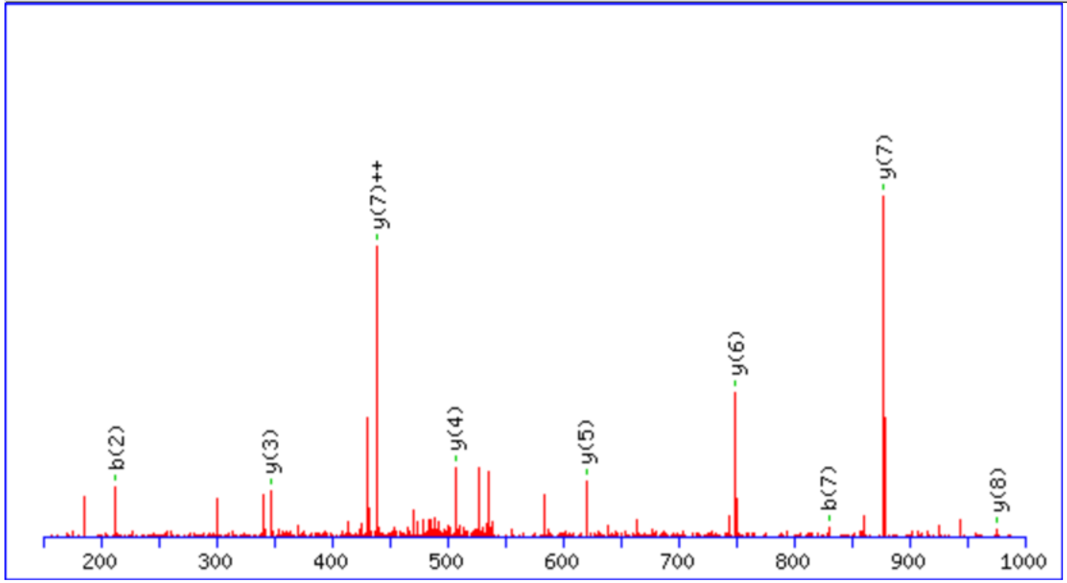
Peptide View

MS/MS Fragmentation of **LVQELCSLK**
Found in **IPI00018275**, Tax_Id=9606 Gene_Symbol=PRND Prion-like protein doppel
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 4974: 1088.588248 from(545.301400,2+)
Title: OECHL100317_31.11553.11553.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1088.589966**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58 **Expect:** 0.00011**Matches :** 9/82 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							9
2	**213.159754**	107.083515					V	***976.513194***	488.760235	959.486645	480.246961	958.502629	479.754953	8
3	341.218332	171.112804	324.191783	162.599529			Q	***877.444780***	439.226028	860.418231	430.712754	859.434215	430.220746	7
4	470.260925	235.634100	453.234376	227.120826	452.250360	226.628818	E	***749.386202***	375.196739	732.359653	366.683465	731.375637	366.191457	6
5	583.344989	292.176133	566.318440	283.662858	565.334424	283.170850	L	***620.343609***	310.675443	603.317060	302.162168	602.333044	301.670160	5

6	743.375638	372.191457	726.349089	363.678183	725.365073	363.186175	**C**	***507.259545***	254.133410	490.232996	245.620136	489.248980	245.128128	**4**
7	**830.407666**	415.707471	813.381117	407.194197	812.397101	406.702189	**S**	***347.228896***	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
8	943.491730	472.249503	926.465181	463.736229	925.481165	463.244221	**L**	260.196868	130.602072	243.170319	122.088797			**2**
9							**K**	147.112804	74.060040	130.086255	65.546765			**1**



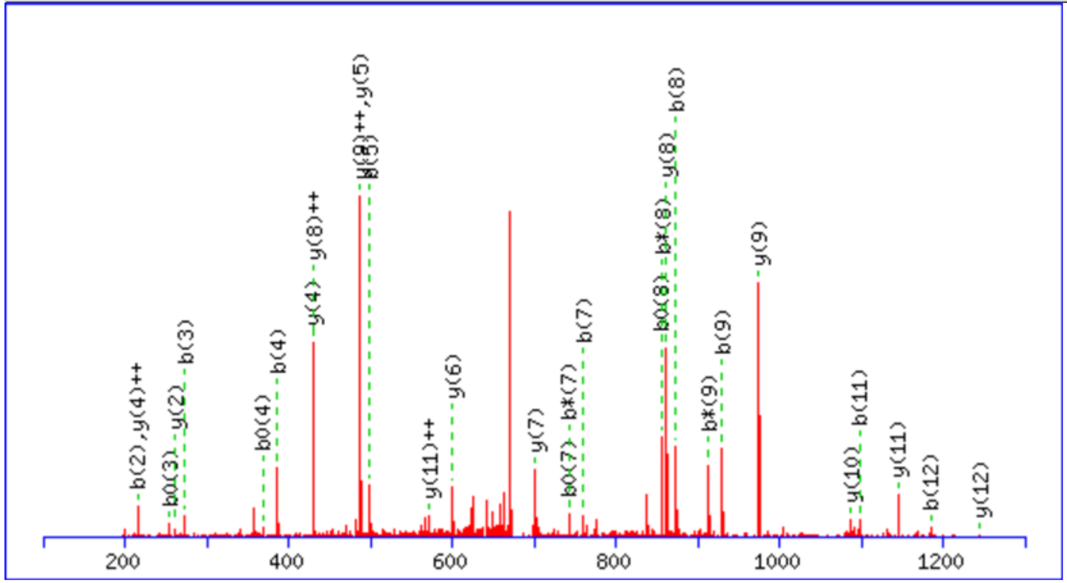
Peptide View

MS/MS Fragmentation of **NTGIICTIGPASR**
Found in **IPI00220644**, Tax_Id=9606 Gene_Symbol=PKM2 Isoform M1 of Pyruvate kinase isozymes M1/M2
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 9060: 1358.696048 from(680.355300,2+)
Title: OECHL100317_31.11775.11775.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1358.697632**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 80 **Expect:** 1.5e-006**Matches :** 30/140 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	115.050203	58.028740	98.023654	49.515465			**N**						

2	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	**T**	***1245.661985***	623.334631	1228.635436	614.821356	1227.651420	614.3293
3	**273.119346**	137.063311	256.092797	128.550037	255.108781	128.058029	**G**	***1144.614306***	572.810791	1127.587757	564.297517	1126.603741	563.8055
4	**386.203410**	193.605343	369.176861	185.092069	368.192845	184.600061	**I**	***1087.592842***	544.300059	1070.566293	535.786785	1069.582277	535.2947
5	**499.287474**	250.147375	482.260925	241.634101	481.276909	241.142093	**I**	***974.508778***	487.758027	957.482229	479.244753	956.498213	478.7527
6	659.318123	330.162700	642.291574	321.649425	641.307558	321.157417	**C**	***861.424714***	431.215995	844.398165	422.702721	843.414149	422.2107
7	**760.365802**	380.686539	743.339253	372.173265	742.355237	371.681257	**T**	***701.394065***	351.200671	684.367516	342.687396	683.383500	342.1953
8	**873.449866**	437.228571	856.423317	428.715297	855.439301	428.223289	**I**	***600.346386***	300.676831	583.319837	292.163557	582.335821	291.6715
9	**930.471330**	465.739303	913.444781	457.226029	912.460765	456.734021	**G**	***487.262322***	244.134799	470.235773	235.621524	469.251757	235.1295
10	1027.524094	514.265685	1010.497545	505.752411	1009.513529	505.260403	**P**	***430.240858***	215.624067	413.214309	207.110792	412.230293	206.6187
11	**1098.561208**	549.784242	1081.534659	541.270968	1080.550643	540.778960	**A**	333.188094	167.097685	316.161545	158.584410	315.177529	158.0924
12	**1185.593236**	593.300256	1168.566687	584.786982	1167.582671	584.294974	**S**	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.5738
13							**R**	175.118952	88.063114	158.092403	79.549839		



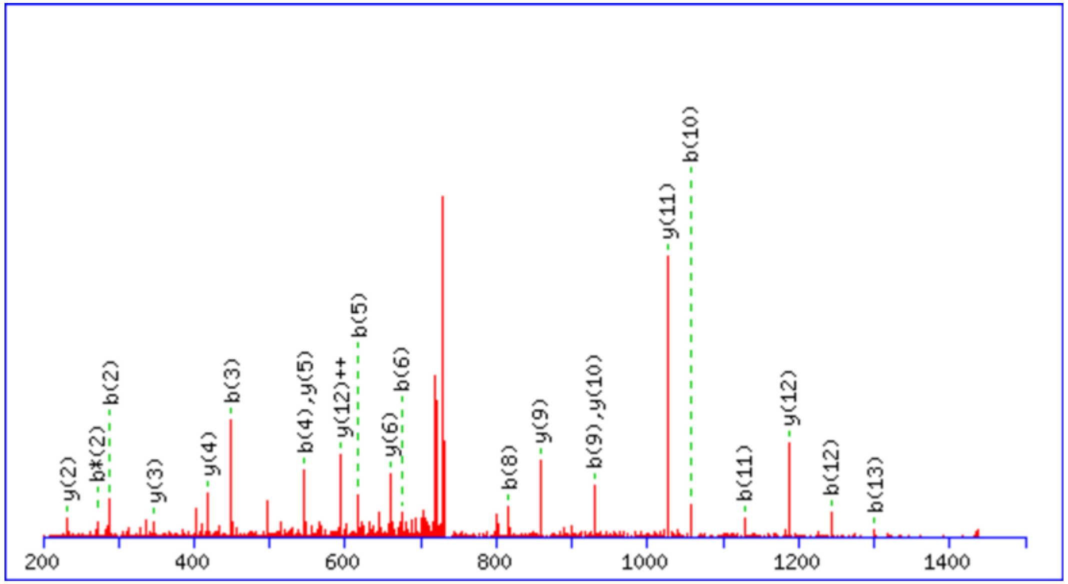
Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**

Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 10230: 1473.645248 from(737.829900,2+)
Title: OECHL100317_31.7372.7372.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 79 **Expect:** 5.6e-007**Matches :** 22/128 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}
1	161.037925	81.022600					**C**						
2	***289.096503***	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.8093
3	***449.127152***	225.067214	432.100603	216.553940			**C**	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.7800
4	***546.179916***	273.593596	529.153367	265.080322			**P**	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.7646
5	***617.217030***	309.112153	600.190481	300.598879			**A**	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.2383
6	***674.238494***	337.622885	657.211945	329.109611			**G**	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.7197
7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.2090
8	***816.312722***	408.659999	799.286173	400.146725			**A**	730.384229	365.695753	713.357680	357.182478	712.373664	356.6904
9	***929.396786***	465.202031	912.370237	456.688757			**L**	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.1719
10	***1057.455364***	529.231320	1040.428815	520.718046			**Q**	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.6298
11	***1128.492478***	564.749877	1111.465929	556.236603			**A**	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.6005
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	**347.167359**	174.087317	330.140810	165.574043	329.156794	165.0820
13	***1300.540885***	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	**232.140416**	116.573846	215.113867	108.060571		
14							**R**	175.118952	88.063114	158.092403	79.549839		



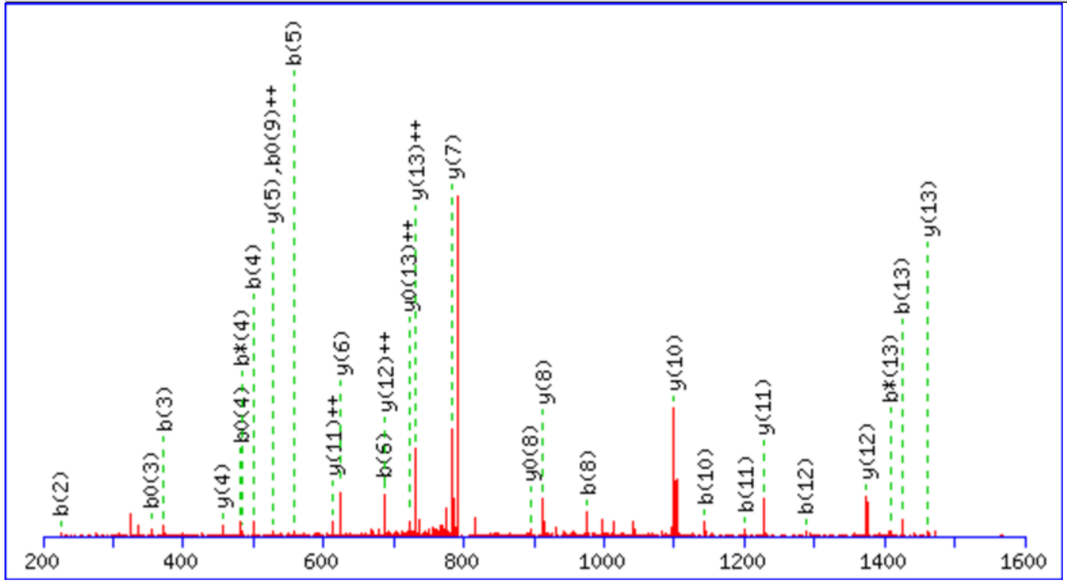
Peptide View

MS/MS Fragmentation of **HSFKGEECPAGSHR**
Found in **IPI00021970**, Tax_Id=9606 Gene_Symbol=MGC31957;TNFRSF10C TNFRSF10C protein
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 11542: 1597.705248 from(799.859900,2+)
Title: OECHL100317_31.2235.2235.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1597.705566**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 70 **Expect:** 6.9e-006**Matches :** 29/144 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	138.066188	69.536732					**H**						
2	***225.098216***	113.052746			207.087651	104.047463	**S**	***1461.653938***	731.330607	1444.627389	722.817333	1443.643373	722.3253
3	***372.166630***	186.586953			354.156065	177.581671	**F**	***1374.621910***	687.814593	1357.595361	679.301319	1356.611345	678.8093
4	***500.261593***	250.634435	483.235044	242.121160	482.251028	241.629152	**K**	***1227.553496***	614.280386	1210.526947	605.767112	1209.542931	605.2751
5	***557.283057***	279.145167	540.256508	270.631892	539.272492	270.139884	**G**	***1099.458533***	550.232905	1082.431984	541.719630	1081.447968	541.2276

6	**686.325650**	343.666463	669.299101	335.153189	668.315085	334.661181	**E**	1042.437069	521.722173	1025.410520	513.208898	1024.426504	512.7168
7	815.368243	408.187760	798.341694	399.674485	797.357678	399.182477	**E**	**913.394476**	457.200876	896.367927	448.687602	895.383911	448.1955
8	**975.398892**	488.203084	958.372343	479.689810	957.388327	479.197802	**C**	**784.351883**	392.679580	767.325334	384.166305	766.341318	383.6742
9	1072.451656	536.729466	1055.425107	528.216192	1054.441091	527.724184	**P**	**624.321234**	312.664255	607.294685	304.150981	606.310669	303.6589
10	**1143.488770**	572.248023	1126.462221	563.734749	1125.478205	563.242741	**A**	**527.268470**	264.137873	510.241921	255.624598	509.257905	255.1325
11	**1200.510234**	600.758755	1183.483685	592.245481	1182.499669	591.753473	**G**	**456.231356**	228.619316	439.204807	220.106041	438.220791	219.6140
12	**1287.542262**	644.274769	1270.515713	635.761495	1269.531697	635.269487	**S**	399.209892	200.108584	382.183343	191.595309	381.199327	191.1033
13	**1424.601174**	712.804225	1407.574625	704.290951	1406.590609	703.798943	**H**	312.177864	156.592570	295.151315	148.079295		
14							**R**	175.118952	88.063114	158.092403	79.549839		



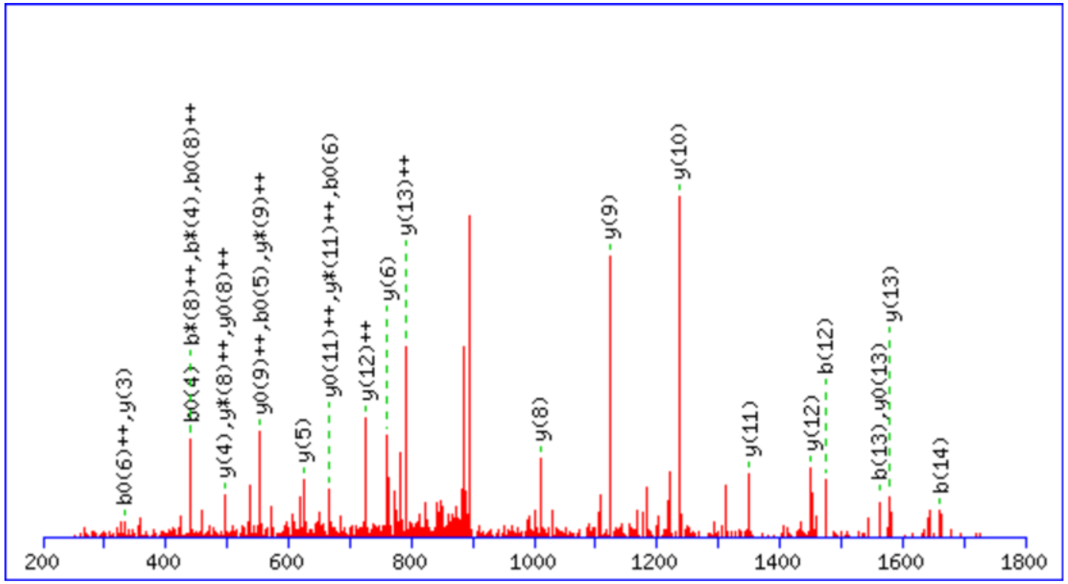
Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 13373: 1805.932848 from(903.973700,2+)

Title: OECHL100317_31.19372.19372.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 74 **Expect:** 4.9e-006**Matches :** 29/160 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	115.050203	58.028740	98.023654	49.515465			**N**						
2	228.134267	114.570771	211.107718	106.057497			**I**	1692.895549	846.951413	1675.869000	838.438138	1674.884984	837.9461
3	357.176860	179.092068	340.150311	170.578793	339.166295	170.086785	**E**	***1579.811485***	790.409381	1562.784936	781.896106	1561.800920	781.4040
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	**T**	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.8828
5	571.308603	286.157940	554.282054	277.644665	553.298038	277.152657	**I**	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.3589
6	684.392667	342.699972	667.366118	334.186697	666.382102	333.694689	**I**	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.8169
7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	**N**	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.2748
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	**T**	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.2534
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	**F**	908.462479	454.734878	891.435930	446.221603	890.451914	445.7295
10	1183.610599	592.308938	1166.584050	583.795663	1165.600034	583.303655	**H**	***761.394065***	381.200671	744.367516	372.687396	743.383500	372.1953
11	1311.669177	656.338227	1294.642628	647.824952	1293.658612	647.332944	**Q**	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.6659
12	**1474.732506**	737.869891	1457.705957	729.356617	1456.721941	728.864609	**Y**	***496.276575***	248.641926	479.250026	240.128651	478.266010	239.6366
13	**1561.764534**	781.385905	1544.737985	772.872631	1543.753969	772.380623	**S**	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.1049
14	**1660.832948**	830.920112	1643.806399	822.406838	1642.822383	821.914830	**V**	246.181218	123.594247	229.154669	115.080973		
15							**K**	147.112804	74.060040	130.086255	65.546765		



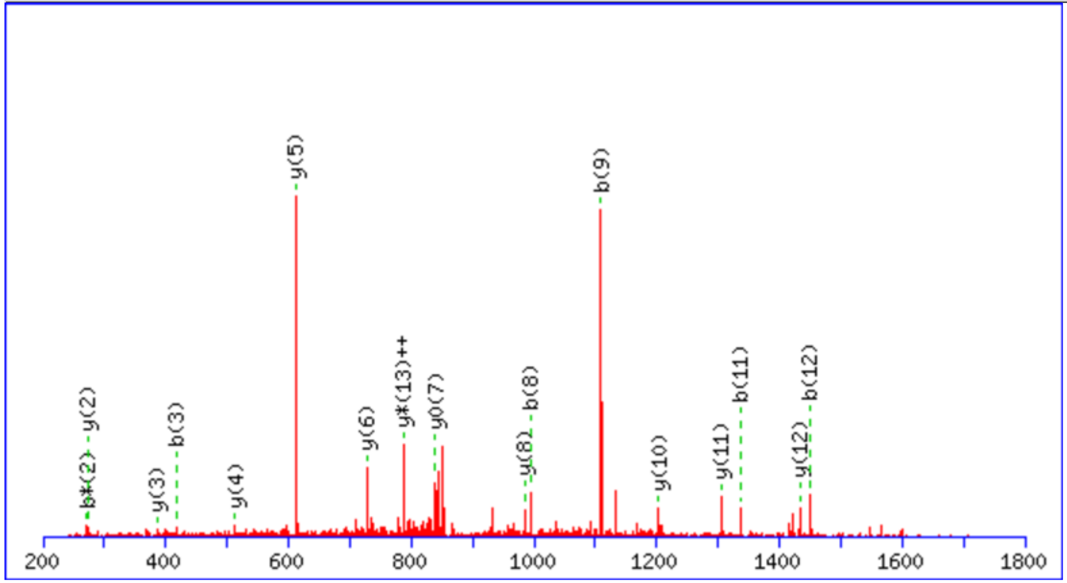
Peptide View

MS/MS Fragmentation of **MRETAFEEDVQLPR**
Found in **IPI00008239**, Tax_Id=9606 Gene_Symbol=GPRC5B cDNA FLJ55176, highly similar to G-protein coupled receptor family C group 5 member B
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 12772: 1719.826048 from(860.920300,2+)
Title: OECHL100317_31.14388.14388.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1719.824997**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60 **Expect:** 0.00014**Matches :** 17/140 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	132.047761	66.527518					**M**						
2	288.148872	144.578074	271.122323	136.064799			**R**	1589.791812	795.399544	1572.765263	786.886270	1571.781247	786.3942
3	**417.191465**	209.099370	400.164916	200.586096	399.180900	200.094088	**E**	***1433.690701***	717.348989	1416.664152	708.835714	1415.680136	708.3437
4	518.239144	259.623210	501.212595	251.109936	500.228579	250.617928	**T**	***1304.648108***	652.827692	1287.621559	644.314417	1286.637543	643.8224
5	589.276258	295.141767	572.249709	286.628492	571.265693	286.136484	**A**	***1203.600429***	602.303852	1186.573880	593.790578	1185.589864	593.2985

6	736.344672	368.675974	719.318123	360.162699	718.334107	359.670691	**F**	1132.563315	566.785296	1115.536766	558.272021	1114.552750	557.7800
7	865.387265	433.197271	848.360716	424.683996	847.376700	424.191988	**E**	***985.494901***	493.251089	968.468352	484.737814	967.484336	484.2458
8	**994.429858**	497.718567	977.403309	489.205292	976.419293	488.713284	**E**	856.452308	428.729792	839.425759	420.216518	838.441743	419.7245
9	**1109.456801**	555.232039	1092.430252	546.718764	1091.446236	546.226756	**D**	***727.409715***	364.208496	710.383166	355.695221	709.399150	355.2032
10	1208.525215	604.766246	1191.498666	596.252971	1190.514650	595.760963	**V**	***612.382772***	306.695024	595.356223	298.181749		
11	**1336.583793**	668.795535	1319.557244	660.282260	1318.573228	659.790252	**Q**	***513.314358***	257.160817	496.287809	248.647542		
12	**1449.667857**	725.337566	1432.641308	716.824292	1431.657292	716.332284	**L**	***385.255780***	193.131528	368.229231	184.618253		
13	1546.720621	773.863948	1529.694072	765.350674	1528.710056	764.858666	**P**	***272.171716***	136.589496	255.145167	128.076221		
14							**R**	175.118952	88.063114	158.092403	79.549839		



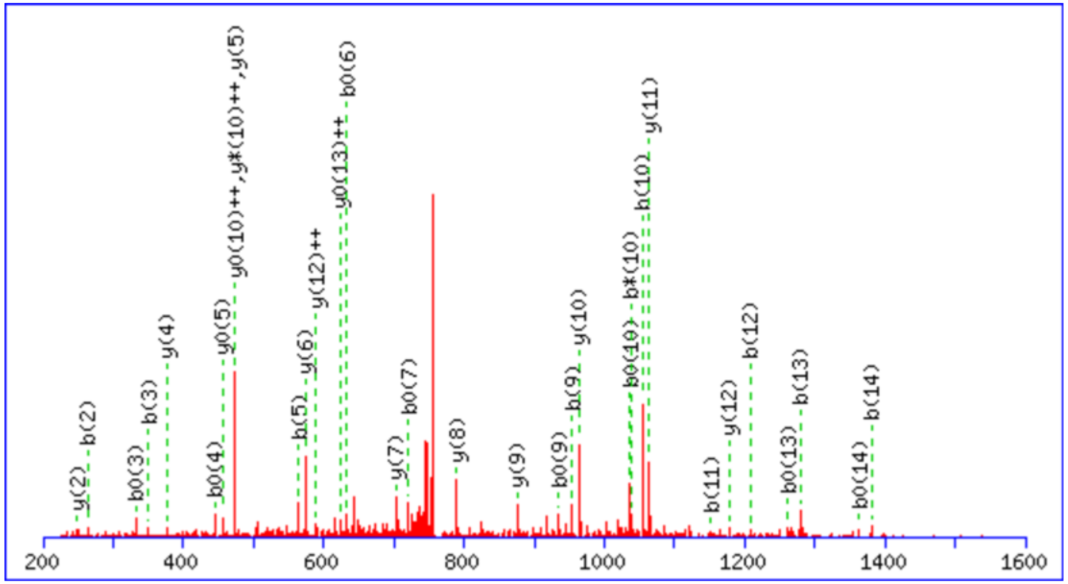
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 10779: 1525.727048 from(763.870800,2+)

Title: OECHL100317_31.10602.10602.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 64 **Expect:** 4.2e-005**Matches :** 33/150 fragment ions using 63 most intense peaks (help)

#	**b**	**b^{++}**	**b***	**b*$^{++}$**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y*$^{++}$**	**y^{0}**	**y^{0++}**
1	116.034219	58.520748			98.023654	49.515465	**D**						
2	***263.102633***	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.3515
3	***350.134661***	175.570968			332.124096	166.565686	**S**	1264.637937	632.822607	1247.611388	624.309332	1246.627372	623.8173
4	463.218725	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.3013
5	***564.266404***	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.7592
6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.2354
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.7194
8	825.362488	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.2034
9	***953.421066***	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.6873
10	***1054.468745***	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.6581
11	***1151.521509***	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.1342
12	***1208.542973***	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.6078
13	***1279.580087***	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	319.197597	160.102436	302.171048	151.589162	301.187032	151.0971
14	***1380.627766***	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.5785
15							**K**	147.112804	74.060040	130.086255	65.546765		



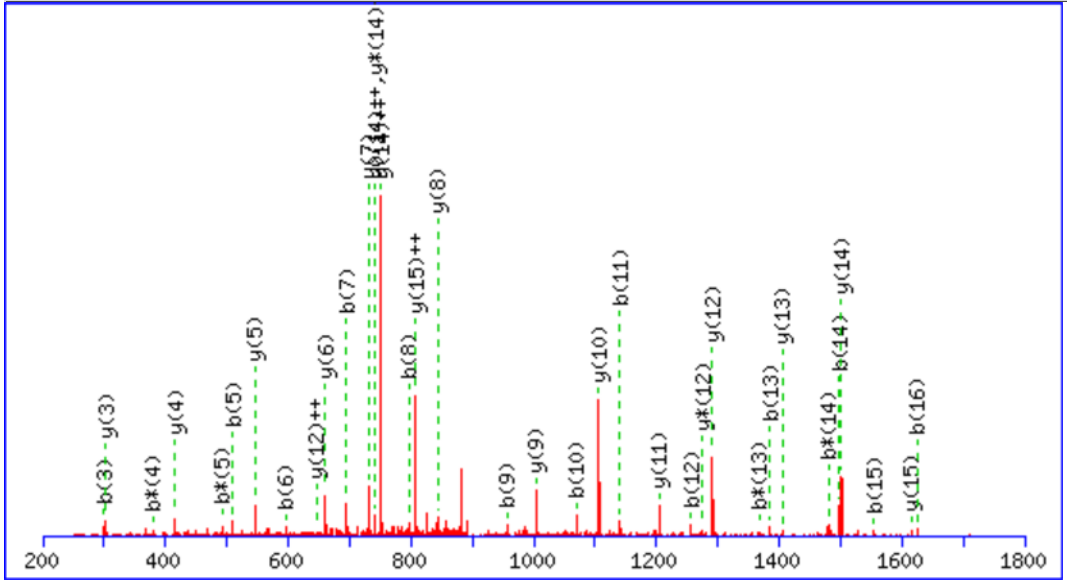
Peptide View

MS/MS Fragmentation of **GQLPISVTCIADEIGAR**
Found in **IPI00240345**, Tax_Id=9606 Gene_Symbol=CLEC14A C-type lectin domain family 14 member A
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 13326: 1798.926448 from(900.470500,2+)
Title: OECHL100317_31.19505.19505.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1798.924728**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 86 **Expect:** 3e-007**Matches :** 36/172 fragment ions using 71 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	58.028740	29.518008					G						
2	186.087318	93.547297	169.060769	85.034023			Q	1742.910548	871.958912	1725.883999	863.445638	1724.899983	862.9536
3	***299.171382***	150.089329	282.144833	141.576055			L	***1614.851970***	807.929623	1597.825421	799.416349	1596.841405	798.9243
4	396.224146	198.615711	379.197597	190.102436			P	***1501.767906***	751.387591	1484.741357	742.874317	1483.757341	742.3823
5	***509.308210***	255.157743	492.281661	246.644468			I	***1404.715142***	702.861209	1387.688593	694.347935	1386.704577	693.8559

6	***596.340238***	298.673757	579.313689	290.160483	578.329673	289.668475	**S**	***1291.631078***	646.319177	1274.604529	637.805903	1273.620513	637.3138
7	***695.408652***	348.207964	678.382103	339.694689	677.398087	339.202681	**V**	***1204.599050***	602.803163	1187.572501	594.289889	1186.588485	593.7978
8	***796.456331***	398.731804	779.429782	390.218529	778.445766	389.726521	**T**	***1105.530636***	553.268956	1088.504087	544.755682	1087.520071	544.2636
9	***956.486980***	478.747128	939.460431	470.233854	938.476415	469.741846	**C**	***1004.482957***	502.745117	987.456408	494.231842	986.472392	493.7398
10	***1069.571044***	535.289160	1052.544495	526.775886	1051.560479	526.283878	**I**	***844.452308***	422.729792	827.425759	414.216518	826.441743	413.7245
11	***1140.608158***	570.807717	1123.581609	562.294443	1122.597593	561.802435	**A**	***731.368244***	366.187760	714.341695	357.674486	713.357679	357.1824
12	***1255.635101***	628.321189	1238.608552	619.807914	1237.624536	619.315906	**D**	***660.331130***	330.669203	643.304581	322.155929	642.320565	321.6639
13	***1384.677694***	692.842485	1367.651145	684.329211	1366.667129	683.837203	**E**	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.1504
14	***1497.761758***	749.384517	1480.735209	740.871243	1479.751193	740.379235	**I**	***416.261594***	208.634435	399.235045	200.121160		
15	***1554.783222***	777.895249	1537.756673	769.381975	1536.772657	768.889967	**G**	***303.177530***	152.092403	286.150981	143.579128		
16	***1625.820336***	813.413806	1608.793787	804.900532	1607.809771	804.408524	**A**	246.156066	123.581671	229.129517	115.068396		
17							**R**	175.118952	88.063114	158.092403	79.549839		



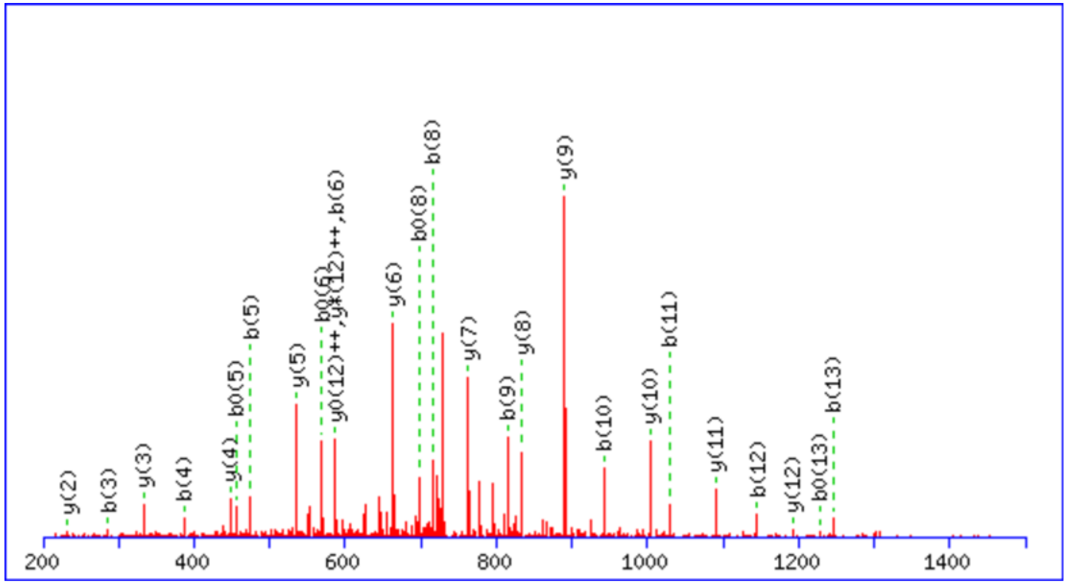
Peptide View

MS/MS Fragmentation of **GLDTSLGAVQSDTGR**

Found in **IPI00289931**, Tax_Id=9606 Gene_Symbol=MADCAM1 MADCAM1 protein
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 10256: 1475.721448 from(738.868000,2+)
Title: OECHL100317_31.11178.11178.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1475.721619**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 85 **Expect:** 4.1e-007**Matches :** 27/142 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	58.028740	29.518008					**G**						
2	171.112804	86.060040					**L**	1419.707414	710.357345	1402.680865	701.844071	1401.696849	701.3520
3	**286.139747**	143.573512			268.129182	134.568229	**D**	1306.623350	653.815313	1289.596801	645.302039	1288.612785	644.8100
4	**387.187426**	194.097351			369.176861	185.092069	**T**	***1191.596407***	596.301842	1174.569858	587.788567	1173.585842	587.2965
5	**474.219454**	237.613365			456.208889	228.608082	**S**	***1090.548728***	545.778002	1073.522179	537.264728	1072.538163	536.7727
6	**587.303518**	294.155397			569.292953	285.150115	**L**	***1003.516700***	502.261988	986.490151	493.748714	985.506135	493.2567
7	644.324982	322.666129			626.314417	313.660847	**G**	***890.432636***	445.719956	873.406087	437.206682	872.422071	436.7146
8	**715.362096**	358.184686			697.351531	349.179404	**A**	***833.411172***	417.209224	816.384623	408.695950	815.400607	408.2039
9	**814.430510**	407.718893			796.419945	398.713611	**V**	***762.374058***	381.690667	745.347509	373.177393	744.363493	372.6853
10	**942.489088**	471.748182	925.462539	463.234908	924.478523	462.742900	**Q**	***663.305644***	332.156460	646.279095	323.643186	645.295079	323.1511
11	**1029.521116**	515.264196	1012.494567	506.750922	1011.510551	506.258914	**S**	***535.247066***	268.127171	518.220517	259.613897	517.236501	259.1218
12	**1144.548059**	572.777668	1127.521510	564.264393	1126.537494	563.772385	**D**	***448.215038***	224.611157	431.188489	216.097882	430.204473	215.6058
13	**1245.595738**	623.301507	1228.569189	614.788233	1227.585173	614.296225	**T**	***333.188095***	167.097685	316.161546	158.584411	315.177530	158.0924
14	1302.617202	651.812239	1285.590653	643.298965	1284.606637	642.806957	**G**	***232.140416***	116.573846	215.113867	108.060571		
15							**R**	175.118952	88.063114	158.092403	79.549839		



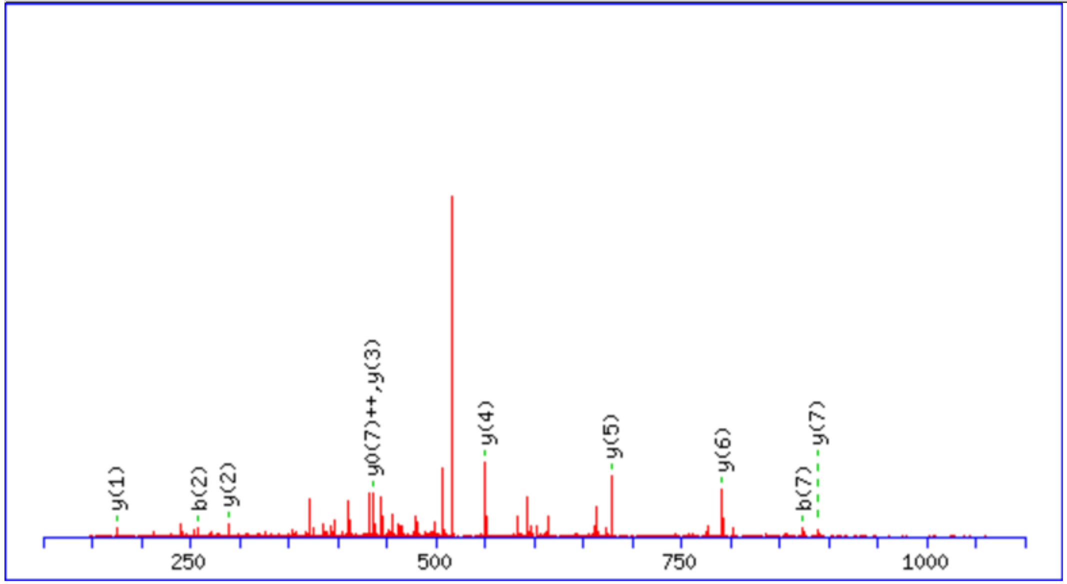
Peptide View

MS/MS Fragmentation of **CPLQDFLR**
Found in **IPI00003807**, Tax_Id=9606 Gene_Symbol=ACP2 Lysosomal acid phosphatase
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 4474: 1047.516648 from(524.765600,2+)
Title: OECHL100317_31.16667.16667.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1047.517151**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53 **Expect:** 0.00044**Matches :** 10/64 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	161.037925	81.022600					**C**							**8**
2	**258.090689**	129.548982					**P**	***888.493779***	444.750528	871.467230	436.237253	870.483214	435.745245	**7**
3	371.174753	186.091015					**L**	***791.441015***	396.224146	774.414466	387.710871	773.430450	387.218863	**6**
4	499.233331	250.120304	482.206782	241.607029			**Q**	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	**5**
5	614.260274	307.633775	597.233725	299.120501	596.249709	298.628493	**D**	***550.298373***	275.652825	533.271824	267.139550	532.287808	266.647542	**4**

6	761.328688	381.167982	744.302139	372.654708	743.318123	372.162700	**F**	***435.271430***	218.139353	418.244881	209.626079			**3**
7	**874.412752**	437.710014	857.386203	429.196740	856.402187	428.704732	**L**	***288.203016***	144.605146	271.176467	136.091872			**2**
8							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



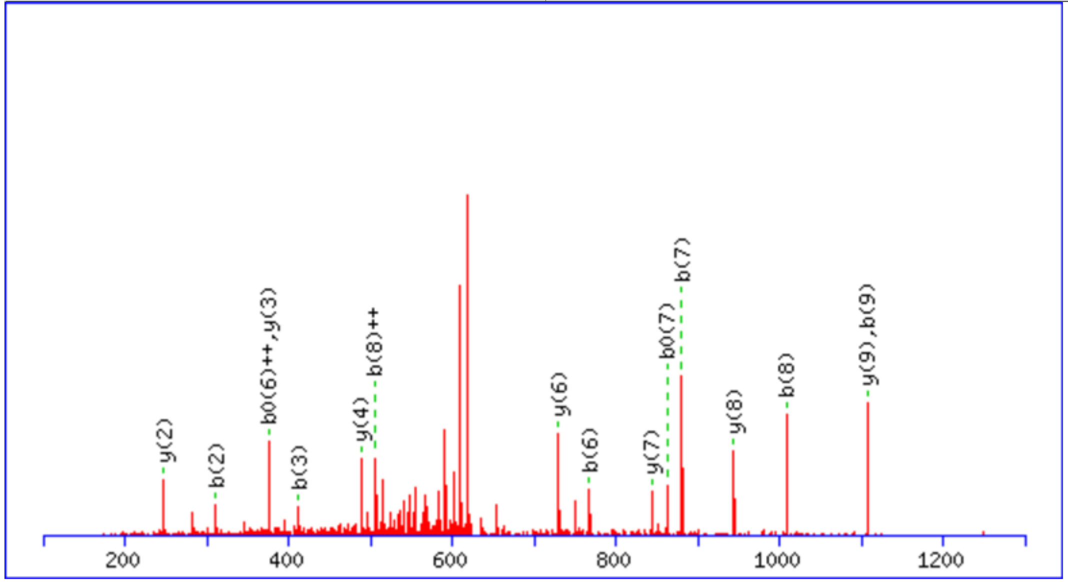
Peptide View

MS/MS Fragmentation of **FYTIEILKVE**
Found in **IPI00022974**, Tax_Id=9606 Gene_Symbol=PIP Prolactin-inducible protein
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 7872: 1253.691648 from(627.853100,2+)
Title: OECHL100317_31.19121.19121.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1253.690720**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54 **Expect:** 0.00025**Matches :** 16/86 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	148.075690	74.541483					**F**						
2	**311.139019**	156.073148					**Y**	***1107.629604***	554.318440	1090.603055	545.805166	1089.619039	545.3131

3	**412.186698**	206.596987			394.176133	197.591705	T	***944.566275***	472.786776	927.539726	464.273501	926.555710	463.7814
4	525.270762	263.139019			507.260197	254.133737	I	***843.518596***	422.262936	826.492047	413.749662	825.508031	413.2576
5	654.313355	327.660316			636.302790	318.655033	E	***730.434532***	365.720904	713.407983	357.207630	712.423967	356.7156
6	**767.397419**	384.202348			749.386854	375.197065	I	601.391939	301.199608	584.365390	292.686333	583.381374	292.1943
7	**880.481483**	440.744380			862.470918	431.739097	L	***488.307875***	244.657576	471.281326	236.144301	470.297310	235.6522
8	**1008.576446**	504.791861	991.549897	496.278587	990.565881	495.786579	K	***375.223811***	188.115544	358.197262	179.602269	357.213246	179.1102
9	**1107.644860**	554.326068	1090.618311	545.812794	1089.634295	545.320786	V	***247.128848***	124.068062			229.118283	115.0627
10							E	148.060434	74.533855			130.049869	65.5285



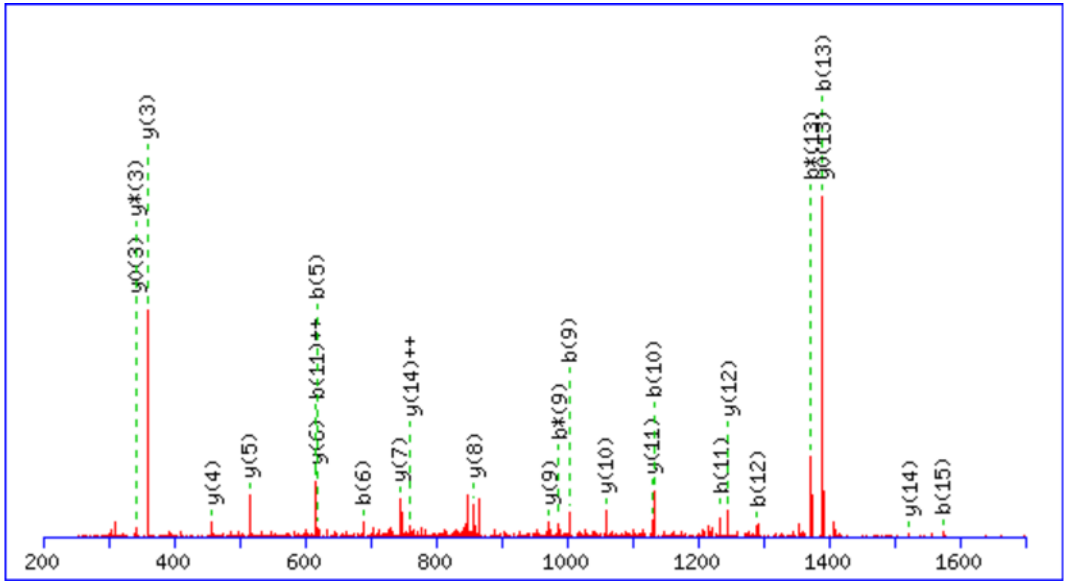
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 12970: 1746.917448 from(874.466000,2+)
Title: OECHL100317_31.16755.16755.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 75 **Expect:** 3e-006**Matches :** 26/156 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	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018
6	**689.386854**	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							**R**	175.118952	88.063114	158.092403	79.549839		



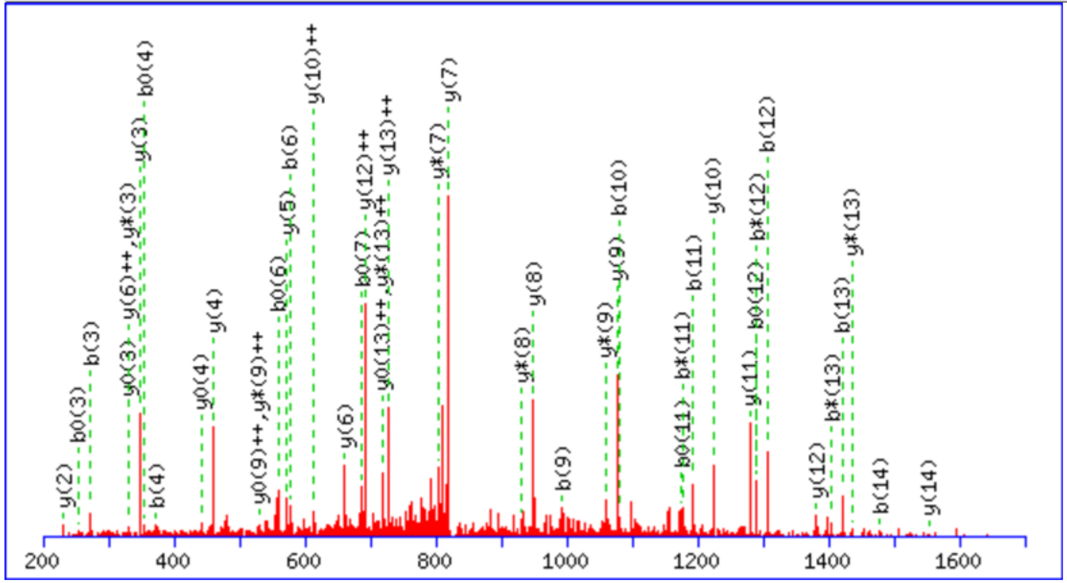
Peptide View

MS/MS Fragmentation of **VTATGFQQCSLIDGR**
Found in **IPI00333140**, Tax_Id=9606 Gene_Symbol=DNER Delta and Notch-like epidermal growth factor-related receptor
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 12182: 1651.799848 from(826.907200,2+)
Title: OECHL100317_31.13606.13606.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1651.798828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 72 **Expect:** 8.3e-006**Matches :** 45/150 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	100.075690	50.541483					**V**						
2	201.123369	101.065322			183.112804	92.060040	**T**	***1553.737670***	777.372473	1536.711121	768.859198	1535.727105	768.3671
3	**272.160483**	136.583879			254.149918	127.578597	**A**	1452.689991	726.848633	1435.663442	718.335359	1434.679426	717.8433
4	**373.208162**	187.107719			355.197597	178.102437	**T**	***1381.652877***	691.330076	1364.626328	682.816802	1363.642312	682.3247
5	430.229626	215.618451			412.219061	206.613169	**G**	***1280.605198***	640.806237	1263.578649	632.292962	1262.594633	631.8009

6	**577.298040**	289.152658			559.287475	280.147376	**F**	***1223.583734***	612.295505	1206.557185	603.782230	1205.573169	603.2902
7	705.356618	353.181947	688.330069	344.668673	687.346053	344.176665	**Q**	***1076.515320***	538.761298	1059.488771	530.248023	1058.504755	529.7560
8	833.415196	417.211236	816.388647	408.697962	815.404631	408.205954	**Q**	***948.456742***	474.732009	931.430193	466.218734	930.446177	465.7267
9	**993.445845**	497.226561	976.419296	488.713286	975.435280	488.221278	**C**	***820.398164***	410.702720	803.371615	402.189445	802.387599	401.6974
10	**1080.477873**	540.742575	1063.451324	532.229300	1062.467308	531.737292	**S**	***660.367515***	330.687395	643.340966	322.174121	642.356950	321.6821
11	**1193.561937**	597.284607	1176.535388	588.771332	1175.551372	588.279324	**L**	***573.335487***	287.171381	556.308938	278.658107	555.324922	278.1660
12	**1306.646001**	653.826638	1289.619452	645.313364	1288.635436	644.821356	**I**	***460.251423***	230.629349	443.224874	222.116075	442.240858	221.6240
13	**1421.672944**	711.340110	1404.646395	702.826836	1403.662379	702.334827	**D**	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.0820
14	**1478.694408**	739.850842	1461.667859	731.337567	1460.683843	730.845559	**G**	***232.140416***	116.573846	215.113867	108.060571		
15							**R**	175.118952	88.063114	158.092403	79.549839		

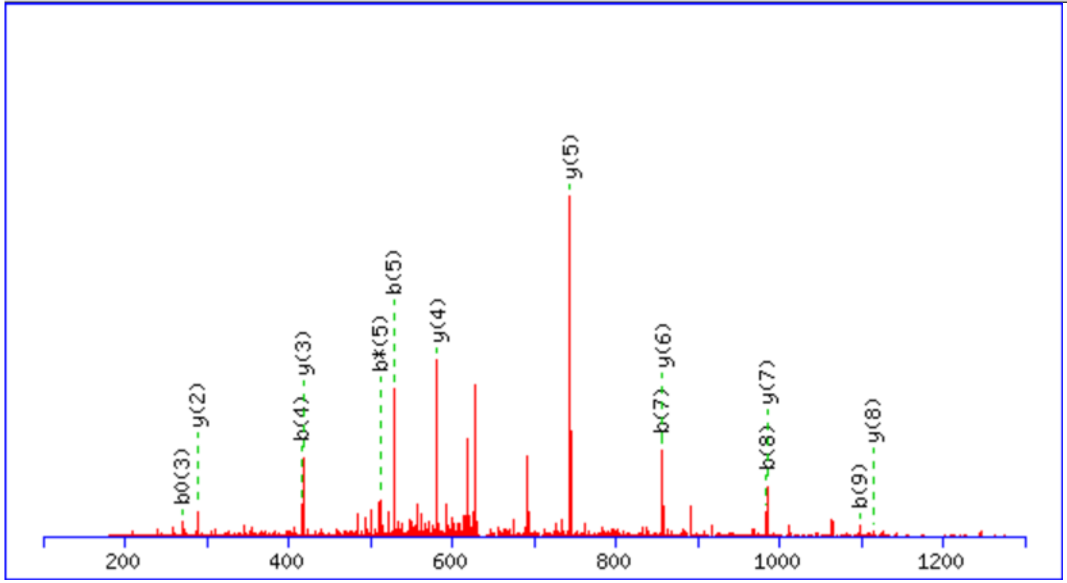


Peptide View

MS/MS Fragmentation of **ASEQIYYENR**
Found in **IPI00030431**, Tax_Id=9606 Gene_Symbol=ANTXR1 Isoform 1 of Anthrax toxin receptor 1
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 8091: 1271.578848 from(636.796700,2+)
Title: OECHL100317_31.7414.7414.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1271.578186**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 51 **Expect:** 0.0004**Matches :** 14/96 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	72.044390	36.525833					A						
2	159.076418	80.041847			141.065853	71.036564	S	1201.548393	601.277835	1184.521844	592.764560	1183.537828	592.2725
3	288.119011	144.563144			270.108446	135.557861	E	***1114.516365***	557.761821	1097.489816	549.248546	1096.505800	548.7565
4	**416.177589**	208.592433	399.151040	200.079158	398.167024	199.587150	Q	***985.473772***	493.240524	968.447223	484.727250	967.463207	484.2352
5	**529.261653**	265.134465	512.235104	256.621190	511.251088	256.129182	I	***857.415194***	429.211235	840.388645	420.697961	839.404629	420.2059
6	692.324982	346.666129	675.298433	338.152855	674.314417	337.660847	Y	***744.331130***	372.669203	727.304581	364.155929	726.320565	363.6639
7	**855.388311**	428.197794	838.361762	419.684519	837.377746	419.192511	Y	***581.267801***	291.137539	564.241252	282.624264	563.257236	282.1322
8	**984.430904**	492.719090	967.404355	484.205816	966.420339	483.713808	E	***418.204472***	209.605874	401.177923	201.092600	400.193907	200.6005
9	**1098.473831**	549.740554	1081.447282	541.227279	1080.463266	540.735271	N	***289.161879***	145.084577	272.135330	136.571303		
10							R	175.118952	88.063114	158.092403	79.549839		

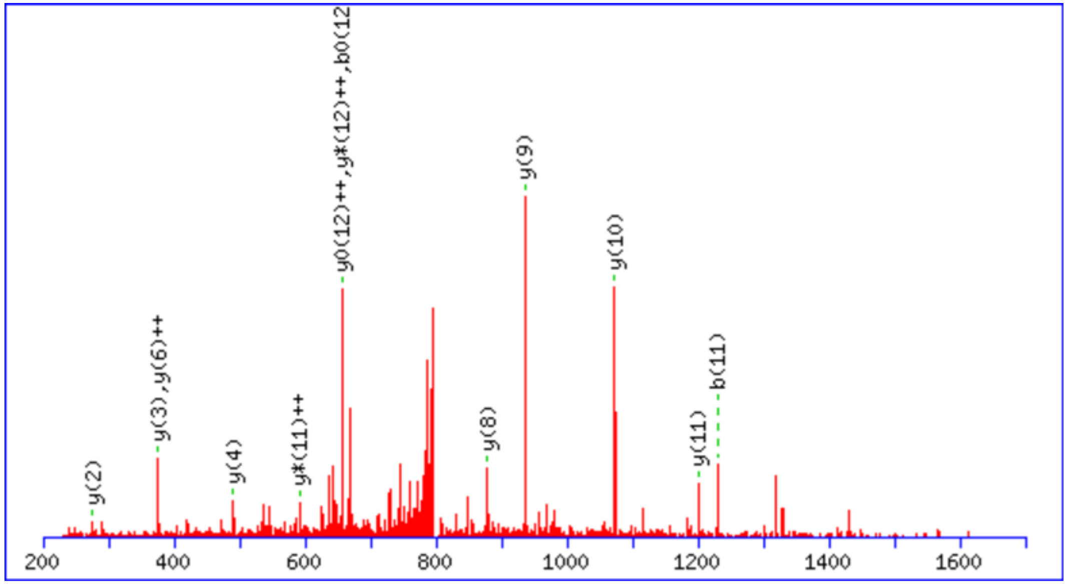


Peptide View

MS/MS Fragmentation of **LYQQHGAGLFDVTR**
Found in **IPI00554538**, Tax_Id=9606 Gene_Symbol=TPP1 Putative uncharacterized protein TPP1
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 11608: 1603.811048 from(802.912800,2+)
Title: OECHL100317_31.13486.13486.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1603.810699**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 51 **Expect:** 0.0011**Matches :** 13/130 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	114.091340	57.549308					L						
2	277.154669	139.080973					Y	1491.733905	746.370591	1474.707356	737.857316	1473.723340	737.3653
3	405.213247	203.110262	388.186698	194.596987			Q	1328.670576	664.838926	1311.644027	656.325652	1310.660011	655.8336
4	533.271825	267.139551	516.245276	258.626276			Q	***1200.611998***	600.809637	1183.585449	592.296363	1182.601433	591.8043
5	670.330737	335.669007	653.304188	327.155732			H	***1072.553420***	536.780348	1055.526871	528.267074	1054.542855	527.7750
6	727.352201	364.179739	710.325652	355.666464			G	***935.494508***	468.250892	918.467959	459.737618	917.483943	459.2456
7	798.389315	399.698296	781.362766	391.185021			A	***878.473044***	439.740160	861.446495	431.226886	860.462479	430.7348
8	855.410779	428.209028	838.384230	419.695753			G	807.435930	404.221603	790.409381	395.708329	789.425365	395.2163
9	968.494843	484.751060	951.468294	476.237785			L	750.414466	375.710871	733.387917	367.197597	732.403901	366.7055
10	1115.563257	558.285267	1098.536708	549.771992			F	637.330402	319.168839	620.303853	310.655565	619.319837	310.1635
11	1230.590200	615.798738	1213.563651	607.285464	1212.579635	606.793456	D	***490.261988***	245.634632	473.235439	237.121358	472.251423	236.6293
12	1329.658614	665.332945	1312.632065	656.819671	1311.648049	656.327663	V	***375.235045***	188.121161	358.208496	179.607886	357.224480	179.1158
13	1430.706293	715.856785	1413.679744	707.343510	1412.695728	706.851502	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.5816
14							R	175.118952	88.063114	158.092403	79.549839		



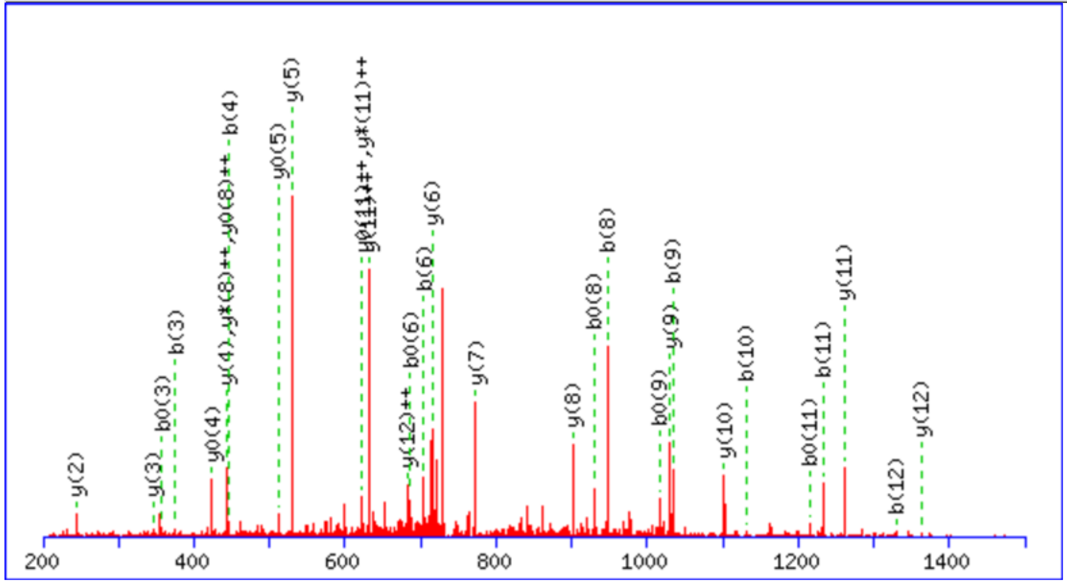
Peptide View

MS/MS Fragmentation of **ITCAEEGWSPTPK**
Found in **IPI00006154**, Tax_Id=9606 Gene_Symbol=CFHR2 Isoform Long of Complement factor H-related protein 2
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 10242: 1474.677248 from(738.345900,2+)
Title: OECHL100317_31.10105.10105.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1474.676224**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 64 **Expect:** 3.8e-005**Matches :** 32/114 fragment ions using 62 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**I**							**13**
2	215.139019	108.073147	197.128454	99.067865	**T**	***1362.599444***	681.803360	1345.572895	673.290086	1344.588879	672.798078	**12**
3	**375.169668**	188.088472	357.159103	179.083190	**C**	***1261.551765***	631.279521	1244.525216	622.766246	1243.541200	622.274238	**11**
4	**446.206782**	223.607029	428.196217	214.601747	**A**	***1101.521116***	551.264196	1084.494567	542.750922	1083.510551	542.258914	**10**
5	575.249375	288.128326	557.238810	279.123043	**E**	***1030.484002***	515.745639	1013.457453	507.232365	1012.473437	506.740357	**9**

6	**704.291968**	352.649622	686.281403	343.644340	**E**	***901.441409***	451.224343	884.414860	442.711068	883.430844	442.219060	**8**
7	761.313432	381.160354	743.302867	372.155072	**G**	***772.398816***	386.703046	755.372267	378.189772	754.388251	377.697764	**7**
8	**947.392745**	474.200011	929.382180	465.194728	**W**	***715.377352***	358.192314	698.350803	349.679040	697.366787	349.187032	**6**
9	**1034.424773**	517.716025	1016.414208	508.710742	**S**	***529.298039***	265.152658	512.271490	256.639383	511.287474	256.147375	**5**
10	**1131.477537**	566.242407	1113.466972	557.237124	**P**	***442.266011***	221.636644	425.239462	213.123369	424.255446	212.631361	**4**
11	**1232.525216**	616.766246	1214.514651	607.760964	**T**	***345.213247***	173.110262	328.186698	164.596987	327.202682	164.104979	**3**
12	**1329.577980**	665.292628	1311.567415	656.287346	**P**	***244.165568***	122.586422	227.139019	114.073148			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**



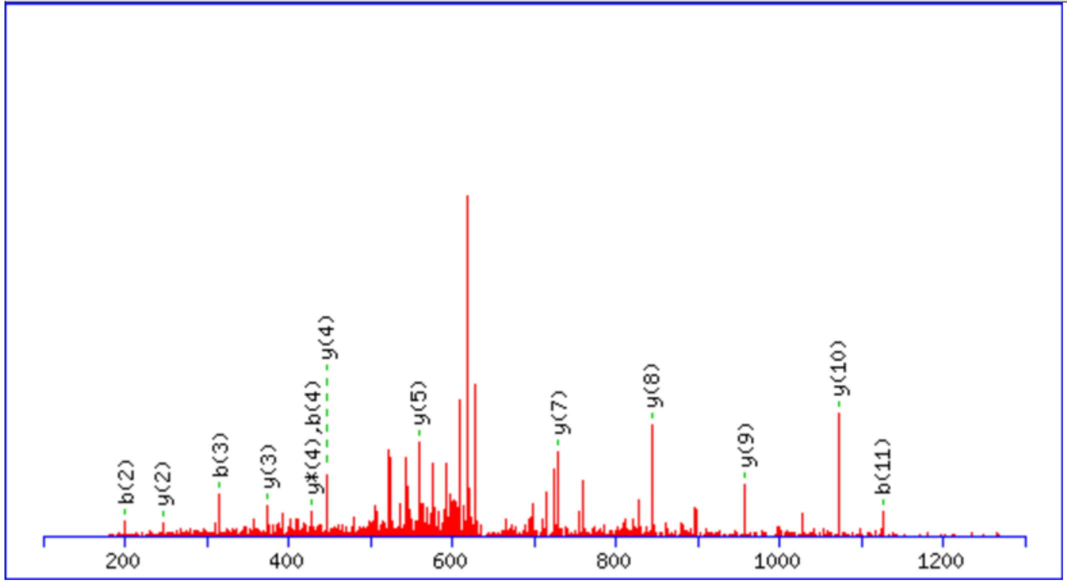
Peptide View

MS/MS Fragmentation of **SLDLDGIIAEVK**
Found in **IPI00306959**, Tax_Id=9606 Gene_Symbol=KRT7 Keratin, type II cytoskeletal 7
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 8105: 1271.696848 from(636.855700,2+)
Title: OECHL100317_31.19355.19355.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1271.697266**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55 **Expect:** 0.00031**Matches :** 13/106 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							12
2	**201.123368**	101.065322	183.112803	92.060039	L	1185.672531	593.339904	1168.645982	584.826629	1167.661966	584.334621	11
3	**316.150311**	158.578793	298.139746	149.573511	D	***1072.588467***	536.797872	1055.561918	528.284597	1054.577902	527.792589	10
4	**429.234375**	215.120826	411.223810	206.115543	L	***957.561524***	479.284400	940.534975	470.771126	939.550959	470.279118	9
5	544.261318	272.634297	526.250753	263.629015	D	***844.477460***	422.742368	827.450911	414.229094	826.466895	413.737086	8
6	601.282782	301.145029	583.272217	292.139747	G	***729.450517***	365.228897	712.423968	356.715622	711.439952	356.223614	7
7	714.366846	357.687061	696.356281	348.681779	I	672.429053	336.718165	655.402504	328.204890	654.418488	327.712882	6
8	827.450910	414.229093	809.440345	405.223811	I	***559.344989***	280.176133	542.318440	271.662858	541.334424	271.170850	5
9	898.488024	449.747650	880.477459	440.742368	A	***446.260925***	223.634101	429.234376	215.120826	428.250360	214.628818	4
10	1027.530617	514.268947	1009.520052	505.263664	E	***375.223811***	188.115544	358.197262	179.602269	357.213246	179.110261	3
11	**1126.599031**	563.803154	1108.588466	554.797871	V	***246.181218***	123.594247	229.154669	115.080973			2
12					K	147.112804	74.060040	130.086255	65.546765			1

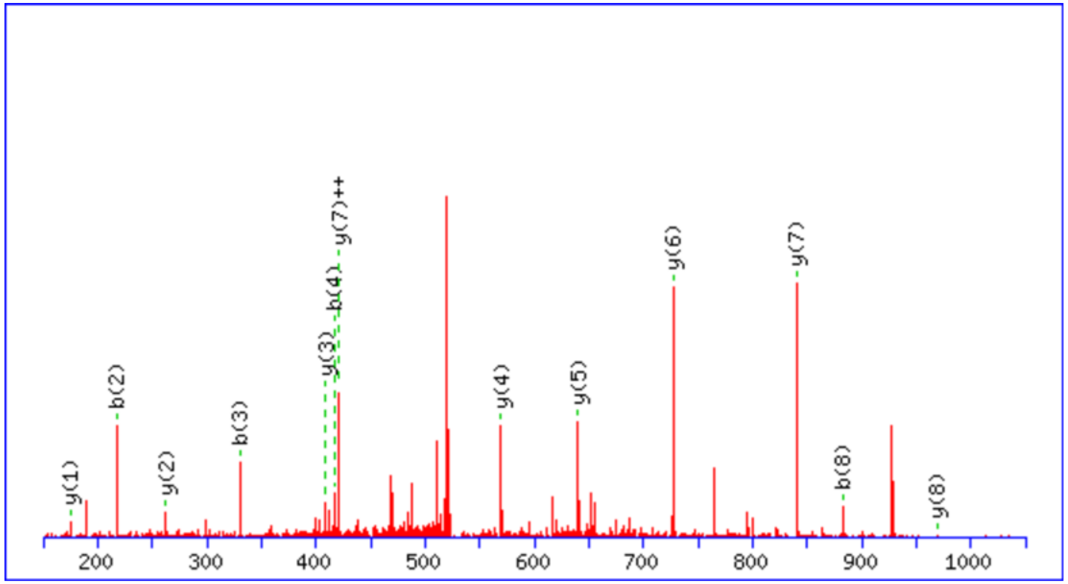


Peptide View

MS/MS Fragmentation of **SELSACFSR**
Found in **IPI00011899**, Tax_Id=9606 Gene_Symbol=BAMBI BMP and activin membrane-bound inhibitor homolog
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 4557: 1055.470648 from(528.742600,2+)
Title: OECHL100317_31.10170.10170.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1055.470581**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 56 **Expect:** 6.9e-005**Matches :** 13/78 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							9
2	**217.081897**	109.044586	199.071332	100.039304	E	***969.445842***	485.226559	952.419293	476.713284	951.435277	476.221276	8
3	**330.165961**	165.586618	312.155396	156.581336	L	***840.403249***	420.705263	823.376700	412.191988	822.392684	411.699980	7
4	**417.197989**	209.102632	399.187424	200.097350	S	***727.319185***	364.163231	710.292636	355.649956	709.308620	355.157948	6
5	488.235103	244.621189	470.224538	235.615907	A	***640.287157***	320.647217	623.260608	312.133942	622.276592	311.641934	5
6	648.265752	324.636514	630.255187	315.631232	C	***569.250043***	285.128660	552.223494	276.615385	551.239478	276.123377	4
7	795.334166	398.170721	777.323601	389.165438	F	***409.219394***	205.113335	392.192845	196.600060	391.208829	196.108052	3
8	**882.366194**	441.686735	864.355629	432.681452	S	***262.150980***	131.579128	245.124431	123.065853	244.140415	122.573845	2
9					R	***175.118952***	88.063114	158.092403	79.549839			1



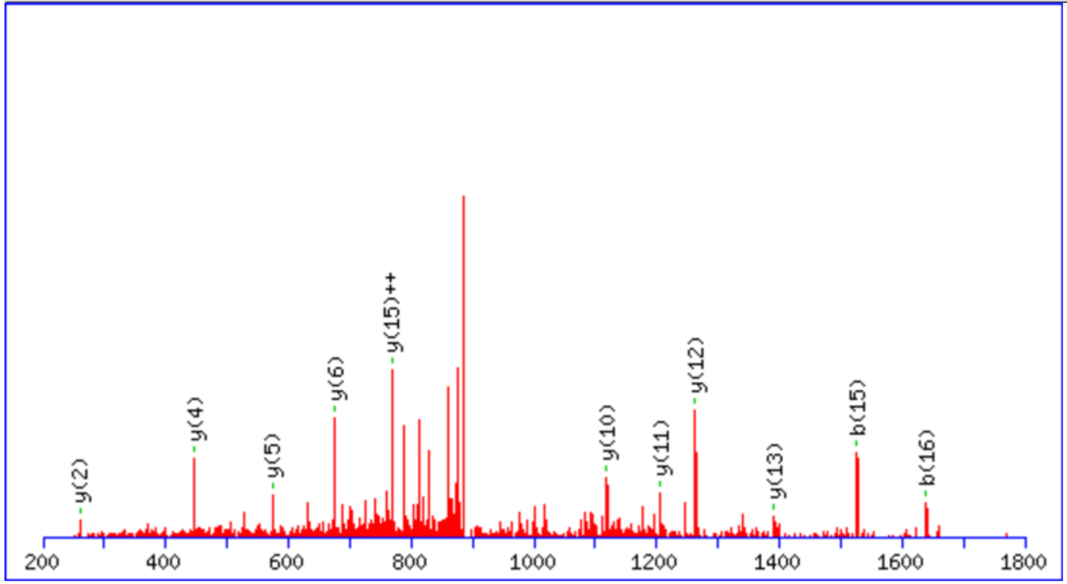
Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 13245: 1784.881048 from(893.447800,2+)
Title: OECHL100317_31.7536.7536.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56 **Expect:** 0.0004**Matches :** 11/170 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	164.070605	82.538940					**Y**						
2	251.102633	126.054954			233.092068	117.049672	**S**	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.9099
3	308.124097	154.565687			290.113532	145.560404	**G**	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.3939
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.8831
5	524.198718	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.3671

6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.8458
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.3351
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.8191
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	1017.593888	509.300582	1000.567339	500.787307	999.583323	500.2952
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.2660
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	788.487631	394.747453	771.461082	386.234179	770.477066	385.7421
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.2001
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.6762
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.6288
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.1180
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		



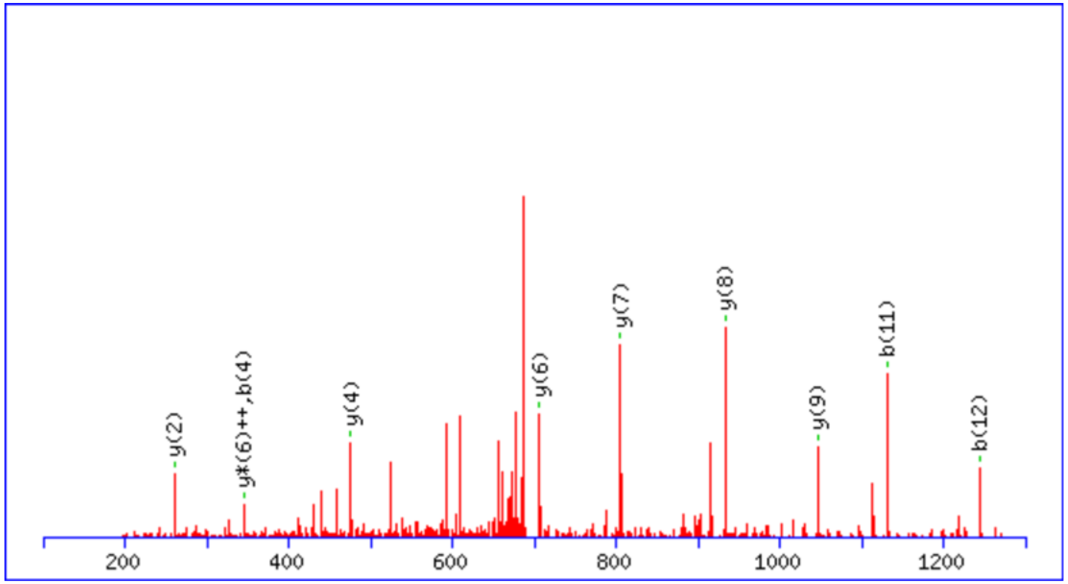
Peptide View

MS/MS Fragmentation of **ATGDIKVTESEIK**

Found in **IPI00302614**, Tax_Id=9606 Gene_Symbol=VTCN1 V-set domain containing T cell activation inhibitor 1
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 9354: 1389.735048 from(695.874800,2+)
Title: OECHL100317_31.8088.8088.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1389.735107**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 53 **Expect:** 0.00057**Matches :** 10/128 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	72.044390	36.525833					A						
2	173.092069	87.049672			155.081504	78.044390	T	1319.705288	660.356282	1302.678739	651.843008	1301.694723	651.3509
3	230.113533	115.560404			212.102968	106.555122	G	1218.657609	609.832442	1201.631060	601.319168	1200.647044	600.8271
4	**345.140476**	173.073876			327.129911	164.068593	D	1161.636145	581.321710	1144.609596	572.808436	1143.625580	572.3164
5	458.224540	229.615908			440.213975	220.610626	I	***1046.609202***	523.808239	1029.582653	515.294964	1028.598637	514.8029
6	586.319503	293.663390	569.292954	285.150115	568.308938	284.658107	K	***933.525138***	467.266207	916.498589	458.752932	915.514573	458.2609
7	685.387917	343.197597	668.361368	334.684322	667.377352	334.192314	V	***805.430175***	403.218725	788.403626	394.705451	787.419610	394.2134
8	786.435596	393.721436	769.409047	385.208162	768.425031	384.716154	T	***706.361761***	353.684518	689.335212	345.171244	688.351196	344.6792
9	915.478189	458.242733	898.451640	449.729458	897.467624	449.237450	E	605.314082	303.160679	588.287533	294.647404	587.303517	294.1553
10	1002.510217	501.758747	985.483668	493.245472	984.499652	492.753464	S	***476.271489***	238.639382	459.244940	230.126108	458.260924	229.6341
11	**1131.552810**	566.280043	1114.526261	557.766769	1113.542245	557.274760	E	389.239461	195.123368	372.212912	186.610094	371.228896	186.1180
12	**1244.636874**	622.822075	1227.610325	614.308800	1226.626309	613.816792	I	***260.196868***	130.602072	243.170319	122.088797		
13							K	147.112804	74.060040	130.086255	65.546765		



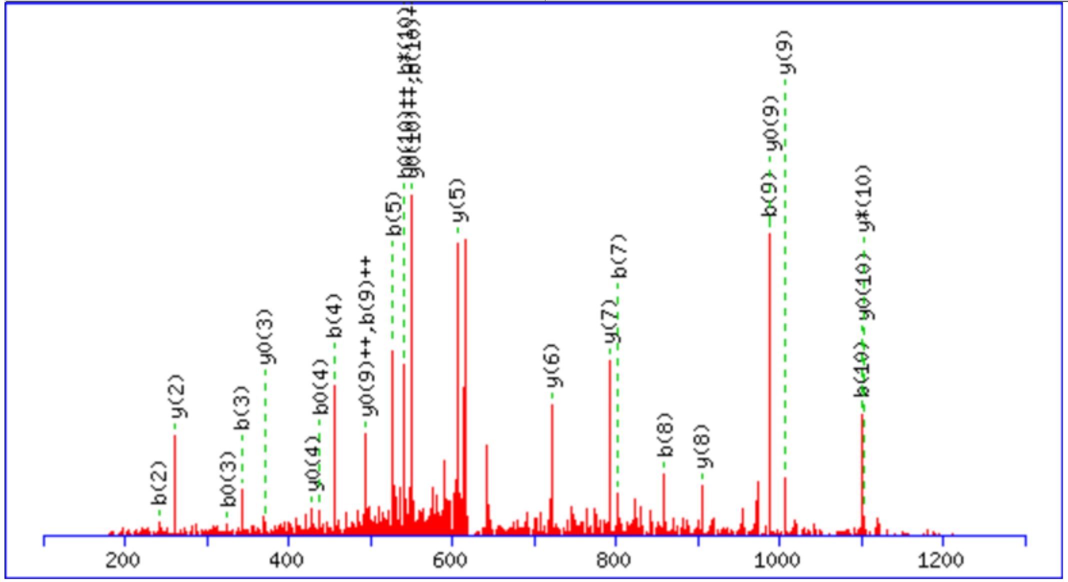
Peptide View

MS/MS Fragmentation of **KITIADCGQLE**
Found in **IPI00419585**, Tax_Id=9606 Gene_Symbol=PPIA Peptidyl-prolyl cis-trans isomerase A
Experiment: 45 - OPE-3 **Fraction:** OPE-3

Match to Query 7727: 1246.623848 from(624.319200,2+)
Title: OECHL100317_31.11214.11214.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_31.raw
Monoisotopic mass of neutral peptide Mr(calc): 1246.622726**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51 **Expect:** 0.0011**Matches :** 27/112 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	129.102239	65.054757	112.075690	56.541483			**K**						
2	***242.186303***	121.596790	225.159754	113.083515			**I**	1119.535053	560.271165	1102.508504	551.757890	1101.524488	551.2658
3	***343.233982***	172.120629	326.207433	163.607355	325.223417	163.115347	**T**	**1006.450989**	503.729133	989.424440	495.215858	988.440424	494.7238
4	***456.318046***	228.662661	439.291497	220.149387	438.307481	219.657379	**I**	**905.403310**	453.205293	888.376761	444.692019	887.392745	444.2000
5	***527.355160***	264.181218	510.328611	255.667944	509.344595	255.175936	**A**	**792.319246**	396.663261	775.292697	388.149987	774.308681	387.6579

6	642.382103	321.694690	625.355554	313.181415	624.371538	312.689407	**D**	**721.282132**	361.144704	704.255583	352.631430	703.271567	352.1394
7	***802.412752***	401.710014	785.386203	393.196740	784.402187	392.704732	**C**	**606.255189**	303.631233	589.228640	295.117958	588.244624	294.6259
8	***859.434216***	430.220746	842.407667	421.707472	841.423651	421.215464	**G**	446.224540	223.615908	429.197991	215.102634	428.213975	214.6106
9	***987.492794***	494.250035	970.466245	485.736761	969.482229	485.244753	**Q**	389.203076	195.105176	372.176527	186.591902	371.192511	186.0998
10	***1100.576858***	550.792067	1083.550309	542.278793	1082.566293	541.786785	**L**	**261.144498**	131.075887			243.133933	122.0706
11							**E**	148.060434	74.533855			130.049869	65.5285

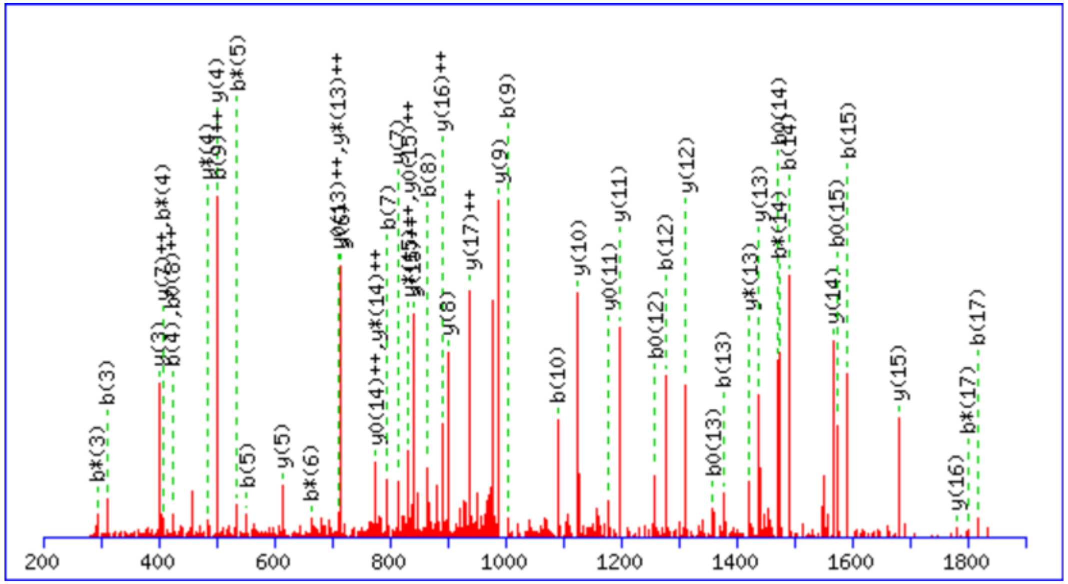


Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 12 - S_D-3 **Fraction:** S_D-3

Match to Query 15799: 1990.024648 from(996.019600,2+)
Title: OECHL100317_29.10278.10278.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 94 **Expect:** 5.5e-008**Matches :** 51/186 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	115.050203	58.028740	98.023654	49.515465			**N**						
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.9921
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.4657
4	**424.255445**	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.9315
5	**552.314023**	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.3895
6	680.372601	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.3602
7	**795.399544**	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.3309
8	**866.436658**	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.8174
9	**1003.495570**	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.2989
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.7694
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.2534
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	***814.478130***	407.742703	797.451581	399.229428	796.467565	398.7374
13	**1377.675719**	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.2032
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.6793
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.1373
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510		
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128		
18							**R**	175.118952	88.063114	158.092403	79.549839		



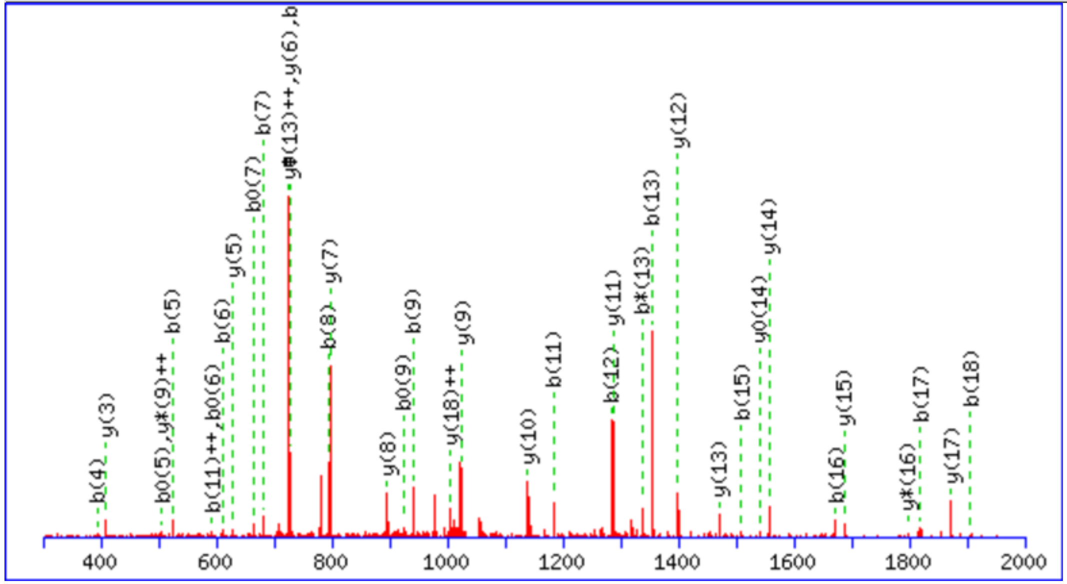
Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 12 - S_D-3 **Fraction:** S_D-3

Match to Query 16362: 2078.985448 from(1040.500000,2+)
Title: OECHL100317_29.17697.17697.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 86 **Expect:** 4.7e-007**Matches :** 39/200 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	72.044390	36.525833					**A**						
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444
4	***394.183344***	197.595310	377.156795	189.082035			**Q**	1814.870790	907.939033	1797.844241	899.425759	1796.860225	898.933
5	***523.225937***	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904

6	***610.257965***	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383
7	***681.295079***	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867
8	***794.379143***	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348
9	***941.447557***	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272
11	***1184.533077***	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	***1025.505072***	513.256174	1008.478523	504.742900	1007.494507	504.250
12	***1283.601491***	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729
13	***1354.638605***	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195
14	1451.691369	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676
15	***1508.712833***	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150
16	***1671.776162***	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	572.282723	286.645000	555.256174	278.131725	554.272158	277.639
17	***1818.844576***	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108
18	***1905.876604***	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573
19							**R**	175.118952	88.063114	158.092403	79.549840		

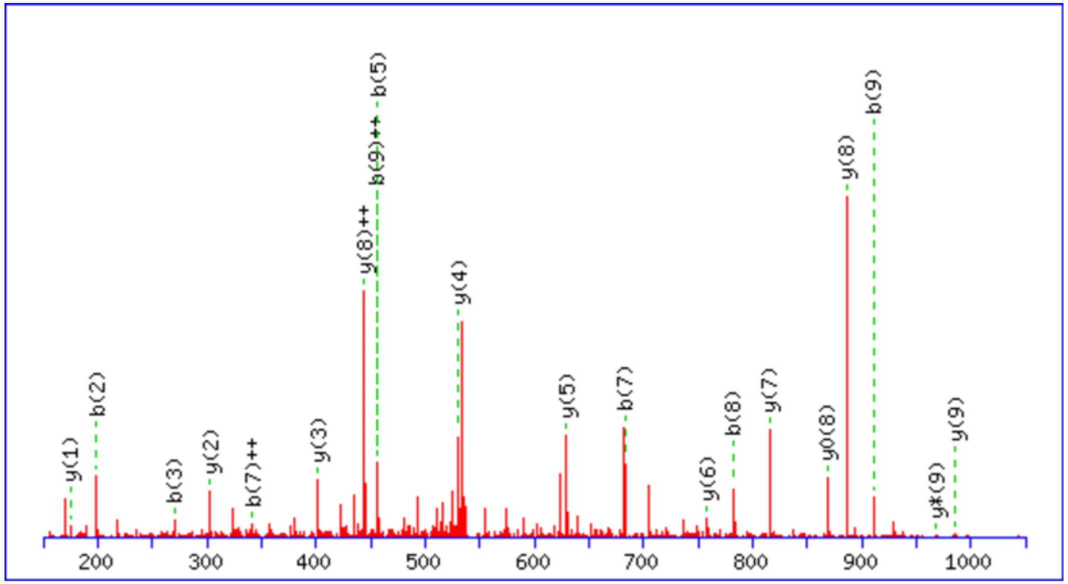


Peptide View

MS/MS Fragmentation of **VVAGEVQVQR**
Found in **IPI00056478**, Tax_Id=9606 Gene_Symbol=IGSF8 Isoform 1 of Immunoglobulin superfamily member 8
Experiment: 12 - S_D-3 **Fraction:** S_D-3

Match to Query 5679: 1083.602848 from(542.808700,2+)
Title: OECHL100317_29.5879.5879.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1083.603668**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 68 **Expect:** 1e-005**Matches :** 20/78 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	$b*^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	100.075690	50.541483					**V**							**10**
2	**199.144104**	100.075690					**V**	***985.542521***	493.274899	968.515972	484.761624	967.531956	484.269616	**9**
3	**270.181218**	135.594247					**A**	***886.474107***	443.740692	869.447558	435.227417	868.463542	434.735409	**8**
4	327.202682	164.104979					**G**	***815.436993***	408.222135	798.410444	399.708860	797.426428	399.216852	**7**
5	**456.245275**	228.626275			438.234710	219.620993	**E**	***758.415529***	379.711403	741.388980	371.198128	740.404964	370.706120	**6**
6	555.313689	278.160483			537.303124	269.155200	**V**	***629.372936***	315.190106	612.346387	306.676832			**5**
7	**683.372267**	**342.189772**	666.345718	333.676497	665.361702	333.184489	**Q**	***530.304522***	265.655899	513.277973	257.142625			**4**
8	**782.440681**	391.723979	765.414132	383.210704	764.430116	382.718696	**V**	***402.245944***	201.626610	385.219395	193.113336			**3**
9	**910.499259**	**455.753268**	893.472710	447.239993	892.488694	446.747985	**Q**	***303.177530***	152.092403	286.150981	143.579129			**2**
10							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**



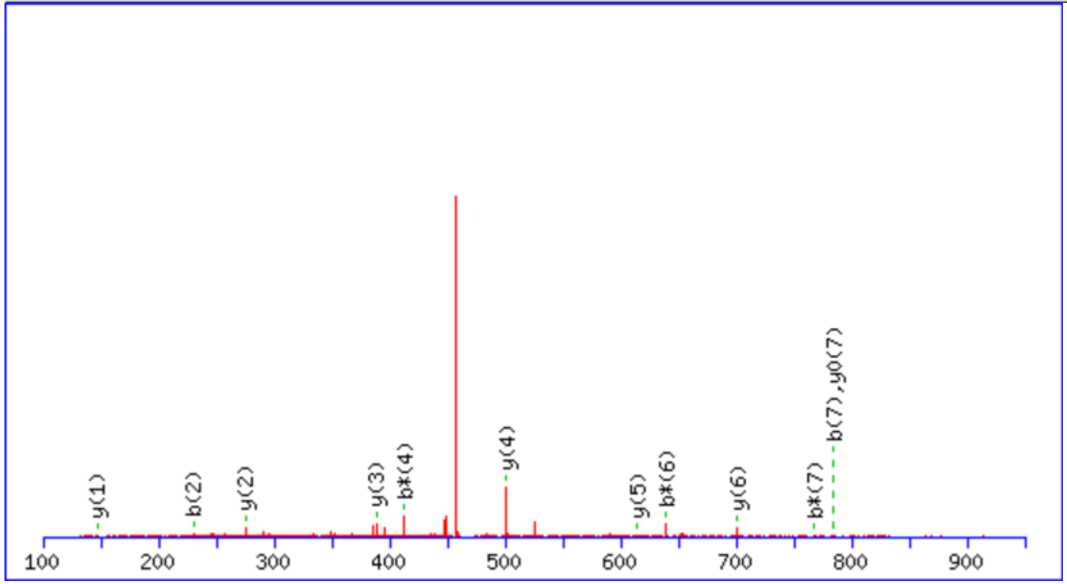
Peptide View

MS/MS Fragmentation of **QTSILIQK**
Found in **IPI00020687**, Tax_Id=9606 Gene_Symbol=SPINK1 Pancreatic secretory trypsin inhibitor
Experiment: 12 - S_D-3 **Fraction:** S_D-3

Match to Query 2766: 929.554848 from(465.784700,2+)
Title: OECHL100317_29.8332.8332.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 929.554565**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55 **Expect:** 0.00012**Matches :** 12/72 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	129.065854	65.036565	112.039305	56.523291			Q							8
2	**230.113533**	115.560405	213.086984	107.047130	212.102968	106.555122	T	802.503281	401.755279	785.476732	393.242004	784.492716	392.749996	7
3	317.145561	159.076418	300.119012	150.563144	299.134996	150.071136	S	***701.455602***	351.231439	684.429053	342.718165	683.445037	342.226157	6
4	430.229625	215.618450	413.203076	207.105176	412.219060	206.613168	I	***614.423574***	307.715425	597.397025	299.202151			5
5	543.313689	272.160483	526.287140	263.647208	525.303124	263.155200	L	***501.339510***	251.173393	484.312961	242.660119			4

6	656.397753	328.702515	639.371204	320.189240	638.387188	319.697232	**I**	***388.255446***	194.631361	371.228897	186.118087			**3**
7	**784.456331**	392.731804	767.429782	384.218529	766.445766	383.726521	**Q**	***275.171382***	138.089329	258.144833	129.576055			**2**
8							**K**	***147.112804***	74.060040	130.086255	65.546765			**1**



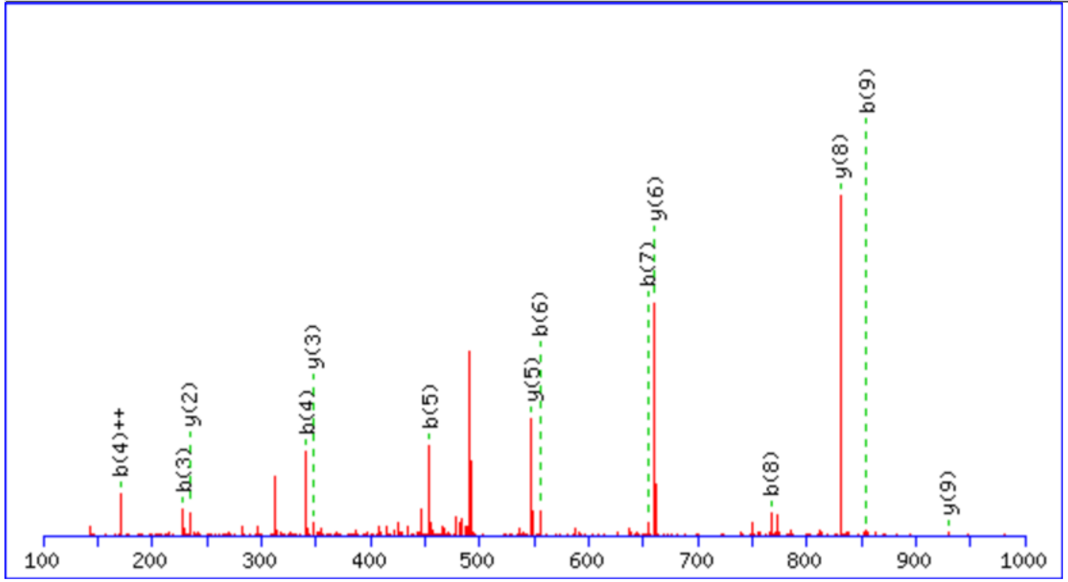
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 12 - S_D-3 **Fraction:** S_D-3

Match to Query 4067: 999.633048 from(500.823800,2+)
Title: OECHL100317_29.17681.17681.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 63 **Expect:** 5.3e-006**Matches :** 15/78 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	**929.602995**	465.305136	912.576446	456.791861	911.592430	456.299853	**9**

3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



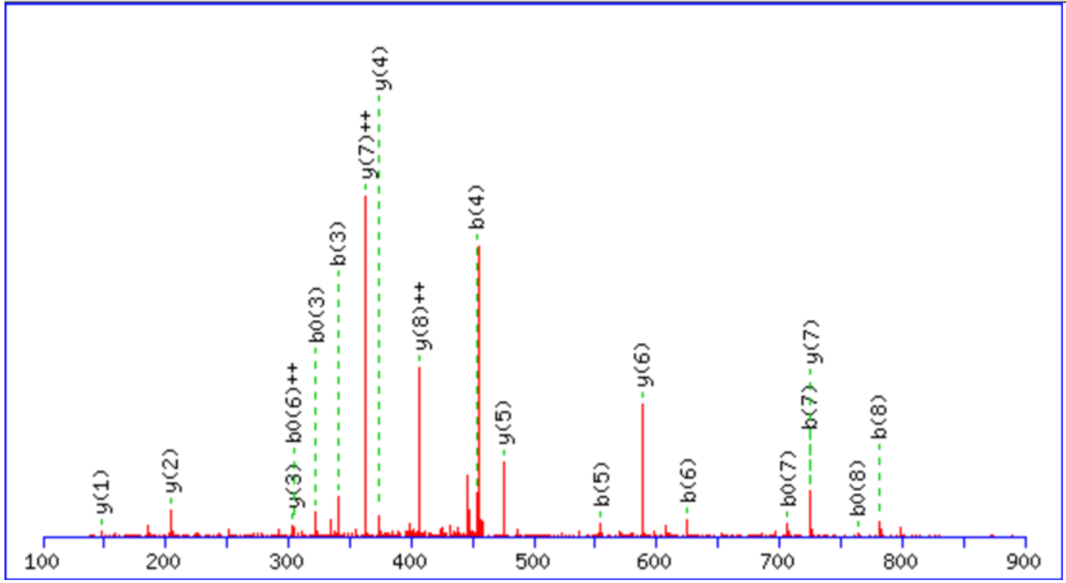
Peptide View

MS/MS Fragmentation of **DSHLTAVGK**
Found in **IPI00031065**, Tax_Id=9606 Gene_Symbol=DNASE1 Deoxyribonuclease-1
Experiment: 12 - S_D-3 **Fraction:** S_D-3

Match to Query 2701: 926.482448 from(464.248500,2+)
Title: OECHL100317_29.3209.3209.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 926.482147**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56 **Expect:** 0.0002**Matches :** 19/72 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	**D**							**9**
2	203.066247	102.036761	185.055682	93.031479	**S**	812.462479	406.734878	795.435930	398.221603	794.451914	397.729595	**8**
3	**340.125159**	170.566217	322.114594	161.560935	**H**	***725.430451***	363.218864	708.403902	354.705589	707.419886	354.213581	**7**
4	**453.209223**	227.108250	435.198658	218.102967	**L**	***588.371539***	294.689408	571.344990	286.176133	570.360974	285.684125	**6**
5	**554.256902**	277.632089	536.246337	268.626807	**T**	***475.287475***	238.147375	458.260926	229.634101	457.276910	229.142093	**5**
6	**625.294016**	313.150646	607.283451	304.145364	**A**	***374.239796***	187.623536	357.213247	179.110261			**4**
7	**724.362430**	362.684853	706.351865	353.679571	**V**	***303.202682***	152.104979	286.176133	143.591704			**3**
8	**781.383894**	391.195585	763.373329	382.190303	**G**	***204.134268***	102.570772	187.107719	94.057498			**2**
9					**K**	***147.112804***	74.060040	130.086255	65.546765			**1**

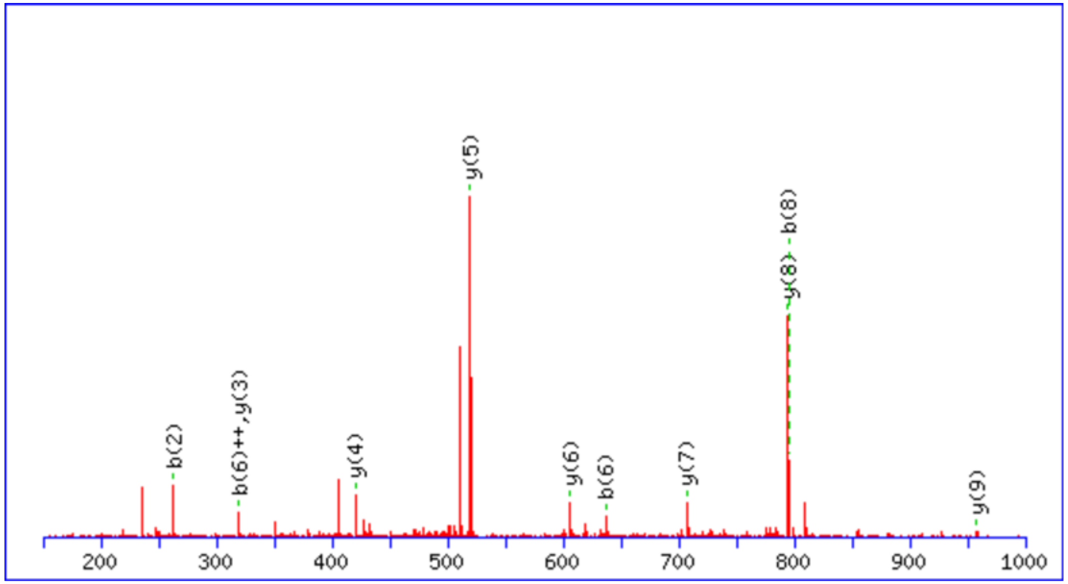


Peptide View

MS/MS Fragmentation of **VYSTSVTGSR**
Found in **IPI00010402**, Tax_Id=9606 Gene_Symbol=SH3BGRL3 Putative uncharacterized protein
Experiment: 12 - S_D-3 **Fraction:** S_D-3

Match to Query 5145: 1055.526048 from(528.770300,2+)
Title: OECHL100317_29.4522.4522.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1055.524750**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 54 **Expect:** 0.0003**Matches :** 11/84 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	100.075690	50.541483			**V**							**10**
2	**263.139019**	132.073148			**Y**	***957.463601***	479.235439	940.437052	470.722164	939.453036	470.230156	**9**
3	350.171047	175.589161	332.160482	166.583879	**S**	***794.400272***	397.703774	777.373723	389.190499	776.389707	388.698491	**8**
4	451.218726	226.113001	433.208161	217.107719	**T**	***707.368244***	354.187760	690.341695	345.674486	689.357679	345.182478	**7**
5	538.250754	269.629015	520.240189	260.623733	**S**	***606.320565***	303.663921	589.294016	295.150646	588.310000	294.658638	**6**
6	**637.319168**	319.163222	619.308603	310.157940	**V**	***519.288537***	260.147907	502.261988	251.634632	501.277972	251.142624	**5**
7	738.366847	369.687062	720.356282	360.681779	**T**	***420.220123***	210.613699	403.193574	202.100425	402.209558	201.608417	**4**
8	**795.388311**	398.197794	777.377746	389.192511	**G**	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	**3**
9	882.420339	441.713808	864.409774	432.708525	**S**	262.150980	131.579128	245.124431	123.065853	244.140415	122.573845	**2**
10					**R**	175.118952	88.063114	158.092403	79.549839			**1**



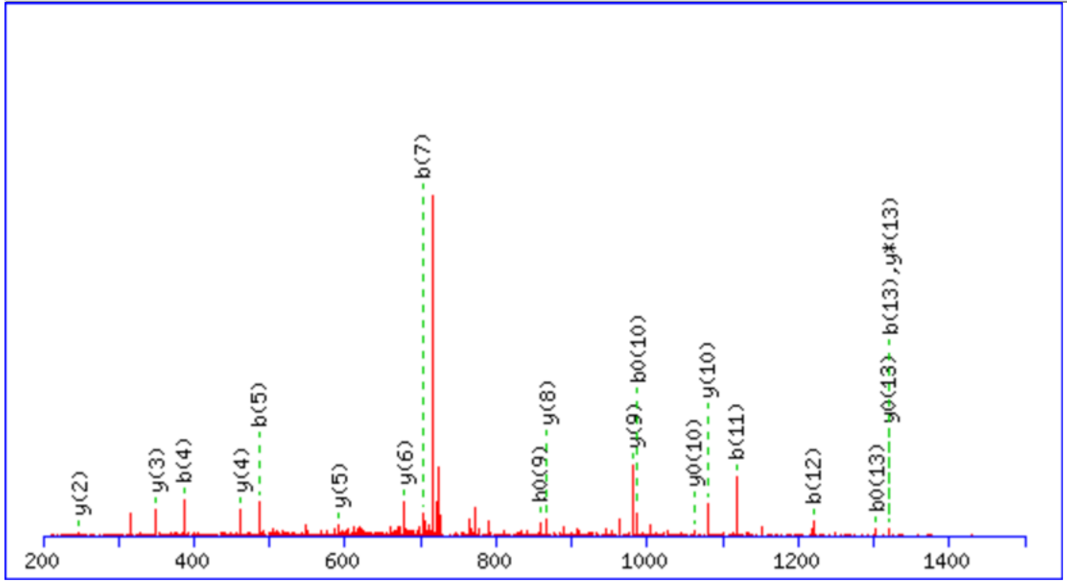
Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 12 - S_D-3 **Fraction:** S_D-3

Match to Query 10983: 1465.677648 from(733.846100,2+)
Title: OECHL100317_29.10378.10378.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 70 **Expect:** 8.1e-006**Matches :** 20/128 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	1337.643082	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	316.113926	158.560601	298.103361	149.555319	**A**	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	***387.151040***	194.079158	369.140475	185.073875	**A**	1151.579025	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	***486.219454***	243.613365	468.208889	234.608082	**V**	***1080.541911***	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**

6	601.246397	301.126837	583.235832	292.121554	D	***981.473497***	491.240387	964.446948	482.727112	963.462932	482.235104	9
7	***702.294076***	351.650676	684.283511	342.645394	T	***866.446554***	433.726915	849.420005	425.213641	848.435989	424.721633	8
8	789.326104	395.166690	771.315539	386.161408	S	765.398875	383.203076	748.372326	374.689801	747.388310	374.197793	7
9	876.358132	438.682704	858.347567	429.677421	S	***678.366847***	339.687062	661.340298	331.173787	660.356282	330.681779	6
10	1005.400725	503.204001	987.390160	494.198718	E	***591.334819***	296.171048	574.308270	287.657773	573.324254	287.165765	5
11	***1118.484789***	559.746033	1100.474224	550.740750	I	***462.292226***	231.649751	445.265677	223.136477	444.281661	222.644469	4
12	***1219.532468***	610.269872	1201.521903	601.264590	T	***349.208162***	175.107719	332.181613	166.594445	331.197597	166.102437	3
13	***1320.580147***	660.793712	1302.569582	651.788429	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
14					K	147.112804	74.060040	130.086255	65.546765			1



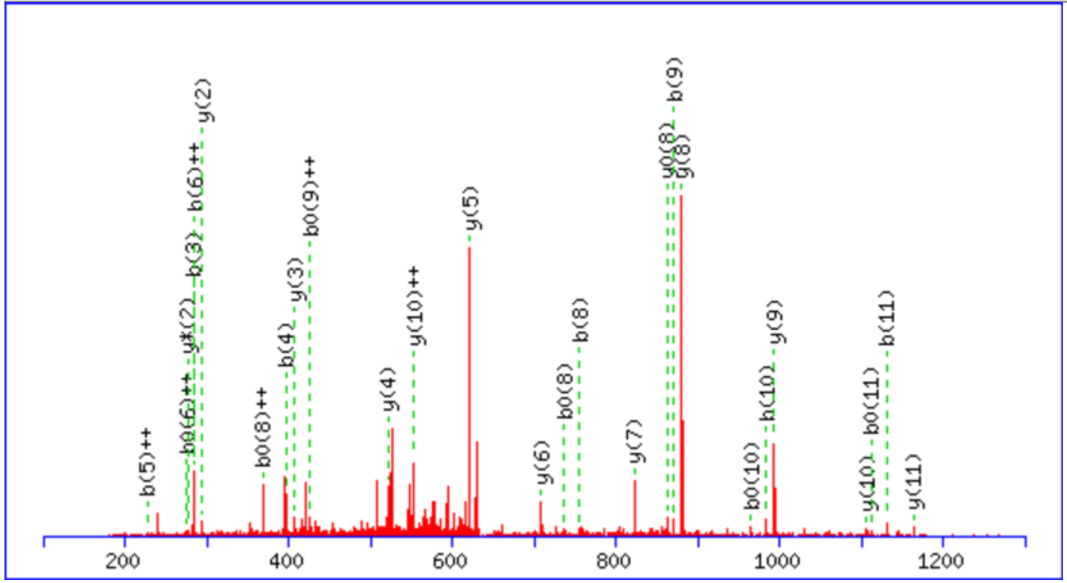
Peptide View

MS/MS Fragmentation of **LGLLGDSVDIFK**
Found in **IPI00099670**, Tax_Id=9606 Gene_Symbol=CEL carboxyl ester lipase precursor
Experiment: 12 - S_D-3 **Fraction:** S_D-3

Match to Query 8692: 1275.704648 from(638.859600,2+)

Title: OECHL100317_29.21485.21485.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1275.707458**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 54 **Expect:** 0.00021**Matches :** 27/94 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							**12**
2	171.112804	86.060040			**G**	***1163.630666***	582.318971	1146.604117	573.805697	1145.620101	573.313689	**11**
3	**284.196868**	142.602072			**L**	***1106.609202***	553.808239	1089.582653	545.294964	1088.598637	544.802956	**10**
4	**397.280932**	199.144104			**L**	***993.525138***	497.266207	976.498589	488.752932	975.514573	488.260924	**9**
5	454.302396	227.654836			**G**	***880.441074***	440.724175	863.414525	432.210900	862.430509	431.718892	**8**
6	569.329339	285.168308	551.318774	276.163025	**D**	***823.419610***	412.213443	806.393061	403.700168	805.409045	403.208160	**7**
7	656.361367	328.684322	638.350802	319.679039	**S**	***708.392667***	354.699972	691.366118	346.186697	690.382102	345.694689	**6**
8	**755.429781**	378.218528	737.419216	369.213246	**V**	***621.360639***	311.183958	604.334090	302.670683	603.350074	302.178675	**5**
9	**870.456724**	435.732000	852.446159	426.726717	**D**	***522.292225***	261.649751	505.265676	253.136476	504.281660	252.644468	**4**
10	**983.540788**	492.274032	965.530223	483.268749	**I**	***407.265282***	204.136279	390.238733	195.623004			**3**
11	**1130.609202**	565.808239	1112.598637	556.802956	**F**	***294.181218***	147.594247	277.154669	139.080972			**2**
12					**K**	147.112804	74.060040	130.086255	65.546765			**1**

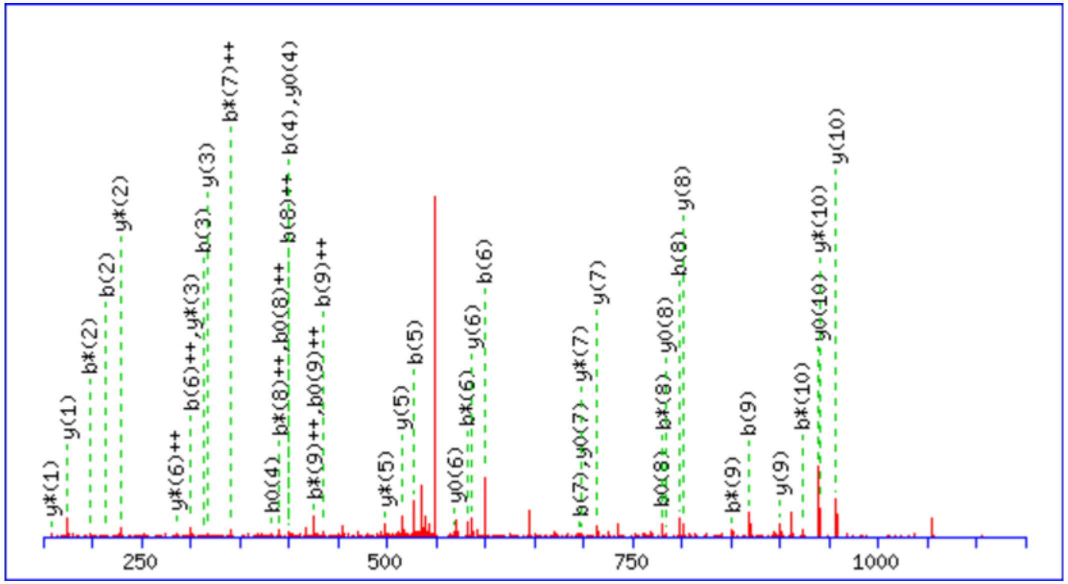


Peptide View

MS/MS Fragmentation of **RGVSQAPTAAR**
Found in **IPI00025365**, Tax_Id=9606 Gene_Symbol=EDN3 Isoform Long of Endothelin-3
Experiment: 12 - S_D-3 **Fraction:** S_D-3

Match to Query 6094: 1112.605248 from(557.309900,2+)
Title: OECHL100317_29.2352.2352.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_29.raw
Monoisotopic mass of neutral peptide Mr(calc): 1112.605042**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 50 **Expect:** 0.00087**Matches :** 44/108 fragment ions using 82 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			**R**							**11**
2	***214.129851***	107.568564	197.103302	99.055289			**G**	**957.511221**	479.259249	940.484672	470.745974	939.500656	470.253966	**10**
3	***313.198265***	157.102770	296.171716	148.589496			**V**	**900.489757**	450.748517	883.463208	442.235242	882.479192	441.743234	**9**
4	***400.230293***	200.618785	383.203744	192.105510	382.219728	191.613502	**S**	**801.421343**	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
5	***528.288871***	264.648074	511.262322	256.134799	510.278306	255.642791	**Q**	**714.389315**	357.698296	697.362766	349.185021	696.378750	348.693013	**7**
6	***599.325985***	**300.166631**	582.299436	291.653356	581.315420	291.161348	**A**	**586.330737**	293.669007	569.304188	285.155732	568.320172	284.663724	**6**
7	***696.378749***	348.693013	679.352200	340.179738	678.368184	339.687730	**P**	**515.293623**	258.150450	498.267074	249.637175	497.283058	249.145167	**5**
8	***797.426428***	**399.216852**	780.399879	390.703578	779.415863	390.211570	**T**	418.240859	209.624068	401.214310	201.110793	400.230294	200.618785	**4**
9	***868.463542***	**434.735409**	851.436993	426.222135	850.452977	425.730127	**A**	**317.193180**	159.100228	300.166631	150.586953			**3**
10	***939.500656***	470.253966	922.474107	461.740692	921.490091	461.248684	**A**	246.156066	123.581671	229.129517	115.068397			**2**
11							**R**	**175.118952**	88.063114	158.092403	79.549840			**1**



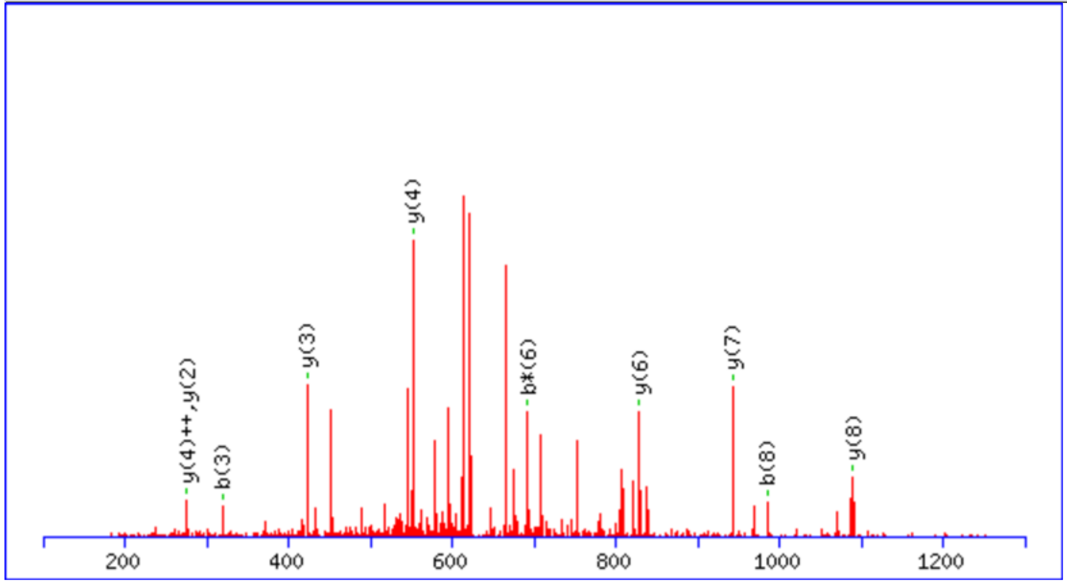
Peptide View

MS/MS Fragmentation of **GNFNYIEFTR**
Found in **IPI00033494**, Tax_Id=9606 Gene_Symbol=MYL12B Myosin regulatory light chain 12B
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 7184: 1259.594048 from(630.804300,2+)
Title: OECHL100317_27.15741.15741.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1259.593475**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 53 **Expect:** 0.00063**Matches :** 10/92 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	58.028740	29.518008					**G**						
2	172.071667	86.539471	155.045118	78.026197			**N**	1203.579299	602.293288	1186.552750	593.780013	1185.568734	593.2880
3	**319.140081**	160.073678	302.113532	151.560404			**F**	***1089.536372***	545.271824	1072.509823	536.758549	1071.525807	536.2665
4	433.183008	217.095142	416.156459	208.581867			**N**	***942.467958***	471.737617	925.441409	463.224342	924.457393	462.7323
5	596.246337	298.626807	579.219788	290.113532			**Y**	***828.425031***	414.716154	811.398482	406.202879	810.414466	405.7108

6	709.330401	355.168839	692.303852	346.655564			**I**	665.361702	333.184489	648.335153	324.671214	647.351137	324.1792
7	838.372994	419.690135	821.346445	411.176861	820.362429	410.684853	**E**	***552.277638***	276.642457	535.251089	268.129182	534.267073	267.6371
8	**985.441408**	493.224342	968.414859	484.711068	967.430843	484.219060	**F**	***423.235045***	212.121160	406.208496	203.607886	405.224480	203.1158
9	1086.489087	543.748181	1069.462538	535.234907	1068.478522	534.742899	**T**	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.5816
10							**R**	175.118952	88.063114	158.092403	79.549839		



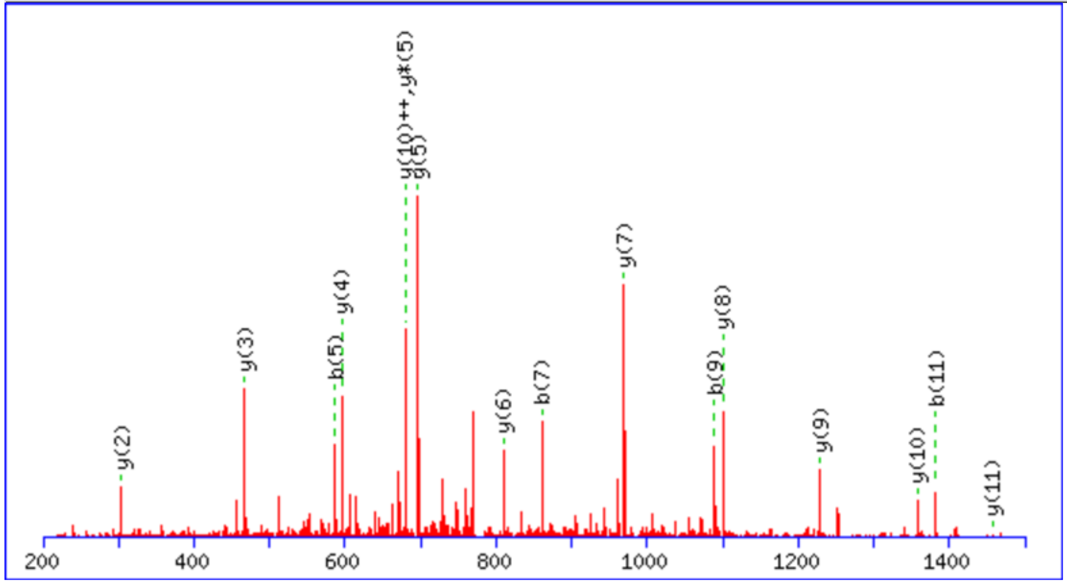
Peptide View

MS/MS Fragmentation of **VVEQMCITQYER**
Found in **IPI00022284**, Tax_Id=9606 Gene_Symbol=PRNP Major prion protein
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 10333: 1554.717848 from(778.366200,2+)
Title: OECHL100317_27.13015.13015.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1554.717041**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 74 **Expect:** 3.6e-006**Matches :** 16/120 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	100.075690	50.541483					**V**						
2	199.144104	100.075690					**V**	***1456.655914***	728.831595	1439.629365	720.318321	1438.645349	719.8263
3	328.186697	164.596987			310.176132	155.591704	**E**	***1357.587500***	679.297388	1340.560951	670.784114	1339.576935	670.2921
4	456.245275	228.626276	439.218726	220.113001	438.234710	219.620993	**Q**	***1228.544907***	614.776092	1211.518358	606.262817	1210.534342	605.7708
5	**587.285760**	294.146518	570.259211	285.633244	569.275195	285.141236	**M**	***1100.486329***	550.746803	1083.459780	542.233528	1082.475764	541.7415
6	747.316409	374.161843	730.289860	365.648568	729.305844	365.156560	**C**	***969.445844***	485.226560	952.419295	476.713286	951.435279	476.2212
7	**860.400473**	430.703875	843.373924	422.190600	842.389908	421.698592	**I**	***809.415195***	405.211236	792.388646	396.697961	791.404630	396.2059
8	961.448152	481.227714	944.421603	472.714440	943.437587	472.222432	**T**	***696.331131***	348.669204	679.304582	340.155929	678.320566	339.6639
9	**1089.506730**	545.257003	1072.480181	536.743729	1071.496165	536.251721	**Q**	***595.283452***	298.145364	578.256903	289.632090	577.272887	289.1400
10	1252.570059	626.788668	1235.543510	618.275393	1234.559494	617.783385	**Y**	***467.224874***	234.116075	450.198325	225.602801	449.214309	225.1107
11	**1381.612652**	691.309964	1364.586103	682.796690	1363.602087	682.304682	**E**	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.5791
12							**R**	175.118952	88.063114	158.092403	79.549839		



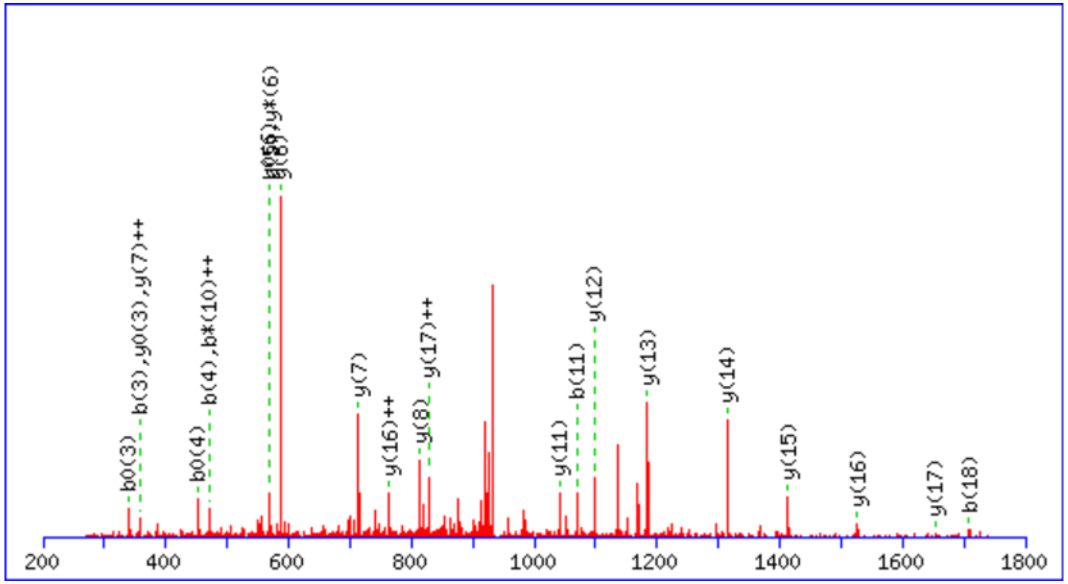
Peptide View

MS/MS Fragmentation of **EVQLVESGGGLVKPGGSLR**

Found in **IPI00783024**, Tax_Id=9606 Gene_Symbol=- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 12862: 1881.033448 from(941.524000,2+)
Title: OECHL100317_27.13579.13579.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1881.031982**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71 **Expect:** 4.5e-006**Matches :** 24/208 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	130.049869	65.528572			112.039304	56.523290	**E**						
2	229.118283	115.062780			211.107718	106.057497	**V**	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.9966
3	**357.176861**	179.092069	340.150312	170.578794	339.166296	170.086786	**Q**	***1653.928246***	827.467761	1636.901697	818.954487	1635.917681	818.4624
4	**470.260925**	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.4331
5	**569.329339**	285.168308	552.302790	276.655033	551.318774	276.163025	**V**	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.8911
6	698.371932	349.689604	681.345383	341.176330	680.361367	340.684322	**E**	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.3569
7	785.403960	393.205618	768.377411	384.692344	767.393395	384.200336	**S**	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.8356
8	842.425424	421.716350	825.398875	413.203076	824.414859	412.711068	**G**	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.3196
9	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	**G**	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.8089
10	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	**G**	983.599641	492.303459	966.573092	483.790184	965.589076	483.2981
11	**1069.552416**	535.279846	1052.525867	526.766572	1051.541851	526.274564	**L**	926.578177	463.792727	909.551628	455.279452	908.567612	454.7874
12	1168.620830	584.814053	1151.594281	576.300779	1150.610265	575.808771	**V**	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.2454
13	1296.715793	648.861535	1279.689244	640.348260	1278.705228	639.856252	**K**	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.7112
14	1393.768557	697.387917	1376.742008	688.874642	1375.757992	688.382634	**P**	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.6637
15	1450.790021	725.898649	1433.763472	717.385374	1432.779456	716.893366	**G**	489.277972	245.142624	472.251423	236.629349	471.267407	236.1373
16	1507.811485	754.409381	1490.784936	745.896106	1489.800920	745.404098	**G**	432.256508	216.631892	415.229959	208.118617	414.245943	207.6266
17	1594.843513	797.925395	1577.816964	789.412120	1576.832948	788.920112	**S**	375.235044	188.121160	358.208495	179.607885	357.224479	179.1158
18	**1707.927577**	854.467427	1690.901028	845.954152	1689.917012	845.462144	**L**	288.203016	144.605146	271.176467	136.091871		
19							**R**	175.118952	88.063114	158.092403	79.549839		



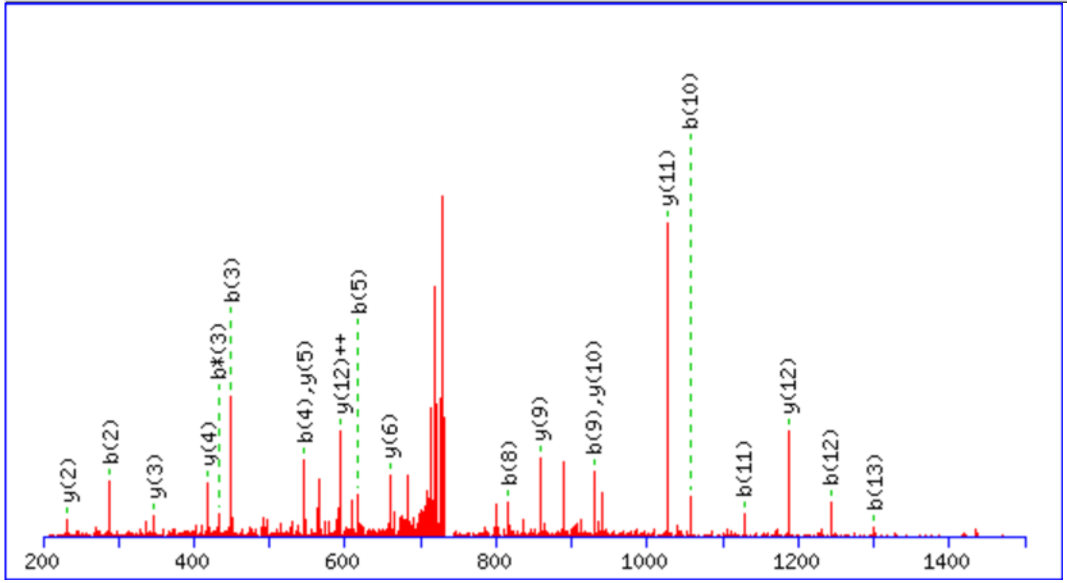
Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 9234: 1473.645048 from(737.829800,2+)
Title: OECHL100317_27.7924.7924.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 63 **Expect:** 2.3e-005**Matches :** 21/128 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	161.037925	81.022600					**C**						
2	***289.096503***	145.051890	272.069954	136.538615			**Q**	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.8093
3	***449.127152***	225.067214	432.100603	216.553940			**C**	**1186.563334**	593.785305	1169.536785	585.272031	1168.552769	584.7800
4	***546.179916***	273.593596	529.153367	265.080322			**P**	**1026.532685**	513.769981	1009.506136	505.256706	1008.522120	504.7646
5	***617.217030***	309.112153	600.190481	300.598879			**A**	**929.479921**	465.243599	912.453372	456.730324	911.469356	456.2383

6	674.238494	337.622885	657.211945	329.109611			**G**	**858.442807**	429.725042	841.416258	421.211767	840.432242	420.7197
7	745.275608	373.141442	728.249059	364.628168			**A**	801.421343	401.214310	784.394794	392.701035	783.410778	392.2090
8	***816.312722***	408.659999	799.286173	400.146725			**A**	730.384229	365.695753	713.357680	357.182478	712.373664	356.6904
9	***929.396786***	465.202031	912.370237	456.688757			**L**	**659.347115**	330.177196	642.320566	321.663921	641.336550	321.1719
10	***1057.455364***	529.231320	1040.428815	520.718046			**Q**	**546.263051**	273.635164	529.236502	265.121889	528.252486	264.6298
11	***1128.492478***	564.749877	1111.465929	556.236603			**A**	**418.204473**	209.605874	401.177924	201.092600	400.193908	200.6005
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	**D**	**347.167359**	174.087317	330.140810	165.574043	329.156794	165.0820
13	***1300.540885***	650.774081	1283.514336	642.260806	1282.530320	641.768798	**G**	**232.140416**	116.573846	215.113867	108.060571		
14							**R**	175.118952	88.063114	158.092403	79.549839		



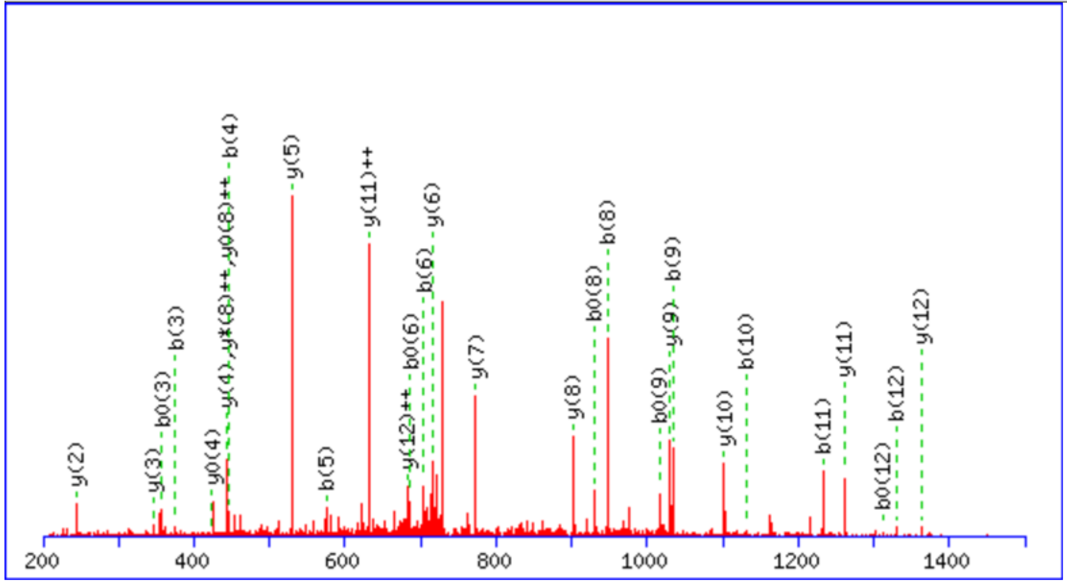
Peptide View

MS/MS Fragmentation of **ITCAEEGWSPTPK**
Found in **IPI00006154**, Tax_Id=9606 Gene_Symbol=CFHR2 Isoform Long of Complement factor H-related protein 2
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 9249: 1474.677648 from(738.346100,2+)

Title: OECHL100317_27.10318.10318.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1474.676224**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 77 **Expect:** 2.3e-006**Matches :** 30/114 fragment ions using 49 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308			**I**							**13**
2	215.139019	108.073147	197.128454	99.067865	**T**	***1362.599444***	681.803360	1345.572895	673.290086	1344.588879	672.798078	**12**
3	**375.169668**	188.088472	357.159103	179.083190	**C**	***1261.551765***	631.279521	1244.525216	622.766246	1243.541200	622.274238	**11**
4	**446.206782**	223.607029	428.196217	214.601747	**A**	***1101.521116***	551.264196	1084.494567	542.750922	1083.510551	542.258914	**10**
5	**575.249375**	288.128326	557.238810	279.123043	**E**	***1030.484002***	515.745639	1013.457453	507.232365	1012.473437	506.740357	**9**
6	**704.291968**	352.649622	686.281403	343.644340	**E**	***901.441409***	451.224343	884.414860	442.711068	883.430844	442.219060	**8**
7	761.313432	381.160354	743.302867	372.155072	**G**	***772.398816***	386.703046	755.372267	378.189772	754.388251	377.697764	**7**
8	**947.392745**	474.200011	929.382180	465.194728	**W**	***715.377352***	358.192314	698.350803	349.679040	697.366787	349.187032	**6**
9	**1034.424773**	517.716025	1016.414208	508.710742	**S**	***529.298039***	265.152658	512.271490	256.639383	511.287474	256.147375	**5**
10	**1131.477537**	566.242407	1113.466972	557.237124	**P**	***442.266011***	221.636644	425.239462	213.123369	424.255446	212.631361	**4**
11	**1232.525216**	616.766246	1214.514651	607.760964	**T**	***345.213247***	173.110262	328.186698	164.596987	327.202682	164.104979	**3**
12	**1329.577980**	665.292628	1311.567415	656.287346	**P**	***244.165568***	122.586422	227.139019	114.073148			**2**
13					**K**	147.112804	74.060040	130.086255	65.546765			**1**

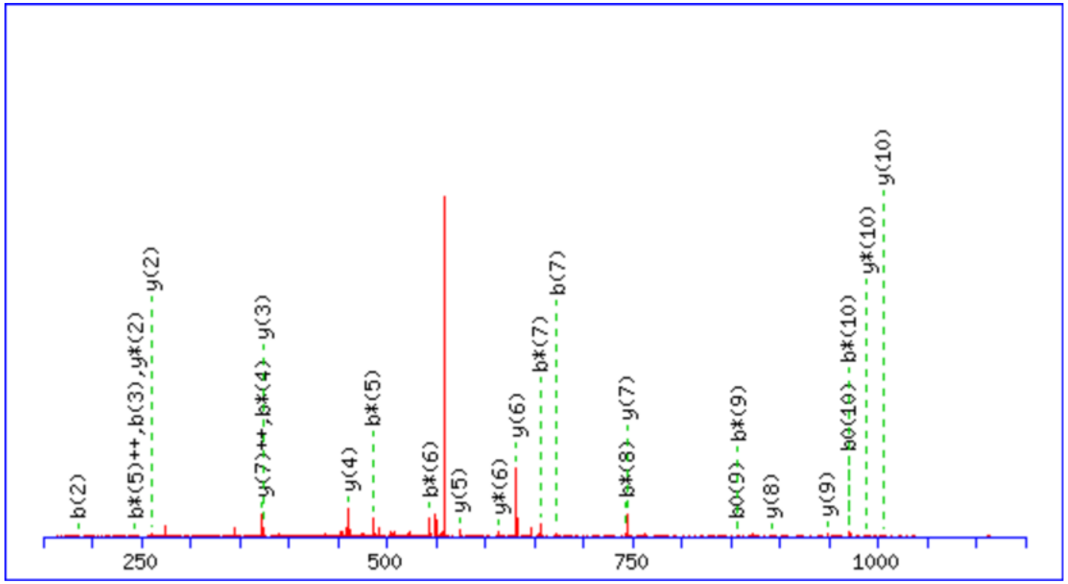


Peptide View

MS/MS Fragmentation of **QGGFLGLSNIK**
Found in **IPI00013955**, Tax_Id=9606 Gene_Symbol=MUC1 Isoform 1 of Mucin-1
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 5243: 1132.624448 from(567.319500,2+)
Title: OECHL100317_27.16278.16278.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1132.624054**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 55 **Expect:** 0.0002**Matches :** 26/100 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			**Q**							**11**
2	**186.087318**	93.547297	169.060769	85.034023			**G**	***1005.572757***	503.290017	988.546208	494.776742	987.562192	494.284734	**10**
3	**243.108782**	122.058029	226.082233	113.544755			**G**	***948.551293***	474.779285	931.524744	466.266010	930.540728	465.774002	**9**
4	390.177196	195.592236	373.150647	187.078962			**F**	***891.529829***	446.268553	874.503280	437.755278	873.519264	437.263270	**8**
5	503.261260	252.134268	486.234711	243.620994			**L**	***744.461415***	372.734346	727.434866	364.221071	726.450850	363.729063	**7**
6	560.282724	280.645000	543.256175	272.131726			**G**	***631.377351***	316.192314	614.350802	307.679039	613.366786	307.187031	**6**
7	**673.366788**	337.187032	656.340239	328.673758			**L**	***574.355887***	287.681582	557.329338	279.168307	556.345322	278.676299	**5**
8	760.398816	380.703046	743.372267	372.189772	742.388251	371.697764	**S**	***461.271823***	231.139550	444.245274	222.626275	443.261258	222.134267	**4**
9	874.441743	437.724510	857.415194	429.211235	856.431178	428.719227	**N**	***374.239795***	187.623536	357.213246	179.110261			**3**
10	987.525807	494.266542	970.499258	485.753267	969.515242	485.261259	**I**	***260.196868***	130.602072	243.170319	122.088798			**2**
11							**K**	147.112804	74.060040	130.086255	65.546766			**1**



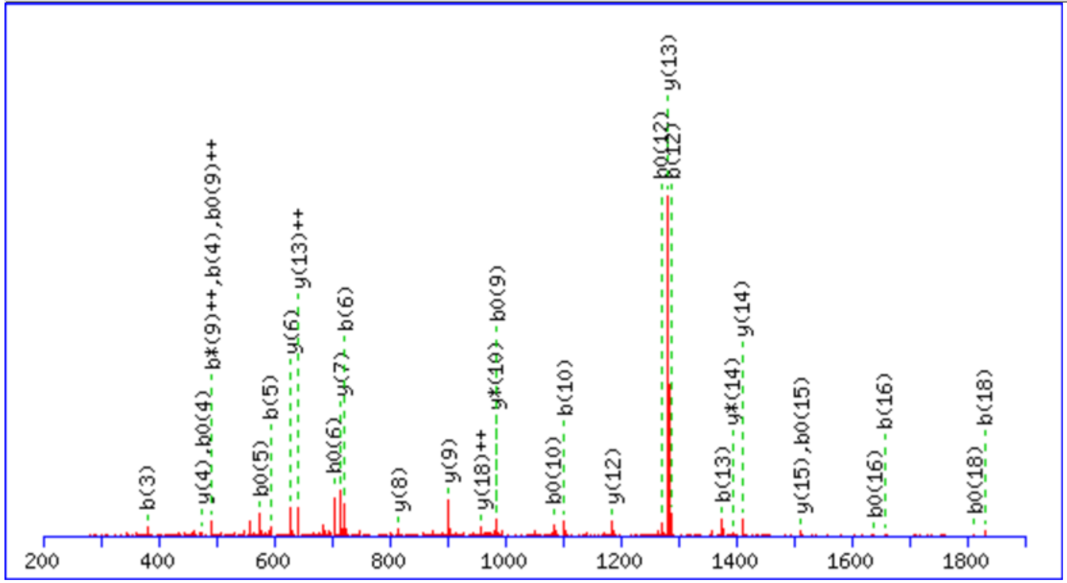
Peptide View

MS/MS Fragmentation of **SYELTQPPSVSVSPGQTAR**
Found in **IPI00382440**, Tax_Id=9606 Gene_Symbol=- Ig lambda chain V-IV region Hil
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 13449: 2002.995448 from(1002.505000,2+)
Title: OECHL100317_27.13143.13143.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 2002.995987**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 60 **Expect:** 0.00019**Matches :** 33/202 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	88.039304	44.523290			70.028739	35.518008	**S**						
2	251.102633	126.054954			233.092068	117.049672	**Y**	1916.971234	958.989255	1899.944685	950.475981	1898.960669	949.9839
3	***380.145226***	190.576251			362.134661	181.570969	**E**	1753.907905	877.457591	1736.881356	868.944316	1735.897340	868.4523
4	***493.229290***	247.118283			475.218725	238.113001	**L**	1624.865312	812.936294	1607.838763	804.423020	1606.854747	803.9310
5	***594.276969***	297.642123			576.266404	288.636840	**T**	***1511.781248***	756.394262	1494.754699	747.880988	1493.770683	747.3889

6	***722.335547***	361.671412	705.308998	353.158137	704.324982	352.666129	**Q**	***1410.733569***	705.870423	1393.707020	697.357148	1392.723004	696.8651
7	819.388311	410.197794	802.361762	401.684519	801.377746	401.192511	**P**	***1282.674991***	641.841134	1265.648442	633.327859	1264.664426	632.8358
8	916.441075	458.724176	899.414526	450.210901	898.430510	449.718893	**P**	***1185.622227***	593.314752	1168.595678	584.801477	1167.611662	584.3094
9	1003.473103	502.240190	986.446554	493.726915	985.462538	493.234907	**S**	1088.569463	544.788370	1071.542914	536.275095	1070.558898	535.7830
10	***1102.541517***	551.774397	1085.514968	543.261122	1084.530952	542.769114	**V**	1001.537435	501.272356	984.510886	492.759081	983.526870	492.2670
11	1189.573545	595.290411	1172.546996	586.777136	1171.562980	586.285128	**S**	***902.469021***	451.738149	885.442472	443.224874	884.458456	442.7328
12	***1288.641959***	644.824618	1271.615410	636.311343	1270.631394	635.819335	**V**	***815.436993***	408.222135	798.410444	399.708860	797.426428	399.2168
13	***1375.673987***	688.340632	1358.647438	679.827357	1357.663422	679.335349	**S**	***716.368579***	358.687928	699.342030	350.174653	698.358014	349.6826
14	1472.726751	736.867014	1455.700202	728.353739	1454.716186	727.861731	**P**	***629.336551***	315.171914	612.310002	306.658639	611.325986	306.1666
15	1529.748215	765.377746	1512.721666	756.864471	1511.737650	756.372463	**G**	532.283787	266.645532	515.257238	258.132257	514.273222	257.6402
16	***1657.806793***	829.407035	1640.780244	820.893760	1639.796228	820.401752	**Q**	***475.262323***	238.134800	458.235774	229.621525	457.251758	229.1295
17	1758.854472	879.930874	1741.827923	871.417600	1740.843907	870.925592	**T**	347.203745	174.105510	330.177196	165.592236	329.193180	165.1002
18	***1829.891586***	915.449431	1812.865037	906.936157	1811.881021	906.444149	**A**	246.156066	123.581671	229.129517	115.068396		
19							**R**	175.118952	88.063114	158.092403	79.549839		

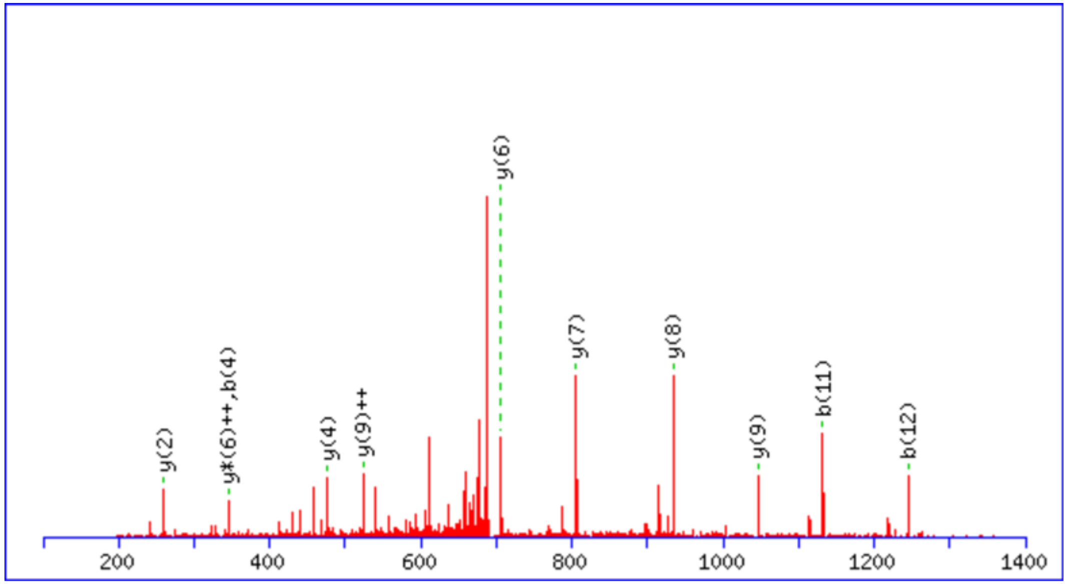


Peptide View

MS/MS Fragmentation of **ATGDIKVTESEIK**
Found in **IPI00302614**, Tax_Id=9606 Gene_Symbol=VTCN1 V-set domain containing T cell activation inhibitor 1
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 8456: 1389.735848 from(695.875200,2+)
Title: OECHL100317_27.8499.8499.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1389.735107**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 49 **Expect:** 0.0011**Matches :** 11/128 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	72.044390	36.525833					**A**						
2	173.092069	87.049672			155.081504	78.044390	**T**	1319.705288	660.356282	1302.678739	651.843008	1301.694723	651.3509
3	230.113533	115.560404			212.102968	106.555122	**G**	1218.657609	609.832442	1201.631060	601.319168	1200.647044	600.8271
4	**345.140476**	173.073876			327.129911	164.068593	**D**	1161.636145	581.321710	1144.609596	572.808436	1143.625580	572.3164
5	458.224540	229.615908			440.213975	220.610626	**I**	***1046.609202***	523.808239	1029.582653	515.294964	1028.598637	514.8029
6	586.319503	293.663390	569.292954	285.150115	568.308938	284.658107	**K**	***933.525138***	467.266207	916.498589	458.752932	915.514573	458.2609
7	685.387917	343.197597	668.361368	334.684322	667.377352	334.192314	**V**	***805.430175***	403.218725	788.403626	394.705451	787.419610	394.2134
8	786.435596	393.721436	769.409047	385.208162	768.425031	384.716154	**T**	***706.361761***	353.684518	689.335212	345.171244	688.351196	344.6792
9	915.478189	458.242733	898.451640	449.729458	897.467624	449.237450	**E**	605.314082	303.160679	588.287533	294.647404	587.303517	294.1553
10	1002.510217	501.758747	985.483668	493.245472	984.499652	492.753464	**S**	***476.271489***	238.639382	459.244940	230.126108	458.260924	229.6341
11	**1131.552810**	566.280043	1114.526261	557.766769	1113.542245	557.274760	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.1180
12	**1244.636874**	622.822075	1227.610325	614.308800	1226.626309	613.816792	**I**	***260.196868***	130.602072	243.170319	122.088797		
13							**K**	147.112804	74.060040	130.086255	65.546765		



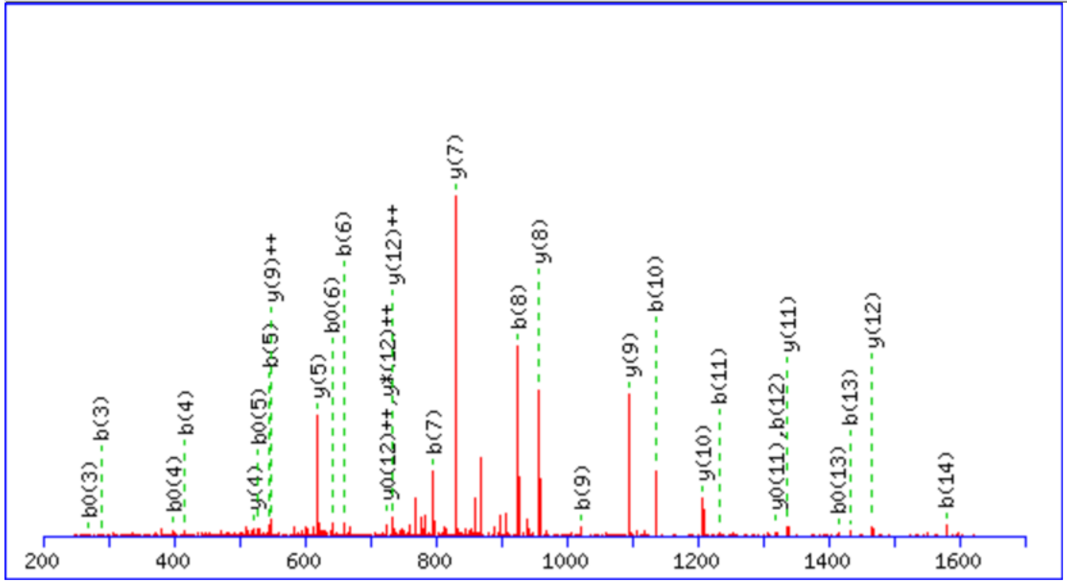
Peptide View

MS/MS Fragmentation of **STVEELHEPIPSLFR**
Found in **IPI00410487**, Tax_Id=9606 Gene_Symbol=TWSG1 Isoform 1 of Twisted gastrulation protein homolog 1
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 12173: 1752.906648 from(877.460600,2+)
Title: OECHL100317_27.16743.16743.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1752.904633**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 74 **Expect:** 4.3e-006**Matches :** 30/134 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	**S**							**15**
2	189.086983	95.047129	171.076418	86.041847	**T**	1666.879898	833.943587	1649.853349	825.430313	1648.869333	824.938304	**14**
3	***288.155397***	144.581336	270.144832	135.576054	**V**	1565.832219	783.419748	1548.805670	774.906473	1547.821654	774.414465	**13**
4	***417.197990***	209.102633	399.187425	200.097351	**E**	**1466.763805**	733.885541	1449.737256	725.372266	1448.753240	724.880258	**12**
5	***546.240583***	273.623930	528.230018	264.618647	**E**	**1337.721212**	669.364244	1320.694663	660.850970	1319.710647	660.358961	**11**

6	***659.324647***	330.165962	641.314082	321.160679	**L**	**1208.678619**	604.842948	1191.652070	596.329673	1190.668054	595.837665	**10**
7	***796.383559***	398.695418	778.372994	389.690135	**H**	**1095.594555**	548.300915	1078.568006	539.787641	1077.583990	539.295633	**9**
8	***925.426152***	463.216714	907.415587	454.211432	**E**	**958.535643**	479.771460	941.509094	471.258185	940.525078	470.766177	**8**
9	***1022.478916***	511.743096	1004.468351	502.737814	**P**	**829.493050**	415.250163	812.466501	406.736889	811.482485	406.244881	**7**
10	***1135.562980***	568.285128	1117.552415	559.279845	**I**	732.440286	366.723781	715.413737	358.210507	714.429721	357.718499	**6**
11	***1232.615744***	616.811510	1214.605179	607.806227	**P**	**619.356222**	310.181749	602.329673	301.668475	601.345657	301.176467	**5**
12	***1319.647772***	660.327524	1301.637207	651.322242	**S**	**522.303458**	261.655367	505.276909	253.142093	504.292893	252.650085	**4**
13	***1432.731836***	716.869556	1414.721271	707.864273	**L**	435.271430	218.139353	418.244881	209.626078			**3**
14	***1579.800250***	790.403763	1561.789685	781.398481	**F**	322.187366	161.597321	305.160817	153.084047			**2**
15					**R**	175.118952	88.063114	158.092403	79.549839			**1**

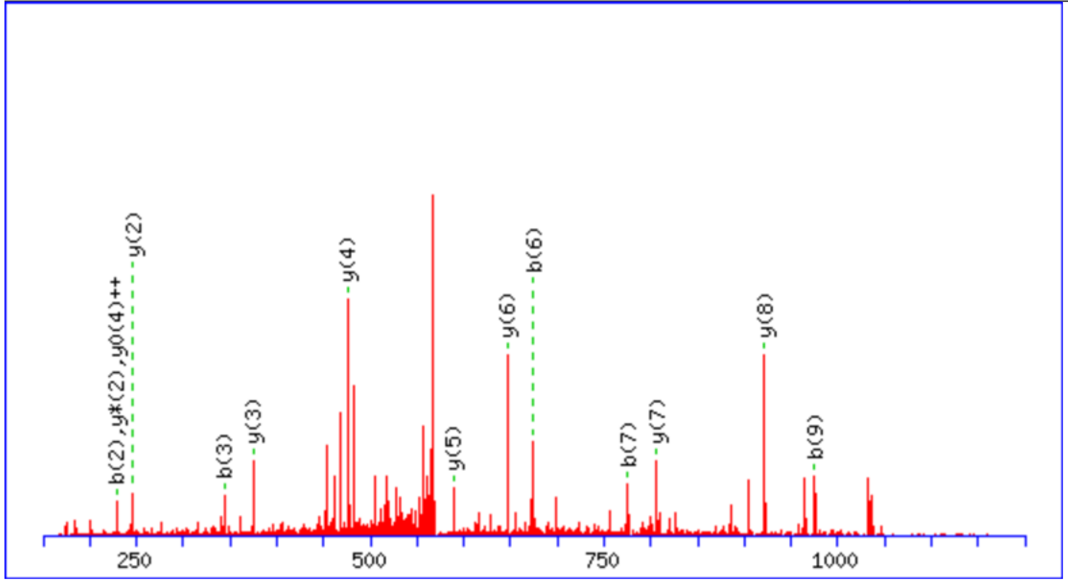


Peptide View

MS/MS Fragmentation of **LDDCGLTEAR**
Found in **IPI00550069**, Tax_Id=9606 Gene_Symbol=RNH1 Ribonuclease inhibitor
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 5419: 1148.511848 from(575.263200,2+)
Title: OECHL100317_27.8317.8317.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1148.513184**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 51 **Expect:** 0.00041**Matches :** 14/84 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							10
2	**229.118283**	115.062779	211.107718	106.057497	D	1036.436401	518.721839	1019.409852	510.208564	1018.425836	509.716556	9
3	**344.145226**	172.576251	326.134661	163.570968	D	***921.409458***	461.208367	904.382909	452.695093	903.398893	452.203085	8
4	504.175875	252.591575	486.165310	243.586293	C	***806.382515***	403.694896	789.355966	395.181621	788.371950	394.689613	7
5	561.197339	281.102308	543.186774	272.097025	G	***646.351866***	323.679571	629.325317	315.166297	628.341301	314.674289	6
6	**674.281403**	337.644340	656.270838	328.639057	L	***589.330402***	295.168839	572.303853	286.655565	571.319837	286.163557	5
7	**775.329082**	388.168179	757.318517	379.162897	T	***476.246338***	238.626807	459.219789	230.113532	458.235773	229.621524	4
8	904.371675	452.689476	886.361110	443.684193	E	***375.198659***	188.102967	358.172110	179.589693	357.188094	179.097685	3
9	**975.408789**	488.208033	957.398224	479.202750	A	***246.156066***	123.581671	229.129517	115.068396			2
10					R	175.118952	88.063114	158.092403	79.549839			1

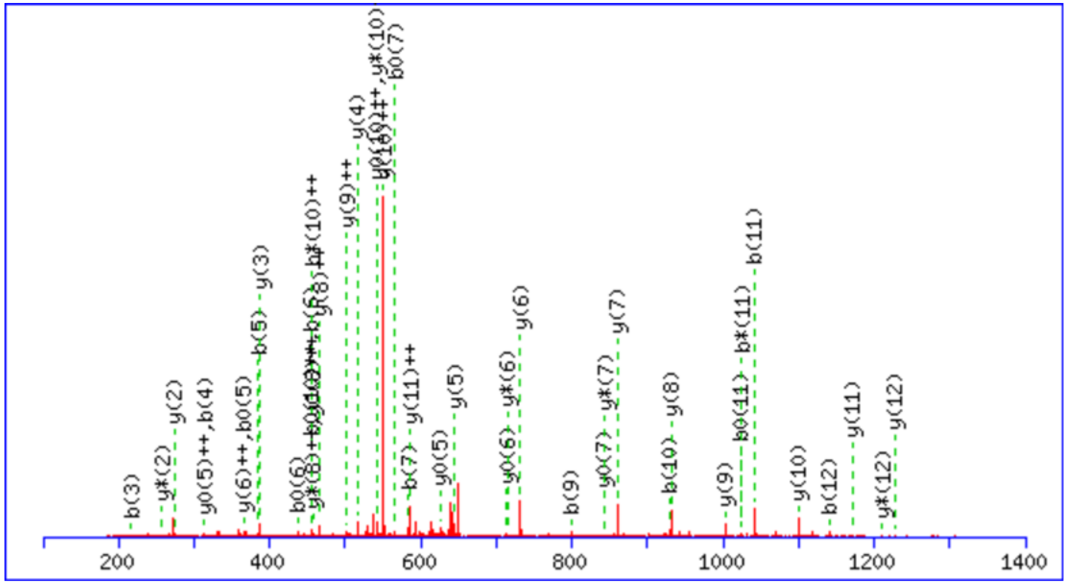


Peptide View

MS/MS Fragmentation of **SGAPAAESKEIVR**
Found in **IPI00299977**, Tax_Id=9606 Gene_Symbol=PHPT1 14 kDa phosphohistidine phosphatase
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 7814: 1313.695448 from(657.855000,2+)
Title: OECHL100317_27.5400.5400.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1313.693893**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 53 **Expect:** 0.0006**Matches :** 44/122 fragment ions using 111 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	88.039304	44.523290			70.028739	35.518008	**S**						
2	145.060768	73.034022			127.050203	64.028740	**G**	***1227.669177***	614.338227	1210.642628	605.824952	1209.658612	605.3329
3	**216.097882**	108.552579			198.087317	99.547296	**A**	***1170.647713***	585.827495	1153.621164	577.314220	1152.637148	576.8222
4	**313.150646**	157.078961			295.140081	148.073679	**P**	***1099.610599***	550.308938	1082.584050	541.795663	1081.600034	541.3036
5	**384.187760**	192.597518			366.177195	183.592235	**A**	***1002.557835***	501.782556	985.531286	493.269281	984.547270	492.7772
6	**455.224874**	228.116075			437.214309	219.110792	**A**	***931.520721***	466.263999	914.494172	457.750724	913.510156	457.2587
7	**584.267467**	292.637372			566.256902	283.632089	**E**	***860.483607***	430.745442	843.457058	422.232167	842.473042	421.7401
8	671.299495	336.153386			653.288930	327.148103	**S**	***731.441014***	366.224145	714.414465	357.710871	713.430449	357.2188
9	**799.394458**	400.200867	782.367909	391.687592	781.383893	391.195585	**K**	***644.408986***	322.708131	627.382437	314.194857	626.398421	313.7028
10	**928.437051**	464.722164	911.410502	456.208889	910.426486	455.716881	**E**	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.6553
11	**1041.521115**	521.264196	1024.494566	512.750921	1023.510550	512.258913	**I**	***387.271430***	194.139353	370.244881	185.626079		
12	**1140.589529**	570.798403	1123.562980	562.285128	1122.578964	561.793120	**V**	***274.187366***	137.597321	257.160817	129.084047		
13							**R**	175.118952	88.063114	158.092403	79.549839		



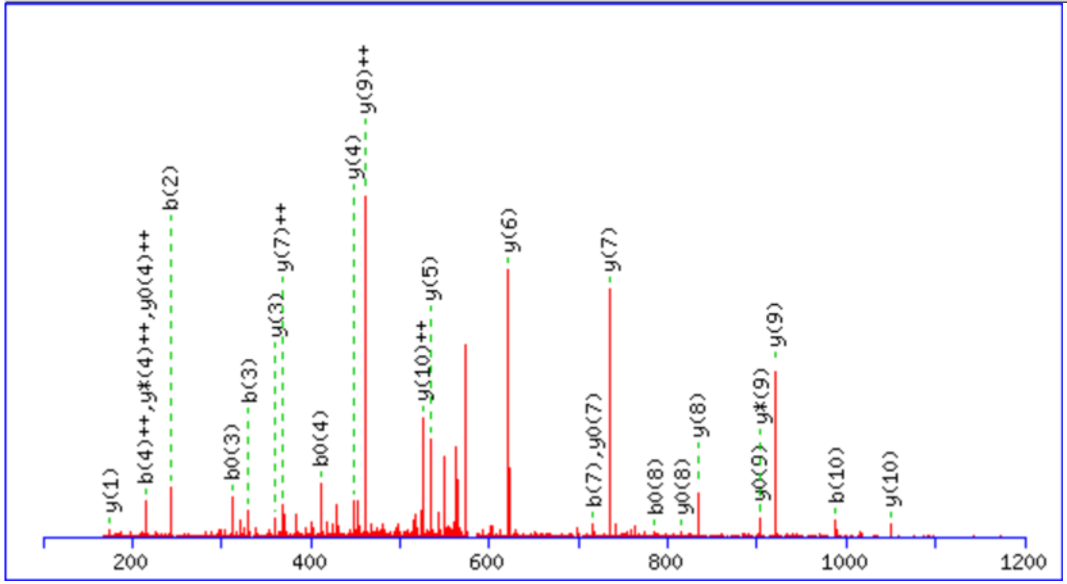
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 5666: 1161.635848 from(581.825200,2+)
Title: OECHL100317_27.5747.5747.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70 **Expect:** 5.9e-006**Matches :** 26/94 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	114.091340	57.549308					I						
2	**243.133933**	122.070605			225.123368	113.065322	E	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637
3	**330.165961**	165.586618			312.155396	156.581336	S	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340
4	429.234375	215.120826			411.223810	206.115543	V	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326
5	542.318439	271.662858			524.307874	262.657575	L	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119

6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087
7	**716.382495**	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073
8	803.414523	402.210899			785.403958	393.205617	**S**	***447.267407***	224.137342	430.240858	215.624067	429.256842	215.132059
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053		
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321		
11							**R**	***175.118952***	88.063114	158.092403	79.549840		

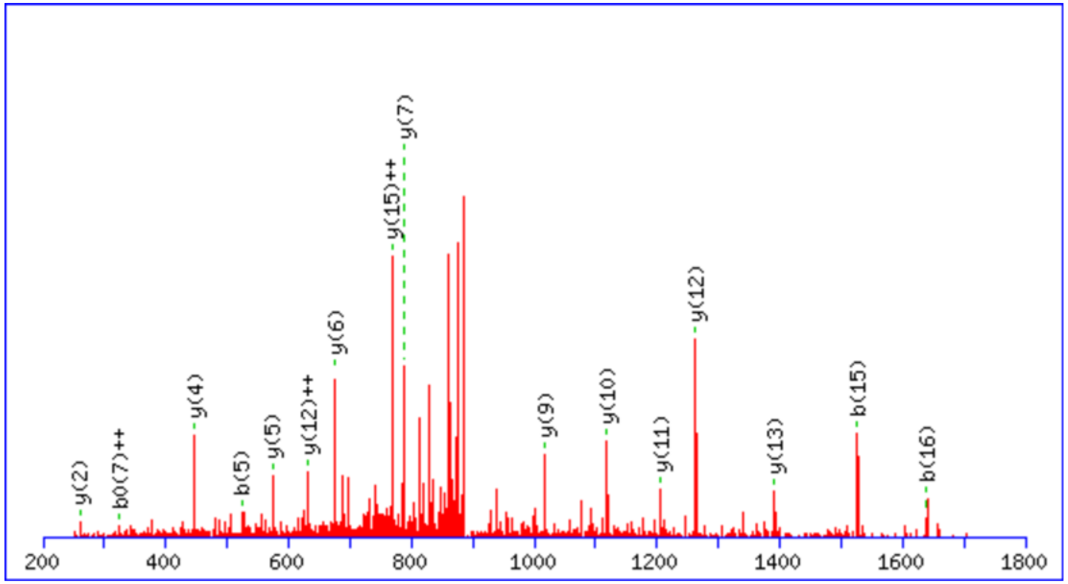


Peptide View

MS/MS Fragmentation of **YSGSEGSTQTLTKGELK**
Found in **IPI00017526**, Tax_Id=9606 Gene_Symbol=S100P Protein S100-P
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 12329: 1784.879648 from(893.447100,2+)
Title: OECHL100317_27.8016.8016.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1784.879211**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 66 **Expect:** 3.8e-005**Matches :** 16/170 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	164.070605	82.538940					**Y**						
2	251.102633	126.054954			233.092068	117.049672	**S**	1622.823172	811.915224	1605.796623	803.401950	1604.812607	802.9099
3	308.124097	154.565687			290.113532	145.560404	**G**	1535.791144	768.399210	1518.764595	759.885936	1517.780579	759.3939
4	395.156125	198.081701			377.145560	189.076418	**S**	1478.769680	739.888478	1461.743131	731.375204	1460.759115	730.8831
5	**524.198718**	262.602997			506.188153	253.597715	**E**	***1391.737652***	696.372464	1374.711103	687.859190	1373.727087	687.3671
6	581.220182	291.113729			563.209617	282.108447	**G**	***1262.695059***	631.851167	1245.668510	623.337893	1244.684494	622.8458
7	668.252210	334.629743			650.241645	325.624461	**S**	***1205.673595***	603.340436	1188.647046	594.827161	1187.663030	594.3351
8	769.299889	385.153583			751.289324	376.148300	**T**	***1118.641567***	559.824421	1101.615018	551.311147	1100.631002	550.8191
9	897.358467	449.182872	880.331918	440.669597	879.347902	440.177589	**Q**	***1017.593888***	509.300582	1000.567339	500.787307	999.583323	500.2952
10	998.406146	499.706711	981.379597	491.193437	980.395581	490.701429	**T**	889.535310	445.271293	872.508761	436.758018	871.524745	436.2660
11	1111.490210	556.248743	1094.463661	547.735469	1093.479645	547.243461	**L**	***788.487631***	394.747453	771.461082	386.234179	770.477066	385.7421
12	1212.537889	606.772583	1195.511340	598.259308	1194.527324	597.767300	**T**	***675.403567***	338.205421	658.377018	329.692147	657.393002	329.2001
13	1340.632852	670.820064	1323.606303	662.306790	1322.622287	661.814782	**K**	***574.355888***	287.681582	557.329339	279.168307	556.345323	278.6762
14	1397.654316	699.330796	1380.627767	690.817522	1379.643751	690.325514	**G**	***446.260925***	223.634100	429.234376	215.120826	428.250360	214.6288
15	**1526.696909**	763.852093	1509.670360	755.338818	1508.686344	754.846810	**E**	389.239461	195.123368	372.212912	186.610094	371.228896	186.1180
16	**1639.780973**	820.394124	1622.754424	811.880850	1621.770408	811.388842	**L**	***260.196868***	130.602072	243.170319	122.088797		
17							**K**	147.112804	74.060040	130.086255	65.546765		



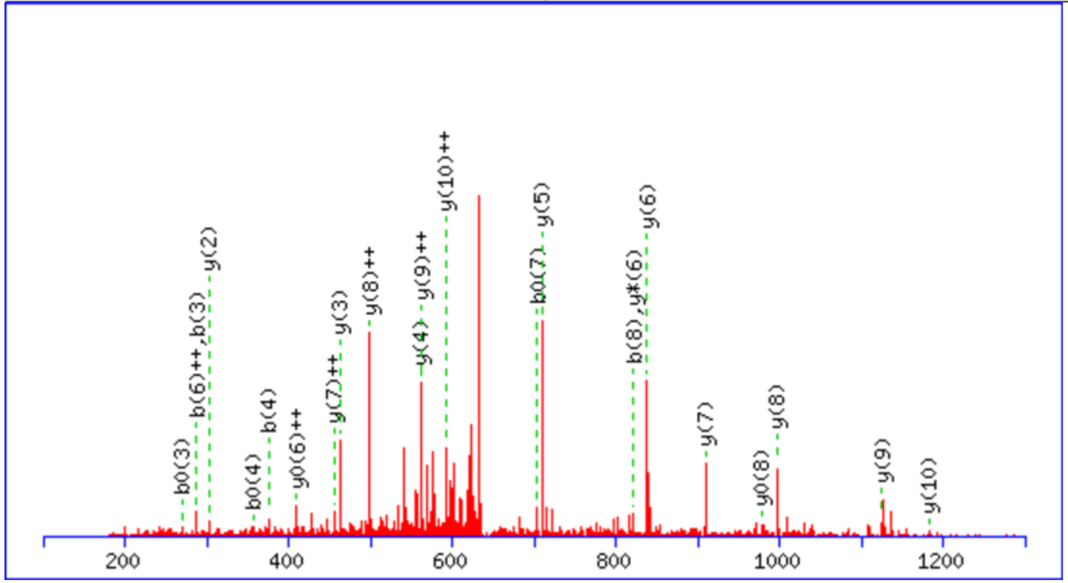
Peptide View

MS/MS Fragmentation of **TGESAEFVCKR**
Found in **IPI00011264**, Tax_Id=9606 Gene_Symbol=CFHR1;LOC100293069 Complement factor H-related protein 1
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 7430: 1282.597648 from(642.306100,2+)
Title: OECHL100317_27.5686.5686.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1282.597580**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56 **Expect:** 0.00013**Matches :** 23/92 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	102.054955	51.531116			84.044390	42.525833	**T**						
2	159.076419	80.041847			141.065854	71.036565	**G**	***1182.557184***	591.782230	1165.530635	583.268956	1164.546619	582.7769
3	**288.119012**	144.563144			270.108447	135.557862	**E**	***1125.535720***	563.271498	1108.509171	554.758224	1107.525155	554.2662
4	**375.151040**	188.079158			357.140475	179.073876	**S**	***996.493127***	498.750202	979.466578	490.236927	978.482562	489.7449
5	446.188154	223.597715			428.177589	214.592433	**A**	***909.461099***	455.234188	892.434550	446.720913	891.450534	446.2289

6	575.230747	288.119012			557.220182	279.113729	**E**	***838.423985***	419.715631	821.397436	411.202356	820.413420	410.7103
7	722.299161	361.653219			704.288596	352.647936	**F**	***709.381392***	355.194334	692.354843	346.681060		
8	**821.367575**	411.187426			803.357010	402.182143	**V**	***562.312978***	281.660127	545.286429	273.146853		
9	981.398224	491.202750			963.387659	482.197468	**C**	***463.244564***	232.125920	446.218015	223.612645		
10	1109.493187	555.250232	1092.466638	546.736957	1091.482622	546.244949	**K**	***303.213915***	152.110595	286.187366	143.597321		
11							**R**	175.118952	88.063114	158.092403	79.549839		

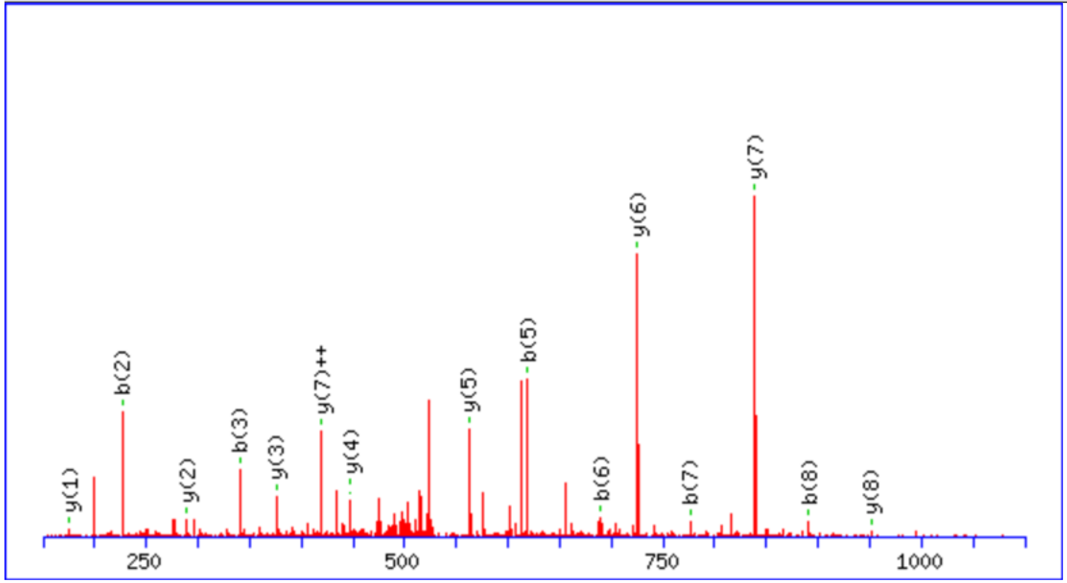


Peptide View

MS/MS Fragmentation of **LLIYDASNR**
Found in **IPI00784430**, Tax_Id=9606 Gene_Symbol=IGKV3D-11 Similar to Ig kappa chain V-III region VG precursor
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 4350: 1063.564448 from(532.789500,2+)
Title: OECHL100317_27.11764.11764.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1063.566177**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51 **Expect:** 0.00062**Matches :** 15/70 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					**L**							**9**
2	**227.175404**	114.091340					**L**	***951.489421***	476.248348	934.462872	467.735074	933.478856	467.243066	**8**
3	**340.259468**	170.633372					**I**	***838.405357***	419.706316	821.378808	411.193042	820.394792	410.701034	**7**
4	503.322797	252.165036					**Y**	***725.321293***	363.164285	708.294744	354.651010	707.310728	354.159002	**6**
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***562.257964***	281.632620	545.231415	273.119345	544.247399	272.627337	**5**
6	**689.386854**	345.197065			671.376289	336.191782	**A**	***447.231021***	224.119148	430.204472	215.605874	429.220456	215.113866	**4**
7	**776.418882**	388.713079			758.408317	379.707796	**S**	***376.193907***	188.600591	359.167358	180.087317	358.183342	179.595309	**3**
8	**890.461809**	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***289.161879***	145.084577	272.135330	136.571303			**2**
9							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**

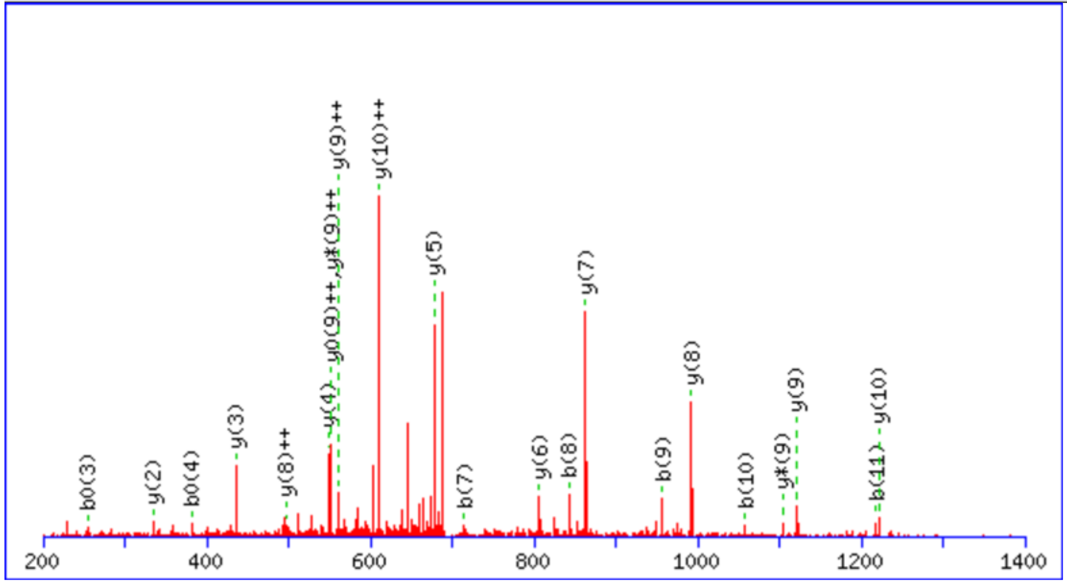


Peptide View

MS/MS Fragmentation of **VATQEGKEITCR**
Found in **IPI00031564**, Tax_Id=9606 Gene_Symbol=GGCT Isoform 1 of Gamma-glutamylcyclotransferase
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 8463: 1390.688648 from(696.351600,2+)
Title: OECHL100317_27.4205.4205.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1390.687454**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 53 **Expect:** 0.00072**Matches :** 22/118 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}
1	100.075690	50.541483					V						
2	171.112804	86.060040					A	1292.626328	646.816802	1275.599779	638.303528	1274.615763	637.8115
3	272.160483	136.583879			254.149918	127.578597	T	***1221.589214***	611.298245	1204.562665	602.784971	1203.578649	602.2929
4	400.219061	200.613169	383.192512	192.099894	382.208496	191.607886	Q	***1120.541535***	560.774406	1103.514986	552.261131	1102.530970	551.7691
5	529.261654	265.134465	512.235105	256.621191	511.251089	256.129183	E	***992.482957***	496.745117	975.456408	488.231842	974.472392	487.7398
6	586.283118	293.645197	569.256569	285.131923	568.272553	284.639915	G	***863.440364***	432.223820	846.413815	423.710546	845.429799	423.2185
7	**714.378081**	357.692679	697.351532	349.179404	696.367516	348.687396	K	***806.418900***	403.713088	789.392351	395.199814	788.408335	394.7078
8	**843.420674**	422.213975	826.394125	413.700701	825.410109	413.208693	E	***678.323937***	339.665607	661.297388	331.152332	660.313372	330.6603
9	**956.504738**	478.756007	939.478189	470.242733	938.494173	469.750725	I	***549.281344***	275.144310	532.254795	266.631036	531.270779	266.1390
10	**1057.552417**	529.279847	1040.525868	520.766572	1039.541852	520.274564	T	***436.197280***	218.602278	419.170731	210.089003	418.186715	209.5969
11	**1217.583066**	609.295171	1200.556517	600.781897	1199.572501	600.289889	C	***335.149601***	168.078438	318.123052	159.565164		
12							R	175.118952	88.063114	158.092403	79.549839		

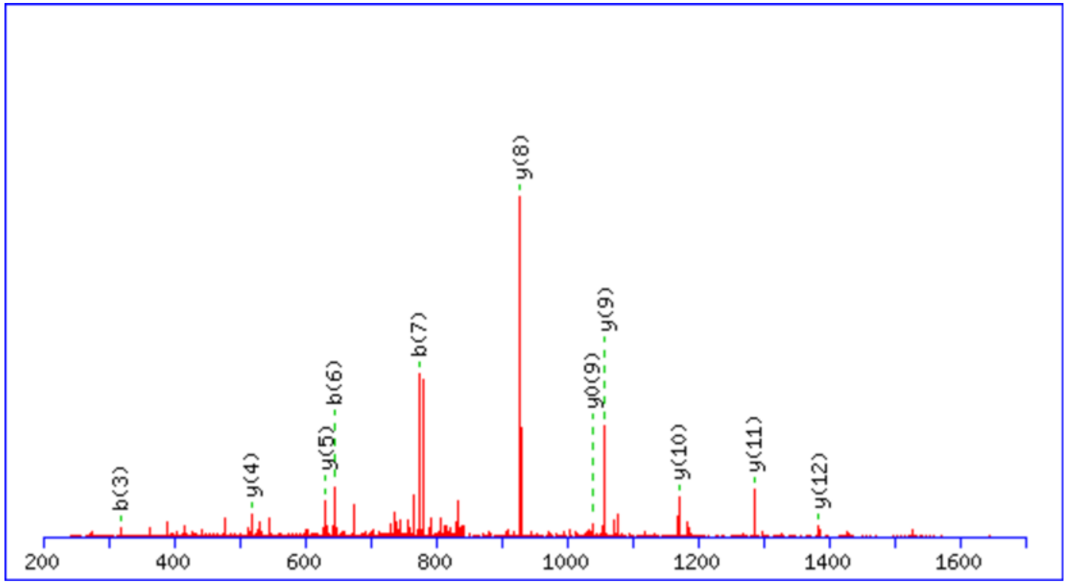


Peptide View

MS/MS Fragmentation of **AVFVDLEPTVIDEVR**
Found in **IPI00909762**, Tax_Id=9606 Gene_Symbol=TUBA1B;TUBA1A cDNA FLJ53765, highly similar to Tubulin alpha chain
Experiment: 51 - PyB-3 **Fraction:** PyB-3

Match to Query 11779: 1700.902848 from(851.458700,2+)
Title: OECHL100317_27.18065.18065.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_27.raw
Monoisotopic mass of neutral peptide Mr(calc): 1700.898514**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51 **Expect:** 0.001**Matches :** 11/128 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**15**
2	171.112804	86.060040			**V**	1630.868665	815.937971	1613.842116	807.424696	1612.858100	806.932688	**14**
3	**318.181218**	159.594247			**F**	1531.800251	766.403764	1514.773702	757.890489	1513.789686	757.398481	**13**
4	417.249632	209.128454			**V**	***1384.731837***	692.869557	1367.705288	684.356282	1366.721272	683.864274	**12**
5	532.276575	266.641926	514.266010	257.636643	**D**	***1285.663423***	643.335350	1268.636874	634.822075	1267.652858	634.330067	**11**
6	**645.360639**	323.183958	627.350074	314.178675	**L**	***1170.636480***	585.821878	1153.609931	577.308604	1152.625915	576.816596	**10**
7	**774.403232**	387.705254	756.392667	378.699972	**E**	***1057.552416***	529.279846	1040.525867	520.766572	1039.541851	520.274564	**9**
8	871.455996	436.231636	853.445431	427.226354	**P**	***928.509823***	464.758550	911.483274	456.245275	910.499258	455.753267	**8**
9	972.503675	486.755476	954.493110	477.750193	**T**	831.457059	416.232168	814.430510	407.718893	813.446494	407.226885	**7**
10	1071.572089	536.289683	1053.561524	527.284400	**V**	730.409380	365.708328	713.382831	357.195054	712.398815	356.703046	**6**
11	1184.656153	592.831715	1166.645588	583.826432	**I**	***631.340966***	316.174121	614.314417	307.660846	613.330401	307.168838	**5**
12	1299.683096	650.345186	1281.672531	641.339904	**D**	***518.256902***	259.632089	501.230353	251.118815	500.246337	250.626807	**4**
13	1428.725689	714.866483	1410.715124	705.861200	**E**	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	**3**
14	1527.794103	764.400690	1509.783538	755.395407	**V**	274.187366	137.597321	257.160817	129.084047			**2**
15					**R**	175.118952	88.063114	158.092403	79.549839			**1**



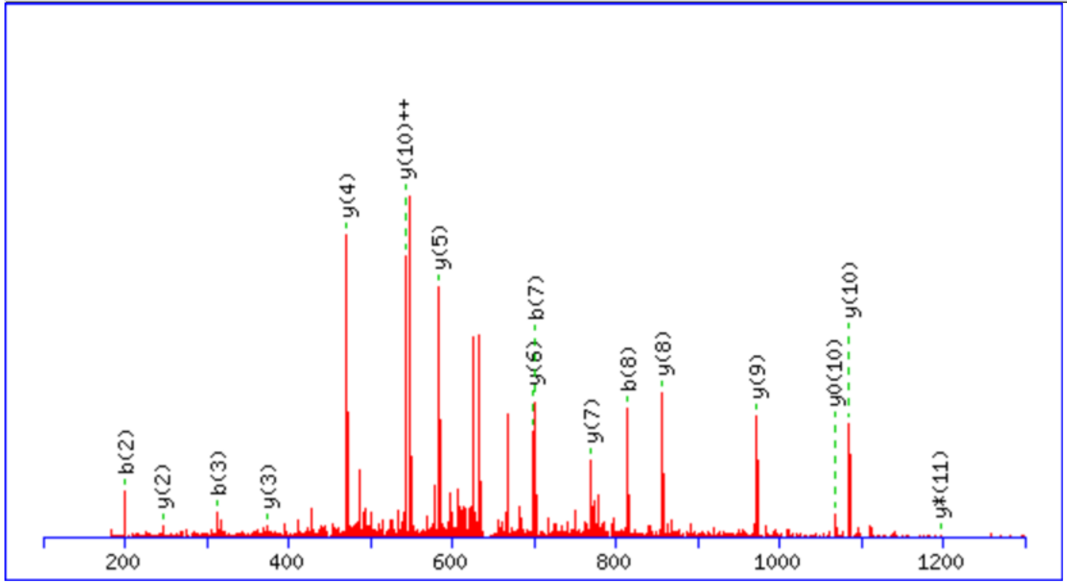
Peptide View

MS/MS Fragmentation of **AQLDSADIPKAR**
Found in **IPI00026303**, Tax_Id=9606 Gene_Symbol=PI15 Peptidase inhibitor 15
Experiment: 24 - NOPC3 **Fraction:** NOPC3

Match to Query 7508: 1283.683848 from(642.849200,2+)
Title: OECHL100317_25.8047.8047.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1283.683334**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 59 **Expect:** 9.3e-005**Matches :** 16/114 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	72.044390	36.525833					A						
2	**200.102968**	100.555122	183.076419	92.041848			Q	1213.653527	607.330402	1196.626978	598.817127	1195.642962	598.3251
3	**313.187032**	157.097154	296.160483	148.583879			L	***1085.594949***	543.301113	1068.568400	534.787838	1067.584384	534.2958
4	428.213975	214.610626	411.187426	206.097351	410.203410	205.605343	D	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
5	515.246003	258.126640	498.219454	249.613365	497.235438	249.121357	S	***857.483942***	429.245609	840.457393	420.732335	839.473377	420.2403

6	586.283117	293.645197	569.256568	285.131922	568.272552	284.639914	**A**	***770.451914***	385.729595	753.425365	377.216321	752.441349	376.7243
7	**701.310060**	351.158668	684.283511	342.645394	683.299495	342.153386	**D**	***699.414800***	350.211038	682.388251	341.697764	681.404235	341.2057
8	**814.394124**	407.700700	797.367575	399.187426	796.383559	398.695418	**I**	***584.387857***	292.697567	567.361308	284.184292		
9	911.446888	456.227082	894.420339	447.713808	893.436323	447.221800	**P**	***471.303793***	236.155535	454.277244	227.642260		
10	1039.541851	520.274564	1022.515302	511.761289	1021.531286	511.269281	**K**	***374.251029***	187.629153	357.224480	179.115878		
11	1110.578965	555.793121	1093.552416	547.279846	1092.568400	546.787838	**A**	***246.156066***	123.581671	229.129517	115.068396		
12							**R**	175.118952	88.063114	158.092403	79.549839		



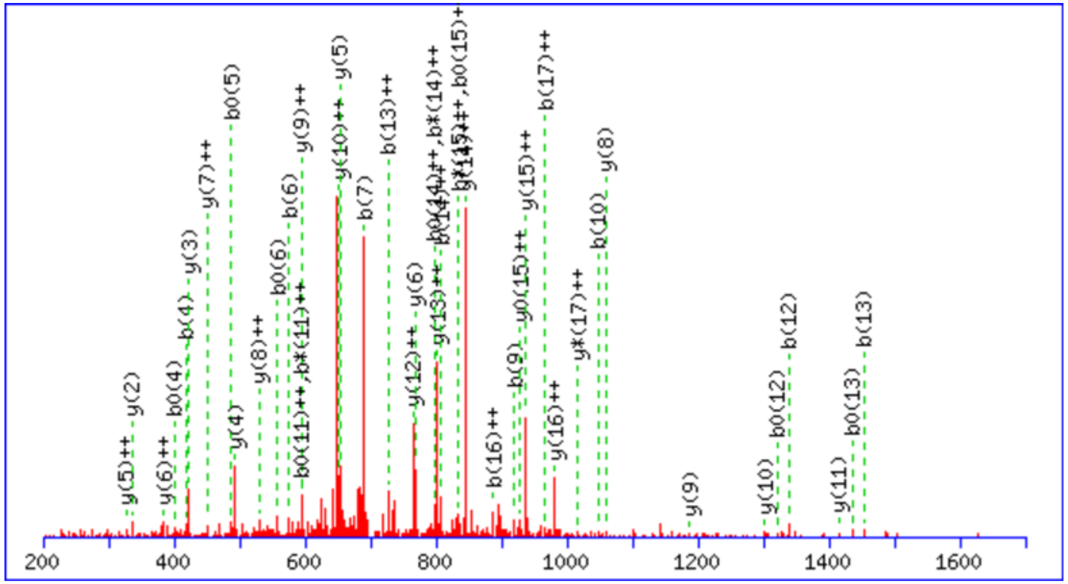
Peptide View

MS/MS Fragmentation of **GSSWSADLDKCMDCASCR**
Found in **IPI00010277**, Tax_Id=9606 Gene_Symbol=TNFRSF12A Isoform 1 of Tumor necrosis factor receptor superfamily member 12A
Experiment: 24 - NOPC3 **Fraction:** NOPC3

Match to Query 14680: 2104.806972 from(702.609600,3+)
Title: OECHL100317_25.14729.14729.3.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 2104.807083**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**

Score: 55 **Expect:** 1.8e-005**Matches :** 44/180 fragment ions using 93 most intense peaks (help)

#	**b**	**b^{++}**	**b***	**b*$^{++}$**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y*$^{++}$**	**y^{0}**	**y^{0}**
1	58.028740	29.518008					**G**						
2	145.060768	73.034022			127.050203	64.028740	**S**	2048.792893	1024.900085	2031.766344	1016.386810	2030.782328	1015.8
3	232.092796	116.550036			214.082231	107.544753	**S**	1961.760865	981.384071	1944.734316	972.870796	1943.750300	972.3
4	**418.172109**	209.589693			400.161544	200.584410	**W**	1874.728837	937.868057	1857.702288	929.354782	1856.718272	928.8
5	505.204137	253.105707			487.193572	244.100424	**S**	1688.649524	844.828400	1671.622975	836.315126	1670.638959	835.8
6	**576.241251**	288.624264			558.230686	279.618981	**A**	1601.617496	801.312386	1584.590947	792.799112	1583.606931	792.3
7	**691.268194**	346.137735			673.257629	337.132453	**D**	1530.580382	765.793829	1513.553833	757.280555	1512.569817	756.7
8	804.352258	402.679767			786.341693	393.674485	**L**	***1415.553439***	708.280358	1398.526890	699.767083	1397.542874	699.2
9	**919.379201**	460.193239			901.368636	451.187956	**D**	***1302.469375***	651.738326	1285.442826	643.225051	1284.458810	642.7
10	**1047.474164**	524.240720	1030.447615	515.727446	1029.463599	515.235437	**K**	***1187.442432***	594.224854	1170.415883	585.711580	1169.431867	585.2
11	1207.504813	604.256045	1190.478264	595.742770	1189.494248	595.250762	**C**	***1059.347469***	530.177373	1042.320920	521.664098	1041.336904	521.1
12	**1338.545298**	669.776287	1321.518749	661.263013	1320.534733	660.771005	**M**	899.316820	450.162048	882.290271	441.648774	881.306255	441.1
13	**1453.572241**	**727.289759**	1436.545692	718.776484	1435.561676	718.284476	**D**	***768.276335***	384.641806	751.249786	376.128531	750.265770	375.6
14	1613.602890	**807.305083**	1596.576341	798.791809	1595.592325	798.299801	**C**	***653.249392***	327.128334	636.222843	318.615060	635.238827	318.1
15	1684.640004	842.823640	1667.613455	834.310366	1666.629439	833.818358	**A**	***493.218743***	247.113010	476.192194	238.599735	475.208178	238.1
16	1771.672032	**886.339654**	1754.645483	877.826380	1753.661467	877.334372	**S**	***422.181629***	211.594453	405.155080	203.081178	404.171064	202.5
17	1931.702681	**966.354979**	1914.676132	957.841704	1913.692116	957.349696	**C**	***335.149601***	168.078439	318.123052	159.565164		
18							**R**	175.118952	88.063114	158.092403	79.549840		



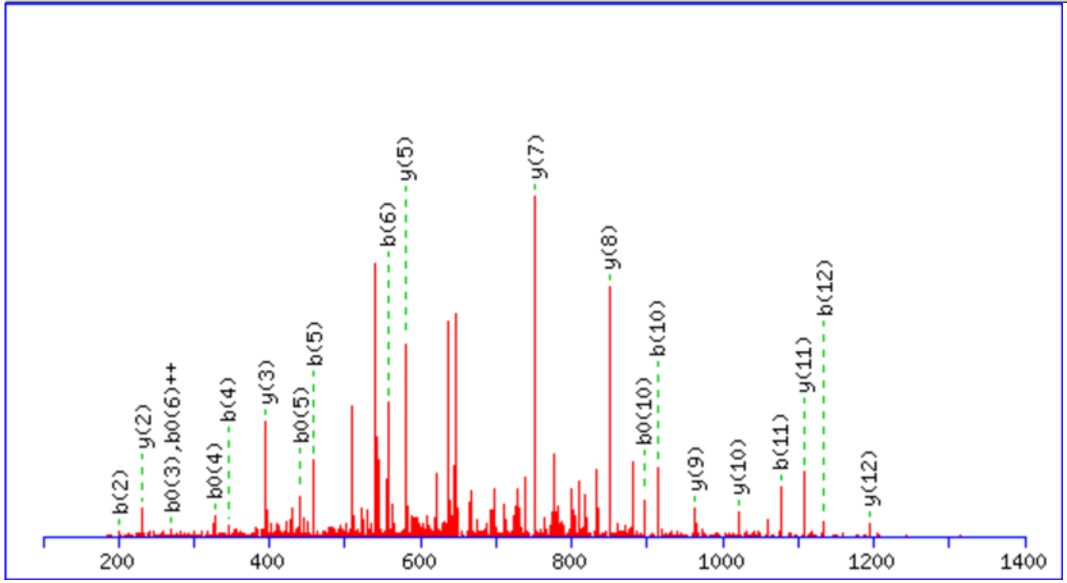
Peptide View

MS/MS Fragmentation of **LSSGLVTAALYGR**
Found in **IPI00218413**, Tax_Id=9606 Gene_Symbol=BTD Biotinidase
Experiment: 24 - NOPC3 **Fraction:** NOPC3

Match to Query 7846: 1306.726248 from(654.370400,2+)
Title: OECHL100317_25.17291.17291.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1306.724487**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67 **Expect:** 9.7e-006**Matches :** 21/106 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			**L**							**13**
2	**201.123368**	101.065322	183.112803	92.060039	**S**	***1194.647714***	597.827495	1177.621165	589.314221	1176.637149	588.822212	**12**
3	288.155396	144.581336	270.144831	135.576053	**S**	***1107.615686***	554.311481	1090.589137	545.798206	1089.605121	545.306198	**11**
4	**345.176860**	173.092068	327.166295	164.086785	**G**	***1020.583658***	510.795467	1003.557109	502.282192	1002.573093	501.790184	**10**
5	**458.260924**	229.634100	440.250359	220.628817	**L**	***963.562194***	482.284735	946.535645	473.771460	945.551629	473.279452	**9**

6	**557.329338**	279.168307	539.318773	270.163025	**V**	***850.478130***	425.742703	833.451581	417.229428	832.467565	416.737420	**8**
7	658.377017	329.692147	640.366452	320.686864	**T**	***751.409716***	376.208496	734.383167	367.695221	733.399151	367.203213	**7**
8	729.414131	365.210704	711.403566	356.205421	**A**	650.362037	325.684656	633.335488	317.171382			**6**
9	800.451245	400.729261	782.440680	391.723978	**A**	***579.324923***	290.166099	562.298374	281.652825			**5**
10	**913.535309**	457.271293	895.524744	448.266010	**L**	508.287809	254.647542	491.261260	246.134268			**4**
11	**1076.598638**	538.802957	1058.588073	529.797674	**Y**	***395.203745***	198.105510	378.177196	189.592236			**3**
12	**1133.620102**	567.313689	1115.609537	558.308406	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
13					**R**	175.118952	88.063114	158.092403	79.549839			**1**



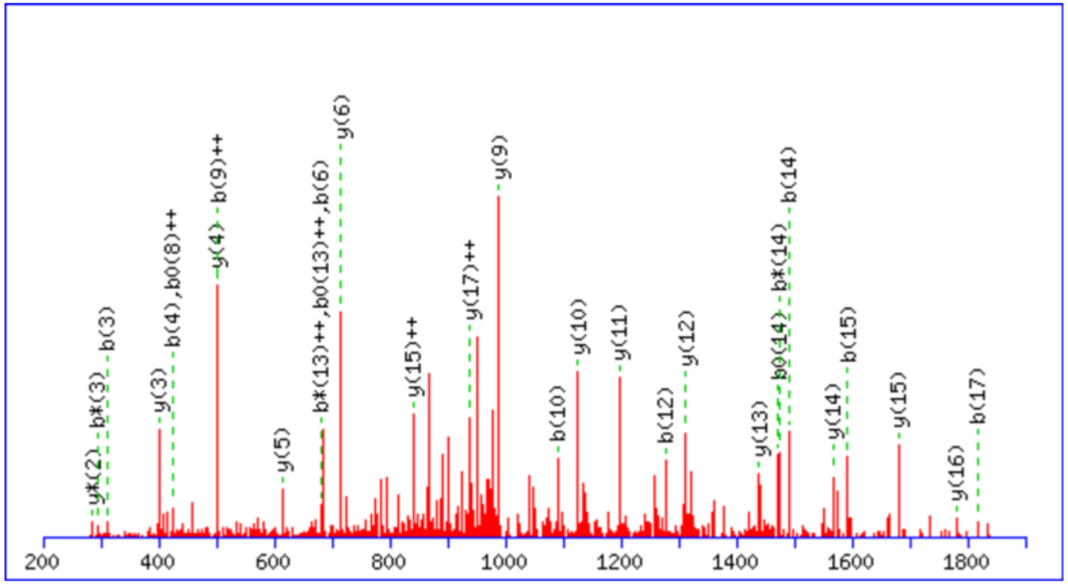
Peptide View

MS/MS Fragmentation of **NPVLQQDAHSSVTITPQR**
Found in **IPI00410488**, Tax_Id=9606 Gene_Symbol=CD276 Isoform 1 of CD276 antigen
Experiment: 24 - NOPC3 **Fraction:** NOPC3

Match to Query 13948: 1990.021848 from(996.018200,2+)
Title: OECHL100317_25.10015.10015.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1990.023209**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 74 **Expect:** 5.9e-006**Matches :** 30/186 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	115.050203	58.028740	98.023654	49.515465			**N**						
2	212.102967	106.555121	195.076418	98.041847			**P**	1876.987553	938.997415	1859.961004	930.484140	1858.976988	929.9921
3	**311.171381**	156.089328	294.144832	147.576054			**V**	***1779.934789***	890.471033	1762.908240	881.957758	1761.924224	881.4657
4	**424.255445**	212.631361	407.228896	204.118086			**L**	***1680.866375***	840.936826	1663.839826	832.423551	1662.855810	831.9315
5	552.314023	276.660650	535.287474	268.147375			**Q**	***1567.782311***	784.394794	1550.755762	775.881519	1549.771746	775.3895
6	**680.372601**	340.689939	663.346052	332.176664			**Q**	***1439.723733***	720.365505	1422.697184	711.852230	1421.713168	711.3602
7	795.399544	398.203410	778.372995	389.690136	777.388979	389.198128	**D**	***1311.665155***	656.336215	1294.638606	647.822941	1293.654590	647.3309
8	866.436658	433.721967	849.410109	425.208693	848.426093	424.716685	**A**	***1196.638212***	598.822744	1179.611663	590.309470	1178.627647	589.8174
9	1003.495570	502.251423	986.469021	493.738149	985.485005	493.246141	**H**	***1125.601098***	563.304187	1108.574549	554.790913	1107.590533	554.2989
10	**1090.527598**	545.767437	1073.501049	537.254163	1072.517033	536.762155	**S**	***988.542186***	494.774731	971.515637	486.261457	970.531621	485.7694
11	1177.559626	589.283451	1160.533077	580.770177	1159.549061	580.278169	**S**	901.510158	451.258717	884.483609	442.745443	883.499593	442.2534
12	**1276.628040**	638.817658	1259.601491	630.304384	1258.617475	629.812376	**V**	814.478130	407.742703	797.451581	399.229428	796.467565	398.7374
13	1377.675719	689.341498	1360.649170	680.828223	1359.665154	680.336215	**T**	***715.409716***	358.208496	698.383167	349.695221	697.399151	349.2032
14	**1490.759783**	745.883530	1473.733234	737.370255	1472.749218	736.878247	**I**	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.6793
15	**1591.807462**	796.407369	1574.780913	787.894095	1573.796897	787.402087	**T**	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.1373
16	1688.860226	844.933751	1671.833677	836.420477	1670.849661	835.928469	**P**	***400.230294***	200.618785	383.203745	192.105510		
17	**1816.918804**	908.963040	1799.892255	900.449766	1798.908239	899.957758	**Q**	303.177530	152.092403	286.150981	143.579128		
18							**R**	175.118952	88.063114	158.092403	79.549839		



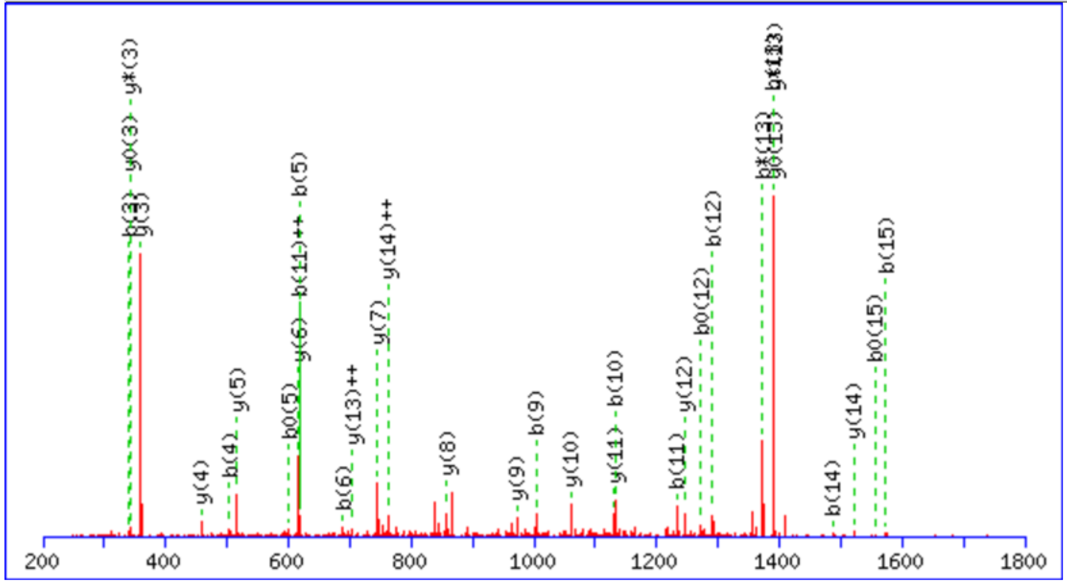
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 24 - NOPC3 **Fraction:** NOPC3

Match to Query 12232: 1746.916448 from(874.465500,2+)
Title: OECHL100317_25.17184.17184.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 77 **Expect:** 2.1e-006**Matches :** 33/156 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	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	***340.259468***	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	***503.322797***	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	***618.349740***	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018

6	***689.386854***	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	***1003.545873***	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	***1132.588466***	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	***1233.636145***	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	***1290.657609***	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	***1389.726023***	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	***1486.778787***	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	***1573.810815***	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							**R**	175.118952	88.063114	158.092403	79.549839		



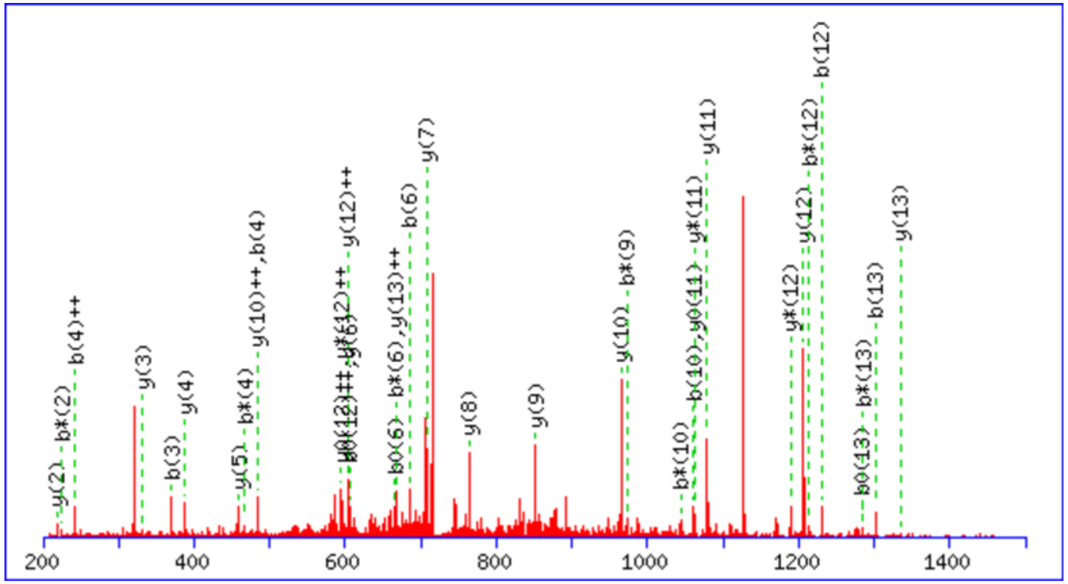
Peptide View

MS/MS Fragmentation of **IQQLNSGTFAGLAK**
Found in **IPI00248596**, Tax_Id=9606 Gene_Symbol=ELFN1 extracellular leucine-rich repeat and fibronectin type III domain containing 1

Experiment: 24 - NOPC3 **Fraction:** NOPC3

Match to Query 9051: 1446.783848 from(724.399200,2+)
Title: OECHL100317_25.15300.15300.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1446.783066**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 81 **Expect:** 5e-007**Matches :** 38/132 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	114.091340	57.549308					**I**						
2	**242.149918**	121.578597	225.123369	113.065323			**Q**	***1334.706292***	667.856784	1317.679743	659.343510	1316.695727	658.8515
3	**370.208496**	185.607886	353.181947	177.094612			**Q**	***1206.647714***	603.827495	1189.621165	595.314221	1188.637149	594.8222
4	**483.292560**	242.149918	466.266011	233.636644			**L**	***1078.589136***	539.798206	1061.562587	531.284931	1060.578571	530.7929
5	597.335487	299.171382	580.308938	290.658107			**N**	***965.505072***	483.256174	948.478523	474.742899	947.494507	474.2508
6	**684.367515**	342.687396	667.340966	334.174121	666.356950	333.682113	**S**	***851.462145***	426.234711	834.435596	417.721436	833.451580	417.2294
7	741.388979	371.198128	724.362430	362.684853	723.378414	362.192845	**G**	***764.430117***	382.718697	747.403568	374.205422	746.419552	373.7134
8	842.436658	421.721967	825.410109	413.208693	824.426093	412.716685	**T**	***707.408653***	354.207965	690.382104	345.694690	689.398088	345.2026
9	989.505072	495.256174	972.478523	486.742900	971.494507	486.250892	**F**	***606.360974***	303.684125	589.334425	295.170850		
10	**1060.542186**	530.774731	1043.515637	522.261457	1042.531621	521.769449	**A**	***459.292560***	230.149918	442.266011	221.636643		
11	1117.563650	559.285463	1100.537101	550.772189	1099.553085	550.280181	**G**	***388.255446***	194.631361	371.228897	186.118086		
12	**1230.647714**	615.827495	1213.621165	607.314221	1212.637149	606.822212	**L**	***331.233982***	166.120629	314.207433	157.607354		
13	**1301.684828**	651.346052	1284.658279	642.832778	1283.674263	642.340769	**A**	***218.149918***	109.578597	201.123369	101.065322		
14							**K**	147.112804	74.060040	130.086255	65.546765		



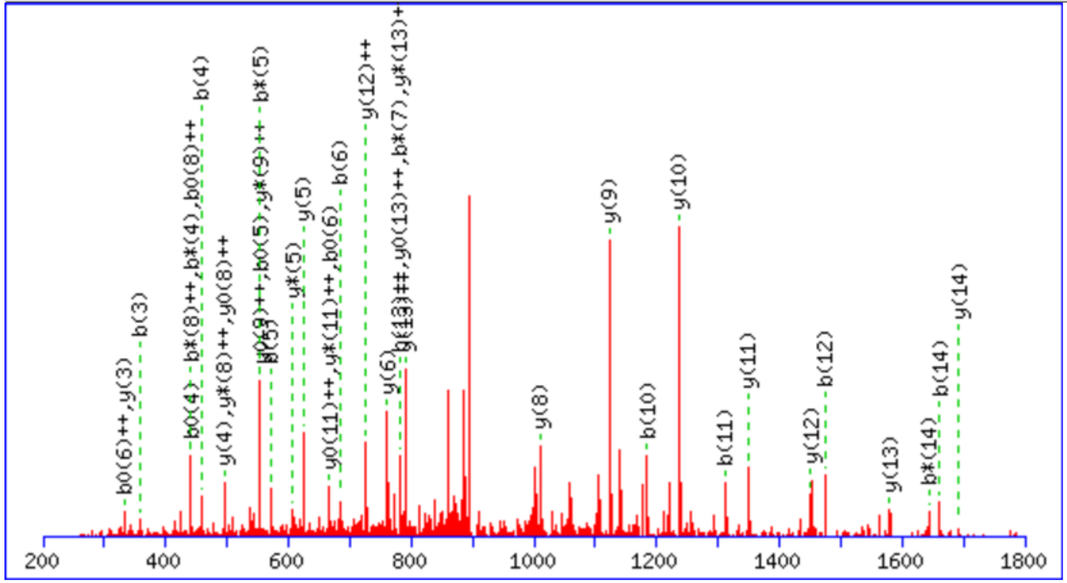
Peptide View

MS/MS Fragmentation of **NIETIINTFHQYSVK**
Found in **IPI00027462**, Tax_Id=9606 Gene_Symbol=S100A9 Protein S100-A9
Experiment: 24 - NOPC3 **Fraction:** NOPC3

Match to Query 12687: 1805.933048 from(903.973800,2+)
Title: OECHL100317_25.20144.20144.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1805.931183**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 71 **Expect:** 9.9e-006**Matches :** 41/160 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	115.050203	58.028740	98.023654	49.515465			N						
2	228.134267	114.570771	211.107718	106.057497			I	***1692.895549***	846.951413	1675.869000	838.438138	1674.884984	837.9461
3	**357.176860**	179.092068	340.150311	170.578793	339.166295	170.086785	E	***1579.811485***	790.409381	1562.784936	781.896106	1561.800920	781.4040
4	**458.224539**	229.615907	441.197990	221.102633	440.213974	220.610625	T	***1450.768892***	725.888084	1433.742343	717.374810	1432.758327	716.8828
5	**571.308603**	286.157940	554.282054	277.644665	553.298038	277.152657	I	***1349.721213***	675.364245	1332.694664	666.850970	1331.710648	666.3589

6	**684.392667**	342.699972	667.366118	334.186697	666.382102	333.694689	**I**	***1236.637149***	618.822213	1219.610600	610.308938	1218.626584	609.8169
7	798.435594	399.721435	781.409045	391.208161	780.425029	390.716153	**N**	***1123.553085***	562.280181	1106.526536	553.766906	1105.542520	553.2748
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	**T**	***1009.510158***	505.258717	992.483609	496.745443	991.499593	496.2534
9	1046.551687	523.779482	1029.525138	515.266207	1028.541122	514.774199	**F**	908.462479	454.734878	891.435930	446.221603	890.451914	445.7295
10	**1183.610599**	592.308938	1166.584050	583.795663	1165.600034	583.303655	**H**	***761.394065***	381.200671	744.367516	372.687396	743.383500	372.1953
11	**1311.669177**	656.338227	1294.642628	647.824952	1293.658612	647.332944	**Q**	***624.335153***	312.671215	607.308604	304.157940	606.324588	303.6659
12	**1474.732506**	737.869891	1457.705957	729.356617	1456.721941	728.864609	**Y**	***496.276575***	248.641926	479.250026	240.128651	478.266010	239.6366
13	1561.764534	781.385905	1544.737985	772.872631	1543.753969	772.380623	**S**	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.1049
14	**1660.832948**	830.920112	1643.806399	822.406838	1642.822383	821.914830	**V**	246.181218	123.594247	229.154669	115.080973		
15							**K**	147.112804	74.060040	130.086255	65.546765		

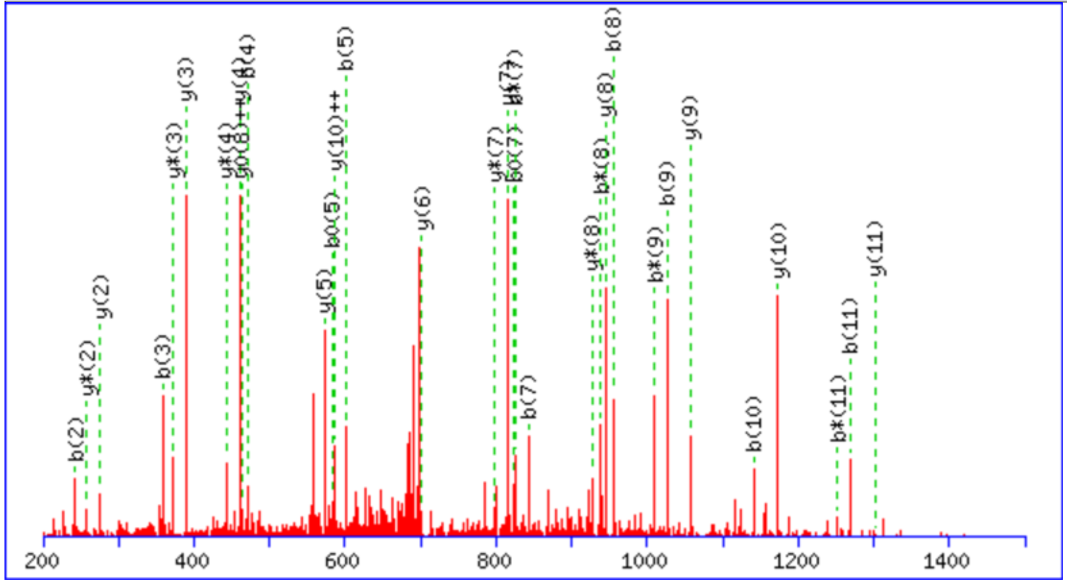


Peptide View

MS/MS Fragmentation of **LEDLENQLANQK**
Found in **IPI00012325**, Tax_Id=9606 Gene_Symbol=MATN4 matrilin 4 isoform 3 precursor
Experiment: 24 - NOPC3 **Fraction:** NOPC3

Match to Query 8755: 1413.711048 from(707.862800,2+)
Title: OECHL100317_25.11967.11967.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1413.709930**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 66 **Expect:** 3.1e-005**Matches :** 32/106 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	114.091340	57.549308					L						
2	**243.133933**	122.070605			225.123368	113.065322	E	***1301.633185***	651.320231	1284.606636	642.806956	1283.622620	642.3149
3	**358.160876**	179.584076			340.150311	170.578794	D	***1172.590592***	586.798934	1155.564043	578.285660	1154.580027	577.7936
4	**471.244940**	236.126108			453.234375	227.120826	L	***1057.563649***	529.285462	1040.537100	520.772188	1039.553084	520.2801
5	**600.287533**	300.647405			582.276968	291.642122	E	***944.479585***	472.743431	927.453036	464.230156	926.469020	463.7381
6	714.330460	357.668868	697.303911	349.155594	696.319895	348.663586	N	***815.436992***	408.222134	798.410443	399.708859		
7	**842.389038**	421.698157	825.362489	413.184883	824.378473	412.692875	Q	***701.394065***	351.200671	684.367516	342.687396		
8	**955.473102**	478.240189	938.446553	469.726915	937.462537	469.234907	L	***573.335487***	287.171382	556.308938	278.658107		
9	**1026.510216**	513.758746	1009.483667	505.245472	1008.499651	504.753464	A	***460.251423***	230.629349	443.224874	222.116075		
10	**1140.553143**	570.780210	1123.526594	562.266935	1122.542578	561.774927	N	***389.214309***	195.110792	372.187760	186.597518		
11	**1268.611721**	634.809499	1251.585172	626.296224	1250.601156	625.804216	Q	***275.171382***	138.089329	258.144833	129.576054		
12							K	147.112804	74.060040	130.086255	65.546765		

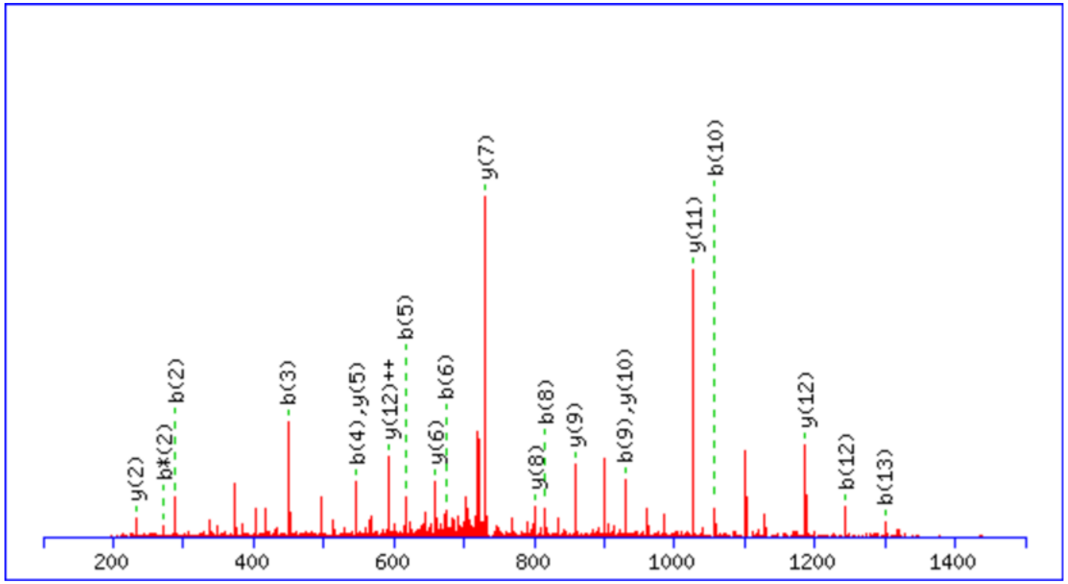


Peptide View

MS/MS Fragmentation of **CQCPAGAALQADGR**
Found in **IPI00010737**, Tax_Id=9606 Gene_Symbol=THBD Thrombomodulin
Experiment: 24 - NOPC3 **Fraction:** NOPC3

Match to Query 9262: 1473.646248 from(737.830400,2+)
Title: OECHL100317_25.7743.7743.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1473.645279**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65 **Expect:** 1.6e-005**Matches :** 21/128 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	161.037925	81.022600					C						
2	***289.096503***	145.051890	272.069954	136.538615			Q	1314.621912	657.814594	1297.595363	649.301320	1296.611347	648.8093
3	***449.127152***	225.067214	432.100603	216.553940			C	***1186.563334***	593.785305	1169.536785	585.272031	1168.552769	584.7800
4	***546.179916***	273.593596	529.153367	265.080322			P	***1026.532685***	513.769981	1009.506136	505.256706	1008.522120	504.7646
5	***617.217030***	309.112153	600.190481	300.598879			A	***929.479921***	465.243599	912.453372	456.730324	911.469356	456.2383
6	***674.238494***	337.622885	657.211945	329.109611			G	***858.442807***	429.725042	841.416258	421.211767	840.432242	420.7197
7	745.275608	373.141442	728.249059	364.628168			A	***801.421343***	401.214310	784.394794	392.701035	783.410778	392.2090
8	***816.312722***	408.659999	799.286173	400.146725			A	***730.384229***	365.695753	713.357680	357.182478	712.373664	356.6904
9	***929.396786***	465.202031	912.370237	456.688757			L	***659.347115***	330.177196	642.320566	321.663921	641.336550	321.1719
10	***1057.455364***	529.231320	1040.428815	520.718046			Q	***546.263051***	273.635164	529.236502	265.121889	528.252486	264.6298
11	1128.492478	564.749877	1111.465929	556.236603			A	418.204473	209.605874	401.177924	201.092600	400.193908	200.6005
12	***1243.519421***	622.263349	1226.492872	613.750074	1225.508856	613.258066	D	347.167359	174.087317	330.140810	165.574043	329.156794	165.0820
13	***1300.540885***	650.774081	1283.514336	642.260806	1282.530320	641.768798	G	***232.140416***	116.573846	215.113867	108.060571		
14							R	175.118952	88.063114	158.092403	79.549839		



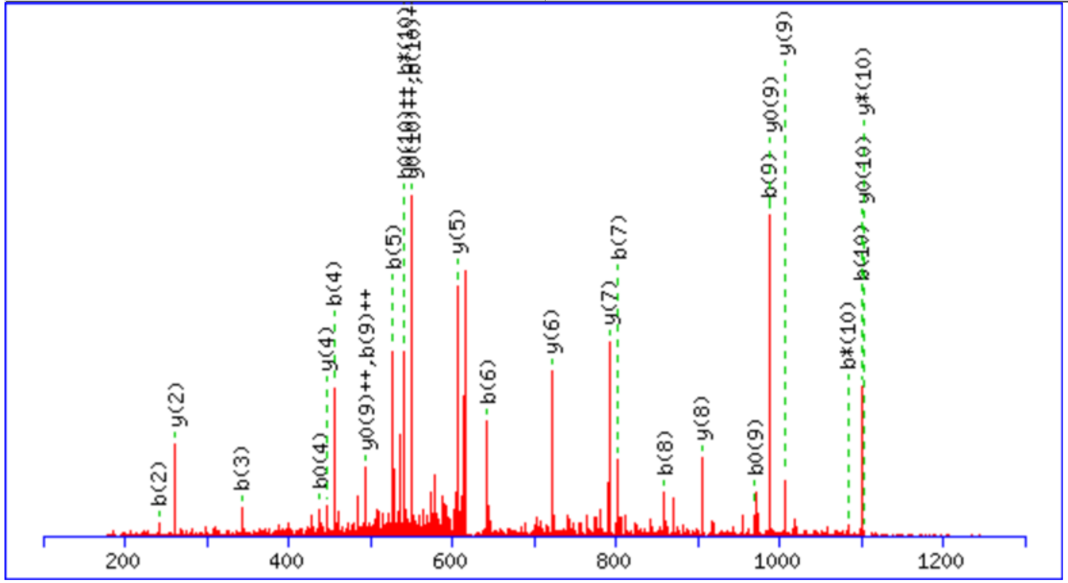
Peptide View

MS/MS Fragmentation of **KITIADCGQLE**
Found in **IPI00419585**, Tax_Id=9606 Gene_Symbol=PPIA Peptidyl-prolyl cis-trans isomerase A
Experiment: 24 - NOPC3 **Fraction:** NOPC3

Match to Query 7093: 1246.622648 from(624.318600,2+)
Title: OECHL100317_25.11401.11401.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1246.622726**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 51 **Expect:** 0.00098**Matches :** 28/112 fragment ions using 55 most intense peaks (help)

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}
1	129.102239	65.054757	112.075690	56.541483			K						
2	***242.186303***	121.596790	225.159754	113.083515			I	1119.535053	560.271165	1102.508504	551.757890	1101.524488	551.2658
3	***343.233982***	172.120629	326.207433	163.607355	325.223417	163.115347	T	**1006.450989**	503.729133	989.424440	495.215858	988.440424	494.7238
4	***456.318046***	228.662661	439.291497	220.149387	438.307481	219.657379	I	**905.403310**	453.205293	888.376761	444.692019	887.392745	444.2000
5	***527.355160***	264.181218	510.328611	255.667944	509.344595	255.175936	A	**792.319246**	396.663261	775.292697	388.149987	774.308681	387.6579

6	***642.382103***	321.694690	625.355554	313.181415	624.371538	312.689407	**D**	**721.282132**	361.144704	704.255583	352.631430	703.271567	352.1394
7	***802.412752***	401.710014	785.386203	393.196740	784.402187	392.704732	**C**	**606.255189**	303.631233	589.228640	295.117958	588.244624	294.6259
8	***859.434216***	430.220746	842.407667	421.707472	841.423651	421.215464	**G**	**446.224540**	223.615908	429.197991	215.102634	428.213975	214.6106
9	***987.492794***	494.250035	970.466245	485.736761	969.482229	485.244753	**Q**	389.203076	195.105176	372.176527	186.591902	371.192511	186.0998
10	***1100.576858***	550.792067	1083.550309	542.278793	1082.566293	541.786785	**L**	**261.144498**	131.075887			243.133933	122.0706
11							**E**	148.060434	74.533855			130.049869	65.5285

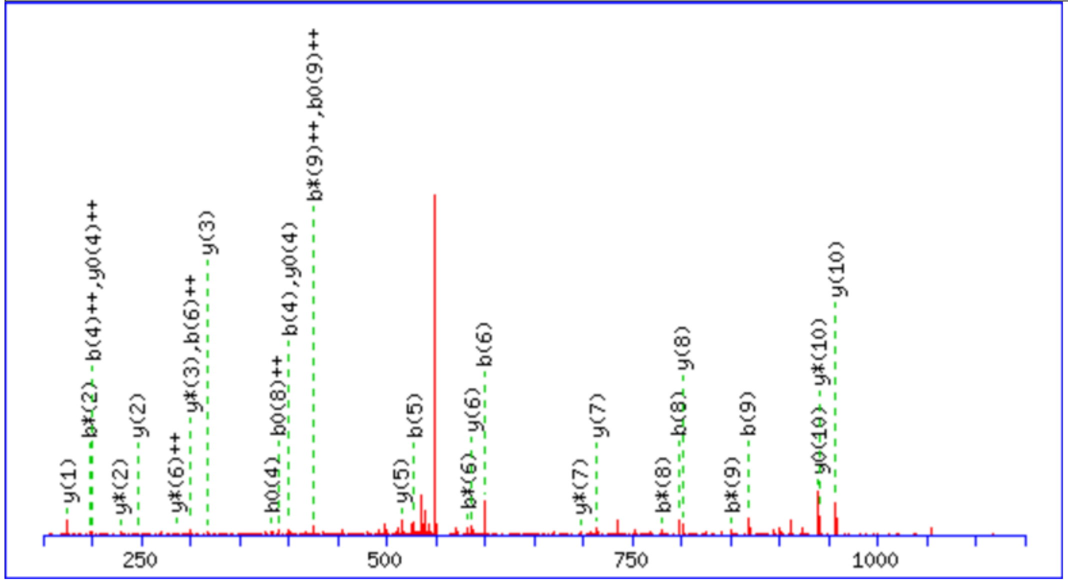


Peptide View

MS/MS Fragmentation of **RGVSQAPTAAR**
Found in **IPI00025365**, Tax_Id=9606 Gene_Symbol=EDN3 Isoform Long of Endothelin-3
Experiment: 24 - NOPC3 **Fraction:** NOPC3

Match to Query 5014: 1112.604048 from(557.309300,2+)
Title: OECHL100317_25.2431.2431.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1112.605042**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 56 **Expect:** 0.00019**Matches :** 32/108 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	157.108387	79.057831	140.081838	70.544557			R							11
2	214.129851	107.568564	197.103302	99.055289			G	***957.511221***	479.259249	940.484672	470.745974	939.500656	470.253966	10
3	313.198265	157.102770	296.171716	148.589496			V	900.489757	450.748517	883.463208	442.235242	882.479192	441.743234	9
4	**400.230293**	200.618785	383.203744	192.105510	382.219728	191.613502	S	***801.421343***	401.214310	784.394794	392.701035	783.410778	392.209027	8
5	**528.288871**	264.648074	511.262322	256.134799	510.278306	255.642791	Q	***714.389315***	357.698296	697.362766	349.185021	696.378750	348.693013	7
6	**599.325985**	300.166631	582.299436	291.653356	581.315420	291.161348	A	***586.330737***	293.669007	569.304188	285.155732	568.320172	284.663724	6
7	696.378749	348.693013	679.352200	340.179738	678.368184	339.687730	P	***515.293623***	258.150450	498.267074	249.637175	497.283058	249.145167	5
8	**797.426428**	399.216852	780.399879	390.703578	779.415863	390.211570	T	418.240859	209.624068	401.214310	201.110793	400.230294	200.618785	4
9	**868.463542**	434.735409	851.436993	426.222135	850.452977	425.730127	A	***317.193180***	159.100228	300.166631	150.586953			3
10	**939.500656**	470.253966	922.474107	461.740692	921.490091	461.248684	A	***246.156066***	123.581671	229.129517	115.068397			2
11							R	***175.118952***	88.063114	158.092403	79.549840			1



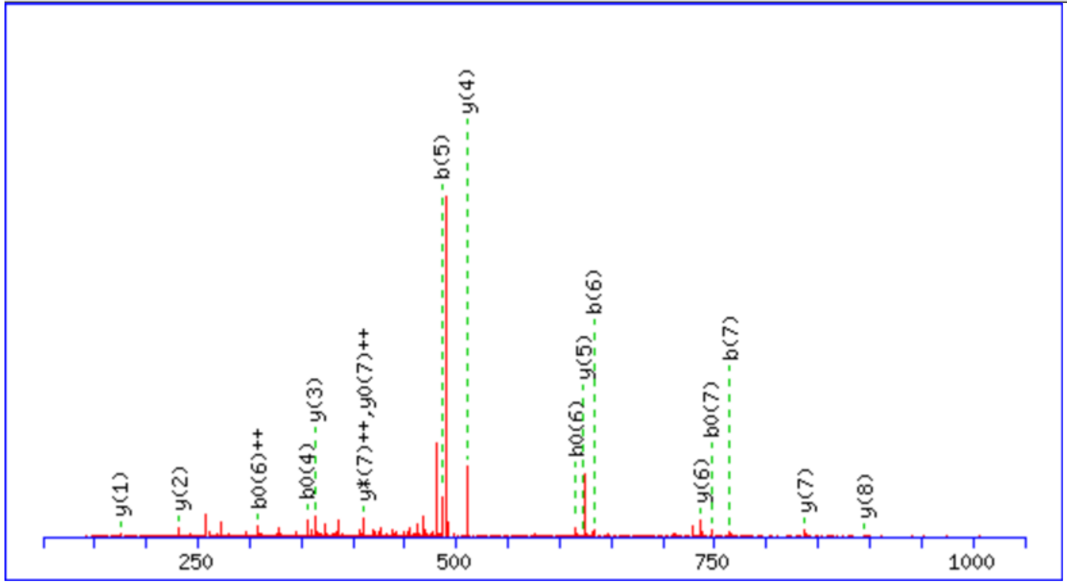
Peptide View

MS/MS Fragmentation of **TGTILFMGR**

Found in **IPI00016150**, Tax_Id=9606 Gene_Symbol=SERPINI1 Neuroserpin
Experiment: 24 - NOPC3 **Fraction:** NOPC3

Match to Query 3420: 994.527448 from(498.271000,2+)
Title: OECHL100317_25.16078.16078.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 994.526993**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58 **Expect:** 7.3e-005**Matches :** 17/68 fragment ions using 35 most intense peaks (help)

#	**b**	**b^{++}**	**b^0**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^0**	**y^{0++}**	**#**
1	102.054955	51.531116	84.044390	42.525833	**T**							**9**
2	159.076419	80.041847	141.065854	71.036565	**G**	***894.486586***	447.746931	877.460037	439.233657	876.476021	438.741649	**8**
3	260.124098	130.565687	242.113533	121.560405	**T**	***837.465122***	419.236199	820.438573	410.722925	819.454557	410.230917	**7**
4	373.208162	187.107719	355.197597	178.102437	**I**	***736.417443***	368.712360	719.390894	360.199085			**6**
5	**486.292226**	243.649751	468.281661	234.644469	**L**	***623.333379***	312.170328	606.306830	303.657053			**5**
6	**633.360640**	317.183958	615.350075	308.178676	**F**	***510.249315***	255.628296	493.222766	247.115021			**4**
7	**764.401125**	382.704201	746.390560	373.698918	**M**	***363.180901***	182.094089	346.154352	173.580814			**3**
8	821.422589	411.214933	803.412024	402.209650	**G**	***232.140416***	116.573846	215.113867	108.060572			**2**
9					**R**	***175.118952***	88.063114	158.092403	79.549840			**1**

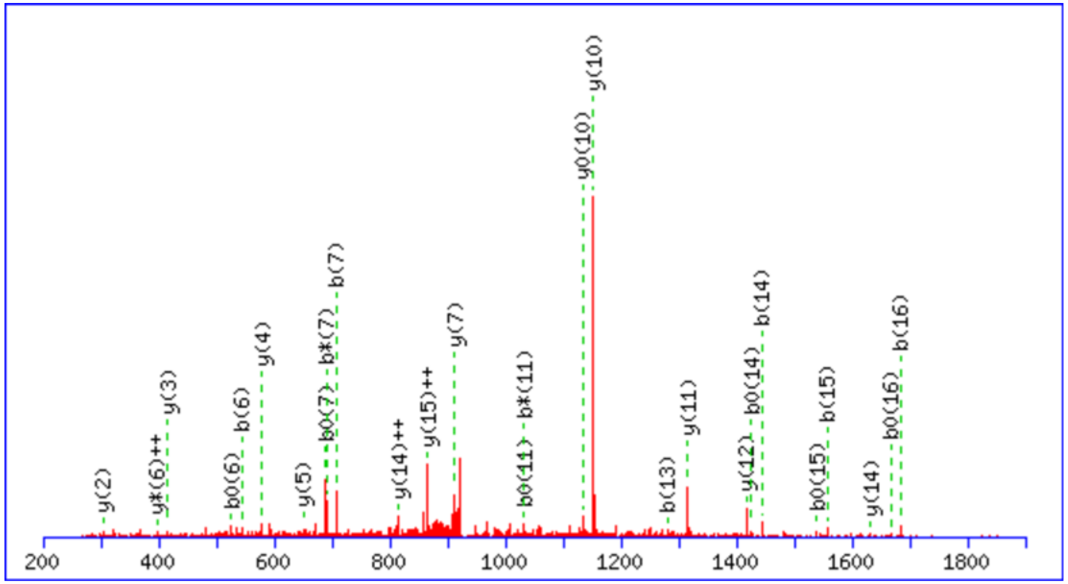


Peptide View

MS/MS Fragmentation of **GAVSQTYPSGTCAYIQR**
Found in **IPI00001759**, Tax_Id=9606 Gene_Symbol=OLR1 Oxidized low-density lipoprotein receptor 1
Experiment: 24 - NOPC3 **Fraction:** NOPC3

Match to Query 13074: 1857.870848 from(929.942700,2+)
Title: OECHL100317_25.11017.11017.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_25.raw
Monoisotopic mass of neutral peptide Mr(calc): 1857.867950**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 50 **Expect:** 0.0011**Matches :** 27/166 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	58.028740	29.518008					**G**						
2	129.065854	65.036565					**A**	1801.853763	901.430520	1784.827214	892.917245	1783.843198	892.4252
3	228.134268	114.570772					**V**	1730.816649	865.911963	1713.790100	857.398688	1712.806084	856.9066
4	315.166296	158.086786			297.155731	149.081504	**S**	***1631.748235***	816.377756	1614.721686	807.864481	1613.737670	807.3724
5	443.224874	222.116075	426.198325	213.602801	425.214309	213.110793	**Q**	1544.716207	772.861742	1527.689658	764.348467	1526.705642	763.8564
6	**544.272553**	272.639915	527.246004	264.126640	526.261988	263.634632	**T**	***1416.657629***	708.832453	1399.631080	700.319178	1398.647064	699.8271
7	**707.335882**	354.171579	690.309333	345.658305	689.325317	345.166297	**Y**	***1315.609950***	658.308613	1298.583401	649.795339	1297.599385	649.3033
8	804.388646	402.697961	787.362097	394.184687	786.378081	393.692679	**P**	***1152.546621***	576.776949	1135.520072	568.263674	1134.536056	567.7716
9	891.420674	446.213975	874.394125	437.700701	873.410109	437.208693	**S**	1055.493857	528.250567	1038.467308	519.737292	1037.483292	519.2452
10	948.442138	474.724707	931.415589	466.211433	930.431573	465.719425	**G**	968.461829	484.734553	951.435280	476.221278	950.451264	475.7292
11	1049.489817	525.248547	1032.463268	516.735272	1031.479252	516.243264	**T**	***911.440365***	456.223821	894.413816	447.710546	893.429800	447.2185
12	1209.520466	605.263871	1192.493917	596.750597	1191.509901	596.258589	**C**	810.392686	405.699981	793.366137	397.186707		
13	**1280.557580**	640.782428	1263.531031	632.269154	1262.547015	631.777146	**A**	***650.362037***	325.684657	633.335488	317.171382		
14	**1443.620909**	722.314093	1426.594360	713.800818	1425.610344	713.308810	**Y**	***579.324923***	290.166100	562.298374	281.652825		
15	**1556.704973**	778.856125	1539.678424	770.342850	1538.694408	769.850842	**I**	***416.261594***	208.634435	399.235045	200.121160		
16	**1684.763551**	842.885414	1667.737002	834.372139	1666.752986	833.880131	**Q**	***303.177530***	152.092403	286.150981	143.579129		
17							**R**	175.118952	88.063114	158.092403	79.549839		



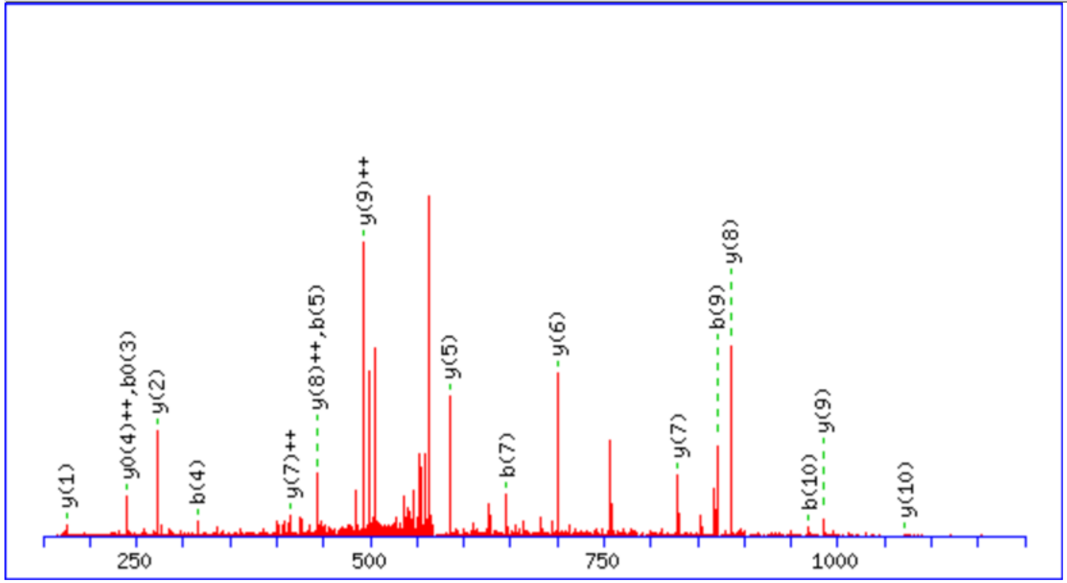
Peptide View

MS/MS Fragmentation of **ASVGQDSPEPR**
Found in **IPI00044369**, Tax_Id=9606 Gene_Symbol=PLXDC2 Isoform 1 of Plexin domain-containing protein 2
Experiment: 15 - S_E-3 **Fraction:** S_E-3

Match to Query 5848: 1141.536448 from(571.775500,2+)
Title: OECHL100317_23.3551.3551.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1141.536362**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 76 **Expect:** 1.5e-006**Matches :** 18/106 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	72.044390	36.525833					A						
2	159.076418	80.041847			141.065853	71.036564	S	***1071.506528***	536.256902	1054.479979	527.743628	1053.495963	527.251620
3	258.144832	129.576054			240.134267	120.570772	V	***984.474500***	492.740888	967.447951	484.227614	966.463935	483.735606
4	**315.166296**	158.086786			297.155731	149.081504	G	***885.406086***	443.206681	868.379537	434.693407	867.395521	434.201399
5	**443.224874**	222.116075	426.198325	213.602801	425.214309	213.110793	Q	***828.384622***	414.695949	811.358073	406.182675	810.374057	405.690667

6	558.251817	279.629547	541.225268	271.116272	540.241252	270.624264	**D**	***700.326044***	350.666660	683.299495	342.153386	682.315479	341.661378
7	**645.283845**	323.145561	628.257296	314.632286	627.273280	314.140278	**S**	***585.299101***	293.153189	568.272552	284.639914	567.288536	284.147906
8	742.336609	371.671943	725.310060	363.158668	724.326044	362.666660	**P**	498.267073	249.637174	481.240524	241.123900	480.256508	240.631892
9	**871.379202**	436.193239	854.352653	427.679965	853.368637	427.187957	**E**	401.214309	201.110792	384.187760	192.597518	383.203744	192.105510
10	**968.431966**	484.719621	951.405417	476.206347	950.421401	475.714339	**P**	***272.171716***	136.589496	255.145167	128.076221		
11							**R**	***175.118952***	88.063114	158.092403	79.549839		

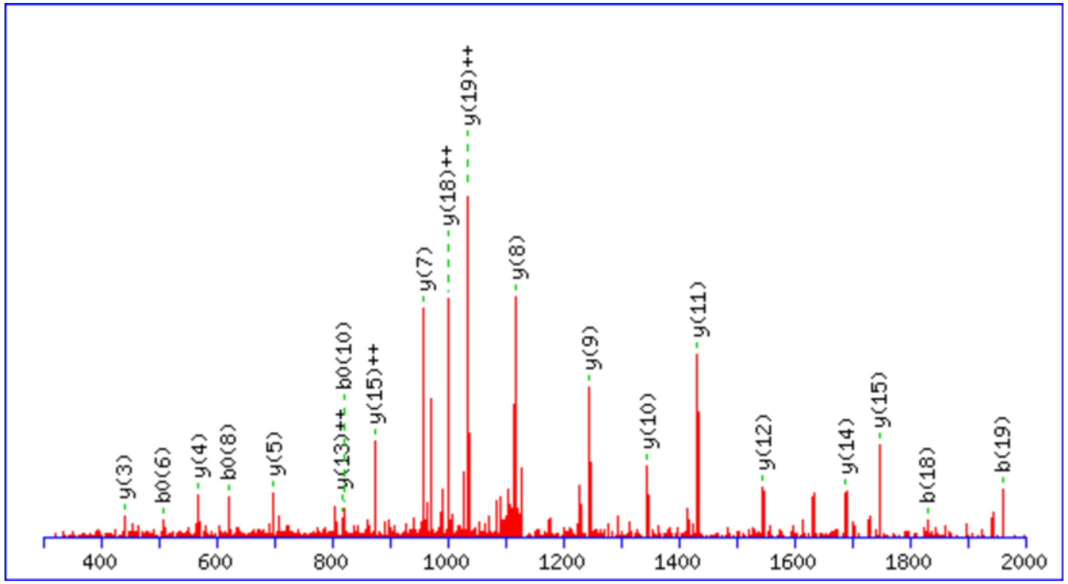


Peptide View

MS/MS Fragmentation of **TVAGPVGGSLSVQCPYEKEHR**
Found in **IPI00414784**, Tax_Id=9606 Gene_Symbol=CD300A Isoform 1 of CMRF35-like molecule 8
Experiment: 15 - S_E-3 **Fraction:** S_E-3

Match to Query 15766: 2270.113448 from(1136.064000,2+)
Title: OECHL100317_23.11185.11185.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.111374**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 70 **Expect:** 1.8e-005**Matches :** 20/212 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}
1	102.054955	51.531116			84.044390	42.525833	**T**					
2	201.123369	101.065322			183.112804	92.060040	**V**	2170.070965	1085.539120	2153.044416	1077.025846	2152.060400
3	272.160483	136.583879			254.149918	127.578597	**A**	2071.002551	1036.004913	2053.976002	1027.491639	2052.991986
4	329.181947	165.094611			311.171382	156.089329	**G**	1999.965437	1000.486357	1982.938888	991.973082	1981.954872
5	426.234711	213.620994			408.224146	204.615711	**P**	1942.943973	971.975625	1925.917424	963.462350	1924.933408
6	525.303125	263.155201			507.292560	254.149918	**V**	1845.891209	923.449243	1828.864660	914.935968	1827.880644
7	582.324589	291.665933			564.314024	282.660650	**G**	***1746.822795***	873.915036	1729.796246	865.401761	1728.812230
8	639.346053	320.176665			621.335488	311.171382	**G**	***1689.801331***	845.404304	1672.774782	836.891029	1671.790766
9	726.378081	363.692679			708.367516	354.687396	**S**	1632.779867	816.893572	1615.753318	808.380297	1614.769302
10	839.462145	420.234711			821.451580	411.229428	**L**	***1545.747839***	773.377558	1528.721290	764.864283	1527.737274
11	926.494173	463.750725			908.483608	454.745442	**S**	***1432.663775***	716.835526	1415.637226	708.322251	1414.653210
12	1025.562587	513.284932			1007.552022	504.279649	**V**	***1345.631747***	673.319512	1328.605198	664.806237	1327.621182
13	1153.621165	577.314221	1136.594616	568.800946	1135.610600	568.308938	**Q**	***1246.563333***	623.785305	1229.536784	615.272030	1228.552768
14	1313.651814	657.329545	1296.625265	648.816271	1295.641249	648.324263	**C**	***1118.504755***	559.756016	1101.478206	551.242741	1100.494190
15	1410.704578	705.855927	1393.678029	697.342653	1392.694013	696.850645	**P**	***958.474106***	479.740691	941.447557	471.227417	940.463541
16	1573.767907	787.387592	1556.741358	778.874317	1555.757342	778.382309	**Y**	861.421342	431.214309	844.394793	422.701035	843.410777
17	1702.810500	851.908888	1685.783951	843.395614	1684.799935	842.903606	**E**	***698.358013***	349.682645	681.331464	341.169370	680.347448
18	**1830.905463**	915.956370	1813.878914	907.443095	1812.894898	906.951087	**K**	***569.315420***	285.161348	552.288871	276.648074	551.304855
19	**1959.948056**	980.477666	1942.921507	971.964392	1941.937491	971.472384	**E**	***441.220457***	221.113867	424.193908	212.600592	423.209892
20	2097.006968	1049.007122	2079.980419	1040.493847	2078.996403	1040.001840	**H**	312.177864	156.592570	295.151315	148.079295	
21							**R**	175.118952	88.063114	158.092403	79.549839	



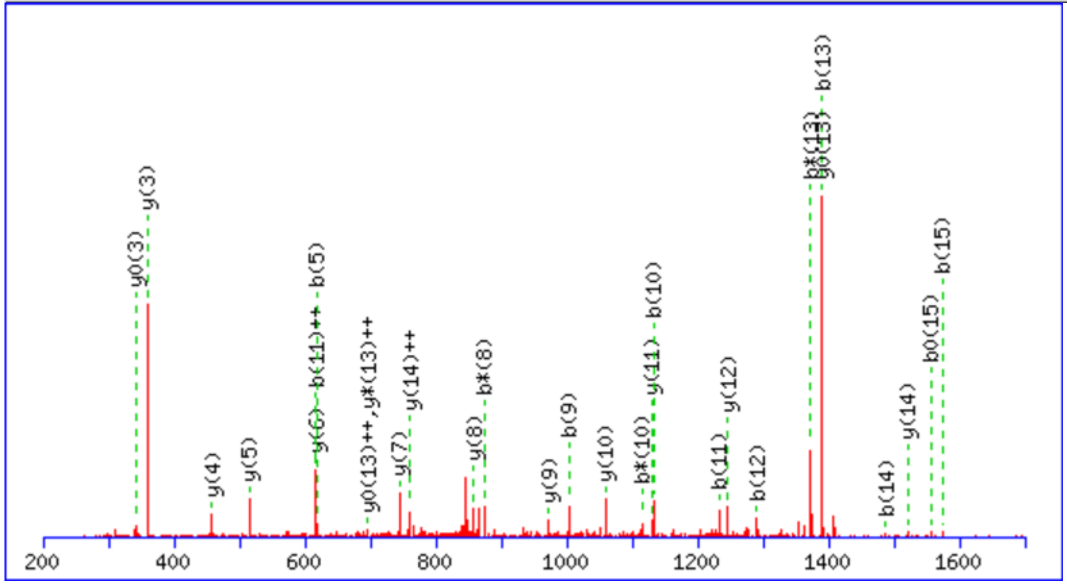
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 15 - S_E-3 **Fraction:** S_E-3

Match to Query 13052: 1746.916048 from(874.465300,2+)
Title: OECHL100317_23.17527.17527.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 79 **Expect:** 1.4e-006**Matches :** 29/156 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	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	503.322797	252.165036					**Y**	1408.670299	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018

6	689.386854	345.197065			671.376289	336.191782	**A**	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	**S**	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	**N**	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	**L**	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	**E**	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	**T**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	**G**	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	**V**	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	**1486.778787**	743.893032	1469.752238	735.379757	1468.768222	734.887749	**P**	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							**R**	175.118952	88.063114	158.092403	79.549839		



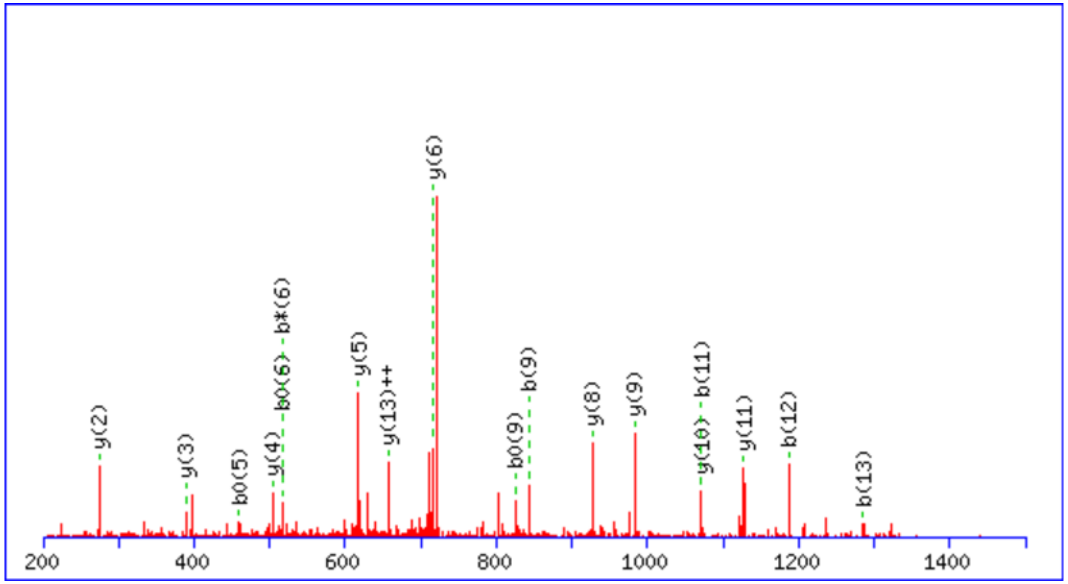
Peptide View

MS/MS Fragmentation of **FGQGSGPIVLDDVR**
Found in **IPI00418512**, Tax_Id=9606 Gene_Symbol=DMBT1 Isoform 4 of Deleted in malignant brain tumors 1 protein

Experiment: 15 - S_E-3 **Fraction:** S_E-3

Match to Query 10117: 1458.750048 from(730.382300,2+)
Title: OECHL100317_23.16064.16064.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1458.746719**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 72 **Expect:** 7.9e-006**Matches :** 18/140 fragment ions using 25 most intense peaks (help)

#	**b**	**b^{++}**	**b***	**b^{*++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**
1	148.075690	74.541483					**F**						
2	205.097154	103.052215					**G**	1312.685556	656.846416	1295.659007	648.333142	1294.674991	647.8411
3	333.155732	167.081504	316.129183	158.568230			**Q**	1255.664092	628.335684	1238.637543	619.822410	1237.653527	619.3304
4	390.177196	195.592236	373.150647	187.078961			**G**	***1127.605514***	564.306395	1110.578965	555.793121	1109.594949	555.3011
5	477.209224	239.108250	460.182675	230.594976	459.198659	230.102968	**S**	***1070.584050***	535.795663	1053.557501	527.282389	1052.573485	526.7903
6	534.230688	267.618982	517.204139	259.105708	516.220123	258.613700	**G**	***983.552022***	492.279649	966.525473	483.766375	965.541457	483.2743
7	631.283452	316.145364	614.256903	307.632090	613.272887	307.140082	**P**	***926.530558***	463.768917	909.504009	455.255643	908.519993	454.7636
8	744.367516	372.687396	727.340967	364.174122	726.356951	363.682114	**I**	829.477794	415.242535	812.451245	406.729261	811.467229	406.2372
9	**843.435930**	422.221603	826.409381	413.708329	825.425365	413.216321	**V**	***716.393730***	358.700503	699.367181	350.187229	698.383165	349.6952
10	956.519994	478.763635	939.493445	470.250361	938.509429	469.758353	**L**	***617.325316***	309.166296	600.298767	300.653022	599.314751	300.1610
11	**1071.546937**	536.277107	1054.520388	527.763832	1053.536372	527.271824	**D**	***504.241252***	252.624264	487.214703	244.110990	486.230687	243.6189
12	**1186.573880**	593.790578	1169.547331	585.277304	1168.563315	584.785296	**D**	***389.214309***	195.110793	372.187760	186.597518	371.203744	186.1055
13	**1285.642294**	643.324785	1268.615745	634.811511	1267.631729	634.319503	**V**	***274.187366***	137.597321	257.160817	129.084047		
14							**R**	175.118952	88.063114	158.092403	79.549839		



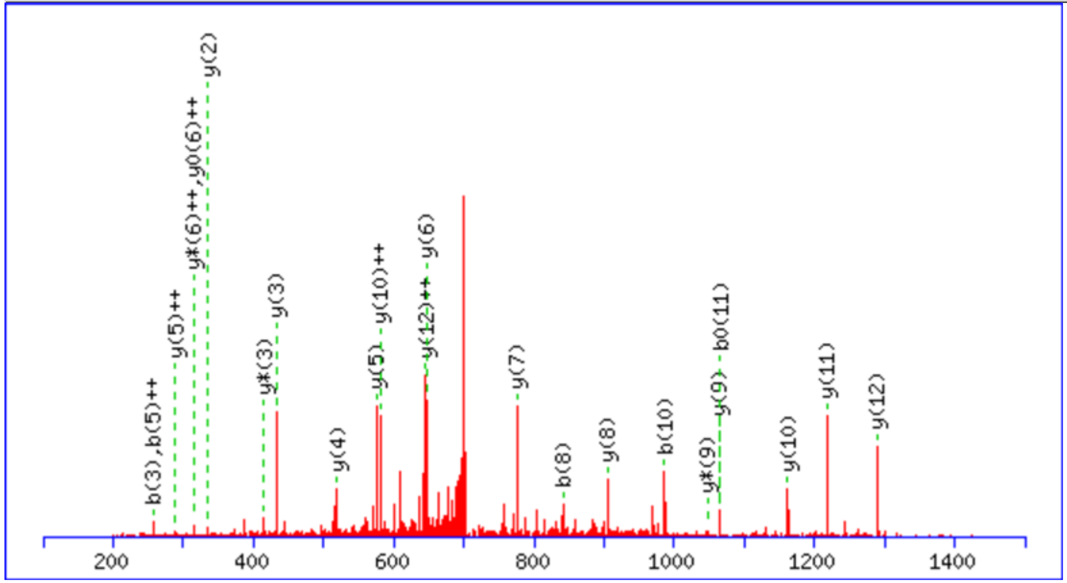
Peptide View

MS/MS Fragmentation of **KAGPCEQAGSPCR**
Found in **IPI00028381**, Tax_Id=9606 Gene_Symbol=DLK2 Isoform 1 of Protein delta homolog 2
Experiment: 15 - S_E-3 **Fraction:** S_E-3

Match to Query 9681: 1416.626048 from(709.320300,2+)
Title: OECHL100317_23.2345.2345.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1416.623810**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 87 **Expect:** 1.3e-007**Matches :** 23/128 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	129.102239	65.054757	112.075690	56.541483			**K**						
2	200.139353	100.573315	183.112804	92.060040			**A**	***1289.536133***	645.271705	1272.509584	636.758430	1271.525568	636.2664
3	**257.160817**	129.084047	240.134268	120.570772			**G**	***1218.499019***	609.753148	1201.472470	601.239873	1200.488454	600.7478
4	354.213581	177.610429	337.187032	169.097154			**P**	***1161.477555***	581.242416	1144.451006	572.729141	1143.466990	572.2371
5	514.244230	257.625753	497.217681	249.112479			**C**	***1064.424791***	532.716034	1047.398242	524.202759	1046.414226	523.7107

6	643.286823	322.147050	626.260274	313.633775	625.276258	313.141767	**E**	***904.394142***	452.700709	887.367593	444.187434	886.383577	443.6954
7	771.345401	386.176339	754.318852	377.663064	753.334836	377.171056	**Q**	***775.351549***	388.179413	758.325000	379.666138	757.340984	379.1741
8	**842.382515**	421.694896	825.355966	413.181621	824.371950	412.689613	**A**	***647.292971***	324.150124	630.266422	315.636849	629.282406	315.1448
9	899.403979	450.205628	882.377430	441.692353	881.393414	441.200345	**G**	***576.255857***	288.631567	559.229308	280.118292	558.245292	279.6262
10	**986.436007**	493.721642	969.409458	485.208367	968.425442	484.716359	**S**	***519.234393***	260.120835	502.207844	251.607560	501.223828	251.1155
11	1083.488771	542.248024	1066.462222	533.734749	1065.478206	533.242741	**P**	***432.202365***	216.604820	415.175816	208.091546		
12	1243.519420	622.263348	1226.492871	613.750074	1225.508855	613.258066	**C**	***335.149601***	168.078438	318.123052	159.565164		
13							**R**	175.118952	88.063114	158.092403	79.549839		



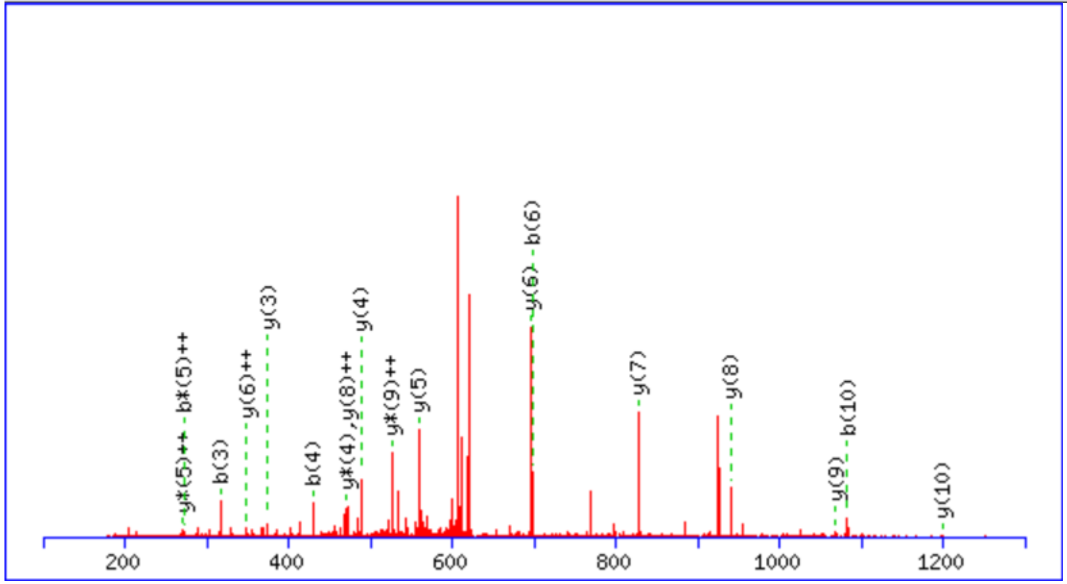
Peptide View

MS/MS Fragmentation of **GMQLMHANAQR**
Found in **IPI00007853**, Tax_Id=9606 Gene_Symbol=IFI30 Gamma-interferon-inducible lysosomal thiol reductase
Experiment: 15 - S_E-3 **Fraction:** S_E-3

Match to Query 7841: 1255.591248 from(628.802900,2+)
Title: OECHL100317_23.7230.7230.2.dta

Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1255.591370**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 52 **Expect:** 0.0005**Matches :** 18/76 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.028740	29.518008			**G**					**11**
2	189.069225	95.038250			**M**	***1199.577209***	600.292243	1182.550660	591.778968	**10**
3	**317.127803**	159.067540	300.101254	150.554265	**Q**	***1068.536724***	534.772000	1051.510175	526.258726	**9**
4	**430.211867**	215.609572	413.185318	207.096297	**L**	***940.478146***	470.742711	923.451597	462.229436	**8**
5	561.252352	281.129814	544.225803	272.616540	**M**	***827.394082***	414.200679	810.367533	405.687404	**7**
6	**698.311264**	349.659270	681.284715	341.145996	**H**	***696.353597***	348.680436	679.327048	340.167162	**6**
7	769.348378	385.177827	752.321829	376.664553	**A**	***559.294685***	280.150981	542.268136	271.637706	**5**
8	883.391305	442.199291	866.364756	433.686016	**N**	***488.257571***	244.632423	471.231022	236.119149	**4**
9	954.428419	477.717848	937.401870	469.204573	**A**	***374.214644***	187.610960	357.188095	179.097685	**3**
10	**1082.486997**	541.747137	1065.460448	533.233862	**Q**	303.177530	152.092403	286.150981	143.579128	**2**
11					**R**	175.118952	88.063114	158.092403	79.549839	**1**

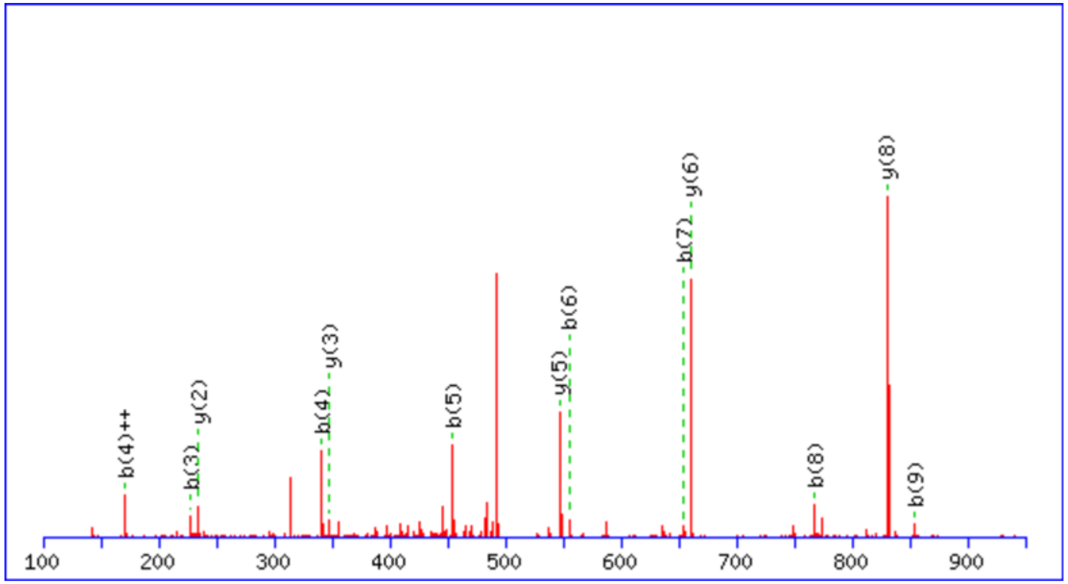


Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 15 - S_E-3 **Fraction:** S_E-3

Match to Query 3773: 999.634648 from(500.824600,2+)
Title: OECHL100317_23.17777.17777.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65 **Expect:** 3.8e-006**Matches :** 14/78 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**
6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	**347.228896**	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



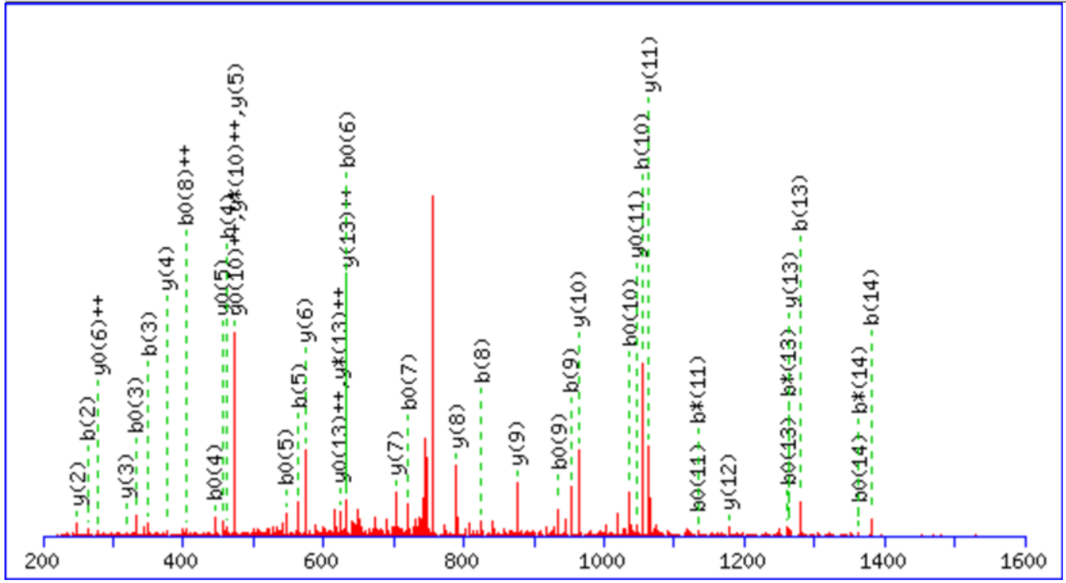
Peptide View

MS/MS Fragmentation of **DFSLTSSSQTPGATK**
Found in **IPI00291300**, Tax_Id=9606 Gene_Symbol=PODXL2 Putative uncharacterized protein PODXL2
Experiment: 15 - S_E-3 **Fraction:** S_E-3

Match to Query 10771: 1525.724648 from(763.869600,2+)
Title: OECHL100317_23.11535.11535.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1525.726028**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 77 **Expect:** 2e-006**Matches :** 43/150 fragment ions using 75 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}
1	116.034219	58.520748			98.023654	49.515465	**D**						
2	**263.102633**	132.054954			245.092068	123.049672	**F**	1411.706351	706.356813	1394.679802	697.843539	1393.695786	697.3515
3	**350.134661**	175.570968			332.124096	166.565686	**S**	***1264.637937***	632.822607	1247.611388	624.309332	1246.627372	623.8173
4	**463.218725**	232.113001			445.208160	223.107718	**L**	***1177.605909***	589.306592	1160.579360	580.793318	1159.595344	580.3013
5	**564.266404**	282.636840			546.255839	273.631558	**T**	***1064.521845***	532.764561	1047.495296	524.251286	1046.511280	523.7592

6	651.298432	326.152854			633.287867	317.147572	**S**	***963.474166***	482.240721	946.447617	473.727446	945.463601	473.2354
7	738.330460	369.668868			720.319895	360.663586	**S**	***876.442138***	438.724707	859.415589	430.211432	858.431573	429.7194
8	**825.362488**	413.184882			807.351923	404.179599	**S**	***789.410110***	395.208693	772.383561	386.695418	771.399545	386.2034
9	**953.421066**	477.214171	936.394517	468.700897	935.410501	468.208889	**Q**	***702.378082***	351.692679	685.351533	343.179404	684.367517	342.6873
10	**1054.468745**	527.738010	1037.442196	519.224736	1036.458180	518.732728	**T**	***574.319504***	287.663390	557.292955	279.150115	556.308939	278.6581
11	1151.521509	576.264392	1134.494960	567.751118	1133.510944	567.259110	**P**	***473.271825***	237.139550	456.245276	228.626276	455.261260	228.1342
12	1208.542973	604.775124	1191.516424	596.261850	1190.532408	595.769842	**G**	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.6078
13	**1279.580087**	640.293681	1262.553538	631.780407	1261.569522	631.288399	**A**	***319.197597***	160.102436	302.171048	151.589162	301.187032	151.0971
14	**1380.627766**	690.817521	1363.601217	682.304246	1362.617201	681.812238	**T**	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.5785
15							**K**	147.112804	74.060040	130.086255	65.546765		

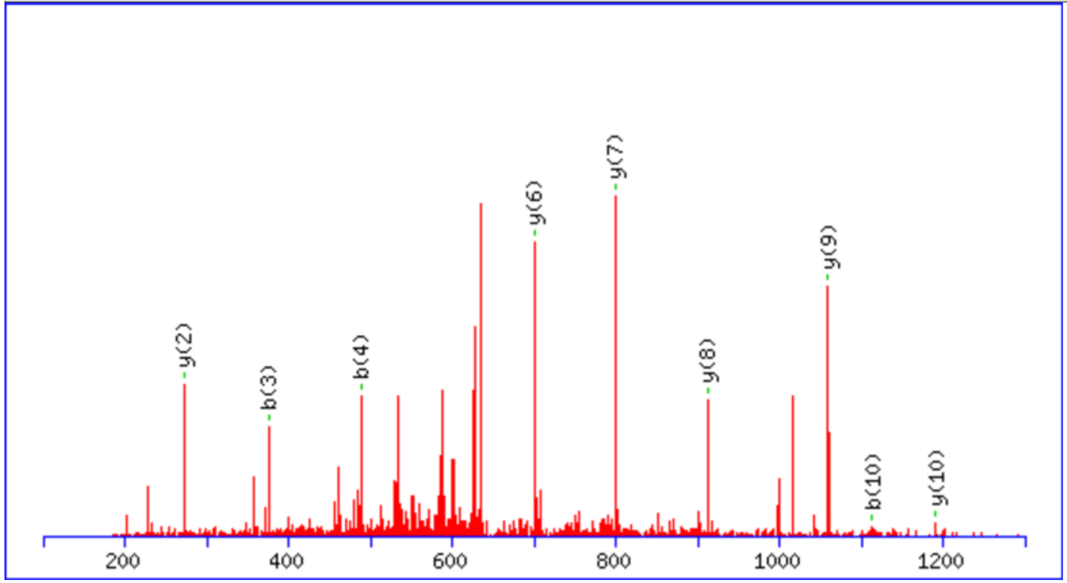


Peptide View

MS/MS Fragmentation of **PMFIVNTNVPR**
Found in **IPI00293276**, Tax_Id=9606 Gene_Symbol=MIF Macrophage migration inhibitory factor
Experiment: 15 - S_E-3 **Fraction:** S_E-3

Match to Query 8262: 1286.680448 from(644.347500,2+)
Title: OECHL100317_23.16181.16181.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1286.680527**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 54 **Expect:** 0.00042**Matches :** 9/90 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	98.060040	49.533658					**P**						
2	229.100525	115.053900					**M**	***1190.635040***	595.821158	1173.608491	587.307884	1172.624475	586.8158
3	**376.168939**	188.588107					**F**	***1059.594555***	530.300915	1042.568006	521.787641	1041.583990	521.2956
4	**489.253003**	245.130139					**I**	***912.526141***	456.766708	895.499592	448.253434	894.515576	447.7614
5	588.321417	294.664347					**V**	***799.442077***	400.224676	782.415528	391.711402	781.431512	391.2193
6	702.364344	351.685810	685.337795	343.172535			**N**	***700.373663***	350.690470	683.347114	342.177195	682.363098	341.6851
7	803.412023	402.209650	786.385474	393.696375	785.401458	393.204367	**T**	586.330736	293.669006	569.304187	285.155732	568.320171	284.6637
8	917.454950	459.231113	900.428401	450.717838	899.444385	450.225830	**N**	485.283057	243.145166	468.256508	234.631892		
9	1016.523364	508.765320	999.496815	500.252045	998.512799	499.760037	**V**	371.240130	186.123703	354.213581	177.610428		
10	**1113.576128**	557.291702	1096.549579	548.778428	1095.565563	548.286419	**P**	***272.171716***	136.589496	255.145167	128.076221		
11							**R**	175.118952	88.063114	158.092403	79.549839		

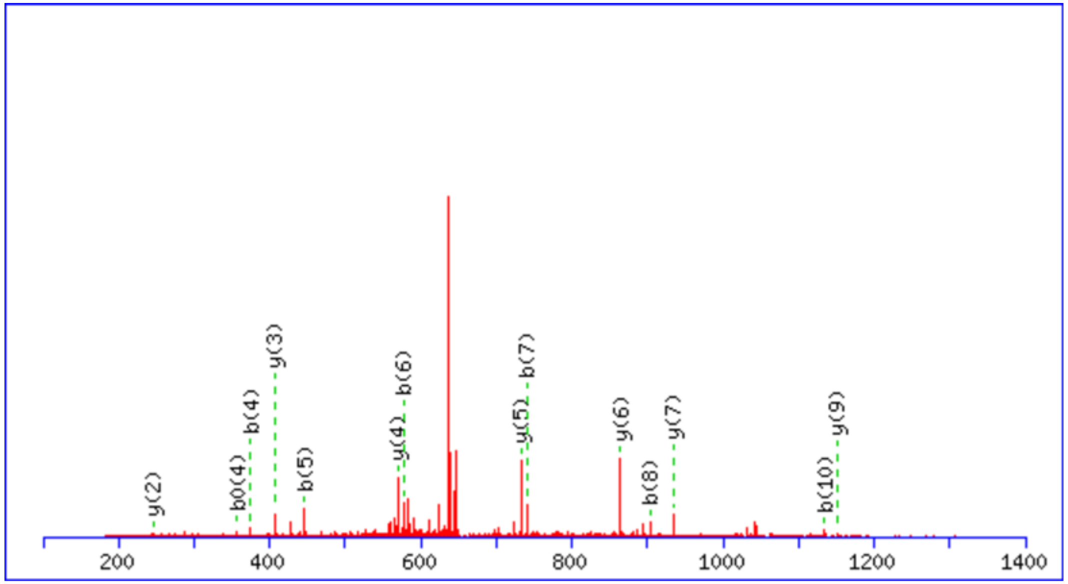


Peptide View

MS/MS Fragmentation of **ASDTAMYYCAR**
Found in **IPI00735451**, Tax_Id=9606 Gene_Symbol=- Putative uncharacterized protein ENSP00000375035
Experiment: 15 - S_E-3 **Fraction:** S_E-3

Match to Query 8545: 1307.527848 from(654.771200,2+)
Title: OECHL100317_23.9467.9467.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1307.527435**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 54 **Expect:** 7.8e-005**Matches :** 14/84 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**11**
2	159.076418	80.041847	141.065853	71.036564	**S**	1237.497622	619.252449	1220.471073	610.739175	1219.487057	610.247167	**10**
3	274.103361	137.555319	256.092796	128.550036	**D**	***1150.465594***	575.736435	1133.439045	567.223161	1132.455029	566.731153	**9**
4	***375.151040***	188.079158	357.140475	179.073876	**T**	1035.438651	518.222964	1018.412102	509.709689	1017.428086	509.217681	**8**
5	***446.188154***	223.597715	428.177589	214.592433	**A**	***934.390972***	467.699124	917.364423	459.185850			**7**
6	***577.228639***	289.117958	559.218074	280.112675	**M**	***863.353858***	432.180567	846.327309	423.667293			**6**
7	***740.291968***	370.649622	722.281403	361.644340	**Y**	***732.313373***	366.660325	715.286824	358.147050			**5**
8	***903.355297***	452.181287	885.344732	443.176004	**Y**	***569.250044***	285.128660	552.223495	276.615386			**4**
9	1063.385946	532.196611	1045.375381	523.191329	**C**	***406.186715***	203.596995	389.160166	195.083721			**3**
10	***1134.423060***	567.715168	1116.412495	558.709886	**A**	***246.156066***	123.581671	229.129517	115.068396			**2**
11					**R**	175.118952	88.063114	158.092403	79.549839			**1**



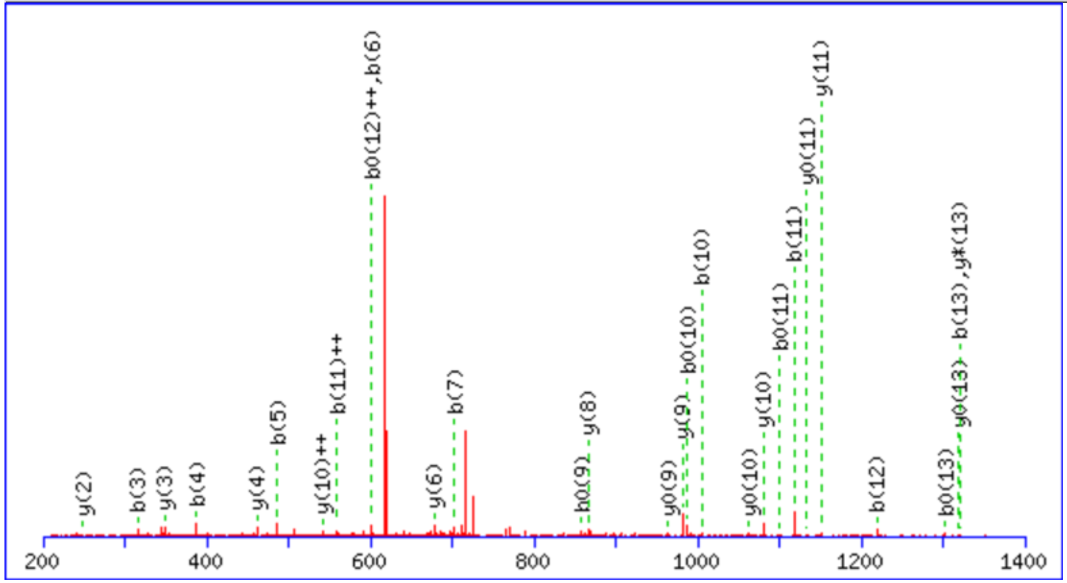
Peptide View

MS/MS Fragmentation of **SDAAVDTSSEITTK**
Found in **IPI00412977**, Tax_Id=9606 Gene_Symbol=- Prothymosin alpha
Experiment: 15 - S_E-3 **Fraction:** S_E-3

Match to Query 10157: 1465.678648 from(733.846600,2+)
Title: OECHL100317_23.10552.10552.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1465.678391**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications: N-term :** Acetyl (N-term)**Ions Score:** 52 **Expect:** 0.00051**Matches :** 29/128 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	**S**							**14**
2	245.076812	123.042044	227.066247	114.036761	**D**	1337.643082	669.325179	1320.616533	660.811905	1319.632517	660.319897	**13**
3	***316.113926***	158.560601	298.103361	149.555319	**A**	1222.616139	611.811708	1205.589590	603.298433	1204.605574	602.806425	**12**
4	***387.151040***	194.079158	369.140475	185.073875	**A**	**1151.579025**	576.293151	1134.552476	567.779876	1133.568460	567.287868	**11**
5	***486.219454***	243.613365	468.208889	234.608082	**V**	**1080.541911**	540.774594	1063.515362	532.261319	1062.531346	531.769311	**10**

6	***601.246397***	301.126837	583.235832	292.121554	**D**	**981.473497**	491.240387	964.446948	482.727112	963.462932	482.235104	**9**
7	***702.294076***	351.650676	684.283511	342.645394	**T**	**866.446554**	433.726915	849.420005	425.213641	848.435989	424.721633	**8**
8	789.326104	395.166690	771.315539	386.161408	**S**	765.398875	383.203076	748.372326	374.689801	747.388310	374.197793	**7**
9	876.358132	438.682704	858.347567	429.677421	**S**	**678.366847**	339.687062	661.340298	331.173787	660.356282	330.681779	**6**
10	***1005.400725***	503.204001	987.390160	494.198718	**E**	591.334819	296.171048	574.308270	287.657773	573.324254	287.165765	**5**
11	***1118.484789***	559.746033	1100.474224	550.740750	**I**	**462.292226**	231.649751	445.265677	223.136477	444.281661	222.644469	**4**
12	***1219.532468***	610.269872	1201.521903	601.264590	**T**	**349.208162**	175.107719	332.181613	166.594445	331.197597	166.102437	**3**
13	***1320.580147***	660.793712	1302.569582	651.788429	**T**	**248.160483**	124.583879	231.133934	116.070605	230.149918	115.578597	**2**
14					**K**	147.112804	74.060040	130.086255	65.546765			**1**



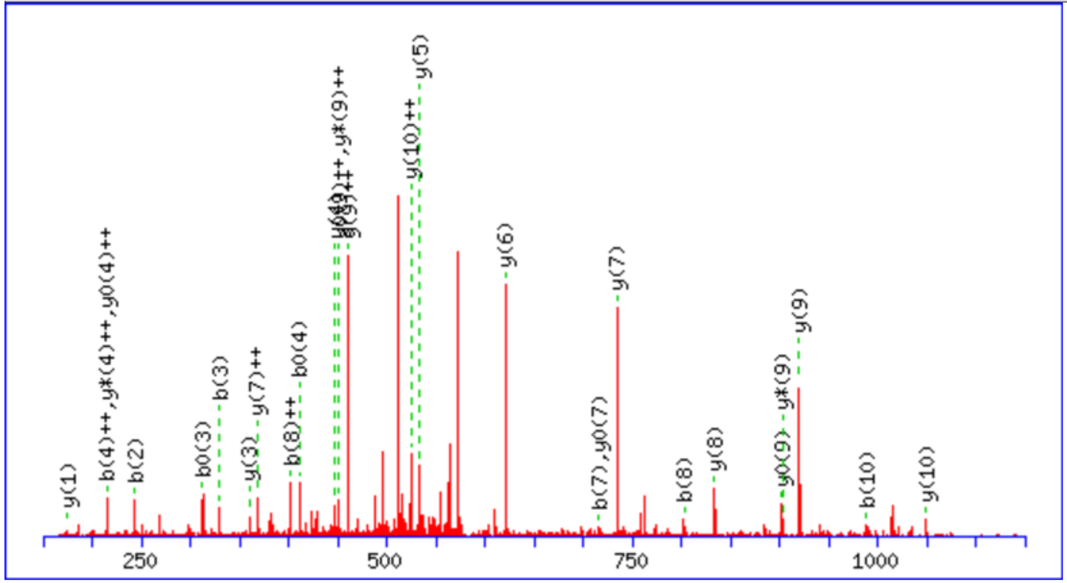
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 15 - S_E-3 **Fraction:** S_E-3

Match to Query 6191: 1161.635048 from(581.824800,2+)

Title: OECHL100317_23.6092.6092.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_23.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51 **Expect:** 0.00055**Matches :** 28/94 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	114.091340	57.549308					**I**						
2	**243.133933**	122.070605			225.123368	113.065322	**E**	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637
3	**330.165961**	165.586618			312.155396	156.581336	**S**	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340
4	429.234375	215.120826			411.223810	206.115543	**V**	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326
5	542.318439	271.662858			524.307874	262.657575	**L**	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119
6	629.350467	315.178872			611.339902	306.173589	**S**	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087
7	**716.382495**	358.694886			698.371930	349.689603	**S**	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073
8	**803.414523**	402.210899			785.403958	393.205617	**S**	***447.267407***	224.137342	430.240858	215.624067	429.256842	215.132059
9	860.435987	430.721632			842.425422	421.716349	**G**	***360.235379***	180.621328	343.208830	172.108053		
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	**K**	303.213915	152.110596	286.187366	143.597321		
11							**R**	***175.118952***	88.063114	158.092403	79.549840		

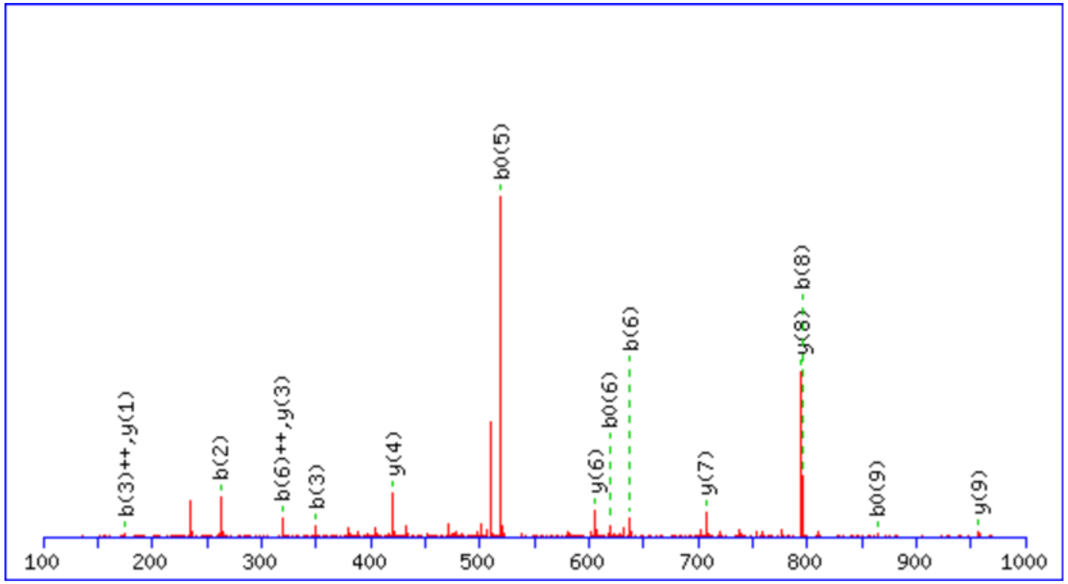


Peptide View

MS/MS Fragmentation of **VYSTSVTGSR**
Found in **IPI00010402**, Tax_Id=9606 Gene_Symbol=SH3BGRL3 Putative uncharacterized protein
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 5002: 1055.523848 from(528.769200,2+)
Title: OECHL100317_21.4349.4349.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1055.524750**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 67 **Expect:** 1.6e-005**Matches :** 16/84 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			**V**							**10**
2	**263.139019**	132.073148			**Y**	***957.463601***	479.235439	940.437052	470.722164	939.453036	470.230156	**9**
3	**350.171047**	**175.589161**	332.160482	166.583879	**S**	***794.400272***	397.703774	777.373723	389.190499	776.389707	388.698491	**8**
4	451.218726	226.113001	433.208161	217.107719	**T**	***707.368244***	354.187760	690.341695	345.674486	689.357679	345.182478	**7**
5	538.250754	269.629015	520.240189	260.623733	**S**	***606.320565***	303.663921	589.294016	295.150646	588.310000	294.658638	**6**
6	**637.319168**	**319.163222**	619.308603	310.157940	**V**	519.288537	260.147907	502.261988	251.634632	501.277972	251.142624	**5**
7	738.366847	369.687062	720.356282	360.681779	**T**	***420.220123***	210.613699	403.193574	202.100425	402.209558	201.608417	**4**
8	**795.388311**	398.197794	777.377746	389.192511	**G**	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	**3**
9	882.420339	441.713808	864.409774	432.708525	**S**	262.150980	131.579128	245.124431	123.065853	244.140415	122.573845	**2**
10					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



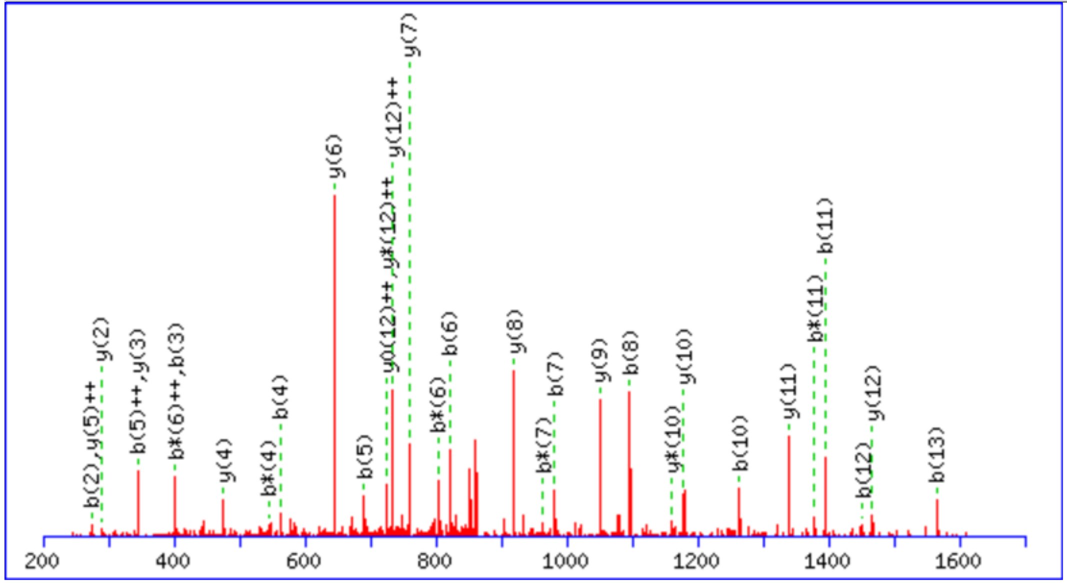
Peptide View

MS/MS Fragmentation of **CLQCQMCDPAMGLR**
Found in **IPI00024331**, Tax_Id=9606 Gene_Symbol=TNFRSF14 Tumor necrosis factor receptor superfamily member 14
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 13141: 1738.708648 from(870.361600,2+)
Title: OECHL100317_21.14164.14164.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1738.708160**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 85 **Expect:** 6.2e-008**Matches :** 32/126 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	161.037925	81.022600					C						
2	***274.121989***	137.564632					L	1579.684789	790.346032	1562.658240	781.832758	1561.674224	781.3407
3	***402.180567***	201.593921	385.154018	193.080647			Q	**1466.600725**	733.804001	1449.574176	725.290726	1448.590160	724.7987
4	***562.211216***	281.609246	545.184667	273.095972			C	**1338.542147**	669.774711	1321.515598	661.261437	1320.531582	660.7694
5	***690.269794***	345.638535	673.243245	337.125261			Q	**1178.511498**	589.759387	1161.484949	581.246113	1160.500933	580.7541

6	***821.310279***	411.158778	804.283730	402.645503			**M**	**1050.452920**	525.730098	1033.426371	517.216824	1032.442355	516.7248
7	***981.340928***	491.174102	964.314379	482.660828			**C**	**919.412435**	460.209856	902.385886	451.696581	901.401870	451.2045
8	***1096.367871***	548.687574	1079.341322	540.174299	1078.357306	539.682291	**D**	**759.381786**	380.194531	742.355237	371.681256	741.371221	371.1892
9	1193.420635	597.213956	1176.394086	588.700681	1175.410070	588.208673	**P**	**644.354843**	322.681059	627.328294	314.167785		
10	***1264.457749***	632.732513	1247.431200	624.219238	1246.447184	623.727230	**A**	547.302079	274.154677	530.275530	265.641403		
11	***1395.498234***	698.252755	1378.471685	689.739481	1377.487669	689.247473	**M**	**476.264965**	238.636120	459.238416	230.122846		
12	***1452.519698***	726.763487	1435.493149	718.250213	1434.509133	717.758205	**G**	**345.224480**	173.115878	328.197931	164.602603		
13	***1565.603762***	783.305519	1548.577213	774.792245	1547.593197	774.300236	**L**	**288.203016**	144.605146	271.176467	136.091871		
14							**R**	175.118952	88.063114	158.092403	79.549839		



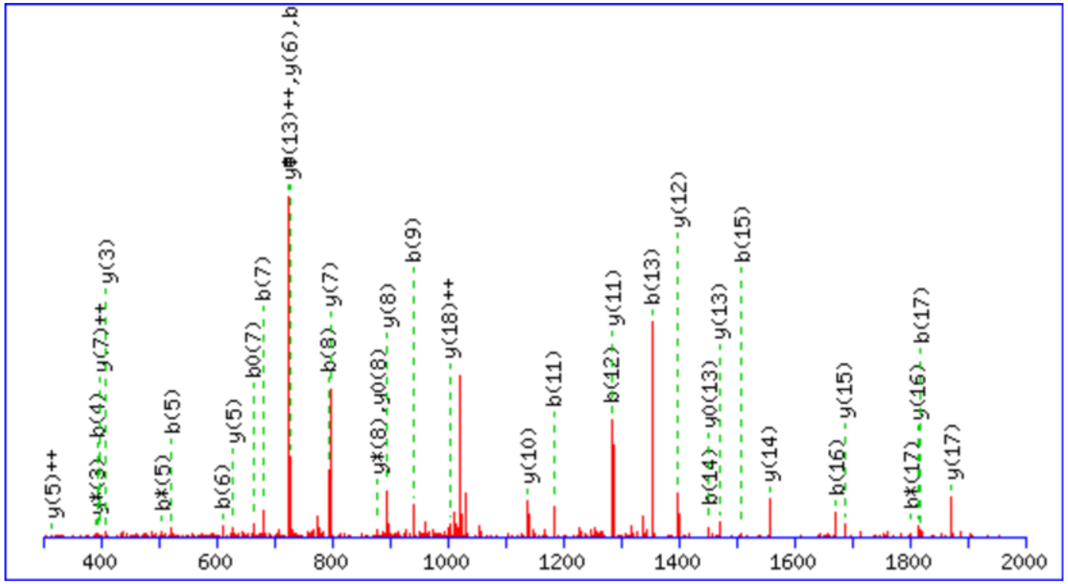
Peptide View

MS/MS Fragmentation of **AHGQESAIFNEVAPGYFSR**
Found in **IPI00170635**, Tax_Id=9606 Gene_Symbol=SECTM1 Secreted and transmembrane protein 1
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 15338: 2078.981448 from(1040.498000,2+)

Title: OECHL100317_21.16990.16990.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 2078.980988**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 86 **Expect:** 4.1e-007**Matches :** 39/200 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	72.044390	36.525833					**A**						
2	209.103302	105.055289					**H**	2008.951166	1004.979221	1991.924617	996.465947	1990.940601	995.973
3	266.124766	133.566021					**G**	***1871.892254***	936.449765	1854.865705	927.936491	1853.881689	927.444
4	***394.183344***	197.595310	377.156795	189.082035			**Q**	***1814.870790***	907.939033	1797.844241	899.425759	1796.860225	898.933
5	***523.225937***	262.116607	506.199388	253.603332	505.215372	253.111324	**E**	***1686.812212***	843.909744	1669.785663	835.396470	1668.801647	834.904
6	***610.257965***	305.632621	593.231416	297.119346	592.247400	296.627338	**S**	***1557.769619***	779.388448	1540.743070	770.875173	1539.759054	770.383
7	***681.295079***	341.151178	664.268530	332.637903	663.284514	332.145895	**A**	***1470.737591***	735.872434	1453.711042	727.359159	1452.727026	726.867
8	***794.379143***	397.693210	777.352594	389.179935	776.368578	388.687927	**I**	***1399.700477***	700.353877	1382.673928	691.840602	1381.689912	691.348
9	***941.447557***	471.227417	924.421008	462.714142	923.436992	462.222134	**F**	***1286.616413***	643.811845	1269.589864	635.298570	1268.605848	634.806
10	1055.490484	528.248880	1038.463935	519.735606	1037.479919	519.243597	**N**	***1139.547999***	570.277638	1122.521450	561.764363	1121.537434	561.272
11	***1184.533077***	592.770176	1167.506528	584.256902	1166.522512	583.764894	**E**	1025.505072	513.256174	1008.478523	504.742900	1007.494507	504.250
12	***1283.601491***	642.304383	1266.574942	633.791109	1265.590926	633.299101	**V**	***896.462479***	448.734878	879.435930	440.221603	878.451914	439.729
13	***1354.638605***	677.822940	1337.612056	669.309666	1336.628040	668.817658	**A**	***797.394065***	399.200671	780.367516	390.687396	779.383500	390.195
14	***1451.691369***	726.349322	1434.664820	717.836048	1433.680804	717.344040	**P**	***726.356951***	363.682114	709.330402	355.168839	708.346386	354.676
15	***1508.712833***	754.860054	1491.686284	746.346780	1490.702268	745.854772	**G**	***629.304187***	315.155732	612.277638	306.642457	611.293622	306.150
16	***1671.776162***	836.391719	1654.749613	827.878445	1653.765597	827.386436	**Y**	572.282723	286.645000	555.256174	278.131725	554.272158	277.639
17	***1818.844576***	909.925926	1801.818027	901.412652	1800.834011	900.920643	**F**	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108
18	1905.876604	953.441940	1888.850055	944.928666	1887.866039	944.436658	**S**	262.150980	131.579128	245.124431	123.065854	244.140415	122.573
19							**R**	175.118952	88.063114	158.092403	79.549840		



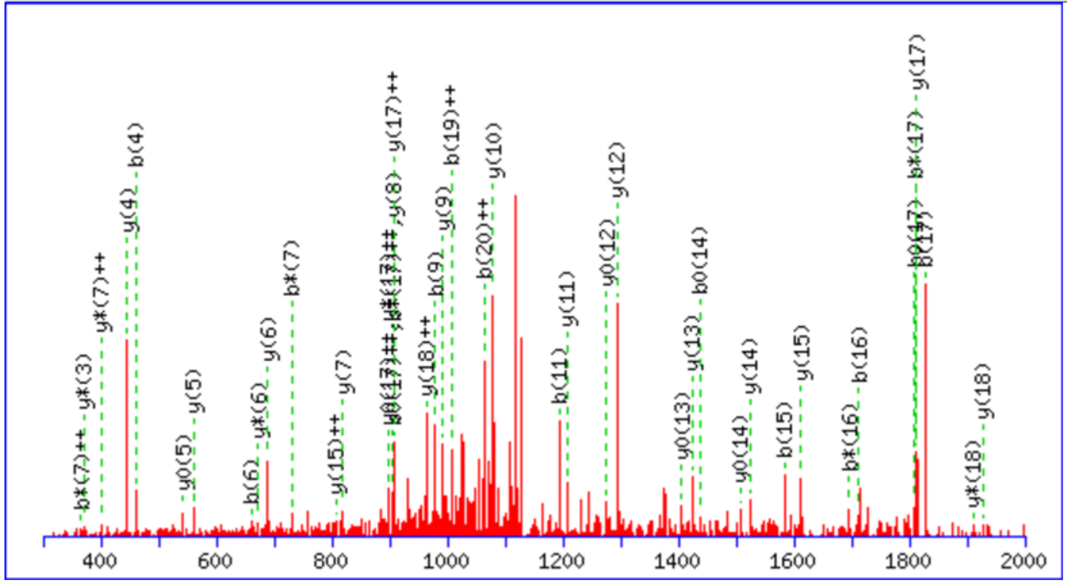
Peptide View

MS/MS Fragmentation of **SKEDSNSTESKSSSEEDGQLK**
Found in **IPI00012734**, Tax_Id=9606 Gene_Symbol=DMP1 Isoform 1 of Dentin matrix acidic phosphoprotein 1
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 16303: 2271.001448 from(1136.508000,2+)
Title: OECHL100317_21.2411.2411.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 2270.998581**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 72 **Expect:** 5.5e-006**Matches :** 44/230 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	
1	88.039304	44.523290			70.028739	35.518008	**S**						
2	216.134267	108.570771	199.107718	100.057497	198.123702	99.565489	**K**	2184.973868	1092.990572	2167.947319	1084.477297	2166.963303	10
3	345.176860	173.092068	328.150311	164.578793	327.166295	164.086785	**E**	2056.878905	1028.943090	2039.852356	1020.429816	2038.868340	10
4	**460.203803**	230.605539	443.177254	222.092265	442.193238	221.600257	**D**	***1927.836312***	964.421794	1910.809763	955.908520	1909.825747	9
5	547.235831	274.121554	530.209282	265.608279	529.225266	265.116271	**S**	***1812.809369***	906.908323	1795.782820	898.395048	1794.798804	8

6	**661.278758**	331.143017	644.252209	322.629743	643.268193	322.137735	**N**	1725.777341	863.392309	1708.750792	854.879034	1707.766776	85
7	748.310786	374.659031	731.284237	366.145757	730.300221	365.653749	**S**	***1611.734414***	806.370845	1594.707865	797.857571	1593.723849	79
8	849.358465	425.182871	832.331916	416.669596	831.347900	416.177588	**T**	***1524.702386***	762.854831	1507.675837	754.341557	1506.691821	75
9	**978.401058**	489.704167	961.374509	481.190893	960.390493	480.698885	**E**	***1423.654707***	712.330992	1406.628158	703.817717	1405.644142	70
10	1065.433086	533.220181	1048.406537	524.706907	1047.422521	524.214899	**S**	***1294.612114***	647.809695	1277.585565	639.296421	1276.601549	63
11	**1193.528049**	597.267663	1176.501500	588.754388	1175.517484	588.262380	**K**	***1207.580086***	604.293681	1190.553537	595.780407	1189.569521	59
12	1280.560077	640.783677	1263.533528	632.270402	1262.549512	631.778394	**S**	***1079.485123***	540.246200	1062.458574	531.732925	1061.474558	53
13	1367.592105	684.299691	1350.565556	675.786416	1349.581540	675.294408	**S**	***992.453095***	496.730186	975.426546	488.216911	974.442530	48
14	1454.624133	727.815705	1437.597584	719.302430	1436.613568	718.810422	**S**	***905.421067***	453.214172	888.394518	444.700897	887.410502	44
15	**1583.666726**	792.337001	1566.640177	783.823727	1565.656161	783.331719	**E**	***818.389039***	409.698158	801.362490	401.184883	800.378474	40
16	**1712.709319**	856.858298	1695.682770	848.345023	1694.698754	847.853015	**E**	***689.346446***	345.176861	672.319897	336.663587	671.335881	33
17	**1827.736262**	914.371769	1810.709713	905.858495	1809.725697	905.366487	**D**	***560.303853***	280.655565	543.277304	272.142290	542.293288	27
18	1884.757726	942.882501	1867.731177	934.369227	1866.747161	933.877219	**G**	***445.276910***	223.142093	428.250361	214.628818		
19	2012.816304	1006.911790	1995.789755	998.398516	1994.805739	997.906508	**Q**	388.255446	194.631361	371.228897	186.118087		
20	2125.900368	1063.453822	2108.873819	1054.940547	2107.889803	1054.448539	**L**	260.196868	130.602072	243.170319	122.088798		
21							**K**	147.112804	74.060040	130.086255	65.546765		

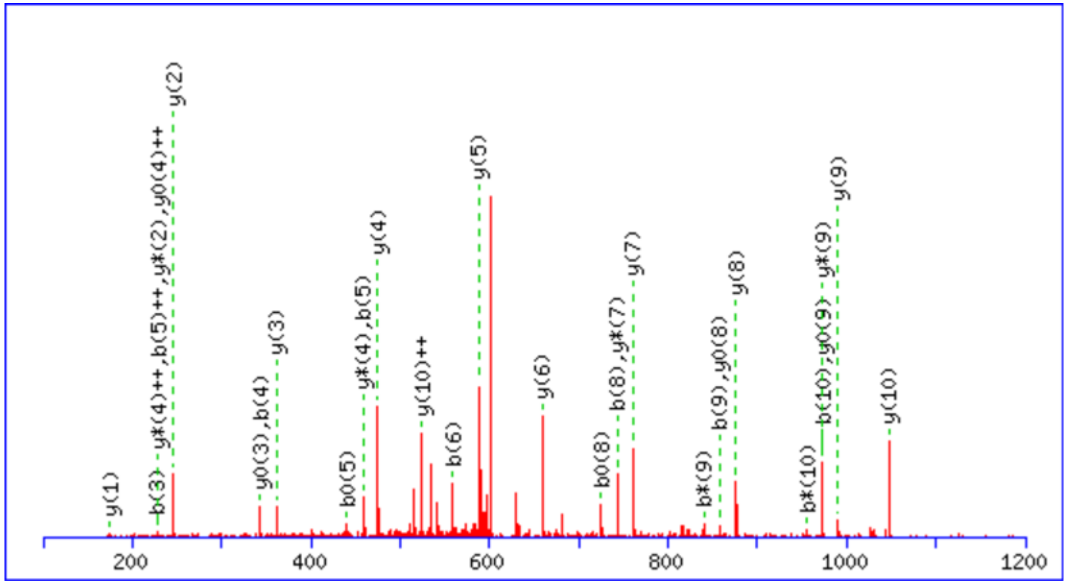


Peptide View

MS/MS Fragmentation of **GLGDDTALNDAR**
Found in **IPI00216914**, Tax_Id=9606 Gene_Symbol=VMO1 Vitelline membrane outer layer protein 1 homolog
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 7254: 1216.568648 from(609.291600,2+)
Title: OECHL100317_21.8678.8678.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1216.568390**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 75 **Expect:** 2.3e-006**Matches :** 32/106 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	58.028740	29.518008					**G**						
2	171.112804	86.060040					**L**	1160.554207	580.780742	1143.527658	572.267467	1142.543642	571.7754
3	**228.134268**	114.570772					**G**	***1047.470143***	524.238710	1030.443594	515.725435	1029.459578	515.2334
4	**343.161211**	172.084243			325.150646	163.078961	**D**	***990.448679***	495.727978	973.422130	487.214703	972.438114	486.7226
5	**458.188154**	229.597715			440.177589	220.592433	**D**	***875.421736***	438.214506	858.395187	429.701232	857.411171	429.2092
6	**559.235833**	280.121555			541.225268	271.116272	**T**	***760.394793***	380.701035	743.368244	372.187760	742.384228	371.6957
7	630.272947	315.640112			612.262382	306.634829	**A**	***659.347114***	330.177195	642.320565	321.663921	641.336549	321.1719
8	**743.357011**	372.182144			725.346446	363.176861	**L**	***588.310000***	294.658638	571.283451	286.145364	570.299435	285.6533
9	**857.399938**	429.203607	840.373389	420.690333	839.389373	420.198325	**N**	***475.225936***	238.116606	458.199387	229.603331	457.215371	229.1113
10	**972.426881**	486.717079	955.400332	478.203804	954.416316	477.711796	**D**	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.0898
11	1043.463995	522.235636	1026.437446	513.722361	1025.453430	513.230353	**A**	***246.156066***	123.581671	229.129517	115.068397		
12							**R**	***175.118952***	88.063114	158.092403	79.549839		



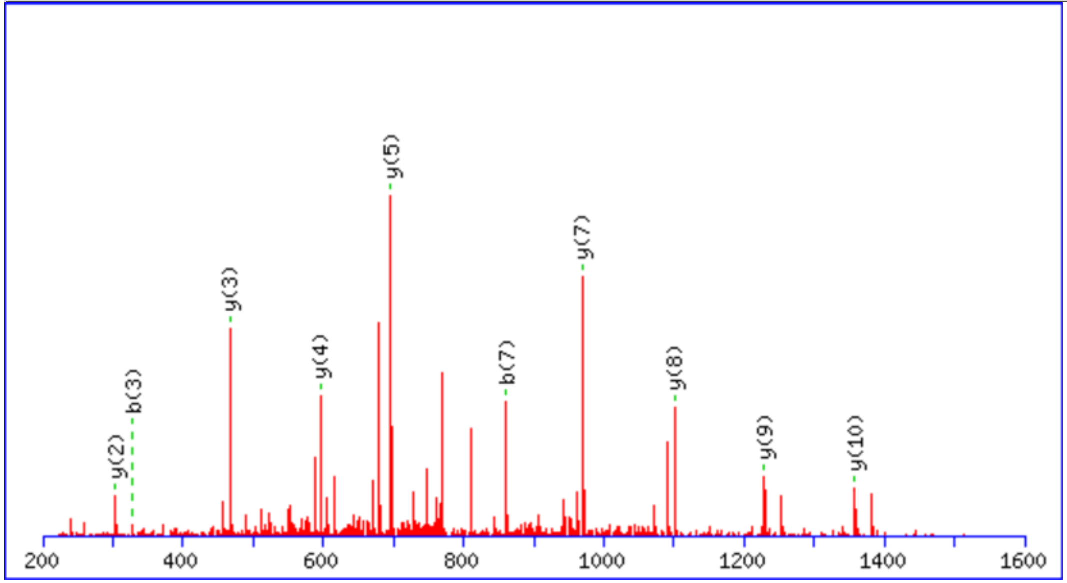
Peptide View

MS/MS Fragmentation of **VVEQMCITQYER**
Found in **IPI00022284**, Tax_Id=9606 Gene_Symbol=PRNP Major prion protein
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 11272: 1554.717448 from(778.366000,2+)
Title: OECHL100317_21.13258.13258.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1554.717041**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 70 **Expect:** 9.3e-006**Matches :** 10/120 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	100.075690	50.541483					V						
2	199.144104	100.075690					V	1456.655914	728.831595	1439.629365	720.318321	1438.645349	719.8263
3	**328.186697**	164.596987			310.176132	155.591704	E	***1357.587500***	679.297388	1340.560951	670.784114	1339.576935	670.2921
4	456.245275	228.626276	439.218726	220.113001	438.234710	219.620993	Q	***1228.544907***	614.776092	1211.518358	606.262817	1210.534342	605.7708
5	587.285760	294.146518	570.259211	285.633244	569.275195	285.141236	M	***1100.486329***	550.746803	1083.459780	542.233528	1082.475764	541.7415

6	747.316409	374.161843	730.289860	365.648568	729.305844	365.156560	C	***969.445844***	485.226560	952.419295	476.713286	951.435279	476.2212
7	**860.400473**	430.703875	843.373924	422.190600	842.389908	421.698592	I	809.415195	405.211236	792.388646	396.697961	791.404630	396.2059
8	961.448152	481.227714	944.421603	472.714440	943.437587	472.222432	T	***696.331131***	348.669204	679.304582	340.155929	678.320566	339.6639
9	1089.506730	545.257003	1072.480181	536.743729	1071.496165	536.251721	Q	***595.283452***	298.145364	578.256903	289.632090	577.272887	289.1400
10	1252.570059	626.788668	1235.543510	618.275393	1234.559494	617.783385	Y	***467.224874***	234.116075	450.198325	225.602801	449.214309	225.1107
11	1381.612652	691.309964	1364.586103	682.796690	1363.602087	682.304682	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.5791
12							R	175.118952	88.063114	158.092403	79.549839		



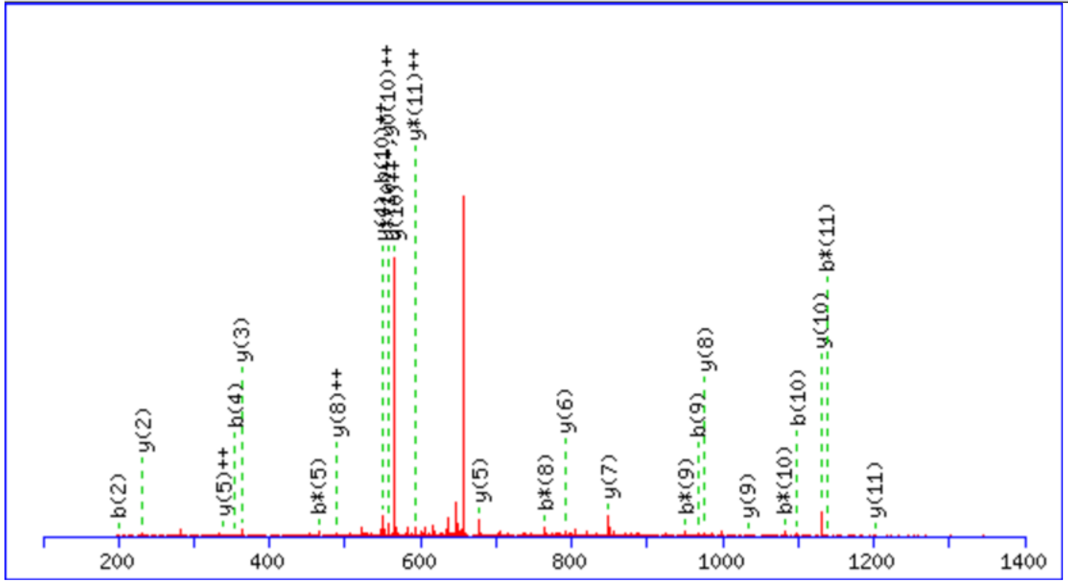
Peptide View

MS/MS Fragmentation of **QAPGQGLEWMGR**
Found in **IPI00009792**, Tax_Id=9606 Gene_Symbol=IGHV1OR15-1 Ig heavy chain V-I region V35
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 8842: 1328.629848 from(665.322200,2+)
Title: OECHL100317_21.14985.14985.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1328.629547**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**

Score: 62 **Expect:** 6.7e-005**Matches :** 26/110 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	129.065854	65.036565	112.039305	56.523291			Q						
2	**200.102968**	100.555122	183.076419	92.041848			A	***1201.578255***	601.292766	1184.551706	592.779491	1183.567690	592.2874
3	297.155732	149.081504	280.129183	140.568230			P	***1130.541141***	565.774208	1113.514592	557.260934	1112.530576	556.7689
4	**354.177196**	177.592236	337.150647	169.078961			G	***1033.488377***	517.247827	1016.461828	508.734552	1015.477812	508.2425
5	482.235774	241.621525	465.209225	233.108251			Q	***976.466913***	488.737095	959.440364	480.223820	958.456348	479.7318
6	539.257238	270.132257	522.230689	261.618983			G	***848.408335***	424.707806	831.381786	416.194531	830.397770	415.7025
7	652.341302	326.674289	635.314753	318.161015			L	***791.386871***	396.197074	774.360322	387.683799	773.376306	387.1917
8	781.383895	391.195586	764.357346	382.682311	763.373330	382.190303	E	***678.302807***	339.655042	661.276258	331.141767	660.292242	330.6497
9	**967.463208**	484.235242	950.436659	475.721968	949.452643	475.229960	W	***549.260214***	275.133745	532.233665	266.620471		
10	**1098.503693**	549.755485	1081.477144	541.242210	1080.493128	540.750202	M	***363.180901***	182.094088	346.154352	173.580814		
11	1155.525157	578.266217	1138.498608	569.752942	1137.514592	569.260934	G	***232.140416***	116.573846	215.113867	108.060571		
12							R	175.118952	88.063114	158.092403	79.549839		

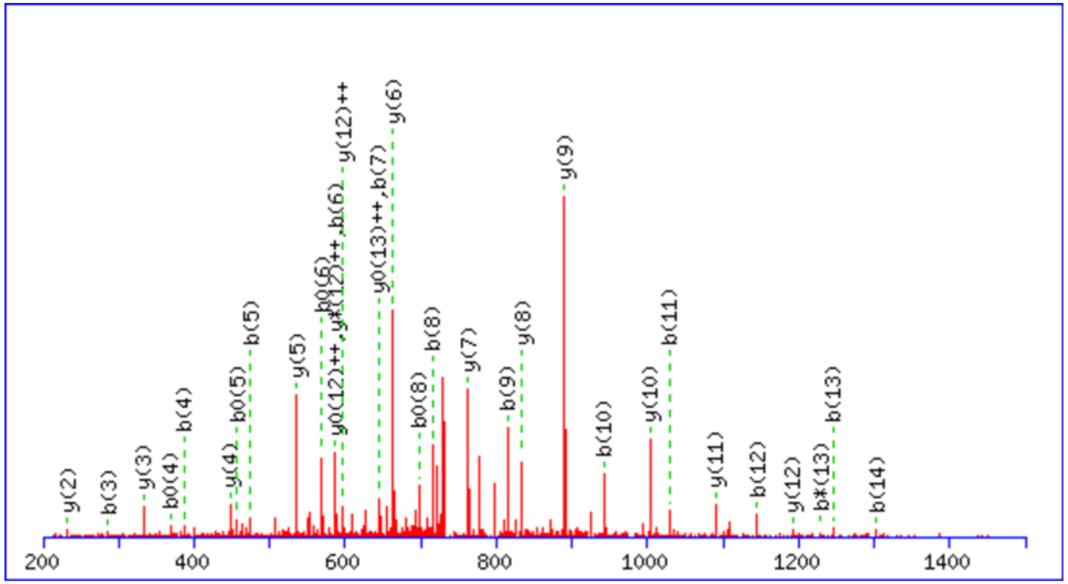


Peptide View

MS/MS Fragmentation of **GLDTSLGAVQSDTGR**
Found in **IPI00289931**, Tax_Id=9606 Gene_Symbol=MADCAM1 MADCAM1 protein
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 10213: 1475.722648 from(738.868600,2+)
Title: OECHL100317_21.11342.11342.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1475.721619**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 88 **Expect:** 2.3e-007**Matches :** 32/142 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	58.028740	29.518008					**G**						
2	171.112804	86.060040					**L**	1419.707414	710.357345	1402.680865	701.844071	1401.696849	701.3520
3	***286.139747***	143.573512			268.129182	134.568229	**D**	1306.623350	653.815313	1289.596801	645.302039	1288.612785	644.8100
4	***387.187426***	194.097351			369.176861	185.092069	**T**	**1191.596407**	596.301842	1174.569858	587.788567	1173.585842	587.2965
5	***474.219454***	237.613365			456.208889	228.608082	**S**	**1090.548728**	545.778002	1073.522179	537.264728	1072.538163	536.7727
6	***587.303518***	294.155397			569.292953	285.150115	**L**	**1003.516700**	502.261988	986.490151	493.748714	985.506135	493.2567
7	***644.324982***	322.666129			626.314417	313.660847	**G**	**890.432636**	445.719956	873.406087	437.206682	872.422071	436.7146
8	***715.362096***	358.184686			697.351531	349.179404	**A**	**833.411172**	417.209224	816.384623	408.695950	815.400607	408.2039
9	***814.430510***	407.718893			796.419945	398.713611	**V**	**762.374058**	381.690667	745.347509	373.177393	744.363493	372.6853
10	***942.489088***	471.748182	925.462539	463.234908	924.478523	462.742900	**Q**	**663.305644**	332.156460	646.279095	323.643186	645.295079	323.1511
11	***1029.521116***	515.264196	1012.494567	506.750922	1011.510551	506.258914	**S**	**535.247066**	268.127171	518.220517	259.613897	517.236501	259.1218
12	***1144.548059***	572.777668	1127.521510	564.264393	1126.537494	563.772385	**D**	**448.215038**	224.611157	431.188489	216.097882	430.204473	215.6058
13	***1245.595738***	623.301507	1228.569189	614.788233	1227.585173	614.296225	**T**	**333.188095**	167.097685	316.161546	158.584411	315.177530	158.0924
14	***1302.617202***	651.812239	1285.590653	643.298965	1284.606637	642.806957	**G**	**232.140416**	116.573846	215.113867	108.060571		
15							**R**	175.118952	88.063114	158.092403	79.549839		



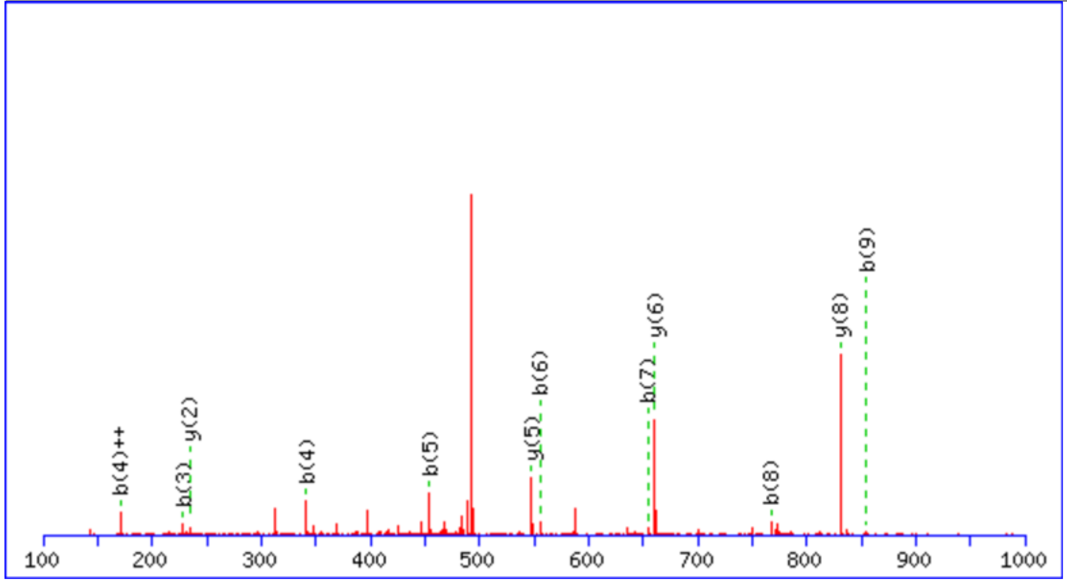
Peptide View

MS/MS Fragmentation of **AVGLLTVISK**
Found in **IPI00013446**, Tax_Id=9606 Gene_Symbol=PSCA Prostate stem cell antigen
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 4012: 999.632448 from(500.823500,2+)
Title: OECHL100317_21.17050.17050.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 999.632828**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 59 **Expect:** 1.4e-005**Matches :** 13/78 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			**A**							**10**
2	***171.112804***	86.060040			**V**	929.602995	465.305136	912.576446	456.791861	911.592430	456.299853	**9**
3	***228.134268***	114.570772			**G**	**830.534581**	415.770929	813.508032	407.257654	812.524016	406.765646	**8**
4	***341.218332***	171.112804			**L**	773.513117	387.260197	756.486568	378.746922	755.502552	378.254914	**7**
5	***454.302396***	227.654836			**L**	**660.429053**	330.718165	643.402504	322.204890	642.418488	321.712882	**6**

6	***555.350075***	278.178676	537.339510	269.173393	**T**	**547.344989**	274.176133	530.318440	265.662858	529.334424	265.170850	**5**
7	***654.418489***	327.712883	636.407924	318.707600	**V**	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	**4**
8	***767.502553***	384.254915	749.491988	375.249632	**I**	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	**3**
9	***854.534581***	427.770929	836.524016	418.765646	**S**	**234.144832**	117.576054	217.118283	109.062779	216.134267	108.570771	**2**
10					**K**	147.112804	74.060040	130.086255	65.546765			**1**



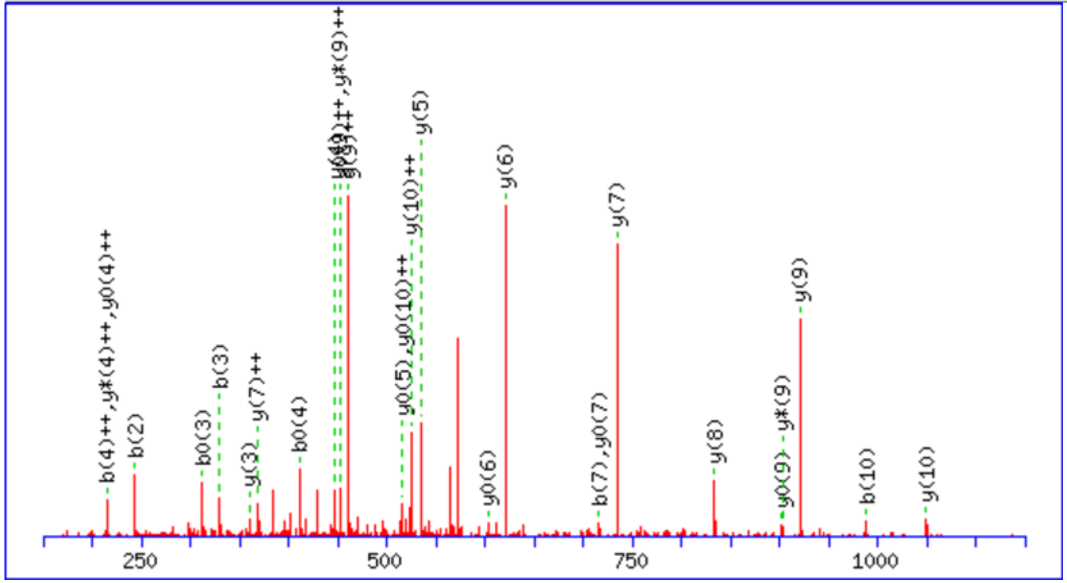
Peptide View

MS/MS Fragmentation of **IESVLSSSGKR**
Found in **IPI00018236**, Tax_Id=9606 Gene_Symbol=GM2A Ganglioside GM2 activator
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 6542: 1161.637048 from(581.825800,2+)
Title: OECHL100317_21.5011.5011.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1161.635330**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 61 **Expect:** 6.1e-005**Matches :** 28/94 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}

1	114.091340	57.549308					I						
2	**243.133933**	122.070605			225.123368	113.065322	E	***1049.558562***	525.282919	1032.532013	516.769645	1031.547997	516.277637
3	**330.165961**	165.586618			312.155396	156.581336	S	***920.515969***	460.761623	903.489420	452.248348	902.505404	451.756340
4	429.234375	215.120826			411.223810	206.115543	V	***833.483941***	417.245609	816.457392	408.732334	815.473376	408.240326
5	542.318439	271.662858			524.307874	262.657575	L	***734.415527***	367.711402	717.388978	359.198127	716.404962	358.706119
6	629.350467	315.178872			611.339902	306.173589	S	***621.331463***	311.169370	604.304914	302.656095	603.320898	302.164087
7	**716.382495**	358.694886			698.371930	349.689603	S	***534.299435***	267.653356	517.272886	259.140081	516.288870	258.648073
8	803.414523	402.210899			785.403958	393.205617	S	***447.267407***	224.137342	430.240858	215.624067	429.256842	215.132059
9	860.435987	430.721632			842.425422	421.716349	G	***360.235379***	180.621328	343.208830	172.108053		
10	**988.530950**	494.769113	971.504401	486.255838	970.520385	485.763830	K	303.213915	152.110596	286.187366	143.597321		
11							R	175.118952	88.063114	158.092403	79.549840		



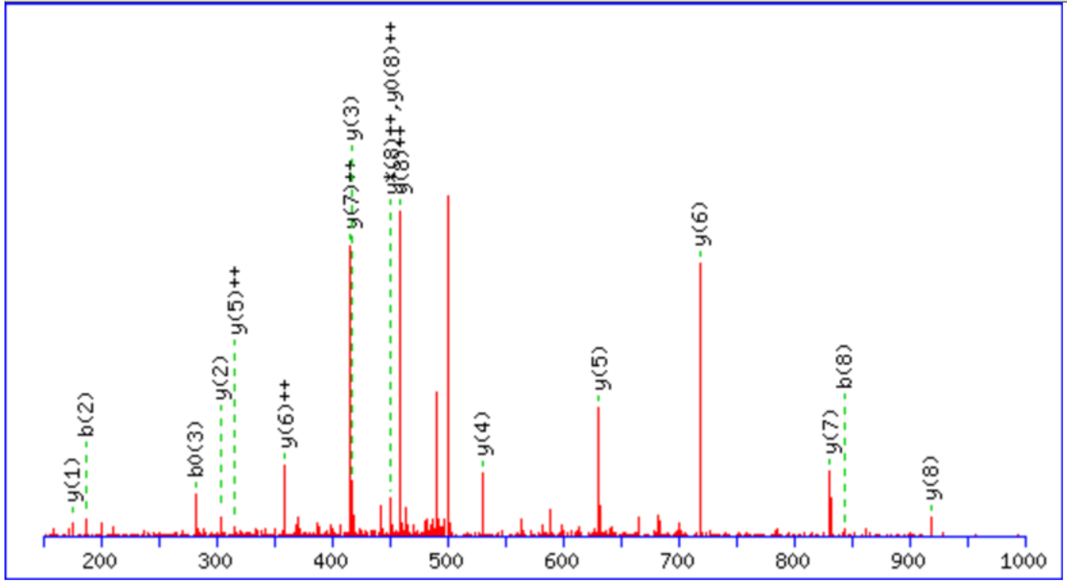
Peptide View

MS/MS Fragmentation of **VSISTLNKR**
Found in **IPI00176221**, Tax_Id=9606 Gene_Symbol=NEGR1 Neuronal growth regulator 1

Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 4387: 1016.597848 from(509.306200,2+)
Title: OECHL100317_21.6067.6067.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1016.597824**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 56 **Expect:** 7.1e-005**Matches :** 17/74 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	100.075690	50.541483					**V**							**9**
2	**187.107718**	94.057497			169.097153	85.052214	**S**	***918.536705***	459.771991	901.510156	451.258716	900.526140	450.766708	**8**
3	300.191782	150.599529			282.181217	141.594247	**I**	***831.504677***	416.255977	814.478128	407.742702	813.494112	407.250694	**7**
4	387.223810	194.115543			369.213245	185.110261	**S**	***718.420613***	359.713945	701.394064	351.200670	700.410048	350.708662	**6**
5	488.271489	244.639383			470.260924	235.634100	**T**	***631.388585***	316.197931	614.362036	307.684656	613.378020	307.192648	**5**
6	601.355553	301.181415			583.344988	292.176132	**L**	***530.340906***	265.674091	513.314357	257.160817			**4**
7	715.398480	358.202878	698.371931	349.689604	697.387915	349.197596	**N**	***417.256842***	209.132059	400.230293	200.618784			**3**
8	**843.493443**	422.250360	826.466894	413.737085	825.482878	413.245077	**K**	***303.213915***	152.110595	286.187366	143.597321			**2**
9							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**

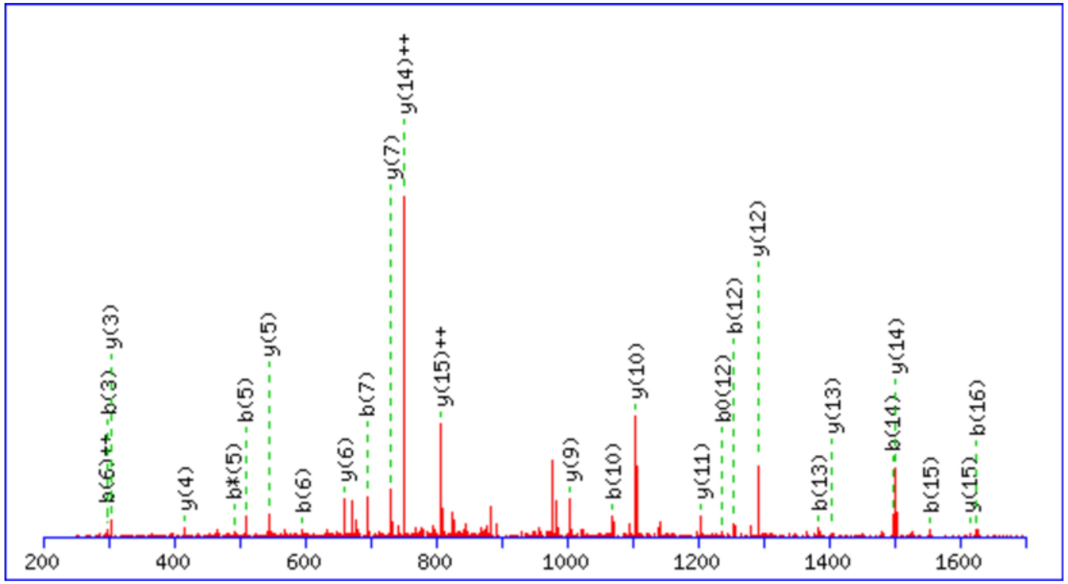


Peptide View

MS/MS Fragmentation of **GQLPISVTCIADEIGAR**
Found in **IPI00240345**, Tax_Id=9606 Gene_Symbol=CLEC14A C-type lectin domain family 14 member A
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 13459: 1798.924848 from(900.469700,2+)
Title: OECHL100317_21.19710.19710.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1798.924728**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 65 **Expect:** 4.4e-005**Matches :** 27/172 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	58.028740	29.518008					**G**						
2	186.087318	93.547297	169.060769	85.034023			**Q**	1742.910548	871.958912	1725.883999	863.445638	1724.899983	862.9536
3	***299.171382***	150.089329	282.144833	141.576055			**L**	***1614.851970***	807.929623	1597.825421	799.416349	1596.841405	798.9243
4	396.224146	198.615711	379.197597	190.102436			**P**	***1501.767906***	751.387591	1484.741357	742.874317	1483.757341	742.3823
5	***509.308210***	255.157743	492.281661	246.644468			**I**	***1404.715142***	702.861209	1387.688593	694.347935	1386.704577	693.8559
6	***596.340238***	298.673757	579.313689	290.160483	578.329673	289.668475	**S**	***1291.631078***	646.319177	1274.604529	637.805903	1273.620513	637.3138
7	***695.408652***	348.207964	678.382103	339.694689	677.398087	339.202681	**V**	***1204.599050***	602.803163	1187.572501	594.289889	1186.588485	593.7978
8	796.456331	398.731804	779.429782	390.218529	778.445766	389.726521	**T**	***1105.530636***	553.268956	1088.504087	544.755682	1087.520071	544.2636
9	956.486980	478.747128	939.460431	470.233854	938.476415	469.741846	**C**	***1004.482957***	502.745117	987.456408	494.231842	986.472392	493.7398
10	***1069.571044***	535.289160	1052.544495	526.775886	1051.560479	526.283878	**I**	844.452308	422.729792	827.425759	414.216518	826.441743	413.7245
11	1140.608158	570.807717	1123.581609	562.294443	1122.597593	561.802435	**A**	***731.368244***	366.187760	714.341695	357.674486	713.357679	357.1824
12	***1255.635101***	628.321189	1238.608552	619.807914	1237.624536	619.315906	**D**	***660.331130***	330.669203	643.304581	322.155929	642.320565	321.6639
13	***1384.677694***	692.842485	1367.651145	684.329211	1366.667129	683.837203	**E**	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.1504
14	***1497.761758***	749.384517	1480.735209	740.871243	1479.751193	740.379235	**I**	***416.261594***	208.634435	399.235045	200.121160		
15	***1554.783222***	777.895249	1537.756673	769.381975	1536.772657	768.889967	**G**	***303.177530***	152.092403	286.150981	143.579128		
16	***1625.820336***	813.413806	1608.793787	804.900532	1607.809771	804.408524	**A**	246.156066	123.581671	229.129517	115.068396		
17							**R**	175.118952	88.063114	158.092403	79.549839		



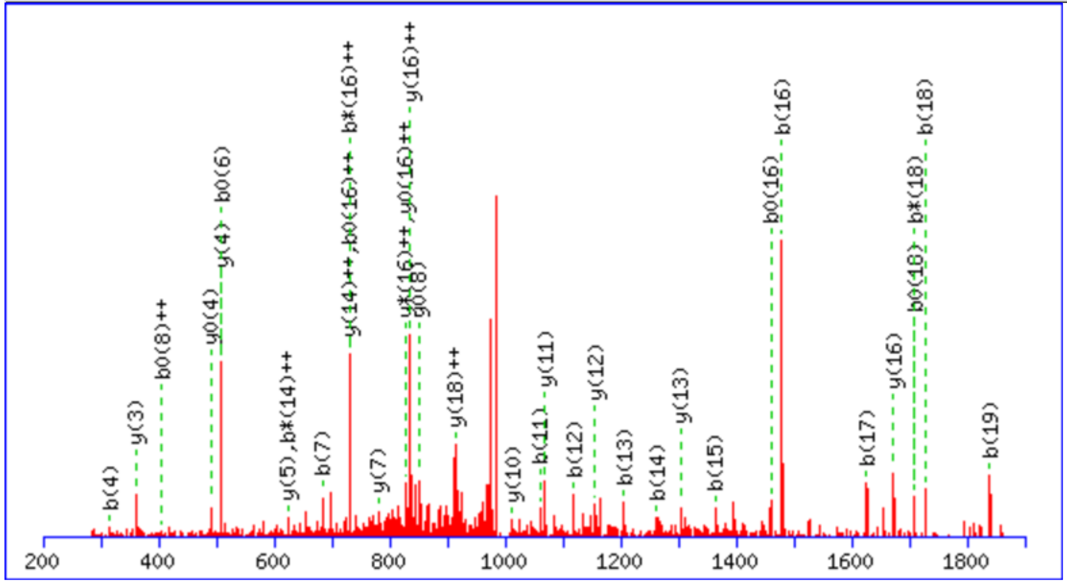
Peptide View

MS/MS Fragmentation of **ASGVPDRFSGSGSGTDFTLK**
Found in **IPI00387107**, Tax_Id=9606 Gene_Symbol=IGKV2-40 Ig kappa chain V-II region Cum
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 14618: 1984.950248 from(993.482400,2+)
Title: OECHL100317_21.13660.13660.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1984.949066**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 61 **Expect:** 0.00012**Matches :** 35/210 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}
1	72.044390	36.525833					A						
2	159.076418	80.041847			141.065853	71.036564	S	1914.919197	957.963236	1897.892648	949.449962	1896.908632	948.9579
3	216.097882	108.552579			198.087317	99.547296	G	1827.887169	914.447222	1810.860620	905.933948	1809.876604	905.4419
4	***315.166296***	158.086786			297.155731	149.081504	V	1770.865705	885.936490	1753.839156	877.423216	1752.855140	876.9312
5	412.219060	206.613168			394.208495	197.607885	P	***1671.797291***	836.402283	1654.770742	827.889009	1653.786726	827.3970

6	527.246003	264.126640			509.235438	255.121357	**D**	1574.744527	787.875902	1557.717978	779.362627	1556.733962	778.8706
7	***683.347114***	342.177195	666.320565	333.663920	665.336549	333.171912	**R**	1459.717584	730.362430	1442.691035	721.849156	1441.707019	721.3571
8	830.415528	415.711402	813.388979	407.198127	812.404963	406.706119	**F**	***1303.616473***	652.311875	1286.589924	643.798600	1285.605908	643.3065
9	917.447556	459.227416	900.421007	450.714141	899.436991	450.222133	**S**	***1156.548059***	578.777668	1139.521510	570.264393	1138.537494	569.7723
10	974.469020	487.738148	957.442471	479.224873	956.458455	478.732865	**G**	***1069.516031***	535.261654	1052.489482	526.748379	1051.505466	526.2563
11	***1061.501048***	531.254162	1044.474499	522.740887	1043.490483	522.248879	**S**	***1012.494567***	506.750922	995.468018	498.237647	994.484002	497.7456
12	***1118.522512***	559.764894	1101.495963	551.251619	1100.511947	550.759611	**G**	925.462539	463.234908	908.435990	454.721633	907.451974	454.2296
13	***1205.554540***	603.280908	1188.527991	594.767633	1187.543975	594.275625	**S**	868.441075	434.724176	851.414526	426.210901	850.430510	425.7188
14	***1262.576004***	631.791640	1245.549455	623.278365	1244.565439	622.786357	**G**	***781.409047***	391.208162	764.382498	382.694887	763.398482	382.2028
15	***1363.623683***	682.315479	1346.597134	673.802205	1345.613118	673.310197	**T**	724.387583	362.697430	707.361034	354.184155	706.377018	353.6921
16	***1478.650626***	739.828951	1461.624077	731.315677	1460.640061	730.823668	**D**	***623.339904***	312.173590	606.313355	303.660316	605.329339	303.1683
17	***1625.719040***	813.363158	1608.692491	804.849884	1607.708475	804.357875	**F**	***508.312961***	254.660118	491.286412	246.146844	490.302396	245.6548
18	***1726.766719***	863.886998	1709.740170	855.373723	1708.756154	854.881715	**T**	***361.244547***	181.125911	344.217998	172.612637	343.233982	172.1206
19	***1839.850783***	920.429029	1822.824234	911.915755	1821.840218	911.423747	**L**	260.196868	130.602072	243.170319	122.088797		
20							**K**	147.112804	74.060040	130.086255	65.546765		

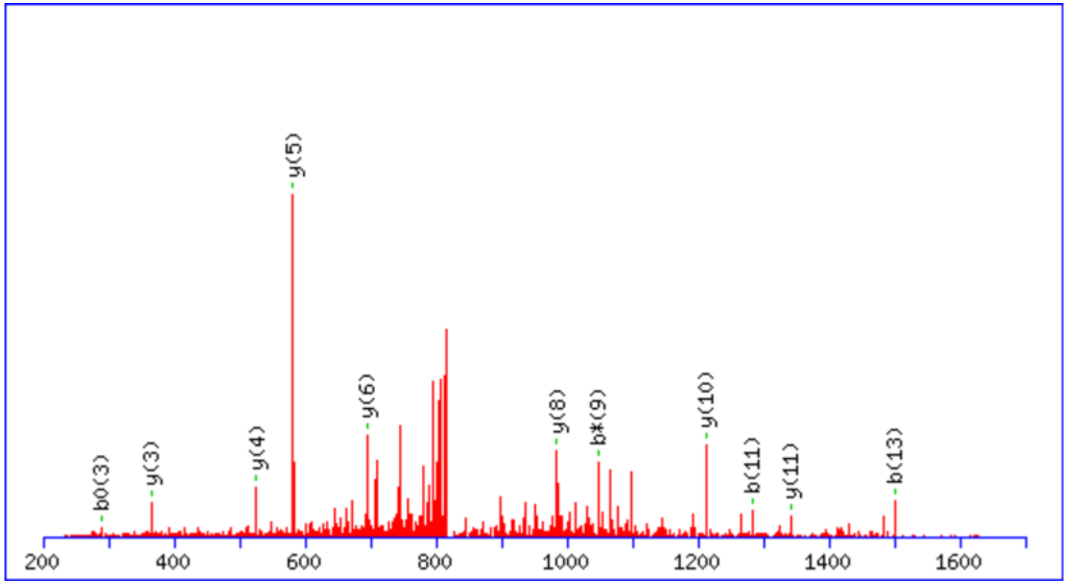


Peptide View

MS/MS Fragmentation of **ASFENNCEIGCFAK**
Found in **IPI00010105**, Tax_Id=9606 Gene_Symbol=EIF6 Eukaryotic translation initiation factor 6
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 12252: 1645.688648 from(823.851600,2+)
Title: OECHL100317_21.13765.13765.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1645.686462**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 57 **Expect:** 6.5e-005**Matches :** 11/134 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	72.044390	36.525833					**A**						
2	159.076418	80.041847			141.065853	71.036564	**S**	1575.656640	788.331958	1558.630091	779.818684	1557.646075	779.3266
3	306.144832	153.576054			288.134267	144.570772	**F**	1488.624612	744.815944	1471.598063	736.302670	1470.614047	735.8106
4	435.187425	218.097351			417.176860	209.092068	**E**	***1341.556198***	671.281737	1324.529649	662.768463	1323.545633	662.2764
5	549.230352	275.118814	532.203803	266.605540	531.219787	266.113532	**N**	***1212.513605***	606.760441	1195.487056	598.247166	1194.503040	597.7551
6	663.273279	332.140278	646.246730	323.627003	645.262714	323.134995	**N**	1098.470678	549.738977	1081.444129	541.225703	1080.460113	540.7336
7	823.303928	412.155602	806.277379	403.642328	805.293363	403.150320	**C**	***984.427751***	492.717514	967.401202	484.204239	966.417186	483.7122
8	952.346521	476.676899	935.319972	468.163624	934.335956	467.671616	**E**	824.397102	412.702189	807.370553	404.188915	806.386537	403.6969
9	1065.430585	533.218931	1048.404036	524.705656	1047.420020	524.213648	**I**	***695.354509***	348.180893	678.327960	339.667618		
10	1122.452049	561.729663	1105.425500	553.216388	1104.441484	552.724380	**G**	***582.270445***	291.638861	565.243896	283.125586		
11	**1282.482698**	641.744987	1265.456149	633.231713	1264.472133	632.739705	**C**	***525.248981***	263.128129	508.222432	254.614854		
12	1429.551112	715.279194	1412.524563	706.765920	1411.540547	706.273912	**F**	***365.218332***	183.112804	348.191783	174.599530		
13	**1500.588226**	750.797751	1483.561677	742.284477	1482.577661	741.792469	**A**	218.149918	109.578597	201.123369	101.065322		
14							**K**	147.112804	74.060040	130.086255	65.546765		



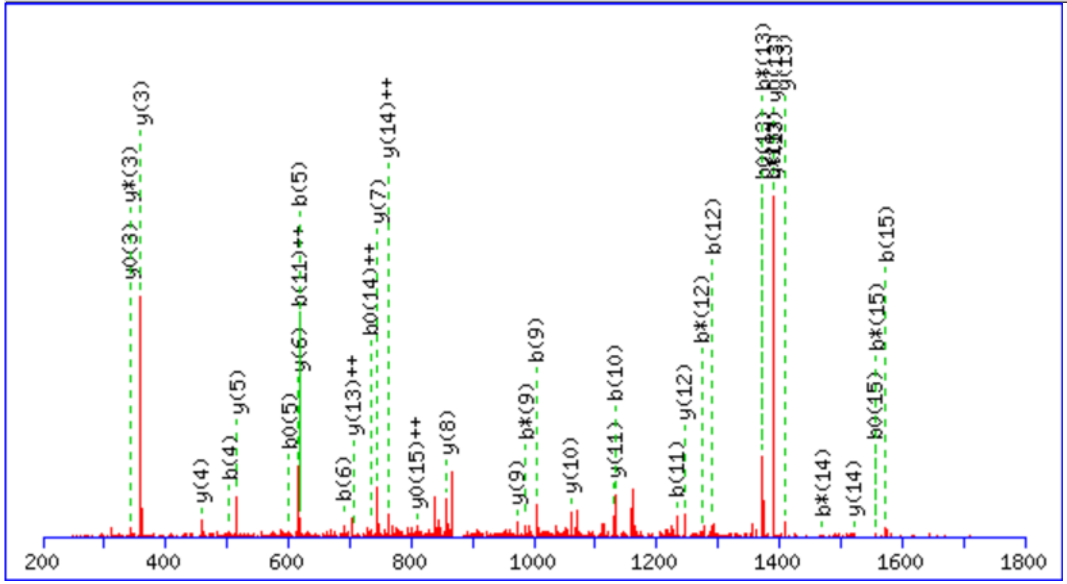
Peptide View

MS/MS Fragmentation of **LLIYDASNLETGVPSR**
Found in **IPI00003111**, Tax_Id=9606 Gene_Symbol=LOC652694 Ig kappa chain V-I region AU
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 13181: 1746.915648 from(874.465100,2+)
Title: OECHL100317_21.16894.16894.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1746.915192**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 53 **Expect:** 0.00055**Matches :** 38/156 fragment ions using 101 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}
1	114.091340	57.549308					**L**						
2	227.175404	114.091340					**L**	1634.838427	817.922852	1617.811878	809.409577	1616.827862	808.9175
3	340.259468	170.633372					**I**	***1521.754363***	761.380820	1504.727814	752.867545	1503.743798	752.3755
4	**503.322797**	252.165036					**Y**	***1408.670299***	704.838788	1391.643750	696.325513	1390.659734	695.8335
5	**618.349740**	309.678508			600.339175	300.673226	**D**	***1245.606970***	623.307123	1228.580421	614.793849	1227.596405	614.3018

6	**689.386854**	345.197065			671.376289	336.191782	A	***1130.580027***	565.793652	1113.553478	557.280377	1112.569462	556.7883
7	776.418882	388.713079			758.408317	379.707796	S	***1059.542913***	530.275095	1042.516364	521.761820	1041.532348	521.2698
8	890.461809	445.734542	873.435260	437.221268	872.451244	436.729260	N	***972.510885***	486.759081	955.484336	478.245806	954.500320	477.7537
9	**1003.545873**	502.276574	986.519324	493.763300	985.535308	493.271292	L	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.7323
10	**1132.588466**	566.797871	1115.561917	558.284597	1114.577901	557.792588	E	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.1903
11	**1233.636145**	617.321710	1216.609596	608.808436	1215.625580	608.316428	T	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.6690
12	**1290.657609**	645.832442	1273.631060	637.319168	1272.647044	636.827160	G	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.1451
13	**1389.726023**	695.366649	1372.699474	686.853375	1371.715458	686.361367	V	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.6344
14	1486.778787	743.893032	1469.752238	735.379757	1468.768222	734.887749	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.1002
15	**1573.810815**	787.409046	1556.784266	778.895771	1555.800250	778.403763	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.5738
16							R	175.118952	88.063114	158.092403	79.549839		



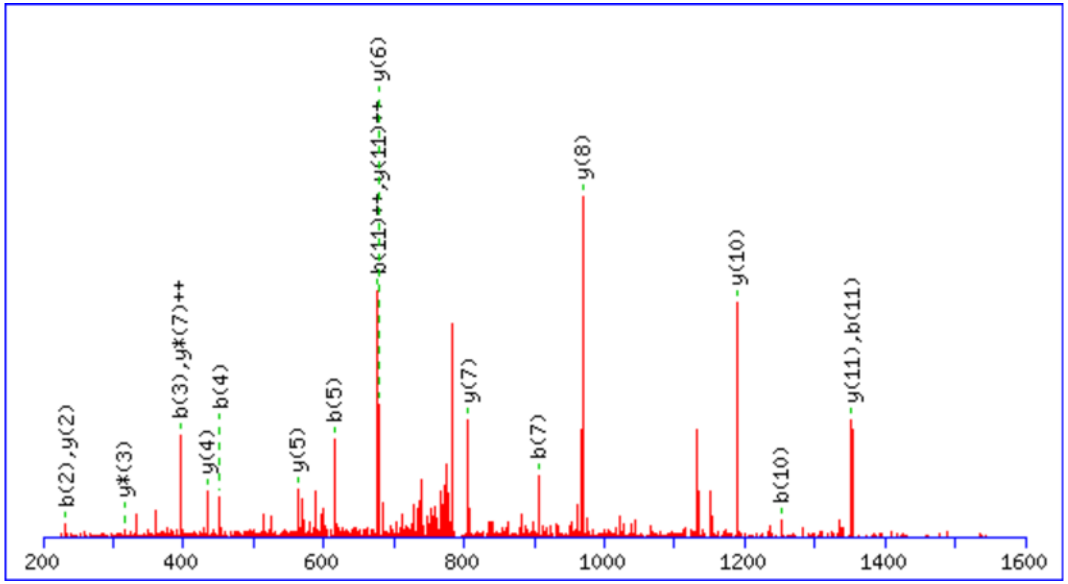
Peptide View

MS/MS Fragmentation of **CAYGYYQDETTGR**
Found in **IPI00027436**, Tax_Id=9606 Gene_Symbol=NGFR Tumor necrosis factor receptor superfamily member 16

Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 11467: 1582.635848 from(792.325200,2+)
Title: OECHL100317_21.8991.8991.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1582.635818**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions**
Score: 52 **Expect:** 9.2e-005**Matches :** 19/114 fragment ions using 28 most intense peaks (help)

#	b	$\mathbf{b}^{++}$	b*	$\mathbf{b*}^{++}$	$\mathbf{b}^{0}$	$\mathbf{b}^{0++}$	Seq.	y	$\mathbf{y}^{++}$	y*	$\mathbf{y*}^{++}$	$\mathbf{y}^{0}$	$\mathbf{y}^{0++}$
1	161.037925	81.022600					**C**						
2	***232.075039***	116.541158					**A**	1423.612453	712.309865	1406.585904	703.796590	1405.601888	703.3045
3	***395.138368***	198.072822					**Y**	***1352.575339***	676.791308	1335.548790	668.278033	1334.564774	667.7860
4	***452.159832***	226.583554					**G**	***1189.512010***	595.259643	1172.485461	586.746369	1171.501445	586.2543
5	***615.223161***	308.115219					**Y**	1132.490546	566.748911	1115.463997	558.235637	1114.479981	557.7436
6	778.286490	389.646883					**Y**	***969.427217***	485.217247	952.400668	476.703972	951.416652	476.2119
7	***906.345068***	453.676172	889.318519	445.162898			**Q**	***806.363888***	403.685582	789.337339	395.172308	788.353323	394.6803
8	1021.372011	511.189644	1004.345462	502.676369	1003.361446	502.184361	**D**	***678.305310***	339.656293	661.278761	331.143019	660.294745	330.6510
9	1150.414604	575.710940	1133.388055	567.197666	1132.404039	566.705658	**E**	***563.278367***	282.142822	546.251818	273.629547	545.267802	273.1375
10	***1251.462283***	626.234780	1234.435734	617.721505	1233.451718	617.229497	**T**	***434.235774***	217.621525	417.209225	209.108250	416.225209	208.6162
11	***1352.509962***	676.758619	1335.483413	668.245345	1334.499397	667.753337	**T**	333.188095	167.097685	316.161546	158.584411	315.177530	158.0924
12	1409.531426	705.269351	1392.504877	696.756077	1391.520861	696.264069	**G**	***232.140416***	116.573846	215.113867	108.060571		
13							**R**	175.118952	88.063114	158.092403	79.549839		



Peptide View

MS/MS Fragmentation of **RGVSQAPTAAR**
Found in **IPI00025365**, Tax_Id=9606 Gene_Symbol=EDN3 Isoform Long of Endothelin-3
Experiment: 60 - PyE-3 **Fraction:** PyE-3

Match to Query 5573: 1112.605448 from(557.310000,2+)
Title: OECHL100317_21.2384.2384.2.dta
Data file \\Boromir\masse\Data LTQ-Orbitrap\Chrystelle Lacroix\Etude clinique sJPU\OECHL100317_21.raw
Monoisotopic mass of neutral peptide Mr(calc): 1112.605042**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 51 **Expect:** 0.00059**Matches :** 28/108 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			**R**							**11**
2	214.129851	107.568564	197.103302	99.055289			**G**	***957.511221***	479.259249	940.484672	470.745974	939.500656	470.253966	**10**
3	313.198265	157.102770	296.171716	148.589496			**V**	***900.489757***	450.748517	883.463208	442.235242	882.479192	441.743234	**9**
4	400.230293	200.618785	383.203744	192.105510	382.219728	191.613502	**S**	***801.421343***	401.214310	784.394794	392.701035	783.410778	392.209027	**8**
5	***528.288871***	264.648074	511.262322	256.134799	510.278306	255.642791	**Q**	***714.389315***	357.698296	697.362766	349.185021	696.378750	348.693013	**7**

6	***599.325985***	300.166631	582.299436	291.653356	581.315420	291.161348	**A**	***586.330737***	293.669007	569.304188	285.155732	568.320172	284.663724	**6**
7	***696.378749***	348.693013	679.352200	340.179738	678.368184	339.687730	**P**	515.293623	258.150450	498.267074	249.637175	497.283058	249.145167	**5**
8	***797.426428***	399.216852	780.399879	390.703578	779.415863	390.211570	**T**	418.240859	209.624068	401.214310	201.110793	400.230294	200.618785	**4**
9	***868.463542***	434.735409	851.436993	426.222135	850.452977	425.730127	**A**	***317.193180***	159.100228	300.166631	150.586953			**3**
10	***939.500656***	470.253966	922.474107	461.740692	921.490091	461.248684	**A**	246.156066	123.581671	229.129517	115.068397			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549840			**1**