

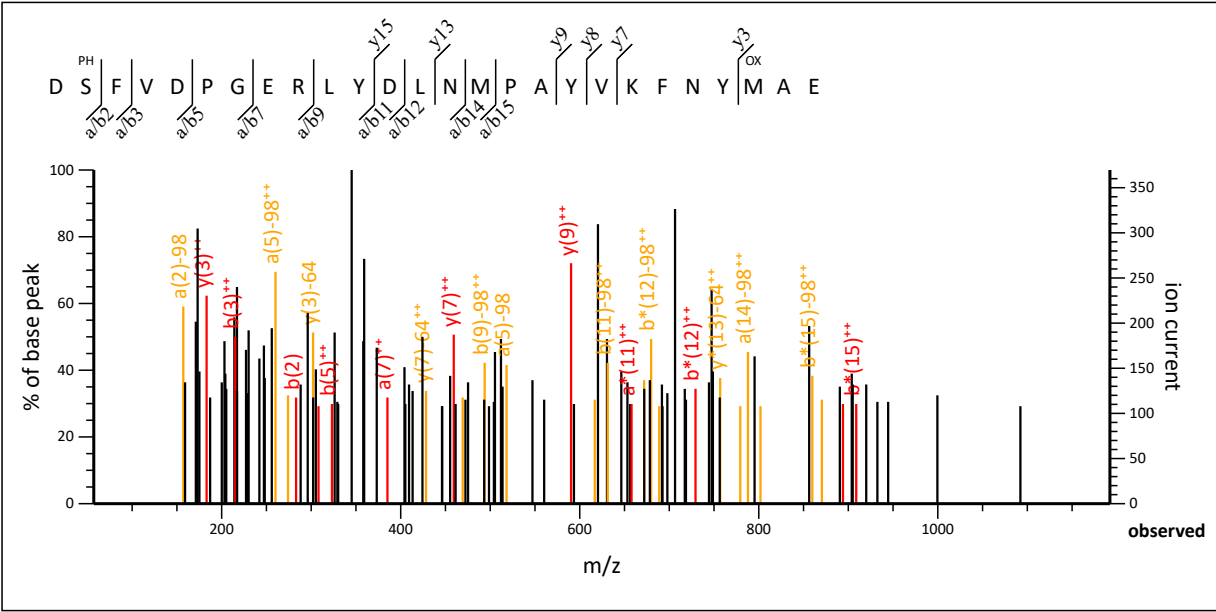
MATRIX SCIENCE

Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSFVDPGERLYDLNMPAYVKFNYMAE**
Found in **Human_Nck1** in **Human_Nck1**, Human_Nck1

Match to Query 10036: 3179.884656 from(795.978440,4+) intensity(4156.0000) rtinseconds(2169.16) scans(MS: 10440 MSMS: 10447) index(8858)
Title: Cmpd 8859, +MS2(795.9784), 35.9eV, 36.2 min #10447
Data file D:\ID proteins\mgf\ID2025\mgf20250102\Jatuporn\Jurkat0min.mgf



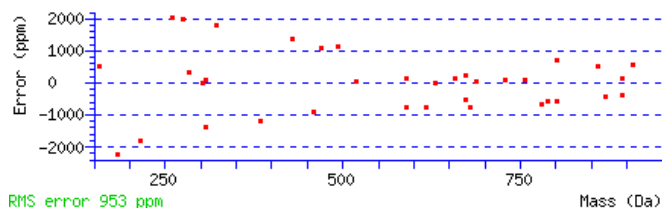
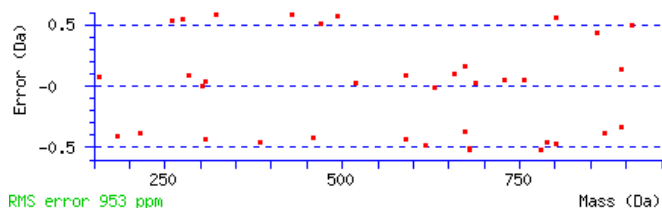
57.14 to 1192.26

Label all possible matches ☒ Label matches used for scoring ☐

Monoisotopic mass of neutral peptide Mr(calc): 3179.3657
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M24 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 1 Expect: 0.88 ([help](#))

#	a	a ⁺⁺	a [*]	a ^{*++}	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	88.0393	44.5233			116.0342	58.5207			D					26
2	157.0608	79.0340			185.0557	93.0315			S	2967.3692	1484.1882	2950.3426	1475.6750	25
3	304.1292	152.5682			332.1241	166.5657			F	2898.3477	1449.6775	2881.3212	1441.1642	24
4	403.1976	202.1024			431.1925	216.0999			V	2751.2793	1376.1433	2734.2528	1367.6300	23
5	518.2245	259.6159			546.2195	273.6134			D	2652.2109	1326.6091	2635.1843	1318.0958	22
6	615.2773	308.1423			643.2722	322.1397			P	2537.1839	1269.0956	2520.1574	1260.5823	21
7	672.2988	336.6530			700.2937	350.6505			G	2440.1312	1220.5692	2423.1046	1212.0560	20
8	801.3414	401.1743			829.3363	415.1718			E	2383.1097	1192.0585	2366.0832	1183.5452	19
9	957.4425	479.2249	940.4159	470.7116	985.4374	493.2223	968.4108	484.7091	R	2254.0671	1127.5372	2237.0406	1119.0239	18
10	1070.5265	535.7669	1053.5000	527.2536	1098.5214	549.7644	1081.4949	541.2511	L	2097.9660	1049.4866	2080.9395	1040.9734	17
11	1233.5899	617.2986	1216.5633	608.7853	1261.5848	631.2960	1244.5582	622.7828	Y	1984.8820	992.9446	1967.8554	984.4313	16
12	1348.6168	674.8120	1331.5903	666.2988	1376.6117	688.8095	1359.5852	680.2962	D	1821.8186	911.4129	1804.7921	902.8997	15
13	1461.7009	731.3541	1444.6743	722.8408	1489.6958	745.3515	1472.6692	736.8383	L	1706.7917	853.8995	1689.7651	845.3862	14
14	1575.7438	788.3755	1558.7172	779.8623	1603.7387	802.3730	1586.7122	793.8597	N	1593.7076	797.3574	1576.6811	788.8442	13
15	1706.7843	853.8958	1689.7577	845.3825	1734.7792	867.8932	1717.7526	859.3800	M	1479.6647	740.3360	1462.6381	731.8227	12
16	1803.8370	902.4222	1786.8105	893.9089	1831.8320	916.4196	1814.8054	907.9063	P	1348.6242	674.8157	1331.5977	666.3025	11
17	1874.8742	937.9407	1857.8476	929.4274	1902.8691	951.9382	1885.8425	943.4249	A	1251.5714	626.2894	1234.5449	617.7761	10

18	2037.9375	1019.4724	2020.9109	1010.9591	2065.9324	1033.4698	2048.9059	1024.9566	Y	1180.5343	590.7708	1163.5078	582.2575	9
19	2137.0059	1069.0066	2119.9794	1060.4933	2165.0008	1083.0040	2147.9743	1074.4908	V	1017.4710	509.2391	1000.4444	500.7259	8
20	2265.1009	1133.0541	2248.0743	1124.5408	2293.0958	1147.0515	2276.0692	1138.5383	K	918.4026	459.7049	901.3760	451.1917	7
21	2412.1693	1206.5883	2395.1427	1198.0750	2440.1642	1220.5857	2423.1376	1212.0725	F	790.3076	395.6574	773.2811	387.1442	6
22	2526.2122	1263.6097	2509.1857	1255.0965	2554.2071	1277.6072	2537.1806	1269.0939	N	643.2392	322.1232	626.2127	313.6100	5
23	2689.2755	1345.1414	2672.2490	1336.6281	2717.2705	1359.1389	2700.2439	1350.6256	Y	529.1963	265.1018			4
24	2836.3109	1418.6591	2819.2844	1410.1458	2864.3059	1432.6566	2847.2793	1424.1433	M	366.1329	183.5701			3
25	2907.3480	1454.1777	2890.3215	1445.6644	2935.3430	1468.1751	2918.3164	1459.6618	A	219.0975	110.0524			2
26									E	148.0604	74.5339			1



NCBI **BLAST** search of [DSFVDPGERLYDLNMPAYVKFNMAE](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
0.6	3179.3657	0.5189	DSFVDPGERLYDLNMPAYVKFNMAE

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