

MATRIX SCIENCE Mascot Search Results

Peptide View

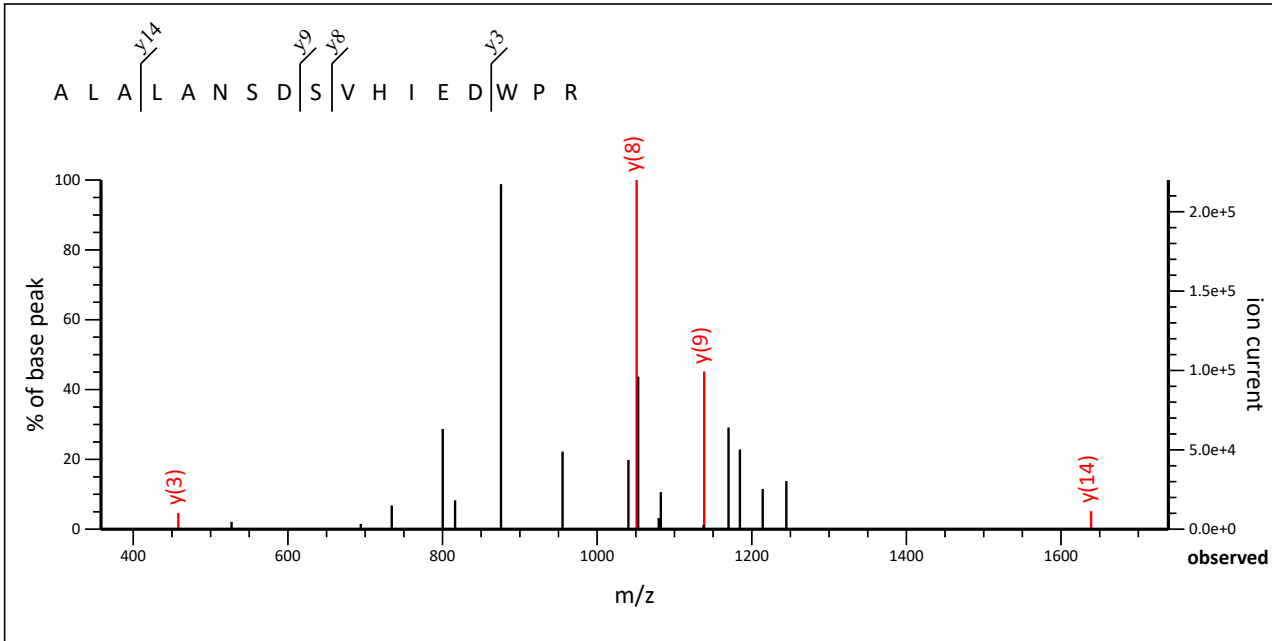
MS/MS Fragmentation of **ALALANSDSVHIEDWPR**

Found in **XP_006176945.2** in **NCBIprot**, PREDICTED: LOW QUALITY PROTEIN: steroid hormone receptor ERR1 [Camelus ferus]

Match to Query 72: 1892.317448 from(947.166000,2+) intensity(6753209.0000) index(86)

Title: Cmpd 87, +MSn(947.17), 10.2 min

Data file LM_26%.mgf



Navigation icons: ? (help), 📄 (document), 🔍 (search), 🔍 (search), 🔍 (search), 🔍 (search), 🔍 (search), 358.24 to 1738.87 (mass range), 🔍 (search), 🏠 (home).

Label all possible matches Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 1892.9380

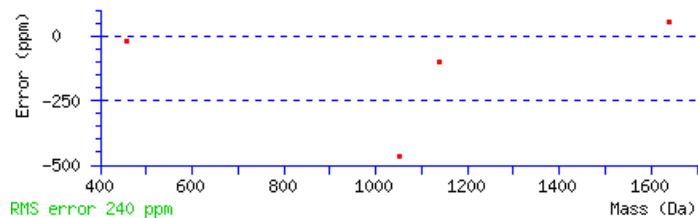
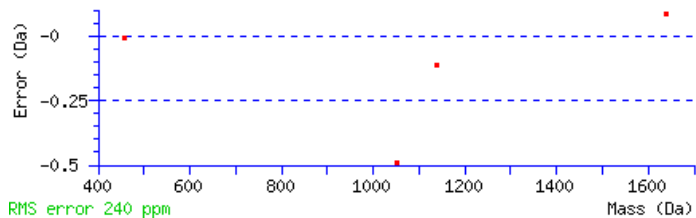
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 18 **Expect:** 5e+02

Matches : 4/164 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							17
2	185.1285	93.0679					L	1822.9082	911.9578	1805.8817	903.4445	1804.8977	902.9525	16
3	256.1656	128.5864					A	1709.8242	855.4157	1692.7976	846.9024	1691.8136	846.4104	15
4	369.2496	185.1285					L	1638.7871	819.8972	1621.7605	811.3839	1620.7765	810.8919	14
5	440.2867	220.6470					A	1525.7030	763.3551	1508.6764	754.8419	1507.6924	754.3499	13
6	554.3297	277.6685	537.3031	269.1552			N	1454.6659	727.8366	1437.6393	719.3233	1436.6553	718.8313	12
7	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	S	1340.6230	670.8151	1323.5964	662.3018	1322.6124	661.8098	11
8	756.3886	378.6980	739.3621	370.1847	738.3781	369.6927	D	1253.5909	627.2991	1236.5644	618.7858	1235.5804	618.2938	10
9	843.4207	422.2140	826.3941	413.7007	825.4101	413.2087	S	1138.5640	569.7856	1121.5374	561.2724	1120.5534	560.7803	9
10	942.4891	471.7482	925.4625	463.2349	924.4785	462.7429	V	1051.5320	526.2696	1034.5054	517.7563	1033.5214	517.2643	8
11	1079.5480	540.2776	1062.5214	531.7644	1061.5374	531.2724	H	952.4635	476.7354	935.4370	468.2221	934.4530	467.7301	7
12	1192.6321	596.8197	1175.6055	588.3064	1174.6215	587.8144	I	815.4046	408.2060	798.3781	399.6927	797.3941	399.2007	6
13	1321.6747	661.3410	1304.6481	652.8277	1303.6641	652.3357	E	702.3206	351.6639	685.2940	343.1506	684.3100	342.6586	5
14	1436.7016	718.8544	1419.6750	710.3412	1418.6910	709.8492	D	573.2780	287.1426	556.2514	278.6293	555.2674	278.1373	4
15	1622.7809	811.8941	1605.7544	803.3808	1604.7703	802.8888	W	458.2510	229.6292	441.2245	221.1159			3

16	1719.8337	860.4205	1702.8071	851.9072	1701.8231	851.4152	P	272.1717	136.5895	255.1452	128.0762			2
17							R	175.1190	88.0631	158.0924	79.5498			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.8	1892.9380	-0.6206	ALALANSDSVHIEDWPR
10.6	1892.0268	0.2906	IHLQTIHDSNYLAVR
8.9	1893.0432	-0.7257	GELQSLQSHLAKLGS LGR
6.2	1892.8727	-0.5552	DPRSFMLGFSLDDEHK
6.2	1891.9500	0.3674	EERPGEGSPAPGRDAVLR
6.2	1891.8583	0.4591	MLLIGFSGEEDYLD MK
6.2	1891.8379	0.4795	SSGFTMSPRAMW SLMR
5.0	1892.8687	-0.5512	NLTEGPLAGAEMDPAHDR
4.9	1891.9925	0.3250	SVTLGPSLSLSNIGMSVK
4.8	1892.9172	-0.5997	SGLVAQMGAMRFMHLGR

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