

Tree hierar Calc. MH+ Meas. Mr Calc. Mr Dev.(Da) Score MascotScc Sequence

F:\Identified saliva phosphopeptides\MSMS_1155\0_M2\0\1155.6000.LIFT.LIFT\ast\pdata\1\1r

Ce_saliva_DHB2_msms1155

DHB

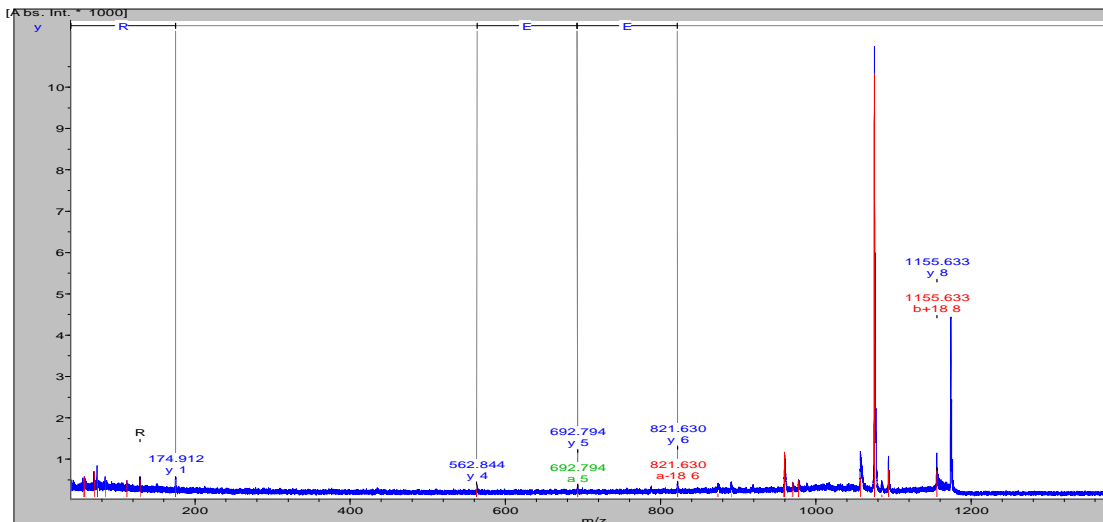
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2 STAT_HUMAN

Digest Matches (Score: 38.57)

Search Parameter: Charge=1+, MS Tol.:250.000000 ppm, MSMS Tol.:1.000000 Da, semiTrypsin, Mascot 2.4.1, SwissProt SwissProt_2013_09.fasta

Modifications: Global: Carboxymethyl (C), Optional: Oxidation (M), Phospho (ST),

MSMS 1 1155,448 1154,593 1154,441 0,152 4 38 SSEEKFLR 1: Phospho (ST) 2: Phospho (ST)



	S	S	E	E	K	F	L	R	Ser	Ser	Glu	Glu	Lys	Phe	Leu	Arg
Ion	1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8
a	S*	S*	E	E	K	F	L	R	140.011	307.009	436.052	565.094	693.189	840.258	953.342	1109.443
a-17	S*	S*	E	E	K	F	L	R	122.984	289.983	419.025	548.068	676.163	823.231	936.315	1092.416
a-18	S*	S*	E	E	K	F	L	R	122.000	288.999	418.041	547.084	675.179	822.247	935.331	1091.432
b	S*	S*	E	E	K	F	L	R	168.006	335.004	464.047	593.089	721.184	868.253	981.337	1137.438
b-17	S*	S*	E	E	K	F	L	R	150.979	317.977	447.020	576.063	704.158	851.226	964.310	1120.411
b-18	S*	S*	E	E	K	F	L	R	149.995	316.993	446.036	575.079	703.174	850.242	963.326	1119.427
b+18	S*	S*	E	E	K	F	L	R	186.016	353.015	482.057	611.100	739.195	886.263	999.347	1155.448
c	S*	S*	E	E	K	F	L	R	185.032	352.031	481.073	610.116	738.211	885.279	998.363	1154.464
x	S*	S*	E	E	K	F	L	R	201.098	314.182	461.251	589.346	718.388	847.431	1014.429	1181.428
y	S*	S*	E	E	K	F	L	R	175.119	288.203	435.271	563.366	692.409	821.452	988.450	1155.448
z	S*	S*	E	E	K	F	L	R	158.092	271.176	418.245	546.340	675.382	804.425	971.423	1138.422
i	S*	S*	E	E	K	F	L	R	140.011	140.010	102.054	102.054	101.107	120.080	86.096	129.113
	8	7	6	5	4	3	2	1	Arg	Leu	Phe	Lys	Glu	Glu	Ser	Ser

Tree hierar Calc. MH+ Meas. Mr Calc. Mr Dev.(Da) Score MascotScc Sequence

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Lift1270

Lift1270

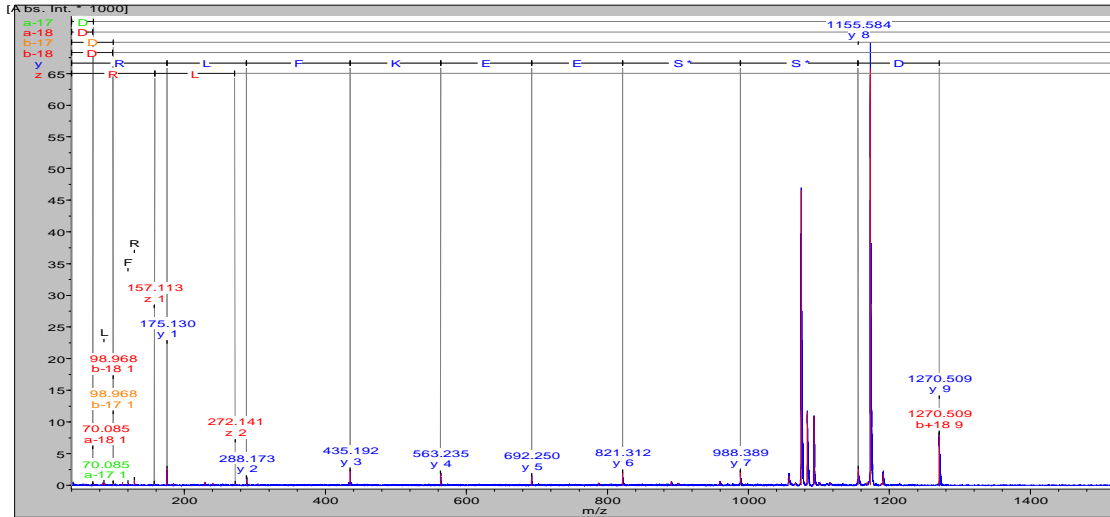
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2 STAT_HUMAN

Digest Matches (Score: 65.32)

Search Parameter: Charge=1+, MS Tol.:250.000000 ppm, MSMS Tol.:1.000000 Da, semiTrypsin, Mascot 2.4.1, SwissProt SwissProt_2013_09.fasta

Modifications: Global: Carboxymethyl (C), Optional: Oxidation (M), Phospho (ST),

MSMS 1 1270,475 1269,493 1269,468 0,025 516 65 DSSEKFLR 2: Phospho (ST) 3: Phospho (ST)



	D	S	S	E	E	K	F	L	R	Asp	Ser	Ser	Glu	Glu	Lys	Phe	Leu	Arg
Ion	1	2	3	4	5	6	7	8	9	1	2	3	4	5	6	7	8	9
a	D	S*	S*	E	E	K	F	L	R	88.039	255.038	422.036	551.079	680.121	808.216	955.285	1068.369	1224.470
a-17	D	S*	S*	E	E	K	F	L	R	71.013	238.011	405.009	534.052	663.095	791.190	938.258	1051.342	1207.443
a-18	D	S*	S*	E	E	K	F	L	R	70.029	237.027	404.025	533.068	662.111	790.206	937.274	1050.358	1206.459
b	D	S*	S*	E	E	K	F	L	R	116.034	283.033	450.031	579.074	708.116	836.211	983.279	1096.364	1252.465
b-17	D	S*	S*	E	E	K	F	L	R	99.008	266.006	433.004	562.047	691.090	819.185	966.253	1079.337	1235.438
b-18	D	S*	S*	E	E	K	F	L	R	98.024	265.022	432.020	561.063	690.106	818.201	965.269	1078.353	1234.454
b+18	D	S*	S*	E	E	K	F	L	R	134.045	301.043	468.042	597.084	726.127	854.222	1001.290	1114.374	1270.475
c	D	S*	S*	E	E	K	F	L	R	133.061	300.059	467.057	596.100	725.143	853.238	1000.306	1113.390	1269.491
x	D	S*	S*	E	E	K	F	L	R	201.098	314.182	461.251	589.346	718.388	847.431	1014.429	1181.428	1296.455
y	D	S*	S*	E	E	K	F	L	R	175.119	288.203	435.271	563.366	692.409	821.452	988.450	1155.448	1270.475
z	D	S*	S*	E	E	K	F	L	R	158.092	271.176	418.245	546.340	675.382	804.425	971.423	1138.422	1253.449
i	D	S*	S*	E	E	K	F	L	R	88.039	140.010	140.010	102.054	102.054	101.107	120.080	86.096	129.113
	9	8	7	6	5	4	3	2	1	Arg	Leu	Phe	Lys	Glu	Glu	Ser	Ser	Asp

Tree hierar Calc. MH+ Meas. Mr Calc. Mr Dev.(Da) Score MascotSco Sequence

F:\Identified saliva phosphopeptides\MSMS_1404\1SRefpdata\1\1r

Lift1404

Lift1404

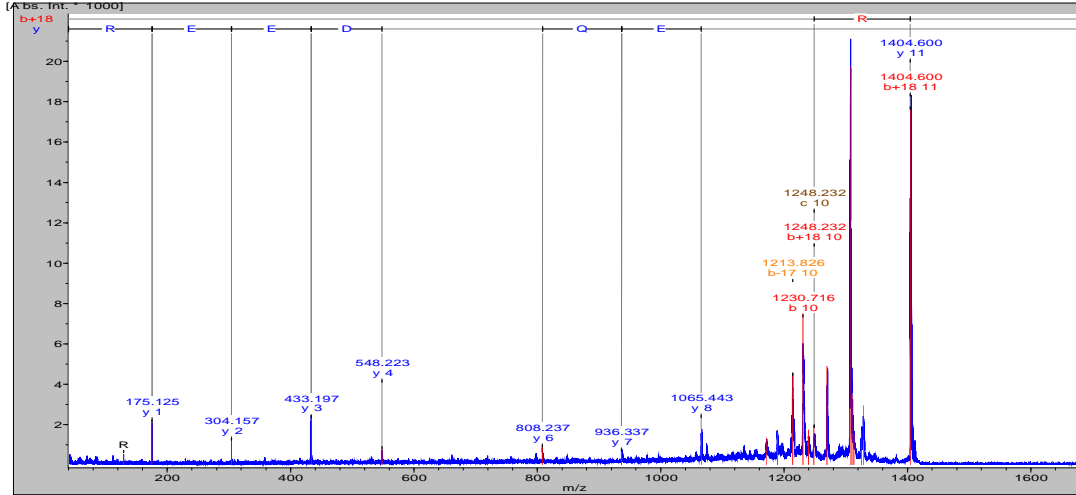
Salivary acidic proline-rich phosphoprotein 1/2 OS=Homo sapiens GN=PRH1 PE=1 SV=2 PRPC_HUMAN

Digest Matches (Score: 71.08)

Search Parameter: Charge=1+, MS Tol.:250.000000 ppm, MSMS Tol.:1.000000 Da, semiTrypsin, Mascot 2.4.1, SwissProt SwissProt_2013_09.fasta

Modifications: Global: Carboxymethyl (C), Optional: Oxidation (M), Phospho (ST),

MSMS 1 1404,531 1403,593 1403,524 0,069 21 71 GDSEQFIDEER 3: Phospho (ST)



	G	D	S	E	Q	F	I	D	E	E	R	Gly	Asp	Ser	Glu	Gln	Phe	Ile	Asp	Glu
Ion	1	2	3	4	5	6	7	8	9	10	11	1	2	3	4	5	6	7	8	9
a	G	D	S*	E	Q	F	I	D	E	E	R	30.034	145.061	312.059	441.102	569.160	716.229	829.313	944.340	1073.382
a-17	G	D	S*	E	Q	F	I	D	E	E	R	13.007	128.034	295.033	424.075	552.134	699.202	812.286	927.313	1056.356
a-18	G	D	S*	E	Q	F	I	D	E	E	R	12.023	127.050	294.049	423.091	551.150	698.218	811.302	926.329	1055.372
b	G	D	S*	E	Q	F	I	D	E	E	R	58.029	173.056	340.054	469.097	597.155	744.224	857.308	972.335	1101.377
b-17	G	D	S*	E	Q	F	I	D	E	E	R	41.002	156.029	323.027	452.070	580.129	727.197	840.281	955.308	1084.351
b-18	G	D	S*	E	Q	F	I	D	E	E	R	40.018	155.045	322.043	451.086	579.145	726.213	839.297	954.324	1083.367
b+18	G	D	S*	E	Q	F	I	D	E	E	R	76.039	191.066	358.065	487.107	615.166	762.234	875.318	990.345	1119.388
c	G	D	S*	E	Q	F	I	D	E	E	R	75.055	190.082	357.081	486.123	614.182	761.250	874.334	989.361	1118.404
x	G	D	S*	E	Q	F	I	D	E	E	R	201.098	330.141	459.183	574.210	687.294	834.363	962.421	1091.464	1258.462
y	G	D	S*	E	Q	F	I	D	E	E	R	175.119	304.162	433.204	548.231	661.315	808.384	936.442	1065.485	1232.483
z	G	D	S*	E	Q	F	I	D	E	E	R	158.092	287.135	416.178	531.205	644.289	791.357	919.416	1048.458	1215.457
i	G	D	S*	E	Q	F	I	D	E	E	R	30.034	88.039	140.010	102.054	101.070	120.080	86.096	88.039	102.054
	11	10	9	8	7	6	5	4	3	2	1	Arg	Glu	Glu	Asp	Ile	Phe	Gln	Glu	Ser

Tree hierar Calc. MH+ Meas. Mr Calc. Mr Dev.(Da) Score MascotScc Sequence

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Lift1426

Lift1426

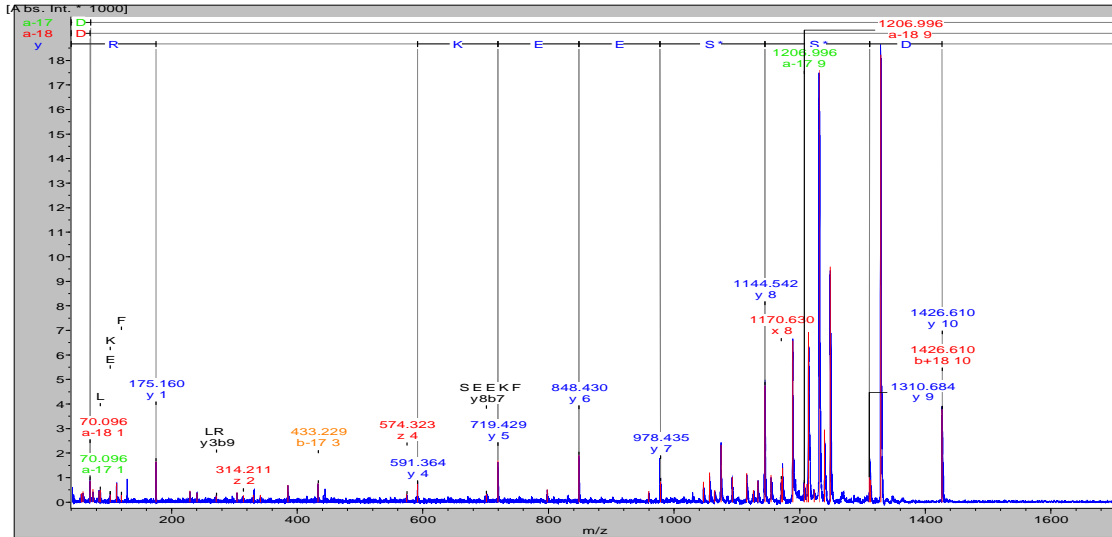
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2 STAT_HUMAN

Digest Matches (Score: 40.19)

Search Parameter: Charge=1+, MS Tol.:250.000000 ppm, MSMS Tol.:1.000000 Da, semiTrypsin, Mascot 2.4.1, SwissProt SwissProt_2013_09.fasta

Modifications: Global: Carboxymethyl (C), Optional: Oxidation (M), Phospho (ST),

MSMS 1 1426,576 1425,593 1425,569 0,024 130 40 DSSEKFLRR 2: Phospho (ST) 3: Phospho (ST)



	D	S	S	E	E	K	F	L	R	R	Asp	Ser	Ser	Glu	Glu	Lys	Phe	Leu	Arg
Ion	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	9
a	D	S*	S*	E	E	K	F	L	R	R	88.039	255.038	422.036	551.079	680.121	808.216	955.285	1068.369	1224.470
a-17	D	S*	S*	E	E	K	F	L	R	R	71.013	238.011	405.009	534.052	663.095	791.190	938.258	1051.342	1207.443
a-18	D	S*	S*	E	E	K	F	L	R	R	70.029	237.027	404.025	533.068	662.111	790.206	937.274	1050.358	1206.459
b	D	S*	S*	E	E	K	F	L	R	R	116.034	283.033	450.031	579.074	708.116	836.211	983.279	1096.364	1252.465
b-17	D	S*	S*	E	E	K	F	L	R	R	99.008	266.006	433.004	562.047	691.090	819.185	966.253	1079.337	1235.438
b-18	D	S*	S*	E	E	K	F	L	R	R	98.024	265.022	432.020	561.063	690.106	818.201	965.269	1078.353	1234.454
b+18	D	S*	S*	E	E	K	F	L	R	R	134.045	301.043	468.042	597.084	726.127	854.222	1001.290	1114.374	1270.475
c	D	S*	S*	E	E	K	F	L	R	R	133.061	300.059	467.057	596.100	725.143	853.238	1000.306	1113.390	1269.491
x	D	S*	S*	E	E	K	F	L	R	R	201.098	357.199	470.283	617.352	745.447	874.489	1003.532	1170.530	1337.529
y	D	S*	S*	E	E	K	F	L	R	R	175.119	331.220	444.304	591.373	719.468	848.510	977.553	1144.551	1311.549
z	D	S*	S*	E	E	K	F	L	R	R	158.092	314.194	427.278	574.346	702.441	831.484	960.526	1127.524	1294.523
i	D	S*	S*	E	E	K	F	L	R	R	88.039	140.010	140.010	102.054	102.054	101.107	120.080	86.096	129.113
	10	9	8	7	6	5	4	3	2	1	Arg	Arg	Leu	Phe	Lys	Glu	Glu	Ser	Ser

Tree hierar Calc. MH+ Meas. Mr Calc. Mr Dev.(Da) Score MascotScc Sequence

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MSMS_1461

MSMS_1461

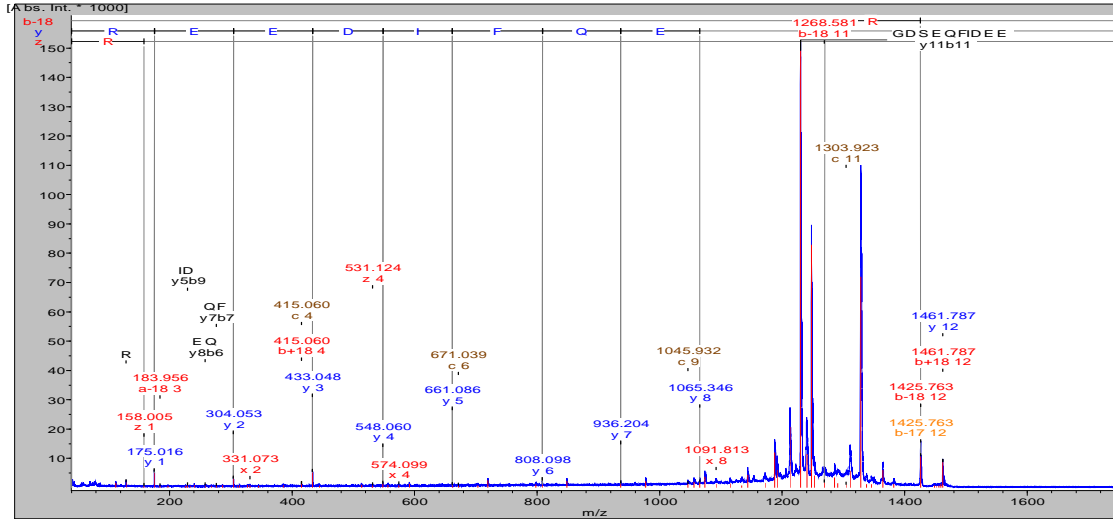
Salivary acidic proline-rich phosphoprotein 1/2 OS=Homo sapiens GN=PRH1 PE=1 SV=2 PRPC_HUMAN

Digest Matches (Score: 28.29)

Search Parameter: Charge=1+, MS Tol.:250.000000 ppm, MSMS Tol.:1.000000 Da, semiTrypsin, Mascot 2.4.1, SwissProt SwissProt_2013_09.fasta

Modifications: Global: Carboxymethyl (C), Optional: Oxidation (M), Phospho (ST),

MSMS 1 1461,553 1460,793 1460,546 0,247 267 28 GGDSEQFIDEER 4: Phospho (ST)



	G	G	D	S	E	Q	F	I	D	E	E	R	Gly	Gly	Asp	Ser	Glu	Gln	Phe	Ile	Asp
Ion	1	2	3	4	5	6	7	8	9	10	11	12	1	2	3	4	5	6	7	8	9
a	G	G	D	S*	E	Q	F	I	D	E	E	R	30.034	87.055	202.082	369.081	498.123	626.182	773.250	886.334	1001.361
a-17	G	G	D	S*	E	Q	F	I	D	E	E	R	13.007	70.029	185.056	352.054	481.097	609.155	756.224	869.308	984.335
a-18	G	G	D	S*	E	Q	F	I	D	E	E	R	12.023	69.045	184.072	351.070	480.113	608.171	755.240	868.324	983.351
b	G	G	D	S*	E	Q	F	I	D	E	E	R	58.029	115.050	230.077	397.076	526.118	654.177	801.245	914.329	1029.356
b-17	G	G	D	S*	E	Q	F	I	D	E	E	R	41.002	98.024	213.051	380.049	509.092	637.150	784.219	897.303	1012.330
b-18	G	G	D	S*	E	Q	F	I	D	E	E	R	40.018	97.040	212.067	379.065	508.108	636.166	783.235	896.319	1011.346
b+18	G	G	D	S*	E	Q	F	I	D	E	E	R	76.039	133.061	248.088	415.086	544.129	672.187	819.256	932.340	1047.367
c	G	G	D	S*	E	Q	F	I	D	E	E	R	75.055	132.077	247.104	414.102	543.145	671.203	818.272	931.356	1046.383
x	G	G	D	S*	E	Q	F	I	D	E	E	R	201.098	330.141	459.183	574.210	687.294	834.363	962.421	1091.464	1258.462
y	G	G	D	S*	E	Q	F	I	D	E	E	R	175.119	304.162	433.204	548.231	661.315	808.384	936.442	1065.485	1232.483
z	G	G	D	S*	E	Q	F	I	D	E	E	R	158.092	287.135	416.178	531.205	644.289	791.357	919.416	1048.458	1215.457
i	G	G	D	S*	E	Q	F	I	D	E	E	R	30.034	30.033	88.039	140.010	102.054	101.070	120.080	86.096	88.039
	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Glu	Glu	Asp	Ile	Phe	Gln	Glu	Ser

Tree hierar Calc. MH+ Meas. Mr Calc. Mr Dev.(Da) Score MascotScc Sequence

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MSMS_1576A

DHB

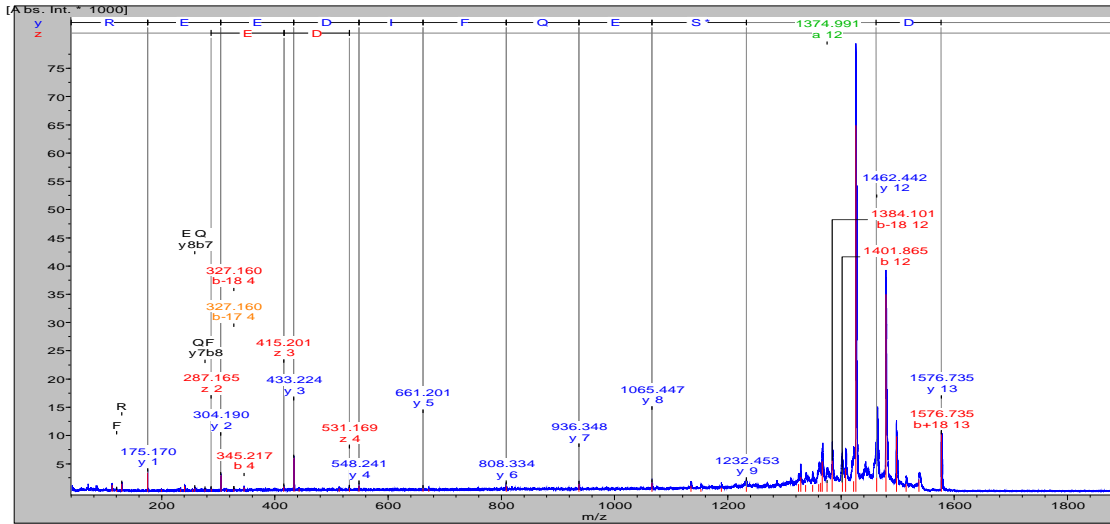
Salivary acidic proline-rich phosphoprotein 1/2 OS=Homo sapiens GN=PRH1 PE=1 SV=2 PRPC_HUMAN

Digest Matches (Score: 71.84)

Search Parameter: Charge=1+, MS Tol.:250.000000 ppm, MSMS Tol.:1.000000 Da, semiTrypsin, Mascot 2.4.1, SwissProt SwissProt_2013_09.fasta

Modifications: Global: Carboxymethyl (C), Optional: Oxidation (M), Phospho (ST),

MSMS 1 1576.58 1575.733 1575.573 0,16 520 71 DGGDSEQFIDEER 5: Phospho (ST)



	D	G	G	D	S	E	Q	F	I	D	E	E	R	Asp	Gly	Gly	Asp	Ser	Glu	Gln	Phe	Ile
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	1	2	3	4	5	6	7	8	9
a	D	G	G	D	S	E	Q	F	I	D	E	E	R	88.039	145.061	202.082	317.109	484.108	613.150	741.209	888.277	1001.361
a-17	D	G	G	D	S	E	Q	F	I	D	E	E	R	71.013	128.034	185.056	300.083	467.081	596.124	724.182	871.251	984.335
a-18	D	G	G	D	S	E	Q	F	I	D	E	E	R	70.029	127.050	184.072	299.099	466.097	595.140	723.198	870.267	983.351
b	D	G	G	D	S	E	Q	F	I	D	E	E	R	116.034	173.056	230.077	345.104	512.102	641.145	769.204	916.272	1029.356
b-17	D	G	G	D	S	E	Q	F	I	D	E	E	R	99.008	156.029	213.051	328.078	495.076	624.118	752.177	899.245	1012.330
b-18	D	G	G	D	S	E	Q	F	I	D	E	E	R	98.024	155.045	212.067	327.094	494.092	623.134	751.193	898.261	1011.346
b+18	D	G	G	D	S	E	Q	F	I	D	E	E	R	134.045	191.066	248.088	363.115	530.113	659.156	787.214	934.283	1047.367
c	D	G	G	D	S	E	Q	F	I	D	E	E	R	133.061	190.082	247.104	362.131	529.129	658.172	786.230	933.299	1046.383
x	D	G	G	D	S	E	Q	F	I	D	E	E	R	201.098	330.141	459.183	574.210	687.294	834.363	962.421	1091.464	1258.462
y	D	G	G	D	S	E	Q	F	I	D	E	E	R	175.119	304.162	433.204	548.231	661.315	808.384	936.442	1065.485	1232.483
z	D	G	G	D	S	E	Q	F	I	D	E	E	R	158.092	287.135	416.178	531.205	644.289	791.357	919.416	1048.458	1215.457
i	D	G	G	D	S	E	Q	F	I	D	E	E	R	88.039	30.033	30.033	88.039	140.010	102.054	101.070	120.080	86.096
	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Glu	Glu	Asp	Ile	Phe	Gln	Glu	Ser

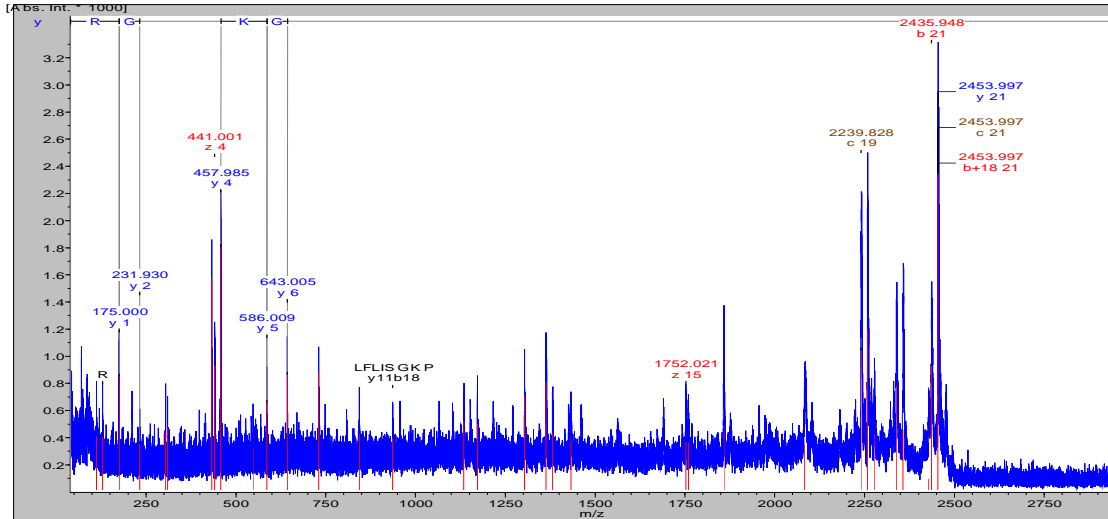
Tree hierar Calc. MH+ Meas. Mr Calc. Mr Dev.(Da) Score MascotScc Sequence

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 MSMS_2454
 MSMS_2454

Basic salivary proline-rich protein 4 OS=Homo sapiens GN=PRB4 PE=1 SV=3 PRB4_HUMAN

Digest Matches (Score: 59.53)

Search Parameter: Charge=1+, MS Tol.:250.000000 ppm, MSMS Tol.:1.000000 Da, semiTrypsin, Mascot 2.4.1, SwissProt SwissProt_2013_09.fasta
 Modifications: Global: Carboxymethyl (C), Optional: Oxidation (M), Phospho (ST),
 MSMS 1 2454,047 2452,993 2453,04 -0,047 39 62 SSEDVSEQEESLFLISGKPEGR 1: Phospho (ST) 6: Phospho (ST)



	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	Ser	Ser	Glu	Asp	Val	Ser	Gln
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	1	2	3	4	5	6	7
a	S*	S	E	D	V	S	Q	E	E	S	L	F	L	I	S*	G	K	P	E	G	R	140.011	227.043	356.085	471.112	570.181	657.213	785.271
a-17	S*	S	E	D	V	S	Q	E	E	S	L	F	L	I	S*	G	K	P	E	G	R	122.984	210.016	339.059	454.086	553.154	640.186	768.245
a-18	S*	S	E	D	V	S	Q	E	E	S	L	F	L	I	S*	G	K	P	E	G	R	122.000	209.032	338.075	453.102	552.170	639.202	767.261
b	S*	S	E	D	V	S	Q	E	E	S	L	F	L	I	S*	G	K	P	E	G	R	168.006	255.038	384.080	499.107	598.176	685.208	813.266
b-17	S*	S	E	D	V	S	Q	E	E	S	L	F	L	I	S*	G	K	P	E	G	R	150.979	238.011	367.054	482.081	581.149	668.181	796.240
b-18	S*	S	E	D	V	S	Q	E	E	S	L	F	L	I	S*	G	K	P	E	G	R	149.995	237.027	366.070	481.097	580.165	667.197	795.256
b+18	S*	S	E	D	V	S	Q	E	E	S	L	F	L	I	S*	G	K	P	E	G	R	186.016	273.048	402.091	517.118	616.186	703.218	831.277
c	S*	S	E	D	V	S	Q	E	E	S	L	F	L	I	S*	G	K	P	E	G	R	185.032	272.064	401.107	516.134	615.202	702.234	830.293
x	S*	S	E	D	V	S	Q	E	E	S	L	F	L	I	S*	G	K	P	E	G	R	201.098	258.120	387.162	484.215	612.310	669.331	836.330
y	S*	S	E	D	V	S	Q	E	E	S	L	F	L	I	S*	G	K	P	E	G	R	175.119	232.140	361.183	458.236	586.331	643.352	810.351
z	S*	S	E	D	V	S	Q	E	E	S	L	F	L	I	S*	G	K	P	E	G	R	158.092	215.114	344.156	441.209	569.304	626.326	793.324
i	S*	S	E	D	V	S	Q	E	E	S	L	F	L	I	S*	G	K	P	E	G	R	140.011	60.044	102.054	88.039	72.080	60.044	101.070
	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Gly	Glu	Pro	Lys	Gly	Ser

Tree hierar Calc. MH+ Meas. Mr Calc. Mr Dev.(Da) Score MascotScc Sequence

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MSMS2534

dhb

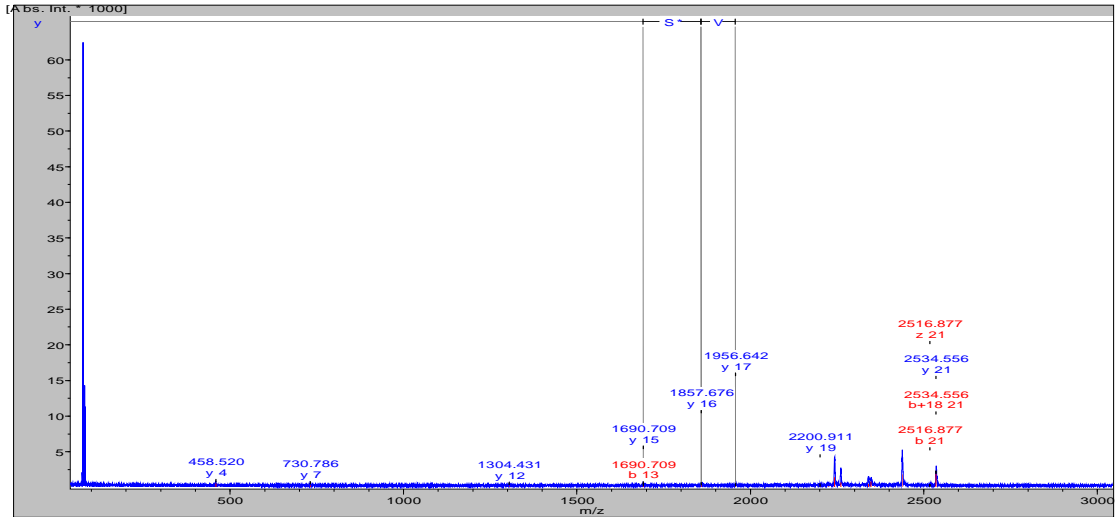
Basic salivary proline-rich protein 3 OS=Homo sapiens GN=PRB3 PE=1 SV=3 PRB4_HUMAN

Digest Matches (Score: 31.06)

Search Parameter: Charge=1+, MS Tol.:250.000000 ppm, MSMS Tol.:1.000000 Da, semiTrypsin, Mascot 2.4.1, SwissProt SwissProt_2013_09.fasta

Modifications: Global: Carboxymethyl (C), Optional: Oxidation (M), Phospho (ST),

MSMS 1 2534,014 2533,593 2533,006 0,586 8 34 QSLNEDVSEQEESPSVISGKPEGR 1: Phospho (ST) 2: Phospho (ST) 6: Phospho (ST)



	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	Ser	Ser	Glu	Asp	Val	Ser	Gln
ln	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	1	2	3	4	5	6	7
a	S*	S*	E	D	V	S*	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	140.011	307.009	436.052	551.079	650.147	817.145	945.204
a-17	S*	S*	E	D	V	S*	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	122.984	289.983	419.025	534.052	633.120	800.119	928.177
a-18	S*	S*	E	D	V	S*	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	122.000	288.999	418.041	533.068	632.136	799.135	927.193
b	S*	S*	E	D	V	S*	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	168.006	335.004	464.047	579.074	678.142	845.140	973.199
b-17	S*	S*	E	D	V	S*	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	150.979	317.977	447.020	562.047	661.115	828.114	956.172
b-18	S*	S*	E	D	V	S*	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	149.995	316.993	446.036	561.063	660.131	827.130	955.188
b+18	S*	S*	E	D	V	S*	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	186.016	353.015	482.057	597.084	696.153	863.151	991.209
c	S*	S*	E	D	V	S*	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	185.032	352.031	481.073	596.100	695.168	862.167	990.225
x	S*	S*	E	D	V	S*	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	201.098	258.120	387.162	484.215	612.310	669.331	756.363
y	S*	S*	E	D	V	S*	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	175.119	232.140	361.183	458.236	586.331	643.352	730.384
z	S*	S*	E	D	V	S*	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	158.092	215.114	344.156	441.209	569.304	626.326	713.358
i	S*	S*	E	D	V	S*	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	140.011	140.010	102.054	88.039	72.080	140.010	101.070
	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Gly	Glu	Pro	Lys	Gly	Ser

Tree hierar Calc. MH+ Meas. Mr Calc. Mr Dev.(Da) Score MascotScoSequence

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MSMS_2830

DHB

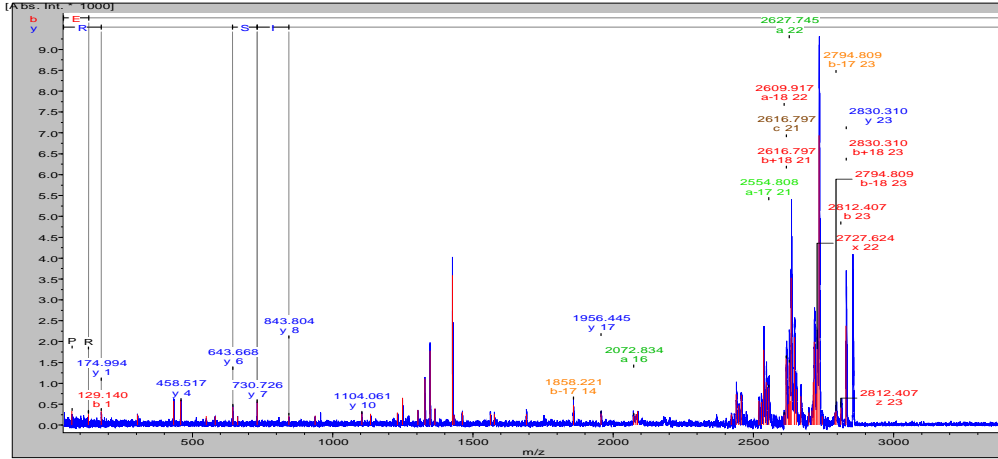
Basic salivary proline-rich protein 4 OS=Homo sapiens GN=PRB4 PE=1 SV=3 PRB4_HUMAN

Digest Matches (Score: 39.53)

Search Parameter: Charge=-1+, MS Tol.:250.000000 ppm, MSMS Tol.:1.000000 Da, semiTrypsin, Mascot 2.4.1, SwissProt SwissProt_2013_09.fasta

Modifications: Global: Carboxymethyl (C), Optional: Oxidation (M), Phospho (ST),

MSMS 1 2830,055 2829,303 2829,047 0,255 39 39 ESSSEDSVQEEESLFLISGKPEGR 2: Phospho (ST) 3: Phospho (ST) 4: Phospho (ST) 8: Phospho (ST)



	E	S	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	Glu	Ser	Ser	Ser	Glu	Asp
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	1	2	3	4	5	6
a	E	S	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	102.055	269.053	436.052	603.050	732.093	847.120
a-17	E	S	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	85.028	252.027	419.025	586.023	715.066	830.093
a-18	E	S	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	84.044	251.043	418.041	585.039	714.082	829.109
b	E	S	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	130.050	297.048	464.047	631.045	760.088	875.114
b-17	E	S	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	113.023	280.022	447.020	614.018	743.061	858.088
b-18	E	S	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	112.039	279.038	446.036	613.034	742.077	857.104
b+18	E	S	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	148.060	315.059	482.057	649.056	778.098	893.125
c	E	S	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	147.076	314.075	481.073	648.071	777.114	892.141
x	E	S	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	201.098	258.120	387.162	484.215	612.310	669.331
y	E	S	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	175.119	232.140	361.183	458.236	586.331	643.352
z	E	S	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	158.092	215.114	344.156	441.209	569.304	626.326
i	E	S	S	S	E	D	V	S	Q	E	E	S	L	F	L	I	S	G	K	P	E	G	R	102.055	140.010	140.010	140.010	102.054	88.039
	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Gly	Glu	Pro	Lys	Gly

Tree hierar Calc. MH+ Meas. Mr Calc. Mr Dev.(Da) Score MascotScc Sequence

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Lift3521

Lift3521

Salivary acidic proline-rich phosphoprotein 1/2 OS=Homo sapiens GN=PRH1 PE=1 SV=2 PRPC_HUMAN

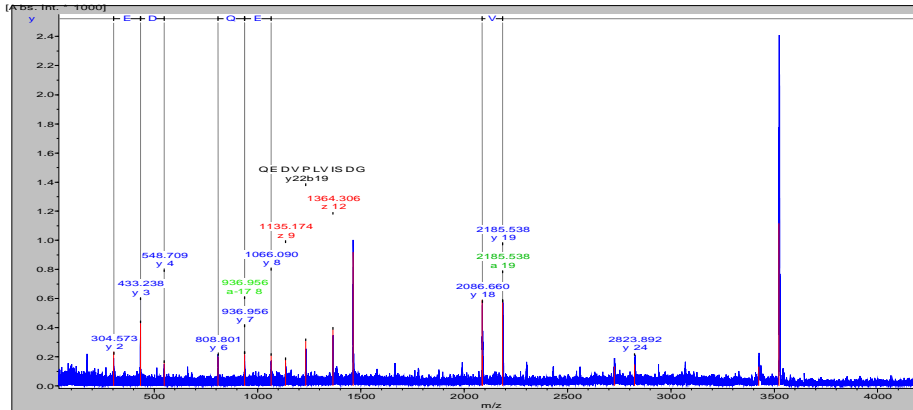
Digest Matches (Score: 89.85)

Search Parameter: Charge=1+, MS Tol.:250.000000 ppm, MSMS Tol.:1.000000 Da, semiTrypsin, Mascot 2.4.1, SwissProt SwissProt_2013_09.fasta

Modifications: Global: Carboxymethyl (C), Optional: Oxidation (M), Phospho (ST)

Unknown: Gln->pyro-Glu (N-term Q), Gln->pyro-Glu (N-term Q), Gln->pyro-Glu (N-term Q), ? (Pls. Synchronize SE and Mascot mod. definitions and reimport result)

MSMS 1 3521,404 3520,703 3520,397 0,306 17 89 QDLDEVDVLSIDGGDSEQFIDEER N-Term: Gln->pyro-Glu (N-term Q) 8: Phospho (ST) 22: Phospho (ST)



	Q	D	L	D	E	D	V	S	Q	E	D	V	P	L	V	I	S	D	G	G	D	S	E	Q	F	I	D	E	E	R	Gln	Asp	Leu	Asp
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	1	2	3	4
a	Q	D	L	D	E	D	V	S*	Q	E	D	V	P	L	V	I	S*	D	G	G	D	S	E	Q	F	I	D	E	E	R	100.063	215.090	328.174	443.201
a-17	Q	D	L	D	E	D	V	S*	Q	E	D	V	P	L	V	I	S*	D	G	G	D	S	E	Q	F	I	D	E	E	R	83.037	198.064	311.148	426.175
a-18	Q	D	L	D	E	D	V	S*	Q	E	D	V	P	L	V	I	S*	D	G	G	D	S	E	Q	F	I	D	E	E	R	82.053	197.079	310.164	425.190
b	Q	D	L	D	E	D	V	S*	Q	E	D	V	P	L	V	I	S*	D	G	G	D	S	E	Q	F	I	D	E	E	R	128.058	243.085	356.169	471.196
b-17	Q	D	L	D	E	D	V	S*	Q	E	D	V	P	L	V	I	S*	D	G	G	D	S	E	Q	F	I	D	E	E	R	111.031	226.058	339.142	454.169
b-18	Q	D	L	D	E	D	V	S*	Q	E	D	V	P	L	V	I	S*	D	G	G	D	S	E	Q	F	I	D	E	E	R	110.047	225.074	338.158	453.185
b+18	Q	D	L	D	E	D	V	S*	Q	E	D	V	P	L	V	I	S*	D	G	G	D	S	E	Q	F	I	D	E	E	R	146.069	261.096	374.180	489.207
c	Q	D	L	D	E	D	V	S*	Q	E	D	V	P	L	V	I	S*	D	G	G	D	S	E	Q	F	I	D	E	E	R	145.085	260.112	373.196	488.223
x	Q	D	L	D	E	D	V	S*	Q	E	D	V	P	L	V	I	S*	D	G	G	D	S	E	Q	F	I	D	E	E	R	201.098	330.141	459.183	574.210
y	Q	D	L	D	E	D	V	S*	Q	E	D	V	P	L	V	I	S*	D	G	G	D	S	E	Q	F	I	D	E	E	R	175.119	304.162	433.204	548.231
z	Q	D	L	D	E	D	V	S*	Q	E	D	V	P	L	V	I	S*	D	G	G	D	S	E	Q	F	I	D	E	E	R	158.092	287.135	416.178	531.205
i	Q	D	L	D	E	D	V	S*	Q	E	D	V	P	L	V	I	S*	D	G	G	D	S	E	Q	F	I	D	E	E	R	100.063	88.039	86.096	88.039
	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Glu	Glu	Asp