A

Sequence data:

riam 1-261

Intensity Coverage:	46.2 % (80764 cnts)	Sequence Coverage MS:	24.0%
Sequence Coverage MS/MS:	0.0%	pI (isoelectric point):	4.1

riam 1-261
MW:29503.480

GAMGESSEDIDQMFSTLLGEMDLLTQSLGVDTLPPPDPNPPRAEFNYSVGFKDLNESLNALEDQDLDALMADLVADISEAEQRTIQAQKESLQNQHHSASLQASIFSGAASLGYGTNVAATGISQYEDDLPPPP
ADPVLDLPLPPPPPEPLSQEEEEAQAKADKIKLALEKLKEAKVKKLVVKVHMNDNSTKSLMVDERQLARDVLDNLFEKTHCDCNVDWCLYEIYPELQIERFFEDHENVVEVLSDWTRDTENKILFLEKE

Mass Search Matches
Search Parameter: MS Tol.:150.000000 ppm, MSMS Tol.:0.500000 Da, Trypsin Specific cleavages only Sequence Editor
Modifications: Optional: Oxidation (M)

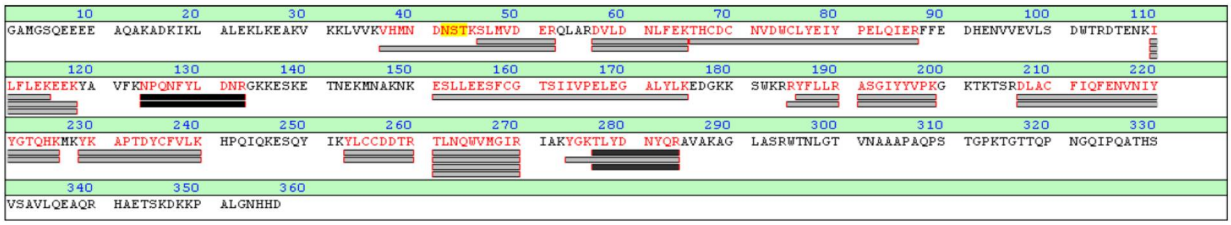
Tree hierarchy	Meas. M/z	Calc. MH+	Int.	Dev. (Da)	Dev. (ppm)	Range	P	Sequence
peak 4	849.395	849.413	18088.978	-0.019	-22.634	193 - 199	0	SLMVDER
peak 5	865.394	865.408	15564.253	-0.015	-17.488	193 - 199	0	SLMVDER 3: Oxidation (M)
peak 8	1045.551	1045.473	4277.279	0.077	73.872	184 - 192	0	VHMNDNSTK
peak 9	1061.465	1061.468	818.171	-0.004	-3.544	184 - 192	0	VHMNDNSTK 3: Oxidation (M)
peak 11	1092.561	1092.557	25145.949	0.003	2.849	204 - 212	0	DVLDNLFEK
peak 23	1317.698	1317.694	5150.648	0.003	2.226	193 - 203	1	SLMVDERQLAR
peak 27	1333.702	1333.689	6696.586	0.012	9.016	193 - 203	1	SLMVDERQLAR 3: Oxidation (M)
peak 29	1478.787	1478.774	4353.589	0.013	8.509	252 - 263	1	DTENKILFLEKE
peak 30	1560.842	1560.838	478.614	0.003	2.080	200 - 212	1	QLARDVLDNLFEK
peak 69	2913.256	2913.264	190.352	-0.009	-3.017	213 - 234	0	THCDCNVDWCLYEIYPELQIER 3: Carbamidomethyl (C) 5: Carbamidomethyl (C) 10: Carbamidomethyl (C)

B

Sequence data:

RIAM150-502

Intensity Coverage:	59.1 % (146360 cnts)	Sequence Coverage MS:	46.8%
Sequence Coverage MS/MS:	0.0%	pI (isoelectric point):	9.3



MW:41439.911

GAMGSQEEEEAQAKADKIKLALEKLKEAKVKKLVVKVHMNDNSTKSLMVDERQLARDVLDNLFEKTHCDCNVDWCLYEIYPELQIERFFEDHENVVEVLSDWTRDTENKILFLEKEEKYAVFKNPQNFYLDNRG
KKESKETNEKMNAKNKESLLEESFCGTSIIVPELEGALYLKEDGKKSWKRRYFLLRASGIYYVPKGKTKTSRDLACFIQFENVNIYYGTQHKMKYKAPTDYCFVLKHPQIQKESQYIKYLCCDDTRTLNQWVMG
IRIAKYGKTLYDNYQRAVAKAGLASRWTNLGTVNAAAPAQPSTGPKTGTTQPNGQIPQATHSVSAVLQEAQRHAETSKDKKPALGNHHD

Mass Search Matches
Search Parameter: MS Tol.: 50.000000 ppm , MSMS Tol.: 0.600000 Da, Trypsin Specific cleavages only Sequence Editor
Modifications: Optional: Oxidation (M)

Tree hierarchy	Meas. M/z	Calc. MH+	Int.	Dev. (Da)	Dev. (ppm)	Range	P	Sequence
peak 1	711.386	711.419	12287.710	-0.034	-47.221	186 - 190	0	YFLLR
peak 2	762.454	762.476	179.642	-0.023	-29.846	110 - 115	0	ILFLEK
peak 7	849.396	849.413	198.565	-0.018	-21.456	46 - 52	0	SLMVDER
peak 9	867.506	867.520	9502.426	-0.015	-16.915	185 - 190	1	RYFLLR
peak 10	997.530	997.535	609.639	-0.006	-6.053	191 - 199	0	ASGIYYVPK
peak 20	1072.495	1072.506	42404.080	-0.011	-9.821	277 - 284	0	TLYDNYQR
peak 21	1092.543	1092.557	676.713	-0.015	-13.641	57 - 65	0	DVLDNLFEK
peak 22	1102.414	1102.429	3242.324	-0.016	-14.462	253 - 260	0	YLCCDDTR 3: Carbamidomethyl (C) 4: Carbamidomethyl (C)
peak 25	1148.640	1148.656	224.069	-0.017	-14.705	110 - 118	1	ILFLEKEEK
peak 36	1217.630	1217.646	7207.119	-0.017	-13.695	261 - 270	0	TLNQWVMGIR
peak 39	1233.627	1233.641	9240.332	-0.015	-11.826	261 - 270	0	TLNQWVMGIR 7: Oxidation (M)
peak 44	1280.590	1280.602	53551.049	-0.013	-9.807	124 - 133	0	NPQNFYLDNR
peak 50	1420.655	1420.686	171.798	-0.031	-22.032	274 - 284	1	YGKTLYDNYQR
peak 54	1504.730	1504.750	2910.046	-0.021	-14.090	229 - 240	1	YKAPTDYCFVLK 8: Carbamidomethyl (C)
peak 67	1907.790	1907.859	799.815	-0.068	-35.823	37 - 52	1	VHMNDNSTKSLMVDER 3: Oxidation (M) 12: Oxidation (M)
peak 95	2460.131	2460.165	1950.580	-0.035	-14.225	207 - 226	0	DLACFIQFENVNIYYGTQHK 4: Carbamidomethyl (C)
peak 97	2797.357	2797.422	112.739	-0.065	-23.356	151 - 175	0	ESLLEESFCGTSIIVPELEGALYLK 9: Carbamidomethyl (C)
peak 101	2913.216	2913.264	1091.337	-0.049	-16.752	66 - 87	0	THCDCNVDWCLYEIYPELQIER 3: Carbamidomethyl (C) 5: Carbamidomethyl (C) 10: Carbamidomethyl (C)