

# Supplementary Materials for

## Assigning significance in label-free quantitative proteomics to include single-peptide-hit proteins with low replicates

*Qingbo Li*

Center for Pharmaceutical Biotechnology, College of Pharmacy, University of Illinois at  
Chicago, Chicago, IL 60607

Department of Microbiology and Immunology, College of Medicine, University of Illinois at  
Chicago, Chicago, IL 60612

### **Description of the Supplementary Materials**

The Supplementary Materials contains three major parts as outlined in the Table of Contents.

- Part I contains the web address to download the raw data of the 20 LC/MS runs for the pH 5 ( $S_P$ ) and pH 7 ( $R_P$ ) samples fractionated with SDS/PAGE gel separation. Descriptions for the data are provided.
- Part II contains the details of PLGEM-STN noise modeling, the use of the combination of MPSP with the PLGEM-STN or the fold-change method, and the list of the differentially regulated proteins selected by the combination of MPSP with PLGEM-STN and fold-change methods.
- Part III contains the lists of peptides and proteins quantified from the 20 LC/MS runs of the SDS/PAGE gel-fractionated  $S_P$  and  $R_P$  samples as described in part I.

## Table of Contents

PART I. Downloadable LC/MS raw data files .....	3
PART II. Details of PLGEM-STN-MPSP and fold-change-MPSP analyses .....	4
Scheme S1. Major steps in PLGEM-STN .....	4
Figure S1. Residual analysis of the PLGEM fitting .....	5
Figure S2. The STN upper and lower thresholds at different confidence levels. ....	6
Figure S3. ROC analysis of the fold-change approach with (pink curves) and without (blue curves) the combination with MPSP. ....	6
Table S1. Examples to select regulated proteins with PLGEM-STN alone or in combintaiotn with MPSP. ....	7
Table S2. The 26 and 44 differentially regulated proteins identified at a false discovery rate of 0.05 by 4-fold-change-MPSP and PLGEM-STN-MPSP respectively. ....	7
PART III. Lists of peptides and proteins quantified from the S <sub>p</sub> and R <sub>p</sub> samples.....	9
Supplemental Table I. List of quantified proteins .....	10
Supplemental Table II. List of quantified peptides.....	94

## PART I. Downloadable LC/MS raw data files

The raw LC/MS data associated with this manuscript may be downloaded from the ProteomeCommons.org Tranche network using the following hash:

xPDQI5X75crsPyDibct4onLk9wYo04dJerHJbnoFM9nSHEy4ZJw+TTg6DwtdSmHxNoDoJk3ekX4HADPJYFiJvGNuXQMAAAAAAAACtA==

The above address contains the raw data of the 20 LC/MS runs for the pH 5 (S<sub>p</sub>) and pH 7 (R<sub>p</sub>) samples fractionated with SDS/PAGE gel separation. The 20 RAW files and one Excel spreadsheet were zipped into one file. The Excel spreadsheet lists the 20 RAW file names, the corresponding samples, 1D SDS/PAGE gel fractions, and LC/MS injections performed for each fraction, as following.

LC/MS injection	LC/MS data file name	Sample	Gel fraction
1	J037ID04	pooled pH7 (R <sub>p</sub> )	1
2	J037ID05		1
3	J037ID09		2
4	J037ID10		2
5	J037ID13		3
6	J037ID14		3
7	J037ID17		4
8	J037ID18		4
9	J037ID21		5
10	J037ID22		5
11	J037ID42	pooled pH5 (S <sub>p</sub> )	1
12	J037ID43		1
13	J037ID47		2
14	J037ID48		2
15	J037ID52		3
16	J037ID53		3
17	J037ID56		4
18	J037ID57		4
19	J037ID61		5
20	J037ID62		5

## PART II. Details of PLGEM-STN-MPSP and fold-change-MPSP analyses

### Scheme S1. Major steps in PLGEM-STN

These steps used the algorithm and followed the procedures described by Pavelka et al. (*BMC Bioinformatics* **2004**, 5, 203).

Step 1: For the 1032 proteins, the measurement noise was fit with the PLGEM by using the four  $A_{\text{PRO}}$  quantitation categories including  $cS_{P,1}$ ,  $cS_{P,2}$ ,  $cR_{P,1}$ , and  $cR_{P,2}$  (Table 1). The PLGEM fitting generated the following error model

$$\ln(STD) = 0.746\ln(\bar{A}_C) - 0.776 + \varepsilon \quad (1)$$

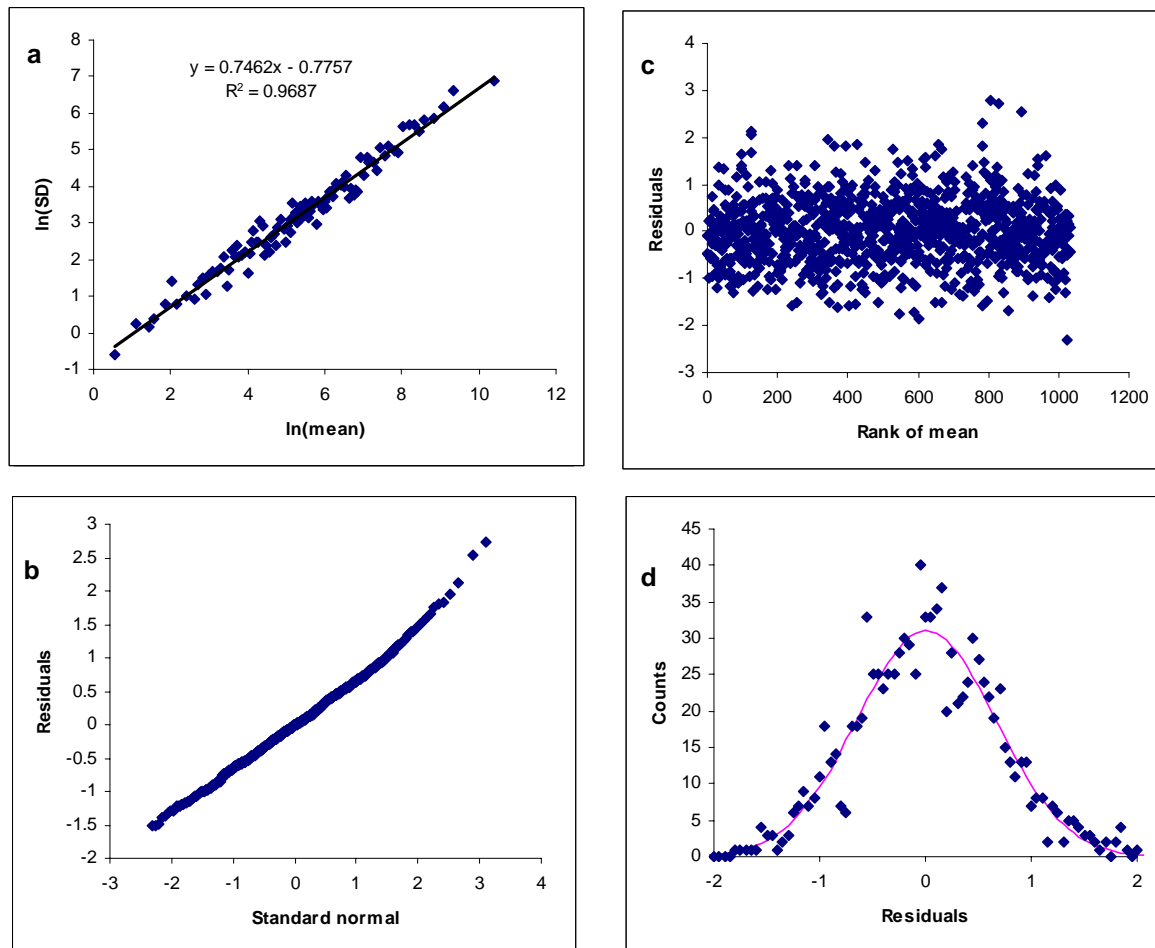
where  $STD$  and  $\bar{A}_C$  respectively were the standard deviation and mean of the  $A_{\text{PRO}}$  values of  $cS_{P,1}$ ,  $cS_{P,2}$ ,  $cR_{P,1}$ , and  $cR_{P,2}$ .  $\varepsilon$  was the error term. The PLGEM fitting was performed with 100 partitions and a 0.5 modeling quantile. The fitting had an  $R^2$  of 0.97 and the distribution of the model residuals  $\varepsilon$  followed a normal distribution as expected (**Figure S1**).

Step 2: For each protein, the 4128  $A_{\text{PRO}}$  values of  $cS_{P,1}$ ,  $cS_{P,2}$ ,  $cR_{P,1}$ , and  $cR_{P,2}$  were re-sampled with replacement for 500 iterations to calculate the null distribution of the PLGEM-STN statistic with the fitted PLGEM parameters from Equation (1). By pooling the statistics from the 500 iterations for the 1032 proteins, a null distribution with 51,600 PLGEM-STN statistics were generated. From the null distribution, STN thresholds were determined at a specific confidence level. A confidence level was a rough estimate of the false positive rate. For example, at a confidence level of 0.01, we would expect approximately 10 false positives from the 1032 proteins.

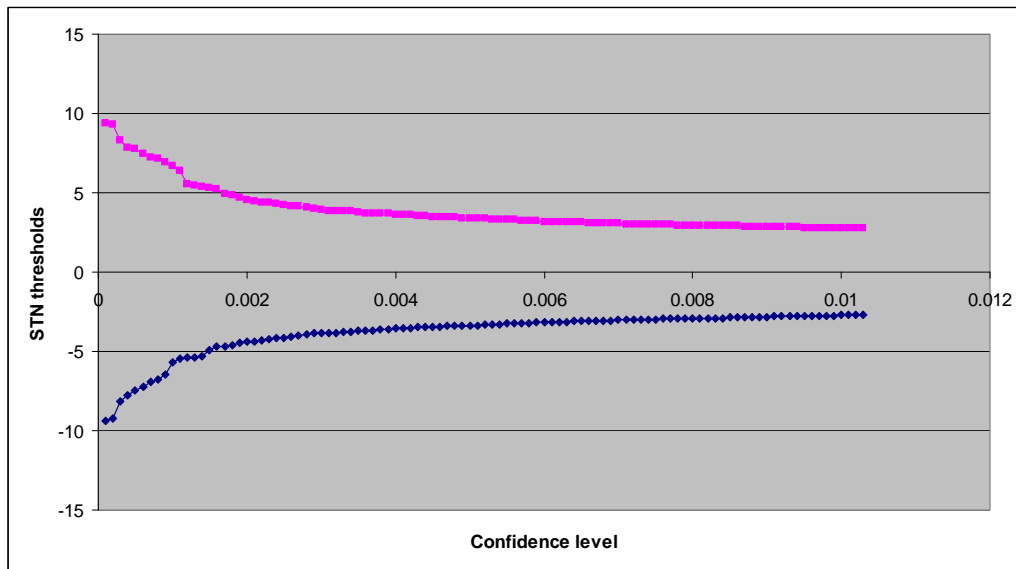
Step 3: The observed PLGEM-STN statistics were calculated for the four permuted pairings among  $cS_{P,1}$ ,  $cS_{P,2}$ ,  $cR_{P,1}$ , and  $cR_{P,2}$  i.e., (I)  $cS_{P,1}/cR_{P,1}$ , (II)  $cS_{P,1}/cR_{P,2}$ , (III)  $cS_{P,2}/cR_{P,1}$ , and (IV)  $cS_{P,2}/cR_{P,2}$ . Similarly, the observed PLGEM-STN statistics were calculated for the four permuted sample pairings of measurements among  $S_{P,1}$ ,  $S_{P,2}$ ,  $R_{P,1}$ , and  $R_{P,2}$  i.e., (I)  $S_{P,1}/R_{P,1}$ , (II)  $S_{P,1}/R_{P,2}$ , (III)  $S_{P,2}/R_{P,1}$ , and (IV)  $S_{P,2}/R_{P,2}$  (see Table 2 in main text).

Step 4: Differentially expressed proteins were selected by choosing a confidence level (**Figure S2**). At a confidence level, a set of STN thresholds were selected. The STN thresholds consisted of a negative threshold for down-regulated proteins and a positive threshold for up-regulated proteins. Based on the assessment of false discovery rates, two confidence levels were selected (see Table 2). At the confidence level of 0.002, the STN thresholds (-4.47, 4.58) result in two false positives in the sample pair  $cS_P/cR_P$  with 44 positives in the sample pair  $S_P/R_P$  when the MPSP rule was applied. At the confidence level of 0.01, the STN thresholds (-2.74, 2.79) result in 13 false positives in the sample pair  $cS_P/cR_P$  with 101 positives in the sample pairs  $S_P/R_P$  when the MPSP rule was applied. Coincidentally, with the combination with the MPSP rule, the false positive rates approximated the STN confidence levels.

**Figure S1. Residual analysis of the PLGEM fitting**



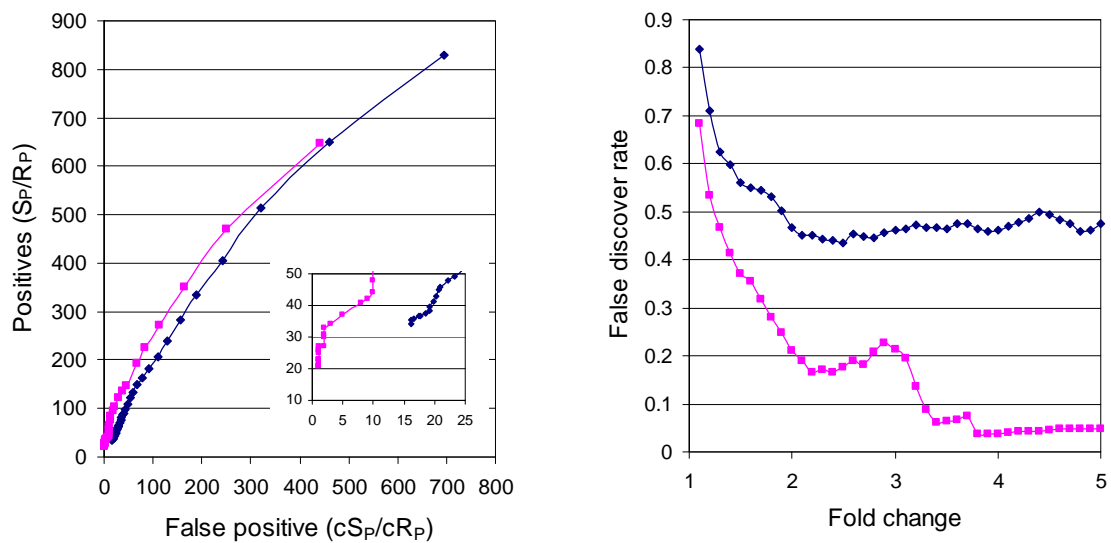
**Figure S2. The STN upper and lower thresholds at different confidence levels.**



**Figure S3. ROC analysis of the fold-change approach with (pink curves) and without (blue curves) the combination with MPSP.**

**Left panel: ROC curves. The insert shows the region with low number of false positives.**

**Right panel: false discovery rate at different fold changes.**



**Table S1.** Numbers of differentially regulated proteins selected with PLGEM-STN alone or in combination with MPSP.<sup>a</sup>

PLGEM-STN confidence level	FP, P, and FDR	PLGEM-STN					PLGEM-STN- MPSP
		Permuted sample pairings				Average	
		I	II	III	IV		
0.01	FP (cS <sub>P</sub> /cR <sub>P</sub> )	31	68	22	46	42	13
	P (S <sub>P</sub> /R <sub>P</sub> )	141	155	134	148	145	101
	FDR	0.22	0.44	0.16	0.31	0.29	0.13
0.002	FP (cS <sub>P</sub> /cR <sub>P</sub> )	6	15	3	9	8	2
	P (S <sub>P</sub> /R <sub>P</sub> )	47	50	46	51	49	44
	FDR	0.13	0.30	0.07	0.18	0.16	0.05

<sup>a</sup> False positives (FP) were selected from sample pair cS<sub>P</sub>/cR<sub>P</sub>. Positives (P) were selected from sample pair S<sub>P</sub>/R<sub>P</sub>. False discovery rate (FDR) was FP/P. The four permuted sample pairings (I-IV) were generated from the four LC/MS injections for a sample pair. See text.

**Table S2.** The 26 and 44 differentially regulated proteins identified at a false discovery rate of 0.05 by 4-fold-change-MPSP and PLGEM-STN-MPSP respectively.

Index	Protein locus	Approach	PCS counts	Average A <sub>PRO</sub>	Fold-change
1	MSMEG_1683	4-fold-change-MPSP	1	0.3	0.02
2	MSMEG_1143	4-fold-change-MPSP	1	0.4	40.73
3	MSMEG_4888	4-fold-change-MPSP	1	1	0.08
4	MSMEG_5244	4-fold-change-MPSP	1	2	3.16
5	MSMEG_1605	4-fold-change-MPSP	1	3	0.01
6	MSMEG_3710	4-fold-change-MPSP	1	4	5.61
7	MSMEG_4075	4-fold-change-MPSP	1	7	0.17
8	MSMEG_6210	4-fold-change-MPSP	1	12	0.16
9	MSMEG_4454	4-fold-change-MPSP	1	14	14.42
10	MSMEG_2116	4-fold-change-MPSP	2	6	0.20
11	MSMEG_1052	4-fold-change-MPSP	2	15	0.08
12	MSMEG_1888	both	1	18	74.03

13	MSMEG_3932	both	1	86	13.19
14	MSMEG_0067	both	1	102	0.17
15	MSMEG_1475	both	2	132	4.49
16	MSMEG_5136	both	2	166	5.85
17	MSMEG2164	both	3	70	91.81
18	MSMEG_5245	both	3	313	6.84
19	MSMEG_3945	both	5	228	4.71
20	MSMEG_5246	both	5	1114	6.89
21	MSMEG_5739	both	6	86	6.24
22	MSMEG_3962	both	8	1770	0.18
23	MSMEG_1037	both	8	6326	6.87
24	MSMEG_1682	both	11	1669	0.24
25	MSMEG_6454	both	12	2064	5.80
26	MSMEG_2956	both	19	513	10.63
27	MSMEG_5243	PLGEM-STN-MPSP	1	168	4.07
28	MSMEG_6097	PLGEM-STN-MPSP	2	1940	0.35
29	MSMEG_0969	PLGEM-STN-MPSP	3	509	2.85
30	MSMEG_3058	PLGEM-STN-MPSP	4	379	0.33
31	MSMEG_5225	PLGEM-STN-MPSP	4	479	0.34
32	MSMEG_4935	PLGEM-STN-MPSP	4	518	0.34
33	MSMEG_2078	PLGEM-STN-MPSP	4	1045	0.42
34	MSMEG_1680	PLGEM-STN-MPSP	5	555	0.27
35	MSMEG_2669	PLGEM-STN-MPSP	5	967	4.00
36	MSMEG_3950	PLGEM-STN-MPSP	5	1157	3.00
37	MSMEG_0919	PLGEM-STN-MPSP	6	1170	0.41
38	MSMEG_5715	PLGEM-STN-MPSP	6	1779	2.01
39	MSMEG_5419	PLGEM-STN-MPSP	7	782	3.01
40	MSMEG_2408	PLGEM-STN-MPSP	7	1163	2.35
41	MSMEG_3106	PLGEM-STN-MPSP	7	2157	2.17
42	MSMEG_4891	PLGEM-STN-MPSP	8	3994	1.85
43	MSMEG_0777	PLGEM-STN-MPSP	8	4362	2.30
44	MSMEG_4298	PLGEM-STN-MPSP	9	12334	0.25
45	MSMEG_3564	PLGEM-STN-MPSP	11	1361	0.47
46	MSMEG_3811	PLGEM-STN-MPSP	11	3688	2.39
47	MSMEG_4281	PLGEM-STN-MPSP	12	3286	2.51
48	MSMEG_0911	PLGEM-STN-MPSP	13	8247	0.31
49	MSMEG_3247	PLGEM-STN-MPSP	14	4396	0.52
50	MSMEG_3642	PLGEM-STN-MPSP	17	3295	0.52
51	MSMEG_4936	PLGEM-STN-MPSP	19	8312	0.29
52	MSMEG_1681	PLGEM-STN-MPSP	20	934	0.31
53	MSMEG_3143	PLGEM-STN-MPSP	20	7199	2.10
54	MSMEG_6759	PLGEM-STN-MPSP	22	20370	0.36
55	MSMEG_6638	PLGEM-STN-MPSP	23	7523	0.48



### **PART III. Lists of peptides and proteins quantified from the S<sub>P</sub> and R<sub>P</sub> samples**

(In the following pages, the following two tables are provided)

**Supplemental Table I. List of quantified proteins**

**Supplemental Table II. List of quantified peptides**

**Supplemental Table I.** List of quantified proteins

Proteins			Protein quantitaion								
Locus	old locus	Description	PCS counts	$A_{PRO}$							
				unlabeled proteins				labeled proteins			
				$S_{P,1}$	$S_{P,2}$	$R_{P,1}$	$R_{P,2}$	$cS_{P,1}$	$cS_{P,2}$	$cR_{P,1}$	$cR_{P,2}$
MSMEG_0001	MSMEG 0001	DNA polymerase III, beta subunit (dnaN)	3	271.6	264.2	308.8	286.0	336.4	288.3	373.4	383.1
MSMEG_0002	MSMEG 0002	gnd	6	275.8	286.0	526.0	498.5	571.9	584.8	693.9	710.1
MSMEG_0005	MSMEG 0005	DNA gyrase, B subunit (gyrB)	14	1778.4	1844.9	2046.6	1962.3	1027.5	1022.2	1020.4	1014.7
MSMEG_0006	MSMEG 0006	DNA gyrase, A subunit (gyrA)	19	2510.5	2600.0	3065.9	3082.2	1072.4	1138.9	1250.9	1439.0
MSMEG_0023	MSMEG 0023	conserved hypothetical protein	3	469.2	540.0	268.0	277.3	384.8	452.1	391.0	383.9
MSMEG_0024	MSMEG 0024	COG0652:Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin	12	5140.5	5341.9	3559.3	3629.5	3524.0	3559.9	3474.5	3561.4
MSMEG_0033	MSMEG 0033	ppp (ppp)	1	316.7	251.6	259.6	232.3	77.2	85.2	48.9	56.2
MSMEG_0034	MSMEG 0034	FHA domain protein	1	11.4	11.7	18.8	21.0	25.5	31.0	21.4	20.1
MSMEG_0042	MSMEG 0042	transcription regulator, TetR family	1	16.4	19.0	9.1	13.0	9.8	10.5	12.5	9.8
MSMEG_0048	MSMEG 0048	conserved hypothetical protein	2	39.0	44.8	94.6	90.9	43.0	54.3	33.7	31.7

MSMEG_0057	MSMEG_0056	conserved hypothetical protein	1	6.9	5.9	18.2	18.1	53.1	45.5	31.6	32.7
MSMEG_0059	MSMEG_0058	ATPase, AAA family	4	85.5	121.9	53.1	112.4	387.0	435.4	234.4	341.0
MSMEG_0065	MSMEG_0064	conserved hypothetical protein	1	12.3	16.7	16.5	25.7	15.7	24.3	8.8	16.2
MSMEG_0066	MSMEG_0065	ea	1	81.1	76.4	159.9	177.5	116.5	101.3	117.6	125.8
MSMEG_0067	MSMEG_0066	conserved hypothetical protein	1	25.9	33.2	175.2	172.2	97.8	113.1	133.9	146.8
MSMEG_0076	MSMEG_0074	conserved hypothetical protein	1	0.2	0.6	0.2	0.7	22.4	33.0	8.6	26.9
MSMEG_0081	MSMEG_0078	conserved hypothetical protein	1	391.5	406.5	175.3	206.3	7.4	11.2	0.6	5.5
MSMEG_0084	MSMEG_0082	phosphocarrier protein HPr, putative	1	4.2	3.4	4.8	6.1	11.9	8.9	16.1	15.1
MSMEG_0091	MSMEG_0089	transcriptional regulatory protein, putative	1	12.2	18.0	15.0	19.0	57.7	54.5	17.9	27.8
MSMEG_0092	MSMEG_0090	transcriptional regulator, TetR family domain protein	10	393.0	462.9	461.7	485.9	674.2	693.2	495.3	546.3
MSMEG_0108	MSMEG_0105	acyl-CoA dehydrogenase (acdA-2)	1	112.1	94.9	108.9	108.8	56.6	53.8	92.5	91.2
MSMEG_0110	MSMEG_0107	NAD(P) transhydrogenase, alpha subunit (pntA)	3	38.6	42.5	80.5	83.9	160.7	151.5	180.3	135.4

MSMEG _0120	MSMEG 0116	transcriptional regulator, TetR family domain protein	1	8.8	8.2	9.9	13.5	99.9	102.9	52.0	70.2
MSMEG _0131	MSMEG 0125	substrate--CoA ligase (fadD5)	1	1.7	1.3	7.1	6.2	7.1	9.1	4.1	13.8
MSMEG _0166	MSMEG 0160	transcription regulator GntR family VC1335	1	23.1	24.1	25.5	31.2	23.8	22.9	41.6	39.1
MSMEG _0215	MSMEG 0205	PUTATIVE PIRIN-LIKE PROTEIN	1	2.9	1.8	0.8	2.0	6.1	3.6	3.7	4.1
MSMEG _0216	MSMEG 0206	3-hydroxyacyl-CoA dehydrogenase type II	7	3042.6	2954.1	2364.7	2533.3	2517.6	2481.8	3143.6	3358.8
MSMEG _0220	MSMEG 0210	lysophospholipase	1	4.5	4.4	3.4	3.0	11.6	17.9	9.4	19.5
MSMEG _0224	MSMEG 0214	O-methyltransferase	2	283.5	270.6	112.9	109.6	180.1	180.9	117.3	136.4
MSMEG _0229	MSMEG 0219	dihydroxy-acid dehydratase (ilvD)	6	2491.7	2401.7	1938.3	1870.8	2347.5	2118.9	2124.5	1892.6
MSMEG _0233	MSMEG 0223	lppS (lppS)	1	90.9	101.6	79.3	110.1	132.2	141.7	182.7	176.3
MSMEG _0234	MSMEG 0224	peptidase, M13 family (pepO)	15	3600.0	3541.5	2259.9	1961.9	1726.7	1681.1	1944.2	1651.3
MSMEG _0238	MSMEG 0229	CoA-binding domain protein	7	988.2	878.7	1162.1	1242.7	329.7	337.2	261.3	286.8
MSMEG _0239	MSMEG 0230	O-acetylhomoserine/O- acetylserine sulfhydrylase family protein (cysD)	3	579.2	521.1	627.6	576.8	462.1	429.1	477.8	470.7

MSMEG _0255	MSMEG 0246	Phosphoenolpyruvate carboxykinase	23	4385.9	4450.2	5396.0	5233.5	911.9	1024.4	911.7	1005.4
MSMEG _0312	MSMEG 0301	2-deydro-3- deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate al	1	13.8	13.0	7.0	10.5	155.6	143.7	130.8	116.0
MSMEG _0317	MSMEG 0306	conserved hypothetical protein	2	47.9	39.6	138.0	167.0	54.5	56.3	98.2	124.2
MSMEG _0356	MSMEG 0347	conserved hypothetical protein	1	24.6	29.9	8.2	9.2	12.9	19.2	9.7	8.0
MSMEG _0363	MSMEG 0355	transcriptional regulator, TetR family domain protein	1	8.7	8.8	1.8	3.1	13.0	10.4	8.9	9.9
MSMEG _0370	MSMEG 0363	conserved hypothetical protein	10	190.3	182.3	157.7	161.1	151.7	146.3	110.7	127.5
MSMEG _0371	MSMEG 0364	MaoC domain protein	3	58.9	64.0	60.3	59.0	145.2	147.2	103.1	107.0
MSMEG _0372	MSMEG 0365	fabG4 (fabG4)	8	2356.9	2008.7	1591.9	1563.1	1754.8	1616.4	2802.0	2426.0
MSMEG _0373	MSMEG 0366	fadA2 (fadA2)	3	716.2	720.4	451.3	452.2	830.6	840.4	786.3	754.6
MSMEG _0380	MSMEG 0373	TmtpA (mmpS1)	1	53.0	80.4	57.8	76.8	54.0	61.9	43.1	46.7
MSMEG _0384	MSMEG 0377	glucose-1-phosphate thymidyltransferase (rfbA)	1	32.9	37.8	50.0	55.8	323.7	314.1	331.9	321.6
MSMEG _0386	MSMEG 0379	UDP-glucose 4-epimerase, putative	1	16.1	23.5	9.4	10.9	25.3	31.1	10.6	18.1

MSMEG_0387	MSMEG_0380	O-methyltransferase I	1	93.2	93.9	68.0	85.3	20.8	24.1	22.0	30.6
MSMEG_0388	MSMEG_0381	methyltransferase	6	287.7	282.5	482.6	534.0	426.9	445.1	566.9	595.9
MSMEG_0391	MSMEG_0384	methyltransferase	2	216.5	215.0	264.6	265.0	349.3	355.9	382.7	387.7
MSMEG_0393	MSMEG_0386	probable glycosyltransferase	4	31.0	40.6	51.1	58.1	216.6	228.5	209.4	206.4
MSMEG_0394	MSMEG_0387	hypothetical protein	4	17.7	12.4	71.0	58.4	41.9	32.3	52.8	54.9
MSMEG_0400	MSMEG_0390	peptide synthetase	51	1423.6	1446.9	2042.5	2110.7	2085.5	2001.0	2361.2	2055.5
MSMEG_0401	MSMEG_0391	pyoverdine synthetase	19	935.6	915.9	1122.6	1157.7	817.0	792.0	779.6	773.5
MSMEG_0402	MSMEG_0392	peptide synthetase	45	1477.5	1457.4	1635.2	1616.7	1504.2	1483.1	1438.3	1356.6
MSMEG_0406	MSMEG_0396	fadE5 (fadE5)	4	190.9	196.8	77.6	85.9	401.7	397.1	280.4	268.9
MSMEG_0408	MSMEG_0398	polyketide synthase	19	215.6	207.4	266.8	263.2	199.1	217.5	217.7	224.5
MSMEG_0415	MSMEG_0405	Flavin reductase like domain, putative	4	204.8	168.8	237.5	230.4	84.1	94.0	82.8	85.5
MSMEG_0422	MSMEG_0413	carboxyphosphoenolpyruvate phosphonmutase-like protein	8	266.5	275.3	320.9	340.4	1047.3	1014.4	859.2	865.6
MSMEG_0456	MSMEG_0447	DNA gyrase, A subunit, putative	2	160.5	166.9	187.7	223.9	190.7	201.5	109.8	68.8
MSMEG_0457	MSMEG_0448	DNA gyrase subunit B, putative	2	68.6	77.7	76.8	93.8	13.9	18.2	13.0	18.6
MSMEG_0464	MSMEG_0456	phosphomethylpyrimidine kinase (thiD)	4	336.3	337.6	304.0	310.8	396.6	392.8	370.8	330.5

MSMEG _0530	MSMEG 0520	oxidoreductase, short-chain dehydrogenase/reductase family (fabG)	2	35.8	49.4	88.1	82.1	277.8	299.1	302.5	286.4
MSMEG _0531	MSMEG 0521	acyl-CoA dehydrogenase (acd-2)	2	262.5	265.3	246.8	224.3	192.9	191.0	154.3	166.2
MSMEG _0550	MSMEG 0541	ABC transporter, periplasmic substrate-binding protein	6	860.7	912.2	1271.2	1275.6	759.9	829.7	466.5	498.2
MSMEG _0551	MSMEG 0542	aliphatic sulfonates ABC transporter, ATP-binding protein	1	36.7	37.5	53.6	56.1	18.5	18.7	17.7	18.9
MSMEG _0572	MSMEG 0563	conserved hypothetical protein	5	70.9	81.1	69.2	79.8	3809.9	4353.6	3506.2	3006.0
MSMEG _0599	MSMEG 0590	fadD2 (fadD2)	2	25.9	34.1	37.8	30.2	168.0	184.1	165.1	151.9
MSMEG _0603	MSMEG 0594	fadE6 (fadE6)	1	18.6	16.7	31.5	39.3	54.4	43.1	49.5	35.3
MSMEG _0613	MSMEG 0603	conserved hypothetical protein	1	1.2	0.8	0.5	0.5	4.0	2.6	6.7	21.3
MSMEG _0614	MSMEG 0604	Mycobacterium tuberculosis paralogous family	1	87.6	98.7	25.1	28.0	32.4	34.0	15.7	24.0
MSMEG _0628	MSMEG 0619	Amidohydrolase family superfamily	1	69.2	74.4	58.9	64.3	78.0	98.7	72.6	81.0
MSMEG _0636	MSMEG 0627	conserved hypothetical protein	4	414.5	411.7	528.7	562.8	128.4	128.9	86.0	91.1

MSMEG _0640	MSMEG 0632	oligopeptide ABC transporter, ATP-binding protein (oppD)	1	11.0	10.3	19.5	15.8	49.3	46.7	20.3	27.9
MSMEG _0643	MSMEG 0635	heme-binding lipoprotein, putative	15	471.5	502.7	886.4	946.4	3387.0	3207.8	2579.2	2775.8
MSMEG _0683	MSMEG 0675	conserved hypothetical protein	2	31.3	36.6	26.9	30.8	47.2	62.2	40.2	48.2
MSMEG _0688	MSMEG 0680	aminotransferase, classes I and II	1	72.7	69.1	71.6	59.1	307.2	370.6	160.9	248.7
MSMEG _0690	MSMEG 0682	ferredoxin, 4Fe-4S	13	426.0	461.6	478.0	489.4	558.5	614.3	474.4	496.3
MSMEG _0692	MSMEG 0684	conserved hypothetical protein	4	94.5	111.5	95.1	109.6	222.3	230.2	237.1	231.5
MSMEG _0695	MSMEG 0689	conserved hypothetical protein	1	22.0	26.3	7.3	14.5	21.5	25.8	15.9	24.0
MSMEG _0702	MSMEG 0697	Luciferase-like monooxygenase superfamily	13	4940.7	5033.1	3123.9	3675.7	2897.4	2807.5	2589.2	2991.9
MSMEG _0703	MSMEG 0698	conserved hypothetical protein	4	71.1	79.5	56.2	67.3	279.2	262.1	249.7	246.6
MSMEG _0709	MSMEG 0704	DNAk protein	18	5357.7	5422.4	5344.4	4749.6	5089.5	5021.7	5512.3	4774.0
MSMEG _0710	MSMEG 0705	grpE protein (grpE)	3	265.1	332.2	148.8	219.5	227.4	283.6	131.4	181.7
MSMEG _0732	MSMEG 0726	heat shock protein	3	170.1	178.0	177.1	194.4	429.5	420.0	471.2	478.6
MSMEG _0741	MSMEG 0736	conserved hypothetical protein	6	388.3	421.9	495.6	482.5	403.0	426.7	397.5	413.5



MSMEG _0759	MSMEG 0755	adenylosuccinate synthetase (purA)	5	393.8	381.8	504.2	542.7	643.3	624.3	733.7	779.0
MSMEG _0760	MSMEG 0756	thioesterase family protein domain protein	2	59.9	64.2	56.4	68.6	104.1	92.3	98.9	107.1
MSMEG _0769	MSMEG 0763	O-succinylhomoserine sulfhydrylase (metZ)	3	647.0	652.3	473.5	480.8	858.4	902.3	784.8	834.6
MSMEG _0777	MSMEG 0772	F420-dependent glucose-6- phosphate dehydrogenase (mer- 2)	8	6045.2	6120.4	2586.2	2696.6	4377.5	4331.6	3767.0	3865.6
MSMEG _0779	MSMEG 0774	3-oxoacyl-(acyl-carrier-protein) reductase	2	163.2	174.6	110.4	116.3	324.3	336.4	315.8	330.9
MSMEG _0783	MSMEG 0778	phosphate acetyltransferase (pta)	1	30.3	36.1	36.5	30.2	26.7	39.5	30.7	34.2
MSMEG _0789	MSMEG 0785	thiamine-phosphate pyrophosphorylase (thiE)	2	128.9	132.8	97.5	93.3	124.5	123.8	114.5	107.9
MSMEG _0793	MSMEG 0788	thiazole biosynthesis protein ThiG (thiG)	2	109.8	118.3	100.0	100.5	85.5	88.3	159.6	167.2
MSMEG _0814	MSMEG 0807	hypothetical protein	5	383.9	408.9	520.0	486.4	418.8	439.5	505.3	474.0
MSMEG _0825	MSMEG 0817	phosphomethylpyrimidine kinase (thiD)	5	556.9	564.6	716.2	760.6	917.0	893.1	851.9	948.0
MSMEG _0826	MSMEG 0818	thiamin biosynthesis protein ThiC	1	111.6	116.1	45.8	53.2	15.3	16.4	5.2	17.5

MSMEG _0832	MSMEG 0826	peptide deformylase (def)	1	145.7	158.1	141.0	139.2	166.1	178.0	205.1	208.6
MSMEG _0834	MSMEG 0828	conserved hypothetical protein	1	75.9	81.9	84.2	98.6	64.4	85.4	21.2	48.2
MSMEG _0835	MSMEG 0829	copper/zinc superoxide dismutase (sodC)	2	699.0	657.1	829.0	730.8	1081.7	950.3	1179.2	1000.1
MSMEG _0858	MSMEG 0852	cell division control protein 48, AAA family (cdc48-1)	2	1398.3	1509.9	1251.2	1153.3	1183.4	1196.1	1113.4	1081.2
MSMEG _0859	MSMEG 0851	Aha1 domain family	5	182.8	189.2	140.8	158.9	209.0	214.5	206.5	215.4
MSMEG _0861	MSMEG 0854	phosphatidylserine decarboxylase (psd)	3	52.2	88.9	28.0	36.7	4.2	5.9	4.1	3.4
MSMEG _0863	MSMEG 0856	oxidoreductase, short-chain dehydrogenase/reductase family	2	114.4	120.2	126.1	144.8	263.9	268.2	308.2	262.8
MSMEG _0876	MSMEG 0871	oxidoreductase, short-chain dehydrogenase/reductase family	2	71.4	83.4	50.4	50.1	85.5	99.3	106.2	116.1
MSMEG _0877	MSMEG 0870	dihydrodipicolinate synthase family protein	2	95.3	105.3	88.6	103.1	64.3	65.3	49.0	62.2
MSMEG _0880	MSMEG 0873	60 kd chaperonin , fragment	24	24758.5	25511.7	25648.9	26468.9	16427.4	17058.2	15398.6	16674.9
MSMEG _0882	MSMEG 0875	conserved hypothetical protein	1	415.7	464.3	449.9	477.5	426.3	467.0	377.2	392.1
MSMEG _0884	MSMEG 0877	glyoxalase family protein	1	21.2	23.7	26.1	31.5	24.6	31.1	27.9	34.6

MSMEG _0887	MSMEG 0880	conserved hypothetical protein	1	149.1	162.2	91.1	108.7	215.2	206.9	164.4	198.9
MSMEG _0889	MSMEG 0882	gabD1 (gabD1)	1	6.9	3.6	9.3	7.9	221.1	208.1	307.2	248.2
MSMEG _0899	MSMEG 0893	prolyl oligopeptidase family protein (pep)	4	188.3	178.2	172.3	127.2	206.1	224.7	223.8	213.7
MSMEG _0903	MSMEG 0897	dihydrolipoamide dehydrogenase (lpdA)	13	7390.5	7313.7	7873.1	8058.1	7997.3	8028.5	9042.2	9388.6
MSMEG _0905	MSMEG 0899	conserved hypothetical protein	2	65.4	75.5	76.2	38.2	88.1	55.1	153.7	67.5
MSMEG _0909	MSMEG 0903	conserved hypothetical protein	2	72.8	80.2	67.9	70.7	57.5	56.9	58.6	64.0
MSMEG _0911	MSMEG 0904	isocitrate lyase (aceA)	13	3803.7	4014.2	12486.0	12684.8	707.5	855.3	595.7	709.7
MSMEG _0912	MSMEG 0905	fadB2 (fadB2)	9	1326.4	1308.0	2031.8	2031.5	1790.3	1694.5	1966.9	1883.2
MSMEG _0913	MSMEG 0906	methoxy mycolic acid synthase 1 (umaA1)	15	2960.1	3072.9	4195.9	4127.8	1531.9	1602.4	1539.5	1641.4
MSMEG _0916	MSMEG 0909	transcriptional regulator, TetR family	1	39.5	37.9	36.8	45.8	53.7	49.2	17.9	31.7
MSMEG _0918	MSMEG 0911	Helix-turn-helix domain protein	3	35.7	40.8	67.5	65.2	369.8	380.5	384.1	368.5
MSMEG _0919	MSMEG 0912	conserved hypothetical protein	6	638.7	717.5	1634.0	1690.6	6661.6	7415.7	6870.1	7187.6
MSMEG _0924	MSMEG 0916	carbon-nitrogen hydrolase family protein, putative	1	66.6	73.0	59.2	70.1	15.2	16.4	12.6	17.2

MSMEG _0927	MSMEG 0919	conserved hypothetical protein	3	34.0	35.6	21.4	25.1	52.2	54.9	36.6	39.2
MSMEG _0930	MSMEG 0922	oxidoreductase, short chain dehydrogenase/reductase family	6	524.6	525.3	423.9	358.3	386.7	399.0	453.6	416.4
MSMEG _0935	MSMEG 0927	phosphoglycerate mutase	15	3506.4	3534.0	3005.8	2927.4	7198.7	7540.3	15103.5	16617.2
MSMEG _0937	MSMEG 0929	DNA-binding response regulator RegX3 (regX3)	1	17.1	21.2	26.2	32.9	4.9	7.5	6.5	7.2
MSMEG _0943	MSMEG 0934	pyrroline-5-carboxylate reductase (proC)	4	653.9	714.8	633.3	646.9	333.8	325.0	372.3	381.2
MSMEG _0944	MSMEG 0935	excisionase, putative	2	61.4	62.7	61.7	58.7	237.5	239.5	225.2	218.4
MSMEG _0948	MSMEG 0939	Actinomycete protein of unknown function (DUF875) superfamily	8	287.1	216.0	251.4	262.3	140.0	99.6	118.9	119.9
MSMEG _0954	MSMEG 0944	uroporphyrin-III C- methyltransferase/uroporphyrinog en-III synthase (h	6	447.5	482.2	534.5	535.2	298.2	317.0	266.5	265.2
MSMEG _0965	MSMEG 0955	mspA-Gen	4	460.7	497.0	298.3	398.1	496.8	533.9	433.3	551.1
MSMEG _0969	MSMEG 0959	glutamate-1-semialdehyde-2,1- aminomutase (hemL)	3	755.0	752.0	270.8	258.0	446.7	573.4	229.4	231.4
MSMEG _0970	MSMEG 0960	phosphoglycerate mutase family protein	1	213.5	204.5	184.7	187.9	136.4	126.7	107.0	105.2

MSMEG_0987	MSMEG_0977	hypothetical protein	1	38.7	0.0	39.8	49.8	114.4	0.0	121.1	110.3
MSMEG_1010	MSMEG_0998	transcriptional regulator, TetR family	3	269.5	283.3	244.7	289.4	444.2	480.3	378.5	413.0
MSMEG_1011	MSMEG_0999	oxidoreductase, short-chain dehydrogenase/reductase family	1	36.8	35.8	50.7	51.0	42.3	40.1	43.5	44.3
MSMEG_1019	MSMEG_1007	ribonucleoside-diphosphate reductase alpha chain (nrdE)	16	2251.5	2203.6	2320.3	2113.5	4569.1	4413.5	4763.6	4449.6
MSMEG_1021	MSMEG_1010	Glyoxalase/Bleomycin resistance protein/Dioxygenase family protein	1	39.6	39.0	56.5	59.5	39.9	42.9	45.8	48.0
MSMEG_1028	MSMEG_1015	probable electron transfer oxidoreductase, putative	7	2963.0	2868.2	2283.2	2360.4	2255.9	2362.1	1810.6	2022.2
MSMEG_1033	MSMEG_1019	ribonucleoside-diphosphate reductase, beta subunit	2	600.0	607.0	413.7	443.3	1210.9	1165.2	824.9	828.3
MSMEG_1037	MSMEG_1024	oxidoreductase, zinc-binding (adhA)	8	10758.9	11327.1	1547.6	1671.9	1518.3	1726.3	1145.6	1357.9
MSMEG_1038	MSMEG_1025	YCII-related domain superfamily	2	368.4	410.9	222.1	208.9	247.6	266.5	239.1	214.0
MSMEG_1041	MSMEG_1028	phosphoserine phosphatase (serB2)	1	118.8	153.6	40.6	63.8	81.8	96.1	41.5	73.7
MSMEG_1046	MSMEG_1033	ABC transporter, ATP-binding protein	5	607.4	617.0	625.6	622.7	960.7	904.8	984.6	1010.9

MSMEG _1047	MSMEG 1034	NUDIX domain protein	7	465.3	496.7	554.0	582.1	423.0	424.5	409.1	444.1
MSMEG _1048	MSMEG 1035	echA17 (echA17)	1	12.6	9.2	4.7	5.7	3.2	4.2	4.9	6.6
MSMEG _1049	MSMEG 1036	conserved hypothetical protein	2	133.3	110.6	121.3	106.1	28.1	26.7	18.9	32.9
MSMEG _1051	MSMEG 1038	immunogenic protein MPB64/MPT64	2	84.2	87.7	60.2	56.5	93.7	91.2	72.8	80.8
MSMEG _1052	MSMEG 1039	sodium:alanine symporter family protein	2	2.4	2.4	28.2	28.8	116.8	93.4	95.5	84.6
MSMEG _1060	MSMEG 1045	lysyl tRNA synthetase-like protein, putative	4	723.2	789.4	840.5	1007.8	1190.8	1317.0	823.1	940.4
MSMEG _1061	MSMEG 1046	Phosphohydrolase (MutT/nudixfamil)	3	227.4	347.8	162.4	176.4	233.2	370.4	162.7	190.1
MSMEG _1075	MSMEG 1059	naphthoate synthase (menB)	2	65.2	58.6	50.0	46.9	12.5	10.7	4.7	3.9
MSMEG _1076	MSMEG 1060	Protein hdeA precursor, putative	1	13.5	12.3	7.3	5.4	10.1	8.9	9.4	6.5
MSMEG _1077	MSMEG 1061	conserved hypothetical protein	1	50.1	54.5	34.4	38.8	72.2	77.8	62.7	65.6
MSMEG _1078	MSMEG 1062	hydrolase, haloacid dehalogenase- like family, putative	1	35.6	35.1	13.9	14.9	34.7	30.3	16.8	25.4
MSMEG _1090	MSMEG 1078	glutamyl-tRNA(Gln) amidotransferase, A subunit	1	14.6	21.5	17.5	25.2	82.5	115.1	97.0	134.0

MSMEG	MSMEG	ubiquinone/menaquinone biosynthesis methlytransferase (ubiE)	1	4.7	3.5	0.9	6.0	19.4	19.1	54.8	32.0
MSMEG	MSMEG	grcC1 (grcC1)	1	32.0	37.9	63.4	72.9	58.3	75.1	79.6	65.1
MSMEG	MSMEG	PROBABLE METALLOPROTEASE ZINC TRANSMEMBRANE PROTEIN	1	31.6	34.0	39.8	40.8	47.9	51.3	29.1	23.4
MSMEG	MSMEG	putative secreted protein	1	0.6	0.8	0.0	0.1	11.3	31.7	10.5	27.8
MSMEG	MSMEG	Protein of unknown function (DUF520) superfamily	6	210.1	180.1	170.0	188.3	354.3	309.3	363.4	380.4
MSMEG	MSMEG	hypothetical protein	1	66.1	57.5	47.0	48.8	61.4	53.5	56.8	51.8
MSMEG	MSMEG	methoxy mycolic acid synthase 1	1	79.8	73.6	104.0	90.9	134.0	129.0	136.5	151.6
MSMEG	MSMEG	probable serine/threonine protein kinase, putative	1	21.3	20.8	19.2	18.3	15.9	19.4	27.8	20.3
MSMEG	MSMEG	conserved hypothetical protein	1	50.3	29.0	17.6	13.6	176.7	153.3	143.7	150.9
MSMEG	MSMEG	hypothetical protein	5	33.6	30.4	39.8	42.0	46.6	39.5	33.6	35.6
MSMEG	MSMEG	hypothetical protein	3	57.7	66.5	159.6	177.3	422.4	419.7	494.4	501.6
MSMEG	MSMEG	hypothetical protein	1	4.8	3.9	2.3	3.5	49.0	48.1	19.6	23.1

MSMEG _1253	MSMEG 1247	conserved hypothetical protein	5	38.5	41.6	66.6	68.6	106.5	113.6	100.9	112.4
MSMEG _1254	MSMEG 1248	RNA helicase, putative	3	61.1	57.4	43.4	28.1	26.6	28.6	38.9	36.5
MSMEG _1255	MSMEG 1249	COG0210:Superfamily I DNA and RNA helicases	6	355.6	312.9	326.9	289.4	517.2	433.5	488.0	472.4
MSMEG _1265	MSMEG 1257	hypothetical protein	5	746.8	770.3	682.6	701.4	819.4	854.6	851.1	908.4
MSMEG _1285	MSMEG 1277	SEC-C motif domain protein	2	27.0	32.8	61.9	54.1	252.8	246.8	338.4	236.6
MSMEG _1292	MSMEG 1284	blr6160	1	12.0	11.0	5.0	5.1	20.8	20.1	23.3	15.9
MSMEG _1295	MSMEG 1287	transthyretin family protein	1	1.5	2.0	2.8	4.6	31.5	32.0	29.8	28.5
MSMEG _1296	MSMEG 1288	uricase	2	175.0	174.5	108.0	112.4	446.4	474.2	276.6	325.6
MSMEG _1331	MSMEG 1324	enoyl-CoA hydratase/isomerase family protein (fad-1)	1	8.6	6.9	12.0	9.3	7.4	5.9	10.6	8.2
MSMEG _1334	MSMEG 1327	metallo-beta-lactamase family protein	3	373.2	436.6	304.5	341.0	196.1	252.6	194.8	240.1
MSMEG _1340	MSMEG 1333	Actinomycete protein of unknown function (DUF875) superfamily	4	398.9	410.2	376.7	420.2	371.5	391.2	340.2	338.5
MSMEG _1341	MSMEG 1334	MaoC like domain, putative	3	805.1	980.9	854.9	935.8	830.4	1023.5	814.6	821.6
MSMEG _1342	MSMEG 1335	conserved hypothetical protein	2	117.6	108.8	118.2	117.0	60.4	55.3	52.6	50.1



MSMEG _1344	MSMEG 1337	preprotein translocase SecE subunit (secE)	1	39.0	50.8	62.6	65.7	15.3	20.9	10.6	13.9
MSMEG _1345	MSMEG 1338	transcription antitermination protein NusG CC3205	3	1578.6	1556.8	1429.2	1395.2	1207.5	1202.4	1299.7	1319.5
MSMEG _1346	MSMEG 1339	ribosomal protein L11 (rplK)	2	898.3	854.8	755.2	818.2	887.7	857.4	831.4	844.0
MSMEG _1347	MSMEG 1340	ribosomal protein L1 (rplA)	12	5653.8	5799.5	6845.4	6718.3	3103.5	3156.6	3636.0	3672.4
MSMEG _1350	MSMEG 1343	cyclopropane-fatty-acyl- phospholipid synthase 1	6	620.1	623.2	1023.2	988.5	333.1	339.4	306.3	326.3
MSMEG _1352	MSMEG 1345	carboxyl esterase	1	5.1	8.2	2.9	6.3	6.2	9.1	5.1	6.5
MSMEG _1364	MSMEG 1357	ribosomal protein L10 (rplJ)	8	2030.8	2153.6	2125.1	2324.0	1543.7	1555.7	1564.5	1558.3
MSMEG _1365	MSMEG 1358	ribosomal protein L7/L12 (rplL)	8	2361.9	2459.4	2425.9	2353.6	1793.1	1858.8	1777.9	1603.0
MSMEG _1367	MSMEG 1360	DNA polymerase (rpoB) (rpoB)	65	10898.8	10871.6	9413.9	9419.9	6709.2	6553.5	6175.8	5977.2
MSMEG _1368	MSMEG 1361	DNA-directed RNA polymerase, beta' subunit (rpoC)	92	12627.2	12407.2	10791.6	10347.5	7929.8	7804.8	8539.1	7951.0
MSMEG _1383	MSMEG 1376	endonuclease IV, putative	2	162.3	153.3	137.7	138.2	91.5	97.0	108.3	105.1
MSMEG _1384	MSMEG 1378	Protein of unknown function (DUF861) family	1	27.8	39.8	23.3	23.8	83.8	93.5	78.0	79.7
MSMEG _1393	MSMEG 1387	conserved hypothetical protein	1	12.2	18.0	14.5	18.5	179.7	203.0	194.3	169.7

MSMEG _1397	MSMEG 1392	transcriptional regulator, putative	1	3.5	6.1	2.1	3.2	85.9	85.6	63.6	56.4
MSMEG _1398	MSMEG 1393	ribosomal protein S12 (rpsL)	1	102.0	92.8	104.9	121.6	46.8	43.5	40.8	42.9
MSMEG _1399	MSMEG 1394	ribosomal protein S7 (rpsG)	11	6966.3	7674.3	6422.3	6712.5	3597.2	4047.4	3524.0	3437.6
MSMEG _1400	MSMEG 1395	translation elongation factor EF-G (fusA) (fusA)	5	833.1	678.9	720.7	601.5	1014.7	790.1	868.7	762.9
MSMEG _1401	MSMEG 1397	translation elongation factor Tu (tuf)	28	29767.6	29016.4	35032.6	34965.8	32108.9	31686.1	33537.3	33587.9
MSMEG _1416	MSMEG 1415	ferredoxin reductase	2	283.2	262.4	298.2	288.7	355.0	274.4	362.7	365.2
MSMEG _1430	MSMEG 1427	transcriptional regulatory protein, putative	1	4.4	3.4	1.7	1.4	7.2	8.6	4.0	4.8
MSMEG _1435	MSMEG 1433	ribosomal protein S10 (rpsJ)	4	1349.3	1431.0	1650.6	1694.9	862.1	885.8	979.3	922.2
MSMEG _1436	MSMEG 1434	ribosomal protein L3 (rplC)	9	2484.4	2118.7	3667.7	3440.1	1277.2	1035.2	1496.9	1417.7
MSMEG _1437	MSMEG 1435	ribosomal protein L4/L1 family (rplD)	4	1387.7	1071.1	1377.7	1400.8	776.1	567.9	736.2	748.4
MSMEG _1438	MSMEG 1436	ribosomal protein L23 (rplW)	2	1155.3	1180.7	1534.5	1588.6	767.5	814.0	841.2	805.7
MSMEG _1439	MSMEG 1437	ribosomal protein L2 (rplB)	7	1900.5	1757.9	1447.5	1424.6	1134.6	1057.9	1061.0	1075.3
MSMEG _1440	MSMEG 1438	ribosomal protein S19 (rpsS)	11	658.8	529.1	721.4	741.2	290.2	246.0	279.3	283.4
MSMEG _1441	MSMEG 1439	ribosomal protein L22	7	1873.5	2096.6	1919.5	1959.3	856.0	934.9	888.1	865.0
MSMEG _1442	MSMEG 1440	rpsC (rpsC)	7	2139.3	2223.0	1708.1	1686.9	1413.7	1636.5	1141.6	1171.1
MSMEG _1443	MSMEG 1441	ribosomal protein L16 (rplP)	5	3114.7	2770.5	3355.2	3190.8	2217.1	1889.5	2237.7	1965.1

MSMEG	MSMEG										
_1445	1443	rpsQ (rpsQ)	1	8.7	0.0	11.5	11.1	4.4	0.0	3.3	3.7
MSMEG	MSMEG										
_1465	1462	ribosomal protein L14 (rplN)	6	984.3	983.4	1190.1	1134.0	594.0	621.7	613.0	567.5
MSMEG	MSMEG										
_1466	1463	ribosomal protein L24 (rplX)	4	564.4	637.9	556.3	558.7	298.5	338.2	250.5	224.9
MSMEG	MSMEG										
_1467	1464	ribosomal protein L5 (rplE)	12	3293.3	3371.4	3847.1	3836.2	2541.9	2628.3	2507.0	2466.7
MSMEG	MSMEG										
_1469	1466	ribosomal protein S8 (rpsH)	3	896.2	947.0	851.0	909.1	489.7	503.3	468.9	462.4
MSMEG	MSMEG										
_1470	1467	ribosomal protein L6 (rplF)	7	3716.9	4025.7	4164.3	4337.2	2244.7	2341.6	2327.8	2280.6
MSMEG	MSMEG										
_1471	1468	ribosomal protein L18 (rplR)	2	211.6	190.4	230.6	238.9	142.0	129.1	147.4	146.8
MSMEG	MSMEG										
_1472	1469	ribosomal protein S5 (rpsE)	11	7926.4	7751.0	8363.6	7987.2	5055.9	4926.6	5165.6	5088.7
MSMEG	MSMEG										
_1473	1470	ribosomal protein L30 (rpmD)	3	797.1	857.2	796.5	833.1	421.5	456.5	507.6	491.6
MSMEG	MSMEG										
_1474	1471	ribosomal protein L15 (rplO)	6	2722.3	3096.4	2574.3	2746.4	2407.1	2747.2	2638.6	2625.1
MSMEG	MSMEG										
_1475	1472	Rif17, putative	2	215.3	214.9	43.5	53.3	71.0	65.7	68.5	77.6
MSMEG	MSMEG										
_1476	1473	signal peptide peptidase SppA, 67K type (sppA)	1	108.9	102.2	33.9	44.4	136.8	128.6	161.7	124.3
MSMEG	MSMEG										
_1479	1476	Mycobacterium tuberculosis paralogous family	2	94.1	114.2	33.5	39.0	61.7	72.7	38.4	64.0
MSMEG	MSMEG										
_1482	1479	Mycobacterium tuberculosis paralogous family	1	162.5	129.6	80.8	87.8	67.2	62.1	70.4	109.5
MSMEG	MSMEG										
_1485	1482	methionine aminopeptidase, type I (map)	4	92.5	108.6	117.3	100.4	28.8	30.1	50.7	52.1
MSMEG	MSMEG										
_1492	1490	transcriptional regulator, MarR family family	1	3.3	3.3	3.5	3.1	3.7	4.3	3.6	3.7

MSMEG _1498	MSMEG 1497	methylmalonate-semialdehyde dehydrogenase (mmsA)	2	283.2	304.2	303.9	301.5	241.1	315.8	294.1	285.3
MSMEG _1512	MSMEG 1511	dTDP-glucose 4,6-dehydratase (rfbB)	2	112.6	117.5	79.6	89.9	141.1	157.2	136.0	144.5
MSMEG _1513	MSMEG 1512	conserved hypothetical protein	7	497.2	505.6	584.5	615.9	802.4	767.0	1721.0	1555.5
MSMEG _1521	MSMEG 1520	ribosomal protein S13p/S18e (rpsM)	9	983.6	841.1	921.0	984.3	542.3	442.5	518.8	535.1
MSMEG _1522	MSMEG 1521	rpsK (rpsK)	6	2671.6	2365.3	2996.3	3015.5	1489.5	1231.5	1414.2	1328.1
MSMEG _1523	MSMEG 1522	ribosomal protein S4 (rpsD)	8	4836.3	4716.1	4910.1	5026.4	2778.6	2713.5	2566.2	2682.1
MSMEG _1524	MSMEG 1523	DNA-directed RNA polymerase, alpha subunit	18	13359.6	12108.1	12236.1	11869.3	9878.1	9281.2	9968.2	9716.3
MSMEG _1525	MSMEG 1524	ribosomal protein L17 (rplQ)	9	1930.4	1993.8	2303.5	2249.1	1014.1	1027.4	1262.5	1202.9
MSMEG _1528	MSMEG 1527	serine esterase, cutinase family	4	220.5	239.4	184.5	198.4	167.6	184.4	167.5	163.3
MSMEG _1536	MSMEG 1535	FtsK/SpoIIIE family protein	1	45.2	40.4	35.9	36.8	25.0	27.3	29.8	31.2
MSMEG _1556	MSMEG 1553	ribosomal protein L13 (rplM)	9	2980.6	2874.7	3061.2	3121.3	1778.0	1654.0	1687.2	1553.0
MSMEG _1557	MSMEG 1554	ribosomal protein S9 (rpsI)	9	7013.5	7462.0	7573.6	7664.4	3777.7	3833.8	4262.2	4143.8
MSMEG _1567	MSMEG 1564	conserved hypothetical protein	2	62.0	62.1	103.2	100.4	168.1	156.8	151.8	158.3
MSMEG _1574	MSMEG 1571	glutamate decarboxylase	7	584.1	570.1	430.4	403.8	739.7	711.1	747.9	681.1

MSMEG _1577	MSMEG 1574	Uncharacterised P-loop hydrolase UPF0079	1	49.4	56.1	22.1	35.2	49.5	60.2	24.9	39.6
MSMEG _1581	MSMEG 1579	hypothetical protein	1	12.3	13.4	9.7	10.5	6.4	9.9	4.3	5.4
MSMEG _1582	MSMEG 1580	chaperonin, 10 kDa (groES)	8	4198.2	4908.0	5099.3	5117.4	3016.9	3365.7	3704.4	3465.0
MSMEG _1583	MSMEG 1581	KCS	14	4682.2	4494.9	4481.3	4347.6	4232.6	4166.8	3723.3	3736.7
MSMEG _1602	MSMEG 1600	inosine-5-monophosphate dehydrogenase (guaB)	6	612.9	559.6	542.1	518.3	581.1	508.1	876.8	770.8
MSMEG _1603	MSMEG 1601	IMP dehydrogenase family protein	5	908.0	852.9	705.8	698.5	1156.9	1085.3	1377.8	1105.7
MSMEG _1605	MSMEG 1603	phosphate transport system regulatory protein, putative	1	0.1	0.1	4.5	5.4	0.4	0.3	0.7	0.7
MSMEG _1610	MSMEG 1608	GMP synthase (guaA)	7	1322.3	1168.8	1040.6	1035.7	1565.4	1480.3	1582.4	1767.3
MSMEG _1614	MSMEG 1612	amino acid ABC transporter, ATP- binding protein (glnQ)	1	76.4	83.8	80.4	84.7	2.0	1.0	1.0	1.9
MSMEG _1634	MSMEG 1633	conserved hypothetical protein	3	1352.7	1445.0	1911.4	1959.6	962.1	1030.3	980.0	958.4
MSMEG _1635	MSMEG 1634	nitroreductase family protein superfamily	9	2864.3	2830.6	1672.3	1670.1	1526.7	1433.0	1607.8	1564.4
MSMEG _1642	MSMEG 1641	ABC transporter, ATP-binding protein	9	275.3	283.5	254.8	281.3	209.2	216.0	173.5	201.8

MSMEG _1647	MSMEG 1645	methylenetetrahydrofolate dehydrogenase/methenyltetrahydr ofolate cycl	7	610.8	640.5	527.1	547.7	780.7	778.1	753.3	788.7
MSMEG _1650	MSMEG 1649	methyltransferase, putative	1	6.0	14.2	5.5	7.1	31.5	29.5	35.6	38.1
MSMEG _1652	MSMEG 1651	metC (metC)	8	2217.4	2304.7	2089.1	2239.6	1387.9	1452.6	1434.5	1487.9
MSMEG _1654	MSMEG 1652	isocitrate dehydrogenase, NADP- dependent	44	14265.5	14955.9	11008.7	10559.0	8088.0	8085.0	9068.2	8476.9
MSMEG _1655	MSMEG 1653	tropinesterase homolog tpeA	2	36.5	36.3	62.6	51.9	6.1	5.6	5.4	9.5
MSMEG _1656	MSMEG 1654	exodeoxyribonuclease III (xth)	1	21.7	18.1	31.2	22.0	23.2	30.0	18.0	21.4
MSMEG _1662	MSMEG 1660	aminotransferase, class III	5	396.7	323.6	597.7	553.1	513.3	456.0	555.1	581.0
MSMEG _1663	MSMEG 1661	regulatory protein AsnC, putative	2	128.2	130.1	127.1	107.6	72.7	72.9	47.1	50.2
MSMEG _1665	MSMEG 1662	aldehyde dehydrogenase family protein	1	291.2	284.9	234.4	207.1	167.1	209.1	248.1	227.8
MSMEG _1669	MSMEG 1666	sdhB (sdhB)	5	854.6	862.6	1527.6	1630.5	825.7	834.3	810.9	860.5
MSMEG _1670	MSMEG 1667	succinate dehydrogenase, flavoprotein subunit (sdhA)	8	1044.7	986.7	1679.9	1458.4	1278.6	1200.1	1055.8	953.9
MSMEG _1671	MSMEG 1668	succinate dehydrogenase, hydrophobic membrane anchor protein	1	9.2	5.8	19.8	23.3	5.1	2.1	4.2	7.2
MSMEG _1672	MSMEG 1669	sdhC (sdhC)	1	230.3	264.8	397.5	393.6	290.3	319.5	263.5	239.4

MSMEG _1676	MSMEG 1673	adenosine deaminase (add)	2	236.7	194.7	97.8	135.4	135.9	90.6	143.2	168.2
MSMEG _1679	MSMEG 1676	amiB (amiB)	3	161.7	184.4	387.2	364.4	476.1	518.3	786.6	783.6
MSMEG _1680	MSMEG 1677	conserved hypothetical protein	5	227.8	243.3	885.2	863.8	618.3	637.9	604.4	591.1
MSMEG _1681	MSMEG 1678	YER057c/YjgF/UK114 family protein	20	448.0	425.5	1378.7	1482.6	2084.2	1993.9	1505.1	1501.3
MSMEG _1682	MSMEG 1679	monooxygenase, putative	11	646.1	632.8	2722.7	2676.2	214.2	188.4	185.3	217.9
MSMEG _1683	MSMEG 1680	cytosine/purine/uracil/thiamine/all antoin permease family protein	1	0.0	0.0	0.8	0.5	34.4	43.3	37.1	31.7
MSMEG _1694	MSMEG 1690	uracil phosphoribosyltransferase	2	39.5	38.5	49.6	55.1	78.4	77.9	41.8	49.7
MSMEG _1696	MSMEG 1692	putative MarR-family transcriptional regulator	1	176.9	182.5	186.4	190.3	177.8	161.8	224.5	207.6
MSMEG _1701	MSMEG 1697	purine nucleotide phosphorylase	2	21.7	22.2	21.5	22.9	30.9	27.6	25.2	34.0
MSMEG _1704	MSMEG 1700	sugar ABC transporter, periplasmic sugar-binding protein	4	182.6	187.8	167.8	145.6	1088.7	1093.9	1031.4	1076.1
MSMEG _1712	MSMEG 1708	periplasmic ribose-binding protein	1	1.3	5.4	2.8	6.0	19.7	16.2	13.6	12.5
MSMEG _1713	MSMEG 1709	L-ribulokinase (araB)	1	18.2	24.0	19.4	25.9	28.7	32.7	14.8	18.1
MSMEG _1734	MSMEG 1730	conserved hypothetical protein	4	91.4	56.6	83.0	85.8	115.1	56.7	83.6	92.8

MSMEG _1735	MSMEG 1731	alpha keto acid dehydrogenase complex, E3 component, lipoamide dehydr	3	322.8	312.1	297.1	266.7	429.5	440.2	397.0	433.2
MSMEG _1753	MSMEG 1750	MTA/SAH nucleosidase	1	88.2	91.6	58.7	55.2	91.7	94.7	84.7	80.4
MSMEG _1757	MSMEG 1754	lhr (lhr)	1	1.6	2.3	2.4	3.6	14.0	14.8	12.7	14.0
MSMEG _1760	MSMEG 1758	bII7251	1	71.8	76.3	43.5	57.6	136.0	134.6	95.7	116.8
MSMEG _1803	MSMEG 1801	rsbW (rsbW)	3	343.9	393.1	289.5	305.8	449.8	537.8	458.9	438.2
MSMEG _1807	MSMEG 1807	biotin carboxylase/biotin carboxyl carrier protein	31	27068.7	27292.5	25172.7	26657.6	32691.1	32943.1	31227.7	32493.4
MSMEG _1808	MSMEG 1808	Fe-S metabolism associated domain subfamily (sufE)	1	81.1	91.4	79.6	73.2	109.6	133.6	63.3	76.1
MSMEG _1809	MSMEG 1809	thiosulfate sulfurtransferase (cysA- 1)	12	2814.1	2713.0	1997.6	1840.6	2299.2	2149.3	1631.4	1572.7
MSMEG _1812	MSMEG 1811	conserved hypothetical protein	1	133.5	124.8	116.4	136.7	97.6	96.3	78.9	85.4
MSMEG _1813	MSMEG 1812	propionyl-CoA carboxylase, beta subunit (accD5)	12	4791.4	4857.2	4043.6	4160.0	5556.5	5490.3	4411.4	4577.8
MSMEG _1819	MSMEG 1818	phosphoribosylaminoimidazole carboxylase, ATPase subunit (purK)	2	207.2	159.5	109.7	119.0	132.2	131.1	249.3	244.7



MSMEG _1822	MSMEG 1821	biotin--acetyl-CoA-carboxylase ligase	1	29.8	30.2	25.0	22.6	38.8	39.1	30.2	35.1
MSMEG _1825	MSMEG 1824	dTDP-4-dehydrorhamnose reductase (rfbD)	1	121.3	119.6	135.5	130.5	57.3	60.6	109.2	105.7
MSMEG _1828	MSMEG 1826	rmlA2 (rmlA2)	2	208.0	166.8	122.9	95.5	80.0	87.2	74.8	76.4
MSMEG _1832	MSMEG 1831	conserved hypothetical protein	1	20.5	0.0	17.9	18.5	36.5	0.0	38.6	39.7
MSMEG _1834	MSMEG 1833	pmmA (pmmA)	1	10.9	9.4	5.8	5.4	5.3	5.6	5.0	4.6
MSMEG _1836	MSMEG 1835	mannose-6-phosphate isomerase, class I (manA)	1	139.3	142.2	105.6	97.9	105.8	131.8	90.7	94.0
MSMEG _1843	MSMEG 1842	adenosylhomocysteinase (ahcY)	11	3786.7	3450.0	5195.4	5273.6	3576.1	3349.7	3634.0	3976.3
MSMEG _1873	MSMEG 1876	Thymidylate kinase	1	65.8	68.7	42.4	48.7	117.0	119.7	65.4	89.7
MSMEG _1874	MSMEG 1877	DNA-binding response regulator MtrA (mtrA)	3	366.1	412.5	308.9	349.7	375.5	367.9	425.7	426.1
MSMEG _1878	MSMEG 1881	S30AE family protein	4	42.1	46.4	46.6	62.5	499.0	549.0	367.9	407.4
MSMEG _1881	MSMEG 1882	preprotein translocase, SecA subunit (secA)	18	2310.9	2296.2	2338.4	2344.1	2716.1	2848.1	2518.8	2194.3
MSMEG _1888	MSMEG 1890	Mycobacterium tuberculosis paralogous family	1	33.6	37.8	1.1	0.3	3.5	3.0	1.3	2.0

MSMEG _1890	MSMEG 1892	3-phosphoshikimate 1- carboxyvinyltransferase (aroA)	1	4.5	4.1	2.1	1.9	2.1	1.6	2.0	1.4
MSMEG _1903	MSMEG 1907	CAIB/BAIF family family	2	74.3	53.0	28.7	8.9	9.4	5.5	21.0	4.2
MSMEG _1913	MSMEG 1917	ybaK/ebcC protein	2	64.6	69.7	38.5	43.6	77.2	87.3	82.8	92.4
MSMEG _1914	MSMEG 1918	RNA polymerase sigma-70 factor, ECF subfamily	4	350.3	396.5	323.4	366.3	342.4	365.1	317.7	338.1
MSMEG _1926	MSMEG 1929	phosphoglycerate mutase family protein	1	40.8	32.4	37.5	22.7	65.7	68.7	65.8	71.2
MSMEG _1927	MSMEG 1930	Soj family protein (probable)	1	29.6	34.0	27.7	27.3	93.3	98.5	110.3	122.4
MSMEG _1934	MSMEG 1938	conserved hypothetical protein	1	168.1	190.8	138.3	153.1	254.9	261.5	250.7	246.8
MSMEG _1935	MSMEG 1939	transcriptional regulator, TetR family domain protein	1	100.5	117.8	74.2	97.9	116.3	128.4	62.9	97.4
MSMEG _1940	MSMEG 1944	hydrolase, alpha/beta hydrolase fold family	1	32.7	32.2	33.9	27.3	67.1	62.2	67.2	75.4
MSMEG _1951	MSMEG 1955	maebl, putative	2	9.1	12.7	31.4	37.8	141.9	151.7	136.8	151.5
MSMEG _1954	MSMEG 1958	ABC transporter, ATP-binding protein, putative	1	28.3	30.6	13.9	24.0	74.1	50.0	57.2	67.6
MSMEG _1959	MSMEG 1961	Uncharacterised protein family (UPF0182) superfamily	7	536.9	514.4	630.1	579.0	907.3	891.0	736.0	805.3

MSMEG _1979	MSMEG 1982	Uncharacterized ACR, YneC family COG1359 subfamily	1	17.6	35.0	10.4	16.2	161.0	320.5	94.6	138.8
MSMEG _1981	MSMEG 1984	conserved hypothetical protein	3	189.3	222.0	186.7	212.1	251.2	248.0	223.0	197.6
MSMEG _1996	MSMEG 1997	putative N5, N10- methylenetetrahydromethanopteri n reductase-related p	9	543.3	549.9	295.1	346.7	490.2	482.6	454.0	484.6
MSMEG _2010	MSMEG 2010	conserved hypothetical protein	2	107.7	106.8	138.1	130.1	143.0	147.5	206.2	184.0
MSMEG _2019	MSMEG 2018	oxidoreductase, short chain dehydrogenase/reductase family	1	10.9	9.8	3.1	6.2	19.8	25.7	14.2	17.1
MSMEG _2025	MSMEG 2027	transcriptional regulator, putative	1	19.1	20.4	16.1	20.2	28.2	28.7	19.8	23.0
MSMEG _2026	MSMEG 2028	oxidoreductase, short-chain dehydrogenase/reductase family	8	2269.2	2296.1	1669.3	1643.4	1233.8	1191.6	1297.9	1332.8
MSMEG _2027	MSMEG 2029	conserved hypothetical protein	2	101.9	108.0	47.2	53.0	114.0	127.0	119.9	114.8
MSMEG _2033	MSMEG 2034	fadB4 (fadB4)	3	476.4	472.1	383.4	354.7	651.5	726.3	492.8	491.2
MSMEG _2045	MSMEG 2046	xenobiotic compound monooxygenase, DszA family	2	150.1	117.8	132.1	113.7	141.4	103.2	440.4	498.4
MSMEG _2078	MSMEG 2080	esterase, putative, antigen 85-B	4	598.3	633.1	1515.3	1434.4	1126.8	1141.8	1322.3	1259.4

MSMEG _2079	MSMEG 2081	alcohol dehydrogenase, zinc- containing	1	206.3	214.9	101.6	125.3	116.3	110.2	74.6	83.3
MSMEG _2080	MSMEG 2082	fadE23 (fadE23)	1	49.1	40.6	31.9	32.2	150.5	150.3	106.6	136.5
MSMEG _2081	MSMEG 2083	fadE24 (fadE24)	4	343.0	355.6	316.4	322.2	611.2	673.4	814.6	784.8
MSMEG _2089	MSMEG 2090	ftsE (ftsE)	1	48.4	32.4	31.7	43.8	29.8	25.8	19.7	39.7
MSMEG _2090	MSMEG 2091	ftsE protein, putative	1	12.3	7.7	11.3	10.3	4.7	2.1	2.6	2.9
MSMEG _2092	MSMEG 2093	D-aminopeptidase putative	2	97.3	66.7	102.1	102.6	149.7	145.0	188.3	185.9
MSMEG _2111	MSMEG 2114	chorismate mutase, putative,	1	30.4	23.4	25.9	30.2	31.5	24.9	26.4	30.9
MSMEG _2112	MSMEG 2115	putative secreted protein	2	16.5	14.4	7.9	9.6	53.0	38.2	53.7	53.5
MSMEG _2116	MSMEG 2119	Phosphotransferase system IIC components, glucose/maltose/N- acetylglu	2	1.9	2.3	9.7	11.8	17.4	18.8	28.4	29.2
MSMEG _2117	MSMEG 2120	PTS system, IIBC components (EC2.7.1.69)	2	143.1	128.2	94.2	89.4	210.3	205.7	191.8	178.6
MSMEG _2118	MSMEG 2121	glucosamine-6-phosphate isomerase (nagB)	1	73.6	72.9	59.3	49.5	84.8	88.4	85.1	84.7
MSMEG _2136	MSMEG 2139	phosphoglucomutase, alpha-D- glucose phosphate-specific (pgm)	3	172.2	136.0	156.9	143.6	259.9	242.1	327.2	321.3

MSMEG _2155	MSMEG 2157	NADPH quinone oxidoreductase, putative	1	1.6	2.7	3.7	3.9	34.2	24.8	34.8	29.5
MSMEG _2171	MSMEG 2175	CAIB/BAIF family protein	1	0.2	0.3	0.1	0.2	5.0	5.0	0.9	1.5
MSMEG _2174	MSMEG 2178	COG3973:Superfamily I DNA and RNA helicases	3	215.8	186.7	138.4	139.3	59.0	56.9	68.4	56.3
MSMEG _2198	MSMEG 2203	HesA/MoeB/ThiF family protein (moeY)	7	519.2	542.7	495.6	506.0	1014.4	1028.5	1131.9	1105.2
MSMEG _2201	MSMEG 2206	MaoC family protein	8	1317.6	1419.7	1404.6	1549.8	1963.3	2081.8	1851.5	1895.6
MSMEG _2225	MSMEG 2230	transcriptional regulator, TetR family, putative	2	44.1	40.8	49.9	61.7	104.6	105.2	85.8	106.0
MSMEG _2263	MSMEG 2266	F420-nonreducing hydrogenase, putative	1	76.7	86.5	249.3	239.3	62.2	69.4	106.7	99.9
MSMEG _2271	MSMEG 2274	hydrogenase accessory protein HypB (hypB)	1	27.0	35.3	61.5	66.6	109.9	152.2	64.8	58.7
MSMEG _2280	MSMEG 2283	pyruvate dehydrogenase	5	145.9	137.8	228.0	170.0	415.9	396.6	297.4	293.4
MSMEG _2351	MSMEG 2350	electron transfer flavoprotein, beta subunit (etfB)	10	4118.4	4359.8	4330.1	4323.6	3104.9	3314.1	3660.5	3753.1
MSMEG _2352	MSMEG 2351	electron transfer flavoprotein, alpha subunit (etfA)	14	12624.2	13306.3	10985.1	11299.6	12476.7	12353.4	9224.6	9681.0
MSMEG _2362	MSMEG 2361	DNA ligase, NAD-dependent (ligA)	9	768.6	724.8	867.7	747.3	714.0	726.9	725.7	718.1

MSMEG _2365	MSMEG 2364	glutamyl-tRNA(Gln) amidotransferase subunit A (gatA)	4	597.2	593.8	375.5	374.0	527.2	594.3	798.0	804.8
MSMEG _2366	MSMEG 2365	Phosphofructokinase	1	62.0	66.7	36.5	38.8	466.1	504.4	335.6	387.0
MSMEG _2367	MSMEG 2366	glutamyl-tRNA(Gln) amidotransferase, B subunit (gatB)	4	555.1	509.5	547.9	486.6	330.4	306.0	476.6	390.4
MSMEG _2372	MSMEG 2371	acetolactate synthase, large subunit, biosynthetic type (ilvB)	2	104.6	93.6	113.7	86.6	47.9	37.8	68.2	58.5
MSMEG _2373	MSMEG 2372	acetolactate synthase, small subunit (ilvN)	5	190.3	170.7	173.0	170.4	34.0	27.5	19.1	22.0
MSMEG _2374	MSMEG 2373	ketol-acid reductoisomerase (ilvC)	16	4212.1	3415.9	4885.9	4546.4	3695.0	3132.8	4371.0	4339.8
MSMEG _2375	MSMEG 2374	tryptophan repressor binding protein (wrbA)	1	91.3	94.0	70.4	231.7	107.3	105.9	108.8	126.3
MSMEG _2378	MSMEG 2377	D-3-phosphoglycerate dehydrogenase (serA)	10	2109.1	1871.5	2164.8	2050.8	2845.0	2485.2	3189.9	2921.8
MSMEG _2379	MSMEG 2378	3-isopropylmalate dehydrogenase (leuB)	4	1340.9	1366.2	832.9	771.1	1041.3	1073.5	951.3	923.7
MSMEG _2382	MSMEG 2381	2-hydroxyhepta-2,4-diene-1,7- dioate isomerase/5-carboxymethyl- 2-oxo-h	4	344.4	363.5	315.3	345.2	365.9	374.8	314.7	413.8

MSMEG _2383	MSMEG 2382	glutamyl-tRNA synthetase (gltX)	5	630.7	597.5	676.1	604.2	697.7	688.6	954.8	893.6
MSMEG _2387	MSMEG 2386	3-isopropylmalate dehydratase, large subunit (IeuC)	1	98.0	132.2	55.9	50.8	108.9	129.7	84.0	89.2
MSMEG _2388	MSMEG 2387	3-isopropylmalate dehydratase, small subunit (IeuD)	8	3016.7	3233.8	2678.8	2776.0	2830.1	2929.8	2711.8	2885.2
MSMEG _2389	MSMEG 2388	histone-like protein	11	2725.2	2647.1	4589.1	4069.9	4321.5	4001.2	5727.8	5105.6
MSMEG _2391	MSMEG 2390	polyphosphate kinase (ppk)	13	1726.7	1741.3	1374.8	1385.3	2566.7	2584.8	2633.6	2637.9
MSMEG _2397	MSMEG 2396	transcriptional regulator, AsnC family, putative	1	28.9	28.5	11.9	12.9	31.5	38.9	39.3	29.4
MSMEG _2399	MSMEG 2398	uracil-DNA glycosylase (ung)	1	88.7	78.1	79.1	77.1	58.9	49.9	54.0	49.8
MSMEG _2407	MSMEG 2405	oxidoreductase, aldo/keto reductase family	8	876.4	795.4	914.7	960.0	663.9	573.2	654.2	679.5
MSMEG _2408	MSMEG 2406	oxidoreductase, aldo/keto reductase family	7	1580.9	1677.0	649.5	746.1	663.9	695.0	642.2	728.9
MSMEG _2410	MSMEG 2408	u0002a	4	311.4	351.0	255.6	308.7	199.3	214.7	171.2	219.5
MSMEG _2412	MSMEG 2410	pyruvate carboxylase (pyc)	42	4319.5	4219.8	3929.2	3870.8	7325.7	7347.2	6443.9	6230.5
MSMEG _2413	MSMEG 2411	methyltransferase, putative	1	22.0	26.8	14.1	13.2	27.7	32.7	19.5	21.6
MSMEG _2414	MSMEG 2412	pantetheine-phosphate adenylyltransferase (coaD)	3	275.4	278.8	233.8	231.9	400.7	417.4	355.7	345.7

MSMEG _2415	MSMEG 2413	conserved hypothetical protein	1	4.7	4.9	2.6	4.7	172.6	161.9	245.4	209.8
MSMEG _2418	MSMEG 2416	ribonuclease III (rnc)	3	115.2	121.9	85.4	79.3	214.6	238.1	213.4	244.4
MSMEG _2421	MSMEG 2420	conserved hypothetical protein	5	161.6	121.3	120.2	132.5	151.2	82.2	149.2	154.2
MSMEG _2423	MSMEG 2422	chromosome partition protein SMC, putative	1	15.4	15.9	14.6	16.0	19.1	19.4	19.2	18.3
MSMEG _2424	MSMEG 2423	signal recognition particle receptor FtsY (ftsY)	2	163.8	185.6	167.2	194.1	135.0	155.7	100.4	180.0
MSMEG _2426	MSMEG 2425	Nitrogen regulatory protein P-II	11	154.0	157.2	138.5	148.9	3182.0	3381.9	3861.3	3603.8
MSMEG _2427	MSMEG 2426	protein-P-II uridylyltransferase (glnD)	11	40.8	48.0	34.8	42.8	1558.7	1534.8	1792.5	1920.2
MSMEG _2435	MSMEG 2433	ribosomal protein S16 (rpsP)	9	4271.6	4436.9	5028.2	5536.0	3100.8	3221.2	3503.8	3678.0
MSMEG _2437	MSMEG 2435	16S rRNA processing protein RimM VC0562	1	10.3	11.9	10.7	13.5	17.0	17.9	12.9	12.4
MSMEG _2440	MSMEG 2438	50S ribosomal protein L19 (rplS)	4	1147.6	1328.3	1401.8	1302.4	605.7	688.5	609.8	532.7
MSMEG _2443	MSMEG 2441	conserved hypothetical protein	4	123.0	136.6	124.0	125.0	116.2	124.9	114.5	99.8
MSMEG _2450	MSMEG 2446	4-aminobutyrate aminotransferase (goaG)	1	23.2	19.8	26.3	23.8	2.2	2.6	1.5	1.8
MSMEG _2468	MSMEG 2467	CAIB/BAIF family protein, putative	1	11.8	12.0	8.6	10.3	7.6	9.0	3.8	5.8



MSMEG _2511	MSMEG 2512	siderophore utilization protein (viuB)	2	391.6	424.7	260.8	283.5	166.7	177.0	146.5	150.9
MSMEG _2516	MSMEG 2520	Luciferase-like monooxygenase superfamily	4	322.7	340.3	145.5	150.1	195.7	220.3	206.5	204.4
MSMEG _2519	MSMEG 2522	ribosomal protein S2 (rpsB)	6	1155.7	1087.1	847.1	823.2	997.7	1128.8	508.4	615.2
MSMEG _2524	MSMEG 2527	ABC transporter, ATP-binding protein homolog	3	3.1	3.2	4.2	3.5	160.4	174.4	203.4	196.4
MSMEG _2525	MSMEG 2528	amino acid permease family protein, putative	1	25.9	33.8	20.5	27.6	472.9	452.2	483.0	466.9
MSMEG _2526	MSMEG 2529	amine oxidase	20	292.3	288.9	277.0	240.8	3106.7	2945.1	3605.6	3377.1
MSMEG _2528	MSMEG 2531	glycerate kinase	3	280.0	250.6	158.9	144.4	728.3	668.7	535.2	527.4
MSMEG _2540	MSMEG 2543	uridylate kinase	3	210.0	213.2	195.2	194.4	254.9	268.7	198.3	197.1
MSMEG _2541	MSMEG 2544	ribosome recycling factor (frr)	3	65.6	70.6	86.6	82.6	170.4	146.0	181.3	188.5
MSMEG _2553	MSMEG 2555	transcriptional regulator, TetR family domain protein	1	10.2	10.1	6.2	6.7	9.4	11.7	3.4	5.7
MSMEG _2580	MSMEG 2581	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (ispG)	3	551.0	539.9	366.6	393.2	421.3	452.4	331.8	375.4
MSMEG _2587	MSMEG 2588	methionine aminopeptidase, type I (map)	1	36.4	37.8	13.0	23.4	5.7	6.4	4.8	5.2

MSMEG _2594	MSMEG 2595	asparagine synthase (glutamine- hydrolyzing)	3	345.5	346.8	304.0	343.6	47.0	55.4	25.8	24.3
MSMEG _2598	MSMEG 2599	oxidoreductase, short-chain dehydrogenase/reductase family	2	86.0	87.0	113.8	138.1	358.1	370.6	322.2	376.2
MSMEG _2606	MSMEG 2607	transcriptional regulator, ArsR family (smtB)	1	8.1	9.6	11.2	9.8	26.4	22.0	21.5	21.3
MSMEG _2613	MSMEG 2614	malate:quinone-oxidoreductase (mqo)	5	408.6	425.5	567.0	501.5	238.8	222.0	284.0	254.2
MSMEG _2616	MSMEG 2617	cob(I)alamin adenosyltransferase (cobO)	1	37.7	37.0	39.1	34.9	54.0	52.0	49.8	54.7
MSMEG _2621	MSMEG 2622	prolyl-tRNA synthetase (proS)	19	2122.7	2107.7	1843.7	1719.9	2535.0	2552.4	2656.2	2769.3
MSMEG _2628	MSMEG 2627	translation initiation factor IF-2 (infB)	20	2250.1	2134.9	2007.8	1826.5	1879.2	1774.3	1827.8	1753.5
MSMEG _2641	MSMEG 2640	EchA16_2 (fad)	4	686.3	711.9	466.1	484.5	470.3	471.9	523.8	526.3
MSMEG _2653	MSMEG 2652	riboflavin biosynthesis protein RibF (ribF)	1	13.6	13.2	12.5	17.5	15.5	15.6	10.9	10.8
MSMEG _2654	MSMEG 2653	ribosomal protein S15 (rpsO)	8	2556.8	2424.1	2763.4	2779.7	1155.4	1117.5	1333.8	1316.9
MSMEG _2656	MSMEG 2655	polyribonucleotide nucleotidyltransferase VC0647	32	8207.5	7959.7	7920.5	7377.8	6056.4	5841.6	7674.9	7217.5
MSMEG _2658	MSMEG 2657	beta-lactamase	3	106.8	120.1	57.5	83.5	23.0	31.2	22.7	34.3

MSMEG _2664	MSMEG 2662	dihydrodipicolinate reductase (dapB)	2	87.9	87.5	81.2	79.9	87.5	87.1	103.1	98.0
MSMEG _2667	MSMEG 2666	conserved hypothetical protein	4	292.2	273.4	160.4	150.8	495.0	535.5	380.1	422.0
MSMEG _2669	MSMEG 2667	dienelactone hydrolase family protein	5	1576.9	1515.3	362.9	413.8	583.8	545.5	521.7	587.2
MSMEG _2671	MSMEG 2669	dihydrofolate reductase (folA)	1	37.5	38.5	21.7	26.4	62.0	58.4	51.6	64.4
MSMEG _2684	MSMEG 2682	dihydrodipicolinate synthase (dapA)	3	208.2	217.3	243.0	232.9	1135.4	1233.4	1438.1	1440.4
MSMEG _2688	MSMEG 2686	Uncharacterized ACR, YneC family COG1359 subfamily	1	58.5	57.4	23.2	29.7	26.0	25.7	22.7	29.1
MSMEG _2698	MSMEG 2697	conserved hypothetical protein	4	238.3	228.5	203.2	207.6	215.2	206.3	180.9	166.6
MSMEG _2723	MSMEG 2725	recA protein (recA)	1	16.0	8.4	2.5	2.6	2.7	0.5	0.2	0.4
MSMEG _2727	MSMEG 2729	glnH, putative	11	1208.2	1278.3	2126.9	2148.0	5105.6	5717.8	4873.5	5160.4
MSMEG _2731	MSMEG 2734	Domain of Unknown Function (DUF349) family	5	1045.3	1189.9	1033.2	1035.5	806.8	981.5	716.2	815.8
MSMEG _2739	MSMEG 2742	conserved hypothetical protein	2	42.5	43.4	56.3	61.7	109.2	101.6	99.4	97.8
MSMEG _2740	MSMEG 2743	LexA repressor (lexA)	1	14.6	12.3	17.3	16.2	52.8	27.4	19.6	21.6

MSMEG _2743	MSMEG 2745	conserved hypothetical protein TIGR00244	1	25.9	24.5	21.2	24.1	35.6	32.1	35.2	27.7
MSMEG _2744	MSMEG 2746	phenazine biosynthesis protein, PhzF family, putative	3	315.2	333.2	230.2	219.2	310.6	320.5	364.6	389.5
MSMEG _2750	MSMEG 2753	siderophore biosynthesis iron binding repressor (dtxR)	1	79.6	85.3	110.7	93.5	171.7	184.0	248.6	239.9
MSMEG _2758	MSMEG 2759	RNA polymerase sigma factor MysA (mysA)	9	810.8	781.6	735.7	659.2	585.5	531.8	526.8	472.8
MSMEG _2760	MSMEG 2760	polyphosphate glucokinase	3	130.4	148.1	180.6	194.0	474.5	500.5	506.2	551.0
MSMEG _2762	MSMEG 2761	inositol monophosphatase family protein (suhB)	8	486.6	489.1	440.9	450.9	443.7	449.2	516.7	569.9
MSMEG _2763	MSMEG 2763	conserved hypothetical protein	1	21.2	22.3	35.8	38.2	18.4	19.2	18.4	17.4
MSMEG _2765	MSMEG 2764	deoxyuridine 5-triphosphate nucleotidohydrolase (dut)	2	326.2	336.2	268.4	284.4	223.6	269.3	216.9	247.8
MSMEG _2766	MSMEG 2765	hypothetical protein	3	185.5	265.0	124.7	175.9	231.1	341.0	160.2	236.7
MSMEG _2769	MSMEG 2769	ceoB protein (trkA)	1	21.1	25.2	13.6	17.9	23.3	27.2	15.0	23.1
MSMEG _2771	MSMEG 2770	ceoB protein	1	93.6	96.7	95.0	110.8	273.2	285.4	189.3	237.6

MSMEG _2776	MSMEG 2775	1-deoxy-D-xylulose-5-phosphate synthase (dxs)	1	12.4	14.1	13.0	9.1	1.2	1.0	2.8	2.6
MSMEG _2780	MSMEG 2780	uroporphyrinogen decarboxylase (hemE)	1	50.0	54.4	16.2	24.8	51.1	44.7	85.2	88.5
MSMEG _2782	MSMEG 2782	conserved hypothetical protein	4	368.5	347.7	190.8	187.3	150.3	143.6	130.4	127.8
MSMEG _2784	MSMEG 2785	methionine-R-sulfoxide reductase (msrB)	2	28.0	18.8	33.8	38.6	49.5	38.4	59.7	55.4
MSMEG _2787	MSMEG 2788	RibD C-terminal domain	1	54.6	61.5	49.4	55.4	62.9	58.4	72.3	73.7
MSMEG _2788	MSMEG 2789	AFG1-like ATPase superfamily	1	44.0	54.5	40.4	50.8	149.5	157.3	136.7	127.6
MSMEG _2789	MSMEG 2790	acetyltransferase, GNAT family	1	16.4	0.0	7.6	8.6	12.0	0.0	9.0	14.1
MSMEG _2800	MSMEG 2802	NADH-dependent FMN reductase, putative	1	90.8	98.0	82.3	103.0	101.0	112.8	108.8	116.5
MSMEG _2839	MSMEG 2841	Predicted RNA binding protein, contains S1 domain	12	762.0	746.6	894.0	938.3	580.1	638.8	422.2	562.0
MSMEG _2897	MSMEG 2903	conserved hypothetical protein	2	19.0	20.6	13.5	11.5	15.0	17.5	22.2	19.3
MSMEG _2900	MSMEG 2908	hydrolase, alpha/beta fold family domain protein	1	17.6	14.0	16.0	14.0	11.4	13.0	3.4	3.8
MSMEG _2931	MSMEG 2941	threonyl-tRNA synthetase (thrS)	8	887.3	871.5	714.4	695.6	874.2	883.8	968.5	952.0

MSMEG _2940	MSMEG 2951	conserved hypothetical protein TIGR01033	2	381.9	374.3	319.7	331.6	141.1	126.5	75.3	93.6
MSMEG _2941	MSMEG 2952	conserved hypothetical protein	2	132.7	150.7	117.9	123.5	160.2	191.5	192.1	197.1
MSMEG _2942	MSMEG 2953	glyoxalase family protein superfamily	1	27.4	0.0	16.6	14.8	152.3	0.0	156.3	137.4
MSMEG _2956	MSMEG 2165	substrate--CoA ligase, putative	19	965.0	908.2	80.7	97.1	751.6	695.9	641.0	563.7
MSMEG _2960	MSMEG 2972	Preprotein translocase subunit, putative	3	170.9	225.2	125.0	168.4	155.4	205.9	106.2	152.8
MSMEG _2961	MSMEG 2973	protein-export membrane protein SecD (secD)	1	96.4	122.5	105.4	123.2	63.0	83.1	65.6	75.4
MSMEG _2964	MSMEG 2976	adenine phosphoribosyltransferase	3	55.1	44.3	26.3	27.3	21.4	20.6	13.6	15.1
MSMEG _2974	MSMEG 2987	peptidyl-prolyl cis-trans isomerase, cyclophilin-type	1	144.6	195.2	110.1	112.6	140.2	218.1	94.5	102.9
MSMEG _2975	MSMEG 2988	1 histidyl-tRNA synthetase (hisS)	3	354.7	354.6	267.3	255.5	312.5	297.4	379.7	381.8
MSMEG _2978	MSMEG 2990	branched-chain amino acid ABC transporter, ATP-binding protein (livF)	1	0.1	0.0	0.0	0.0	26.6	30.3	8.9	19.5
MSMEG _2982	MSMEG 2994	urea/short-chain amide ABC transporter, periplasmic urea/short-chain	9	438.1	524.3	313.2	348.1	3646.3	3677.7	3843.3	3937.1

MSMEG _2983	MSMEG 2995	conserved hypothetical protein	1	16.9	18.9	17.0	17.4	7.8	8.4	12.3	8.5
MSMEG _3003	MSMEG 3017	aspartyl-tRNA synthetase (aspS)	7	1626.8	1681.4	1147.2	1208.5	2360.2	2240.0	1571.5	1824.2
MSMEG _3004	MSMEG 3018	conserved hypothetical protein	1	22.5	24.9	12.5	16.2	13.1	14.8	7.0	8.8
MSMEG _3013	MSMEG 3027	Transcriptional regulator family	1	10.5	10.6	5.0	9.5	6.9	9.0	9.9	9.7
MSMEG _3016	MSMEG 3030	transglutaminase family protein	11	42.1	41.4	54.1	61.2	265.8	241.6	241.7	250.1
MSMEG _3019	MSMEG 3033	conserved hypothetical protein	1	26.4	31.5	24.1	22.4	62.3	67.7	59.1	54.9
MSMEG _3025	MSMEG 3039	alanyl-tRNA synthetase (alaS)	16	2115.6	2189.7	2480.7	2522.1	1221.1	1280.1	1284.6	1365.9
MSMEG _3026	MSMEG 3040	DNA integration/recombination/invertio n protein	1	9.3	8.7	7.0	6.3	19.7	18.9	14.7	18.4
MSMEG _3033	MSMEG 3046	3-dehydroquinate synthase (aroB)	2	161.9	160.0	104.9	116.5	242.1	285.7	161.4	169.8
MSMEG _3035	MSMEG 3049	translation elongation factor P (efp)	1	204.7	223.0	181.7	201.2	179.4	185.6	149.5	172.0
MSMEG _3045	MSMEG 3059	conserved hypothetical protein	1	18.3	18.2	20.0	31.5	25.7	26.2	11.9	19.5
MSMEG _3046	MSMEG 3060	carbamoyl-phosphate synthase, small subunit (carA)	2	453.0	547.8	392.3	493.9	327.8	354.6	324.3	349.4

MSMEG _3047	MSMEG 3061	carbamoyl-phosphate synthase, large subunit (carB)	34	1735.4	1694.8	1356.1	1368.6	2569.5	2452.5	2343.8	2287.9
MSMEG _3050	MSMEG 3063	integration host factor (mIHF)	4	684.6	708.2	771.6	757.7	588.4	607.5	690.5	644.0
MSMEG _3054	MSMEG 3065	phosphopantothenoylcysteine decarboxylase/phosphopantothen ate--cystei	1	75.3	76.7	65.4	69.1	107.1	82.4	94.4	113.3
MSMEG _3055	MSMEG 3066	S-adenosylmethionine synthetase (metK)	22	15934.0	14837.9	12951.0	11986.5	8464.1	8083.1	9320.3	8848.9
MSMEG _3058	MSMEG 3069	D-methionine-binding lipoprotein MetQ	4	186.8	192.4	595.0	541.1	279.4	281.2	268.2	255.1
MSMEG _3066	MSMEG 3077	ribulose-phosphate 3-epimerase (rpe)	1	76.2	78.3	66.1	66.3	112.7	120.0	104.9	114.6
MSMEG _3070	MSMEG 3080	lipoprotein, 27 kDa	4	723.2	733.9	484.6	497.3	787.2	769.2	682.8	651.2
MSMEG _3071	MSMEG 3081	riboflavin synthase, alpha subunit (ribE)	3	125.4	115.2	101.6	94.4	92.1	71.0	57.0	60.2
MSMEG _3072	MSMEG 3082	3,4-dihydrox	5	472.6	462.6	420.5	425.5	221.1	263.6	196.8	245.2
MSMEG _3073	MSMEG 3083	6,7-dimethyl-8-ribityllumazine synthase (ribE)	6	614.3	644.5	405.5	449.5	756.3	784.0	633.5	660.4
MSMEG _3081	MSMEG 3090	Uncharacterized BCR, COG1481	2	216.5	213.5	117.8	115.3	316.8	403.0	199.3	200.8
MSMEG _3084	MSMEG 3093	glyceraldehyde-3-phosphate dehydrogenase, type I (gap)	20	23839.1	23167.3	17589.7	18172.6	30114.8	28999.0	26785.4	27859.8



MSMEG _3085	MSMEG 3094	phosphoglycerate kinase (pgk)	17	7334.3	7169.7	6312.7	6158.5	7285.9	7090.7	7836.6	7385.0
MSMEG _3086	MSMEG 3095	triosephosphate isomerase (tpiA)	14	2053.3	2140.4	2092.5	2038.8	2594.7	2613.9	2678.3	2592.3
MSMEG _3097	MSMEG 3107	phosphoenolpyruvate carboxylase (ppc)	7	325.4	349.2	300.2	380.8	534.4	513.1	639.2	622.1
MSMEG _3099	MSMEG 3109	6-phosphogluconolactonase (pgl)	3	308.3	283.2	257.9	257.7	1203.9	1182.3	1358.1	1333.7
MSMEG _3100	MSMEG 3110	opcA protein (opcA)	1	126.3	137.6	66.8	81.2	214.9	209.4	78.9	101.4
MSMEG _3101	MSMEG 3111	glucose-6-phosphate 1-dehydrogenase (zwf)	3	207.8	186.7	212.6	204.2	152.7	175.5	159.3	176.7
MSMEG _3102	MSMEG 3112	transaldolase (tal)	11	4289.7	4076.3	4154.3	3744.0	2872.4	2764.4	3089.9	2850.9
MSMEG _3103	MSMEG 3113	transketolase (tkt)	35	11537.0	11624.4	9263.4	9301.0	11329.9	11298.6	10124.2	10212.8
MSMEG _3106	MSMEG 3115	quinone oxidoreductase CC3759	7	2993.3	2911.5	1338.9	1384.7	3030.7	2897.0	2177.0	2258.1
MSMEG _3122	MSMEG 3131	Pps1 sans inteine	1	68.2	58.0	51.6	61.3	6.1	2.6	5.0	4.7
MSMEG _3124	MSMEG 3133	MW07	3	301.6	293.7	368.0	335.5	170.1	195.2	226.7	230.9
MSMEG _3127	MSMEG 3136	mrp protein homolog	2	60.8	59.5	64.3	65.7	37.8	34.7	42.7	45.5
MSMEG _3142	MSMEG 3149	transcriptional regulator, TetR family domain protein	1	14.2	13.0	5.3	3.7	14.6	16.2	17.1	15.3
MSMEG _3143	MSMEG 3151	acn (acn)	20	9235.6	10268.2	4569.6	4720.7	4895.7	5198.7	4810.3	4951.8
MSMEG _3147	MSMEG 3155	ATPase, MoxR family (moxR)	4	1468.7	1282.4	1173.9	1066.1	1265.4	1088.9	1384.7	1361.0

MSMEG _3150	MSMEG 3158	hypothetical protein	6	1907.2	1980.4	1893.1	1764.7	1930.0	1917.9	1869.2	1771.3
MSMEG _3151	MSMEG 3159	enoyl-(acyl-carrier-protein) reductase (NADH)	7	1865.1	1864.3	2213.9	2049.5	1452.6	1487.2	1861.7	1674.8
MSMEG _3155	MSMEG 3163	Membrane protease subunits, stomatin/prohibitin homologs	2	75.8	64.3	99.3	94.9	192.4	230.9	157.1	145.7
MSMEG _3158	MSMEG 3166	methylmalonyl-CoA mutase, small subunit (mutA)	7	342.7	354.8	842.8	764.9	959.6	833.6	752.1	711.4
MSMEG _3159	MSMEG 3167	Methylmalonyl-CoA mutase, N- terminal domain/subunit (mutA)	18	1513.7	1663.6	2696.4	2775.3	2870.4	2935.1	2349.7	2411.6
MSMEG _3160	MSMEG 3168	LAO/AO transport system ATPase	1	3.8	3.3	5.4	4.4	1.6	2.4	2.7	1.8
MSMEG _3169	MSMEG 3176	isoleucyl-tRNA synthetase (ileS)	15	605.9	642.9	540.6	574.8	534.1	580.8	430.7	517.4
MSMEG _3178	MSMEG 3185	DNA polymerase III, alpha subunit (dnaE)	3	46.5	44.1	32.9	36.8	44.7	42.1	72.9	66.5
MSMEG _3183	MSMEG 3190	threonine dehydratase, biosynthetic (ilvA)	2	303.5	286.3	218.1	250.4	264.8	288.3	173.3	243.5
MSMEG _3185	MSMEG 3193	glycosyl hydrolase, family 13 (treY)	2	32.3	39.2	32.3	21.9	18.5	22.3	32.0	20.6
MSMEG _3204	MSMEG 3214	conserved hypothetical protein	3	11.2	13.5	7.6	11.6	32.0	31.2	25.9	33.9

MSMEG _3205	MSMEG 3215	histidinol dehydrogenase (hisD)	1	40.8	33.9	53.1	41.8	30.6	28.2	57.2	48.0
MSMEG _3208	MSMEG 3218	imidazole glycerol phosphate synthase, glutamine amidotransferase sub	1	28.4	38.9	18.6	21.0	39.2	30.0	44.1	45.5
MSMEG _3209	MSMEG 3219	bifunctional HisA/TrpF protein	6	455.6	488.8	457.0	468.3	314.1	339.8	304.5	346.7
MSMEG _3210	MSMEG 3220	inositol monophosphatase family protein	1	14.0	15.0	8.4	9.3	24.0	33.1	20.1	30.9
MSMEG _3211	MSMEG 3221	imidazoleglycerol phosphate synthase, cyclase subunit (hisF)	1	9.8	9.4	8.4	11.5	8.8	10.6	7.9	11.7
MSMEG _3215	MSMEG 3225	ABC transporter, ATP-binding protein	2	392.2	416.4	178.8	186.9	161.4	175.4	222.2	206.9
MSMEG _3219	MSMEG 3229	indole-3-glycerol phosphate synthase (trpC)	5	386.5	422.3	504.7	504.9	51.0	64.8	49.1	68.3
MSMEG _3220	MSMEG 3230	tryptophan synthase, beta subunit (trpB)	3	55.4	53.4	40.2	54.7	138.0	145.0	182.2	195.2
MSMEG _3221	MSMEG 3231	tryptophan synthase, alpha subunit (trpA)	1	122.8	110.8	116.6	112.3	156.8	139.5	177.2	166.6
MSMEG _3222	MSMEG 3232	lgt (lgt)	3	46.6	44.3	28.3	31.9	46.5	50.7	25.7	38.4
MSMEG _3225	MSMEG 3235	glutamate synthase, large subunit	18	376.9	394.1	183.9	210.8	925.7	912.5	1245.7	1161.2

MSMEG _3227	MSMEG 3237	pyruvate kinase (pyk)	15	4777.7	4707.9	5243.4	5369.9	7627.2	7824.2	8471.8	8030.5
MSMEG _3234	MSMEG 3244	conserved hypothetical protein	1	2.8	3.2	3.6	4.6	13.5	14.6	14.8	13.2
MSMEG _3235	MSMEG 3245	glutamine ABC transporter, periplasmic glutamine-binding protein (gln	8	3004.0	3192.6	3888.8	4046.4	4849.7	5000.7	4213.8	4387.4
MSMEG _3244	MSMEG 3254	hypothetical protein	1	17.8	21.4	21.6	39.7	64.4	61.4	60.3	47.2
MSMEG _3246	MSMEG 3257	response regulator	6	496.2	523.0	462.9	431.1	809.4	872.6	750.2	788.7
MSMEG _3247	MSMEG 3258	branched-chain amino acid ABC transporter, periplasmic amino acid-bin	14	2999.8	2998.5	5766.5	5820.5	7886.7	8031.3	9444.4	9871.1
MSMEG _3253	MSMEG 3264	conserved hypothetical protein	5	666.1	738.6	611.2	659.8	990.1	1029.6	965.4	1017.7
MSMEG _3255	MSMEG 3266	Tat (twin-arginine translocation) pathway signal sequence domain prot	2	122.3	148.6	71.5	72.7	357.0	381.3	318.0	351.3
MSMEG _3257	MSMEG 3269	xylulokinase (xylB)	3	740.3	740.2	544.5	582.1	486.0	537.9	383.0	438.0
MSMEG _3278	MSMEG 3290	hypothetical protein	3	54.2	54.5	60.1	58.2	80.0	80.8	71.6	71.7
MSMEG _3280	MSMEG 3293	Bacterial extracellular solute- binding protein domain protein	4	170.3	162.7	193.5	204.4	487.7	493.8	277.5	368.1

MSMEG _3284	MSMEG 3296	transcriptional regulator, MarR family family	1	19.7	23.2	12.9	16.2	50.7	61.6	38.9	53.0
MSMEG _3287	MSMEG 3299	ephB (ephA)	2	82.5	90.7	112.1	129.3	90.4	103.4	79.8	101.1
MSMEG _3309	MSMEG 3318	pyridoxal-phosphate dependent TrpB-like enzyme	1	232.7	176.4	158.6	221.6	116.4	77.3	158.3	223.6
MSMEG _3379	MSMEG 3385	oxidoreductase, short chain dehydrogenase/reductase family	1	30.5	32.5	20.7	20.3	33.7	33.2	21.3	25.3
MSMEG _3380	MSMEG 3387	conserved hypothetical protein	1	163.2	180.8	114.3	131.9	144.1	149.0	234.2	219.2
MSMEG _3381	MSMEG 3388	acyl carrier protein phosphodiesterase	1	175.1	182.1	117.0	126.9	214.8	216.9	269.6	281.0
MSMEG _3394	MSMEG 3400	cupin domain protein	1	11.7	9.4	13.8	17.8	3.3	4.9	1.6	3.6
MSMEG _3434	MSMEG 3442	putative FK-506 binding protein, peptidyl-prolyl cis-trans isomerase	1	91.1	85.6	109.5	114.2	36.5	45.9	74.4	82.8
MSMEG _3461	MSMEG 3467	catalase/peroxidase HPI (katG)	23	2658.2	2565.4	2620.8	2810.2	6105.1	5786.4	6293.2	6306.4
MSMEG _3465	MSMEG 3471	acyl-CoA synthase (fadD28)	1	1623.0	1669.7	978.8	993.6	92.2	71.0	55.5	65.0
MSMEG _3478	MSMEG 3483	transcriptional regulator, putative	4	176.2	162.1	133.9	127.5	145.0	147.7	127.8	134.2
MSMEG _3479	MSMEG 3484	thiol peroxidase (tpx)	13	3661.3	4011.8	5089.5	5512.1	4580.6	5057.5	5365.7	5285.5

MSMEG _3489	MSMEG 3494	GDSL-like Lipase/Acylhydrolase, putative	2	23.5	5.2	22.3	24.8	181.5	6.8	160.1	148.7
MSMEG _3500	MSMEG 3504	Uncharacterized BCR	2	12.3	10.2	22.4	23.5	6.0	7.2	9.5	11.4
MSMEG _3505	MSMEG 3509	6-aminohexanoate-cyclic-dimer hydrolase (nylA)	1	210.2	202.9	74.4	80.4	247.8	255.1	171.9	175.2
MSMEG _3507	MSMEG 3511	Fructose-bisphosphate aldolase class-I	14	4026.5	4267.4	4766.6	4753.6	4723.7	4877.0	3205.0	3202.2
MSMEG _3512	MSMEG 3516	competence/damage-inducible protein CinA	1	93.9	86.8	121.9	79.4	98.9	85.5	133.3	110.6
MSMEG _3515	MSMEG 3518	oxidoreductase, short-chain dehydrogenase/reductase family (fabG3)	1	57.1	67.0	40.9	56.2	43.7	60.5	41.7	44.9
MSMEG _3564	MSMEG 3564	bacterioferritin (bfr)	11	837.2	894.7	1822.0	1890.7	4388.5	4579.8	4337.3	4209.4
MSMEG _3569	MSMEG 3569	conserved hypothetical protein	1	11.9	11.6	6.8	6.8	4.4	3.4	4.9	6.1
MSMEG _3574	MSMEG 3574	TPR Domain domain protein	2	159.9	159.8	183.8	174.0	104.5	108.8	108.5	110.4
MSMEG _3575	MSMEG 3576	yfhC protein VC0864	1	71.1	74.8	74.6	64.4	90.3	94.1	95.5	92.4
MSMEG _3580	MSMEG 3581	esterase, putative, antigen 85-C	3	473.7	441.2	300.8	291.0	35.5	30.0	29.1	34.1
MSMEG _3595	MSMEG 3599	hypothetical protein	1	12.0	7.9	7.2	8.9	9.4	5.3	9.2	10.2
MSMEG _3596	MSMEG 3600	hypothetical protein	4	46.1	49.1	32.8	39.9	56.5	62.0	50.3	56.4

MSMEG _3598	MSMEG 3602	sugar-binding transcriptional regulator, LacI family	1	110.4	96.2	147.3	130.4	173.8	176.1	167.4	157.8
MSMEG _3609	MSMEG 3614	Luciferase-like monooxygenase superfamily	1	27.6	29.3	28.9	26.5	41.3	41.0	79.9	88.4
MSMEG _3618	MSMEG 3624	hypothetical protein	2	1119.4	1096.9	724.9	784.7	1308.8	1337.4	1018.8	1240.4
MSMEG _3619	MSMEG 3625	oxidoreductase, short chain dehydrogenase/reductase family superfamil	2	324.6	331.0	260.0	283.8	90.0	102.9	127.6	127.2
MSMEG _3620	MSMEG 3626	Luciferase-like monooxygenase superfamily	8	1946.8	2043.9	989.8	1037.0	1326.0	1458.7	796.8	914.8
MSMEG _3621	MSMEG 3627	NADH dehydrogenase (ndh)	2	47.0	46.3	57.2	58.0	38.7	36.9	44.7	55.5
MSMEG _3623	MSMEG 3628	urease accessory protein UreG (ureG)	1	223.3	239.4	391.1	310.8	328.9	344.4	434.5	418.4
MSMEG _3625	MSMEG 3631	urease, alpha subunit (ureC)	6	376.1	349.0	257.4	272.7	713.0	724.1	380.7	368.4
MSMEG _3627	MSMEG 3633	urease, gamma subunit (ureA)	1	4.2	5.5	8.6	7.5	10.1	9.3	16.9	16.5
MSMEG _3628	MSMEG 3634	ComA2 protein, putative	2	117.6	114.2	89.3	100.2	89.5	79.0	80.8	85.8
MSMEG _3632	MSMEG 3638	6-phosphogluconate dehydrogenase, decarboxylating (gnd)	10	2145.9	2026.0	2447.9	2157.4	3292.2	3321.0	3472.3	3193.0

MSMEG _3634	MSMEG 3639	IMP dehydrogenase family protein	5	690.5	634.4	511.4	481.8	473.7	477.6	652.2	579.6
MSMEG _3640	MSMEG 3646	malate synthase G (glcB)	19	5180.1	5406.0	3809.9	3688.9	2737.0	2702.0	2926.6	2744.0
MSMEG _3642	MSMEG 3648	glycine dehydrogenase (gcvP)	17	2286.0	2194.4	4507.4	4192.3	2241.2	2157.4	2501.3	2362.9
MSMEG _3647	MSMEG 3653	FHA-domain-containing proteins	4	886.3	960.7	741.0	760.1	1178.4	1183.2	1358.1	1386.7
MSMEG _3648	MSMEG 3654	glycine cleavage system H protein (gcvH)	2	752.1	878.4	674.3	748.9	913.8	1024.4	861.4	870.6
MSMEG _3654	MSMEG 3660	preprotein translocase, SecA subunit (ATPase,RNAhelic)	7	423.3	414.9	383.5	391.4	501.6	489.6	606.1	626.2
MSMEG _3673	MSMEG 3679	4-alpha-glucanotransferase (malQ)	1	16.1	20.8	26.9	20.0	47.0	56.6	50.7	49.2
MSMEG _3710	MSMEG 3716	cytochrome b561, putative	1	14.1	0.0	0.9	2.1	4.2	0.0	1.1	1.4
MSMEG _3715	MSMEG 3722	non-ribosomal peptide synthetase	1	29.7	29.2	21.4	22.6	64.0	69.8	49.4	50.5
MSMEG _3740	MSMEG 3746	ribosomal large subunit pseudouridine synthase B (rluB)	2	130.7	147.7	158.9	154.3	164.2	171.5	165.4	176.6
MSMEG _3745	MSMEG 3751	MutT/nudix family protein	1	66.4	73.5	35.7	23.7	47.1	54.0	27.5	6.0
MSMEG _3746	MSMEG 3752	CTP synthase (pyrG)	10	648.7	655.5	769.9	717.6	2225.1	2219.2	2263.1	2098.2



MSMEG _3754	MSMEG 3760	conserved hypothetical protein	1	60.5	61.5	41.6	51.3	55.1	42.9	20.5	29.3
MSMEG _3758	MSMEG 3764	tyrosyl-tRNA synthetase (tyrS)	2	76.2	85.3	62.9	60.4	143.8	143.4	194.6	181.5
MSMEG _3767	MSMEG 3773	poly-beta-hydroxybutyrate polymerase/very long chain acyl- CoA dehydro	6	127.3	144.4	98.8	116.3	275.0	281.8	240.3	257.0
MSMEG _3770	MSMEG 3776	argininosuccinate synthase (argG)	7	3020.4	3092.0	2663.7	2729.4	886.2	985.2	942.1	993.0
MSMEG _3773	MSMEG 3779	acetylornithine aminotransferase	1	35.9	18.2	27.2	31.7	12.2	10.9	21.4	27.5
MSMEG _3775	MSMEG 3781	arginine biosynthesis bifunctional protein ArgJ (argJ)	4	588.4	699.7	552.9	585.4	318.8	345.3	301.4	324.7
MSMEG _3776	MSMEG 3782	N-acetyl-gamma-glutamyl- phosphate reductase (argC)	1	19.0	20.7	8.9	6.2	86.1	96.1	62.6	111.9
MSMEG _3777	MSMEG 3783	phenylalanyl-tRNA synthetase, beta subunit (pheT)	14	2247.7	2347.4	2516.4	2437.9	2043.8	2170.3	2480.6	2559.6
MSMEG _3778	MSMEG 3784	phenylalanyl-tRNA synthetase, alpha subunit (pheS)	1	33.4	36.9	22.2	28.4	18.2	21.0	25.5	8.1
MSMEG _3791	MSMEG 3797	ribosomal protein L20 (rpIT)	5	902.3	884.8	807.2	917.3	595.9	576.3	556.6	583.0
MSMEG _3793	MSMEG 3799	translation initiation factor IF-3 (infC)	4	852.7	879.6	1064.1	1046.1	4362.8	4921.7	4523.2	4833.0

MSMEG _3808	MSMEG 3814	excinuclease ABC, A subunit (uvrA)	4	205.6	197.2	215.1	178.3	431.5	379.9	469.7	444.3
MSMEG _3810	MSMEG 3815	metallo-beta-lactamase superfamily protein	3	154.2	174.3	230.8	270.8	150.1	151.8	163.5	180.6
MSMEG _3811	MSMEG 3816	universal stress protein family domain protein	11	4651.0	5750.7	2128.5	2221.2	4640.6	5545.3	4298.2	4284.6
MSMEG _3816	MSMEG 3820	excinuclease ABC, B subunit (uvrB)	1	6.5	8.0	13.0	11.0	34.8	30.4	61.4	39.2
MSMEG _3831	MSMEG 3837	dephospho-CoA kinase, putative	1	10.0	7.8	7.7	6.0	7.1	5.4	6.7	5.0
MSMEG _3833	MSMEG 3838	rpsA (rpsA)	18	8923.2	8541.4	8540.4	7728.0	8084.7	7790.2	6975.7	6900.7
MSMEG _3839	MSMEG 3843	DNA polymerase I (polA)	13	1344.4	1327.0	1402.9	1237.9	1552.7	1594.0	1863.2	1647.2
MSMEG _3859	MSMEG 3862	apolipoprotein n-acyltransferase Lnt/dolichol-phosphate-mannosyl tra	1	16.9	19.6	15.6	15.1	33.8	35.6	19.4	16.7
MSMEG _3863	MSMEG 3866	conserved hypothetical protein	2	12.4	9.2	15.9	15.1	19.3	14.1	27.2	24.2
MSMEG _3864	MSMEG 3867	cobalamin biosynthesis protein N	6	167.7	160.0	105.4	111.4	117.2	128.8	107.4	110.7
MSMEG _3872	MSMEG 3875	precorrin-8X methylmutase	1	20.1	21.7	35.2	37.3	50.8	51.4	58.1	61.3
MSMEG _3881	MSMEG 3884	proline dipeptidase (pepQ)	2	304.6	233.3	247.4	248.2	344.2	298.0	379.3	384.2
MSMEG _3889	MSMEG 3893	repressor protein, putative	1	17.6	19.2	4.8	6.7	4.6	7.0	0.4	2.4

MSMEG _3895	MSMEG 3899	proteasome beta subunit	5	939.7	929.2	544.8	554.8	672.0	627.5	633.3	670.3
MSMEG _3897	MSMEG 3901	Putative proteasome component family	2	226.8	231.9	214.3	231.6	303.6	323.1	262.1	308.6
MSMEG _3902	MSMEG 3906	COG0464:ATPases of the AAA+ class	12	1888.0	1981.4	1636.4	1636.6	926.1	970.1	811.1	854.1
MSMEG _3906	MSMEG 3910	conserved hypothetical protein	2	59.8	50.9	94.7	93.7	89.0	89.9	104.3	99.1
MSMEG _3918	MSMEG 3923	hypothetical protein	1	6.7	6.9	10.6	16.7	75.7	77.1	64.2	81.0
MSMEG _3932	MSMEG 3937	heat shock protein, Hsp20 family (hsp)	1	168.0	149.7	10.8	13.7	3.9	3.7	3.5	4.6
MSMEG _3945	MSMEG 3950	universal stress protei	5	373.7	377.8	75.7	84.3	33.5	33.2	40.0	49.2
MSMEG _3950	MSMEG 3957	universal stress protei	5	1721.1	1750.7	572.7	584.0	152.7	144.3	146.0	143.0
MSMEG _3962	MSMEG 3970	lactate 2-monooxygenase	8	520.5	558.5	2994.6	3004.6	2952.5	2966.4	3174.4	2997.8
MSMEG _3980	MSMEG 3987	transcriptional regulator, GntR family	1	10.7	12.9	8.0	10.4	13.7	10.5	8.5	8.5
MSMEG _4042	MSMEG 4047	transcriptional regulator, GntR family, putative	2	106.7	104.6	140.9	116.9	150.0	143.0	131.3	155.1
MSMEG _4075	MSMEG 4082	blr3446	1	1.8	2.1	10.8	12.1	46.5	29.2	64.3	61.0
MSMEG _4125	MSMEG 4132	oxidoreductase, short-chain dehydrogenase/reductase family, putative	1	28.5	27.3	39.2	34.0	16.1	12.0	19.9	18.9

MSMEG _4180	MSMEG 4185	ATP phosphoribosyltransferase (hisG)	2	124.3	137.4	111.3	116.3	99.7	101.1	98.8	108.1
MSMEG _4185	MSMEG 4189	5-methyltetrahydrofolate-- homocysteine methyltransferase (metH)	10	322.7	307.7	310.5	305.8	503.8	314.5	143.0	149.9
MSMEG _4188	MSMEG 4192	oxidoreductase, short-chain dehydrogenase/reductase family	3	82.4	77.9	77.7	79.3	123.8	119.0	92.0	112.7
MSMEG _4189	MSMEG 4193	cysteinyl-tRNA synthetase (cysS)	2	367.4	397.0	246.5	263.1	183.3	207.1	161.7	184.3
MSMEG _4193	MSMEG 4198	alpha-ribazole-5-phosphate phosphatase	2	99.9	90.8	66.8	64.3	107.3	78.4	84.6	90.7
MSMEG _4199	MSMEG 4204	conserved hypothetical protein TIGR00481	3	145.4	145.4	115.5	111.1	204.8	209.9	177.9	201.8
MSMEG _4205	MSMEG 4210	transcriptional regulator, LuxR family domain protein	1	60.5	64.0	35.6	37.5	90.9	100.8	71.3	81.1
MSMEG _4207	MSMEG 4213	universal stress protein family, putative	4	40.1	45.5	32.5	42.8	1020.8	1082.7	1019.5	982.9
MSMEG _4208	MSMEG 4214	COG3333:Uncharacterized BCR	1	36.9	39.0	6.2	29.1	83.3	129.4	18.7	77.7
MSMEG _4210	MSMEG 4216	Uncharacterized BCR	16	366.8	412.1	343.1	393.3	4426.2	4495.8	3840.4	3965.2
MSMEG _4217	MSMEG 4223	cell division protein DivIVA	7	788.7	742.0	749.3	794.1	1253.5	1151.2	1061.7	1215.5

MSMEG _4222	MSMEG 4228	cell division protein FtsZ (ftsZ)	3	176.4	177.4	109.8	99.4	330.0	331.6	320.4	338.0
MSMEG _4237	MSMEG 4241	SEQ ID NO 45F	1	27.3	28.2	14.5	19.6	12.6	15.6	12.1	16.6
MSMEG _4240	MSMEG 4244	idsA2 (idsA2)	5	601.9	619.1	464.0	470.5	580.9	599.4	496.4	527.3
MSMEG _4244	MSMEG 4247	3-deoxy-7-phosphoheptulonate synthase	1	364.5	351.8	327.3	331.6	262.4	271.1	276.4	284.2
MSMEG _4251	MSMEG 4254	conserved hypothetical protein	1	16.6	20.7	16.9	11.6	22.2	28.1	28.3	21.4
MSMEG _4254	MSMEG 4256	long-chain-fatty-acid--CoA ligase (fadD-2)	8	1285.1	1205.3	873.7	910.1	1190.5	1085.6	941.4	913.3
MSMEG _4258	MSMEG 4262	anthranilate phosphoribosyltransferase (trpD)	3	695.0	663.3	555.4	507.3	469.3	485.7	579.5	525.0
MSMEG _4262	MSMEG 4265	Rieske Fe-S Protein	5	908.0	782.5	921.1	1042.3	542.3	389.3	690.3	548.8
MSMEG _4263	MSMEG 4266	cytochrome B6, putative	2	47.7	44.7	69.4	61.3	45.3	41.6	84.2	73.7
MSMEG _4268	MSMEG 4271	cytochrome c oxidase, subunit II, putative	1	98.6	103.3	41.7	40.9	26.7	30.9	44.4	53.2
MSMEG _4269	MSMEG 4272	asparagine synthase (glutamine-hydrolyzing)	4	214.8	223.8	218.7	163.0	238.1	237.9	365.0	280.5
MSMEG _4270	MSMEG 4273	probable carbohydrate kinase	5	1511.7	1489.3	1781.7	1745.2	959.9	986.0	915.8	943.1
MSMEG _4272	MSMEG 4275	HesB/YadR/YfhF family protein	4	175.1	177.7	112.5	117.8	14.9	25.7	13.7	15.6
MSMEG _4273	MSMEG 4276	conserved hypothetical protein	1	13.7	17.2	13.1	17.2	7.8	10.0	6.7	10.2

MSMEG _4276	MSMEG 4280	branched-chain amino acid aminotransferase (ilvE)	6	1193.8	1082.0	853.4	796.0	1322.9	1257.6	1184.6	1231.3
MSMEG _4278	MSMEG 4281	glycine cleavage system T protein (gcvT)	4	719.8	657.4	360.1	340.1	700.9	727.6	492.6	554.9
MSMEG _4281	MSMEG 4283	cytosol aminopeptidase (pepA)	12	4788.3	4610.7	1886.3	1860.5	1896.6	1785.6	2010.9	2081.0
MSMEG _4283	MSMEG 4286	2-oxo acid dehydrogenases acyltransferase (catalytic domain) protein	19	5757.5	5669.6	6353.9	6768.9	8815.4	8503.2	10561.4	10900.3
MSMEG _4287	MSMEG 4290	conserved hypothetical protein	1	47.5	43.4	72.9	75.7	29.1	17.6	31.3	38.1
MSMEG _4288	MSMEG 4292	conserved hypothetical protein	1	13.7	15.4	14.6	20.8	6.3	7.0	2.6	7.6
MSMEG _4290	MSMEG 4293	glutamine synthetase, type I (glnA)	24	11712.2	11947.1	8646.5	8716.8	38488.9	39697.5	36050.3	35924.0
MSMEG _4291	MSMEG 4294	D-tyrosyl-tRNA(Tyr) deacylase (dtd)	1	29.1	12.0	21.8	23.9	48.0	16.2	37.2	39.8
MSMEG _4293	MSMEG 4296	glutamate-ammonia-ligase adenylyltransferase, putative	1	16.8	27.8	16.3	22.5	84.5	100.6	84.2	92.7
MSMEG _4294	MSMEG 4297	glutamine synthetase, type I (glnA)	4	464.1	475.3	559.1	576.9	1064.6	1098.4	1230.5	1276.1

MSMEG _4298	MSMEG 4301	3-methyl-2-oxobutanoate hydroxymethyltransferase (panB)	9	5011.7	4740.7	19350.9	20231.2	252.0	258.9	371.7	289.5
MSMEG _4299	MSMEG 4302	enoyl-CoA hydratase/isomerase PhaB (b1394)	2	211.1	221.6	158.5	175.8	63.6	64.5	54.4	60.6
MSMEG _4301	MSMEG 4304	acyl-CoA synthase (fadD28)	3	344.9	342.9	336.5	328.1	187.6	211.8	129.8	154.1
MSMEG _4302	MSMEG 4305	Adenylate cyclase, putative	1	124.6	127.3	94.1	111.1	182.0	190.6	183.4	206.3
MSMEG _4306	MSMEG 4311	Uncharacterized ACR, COG1579 superfamily	2	54.0	57.7	77.4	76.7	65.4	68.7	73.1	74.7
MSMEG _4313	MSMEG 4318	fosfomycin resistance protein fosB, putative	6	1100.5	1090.6	899.4	936.9	882.9	887.0	887.3	877.8
MSMEG _4320	MSMEG 4325	bacterioferritin comigratory protein, ahpC/TSA family (ahpE)	2	50.7	33.5	40.9	45.0	127.8	37.0	69.2	79.0
MSMEG _4321	MSMEG 4326	conserved hypothetical protein	1	36.8	43.2	29.7	35.8	60.9	73.2	62.1	74.1
MSMEG _4323	MSMEG 4328	pyruvate dehydrogenase E1 component (aceE)	18	4139.1	4358.0	3426.9	3641.9	5655.4	5782.0	5518.8	5912.3
MSMEG _4325	MSMEG 4330	malonyl CoA-acyl carrier protein transacylase (fabD)	4	589.4	613.8	658.9	615.1	505.1	515.6	636.8	583.7

MSMEG_4326	MSMEG_4331	acyl carrier protein (acpP)	4	1008.4	1065.7	1038.4	1118.1	1144.2	1241.7	1392.0	1390.7
MSMEG_4328	MSMEG_4334	3-oxoacyl- synthase (kasB)	6	1817.2	1959.8	1642.6	1644.6	1853.6	1847.3	1914.9	1916.9
MSMEG_4329	MSMEG_4335	methyalmalonyl-CoA decarboxylase, subunit alpha (mmdA)	4	340.7	314.3	478.4	435.4	413.2	385.7	417.4	492.4
MSMEG_4330	MSMEG_4336	short chain dehydrogenase	1	3.7	3.4	6.3	4.9	7.5	5.4	8.0	5.3
MSMEG_4337	MSMEG_4343	conserved hypothetical protein	2	321.3	336.6	292.1	307.4	150.3	149.4	179.6	190.0
MSMEG_4340	MSMEG_4346	adhE2 (adhE2)	8	1545.7	1444.3	1134.3	987.4	1395.6	1280.6	1608.9	1346.0
MSMEG_4342	MSMEG_4347	metallo-beta-lactamase family protein	1	184.7	235.7	99.3	98.2	189.5	190.2	268.0	237.7
MSMEG_4358	MSMEG_4364	short chain dehydrogenase	1	28.3	34.3	28.6	37.6	48.5	113.3	54.3	53.1
MSMEG_4362	MSMEG_4368	universal stress protein family domain protein	2	60.1	66.2	59.3	58.4	99.1	99.2	92.1	92.5
MSMEG_4367	MSMEG_4372	formamidase	3	518.0	508.2	248.6	310.2	1496.7	1554.7	1181.3	1292.1
MSMEG_4381	MSMEG_4385	AMIDASE	1	18.2	19.8	6.3	7.0	58.4	67.4	31.9	53.3
MSMEG_4396	MSMEG_4399	isochorismatase family protein family	7	1556.9	1613.5	1724.9	1791.9	1121.8	1095.3	1234.1	1360.1
MSMEG_4401	MSMEG_4404	phosphoglycolate phosphatase, putative	5	852.7	866.8	581.7	619.6	558.4	599.6	487.5	526.0
MSMEG_4454	MSMEG_4449	low-specificity L-threonine aldolase	1	24.5	28.7	1.3	3.3	0.1	1.0	0.9	0.2



MSMEG _4463	MSMEG 4458	conserved hypothetical protein	2	21.7	22.5	10.5	10.8	13.1	13.6	8.4	10.9
MSMEG _4471	MSMEG 4466	transcriptional regulator, MarR family	1	38.4	45.4	28.9	34.0	73.8	83.8	58.0	59.5
MSMEG _4474	MSMEG 4469	acyl-CoA oxidase homolog (proteinforMGC:9)	9	1112.1	1058.7	940.6	796.6	1112.0	1076.7	1363.4	1156.3
MSMEG _4475	MSMEG 4470	conserved hypothetical protein	1	11.8	8.5	6.0	8.4	15.9	13.0	12.5	16.3
MSMEG _4476	MSMEG 4471	hypothetical protein	1	19.2	0.0	15.6	17.0	15.7	0.0	8.6	5.6
MSMEG _4485	MSMEG 4480	glycyl-tRNA synthetase (glyS)	5	694.3	726.9	538.1	468.1	516.4	583.2	477.4	487.5
MSMEG _4486	MSMEG 4481	transcriptional regulator (smtB)	2	25.7	26.4	31.2	29.4	11.1	11.9	16.4	16.8
MSMEG _4487	MSMEG 4482	furB (furB)	1	453.1	513.7	392.8	402.7	37.8	43.3	36.7	35.0
MSMEG _4489	MSMEG 4484	conserved hypothetical protein	1	28.4	33.5	35.5	35.8	58.8	56.4	63.9	56.6
MSMEG _4490	MSMEG 4485	undecaprenyl diphosphate synthase (uppS)	1	27.4	27.6	25.7	21.7	30.0	24.1	10.2	8.7
MSMEG _4527	MSMEG 4520	nitrite reductase (nirA)	4	402.5	426.5	193.3	204.1	240.0	237.6	124.2	133.9
MSMEG _4528	MSMEG 4521	phosphoadenylyl-sulfate reductase (cysH)	2	170.1	192.4	123.0	123.4	60.2	58.3	66.4	72.9
MSMEG _4533	MSMEG 4526	subl (subl)	8	2169.4	2352.7	1875.1	1806.2	1589.4	1687.5	1406.1	1552.7
MSMEG _4535	MSMEG 4528	glycosyl hydrolase, family 15	19	1939.8	1983.1	1736.5	1692.6	3300.2	3278.2	3363.9	3127.2

MSMEG _4553	MSMEG 4547	GGDEF family protein VCA0785	2	96.9	105.2	96.3	100.5	98.3	102.1	85.9	80.1
MSMEG _4569	MSMEG 4566	conserved hypothetical protein	1	12.7	13.6	8.1	6.5	49.3	51.7	33.2	35.2
MSMEG _4570	MSMEG 4567	u1937b; B1937_F1_4	1	100.0	102.4	99.2	153.1	163.6	181.3	95.1	224.3
MSMEG _4571	MSMEG 4568	ribosomal protein S20 (rpsT)	1	138.4	131.5	279.5	262.8	43.9	45.1	97.2	96.9
MSMEG _4617	MSMEG 4609	glutamine-dependent NAD+ synthetase (nadE)	4	420.6	404.0	432.7	312.2	1828.0	1874.4	1411.5	1649.9
MSMEG _4624	MSMEG 4616	ribosomal protein L27 (rpmA)	4	932.4	942.4	855.6	943.4	391.5	391.4	398.2	406.0
MSMEG _4625	MSMEG 4617	ribosomal protein L21 (rplU)	4	1094.3	1000.5	1353.3	1453.6	807.0	724.8	742.9	810.1
MSMEG _4626	MSMEG 4618	rne (rne)	9	346.7	350.3	292.8	280.6	261.8	278.1	272.4	279.4
MSMEG _4627	MSMEG 4619	nucleoside diphosphate kinase (ndk)	3	1118.1	1140.2	954.8	993.1	629.2	626.6	745.9	684.0
MSMEG _4630	MSMEG 4622	valyl-tRNA synthetase (valS)	12	1845.3	1850.3	1603.6	1548.4	1146.7	1212.4	1327.4	1352.9
MSMEG _4636	MSMEG 4627	hypothetical protein	1	0.3	0.0	0.0	0.1	309.1	0.0	297.9	321.0
MSMEG _4645	MSMEG 4636	alpha oxoglutarate ferredoxin oxidoreductase, beta subunit (orB)	4	737.6	719.1	987.6	956.2	356.2	333.8	301.6	305.1
MSMEG _4646	MSMEG 4637	ferredoxin oxidoreductase, alpha subunit	15	1942.8	1951.1	3218.5	2991.5	934.4	942.3	978.7	952.2
MSMEG _4647	MSMEG 4638	putative sugar kinase	1	18.5	17.2	22.2	17.2	13.1	15.6	24.5	13.9

MSMEG _4664	MSMEG 4654	iolD protein	1	13.2	10.9	27.0	18.9	61.0	67.5	90.5	51.4
MSMEG _4668	MSMEG 4658	oxidoreductase alpha (molybdopterin) subunit	1	8.0	18.8	15.4	19.9	0.8	1.6	0.9	0.8
MSMEG _4672	MSMEG 4662	ATP-dependent Clp protease, proteolytic subunit ClpP (clpP)	6	2276.5	2260.3	1814.9	1916.3	1602.4	1540.2	1476.4	1418.0
MSMEG _4673	MSMEG 4663	ATP-dependent Clp protease, proteolytic subunit ClpP (clpP)	9	5605.8	5772.7	4743.9	4662.0	5780.4	5740.6	5551.5	5394.9
MSMEG _4674	MSMEG 4664	trigger factor (tig)	10	4105.1	4340.8	2914.1	2901.0	3150.9	3231.6	2601.9	2560.1
MSMEG _4679	MSMEG 4669	hypothetical protein	1	4.1	6.4	7.9	10.6	2.4	5.5	5.6	2.5
MSMEG _4687	MSMEG 4676	cytosine deaminase	4	162.5	155.6	165.1	178.1	325.1	303.1	282.8	277.7
MSMEG _4688	MSMEG 4677	DSBA-like thioredoxin domain family	1	59.5	69.9	48.3	37.2	29.4	44.3	40.2	33.5
MSMEG _4690	MSMEG 4679	pepD (pepD)	16	3104.3	2986.0	2944.6	2664.0	2214.2	2196.5	2674.2	2500.4
MSMEG _4692	MSMEG 4681	conserved hypothetical protein	4	662.2	681.3	688.5	713.2	358.0	371.5	330.6	329.0
MSMEG _4693	MSMEG 4682	conserved hypothetical protein	1	35.0	35.6	30.5	33.6	6.3	7.5	7.1	5.7
MSMEG _4698	MSMEG 4687	conserved hypothetical protein	1	169.2	162.7	138.0	140.2	191.6	250.6	158.1	175.7

MSMEG _4699	MSMEG 4688	NAD-glutamate dehydrogenase (NAD-GDH)	20	494.2	490.0	531.8	538.3	569.1	593.6	778.1	784.2
MSMEG _4700	MSMEG 4689	ABC-type transport system, ATPase component (AB041227)	11	1333.2	1272.7	841.7	731.0	1887.8	1866.8	1993.2	1727.8
MSMEG _4709	MSMEG 4698	enoyl-CoA hydratase/isomerase family protein (crt)	5	289.6	296.6	213.8	248.6	463.5	462.6	520.4	552.3
MSMEG _4714	MSMEG 4704	maoC protein (maoC)	1	15.8	17.2	14.1	19.4	22.2	20.1	7.1	16.2
MSMEG _4716	MSMEG 4706	biotin carboxylase (accA2)	1	11.0	14.7	17.7	22.5	26.7	35.6	31.0	35.6
MSMEG _4722	MSMEG 4713	oxidoreductase, short chain dehydrogenase/reductase family	6	592.9	589.9	555.1	550.5	645.9	673.9	693.5	720.6
MSMEG _4724	MSMEG 4715	exonuclease family	1	24.1	27.8	18.6	20.0	33.3	33.4	28.7	31.7
MSMEG _4727	MSMEG 4717	pks2 (pks2)	2	5.2	5.2	10.4	8.9	122.7	114.0	155.1	164.3
MSMEG _4742	MSMEG 4734	oxidoreductase, short-chain dehydrogenase/reductase family, putative	7	744.3	689.0	918.3	924.1	1342.4	1221.4	1227.1	1248.7
MSMEG _4752	MSMEG 4742	conserved hypothetical protein	1	220.0	228.2	209.0	205.9	229.0	249.5	229.1	217.2
MSMEG _4753	MSMEG 4743	bcp (bcp)	13	3255.8	3501.9	2274.8	2434.0	3881.1	4207.1	3563.0	3527.3
MSMEG _4755	MSMEG 4745	ArgE/DapE/Acy1 family protein	2	181.0	173.7	107.4	105.4	232.3	229.3	244.5	244.1

MSMEG _4757	MSMEG 4747	fatty-acid synthase (fas)	164	15609.0	15000.1	19787.8	19270.5	17072.0	16547.1	17004.2	15853.9
MSMEG _4847	MSMEG 4835	transcriptional regulator, TetR family domain protein	3	59.5	52.4	38.2	32.3	57.5	44.8	26.0	30.2
MSMEG _4888	MSMEG 4874	transcription regulator, LacI family	1	0.1	0.1	1.2	2.0	1.7	1.4	0.7	1.1
MSMEG _4891	MSMEG 4876	alkyl hydroperoxide reductase C	8	5046.3	5321.6	2821.1	2788.2	183.8	180.6	132.6	157.3
MSMEG _4901	MSMEG 4886	ribonuclease PH	2	173.2	201.4	231.8	238.4	242.2	289.0	240.9	293.8
MSMEG _4905	MSMEG 4890	cysteine synthase B	2	146.4	142.7	109.5	125.7	75.5	78.0	32.9	41.1
MSMEG _4906	MSMEG 4891	ThiS family domain protein nicotinate	2	111.2	132.6	107.0	118.9	57.4	57.5	50.2	63.4
MSMEG _4911	MSMEG 4896	phosphoribosyltransferase, putative	1	30.3	26.1	35.2	35.7	61.3	42.3	87.0	66.9
MSMEG _4914	MSMEG 4899	unnamed protein product	1	24.2	26.5	26.0	31.2	15.0	10.5	13.7	14.6
MSMEG _4915	MSMEG 4900	glycogen phosphorylase family protein (glgP)	19	1593.3	1603.3	1878.1	1778.7	2551.5	2515.6	3180.0	2860.7
MSMEG _4916	MSMEG 4901	alpha-amylase family protein	2	42.1	46.0	56.1	56.9	14.6	13.2	13.4	13.4
MSMEG _4917	MSMEG 4903	thioredoxin, putative	2	60.9	46.4	36.9	44.6	49.3	33.1	34.9	41.4
MSMEG _4918	MSMEG 4902	1,4-alpha-glucan branching enzyme (glgB)	3	244.5	231.1	180.6	212.8	314.3	316.5	301.1	334.1
MSMEG _4920	MSMEG 4905	acetyl-CoA acetyltransferase (atoB-1)	24	12838.6	11985.0	16220.4	15867.1	11936.8	11349.0	11340.5	10998.0

MSMEG _4921	MSMEG 4906	4-hydroxyphenylpyruvate dioxygenase C terminal domain containing prot	5	677.1	741.3	832.7	888.2	550.9	617.8	495.6	548.0
MSMEG _4932	MSMEG 4917	UDP-N-acetylglucosamine 1- carboxyvinyltransferase (murA)	4	334.4	336.5	314.5	339.9	298.7	268.2	213.5	229.0
MSMEG _4934	MSMEG 4918	ATP:cob(I)alamin adenosyltransferase, putative	3	421.5	423.6	356.7	373.7	247.9	257.9	222.8	242.0
MSMEG _4935	MSMEG 4920	ATP synthase F1, epsilon subunit (atpC)	4	261.2	268.7	793.6	749.6	305.6	325.9	379.5	344.5
MSMEG _4936	MSMEG 4921	ATP synthase F1, beta subunit (atpD)	19	3670.3	3748.4	12917.0	12912.8	8423.8	8748.2	9190.1	9573.7
MSMEG _4937	MSMEG 4922	ATP synthase F1, gamma subunit (atpG)	6	111.2	139.3	298.1	326.9	197.8	225.6	175.6	214.2
MSMEG _4940	MSMEG 4926	ATP synthase b chain (atpF)	2	92.2	114.8	234.1	243.8	82.0	101.4	83.4	83.8
MSMEG _4950	MSMEG 4935	peptide chain release factor 1 (prfA)	1	16.6	18.1	7.4	14.7	2.5	2.4	1.5	0.5
MSMEG _4951	MSMEG 4936	ribosomal protein L31 (rpmE)	3	693.3	782.3	763.5	779.8	360.3	428.9	381.5	408.5
MSMEG _4955	MSMEG 4941	homoserine kinase (thrB)	1	46.7	49.8	56.2	56.4	45.8	42.5	63.6	66.4
MSMEG _4956	MSMEG 4942	threonine synthase (thrC)	4	586.5	499.6	379.4	409.1	339.8	309.1	223.2	294.9
MSMEG _4957	MSMEG 4943	homoserine dehydrogenase	2	299.0	269.0	310.4	290.6	360.6	329.2	464.6	407.8

MSMEG _4958	MSMEG 4944	diaminopimelate decarboxylase (lysA)	2	144.3	131.5	152.5	126.1	443.4	445.5	417.7	427.7
MSMEG _4959	MSMEG 4945	arginyl-tRNA synthetase (argS)	3	248.6	240.5	266.2	259.5	325.7	309.9	370.9	340.8
MSMEG _4971	MSMEG 4957	enoyl-(acyl-carrier-protein) reductase II (fabK)	1	33.2	41.9	11.1	13.3	97.7	96.8	149.6	153.0
MSMEG _4974	MSMEG 4960	RrF2 family protein	2	15.2	16.3	16.5	20.1	17.3	16.9	21.4	21.1
MSMEG _4976	MSMEG 4962	isochorismatase family protein	10	1453.4	988.7	1621.3	1723.8	1305.6	1172.8	1127.4	1191.8
MSMEG _4978	MSMEG 4965	sulfate adenylytransferase, large subunit/adenylylsulfate kinase (cys	1	9.1	10.2	3.9	9.5	4.8	3.9	1.2	3.9
MSMEG _4985	MSMEG 4972	carbonic anhydrase-related protein	6	2222.3	1831.3	1817.4	1829.9	1643.6	1379.1	1557.7	1427.4
MSMEG _4997	MSMEG 4983	ABC transporter, ATP-binding protein	1	1.4	0.2	0.1	0.0	2.3	0.8	0.6	0.6
MSMEG _5005	MSMEG 4993	conserved hypothetical protein	2	154.0	169.3	115.1	131.0	109.0	113.8	100.0	97.2
MSMEG _5006	MSMEG 4992	phosphohistidine phosphatase SixA, putative	1	3.9	0.0	4.4	5.2	3.0	0.0	2.8	2.6
MSMEG _5022	MSMEG 5007	flavin-containing monooxygenase	3	11.1	11.3	43.8	35.3	63.9	70.4	112.3	75.8
MSMEG _5037	MSMEG 5024	glycolate oxidase, subunit GlcD (glcD)	1	118.4	150.3	87.1	113.0	46.1	61.0	46.7	63.8

MSMEG _5042	MSMEG 5030	ATP-dependent RNA helicase DeaD	11	481.5	488.3	322.1	394.9	499.1	521.4	511.2	618.0
MSMEG _5048	MSMEG 5036	conserved hypothetical protein	1	8.3	12.6	3.9	4.5	16.4	23.2	9.0	17.1
MSMEG _5049	MSMEG 5037	2-oxoglutarate dehydrogenase E1 component	54	6644.3	6329.4	5708.7	5617.2	7350.1	6826.6	6972.3	6472.8
MSMEG _5053	MSMEG 5041	short chain dehydrogenase family protein	1	14.6	10.7	16.4	16.0	21.8	20.6	24.2	23.3
MSMEG _5055	MSMEG 5043	malate oxidoreductase (oxaloacetatedec)	4	1131.6	1065.4	955.3	954.0	1273.6	1193.4	1218.4	1146.6
MSMEG _5058	MSMEG 5046	sugC (sugC)	2	83.7	83.0	165.1	145.1	139.3	151.7	224.9	186.4
MSMEG _5062	MSMEG 5050	conserved hypothetical protein	1	48.0	55.4	56.8	66.0	90.6	100.4	81.0	77.3
MSMEG _5064	MSMEG 5052	citrate lyase, beta subunit	3	157.2	176.6	128.2	137.4	135.3	145.0	95.1	96.6
MSMEG _5073	MSMEG 5061	O-methyltransferase superfamily	3	32.4	31.8	20.1	21.6	174.9	190.3	146.3	168.9
MSMEG _5086	MSMEG 5074	fadD6 (fadD6)	5	378.9	348.8	287.8	311.8	439.7	400.1	352.6	358.9
MSMEG _5104	MSMEG 5090	tetrahydrodipicolinate N- succinyltransferase (dapD)	5	1116.5	1157.0	612.9	646.5	708.7	758.4	711.5	667.7
MSMEG _5117	MSMEG 5103	Proline dehydrogenase superfamily	1	47.7	46.5	66.5	60.6	40.3	27.0	56.2	37.7



MSMEG _5119	MSMEG 5104	delta-1-pyrroline-5-carboxylate dehydrogenase (pruA)	7	81.8	79.0	97.8	91.7	916.1	832.5	589.2	523.1
MSMEG _5121	MSMEG 5107	aminotransferase, classes I and II	3	303.2	313.9	255.5	267.4	229.5	253.7	212.9	234.4
MSMEG _5122	MSMEG 5108	ferredoxin	1	198.0	204.9	212.7	233.9	282.0	276.4	316.4	300.6
MSMEG _5129	MSMEG 5117	Uncharacterized LmbE-like protein, COG2120 superfamily	4	361.3	333.6	231.5	253.7	294.6	304.0	270.2	291.6
MSMEG _5132	MSMEG 5120	GTP-binding protein TypA (typA)	5	265.2	289.5	156.5	208.8	745.0	730.0	579.6	655.5
MSMEG _5136	MSMEG 5121	conserved hypothetical protein	2	264.0	304.6	47.0	50.3	4.2	6.9	4.8	2.6
MSMEG _5150	MSMEG 5135	pterin-4-alpha-carbinolamine dehydratase	1	9.8	10.6	15.7	17.1	31.6	29.6	36.8	34.9
MSMEG _5164	MSMEG 5148	alcohol dehydrogenase, zinc- containing	2	101.6	103.9	19.5	32.1	993.1	971.9	429.3	504.7
MSMEG _5170	MSMEG 5154	conserved hypothetical protein	2	154.2	202.7	104.1	119.3	475.9	697.2	370.5	445.3
MSMEG _5183	MSMEG 5166	3-hydroxyacyl-CoA dehydrogenase FadB2x	7	1068.7	1079.6	769.3	781.3	1401.2	1378.7	1559.7	1553.9
MSMEG _5184	MSMEG 5167	alpha-methylacyl-CoA racemase, putative	1	64.6	71.5	41.7	45.7	438.2	638.3	258.5	260.2
MSMEG _5191	MSMEG 5175	anhydrase, family 3 protein	3	123.4	110.1	80.0	84.5	62.1	50.2	56.2	55.1

MSMEG_5197	MSMEG_5179	acyl-CoA dehydrogenase (fadE20)	2	71.0	69.8	98.9	97.9	67.4	104.8	61.7	82.2
MSMEG_5198	MSMEG_5180	echA1 (echA1)	2	70.6	83.5	117.5	136.0	52.1	58.0	53.3	78.5
MSMEG_5199	MSMEG_5181	thiolase family protein	2	435.2	435.5	519.1	531.8	406.1	384.0	375.0	434.8
MSMEG_5211	MSMEG_5192	aminotransferase, class III	7	499.8	491.8	479.7	487.9	547.7	551.4	581.0	608.8
MSMEG_5215	MSMEG_5199	conserved hypothetical protein	1	3.4	2.7	2.9	3.6	2.2	3.7	2.3	1.5
MSMEG_5225	MSMEG_5209	conserved hypothetical protein	4	244.3	242.4	675.3	754.9	873.9	882.0	936.2	938.6
MSMEG_5239	MSMEG_5224	fructose-1,6-bisphosphatase, class II (glpX)	4	1019.0	1028.6	610.1	601.7	1029.2	1059.7	805.8	840.4
MSMEG_5240	MSMEG_5225	fum (fum)	11	3706.6	3464.2	3787.2	3569.9	4030.1	3917.4	4933.0	4722.4
MSMEG_5243	MSMEG_5228	conserved hypothetical protein	1	263.5	274.0	61.2	71.8	15.7	17.8	19.4	17.8
MSMEG_5244	MSMEG_5229	DNA-binding response regulator,	1	6.6	0.0	1.2	0.9	8.7	0.0	2.0	2.7
MSMEG_5245	MSMEG_5230	universal stress protein family domain protein	3	537.1	555.2	76.2	83.7	41.7	51.0	31.0	37.0
MSMEG_5246	MSMEG_5231	conserved hypothetical protein	5	1936.4	1954.3	267.8	298.4	529.5	461.9	857.7	857.1
MSMEG_5248	MSMEG_5233	acyl-	6	895.5	939.4	726.2	786.6	393.0	420.4	420.1	469.8
MSMEG_5249	MSMEG_5234	serine hydroxymethyltransferase	9	3714.6	4001.3	3373.7	3404.1	4253.2	4573.5	4598.2	4794.2

MSMEG _5252	MSMEG 5236	pantothenate kinase VC0320	2	79.3	82.1	61.6	62.1	76.6	78.6	37.5	58.1
MSMEG _5258	MSMEG 5243	steroid Delta-isomerase	1	70.4	88.8	65.4	85.1	64.2	82.7	54.9	62.5
MSMEG _5263	MSMEG 5248	transcription elongation factor G greA	2	421.2	480.9	417.8	441.8	333.6	361.1	291.5	286.4
MSMEG _5265	MSMEG 5251	cystathionine beta-lyase	4	1757.5	1586.7	1280.8	1279.2	1116.8	1050.3	1130.8	1215.3
MSMEG _5270	MSMEG 5255	cystathionine beta-synthase	4	641.3	573.8	467.6	426.7	518.2	481.5	413.8	416.3
MSMEG _5273	MSMEG 5258	thiolase, putative	9	6050.6	5837.2	4485.1	4341.0	6404.6	6524.6	5928.3	6004.2
MSMEG _5274	MSMEG 5259	phosphoribosylglycinamide formyltransferase 2 (purT)	1	117.5	114.3	150.2	136.3	328.1	359.6	339.7	360.9
MSMEG _5285	MSMEG 5270	Patatin-like phospholipase family	1	161.4	164.7	39.2	46.7	22.7	23.1	14.4	17.1
MSMEG _5358	MSMEG 5339	Acetamidase/Formamidase family	2	192.3	213.1	134.4	131.9	96.6	99.6	117.3	106.1
MSMEG _5359	MSMEG 5340	cyanate hydratase (cynS)	7	50.2	53.0	60.8	64.8	1050.3	1129.9	1124.2	1041.8
MSMEG _5397	MSMEG 5377	ATP-dependent DNA helicase RecQ, interruption-C	1	7.9	6.2	7.5	5.2	35.9	21.3	43.1	20.4
MSMEG _5404	MSMEG 5383	prpE protein VC1340	3	259.4	262.4	93.4	109.1	145.9	181.2	128.7	198.8
MSMEG _5413	MSMEG 5393	exopolyphosphatase	1	22.9	27.1	26.0	26.3	294.8	325.0	171.6	186.4
MSMEG _5415	MSMEG 5395	enolase (eno)	14	12106.2	11488.7	9458.8	8682.8	10548.6	10209.8	11963.1	11385.6
MSMEG _5419	MSMEG 5399	putative lipoprotein	7	1215.7	1133.2	396.9	383.8	415.0	422.3	465.2	400.1

MSMEG _5423	MSMEG 5404	transcription-repair coupling factor (mfd)	9	209.7	202.7	128.5	130.3	225.9	226.5	204.0	211.8
MSMEG _5424	MSMEG 5405	transcriptional regulator, TetR family	1	7.6	6.6	2.1	2.5	27.0	27.1	25.1	34.1
MSMEG _5427	MSMEG 5408	ribose-phosphate pyrophosphokinase (PRPPsynthetase)	10	1088.0	1209.9	968.9	971.8	570.4	623.1	323.0	348.2
MSMEG _5431	MSMEG 5412	ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5	3	1877.8	1827.8	2318.4	2376.1	1445.1	1384.4	1529.0	1546.3
MSMEG _5435	MSMEG 5415	pks16 (pks16)	8	1102.1	1021.2	1336.0	1507.5	704.4	772.1	392.3	498.3
MSMEG _5438	MSMEG 5418	dimethyladenosine transferase (ksgA)	1	182.5	162.2	219.1	198.8	527.8	496.8	451.0	444.7
MSMEG _5441	MSMEG 5421	methionyl-tRNA synthetase (metG)	1	87.1	87.9	87.9	76.1	88.3	72.4	68.2	69.5
MSMEG _5471	MSMEG 5450	UTP-glucose-1-phosphate uridylyltransferase (galU)	2	171.0	171.0	174.3	209.7	154.0	148.3	212.8	201.8
MSMEG _5479	MSMEG 5458	conserved hypothetical protein	1	43.2	46.5	31.9	30.8	0.4	0.6	0.0	1.1
MSMEG _5485	MSMEG 5465	molybdopterin biosynthesis protein (mog)	3	453.1	484.0	492.6	494.2	693.5	707.2	774.8	704.3
MSMEG _5486	MSMEG 5466	heat shock protein HtrA, putative	1	29.2	19.7	11.2	13.0	26.8	14.2	14.9	21.4

MSMEG_5488	MSMEG_5468	DNA-binding response regulator	1	45.8	52.3	37.2	39.2	90.7	88.3	112.3	116.7
MSMEG_5489	MSMEG_5469	ribosomal protein L32, putative	2	550.8	561.5	519.6	584.0	229.8	229.0	256.1	278.7
MSMEG_5512	MSMEG_5490	Mg-chelatase subunit ChlI	6	534.2	529.8	365.1	375.5	543.9	547.0	605.9	600.0
MSMEG_5515	MSMEG_5493	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohy	4	120.7	116.7	97.5	92.5	94.4	93.1	90.5	106.9
MSMEG_5520	MSMEG_5498	N5,N10-methylenetetrahydromethanopterin reductase-related protein	3	231.0	210.0	324.0	302.8	122.8	118.6	85.9	103.9
MSMEG_5524	MSMEG_5502	hypothetical protein	15	3426.2	3383.8	5592.9	5294.5	4452.4	4459.5	4674.9	4374.8
MSMEG_5525	MSMEG_5503	carbamoyl-phosphate synthase, large subunit (carB)	13	12254.2	11646.1	12668.7	12267.9	11324.9	11027.3	11061.8	10519.7
MSMEG_5534	MSMEG_5512	ATP-dependent DNA helicase PcrA (pcrA)	1	4.0	4.2	8.2	9.5	0.1	0.0	0.2	0.1
MSMEG_5538	MSMEG_5516	NAD-dependent aldehyde dehydrogenases	6	1127.2	1066.8	851.1	705.7	675.1	638.9	694.6	674.0
MSMEG_5541	MSMEG_5517	glucose-6-phosphate isomerase (pgi)	5	1804.1	1755.4	1438.7	1286.8	1161.3	1161.2	1357.9	1203.2
MSMEG_5553	MSMEG_5530	methyltransferase (multi-domain)	1	60.8	55.7	71.0	74.1	153.4	138.6	110.1	115.2
MSMEG_5592	MSMEG_5572	Rif11	3	73.2	100.2	68.8	92.8	200.0	238.1	229.1	262.2

MSMEG _5612	MSMEG 5590	acetyltransferase, GNAT family	2	138.2	131.2	220.9	226.8	84.5	94.4	59.1	88.1
MSMEG _5615	MSMEG 5592	conserved hypothetical protein	1	34.2	44.1	25.4	33.1	58.4	67.9	46.4	51.5
MSMEG _5634	MSMEG 5613	conserved hypothetical protein	1	23.6	15.5	18.2	19.0	20.6	13.0	10.6	12.9
MSMEG _5639	MSMEG 5618	enoyl-CoA hydratase (fad-1)	12	1979.6	1985.5	1682.1	1685.3	1463.5	1433.9	1298.4	1309.3
MSMEG _5650	MSMEG 5630	acetyl-CoA synthetase (acs-6)	1	2.0	3.1	4.8	5.7	22.2	38.4	5.4	10.4
MSMEG _5662	MSMEG 5641	DNA-binding response regulator PrrA (prpA)	5	443.7	483.6	433.0	470.4	695.1	707.9	763.1	761.9
MSMEG _5664	MSMEG 5643	peptidyl-prolyl cis-trans isomerase FkpP	5	332.5	300.1	266.3	285.7	252.1	238.6	280.3	271.9
MSMEG _5672	MSMEG 5650	citrate synthase I (gltA)	15	8510.7	8503.2	5881.6	5877.6	7366.9	7400.8	7112.2	7159.4
MSMEG _5675	MSMEG 5653	pyridoxamine 5-phosphate oxidase (pdxH)	2	226.1	253.5	186.0	181.6	122.0	147.6	134.6	144.5
MSMEG _5676	MSMEG 5654	putative citrate synthase 2 (citA)	2	200.8	186.5	84.2	78.2	259.5	226.4	132.9	125.5
MSMEG _5680	MSMEG 5658	glyoxalase family protein	8	585.3	524.7	433.2	451.0	567.7	523.2	477.7	468.2
MSMEG _5684	MSMEG 5662	phosphoserine aminotransferase, putative	6	1667.0	1455.0	1334.7	1224.0	1277.1	1081.6	1274.1	1280.2
MSMEG _5690	MSMEG 5667	hypothetical protein	3	249.2	274.2	253.5	278.7	325.1	354.9	283.7	296.9
MSMEG _5694	MSMEG 5670	conserved hypothetical protein	1	26.8	0.0	13.5	15.9	98.4	0.0	159.6	132.1

MSMEG _5696	MSMEG 5672	cspB (cspB)	2	178.2	186.7	197.1	209.3	208.9	219.7	183.2	190.9
MSMEG _5701	MSMEG 5677	molybdopterin converting factor, subunit 2	1	23.6	26.0	22.0	22.3	28.8	28.9	27.9	24.8
MSMEG _5702	MSMEG 5678	mog (mog)	3	117.2	123.4	55.4	58.7	130.5	133.7	131.0	126.9
MSMEG _5703	MSMEG 5679	molybdenum cofactor biosynthesis protein C (moaC)	1	105.3	0.0	42.8	72.2	89.6	0.0	43.7	74.9
MSMEG _5706	MSMEG 5682	Helicase conserved C-terminal domain protein	1	51.2	52.9	35.2	34.6	39.0	39.1	25.3	34.3
MSMEG _5707	MSMEG 5683	conserved hypothetical protein	2	166.2	136.5	164.6	175.8	197.6	166.8	208.0	211.4
MSMEG _5715	MSMEG 5691	Luciferase-like monooxygenase superfamily	6	2379.2	2375.8	1167.9	1194.2	2476.0	2331.5	1936.1	1873.6
MSMEG _5720	MSMEG 5695	fatty oxidation complex, alpha subunit (fadB)	20	1958.0	1877.3	2636.2	2290.2	875.8	835.6	1032.7	895.8
MSMEG _5721	MSMEG 5696	thiolase	3	434.0	474.0	435.0	422.9	190.6	218.2	175.6	197.3
MSMEG _5725	MSMEG 5700	aminotransferase, class I	2	331.0	339.1	199.4	196.3	220.0	257.6	276.2	318.8
MSMEG _5727	MSMEG 5702	allantoicase	1	51.6	48.0	36.1	36.4	98.6	98.2	89.7	73.2
MSMEG _5732	MSMEG 5707	N5,N10-methylene- tetrahydromethanopterin reductase (mer), putative	1	45.9	53.2	21.2	29.1	59.3	76.5	47.9	59.8

MSMEG_5733	MSMEG_5708	universal stress protein family domain protein	2	125.1	123.5	54.0	48.9	4.0	2.9	2.0	2.0
MSMEG_5734	MSMEG_5709	far (far)	2	363.7	334.8	206.0	199.6	244.0	249.1	149.8	200.3
MSMEG_5739	MSMEG_5713	substrate--CoA ligase, putative	6	155.0	141.1	22.6	25.0	52.7	47.1	38.9	34.6
MSMEG_5773	MSMEG_5743	fatty acid desaturase (desA1)	1	206.6	219.8	149.7	144.5	2.4	4.5	1.9	1.8
MSMEG_5776	MSMEG_5747	phosphate transport system regulatory protein, putative	3	295.6	326.4	195.6	197.6	370.9	403.8	375.2	398.8
MSMEG_5784	MSMEG_5755	transcriptional regulator (drrA)	2	77.0	86.0	98.2	105.6	243.1	265.7	244.2	270.8
MSMEG_5789	MSMEG_5759	thiosulfate sulfurtransferase (cysA-1)	16	9903.7	9840.0	9702.1	9446.5	4363.8	4447.5	4109.9	4146.9
MSMEG_5790	MSMEG_5760	conserved hypotheticala	3	2104.9	2348.3	1742.3	1792.2	354.5	399.7	439.9	426.6
MSMEG_5792	MSMEG_5762	conserved hypothetical protein	2	124.2	126.9	104.4	114.0	141.3	158.1	112.7	118.7
MSMEG_5795	MSMEG_5764	aminotransferase, class IV	2	70.1	65.7	66.4	68.9	52.6	45.3	44.3	47.3
MSMEG_5798	MSMEG_5766	phosphoribosylformylglycinamidin e cyclo-ligase (purM)	2	151.1	141.2	146.3	121.6	601.6	548.2	675.8	609.3
MSMEG_5804	MSMEG_5771	hypothetical protein	1	308.8	303.3	336.9	326.2	4.5	9.5	1.1	4.0
MSMEG_5824	MSMEG_5789	phosphoribosylformylglycinamidin e synthase II (purL)	16	2922.0	3087.7	2215.8	2568.4	1992.9	2067.5	1926.2	2238.6



MSMEG _5830	MSMEG 5795	Linocin_M18 bacteriocin protein superfamily	4	592.6	618.9	750.5	748.1	894.0	878.3	962.7	963.7
MSMEG _5831	MSMEG 5796	phosphoribosylformylglycinamidin e synthase I (purQ)	4	1036.0	1100.8	793.8	793.5	625.2	658.8	648.8	641.4
MSMEG _5832	MSMEG 5797	phosphoribosylformylglycinamidin e synthase, PurS protein (purS)	1	136.9	179.8	94.0	107.7	233.6	303.6	228.0	250.6
MSMEG _5834	MSMEG 5800	metallo-beta-lactamase superfamily domain protein	1	21.5	16.1	9.9	14.6	22.5	17.7	16.2	19.4
MSMEG _5835	MSMEG 5801	3-ketosteroid-delta-1- dehydrogenase, putative	1	16.3	13.0	54.9	53.1	5.3	7.8	20.5	25.1
MSMEG _5837	MSMEG 5803	glutathione peroxidase family protein	2	439.1	499.7	243.7	266.6	338.7	382.0	261.4	268.2
MSMEG _5839	MSMEG 5806	protease II	5	430.7	441.0	407.7	413.4	258.2	281.7	234.2	298.7
MSMEG _5841	MSMEG 5807	phosphoribosylaminoimidazole- succinocarboxamide synthase (purC)	7	443.0	478.8	371.7	395.9	562.7	600.2	481.0	500.3
MSMEG _5847	MSMEG 5813	adenylosuccinate lyase (purB)	4	649.6	580.5	544.6	534.1	1212.1	1246.5	1623.7	1580.4
MSMEG _5852	MSMEG 5818	phosphoribosylamine--glycine ligase (purD)	9	1437.6	1166.3	1133.1	1173.0	1148.9	946.4	1322.3	1354.7
MSMEG _5871	MSMEG 5835	HIT family protein (pkcl)	7	634.9	663.7	804.3	808.5	604.2	618.5	760.5	697.8

MSMEG _5872	MSMEG 5837	DNA-binding response regulator PhoP (phoP)	2	405.6	394.6	174.0	171.8	166.5	171.9	135.3	146.0
MSMEG _5873	MSMEG 5838	conserved hypothetical protein	1	39.6	34.0	22.4	28.5	34.0	36.1	29.1	34.3
MSMEG _5884	MSMEG 5848	2-hydroxy-3-oxopropionate reductase, putative	3	258.3	239.9	190.7	190.9	246.5	247.7	177.0	183.3
MSMEG _5892	MSMEG 5854	alpha,alpha-trehalose-phosphate synthase (otsA)	2	90.4	98.3	103.7	102.3	138.7	152.2	157.1	156.6
MSMEG _5893	MSMEG 5856	conserved hypothetical protein	1	68.6	82.5	70.3	73.4	23.4	21.2	16.6	15.5
MSMEG _5925	MSMEG 5884	iron-sulfur cluster-binding protein, rieske family domain protein	1	35.5	31.6	20.5	32.5	4.7	2.6	5.0	5.2
MSMEG _5935	MSMEG 5893	ATP-dependent DNA helicase RecQ (recQ-1)	1	21.1	21.4	23.9	28.2	29.4	30.1	28.5	35.1
MSMEG _5937	MSMEG 5895	HMGL-like domain protein	2	400.4	360.5	408.8	375.0	260.0	225.1	201.9	189.0
MSMEG _5939	MSMEG 5896	acetaldehyde dehydrogenase (acetylating) (EC 1.2.1.10) Rv3535c	3	178.9	188.0	204.2	227.2	107.7	118.5	96.5	119.8
MSMEG _5940	MSMEG 5897	2-oxo-hepta-3-ene-1,7-dioate hydratase (hpaH)	2	158.6	166.2	300.7	266.5	295.2	312.5	344.1	340.7
MSMEG _5943	MSMEG 5899	MaoC family protein (ufaA2)	3	220.0	244.3	348.1	391.1	380.1	389.1	374.5	381.7

MSMEG _6008	MSMEG 5965	fadA6 (fadA6)	2	123.7	161.7	96.5	126.8	147.5	144.0	175.0	186.4
MSMEG _6024	MSMEG 5983	acetoacetyl-CoA synthase	3	108.2	106.3	71.4	80.0	71.8	69.8	42.8	70.4
MSMEG _6073	MSMEG 6035	spoU rRNA methylase family protein	1	19.1	16.1	9.8	9.0	13.9	12.1	7.6	8.2
MSMEG _6075	MSMEG 6037	2C-methyl-D-erythritol 2,4- cyclodiphosphate synthase (ispF)	1	5.8	0.0	5.4	4.4	21.4	0.0	12.0	15.9
MSMEG _6076	MSMEG 6038	2-C-methyl-D-erythritol 4- phosphate cytidyltransferase (ispD)	2	40.8	39.2	34.8	34.2	94.6	87.5	101.4	125.0
MSMEG _6077	MSMEG 6039	CarD-like transcriptional regulator family	1	30.6	26.1	18.5	20.7	1.9	1.7	0.5	0.2
MSMEG _6082	MSMEG 6044	carbonic anhydrase (icfA)	4	291.7	307.3	419.0	417.5	612.4	659.1	614.8	574.4
MSMEG _6086	MSMEG 6049	Antibiotic biosynthesis monooxygenase domain protein	4	500.7	597.7	491.9	461.2	455.4	529.2	648.9	606.1
MSMEG _6091	MSMEG 6054	clpC (clpC)	25	3502.1	3281.9	3883.1	3651.7	5182.1	4894.8	6314.3	6124.2
MSMEG _6092	MSMEG 6056	LSR2 protein precursor (15 kDa antigen) (A15)	3	555.2	448.8	501.9	529.3	259.2	276.7	324.2	315.5
MSMEG _6094	MSMEG 6057	lysyl-tRNA synthetase (lysS)	5	432.3	432.5	185.8	225.8	505.8	497.1	310.5	394.1
MSMEG _6096	MSMEG 6059	transcriptional activator, putative, Baf family subfamily	1	75.4	75.1	103.2	93.0	41.3	49.5	42.8	57.5

MSMEG _6097	MSMEG 6060	pantoate--beta-alanine ligase (panC)	2	989.8	1004.7	2888.0	2875.8	1387.3	1308.3	1635.2	1616.1
MSMEG _6105	MSMEG 6068	ATP-dependent metalloprotease FtsH	5	395.6	406.1	560.7	518.8	396.6	399.6	315.1	322.0
MSMEG _6110	MSMEG 6073	hypoxanthine phosphoribosyltransferase (hpt)	3	28.8	31.8	25.5	34.6	95.4	96.1	42.1	59.2
MSMEG _6114	MSMEG 6077	inorganic pyrophosphatase (ppa)	6	414.3	346.2	425.2	468.1	410.9	331.7	398.6	432.5
MSMEG _6127	MSMEG 6090	anti-anti-sigma factor family	2	7.9	1.2	12.3	16.6	12.3	7.5	20.0	22.6
MSMEG _6128	MSMEG 6092	response regulator	1	16.4	18.1	35.6	39.4	29.7	36.5	30.4	31.4
MSMEG _6142	MSMEG 6105	NAD-dependent epimerase/dehydratase family protein	10	1161.0	1116.4	732.6	760.0	748.5	756.0	619.4	627.9
MSMEG _6157	MSMEG 6120	DNA topoisomerase I (topA)	13	667.9	662.1	683.0	649.6	784.7	816.1	757.5	849.7
MSMEG _6159	MSMEG 6122	probable cold shock protein	1	10.7	15.0	33.5	38.3	7.9	10.0	31.9	35.4
MSMEG _6179	MSMEG 6139	acetyl-CoA synthase	16	2127.0	2140.0	2827.0	2713.6	4649.9	4332.5	4787.4	4495.6
MSMEG _6189	MSMEG 6148	cyclic nucleotide-binding domain protein	7	3634.0	3792.3	3803.1	3567.2	4352.4	4325.3	4330.0	4149.2
MSMEG _6191	MSMEG 6150	Putative translation initiation inhibitor	5	445.8	364.2	330.1	296.2	289.6	225.4	285.4	237.1
MSMEG _6195	MSMEG 6153	Anion-transporting ATPase superfamily	1	150.2	144.7	151.8	162.0	192.5	208.7	206.0	226.5

MSMEG_6207	MSMEG_6167	conserved hypothetical protein	6	73.2	53.7	74.2	72.7	171.8	130.9	167.5	164.8
MSMEG_6210	MSMEG_6170	hypothetical protein	1	2.5	3.9	18.0	22.7	110.0	124.1	99.6	109.6
MSMEG_6213	MSMEG_6172	Mn-containing catalase (dividedwithOB16)	1	11.3	14.5	6.7	12.2	93.9	110.0	109.7	118.2
MSMEG_6215	MSMEG_6174	Protein of unknown function (DUF541) superfamily	1	143.6	135.4	166.0	158.7	178.9	153.0	139.3	161.8
MSMEG_6229	MSMEG_6190	glycerol kinase (glpK)	4	277.0	265.8	658.1	683.1	398.7	405.4	411.9	444.1
MSMEG_6242	MSMEG_6203	alcohol dehydrogenase II	1	449.0	424.8	476.7	443.2	60.3	73.4	109.3	106.8
MSMEG_6243	MSMEG_6204	conserved hypothetical protein	1	7.4	6.7	24.0	10.1	10.1	12.2	11.8	11.7
MSMEG_6256	MSMEG_6217	aspartate-semialdehyde dehydrogenase (asd)	7	1305.0	1226.9	1178.4	1152.0	1554.7	1487.1	1414.1	1475.3
MSMEG_6257	MSMEG_6218	aspartate kinase, monofunctional class	3	928.3	1008.2	753.6	742.2	1246.4	1383.8	1198.0	1167.2
MSMEG_6271	MSMEG_6231	2-isopropylmalate synthase (leuA)	4	404.3	439.3	299.9	430.8	205.6	213.1	185.2	224.7
MSMEG_6280	MSMEG_6240	conserved hypothetical protein TIGR00103, putative	3	65.0	69.5	60.2	73.6	113.2	101.1	120.0	144.6
MSMEG_6282	MSMEG_6242	conserved hypothetical protein	6	784.4	882.9	518.3	557.3	2557.3	3016.3	2680.7	2582.9

MSMEG _6283	MSMEG 6243	FAD binding domain protein	1	32.0	25.0	71.0	55.3	37.6	34.8	23.2	23.2
MSMEG _6284	MSMEG 6244	cyclopropane-fatty-acyl- phospholipid synthase	4	1141.1	1077.3	1087.2	996.0	1076.7	1081.4	1298.2	1257.3
MSMEG _6285	MSMEG 6245	DNA polymerase III, subunit	3	192.2	198.3	193.0	196.9	180.2	191.8	186.7	208.5
MSMEG _6286	MSMEG 6246	conserved hypothetical protein	3	284.3	242.2	258.3	256.3	146.9	142.7	239.7	252.3
MSMEG _6288	MSMEG 6249	conserved hypothetical protein	1	10.5	13.8	1.8	12.4	6.9	11.1	0.1	9.5
MSMEG _6309	MSMEG 6269	amino acid ABC transporter, ATP- binding protein	1	43.8	44.4	60.0	56.1	251.4	233.3	255.6	195.2
MSMEG _6317	MSMEG 6277	arylesterase	2	638.6	695.8	436.2	460.8	454.2	464.5	348.9	373.0
MSMEG _6329	MSMEG 6290	conserved hypothetical protein	2	29.7	34.2	56.0	54.7	38.5	48.1	42.1	39.8
MSMEG _6337	MSMEG 6297	fadE36 (fadE36)	1	45.8	58.6	42.3	54.3	340.7	332.4	231.1	251.7
MSMEG _6351	MSMEG 6314	histidinol-phosphate aminotransferase (hisC)	4	1143.0	1092.2	933.8	883.0	697.2	722.9	640.4	611.6
MSMEG _6352	MSMEG 6315	conserved hypothetical protein	3	87.1	94.7	64.6	78.1	45.9	58.6	41.1	47.1
MSMEG _6353	MSMEG 6316	enoyl-CoA hydratase/isomerase family protein (fad-1)	8	672.9	718.6	644.1	657.5	684.3	733.4	608.6	680.7
MSMEG _6354	MSMEG 6317	serine esterase, cutinase family	1	5.1	3.7	6.1	5.2	53.8	48.8	61.3	52.2

MSMEG _6363	MSMEG 6325	conserved hypothetical protein	3	261.0	254.8	175.4	178.1	143.1	206.3	98.4	124.3
MSMEG _6365	MSMEG 6327	conserved hypothetical protein	1	115.9	124.3	123.0	126.3	108.2	123.7	137.8	142.9
MSMEG _6384	MSMEG 6346	catalase/oxidoreductase HPI (katG)	10	1355.4	1376.5	2392.4	2210.0	1121.3	1168.9	1431.4	1195.3
MSMEG _6385	MSMEG 6347	putative protein belonging to the short-chain alcohol dehydrogenase	3	367.6	353.4	274.0	308.5	380.1	348.5	311.7	344.2
MSMEG _6391	MSMEG 6353	propionyl-CoA carboxylase, beta subunit (pccB)	11	3131.8	2948.2	3140.8	2855.8	3389.0	3260.6	2999.8	2698.6
MSMEG _6392	MSMEG 6354	POLYKETIDE SYNTHASE PKS13	56	2971.6	2870.5	3227.1	3257.4	5675.2	5399.8	5144.1	4852.1
MSMEG _6393	MSMEG 6355	acyl-CoA synthase (fadD32)	26	6175.9	5755.1	7214.2	7245.2	9720.8	8839.8	9187.1	8986.5
MSMEG _6398	MSMEG 6360	esterase, putative, antigen 85-A	9	1520.5	1598.7	2290.2	2480.5	525.0	566.4	443.3	484.4
MSMEG _6399	MSMEG 6361	esterase, putative, antigen 85-C	2	26.3	29.4	73.3	69.5	29.5	44.0	37.7	38.4
MSMEG _6402	MSMEG 6364	PAP2 superfamily domain protein	5	119.6	97.6	95.4	90.8	92.6	77.5	75.9	75.2
MSMEG _6403	MSMEG 6365	conserved hypothetical protein	5	196.9	104.2	181.1	111.1	107.5	58.2	111.0	82.4

MSMEG _6404	MSMEG 6366	UDP-galactopyranose mutase (glf)	6	538.0	461.9	600.8	583.5	367.8	345.3	670.4	689.7
MSMEG _6408	MSMEG 6371	Acyltransferase domain protein	1	110.5	136.2	166.5	162.3	219.3	283.1	228.4	262.4
MSMEG _6409	MSMEG 6372	Acyltransferase domain protein	1	71.5	73.6	56.7	81.7	834.4	873.0	1192.1	1196.5
MSMEG _6410	MSMEG 6373	iron-sulfur cluster-binding protein, rieske family domain protein	3	263.9	249.7	324.4	288.3	249.8	274.7	272.9	252.5
MSMEG _6412	MSMEG 6375	conserved hypothetical protein	6	697.0	688.0	819.2	821.9	751.5	760.6	762.2	777.2
MSMEG _6413	MSMEG 6376	seryl-tRNA synthetase (serS)	1	128.7	119.4	130.4	130.1	23.5	26.6	17.8	16.8
MSMEG _6418	MSMEG 6381	pheA (pheA)	2	94.7	103.8	134.5	136.0	88.7	89.1	68.2	80.7
MSMEG _6422	MSMEG 6385	bfrB (bfrB)	3	58.4	71.3	167.2	170.0	418.1	461.1	452.1	444.8
MSMEG _6425	MSMEG 6388	rhodanese-like domain protein	1	31.5	37.7	25.0	27.2	76.0	56.7	46.9	63.3
MSMEG _6427	MSMEG 6390	superoxide dismutase (mn)	5	11360.2	12830.2	6802.7	8154.8	5403.9	6087.0	3957.8	4732.8
MSMEG _6431	MSMEG 6392	conserved hypothetical protein	13	1507.7	1442.4	1492.3	1555.2	927.4	903.9	938.8	959.5
MSMEG _6434	MSMEG 6397	conserved hypothetical protein	2	379.1	367.8	323.6	345.0	515.4	538.3	271.5	331.0
MSMEG _6439	MSMEG 6402	protein of unknown function, TIGR01935	2	576.1	587.1	444.3	422.7	387.6	378.9	401.6	344.9
MSMEG _6440	MSMEG 6403	arylesterase/monooxygenase	1	30.7	22.2	6.7	5.3	8.4	5.8	0.7	1.8



MSMEG _6452	MSMEG 6415	aldehyde dehydrogenase family protein	6	1705.9	1574.7	1795.3	1580.8	1546.2	1431.6	1878.9	1728.1
MSMEG _6454	MSMEG 6416	Luciferase-like monooxygenase superfamily	12	3758.4	3282.9	609.6	605.1	379.9	334.9	408.1	421.2
MSMEG _6457	MSMEG 6419	conserved hypothetical protein	1	8.9	14.5	42.9	52.0	37.5	44.9	37.4	53.1
MSMEG _6458	MSMEG 6420	gltD (gltD)	1	115.3	124.9	129.0	125.8	73.6	81.6	9.2	14.2
MSMEG _6459	MSMEG 6421	glutamate synthase, large subunit	19	592.2	561.8	772.4	740.0	674.2	673.1	651.8	719.5
MSMEG _6464	MSMEG 6424	uncharacterized domain 1 protein	1	1.3	1.4	3.9	2.9	4.7	3.2	5.7	4.4
MSMEG _6467	MSMEG 6427	Dps family protein, putative	1	108.1	106.8	62.7	63.2	255.7	235.2	259.6	226.8
MSMEG _6471	MSMEG 6431	conserved hypothetical protein	1	84.6	80.7	59.1	45.0	30.9	25.1	57.7	36.0
MSMEG _6477	MSMEG 6437	peptide methionine sulfoxide reductase (msrA)	1	44.5	48.9	30.4	31.3	6.6	10.7	2.9	5.4
MSMEG _6502	MSMEG 6463	hypothetical protein	4	354.4	283.9	394.5	411.4	304.9	282.1	326.7	297.0
MSMEG _6506	MSMEG 6467	unnamed protein product	1	39.3	44.9	29.9	30.7	288.7	309.1	430.3	313.7
MSMEG _6507	MSMEG 6469	glycogen operon protein GlgX (glgX)	9	778.0	792.4	468.0	458.0	764.3	828.2	730.0	731.8
MSMEG _6511	MSMEG 6473	bII7818 (fadE26)	1	185.1	194.2	143.6	153.9	136.8	138.7	101.3	106.3
MSMEG _6512	MSMEG 6474	bII7817 (fadE18)	5	634.5	601.8	486.8	462.3	928.8	846.4	825.5	805.0

MSMEG _6515	MSMEG 6477	alpha-amylase family protein	1	50.3	72.7	19.1	42.7	58.3	96.5	33.5	94.0
MSMEG _6520	MSMEG 6479	orotate phosphoribosyltransferase (EC 2.4.2.10)	3	130.3	109.7	131.0	146.2	305.2	271.4	273.2	291.0
MSMEG _6524	MSMEG 6483	ABC transporter, periplasmic binding protein	1	103.0	109.7	178.1	167.1	374.6	390.2	350.4	406.2
MSMEG _6535	MSMEG 1396	translation elongation factor G (fusA)	30	8506.0	8169.9	9041.9	8032.6	10787.6	10293.7	10491.8	9816.5
MSMEG _6561	MSMEG 6523	ltp2, putative	1	3.7	0.0	1.6	1.5	6.0	0.0	5.1	5.7
MSMEG _6565	MSMEG 6527	conserved hypothetical protein	5	736.0	783.8	584.9	598.3	649.5	686.1	619.4	621.9
MSMEG _6574	MSMEG 6535	conserved hypothetical protein	1	66.4	66.7	29.2	31.0	49.4	52.2	33.9	35.4
MSMEG _6587	MSMEG 6549	ATP-dependent helicase hrpA (hrpA)	1	3.7	4.4	1.8	2.7	5.9	6.5	3.2	5.0
MSMEG _6596	MSMEG 6557	conserved hypothetical protein	5	709.3	746.0	603.9	701.2	278.1	289.4	191.0	194.9
MSMEG _6622	MSMEG 6584	P450 heme-thiolate protein	1	235.3	286.3	177.9	164.1	35.2	46.3	42.8	45.9
MSMEG _6630	MSMEG 6591	glyoxalase family protein superfamily	5	298.0	88.3	293.3	308.8	304.7	139.2	356.8	314.4
MSMEG _6636	MSMEG 6597	superoxide dismutase (mn)	4	1738.9	1771.1	1406.5	1392.7	1423.3	1395.8	1116.5	1095.5

MSMEG _6638	MSMEG 6600	5- methyltetrahydropteroyltriglutamat e--homocysteine S- methyltransfera	23	4736.4	5085.6	10217.6	10050.7	1772.5	1880.5	2128.0	2035.7
MSMEG _6733	MSMEG 6692	carbon-nitrogen hydrolase family protein	1	82.1	87.0	78.6	97.0	92.6	97.4	95.6	112.9
MSMEG _6740	MSMEG 6701	1-aminocyclopropane-1- carboxylate deaminase	3	243.5	281.3	167.6	185.8	342.0	410.6	340.8	336.3
MSMEG _6741	MSMEG 6702	ANTAR domain protein	1	36.9	43.1	32.2	38.9	56.3	65.9	66.3	83.8
MSMEG _6743	MSMEG 6704	glyoxalase family protein, putative	1	40.0	39.7	53.1	49.8	35.8	38.0	36.6	31.5
MSMEG _6746	MSMEG 6707	oxidoreductase, aldo/keto reductase family	10	2381.4	2320.5	1546.8	1540.2	2409.3	2334.9	2561.4	2400.5
MSMEG _6754	MSMEG 6715	MaoC like domain protein	2	390.6	402.4	295.7	322.3	197.4	230.7	141.8	176.3
MSMEG _6756	MSMEG 6717	glycerol kinase (glpK)	1	24.8	20.2	30.3	28.4	51.0	46.8	47.0	43.2
MSMEG _6759	MSMEG 6720	glycerol kinase (glpK)	22	10985.4	10760.3	29889.0	29843.9	17852.3	17052.6	18325.0	18830.9
MSMEG _6760	MSMEG 6722	Aha1 domain superfamily	1	78.4	76.9	36.1	43.3	22.0	17.6	17.1	19.4
MSMEG _6761	MSMEG 6721	glpD2 (glpD2)	5	342.0	366.1	708.5	742.3	175.3	198.0	119.8	162.4
MSMEG _6776	MSMEG 6737	transcription regulator LysR family VC0896	1	81.7	61.5	71.2	62.4	181.3	117.4	77.3	74.0
MSMEG _6787	MSMEG 6749	sugar-phosphate isomerases, RpiB/LacA/LacB family	2	36.7	21.0	27.1	32.4	244.9	205.7	306.4	294.6

MSMEG _6816	MSMEG 6779	molybdopterin oxidoreductase	10	209.8	238.5	102.5	178.3	2213.4	2093.3	2019.7	1882.6
MSMEG _6822	MSMEG 6786	conserved hypothetical protein	3	589.7	718.2	502.6	674.9	766.6	866.8	745.0	799.7
MSMEG _6854	MSMEG 6817	aconitase (acn)	2	133.9	155.1	93.1	120.5	1.7	1.9	0.8	1.2
MSMEG _6875	MSMEG 6839	Endoribonuclease L-PSP family	1	71.0	71.4	30.0	32.6	102.1	115.8	70.0	112.0
MSMEG _6894	MSMEG 6855	ribosomal protein L9 (rplI)	8	2354.4	2556.9	2372.6	2453.8	1501.4	1647.5	1626.2	1462.8
MSMEG _6896	MSMEG 6857	single-strand binding protein homolog	5	1549.5	1680.8	1293.1	1457.8	804.5	840.8	840.5	855.3
MSMEG _6897	MSMEG 6858	ribosomal protein S6 (rpsF)	5	430.1	375.9	494.0	487.3	361.2	313.7	413.5	377.5
MSMEG _6904	MSMEG 6866	1L-myo-inositol-1-phosphate synthase	12	2975.1	2919.7	3401.1	3365.2	930.4	1017.2	962.7	1190.6
MSMEG _6907	MSMEG 6868	conserved hypothetical protein	2	163.6	148.3	124.9	127.9	191.7	175.3	209.4	176.4
MSMEG _6913	MSMEG 6872	transcriptional regulator, MarR family	1	11.2	0.0	11.1	12.1	12.9	0.0	9.2	9.9
MSMEG _6917	MSMEG 6875	leucyl-tRNA synthetase (leuS)	20	1716.7	1502.8	1190.7	1322.2	2054.4	2184.7	1760.2	2127.8
MSMEG _6926	MSMEG 6882	pcnA (pcnA)	1	0.7	0.6	1.2	1.2	1.8	1.4	0.3	0.4
MSMEG _6929	MSMEG 6886	integral membrane protein MviN, putative	1	16.0	13.3	16.8	16.9	42.5	46.3	33.2	43.7
MSMEG _6933	MSMEG 6889	thioredoxin-disulfide reductase (trxB)	3	417.4	433.6	406.6	424.1	230.2	218.6	119.5	131.2

MSMEG_6934	MSMEG_6890	thioredoxin (trx)	4	146.7	103.3	93.1	102.0	234.5	175.7	183.9	193.3
MSMEG_6941	MSMEG_6896	R3H domain protein	6	517.4	506.3	552.3	549.2	307.9	297.3	382.0	392.0
MSMEG_6947	MSMEG_6901	chromosomal replication initiator protein DnaA (dnaA)	2	32.0	38.3	8.6	19.1	108.2	124.0	33.7	51.0
MSMEG_1843	MSMEG_1843	adenosylhomocysteinase	3	906.3	977.0	1142.5	1202.9	1005.5	1070.7	764.0	880.3
MSMEG_2968	MSMEG_2968	substrate--CoA ligase, putative	3	149.7	126.6	1.3	1.8	17.6	18.4	3.1	7.5
MSMEG_3192	MSMEG_3192	maltooligosyltrehalose synthase (treY)	2	176.9	181.7	113.8	119.4	176.0	178.5	205.5	178.1
MSMEG_3892	MSMEG_3892	conserved hypothetical protein	1	22.1	19.6	8.9	11.4	7.5	8.0	1.7	3.9
MSMEG_5534	MSMEG_5534	conserved hypothetical protein	2	112.2	119.9	72.5	79.3	68.3	72.7	45.2	51.1

**Supplemental Table II.** List of quantified peptide charge states (PCSs).

Proteins		PCS quantitaion									
		PCS		$A_{PCS}$							
				from protein sample $S_p$				from protein sample $R_p$			
Locus	old locus	Tryptic peptide sequence	Chai	$S_{P,1}$	$S_{P,2}$	$cS_{P,1}$	$cS_{P,2}$	$R_{P,1}$	$R_{P,2}$	$cR_{P,1}$	$cR_{P,2}$
MSMEG _0001	MSMEG 0001	K.AGTDGNQVHLALGSGAS VGK.D	2	31.7	22.0	119.1	57.9	32.2	35.9	126.5	142.4
		K.AGTDGNQVHLALGSGAS VGK.D	3	139.7	143.2	146.8	149.6	169.0	141.4	175.3	161.8
		R.EDFADAVAWVAR.S	2	100.3	99.1	70.5	80.9	107.5	108.7	71.6	78.9
MSMEG _0002	MSMEG 0002	-.MQLGLIGLGK.M	2	21.3	24.7	58.8	62.8	48.8	50.2	62.2	65.6
		K.ALKEDPGFAEISGYTEDS GEGR.W	3	132.2	140.4	222.3	227.2	270.4	257.4	332.2	341.9
		K.EDPGFAEISGYTEDSGEG R.W	2	26.1	26.2	51.9	51.8	23.4	25.0	22.9	27.8
		R.SWLQSLLAK.A	2	33.1	31.8	62.4	59.4	60.3	54.2	68.5	58.5
		R.VPMPVIAASLFAR.F	2	61.0	62.9	172.3	182.7	114.7	105.1	206.0	212.2
		R.WTVEEAIAHR.V	3	2.1	0.1	4.2	0.8	8.4	6.6	2.1	4.0
MSMEG _0005	MSMEG 0005	K.EYGADSITILEGLEAVR.K	2	193.3	184.6	71.9	58.9	231.9	192.3	80.0	72.8
		K.FDGETYAVSGGLHGVGV SVVNALSTR.L	3	261.1	243.9	124.9	122.2	302.3	275.2	120.0	125.1
		K.GLTIELTDER.V	2	19.4	14.7	10.6	11.7	25.9	13.8	5.1	10.2
		K.IC#NEQLQHWFEANPAEA K.T	3	229.0	262.4	112.6	106.6	244.6	267.2	144.6	115.5
		K.IHADGSVEVR.D	2	4.6	3.3	1.0	0.7	5.3	4.7	1.1	1.3
		K.NTEVQSIITALGTGIHDEF DISK.L	3	312.0	366.7	120.4	136.9	357.3	372.4	154.3	154.0
		K.SELYVVEGDSAGGSAK.S	2	17.3	13.9	2.3	3.6	8.2	11.0	0.5	1.1
		K.TPIQQSIIDFDGK.G	2	200.5	220.0	401.9	406.1	153.2	177.9	268.9	282.2

		R.DSMFQAILPLR.G	2	79.7	71.0	15.6	15.7	92.4	70.3	22.1	15.8
		R.EGLAAVISVK.V	2	20.4	14.7	14.5	11.7	28.6	20.0	7.0	6.5
		R.STDPSKSELYVVEGDSAG									
		GSAK.S	3	29.7	32.6	30.2	19.4	42.6	49.6	27.6	23.5
		R.VFHYPGGLVDYVK.H	2	95.2	98.0	41.6	50.6	105.0	111.4	54.8	66.3
		R.VTAEEVVDDVVKDTAEAP									
		K.T	2	96.9	98.4	30.2	29.1	143.7	122.6	45.2	75.2
		R.VTAEEVVDDVVKDTAEAP									
		K.T	3	219.1	220.8	49.8	49.0	305.8	273.8	89.1	65.4
MSMEG	MSMEG										
_0006	0006	K.ALDALDEVIALIR.A	2	147.2	146.2	62.6	59.3	226.9	170.7	98.9	70.7
		K.ALDALDEVIALIR.A	3	10.1	8.7	0.3	0.3	11.5	13.6	0.9	1.7
		K.IEAEIADLEDILAKPER.Q	2	68.2	70.8	104.8	95.1	80.6	84.7	167.0	249.0
		K.IEAEIADLEDILAKPER.Q	3	126.3	119.1	43.3	44.4	151.4	135.8	47.9	46.4
		K.LAGISNIEDQSSDR.V	2	37.5	30.2	11.7	9.0	30.9	32.3	14.3	12.5
		K.SYEDAPYLVLATR.N	2	175.1	201.4	50.2	52.4	247.3	227.3	70.5	77.7
		R.EIDEETVDFIPNYDGR.V	2	116.8	116.9	21.0	30.6	127.7	145.1	26.9	34.3
		R.GQHVANLLAFQPEER.I	2	81.5	79.6	10.3	10.7	106.2	117.6	14.0	21.1
		R.GVVEIEEDSR.G	2	1.5	0.8	0.6	0.1	1.0	2.0	0.1	0.2
		R.IEPVDIQQEMQR.S	2	115.8	102.0	26.5	27.3	94.0	94.4	13.7	20.8
		R.IVPADGEVSEDEDLIAR.E	2	591.8	565.4	220.5	206.4	625.5	668.0	221.8	244.3
		R.LLSLNVVRPDTYLLVATSG									
		GYAK.R	3	288.4	318.9	106.6	128.3	355.4	407.4	136.2	147.6
		R.LMNLAEGDTLIAIAR.N	2	135.0	121.3	160.1	116.8	210.5	135.8	186.7	132.1
		R.LYVDHQLDVIVR.R	3	54.8	46.5	4.6	3.7	78.6	56.4	5.4	3.7
		R.NADEDEAAESISESDADT									
		AESPEA	2	12.9	24.0	0.2	1.6	2.6	22.8	0.1	3.1
		R.SGGIVAINLR.E	2	6.1	2.8	3.4	2.5	8.6	8.3	10.9	6.1
		R.SVAETMGNYHPHGDASIY									
		DTLVR.M	3	100.3	110.7	33.8	53.3	114.6	123.9	24.2	57.4
		R.TSIVITELPYQVNHDNFITS									
		IAEQVR.D	3	193.7	249.0	98.2	166.7	238.5	282.6	96.1	155.8
		R.VKGPDPFPTSGLIVGTQGIE									
		DTYK.T	3	247.6	285.8	113.7	130.7	354.1	353.7	115.3	154.6
MSMEG	MSMEG	R.GVLGIGADTAQATAAELR.									
_0023	0023	R	2	237.3	284.0	175.7	216.3	148.5	145.3	215.5	199.4

		R.SRPQEPPTLAPSVEVAPK P	2	23.5	22.5	11.6	13.9	9.0	8.2	4.5	5.3
		R.SRPQEPPTLAPSVEVAPK P	3	208.4	233.5	197.6	221.9	110.6	123.8	171.0	179.2
MSMEG	MSMEG	K.DYSTENASGGTSGPFYD GAVFHR.V	2	194.5	189.1	83.2	88.0	119.3	111.7	65.3	82.4
_0024	0024	K.DYSTENASGGTSGPFYD GAVFHR.V	3	1935.2	2251.3	1318.3	1484.3	1253.2	1364.6	1228.1	1307.4
		K.TVNNFVGLAQGTK.D	2	99.5	85.2	245.1	221.7	75.6	74.8	197.3	215.3
		K.VVDAIASTPTDR.S	2	3.1	2.8	0.5	0.5	2.9	2.4	0.7	0.8
		R.HTIFGEVVDEESQK.V	2	646.9	453.0	462.5	316.8	506.6	467.2	483.6	452.4
		R.HTIFGEVVDEESQK.V	3	413.9	349.8	240.0	208.5	329.9	287.8	299.4	248.6
		R.RHTIFGEVVDEESQK.V	3	86.7	95.8	19.5	24.2	48.2	54.5	19.0	26.7
		R.SDRPTEPVVIESITIA	2	91.8	99.2	30.4	29.5	67.8	72.7	28.0	29.2
		R.VIDGFM#IQGGDPTGTGR. G	2	201.5	195.6	102.2	110.3	123.7	138.0	100.2	111.7
		R.VIDGFM*IQGGDPTGTGR. G	2	219.7	221.9	103.6	113.3	130.9	144.3	100.3	112.4
		R.VIDGFMIQGGDPTGTGR. G	2	1158.7	1306.7	870.0	921.5	840.1	860.5	912.3	931.1
		R.VIDGFMIQGGDPTGTGR. G	3	89.1	91.4	48.8	41.3	61.2	50.9	40.4	43.4
MSMEG	MSMEG	K.EALQIEDVAESADR.L	2	316.7	251.6	77.2	85.2	259.6	232.3	48.9	56.2
_0033	0033										
MSMEG	MSMEG	R.ITLGNQPVLIGR.A	2	11.4	11.7	25.5	31.0	18.8	21.0	21.4	20.1
_0034	0034										
MSMEG	MSMEG	R.FAADDTPSPLTEAFAQLR. D	2	16.4	19.0	9.8	10.5	9.1	13.0	12.5	9.8
_0042	0042										
MSMEG	MSMEG	R.DPTVTVLIEDGHTYDTLR. G	2	5.9	11.8	12.3	19.6	16.0	15.9	4.4	7.1
_0048	0048										
		R.GVSIDGTAEIVDDPETLLR. V	2	33.0	33.0	30.7	34.6	78.6	75.0	29.3	24.6
MSMEG	MSMEG	R.ALEGLVEFLPSK.T	2	6.9	5.9	53.1	45.5	18.2	18.1	31.6	32.7
_0057	0056										
MSMEG	MSMEG	R.ALGGVLFIDEAYTLVQER. N	2	1.4	4.0	39.6	51.5	1.1	2.8	14.4	36.9
_0059	0058										
		R.IEFDSYSPDEIVEISK.V	2	28.5	38.0	195.7	210.2	20.2	37.1	127.6	162.2



		R.NGQTDPPFGAEALDTLLAR									
		.M	2	28.7	43.5	60.8	64.7	16.5	28.2	38.3	58.6
		R.SDPWDPSSVVADTSAR.D	2	27.0	36.3	90.8	108.9	15.3	44.3	54.0	83.3
MSMEG	MSMEG	K.GVIAQVESTGSALAAQMV									
_0065	0064	GQAGTAAQAALAR.F	3	12.3	16.7	15.7	24.3	16.5	25.7	8.8	16.2
MSMEG	MSMEG	K.ASLTTLASAWGGTGSEAY									
_0066	0065	QAVQAR.W	3	81.1	76.4	116.5	101.3	159.9	177.5	117.6	125.8
MSMEG	MSMEG										
_0067	0066	R.ILAIDADPDGGNLADR.A	2	25.9	33.2	97.8	113.1	175.2	172.2	133.9	146.8
MSMEG	MSMEG										
_0076	0074	R.EFEETEWASEWDR.Q	2	0.2	0.6	22.4	33.0	0.2	0.7	8.6	26.9
MSMEG	MSMEG										
_0081	0078	R.ERLDALVADITAEDV	2	391.5	406.5	7.4	11.2	175.3	206.3	0.6	5.5
MSMEG	MSMEG										
_0084	0082	K.GAQVTVSSDDADVLAK.V	2	4.2	3.4	11.9	8.9	4.8	6.1	16.1	15.1
MSMEG	MSMEG	R.VWSSLDPDVYTVQSVVD									
_0091	0089	R.L	2	12.2	18.0	57.7	54.5	15.0	19.0	17.9	27.8
MSMEG	MSMEG										
_0092	0090	K.FVAWAVNDAIER.G	2	52.4	63.1	120.4	141.2	34.3	43.6	55.3	64.4
		K.FVAWAVNDAIER.G	3	7.1	5.6	1.3	0.4	6.6	7.3	1.7	1.5
		R.ADLTRPAINHYFGSK.R	3	24.1	23.0	74.0	65.1	39.4	42.1	61.6	76.1
		R.EVVEQTNATVIAAGVAR.A	2	17.2	22.3	155.3	155.0	32.3	33.0	120.1	131.2
		R.HPDLVSEEQDALLNSR.K	2	112.3	133.7	154.2	142.4	80.2	89.8	98.6	116.1
		R.KFVAWAVNDAIER.G	2	83.9	112.9	77.9	95.2	150.0	157.3	72.1	75.1
		R.KFVAWAVNDAIER.G	3	37.9	33.6	22.3	22.7	47.3	40.1	25.2	25.8
		R.SEELAAIVDKFEMLMANK.									
		L	2	3.3	4.9	11.2	8.0	5.3	5.0	7.0	5.3
		R.SEELAAIVDKFEMLMANK.									
		L	3	9.6	9.1	29.4	30.6	16.5	13.4	26.1	23.7
		R.SSA AFLVTSVLESQR.H	2	45.3	54.7	28.2	32.7	49.8	54.1	27.5	27.1
MSMEG	MSMEG	K.GVSC#FLVPGDLPGLSFG									
_0108	0105	KPEEK.M	3	112.1	94.9	56.6	53.8	108.9	108.8	92.5	91.2
MSMEG	MSMEG										
_0110	0107	K.VNAPSEGEIAALR.D	2	13.0	17.9	123.9	111.0	31.7	34.8	137.0	101.6

		R.DGATLISLISPALRPDLVE									
		QLGTR.N	3	4.3	4.1	4.0	5.5	5.7	7.0	2.8	4.5
		R.LPAQSSQLYGTNLVNLLK.									
		L	2	21.3	20.5	32.9	35.0	43.1	42.1	40.5	29.3
MSMEG	MSMEG										
_0120	0116	R.VESPLGIDVQAGSEEQR	2	8.8	8.2	99.9	102.9	9.9	13.5	52.0	70.2
MSMEG	MSMEG										
_0131	0125	K.ALEVVDALPR.N	2	1.7	1.3	7.1	9.1	7.1	6.2	4.1	13.8
MSMEG	MSMEG										
_0166	0160	K.AIAAHDVEQATDIMR.R	2	23.1	24.1	23.8	22.9	25.5	31.2	41.6	39.1
MSMEG	MSMEG										
_0215	0205	R.GVSVTDWLQSR.H	2	2.9	1.8	6.1	3.6	0.8	2.0	3.7	4.1
MSMEG	MSMEG										
_0216	0206	K.GGVVGLTLPVAR.D	2	556.6	536.9	332.4	310.3	499.8	443.0	378.6	331.1
		K.VLAINLVGTFDC#IR.I	2	270.8	238.3	416.3	387.6	179.4	153.4	435.3	381.3
		K.VLAINLVGTFDC*IR.I	2	270.8	238.3	416.3	387.6	179.0	153.4	435.3	381.3
		K.VVIADLQADKGEALAK.E	2	356.9	315.8	379.6	399.5	347.3	303.1	1042.5	1278.8
		R.ALVNSAGIGWAQR.T	2	914.6	868.1	519.6	518.5	707.4	975.1	480.2	566.8
		R.VNTVAPGLIDTPIYGEGEG									
		SEAFK.A	2	300.1	341.4	201.8	214.2	206.2	236.1	185.7	202.3
		R.VNTVAPGLIDTPIYGEGEG									
		SEAFK.A	3	373.0	415.3	251.7	264.1	245.7	269.2	186.0	217.2
MSMEG	MSMEG										
_0220	0210	K.LVLDDVTSWIVSHL	2	4.5	4.4	11.6	17.9	3.4	3.0	9.4	19.5
MSMEG	MSMEG										
_0224	0214	K.LLSLLAGISGAR.R	2	96.5	89.0	36.1	31.2	44.8	41.2	27.7	29.2
		R.VEILVGTALDTLPK.L	2	187.0	181.6	144.0	149.7	68.1	68.4	89.6	107.1
MSMEG	MSMEG										
_0229	0219	K.GTLDVLVDEEEFEAR.K	2	396.0	366.6	348.7	316.5	263.4	254.1	364.4	303.0
		K.SAGFSDSVFEGTAR.V	2	75.6	60.6	331.3	249.9	37.2	30.5	167.4	119.8
		R.AMNNPIHPTGGITILHGSL									
		APEGAVVK.S	4	163.9	147.5	284.9	250.7	98.5	89.9	147.6	153.3
		R.EAEVELTLDDFTR.V	2	68.9	74.9	77.4	80.2	40.8	37.7	51.7	40.7
		R.EVIADSVETVVQAER.L	2	1753.8	1710.2	1267.8	1185.8	1488.3	1436.6	1381.0	1247.0
		R.LDLASVFFYNGSIMPQVA									
		K.L	2	33.5	41.8	37.4	35.8	10.1	21.9	12.4	28.8

MSMEG	MSMEG	R.VGDYLVATVDDSTHQMEI									
_0233	0223	R.R	3	90.9	101.6	132.2	141.7	79.3	110.1	182.7	176.3
MSMEG	MSMEG										
_0234	0224	K.ALIEQYEQFTPR.G	2	649.2	697.0	319.5	332.7	378.0	373.8	336.4	302.5
		K.EAPVIDGLTGVQR.V	2	333.3	244.7	192.3	122.3	247.3	105.7	250.5	107.7
		K.MFGLIYGGDHTDTAAR.I	2	104.1	107.4	12.1	20.3	44.8	63.7	19.9	39.5
		K.MFGLIYGGDHTDTAAR.I	3	130.0	118.6	36.7	34.9	88.1	85.4	50.0	53.5
		K.YDGDGNLVDWWTDADR.									
		T	2	205.5	231.1	72.2	79.2	95.6	117.1	78.6	88.8
		R.AGLLTDDLVAEDFAFYGR.									
		T	2	402.8	371.3	193.5	173.5	279.0	238.3	256.0	201.7
		R.AVSVVENLMGDALGK.L	2	613.6	616.3	440.0	423.0	523.9	377.0	508.4	413.0
		R.DEQHAEILAGYPVHIAK.M	2	38.8	40.1	6.2	6.5	16.8	18.8	3.1	8.3
		R.DEQHAEILAGYPVHIAK.M	3	190.1	191.9	49.1	65.1	101.0	101.8	48.3	48.3
		R.DLITEAAASGAADGTDEQ									
		R.I	2	260.2	259.4	74.5	77.4	111.5	125.6	59.9	81.5
		R.IGDLYASFMDTQTIAER.G	2	169.2	153.1	45.8	37.8	111.4	86.7	59.7	37.4
		R.TGVGGGAGVYVDTDSK.N	2	117.1	103.0	52.1	47.4	59.0	68.9	44.1	54.3
		R.VFFGWAQVWR.T	2	54.3	65.1	8.7	16.4	34.4	37.4	10.6	18.8
		R.VSIDELDWM*TPETR.A	2	33.4	29.6	7.6	9.2	11.1	12.6	5.9	0.8
		R.VSIDELDWMTPETR.A	2	298.4	312.9	216.2	235.3	158.1	149.2	212.8	195.0
MSMEG	MSMEG	K.EIEGTPVYPSLSELPVVPD									
_0238	0229	LVDVFR.R	3	52.1	62.9	46.5	57.4	43.9	85.6	29.8	55.2
		K.STGDYDIYLVNPTIK.E	2	160.0	168.6	174.0	181.1	190.2	198.8	137.1	131.4
		K.TLWLQLGLR.H	2	17.9	16.2	8.1	7.7	24.2	25.2	5.6	6.2
		R.ASYFVWTYLK.S	2	642.5	524.1	20.1	21.4	763.1	785.2	18.8	23.0
		R.DGEAAGLQVVQDR.C	2	50.0	48.7	46.6	43.1	52.5	60.9	40.9	43.1
		R.FAGGLHLAGFNTGVIDSR.									
		R	3	62.7	56.1	33.1	25.4	83.9	84.5	27.7	27.2
		R.SVAIVGASANTSR.A	2	3.0	2.2	1.4	1.0	4.4	2.6	1.4	0.6
MSMEG	MSMEG	K.FIGGHGTTLGGVAVDAGR									
_0239	0230	.F	3	470.6	405.9	425.8	388.3	426.5	403.5	429.2	425.7

MSMEG _0255	MSMEG 0246	K.FINSVQLASHLANIGDVR.T	3	43.0	36.2	11.9	1.8	100.5	80.8	23.9	19.2
		R.FGIDTTFVGGTDPADYAA AVTDR.T	2	65.6	79.0	24.5	39.0	100.6	92.5	24.6	25.9
MSMEG _0255	MSMEG 0246	K.AYFIAAAFPSAC#GK.T	2	615.1	598.0	49.7	56.1	693.7	645.0	69.6	53.1
		K.HQGLLAWVQEVAELTQP DR.V	2	41.3	48.8	1.8	2.1	38.3	159.8	0.6	3.2
MSMEG _0255	MSMEG 0246	K.HQGLLAWVQEVAELTQP DR.V	3	187.4	239.9	24.9	34.1	199.8	289.0	26.2	30.7
		K.LPTGLKDEFDALK.H	2	309.7	304.1	274.2	316.0	414.0	419.3	218.3	300.9
MSMEG _0255	MSMEG 0246	K.LPTGLKDEFDALK.H	3	367.6	330.4	41.2	30.7	486.0	446.8	42.9	49.0
		K.QPNSYLALSDPSDVAR.V	2	22.9	27.7	15.2	4.9	48.5	58.2	40.2	13.6
MSMEG _0255	MSMEG 0246	K.TDDGDVWWEGLEGDPQ HLIDWK.G	3	118.2	185.5	8.0	24.9	114.4	177.2	7.8	15.8
		K.TIAAGNTVFTNVAK.T	2	238.7	187.9	138.7	133.6	341.6	172.2	145.8	142.5
MSMEG _0255	MSMEG 0246	K.TNLAM*LQPTIEGWR.A	2	74.5	76.0	7.0	7.2	69.6	76.8	6.9	5.2
		K.VFFVNWFR.R	2	206.1	243.7	17.9	22.3	333.3	277.0	30.7	19.1
MSMEG _0255	MSMEG 0246	R.AELPLIEEWFEFVGEK.L	2	65.8	89.9	10.0	14.1	63.7	105.9	5.5	15.0
		R.AELPLIEEWFEFVGEK.L	3	13.2	18.2	0.8	0.6	13.8	18.8	0.7	1.0
MSMEG _0255	MSMEG 0246	R.AETVGDDIAWMR.F	2	235.6	241.3	22.6	31.5	293.3	254.6	26.6	25.0
		R.DWQHGVFIGATLGSEQT AAAEKG.V	3	340.1	323.2	21.0	38.4	449.1	398.0	27.2	63.1
MSMEG _0255	MSMEG 0246	R.EIDAGPTNNWM*DPAEM* R.G	2	15.5	13.8	0.7	1.0	10.3	13.3	1.3	3.7
		R.EIDAGPTNNWMDPAEMR. G	2	169.8	160.8	5.2	3.8	147.2	159.1	1.3	3.7
MSMEG _0255	MSMEG 0246	R.EIWSFGSGYGGNALLGK. K	2	440.7	433.0	145.7	156.6	636.5	510.0	159.1	153.8
		R.FLWPGFGENSR.V	2	320.1	326.5	31.7	40.0	459.1	418.6	50.9	40.2
MSMEG _0255	MSMEG 0246	R.IASAMAHDEGWLAEHMLI LK.L	3	173.2	162.6	44.2	52.4	202.8	170.3	30.5	31.5
		R.LC#AHLVEAGTFQK.L	2	88.4	67.5	15.6	9.2	110.9	83.9	3.0	4.0
MSMEG _0255	MSMEG 0246	R.LC#AHLVEAGTFQK.L	3	129.5	105.7	21.9	22.7	162.8	138.4	12.2	14.2
		R.LYATNPEFGFFGVAPGTN WSSNPNAMK.T	3	187.5	246.0	11.9	21.6	89.0	215.4	4.1	16.7

		R.VVFADGSDEEYER.L	2	25.0	19.6	2.1	0.6	18.2	25.9	0.4	0.6
MSMEG	MSMEG										
_0312	0301	K.ALVEGGLPVIELTLR.T	2	13.8	13.0	155.6	143.7	7.0	10.5	130.8	116.0
MSMEG	MSMEG	K.VTTNEESVESQVAAASDE									
_0317	0306	RDR.I	3	36.1	26.5	43.4	40.5	117.2	144.5	89.2	113.7
		K.YSSLYEDDADASVTAR.A	2	11.8	13.2	11.1	15.8	20.8	22.5	9.0	10.5
MSMEG	MSMEG	K.FSGQGLAGELVSAGLSDA									
_0356	0347	K.A	2	24.6	29.9	12.9	19.2	8.2	9.2	9.7	8.0
MSMEG	MSMEG										
_0363	0355	R.TAVLAFLTYIDR.N	2	8.7	8.8	13.0	10.4	1.8	3.1	8.9	9.9
MSMEG	MSMEG										
_0370	0363	K.FGVIDTIDNAMVR.D	2	31.8	26.0	47.5	38.6	23.6	26.4	34.8	43.4
		K.LRPSDYIFVGGTEAK.V	2	7.3	8.9	6.0	8.5	14.1	8.5	6.6	6.3
		K.SDPQFAQQALSAFR.K	2	44.2	45.7	41.1	42.3	36.4	40.3	25.5	30.6
		K.SSLLDAISLAFLPSHR.R	2	9.3	9.2	9.9	10.2	9.8	6.9	2.1	3.4
		K.SSLLDAISLAFLPSHR.R	3	10.3	9.7	0.8	1.2	9.2	7.6	1.1	1.0
		K.SVGGLEQFVR.E	2	19.6	16.0	13.5	13.0	11.1	12.0	8.5	12.9
		K.VAALQADLAAAEDVYAAA									
		R.K	2	19.9	17.9	5.9	9.7	18.8	19.0	5.9	10.1
		R.LQDELDLLVSDNPDVEK.L	2	17.8	18.3	1.1	0.8	15.9	14.4	1.2	1.3
		R.VNTGLGAVEFNR.G	2	26.2	26.2	6.3	6.8	15.0	19.1	8.1	6.2
		R.WAAGGYDASVFR.E	2	3.7	4.2	19.6	15.2	3.7	6.8	16.8	12.3
MSMEG	MSMEG										
_0371	0364	R.AVVGALPFVTR.S	2	55.7	62.4	143.9	146.8	54.2	54.7	99.9	104.5
		R.HYAAVGGDHNPIHTNAIA									
		AK.L	3	0.3	0.1	0.2	0.1	1.1	0.4	0.2	0.4
		R.HYAAVGGDHNPIHTNAIA									
		AK.L	4	2.9	1.6	1.1	0.3	5.1	3.9	3.0	2.1
MSMEG	MSMEG										
_0372	0365	K.AGMIGLAEALAPVLADK.G	2	251.8	216.8	173.9	152.4	124.5	107.7	144.4	117.4
		K.ELYTFFTPLL.R.N	2	114.8	103.5	66.9	74.5	94.5	82.9	97.7	79.3
		R.GIGATIAEVFAR.D	2	137.9	119.7	50.1	51.0	87.8	73.5	70.6	59.6
		R.TALADDYNLVSNNIGGR.									
		W	2	239.3	228.2	246.4	234.3	178.9	161.1	423.3	372.2

		R.TALADDYNLVSNNIGGR.									
		W	3	28.9	25.6	59.0	27.5	125.6	92.7	806.1	480.2
		R.VVVVGTTPAEAGSVHAQV									
		VQR.A	2	36.4	18.5	14.9	4.0	16.8	17.7	16.7	13.4
		R.VVVVGTTPAEAGSVHAQV									
		VQR.A	3	1472.1	1232.5	1112.4	1040.3	921.2	984.3	1218.0	1278.0
		R.YRPGDPPLAGSLLIGGSG									
		R.V	3	75.8	63.8	31.2	32.4	42.6	43.1	25.3	25.9
MSMEG	MSMEG	K.LNVNGSSLAAGHPFAATG									
_0373	0366	GR.I	3	135.7	159.2	127.3	104.3	111.1	122.6	157.0	153.0
		K.LPASLGVEIPVNSEPR.T	2	348.1	353.9	500.8	558.4	201.6	200.6	380.5	380.9
		R.FNLAGEQLGAVIGGAVLK.									
		H	2	232.5	207.3	202.5	177.7	138.6	129.1	248.8	220.7
MSMEG	MSMEG										
_0380	0373	K.VSNQTNFTSC#LLK.A	2	53.0	80.4	54.0	61.9	57.8	76.8	43.1	46.7
MSMEG	MSMEG										
_0384	0377	R.DILVITTPADAPAFR.R	2	32.9	37.8	323.7	314.1	50.0	55.8	331.9	321.6
MSMEG	MSMEG										
_0386	0379	K.WTLDDGLPALLDWIAK.S	2	16.1	23.5	25.3	31.1	9.4	10.9	10.6	18.1
MSMEG	MSMEG	R.SVTMTADDSVPEETSIGR.									
_0387	0380	I	2	93.2	93.9	20.8	24.1	68.0	85.3	22.0	30.6
MSMEG	MSMEG	R.DLGLDWPADALTMIGMTR									
_0388	0381	.L	2	25.1	26.1	31.9	39.6	47.2	57.6	40.5	47.4
		R.LDGDLYESTIQALDGLYER									
		.L	2	56.4	44.2	57.2	63.8	77.0	97.8	62.8	71.0
		R.LHLAAPILAVSEQDVR.A	2	38.2	42.6	67.9	69.7	79.7	73.8	80.6	81.1
		R.LHLAAPILAVSEQDVR.A	3	89.6	91.1	134.5	131.4	178.7	174.0	171.0	166.8
		R.VWLC#DSFAGVPAPDAAK									
		.Y	2	41.1	40.8	67.7	70.3	50.8	65.6	106.0	114.8
		R.VWLC*DSFAGVPAPDAAK									
		.Y	2	37.4	37.6	67.7	70.3	49.2	65.1	106.0	114.8
MSMEG	MSMEG										
_0391	0384	K.TFYLLDTFAGLDPR.Y	2	69.7	66.7	101.5	92.0	74.4	73.3	105.9	107.2
		R.LSPGAFVLLDDYANR.G	2	146.9	148.3	247.8	263.9	190.2	191.8	276.8	280.5
MSMEG	MSMEG										
_0393	0386	K.NLDALESVVDR.V	2	18.1	22.8	55.1	58.0	24.5	34.1	51.2	58.0
		R.FDVFLTEVAR.V	2	0.8	2.2	50.4	42.6	4.1	4.2	74.6	60.8

MSMEG _0394	MSMEG 0387	R.TFRPATYTGGLDNLNSDGINF									
		C*R.R	3	7.4	6.4	76.6	93.8	12.4	14.7	60.1	71.5
		R.VLRPGGYFLYTDAR.P	3	4.7	9.2	34.5	34.1	10.1	5.1	23.5	16.1
		R.GLDWLAAPK.R	2	10.9	7.0	22.5	15.9	55.2	45.1	29.3	27.3
		R.GSSPIEGTQVSAEDSAVD									
		GK	2	5.5	4.3	15.3	13.0	8.6	10.1	17.4	21.8
MSMEG _0400	MSMEG 0390	R.GSSPIEGTQVSAEDSAVD									
		GK	3	0.8	0.6	2.6	1.3	1.3	1.8	2.2	3.7
		R.VPLFFMLMPR.G	2	0.4	0.5	1.6	2.1	5.8	1.5	3.9	2.1
		K.AGAAYVPVDPAPPAAR.V	2	106.8	101.5	138.5	130.6	170.5	154.2	158.1	135.9
		K.DAAPVAAVSSADLC#TR.L	2	28.7	31.5	21.0	22.9	36.4	42.7	22.7	25.8
		K.DAAPVAAVSSADLC#TR.L	3	6.3	6.5	0.9	1.9	11.0	15.8	0.3	1.4
		K.DAAPVAAVSSADLC*TR.L	2	27.9	30.3	21.0	22.7	36.4	42.2	22.5	25.7
		K.IDGVVDHGLLQQAIR.Q	2	9.7	10.7	53.2	42.1	25.8	20.6	81.4	47.8
		K.IDGVVDHGLLQQAIR.Q	3	29.4	32.2	24.2	22.8	41.1	46.8	27.8	29.7
		K.LQTVVFGGEALEPHR.L	2	14.8	14.6	26.6	20.4	36.4	25.9	20.0	16.7
		K.LQTVVFGGEALEPHR.L	3	74.4	70.4	43.6	43.7	99.8	108.3	48.1	53.8
		K.NAYTPSASVPMDDPAIVGR.									
		I	2	22.2	23.3	19.2	20.0	31.5	33.8	18.7	18.5
		K.NLTHLIAVLEER.L	2	15.2	13.0	11.3	12.0	26.6	24.5	14.9	13.4
K.NLTHLIAVLEER.L	3	11.8	9.0	8.4	7.0	18.5	18.3	6.7	8.6		
		K.PAALPAVQPDTHASAG									
		R.F	3	3.0	3.3	1.0	1.7	4.2	5.0	0.5	1.5
		K.TGAAYLPIDPAHPDAR.I	2	11.8	8.9	4.5	14.9	42.0	21.1	22.5	10.9
		K.TGAAYLPIDPAHPDAR.I	3	48.4	45.6	39.4	39.9	68.6	72.4	41.8	41.5
		K.YPVALTVADVPWAQVVA									
		GEATLGAVVK.D	3	11.3	13.5	10.5	13.6	10.5	19.4	5.4	11.9
		R.ATSGVATTVTDLLGQLQR									
		.D	2	69.6	65.1	102.2	118.1	114.9	93.5	166.2	140.1
		R.AVPDGLTYGLLR.Y	2	36.9	34.3	40.2	33.0	62.1	54.8	47.8	40.7
		R.DAAQAAWGSVLEGFETP									
		TLVAPPAQAGPR.G	3	33.3	47.9	41.0	51.4	22.9	52.4	11.6	38.7

R.DHNDTVDHEHM*ALNEIH									
R.L	4	3.6	1.7	2.8	0.9	2.9	3.0	1.0	1.3
R.DHNDTVDHEHM*ALNEIH									
R.L	5	3.0	1.2	1.7	0.6	2.4	2.3	0.5	0.8
R.DHNDTVDHEHMALNEIHR									
.L	3	2.9	2.1	2.4	2.0	8.0	4.2	5.0	3.6
R.DHNDTVDHEHMALNEIHR									
.L	4	10.7	10.9	8.8	9.9	12.0	15.8	6.9	8.9
R.DHNDTVDHEHMALNEIHR									
.L	5	9.2	9.0	7.6	7.2	11.2	13.0	6.0	7.6
R.EYNHYPLSMVATPGHEVV									
LR.V	4	15.7	18.8	10.1	12.9	19.3	25.6	10.3	14.9
R.FILDDASPVAVVTTAELR.									
S	2	50.6	43.2	69.0	52.2	83.6	76.4	74.1	55.8
R.FILDDASPVAVVTTAELR.									
S	3	5.9	7.4	6.5	13.2	9.8	13.3	4.4	12.7
R.FVAC#PFGAPGAR.M	2	13.4	15.5	8.9	10.0	18.6	22.1	5.3	10.0
R.IELGEVQSALAALDGVESA									
AAIM*R.E	3	11.7	14.8	8.4	13.3	11.8	16.5	10.6	11.0
R.IILEDLNIAWAQHHSGQQ									
VQLPAGGTSFLR.W	4	21.2	20.8	31.0	26.5	25.6	29.4	30.5	31.1
R.ISTIYTSLVTK.P	2	36.3	33.9	19.1	17.9	19.7	22.5	8.2	7.1
R.ISTIYTSLVTKPVPEAYF									
GSLR.D	3	16.6	16.8	14.3	11.3	35.4	39.0	18.4	20.0
R.LADHAHTAEVTAQADAW									
R.E	3	13.7	12.8	11.3	9.3	21.3	22.7	10.0	13.9
R.LADHAHTAEVTAQADAW									
R.E	4	14.2	14.7	8.9	8.1	16.6	22.6	5.8	8.7
R.LATIGNHSALSSESAPDAVS									
IPER.F	3	91.3	110.9	111.5	125.4	130.2	131.8	91.2	90.9
R.LAVNFIPSR.L	2	35.0	33.3	30.7	31.6	51.5	50.3	26.6	29.3
R.LGAGAGELSEELWR.I	2	133.8	148.5	136.4	141.3	154.6	200.5	127.3	146.0
R.LGAIVAAMAADPAMPLAA									
VR.L	2	14.5	12.7	469.5	396.6	18.8	18.6	646.2	409.5
R.LLM*VPDAVVR.S	2	7.9	8.2	47.2	41.9	13.8	13.1	54.0	47.7
R.LPPYMVPTAIVVLPALPLT									
SSNK.L	3	18.0	26.3	13.1	22.3	19.9	29.5	5.7	15.5



		R.LSGWMHAHPGMPR.M	3	3.8	4.3	7.1	4.1	4.2	5.6	1.8	1.3
		R.LSTIDLLDPQEHDRLDEW									
		GNR.A	3	10.8	11.2	12.3	11.9	26.0	23.1	10.3	10.2
		R.LVGYITGTADPVDIR.A	2	71.1	69.8	142.5	126.1	98.3	101.7	172.9	135.3
		R.NFVTWLGAQDR.D	2	31.9	25.8	27.4	23.9	40.2	40.8	19.3	21.6
		R.PAPALESIPASFAESVR.R	2	59.1	52.3	97.4	81.4	83.6	75.7	106.7	88.4
		R.PAPALESIPASFAESVR.R	3	7.8	7.7	2.8	5.3	8.4	12.1	0.7	3.1
		R.PVDLAGADSMVGLLINTV									
		PVR.A	3	9.5	10.0	9.4	9.4	6.3	7.6	3.6	5.5
		R.SVIAILGAFK.A	2	23.7	19.5	19.3	15.5	42.1	35.2	25.5	19.1
		R.TGEAVVTILAILK.T	2	3.0	3.1	1.4	1.8	16.2	10.8	6.5	3.5
		R.VAEAPDAAAALTFEGR.T	2	71.7	74.0	84.3	86.0	118.4	107.4	101.4	94.4
		R.VQDSGDGEWSLLVPDAAT									
		VDAR.D	2	14.3	14.0	11.7	12.0	21.5	24.5	5.8	12.0
		R.WGADGQLQYVGR.A	2	26.4	30.5	44.1	50.4	31.0	42.2	41.7	52.3
MSMEG	MSMEG										
_0401	0391	K.YPVALDFDR.N	2	33.9	31.2	26.0	29.7	51.3	53.5	31.4	30.4
		R.ALPAPEYQDADQYR.A	2	79.2	79.6	73.3	72.3	105.0	106.4	76.6	70.6
		R.ALPAPEYQDADQYR.A	3	4.7	6.9	3.2	3.1	3.9	9.8	0.5	4.2
		R.AQLNPATGSMLTAAWVP									
		ETR.Q	2	13.5	13.0	64.5	67.4	20.0	21.4	70.7	62.4
		R.AQLNPATGSMLTAAWVP									
		ETR.Q	3	14.9	21.3	12.6	22.6	19.7	26.2	6.5	17.3
		R.AVESFQVSAETTQALGEL									
		AR.S	2	13.6	12.6	2.1	2.2	19.5	17.2	5.5	3.5
		R.EYNHYPLSVQAVPGHEL									
		LR.V	3	28.9	26.8	54.8	45.4	48.8	45.1	60.6	53.9
		R.FVSWLAEQDNDAAR.A	2	186.7	166.0	151.4	132.7	140.4	139.5	118.9	110.9
		R.GVFSGFETPTLVGTPGLA									
		LGR.R	2	81.2	75.2	64.9	56.6	98.1	92.1	66.4	60.7
		R.ILLEDLNIAWAQHR.S	2	5.5	3.1	4.3	4.3	21.6	10.4	7.9	4.1
		R.ILLEDLNIAWAQHR.S	3	22.7	21.2	17.2	19.4	45.0	40.0	21.3	21.1
		R.LDPDAVSLTAAGGR.V	2	39.3	34.4	28.6	25.2	31.3	37.4	16.1	18.6
		R.LGAGAADLSDDLWR.L	2	141.8	151.7	40.3	41.5	147.9	174.5	36.1	50.0
		R.SDIDAQIAQISAAER.A	2	41.7	48.1	46.1	45.0	58.6	59.1	45.2	44.1

		R.SGQPVVLPTPGTSFGR.W	2	87.0	87.1	93.5	89.8	129.9	124.1	97.2	83.8
		R.SVPDGLTYGLLR.Y	2	31.7	29.9	23.9	22.9	48.1	47.3	21.3	25.3
		R.TADVLTADVWR.T	2	26.9	24.5	36.8	34.5	33.4	38.6	36.2	40.3
		R.TEELFGDADLSR.T	2	56.5	57.0	55.1	55.7	81.1	75.3	52.9	50.1
		R.YLNPDVELDNPDPDTIGFN									
		YLGR.L	3	26.0	26.4	18.4	21.6	19.1	39.7	8.1	22.2
MSMEG	MSMEG										
_0402	0392	K.GATFVLDEWLR.P	2	5.3	4.6	1.4	1.9	5.0	4.0	1.5	1.7
		K.GQPNLGLDEQTWQR.L	2	29.1	30.0	13.9	14.6	27.2	30.8	9.1	13.4
		K.LDGVDAQAVVIAR.E	2	67.1	59.0	38.1	41.4	73.4	66.1	39.8	37.3
		K.LKPFNFVSTSDVGR.Q	3	23.5	24.3	31.2	30.6	23.9	27.0	21.0	20.7
		K.PGATVAFLIPR.S	2	17.1	16.2	14.4	15.6	23.7	20.5	17.6	18.0
		K.TGAAYLPIDPSVPAAR.L	2	84.4	84.6	76.7	69.5	91.9	90.4	79.5	73.9
		K.TGAAYLPVDPAPHPDAR.I	2	30.3	23.7	65.1	45.8	34.4	29.1	49.5	44.5
		K.TGAAYLPVDPAPHPDAR.I	3	32.8	33.1	22.0	23.0	37.5	38.6	19.6	24.1
		K.TLAGIFAHVLGVER.I	2	5.2	4.6	2.2	2.2	15.8	10.3	8.5	5.5
		K.TLAGIFAHVLGVER.I	3	2.8	2.3	0.6	0.5	7.2	5.7	2.8	1.7
		K.VSADTTVGDLLR.Q	2	31.6	28.8	32.8	32.1	36.1	34.5	21.7	21.9
		K.WAGEVLLR.E	2	16.9	13.9	0.3	0.0	1.8	2.3	0.4	0.1
		K.YPVALTVENLPWEQVVAG									
		DAALGGIVK.A	3	31.2	35.6	24.9	26.9	19.8	36.0	12.4	23.5
		R.APSTPAEQILADVYAQVL									
		GVER.V	3	12.4	15.8	10.8	14.8	12.0	14.9	6.4	10.3
		R.ASWTWAPSAFDEEQATR									
		.L	2	28.5	30.2	24.5	24.8	36.6	39.2	17.5	25.7
		R.AVLTDPGPTPVTIPALFAE									
		QVVR.A	3	21.9	26.7	17.6	23.9	23.5	33.4	17.4	23.3
		R.AVLTPVDSPQSIPEVFA									
		R.Q	2	26.6	25.3	16.9	17.0	32.1	29.9	13.8	16.3
		R.EVLDPGFETPTLVAPPGVP									
		GPR.G	2	27.4	26.5	24.3	42.3	39.5	35.4	73.1	24.6
		R.FEALQGLSDQQR.Q	2	41.8	43.8	37.1	37.9	43.7	48.7	36.6	41.2
		R.GDDLTPDHEIEQLC#AAE									
		R.S	3	12.8	14.7	13.0	17.0	16.8	19.6	12.9	14.9
		R.IEDFGEWLQR.F	2	15.4	14.4	10.3	9.8	16.3	16.4	10.4	8.1
		R.IELGEIQAALAK.L	2	34.5	31.8	22.7	30.9	48.9	41.9	35.4	37.9

	R.LEATFDTDPLLR.K	2	70.7	60.1	89.1	67.6	67.0	59.1	91.1	68.8
	R.LEFMLGDAKPVAAVTTGD									
	LR.S	3	27.7	30.9	73.1	58.3	34.8	30.9	90.1	66.7
	R.LLEAMIDDPAR.R	2	11.1	12.1	160.1	178.9	8.9	11.7	75.1	70.4
	R.LVGYITGTADPAAAR.S	2	60.1	65.8	51.5	53.9	62.6	67.1	46.3	50.7
	R.LVGYITGTADPAQLR.T	2	48.2	50.8	43.1	46.5	62.8	56.8	45.1	49.0
	R.LVVVPESVGSSPDDLHNL									
	LITEK.V	3	130.3	130.3	120.1	111.6	154.7	161.1	120.4	120.5
	R.NFVNWLATQDATAAK.A	2	45.1	46.1	50.7	52.1	68.9	61.6	63.9	61.1
	R.PADLAGAESMVGLLINTV									
	PIR.A	3	20.0	19.0	13.1	15.2	14.0	15.8	9.9	11.2
	R.RLEATFDTDPLLR.K	3	3.4	2.9	4.2	3.3	5.2	6.4	7.3	5.9
	R.SADAIVAILAVLK.T	2	4.4	3.5	2.5	2.1	11.0	6.8	6.8	4.2
	R.SGEAILSILSVLK.T	2	16.0	15.6	12.3	11.7	20.5	15.9	14.2	10.5
	R.SLPEGLTYGLLR.Y	2	25.0	23.4	12.6	11.6	29.1	30.0	10.5	11.1
	R.TATTLPRPDGAVQTVLLT									
	GATGFLGR.Y	3	42.9	57.3	57.5	50.8	61.6	60.3	64.4	55.5
	R.TVDALTDDVLVEAR.N	2	35.1	34.6	34.1	30.2	42.6	44.4	33.4	29.5
	R.VAVAAGESHVVDGVP									
	VVATPIMR.W	3	110.4	107.8	63.4	68.5	103.6	82.0	59.1	61.6
	R.VEYDTSVFDVSEIETLIDR.									
	F	2	77.3	70.8	101.3	93.0	65.6	64.3	83.4	81.9
	R.VSFAAVHGSDVTEVHAR.									
	D	3	5.8	5.4	5.7	3.2	9.4	7.1	5.7	5.2
	R.VSFAAVHGSDVTEVHAR.									
	D	4	13.7	11.1	7.3	5.8	14.5	15.0	5.3	6.3
	R.YDELASDVDLR.T	2	40.5	36.8	32.5	29.3	32.5	39.7	23.8	27.6
	R.YDVTDLPLTPVQQGLLF									
	HSTFAR.G	3	51.6	47.3	44.2	40.1	56.7	60.2	51.0	46.2
	R.YLLLEWLR.Q	2	7.3	6.4	3.1	3.0	10.9	8.4	5.2	3.3
	R.YLNPEVDLGGSDPTIGFN									
	YLGR.L	2	12.5	9.9	6.4	5.3	10.0	14.8	3.6	4.8
	R.YLNPEVDLGGSDPTIGFN									
	YLGR.L	3	20.0	19.4	15.5	18.7	21.2	22.8	16.1	16.0
MSMEG MSMEG										
_0406 0396	K.AIATLSTGYLNALEYAK.E	2	105.0	109.8	172.1	160.7	36.7	45.9	99.7	87.0

MSMEG _0408	MSMEG 0398	R.DKGQALAYVAGEIEQFIK.									
		N	2	3.5	4.4	32.1	32.9	1.5	1.0	21.7	25.8
		R.DQVFNLFEVFGVDK.V	2	58.6	60.7	127.5	140.1	34.1	35.8	124.4	127.5
		R.VNDLLLPIVK.G	2	23.8	21.9	70.0	63.3	5.3	3.2	34.6	28.7
		K.DLESAVATLVADGVR.C	2	6.1	7.8	5.2	4.9	8.8	10.2	4.3	4.9
		K.DLESAVATLVADGVR.C	3	1.3	1.6	0.2	0.1	2.3	2.7	0.1	0.1
		K.TFDASADGYVR.S	2	2.1	1.3	0.2	0.1	1.2	1.9	0.0	0.0
		K.VLGSARPPILDLVLP									
		EATGDSELLK.Q	3	30.2	33.0	28.3	33.9	37.7	37.4	38.1	38.9
		R.AGFVTEFLQR.E	2	8.9	9.4	1.1	1.2	11.2	10.3	0.4	1.7
		R.ELFDTEPVFAETVR.K	2	17.7	17.6	43.0	45.8	22.3	24.4	49.8	51.1
		R.ELFDTQPVFAQTVR.Q	2	41.9	26.2	66.0	63.4	35.5	25.7	55.1	60.6
		R.ESAIELLGALADDRPAPGL									
		VR.G	3	11.0	12.3	3.8	6.1	24.0	17.5	9.3	7.7
		R.FPGAASAEYWALLR.D	2	8.3	7.9	5.0	3.7	9.3	11.6	3.7	4.7
		R.GAGFSGVVR.C	2	2.5	2.1	2.3	1.1	2.3	4.2	0.2	0.1
		R.IHTYAADVGDEAQVADLL									
		AR.I	3	12.1	14.8	2.9	4.0	18.1	19.6	4.0	5.6
		R.KLDLPTYPFHR.Q	3	4.7	4.1	0.3	0.4	5.8	6.0	0.2	1.1
		R.LEAEITNLLSAVHAAQGPS									
		VK.L	3	18.2	18.1	16.1	20.8	26.9	25.6	21.9	21.8
		R.LKDVFFYEPIILPEK.A	3	5.2	6.0	6.1	8.2	8.6	9.1	6.5	7.8
		R.LSDAADYLLVEVLGLGEQ									
		TNVR.Q	3	5.1	5.8	1.2	1.0	8.6	8.4	3.1	2.6
		R.LTETDVPEPDEGYVQVR.									
		V	2	15.8	17.5	10.6	11.5	17.2	19.6	12.2	8.9
		R.PLLDVLFATDR.E	2	8.3	6.8	1.2	1.0	9.9	7.3	1.3	0.8
		R.SPIWLVR.D	2	5.0	4.5	3.0	7.9	5.2	7.1	5.6	3.9
R.TGAVLTGQTPLDAQYWR.											
R	2	11.3	10.6	2.7	2.5	12.0	14.8	1.9	2.0		
MSMEG _0415	MSMEG 0405	K.DLPSLGISVLGEAHD									
		T	2	31.8	0.0	4.6	0.0	25.8	27.1	3.5	
		K.LKDLPSLGISVLGEAHD									
		A	3	28.4	29.1	13.1	13.5	43.3	44.5	13.8	
		R.VSDIVVNDDVAPIV	2	10.1	10.0	17.5	21.0	31.6	18.2	17.8	
		FHR.S									

		R.VSDIVNDDVAPIVFHR.S	3	134.5	129.8	48.8	59.4	136.8	140.6	47.8	47.9
MSMEG	MSMEG										
_0422	0413	K.SDGENMAFEDLLTR.V	2	62.1	68.3	174.8	170.3	55.0	59.6	161.5	173.1
		R.AAADAAGVHVVINAR.T	2	5.4	5.3	30.4	24.0	5.1	4.9	19.4	13.5
		R.AAADAAGVHVVINAR.T	3	18.3	16.5	64.9	58.3	28.7	23.5	52.2	47.1
		R.FTSAVSLPVSVTVPPEDT									
		DK.A	2	7.3	6.7	51.6	53.2	2.3	5.2	8.0	14.0
		R.ITFGPFLQWALGAQAK.E	2	44.6	40.3	224.7	203.8	72.0	69.3	188.0	190.4
		R.LAVDAGFAALTVGSHOVA									
		DSIGK.S	3	87.5	96.1	286.9	286.7	104.8	111.6	277.0	270.8
		R.LIEGLLDAGVVGFNLEDTV									
		HK.E	3	11.7	12.0	87.4	85.6	16.7	14.2	59.9	53.3
		R.MSEAAAAGADSLFPAGLR									
		.D	2	29.6	30.2	126.7	132.5	36.2	52.2	93.1	103.3
MSMEG	MSMEG	K.LIPGPDWGSGASVVGTA									
_0456	0447	GLR.E	2	66.5	62.8	171.1	171.6	85.5	78.9	97.9	39.4
		R.VDPASVNPQGVAGNGVA									
		GVK.L	2	94.0	104.1	19.6	29.9	102.1	145.0	11.9	29.4
MSMEG	MSMEG	R.ILFDPAIAPDSTLDIGEVL									
_0457	0448	R.A	2	40.4	45.6	3.3	5.1	39.9	60.1	1.9	6.2
		R.LRPAVNLGLDVLNTALR.E	3	28.2	32.1	10.6	13.1	36.9	33.7	11.0	12.3
MSMEG	MSMEG	K.GGVEFPGSDAVDVLFR.									
_0464	0456	D	2	109.5	114.8	96.8	94.8	95.2	96.9	81.6	81.8
		R.EILPLATVTTPNLFAR.T	2	140.7	137.4	171.7	173.9	117.2	122.9	175.3	144.0
		R.TLSGMDEITTVDDLIEAAR.									
		R	2	47.5	47.0	41.2	38.7	52.0	49.3	50.7	46.2
		R.VAGAGC*TLAAAITAELAK.									
		G	2	38.5	38.4	86.9	85.4	39.6	41.8	63.3	58.5
MSMEG	MSMEG	R.GIGAEVAQQLATSGTHSIV									
_0530	0520	NYR.A	3	32.8	45.5	266.4	289.2	78.2	71.4	284.2	273.1
		R.LDALVLTALGGPR.V	2	2.9	4.0	11.3	9.9	9.9	10.8	18.4	13.3
MSMEG	MSMEG										
_0531	0521	K.IFTIFEGTSEIQR.L	2	159.1	156.8	53.2	49.7	147.7	118.3	60.0	61.7

MSMEG _0550	MSMEG 0541	K.LGAFC#SSEPDA GSDVGA									
		IR.T	2	103.4	108.5	139.7	141.3	99.1	106.0	94.3	104.5
		K.VVDVYSQPEWTALVVAK.									
		D	2	224.6	219.1	141.2	152.2	255.3	261.2	105.4	104.0
		R.EDFSAAHPDTVQAVVNSY									
		EEAR.T	3	193.7	208.7	180.8	212.6	386.9	410.9	106.5	126.7
		R.LDYAYYNPLSLVVR.D	2	144.4	165.4	146.1	173.0	171.7	169.7	80.1	89.1
		R.NPEFNSYGVNLNR.E	2	87.9	98.5	95.2	96.3	119.6	117.2	67.0	72.0
MSMEG _0551	MSMEG 0542	R.SNALDFGSTAGSAALVAR									
		.A	2	130.0	139.1	118.0	124.9	213.1	206.3	68.0	73.7
		R.TWALEHPAELTTLLAQEA									
		K.I	3	80.1	81.3	78.6	70.8	124.7	110.3	39.5	32.8
		R.VLLLDEPLAALDALTR.L	2	36.7	37.5	18.5	18.7	53.6	56.1	17.7	18.9
		K.GFESAIFYGPGSINC*LA									
		TR.G	2	13.3	18.8	145.8	160.1	18.8	17.6	148.3	144.0
		K.SSLAEIPHPALPK.G	2	1.5	1.9	1719.2	2141.9	0.9	1.8	1944.1	1508.1
MSMEG _0572	MSMEG 0563	K.TGDSGFPGEQNINDALAT									
		FIK.E	2	10.0	13.1	1049.9	1126.6	8.3	10.2	919.4	820.3
		K.TGDSGFPGEQNINDALAT									
		FIK.E	3	0.9	1.0	352.9	276.7	1.1	1.0	292.5	273.0
		R.EEDLIEGVIPAHPLDVQDA									
		LIYYAR.K	3	45.2	46.2	542.1	648.3	40.0	49.2	201.8	260.6
		R.EVIFLDELPR.N	2	6.7	12.2	27.3	26.8	9.9	9.4	32.9	33.2
		R.IIMLNTEFSGPQIK.E	2	19.2	21.9	140.7	157.3	27.9	20.8	132.2	118.7
MSMEG _0603	MSMEG 0594	R.DGQFDQIEQNHAGQLIAE									
		GHAAK.V	3	18.6	16.7	54.4	43.1	31.5	39.3	49.5	35.3
MSMEG _0613	MSMEG 0603	R.LDGIALLITTGFLPQR.F	2	1.2	0.8	4.0	2.6	0.5	0.5	6.7	21.3
MSMEG _0614	MSMEG 0604	R.LPWADGTVVYELDVPK.V	2	87.6	98.7	32.4	34.0	25.1	28.0	15.7	24.0
MSMEG _0628	MSMEG 0619	R.YVAEAIDAGTQIFK.A	2	69.2	74.4	78.0	98.7	58.9	64.3	72.6	81.0
MSMEG _0636	MSMEG 0627	K.NWDEFADTLTEDVR.G	2	91.7	60.0	27.8	19.3	119.3	135.9	21.7	24.4

		R.GDYGQSLGEALHFTDR.A	2	71.4	80.2	12.6	16.7	85.0	78.7	7.8	5.3
		R.GDYGQSLGEALHFTDR.A	3	65.8	62.6	20.4	17.1	94.4	93.3	11.6	12.6
		R.VAHPEITVDGDEATGTWY									
		LQDR.V	3	185.6	208.9	67.7	75.7	230.1	254.9	44.9	48.8
MSMEG	MSMEG										
_0640	0632	K.SVTAQTLIGLTR.A	2	11.0	10.3	49.3	46.7	19.5	15.8	20.3	27.9
MSMEG	MSMEG										
_0643	0635	K.DAGADEVADAHVDK.I	2	1.7	1.1	10.0	5.1	9.0	6.6	9.8	8.1
		K.DAGADEVADAHVDK.I	3	3.6	2.2	19.9	12.4	12.1	10.9	17.2	18.9
		K.GEEGAEVAPGLAEDMPE									
		VSPDGK.T	2	43.9	52.5	385.9	374.5	25.5	63.1	166.6	241.5
		K.MNELLTQQLTDETK.K	2	109.1	104.5	676.8	668.9	262.0	293.9	666.1	739.3
		K.MNELLTQQLTDETKK.G	2	11.3	13.4	94.2	79.5	24.0	27.1	85.3	95.7
		K.MNELLTQQLTDETKK.G	3	29.1	35.9	201.6	186.5	39.9	39.4	156.6	190.8
		K.TDFM#HDPPDADRLPEVK									
		.A	4	3.3	4.1	26.6	28.5	0.7	2.3	2.9	10.3
		K.TDFMHDPPDADRLPEVK.									
		A	4	9.3	9.7	99.1	92.0	5.0	8.6	27.9	32.4
		R.AYMEQAVWAPYGNEQLA									
		TFLSDR.M	2	3.7	8.2	47.2	64.1	1.2	7.9	14.6	36.4
		R.DITVWTDDEPDR.K	2	35.8	40.4	339.1	263.9	17.4	20.6	124.7	109.1
		R.IGEYYHDVLTQLGFNATLK									
		.V	2	16.0	13.6	104.6	102.7	16.5	16.4	71.4	88.4
		R.IGEYYHDVLTQLGFNATLK									
		.V	3	144.5	151.1	746.5	722.5	323.8	297.2	724.1	652.1
		R.QAVNYAIDPEALNR.V	2	23.0	30.5	230.1	225.2	40.9	46.3	197.2	221.7
		R.SYHHVLFNQDFTSFALK	2	2.3	4.0	93.2	100.3	4.2	5.5	49.9	87.7
		R.SYHHVLFNQDFTSFALK	3	34.8	31.5	312.3	281.7	104.2	100.7	264.9	243.2
MSMEG	MSMEG	R.HDDLASALAATDLDEDDL									
_0683	0675	AG	2	21.0	24.7	32.4	42.9	16.8	20.9	29.1	35.2
		R.WAEAAGISVTPGR.M	2	10.3	11.8	14.8	19.4	10.0	9.9	11.1	13.0
MSMEG	MSMEG										
_0688	0680	K.AIVVINPNNPTGAVYSR.E	2	72.7	69.1	307.2	370.6	71.6	59.1	160.9	248.7
MSMEG	MSMEG	K.AEAAAPPVEEAPEAEAP									
_0690	0682	AAPAAGGAEEK.P	3	26.9	36.5	31.7	43.0	11.9	20.8	13.7	26.7

		K.AEVLDDVAQLLLNSLDTSK. V	2	39.9	38.7	44.4	44.2	40.3	38.7	39.6	36.4
		K.AEVLDDVAQLLLNSLDTSK. V	3	17.2	17.7	20.7	19.4	17.9	16.4	18.5	15.7
		K.APYILGEKPSPLESTPEGGLGEK.A	3	96.5	108.5	135.8	154.9	111.2	115.7	120.6	134.2
		K.AVAELLATAGVK.F	2	27.4	26.7	25.1	26.4	35.7	31.8	21.6	23.4
		K.FLVLTGTGETC#TGDSAR.R	2	32.6	37.5	47.4	52.2	38.4	39.8	39.5	40.9
		K.FLVLTGTGETC*TGDSAR.R	2	32.6	37.5	47.3	52.2	38.4	39.8	39.5	40.9
		K.GYLDFTTC#TEC#GR.C	2	27.3	26.7	31.0	33.4	31.1	29.9	28.5	27.0
		K.GYLDFTTC*TEC*GR.C	2	27.3	26.7	31.0	33.4	31.1	29.9	28.5	27.0
		K.KTAAAPAEKPAATEAPE ASATPAAPAPVK.G	4	0.7	1.4	0.1	0.1	7.0	9.8	0.2	0.3
		K.TAAAPAEKPAATEAPEA SATPAAPAPVK.G	3	5.5	6.6	4.8	6.7	20.0	24.5	3.4	5.5
		R.ITTQITEVFGQTR.L	2	52.1	49.2	79.7	82.2	54.4	50.8	65.7	65.3
		R.VMITDGVDDVAASR.N	2	40.2	47.8	59.6	66.1	40.5	41.5	55.0	52.9
MSMEG	MSMEG	R.DRAPEVGELGGDGLALT GFVER.T	3	55.8	64.5	134.8	119.9	42.8	58.5	167.3	153.9
_0692	0684	R.GELALAEALDAMAR.E	2	6.3	5.4	10.4	8.9	5.8	4.5	7.5	5.8
		R.LRAPVVTSPQPQLVAAAG AALLADR.A	3	16.2	15.1	38.1	34.6	24.8	23.5	42.9	39.7
		R.NKPAFAPDGIPAALVPDS MAALAALK.A	3	16.1	26.5	38.9	66.9	21.7	23.2	19.3	32.1
MSMEG	MSMEG	R.SAAEHLLLAVESELSSFND PGER.E	3	22.0	26.3	21.5	25.8	7.3	14.5	15.9	24.0
_0695	0689	K.DSPGLPKPVQTPHPPIIIG GQGAK.R	3	1001.5	915.4	635.1	533.2	612.9	728.6	564.8	647.9
MSMEG	MSMEG	K.DSPGLPKPVQTPHPPIIIG GQGAK.R	4	717.3	687.6	406.2	340.5	425.6	521.9	308.6	425.5
_0702	0697	K.LGPFIEAGVQR.V	2	121.8	85.4	57.8	32.2	81.4	83.0	46.9	54.3
		K.MAGDGLPGPTDSWVTLA GIAR.E	2	285.4	306.5	165.7	181.6	217.2	230.1	162.0	194.4
		K.RTPALAAQFASEFNIPFVP LDTLK.T	3	297.8	311.8	154.5	166.6	169.9	190.5	128.0	150.1



		R.LGYSAFFR.S	2	210.5	196.4	101.8	91.5	178.6	174.3	138.5	123.3
		R.SNSPLVGTSTEIVDK.L	2	92.9	73.4	34.0	32.3	47.2	47.7	30.3	31.4
		R.TPALAAQFASEFNIPFVPL									
		DTLK.T	3	118.9	118.6	67.1	70.1	52.3	68.0	42.6	51.4
		R.VFVEPQQGATYSDQLAVA									
		QAAER.L	2	322.5	377.4	171.6	200.1	189.3	238.4	144.1	180.8
		R.VFVEPQQGATYSDQLAVA									
		QAAER.L	3	1185.0	1382.9	794.7	866.9	762.9	999.6	736.1	845.1
		R.VYLQVLDMSDLHVEFFA									
		NEVVR.Q	3	62.2	48.4	40.9	34.8	13.9	20.5	12.1	20.9
		R.YPGPLAISVAQVDEM*SG									
		GR.V	2	93.8	99.6	5.4	8.3	68.9	64.7	5.2	4.7
		R.YPGPLAISVAQVDEMSGG									
		R.V	2	431.3	429.5	262.7	249.2	303.7	308.5	269.8	262.2
MSMEG	MSMEG	K.GPAVTVTGAPGELLLFVA									
_0703	0698	GR.D	2	14.7	15.8	82.7	76.3	9.7	10.1	57.8	65.8
		K.LLDPLVNVAEMFIHHEDVR									
		.R	4	11.2	10.3	32.7	29.9	8.6	7.3	26.0	23.3
		R.IASGPPLLSPFK.L	2	11.1	12.1	75.4	78.1	6.6	6.7	52.3	46.4
		R.VEFTGDENSIAALR.A	2	34.1	41.4	88.5	77.8	31.3	43.2	113.6	111.1
MSMEG	MSMEG										
_0709	0704	K.ALEGTDISAIK.S	2	10.6	11.2	14.4	21.1	10.4	10.0	17.5	25.1
		K.DAGISVSDIDHVVLVGGST									
		R.M	2	198.8	186.4	170.1	162.9	191.5	189.1	210.1	199.5
		K.DAGISVSDIDHVVLVGGST									
		R.M	3	384.5	363.5	407.4	343.2	488.7	311.7	507.9	327.8
		K.DVLLLDVTPLSLGIETK.G	2	577.4	612.7	644.3	688.6	668.3	629.9	838.3	738.7
		K.EAGQIAGLNVLR.I	2	684.3	601.0	788.1	661.0	799.4	486.6	878.3	511.5
		K.GVNPDEVVAVGAALQAG									
		VLK.G	2	1021.5	956.0	917.7	844.2	970.5	765.9	964.9	763.7
		K.GVNPDEVVAVGAALQAG									
		VLK.G	3	329.7	371.6	267.3	270.6	339.8	259.2	305.0	221.1
		K.LLGSFELTGIPPAPR.G	2	328.3	388.8	311.6	343.2	446.0	353.2	503.0	382.9
		K.RHVGTDWNIEIDDK.Y	4	27.6	32.8	8.3	13.1	22.9	41.4	7.6	23.1
		R.AVGIDLGTNSVVAVLEG									
		GDPVVVANSEGSR.T	3	236.7	348.6	175.1	280.1	172.6	306.0	129.6	267.4
		R.HVGTDWNIEIDDK.K	2	57.1	49.8	40.3	43.0	52.1	58.0	23.2	44.9

		R.HVGTDWNIEIDDKK.Y	2	84.1	76.1	99.9	75.8	89.4	85.3	86.0	83.1
		R.HVGTDWNIEIDDKK.Y	3	530.2	464.7	476.3	405.3	440.0	453.6	410.6	415.1
		R.IVNEPTAAALAYGLDK.G	2	182.2	177.4	272.2	251.6	133.6	154.3	241.7	243.4
		R.IVNEPTAAALAYGLDK.G	3	178.1	168.7	130.9	123.7	155.8	133.3	107.8	108.0
		R.NQAESLVYQTEK.F	2	22.9	19.8	12.7	9.6	15.5	18.8	9.9	11.7
		R.SETFTTADDNQPSVQIQV									
		YQGER.E	2	162.8	204.2	107.2	164.3	98.4	182.7	64.3	151.9
		R.SETFTTADDNQPSVQIQV									
		YQGER.E	3	340.8	389.1	245.7	320.3	249.6	310.4	206.7	254.9
MSMEG	MSMEG										
_0710	0705	K.ANVVSELLGVLDLDR.A	2	65.8	71.4	62.7	79.0	40.7	49.0	41.0	49.2
		K.ANVVSELLGVLDLDR.A	3	13.7	10.9	6.7	4.8	7.9	8.6	4.6	4.4
		R.EPAATPQGSAPASAAPET									
		GGDSDEVTELK.A	3	185.5	250.0	158.0	199.7	100.2	161.9	85.8	128.2
MSMEG	MSMEG										
_0732	0726	K.AHPDVFDVLLQVLDEGR.L	3	13.4	15.6	11.0	11.7	19.5	26.2	26.3	30.9
		R.ITDSALVAAATLSDR.Y	2	47.8	57.9	274.5	279.6	70.2	57.0	315.5	294.5
		R.VTSPDPEGTYQALEK.Y	2	109.0	104.4	144.0	128.6	87.4	111.2	129.4	153.1
MSMEG	MSMEG										
_0741	0736	K.EC#LTQSAAFLAATER.L	2	62.2	67.6	51.6	57.0	92.1	81.4	51.9	53.0
		K.EC*LTQSAAFLAATER.L	2	62.2	67.6	51.6	57.0	92.1	81.4	51.9	53.0
		R.AHQHLEVYSGLPNYR.N	3	44.4	51.3	40.6	49.3	52.7	60.0	27.5	30.6
		R.EIEALGFGSLFLPETVAK.E	2	157.4	159.5	185.0	187.2	190.3	185.3	206.7	204.4
		R.FVLGLGVSHGPLVER.G	2	39.4	48.9	46.2	46.7	46.0	56.6	45.4	51.8
		R.IGVWWASDTWSMR.D	2	22.7	26.9	28.0	29.5	22.4	17.8	14.0	20.8
MSMEG	MSMEG	K.ALEPAEVLENLLEQAEGF									
_0759	0755	K.H	2	85.1	102.1	101.0	112.2	77.6	90.4	72.5	93.8
		K.ALEPAEVLENLLEQAEGF									
		K.H	3	93.0	101.2	84.1	97.1	82.6	102.5	78.0	90.0
		R.KALEPAEVLENLLEQAEG									
		FK.H	3	55.2	60.3	61.1	60.8	75.9	70.6	74.3	78.3
		R.VADVLDEQVLAEK.I	2	145.2	98.0	389.2	344.5	249.0	253.5	496.2	504.3
		R.VNGITDYFLTK.L	2	15.4	20.3	7.8	9.7	19.0	25.7	12.6	12.6
MSMEG	MSMEG	R.AQDLAVSADPDAATWDK.									
_0760	0756	A	2	26.3	29.5	8.3	9.4	26.5	31.4	2.7	7.1

		R.VPELPGAGSLLAPPWTV									
		K.F	2	33.6	34.7	95.8	83.0	29.9	37.2	96.2	100.0
MSMEG	MSMEG										
_0769	0763	K.YPFLQSHQPQYELAK.R	3	79.8	83.1	30.9	26.7	64.5	65.0	34.3	33.2
		R.IPAPLPDGVVSQATIGVR.G	2	352.4	345.8	603.6	608.7	272.0	261.6	542.1	571.2
		R.VLGGAILGDQEYIDGPVQ									
		K.L	2	214.8	223.4	223.9	266.9	136.9	154.2	208.4	230.2
MSMEG	MSMEG	K.GASIYDVPEGGIPVYIAAG									
_0777	0772	GPVVAK.Y	2	676.0	769.5	507.6	593.1	264.9	253.1	400.5	413.2
		K.GASIYDVPEGGIPVYIAAG									
		GPVVAK.Y	3	474.0	513.0	438.2	461.9	262.2	265.3	438.8	488.9
		K.ISYDTDPELALENT.R.F	2	1864.6	1941.5	1205.4	1229.6	829.7	842.1	1068.6	1047.2
		K.NLVLGTSVLTPTFR.Y	2	1454.0	1337.9	1178.3	1021.0	572.2	574.4	990.3	973.6
		K.WGLNHLVFHAPGHDQR.									
		R	4	113.4	83.1	44.3	35.9	19.3	36.8	8.6	40.0
		R.FWAPLSLTAEQK.H	2	799.4	737.9	669.7	563.5	403.1	396.0	661.1	624.6
		R.IFLGVGTGEALNEIATGYA									
		GEWPEFK.E	3	530.6	620.9	294.4	369.7	178.4	257.1	175.3	241.9
		R.WIVASDPDEAVEK.V	2	133.5	116.6	39.5	56.9	56.3	71.9	23.8	36.3
MSMEG	MSMEG	R.STADIDAC*VADLDQLGS									
_0779	0774	GK.V	2	23.3	15.5	44.9	43.2	4.0	4.7	47.6	47.3
		R.VVLTSSITGPITGYPGWS									
		HYGATK.A	3	139.9	159.1	279.4	293.2	106.4	111.6	268.2	283.6
MSMEG	MSMEG	R.GALVEDIVNTVAITAIQAQ									
_0783	0778	GR.S	3	30.3	36.1	26.7	39.5	36.5	30.2	30.7	34.2
MSMEG	MSMEG	R.ADIALAAGADVLHLGQDD									
_0789	0785	LPLDVAR.G	3	115.3	120.0	114.7	115.6	93.1	88.1	110.9	104.1
		R.GDLAEFADAALAGGVDLI									
		QLR.D	3	13.6	12.8	9.8	8.2	4.4	5.2	3.6	3.8
MSMEG	MSMEG										
_0793	0788	R.GAAEAVLTAQLAR.E	2	34.2	36.5	19.6	23.5	35.4	33.3	42.0	39.9
		R.VDAETGTGVLDLLNR.L	2	75.7	81.9	65.9	64.7	64.6	67.2	117.6	127.3
MSMEG	MSMEG										
_0814	0807	K.LAGLGLAGVGVAHFAK.P	2	29.9	34.2	21.0	19.6	48.0	42.5	19.8	24.5
		K.LAGLGLAGVGVAHFAK.P	3	81.9	72.0	72.3	59.0	110.0	105.9	90.3	83.8

		K.PQLFESITKPAFPR.D	3	103.9	104.8	92.4	76.4	143.8	143.0	109.7	103.5
		R.IGAVGAVGYLTYLAGNAV									
		R.N	2	106.9	156.2	183.8	253.0	145.3	121.2	225.5	210.0
		R.IGAVGAVGYLTYLAGNAV									
		R.N	3	61.3	41.6	49.4	31.5	73.0	73.9	60.0	52.3
MSMEG	MSMEG	K.GFHEVPVDIIAGQIQVVAE									
_0825	0817	DIGIQA.K.T	3	127.8	147.6	208.2	226.2	87.9	118.8	111.6	150.4
		K.LLPLTPPGQTPTR.V	2	156.8	124.0	258.5	213.0	223.8	236.2	244.0	288.8
		R.LITGIEVVDEATQR.D	2	129.7	140.2	196.9	205.1	179.5	181.7	198.0	205.1
		R.NELFPIASLVTPNLDEV.R.L	2	111.1	114.1	194.2	182.1	168.7	167.7	224.1	218.2
		R.VMTIAGTDSGGGAGIQAD									
		LR.T	2	31.6	38.7	59.2	66.7	56.4	56.2	74.2	85.5
MSMEG	MSMEG	R.NSPVPVGTVPMYQALEK.									
_0826	0818	V	2	111.6	116.1	15.3	16.4	45.8	53.2	5.2	17.5
MSMEG	MSMEG	R.VTGLDADGSPITLEGEDLF									
_0832	0826	AR.M	2	145.7	158.1	166.1	178.0	141.0	139.2	205.1	208.6
MSMEG	MSMEG										
_0834	0828	R.VFNISDVAGAAENTANR.L	2	75.9	81.9	64.4	85.4	84.2	98.6	21.2	48.2
MSMEG	MSMEG	K.LVTTTDAFTAEDLLDGAK.									
_0835	0829	T	2	693.8	651.2	1071.5	940.0	828.1	728.9	1178.9	997.7
		R.YQQVNGAPGPDQTTMAT									
		GDAGSR.V	3	5.1	5.9	10.2	10.3	0.9	2.0	0.4	2.5
MSMEG	MSMEG	R.EIAAPSDVIFELIADPAQQP									
_0859	0851	R.W	2	13.3	15.7	14.1	17.8	11.9	10.8	16.1	15.8
		R.EIAAPSDVIFELIADPAQQP									
		R.W	3	75.4	68.2	91.0	82.5	54.0	65.8	84.3	99.7
		R.IAWRPAVAGEQPLGHLW									
		R.W	4	40.6	39.8	33.0	33.5	38.6	41.7	44.8	44.1
		R.PAVAGEQPLGHLWR.W	3	21.6	25.4	30.0	30.0	9.8	11.6	15.2	16.1
		R.TLVTHTYDWTQLTDEKR.									
		F	3	31.9	40.0	40.9	50.6	26.5	29.0	46.1	39.6
MSMEG	MSMEG	R.DSAPSLVFLDEIDALAPR.									
_0858	0852	R	2	44.8	49.6	54.9	57.4	46.6	48.8	53.4	59.3
		R.ENAAVLVSPVTVYGAR.S	2	1353.5	1460.3	1128.5	1138.7	1204.6	1104.5	1060.0	1021.9

MSMEG	MSMEG										
_0861	0854	K.LSIGDTYGLIR.Y	2	40.3	77.7	1.9	3.6	20.3	24.1	2.2	1.9
		R.AGLISAGANAAFFR.H	2	10.8	10.3	2.3	2.3	6.9	12.0	1.8	1.5
		R.FHSAELEAASEDNER.N	3	1.1	0.9	0.0	0.0	0.9	0.6	0.1	0.1
MSMEG	MSMEG										
_0863	0856	K.LANLLFAYELQR.R	2	19.8	20.8	210.2	206.0	24.9	23.9	266.1	214.0
		R.VAIVTGSNTGLGYETAR.A	2	94.6	99.3	53.7	62.1	101.2	120.9	42.1	48.8
MSMEG	MSMEG	K.AGADAVVATPPFYVAPHA									
_0877	0870	DEVIR.H	3	84.8	89.3	51.8	55.2	74.4	86.3	42.2	53.9
		R.IGLTAGALGAFK.A	2	10.5	16.0	12.5	10.1	14.1	16.7	6.8	8.3
MSMEG	MSMEG										
_0876	0871	K.LANLLFTYELQR.R	2	33.7	36.2	74.2	84.0	29.0	24.7	94.0	101.2
		R.VAIVTGANTGLGLETAK.A	2	37.7	47.2	11.3	15.3	21.4	25.4	12.2	14.9
MSMEG	MSMEG										
_0880	0873	K.AGAATEVELK.E	2	88.4	65.4	43.5	29.9	101.1	76.0	87.0	71.3
		K.DETTIVEGAGDAEAIQGR.									
		V	2	3348.0	3869.0	2045.3	2291.2	2719.5	2868.0	1471.1	1737.2
		K.DETTIVEGAGDAEAIQGR.									
		V	3	444.5	489.4	243.0	282.8	395.5	408.7	176.0	177.5
		K.EQIAATAGISAGDQSIGDLI									
		AEAMDK.V	2	111.5	114.4	142.3	154.0	46.2	70.3	51.5	75.6
		K.EQIAATAGISAGDQSIGDLI									
		AEAMDK.V	3	1558.7	1596.5	1036.8	1131.3	1184.0	1185.7	735.1	748.5
		K.GYISGYFVTDAR.Q	2	2103.4	2181.6	1134.7	1177.2	2130.4	2109.3	980.9	972.9
		K.KTDDVAGDGTTTATVLAQ									
		ALVR.E	2	275.8	353.0	67.3	94.7	363.1	357.2	145.6	136.7
		K.KTDDVAGDGTTTATVLAQ									
		ALVR.E	3	2725.0	2527.9	1432.5	1386.5	3724.7	3115.6	1812.3	1599.9
		K.KWGAPTITNDGVSIK.E	2	294.4	267.4	231.4	216.4	309.3	317.9	228.2	256.4
		K.KWGAPTITNDGVSIK.E	3	247.4	216.3	142.1	127.4	278.0	296.2	150.8	174.0
		K.LAGGVAVIK.A	2	11.4	8.2	0.6	0.3	17.7	15.7	1.2	0.6
		K.QIALNGGLEPGVVAEK.V	2	609.6	653.1	497.7	499.2	840.1	829.1	558.0	597.4
		K.TDDVAGDGTTTATVLAQA									
		LVR.E	2	401.2	392.6	221.9	227.2	319.6	312.1	214.9	200.2

		K.TDDVAGDGTATVLAQA LVR.E	3	350.2	345.3	224.0	230.7	350.0	289.1	188.7	180.8
		K.VIQSGKPLIIAEDVEGEAL STLVVNK.I	3	2378.4	2404.1	1902.4	2052.4	1664.2	2257.5	1357.8	1920.3
		K.VIQSGKPLIIAEDVEGEAL STLVVNK.I	4	398.5	409.7	235.3	272.5	390.4	403.8	222.8	259.1
		K.VSNLPAGHGLNAATGEYE DLLAAGVADPVK.V	3	548.6	549.3	165.1	153.8	675.0	685.5	146.1	150.6
		K.VVVTKDETTIVEGAGDAE AIQGR.V	3	999.4	1017.1	1004.9	1029.9	1666.9	1753.8	1197.7	1368.9
		K.WGAPTITNDGVSIK.E	2	2308.4	2314.8	1850.2	1760.6	2280.6	2289.8	1678.0	1586.1
		R.KVVVTKDETTIVEGAGDA EAIQGR.V	3	210.4	242.1	51.7	56.9	877.2	1030.9	245.6	296.9
		R.KVVVTKDETTIVEGAGDA EAIQGR.V	4	93.5	97.0	221.4	213.2	465.4	463.3	375.4	433.0
		R.QEAVLEDPYILLVSSK.V	2	920.3	930.1	904.5	856.0	1044.5	1023.9	995.6	1002.4
		R.SALQNAASIAALFLTTEAV VADKPEK.A	3	3807.3	3910.0	2321.0	2458.2	3376.0	3787.1	2124.3	2405.9
		R.SALQNAASIAALFLTTEAV VADKPEK.A	4	524.2	557.4	307.7	355.9	429.4	522.0	254.1	322.7
MSMEG	MSMEG	R.VVDGVIEVGS LGDR.T	2	415.7	464.3	426.3	467.0	449.9	477.5	377.2	392.1
MSMEG	MSMEG	K.ASGVDAVQAFYDAALELG AESLHAPR.L	3	21.2	23.7	24.6	31.1	26.1	31.5	27.9	34.6
MSMEG	MSMEG	R.VVDTNWNPPVTASAR.L	2	149.1	162.2	215.2	206.9	91.1	108.7	164.4	198.9
MSMEG	MSMEG	R.TPLTAEVLLR.G	2	6.9	3.6	221.1	208.1	9.3	7.9	307.2	248.2
MSMEG	MSMEG	K.GALTYEFLWR.M	2	10.9	11.7	2.6	4.2	11.2	10.5	3.0	3.1
		K.YPPILITTSTR.D	2	49.9	36.4	25.8	34.1	38.8	19.4	35.1	22.5
		R.HLVYEDFAAIAADLVR.R	3	21.6	22.5	12.7	11.7	18.8	15.7	16.2	12.0
		R.LLYGTAGGPLVQLK.S	2	105.9	107.7	165.0	174.7	103.5	81.7	169.4	176.1
MSMEG	MSMEG	K.FTGPNSLEVALNDGGTEK .V	2	1004.4	1030.0	1001.4	1023.5	1042.5	936.7	968.7	898.5
_0903	0897	K.NYGVDVTIVEFLPR.A	2	111.0	106.6	95.8	106.0	49.0	99.1	60.2	119.4
		K.VEFSNAIIATGSSTR.L	2	861.4	818.4	1042.0	1026.8	845.2	800.4	1123.5	1116.5

		K.WDLTVNELAR.N	2	130.3	109.1	120.8	109.1	169.3	143.8	139.7	134.3
		K.YGELLGGHLIGPDVSELLP									
		ELTLAQK.W	3	2111.4	2252.5	2137.9	2163.2	1895.0	2177.9	2264.8	2319.8
		K.YWGGVC#LNVGC#IPSK.A	2	415.6	396.1	566.7	586.1	484.6	472.4	616.7	678.5
		K.YWGGVC*LNVGC*IPSK.A	2	412.7	396.1	555.4	584.2	483.3	471.5	608.7	676.0
		R.AAQLGLNTAIVEPK.Y	2	738.6	538.9	784.5	633.3	1282.5	1253.5	1357.5	1412.4
		R.ATFC#QPQVASFGLTEEQ									
		AR.D	2	171.6	205.5	173.7	230.4	135.0	153.2	129.5	154.1
		R.ATFC*QPQVASFGLTEEQ									
		AR.D	2	171.6	205.5	173.7	230.4	135.0	153.2	129.5	154.0
		R.LVPGTSLSENVVYETQIL									
		SR.E	2	802.1	851.9	807.4	848.3	734.7	837.4	845.1	935.6
		R.TNVGHIYAIGDVTGK.L	2	226.5	206.1	348.4	319.7	310.9	303.4	572.5	597.9
		R.TNVGHIYAIGDVTGK.L	3	233.5	197.1	189.6	167.5	306.2	255.6	225.7	191.8
MSMEG	MSMEG										
_0905	0899	R.ALGPIGWIAAR.A	2	9.0	8.2	9.7	6.7	5.6	6.6	17.9	14.1
		R.TLITATDEFVVTR.S	2	56.4	67.3	78.4	48.3	70.6	31.6	135.9	53.4
MSMEG	MSMEG										
_0909	0903	R.IADDFLAGLR.R	2	28.5	28.4	12.0	12.6	27.5	26.4	21.3	19.5
		R.TMIDMIEPIEFPELLR.L	2	44.3	51.8	45.5	44.3	40.4	44.3	37.3	44.5
MSMEG	MSMEG										
_0911	0904	K.AMIAAGVAGSHWEDQLA									
		SEK.K	3	470.6	426.8	70.2	88.0	798.8	740.2	47.2	74.2
		K.VEGDTSVENWLAPIVADG									
		EAGFGGALNVYELQK.A	3	52.7	82.8	6.2	7.1	77.7	173.9	0.5	5.6
		R.DYTPEDVVALQGTVVEEH									
		TLAR.R	3	75.7	67.0	8.6	5.5	41.2	49.9	8.8	6.9
		R.IATTVDPNSSTTALAGSTE									
		EGQFH.-	3	514.1	597.3	116.2	136.8	1718.5	1903.8	48.9	97.1
		R.IATTVDPNSSTTALAGSTE									
		EGQFH	2	330.3	419.4	4.6	4.4	1147.8	1230.3	1.5	4.5
		R.IATTVDPNSSTTALAGSTE									
		EGQFH	3	515.9	603.0	112.3	133.2	1768.0	1964.6	50.6	105.1
		R.LAADVADVPTTVVIAR.T	2	1084.8	1049.1	204.1	255.4	4001.7	3969.7	325.6	270.1
		R.LAADVADVPTTVVIAR.T	3	49.8	40.4	0.3	1.0	289.9	246.5	0.7	0.6
		R.NQM*SAYVELQER.E	2	13.6	10.4	35.5	24.5	47.9	54.8	0.9	0.8

		R.NQMSAYVELQER.E	2	118.6	150.4	61.0	95.0	277.2	269.6	39.9	50.8
		R.TDAEAATLITSDVDER.D	2	559.3	537.1	81.6	93.7	1759.6	1589.2	56.0	83.4
		R.TDAEAATLITSDVDER.D	3	3.5	14.2	0.0	0.5	85.4	53.9	0.0	0.1
		R.TDAEAATLITSDVDERDQ									
		PFITGER.T	3	14.7	16.3	6.9	10.2	472.2	438.4	14.9	10.4
MSMEG	MSMEG										
_0912	0905	K.AVVAGLSHPMGPLR.L	2	104.0	81.7	69.6	57.2	115.8	152.6	40.7	52.8
		R.AGVVDLVYDTTDAFVTAG									
		R.N	2	123.2	110.1	209.0	182.7	287.3	217.3	226.9	161.2
		R.LSDLVGLDTLK.L	2	245.0	250.4	351.5	360.5	399.8	364.3	406.1	354.8
		R.MVEGGVATIEDVDK.A	2	219.1	203.7	340.9	290.0	256.4	299.2	318.5	349.9
		R.VGVVGAGQM#GSGIAEV									
		SAR.A	2	35.0	30.6	30.1	28.5	48.3	51.2	30.2	34.0
		R.VGVVGAGQM*GSGIAEVS									
		AR.A	2	35.0	30.6	30.1	28.5	47.9	51.0	30.2	34.0
		R.VGVVGAGQM#GSGIAEVS									
		AR.A	2	318.9	356.9	434.6	457.9	487.0	506.4	518.0	532.6
		R.VGVVGAGQM#GSGIAEVS									
		AR.A	3	50.5	39.8	47.4	38.7	85.1	70.5	66.5	51.6
		R.VITDPDAVLASNTSSIPIMK									
		.I	2	195.7	204.1	277.1	250.4	304.2	319.1	329.9	312.2
MSMEG	MSMEG	K.FIGEEIFPGGQLPAVEDIE									
_0913	0906	K.L	2	432.3	465.5	195.9	195.2	628.4	607.5	200.8	197.0
		K.KDEAIAMQGQEVYDR.Y	2	5.1	3.7	0.7	0.4	12.8	6.8	1.2	0.3
		K.KDEAIAMQGQEVYDR.Y	3	33.2	27.2	13.5	11.4	54.1	41.8	13.4	12.3
		K.LDLKPGM*TLLDVGC#GW									
		GGALER.A	3	43.4	51.8	7.2	11.6	43.5	50.2	8.8	8.3
		K.LDLKPGMTLLDVGC#GW									
		GGALER.A	3	161.5	166.4	70.8	73.1	242.5	241.5	78.6	74.0
		K.LDLKPGMTLLDVGC*GWG									
		GALER.A	3	161.5	166.4	70.8	73.1	242.5	241.5	78.6	74.0
		K.YDVNVIGITLSK.A	2	346.6	364.2	285.5	309.8	451.0	441.0	308.6	366.4
		K.YLTGC#ADFFR.R	2	200.3	198.1	75.7	78.7	291.7	286.4	77.2	76.1
		R.GITNVGQFTLVK	2	267.4	278.3	230.6	226.9	423.8	389.5	218.7	221.7
		R.LQGWEFNEPVDR.I	2	694.2	758.5	339.5	372.5	955.6	965.3	340.6	366.5
		R.M*LLHTILAHTQK.F	3	100.5	77.9	57.7	51.9	111.9	111.1	47.0	53.1
		R.MLLHTILAHTQK.F	2	87.6	81.5	19.6	20.3	102.8	116.0	14.5	24.8



		R.MLLHTILAHTQK.F	3	143.0	132.5	57.7	57.7	214.4	211.1	47.0	53.1
		R.TLDMWAANLEAK.K	2	242.2	279.6	103.9	119.2	366.4	361.7	103.6	112.7
		R.YPVFFER.A	2	41.3	21.2	2.7	0.6	54.4	56.5	1.0	0.9
MSMEG	MSMEG										
_0916	0909	R.VYVETVAAEPEPYR.F	2	39.5	37.9	53.7	49.2	36.8	45.8	17.9	31.7
MSMEG	MSMEG										
_0918	0911	K.AGVSNPYLSQIER.G	2	14.3	20.0	286.7	314.6	49.8	43.3	305.3	287.1
		R.AGILEPSEPSEVR.D	2	0.8	0.1	21.0	19.0	1.9	3.8	18.6	24.5
		R.DAIVNDVSITER.Q	2	20.6	20.7	62.0	46.9	15.8	18.1	60.2	56.9
MSMEG	MSMEG										
_0919	0912	K.AAESYADQATATYNK.L	2	1.1	0.6	41.0	30.7	6.9	5.2	35.1	26.3
		K.LQEELPSQFGELR.E	2	545.1	593.2	5463.7	6006.0	1306.9	1293.3	5794.8	5882.0
		K.LVGVELPK.R	2	0.0	0.2	57.4	53.7	4.8	7.5	75.4	82.5
		R.KAAESYADQATATYNK.L	3	1.4	1.5	5.2	4.1	3.7	3.6	7.3	6.2
		R.VETYTDQAVELTQEALGT									
		VASQTR.A	2	24.9	28.3	351.8	402.3	85.8	100.9	323.1	375.7
		R.VETYTDQAVELTQEALGT									
		VASQTR.A	3	66.2	93.7	742.5	919.0	225.8	280.1	634.4	814.9
MSMEG	MSMEG	R.FGVPLGPVAQPLDGPWA									
_0924	0916	R.A	2	66.6	73.0	15.2	16.4	59.2	70.1	12.6	17.2
MSMEG	MSMEG										
_0927	0919	K.IENFIGSQLVDLLVAEQR.F	2	11.6	15.5	17.9	22.5	9.2	10.9	13.7	15.7
		K.IENFIGSQLVDLLVAEQR.F	3	10.9	10.3	15.2	14.0	7.6	7.9	11.0	11.3
		R.LPGLVSQFHPGDLSIR.R	3	11.5	9.8	19.1	18.5	4.5	6.3	11.9	12.2
MSMEG	MSMEG	K.EIDGTAVVADVTDDSVN									
_0930	0922	ALAAQLDR.V	3	93.2	101.0	46.4	55.3	58.9	8.9	31.8	19.4
		K.GITPLVAEDIAEVIGFVASR									
		.P	2	31.9	33.5	22.2	24.0	13.2	19.0	13.9	17.2
		K.GITPLVAEDIAEVIGFVASR									
		.P	3	17.8	17.2	13.3	11.9	7.3	9.8	6.3	10.3
		K.TLASLGFHVIC*AAR.R	2	45.8	41.7	54.9	61.4	42.0	43.6	89.6	54.6
		R.LTEIAPGAVETEFSLVR.F	2	236.4	237.4	195.2	196.3	200.0	191.4	238.4	251.2
		R.PSHVNLDQIVIRPR.D	4	99.5	94.5	54.8	50.2	102.4	85.6	73.6	63.6

MSMEG	MSMEG										
_0935	0927	K.EKYGEEQFMAWR.R	2	34.1	26.2	10.5	8.0	27.7	33.1	6.7	12.3
		K.IGGEYLDPEAAAAGAAAV									
		AAQGAK.K	2	436.1	435.9	1869.7	1988.1	352.7	393.6	5471.7	6051.5
		K.IGGEYLDPEAAAAGAAAV									
		AAQGAK.K	3	383.0	419.6	2478.1	2737.6	319.7	316.9	6703.0	7654.0
		K.NLFTGWVDVLDLTDK.G	2	84.8	73.6	75.5	69.6	51.6	44.5	51.7	43.4
		K.YGEEQFMAWR.R	2	113.8	142.0	103.2	130.7	75.6	86.7	95.6	107.6
		K.YLDGMSDEEVVGLNIPTGI									
		PLR.Y	2	101.9	103.0	94.9	89.5	85.1	76.2	92.2	88.5
		K.YLDGMSDEEVVGLNIPTGI									
		PLR.Y	3	156.2	152.8	170.6	165.7	119.7	115.5	171.8	165.0
		R.AITTAHLALDAADR.L	2	67.2	54.6	57.7	49.0	68.3	41.8	83.6	56.1
		R.AITTAHLALDAADR.L	3	140.5	119.0	89.2	78.5	138.8	117.9	114.8	90.2
		R.FVPYYESAILPDLK.A	2	788.0	810.9	897.7	913.5	790.8	787.6	1046.0	1089.4
		R.FVPYYESAILPDLK.A	3	20.5	16.9	6.6	14.6	18.3	18.2	12.9	15.7
		R.GGQLMAEQGVLPDVLYT									
		SLLR.R	2	184.2	183.2	190.8	196.1	178.9	161.9	224.3	219.0
		R.GGQLMAEQGVLPDVLYT									
		SLLR.R	3	169.0	163.9	172.0	158.2	133.6	135.6	173.0	167.0
		R.YADIDGGPLTEC#LK.D	2	414.2	417.0	491.2	471.0	325.5	299.5	429.4	429.1
		R.YADIDGGPLTEC*LK.D	2	412.8	415.4	491.2	470.3	319.6	298.4	426.9	428.3
MSMEG	MSMEG										
_0937	0929	R.SKIEEDPANPVHLVTVR.G	3	17.1	21.2	4.9	7.5	26.2	32.9	6.5	7.2
MSMEG	MSMEG	R.AVATDLVAQTMAGSAAML									
_0943	0934	LDR.L	2	373.1	429.0	23.8	28.5	303.2	331.7	24.4	32.1
		R.AVATDLVAQTMAGSAAML									
		LDR.L	3	103.5	101.0	49.6	45.2	107.4	95.7	73.8	66.2
		R.LDQVNAAGGAALDTTPAQ									
		LR.A	2	75.3	82.4	68.5	63.4	95.3	95.1	84.9	95.1
		R.VMPNAPVIVGGGV SALAP									
		GR.F	2	102.0	102.4	191.9	187.9	127.4	124.5	189.2	187.8
MSMEG	MSMEG										
_0944	0935	K.AVHDLLETSYFDAG	2	37.8	39.6	180.7	188.8	41.1	40.7	179.4	176.9
		R.AQFLTVAEVASLMR.V	2	23.5	23.1	56.8	50.7	20.5	18.0	45.9	41.5
MSMEG	MSMEG	K.EC#GHDNLIAPLTFLAVAG									
_0948	0939	R.R	3	27.1	28.6	19.9	22.3	20.4	23.1	12.7	15.5

MSMEG _0954	MSMEG 0944	K.ECGHDNLIAPLTFLAVAGR										
		.R	3	27.2	0.0	19.9	0.0	20.4	23.0	12.6	15.5	
		K.FDVPINLER.V	2	12.1	13.4	3.6	2.8	6.6	7.4	3.5	2.2	
		K.LIFHRPIVVGDK.L	3	67.5	52.1	29.0	19.9	56.6	59.8	24.7	25.1	
		R.EFSAAVKDDHPAHFDEAA										
		AK.E	3	4.6	1.8	1.4	0.3	9.4	7.1	4.5	3.1	
		R.EFSAAVKDDHPAHFDEAA										
		AK.E	4	17.4	9.8	6.8	3.2	25.9	27.6	11.4	10.9	
	MSMEG _0965	MSMEG 0955	R.VQLDLFDKFDVPINLER.V	3	52.2	45.5	32.0	28.4	37.5	38.7	24.4	22.5
			R.YPDYFEVGR.E	2	79.0	64.7	27.5	22.6	74.5	75.6	25.1	25.0
			R.ALYGWTVLVPR.T	2	33.9	37.8	19.2	18.2	34.0	35.7	20.5	13.5
			R.GWEIEDVTAYR.T	2	29.1	38.2	1.5	3.0	17.4	21.0	0.4	1.0
			R.ITFVGSGPGDPGLLTTR.A	2	196.1	191.7	57.3	56.3	253.3	227.4	29.9	37.6
			R.LIAGDPLSVDVITEINALA									
			K.T	2	49.6	57.8	5.9	5.8	55.7	80.3	4.8	10.4
			R.LIAGDPLSVDVITEINALA									
	MSMEG _0969	MSMEG 0959	K.T	3	34.2	53.7	2.9	5.1	44.8	58.8	6.1	6.6
			R.LVTHGALPIEVPTIAVEPP									
			R.S	3	104.5	103.1	211.4	228.6	129.2	112.0	204.9	196.1
			R.LIASTGDSVTTYGEPWNM									
*N			2	26.5	32.7	24.3	34.3	23.1	36.1	8.2	18.8	
R.LIASTGDSVTTYGEPWNM												
N			2	39.4	0.0	42.7	0.0	27.1	43.4	10.8	27.4	
R.TLTVQQWDTFLNGVFPLD												
R.N	2	303.9	359.2	319.9	376.9	214.5	270.7	322.0	375.6			
R.TLTVQQWDTFLNGVFPLD												
R.N	3	90.8	105.0	110.0	122.7	33.6	48.0	92.4	129.3			
K.VAEHGLSFGAPTPSETEL												
AAEI.DR.V	3	351.6	338.5	192.5	246.0	116.0	104.0	74.4	84.9			
R.FITSAGGYWLTDADGNR.												
Y	2	148.2	147.6	186.4	245.6	46.4	52.3	74.3	71.8			
R.SGWYGLDPVEADLLTFG												
K.V	2	255.2	265.9	67.7	81.7	108.4	101.7	80.7	74.7			

MSMEG	MSMEG	K.AAGHEAVC#VSHQLPVET									
_0970	0960	LR.R	3	213.5	204.5	136.4	126.7	184.7	187.9	107.0	105.2
MSMEG	MSMEG	R.ATGTDAEESAVAVLPAAE									
_0987	0977	TAVAR.E	3	38.7	0.0	114.4	0.0	39.8	49.8	121.1	110.3
MSMEG	MSMEG	K.IVGVIEQDTGARPIDDL									
_1010	0998	ALVR.T	3	233.9	243.5	426.5	460.3	232.3	268.4	366.7	396.3
		R.LWLSALWGGLPE	2	12.6	13.9	14.5	15.2	8.6	11.7	10.1	15.1
		R.PISDDLALVR.T	2	23.1	25.9	3.3	4.8	3.8	9.3	1.7	1.5
MSMEG	MSMEG										
_1011	0999	R.IGVSVVVPGAVK.T	2	36.8	35.8	42.3	40.1	50.7	51.0	43.5	44.3
MSMEG	MSMEG										
_1019	1007	K.AMDSPDFAQTIEVAIR.A	2	112.2	103.9	338.3	297.1	139.6	106.8	354.7	280.3
		K.DISC#NLGSLNIAK.A	2	170.7	177.1	289.0	282.2	168.7	163.6	305.5	308.3
		K.DISC*NLGSLNIAK.A	2	153.1	163.4	280.9	273.5	152.0	155.6	297.5	308.3
		K.KNEDMYLFSPYDVER.V	2	46.6	54.5	71.5	78.0	21.9	41.2	45.0	72.7
		K.KNEDMYLFSPYDVER.V	3	61.7	55.4	100.4	88.3	36.9	40.5	76.7	86.3
		K.LDYLIENEYER.E	2	190.5	202.3	412.4	406.4	126.2	148.9	363.2	324.9
		K.LLEDSEFSYANQLGAR.Q	2	339.0	327.2	656.7	585.6	374.3	345.8	756.4	647.3
		K.NIENQSSGVIPIK.L	2	311.1	287.3	757.5	714.6	288.4	281.0	676.7	629.1
		K.RGGGVALLLSNIR.E	3	17.7	11.1	20.7	16.1	31.9	28.6	45.0	39.7
		K.TLSLGVVIPDITFELAK.K	2	103.6	110.9	237.9	262.2	133.0	125.5	304.1	297.6
		K.YASGEFFDKYTDQVWEP									
		K.T	3	93.2	50.3	56.4	89.8	125.2	64.8	109.8	135.3
		R.FPTFLGAFK.Y	2	48.9	46.0	113.5	108.2	47.1	39.2	109.0	92.1
		R.GEPVSC#FLLR.I	2	55.2	56.2	116.7	106.6	64.4	48.4	106.5	95.3
		R.GGGVALLLSNIR.E	2	94.3	85.5	198.6	174.0	107.7	88.9	211.4	169.4
		R.LFADADIHIPTQDDWK.Q	3	111.0	104.3	126.6	135.2	110.6	84.1	101.3	114.1
		R.VYGVVPFADVSVTEK.Y	2	342.7	368.1	791.9	795.7	392.5	350.4	900.5	849.2
MSMEG	MSMEG										
_1021	1010	R.ISLITLGVDNLAASR.R	2	39.6	39.0	39.9	42.9	56.5	59.5	45.8	48.0
MSMEG	MSMEG										
_1028	1015	K.IDSEYNGYSAIAIR.S	2	391.4	408.3	182.1	212.1	401.8	414.4	190.4	252.5
		K.NWQSINATQFLGEFLR.S	2	418.9	429.1	301.2	320.1	277.5	294.5	262.0	285.3
		K.VYGDAVIAADGAYSPIK.R	2	333.4	326.3	433.0	528.9	247.2	258.1	113.1	140.2

MSMEG _1033	MSMEG 1019	K.VYGDVIAADGAYSPIKR. A	3	135.7	136.4	169.5	198.0	166.6	148.1	239.6	221.0
		R.SEMHANRPDSDSLDIYLK. L	3	322.0	283.8	195.8	174.1	154.8	172.0	84.4	106.4
		R.VTVFSPSEWELSFPR.R	2	1019.2	952.0	692.5	654.5	853.5	787.9	792.4	692.9
		R.YDLVIAGGGPSGSAAAW QAAQTGAK.V	3	342.4	332.3	281.7	274.4	181.8	285.5	128.7	323.9
		K.ALMNLGYEALFPR.D	2	70.3	67.3	217.8	197.2	24.8	30.3	95.6	96.8
MSMEG _1037	MSMEG 1024	K.VPVSNDIQSWHTLTDNEK .Q	3	529.8	539.7	993.1	968.0	388.9	413.0	729.3	731.5
		K.AMGADVTVLSQSLK.K K.LDGALVELGLPEHPMEVP AFPLLAQR.R	2 3	1359.9 2375.9	1357.8 2643.9	189.3 399.2	207.1 438.2	216.2 327.0	201.1 376.2	225.0 280.6	213.4 319.9
MSMEG _1038	MSMEG 1025	K.VAVIGLGGLGHVAVK.L	2	416.3	375.2	60.0	72.2	21.5	16.8	36.1	60.3
		K.VAVIGLGGLGHVAVK.L	3	1012.1	867.8	24.5	25.2	121.9	111.9	14.1	14.8
		R.FVIDTASLR.S	2	76.2	43.7	16.5	12.5	11.9	14.1	17.8	20.9
		R.IPDSLPLDAAAPLLC#AGIT TYSPLR.H	3	1301.0	1445.6	149.4	171.0	174.7	201.9	111.5	155.4
		R.IPDSLPLDAAAPLLC*AGIT TYSPLR.H	3	1301.0	1445.6	149.4	171.0	174.7	201.9	111.5	155.4
		R.LGASAYYATSDPETFDK.L	2	2916.5	3147.8	530.0	629.0	499.8	547.9	349.0	417.7
		R.PAHVAWLNDEVAAGR.I	2	121.0	128.3	87.2	88.8	75.8	60.7	87.5	70.7
		R.PAHVAWLNDEVAAGR.I	3	247.3	282.6	160.5	177.7	146.4	148.2	151.6	143.3
		R.VATLAGLPASVLDEVAEQ LELTGAR.T	3	118.8	153.6	81.8	96.1	40.6	63.8	41.5	73.7
		MSMEG _1046	MSMEG 1033	K.AFGQAIALEVIDGR.Y	2	125.0	135.6	259.3	275.9	118.4	125.2
K.VVASGLLTDVLTSENLSK. A	2			211.3	212.6	405.3	382.3	194.3	192.1	378.8	378.5
K.VVASGLLTDVLTSENLSK. A	3			31.8	33.2	54.5	53.4	28.7	31.1	58.2	55.0
R.DLVVSAGYAVLGR.W	2			169.1	181.8	136.5	128.4	223.8	203.1	138.5	137.5

MSMEG _1047	MSMEG 1034	R.IAAATEHPSSGTAYVLGE R.L	3	70.1	53.7	104.9	64.8	60.4	71.1	97.9	99.7
		R.AALANHSLSFADFLR.D	2	39.4	47.5	65.8	80.3	72.6	66.5	70.1	73.5
		R.AALANHSLSFADFLR.D	3	64.3	65.5	30.7	33.8	80.1	81.9	28.4	33.4
		R.ADLEVFLMR.R	2	20.8	18.4	68.6	47.0	25.7	22.6	41.4	37.8
		R.ADLLRPWANWVTPK.E	2	182.3	203.7	139.1	136.1	199.2	228.2	140.3	169.5
		R.ADLLRPWANWVTPK.E	3	43.4	41.0	13.8	17.6	58.9	65.2	19.2	24.4
		R.LGVDEGLAEALVC#AAAR. E	2	105.1	107.6	103.6	107.6	102.8	103.3	109.4	102.5
		R.LGVDEGLAEALVC#AAAR. E	3	10.0	12.9	1.5	2.0	14.6	14.4	0.3	3.0
		R.FSDHPVDVLAAAK.A	3	12.6	9.2	3.2	4.2	4.7	5.7	4.9	6.6
MSMEG _1049	MSMEG 1036	K.LPFLSGWR.R	2	40.7	35.0	1.3	0.7	38.6	35.8	0.5	0.0
		R.AAALEAVVDLHTFDPADL ER.M	3	92.5	75.5	26.8	26.0	82.7	70.3	18.4	32.9
		K.RAPITFDTLFK.P	2	8.8	9.4	30.2	26.0	6.0	3.2	26.3	36.9
MSMEG _1051	MSMEG 1038	R.PLDVIFPIVAR.E	2	75.5	78.3	63.5	65.2	54.2	53.3	46.5	43.9
		R.GIYSNEAGQGTGPHAAAA AEVTHPAK.Q	3	0.2	0.3	12.2	10.5	3.9	3.4	13.0	9.6
		R.GIYSNEAGQGTGPHAAAA AEVTHPAK.Q	4	2.2	2.1	104.6	82.9	24.4	25.4	82.5	75.0
MSMEG _1060	MSMEG 1045	K.DVDTVEFSYR.G	2	54.2	40.7	86.4	63.1	68.6	74.5	50.0	59.5
		K.IVTIDYIDDLGVPIDEK.D	2	363.6	459.5	652.9	817.6	340.7	464.8	325.2	438.0
		K.IVTIDYIDDLGVPIDEKDV DTVEFSYR.G	3	94.1	96.0	99.5	114.1	96.7	109.5	98.4	105.7
		R.GEDYTLVLTTK.N	2	211.3	193.1	352.0	322.1	334.6	359.0	349.4	337.3
		R.SDTWKPETWNPTAVPSV AQLAK.A	3	180.0	321.2	197.4	345.2	124.6	137.5	130.9	154.2
MSMEG _1061	MSMEG 1046	R.VIDDTTIAIPERPGNK.R	2	32.2	26.6	27.4	25.2	26.2	25.6	25.4	27.4
		R.VIDDTTIAIPERPGNK.R	3	15.2	0.0	8.3	0.0	11.7	13.3	6.3	8.5
		R.TGYQYASGETAETVDPAR .A	2	11.6	8.7	4.9	3.0	5.8	8.0	0.8	2.1

		R.VPGFDDLTDTITYHR.H	3	53.6	49.9	7.6	7.7	44.2	38.9	3.9	1.8
MSMEG	MSMEG										
_1076	1060	K.GTDAAQLEITGTR.V	2	13.5	12.3	10.1	8.9	7.3	5.4	9.4	6.5
MSMEG	MSMEG										
_1077	1061	R.YVVGGGLPGADWTANLR.A	2	50.1	54.5	72.2	77.8	34.4	38.8	62.7	65.6
MSMEG	MSMEG	R.VIDPDSWTAYPDTATVLK.									
_1078	1062	S	2	35.6	35.1	34.7	30.3	13.9	14.9	16.8	25.4
MSMEG	MSMEG	R.LEEVEPLLTAFTTTPELA									
_1090	1078	LEQAK.A	3	14.6	21.5	82.5	115.1	17.5	25.2	97.0	134.0
MSMEG	MSMEG										
_1115	1105	R.NLTGGIVALHAATKPA	2	4.7	3.5	19.4	19.1	0.9	6.0	54.8	32.0
MSMEG	MSMEG										
_1133	1122	R.FGATFSGANDEQUIER.L	2	32.0	37.9	58.3	75.1	63.4	72.9	79.6	65.1
MSMEG	MSMEG										
_1134	1123	R.LYISDTANPNAFATGR.N	2	31.6	34.0	47.9	51.3	39.8	40.8	29.1	23.4
MSMEG	MSMEG	R.QLLACGLAVLVVAGLISTV									
_1143	1133	LLVK.A	2	0.6	0.8	11.3	31.7	0.0	0.1	10.5	27.8
MSMEG	MSMEG										
_1165	1158	K.GADLDVALQFVNRY	2	96.7	88.9	192.5	177.8	88.9	93.2	215.2	218.9
		K.GDEVIELTSSTEER.V	2	42.3	36.9	65.5	60.1	27.8	29.8	60.5	62.6
		K.KRDDLQAVIALLK.G	3	20.3	21.3	24.6	27.7	13.5	16.0	22.7	27.1
		K.VDRQEVDNALNQAQK.E	2	11.9	3.9	18.3	6.3	11.2	14.1	19.0	19.4
		K.VDRQEVDNALNQAQK.E	3	21.4	10.4	31.6	14.0	20.2	27.0	34.0	40.6
		R.DDLQAVIALLK.G	2	17.5	18.8	21.9	23.4	8.3	8.3	12.0	11.8
MSMEG	MSMEG										
_1188	1181	R.LDLDSVAAELR.S	2	66.1	57.5	61.4	53.5	47.0	48.8	56.8	51.8
MSMEG	MSMEG										
_1203	1198	K.YDVDVIGLTLTK.N	2	79.8	73.6	134.0	129.0	104.0	90.9	136.5	151.6
MSMEG	MSMEG										
_1215	1208	R.FVEQIFSAEQQPK.E	2	21.3	20.8	15.9	19.4	19.2	18.3	27.8	20.3
MSMEG	MSMEG										
_1225	1218	R.QYASTALHPRWR.A	2	50.3	29.0	176.7	153.3	17.6	13.6	143.7	150.9
MSMEG	MSMEG										
_1244	1236	K.TIGLLNLVSSGGR.I	2	2.8	2.1	10.4	8.1	3.1	3.8	16.3	14.7
		R.LAAEHAPSEDSTAVAQMP									
		GR.K	3	6.1	5.9	4.3	4.5	4.7	6.4	3.4	3.6

		R.LGLSSLLSDVADTVYLR.T	2	4.7	5.2	3.6	4.8	5.0	5.9	1.8	3.0
		R.TAGPTFLNVATALFR.E	2	5.2	4.9	16.7	11.6	11.1	8.7	7.0	4.7
		R.TLFSFVTGAEPALPR.Y	2	14.8	12.2	11.7	10.6	16.0	17.3	5.1	9.6
MSMEG	MSMEG										
_1247	1240	K.VVQVGGVEILDELPK.K	2	10.5	11.8	227.1	210.3	61.4	47.6	279.6	235.2
		R.LAQDLGDQPWTVVLEILD									
		SK.K	2	18.3	21.5	70.1	80.7	33.6	56.4	67.6	111.2
		R.SDVSDEELFTAVLQTFGR.									
		R	2	28.9	33.3	125.1	128.7	64.6	73.3	147.3	155.2
MSMEG	MSMEG										
_1252	1245	R.TFDAADTGQVGGLR.R	2	4.8	3.9	49.0	48.1	2.3	3.5	19.6	23.1
MSMEG	MSMEG										
_1253	1247	R.AAGTGFTNVDMPVQR.F	2	34.0	35.4	37.4	39.5	36.9	34.7	13.9	19.2
		R.FLAGDYSQPVEIDFER.L	2	0.6	0.9	9.6	9.6	7.3	9.3	11.0	11.3
		R.LTEFAEPNALWK.L	2	2.9	3.6	17.1	16.0	5.2	5.1	31.9	29.7
		R.LVLDPYGQGLLR.L	2	0.3	0.6	19.0	18.9	6.9	7.2	20.5	23.4
		R.VSTESLEPGSTEPAPQTD									
		VAIGKPV.R.S	3	0.7	1.1	23.4	29.5	10.3	12.3	23.6	28.8
MSMEG	MSMEG										
_1254	1248	K.GVWEFLVR.R	2	0.4	0.3	0.6	1.3	2.2	1.9	1.8	2.5
		K.TESFLLPILDSLVR.E	2	1.0	0.9	12.0	11.7	7.4	6.4	18.8	14.6
		R.VLQALQC*EVD AEQLLK.G	2	59.8	56.2	14.0	15.7	33.7	19.7	18.2	19.4
MSMEG	MSMEG	K.SWLVEDGVEPESIAVLTR.									
_1255	1249	S	2	39.9	49.4	45.4	50.2	28.8	37.3	37.4	57.2
		R.IADKPGDPGVYVGGIDAL									
		GR.D	3	161.2	150.2	256.4	217.5	112.5	109.9	171.9	172.7
		R.IVLTTFNATLAQGLK.T	2	22.7	25.3	60.2	56.2	57.7	37.1	101.4	76.9
		R.SVVPSPKPVLSYLAGVG									
		YTLADLTER.L	3	4.1	6.2	17.6	20.6	15.7	27.3	35.9	57.0
		R.VFGHVFEFGSK.R	3	116.8	68.6	125.6	66.5	95.8	56.3	117.5	78.7
		R.VIEGGDFAAWR.T	2	10.9	13.3	11.9	22.5	16.4	21.5	23.9	29.9
MSMEG	MSMEG	K.IAC#DAVLVPTDDHFTIEA									
_1265	1257	PWR.G	3	190.3	194.8	148.3	145.5	182.1	193.6	189.0	183.7



		K.IAC*DAVLVPTDDHFTIEAP									
		WR.G	3	190.3	194.1	147.7	145.5	181.1	193.6	189.0	182.5
		K.TAGSPLDSVGHLVEEFLK.									
		D	2	73.3	67.7	116.9	106.9	83.2	65.4	140.1	120.3
		K.TAGSPLDSVGHLVEEFLK.									
		D	3	138.0	133.5	163.1	149.1	132.9	117.6	179.6	169.6
		R.GVALTLYADPLDR.Q	2	154.9	180.2	243.4	307.6	103.4	131.2	153.4	252.3
MSMEG	MSMEG										
_1285	1277	R.ALAEQWLLVDR.S	2	14.0	14.4	223.0	200.8	34.4	28.9	306.8	190.3
		R.VLPTGSIMQFFGGIER.V	2	13.1	18.4	29.7	45.9	27.4	25.2	31.6	46.4
MSMEG	MSMEG	R.LPVAALVTGAGTNLLAAA									
_1292	1284	DVLR.S	3	12.0	11.0	20.8	20.1	5.0	5.1	23.3	15.9
MSMEG	MSMEG										
_1295	1287	R.IPDLYTGPASGIHR.L	3	1.5	2.0	31.5	32.0	2.8	4.6	29.8	28.5
MSMEG	MSMEG	R.GDFSGAHLTGDQSQVLP									
_1296	1288	TDSQK.Q	3	171.9	170.8	408.8	431.1	105.9	109.8	257.7	308.8
		R.VMATSLIAQWR.F	2	3.0	3.7	37.6	43.1	2.1	2.5	18.9	16.8
MSMEG	MSMEG	R.AQQVATEAAALHTNAHVA									
_1331	1324	SK.L	4	8.6	6.9	7.4	5.9	12.0	9.3	10.6	8.2
MSMEG	MSMEG	K.LPGDPTVYPGHWYSAEP									
_1334	1327	SAPLEEVR.S	4	140.9	173.6	66.2	96.0	117.9	135.8	85.9	112.1
		R.LVAGDTLFLEGC#GR.T	2	98.0	109.9	76.3	93.7	77.8	82.2	63.4	76.4
		R.SVPVHVNSHEADWVSQV									
		TGIAR.S	3	134.2	153.1	53.6	63.0	108.8	123.1	45.5	51.6
MSMEG	MSMEG	K.NIITNDAGEIVQEAYTTLA									
_1340	1333	GR.A	2	120.0	198.8	129.1	197.0	138.4	138.9	138.9	123.9
		K.NIITNDAGEIVQEAYTTLA									
		GR.A	3	186.7	131.8	191.0	146.4	158.8	190.4	159.9	167.0
		R.LYC#DVYVHAVR.R	3	17.9	13.1	6.6	4.7	17.8	16.8	4.1	3.8
		R.YPDFYEVGR.E	2	74.2	66.6	44.6	43.1	61.7	74.1	37.3	43.7
MSMEG	MSMEG										
_1341	1334	K.LVTIAISATAGGK.K	2	111.6	118.4	114.2	116.6	114.7	112.9	103.0	92.6
		R.FTAVVPVPNDGVGAEITF									
		NGR.V	2	102.9	100.7	98.2	94.4	112.6	117.7	98.8	99.2
		R.GDLVNYAGVSGDLNPIHW									
		DDEIAK.Q	3	590.6	761.7	618.0	812.5	627.6	705.3	612.7	629.8

MSMEG	MSMEG										
_1342	1335	K.YDPDFLIGR.E	2	86.8	84.0	49.4	45.7	90.6	93.0	43.8	42.5
		R.FGADIVVTR.N	2	30.8	24.8	11.1	9.6	27.7	24.0	8.8	7.6
MSMEG	MSMEG	R.RGVAESTDEPETAAEAAA									
_1344	1337	AVEAGGK.A	3	39.0	50.8	15.3	20.9	62.6	65.7	10.6	13.9
MSMEG	MSMEG										
_1345	1338	R.ETPVELTFNQVAK.-	2	781.6	723.7	624.9	585.8	687.8	666.5	648.5	652.6
		R.ETPVELTFNQVAK.I	2	751.0	778.9	555.7	599.9	706.9	683.7	631.2	651.6
		R.LKPGDWYVIHSYAGYENK									
		.V	4	46.0	54.2	26.9	16.7	34.5	44.9	20.1	15.2
MSMEG	MSMEG										
_1346	1339	K.ADLNANDIDAAAK.I	2	0.5	0.0	2.7	0.0	0.2	0.4	2.2	1.9
		R.GNVIPVEITVYEDR.S	2	897.8	854.8	885.0	857.4	754.9	817.9	829.2	842.0
MSMEG	MSMEG	K.AEQAQAAGADIVGSDDLIE									
_1347	1340	K.I	2	846.4	899.8	462.9	490.3	1032.6	1085.9	549.0	591.6
		K.AEQAQAAGADIVGSDDLIE									
		K.I	3	261.3	274.2	145.2	138.3	331.8	334.3	200.4	190.6
		K.IQGGFLDFDAAIATPDQM*									
		AK.V	2	60.2	56.6	18.0	21.5	68.9	63.6	6.1	12.1
		K.IQGGFLDFDAAIATPDQM									
		AK.V	2	410.7	402.0	214.7	204.9	567.6	503.4	263.7	256.7
		K.KQDATVEVAIR.L	2	23.0	17.5	11.9	8.7	45.3	32.3	16.0	12.6
		K.KQDATVEVAIR.L	3	45.6	32.1	29.0	24.1	80.5	51.4	46.0	34.6
		K.KVTVSTTTGPGIPVDPSVT									
		R.N	2	93.1	90.6	51.2	50.1	134.7	139.0	98.5	90.2
		K.KVTVSTTTGPGIPVDPSVT									
		R.N	3	592.3	656.5	417.2	443.1	698.8	622.6	523.6	484.2
		K.LAENYGAALDEVLR.A	2	1426.3	1518.9	776.2	776.7	1714.9	1622.2	923.7	888.8
		K.LAENYGAALDEVLR.A	3	35.0	38.5	11.4	6.3	43.1	40.0	5.7	8.8
		K.VTVSTTTGPGIPVDPSVT									
		R.N	2	1632.5	1597.6	875.9	902.1	1871.9	1958.2	919.8	1008.9
		K.VTVSTTTGPGIPVDPSVT									
		R.N	3	227.5	215.1	90.0	90.4	255.2	265.3	83.5	93.2
MSMEG	MSMEG										
_1350	1343	K.LGLHMTFEDAR.F	3	28.6	25.3	8.5	6.5	60.4	55.4	6.7	9.5
		K.LTQLQEIGPHYVR.T	2	28.5	17.6	112.9	106.5	69.8	64.9	88.4	88.0
		K.LTQLQEIGPHYVR.T	3	119.7	108.6	65.8	60.9	258.1	266.8	70.7	73.5

		K.YDVNVIGLTLSGEQR.E	2	125.5	132.4	87.2	91.6	176.9	161.4	79.2	81.6
		R.FIMTEIFPGGR.L	2	54.6	61.3	25.1	25.4	143.3	142.6	30.7	32.1
		R.IVSIGAFEHFGFER.Y	2	263.2	278.0	33.5	48.6	314.7	297.4	30.6	41.6
MSMEG	MSMEG	R.SPAVYTLEDM#ADDAAAL									
_1352	1345	LDHLEIDR.A	3	5.1	8.2	6.2	9.1	2.9	6.3	5.1	6.5
MSMEG	MSMEG										
_1364	1357	K.AAGLFNAPASQVAR.L	2	216.3	173.1	141.9	111.4	224.5	293.8	143.4	172.4
		K.ASTATVVTEYR.G	2	5.3	5.2	3.8	3.1	5.7	5.1	2.0	2.5
		K.ATAVADIAEQFK.A	2	477.9	561.6	350.2	399.6	547.7	546.9	394.5	392.3
		K.RAASEAGIEGLDELFAFP									
		TAIAFVK.G	3	13.7	13.9	7.9	9.9	38.8	41.3	21.9	23.2
		R.AASEAGIEGLDELFAFP									
		AIAFVK.G	2	300.2	342.8	215.9	242.4	299.8	316.6	197.7	187.3
		R.AASEAGIEGLDELFAFP									
		AIAFVK.G	3	446.1	457.7	380.2	367.8	389.5	490.1	321.3	361.7
		R.ALGDSATYTVAK.N	2	5.6	5.4	3.0	2.5	5.4	5.6	1.7	2.0
		R.GLTVANLAELR.R	2	565.7	593.9	440.8	418.9	613.6	624.7	482.0	416.9
MSMEG	MSMEG										
_1365	1358	K.AKLEAAGASVTVK.-	2	1.4	1.0	0.4	0.2	2.2	1.5	2.0	0.8
		K.AKLEAAGASVTVK	2	31.2	23.3	41.5	29.3	46.4	36.6	55.8	40.1
		K.AKLEAAGASVTVK	3	26.6	9.8	19.3	7.3	42.1	33.1	29.0	21.9
		K.DLVDSAPKPLLEK.V	2	905.1	1133.2	654.9	837.4	988.8	1011.8	687.3	644.7
		K.EM*TLLELSEFVK.Q	2	280.3	232.0	207.8	168.9	233.1	210.5	175.0	141.3
		K.EMTLLELSEFVK.Q	2	674.8	648.1	549.6	526.1	565.4	575.7	436.9	427.9
		K.LEAAGASVTVK	2	47.5	38.2	51.7	41.9	47.9	34.5	50.6	34.4
		K.LSTEELDAFK.E	2	395.0	373.9	267.9	247.9	500.1	450.0	341.3	291.9
MSMEG	MSMEG	K.AGWNIDVAAGVPDWASK.									
_1367	1360	L	2	281.6	249.4	166.1	146.7	256.7	277.0	172.9	168.6
		K.ALGWTNEQIVER.F	2	951.1	975.9	579.9	529.3	983.1	652.7	518.2	440.6
		K.DMTYAAPLFVTAEFINNNT									
		GEIK.S	3	44.5	56.0	22.0	25.9	19.8	34.1	9.5	18.4
		K.DTTSGTDEALLDIYR.K	2	548.9	569.2	368.9	353.6	429.9	462.2	337.2	308.3
		K.DTTSGTDEALLDIYRK.L	2	15.3	14.1	23.9	23.8	33.7	26.9	40.1	40.9
		K.EFFGTSQLSQFM*DQNNP									
		LSGLTHK.R	3	264.0	248.7	147.9	150.2	206.4	200.1	119.2	109.9
		K.EFFGTSQLSQFMDQNNPL									
		SGLTHK.R	3	476.4	546.8	287.6	339.4	371.6	420.3	242.3	270.4

K.ESAQTLLLENLFFK.E	2	310.9	254.8	174.3	136.1	360.5	230.8	220.8	132.8
K.ESAQTLLLENLFFK.E	3	4.1	6.3	1.4	2.0	3.2	4.9	0.4	2.1
K.GENIPEPGIPESFK.V	2	579.0	690.6	380.9	423.2	551.6	665.6	406.7	433.7
K.GGEVEFVSADQVDYMDV SPR.Q	2	63.0	52.9	40.5	34.0	46.8	42.6	24.5	22.8
K.ILPVEDM#PFLPDGTPVDII LNTHGVPR.R	3	185.3	189.5	120.6	116.8	130.6	148.9	88.7	100.1
K.ILPVEDM*PFLPDGTPVDII LNTHGVPR.R	3	185.3	187.3	120.6	116.8	129.0	146.6	88.7	100.1
K.ILPVEDMPFLPDGTPVDIIL NTHGVPR.R	3	436.5	498.0	295.2	308.9	217.4	374.2	169.1	257.1
K.LGLNAGKPITSSTLTEEDV VATIEYLV.R.L	3	284.5	365.7	156.1	207.4	197.0	294.5	119.5	177.9
K.LGLNAGKPITSSTLTEEDV VATIEYLV.R.L	4	12.2	15.8	6.7	9.6	10.7	12.5	6.4	8.3
K.LREPLEVPGLLDVQTDSF EWLVGSDR.W	3	69.2	67.2	35.8	36.0	52.5	67.5	31.6	37.2
K.PITSSTLTEEDVVATIEYLV R.L	3	19.8	21.3	8.9	11.0	16.1	15.5	7.9	8.0
K.SNAITNNSVPGAPNR.V	2	1.5	1.5	0.7	0.8	1.2	1.5	0.5	0.9
K.SQTVFM*GDFPMMTEK.G	2	38.0	30.9	12.2	13.7	18.4	20.2	3.4	5.2
K.SQTVFMGDFPM*M*TEK. G	2	37.0	34.4	8.3	12.4	19.9	20.4	3.6	5.0
K.SQTVFMGDFPM*MTEK.G	2	39.6	34.4	12.8	15.6	19.9	20.4	3.6	5.2
K.SQTVFMGDFPMM*TEK.G	2	40.2	35.6	12.8	15.9	20.9	21.1	3.7	5.0
K.SQTVFMGDFPMMTEK.G	2	122.4	110.6	82.5	70.3	82.2	82.2	60.1	56.8
K.TGVIEEVSADYITVMADDG TR.Q	2	102.4	104.1	67.8	66.2	84.2	101.6	53.3	56.3
R.AAANLGINLSR.N	2	72.3	54.6	30.2	27.2	60.2	50.2	27.1	26.1
R.AAIDAGDVVVADK.T	2	24.2	26.1	11.9	14.0	23.2	22.9	11.0	12.0
R.DIPNVSDEVLADLDER.G	2	575.2	539.7	352.0	314.6	551.7	573.9	350.3	336.7
R.DIPNVSDEVLADLDER.G	3	46.1	47.0	18.3	22.5	25.3	45.1	8.7	22.3
R.EDDDELPAGVNELVR.V	2	375.2	363.0	233.4	214.2	239.5	258.3	152.4	160.5

R.FGFSEIM*M*GTLEK.D	2	34.7	30.9	14.0	13.0	28.0	24.5	11.8	9.6
R.FGFSEIM*MGTLK.D	2	45.8	42.3	19.8	18.0	32.0	30.2	11.8	12.7
R.FGFSEIMM#GTLEK.D	2	34.7	30.9	14.0	13.0	28.0	24.5	14.3	9.6
R.FGFSEIMM*GTLEK.D	2	34.7	30.9	14.0	13.0	28.0	24.5	14.3	9.6
R.FGFSEIMMGTLEK.D	2	149.5	134.2	100.5	85.6	141.2	109.7	107.3	73.7
R.GAWLEFDVDKR.D	2	65.1	61.6	29.1	30.5	66.1	74.7	33.8	42.9
R.KKGGEVEFVSADQVDYM									
DVSPR.Q	3	31.0	30.4	5.2	6.0	32.8	31.2	7.0	8.5
R.LSALPGGLSR.E	2	3.2	4.4	16.7	15.6	2.7	3.5	13.5	19.2
R.LVEEDVLTSIHIEEHEIDAR									
.D	3	289.1	223.4	149.1	114.5	375.8	294.1	240.3	165.0
R.LVEEDVLTSIHIEEHEIDAR									
.D	4	198.0	162.8	100.3	84.4	215.7	193.1	118.2	98.4
R.M#NIGQILETHLGWVAK.A	3	54.9	61.0	37.2	39.0	34.4	41.3	23.3	25.8
R.M#TTQDVEAITPQTLINIR									
PVVAIAK.E	3	168.8	163.8	122.9	117.7	118.9	103.1	86.9	75.7
R.M*NIGQILETHLGWVAK.A	3	54.9	61.0	32.6	32.8	34.4	40.6	23.3	25.8
R.M*TTQDVEAITPQTLINIR.									
P	2	47.1	42.4	20.9	21.7	21.2	19.0	12.7	19.2
R.M*TTQDVEAITPQTLINIRP									
VVAAIAK.E	3	130.9	122.4	82.3	74.2	118.6	103.1	86.9	75.7
R.MNIGQILETHLGWVAK.A	2	23.4	20.0	18.5	16.6	42.1	26.1	33.8	18.6
R.MNIGQILETHLGWVAK.A	3	63.6	61.3	32.6	32.8	86.0	73.4	52.6	38.9
R.MTTQDVEAITPQTLINIR.P	2	47.6	46.6	20.9	21.7	52.4	49.7	32.3	41.1
R.MTTQDVEAITPQTLINIR.P	3	54.6	47.6	9.0	14.9	24.9	35.2	5.1	15.1
R.MTTQDVEAITPQTLINIRP									
VVAAIAK.E	3	130.9	122.4	82.3	74.2	154.6	143.2	105.5	96.9
R.RMNIGQILETHLGWVAK.A	3	2.7	2.1	0.2	0.0	7.8	8.1	1.6	1.5
R.SEAPLVGTGMELR.A	2	344.3	334.7	204.8	189.7	290.5	273.0	185.7	154.4
R.SGEPFPYPVTVGYMYILK.									
L	2	154.6	148.8	97.0	85.8	142.4	155.0	109.1	103.8
R.SPGVYFDETIDK.S	2	436.0	408.0	343.0	307.6	340.3	387.0	277.4	241.9

		R.SPGVYFDETIDKSTEK.T	3	47.4	54.9	1.2	2.1	49.2	53.1	9.1	15.2
		R.STGPYSM#ITQQPLGGK.A	2	105.1	96.7	57.5	53.8	64.3	62.2	35.9	38.1
		R.STGPYSM*ITQQPLGGK.A	2	102.9	95.2	54.0	49.2	62.2	60.9	33.8	36.2
		R.STGPYSMITQQPLGGK.A	2	329.7	306.9	218.9	201.4	287.2	247.4	202.1	166.0
		R.TVGELIQNQIR.V	2	423.0	427.0	318.1	312.7	376.9	347.2	315.3	266.9
		R.VEAGQVIADGPC#TQNGE									
		MALGK.N	2	66.3	64.5	39.0	40.6	62.4	64.8	40.3	35.4
		R.VEAGQVIADGPC#TQNGE									
		MALGK.N	3	141.6	178.7	103.3	132.5	91.4	134.6	64.9	96.4
		R.VEAGQVIADGPC*TQNGE									
		MALGK.N	3	141.6	178.7	103.3	132.5	91.4	134.6	64.9	96.4
		R.VFSREDDDELPAAGVNELV									
		R.V	2	19.2	20.3	4.2	4.9	37.2	35.1	12.1	14.1
		R.VFSREDDDELPAAGVNELV									
		R.V	3	290.0	308.2	167.3	192.8	336.0	361.9	212.8	242.5
		R.VNPFPGFIETPYR.K	2	426.6	355.1	295.4	250.9	373.9	355.6	294.4	257.3
MSMEG	MSMEG										
_1368	1361	-.M#LDVNFFDEL.R.I	2	102.5	96.0	52.8	47.6	64.3	56.1	37.4	30.5
		-.M*LDVNFFDEL.R.I	2	44.6	48.7	23.5	24.0	50.1	47.7	35.2	28.8
		-.MLDVNFFDEL.R.I	2	44.6	48.7	23.5	24.0	50.1	47.7	35.2	28.8
		K.ALEEFYPADNPIITIVK.S	2	847.0	779.7	684.6	658.8	911.0	697.8	1032.3	816.9
		K.ALEEFYPADNPIITIVK.S	3	49.0	60.3	26.7	32.0	31.3	49.0	18.9	39.8
		K.ASLATDSWLSAASFQETT									
		R.V	2	285.4	246.2	138.9	123.6	248.1	227.9	157.5	138.2
		K.ASLATDSWLSAASFQETT									
		R.V	3	267.3	233.9	14.5	22.3	56.3	83.2	3.3	23.3
		K.DAPEQGVYSSPAEAIMAM									
		DR.G	2	118.2	107.3	54.3	52.4	75.8	77.5	36.6	45.6
		K.DAPEQGVYSSPAEAIMAM									
		DR.G	3	81.2	79.5	40.1	39.8	29.9	49.6	13.9	31.9
		K.HIEVIVR.Q	2	5.8	4.2	1.5	1.3	4.4	3.7	1.1	1.3
		K.ITIVPDDGGEEVVYDK.L	2	894.2	964.7	632.4	671.0	727.5	786.1	603.5	647.6
		K.LEADLAELEAEGAK.S	2	665.5	716.3	465.5	528.3	541.2	532.6	479.2	444.9
		K.LEADLAELEAEGAK.S	3	8.1	11.8	0.9	2.6	3.6	8.5	0.3	2.0

K.LIENFDIDAEAESLR.E	2	458.7	446.0	264.2	231.5	441.9	407.9	287.4	254.1
K.LIENFDIDAEAESLR.E	3	24.6	25.5	6.7	9.0	14.5	23.1	3.2	9.0
K.LM*ALELFKPFVM*K.R	3	11.9	10.5	0.8	1.7	8.2	9.7	0.7	2.6
K.LM*ALELFKPFVMK.R	3	20.8	25.6	3.7	5.8	19.3	18.6	5.1	5.4
K.LMALELFK.P	2	22.1	19.2	4.9	5.7	13.7	11.7	4.5	3.4
K.LMALELFKPFVM*K.R	2	5.3	6.9	7.9	10.0	7.9	8.4	9.0	10.9
K.LMALELFKPFVMK.R	2	16.1	15.6	12.0	12.2	28.4	15.1	22.5	13.7
K.LVDIGEAVGIVAAQSIGEP									
GTQLTM*R.T	3	34.4	56.6	81.0	65.7	38.6	42.1	84.0	78.4
K.LVDIGEAVGIVAAQSIGEP									
GTQLTMR.T	3	175.1	182.1	111.7	116.1	131.7	136.2	111.9	106.4
K.LVDIGEAVGIVAAQSIGEP									
GTQLTMR.T	4	26.7	28.2	9.8	11.9	19.6	22.3	8.4	9.6
K.QLIVDEVLYR.E	2	59.6	48.9	34.5	27.8	77.4	70.8	57.1	47.8
R.AQKLEADLAELEAEGAK.S	2	10.8	8.2	9.6	6.5	27.6	19.7	26.5	18.0
R.AQKLEADLAELEAEGAK.S	3	8.2	9.8	17.4	16.3	24.6	28.0	29.3	30.0
R.DAHVETSAFAR.T	2	1.4	0.9	0.3	0.1	0.9	0.7	0.1	0.1
R.DAHVETSAFAR.T	3	1.4	0.7	0.1	0.0	0.6	0.6	0.0	0.0
R.EGLTVLEYFINTHGAR.K	2	72.3	73.7	42.9	44.0	102.8	74.8	80.2	59.9
R.EGLTVLEYFINTHGAR.K	3	172.3	191.4	79.4	87.5	202.7	177.2	119.9	96.6
R.ELDRLDEIWNTFTK.L	2	88.9	81.1	40.9	41.4	99.6	80.8	56.8	44.5
R.ELDRLDEIWNTFTK.L	3	56.4	67.8	27.0	30.2	55.2	57.3	33.2	32.8
R.FATSDLNDLYR.R	2	494.0	484.1	270.9	275.3	354.6	350.9	232.6	242.7
R.FPM*IVVAQTVDK.L	2	114.7	122.7	51.4	67.2	77.0	82.1	39.5	46.3
R.FPMIVVAQTVDK.L	2	411.3	411.0	276.8	238.2	361.2	294.4	301.8	214.8
R.GHDLGDPAIDALLAAGITT									
VK.V	2	37.0	36.9	33.4	31.3	39.5	35.0	50.0	45.5
R.GHDLGDPAIDALLAAGITT									
VK.V	4	5.9	6.3	33.2	12.7	11.1	9.4	7.2	19.2
R.HNELSTLEAEM*AVEK.K	2	16.5	13.8	4.7	3.8	12.2	9.7	2.8	1.1
R.HNELSTLEAEM*AVEKK.A	3	1.7	2.0	0.9	1.3	2.9	3.5	0.7	2.0
R.HNELSTLEAEMAVEK.K	2	105.2	100.5	48.8	47.5	70.6	78.2	41.5	43.0
R.HNELSTLEAEMAVEK.K	3	104.2	95.7	44.3	40.5	61.7	68.3	29.3	34.0
R.IGLATADDIR.N	2	18.8	20.6	7.9	11.0	15.3	16.3	7.4	9.0

R.ILM*LSSNNILSPASGK.P	2	48.9	58.3	14.5	14.8	43.4	43.7	5.4	6.2
R.ILM*LSSNNILSPASGKPLA									
M*PR.L	3	42.0	43.7	25.4	32.8	23.4	30.0	23.6	28.6
R.ILMLSSNNILSPASGK.P	2	172.4	167.2	91.7	89.7	84.1	85.8	52.7	55.5
R.ILMLSSNNILSPASGKPLA									
M*PR.L	3	141.7	121.5	174.9	160.6	88.2	82.6	147.7	154.3
R.ILMLSSNNILSPASGKPLA									
MPR.L	3	291.7	281.5	174.9	160.6	204.1	220.0	147.7	154.3
R.LDEIWNTFTK.L	2	61.4	55.3	31.1	26.9	32.5	30.7	14.6	14.6
R.LDM*VTGLYYLTTLVEGAT									
GEYQAATK.D	3	35.8	45.8	19.4	24.3	10.9	23.4	7.0	14.3
R.LGIQAFEPQLVEGK.A	2	472.7	544.4	288.7	310.7	413.3	477.3	347.4	373.8
R.LGYLLDLAPK.D	2	418.9	389.3	203.0	179.1	397.4	364.7	229.1	203.8
R.LIDLGAPEIIVNNEK.R	2	1202.8	1213.7	1032.4	1041.9	1119.2	1182.7	1044.5	1020.9
R.LIDLGAPEIIVNNEKR.M	2	13.0	9.8	0.8	1.8	28.4	18.8	6.7	6.7
R.LVDVSQDVIVR.E	2	421.0	416.6	280.0	272.3	352.3	323.1	281.2	246.2
R.M#GHIELAAPVTHIWYFK.									
G	3	74.9	59.6	27.0	23.1	59.6	44.7	24.6	16.0
R.M#LQESVDALFDNGR.R	2	63.2	60.6	26.4	26.6	19.5	21.0	9.1	9.2
R.M*GHIELAAPVTHIWYFK.									
G	3	47.3	37.3	23.1	17.2	58.0	43.2	24.6	16.0
R.M*GHIELAAPVTHIWYFK.									
G	4	59.5	50.5	22.3	18.9	36.9	38.3	17.9	21.5
R.M*LQESVDALFDNGR.R	2	63.2	60.6	26.4	26.6	19.5	21.0	9.1	9.2
R.MGHIELAAPVTHIWYFK.G	3	47.3	37.3	23.1	17.2	59.4	46.3	44.0	30.5
R.MGHIELAAPVTHIWYFK.G	4	59.5	50.5	22.3	18.9	59.7	65.5	30.1	32.4
R.MLQESVDALFDNGR.R	2	72.2	68.6	32.2	31.4	50.7	51.4	31.4	31.2
R.QRPQVWDVLEEVI AHPV									
LLNR.A	3	9.3	9.4	3.3	3.9	11.1	10.3	6.8	5.6
R.QRPQVWDVLEEVI AHPV									
LLNR.A	4	9.2	10.2	3.1	4.2	8.9	11.4	5.4	6.2
R.RLVDVSQDVIVR.E	2	26.9	25.7	55.1	43.6	56.9	43.5	109.4	80.3
R.RLVDVSQDVIVR.E	3	33.4	33.4	61.1	45.1	46.7	48.6	84.7	79.4
R.RVTIIDSGSTEFLPGSLTE									
R.A	2	3.1	4.3	1.4	1.1	7.9	7.8	1.0	0.8



R.RVTIIDSGSTEFPLPGSLTE									
R.A	3	102.3	105.9	57.4	64.3	148.6	168.4	93.6	112.6
R.RVVAEGGEPAAGRPVLM*									
GITK.A	3	13.6	12.6	3.1	3.2	13.6	10.9	3.5	3.5
R.RVVAEGGEPAAGRPVLM									
GITK.A	3	49.6	46.3	16.1	16.9	61.7	54.9	21.8	26.1
R.SVIVVGPQLK.L	2	24.4	24.7	5.8	9.2	21.0	19.7	4.1	6.1
R.SVLTC#TSATGVC#AMC#									
YGR.S	2	37.6	34.2	16.7	20.3	36.1	28.3	22.7	19.8
R.SVLTC*TSATGVC*AMC*Y									
GR.S	2	37.6	34.2	16.7	20.3	36.1	28.3	22.7	19.8
R.TFHQGGVTGGADIVGGLP									
R.V	2	65.3	59.5	36.2	35.3	82.2	52.3	53.0	37.8
R.TFHQGGVTGGADIVGGLP									
R.V	3	441.3	392.8	258.4	244.2	370.1	326.8	265.7	246.6
R.TLATDAVDANGNVIIER.G	2	352.2	354.7	220.9	218.1	331.3	308.4	294.0	238.5
R.TLATDAVDANGNVIIER.G	3	46.1	45.2	43.5	51.4	32.6	45.4	42.3	56.9
R.VM*FNELLPK.S	2	57.4	52.6	25.4	28.2	40.4	39.4	22.8	23.0
R.VM*FNELLPK.S	2	217.5	197.9	130.0	124.6	173.1	158.1	131.1	119.7
R.VRLEESDKFFK.I	2	15.6	13.1	1.8	0.9	29.9	18.1	14.7	7.8
R.VRLEESDKFFK.I	3	48.6	43.8	18.4	17.3	61.7	65.6	33.3	36.1
R.VTIIDSGSTEFPLPGSLTER.									
A	2	623.3	563.7	352.3	316.1	465.8	442.7	344.8	301.5
R.VVAEGGEPAAGRPVLM*G									
ITK.A	2	3.6	3.0	8.0	6.8	5.3	2.8	11.9	6.4
R.VVAEGGEPAAGRPVLMGI									
TK.A	2	39.0	32.8	15.0	9.3	54.1	29.0	25.5	12.1
R.YGEYFTGAM#GAESIK.K	2	65.1	64.4	25.1	29.6	43.5	37.0	16.1	18.6
R.YGEYFTGAM#GAESIKK.L	3	44.1	42.6	20.7	20.9	30.8	33.7	18.8	20.1
R.YGEYFTGAM*GAESIK.K	2	65.1	64.4	24.7	29.2	43.5	37.0	15.8	18.3
R.YGEYFTGAM*GAESIKK.L	2	5.8	5.7	1.4	2.5	9.1	6.6	5.9	3.0

		R.YGEYFTGAM*GAESIKK.L	3	44.1	42.6	20.7	20.9	30.8	33.7	18.8	20.1
		R.YGEYFTGAMGAESIK.K	2	204.0	191.7	168.6	157.9	125.1	119.3	135.9	127.7
		R.YGEYFTGAMGAESIKK.L	2	56.1	53.5	50.6	47.2	58.9	47.2	61.4	47.3
		R.YGEYFTGAMGAESIKK.L	3	87.0	80.5	42.1	37.3	79.4	78.0	45.8	43.6
MSMEG	MSMEG	K.ALDALDTDVPVYLENTAG									
_1383	1376	GDHAMAR.H	3	118.5	116.0	78.3	86.8	101.8	102.7	95.5	94.9
		R.HANFGAGQIDPQLLAADV									
		K.A	3	43.8	37.3	13.2	10.2	35.9	35.5	12.8	10.3
MSMEG	MSMEG	K.AGTSTVWTVTETLR.K	2	27.8	39.8	83.8	93.5	23.3	23.8	78.0	79.7
_1384	1378										
MSMEG	MSMEG	K.IDKDLTVVGLNNTITYR.D	3	12.2	18.0	179.7	203.0	14.5	18.5	194.3	169.7
_1393	1387										
MSMEG	MSMEG	R.VIDDIISMLNR.V	2	3.5	6.1	85.9	85.6	2.1	3.2	63.6	56.4
_1397	1392										
MSMEG	MSMEG	K.LTSQVEVTAYIPGEGHNL									
_1398	1393	QEHSMLVLR.G	4	102.0	92.8	46.8	43.5	104.9	121.6	40.8	42.9
MSMEG	MSMEG	K.RPLVNDPVYGSQVLVTQLV									
_1399	1394	NK.V	2	231.9	168.4	105.4	75.5	216.3	186.3	98.2	78.3
		K.RPLVNDPVYGSQVLVTQLV									
		NK.V	3	3090.8	3241.0	1548.5	1683.7	2795.7	3051.6	1502.9	1504.5
		R.ALDNVKPALEVR.S	2	22.9	20.8	11.9	14.1	22.8	23.8	11.4	12.3
		R.ALDNVKPALEVR.S	3	98.8	0.0	31.0	0.0	102.3	113.7	32.3	31.6
		R.IVYGALEQAR.E	2	30.1	31.3	10.7	12.3	29.6	34.2	10.1	12.7
		R.LANEILDASNGLGASVK.R	2	1020.9	1243.2	622.0	708.5	883.5	922.4	594.1	575.0
		R.LANEILDASNGLGASVK.R	3	134.5	128.2	50.8	52.5	117.2	117.4	44.3	48.1
		R.RVGGATYQVPVEVRPDR.									
		S	3	272.1	256.0	103.9	101.7	294.2	289.9	123.3	113.6
		R.RVGGATYQVPVEVRPDR.									
		S	4	342.0	309.9	137.7	127.1	353.8	371.3	157.0	152.7
		R.VGGATYQVPVEVRPDR.S	2	322.0	301.6	177.4	166.6	348.0	277.5	200.5	158.2

MSMEG _1400	MSMEG 1395	R.VGGATYQVPVEVRPDR.S	3	1400.3	1973.9	797.9	1105.4	1258.9	1324.4	749.9	750.6
		K.IGETHDGASTTDWM*EQE									
		QER.G	3	34.4	37.9	35.2	37.2	30.4	35.5	21.9	25.9
		K.IGETHDGASTTDWMEQE									
		QER.G	3	582.1	503.5	630.3	511.0	419.5	419.2	484.1	447.5
		R.ILYYTGVNYK.I	2	170.5	100.5	229.0	165.2	211.7	98.3	268.8	166.0
MSMEG _6535	MSMEG 1396	R.NIGIM*AHIDAGK.T	2	4.5	2.8	60.1	38.3	3.8	5.1	21.8	54.1
		R.NIGIMAHIDAGK.T	2	41.6	34.2	60.1	38.3	55.4	43.5	72.1	69.4
		K.AQVPLSEM*FGYVGDLR.S	2	179.8	190.2	97.1	97.4	150.0	153.1	84.5	80.6
		K.AQVPLSEMFGYVGDLR.S	2	634.6	715.9	721.3	789.1	683.5	634.7	781.6	683.3
		K.AQVPLSEMFGYVGDLR.S	3	40.8	57.9	35.6	49.0	51.9	42.1	41.4	45.2
		K.LGADFYFTVR.T	2	63.3	52.2	44.1	34.9	143.1	86.0	115.7	70.7
		K.LLETVAESDEALLEK.Y	2	1226.0	1186.9	1439.0	1335.9	1445.4	1229.7	1725.7	1473.8
		K.LLETVAESDEALLEK.Y	3	100.4	87.7	96.9	94.8	102.9	94.9	109.8	98.8
		K.LTVNSELYPVLC#GSAFK.									
		N	2	161.0	151.2	191.9	185.3	142.8	140.1	183.8	185.8
		K.LTVNSELYPVLC*GSAFK.									
		N	2	160.8	151.2	191.5	184.3	142.8	139.6	183.8	185.4
		K.VLIDLEPFVGEDGATYEF									
		NK.V	2	422.1	432.7	508.0	509.7	440.6	423.1	521.3	561.7
		K.VLIDLEPFVGEDGATYEF									
		NK.V	3	193.6	256.5	205.2	271.4	201.4	210.8	199.8	261.3
		K.VTLLDGAYHEVDSSEM*A									
		FK.V	3	69.4	86.7	57.2	67.1	64.4	70.5	53.7	52.7
		K.VTLLDGAYHEVDSSEMAF									
		K.V	2	65.9	60.8	59.8	63.5	81.0	60.5	77.9	67.1
		K.VTLLDGAYHEVDSSEMAF									
		K.V	3	372.2	360.1	426.6	387.7	379.8	337.0	466.8	390.2
		K.YEVEDIPADLADK.A	2	305.0	282.2	413.2	329.6	148.7	253.5	199.9	351.1
		K.YEVEDIPADLADKAEYR.									
		T	2	194.0	202.2	118.2	132.5	185.2	155.3	119.7	141.2
		K.YEVEDIPADLADKAEYR.									
		T	3	605.3	603.8	663.1	642.2	640.5	566.6	694.0	624.6

		K.YFGGEELSVDEIK.G	2	778.3	832.1	857.3	959.0	764.4	736.9	945.2	901.5
		R.ANYSMVFD SYAEVPANVS									
		K.E	2	319.5	289.3	284.7	259.6	282.2	254.0	324.5	259.5
		R.ASAGHIYAVIGLK.D	2	100.4	83.4	182.8	178.1	131.1	107.4	219.5	196.0
		R.ASAGHIYAVIGLK.D	3	145.5	112.5	100.6	64.0	177.5	150.6	144.1	101.6
		R.EFKVEANVGKPVAYR.E	3	9.2	11.9	55.7	43.8	27.3	38.8	38.7	63.9
		R.GETALGEKYEVEDIPADLA									
		DKAEEYR.T	3	39.5	58.1	30.4	34.3	121.6	142.8	102.2	131.1
		R.GETALGEKYEVEDIPADLA									
		DKAEEYR.T	4	116.9	117.1	121.2	154.8	296.6	294.3	335.8	353.0
		R.KLTVNSELYPVLC#GSAFK									
		.N	2	63.2	71.9	338.0	351.4	73.9	105.1	139.7	209.5
		R.KLTVNSELYPVLC*GSAFK									
		.N	2	63.2	71.3	337.2	347.4	73.7	104.9	139.7	209.5
		R.KLTVNSELYPVLC*GSAFK									
		.N	3	126.5	124.3	982.5	999.1	168.8	155.1	194.7	308.8
		R.KPSVDEPFSALAFK.I	2	660.7	562.4	695.1	635.2	608.2	399.9	787.6	727.2
		R.KPSVDEPFSALAFK.I	3	363.8	316.6	429.3	369.0	454.0	389.6	555.7	464.1
		R.VYSGVVESGSQVVNSTK.									
		G	2	651.3	422.9	772.5	481.5	615.1	393.0	719.3	437.5
		R.VYSGVVESGSQVVNSTK.									
		G	3	273.7	218.1	331.9	241.9	243.6	162.8	285.4	180.0
MSMEG	MSMEG										
_1401	1397	K.LIQPVAMDEGLR.F	2	2067.4	1676.0	2361.2	1862.2	2088.5	2519.8	2282.5	2738.7
		K.LLDQGGQAGDNVGLLLR.G	2	4169.4	3997.8	4656.2	4486.7	5452.4	5134.1	5314.6	4906.1
		K.LLDQGGQAGDNVGLLLR.G	3	193.4	187.0	199.2	184.5	276.0	275.2	226.2	248.2
		K.SDAVDDEELIELVEM#EVR									
		.E	2	113.5	115.9	86.1	96.0	88.9	106.1	55.2	66.2
		K.SDAVDDEELIELVEM*EVR									
		.E	3	103.4	110.8	99.0	104.9	88.9	96.5	51.1	62.7
		K.SDAVDDEELIELVEMEVR.									
		E	2	466.6	471.0	496.7	505.3	487.2	571.5	435.8	561.0
		K.SDAVDDEELIELVEMEVR.									
		E	3	223.4	227.8	234.8	243.8	229.9	293.2	221.0	266.6

MSMEG _1416	MSMEG 1415	K.SVEELMEAVDASIPDPVR. E	2	1472.8	1353.1	1632.8	1566.7	1339.2	1201.7	1322.4	1220.1
		K.SVEELMEAVDASIPDPVR. E	3	15.0	22.1	26.0	38.3	19.2	16.2	10.5	11.3
		K.TTVTGVEMFR.K	2	75.2	56.4	44.7	46.9	43.5	38.7	50.8	27.8
		K.VLHDKFPDLNESR.A	3	59.2	41.9	38.8	26.3	94.9	102.1	96.9	114.0
		R.AFDQIDNAPEER.Q	2	43.0	29.4	22.9	21.8	65.2	73.3	50.7	57.2
		R.ELLAAQDFDEEAPVVR.V	2	6036.0	6152.8	6773.3	6827.6	7979.5	7852.6	7977.9	7790.8
		R.ELLAAQDFDEEAPVVR.V	3	236.9	236.9	210.1	197.0	336.6	329.6	258.4	245.1
		R.ETDKPFLMPVEDVFTITG R.G	2	637.1	726.7	752.6	855.7	359.5	361.7	362.3	378.2
		R.ETDKPFLMPVEDVFTITG R.G	3	2640.2	2867.0	3025.5	3175.8	2160.7	1905.8	2240.1	1941.0
		R.GITINISHVEYQTDK.R	2	358.3	340.4	415.0	482.5	297.1	301.6	396.5	484.0
		R.GITINISHVEYQTDK.R	3	185.5	174.4	169.7	169.5	173.2	161.2	129.0	141.9
		R.GITINISHVEYQTDKR.H	3	1082.6	817.0	1051.0	830.2	1805.6	1863.0	1396.6	1705.8
		R.GQVVVKPGTTTTPHTEFEG QVYILSK.D	3	2454.0	2587.0	2536.3	2658.8	2756.5	2835.5	2647.5	2656.0
		R.GQVVVKPGTTTTPHTEFEG QVYILSK.D	4	2971.1	2958.7	3101.8	3305.2	3809.0	3770.0	3517.8	3438.0
		R.GVINVNEEVEIVGIRPETT K.T	2	413.9	464.3	391.8	467.5	465.0	463.3	318.3	362.2
		R.GVINVNEEVEIVGIRPETT K.T	3	3341.3	3171.8	3458.4	3337.9	3925.6	4148.5	3673.7	3783.2
		R.HYAHVDAPGHADYIK.N	3	41.7	19.8	32.8	14.0	62.2	40.5	44.4	28.3
		R.HYAHVDAPGHADYIK.N	4	102.2	50.9	74.2	36.8	135.2	102.8	85.1	62.8
		R.KLLDQQGAGDNVGLLLR. G	2	41.0	48.8	48.8	64.0	138.2	154.9	128.8	130.0
		R.TKPHVNIGTIGHVDHGK.T	3	28.6	11.7	18.2	6.8	64.3	34.3	48.5	22.7
		R.TKPHVNIGTIGHVDHGK.T	4	194.7	99.3	150.8	73.4	290.6	211.8	194.7	138.1
		R.IGSFDDLQGIR.V	2	112.8	90.3	153.8	113.5	119.3	113.9	99.8	144.9

		R.LADGSELPHYDELVIATGLV PK.R	2	170.4	172.1	201.2	160.9	178.8	174.8	262.9	220.3
MSMEG	MSMEG										
_1430	1427	R.LLEAATVLLR.S	2	4.4	3.4	7.2	8.6	1.7	1.4	4.0	4.8
MSMEG	MSMEG										
_1435	1433	K.AYDHEAIDASAR.K	2	0.1	0.0	0.0	0.0	0.3	0.1	0.0	0.0
		K.AYDHEAIDASAR.K	3	1.3	0.8	0.2	0.1	1.7	1.1	0.4	0.1
		R.LIDILDPTPK.T	2	357.1	376.4	226.1	237.5	458.6	443.7	274.2	247.4
		R.TGASVVGVPVPLPTEK.N	2	990.9	1053.7	635.7	648.1	1190.0	1250.1	704.7	674.7
MSMEG	MSMEG										
_1436	1434	K.LGMTQVFDENNK.V	2	135.3	101.7	89.6	60.0	161.0	175.2	59.0	70.4
		K.VHKVDAENGVLLIK.G	3	32.9	25.6	28.9	34.9	87.3	76.3	40.1	41.0
		K.VIKPVAGQFAAAGVNPR.R	2	92.2	69.2	30.3	20.2	97.4	91.0	14.5	22.9
		K.VIKPVAGQFAAAGVNPR.R	3	462.8	429.0	223.5	187.2	472.2	511.7	157.0	181.5
		R.DGYSAVQLAYGEISPR.K	2	730.0	795.4	427.4	427.3	904.5	988.3	470.6	477.5
		R.DGYSAVQLAYGEISPR.K	3	192.9	178.5	72.4	60.1	279.0	254.4	88.7	77.8
		R.KVIKPVAGQFAAAGVNPR. R	2	48.0	23.0	33.6	15.2	127.1	93.4	47.9	33.0
		R.KVIKPVAGQFAAAGVNPR. R	3	429.5	278.0	198.1	128.7	833.0	672.1	329.6	282.3
		R.KVIKPVAGQFAAAGVNPR. R	4	360.8	218.4	173.5	101.5	706.1	577.8	289.5	231.3
MSMEG	MSMEG	K.TDGSVELPAELFDVEPNIA LMHQVVTAQLAAK.R	4	141.2	141.1	62.8	65.0	74.7	109.5	29.3	49.9
_1437	1435										
		R.APQFTGGGTVHGPVKPR.D	4	1.9	1.1	0.2	0.1	3.1	2.2	0.5	0.2
		R.IHAVTELVEGQTPSTK.S	2	412.5	286.9	267.4	179.9	457.7	435.7	274.6	269.4
		R.IHAVTELVEGQTPSTK.S	3	832.1	641.9	445.7	323.0	842.2	853.3	431.8	428.9
MSMEG	MSMEG	K.SYGLIEDNVYTFVHPDS NK.T	2	60.7	46.7	37.0	30.9	88.7	72.0	38.0	32.0
_1438	1436	K.SYGLIEDNVYTFVHPDS NK.T	3	1094.6	1134.0	730.5	783.2	1445.7	1516.6	803.2	773.7

MSMEG	MSMEG	R.ATVGEVGNAEQSNINWG									
_1439	1437	K.A	2	1087.5	946.4	540.7	455.1	830.8	821.4	477.8	504.7
		R.ATVGEVGNAEQSNINWG									
		K.A	3	122.7	129.4	14.8	19.3	70.9	76.3	13.6	13.2
		R.GASVSDFAEITR.S	2	11.9	11.9	8.9	15.9	14.7	19.5	7.3	11.4
		R.SAGVSIQLLGK.E	2	9.0	9.2	200.0	188.2	10.6	14.1	260.7	241.1
		R.TANIALHLYLDGEK.R	2	220.7	223.5	152.9	157.9	202.8	199.7	104.5	102.2
		R.TANIALHLYLDGEK.R	3	163.6	158.1	42.8	43.5	69.2	61.6	7.9	13.7
		R.TANIALHLYLDGEKR.Y	3	285.1	279.2	174.6	177.9	248.4	232.1	189.2	189.1
MSMEG	MSMEG										
_1440	1438	K.HVPVFEVTEAM#VGHK.L	3	51.5	28.3	19.1	10.4	50.1	48.2	15.3	17.2
		K.HVPVFEVTEAM*VGHK.L	3	51.5	28.3	18.1	9.7	50.1	48.2	14.5	16.1
		K.HVPVFEVTEAMVGHK.L	3	187.8	222.5	112.9	131.5	162.1	191.3	102.0	109.7
		K.KGPFVDDHLLK.K	3	13.7	10.3	1.3	0.7	17.7	18.1	1.0	1.7
		R.KHVPVFEVTEAM#VGHK.L	4	17.0	9.8	4.8	2.6	17.4	15.7	4.1	3.4
		R.KHVPVFEVTEAM*VGHK.L	3	6.5	4.1	1.5	0.9	7.2	5.6	1.2	1.0
		R.KHVPVFEVTEAM*VGHK.L	4	17.0	9.8	4.8	2.6	17.4	15.7	4.1	3.4
		R.KHVPVFEVTEAMVGHK.L	4	25.7	29.3	8.6	10.9	25.4	27.5	4.9	6.2
		R.RSTIIPDFIGHTFAVHDGR.K	4	38.5	44.2	9.7	14.5	82.1	89.5	22.0	25.1
		R.STIIPDFIGHTFAVHDGR.K	2	37.6	24.7	19.2	13.0	44.1	32.1	16.4	12.9
		R.STIIPDFIGHTFAVHDGR.K	4	211.9	117.9	90.1	49.2	247.5	249.2	93.9	86.6
MSMEG	MSMEG										
_1441	1439	K.RTSHITVIVESRPPK.Q	4	8.7	7.8	1.6	1.7	8.4	8.8	1.7	1.6
		K.SVEEALDILR.W	2	707.4	762.9	360.9	367.2	772.9	762.4	423.2	393.5
		K.VIASAAAANAQNNEGLDPS									
		TLVVATVYADEGPTAK.R	3	516.6	769.6	238.8	343.6	516.4	577.6	216.3	244.2
		K.VIASAAAANAQNNEGLDPS									
		TLVVATVYADEGPTAK.R	4	485.6	424.3	186.0	165.1	454.8	473.1	166.3	167.3
		R.TSHITVIVESRPPK.Q	2	22.4	17.4	7.0	5.5	26.4	15.9	8.3	2.9
		R.TSHITVIVESRPPK.Q	3	128.1	110.2	61.1	51.4	135.7	116.2	71.5	55.1
		R.WAPQAASEPVAK.V	2	4.7	4.5	0.4	0.4	5.0	5.3	0.7	0.4

MSMEG	MSMEG										
_1442	1440	K.DYVKEDVAIR.K	2	14.5	8.8	14.0	8.6	13.6	12.8	16.1	14.5
		K.NPESQAQLVAQGVAEQLS									
		NR.V	2	337.1	371.8	352.9	605.5	296.9	273.4	242.0	272.3
		K.NPESQAQLVAQGVAEQLS									
		NR.V	3	1633.1	1715.3	942.7	929.8	1270.6	1248.6	852.1	799.3
		R.AATSDAPAAGTAAAAEAP									
		AESTES	2	37.8	35.9	18.7	17.4	22.3	35.7	5.8	16.9
		R.AATSDAPAAGTAAAAEAP									
		AESTES	3	25.1	25.5	8.8	9.7	13.9	22.7	2.8	7.9
		R.AGIADVEIER.T	2	41.3	34.9	68.2	61.3	27.7	30.2	14.2	51.7
		R.VDIHTARPGIVIGR.R	3	50.4	30.9	8.4	4.2	63.1	63.6	8.6	8.6
MSMEG	MSMEG										
_1443	1441	K.GSPEWWVANVPGR.V	2	331.3	406.3	521.9	516.1	399.3	363.3	491.8	410.0
		K.VWINIFPDRPLTK.K	2	371.6	343.1	217.5	205.1	383.9	323.3	220.2	175.1
		K.VWINIFPDRPLTK.K	3	884.4	901.6	456.2	445.0	858.0	897.3	426.4	409.5
		R.GIASGGTSVSFGDYGIQA									
		LEHAYITNR.Q	3	337.2	0.0	200.1	0.0	509.9	366.1	321.5	203.5
		R.VLFELSYNDEK.T	2	1190.3	1119.4	821.5	723.2	1204.0	1240.8	777.9	767.1
MSMEG	MSMEG										
_1445	1443	K.TAIGYVVS DK.M	2	8.7	0.0	4.4	0.0	11.5	11.1	3.3	3.7
MSMEG	MSMEG										
_1465	1462	K.FDENAAV I K.N	2	167.6	160.9	121.3	112.0	197.2	185.6	118.2	106.4
		K.IVSLAPEVL	2	7.5	1.7	8.2	2.3	11.6	15.1	10.2	15.6
		R.RYAGIGDVIVATVK.D	2	94.3	98.5	104.7	110.0	147.1	132.8	111.6	95.2
		R.RYAGIGDVIVATVK.D	3	79.2	70.7	26.5	25.6	145.3	130.0	49.6	47.1
		R.YAGIGDVIVATVK.D	2	613.6	638.7	329.6	369.5	662.7	644.3	319.8	299.2
		R.YAGIGDVIVATVK.D	3	22.1	12.8	3.7	2.3	26.1	26.3	3.6	4.1
MSMEG	MSMEG	R.GASSGGIVTQEAPIHVS N									
_1466	1463	VM*VVDSDGKPTR.V	3	27.5	34.7	6.5	7.9	26.5	26.3	1.9	4.7
		R.GASSGGIVTQEAPIHVS N									
		VM*VVDSDGKPTR.V	4	183.4	210.0	84.8	106.2	175.8	187.0	78.2	67.1
		R.GASSGGIVTQEAPIHVS N									
		VMVVDSDGKPTR.V	3	63.5	72.3	34.6	36.1	62.8	57.1	23.1	22.1
		R.GASSGGIVTQEAPIHVS N									
		VMVVDSDGKPTR.V	4	290.0	320.9	172.6	188.0	291.1	288.3	147.3	131.1



MSMEG	MSMEG	K.LINGAINDLALITGQKPEVR									
_1467	1464	.R	2	51.4	53.6	12.5	12.3	46.4	39.4	11.3	12.3
		K.LINGAINDLALITGQKPEVR									
		.R	3	1392.4	1426.1	1202.0	1281.5	1648.7	1650.0	1231.5	1163.7
		K.VVVNMGVGDAAR.D	2	8.3	7.3	17.4	12.6	5.7	5.3	20.7	22.9
		R.ALGFPFKEN	2	112.4	106.9	33.2	27.8	151.9	173.3	33.8	45.4
		R.EALQQEFNYANVM*QIPG									
		VVK.V	3	74.6	78.6	32.4	33.4	59.7	69.5	20.4	23.7
		R.EALQQEFNYANVMQIPGV									
		VK.V	2	149.5	156.9	165.6	177.4	202.2	178.3	148.9	156.5
		R.EALQQEFNYANVMQIPGV									
		VK.V	3	114.0	117.4	43.6	42.2	78.8	93.1	20.4	23.7
		R.GM#DITVVTTATNDAEGR.									
		A	2	177.6	197.3	105.1	114.2	176.1	199.0	84.9	101.1
		R.GM*DITVVTTATNDAEGR.									
		A	2	170.8	192.4	105.1	114.2	169.2	191.1	84.9	101.1
		R.GMDITVVTTATNDAEGR.									
		A	2	380.5	399.3	348.0	352.1	439.2	444.0	362.5	346.8
		R.LISIALPR.I	2	580.9	552.8	415.9	395.9	769.6	689.3	422.1	402.6
		R.MWEFLDR.L	2	80.9	82.9	61.2	64.5	99.6	104.1	65.4	66.9
MSMEG	MSMEG										
_1469	1466	R.NANSAYHDEVTLPHSK.L	3	6.0	5.6	1.5	1.4	7.2	7.3	1.5	1.6
		R.VLGGLGVAIISTSSGLLTD									
		R.Q	2	513.7	716.0	289.9	390.3	505.2	544.0	280.5	284.2
		R.VLGGLGVAIISTSSGLLTD									
		R.Q	3	376.5	225.4	198.3	111.5	338.6	357.8	186.9	176.5
MSMEG	MSMEG										
_1470	1467	K.GTLTLDVAEPISVSR.A	2	1747.0	1798.6	1119.8	1104.4	2016.6	2094.9	1193.3	1198.6
		K.M*EIFGVGYR.V	2	108.3	95.5	77.5	92.4	174.0	177.3	100.7	102.3
		K.MEIFGVGYR.V	2	185.8	184.8	107.5	123.6	239.8	240.8	122.1	122.3
		K.VGQISAVIR.R	2	4.8	4.9	0.3	0.5	4.2	4.7	0.4	0.5
		R.AEDGAIVVTRPDDERR.S	3	0.3	0.2	0.0	0.0	0.7	0.7	0.0	0.0
		R.TLIANLVTGVTEGYTQK.M	2	1066.8	1367.9	667.4	767.8	1109.5	1140.5	647.2	606.6
		R.TLIANLVTGVTEGYTQK.M	3	603.8	573.9	272.2	252.8	619.5	678.3	264.2	250.3

MSMEG	MSMEG										
_1471	1468	K.AAGVETVVFDR.G	2	207.6	187.0	140.1	127.6	226.1	234.2	145.2	144.9
		K.TEGTVAHKPVGQNISEVR.									
		R	3	4.0	3.4	1.9	1.5	4.5	4.8	2.2	1.8
MSMEG	MSMEG	K.SLGSDNAINVVHATVAALK									
_1472	1469	.L	2	651.3	616.4	388.1	358.1	704.7	624.1	442.3	393.1
		K.SLGSDNAINVVHATVAALK									
		.L	3	1180.8	1161.2	530.7	507.0	1316.1	1185.6	565.9	521.6
		R.AVLEC#AGVHDILAK.S	2	513.4	412.5	376.0	307.5	559.1	492.4	389.0	355.9
		R.AVLEC*AGVHDILAK.S	2	513.4	412.5	376.0	306.9	559.1	492.4	389.0	355.9
		R.GLPIEDVAPAGMLK.A	2	981.7	1009.3	725.9	731.7	1011.0	959.6	669.8	679.8
		R.RGLPIEDVAPAGMLK.A	2	50.8	52.6	324.5	340.3	86.0	73.4	462.1	423.6
		R.VPLIGSTITHPVQGEAAAG									
		VVM*LR.P	3	111.2	131.6	81.8	90.9	44.8	49.5	65.2	81.8
		R.VPLIGSTITHPVQGEAAAG									
		VVM*LRPASPGTGVIAGGAA									
		R.A	4	621.5	638.4	251.5	272.8	594.8	657.0	220.3	269.5
		R.VPLIGSTITHPVQGEAAAG									
		VVMLR.P	3	686.5	673.6	632.1	657.8	386.6	391.0	406.6	445.5
		R.VPLIGSTITHPVQGEAAAG									
		VVMLRPASPGTGVIAGGAA									
		R.A	4	1901.2	1946.2	1035.3	1045.6	2272.3	2286.2	1164.6	1192.1
		R.VPLIGSTITHPVQGEAAAG									
		VVMLRPASPGTGVIAGGAA									
		R.A	5	714.5	696.7	333.9	308.1	829.1	776.0	390.8	369.9
MSMEG	MSMEG										
_1473	1470	R.GLINTVHHLVEVEEVGK	2	163.5	131.3	78.5	68.5	173.3	144.5	101.7	79.1
		R.GLINTVHHLVEVEEVGK	3	543.9	673.7	297.3	362.4	512.6	584.4	331.9	346.5
		R.GLINTVHHLVEVEEVGK	4	89.7	52.2	45.7	25.6	110.6	104.2	73.9	66.0
MSMEG	MSMEG										
_1474	1471	K.AFPQGGTVGVDELVAK.G	2	1110.1	1505.6	1165.5	1456.8	1159.1	1250.1	1431.8	1445.7
		K.AFPQGGTVGVDELVAK.G	3	64.2	57.2	180.1	190.2	53.3	52.8	152.3	159.8
		R.FRTEYQVVNVGDINK.A	2	64.5	63.9	326.0	345.0	108.2	89.4	377.9	342.6
		R.FRTEYQVVNVGDINK.A	3	107.6	121.5	39.7	41.9	185.3	180.3	77.6	71.8
		R.KNVPVMFEGGQM*PIHM*									
		R.L	3	7.9	7.3	2.0	2.5	3.8	7.0	1.5	2.3

		R.TEYQVVNVGDINK.A	2	1368.0	1340.9	694.0	710.9	1064.7	1166.8	597.5	602.8
MSMEG	MSMEG	K.ADYADVAVAGTPGEVVR.									
_1475	1472	G	2	153.6	160.5	44.5	42.2	41.4	50.1	22.7	49.4
		R.LGVAVLVTSLHDPLQLAS									
		SITAVDR.L	3	61.7	54.4	26.5	23.5	2.1	3.2	45.8	28.2
MSMEG	MSMEG										
_1476	1473	R.VQLPAAAPGPVQELR.D	2	108.9	102.2	136.8	128.6	33.9	44.4	161.7	124.3
MSMEG	MSMEG										
_1479	1476	R.AVGIEALTMLADGK.F	2	20.2	23.8	13.3	7.5	8.7	10.0	15.8	15.1
		R.GVGQAVILASGLDSR.A	2	73.9	90.4	48.4	65.2	24.9	29.1	22.5	48.9
MSMEG	MSMEG										
_1482	1479	K.ALADLGALPTTDR.R	2	162.5	129.6	67.2	62.1	80.8	87.8	70.4	109.5
MSMEG	MSMEG										
_1485	1482	R.AAHWEHTVAVTEDGPR.I	3	5.5	3.5	1.9	1.8	10.7	7.7	3.8	3.5
		R.LTDVSHAIEVETHAAEK.R	3	30.2	41.1	10.7	9.0	38.9	35.3	20.5	20.2
		R.LTDVSHAIEVETHAAEK.R	4	45.5	52.0	7.0	7.4	56.6	46.3	5.6	6.1
		R.TSAELDAMAVAGALVASA									
		LR.A	2	11.3	12.1	9.2	11.8	10.9	11.1	20.8	22.2
MSMEG	MSMEG										
_1492	1490	R.LQVHVTSVTHAIR.R	3	3.3	3.3	3.7	4.3	3.5	3.1	3.6	3.7
MSMEG	MSMEG										
_1498	1497	K.ADYGPLVTEAALNR.V	2	114.4	133.4	94.4	150.0	108.2	129.3	105.5	119.4
		K.FIDLNVQNADELAR.L	2	168.7	170.8	146.8	165.7	195.7	172.2	188.6	165.9
MSMEG	MSMEG										
_1512	1511	R.FNETTPYNPSSPYSTK.A	2	7.5	7.0	3.3	1.8	6.1	8.0	1.3	2.6
		R.YAIDPSTLQDELGWAPK.H	2	105.2	110.5	137.7	155.4	73.5	82.0	134.7	141.9
MSMEG	MSMEG										
_1513	1512	K.LIDAVVAHGTTAGDIAAR.L	2	55.0	52.8	188.6	166.2	63.6	76.0	1039.1	869.6
		K.LIDAVVAHGTTAGDIAAR.L	3	163.7	169.0	231.2	226.1	182.4	188.9	217.6	225.5
		R.AVLGEAVFLAPEHK.V	3	84.2	74.2	95.9	90.0	111.2	105.0	119.5	115.6
		R.FVLGVGVGHPEHTGEYR.									
		K	2	58.4	66.0	26.2	21.4	58.5	72.8	21.8	26.9

		R.FVLGVGVGHPEHTGEYR. K	3	47.9	55.3	76.2	80.6	55.5	63.2	78.4	86.2
		R.KPYDALVEYLDVLDAAK.V	2	41.4	41.5	116.1	117.3	58.9	51.0	166.9	156.1
		R.KPYDALVEYLDVLDAAK.V	3	46.8	46.9	68.4	65.5	54.4	59.0	77.8	75.6
MSMEG	MSMEG										
_1521	1520	K.DLTDDQVTVLR.D	2	187.9	137.3	100.1	70.1	155.4	181.5	93.1	98.6
		K.IEIGC*YQGLR.H	2	161.6	119.8	76.6	56.6	131.8	157.1	62.4	75.4
		R.KIEIGC#YQGLR.H	2	36.4	17.1	24.9	10.9	45.9	46.7	24.4	29.0
		R.LVGVDLPR.D	2	57.4	54.4	28.1	24.8	63.9	65.5	21.0	27.7
		R.M#EIALTYIYGIGR.T	2	252.2	266.5	150.8	142.7	200.6	202.6	124.6	117.2
		R.M*EIALTYIYGIGR.T	2	59.3	50.4	28.4	25.8	73.5	67.9	41.5	36.0
		R.MEIALTYIYGIGR.T	2	59.3	50.4	28.4	25.8	73.5	67.9	41.5	36.0
		R.SNEILAAATGIDK.N	2	165.3	141.0	97.1	80.6	167.6	187.5	98.5	105.7
		R.TKDLTDDQVTVLR.D	2	4.4	4.2	7.9	5.3	8.9	7.6	11.7	9.4
MSMEG	MSMEG	K.STFNNTIVSITDPQGNVIA									
_1522	1521	WASSGHVGF.K	3	223.8	223.3	107.5	100.3	229.7	248.6	96.0	94.3
		K.STPFAAQLAAENAAR.K	2	1680.1	1881.7	924.0	982.7	1775.2	1820.9	879.4	816.5
		K.STPFAAQLAAENAAR.K	3	176.9	189.3	64.6	75.3	196.0	198.1	60.5	55.8
		R.KSTPFAAQLAAENAAR.K	2	28.8	18.1	17.6	11.9	56.7	57.5	24.8	24.0
		R.KSTPFAAQLAAENAAR.K	3	87.5	52.9	72.1	61.4	148.2	164.8	70.6	83.2
		R.SLQAAGLEVGTISDVTPQ PHNGC*RP.PK.R	3	474.5	0.0	303.7	0.0	590.5	525.7	283.0	254.3
MSMEG	MSMEG										
_1523	1522	K.SLNTLPFQIAR.E	2	990.5	941.2	515.4	495.1	992.6	1088.7	433.0	527.4
		R.AQIDVPLTEQLLIVELYSK	2	362.2	320.5	289.0	243.3	350.7	308.3	267.7	221.9
		R.AQIDVPLTEQLLIVELYSK	3	78.1	73.1	72.0	66.7	67.7	65.1	45.9	57.4
		R.ETAGERPIPSWLQVVGER .Q	2	284.5	269.0	166.0	174.3	323.0	300.0	156.4	161.2
		R.ETAGERPIPSWLQVVGER .Q	3	1069.2	1056.2	566.3	572.8	1115.5	1094.6	540.2	566.3
		R.LGVDLVGGDQSFEK.R	2	1540.1	1630.7	937.9	971.0	1341.5	1503.1	740.7	807.5
		R.LGVDLVGGDQSFEK.R.P	3	220.2	212.5	118.1	115.9	362.9	331.8	193.8	175.2
		R.RLGVDLVGGDQSFEK.R	2	291.6	212.8	113.9	74.4	356.2	334.6	188.7	165.3

MSMEG	MSMEG	-									
_1524	1523	.M#LISQRPTLSEETVAENR. S	3	607.4	380.1	368.4	249.9	448.8	506.6	253.8	304.9
		-									
		.M*LISQRPTLSEETVAENR. S	3	604.8	373.0	369.5	251.4	435.9	494.6	254.1	306.1
		-									
		.MLISQRPTLSEETVAENR.S	2	169.8	177.2	96.1	100.0	143.2	133.6	59.6	74.7
		-									
		.MLISQRPTLSEETVAENR.S	3	2018.3	1731.5	1305.8	1150.7	1868.7	1906.2	1186.6	1320.4
		K.EDVTDIILNLK.G	2	666.3	606.3	435.3	378.8	584.4	519.6	464.4	364.3
		K.GLVVSSDDDEPVTMYLR. K	2	851.3	794.5	563.1	575.9	551.3	563.4	354.1	359.7
		K.LIIDVETK.N	2	80.6	65.1	52.6	43.1	63.9	52.3	54.0	68.7
		R.DALASAGGTLVELFGLAR. E	2	1652.3	1530.2	1198.7	1074.9	1591.1	1513.8	1298.7	1209.7
		R.DALASAGGTLVELFGLAR. E	3	257.6	240.5	143.6	140.7	318.8	280.2	208.1	179.6
		R.EGVHTVGELVAR.T	2	99.9	68.9	177.9	210.2	108.2	79.8	69.6	58.6
		R.FVIEPLEPGFGYTLGNSLR .R	2	734.9	773.0	488.0	518.6	844.9	818.9	622.1	609.4
		R.FVIEPLEPGFGYTLGNSLR .R	3	97.2	119.5	63.7	72.9	134.2	127.9	71.6	82.2
		R.IDGVLHEFTTVPGVK.E	2	1693.9	1691.3	1630.6	1656.6	1364.8	1322.8	1828.0	1808.1
		R.IDGVLHEFTTVPGVK.E	3	595.4	538.1	344.7	336.9	546.9	486.2	356.8	316.2
		R.IPVDSIYSPVLK.V	2	1439.9	1417.4	1434.6	1413.9	1612.2	1494.7	1638.0	1507.8
		R.PTLSEETVAENR.S	2	17.3	15.4	9.3	10.0	8.7	6.5	2.1	3.3
		R.TLLSSIPGAAVTSIR.I	2	1680.9	1508.0	1156.1	1060.0	1533.9	1488.6	1209.5	1112.3
		R.TLLSSIPGAAVTSIR.I	3	91.8	78.0	40.1	36.7	76.2	73.4	37.1	30.5
MSMEG	MSMEG										
_1525	1524	K.DVVHTLFAEIGPFYADR.N	3	26.9	27.8	7.9	8.8	26.1	23.4	3.2	4.5
		K.GDNAPMAVIELVR.E	2	42.0	42.1	26.0	29.9	33.5	34.6	11.6	19.9
		R.DKDVVHTLFAEIGPFYAD R.N	4	84.9	95.8	23.9	28.6	86.0	83.3	19.3	27.7
		R.KGDNAPM*AVIELVR.E	2	122.5	122.0	83.9	107.6	177.6	197.9	98.2	108.7

		R.KGDNAPM*AVIELVR.E	3	71.3	60.4	8.7	4.8	35.2	63.0	1.7	11.2
		R.KGDNAPMAVIELVR.E	2	357.5	404.0	208.8	220.3	421.4	408.9	266.4	254.5
		R.KGDNAPMAVIELVR.E	3	326.3	307.7	153.9	131.5	415.8	380.7	193.6	166.4
		R.LGGSSSHQSALLANLATS									
		LFEHGR.I	3	387.6	394.5	238.3	237.5	478.5	444.3	304.1	278.7
		R.LGGSSSHQSALLANLATS									
		LFEHGR.I	4	511.5	539.5	262.6	258.3	629.4	613.1	364.4	331.2
MSMEG	MSMEG										
_1528	1527	K.LGLPLTASPVYGSRA	2	81.0	86.7	60.2	67.9	64.8	71.0	51.4	51.0
		R.AIDLC#NAGDPVC#GSGD									
		SVPAHR.A	3	58.1	66.9	42.2	46.9	48.4	50.5	45.1	42.0
		R.AIDLC*NAGDPVC*GSGDS									
		VPAHR.A	3	57.9	66.7	41.5	46.5	48.3	50.4	44.4	40.7
		R.IGNAFVQALR.G	2	23.5	19.2	23.7	23.1	23.0	26.5	26.6	29.7
MSMEG	MSMEG	R.QELLRAANVGSAAEYTR.									
_1536	1535	T	3	45.2	40.4	25.0	27.3	35.9	36.8	29.8	31.2
MSMEG	MSMEG	K.HKPTFTPNVDGGDFVIVIN									
_1556	1553	ADK.I	3	1094.4	844.8	661.5	522.4	1137.0	1136.9	641.1	535.9
		K.VYAGPDHPHAAQQPIPFEI									
		K.Q	3	986.0	1141.1	508.5	558.5	1067.4	1035.9	507.4	457.1
		R.LASAAATLLR.G	2	36.8	36.7	10.2	9.1	39.6	39.2	10.6	9.6
		R.SWYVIDASDVVLGR.L	2	414.7	411.3	246.6	230.5	401.4	454.6	238.7	237.9
		R.SWYVIDASDVVLGR.L	3	29.2	16.0	10.0	3.7	25.4	29.7	2.3	7.6
		R.VVENAIIGM#LPHNK.L	3	229.6	251.1	81.9	90.6	188.6	236.6	62.3	71.2
		R.VVENAIIGM*LPHNK.L	2	35.4	37.8	37.8	41.0	37.1	31.6	42.3	41.1
		R.VVENAIIGMLPHNK.L	2	35.4	37.8	171.3	150.2	37.1	31.6	129.0	142.4
		R.VVENAIIGMLPHNK.L	3	119.1	98.1	50.1	47.9	127.8	125.3	53.5	50.4
MSMEG	MSMEG	K.APLVTVDRVDQFDIYAHLD									
_1557	1554	GGGPSGQAGALR.L	4	97.3	82.8	83.2	77.0	218.6	210.1	132.1	132.5
		R.ALILVQPEDRPALK.K	2	436.4	466.2	303.0	301.0	491.0	436.3	333.1	304.5
		R.ALILVQPEDRPALK.K	3	1570.7	1707.8	518.8	547.3	1529.1	1469.8	491.6	427.7
		R.ALILVQPEDRPALKK.A	2	5.2	7.3	0.1	0.2	16.9	12.4	0.3	0.2
		R.ALILVQPEDRPALKK.A	4	107.5	111.3	28.8	30.7	260.0	234.5	92.9	85.2
		R.EPVIIDRPIQTVGR.R	2	691.7	67.7	408.0	81.1	792.8	686.7	472.2	416.6
		R.LVPGTGQFNLDGR.T	2	2357.3	3238.7	1596.4	2000.3	2565.0	2943.1	1975.6	2015.3
		R.VDQFDIYAHLDGGGPSG									
		QAGALR.L	2	118.1	96.9	37.5	31.3	97.6	88.0	29.6	23.4

		R.VDQFDIYAHLDGGGPSG									
		QAGALR.L	3	1629.2	1683.2	801.9	764.8	1602.6	1583.5	734.7	738.5
MSMEG	MSMEG										
_1567	1564	R.ALLTGFLATLAGDK.T	2	14.0	11.7	25.2	19.6	30.6	27.0	24.8	20.4
		R.IPGLVLTDPGDR.M	2	48.0	50.4	142.9	137.2	72.6	73.5	126.9	137.9
MSMEG	MSMEG										
_1574	1571	K.YGLTYPGVGFVVR.N	2	62.4	61.0	115.3	108.0	83.5	73.1	162.1	140.9
		R.AGYTQVMQC#LSQTAR.									
		W	2	97.1	116.6	119.9	123.6	50.1	56.2	54.3	77.0
		R.ALKDDIITVLGQLDALKPR.									
		G	3	135.6	131.6	187.1	170.9	113.0	95.2	224.7	167.5
		R.ALKDDIITVLGQLDALKPR.									
		G	4	29.3	21.0	22.8	20.7	30.3	24.4	31.8	30.5
		R.GQFDQLQPFAH	2	6.9	3.2	13.8	18.6	6.7	11.9	36.9	39.4
		R.LNLATFVTTWMDPEAEK.									
		L	2	95.5	85.9	103.9	98.7	47.9	49.0	78.7	73.8
		R.PGNQVVGQYYNFLR.L	2	157.3	150.7	176.9	170.7	99.0	94.1	159.3	152.1
MSMEG	MSMEG										
_1577	1574	K.AGDVVVLGSGPLGAGK.T	2	49.4	56.1	49.5	60.2	22.1	35.2	24.9	39.6
MSMEG	MSMEG										
_1581	1579	R.YAELVDAGDFDGVGQLL									
		GR.G	2	12.3	13.4	6.4	9.9	9.7	10.5	4.3	5.4
MSMEG	MSMEG										
_1582	1580	K.EKPQEGTVVAVGPGR.W	3	4.0	4.0	1.6	1.4	5.2	5.4	2.1	2.4
		K.ILVQANEAEATTTASGLVIP									
		DTAK.E	2	525.9	558.9	315.5	349.8	633.6	585.3	393.5	348.8
		K.ILVQANEAEATTTASGLVIP									
		DTAK.E	3	758.6	581.2	528.2	402.8	933.4	883.3	631.3	597.5
		K.RIPLDVAEGDTVIYSK.Y	2	478.0	517.3	594.9	545.1	852.5	751.5	887.4	703.5
		K.RIPLDVAEGDTVIYSK.Y	3	606.9	654.4	420.6	426.4	1044.3	1061.3	688.2	659.0
		K.YNGEYLLSAR.D	2	404.7	378.5	273.7	255.7	400.1	443.7	304.5	304.0
		K.YNGEYLLSAR.D	3	64.4	42.7	17.3	10.4	76.2	57.3	24.4	17.8
		R.IPLDVAEGDTVIYSK.Y	2	1355.5	2171.0	865.1	1374.0	1154.0	1329.5	773.0	831.8
MSMEG	MSMEG										
_1583	1581	K.AADAVSEALLASATPVDD									
		KK.A	2	108.3	104.7	81.8	68.0	76.7	77.3	48.5	53.4
		K.AADAVSEALLASATPVDD									
		KK.A	3	454.1	441.8	239.8	220.4	474.2	438.6	262.1	252.5

		K.AAVEEGIVTGGGAALVQA R.S	2	323.6	303.0	182.0	200.7	255.8	254.7	112.1	174.7
		K.AFLDDLAIVTGGQVNP VGLLR.E	3	164.7	221.3	125.2	184.0	217.0	208.0	78.6	120.7
		K.ISSLPDLLPLEK.V	2	597.0	558.9	344.4	336.1	473.5	404.1	311.4	244.9
		K.SFGGPQVTNDGVTIAR.E	2	867.8	721.6	562.6	497.3	915.4	921.9	499.0	552.2
		K.TNDVAGDGTATVLAQA LVR.A	2	149.3	154.5	177.6	182.0	66.5	73.0	64.3	57.0
		K.TNDVAGDGTATVLAQA LVR.A	3	307.0	360.1	231.9	259.1	374.6	335.8	213.1	203.1
		R.DEQVGELVGEAMTK.V	2	283.4	327.3	406.0	462.6	172.0	204.7	222.9	245.8
		R.DKISSLPDLLPLEK.V	2	61.9	75.6	44.2	64.5	107.5	92.5	50.7	52.3
		R.EIDLEDPYENLGAQLVK.S	2	602.9	586.1	932.6	839.3	480.2	477.3	1015.0	940.9
		R.EVGLEVLGSAR.R	2	60.0	54.7	114.6	96.5	58.3	50.1	126.9	109.6
		R.M*ILTETAVVDKPADEDE HGHGHHHGH	5	43.2	43.0	14.3	18.2	15.1	12.6	0.4	3.5
		R.NVAAGANPIALGSGISK.A	2	658.9	542.2	775.7	738.0	794.5	796.9	718.3	726.1
MSMEG	MSMEG										
_1602	1600	K.EGVSAEAAALGLLR.R	2	82.8	82.0	23.7	24.0	77.7	77.8	39.4	34.0
		R.AAAAALVEAGADAVK.V	2	170.8	133.1	330.5	247.9	180.8	162.5	441.3	405.5
		R.GPLGTVIHQTLGGLR.A	3	29.6	22.3	2.6	2.4	15.0	18.6	0.9	2.4
		R.ISGLPVVDDTGELVGIITN R.D	2	206.0	196.7	105.9	113.8	164.4	159.5	304.1	230.4
		R.ISGLPVVDDTGELVGIITN R.D	3	107.5	114.3	68.3	63.6	98.4	96.9	67.5	65.8
		R.NLPVAEQAGQVETVK.R	2	16.1	11.2	50.1	56.4	5.7	3.0	23.6	32.7
MSMEG	MSMEG										
_1603	1601	K.TFISELDVPVAGGVLDH R.T	3	204.0	173.4	196.9	189.0	197.2	154.4	189.3	168.5
		R.FEIPVIAHPTDALVSPEFAI EMGR.L	3	317.9	313.4	279.4	253.1	159.3	211.7	177.6	198.6
		R.LLQQLHAAPLDPDLLGAA VAR.I	3	253.5	243.0	466.0	406.1	256.5	234.9	904.3	605.3
		R.YVHVLAADGDIHSSGDLAK. A	3	60.7	57.2	160.6	180.6	35.3	44.2	33.7	53.7



		R.YVHVLADGDIHSSGDLAK.A	4	71.9	65.9	54.0	56.5	57.6	53.2	72.9	79.6
MSMEG	MSMEG	R.DPDTAARLRAEDDAVDAE									
_1605	1603	HR.H	3	0.1	0.1	0.4	0.3	4.5	5.4	0.7	0.7
MSMEG	MSMEG										
_1610	1608	R.FLEALTGVTNPEGK.R	2	758.8	698.5	627.5	580.9	668.5	643.1	656.5	659.0
		R.LAGVQYHPEVLHSPHGQ									
		QVLSR.F	3	72.8	47.7	142.0	158.4	46.5	45.5	480.1	547.9
		R.LAGVQYHPEVLHSPHGQ									
		QVLSR.F	4	44.8	49.1	108.8	109.9	9.6	22.9	31.4	54.0
		R.LAGVQYHPEVLHSPHGQ									
		QVLSR.F	5	343.1	268.2	251.7	200.6	279.2	272.8	197.2	228.0
		R.VVLDITSKPPGTIEWE	2	12.6	15.4	166.5	175.6	1.2	6.6	79.0	92.9
		R.VYSEVVPHTAGVEEIK.A	2	18.7	15.7	77.8	67.0	5.4	6.9	44.1	55.9
		R.VYSEVVPHTAGVEEIK.A	3	71.5	74.3	191.1	187.9	30.2	37.8	94.0	129.6
MSMEG	MSMEG										
_1614	1612	R.TVLDDVSLDVRR.G	2	76.4	83.8	2.0	1.0	80.4	84.7	1.0	1.9
MSMEG	MSMEG	R.ETIAALGGLPGADHGEHE									
_1634	1633	GR.H	3	9.5	0.0	0.4	0.0	14.8	15.1	0.5	1.3
		R.SALTEAASAQRPSPAVAA									
		ALSGVR.Q	3	1129.1	1204.5	728.1	785.6	1591.1	1632.4	783.1	756.9
		R.YDSLMAHAAAAPGSSLG									
		QQIYVTR.V	3	214.1	240.6	233.6	244.7	305.5	312.1	196.5	200.1
MSMEG	MSMEG										
_1635	1634	K.APVLLIPC#LEGR.P	2	35.1	34.8	90.2	87.1	0.6	3.2	101.3	91.4
		K.QAAEVVGIPFDK.Y	2	53.6	46.8	15.4	10.0	21.6	19.0	14.2	10.5
		K.RLPAEQFAHWDTW	2	176.5	143.7	71.7	54.9	81.4	97.7	69.2	65.6
		K.YSQAGLFPIAYTIGTDFK.K	2	41.9	46.6	17.4	22.5	62.1	60.4	54.2	58.2
		R.GLGSAWTTLHLLGEGEK.									
		Q	2	547.8	539.3	385.8	360.5	289.0	254.9	398.5	396.6
		R.GLGSAWTTLHLLGEGEK.									
		Q	3	599.1	517.9	280.0	247.8	304.4	271.2	288.4	263.5
		R.LPAEQFAHWDTW	2	119.7	127.8	67.2	73.3	54.7	59.4	58.5	67.9
		R.SNAIPYLEQEAAER.G	2	1218.8	1310.0	585.3	558.1	825.3	868.9	610.0	599.2

MSMEG _1642	MSMEG 1641	R.SNAIPYLEQEAAER.G	3	71.8	63.5	13.6	18.7	33.0	35.4	13.6	11.5
		K.FEGHDVHAEYASLR.S	3	4.7	3.6	6.8	4.0	4.4	4.3	4.8	4.2
		K.FEGHDVHAEYASLR.S	4	5.0	3.2	5.0	3.1	2.9	3.7	2.3	3.5
		K.TLLDNISIDAR.P	2	20.3	24.5	54.7	61.6	17.0	18.5	38.2	33.2
		R.ATDNDIVIPDVLASR.H	2	11.4	10.7	19.0	19.6	13.1	12.5	18.3	19.9
		R.IGLDQLSWITPAR.W	2	13.6	12.8	11.2	11.7	12.3	14.4	9.0	14.6
		R.TPEAPPASASSEAPADLG APAK.T	2	99.1	96.9	29.8	26.8	104.2	96.5	31.2	28.4
		R.TPEAPPASASSEAPADLG APAK.T	3	26.2	31.3	9.0	11.5	22.2	30.9	7.6	14.1
		R.TPPPAPANSSQAPTTMGP AAAPR.G	3	6.1	9.8	7.2	8.6	4.0	7.1	3.7	6.6
		R.YPSAPQHGYPNGPQTGY PSGPQR.G	3	88.9	90.7	66.6	69.2	74.8	93.4	58.3	77.3
MSMEG _1647	MSMEG 1645	K.LTGDVAPDVWEVAGHVS PNPGGVGPLTR.A	3	283.0	293.5	295.4	289.6	256.9	264.1	302.1	313.7
		R.AFLLTNVVEAEESK.L	2	194.3	198.3	348.8	344.7	159.8	154.0	311.0	326.6
MSMEG _1650	MSMEG 1649	R.IDPAKDADGLHPTNLGR.L	3	2.6	1.8	6.5	3.6	4.6	6.6	11.1	11.1
		R.RFDVPIAGAHVVVIGR.G	3	55.4	55.4	27.9	33.7	35.2	44.5	32.5	30.3
		R.RSENATVTLC#HTGTR.D	3	1.3	0.7	1.2	0.4	2.1	1.2	2.5	1.1
		R.RSENATVTLC*HTGTR.D	3	1.3	0.7	1.2	0.4	2.1	1.2	2.5	1.1
		R.TPGLGTVLVGDDPGSQA YVR.G	2	72.8	90.0	99.8	105.6	66.3	76.2	91.6	104.8
		R.GRPSYPPEAIDWLLPDGA HDVLDLGAGTGK.L	3	6.0	14.2	31.5	29.5	5.5	7.1	35.6	38.1
MSMEG _1652	MSMEG 1651	K.AFVNALTLHSHVANIGDV R.S	3	168.6	153.6	344.3	333.1	230.4	210.7	274.5	255.4
		K.FPGFTEPDPSYHGTVFAE LGAPAYALK.A	3	996.2	1051.8	573.9	594.0	842.4	982.9	591.4	667.6
		K.LGIETTFVENPDDLESWR. A	2	563.7	575.9	232.8	242.5	578.5	578.6	316.4	302.0
		K.LGIETTFVENPDDLESWR. A	3	25.5	31.6	5.2	5.2	25.7	26.1	3.7	4.6
		R.DLGSAAAPFNAFLIAQGLE TLSLR.V	3	114.1	133.2	59.1	76.5	114.0	155.5	70.2	96.5

		R.IGNPTTDVVEQR.I	2	6.7	5.4	8.4	8.1	4.5	7.1	4.0	3.8
		R.LAVGLEGIDDIIADLEQGF									
		AAAR.P	3	26.2	35.3	10.8	16.9	6.7	14.3	3.0	6.9
		R.LYGGTYNLLHYTLPK.L	2	316.5	317.9	153.5	176.3	286.8	264.5	171.3	151.1
MSMEG	MSMEG	K.ALAEQEEAIVSELNSVQG									
_1654	1652	K.T	2	1043.0	1097.2	649.3	642.1	723.6	821.9	580.4	708.0
		K.ALAEQEEAIVSELNSVQG									
		K.T	3	450.1	554.7	250.8	309.2	407.0	367.3	362.1	294.9
		K.ALIAFYEEQIEDAYK.T	2	1110.6	1127.3	707.1	669.1	811.6	820.7	746.5	721.9
		K.ALIAFYEEQIEDAYK.T	3	63.6	85.9	21.1	31.2	44.3	45.2	22.8	29.2
		K.FAEAAGIDVK.T	2	96.9	69.8	42.7	30.4	61.6	67.8	38.7	46.7
		K.GISNFHSPSDVIVDASM*P									
		AM*IR.L	3	227.1	228.1	56.9	75.9	99.2	141.6	34.8	54.3
		K.GISNFHSPSDVIVDASMPA									
		MIR.L	3	710.8	778.0	407.7	419.7	509.6	379.6	417.3	317.5
		K.GYNVPDYPANPK.T	2	40.1	32.1	39.5	34.7	25.9	22.8	33.6	38.4
		K.HVHQLVEENHLR.W	2	3.0	0.2	0.6	0.2	3.4	0.1	2.1	0.4
		K.HVHQLVEENHLR.W	3	27.2	7.8	11.5	2.3	17.1	4.9	9.5	2.2
		K.ILGSAVNPVLR.E	2	295.6	217.2	110.7	79.4	308.0	123.8	171.4	63.6
		K.IQIMPQVWAMR.Y	2	393.8	387.2	252.2	226.6	325.4	253.4	304.2	219.8
		K.KALIAFYEEQIEDAYK.T	2	71.5	75.7	107.8	91.9	75.6	82.4	213.6	168.2
		K.KALIAFYEEQIEDAYK.T	3	33.0	32.1	14.9	17.1	39.7	35.0	38.0	20.1
		K.LDAGDIIDSM*YMSK.K	2	315.8	381.7	45.4	62.6	215.7	249.9	36.4	57.6
		K.LDAGDIIDSMYM*SK.K	2	56.9	63.6	30.9	32.6	46.0	30.4	29.4	25.1
		K.LDAGDIIDSMYMSK.K	2	572.9	553.4	340.1	319.3	407.4	328.7	359.4	269.8
		K.LDAGDIIDSMYMSK.K	3	14.1	18.6	1.3	2.1	5.0	6.5	0.7	0.8
		K.LFDELGVNVNNGLSLDLYD									
		K.I	2	274.1	306.0	154.0	153.7	118.5	161.3	62.3	118.1
		K.LPNISASVPQLLAIAIK.E	2	1103.9	992.2	778.6	584.0	1386.9	771.0	1285.9	674.2
		K.LPNISASVPQLLAIAIK.E	3	58.0	83.6	9.5	30.2	61.5	53.8	33.7	31.3
		K.MLSIVPLMAGGGLYETGA									
		GGSA PK.H	2	197.5	182.0	111.0	112.1	198.1	208.9	132.9	162.9
		K.SGEEIVLKPEVK.L	3	39.4	30.8	2.4	2.8	26.8	27.3	3.3	5.7
		K.TGVMFSLHVK.A	2	47.9	46.2	5.2	5.4	41.6	38.2	11.3	8.7
		K.THGQFDPTTM*GTVPNVG									
		LM*AQK.A	3	160.6	178.8	39.7	40.1	89.4	93.6	16.8	35.4

		K.THGQFDPTTM*GTVPNVG									
		LMAQK.A	3	160.6	178.8	54.9	54.7	95.3	114.0	39.2	48.4
		K.THGQFDPTTMGTVPNVG									
		LMAQK.A	3	786.4	816.2	438.2	420.9	411.1	478.6	327.1	382.0
		K.TSDISVAAR.I	2	0.2	0.1	0.0	0.0	0.1	0.1	0.0	0.0
		K.TVDIGGYYPDPEK.T	2	1131.8	1119.6	773.7	746.0	894.6	883.7	909.4	800.8
		K.VSHPIVFGHAVK.V	3	5.2	3.4	0.2	0.2	4.5	3.3	0.6	0.6
		R.DYLTDLFPILELGTSAK.M	2	925.7	1188.2	614.1	723.7	751.0	973.1	716.6	894.6
		R.DYLTDLFPILELGTSAK.M	3	54.7	65.7	27.8	36.7	46.1	58.9	32.9	49.6
		R.ILAEFGDHLTEEQR.V	2	457.9	418.7	273.2	264.4	336.1	326.1	278.5	253.7
		R.ILAEFGDHLTEEQR.V	3	781.9	750.1	385.9	373.5	511.4	520.1	336.7	377.1
		R.KFAEAAGIDVK.T	2	27.4	17.2	8.6	6.6	21.2	21.7	10.0	13.1
		R.LSGM*PVVFWLDTERPHE									
		VELR.K	4	112.0	125.9	29.0	34.0	103.5	87.4	28.0	36.2
		R.LSGMPVVFWLDTERPHE									
		VELR.K	3	304.2	335.3	154.0	147.3	218.0	273.4	125.7	218.0
		R.LSGMPVVFWLDTERPHE									
		VELR.K	4	397.0	450.3	181.8	220.4	221.7	407.1	138.6	287.3
		R.MYQEMINFC#K.T	2	196.7	192.9	112.2	108.5	160.1	144.9	119.1	125.8
		R.MYQEMINFC*K.T	2	196.7	192.9	112.2	108.5	160.1	144.9	119.1	125.8
		R.VPDNLGELGALTQDPSAN									
		IIK.L	2	577.9	621.4	273.1	312.6	411.1	390.6	337.3	307.1
		R.VPDNLGELGALTQDPSAN									
		IIK.L	3	615.6	810.0	406.1	497.9	505.1	463.5	551.5	392.9
		R.WDSLGEFLALGASLEDM*									
		GNK.T	2	36.2	42.2	8.1	7.2	50.5	26.3	5.9	10.6
		R.WDSLGEFLALGASLEDM									
		GNK.T	2	90.2	96.8	43.8	47.4	58.4	105.5	45.0	78.6
MSMEG	MSMEG										
_1655	1653	R.GPFLLDVAHLADDIER.R	3	15.5	14.2	0.9	1.6	27.3	22.9	1.1	2.1
		R.VTEliteFVDR.H	2	21.0	22.1	5.2	4.0	35.4	29.0	4.3	7.4
MSMEG	MSMEG										
_1656	1654	R.IDYHLVTPGLAGR.L	2	21.7	18.1	23.2	30.0	31.2	22.0	18.0	21.4
MSMEG	MSMEG										
_1662	1660	K.APFEPLTPGGFR.A	2	78.9	55.1	72.4	55.8	112.1	103.1	90.4	95.6

		K.LYDLPIVGDVR.G	2	51.2	56.1	81.1	84.7	68.3	62.1	71.0	79.2
		R.GEGFFYGIELVK.D	2	22.4	19.0	32.9	53.2	33.4	32.7	30.1	45.4
		R.GFLTPALWEAGLYC#R.A	2	146.9	109.9	88.7	74.3	238.7	238.0	144.0	129.7
		R.VFFTTGGGEAVESAWK.L	2	97.3	83.6	238.3	188.0	145.3	117.2	219.5	231.1
MSMEG	MSMEG										
_1663	1661	R.ALPGVISTETLVYLK.L	2	30.5	27.0	66.0	64.0	28.8	26.4	40.1	42.0
		R.PGAFQLDELSK.A	2	97.7	103.1	6.6	8.8	98.4	81.1	7.0	8.2
MSMEG	MSMEG	K.LADEHAEQFVAEEVSQTG									
_1665	1662	KPVR.L	3	291.2	284.9	167.1	209.1	234.4	207.1	248.1	227.8
MSMEG	MSMEG										
_1669	1666	K.DLVVNMEPFFDAYR.A	2	104.6	114.6	90.8	102.3	174.9	167.5	90.5	86.4
		R.FNPENPDAAGWQSFR.V	2	398.1	430.1	299.3	298.2	663.8	713.1	319.5	314.0
		R.GIQVTQAIQEVK.R	2	209.4	184.4	261.3	252.5	378.4	447.2	217.1	268.4
		R.LDILNEVDGVWR.C	2	107.0	96.4	148.2	148.0	230.5	223.3	156.7	159.8
		R.LLNLLHYVK.W	2	35.6	37.2	26.1	33.3	80.0	79.4	27.1	31.8
MSMEG	MSMEG										
_1670	1667	K.EAIDAVLDLEK.M	2	200.0	201.4	117.7	94.8	307.2	259.6	104.7	77.9
		K.LPDITEFAR.T	2	142.4	124.0	112.6	104.1	274.7	260.9	88.2	79.1
		K.TTSNAHTLTGDGLGIVFR.									
		K	2	135.0	156.8	202.9	246.0	207.2	221.2	185.2	207.9
		K.TTSNAHTLTGDGLGIVFR.									
		K	3	148.7	141.5	171.3	168.9	273.4	249.8	180.2	153.8
		R.GALQQSMDNNAAVFR.T	2	90.8	78.9	171.6	144.3	110.5	92.8	97.4	96.2
		R.LGTNSLLDINVFGR.R	2	141.0	125.7	217.5	193.1	211.6	141.1	202.0	129.1
		R.SMVLEVLEGR.G	2	71.6	55.3	113.8	94.8	127.7	98.7	97.1	99.9
		R.YAPTIVDLAPR.D	2	115.2	103.1	171.3	154.1	167.5	134.4	101.1	110.0
MSMEG	MSMEG										
_1671	1668	R.IDFNYVAER.W	2	9.2	5.8	5.1	2.1	19.8	23.3	4.2	7.2
MSMEG	MSMEG										
_1672	1669	R.VSPQAYNEVIETYK.T	2	230.3	264.8	290.3	319.5	397.5	393.6	263.5	239.4
MSMEG	MSMEG										
_1676	1673	R.IVDDISETPDGTQQLGR.L	2	210.8	169.8	127.0	80.6	96.8	134.5	137.7	162.4
		R.LAIIDEVIKPR.Y	2	25.9	24.9	9.0	10.0	1.0	0.9	5.4	5.8

MSMEG	MSMEG	R.GVNAADAFTIAQVAIGLLR									
_1679	1676	.Q	2	23.5	24.7	165.0	176.9	76.7	92.9	502.1	477.3
		R.GVNAADAFTIAQVAIGLLR									
		.Q	3	7.3	5.9	35.7	34.2	38.3	41.9	53.1	55.6
		R.VASTLAEGGFDVTER.Y	2	130.8	153.8	275.4	307.3	272.2	229.6	231.4	250.7
MSMEG	MSMEG										
_1680	1677	R.AALAAGGEAGPVR.S	2	0.2	0.2	4.9	3.2	4.9	3.2	7.3	5.4
		R.SAGM#IVVEDVSWPVTDL									
		R.V	2	28.1	32.4	50.4	58.5	60.2	61.3	44.2	38.9
		R.SAGM*IVVEDVSWPVTDL									
		R.V	2	35.7	41.3	69.6	80.3	108.3	106.5	59.0	54.1
		R.SAGMIVVEDVSWPVTDLR									
		.V	2	155.6	158.2	469.4	465.4	664.1	621.8	459.9	431.5
		R.VDFADDPIGDLAALWQV									
		WQPQKK.D	3	8.2	11.2	24.0	30.4	47.7	71.0	33.9	61.2
MSMEG	MSMEG	K.AM#SNIAM#LLEEAGSSLR									
_1681	1678	.D	2	26.1	27.7	99.0	114.4	66.2	66.0	53.3	52.0
		K.AM#SNIAM#LLEEAGSSLR									
		.D	3	7.3	0.0	33.1	0.0	21.1	24.5	15.2	16.5
		K.AM#SNIAMLLEEAGSSLR.									
		D	2	8.9	9.7	41.6	44.8	21.9	20.9	20.8	20.6
		K.AM#SNIAMLLEEAGSSLR.									
		D	3	2.6	1.8	15.4	13.9	7.8	8.4	4.6	6.8
		K.AM*SNIAM*LLEEAGSSLR.									
		D	2	8.7	9.7	41.6	44.8	21.8	20.9	20.8	20.6
		K.AM*SNIAM*LLEEAGSSLR.									
		D	3	2.7	1.8	22.3	21.3	9.4	10.2	13.0	14.1
		K.AM*SNIAMLLEEAGSSLR.									
		D	2	8.7	9.7	41.6	44.8	21.8	20.9	20.8	20.6
		K.AM*SNIAMLLEEAGSSLR.									
		D	3	2.7	1.8	22.3	21.3	9.4	10.2	13.0	14.1
		K.AMSNIAM#LLEEAGSSLR.									
		D	2	10.8	14.6	55.0	69.6	29.9	30.7	26.8	26.6
		K.AMSNIAM#LLEEAGSSLR.									
		D	3	5.5	1.8	29.6	13.9	16.9	17.6	13.3	15.1
		K.AMSNIAM*LLEEAGSSLR.									
		D	2	10.8	14.6	55.0	69.6	29.8	30.7	26.8	26.6

MSMEG _1682	MSMEG 1679	K.AMSNIAM*LLEEAGSSLR.D	3	5.6	1.8	36.6	21.3	18.4	19.4	21.6	22.4
		K.AMSNIAMLLEEAGSSLR.D	2	34.2	51.8	167.6	256.4	83.2	88.7	96.1	93.9
		K.AMSNIAMLLEEAGSSLR.D	3	26.6	21.8	152.0	125.0	64.7	67.6	87.4	84.4
		K.DTYPEQNLNDLDC#QAVV AGGVVYLR.G	3	2.8	3.1	17.5	25.0	12.1	27.9	16.6	18.7
		K.GVFPVSTGLVVEALAR.P	2	58.7	53.9	259.5	245.5	134.3	130.5	147.0	142.0
		K.GVFPVSTGLVVEALAR.P	3	1.6	0.5	9.5	5.3	4.4	6.2	1.9	2.2
		K.VTVYLTDIR.Y	2	184.8	163.0	799.9	683.8	647.0	710.3	718.6	719.2
		R.ESVGIGDVAAQTEK.A	2	38.8	36.5	183.0	170.7	157.4	169.7	184.1	181.7
		R.GQIGQDLETR.E	2	0.1	0.0	2.2	2.5	1.3	1.3	3.3	3.2
		K.IHGRPGFHAETSAGTIDAR .Y	3	0.1	1.6	3.1	2.4	12.6	8.7	0.9	1.5
		K.IHGRPGFHAETSAGTIDAR .Y	4	0.0	0.0	0.0	0.0	6.6	5.5	0.0	0.1
		R.GAEHVTIAVSGAHGGHTV DFR.S	2	1.5	0.8	3.1	2.9	41.3	32.8	2.3	3.5
		R.GAEHVTIAVSGAHGGHTV DFR.S	3	67.8	43.6	27.4	28.5	502.1	448.5	36.3	47.8
		R.GAEHVTIAVSGAHGGHTV DFR.S	4	112.6	106.6	58.9	52.2	738.4	838.1	40.1	60.0
		R.GAEHVTIAVSGAHGGHTV DFR.S	5	70.6	48.9	26.5	17.3	596.0	594.4	23.0	25.2
		R.GSSFLWGVWHDAK.Y	2	344.0	388.0	7.5	7.0	162.4	166.1	10.0	6.2
		R.PGFHAETSAGTIDAR.Y	2	3.4	2.2	4.9	5.7	44.0	28.7	1.3	1.8
		R.PGFHAETSAGTIDAR.Y	3	25.5	21.0	12.2	12.5	153.5	143.1	10.9	11.5
		R.RGSSFLWGVWHDAK.Y	3	7.2	13.2	12.4	7.5	58.8	55.4	4.6	5.4
		R.SLAASGITLLGR.A	2	13.4	6.8	58.2	52.2	407.1	355.0	55.9	54.9
MSMEG _1683	MSMEG 1680	K.GVYDLESIFR.F	2	0.0	0.0	34.4	43.3	0.8	0.5	37.1	31.7
MSMEG _1694	MSMEG 1690	R.LANPPLLVPVLR.A	2	20.9	19.2	68.5	67.6	31.8	27.0	35.1	38.6

		R.LITATVDEGLNEIAYIVPGL									
		GDAGDR.Q	3	18.6	19.3	9.9	10.4	17.8	28.1	6.7	11.1
MSMEG	MSMEG	R.ENLSELEFNLLMLVAPVLR									
_1696	1692	.K	2	176.9	182.5	177.8	161.8	186.4	190.3	224.5	207.6
MSMEG	MSMEG										
_1701	1697	R.IHAYEGHDLAHVVHPVR.T	3	3.8	2.6	18.0	14.4	4.6	4.0	13.2	16.2
		R.IHAYEGHDLAHVVHPVR.T	4	17.9	19.7	12.9	13.2	17.0	18.9	11.9	17.8
MSMEG	MSMEG										
_1704	1700	K.PLPIVTGQDAELASVK.S	2	3.3	3.1	218.8	192.2	1.3	0.7	200.7	250.7
		K.SIVAGEQTQTVFK.D	2	1.9	3.6	237.5	233.5	3.4	4.2	205.3	224.1
		K.VGVLLQANYIVDTLGVADG									
		K.G	2	28.7	31.5	251.8	286.0	19.3	26.0	259.7	243.9
		K.VVPSYLLDPVSVDK.S	2	148.6	149.6	380.6	382.3	143.8	114.7	365.7	357.4
MSMEG	MSMEG										
_1712	1708	R.TGWDAVLQETK.N	2	1.3	5.4	19.7	16.2	2.8	6.0	13.6	12.5
MSMEG	MSMEG										
_1713	1709	R.AFLAELNPGFASFVEDK.I	2	18.2	24.0	28.7	32.7	19.4	25.9	14.8	18.1
MSMEG	MSMEG	K.EDEEALDRWEGAELGIHK									
_1734	1730	.K	3	8.0	0.0	10.7	0.0	12.2	10.4	14.7	15.0
		K.VFVVLYDMTK.E	2	14.7	14.2	5.3	5.4	16.5	16.9	0.9	2.1
		R.LTFGGEDIGWEGALATVV									
		EDPLSK.V	3	16.8	0.0	23.6	0.0	16.4	22.2	19.9	25.2
		R.YIGVMADAAEIAGAPPEYV									
		HDLR.T	3	51.8	42.4	75.4	51.3	38.0	36.3	48.0	50.5
MSMEG	MSMEG	R.DQILPHEDSDAAAVLEQV									
_1735	1731	FAQR.G	3	146.6	153.7	153.0	157.7	116.9	112.6	163.0	143.2
		R.IAMYHALGEAVAPIR.L	3	43.6	40.2	19.3	21.8	15.7	16.5	12.8	9.0
		R.IVILGGGPAGYEAAALVAAA									
		R.G	2	132.6	118.2	257.2	260.7	164.4	137.6	221.2	281.0
MSMEG	MSMEG	R.IAYGTVLSGDQYLHSVPT									
_1753	1750	R.D	3	88.2	91.6	91.7	94.7	58.7	55.2	84.7	80.4
MSMEG	MSMEG										
_1757	1754	R.LLGPLTEADIAQR.C	2	1.6	2.3	14.0	14.8	2.4	3.6	12.7	14.0
MSMEG	MSMEG										
_1760	1758	R.VVVADLDEPGAAATAAR.I	2	71.8	76.3	136.0	134.6	43.5	57.6	95.7	116.8



MSMEG	MSMEG										
_1803	1801	R.LAVDEAC#TTLIR.S	2	141.0	167.6	287.7	370.7	127.7	132.7	319.5	302.9
		R.VAAM*LENLAVVR.T	2	37.7	41.4	48.1	51.6	27.5	24.9	40.4	40.5
		R.VAAMLENLAVVR.T	2	165.2	184.0	114.0	115.5	134.4	148.2	99.0	94.8
MSMEG	MSMEG	K.AASGDAVTAPMQGTVVK.									
_1807	1807	V	2	71.3	66.4	88.6	82.4	41.7	37.0	60.7	61.6
		K.APLVPGTPDPVKDADEVV									
		AFAK.E	2	180.3	159.6	246.5	228.8	143.4	111.0	234.9	209.0
		K.APLVPGTPDPVKDADEVV									
		AFAK.E	3	3512.6	3731.4	5757.9	5943.0	2859.0	2749.0	6234.7	6070.8
		K.DAGLASVAVYAEPDADAP									
		HVR.L	2	552.7	559.5	432.9	463.5	510.5	571.6	390.1	502.8
		K.DAGLASVAVYAEPDADAP									
		HVR.L	3	2380.1	2103.7	2878.9	2619.0	1909.3	1592.0	2480.9	2333.0
		K.DAGLASVAVYAEPDADAP									
		HVR.L	4	111.5	94.5	65.1	52.8	75.1	73.8	63.0	57.3
		K.DGTITGLAVEAGAAITQGT									
		VIAEIK	3	104.0	107.0	113.1	125.0	96.4	75.8	139.0	110.6
		K.IANGEPLDITEDPTPR.G	2	2323.9	2214.9	2473.2	2348.4	2711.1	2722.7	2887.9	2912.8
		K.IANGEPLDITEDPTPR.G	3	88.6	108.4	71.6	104.1	54.0	69.0	69.4	89.7
		K.LVEEAPAPFLTDAQR.K	2	3372.0	3278.7	3210.6	3121.1	3791.3	3834.1	3657.5	3652.1
		K.LVEEAPAPFLTDAQR.K	3	206.7	205.9	179.4	179.4	182.6	166.9	171.9	172.7
		R.AKAPLVPGTPDPVKDADE									
		VVAFAK.E	3	590.2	614.8	3576.6	3759.3	1071.5	1058.1	1329.4	1405.8
		R.AKAPLVPGTPDPVKDADE									
		VVAFAK.E	4	338.6	323.1	356.4	344.4	595.1	598.6	536.2	626.2
		R.ALAEFTVEGLATVIPFHR.									
		A	3	64.4	69.6	66.8	71.5	116.4	103.0	141.9	129.0
		R.AVVSDPAFIGDGEK.F	2	240.4	196.6	343.9	298.3	159.5	98.2	335.5	273.1
		R.AVVSDPAFIGDGEKFVDH									
		TR.W	3	94.4	94.0	121.8	140.3	180.3	183.1	275.1	297.9
		R.AVVSDPAFIGDGEKFVDH									
		TR.W	4	159.1	137.1	164.4	151.7	496.3	486.4	443.1	449.1
		R.HVEAQVIADQHGNVVVAG									
		TR.D	2	29.9	17.6	22.3	20.6	38.3	47.3	25.5	45.2
		R.HVEAQVIADQHGNVVVAG									
		TR.D	3	1098.7	889.2	867.1	739.3	1220.0	1480.3	1055.4	1312.8

MSMEG _1808 MSMEG _1809	MSMEG 1808 MSMEG 1809	R.HVEAQVIADQHGNVVVAG										
		TR.D	4	608.2	449.7	498.4	408.3	569.4	709.7	435.1	619.5	
		R.LEVSLPGDLAIGGGGGAA										
		APGVVR.K	2	238.2	255.4	242.9	261.6	110.2	111.0	141.7	156.2	
		R.LQVEHPVTEETSGIDLVR.										
		Q	2	1133.3	1128.3	1062.9	988.2	1119.1	1274.6	1090.2	1231.7	
		R.LQVEHPVTEETSGIDLVR.										
		Q	3	4950.5	5456.6	4591.5	5106.6	3448.0	4885.4	3958.6	5069.3	
		R.M#DSGVETGSVIGGQFDS										
		MLAK.L	2	104.3	115.2	95.5	104.2	21.2	43.5	13.1	16.2	
		R.M*DSGVETGSVIGGQFDS										
		MLAK.L	2	104.3	115.2	95.5	104.2	21.2	43.5	13.1	16.2	
		R.MDSGVETGSVIGGQFDS										
		MLAK.L	2	210.7	202.9	223.6	202.2	185.9	158.7	220.6	210.9	
		R.QTVVVEVGGR.R	2	5.8	4.0	4.2	3.4	4.9	5.9	4.0	6.0	
		R.RLEVSLPGDLAIGGGGGA										
		AAPGVVR.K	2	135.1	187.0	113.7	195.3	86.1	142.3	118.6	187.1	
		R.RLEVSLPGDLAIGGGGGA										
		AAPGVVR.K	3	2073.3	2242.8	2254.5	2183.4	1670.0	1697.4	2279.0	2103.5	
		R.TLEEIPELFESATR.E	2	1741.4	1892.0	2225.6	2333.6	1393.8	1291.4	2144.2	1946.6	
		R.TLEEIPELFESATR.E	3	244.4	271.4	245.5	258.8	291.3	236.3	277.4	218.9	
		R.LYFSAPAEAPTTR.G	2	81.1	91.4	109.6	133.6	79.6	73.2	63.3	76.1	
		K.IDWHTDLNDPHVR.D	2	111.7	115.8	19.7	14.9	116.7	122.5	9.8	10.2	
		K.IDWHTDLNDPHVR.D	3	130.0	121.2	89.0	69.9	83.7	90.1	57.7	56.3	
		K.IDWHTDLNDPHVR.D	4	198.6	170.0	91.9	76.4	158.4	134.3	69.2	64.3	
		R.AFKEDVLEILGK.Q	2	73.7	72.7	42.0	35.8	65.4	51.6	44.4	28.9	
		R.AFKEDVLEILGK.Q	3	36.3	35.7	9.2	9.6	37.1	34.7	11.2	8.3	
		R.DYINGEQFAALMDR.K	2	216.0	237.2	125.0	145.4	139.4	144.0	69.5	78.0	
R.LVTADWLASNLGR.P	2	501.0	521.1	533.1	544.9	371.3	341.2	351.4	381.0			
R.NYDGSWTEWGNVAVR.V	2	188.8	225.7	138.9	146.8	124.6	134.3	71.5	95.2			
R.PGLAIVESDEDVLLYDTGH												
IPGAVK.I	3	1197.4	1069.0	1172.7	1033.4	820.1	707.4	911.3	819.5			
R.SSHTWFLVTHLLGLPGVR												
.N	3	110.0	102.3	55.6	53.8	55.2	55.3	27.5	24.8			

		R.SSHTWFLVTHLLGLPGVR									
		.N	4	36.3	32.1	15.0	14.8	17.3	15.6	5.3	4.2
		R.THMPDYPEEGALR.G	3	14.3	10.4	7.0	3.6	8.3	9.7	2.7	2.2
MSMEG	MSMEG										
_1812	1811	R.YSVFSWQR.V	2	133.5	124.8	97.6	96.3	116.4	136.7	78.9	85.4
MSMEG	MSMEG										
_1813	1812	K.LLYAYGEATVAK.V	2	544.9	568.7	643.3	704.8	504.0	498.3	545.0	607.9
		K.NRPLGDGVITGYGTIDGR.									
		D	2	403.1	430.5	483.0	572.2	361.9	382.8	254.5	301.6
		K.NRPLGDGVITGYGTIDGR.									
		D	3	613.0	594.9	630.8	581.9	587.9	553.6	562.5	471.6
		K.SGTAHYVASGEQDAFDYV									
		R.D	2	398.6	488.7	287.1	342.9	318.8	384.6	213.4	283.5
		K.SGTAHYVASGEQDAFDYV									
		R.D	3	1158.7	1190.5	1167.5	1148.8	1150.5	1248.1	1128.7	1083.7
		K.TVTGEDVTMEELGGAHT									
		HMAK.S	3	149.3	174.3	199.3	213.4	78.4	106.9	88.1	124.6
		K.TVTGEDVTMEELGGAHT									
		HMAK.S	4	272.5	204.1	291.0	245.1	128.4	145.9	114.1	141.3
		R.ILALLDEGSFVELDALAK.H	2	186.8	179.4	183.3	155.3	137.3	127.7	128.8	108.8
		R.IQEGVVSLGLYSR.I	2	1007.5	937.5	1605.3	1430.2	739.2	668.3	1354.5	1384.2
		R.LELQQTIEDTLVNPYIAAE									
		R.G	3	56.2	88.2	65.1	95.1	36.5	42.9	21.6	70.5
		R.RTEETLHPVGEEAAVDK.V	3	1.0	0.5	0.7	0.5	0.2	0.1	0.1	0.1
		R.RTEETLHPVGEEAAVDKVH									
		AK.G	4	0.0	0.0	0.0	0.0	0.4	0.7	0.0	0.1
MSMEG	MSMEG	K.VAQGATVVTDFDHEHVPTE									
_1819	1818	HLDR.L	3	83.4	76.8	74.1	89.0	38.5	50.4	192.3	196.6
		K.VAQGATVVTDFDHEHVPTE									
		HLDR.L	5	123.8	82.7	58.1	42.1	71.3	68.5	57.0	48.1
MSMEG	MSMEG										
_1822	1821	R.SALLTEFLTR.L	2	29.8	30.2	38.8	39.1	25.0	22.6	30.2	35.1
MSMEG	MSMEG	K.LAGEQAVLAAKPDAYVVR.									
_1825	1824	T	3	121.3	119.6	57.3	60.6	135.5	130.5	109.2	105.7

MSMEG	MSMEG										
_1828	1826	R.EVFPALLADGLR.I	2	101.1	92.7	70.8	74.9	74.5	62.8	51.9	62.2
		R.LDGAVIFDGVR.V	2	106.9	74.2	9.1	12.4	48.5	32.7	22.9	14.2
MSMEG	MSMEG										
_1832	1831	R.VSSLDVAVDEIPR.M	2	20.5	0.0	36.5	0.0	17.9	18.5	38.6	39.7
MSMEG	MSMEG										
_1834	1833	R.TTEEVDVAVDR.I	2	10.9	9.4	5.3	5.6	5.8	5.4	5.0	4.6
MSMEG	MSMEG	K.VLAADEPLSLQAHPSAAQ									
_1836	1835	AQEGFER.E	3	139.3	142.2	105.8	131.8	105.6	97.9	90.7	94.0
MSMEG	MSMEG										
_1843	1842	K.AGVVPPAEDDDPAEWK.V	2	1453.1	1220.0	1474.3	1237.6	2171.6	2164.9	1667.2	1788.3
		K.GVTEETTTGVLRL	2	5.2	5.1	5.6	4.7	8.8	10.6	19.3	20.7
		K.INIKPQVDQWIFDDGK.S	2	267.9	222.0	291.0	250.0	452.0	494.5	261.4	318.2
		K.INIKPQVDQWIFDDGK.S	3	111.3	115.6	86.5	91.3	175.2	184.5	91.1	108.7
		K.KINIKPQVDQWIFDDGK.S	3	571.7	640.3	458.4	557.6	659.9	738.1	437.8	594.1
		K.NQAILGNIGHFDNEIDMAA									
		LER.S	3	405.1	363.9	341.9	324.0	470.2	407.4	274.1	252.7
		K.VADLSLADFGK	2	532.6	460.0	488.1	446.2	868.3	774.3	599.2	554.4
		K.VLIC#GYGDVGK.G	2	156.0	136.0	229.9	210.5	191.3	226.8	179.6	178.4
		R.LAEHEMPGLMALR.R	3	87.6	42.5	33.9	11.7	39.6	43.7	6.1	6.9
		R.VSVTEIDPINALQALMDGF									
		DVR.T	2	102.7	133.4	94.7	127.6	79.9	118.0	53.7	86.1
		R.VSVTEIDPINALQALMDGF									
		DVR.T	3	93.4	111.1	71.8	88.5	78.6	110.8	44.6	67.7
MSMEG	MSMEG	K.DQAEYIGVDVEGPYKPEH									
1843	1843	YR.Y	3	621.1	701.1	739.9	802.4	711.1	804.2	523.2	608.2
		K.DQAEYIGVDVEGPYKPEH									
		YR.Y	4	270.2	267.4	243.7	242.0	398.0	370.3	225.3	252.9
		R.IHVEALGGTLTK.L	2	15.1	8.5	22.0	26.4	33.4	28.4	15.6	19.1
MSMEG	MSMEG	R.LHLPVPDWQVLLNVPTL									
_1873	1876	AAQR.A	3	65.8	68.7	117.0	119.7	42.4	48.7	65.4	89.7
MSMEG	MSMEG	R.AKVEKDPENPQVVLTVR.									
_1874	1877	G	3	4.6	2.6	23.2	14.2	11.6	9.7	45.7	36.7
		R.DVLEQVWGYR.H	2	36.1	36.3	70.6	74.6	33.5	41.3	66.3	80.7
		R.GEGFDTAVIGDGSQALTA									
		VR.E	2	325.3	373.6	281.8	279.1	263.8	298.7	313.7	308.8

MSMEG	MSMEG										
_1878	1881	K.TIYLFDVELDHER.N	2	36.4	39.3	84.8	86.4	20.8	28.3	54.4	48.0
		R.GEAC*ADSFYTAFESAVQ									
		K.L	2	0.5	0.4	134.3	136.7	1.9	2.6	111.3	104.9
		R.TM*VVEDDRESTAGTTPE									
		RPHAEVVVK.G	4	1.0	0.9	40.9	41.5	3.5	4.1	33.3	37.4
		R.TMVVEDDRESTAGTTPER									
		PHAEVVVK.G	4	4.3	5.8	238.9	284.4	20.4	27.4	169.0	217.1
MSMEG	MSMEG										
_1881	1882	K.AENQTLATITLQNYFR.L	2	7.9	7.9	22.5	21.3	9.0	7.0	19.9	19.6
		K.FLAVVDDVAER.H	2	142.9	131.4	110.7	114.3	179.8	151.3	129.7	118.9
		K.GIDNEAPPLTYTGPSEDG									
		TAQVQR.S	3	124.5	124.9	122.8	111.2	92.9	109.2	77.0	100.2
		K.GVHVVTVNDYLAR.R	2	94.5	90.9	82.9	88.6	86.0	92.6	58.5	75.9
		K.GVHVVTVNDYLAR.R	3	102.7	87.5	81.9	66.4	108.3	101.6	75.5	77.0
		K.LSGMTGTAETEAELHEY									
		K.L	3	205.6	200.3	734.4	903.6	178.3	206.4	639.4	282.2
		K.TLTAVLP SYLNALSGK.G	2	275.1	253.9	344.2	319.9	322.6	280.6	430.6	361.2
		K.VADYVNALSDDVEK.L	2	243.1	236.8	151.5	137.6	252.6	270.5	159.2	189.2
		R.DLIDSDAVGEPGELTR.E	2	214.5	213.7	194.8	200.9	227.0	229.5	164.3	162.1
		R.EGYDMFVGMLEALK.E	2	23.5	28.1	6.9	8.5	20.6	17.7	10.6	6.2
		R.GHNFAIVDEVDSILIDEAR.									
		T	3	78.3	79.5	47.4	47.2	93.4	78.1	55.3	46.6
		R.GLDPVETPEEYEA AWHE									
		VLPQVK.A	3	286.2	297.7	199.4	220.9	247.3	274.3	163.8	214.8
		R.KVADYVNALSDDVEK.L	2	34.1	32.6	32.7	49.8	27.5	25.0	46.4	64.4
		R.LNLPPDDVPIEAK.M	2	23.0	25.0	39.4	45.6	19.3	23.8	20.8	34.6
		R.NGEVLIVDEFTGR.V	2	73.9	76.0	179.1	152.1	73.3	57.0	113.2	82.7
		R.NVLLNVIDR.K	2	62.9	52.7	35.4	22.9	51.8	40.3	25.4	18.4
		R.TPLISGPADGASHWYQE									
		FAR.I	3	206.3	216.3	240.0	225.2	233.4	229.6	248.6	231.2
		R.VADGEDLDDLLPEAFAVA									
		R.E	2	112.1	141.1	89.9	112.1	115.3	149.6	80.7	108.9
MSMEG	MSMEG	R.TPLAALLDAAGLEVPRPA									
_1888	1890	DGR.K	3	33.6	37.8	3.5	3.0	1.1	0.3	1.3	2.0
MSMEG	MSMEG										
_1890	1892	R.SSVTFDGDEQAR.S	2	4.5	4.1	2.1	1.6	2.1	1.9	2.0	1.4

MSMEG	MSMEG	R.FGLSTVDLDTSTADGAR.										
_1903	1907	R	2	68.5	47.4	9.4	5.5	26.9	8.4	20.9	4.1	
		R.IGALTALTLLLR.R	2	5.8	5.6	0.0	0.0	1.7	0.5	0.1	0.0	
MSMEG	MSMEG											
_1913	1917	K.GLAVAVVPVPTK.L	2	23.3	26.8	17.3	18.5	13.7	15.4	14.9	14.9	
		R.STGYVVGGISPLGQR.K	2	41.3	42.9	59.9	68.8	24.7	28.1	67.9	77.5	
MSMEG	MSMEG											
_1914	1918	K.EIAEIMETPIGTVMSR.L	2	82.5	90.2	44.5	52.9	88.6	97.0	44.0	57.5	
		R.DAIPLLDQLYGGALR.M	2	54.3	59.7	42.6	52.7	20.5	64.2	21.0	43.4	
		R.MAVYYADVEGFYK.E	2	32.5	39.8	29.2	30.2	35.7	35.5	25.2	25.2	
		R.SAEVEALEALPDTEIK.A	2	181.0	206.9	226.2	229.3	178.6	169.7	227.4	211.9	
MSMEG	MSMEG											
_1926	1929	K.LAAEPLAELQLR.D	2	40.8	32.4	65.7	68.7	37.5	22.7	65.8	71.2	
MSMEG	MSMEG											
_1927	1930	K.LLGALPTLYDSR.T	2	29.6	34.0	93.3	98.5	27.7	27.3	110.3	122.4	
MSMEG	MSMEG											
_1934	1938	K.IAYVEIGAADV.R	2	168.1	190.8	254.9	261.5	138.3	153.1	250.7	246.8	
MSMEG	MSMEG	R.LIFENDYVTEPQVAAQVK.										
_1935	1939	V	2	100.5	117.8	116.3	128.4	74.2	97.9	62.9	97.4	
MSMEG	MSMEG											
_1940	1944	R.PVVLPHPNPIPTVLVR.A	3	32.7	32.2	67.1	62.2	33.9	27.3	67.2	75.4	
MSMEG	MSMEG											
_1951	1955	K.IVEADQIEEWAEAEK.A	2	6.6	9.6	76.3	87.7	17.5	21.5	75.9	83.0	
		R.LPLQLIEDQVMTR.L	2	2.5	3.1	65.6	64.0	13.9	16.3	60.9	68.4	
MSMEG	MSMEG											
_1954	1958	K.AAQQLFTVLGELK.G	2	28.3	30.6	74.1	50.0	13.9	24.0	57.2	67.6	
MSMEG	MSMEG	K.AEALQDLESALTAAQEAQ										
_1959	1961	R.S	3	43.4	45.1	13.2	14.8	86.3	50.6	14.9	19.7	
		K.NFYYPDQLSIDR.Y	2	24.4	25.4	20.4	25.9	57.9	52.5	28.8	25.1	
		R.IYFGPVISNTPADYAIVGK.										
		T	2	68.2	61.0	264.0	229.1	111.3	91.0	229.2	231.3	
		R.LLDPTIVSPAFTQFQQGK.										
		N	2	283.5	279.9	483.6	465.2	214.1	236.5	366.7	417.4	
		R.NFLFSNVIGENSK.I	2	47.4	57.7	25.0	40.9	85.4	74.7	22.6	32.0	
		R.PAQAPPPPSAATPTGPVQ										
		ISQAK.A	3	51.6	29.5	13.3	25.6	33.7	33.6	6.1	18.1	

		R.TRPV FVPTAGPNDPVAR. Y	3	18.3	15.8	87.7	89.6	41.4	40.2	67.5	61.7
MSMEG	MSMEG										
_1979	1982	R.SLDDPNEYVLVEAFR.D	2	17.6	35.0	161.0	320.5	10.4	16.2	94.6	138.8
MSMEG	MSMEG	R.EVVLEVVEHDPQTGAYTV									
_1981	1984	ASGWGPK.A	3	62.3	73.6	122.8	115.5	72.8	80.3	129.1	102.9
		R.TIAVTALPLDQAEGADIFA									
		R.Y	2	82.2	98.0	99.0	106.9	81.9	87.8	72.6	70.9
		R.TIAVTALPLDQAEGADIFA									
		R.Y	3	44.8	50.3	29.4	25.6	32.0	43.9	21.3	23.8
MSMEG	MSMEG	K.IGISTFVNDDTIDAVTLAR.									
_1996	1997	A	2	76.0	80.0	74.1	77.1	57.1	56.8	87.5	80.4
		K.PVQKPHPPPIYIGGASEATV									
		K.R	3	47.1	47.2	46.1	44.9	36.4	30.5	54.0	46.6
		K.PVQKPHPPPIYIGGASEATV									
		K.R	4	43.5	47.4	36.3	34.3	24.6	27.5	40.5	41.6
		R.GFHSLVIAEHSHIPASR.E	3	31.9	35.3	25.4	27.9	15.4	23.7	31.7	31.1
		R.GFHSLVIAEHSHIPASR.E	4	87.4	98.1	47.0	49.6	47.4	59.0	48.7	56.3
		R.HDAGWISNPLPVDFLSK.F	2	45.3	41.4	55.2	49.6	23.3	33.4	49.5	51.1
		R.LLDEQIEAIK.A	2	75.3	56.7	73.0	47.6	45.2	48.3	70.9	77.0
		R.PKPVQKPHPPPIYIGGASEA									
		TVK.R	4	54.8	60.8	54.0	56.8	23.1	27.0	39.3	46.7
		R.TLDPFVTLAAAAVTTK.I	2	82.1	83.0	79.0	94.8	22.6	40.4	31.8	53.8
MSMEG	MSMEG	R.EGNADYAVIALQNPEDV									
_2010	2010	DTYVDHPAHVELSR.Q	4	61.8	72.1	79.7	95.2	74.4	76.0	123.0	112.0
		R.SAVQFALPENAVLDL	2	46.0	34.7	63.3	52.3	63.6	54.2	83.2	72.0
MSMEG	MSMEG										
_2019	2018	R.ALFAVATFGR.V	2	10.9	9.8	19.8	25.7	3.1	6.2	14.2	17.1
MSMEG	MSMEG	R.ILSAPLEPLTEGTVTSAED									
_2025	2027	LAALIAK.A	3	19.1	20.4	28.2	28.7	16.1	20.2	19.8	23.0
MSMEG	MSMEG	K.AVESPEPPAFLLLGSDALS									
_2026	2028	AYR.R	2	264.8	271.3	158.5	152.8	178.1	180.1	160.2	173.5
		K.AVESPEPPAFLLLGSDALS									
		AYR.R	3	134.3	132.0	56.0	57.4	94.1	90.8	51.7	57.7

		R.DVSSVADIAETAPDR.V	2	343.5	331.8	195.5	191.5	252.5	256.5	204.8	208.7
		R.FGGVDLVNAGYGYR.A	2	326.2	333.5	96.5	103.6	320.3	294.5	106.2	117.6
		R.TLAEAVAAAGHNLVVTAR.									
		D	2	175.4	174.5	110.9	104.1	111.6	111.7	99.6	83.1
		R.TLFDTHIFGTVATIK.A	2	63.7	68.9	127.6	105.1	43.9	42.6	163.8	184.4
		R.TLFDTHIFGTVATIK.A	3	65.3	62.9	20.1	20.9	32.3	32.3	12.5	17.8
		R.VVAAPLDVTRPEQVTAQA									
		QLADER.F	3	896.0	921.2	468.9	456.2	636.5	634.8	499.1	490.1
MSMEG	MSMEG										
_2027	2029	K.LAVEAYPPYAEYQTK.T	2	55.2	64.7	48.6	63.7	24.8	26.1	43.6	43.9
		R.ILEQGTDDGVHVLDRPIVL									
		FTTTGAK.S	4	46.6	43.3	65.4	63.3	22.4	26.9	76.3	70.9
MSMEG	MSMEG	R.GLYQYKPDLPFSPGAEVA									
_2033	2034	GVVR.S	3	248.9	257.0	411.2	457.1	217.6	204.5	380.1	359.3
		R.LLVVGFTGGEIPQVK.V	2	148.4	145.0	193.9	232.7	103.8	96.6	96.9	115.8
		R.LSGGETVLVHGAAGGIGS									
		SVLR.L	3	79.2	70.2	46.5	36.5	62.1	53.6	15.8	16.1
MSMEG	MSMEG	R.GPVLVGSATEVADELER.									
_2045	2046	W	2	57.4	50.8	8.2	9.8	72.2	60.1	28.5	10.2
		R.VAWNIVTSYLDAAAR.N	2	92.8	67.0	133.2	93.4	59.9	53.6	411.9	488.2
MSMEG	MSMEG	K.ANDMWGPTEDPNSAWK.									
_2078	2080	R	2	68.0	81.8	129.2	142.6	158.7	182.9	135.8	142.9
		K.VQFQSGGPGSHAVYLLD									
		GLR.A	3	325.1	337.1	611.6	613.2	837.7	777.2	741.0	689.0
		K.WETFLTSELPEWLAANR.									
		D	2	112.0	112.5	153.1	160.8	195.6	213.4	151.8	149.1
		R.ELQAMVPDLQR.V	2	93.3	101.6	232.9	225.2	323.3	260.9	293.7	278.4
MSMEG	MSMEG										
_2079	2081	R.LPADQIVALGALTTPR.E	2	206.3	214.9	116.3	110.2	101.6	125.3	74.6	83.3
MSMEG	MSMEG										
_2080	2082	K.ILDIFEGTQQIQQLVVAR.R	2	49.1	40.6	150.5	150.3	31.9	32.2	106.6	136.5
MSMEG	MSMEG	K.AAELGITAVNVPEDFEGIA									
_2081	2083	EHR.S	3	161.6	151.7	309.9	304.6	159.7	165.9	428.6	382.8
		K.ASGADLFDLTPDDDDQK.M	2	53.4	50.3	78.6	105.6	27.4	41.0	86.7	103.3



		R.LGEDGATDQDYSEIALA									
		R.L	2	72.7	88.4	124.4	147.8	76.2	56.5	160.3	159.5
		R.TATDIGLALITPIVGQEWL									
		DR.Y	3	55.3	65.2	98.3	115.4	53.2	58.8	139.0	139.2
MSMEG	MSMEG										
_2089	2090	R.LLLGADTPTSGDVR.V	2	48.4	32.4	29.8	25.8	31.7	43.8	19.7	39.7
MSMEG	MSMEG										
_2090	2091	R.FGFLINEVLTGLR.R	2	12.3	7.7	4.7	2.1	11.3	10.3	2.6	2.9
MSMEG	MSMEG										
_2092	2093	R.EEPWNRPLFAAPHR.L	3	82.1	51.2	72.6	57.9	72.6	68.8	86.8	83.8
		R.LMIDGVPVGR.L	2	15.3	15.5	77.1	87.1	29.4	33.8	101.6	102.1
MSMEG	MSMEG										
_2111	2114	K.LDPAAAPSSAPDLSES.R.Q	2	30.4	23.4	31.5	24.9	25.9	30.2	26.4	30.9
MSMEG	MSMEG	R.AAHVLHLAQEHGEIGTEA									
_2112	2115	QR.E	3	8.4	8.7	16.1	10.4	3.2	5.0	18.3	15.5
		R.AAHVLHLAQEHGEIGTEA									
		QR.E	4	8.1	5.7	36.9	27.9	4.6	4.6	35.4	38.0
MSMEG	MSMEG										
_2116	2119	K.SLMLPIAVLPAAGILLR.I	2	1.9	2.3	16.8	18.4	9.6	10.7	27.5	28.3
		R.IPGFAQLQR.L	2	0.0	0.0	0.6	0.4	0.0	1.2	0.9	1.0
MSMEG	MSMEG										
_2117	2120	K.GLNPIVPVIMDER.E	2	51.3	54.9	72.0	74.1	22.2	23.8	39.8	54.1
		R.TGADIATGAELFTAACK	2	91.9	73.2	138.3	131.6	72.0	65.5	152.0	124.5
MSMEG	MSMEG										
_2118	2121	R.IGSLAADAITALITR.K	2	73.6	72.9	84.8	88.4	59.3	49.5	85.1	84.7
MSMEG	MSMEG	K.YNPPNGGPADSDATSVIA									
_2136	2139	K.R	2	14.8	10.6	31.9	17.7	13.0	23.6	22.2	34.6
		R.IGADPLGGASVDYWGAIA									
		ER.H	2	37.5	39.6	71.1	75.0	21.7	29.7	123.3	123.8
		R.YAELAEQYGAPSYAR.I	2	119.9	85.7	157.0	149.4	122.2	90.3	181.7	162.9
MSMEG	MSMEG										
_2155	2157	R.HEIVDTLDYLAR.L	3	1.6	2.7	34.2	24.8	3.7	3.9	34.8	29.5
MSMEG	MSMEG										
2968	2968	R.AAGLQSYEIPR.D	2	19.3	12.6	16.5	17.7	0.3	0.4	2.3	6.5
		R.TVLLTGATGFLGR.Y	2	100.8	87.0	0.8	0.6	1.0	1.3	0.6	0.9
		R.YLALEWLER.M	2	29.6	27.1	0.3	0.1	0.0	0.0	0.2	0.0

MSMEG	MSMEG										
_2171	2175	K.SPLGRDALTELLRR.A	3	0.2	0.3	5.0	5.0	0.1	0.2	0.9	1.5
MSMEG	MSMEG										
_2174	2178	R.PFYVATAANPENMR.R	2	118.0	102.0	4.7	10.0	101.4	106.1	3.9	10.3
		R.SFTIVGDLAQR.R	2	29.4	23.5	42.2	38.8	18.7	13.6	37.7	28.0
		R.VAYLLYTYR.K	2	68.4	61.2	12.0	8.1	18.3	19.6	26.7	17.9
MSMEG	MSMEG	K.LADWGSALGDDTYER.									
_2198	2203	V	2	16.9	18.9	130.4	127.6	19.2	30.1	90.7	137.2
		R.FDLDPGRPILHGLVGDIDA									
		AR.L	3	32.3	32.8	111.5	104.9	42.4	45.9	118.1	123.3
		R.FDLDPGRPILHGLVGDIDA									
		AR.L	4	18.3	17.4	55.9	58.5	23.7	23.4	68.4	59.5
		R.GSAVALGAAAFNAR.V	2	62.9	51.7	56.9	39.5	21.0	18.3	60.5	34.9
		R.LLTQYTSAMDVGYS.G	2	234.4	246.9	176.2	206.7	166.9	173.6	208.9	265.1
		R.LTDFDEIELPNLR.V	2	139.9	162.9	308.4	327.8	173.3	178.6	347.8	316.8
		R.VPGTVFDLGVNK.A	2	14.5	12.1	175.2	163.4	49.1	36.1	237.5	168.4
MSMEG	MSMEG	K.TGPFGGTIAHGLLTLSELLP									
_2201	2206	HFTHQLYR.V	4	61.8	61.6	80.1	73.6	82.8	88.0	94.4	87.0
		K.TGPFGGTIAHGLLTLSELLP									
		HFTHQLYR.V	5	25.9	12.7	39.5	20.1	33.1	35.3	41.5	43.2
		K.VFDNLDALAAAAGTELGP									
		TDWLEVTQDR.V	3	175.7	234.6	235.0	333.0	142.2	252.4	153.9	282.6
		R.VDNITM#AINYGYNK.V	2	81.1	96.4	100.2	113.5	72.1	73.1	79.2	69.0
		R.VDNITM*AINYGYNK.V	2	81.1	96.4	100.2	113.5	72.1	73.1	79.1	69.0
		R.VDNITMAINYGYNK.V	2	197.7	213.6	343.8	386.9	178.9	167.1	297.4	269.1
		R.VNLFADATEDHQQWIVDP									
		EK.A	3	358.1	437.3	554.6	661.5	405.7	426.6	565.9	542.7
		R.VNLFADATEDHQQWIVDP									
		EK.A	4	336.3	267.2	509.9	379.8	417.7	434.2	540.1	532.9
MSMEG	MSMEG										
_2225	2230	K.AFMGNPILC*DLILIR.S	2	14.8	15.1	38.3	38.9	17.0	16.7	38.6	37.4
		R.EFVVATPYVEAK.D	2	29.2	25.7	66.3	66.3	32.9	45.0	47.2	68.6
MSMEG	MSMEG	R.YAVPGLGNVPLETGPLAR.									
_2263	2266	R	2	76.7	86.5	62.2	69.4	249.3	239.3	106.7	99.9
MSMEG	MSMEG										
_2271	2274	R.EVNPTTEILPVSAR.T	2	27.0	35.3	109.9	152.2	61.5	66.6	64.8	58.7

MSMEG	MSMEG										
_2280	2283	R.SDELLDLITTNVAR.R	2	14.8	16.4	68.5	66.9	50.1	35.9	102.3	75.6
		R.TPIRPEYLAGLIDR.L	2	26.6	35.4	93.9	104.6	38.7	46.9	48.0	63.8
		R.TPIRPEYLAGLIDR.L	3	96.0	77.7	120.3	115.6	125.6	75.1	99.7	108.0
		R.VPVLAIAAHIPR.S	3	2.8	1.0	43.6	29.6	3.9	3.9	10.2	8.3
		R.VYGLPGDSLNGFTDAIR.R	2	5.6	7.2	89.6	80.0	9.8	8.2	37.2	37.7
MSMEG	MSMEG	K.DDGLHGSDLIQTAWTLAR									
_2351	2350	.A	2	201.5	195.3	137.8	140.5	234.0	229.4	188.6	176.2
		K.DDGLHGSDLIQTAWTLAR									
		.A	3	386.1	388.3	266.2	254.1	463.9	422.1	348.9	335.4
		K.EVTVLSLAEIGVEPDEVG									
		ANAGSK.V	2	357.2	370.0	237.5	250.8	307.4	305.9	246.0	240.9
		K.EVTVLSLAEIGVEPDEVG									
		ANAGSK.V	3	636.1	690.2	453.7	481.2	514.1	548.7	422.1	462.9
		K.IAEYLVAQK.L	2	4.5	4.1	0.9	1.2	2.7	3.4	0.1	1.2
		R.AVEEALLIK.E	2	17.4	17.5	4.6	4.6	23.5	19.7	11.3	7.2
		R.EAADAVLDEINER.A	2	1954.5	2190.4	1621.9	1867.6	2206.1	2259.3	2035.6	2163.3
		R.EAADAVLDEINER.A	3	66.3	42.6	37.9	18.4	72.2	60.5	42.9	42.9
		R.EGGDSTVTVLTAGPER.A	2	202.0	168.0	90.7	67.6	212.1	203.0	99.8	90.7
		R.ETDEGVFTLEASLPAVVS									
		VNEK.I	2	292.8	293.4	253.6	228.2	294.2	271.7	265.1	232.3
MSMEG	MSMEG										
_2352	2351	K.IVEELADSLGGAVGASR.A	2	1442.7	1403.3	1386.0	1443.2	1169.2	1120.6	1123.4	1539.1
		K.IVEELADSLGGAVGASR.A	3	481.4	487.0	244.5	243.1	448.2	397.0	172.0	162.3
		K.REPAVAGDRPELTEASV									
		VAGGR.G	3	583.9	571.1	2682.6	1906.7	536.9	513.7	873.8	845.4
		K.REPAVAGDRPELTEASV									
		VAGGR.G	4	450.7	466.1	198.3	218.3	390.5	390.3	121.2	115.9
		K.TIVAVNKGDEEAPIFEIADLG									
		IVGDLFK.V	3	973.4	1087.7	834.3	913.9	429.2	675.3	418.4	606.7
		K.VSAELLTAAR.A	2	37.3	32.5	29.9	24.8	34.0	24.9	13.2	16.2
		R.AAVDSGYYPGQFQVGQT									
		GK.T	2	1873.0	1838.9	1723.5	1736.0	1577.0	1597.9	1279.4	1320.6

		R.AAVDSGYYPGQFQVGQT GK.T	3	466.6	513.0	198.4	241.2	310.6	347.8	76.1	114.0
		R.ALGEPSAVVVGKPGTAAG LTDGLK.A	2	144.9	141.5	58.3	50.2	181.7	153.0	66.1	48.4
		R.ALGEPSAVVVGKPGTAAG LTDGLK.A	3	2692.3	2957.4	1993.6	2094.7	3088.5	3321.4	2174.6	2254.7
		R.EPAVAGDRPELTEASVVV AGGR.G	2	153.3	96.0	75.1	47.8	112.5	105.6	36.3	30.7
		R.EPAVAGDRPELTEASVVV AGGR.G	3	2033.7	2369.2	2025.9	2426.6	1677.0	1618.5	2114.2	1857.2
		R.IGSGLLVDTVIEVK.E	2	1041.6	1051.0	903.6	860.9	925.4	917.7	729.5	740.0
		R.PGSVEAVPADGAGEVVN VEVPAQAENATR.I	3	249.4	291.7	122.8	146.2	104.4	115.7	26.5	29.6
MSMEG	MSMEG	K.ATGEVEAELPEHPDADER .R	3	22.3	14.4	17.1	10.7	18.6	12.4	11.9	9.6
_2362	2361	K.IDGVALSLVYR.D	2	11.7	8.2	8.3	7.1	18.5	13.5	3.4	15.3
		K.VAGSTVGLATLHNASEVK. R	2	21.5	20.7	26.5	26.4	26.8	19.1	33.3	37.0
		K.VAGSTVGLATLHNASEVK. R	3	101.1	94.4	96.3	103.8	80.4	74.5	76.7	77.7
		R.EFEFPTH#PEC#GTELA PAK.E	3	78.4	77.3	84.5	109.5	50.6	50.5	63.7	79.0
		R.LTPSDEFPVPAVLEVR.G	2	201.5	193.0	162.3	152.5	214.7	221.9	165.2	156.6
		R.M#LSLDNVFDSDELTAWA AR.I	2	42.0	35.8	50.1	48.2	62.5	43.8	49.9	57.3
		R.TPDSPTQLVGGAGFATEF APAEHLER.M	3	122.2	117.5	101.7	107.4	114.7	103.2	126.2	108.3
		R.VADFEELNAGLVAEGKPP FANPR.N	3	167.9	163.4	167.2	161.4	280.8	208.3	195.4	177.3
MSMEG	MSMEG	K.EVSSTEVTQAHLDQIAAT DDR.F	3	387.5	409.0	260.9	327.9	253.7	265.9	225.1	274.9
_2365	2364	R.TVLDTALLHAVIAGHDAR. D	3	71.8	53.8	220.6	215.5	65.1	68.3	554.5	509.3
		R.VGDDGTHSAEEVMALTR. A	2	60.1	56.4	14.5	18.5	19.0	19.8	0.0	1.3

		R.VGDDGTHSAEEVMALTR.									
		A	3	77.7	74.6	31.1	32.3	37.7	20.0	18.4	19.4
MSMEG	MSMEG	R.IGVLTGGGDC*PGLNAVIR									
_2366	2365	.A	2	62.0	66.7	466.1	504.4	36.5	38.8	335.6	387.0
MSMEG	MSMEG										
_2367	2366	K.VQAAGAIVGAVMK.A	2	44.6	36.6	47.6	47.5	38.3	23.9	53.2	63.8
		R.AWWGNFLVQK.A	2	65.2	63.7	14.9	20.7	54.6	71.8	21.5	15.8
		R.DLVNAGAVELVAATVDHG									
		VSSEAAR.A	3	346.1	314.4	187.9	158.5	353.7	292.1	281.8	236.9
		R.IGLALNC#EITPWGR.F	2	99.1	94.7	79.9	79.3	101.3	98.8	120.2	73.9
MSMEG	MSMEG										
_2372	2371	K.AVIAELVQSLR.K	2	85.9	80.7	36.9	29.1	97.0	77.4	40.8	30.4
		K.LAEALGC#VGLR.C	2	18.7	12.9	11.0	8.7	16.7	9.1	27.4	28.1
MSMEG	MSMEG	K.VVDVSTESLTIEATGTPEK									
_2373	2372	.L	2	62.3	62.5	4.0	5.4	44.3	43.2	0.5	1.0
		R.EIAQSGVVSRSR.G	2	6.8	5.5	1.5	1.1	7.6	4.6	1.4	0.9
		R.GQIEAVNLFR.A	2	66.9	65.3	6.8	9.2	74.7	69.1	6.3	6.7
		R.M*TIVVSVEDSPLEQITK.Q	2	21.4	0.0	17.5	0.0	12.8	13.5	5.1	6.3
		R.RGFNIQSLAVGATEQK.D	3	32.9	37.4	4.2	11.7	33.6	40.1	5.7	7.1
MSMEG	MSMEG										
_2374	2373	K.AEEQGLEVDTPAEVAK.W	2	45.7	43.8	14.7	10.8	27.2	35.2	5.2	6.1
		K.APENVTVMVAPK.G	2	31.7	33.3	8.4	12.9	7.2	9.6	3.9	6.5
		K.GEGQALALSYAAAIGGAR.									
		A	2	1351.7	1205.3	1063.2	989.7	1275.3	1112.4	1164.2	1010.8
		K.GEGQALALSYAAAIGGAR.									
		A	3	148.5	140.4	76.6	86.3	149.2	131.0	96.9	82.0
		K.GVPC#LIAIDQDPK.G	2	630.0	495.8	663.3	519.6	648.7	681.0	755.5	861.1
		K.GVPC*LIAIDQDPK.G	2	629.5	491.6	662.9	518.2	637.3	679.8	752.2	860.3
		K.LIVDLIYEGGIAR.M	2	265.8	210.0	229.3	187.8	276.7	273.1	240.0	258.1
		K.VAVIGYGSQGHASLSLR.									
		D	4	371.8	238.9	106.2	60.0	413.9	333.4	186.9	142.5
		R.DLMSWVDRPITETA	2	333.5	282.4	577.5	521.6	342.6	268.3	416.2	329.5
		R.EKAAEQGLEVDTPAEVAK									
		.W	2	24.8	14.6	11.8	6.2	25.5	24.7	9.4	11.4

MSMEG _2375 MSMEG _2378  <
---

		R.LYPGVTGPLVGNPPIDFV VVR.E	3	273.3	314.9	205.6	220.1	180.0	152.3	214.2	193.5
MSMEG	MSMEG										
_2382	2381	K.EIAEHFPGNPNFTGR.S	2	36.6	25.4	38.9	26.8	63.2	54.3	32.3	42.1
		K.EIAEHFPGNPNFTGR.S	3	91.2	69.7	78.6	57.5	81.9	80.7	73.2	94.0
		K.GHDTFC#PLGPWIVTDLD PSDVELR.T	3	109.0	135.1	124.2	145.9	85.2	106.1	104.6	138.9
		K.GHDTFC*PLGPWIVTDLD PSDVELR.T	3	107.5	133.3	124.2	144.6	85.0	104.1	104.5	138.8
MSMEG	MSMEG										
_2383	2382	K.TALLEGLELKPR.K	3	24.4	6.9	3.6	3.3	43.9	28.9	16.2	14.7
		R.GPTTFAAGSVPDFAITR.S	2	410.2	411.7	564.2	573.0	467.2	420.6	768.0	710.3
		R.IGVAEFVPEFAHLPSVLGE GNK.K	3	72.6	76.2	27.2	32.0	45.1	43.7	24.1	25.1
		R.TALFNWAYAR.H	2	58.5	43.9	75.9	59.7	54.1	51.9	109.2	117.3
		R.VVVLGDAWGLLK.F	2	65.0	58.8	26.8	20.6	65.8	59.1	37.2	26.3
MSMEG	MSMEG	K.TMAVNVDGELPPGVSAC. D	2	98.0	132.2	108.9	129.7	55.9	50.8	84.0	89.2
MSMEG	MSMEG	K.AGLLAAEVAQDDVELLWK .V	2	96.1	97.0	125.2	113.1	129.3	119.9	107.5	100.2
		K.GSVLVAGPDFGTGSSR.E	2	186.9	162.5	130.9	104.4	157.0	189.3	68.8	94.6
		K.VIEQNPGLEITVNLQDR.T	2	119.1	123.2	73.8	63.2	83.6	95.2	60.2	58.3
		R.LLEGLDDIGLTR.K	2	126.2	122.3	134.1	129.2	143.6	135.6	92.5	92.4
		R.NDPSFILNLSPFDK.G	2	294.7	284.2	181.1	169.6	333.3	298.9	176.3	164.9
		R.SNVDTDQIIPAVYLK.R	2	2046.0	2312.8	2015.4	2188.6	1638.9	1740.7	2058.1	2229.9
		R.TGFEDGLFAAWR.N	2	66.9	62.2	46.4	50.0	70.6	73.8	29.1	38.8
		R.TVTAGTVVVPFR.I	2	80.8	69.5	123.1	111.8	122.6	122.6	119.2	106.2
MSMEG	MSMEG										
_2389	2388	-.MNKAELIDVLTTK.M	2	67.0	79.7	75.9	66.7	251.7	266.2	290.0	268.0
		-.MNKAELIDVLTTK.M	3	9.9	10.3	10.6	13.6	167.9	145.1	181.9	173.4
		K.AELIDVLTTK.M	2	1259.0	1237.4	1986.6	1874.3	1782.9	1571.3	2214.9	1988.6
		K.GDSVTITGFGVFQR.R	2	400.8	384.4	569.6	531.3	533.2	501.0	600.8	572.9
		K.LPADGPAVK.R	2	0.5	0.5	0.6	0.4	1.3	1.1	0.7	0.8
		K.VKPTSVPAFRPGAQFK.A	2	196.0	132.3	322.9	209.4	429.6	318.0	547.8	396.4

MSMEG _2391	MSMEG 2390	R.AVHKGDSVTITGFGVFEQ									
		R.R	3	11.1	16.2	10.7	14.7	140.1	137.3	192.2	191.4
		R.QATAAVENVVDTIVR.A	2	641.1	654.0	1167.9	1131.3	955.9	831.3	1411.4	1239.9
		R.QATAAVENVVDTIVR.A	3	61.0	60.5	82.6	76.1	89.3	83.5	90.4	84.8
		R.RQATAAVENVVDTIVR.A	2	45.3	41.2	56.0	46.7	133.0	130.9	111.5	107.3
		R.RQATAAVENVVDTIVR.A	3	33.4	30.6	38.3	36.8	104.1	84.4	86.2	82.2
		K.ANALVDEQVIDALYR.A	2	250.1	253.7	346.6	328.0	269.7	227.2	429.1	366.1
		K.DRPFVPATPPAFGER.E	2	61.4	64.2	61.0	76.4	44.7	60.9	76.3	95.1
		R.DGDVLVHHPYDSFSTTVQ									
		R.F	3	104.1	98.9	122.9	130.7	60.9	82.7	124.6	155.5
		R.FIEQAAADPNVLAIK.Q	2	230.4	225.2	432.0	423.0	164.8	189.5	381.9	389.6
		R.GIC*ALRPGVPGYSDNITV									
		R.S	3	246.0	277.0	351.3	355.7	171.6	219.4	246.9	334.9
		R.HDSHWVALPQEGQTVR.									
		D	3	51.7	36.3	74.5	58.9	21.5	22.1	44.6	46.7
		R.HDSHWVALPQEGQTVR.									
		D	4	38.6	28.3	32.2	21.3	21.4	18.2	22.6	21.8
		R.LEVSDDMTESMLELLLR.E	2	43.3	46.8	56.1	64.9	29.0	38.1	54.2	69.0
		R.NADFEVEEDRDEDLLQAL									
		ER.E	3	175.5	169.6	182.1	180.3	131.0	110.8	198.7	167.0
R.TLEQAGVHVYGLIGLK.T	2	39.0	35.2	256.7	294.2	36.8	27.2	217.3	302.3		
R.TLEQAGVHVYGLIGLK.T	3	61.1	63.6	85.1	95.9	45.3	52.7	85.5	112.1		
R.TSGDSPIVNALIDAAEAGK											
.Q	2	185.3	224.9	187.4	202.4	147.2	188.2	216.3	226.4		
R.VLALAADPSLPLLER.A	2	240.3	217.6	378.7	353.0	231.0	148.4	535.6	351.5		
MSMEG _2397	MSMEG 2396	R.ADVVPSVQQVAGITR.T	2	28.9	28.5	31.5	38.9	11.9	12.9	39.3	29.4
MSMEG _2399	MSMEG 2398	R.ALEPVADQVAQMGEFLR.									
		T	2	88.7	78.1	58.9	49.9	79.1	77.1	54.0	49.8
MSMEG _2407	MSMEG 2405	K.LATPDQGFTSSQAAAR.A	2	8.7	7.8	7.2	6.5	9.7	11.2	8.3	9.2
		K.YVDSWGGLMK.V	2	62.5	59.0	24.4	20.1	54.2	63.7	19.3	19.5



MSMEG _2408	MSMEG 2406	R.EVNAGYNIVTEAYGPLGV									
		GR.L	2	119.6	127.2	76.8	71.8	125.4	123.3	89.0	78.1
		R.LGLDYVDLYLIHWPGGDT									
		SK.Y	3	98.4	103.1	71.4	75.0	83.0	89.4	60.0	63.4
		R.LIDTAAAYGNEAAVGR.A	2	295.6	250.0	279.7	230.4	293.8	332.3	252.9	294.5
		R.LLDHPAVTAIAEAHGR.T	3	102.9	85.2	89.9	79.1	112.4	117.7	85.3	95.4
		R.LLDHPAVTAIAEAHGR.T	4	163.9	142.4	97.6	75.4	208.7	201.8	126.9	110.9
		R.SVSAALEAGYR.L	2	24.8	20.6	16.9	14.9	27.4	20.7	12.3	8.4
		K.LWNSDQGYDATLAAFDA									
		SVQR.L	3	195.6	193.3	70.9	66.1	106.8	121.6	87.1	116.9
		R.AVAAAALQAGYR.H	2	67.6	52.2	31.6	24.7	51.2	35.5	52.8	32.7
		R.ITLNDGNSIPQVGLGVWQ									
MSMEG _2410	MSMEG 2408	TPAEDTER.A	2	66.8	74.3	10.4	14.1	21.4	22.2	11.0	12.1
		R.ITLNDGNSIPQVGLGVWQ									
		TPAEDTER.A	3	476.1	543.9	192.1	224.5	201.9	268.4	173.9	216.9
		R.LGVDYLDLYLIHWVPEN									
		NK.F	3	587.0	627.9	296.5	297.2	209.1	238.8	206.1	248.1
		R.WHIQLGNIVIPK.S	2	90.1	89.7	50.4	59.0	21.6	23.7	102.8	92.1
		R.WHIQLGNIVIPK.S	3	97.6	95.8	12.0	9.5	37.3	36.0	8.5	10.0
		K.VKEIVGEVPGL	2	11.2	15.3	21.0	18.8	23.0	24.3	46.3	56.4
		K.VVLGLYEDFLC*PAC*GNF									
		ER.S	2	36.8	38.9	31.6	31.2	10.3	29.5	9.7	22.5
		R.FHTALYTPELQPQENSGI									
		YPDNR.L	3	192.0	212.3	103.4	118.5	155.5	180.6	83.3	101.6
MSMEG _2412	MSMEG 2410	R.INGEDYSPTTPDALVAK.V	2	71.4	84.5	43.3	46.2	66.9	74.3	31.9	39.0
		K.HSGADAVYPGYGFLSENP									
		DLAAK.C	3	207.7	204.8	276.0	262.6	132.6	151.8	231.1	237.3
		K.LAEQIVEAGAHVLAIK.D	2	55.6	39.9	70.9	47.8	77.4	48.1	125.5	68.4
		K.LAEQIVEAGAHVLAIK.D	3	172.5	161.0	186.7	162.6	187.2	175.0	260.5	212.6
		K.LPPLDLQAPPPAGSK.Q	2	171.7	174.0	249.3	241.8	153.8	159.3	311.3	331.8
		K.LPPLDLQAPPPAGSK.Q	3	40.1	43.3	56.3	68.0	29.0	34.8	51.9	66.9
		K.LTADDEALLAQPGPK.R	2	145.1	140.1	194.0	184.6	133.9	131.7	219.6	191.0
		K.LTADDEALLAQPGPK.R	3	17.1	19.3	21.4	25.2	11.5	15.7	16.9	23.5
		K.VVELAPAPNLSDELR.Q	2	439.2	430.0	540.6	544.3	471.4	453.1	711.0	646.5

K.VVGDLALALVGAGITAEFF									
AEDPAK.Y	3	34.4	38.1	43.3	48.1	19.7	22.5	29.0	34.0
K.VYAPFESGLPGPTGR.V	2	250.9	253.2	392.9	380.5	223.1	231.1	421.7	444.9
K.VYAPFESGLPGPTGR.V	3	10.9	14.0	13.7	17.0	7.0	9.4	8.7	10.8
K.YDIPDSVIGFLR.G	2	14.9	19.1	21.6	28.6	9.9	9.3	23.4	19.7
R.AAYEMGIATVAVYPYEDR.									
N	2	72.8	50.0	68.4	58.3	61.2	50.9	70.0	63.3
R.AVC#DLEPYWEAVR.K	2	115.2	113.1	93.6	94.1	93.3	102.4	103.1	106.2
R.AVC*DLEPYWEAVR.K	2	113.2	111.4	93.5	94.1	93.0	102.0	103.1	106.2
R.AYLSVDEIIR.V	2	57.7	50.7	78.1	70.6	47.7	46.2	76.0	74.1
R.EAESAFGDASVYLEQAVL									
NPR.H	3	50.4	46.2	45.7	49.1	38.5	41.8	53.9	53.1
R.ESLAEAIEAASR.E	2	54.6	39.7	83.6	66.2	41.5	32.4	80.9	66.7
R.ETYGDTSSLSANQFFYGL									
R.Y	2	47.9	40.7	61.0	47.8	38.8	34.8	63.9	47.9
R.ETYGDTSSLSANQFFYGL									
R.Y	3	13.7	17.4	23.3	27.4	5.0	11.6	11.2	21.1
R.FEEIEANYAAADR.V	2	61.1	62.2	46.3	41.0	20.4	25.2	17.8	23.3
R.GELGDPPGGWPEPLR.T									
R.GVSTNIPFLQAVIDDPDFR	2	112.2	114.1	146.2	145.2	88.7	96.7	152.7	164.2
.A	2	122.1	108.9	140.1	127.3	121.3	132.0	160.3	173.9
R.GVSTNIPFLQAVIDDPDFR									
.A	3	28.0	33.2	31.6	36.4	17.2	27.4	26.5	36.1
R.IAAGETLADLGLSQDR.L	2	444.2	428.7	310.2	312.5	411.3	386.9	351.5	366.1
R.IAAGETLADLGLSQDR.L	3	27.1	30.2	34.8	40.4	12.3	21.6	22.5	33.9
R.IFDALNNVESMR.P	2	21.9	19.8	19.9	16.0	8.2	7.2	4.3	5.9
R.IFDALNNVESMRPAIDAVR									
.E	3	224.5	240.4	270.2	266.9	228.5	204.9	313.4	250.2
R.ILNYLADITVKNKPHGERPS									
TVYPQDK.L	4	78.1	84.9	110.2	104.1	73.1	66.5	114.7	107.7
R.IQVEHTVTEEITDVDLVSS									
QLR.I	3	366.2	358.4	504.9	515.5	310.4	337.9	553.3	589.0
R.KVYAPFESGLPGPTGR.V									
	3	11.2	11.3	20.8	19.1	11.2	14.1	28.1	27.1
R.LKADESQIGEVGHPVR.A									
	2	2.7	1.5	3.9	3.7	7.2	2.7	9.0	2.5

		R.LKADESYQIGEVGHPVR.A	3	72.0	62.4	153.0	133.4	74.1	56.6	109.1	90.2
		R.LKADESYQIGEVGHPVR.A	4	63.7	49.5	71.5	59.5	52.4	49.4	67.4	65.1
		R.LLFPGPATAEFEAHR.E	2	20.3	16.5	34.7	31.6	25.9	17.6	51.7	35.5
		R.LVELGPEGFAGWLR.E	2	161.0	179.8	273.8	281.8	211.3	188.5	386.2	340.1
		R.TTGLLM#VAPYVAR.S	2	17.8	17.3	78.4	81.0	12.0	13.6	37.2	41.2
		R.TTGLLM*VAPYVAR.S	2	17.8	17.3	78.4	81.0	12.0	13.6	37.2	41.2
		R.TTGLLMVAPYVAR.S	2	66.8	63.6	98.4	88.8	55.8	52.4	114.6	89.4
		R.VTTSFIDDRPHLLTSR.S	3	51.6	68.2	1931.8	2100.2	48.1	47.5	532.5	560.7
		R.VYTHERIPGGQLSNLR.Q	2	45.6	36.5	89.1	85.9	55.2	49.2	90.2	87.0
		R.VYTHERIPGGQLSNLR.Q	3	217.8	208.9	263.7	256.7	197.2	195.5	291.1	274.1
MSMEG	MSMEG										
_2413	2411	K.NIAALDVAGATVR.R	2	22.0	26.8	27.7	32.7	14.1	13.2	19.5	21.6
MSMEG	MSMEG	K.EVASLGGDVSALLPSPVN									
_2414	2412	R.R	2	80.3	87.8	117.1	150.9	67.6	67.6	98.6	99.7
		K.HVAGVDTFFVATTPQYSF									
		VSSSLAK.E	3	106.5	107.2	123.6	122.4	85.8	83.3	105.5	100.8
		R.VESGQGLVVDFVK.S	2	88.6	83.9	160.0	144.2	80.3	80.9	151.6	145.2
MSMEG	MSMEG										
_2415	2413	K.LDIGSAEFITELEK.F	2	4.7	4.9	172.6	161.9	2.6	4.7	245.4	209.8
MSMEG	MSMEG	K.SSILADGVESLLGAIYLEH									
_2418	2416	GLTVVR.E	3	15.3	15.9	18.3	18.4	4.8	5.1	12.4	15.7
		R.ASIVNTQALADVGR.G	2	65.6	68.3	149.3	177.4	66.0	54.8	177.5	195.5
		R.LFGELLDAPTTLGAGLDW									
		K.S	2	34.3	37.8	47.0	42.3	14.7	19.5	23.4	33.2
MSMEG	MSMEG	K.IALAAC#TGM*ASDQPLSR									
_2421	2420	.R	2	11.9	13.2	4.8	5.3	5.2	6.6	5.7	4.8
		K.IALAAC#TGMASDQPLSR.									
		R	2	13.0	0.0	6.1	0.0	5.2	6.6	20.5	7.0
		K.IALAAC*TGM#ASDQPLSR									
		.R	2	12.0	0.0	4.5	0.0	7.8	10.7	5.4	4.5
		K.LEIDL SGLSEADV K.R	2	18.3	0.0	58.4	0.0	8.7	10.0	42.2	51.4
		K.SGTEVTFSVADTVLPK	2	106.4	108.1	77.5	76.9	93.4	98.6	75.6	86.4
MSMEG	MSMEG										
_2423	2422	R.VNPLALEEFAALEER.Y	2	15.4	15.9	19.1	19.4	14.6	16.0	19.2	18.3

MSMEG	MSMEG	K.RPIADVQLPEPAVEPEAPP										
_2424	2423	AR.D	3	109.4	124.8	80.1	92.6	117.6	127.5	51.2	104.3	
		R.IDTTGLPAVGDDATIPR.D	2	54.4	60.9	54.9	63.1	49.7	66.5	49.1	75.7	
MSMEG	MSMEG											
_2426	2425	K.LITAIVKPFTLEDVK.T	2	6.0	8.6	217.5	240.9	6.2	4.7	435.6	320.7	
		K.LITAIVKPFTLEDVK.T	3	17.6	13.5	518.6	431.2	16.2	17.1	689.0	683.8	
		K.TGLEQTGILGM#TVSEVQ										
		GYGR.Q	3	11.8	11.8	119.6	95.5	13.3	16.2	85.0	95.0	
		K.TGLEQTGILGMTVSEVQG										
		YGR.Q	2	2.7	5.2	258.9	276.0	2.2	1.8	254.6	215.2	
		K.TGLEQTGILGMTVSEVQG										
		YGR.Q	3	9.9	9.5	212.4	175.6	5.4	7.5	183.3	193.8	
		K.VRVEVVVDDSAVDK.V	2	1.3	1.2	33.1	30.0	2.0	1.7	63.3	41.9	
		K.VVDVIVQAAR.T	2	3.2	3.1	92.2	79.0	2.1	1.8	87.6	64.2	
		K.VWVSPVETVVR.V	2	70.1	80.6	1613.5	1942.6	64.8	66.4	1898.8	1824.7	
		R.GAEYSVDFVPK.V	2	30.4	21.7	39.6	31.6	24.8	30.5	48.9	54.0	
		R.VEVVVDDSAVDK.V	2	0.9	1.4	42.5	48.4	0.6	0.4	35.1	24.4	
		R.VEVVVDDSAVDKVVDVIV										
		QAAR.T	3	0.2	0.5	34.2	30.9	0.8	0.7	80.1	86.1	
MSMEG	MSMEG											
_2427	2426	K.LWYPLWDANIR.L	2	0.4	0.4	60.8	67.0	0.1	0.1	91.3	105.1	
		K.VAGEDISVGLAMLDVR.H	2	10.1	9.1	118.2	140.7	15.5	12.3	126.0	117.9	
		R.AGEILAAVPANHVPAPPR.										
		L	3	0.4	0.1	120.0	109.3	1.1	0.5	137.7	146.6	
		R.DALLDLYEFWLTTK.A	2	4.1	9.5	9.6	19.7	2.3	9.6	7.1	15.0	
		R.ELLLAQHADEIGAALR.I	2	3.6	3.5	179.7	202.5	3.7	2.1	92.3	175.9	
		R.ELLLAQHADEIGAALR.I	3	0.7	0.3	43.8	48.5	0.2	0.7	66.7	47.3	
		R.HIAGDADLSSLLVGGAR.R	2	14.2	16.3	647.1	572.9	6.8	11.1	888.1	902.3	
		R.LLWADGSNPGEIVQIR.T	2	6.7	8.3	95.5	99.9	4.1	5.6	132.4	109.4	
		R.PANDLAAAVSQLLTGGPR										
		.Q	3	0.0	0.1	28.2	30.2	0.2	0.0	28.9	24.3	
		R.VAAASATTGLPIAVSTLSR										
		.L	2	0.4	0.2	229.1	219.5	0.3	0.5	189.6	242.9	

		R.VSRPDLLLLGALC*HDIGK. G	3	0.2	0.1	26.6	24.7	0.4	0.1	32.5	33.6
MSMEG	MSMEG										
_2435	2433	K.EEPSLIQIDSER.A	2	732.0	563.2	489.8	365.3	793.1	911.5	436.2	482.4
		K.KDEAAEAPAEAAEAPAEA ADAASES	2	388.7	467.1	335.0	410.1	543.4	585.4	441.3	467.6
		K.KDEAAEAPAEAAEAPAEA ADAASES	3	477.7	630.3	386.6	477.3	542.2	688.8	412.8	528.0
		K.LDLFNAALAEAESGTAA ATTPK.K	2	576.8	727.7	404.1	464.2	728.6	738.8	486.0	443.3
		K.LDLFNAALAEAESGTAA ATTPK.K	3	1150.0	1103.6	649.7	627.8	1204.9	1356.7	631.3	646.1
		K.PSKLDLFNAALAEAESGT TAAATTPK.K	3	27.1	33.1	56.7	92.4	202.9	201.3	282.6	288.5
		R.AQYWLGVGQAQPTPEVLA LLK.I	2	610.1	647.0	550.6	573.1	706.1	704.9	592.4	584.7
		R.AQYWLGVGQAQPTPEVLA LLK.I	3	297.0	252.0	196.9	166.4	248.1	283.7	155.7	159.2
		R.YHPKEEPSLIQIDSER.A	3	12.2	12.8	31.1	44.6	58.9	65.1	65.6	78.3
MSMEG	MSMEG										
_2437	2435	R.EILVPFVGAIVTSVSR.Q	2	10.3	11.9	17.0	17.9	10.7	13.5	12.9	12.4
MSMEG	MSMEG										
_2440	2438	R.DDIPTFSPGDTVNVHVK.V	2	383.5	397.8	227.3	235.3	441.2	394.7	233.2	185.9
		R.RQGGGISETFTVR.K	3	3.1	2.6	3.4	1.4	11.9	10.8	2.4	2.8
		R.TFPVHSPNIDHIDVLTR.G	2	101.4	88.5	37.9	32.8	138.0	115.3	40.5	27.6
		R.TFPVHSPNIDHIDVLTR.G	3	659.7	839.3	337.0	418.9	810.7	781.6	333.8	316.3
MSMEG	MSMEG										
_2443	2441	K.DIVGQFSYVVETER.R	2	45.5	50.4	28.7	29.9	41.4	37.9	25.4	23.1
		K.DVNIEEVEKPELR.L	2	33.1	36.9	54.1	57.8	35.3	35.3	53.4	42.4
		R.FYLANSVELIPR.N	2	36.6	40.5	30.8	32.0	39.3	42.1	31.0	30.5
		R.NADGEVYFELR.L	2	7.7	8.8	2.6	5.1	8.0	9.6	4.6	3.7
MSMEG	MSMEG										
_2450	2446	R.SSFYAETEEQESQR.A	2	23.2	19.8	2.2	2.6	26.3	23.8	1.5	1.8
MSMEG	MSMEG										
_2468	2467	K.IAELTESGTVATGSAQK	2	11.8	12.0	7.6	9.0	8.6	10.3	3.8	5.8
MSMEG	MSMEG										
_2511	2512	K.AFIEVAGPDDELELK.A	2	269.9	289.1	116.1	116.4	153.9	170.6	101.7	101.0

		R.LVLGGNNAGSGTGFGTF									
		KPSEFSDSYVK.L	3	121.7	135.6	50.6	60.6	106.9	113.0	44.8	49.9
MSMEG	MSMEG										
_2516	2520	R.LHTGTLVLNNDLR.H	3	27.1	18.9	1.9	1.9	5.0	3.6	3.1	2.6
		R.LTHFGPAGLLDR.I	2	68.6	65.6	135.2	157.5	32.9	41.0	132.5	141.4
		R.LTHFGPAGLLDR.I	3	98.0	94.1	9.0	5.4	31.4	30.1	9.5	7.0
		R.VADIAGLAGFSHNHDATEI									
		R.L	3	129.0	161.7	49.7	55.5	76.3	75.3	61.3	53.4
MSMEG	MSMEG										
_2519	2522	K.ETVAHGGTVLFGTK.K	2	182.9	205.5	323.6	443.3	80.0	67.6	90.3	108.9
		K.VIASAVAEGQLQAR.A	2	41.4	30.8	10.7	11.3	30.0	32.2	16.3	18.2
		K.VPSAVWVVDTNK.E	2	230.5	176.9	127.6	123.9	127.0	132.9	83.9	119.7
		K.VPSAVWVVDTNKEHIAVG									
		EAR.K	4	79.9	83.4	25.7	26.0	178.3	173.3	84.0	101.8
		R.LKELEAMEQTGGFEGR.T	2	341.2	317.8	301.7	310.8	229.9	211.0	122.8	145.8
		R.LKELEAMEQTGGFEGR.T	3	279.9	272.8	208.4	213.5	201.9	206.2	110.9	120.8
MSMEG	MSMEG	K.ISGQDTAQLTESQFAALR.									
_2524	2527	H	2	1.6	0.6	116.1	133.8	0.3	0.9	147.9	141.0
		K.STLLNIIGGLDRPTK.G	3	0.0	0.0	25.8	24.0	0.0	0.0	32.8	40.3
		R.ATELLEMVGLGHR.I	3	1.5	2.5	18.5	16.6	3.8	2.6	22.8	15.1
MSMEG	MSMEG	K.VSQDDALAH LAVFDLTNQ									
_2525	2528	DEAQK	3	25.9	33.8	472.9	452.2	20.5	27.6	483.0	466.9
MSMEG	MSMEG	K.AGNYTEQFMFDADNRPA									
_2526	2529	FTEFR.Q	3	9.4	7.5	198.9	174.2	5.8	10.8	235.7	223.7
		K.DVIPVM#VQEGSVIYDR.A	2	0.2	0.3	43.0	38.8	0.2	0.1	41.8	46.7
		K.DVIPVMVQEGSVIYDR.A	2	1.8	1.3	367.1	331.1	2.0	0.5	423.2	385.4
		K.FVM#IQLAEPEKNEK.L	3	4.0	3.0	24.1	26.4	1.5	0.2	29.5	31.6
		K.FVMIQLAEPEKNEK.L	2	6.1	9.1	41.6	30.7	3.6	5.1	85.4	49.1
		K.FVMIQLAEPEKNEK.L	3	11.1	13.1	181.2	162.8	7.4	11.5	237.4	210.3
		K.IEITQPDGPSFTVDGWNV									
		TWQK.W	3	17.5	16.9	27.0	34.2	23.9	22.6	14.0	35.6
		K.LIYEAIVDLGAR.V	2	0.6	0.8	99.3	74.9	0.1	0.4	173.2	150.5
		K.LNEFGAPVGYK.I	2	0.1	0.4	66.6	53.7	0.3	0.3	48.5	53.5
		K.LTFVGMDVPR.R	2	10.6	11.1	226.1	207.7	5.8	9.4	244.5	226.8

		K.LTGVLTTGSIPEGETPR.W	2	0.5	0.5	1009.6	965.3	1.1	1.0	1125.5	1014.7
		K.M#VAPGMYGPNHQHFFN									
		FR.M	4	12.8	9.9	23.4	26.7	10.5	11.8	9.0	16.5
		K.MVAPGMYGPNHQHFFNF									
		R.M	4	0.0	0.1	15.2	18.7	0.2	0.1	23.5	28.2
		R.AALSEM#VVPYGDSSPTH									
		WNK.N	3	4.0	4.1	53.6	55.8	0.1	0.9	43.9	55.7
		R.AALSEMVVPYGDSSPTH									
		WNK.N	3	6.0	9.2	210.4	238.4	4.6	8.1	230.5	237.4
		R.EGLTLHEITYNDR.G	2	81.2	91.1	129.5	105.6	81.2	82.3	173.8	110.9
		R.FPSYLVEHM#TGVEEK.V	3	0.0	0.0	34.5	36.7	0.0	0.0	44.0	46.5
		R.FPSYLVEHMTGVEEK.V	2	118.5	102.5	236.2	237.6	125.9	71.4	284.9	301.4
		R.FPSYLVEHMTGVEEK.V	3	7.8	7.9	115.7	123.1	2.8	4.2	132.4	146.9
		R.FVQHNLWVTK.Y	3	0.0	0.2	3.8	2.6	0.0	0.1	4.7	5.7
MSMEG	MSMEG										
_2528	2531	K.GATPFDVETLEAALTR.L	2	98.6	88.0	228.1	221.8	52.3	44.2	186.9	151.2
		R.DVLSASTFGVGQLIASALD									
		R.G	2	35.5	36.4	94.7	92.2	10.2	13.5	35.2	46.0
		R.LVAITVPGTPIEQALR.E	2	145.9	126.2	405.4	354.7	96.5	86.8	313.1	330.1
MSMEG	MSMEG										
_2540	2543	R.SGAQVAVVIGGGNFFR.G	2	31.7	31.9	69.5	67.7	22.5	19.6	29.6	31.7
		R.TNPDAELITAISHR.E	2	101.7	101.6	79.9	90.3	113.6	111.6	82.2	78.2
		R.VQTAITMGQVAEPIPLR.									
		A	2	76.6	79.7	105.6	110.6	59.1	63.2	86.5	87.1
MSMEG	MSMEG										
_2541	2544	K.STHTYTAQIDELVK.H	2	6.5	9.7	47.4	37.5	9.7	7.8	30.3	46.4
		R.LVVIKPYEASQLR.A	3	39.7	43.2	108.6	95.9	57.7	50.6	138.7	126.0
		R.NSDLGVNPSNDGNIIR.V	2	19.4	17.7	14.3	12.6	19.2	24.2	12.3	16.0
MSMEG	MSMEG										
_2553	2555	R.ILVATAEVLAR.S	2	10.2	10.1	9.4	11.7	6.2	6.7	3.4	5.7
MSMEG	MSMEG										
_2580	2581	K.TVPEAQIVETLIEEAMR.L	2	118.6	114.9	72.1	70.1	55.4	67.2	44.5	60.6
		K.VGNQILESINLRPR.G	3	359.9	361.4	287.0	308.9	262.2	280.3	259.9	263.0
		R.HSQIPVIADIHFPK.Y	3	72.5	63.6	62.2	73.3	48.9	45.7	27.4	51.9

MSMEG	MSMEG	R.IAHEYMIDHGAYPSTLGYK									
_2587	2588	.G	3	36.4	37.8	5.7	6.4	13.0	23.4	4.8	5.2
MSMEG	MSMEG										
_2594	2595	K.YSDIVAQHFGTDHHQIR.I	3	18.5	15.8	3.6	3.0	16.6	12.5	2.0	1.2
		K.YSDIVAQHFGTDHHQIR.I	4	26.1	24.2	14.7	12.1	9.8	6.2	3.7	4.0
		R.VDGDPSGVFVTDHFGAP									
		GAETGVDR.A	3	300.9	306.8	28.7	40.4	277.6	324.9	20.1	19.2
MSMEG	MSMEG										
_2598	2599	K.VAVITGGASGIGLATGR.R	2	45.7	49.9	167.8	184.1	53.2	63.2	174.8	194.8
		R.AEGATVVVGIDPTTGK.A	2	40.3	37.1	190.3	186.6	60.6	74.9	147.4	181.4
MSMEG	MSMEG										
_2606	2607	R.APGIFVGDIAEVLGR.S	2	8.1	9.6	26.4	22.0	11.2	9.8	21.5	21.3
MSMEG	MSMEG										
_2613	2614	K.AVNVNEQFQVSR.Q	2	102.3	94.0	70.4	64.7	124.2	114.8	72.1	66.2
		K.FVFGAGGGALPLLQK.S	2	103.4	90.5	64.0	51.4	163.2	128.5	75.2	63.3
		K.GFGGFPVGGAFLR.T	2	46.5	44.4	17.6	21.3	75.3	70.0	26.3	27.0
		K.LFEEVWSWGK.V	2	62.5	55.9	6.6	6.0	50.7	60.8	4.9	4.2
		K.YLIGQLLLSEPAR.V	2	93.9	140.6	80.1	78.6	153.8	127.4	105.5	93.5
MSMEG	MSMEG										
_2616	2617	R.DAPQALIDAADLVTEMTK.I	2	37.7	37.0	54.0	52.0	39.1	34.9	49.8	54.7
MSMEG	MSMEG										
_2621	2622	K.DFPVILYQIQTK.Y	2	178.0	180.8	209.1	209.3	150.9	101.8	251.0	172.8
		K.DSYSFDVDDGLK.N	2	119.1	136.5	83.1	107.6	63.1	74.2	71.9	101.4
		K.FKDAELLGMPWIVVVGR.									
		G	3	43.1	46.3	22.2	28.0	42.3	47.5	35.3	34.6
		K.TREPGGEWELLAVGVPG									
		DR.E	2	120.0	118.0	257.7	248.2	193.8	211.2	101.9	165.8
		R.AGAAELVADLDR.L	2	185.0	170.0	175.7	169.9	165.6	130.7	241.7	181.9
		R.AVGPGIYSWLPLGLR.V	2	157.9	152.2	170.1	159.5	187.5	152.2	293.1	243.0
		R.DFTPDGTIEAAEVR.D	2	263.9	248.6	447.0	450.1	206.9	204.3	452.3	600.7
		R.GIEIGHIFQLGR.K	2	50.3	47.9	111.6	104.0	38.0	36.2	107.3	108.2
		R.GIEIGHIFQLGR.K	3	58.1	44.1	36.0	27.6	57.9	45.8	68.6	51.9
		R.GWADGVVELR.N	2	73.2	66.4	62.0	59.1	63.5	53.3	88.1	81.3
		R.KYTDAFSADVLGEDGKPL									
		R.L	3	136.9	135.8	137.9	153.5	119.8	109.4	151.9	183.8



MSMEG _2628	MSMEG 2627	R.KYTDAFSADVLGEDGKPL										
		R.L	4	41.2	34.1	14.5	17.3	35.9	38.1	30.5	27.2	
		R.LGAALEPAEFALLDDADF										
		AANPFLVK.G	3	106.7	172.8	107.5	187.1	50.9	119.1	74.0	176.1	
		R.LTMGSYGIGVSR.L	2	198.9	175.6	293.6	247.8	152.4	107.8	233.4	181.8	
		R.LVAVIAEQQHDQLGLR.W	3	96.5	72.7	85.1	55.1	83.0	77.2	84.1	96.5	
		R.NNDYLLGPTHEELFTLTV										
		K.G	3	116.7	129.8	105.8	115.0	123.5	86.6	159.3	121.9	
		R.SEMNAIGAQEILLPALLPR.										
		G	2	122.9	115.5	176.0	155.9	78.2	80.3	175.1	172.6	
		R.SEMNAIGAQEILLPALLPR.										
		G	3	16.5	21.5	7.1	17.7	10.2	9.5	9.4	14.1	
		R.WTEYGDTLFR.L	2	37.7	39.1	32.9	39.4	20.5	34.6	27.5	53.8	
		K.EGDVIETYELVEK.A	2	294.1	308.9	358.2	341.8	249.8	271.9	401.4	347.2	
		K.PAAPKPAAPQPPAAPATP										
		AAPAAEATPAAPAKPSAPK.										
		P	4	100.0	103.6	68.6	72.1	76.6	94.9	63.7	73.9	
		K.PAAPKPAAPQPPAAPATP										
		AAPAAEATPAAPAKPSAPK.										
		P	5	36.5	44.1	34.3	45.1	30.1	40.7	33.8	46.6	
		K.PAAPQPPAAPATPAAPAA										
		EATPAAPAKPSAPK.P	3	60.6	63.5	37.2	39.8	27.3	30.7	19.8	20.6	
		K.PAAPQPPAAPATPAAPAA										
		EATPAAPAKPSAPK.P	4	51.9	66.7	41.7	49.3	19.6	24.4	21.9	23.2	
		K.RAEYENMQAPVVGGVR.L	2	18.4	16.1	6.4	5.2	12.3	8.4	9.6	5.1	
		K.RAEYENMQAPVVGGVR.L	3	47.2	49.4	28.4	27.7	26.7	29.4	24.9	27.7	
K.VGNIAGC#LVTSGIMR.R	2	243.6	228.9	186.4	190.9	263.5	241.5	182.1	213.5			
K.VGNIAGC*LVTSGIMR.R	2	242.9	228.5	186.4	190.9	263.2	241.0	182.1	213.5			
R.AASAAPSAPAAPAPGATP												
GPR.P	2	1.1	1.3	0.6	0.5	0.4	0.5	0.2	0.2			
R.AASAAPSAPAAPAPGATP												
GPRPTPGATPGPR.P	4	87.0	101.6	60.5	65.1	66.1	81.3	58.4	59.7			

		R.AEYENMQAPVVGVR.L	2	61.9	55.4	30.9	30.1	39.7	33.2	25.1	21.5
		R.DGYEC#GLTLTYNDIK.E	2	22.7	21.8	38.3	40.7	15.0	19.3	33.4	37.2
		R.DGYEC*GLTLTYNDIK.E	2	22.7	21.8	38.2	40.7	15.0	19.3	33.4	37.2
		R.DNVVVAQNLTVSSLR.R	2	260.9	244.4	176.1	165.7	288.4	234.6	207.0	182.8
		R.GQGGNGASAPAAPKPGA									
		PAPSPATAAK.P	3	9.0	9.4	6.1	6.7	7.2	7.4	6.6	6.5
		R.ISLEDLDSALK.E	2	160.4	143.2	93.6	91.7	149.5	126.6	108.1	88.9
		R.ISLEDLDSALKETSQNLNLL									
		K.G	3	2.1	2.3	2.5	2.3	12.7	9.2	12.6	8.0
		R.VGNNPFSTQQPADRPIPR									
		.P	2	8.2	6.4	2.5	3.7	10.8	5.7	5.7	2.4
		R.VGNNPFSTQQPADRPIPR									
		.P	3	518.7	417.8	482.3	364.2	433.9	306.5	397.8	338.0
MSMEG	MSMEG										
_2641	2640	K.ELGDTTELPDISPK.W	2	387.6	370.7	292.4	282.7	287.2	290.7	315.4	308.8
		R.AGLVTEVVAHDDLTAAR.									
		R	2	56.5	60.5	59.8	59.8	36.4	36.1	71.2	87.3
		R.IDALQTGGALWAEAEAAR									
		.Q	3	84.5	95.6	12.2	12.5	36.2	40.3	20.0	12.3
		R.MSLTGDYLSAQDALR.A	2	157.7	185.0	105.8	116.8	106.4	117.4	117.3	117.9
MSMEG	MSMEG										
_2653	2652	R.YQAAVSVGTNPTFSGR.T	2	13.6	13.2	15.5	15.6	12.5	17.5	10.9	10.8
MSMEG	MSMEG	K.EILGQYGLHDTDTGSPEA									
_2654	2653	QVALLTK.R	2	74.6	66.3	19.8	17.7	77.9	73.3	21.2	17.4
		K.EILGQYGLHDTDTGSPEA									
		QVALLTK.R	3	2002.9	2069.0	968.7	1006.9	2205.0	2215.0	1131.9	1114.5
		K.KEILGQYGLHDTDTGSPE									
		AQVALLTK.R	3	82.5	76.4	20.1	19.1	81.1	84.7	18.2	24.4
		K.KEILGQYGLHDTDTGSPE									
		AQVALLTK.R	4	109.2	0.0	46.2	0.0	109.9	130.6	54.2	61.4
		K.RIQDLTEHLK.V	3	5.2	3.5	0.7	0.3	6.2	5.4	0.9	1.4
		K.YVAQVDVAR.Y	2	8.1	6.2	2.7	1.9	9.2	6.7	3.2	1.8
		R.GLLLLVGR.R	2	228.8	170.6	90.4	67.1	212.9	205.9	88.1	82.3
		R.RGLLLLLVGR.R	2	45.4	32.0	6.8	4.4	61.2	58.1	16.1	13.5
MSMEG	MSMEG										
_2656	2655	K.ALC#AAQQELADR.A	2	5.1	4.5	4.0	4.4	3.9	4.8	3.7	4.4

K.APVAGIAMGLVSDDVDVD									
GK.V	2	382.0	351.3	269.1	258.9	300.2	239.7	253.3	212.2
K.APVAGIAMGLVSDDVDVD									
GK.V	3	155.8	168.4	81.7	85.5	128.3	110.0	91.8	56.4
K.DFVTALQLDTK.L	2	307.8	275.5	212.6	208.3	360.7	256.4	338.9	288.1
K.DHFDFPLTVDVEER.M	2	158.4	183.1	94.3	114.1	168.4	187.3	149.6	164.0
K.DHFDFPLTVDVEER.M	3	168.1	160.8	93.6	98.1	198.8	166.7	167.0	133.4
K.INAIANPQLPK.V	2	32.9	30.6	11.9	15.9	29.8	23.7	15.1	12.4
K.ISLVLVAEESAESAESAGD									
K.G	2	165.1	137.8	110.8	92.1	134.8	102.8	106.4	81.1
K.ISLVLVAEESAESAESAGD									
KGAEK.A	3	272.0	256.7	275.2	323.1	455.0	384.9	439.8	455.6
K.LDGIPSQVLGALSQAK.D	2	893.1	894.8	678.7	701.0	940.7	883.7	963.7	992.6
K.LDGIPSQVLGALSQAK.D	3	126.2	149.1	72.3	83.5	133.4	126.0	98.3	93.4
K.LRVEIADIDNR.G	3	57.8	35.9	19.0	9.5	61.0	44.4	40.8	20.8
K.TTDFGAFVSLLPGR.D	2	563.8	560.9	521.8	514.8	612.4	521.9	771.4	674.9
K.TTDFGAFVSLLPGR.D	3	20.4	21.6	2.5	4.8	28.6	24.1	10.5	11.2
R.ALSAEVAVIPR.A	2	418.3	306.1	334.5	235.8	490.2	246.9	477.8	242.1
R.ALVPVLPSIEEFPYAIR.Q	2	1542.5	1454.9	1094.6	944.3	1341.6	1537.4	1286.6	1354.2
R.ALVPVLPSIEEFPYAIR.Q	3	117.7	151.4	75.9	104.6	99.4	124.3	100.2	111.5
R.AVFDMVVAGR.I	2	279.3	197.8	159.6	113.9	302.3	169.3	238.4	128.1
R.GETQILGVTTLDM*IK.M	2	132.4	134.8	85.7	91.6	106.3	99.3	107.2	94.5
R.GETQILGVTTLDMIK.M	2	550.3	531.4	478.2	440.5	612.4	453.1	639.3	490.4
R.IALIDGTWVAFPTVEQLER									
.A	2	527.7	527.9	406.6	386.9	470.2	591.9	481.3	577.9
R.LAQQAAAGSAVAYLDDETM									
*LLSATTASK.N	3	136.4	146.1	74.7	78.3	116.6	104.9	62.8	70.7
R.LIDRPLRPSFVDGLR.N	4	14.4	13.9	7.0	8.6	7.8	9.5	4.2	6.7
R.LTILDVMAEAIDRPDEM#S									
PYAPR.I	3	101.5	109.4	63.6	64.0	70.3	73.2	57.9	66.0
R.LTILDVMAEAIDRPDEM*S									
PYAPR.I	3	101.5	109.0	63.6	64.0	70.2	73.1	57.9	66.0

MSMEG _2658	MSMEG 2657	R.LTILDVMAEAIDRPDEMSP YAPR.I	3	354.1	467.6	249.2	315.7	215.9	356.6	208.7	328.3
		R.LTILDVMAEAIDRPDEMSP YAPR.I	4	11.9	23.1	1.9	7.4	7.1	10.7	2.6	5.1
		R.PLRPSFVDGLR.N	3	60.3	33.5	17.6	4.2	39.6	9.1	11.0	0.7
		R.TDEIKVEVLER.L	2	123.1	94.8	228.0	195.3	123.4	90.2	261.5	176.3
		R.TDEIKVEVLER.L	3	26.7	21.0	4.8	2.9	30.7	30.2	10.1	11.3
		R.YMHYFNFPYSTGETGR. V	3	165.5	163.4	102.2	105.9	86.8	119.9	72.4	105.2
		R.YVALTDILGAEDAFGDMD FK.V	2	235.7	242.6	161.2	163.6	173.7	201.9	144.7	181.9
		K.TGSGDYGSTNDVGIAYGP QGQR.I	3	26.8	25.9	10.3	9.6	12.6	21.3	5.3	12.1
		R.NNASIGIYAVDLDSNR.T	2	39.8	46.6	4.4	10.8	16.7	27.6	6.0	9.5
		R.WETELNSAVPGDPR.D	2	40.2	47.7	8.2	10.9	28.2	34.6	11.3	12.8
MSMEG _2664	MSMEG 2662	R.KGLPPNPDATSTGLDGAR .G	3	5.4	4.0	2.8	2.2	5.3	5.8	3.4	4.5
MSMEG _2667	MSMEG 2666	R.KISGLQGLTVGIEPLDLS K.AAHLPSAIDGPTVGSSPLK .L	2	82.5	83.5	84.7	84.9	75.9	74.1	99.8	93.6
		K.GTSVGGIMLAMVESVDHV TETANR.L	3	114.1	90.4	146.0	147.8	63.9	58.2	198.0	228.7
		R.DTGFGENPATLAYAR.S	2	34.6	39.8	31.7	37.8	15.4	21.6	17.4	22.9
		R.LPDVPIVALVETAR.G	2	112.5	115.3	304.6	334.9	70.0	59.7	158.5	164.0
MSMEG _2669	MSMEG 2667	K.LAGFGYVVLVPDVYYR.I R.IAVEDDPDSPHLLADK.I R.IAVEDDPDSPHLLADK.I R.IPNWGPINLNTVFSQDE R.K R.VAAALSFGHGR.I	2	328.9	364.1	129.8	137.2	49.0	59.1	76.7	104.9
		2	243.6	182.8	93.4	73.9	67.5	71.2	90.6	89.7	
		3	588.3	526.7	217.8	204.5	133.5	153.1	206.0	238.3	
		2	403.1	432.0	135.0	123.5	110.0	128.6	141.0	146.3	
		2	13.0	9.7	7.8	6.4	2.8	1.7	7.4	8.1	
MSMEG _2671	MSMEG 2669	R.LIWAQSTSGIIGR.D	2	37.5	38.5	62.0	58.4	21.7	26.4	51.6	64.4
MSMEG _2684	MSMEG 2682	R.DMLTAFNSGDVATAR.K R.KINVNLAPLAAAQAR.L	2	85.6	88.9	67.3	66.4	117.2	112.4	71.0	77.0
		2	20.1	19.0	846.4	966.7	32.4	28.4	923.1	965.0	

		R.LPQIPATTEEVEALAADM									
		R.A	2	102.5	109.5	221.7	200.2	93.4	92.1	444.0	398.3
MSMEG	MSMEG	K.THGGAPAIGALFGAIGSLL									
_2688	2686	DGAPDIK.T	3	58.5	57.4	26.0	25.7	23.2	29.7	22.7	29.1
MSMEG	MSMEG										
_2698	2697	R.DYFDYLDIFK.A	2	64.5	66.8	65.2	64.6	56.8	60.2	57.1	52.4
		R.GLLGM*VVPSLR.A	2	36.0	34.6	31.4	28.2	26.9	28.2	20.6	19.5
		R.GLLGMVVPSLR.A	2	36.0	34.6	31.4	28.2	26.9	28.2	20.6	19.5
		R.TDVLTFGPLR.V	2	101.9	92.5	87.2	85.3	92.5	91.0	82.6	75.2
MSMEG	MSMEG	R.AEIEGEMGDSHVGLQAR.									
_2723	2725	L	2	16.0	8.4	2.7	0.5	2.5	2.6	0.2	0.4
MSMEG	MSMEG	K.EKVDFAGPYLITGQSLLVR									
_2727	2729	.A	2	31.8	37.2	68.4	77.9	51.2	53.2	93.9	105.5
		K.EKVDFAGPYLITGQSLLVR									
		.A	3	78.2	76.0	143.0	144.9	139.1	135.8	192.2	177.7
		K.NGAVDALTTDEVILAGYAA									
		QSPGTFK.L	3	226.6	284.7	2689.8	3302.0	571.9	658.1	2356.4	2754.9
		K.NLGPAQIQAPQPPAVDRD									
		.-	2	1.1	3.9	127.7	129.4	3.6	4.3	150.8	115.3
		K.NLGPAQIQAPQPPAVDRD	2	158.0	150.1	685.0	721.0	247.0	237.9	381.3	411.8
		K.QPDGTLTGFDVDVAK.Y	2	42.1	43.7	96.5	92.5	55.7	54.3	104.0	96.9
		K.VDFAGPYLITGQSLLVR.A	2	237.0	250.2	468.7	451.7	312.2	309.5	500.4	478.9
		K.VDFAGPYLITGQSLLVR.A	3	11.6	14.3	29.1	26.9	21.3	20.9	20.8	27.3
		K.YVANELGYSEDQIEWK.E	2	131.5	135.4	256.6	268.5	199.8	216.3	309.5	319.3
		R.IKDEYPGVQLQQYDTYSA									
		C#VEALK.N	3	145.6	141.5	270.8	251.8	263.5	229.3	384.4	337.3
		R.IKDEYPGVQLQQYDTYSA									
		C*VEALK.N	3	144.7	141.3	269.9	251.1	261.4	228.5	379.8	335.3
MSMEG	MSMEG	K.EALAAEAEDIAANSTQWK.									
_2731	2734	A	2	92.2	90.4	79.0	49.8	87.4	75.6	83.4	63.9
		K.SAAAALAESLPTASVLGD									
		VDALSAR.L	3	87.2	97.0	107.0	110.0	110.1	90.2	145.5	119.0

		R.AEALADSTDWGATSAAF									
		R.D	2	165.0	167.5	70.9	93.9	155.2	147.1	84.3	104.5
		R.LSSILEQADEAAQNER.A	2	172.9	160.5	178.8	193.1	201.5	175.6	188.4	191.3
		R.VDPDGTVWLITGSGER.V	2	528.0	674.5	371.1	534.7	479.1	547.0	214.6	337.1
MSMEG	MSMEG										
_2739	2742	K.DLQIPDDPASAIAAAR.R	2	22.5	22.8	89.7	81.6	37.6	35.2	87.5	80.5
		R.YRDEDAAGVSDADPYAP									
		GADTR.A	3	20.0	20.6	19.5	20.1	18.7	26.4	11.9	17.3
MSMEG	MSMEG										
_2740	2743	R.ELVGEGSLFLLK.V	2	14.6	12.3	52.8	27.4	17.3	16.2	19.6	21.6
MSMEG	MSMEG										
_2743	2745	R.FTTVETAVLAVVK.R	2	25.9	24.5	35.6	32.1	21.2	24.1	35.2	27.7
MSMEG	MSMEG	K.FGNPLGVVDNSTVDPADR									
_2744	2746	.Q	2	120.7	124.1	112.2	120.9	77.1	75.0	141.0	133.0
		R.IFTPASELPFAGHPTVGAA									
		WYLR.D	3	164.3	170.1	167.4	166.3	144.1	127.5	200.4	220.1
		R.WSPEGWVQVAGR.V	2	30.3	39.0	31.0	33.2	8.9	16.6	23.2	36.4
MSMEG	MSMEG										
_2750	2753	R.LTELPVGMPVAVVVR.Q	2	79.6	85.3	171.7	184.0	110.7	93.5	248.6	239.9
MSMEG	MSMEG										
_2758	2759	K.ASGDFVWDEEESEALR.Q	2	90.1	91.3	35.2	31.3	79.0	63.7	29.6	26.3
		K.RIEAGLYATQK.L	2	0.5	0.4	0.3	0.1	0.3	0.8	1.1	1.1
		K.RIEAGLYATQK.L	3	1.1	0.6	0.1	0.0	0.5	0.9	0.1	0.2
		K.VALLNAEEEEVELAK.R	2	240.2	221.3	158.9	124.0	219.9	166.6	151.3	122.7
		R.ELLQDLGREPTPEELAK.E	3	107.6	97.1	136.2	114.8	111.8	126.0	116.8	123.0
		R.GMAFLDLIQEGNLGLIR.A	2	101.7	98.3	75.7	72.6	100.6	98.9	77.7	75.8
		R.IEAGLYATQK.L	2	2.1	1.5	2.8	2.8	1.0	1.7	0.6	2.4
		R.IPVHMOVEVINK.L	3	35.6	20.6	9.4	4.4	40.1	10.0	11.7	1.5
		R.TLDEIGQVYGVTR.E	2	232.0	250.5	166.9	181.8	182.5	190.6	138.1	119.7
MSMEG	MSMEG										
_2760	2760	K.LGVTYPGVVTGGIVR.T	2	66.2	81.1	293.5	324.7	108.2	110.4	315.0	347.2
		R.FKLDTPQPATPEAVAK.T	2	10.3	8.7	72.2	68.8	16.4	17.2	74.3	79.2
		R.FKLDTPQPATPEAVAK.T	3	53.9	58.3	108.8	106.9	56.0	66.4	116.9	124.5

MSMEG	MSMEG										
_2762	2761	K.STPTDPVTTVDTETER.W	2	139.3	138.5	110.1	122.9	118.7	127.2	130.0	142.4
		K.VIAAAPGVATALR.D	2	14.6	9.4	4.0	0.8	12.1	12.2	3.8	7.0
		R.AEVFGAAGASNDDAAGG									
		QAVR.T	2	4.8	4.5	3.3	2.5	2.2	2.7	13.3	41.4
		R.AVAEQLADEAAELVLR.R	2	125.2	131.0	125.2	124.1	105.0	94.1	124.8	114.5
		R.AVAEQLADEAAELVLR.R	3	24.2	24.5	13.7	17.7	19.8	20.9	16.1	20.0
		R.LAVLRPGEHVLGEEEGGK									
		QEGR.A	3	43.2	37.8	56.5	46.5	49.5	47.6	96.4	91.3
		R.LAVLRPGEHVLGEEEGGK									
		QEGR.A	4	129.3	136.3	127.6	131.2	126.0	138.9	127.8	148.7
		R.RAEVFGAAGASNDDAAG									
		GQAVR.T	3	6.0	7.3	3.1	3.4	7.6	7.3	4.3	4.6
MSMEG	MSMEG										
_2763	2763	R.RTETDDVSEDSLEELK.A	3	21.2	22.3	18.4	19.2	35.8	38.2	18.4	17.4
MSMEG	MSMEG										
_2765	2764	K.VSLINLDPQTPVVISR.G	2	158.7	157.1	144.4	176.1	151.5	159.0	170.4	193.2
		R.VGLSIVNSPGTIDAGYR.G	2	167.6	179.1	79.1	93.1	116.9	125.4	46.5	54.6
MSMEG	MSMEG	R.AAAAAQAAAQQNPAAQQ									
_2766	2765	PQQQEGEQPQPPEPVAR.R	3	26.4	38.0	46.5	58.4	15.5	25.1	29.1	45.8
		R.AAAAAQAAAQQNPAAQQ									
		PQQQEGEQPQPPEPVAR.R	4	138.2	203.7	158.4	252.8	94.7	134.3	111.4	167.0
		R.AAAAAQAAAQQNPAAQQ									
		PQQQEGEQPQPPEPVAR.R	5	20.9	23.3	26.2	29.7	14.6	16.5	19.7	23.8
MSMEG	MSMEG										
_2769	2769	R.MLASLVEEAVAVGDLVR.L	2	21.1	25.2	23.3	27.2	13.6	17.9	15.0	23.1
MSMEG	MSMEG										
_2771	2770	R.LGIPTVATVPWTTDR.L	2	93.6	96.7	273.2	285.4	95.0	110.8	189.3	237.6
MSMEG	MSMEG										
_2776	2775	R.SYAPTIGGLAEHLAALR.L	3	12.4	14.1	1.2	1.0	13.0	9.1	2.8	2.6

MSMEG	MSMEG	K.AAGIGLDIVPDVGPVIDNPI									
_2780	2780	R.T	2	50.0	54.4	51.1	44.7	16.2	24.8	85.2	88.5
MSMEG	MSMEG										
_2782	2782	R.ADVIDEAATFLK.Q	2	168.2	158.0	91.6	86.4	79.1	73.3	72.6	64.5
		R.ISDPVWSSVALHR.P	3	76.7	73.4	20.2	23.5	35.1	34.7	5.6	8.8
		R.ISDPVWSSVALHRPAEFN									
		K.S	4	75.8	81.2	27.3	23.0	57.1	56.8	35.6	35.0
		R.ISVENLIAK.L	2	47.9	35.0	11.2	10.7	19.5	22.5	16.6	19.5
MSMEG	MSMEG										
_2784	2785	K.LSLTDDEWR.E	2	17.7	11.5	45.6	37.0	14.7	18.5	55.2	47.4
		R.YC#INSISLR.L	2	10.4	7.3	3.9	1.4	19.0	20.1	4.5	8.0
MSMEG	MSMEG										
_2787	2788	R.IENYSGVQLSVPQR.Q	2	54.6	61.5	62.9	58.4	49.4	55.4	72.3	73.7
MSMEG	MSMEG	R.GVSIAATSNTLPEQLGEG									
_2788	2789	R.F	2	44.0	54.5	149.5	157.3	40.4	50.8	136.7	127.6
MSMEG	MSMEG										
_2789	2790	R.LGAGIENDYVMVRPV	2	16.4	0.0	12.0	0.0	7.6	8.6	9.0	14.1
MSMEG	MSMEG	K.LTGSAPEHVIDVVDLGAG									
_2800	2802	LLGWGDPK.V	3	90.8	98.0	101.0	112.8	82.3	103.0	108.8	116.5
MSMEG	MSMEG										
_2839	2841	K.LMISASVDAR.I	2	10.8	10.5	253.5	241.6	10.0	11.7	155.5	214.2
		K.SIGVGQYQHDTVPGSLAR									
		.S	2	32.7	26.9	38.0	38.6	29.5	37.2	28.9	55.1
		K.SIGVGQYQHDTVPGSLAR									
		.S	3	158.6	144.1	31.6	35.8	151.8	165.2	30.4	41.7
		R.AGVTLAELIGDTR.T	2	84.3	78.5	9.6	11.5	118.7	89.8	11.8	12.6
		R.ELPDLDVTVR.G	2	63.1	51.6	19.8	34.9	79.0	68.8	28.0	24.9
		R.IRDGEDPLDASGVHPESY									
		PVVR.R	3	64.6	61.9	10.1	15.7	63.2	85.2	10.9	13.6
		R.LLADPNLVPEEVAGEFLN									
		ENVADAAAALGAR.H	3	40.2	70.3	4.5	11.2	21.6	74.6	1.3	13.2
		R.PAFSTATFAAGVEK.V	2	146.4	137.6	53.7	80.6	222.1	210.0	61.5	69.0
		R.RLQDPLAELVK.I	2	16.6	12.1	142.5	145.2	34.0	24.4	74.0	90.7
		R.SLDAVVEDAVNAVGVDLN									
		TASVPLLAR.V	3	43.5	65.7	6.5	12.8	32.9	68.9	4.5	16.9
		R.TTLGLDPGFR.T	2	11.5	10.7	1.9	3.4	8.6	10.5	2.3	3.2
		R.VSGVTESLAEIIVHR.E	3	89.7	76.8	8.4	7.5	122.5	92.0	13.1	7.1



MSMEG	MSMEG										
_2897	2903	K.ATAVSVLEAAGHTVR.E	2	5.5	8.5	8.9	10.6	2.8	2.9	9.1	9.0
		K.ATAVSVLEAAGHTVR.E	3	13.6	12.1	6.1	7.0	10.7	8.6	13.0	10.3
MSMEG	MSMEG										
_2900	2908	R.AAVVFADALGLDR.V	2	17.6	14.0	11.4	13.0	16.0	14.0	3.4	3.8
MSMEG	MSMEG										
_2931	2941	K.DYGLDDYYLELSTK.D	2	74.1	77.0	208.3	219.5	60.2	52.1	215.6	193.4
		K.HLEAGYEFVNTPHITK.E	3	131.0	122.7	100.4	97.4	101.2	129.9	88.1	135.5
		K.VPFMLLAGDKDAEAGAVS									
		FR.F	3	53.7	60.2	35.5	27.2	52.1	38.9	69.5	37.0
		K.YVGSDEIWEEATETLR.E	2	170.3	165.6	154.2	141.4	135.4	126.6	174.0	161.8
		R.EVAEASGLDLVPDPGGAA									
		FYGP.K.I	2	118.9	123.4	87.1	93.4	88.5	87.2	106.5	104.5
		R.IYGTAWESQEALDR.H	2	211.2	202.1	186.9	195.7	151.4	168.4	163.2	193.2
		R.LFEFGSVYR.Y	2	109.1	97.3	90.0	93.4	103.4	74.1	130.8	108.1
		R.LLEFVLSLLK.D	2	19.0	23.3	11.9	15.8	22.3	18.5	20.6	18.6
MSMEG	MSMEG	R.NGGNMADPGSVAYLFSR.									
_2940	2951	K	2	143.0	150.5	21.5	24.3	114.1	104.6	14.6	14.0
		R.VGGGDPGGNPTLYDAIQK									
		.A	2	238.9	223.8	119.5	102.2	205.6	227.0	60.7	79.6
MSMEG	MSMEG	R.TTIVRPGGLTNDAGTGLV									
_2941	2952	R.I	3	48.2	57.2	55.2	66.8	43.4	48.3	64.8	74.5
		R.VLVAVLDAPQTAGR.T	2	84.6	93.5	105.0	124.6	74.5	75.2	127.2	122.6
MSMEG	MSMEG										
_2942	2953	R.HFYGGVLGLPQGR.S	2	27.4	0.0	152.3	0.0	16.6	14.8	156.3	137.4
MSMEG	MSMEG										
_2956	2165	K.IGPDKDIPHVTADVIVK.Y	3	25.8	25.0	464.4	403.8	0.4	0.2	423.6	342.7
		K.IGPDKDIPHVTADVIVK.Y	4	27.5	27.6	9.2	8.1	0.2	0.2	9.2	7.4
		K.LEAVFGDSPLVR.Q	2	127.3	112.2	23.9	20.4	15.1	16.2	33.5	33.0
		K.RPEITAEMFDEDGYR.T	3	31.0	30.5	2.8	2.4	15.3	11.6	2.8	2.6
		K.VIASSVDFLADAVALVESG									
		PAPSR.L	3	21.1	23.6	0.7	0.9	2.5	2.7	2.4	1.7
		R.ALAADHLEVIAGDKGEAD									
		LGLDHDWTWQR.L	4	32.3	22.7	2.9	2.1	2.6	2.2	1.0	1.6
		R.FVSALTGSAPISAEMK.S	2	133.2	140.2	220.6	230.5	4.3	4.4	152.2	152.6

MSMEG _2960	MSMEG 2972	R.IDHLFETDPQFAAARPDE											
		AISAAAADPELR.L	4	45.9	47.6	10.9	11.2	1.3	1.7	4.3	5.9		
		R.IQAVTNAWHNHPVNAGD											
		R.V	3	39.1	23.2	3.4	3.9	0.0	0.1	2.5	3.6		
		R.IWDMLFQEYQSR.L	2	35.1	35.8	1.6	1.2	3.6	3.9	1.3	1.3		
		R.LDATFDTGDATLLEHYR.A	3	139.9	125.5	0.4	0.3	29.5	43.2	0.4	0.4		
		R.LEQLYTDLAEGQANELR.E	2	73.1	70.8	0.1	0.2	1.1	1.5	0.6	0.0		
		R.LEQLYTDLAEGQANELR.E	3	20.7	22.2	1.7	2.3	0.1	0.0	1.4	2.6		
		R.LVVFDYSHEVDDQR.E	2	19.5	17.5	0.2	0.3	0.2	0.1	0.4	0.8		
		R.RIDHLFETDPQFAAARPD											
		EASAAAADPELR.L	4	43.7	39.2	1.3	2.0	2.5	5.9	1.7	2.6		
		R.SDLSTFLEDLALVR.P	2	2.8	2.8	0.6	0.4	0.2	0.5	0.1	0.3		
		R.SDLSTFLEDLALVRPTQLN											
		FVPR.I	3	11.5	12.4	1.9	3.2	0.4	0.6	2.5	1.9		
		R.SYLLAVVVPTEEALSR.W	2	97.8	94.4	4.6	1.9	1.0	1.3	0.6	1.7		
		R.VDDYATWLSR.F	2	37.5	35.0	0.5	0.9	0.3	0.6	0.6	1.2		
		R.DRIDSGLAQDDDELSEHT											
		NDTDGYKND	4	37.6	54.7	29.7	41.9	37.3	52.7	26.3	40.5		
		R.IDSGLAQDDDELSEHTND											
		TDGYK.N	3	40.0	51.0	33.3	42.4	16.8	19.9	11.0	18.7		
		R.IDSGLAQDDDELSEHTND											
		TDGYKND	3	93.3	119.6	92.4	121.6	70.9	95.7	68.9	93.6		
		MSMEG _2961	MSMEG 2973	R.DALNQAQQIISAR.V	2	96.4	122.5	63.0	83.1	105.4	123.2	65.6	75.4
		MSMEG _2964	MSMEG 2976	R.GFLLGAAVATR.L	2	11.3	12.7	6.1	11.0	4.9	4.9	4.1	6.9
				R.NVVIIDDLATGGTLAAAA									
				R.L	3	17.8	14.7	5.8	4.9	8.7	9.1	4.9	3.2
		R.VVTDALADIASGADLVAGL											
		DAR.G	3	26.0	16.9	9.6	4.7	12.7	13.3	4.5	4.9		
MSMEG 2974	MSMEG 2987	K.IAAGGVEGGGPDGKPALD											
		VELK.S	3	144.6	195.2	140.2	218.1	110.1	112.6	94.5	102.9		

MSMEG	MSMEG	K.GVPDYLPDSDAQFVAVR.									
_2975	2988	D	2	117.7	114.4	85.6	86.3	81.6	80.2	119.6	101.6
		R.AGYGDIELPIFEDTALFAR.									
		G	2	183.9	191.3	191.7	181.1	138.9	139.8	211.0	246.7
		R.ELLQEFLFK.L	2	53.2	48.9	35.2	30.0	46.8	35.6	49.0	33.5
MSMEG	MSMEG	K.ALIAEQLDLFPALK.E	2	0.1	0.0	26.6	30.3	0.0	0.0	8.9	19.5
_2978	2990										
MSMEG	MSMEG	K.AIQDNADGVSFDAPEGK.V	2	25.1	15.9	218.2	167.5	16.8	22.6	243.7	279.7
_2982	2994	K.ASETDAANAESC*VDTSG									
		PTIK.V	2	0.0	0.0	68.6	62.0	1.7	3.6	76.7	90.3
		K.GEDYTPLGSTDFSTIVNK.									
		V	2	3.1	7.6	716.7	795.2	16.2	2.6	815.6	844.5
		K.LAVEEINADGGVLGK.Q	2	94.6	129.6	1049.7	970.0	26.9	30.6	1136.1	1072.7
		K.QIELIGEDGASEPTVFAEK.									
		A	2	250.6	300.9	77.3	90.7	175.7	199.7	92.2	105.4
		K.SLYLVGSDYVFPQTANR.I	2	31.5	21.4	656.6	702.1	58.2	68.1	615.0	660.3
		K.VGSLNSLSGTMAISEVTV									
		R.D	2	9.7	13.2	248.4	292.3	1.6	1.2	159.3	171.2
		R.IGEIRPDGLIYTVWESK.G	2	12.3	21.5	237.5	266.6	8.8	10.3	248.7	283.7
		R.IGEIRPDGLIYTVWESK.G	3	11.1	14.2	373.5	331.3	7.4	9.4	456.2	429.2
MSMEG	MSMEG	K.AAYDADPYAYLQK.A	2	16.9	18.9	7.8	8.4	17.0	17.4	12.3	8.5
_2983	2995										
MSMEG	MSMEG	K.AVWATIGYDLPLPLPR.I	2	85.5	77.3	1082.3	937.1	94.1	90.9	513.3	605.8
_3003	3017	K.GLAYVLVGEDGTLGGPVA									
		K.N	2	252.3	260.6	573.6	541.7	203.9	198.6	395.1	392.3
		K.SGGGVDPLTDAPAPITPQ									
		QR.K	2	131.9	134.8	215.3	234.5	115.1	144.3	184.1	303.1
		R.ITALLAGVDSIR.E	2	131.2	119.6	138.9	150.4	162.3	119.9	164.3	135.5
		R.LQPGSFYALPQSPQLFK.									
		Q	2	223.5	222.0	200.8	186.6	222.1	198.7	192.1	199.0
		R.THAAGSLRPADAGQTVTL									
		AGWVAR.R	3	772.7	824.2	82.0	99.0	330.6	425.4	70.8	105.5

		R.VFQAPYVGAVVMPGGAS									
		QPR.R	3	29.6	42.8	67.3	90.7	19.1	30.6	51.8	83.1
MSMEG	MSMEG										
_3004	3018	K.LYSDTAALDDFNSK.V	2	22.5	24.9	13.1	14.8	12.5	16.2	7.0	8.8
MSMEG	MSMEG										
_3013	3027	R.LSDLVEAGLLER.R	2	10.5	10.6	6.9	9.0	5.0	9.5	9.9	9.7
MSMEG	MSMEG										
_3016	3030	R.DIADVAADLR.A	2	0.7	1.1	11.1	9.2	1.1	2.9	9.2	10.2
		R.GAIEPWNVLGEESTAGGT									
		AR.Y	2	14.1	11.5	109.0	88.0	8.8	9.2	104.6	89.9
		R.HLLTDITGNTHR.A	3	0.4	0.0	4.4	0.8	0.4	0.1	2.2	1.4
		R.IVLLDGDSPAGLR.L	2	1.7	2.2	31.0	28.6	3.2	3.8	29.2	35.2
		R.LGLLELR.G	2	0.0	0.0	3.9	2.9	0.1	0.1	0.8	2.6
		R.LPAGDPVGADEDLAEDGA									
		DAR.A	2	0.1	0.5	10.7	12.2	0.0	0.8	7.7	10.4
		R.LTATDAPQPWVLDR.A	2	4.0	3.8	38.4	39.3	3.4	6.0	39.5	43.5
		R.SLVAWFWDPLR.A	2	0.3	0.1	6.4	6.3	0.9	1.0	9.3	7.9
		R.SYDTSPVNAVEAESR.R	2	14.3	14.4	20.2	20.0	27.2	28.6	16.4	20.2
		R.TATVVDADGAPTTALVAEI									
		R.D	2	0.3	0.7	15.8	18.8	0.7	0.8	11.9	13.8
		R.VTLPTYDAAWASIVDLGG									
		R.V	2	6.2	7.0	14.9	15.6	8.2	7.9	10.9	15.1
MSMEG	MSMEG	R.AEDPEYGLAFDLSSEFD									
_3019	3033	K.V	2	26.4	31.5	62.3	67.7	24.1	22.4	59.1	54.9
MSMEG	MSMEG										
_3025	3039	K.EDFEILGPLPR.K	2	26.5	25.2	8.0	13.4	16.6	13.7	14.5	10.4
		K.GAAGIDAALAALR.A	2	99.1	88.0	29.4	25.9	126.4	90.9	56.7	42.2
		K.LLGVEQPVMGDLIATVR.D	2	240.4	237.7	217.6	227.2	254.6	226.5	247.6	243.2
		K.LLGVEQPVMGDLIATVR.D	3	19.4	21.9	1.5	6.4	21.4	17.8	2.2	4.8
		K.RVPVVSHDGLEADRVELIL									
		DR.T	4	65.5	63.8	29.4	37.3	65.8	86.7	30.6	61.6
		R.AAAVNAVAGAETVGK.V	2	7.4	4.6	8.1	7.0	6.3	5.9	8.9	10.1
		R.ALMAGLASSLK.V	2	56.0	33.0	16.1	8.9	68.2	23.8	37.2	5.5
		R.FDFNWQGPLSDDQR.T	2	124.5	131.3	41.9	50.4	127.8	133.7	62.0	66.9

		R.GEGTSKEDFEILGPLPR.K	2	38.7	43.6	14.0	9.0	37.0	46.2	7.7	12.6
		R.GEGTSKEDFEILGPLPR.K	3	66.7	62.5	21.6	23.2	86.3	68.7	45.4	32.7
		R.IAVAEETAFNR.T	2	29.5	25.8	14.8	9.6	24.7	30.7	13.6	18.1
		R.TAIIADGVSPGNEGR.G	2	648.9	600.0	357.1	315.7	1044.3	1080.7	374.0	341.9
		R.TPDIDEVGITTR.H	2	33.4	27.4	12.9	15.0	33.0	22.0	10.8	7.4
		R.TQIEEVTNQAVEADYEVH									
		TFVTELEK.A	3	341.6	377.7	205.5	220.7	245.7	315.2	164.5	223.4
		R.VAC#LLQGVDNVYETDLL									
		RPVIDK.V	3	159.0	223.7	121.6	155.3	162.7	179.8	106.6	142.7
		R.VAC*LLQGVDNVYETDLL									
		RPVIDK.V	3	159.0	223.7	121.6	155.3	159.9	179.8	102.5	142.7
MSMEG	MSMEG	R.ASASAHDAVDVAEQLAR.									
_3026	3040	R	3	9.3	8.7	19.7	18.9	7.0	6.3	14.7	18.4
MSMEG	MSMEG										
_3033	3046	K.VAVLHQPVLNQTAEAIR.S	3	107.5	104.5	183.4	229.1	78.6	95.4	125.4	136.6
		R.GVDIVHVPTLLGMVDAA									
		VGGK.T	3	54.4	55.5	58.7	56.6	26.2	21.1	36.0	33.2
MSMEG	MSMEG	R.DGSDFVFMDSDFEQHP									
_3035	3049	LPESLVGR.L	3	204.7	223.0	179.4	185.6	181.7	201.2	149.5	172.0
MSMEG	MSMEG										
_3045	3059	R.LPALPDSVGPALVAPTK.G	2	18.3	18.2	25.7	26.2	20.0	31.5	11.9	19.5
MSMEG	MSMEG	K.AGVFSGDALADVDALLER.									
_3046	3060	V	2	351.0	424.0	212.8	211.9	349.5	421.2	270.4	277.2
		R.VAITAQNHGFALEGEAGE									
		K.F	3	102.0	123.8	115.0	142.7	42.8	72.7	53.9	72.2
MSMEG	MSMEG	K.AGEVNMVINTPYGNSGPR									
_3047	3061	.V	2	47.0	45.1	52.3	51.5	37.7	32.8	46.5	40.6
		K.ETPAC#FEPTLDYVVVK.A	2	56.1	48.9	111.5	98.7	56.3	48.9	124.0	107.1
		K.ETPAC*FEPTLDYVVVK.A	2	55.8	48.9	110.6	98.7	56.3	48.9	123.8	107.1
		K.FPGADATLTTTMMK.S	2	92.6	96.7	101.5	108.2	66.1	70.3	85.9	97.7
		K.HYEDPSAADPRPSAVEVI									
		K.A	3	76.3	69.6	93.1	77.6	66.4	70.8	96.4	86.8

K.LAIGYTLDEILNDITK.E	2	45.5	52.5	49.2	50.2	34.9	42.7	50.5	57.4
K.LAIGYTLDEILNDITK.E	3	5.7	7.1	6.4	7.4	4.5	5.4	6.0	6.1
K.RLEDAGVPIVGTSPK.A	2	22.2	18.9	26.9	20.5	21.8	16.6	32.5	21.4
K.RLEDAGVPIVGTSPK.A	3	45.2	40.5	53.6	46.0	25.4	31.2	38.6	46.8
K.SQTAAYGSLPTEGTVFVS									
VANR.D	2	18.6	17.2	26.4	24.9	13.8	13.6	18.0	23.6
K.SQTAAYGSLPTEGTVFVS									
VANR.D	3	80.5	87.8	94.5	100.2	45.6	66.1	64.9	82.4
K.STGEVMGIDHDFGTAFAK.									
S	2	12.2	10.4	8.2	7.9	10.9	7.8	6.9	8.6
K.TPYHYSSYELDPAAEDEV									
APQTEKPK.V	4	185.8	214.4	219.0	237.7	112.4	129.5	167.6	185.9
R.ADGAQIDSLLGPEMK.S	2	36.6	33.1	47.7	46.8	24.7	24.9	36.4	39.3
R.AELVEAPVLDADLLR.R	2	201.5	189.0	377.1	375.6	192.9	181.9	431.1	400.4
R.AGFWTAPDPDTTVEQLLT									
NLR.T	2	34.3	32.2	45.3	40.2	15.5	25.2	23.8	39.8
R.AGFWTAPDPDTTVEQLLT									
NLR.T	3	26.6	33.9	34.3	46.1	13.5	26.0	17.1	39.0
R.DLGIAILR.E	2	38.7	33.4	40.6	34.0	28.7	27.9	38.1	36.4
R.ETVAELGLPVVVR.P	2	16.7	17.4	25.1	29.3	12.4	12.9	25.7	27.5
R.EVGVDGTGGC#NIQFAVNP									
R.D	2	38.4	39.0	49.2	47.9	41.4	38.9	57.9	54.1
R.EVGVDGTGGC*NIQFAVNP									
R.D	2	38.4	39.0	49.2	47.9	41.4	38.9	57.9	54.1
R.GDIGVMSLQELHSELGSR									
.R	2	23.3	19.5	19.0	12.9	19.2	14.2	20.6	11.8
R.GDIGVMSLQELHSELGSR									
.R	3	50.1	49.2	55.6	48.7	40.4	35.9	56.5	51.6
R.GHFGEVLTAAGLPAPK.Y	2	31.5	26.6	43.9	39.5	31.8	25.6	51.0	45.1
R.GHFGEVLTAAGLPAPK.Y	3	78.4	72.1	70.3	63.4	61.1	59.7	64.5	62.5
R.GMEIVYDEETLR.G	2	68.4	73.7	95.2	94.4	45.2	49.9	80.5	80.1
R.IAADIGYPVLVR.P	2	61.7	58.2	231.0	198.7	36.1	36.3	73.4	69.0
R.IYDMELALR.L	2	47.9	41.9	63.1	51.7	35.3	34.9	55.6	52.5
R.KHYEDPSAADPRPSAVEV									
IK.A	3	9.9	6.5	5.9	3.9	10.2	7.2	12.8	7.1

		R.LEDAGVPIVGTSPK.A	2	19.8	20.8	21.7	20.7	11.3	13.9	24.0	18.5
		R.LIVIEMNPR.V	2	31.6	35.6	87.2	97.9	22.1	25.7	90.9	92.3
		R.QISALRPELAGEAGVR.A	3	9.5	10.0	47.1	40.1	10.6	10.4	19.7	16.1
		R.VMLGATITQLR.D	2	45.1	39.6	81.4	80.3	23.7	24.2	86.7	95.4
		R.YGVELIGADFEAIQR.G	2	83.9	66.0	126.5	103.0	86.1	69.3	157.9	123.9
MSMEG	MSMEG										
_3050	3063	K.AQEIM#TELEIAPTR.R	2	114.1	127.0	91.1	102.6	103.5	102.9	84.5	82.9
		K.AQEIM*TELEIAPTR.R	2	112.2	125.0	91.1	102.6	101.3	100.9	84.5	82.9
		K.QVLTAETDEVLGK.M	2	147.0	152.7	145.8	149.6	158.8	162.0	169.1	157.4
		K.VSALLEALPK.V	2	311.2	303.5	260.4	252.7	408.1	392.0	352.4	320.7
MSMEG	MSMEG										
_3054	3065	R.LPEAEEITTLAQLLLER.A	2	75.3	76.7	107.1	82.4	65.4	69.1	94.4	113.3
MSMEG	MSMEG	K.AAPVGLFVETFGSETVDP									
_3055	3066	AK.I	2	1623.9	1454.6	741.5	610.7	1386.7	1220.5	905.4	775.8
		K.AIGEVDLRPAIVR.D	2	698.0	680.6	355.9	367.0	615.5	526.7	402.6	371.5
		K.AIGEVDLRPAIVR.D	3	1059.1	925.7	440.2	383.7	967.2	846.4	606.6	522.3
		K.FVLGGPM*GDAGLTGR.K	2	210.9	195.0	491.7	576.0	264.2	277.4	501.2	458.1
		K.FVLGGPMGDAGLTGR.K	2	1361.3	1376.9	709.7	727.8	715.7	675.1	501.2	458.1
		K.GFDGASC#GVNVAIGAQS									
		PDIAQGVDTAHETR.V	3	384.0	426.3	274.4	306.8	349.6	349.6	301.9	315.3
		K.IC*DAISDSVLDALLEQDPK									
		.S	2	301.5	324.6	151.9	165.7	165.3	168.9	108.4	100.5
		K.IC*DAISDSVLDALLEQDPK									
		.S	3	227.0	219.6	77.2	81.0	137.0	124.2	74.1	62.6
		K.IIVDTYGGWAR.H	2	393.0	259.6	146.7	106.1	292.4	277.7	164.3	159.8
		K.NVVAAGLAER.V	2	9.8	6.2	2.5	3.1	9.2	10.7	1.1	2.2
		K.TQVTIQYDGTTPVR.L	2	1793.8	1687.2	1161.4	1103.5	1465.9	1357.7	1368.7	1348.9
		K.VVNTVLADLGHETLDTSD									
		YR.L	2	472.1	422.1	225.6	205.4	309.5	310.6	182.0	188.4
		K.VVNTVLADLGHETLDTSD									
		YR.L	3	3394.3	3103.3	1481.4	1303.9	2800.1	2650.4	1737.6	1642.3
		R.DLDLLRPIYAPTAAYGHFG									
		R.T	3	1117.1	1124.1	498.0	492.1	961.6	874.7	591.7	578.4
		R.DLDLLRPIYAPTAAYGHFG									
		R.T	4	562.3	535.6	253.0	219.8	485.5	477.8	310.0	310.4

MSMEG _3058	MSMEG 3069	R.EKVVNTVLADLGHETLDT												
		SDYR.L	3	291.6	226.6	265.3	212.9	391.4	364.3	342.7	309.2			
		R.ILDIGYDSSTK.G	2	20.9	19.9	196.8	238.8	12.7	8.7	265.8	256.5			
		R.KIIVDTYGGWAR.H	3	32.6	12.5	0.7	0.0	61.5	49.1	20.8	8.4			
		R.LDTVVLSTQHADGIDLEG												
		TLTPDIR.E	3	683.6	528.8	458.1	384.0	603.1	530.5	493.7	456.4			
		R.TDIELPWEQTNK.V	2	716.4	671.3	383.6	378.1	558.9	508.1	280.2	293.9			
		R.TDIELPWEQTNKVDDLK.S	3	305.9	332.9	38.6	66.9	134.5	123.3	55.3	96.3			
		R.VEVQVAYAIGK.A	2	274.9	304.4	109.9	149.7	263.7	254.0	105.1	133.8			
		K.DAGLDFDIR.V	2	1.9	1.4	2.8	1.5	21.8	17.7	3.3	1.6			
		K.HLVTLPTDGPVNVHTIGN PK.N	3	126.2	132.3	181.5	190.9	430.3	374.8	197.4	174.3			
		K.KLTVAATQVPHAEILEFIK. N	3	16.5	13.0	19.7	14.5	46.3	54.1	18.0	27.8			
	MSMEG _3066	MSMEG 3077	K.LTVAATQVPHAEILEFIK.N	3	42.1	45.7	75.4	74.3	96.6	94.5	49.5	51.4		
			K.AGLSVKPGTPLEPYLEILR. E	3	76.2	78.3	112.7	120.0	66.1	66.3	104.9	114.6		
			MSMEG _3070	MSMEG 3080	K.LDGDLTNAPAVAAEGTAD LIAFGQK.I	2	96.6	106.3	127.0	123.4	58.0	65.5	106.9	98.1
					K.LDGDLTNAPAVAAEGTAD LIAFGQK.I	3	463.0	495.2	546.6	566.9	317.2	333.4	501.7	488.1
					K.TQQSVHLLLTVQGK.V	2	52.5	35.4	53.4	30.1	29.8	25.2	35.0	23.7
					K.TQQSVHLLLTVQGK.V	3	111.1	97.0	60.1	48.8	79.6	73.2	39.1	41.3
MSMEG _3071	MSMEG 3081	-.M*FTGIVEELGVLVDK.A	2	56.4	46.7	72.0	53.2	37.6	37.6	31.9	36.9			
		R.LGGHIVQGHVDGTGSVIS R.T	2	2.1	0.0	0.1	0.0	1.7	1.0	0.0	0.1			
		R.LGGHIVQGHVDGTGSVIS R.T	3	66.8	68.5	19.9	17.8	62.3	55.8	25.1	23.2			
		MSMEG _3072	MSMEG 3082	K.HGTAYTVTVDAK.K	2	13.3	9.1	9.9	8.7	10.7	10.0	2.6	2.9	
K.LQAYQLQDAGEDTVDANL K.L	2			131.6	143.9	25.8	59.9	84.8	105.1	24.8	39.0			
K.SIYEDVEHVALVR.G	2			96.9	89.1	120.6	120.3	93.6	75.2	90.6	93.8			



		R.ALANPGSVADDFTKPGHV									
		VPLR.A	4	203.3	191.5	60.6	72.3	193.1	199.3	73.5	97.9
		R.VGLDGYGLHIIER.V	3	27.4	29.1	4.2	2.5	38.3	35.8	5.3	11.6
MSMEG	MSMEG										
_3073	3083	K.GAQAAAAALSTAVTLR.E	2	68.3	85.4	46.2	68.3	36.2	34.8	34.0	32.8
		K.VAADAGIPDPTVVR.V	2	171.6	164.6	225.7	222.2	97.8	115.2	176.2	196.5
		R.AGLPGSTEDKGAQAAAA									
		ALSTAVTLR.E	3	63.2	70.6	68.1	72.9	75.7	82.3	92.0	95.0
		R.VLGAIEIPVVAQALAR.T	2	248.1	256.8	327.6	328.5	164.7	176.7	282.7	278.1
		R.VLGAIEIPVVAQALAR.T	3	10.8	0.0	7.8	0.0	4.0	5.2	2.3	5.2
		R.VSLDEATPVANGVLTTNT									
		EEQAR.A	3	52.2	67.1	80.8	92.2	27.1	35.4	46.2	52.8
MSMEG	MSMEG										
_3081	3090	R.FAGGLHIVAGR.V	2	11.9	11.7	6.2	8.8	11.9	17.3	18.2	23.3
		R.GLPAQVVGGSVGDAEAA									
		WR.G	2	204.6	201.9	310.6	394.2	105.9	98.0	181.1	177.5
MSMEG	MSMEG										
_3084	3093	K.AIGLVLPELK.G	2	1347.6	1229.3	1619.7	1477.6	1200.9	1082.5	1776.1	1594.1
		K.EGPAALPWGDLGVDVVV									
		ESTGIFTNAAK.A	2	73.7	75.4	78.1	88.0	15.0	45.3	14.8	57.5
		K.EGPAALPWGDLGVDVVV									
		ESTGIFTNAAK.A	3	399.5	412.2	468.2	488.9	145.7	276.0	203.9	399.0
		K.GLM#TTIHAYTQDQNLQD									
		GPHK.D	3	278.0	210.2	284.1	222.0	206.1	200.1	221.9	228.5
		K.GLM#TTIHAYTQDQNLQD									
		GPHK.D	4	269.5	217.1	227.4	163.3	216.9	219.8	183.1	175.3
		K.GLM*TTIHAYTQDQNLQD									
		GPHK.D	3	495.7	437.6	457.8	402.9	469.3	459.7	490.5	498.7
		K.GLM*TTIHAYTQDQNLQD									
		GPHK.D	4	269.5	217.1	227.4	163.3	216.9	219.8	183.1	175.3
		K.GLMTTIHAYTQDQNLQDG									
		PHK.D	2	179.7	256.9	209.8	326.0	46.3	56.7	58.7	84.4
		K.GLMTTIHAYTQDQNLQDG									
		PHK.D	3	2908.0	3013.2	3684.2	3802.3	1282.0	1261.2	1901.6	1875.7
		K.NTDIEIVAVNDLTDNATLA									
		HLLK.F	2	125.2	153.5	175.4	206.6	77.3	89.3	107.6	155.4

MSMEG _3085	MSMEG 3094	K.NTDIEIVAVNDLTDNATLA										
		HLLK.F	3	1458.6	1391.2	2050.7	1897.8	1187.2	1122.3	1988.8	1968.8	
		K.VLNDEFGIVK.G	2	88.9	71.4	202.3	190.8	90.2	94.7	179.6	195.7	
		K.VVSWYDNEWGYSNR.L	2	1676.9	1810.9	2085.9	2252.5	1088.7	1240.0	1599.7	1953.9	
		K.YYDAPIVSSDIVTDPHSSL										
		YDAGLTK.V	2	459.8	578.6	565.8	654.8	281.6	335.4	430.3	493.5	
		K.YYDAPIVSSDIVTDPHSSL										
		YDAGLTK.V	3	5939.0	5492.0	6941.5	6339.5	4640.2	4891.5	7082.3	7082.5	
		R.AAALNIVPTSTGAAK.A	2	160.2	119.2	275.6	251.3	137.7	131.7	273.4	288.2	
		R.LADLVALVGK.S	2	853.7	591.8	1163.5	687.3	879.2	834.0	1464.8	1344.2	
		R.LPQDVSLEGDDTIVIGDTK										
		.I	2	587.8	590.9	745.5	808.9	485.6	464.1	740.4	773.2	
		R.VPIPTGSVTDLTAEELAK.S	2	5700.5	5740.0	7947.2	7867.8	4565.1	4691.8	7354.0	7803.8	
		R.VPIPTGSVTDLTAEELAK.S	3	567.5	558.9	704.6	707.5	357.8	456.8	530.6	712.2	
		K.ALAALVEGPDGSPGVFVS										
		DGFGVVHR.K	3	1552.4	1365.1	1051.2	976.2	1293.8	1251.3	1190.3	1090.4	
		K.FAADAEAEETVAADR.I	2	336.9	334.2	320.6	305.5	235.6	223.6	230.8	227.1	
		K.FAADAEAEETVAADRIPDG										
		K.M	3	311.1	341.6	260.0	340.7	419.2	370.1	460.5	413.7	
		K.GAFSVVGGGDSAAAVR.R	2	310.5	301.7	360.3	378.4	287.3	258.3	320.0	346.0	
		K.GVAEAIIGATGK.G	2	26.4	15.2	6.7	6.7	21.4	20.0	20.2	6.3	
		K.LAVIENLTK.A	2	27.2	20.4	13.7	21.6	15.4	10.1	16.0	22.4	
		K.LSLAPVAAALGEK.L	2	502.7	432.0	600.6	550.7	437.7	384.2	671.2	585.1	
		K.TLDDLLAEGVQGR.G	2	300.1	271.3	384.0	366.6	288.7	269.9	523.9	442.0	
		K.TVFWNGPMGVFEFPFAFA										
		AGTK.G	2	161.2	184.8	162.8	202.4	63.8	81.8	66.3	99.2	
		K.VLQQLTSSTDRPYAVVLG										
		GSK.V	2	280.3	317.1	269.1	313.7	233.2	213.8	234.0	238.3	
		K.VLQQLTSSTDRPYAVVLG										
		GSK.V	3	1360.8	1323.1	1112.5	1142.5	1027.9	1167.3	1045.6	1139.0	
R.AEGLTDGDVLLLENIR.F	2	360.9	357.2	329.8	337.9	413.8	369.5	430.7	384.4			
R.HVQLAGDVVGTDALAR.A	2	336.1	400.8	376.7	331.3	352.5	375.7	462.5	478.8			

MSMEG _3086	MSMEG 3095	R.LGLPEDGFSHISTGGGAS									
		LEYLEGK.E	3	474.4	437.1	469.9	455.2	389.2	357.1	448.8	426.1
		R.LLDEYADVIHLPVDIVVAD									
		K.F	3	330.0	339.2	306.1	321.2	253.6	212.7	298.7	258.2
		R.RLLDEYADVIHLPVDIVVA									
		DK.F	3	82.5	82.0	764.9	494.7	56.4	58.3	883.5	770.4
		R.SDLNVPLDDDGNITDPGR.									
		V	2	580.8	647.0	497.1	545.2	523.3	534.8	533.5	457.6
		K.HGLTPIVC#IGEQLVR.E	3	35.3	36.9	12.1	9.6	27.3	19.3	14.0	12.5
		K.IAFALPDKYFDK.V	3	25.6	23.7	33.0	33.8	30.6	28.4	42.9	40.7
MSMEG _3097	MSMEG 3107	K.LGC#TFVIVGHSER.R	3	56.6	44.2	29.1	22.4	61.5	49.2	37.3	28.6
		K.LGC*TFVIVGHSER.R	2	26.9	27.6	43.6	27.2	29.6	28.0	49.7	47.9
		K.M#NLNHFEAIALVQK.I	3	52.1	56.1	37.1	38.8	36.4	41.5	30.2	31.8
		K.M*NLNHFEAIALVQK.I	2	73.2	83.3	142.9	145.2	73.3	74.3	133.4	117.6
		K.M*NLNHFEAIALVQK.I	3	52.1	56.1	37.1	38.8	36.4	41.5	30.2	31.8
		K.MNLNHFEAIALVQK.I	2	108.1	105.2	162.4	145.2	112.0	106.9	182.9	179.8
		K.MNLNHFEAIALVQK.I	3	177.1	180.3	210.3	209.0	179.4	169.1	223.8	207.4
		R.EAGNHVEFNVNSLR.G	2	110.1	76.0	70.3	46.5	106.0	95.7	88.5	77.0
		R.GELANLSSSEIAAGVR.V	2	635.5	725.3	1118.5	1190.4	693.6	690.1	1037.5	1027.6
		R.GELANLSSSEIAAGVR.V	3	49.7	43.5	63.7	51.8	47.5	52.1	43.6	44.4
MSMEG _3097	MSMEG 3107	R.GSLAGLTPEQIGQTVIAYE									
		PVWAIGTGR.V	2	24.8	39.0	23.3	34.7	12.4	28.7	15.4	32.7
		R.LTYGAQDLSQHDSGAYT									
		GEISGAFLAK.L	3	626.2	643.4	611.2	620.6	646.5	614.2	748.9	712.5
		R.AVHVAAGKPPQDSSLAAT									
		YR.K	3	37.2	44.6	66.2	49.7	28.8	35.9	89.1	53.2
		R.FPYLEPLNHLQVELLR.R	3	14.1	20.6	60.3	54.0	15.1	19.1	102.1	60.3
		R.GGGPSYDAILAQPPGAVK									
		.G	2	109.9	118.9	178.6	182.4	102.9	132.4	166.8	210.5
		R.LITGQDDLLADNAALAR.S	2	72.7	70.4	140.6	136.8	61.9	88.2	157.6	182.6
R.LLGAILGDTV.R.E	2	32.6	27.9	45.3	44.7	40.8	30.2	69.4	57.3		
R.YQTPAEFLADLDAVDGSL											
R.A	2	54.8	61.6	36.6	35.2	46.1	70.4	47.8	47.8		
R.YQTPAEFLADLDAVDGSL											
R.A	3	4.0	5.2	6.8	10.2	4.6	4.5	6.3	10.4		

MSMEG	MSMEG	K.ADAVAAAVGGADPVDIPA									
_3099	3109	AGAVGR.E	2	91.7	102.9	93.4	100.4	77.3	89.2	102.6	117.1
		R.GQATIVLTGGGTGIGLLK.									
		R	2	91.6	81.9	985.2	982.1	70.4	63.8	1114.4	1072.8
		R.LVDAISSAIGER.G	2	125.0	98.4	125.3	99.8	110.1	104.8	141.2	143.8
MSMEG	MSMEG	R.VLTLVIAPHTEDLVEDSIEA									
_3100	3110	ANFASR.E	3	126.3	137.6	214.9	209.4	66.8	81.2	78.9	101.4
MSMEG	MSMEG										
_3101	3111	K.LMPAIYDLANR.G	2	37.2	33.4	22.7	25.9	10.9	17.1	5.4	6.8
		K.VVGLLDEEGFAK.D	2	38.1	21.9	58.3	46.2	61.0	55.7	68.3	75.9
		R.FVQGTFFDDDTAFTR.L	2	132.6	131.4	71.6	103.4	140.7	131.3	85.6	94.0
MSMEG	MSMEG										
_3102	3112	K.GTAYDAQVNELAAR.G	2	61.9	54.0	225.1	165.0	69.6	84.4	128.0	166.6
		K.IHSVASFFVSR.V	2	283.7	219.1	109.9	104.2	302.0	216.7	185.2	124.2
		K.LAAIGIDLDPDVFR.V	2	572.6	547.8	350.1	333.2	498.8	446.6	347.8	304.3
		K.SWQELLDATQGQLDAAK.									
		K	2	517.1	477.8	299.0	312.0	450.7	406.2	290.8	278.9
		K.SWQELLDATQGQLDAAK.									
		K	3	73.3	72.8	20.8	26.9	53.0	66.0	13.6	17.9
		K.TILQAIELWK.I	2	321.9	266.4	188.0	142.0	236.7	218.8	154.3	143.2
		K.TLEAVADHGEITGNTIAGT									
		AASSQETFDK.L	3	794.1	768.9	449.1	431.3	817.9	726.0	529.2	498.7
		R.LAHDTDKTILQAIELWK.I	3	24.1	29.8	12.8	12.4	77.0	83.2	59.3	58.8
		R.LAYAAYEEVFGSDR.F	2	475.5	434.3	385.5	387.9	496.4	474.0	429.5	444.6
		R.LQTGNLTELINTR.S	2	928.6	984.8	664.8	700.1	959.5	852.9	764.0	626.3
		R.LVMDAYLEGLEK.A	2	236.9	220.7	167.4	149.4	192.6	169.2	188.1	187.3
MSMEG	MSMEG	K.AHDEWQVSFDEWAEREP									
_3103	3113	ER.K	3	78.7	91.0	53.9	80.0	33.7	49.8	23.6	45.2
		K.AHDEWQVSFDEWAEREP									
		ERK.E	3	48.4	67.3	57.5	45.9	39.0	83.9	51.2	93.7
		K.AHDEWQVSFDEWAEREP									
		ERK.E	4	54.5	51.8	57.2	55.4	71.1	42.5	71.2	57.3
		K.GANSFGPPSISTEDWNAT									
		WYGR.T	2	236.9	264.4	186.8	226.3	153.2	243.9	125.9	245.0
		K.GANSFGPPSISTEDWNAT									
		WYGR.T	3	180.0	222.1	114.4	168.7	195.7	171.0	80.5	141.2

K.GVEITTGPLGQGLASAVG MAMAAR.Y	2	129.4	122.4	108.5	112.0	107.3	111.9	104.5	121.7
K.GVEITTGPLGQGLASAVG MAMAAR.Y	3	193.9	224.6	186.6	198.3	186.6	154.1	211.6	166.0
K.ILGFDPEKNFEVR.D	2	44.1	46.9	113.3	117.1	74.9	52.8	218.7	193.5
K.ISIEHNTDIAFSEDVVAR.Y	3	268.1	238.7	220.1	202.6	241.6	204.5	240.4	193.9
K.LPEGWDADLPHWDLDAK. P	3	79.4	89.8	64.9	70.4	35.9	36.6	28.4	34.9
K.LPEGWDADLPHWDLDAK PVATR.A	3	389.5	405.8	343.7	353.4	416.8	407.5	386.9	388.8
K.LPEGWDADLPHWDLDAK PVATR.A	4	666.9	718.7	531.3	542.1	640.9	645.6	524.3	557.9
K.LPELWGGSADLAGSNNT TIK.G	2	649.3	637.2	641.4	604.7	606.9	579.7	622.0	633.1
K.LVGDTGEIVSIEHYGESAD DK.T	2	138.7	152.4	108.8	120.6	113.6	100.3	89.2	89.4
K.LVGDTGEIVSIEHYGESAD DK.T	3	2751.3	2937.0	2513.6	2660.0	1595.1	2008.6	1757.9	2030.8
K.M*NTGGVHGSALGADEVA ATK.K	3	10.3	8.7	5.0	4.6	2.7	3.4	1.5	0.8
K.MNTGGVHGSALGADEVA ATK.K	3	50.3	39.6	39.9	32.0	33.6	34.2	29.9	34.5
K.MNTGGVHGSALGADEVA ATKK.I	3	4.1	2.8	3.4	2.4	5.7	5.1	4.6	5.1
K.NFEVRDEVIAHTR.E	3	28.0	17.9	7.7	10.5	36.1	34.1	25.9	25.2
R.AASGAVLSAVGPK.L	2	10.5	9.2	3.1	2.1	7.4	14.6	2.6	4.5
R.AYGGTFLQFSDYM#R.P	2	76.4	77.5	92.4	77.5	50.4	41.4	57.7	43.0
R.AYGGTFLQFSDYM*R.P	2	76.4	77.5	85.4	72.7	50.4	41.4	50.3	40.9
R.AYGGTFLQFSDYMR.P	2	549.2	522.1	544.2	504.5	494.8	382.0	554.3	412.9
R.AYGWHVQEVQGGENVV GIEQALEEAR.K	3	1493.8	1530.5	1338.6	1341.2	1158.1	1267.6	1104.5	1251.2
R.EFGFTPEAVAAAAAER.S	2	1384.0	1353.7	1348.4	1351.8	1222.5	1100.5	1432.2	1225.1
R.EFGFTPEAVAAAAAER.S	3	35.3	34.5	20.4	24.3	34.4	29.0	27.2	24.8
R.EHAM*GAILSGIVLHGPTR. A	3	54.8	50.7	20.8	29.1	37.0	40.4	19.4	21.9

		R.EHAMGAILSGIVLHGPTR. A	2	75.4	74.2	330.2	313.7	55.2	66.2	339.6	312.8
		R.EHAMGAILSGIVLHGPTR. A	3	356.6	337.6	431.3	415.7	237.8	264.8	355.6	373.0
		R.EHAMGAILSGIVLHGPTR. A	4	166.2	125.5	91.4	57.5	97.1	117.8	67.0	68.0
		R.GSSSGPVGMILTR.Q	2	111.4	69.9	55.1	30.1	141.2	44.6	96.7	20.1
		R.KVTDKPSFIALR.T	3	116.4	54.5	106.1	58.7	98.0	38.6	89.5	35.3
		R.QPIPVLEGTDPGVAR.G	2	114.0	116.4	403.0	403.1	136.1	152.2	299.6	359.4
		R.TIIGYPAPNK.M	2	5.8	5.7	34.2	16.9	3.8	4.9	47.6	16.5
		R.VAVEAAVAQSWYK.L	2	909.0	845.6	1067.4	993.0	848.7	725.6	982.4	945.2
MSMEG	MSMEG										
_3106	3115	K.ADAIGVNFIDTYFR.S	2	370.5	364.0	424.2	408.0	173.2	165.1	291.5	277.3
		K.ITVGGTYPLAEASR.A	2	643.5	600.9	449.4	418.8	270.5	307.9	266.2	320.5
		R.AGELINAIADGSIK.I	2	453.1	464.3	574.4	562.7	222.2	224.4	457.7	491.7
		R.ELPFVVGTEVC#GTVAAG NDVAALK.V	3	445.2	412.4	446.9	398.6	200.0	194.3	313.1	305.1
		R.ELPFVVGTEVC*GTVAAG NDVAALK.V	3	443.7	412.4	443.1	398.4	200.0	194.3	311.5	302.4
		R.GTLALFGASSGPVPPFDP QR.L	2	598.0	622.1	655.5	683.4	266.9	290.9	483.9	520.9
		R.LNAAGSVFLTR.P	2	39.3	35.4	37.1	27.1	5.9	7.8	53.1	40.3
MSMEG	MSMEG	K.YGYGWADSDVAGASAQR									
_3122	3131	.G	2	68.2	58.0	6.1	2.6	51.6	61.3	5.0	4.7
MSMEG	MSMEG										
_3124	3133	K.AAMDELEIDPAFGER.S	2	119.7	111.7	68.0	74.1	142.9	134.5	95.0	96.7
		K.IAILEDTDSGLDVDALR.V	2	147.9	152.1	90.8	108.5	187.4	170.8	119.9	120.6
		R.HEILQLSLLKPK.I	3	34.1	29.8	11.4	12.6	37.7	30.2	11.9	13.7
MSMEG	MSMEG										
_3127	3136	R.INVWVNPPWGPDK.I	2	21.9	22.7	3.1	3.0	21.4	22.1	1.0	1.9
		R.TALVGAGLVDELRI	2	38.9	36.8	34.8	31.7	42.9	43.6	41.8	43.7
MSMEG	MSMEG										
_3142	3149	K.NLSAVLDLVEASVR.Q	2	14.2	13.0	14.6	16.2	5.3	3.7	17.1	15.3
MSMEG	MSMEG	K.DHIEAIANWDPNAEPSIEI									
_3143	3151	QFTPAR.V	3	253.6	264.5	431.7	384.2	115.3	148.2	419.6	352.6
		K.DIHNYVEQNHPTPETK.L	3	30.9	27.8	13.0	10.1	12.2	12.7	10.7	11.3

		K.LSGEIKPGVTATDVVLTVT DM#LR.R	3	39.1	43.1	26.8	26.8	18.7	14.5	23.4	15.6
		K.LSGEIKPGVTATDVVLTVT DM*LR.R	3	221.5	268.0	100.9	121.9	105.2	83.8	95.4	80.3
		K.LSGEIKPGVTATDVVLTVT DMLR.R	2	60.2	74.9	10.9	18.8	30.5	31.6	18.4	20.2
		K.LSGEIKPGVTATDVVLTVT DMLR.R	3	2424.2	3109.4	1182.8	1389.2	1215.2	1293.5	1259.4	1266.3
		K.LSGEIKPGVTATDVVLTVT DMLR.R	4	64.7	90.2	14.6	23.4	28.3	34.9	17.1	21.8
		K.PGVTATDVVLTVTDMLR.R	2	15.7	18.0	25.6	20.3	2.4	2.8	30.4	30.9
		K.VLAENLLR.T	2	34.9	28.8	8.7	15.7	17.7	11.8	7.2	8.2
		K.VVPPGTGIVHQQVNIEYLAR .T	2	282.1	279.0	148.7	154.1	167.8	162.4	108.4	136.9
		R.ATLGNMSPEFGSTAAIFPI DEETINYLR.L	3	563.0	837.9	268.0	380.8	132.5	302.7	130.9	302.3
		R.DTLTVGDQSYEIYR.L	2	2094.4	2154.7	1201.7	1198.1	1046.6	1063.9	1188.2	1202.0
		R.DTLTVGDQSYEIYR.L	3	40.6	44.4	5.0	2.1	17.4	18.1	0.5	2.8
		R.KDIHNYVEQNHPTPETK.L	4	3.7	1.9	0.4	0.2	0.8	0.6	0.3	0.2
		R.TDEQLALVEAYAK.A	2	1993.2	1948.6	1020.1	1002.2	1069.2	1003.9	1004.9	1023.3
		R.TDEQLALVEAYAK.A	3	10.3	9.5	3.6	3.6	0.3	2.8	0.6	2.6
		R.VIMQDFTGVPC#IVDLATM R.E	3	141.2	190.0	58.0	78.4	69.7	75.1	60.2	69.2
		R.VIMQDFTGVPC*IVDLATM R.E	2	283.7	279.2	119.0	123.7	118.4	140.8	107.7	134.8
		R.VIMQDFTGVPC*IVDLATM R.E	3	162.0	213.6	75.5	101.9	77.3	86.3	71.5	87.0
		R.WGQGAFFDDFK.V	2	516.7	384.9	180.7	143.1	324.0	230.4	255.5	183.7
MSMEG	MSMEG										
_3147	3155	R.DYVIPQDVVEVIPDVL.R.H	2	325.2	238.5	262.3	171.6	234.1	186.3	246.5	220.1
		R.IQFTPDLDVPTDIVGTR.I	2	763.6	727.3	768.4	729.3	635.3	575.5	795.7	815.5
		R.LQDVAANTFVHHALVDYV VR.I	3	280.1	253.0	203.6	163.6	204.5	210.5	282.8	264.0
		R.LQDVAANTFVHHALVDYV VR.I	4	99.8	63.6	31.1	24.4	100.1	93.8	59.7	61.5

MSMEG	MSMEG	K.AGVTANVVAPGYIDTEM									
_3150	3158	R.A	2	334.3	364.7	268.2	300.9	360.5	358.1	280.1	303.4
		K.EVEEHQGPVEVLVANAGI									
		SK.D	2	119.9	124.9	76.1	71.0	108.0	107.3	78.1	65.6
		K.EVEEHQGPVEVLVANAGI									
		SK.D	3	685.1	687.6	661.3	663.5	668.7	610.2	658.7	613.3
		R.FEEVINTNLTGAFR.C	2	343.6	358.2	277.7	262.5	313.1	271.9	246.4	209.9
		R.IQAGALDFIPAK.R	2	365.7	388.0	616.5	588.4	298.1	286.0	526.7	501.6
		R.IQAGALDFIPAKR.V	3	58.6	56.9	30.1	31.5	144.8	131.2	79.1	77.5
MSMEG	MSMEG	K.AVLPIMNPPGGGIVGMDFD									
_3151	3159	PTR.A	2	283.6	297.4	205.7	227.1	312.2	324.2	264.5	266.1
		K.PAPLLELDVQNEEHLSTLA									
		DR.I	3	707.3	714.1	534.8	543.1	678.7	607.5	547.6	463.3
		K.VAQEAGAELVLTGFDR.L	2	364.8	355.1	368.9	376.0	486.7	389.3	485.1	415.1
		R.AMPAYNWMTVAK.S	2	159.6	167.5	132.5	144.8	170.8	189.8	170.4	182.7
		R.APLGWNMKDPTPVAK.T	3	24.4	26.2	30.4	48.9	97.8	92.8	109.2	96.7
		R.LPKPAPLLELDVQNEEHL									
		STLADR.I	3	147.7	153.7	93.7	80.5	229.7	217.2	147.7	140.6
		R.LPKPAPLLELDVQNEEHL									
		STLADR.I	4	177.9	150.4	86.7	66.8	238.1	228.8	137.2	110.5
MSMEG	MSMEG	K.VWLVPSTDFGTALQGFTK.									
_3155	3163	M	2	70.4	59.6	185.6	225.5	93.8	89.7	152.7	140.8
		R.AAAYLQAQQQAK.A	2	5.4	4.7	6.8	5.5	5.5	5.2	4.3	4.9
MSMEG	MSMEG										
_3158	3166	K.INAVEVLSNLLTGLGA	2	4.8	0.0	141.7	0.0	0.0	0.0	0.0	0.0
		K.VVESFPALGADGGADGD									
		VK.F	2	48.9	55.1	115.4	135.0	71.1	80.6	72.4	102.7
		R.DPWVNMLR.T	2	2.9	0.9	3.4	5.3	8.1	4.6	1.5	2.9
		R.ILVDGGLSVPDALR.Q	2	99.1	108.1	291.9	310.7	324.4	284.9	268.0	242.3
		R.LSIDFGADPLTAPLSGR.A	2	140.3	145.7	268.8	261.0	324.5	309.9	285.3	269.9
		R.VLLLPLGPLAEHNIR.A	3	41.2	40.0	126.7	113.1	93.2	64.5	112.7	81.3
		R.YGTEASAAVAAAR.A	2	5.5	5.1	11.6	8.5	21.4	20.4	12.3	12.3
MSMEG	MSMEG										
_3159	3167	K.AGLDAGLDIDK.F	2	4.6	2.0	14.5	11.4	16.8	17.9	13.8	15.3
		K.AGLDAGLDIDKFAPR.L	2	1.6	2.0	136.4	160.6	31.4	38.0	135.7	157.7



		K.AGLDAGLDIDKFAPR.L	3	3.2	5.7	5.8	5.0	76.8	77.4	17.4	24.0
		K.EVAEHGGMAQAISEGIPK.L	2	144.3	189.0	204.9	247.3	73.8	150.5	69.6	188.5
		K.GLSVAFDLATHR.G	2	4.4	4.7	60.0	56.8	43.2	32.9	47.9	48.4
		K.YQVDEDTEIEVLK.V	2	106.3	108.2	80.4	73.8	188.2	187.3	81.1	85.3
		R.AAAASGPAGEDGLGNLLALAIDAAR.A	2	15.4	18.6	39.4	38.1	68.8	75.3	35.0	54.9
		R.AAAASGPAGEDGLGNLLALAIDAAR.A	3	70.6	78.6	154.8	145.8	271.6	235.9	231.6	170.3
		R.AERDEAATQAALDELTR.A	2	518.2	510.2	777.9	739.8	339.7	316.6	459.2	413.6
		R.AERDEAATQAALDELTR.A	3	111.2	125.6	192.0	180.7	155.5	188.8	121.3	136.3
		R.GPYPTMYVNQPWTIR.Q	2	76.3	83.3	266.9	285.7	148.3	171.9	125.6	177.9
		R.IISDIFAYTSK.M	2	90.0	92.2	154.4	165.2	304.9	263.0	195.9	190.9
		R.LLWSELVSEFEPK.S	2	107.6	128.2	230.8	266.6	387.7	371.0	328.8	306.4
		R.PIDPWGGSYYVEWLTHQLAER.A	3	58.4	70.5	78.0	106.8	83.5	140.9	49.0	82.6
		R.SFADVPLEGETPAAAATPEAR.D	2	89.3	97.6	286.7	248.4	192.4	237.9	238.5	223.1
		R.THSQTSGWSLTAQDVFNVAR.T	3	72.8	103.1	142.4	153.6	209.7	172.8	151.0	81.4
		R.VQGDVGMAGVAIDSILDMR.Q	2	30.7	29.5	39.3	43.7	71.6	71.4	39.8	48.5
		R.VQGDVGMAGVAIDSILDMR.Q	3	8.7	14.7	5.7	5.8	32.6	25.9	8.5	6.4
MSMEG	MSMEG										
_3160	3168	K.STTIEALGMHLIEAGHR.V	2	3.8	3.3	1.6	2.4	5.4	4.4	2.7	1.8
MSMEG	MSMEG										
_3169	3176	K.AGEGVVNPDGTLTAGPVV									
		LQPEEYTSK.L	3	55.7	66.3	30.0	39.8	25.5	48.3	15.4	30.5
		K.AVELSDDVPAYGR.F	2	89.3	90.1	91.2	98.1	76.4	79.5	87.8	85.9
		K.DPDLVAAMDQVR.E	2	15.3	19.7	10.6	13.7	8.7	14.7	8.2	16.5
		K.LTVAVQDPDSLRFADLIADELNVK.A	3	33.7	43.7	104.3	115.6	24.3	33.8	34.4	91.6
		K.YTNEWQAYVTR.Q	2	46.2	45.6	39.1	36.8	35.5	37.2	28.1	33.8
		R.FGWDTHGLPAELEVQR.Q	3	33.2	29.8	30.0	28.7	23.3	27.7	23.7	26.6

		R.FWDEDPDAIDTLHTVLEV									
		TC#R.L	3	14.1	19.2	5.9	10.6	14.4	13.3	6.2	7.9
		R.HETYEHSYPHC#WR.C	4	4.7	2.0	1.9	0.9	1.3	1.4	0.2	0.5
		R.IDVYGSLDELER.D	2	156.3	153.1	96.2	89.0	166.1	154.9	76.6	75.0
		R.LAAPLLPLATEVIWR.G	2	86.5	92.9	82.9	92.0	113.2	105.1	117.8	107.4
		R.LAAPLLPLATEVIWR.G	3	11.9	13.0	6.6	6.9	13.3	10.9	9.6	6.8
		R.M*VELNQQITWYPEHVK.D	3	15.8	20.6	11.7	14.7	7.2	11.1	2.1	6.5
		R.MVELNQQITWYPEHVK.D	3	15.8	20.6	11.7	14.7	14.6	18.2	16.0	19.1
		R.PFIDQLTRPNPDDPTGK.S	3	27.3	26.4	12.2	19.5	16.6	18.7	4.6	9.3
		R.YWGTPIPVWK.S	2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
MSMEG	MSMEG										
_3178	3185	K.ALWDTILPFAGYAFNK.S	2	3.3	3.6	4.5	3.8	3.2	5.0	7.1	4.2
		R.GDTLGVFQLDGGPMR.D	2	27.5	25.6	14.8	14.9	18.0	19.5	23.1	20.6
		R.VAQVITFGTIK.T	2	15.7	14.9	25.4	23.4	11.7	12.3	42.7	41.7
MSMEG	MSMEG										
_3183	3190	R.ITALTAPLSAADIDEAAR.R	2	220.5	220.1	195.5	198.8	161.6	189.2	163.8	222.0
		R.LSEATGANVYLK.R	2	83.0	66.2	69.3	89.5	56.5	61.2	9.6	21.5
MSMEG	MSMEG										
3192	3192	R.ADELFAELPVALLER.L	2	53.8	64.0	48.3	51.0	42.6	39.1	69.5	53.7
		R.LVSLNEVGGEPALEFGVTT									
		AEFHQR.A	3	123.1	117.7	127.6	127.5	71.2	80.2	136.0	124.4
MSMEG	MSMEG										
_3185	3193	R.FFSITSLAALR.Q	2	13.2	13.0	13.2	12.3	11.0	8.9	24.9	10.6
		R.IDHPDGLTDPAGYLAWLR									
		.E	3	19.1	26.3	5.3	10.0	21.3	13.0	7.1	9.9
MSMEG	MSMEG										
_3204	3214	K.DNVFAVILAHGK.T	2	1.3	5.1	4.3	10.6	1.1	0.7	3.2	3.6
		K.DNVFAVILAHGK.T	3	1.4	0.3	4.5	1.2	1.1	1.2	5.1	3.9
		R.ILPAGSDDPSLPR.I	2	8.6	8.1	23.1	19.5	5.3	9.6	17.5	26.5
MSMEG	MSMEG										
_3205	3215	R.ELLSQALENLDADVR.A	2	40.8	33.9	30.6	28.2	53.1	41.8	57.2	48.0
MSMEG	MSMEG										
_3208	3218	R.VVVL DYGSGNLR.S	2	28.4	38.9	39.2	30.0	18.6	21.0	44.1	45.5

MSMEG	MSMEG	K.DGTLTGPNLDLLAAVAGR.	2	107.8	110.8	57.6	61.6	97.0	89.4	62.1	61.1
_3209	3219	T									
		R.GLILLPAVDVVNGQAVR.L	2	66.6	80.3	81.7	86.4	83.6	86.1	80.6	94.6
		R.GWETDGGDLWEVLDR.L	2	22.0	22.9	11.8	12.7	14.7	18.0	5.7	9.9
		R.TDAPVIASGGVSSLDDL.R.									
		A	2	156.0	160.6	108.8	123.6	141.5	154.5	107.2	113.6
		R.VAVGLDAQTDGAGGFR.L	2	52.2	54.1	12.6	15.4	56.4	54.2	10.3	18.6
		R.VNIGTAALENPQWC#AR.									
		A	2	50.9	60.2	41.5	40.0	63.9	66.1	38.6	48.9
MSMEG	MSMEG	K.LTALVATAAEILDAASVPF									
_3210	3220	VAGHR.A	3	14.0	15.0	24.0	33.1	8.4	9.3	20.1	30.9
MSMEG	MSMEG										
_3211	3221	R.GTGIDAIEWATR.G	2	9.8	9.4	8.8	10.6	8.4	11.5	7.9	11.7
MSMEG	MSMEG	R.AVETVTTDHSVTTAFHPV									
_3215	3225	TVTYDEGR.W	3	88.1	84.9	22.1	36.6	25.6	31.5	24.6	18.9
		R.LLLLDEPTTGLDVAAR.E	2	304.1	331.5	139.3	138.8	153.2	155.4	197.6	187.9
MSMEG	MSMEG										
_3219	3229	R.FNGSLDDLDVAVR.A	2	18.6	14.4	4.7	5.6	25.5	34.7	2.4	8.7
		R.GALASIGDPAELAQAYQD									
		GGAR.V	2	46.1	47.9	10.1	8.9	64.8	68.8	13.0	15.5
		R.SAVADLVTAGTHPSC#PK.									
		P	2	25.9	31.8	15.4	23.8	21.1	22.0	10.2	10.3
		R.SAVADLVTAGTHPSC#PK									
		PAR	3	277.0	306.7	9.8	14.3	340.9	325.8	10.7	16.1
		R.SAVADLVTAGTHPSC#PK									
		PAR	4	19.0	21.5	11.1	12.2	52.4	53.5	12.8	17.8
MSMEG	MSMEG										
_3220	3230	K.INNVLGQALLAR.Q	2	35.6	28.6	110.6	109.4	31.1	36.9	168.9	171.4
		R.LVPEALMAVIEEVTAAYEK									
		.C	2	10.7	14.6	14.6	22.0	2.3	7.6	4.3	10.7
		R.LVPEALMAVIEEVTAAYEK									
		.C	3	9.1	10.2	12.8	13.6	6.8	10.3	9.0	13.0
MSMEG	MSMEG										
_3221	3231	R.EVSDIPVGVGLGVR.S	2	122.8	110.8	156.8	139.5	116.6	112.3	177.2	166.6

MSMEG _3222	MSMEG 3232	K.AADETEEGDEESLVDEAG K.E	2	10.8	9.3	9.5	8.4	4.7	7.0	3.3	4.4
		R.AEPAAPAAVATAPVEPEK. G	2	22.1	21.8	20.1	19.7	16.9	18.4	14.0	13.9
		R.LGNYFNQELYGR.P	2	13.7	13.1	16.8	22.6	6.7	6.5	8.3	20.1
MSMEG _3225	MSMEG 3235	K.AQLSAAEPYEEWLHAGLL DLK.T	3	21.7	27.6	46.6	49.3	9.3	12.1	65.0	62.6
		K.GMLTTMQLPQYFLDLR.D	2	8.6	7.2	19.5	18.3	6.7	5.9	20.0	21.0
		K.LVSSVGVGTVAAGVSK.A K.TGVRPPVPLEEVEPVESIV TR.F	2 3	34.7 76.2	33.8 80.7	84.1 164.0	88.4 152.2	16.5 39.7	14.3 47.3	115.7 216.4	103.9 209.1
		R.AIPSELLAVSAVHHHLVR. T	4	9.5	10.2	22.1	19.2	1.8	3.7	26.5	29.8
		R.EGELTGIEPAAAVR.N	2	37.2	37.4	88.5	99.1	21.1	21.9	110.0	112.7
		R.FGVTS DYLVNATDIQIK.M	2	27.6	27.9	62.5	58.1	13.6	20.3	78.9	80.9
		R.GGEGLAEALDDL.R	2	7.1	4.9	9.7	9.8	3.1	2.9	17.7	15.7
		R.IVSDGLIALENLEHR.G	2	4.3	3.2	44.1	29.1	2.2	2.0	84.8	38.7
		R.IVSDGLIALENLEHR.G	3	16.8	14.4	39.5	38.8	6.1	7.4	56.9	55.0
		R.LEVGGEYAFR.R	2	11.0	11.5	7.5	7.1	10.9	14.0	6.4	9.2
		R.TLIQLAEGALED AHPVR.L	3	16.7	18.6	40.2	42.4	9.8	8.9	60.2	47.6
		R.VC#HLDTC#PVGVATQNP ELR.A	3	24.4	30.9	76.6	84.6	11.5	12.9	94.0	96.2
		R.VC*HLDTC*PVGVATQNP ELR.A	3	24.4	30.9	76.0	84.4	11.5	12.9	93.6	94.5
		R.VILASEAGVLDVPSGEIVA K.G	2	27.3	24.6	70.6	62.5	11.4	10.4	105.1	92.9
		R.VMGPEENLLEPTAASC*R. Q	2	1.8	4.8	13.8	16.1	0.3	0.9	13.6	18.0
		R.YLAELGFR.S	2	7.5	7.1	22.0	17.2	1.7	2.8	24.8	21.8
		R.YTGSTLGTSLSDWPR.R	2	20.1	18.5	38.4	36.2	6.9	10.2	56.0	51.6
MSMEG 3227	MSMEG 3237	K.ALVAFTQSGDTV.R	2	63.5	53.3	320.8	262.6	133.3	87.3	400.5	330.9

		K.DIEDLEFAVR.L	2	129.4	115.0	159.3	166.0	176.6	166.0	182.1	160.1
		K.GVSLPGMNVSVAMSEK.D	2	766.2	920.1	570.3	586.9	746.0	783.5	292.9	362.5
		K.IVC#TLGPATSTDETVR.A	2	20.5	20.3	29.7	26.8	32.7	35.6	40.2	48.7
		R.AASDVTGHAVGIMADLQGPK.I	2	99.1	106.3	134.6	170.8	72.6	69.7	71.9	93.9
		R.AEASDVANAVLDGADAV									
		MLSGETSVGK.Y	3	423.2	423.6	623.8	611.9	373.9	319.4	460.7	382.1
		R.ALVEAGMDVAR.L	2	180.1	168.5	201.3	205.3	113.7	106.5	141.7	154.8
		R.GDLGVELPLEEVPLVQK.R	2	729.2	660.0	1166.2	1094.3	1047.4	932.3	1588.7	1422.1
		R.IIQAVEDNSVVVPPLTHVP									
		R.T	2	110.0	125.5	249.6	333.7	119.6	127.4	296.7	310.6
		R.IIQAVEDNSVVVPPLTHVP									
		R.T	3	1717.2	1576.3	3525.3	3703.4	1901.8	2221.3	4430.1	4188.3
		R.IIQAVEDNSVVVPPLTHVP									
		R.T	4	40.1	39.0	28.0	36.6	51.1	53.6	42.4	44.5
		R.LGVDLVALSFVR.S	2	79.1	74.9	117.9	112.7	128.1	124.9	151.2	159.4
		R.SPADIELVHEVM#DR.V	3	1.8	0.8	6.9	3.7	5.2	6.3	10.0	11.4
		R.SPADIELVHEVMR.V	2	272.6	292.7	332.2	365.3	210.1	205.2	223.9	232.3
		R.SPADIELVHEVMR.V	3	145.8	131.5	161.3	144.2	131.3	131.0	138.5	128.7
MSMEG	MSMEG										
_3234	3244	R.KLGAALSTGSPSAPPVS	2	2.8	3.2	13.5	14.6	3.6	4.6	14.8	13.2
MSMEG	MSMEG										
_3235	3245	K.AGEVFDSAPYGWPVAK.G	2	1117.6	1220.2	850.8	880.2	1224.1	1250.6	737.4	780.9
		K.GSPLAQSLQQALQHLIDN									
		GEYEK.I	3	390.4	409.2	817.8	813.4	516.8	564.0	605.3	610.3
		K.IIPSIQGGTFNVGMSSFTD									
		TK.E	2	106.9	107.0	188.5	192.5	219.8	185.2	167.2	164.5
		K.KVAVQATTVQETDELPAR.									
		S	3	39.9	31.9	51.0	43.7	59.4	70.3	35.2	48.3
		K.LIVGVNIPYAPNEFK.D	2	450.9	454.5	1241.2	1245.7	474.1	454.0	1277.5	1227.3
		K.LIVGVNIPYAPNEFKDPSG									
		K.I	3	438.1	455.5	774.9	822.6	657.3	700.0	608.9	642.4
		K.VAVQATTVQETDELPAR.S	2	379.5	418.8	820.4	868.0	620.0	700.7	706.2	825.1

		K.VAVQATTVQETDELPAR.S	3	80.7	95.5	105.2	134.6	117.3	121.6	76.1	88.6
MSMEG	MSMEG	R.DPRRDGEHALSAGNPVG									
_3244	3254	VVPR.A	2	17.8	21.4	64.4	61.4	21.6	39.7	60.3	47.2
MSMEG	MSMEG										
_3246	3257	R.FAELSALETEVATLSER.L	2	120.1	117.7	188.2	194.4	97.6	94.7	188.1	177.1
		R.FAELSALETEVATLSER.L	3	28.7	29.6	34.7	37.9	25.3	22.3	35.8	37.9
		R.IAPIVILTAFSQR.E	2	53.3	53.9	100.7	95.6	32.5	34.6	74.6	83.6
		R.LDLAEMLR.E	2	21.6	21.2	30.2	30.4	13.2	14.4	23.4	25.4
		R.VAEVVLETLDLDTK.Q	2	175.1	200.3	280.2	350.7	162.6	165.2	277.2	287.7
		R.VLIAEDEALIR.L	2	97.4	100.2	175.5	163.6	131.7	99.9	151.1	177.0
MSMEG	MSMEG	K.ATGVAPQIVDEPFIIGVVG									
_3247	3258	PAFSGETK.A	2	124.8	159.8	647.2	735.5	111.2	190.3	611.6	779.0
		K.ATGVAPQIVDEPFIIGVVG									
		PAFSGETK.A	3	359.7	347.0	1516.6	1506.4	595.5	660.4	2064.5	2290.8
		K.DGGVEATFISADGTKDPE									
		FVK.Q	3	133.4	149.6	224.1	242.3	316.0	359.0	457.7	427.3
		K.FGQEPGTYSTEGYDLGTI									
		LLK.G	2	297.1	302.3	691.3	694.0	498.1	448.3	755.3	694.5
		K.GAAPDSVFYSGYYSEAAP									
		FVQQLK.D	2	118.1	140.5	270.9	325.3	214.9	194.1	307.1	288.8
		K.GAAPDSVFYSGYYSEAAP									
		FVQQLK.D	3	244.6	234.0	379.8	356.4	365.5	374.8	424.6	439.5
		K.GALLSC#PC#GPATAEFA									
		EEYTQK.F	2	94.8	111.0	250.6	330.9	173.8	202.2	279.2	316.2
		K.GALLSC*PC*GPATAEFAE									
		EYTQK.F	2	94.8	111.0	250.6	330.9	173.7	202.2	278.9	316.2
		K.GALLSC*PC*GPATAEFAE									
		EYTQK.F	3	64.5	81.5	210.0	231.5	155.2	176.6	248.7	268.9
		K.VC#VVDDSTDYGLGLAEA									
		VR.T	2	249.3	227.1	552.3	520.4	765.8	688.1	674.4	656.4
		K.VC#VVDDSTDYGLGLAEA									
		VR.T	2	246.9	215.9	546.6	501.2	735.0	662.2	656.0	639.3
		R.GLANDGVQGPPSVANYMK.									
		N	2	353.8	371.1	748.1	843.9	341.8	362.9	507.6	552.9

		R.TTLGPVADASC#NISVK.K	2	307.5	272.3	797.2	703.7	659.4	648.7	1089.4	1100.1
MSMEG _3253	MSMEG 3264	R.TTLGPVADASC*NISVK.K	2	310.9	275.4	801.4	708.8	660.7	650.9	1089.5	1101.2
		K.TLPAVWDLAAPSTVLAVR.									
		S	2	40.5	43.3	93.9	105.4	55.5	63.6	103.7	112.7
		R.GFWQGYFAAR.S	2	16.3	11.4	10.1	11.2	20.8	23.9	10.1	15.3
		R.LEPVHAVTYFSGESR.S	2	60.1	56.6	38.6	32.0	66.4	70.8	29.4	35.2
		R.LEPVHAVTYFSGESR.S	3	37.3	43.0	59.5	50.2	55.6	56.3	54.0	55.6
MSMEG _3255	MSMEG 3266	R.LVVAAAGDIPVDTPMGLR.R	2	512.0	584.3	787.9	830.8	412.9	445.2	768.0	798.9
		K.VTASVAAAALPAGAAAASESI									
		ADSAVAEK.L	3	63.6	87.2	234.2	258.3	33.5	37.4	212.9	246.1
MSMEG _3257	MSMEG 3269	R.LTAAALALSVPGLSH									
		SFWK.E	3	58.7	61.4	122.7	123.0	38.0	35.2	105.2	105.3
MSMEG _3278	MSMEG 3290	R.GADGLTLVPYLEGER.S	2	136.7	133.4	114.5	113.2	150.5	143.8	168.3	159.0
		R.PVDVPPPGEYVALGAAR.									
		Q	2	396.5	387.0	289.3	315.0	241.3	265.1	121.8	171.1
		R.SASSADDLVSELGGPDE									
		WAK.T	2	207.1	219.8	82.2	109.7	152.7	173.2	92.9	107.9
MSMEG _3280	MSMEG 3293	K.VSVTVQLDAR	2	0.0	0.3	2.5	3.1	0.3	0.1	1.7	1.4
		R.NFLGEGSSITLVGLDGAD									
		R.T	2	30.4	32.7	48.1	50.7	34.3	33.3	46.6	45.5
		R.VPILGSLVR.R	2	23.8	21.5	29.5	27.0	25.4	24.7	23.3	24.8
MSMEG _3284	MSMEG 3296	K.IDDLWDPAFK.G	2	5.4	4.4	26.9	33.0	24.9	26.1	21.0	33.0
		K.LVAFTQFVPVLSDMTDEL									
		AK.I	2	37.8	39.0	206.4	200.4	21.8	26.7	125.8	182.8
		R.KQDIGADLVVPTEFMAAR.									
		L	2	75.9	69.4	85.7	104.9	95.5	98.9	27.2	57.2
		R.LMGLNWLNEINESR.V	2	51.2	49.8	168.7	155.5	51.3	52.8	103.5	95.1
MSMEG 3287	MSMEG 3299	R.LLQLQPSNVSTTVR.H	2	19.7	23.2	50.7	61.6	12.9	16.2	38.9	53.0
		R.VGELVEDVVALIDASGAD									
		R.V	2	69.1	78.6	70.3	83.9	95.8	110.5	64.2	83.8

		R.VGELVEDVVALIDASGAD									
		R.V	3	13.4	12.1	20.1	19.5	16.3	18.8	15.6	17.3
MSMEG	MSMEG	K.VIAAEPAAC#PSITQGEYR.									
_3309	3318	Y	2	116.4	88.2	58.2	38.7	79.3	110.8	79.2	111.8
		K.VIAAEPAAC*PSITQGEYR.									
		Y	2	116.4	88.2	58.2	38.7	79.3	110.8	79.2	111.8
MSMEG	MSMEG										
_3379	3385	K.AGVASLIDSMAVELAR.H	2	30.5	32.5	33.7	33.2	20.7	20.3	21.3	25.3
MSMEG	MSMEG										
_3380	3387	R.GLVEDIVPDPTGAFYLK.L	2	163.2	180.8	144.1	149.0	114.3	131.9	234.2	219.2
MSMEG	MSMEG	K.AWLDYVHVIGQTSPAAQG									
_3381	3388	VC#PLK.G	3	175.1	182.1	214.8	216.9	117.0	126.9	269.6	281.0
MSMEG	MSMEG										
_3394	3400	K.VISLADAPEIPGR.R	2	11.7	9.4	3.3	4.9	13.8	17.8	1.6	3.6
MSMEG	MSMEG	R.GAPVDFPLNGVVAGFQK.									
_3434	3442	A	2	91.1	85.6	36.5	45.9	109.5	114.2	74.4	82.8
MSMEG	MSMEG	K.DGAGAGTIPDPFGGPGR.									
_3461	3467	N	2	328.1	324.9	581.8	537.8	499.8	473.2	698.6	635.1
		K.DGGYNVTVPFAPGR.T	2	172.3	156.5	486.1	463.9	143.3	156.3	482.6	488.6
		K.GPDTITSGLEVWWTNTPT									
		K.W	2	162.3	90.8	315.3	212.5	84.6	234.7	286.6	418.7
		K.NWDVNEPAELATVLPVLE									
		R.I	2	66.0	68.3	192.6	184.0	61.4	71.0	189.5	214.7
		K.STVLDSGLSTGQLIK.T	2	198.8	212.1	628.8	635.0	222.5	201.1	711.7	664.3
		K.THGAGDASLVGPEPEAAP									
		IEQQGLGWK.S	3	209.2	225.2	658.7	649.7	154.8	210.5	415.3	568.4
		K.VSLADLIVLAGSAAIEK.A	2	71.9	72.1	191.4	196.8	84.5	78.4	237.6	223.9
		K.VSLADLIVLAGSAAIEK.A	3	25.7	24.5	63.0	57.1	37.0	29.2	93.9	75.2
		K.WTATANDLVFGSHSVLR.									
		A	2	24.5	24.9	198.6	196.8	33.3	36.8	228.2	216.9
		K.WTATANDLVFGSHSVLR.									
		A	3	133.4	114.5	141.7	119.9	133.9	142.0	209.6	145.4
		R.AVAEVYAQSDNGER.F	2	6.3	5.0	23.4	17.0	3.8	5.1	17.5	21.5
		R.AYFLGVTAPQLTALVGGL									
		R.A	2	110.9	114.9	231.6	226.1	109.4	139.0	276.3	314.5
		R.AYFLGVTAPQLTALVGGL									
		R.A	3	11.2	17.1	25.4	33.7	18.0	18.1	35.7	40.0



		R.EDIWEPEEILFGEEDEWL								
		GTDKR.Y	3	26.6	44.5	61.4	97.5	18.5	40.8	109.1
		R.FAPINSWPDNVSLDK.A	2	363.2	359.3	672.5	657.8	313.7	317.5	686.1
		R.IQQDFNASASGGK.K	2	6.3	4.1	19.6	12.1	3.0	2.9	13.1
		R.LHPHPPQGNPLGEDFDYA								
		EEFAK.L	3	239.6	244.6	531.4	486.8	207.9	220.7	452.8
		R.LHPHPPQGNPLGEDFDYA								
		EEFAK.L	4	73.3	45.9	186.9	123.3	99.8	10.1	44.8
		R.NPTMLVTDISMR.V	2	50.7	54.1	201.4	164.3	52.1	34.2	137.1
		R.NQDWWPQNQIDVSR.L	2	130.7	138.0	277.6	303.9	108.1	128.3	323.1
		R.TDASQENTDVESFAVLEP								
		R.A	2	123.0	113.9	179.6	187.3	105.1	121.9	224.1
		R.WLDHPEELSEAF.A	2	83.2	71.0	148.2	138.8	76.6	93.5	179.4
		R.WLDHPEELSEAF.A	3	40.9	39.3	88.1	84.4	49.4	45.1	109.6
MSMEG	MSMEG									
_3465	3471	R.VITAAPNFAYEWTAQR.G	2	1623.0	1669.7	92.2	71.0	978.8	993.6	65.0
MSMEG	MSMEG									
_3478	3483	K.APTLADTAMFAR.H	2	60.3	51.5	49.7	48.1	45.8	46.6	47.1
		K.TFAHYVAQDVHYLR.D	3	52.9	58.0	51.9	56.8	38.6	41.4	46.5
		K.TFAHYVAQDVHYLR.D	4	39.4	33.0	20.8	22.9	29.1	25.8	22.0
		R.LGATLGETEQATAQR.H	2	23.7	19.6	22.7	19.9	20.4	13.7	18.5
MSMEG	MSMEG									
_3479	3484	K.AASSGATVLC#VSK.D	2	8.9	7.7	7.6	6.3	11.9	7.7	4.9
		K.AASSGATVLC*VSK.D	2	8.9	7.7	7.6	6.3	11.9	7.7	4.9
		K.SVLLNIFPSVDTPVC#ATS								
		VR.T	2	543.2	771.5	713.2	993.7	993.7	947.5	827.9
		K.SVLLNIFPSVDTPVC#ATS								
		VR.T	3	227.3	170.5	307.6	223.3	316.1	388.1	367.2
		K.SVLLNIFPSVDTPVC*ATS								
		VR.T	2	575.2	806.5	843.1	1129.4	1089.5	1040.6	1068.8
		K.SVLLNIFPSVDTPVC*ATS								
		VR.T	3	229.9	173.8	341.3	259.2	329.6	407.8	434.4
		R.FC#GAEGIENVTTASAFR.								
		S	2	870.5	887.4	1059.0	1049.3	992.2	1061.7	1055.3
		R.FC#GAEGIENVTTASAFR.								
		S	3	116.7	88.0	116.8	98.3	124.1	120.9	92.3

		R.FC*GAEGIENVTTASAFR.S	2	98.3	115.4	172.2	193.2	203.9	227.5	328.9	322.1
		R.FCGAEGIENVTTASAFR.S	2	98.5	115.4	172.2	193.2	205.4	230.4	329.7	322.1
		R.GNPINTVGELPAVGSSAP									
		GFTLTGTDLGEVTNDQFSG									
		K.S	3	752.5	737.0	732.8	798.8	650.3	928.0	493.4	694.6
		R.SSFGEDFGITIADGPM*AG									
		LLGR.A	2	62.9	65.4	47.2	50.6	69.8	60.9	41.7	34.1
		R.SSFGEDFGITIADGPMAG									
		LLGR.A	2	68.5	65.4	60.1	55.8	91.2	83.3	64.6	56.9
MSMEG	MSMEG										
_3489	3494	R.AVKPDDSLVVFYGSR.N	2	18.4	0.0	172.5	0.0	10.8	13.4	153.1	137.5
		R.GSIFADLTPR.A	2	5.1	5.2	9.0	6.8	11.5	11.4	7.0	11.2
MSMEG	MSMEG										
_3500	3504	K.LAAEQLIVDLR.S	2	7.0	5.9	5.3	6.1	11.2	14.4	7.0	8.1
		R.LAVGSALFGLVR.A	2	5.3	4.2	0.7	1.1	11.2	9.1	2.5	3.3
MSMEG	MSMEG										
_3505	3509	R.HLNAVITDLFER.G	2	210.2	202.9	247.8	255.1	74.4	80.4	171.9	175.2
MSMEG	MSMEG										
_3507	3511	K.GLAEEDGVQLMK.P	2	209.8	211.6	151.4	139.5	159.9	145.7	77.2	80.6
		K.GLAEEDGVQLMKPMPTL									
		DDLLAR.G	3	90.0	107.7	100.9	119.0	120.5	120.3	100.1	112.6
		K.LLAQNTGVASFSA.A	2	1205.3	1374.4	1401.5	1550.9	1439.4	1511.4	1146.7	1215.0
		K.LSLPTVANHYK.S	3	66.5	39.3	37.6	18.2	66.7	70.6	11.4	12.0
		K.M#TSGQGFIALDQSGGS									
		TPK.A	2	93.0	95.4	102.9	110.9	87.8	81.6	39.3	47.0
		K.M*TSGQGFIALDQSGGS									
		TPK.A	2	92.9	95.4	102.9	110.9	87.8	81.6	39.3	47.0
		K.MTSGQGFIALDQSGGST									
		PK.A	2	152.2	158.7	132.0	138.5	225.5	216.1	99.8	92.8
		K.PMPTLDDLLAR.G	2	130.4	134.5	162.8	165.2	96.5	99.4	19.2	22.5
		R.LYGVEESAYSNEDEMFDL									
		IHQMR.S	3	328.1	356.0	320.8	320.4	390.7	408.4	176.9	161.7
		R.SVIGAANPTGVAAVVAQQ									
		FEVAK.Q	2	402.9	434.4	549.8	551.4	497.9	503.4	369.6	351.4

		R.SVIGAANPTGVAAVVAQQ									
		FEVAK.Q	3	546.5	546.7	671.8	683.0	725.6	692.3	450.0	437.5
		R.TIEGKPSATYLWEDK.G	2	96.3	99.7	71.8	82.7	73.6	88.6	62.6	86.5
		R.VLAAILFEQTM*DR.T	2	142.7	146.1	293.0	276.4	251.5	221.6	243.6	199.5
		R.VLAAILFEQTMDR.T	2	469.7	467.6	624.4	610.0	543.2	512.6	369.4	335.9
MSMEG	MSMEG	R.YEPAAADAYGQLLDVLR.									
_3512	3516	D	2	93.9	86.8	98.9	85.5	121.9	79.4	133.3	110.6
MSMEG	MSMEG										
_3515	3518	K.AAGGGSIIINVSSIEGLR.G	2	57.1	67.0	43.7	60.5	40.9	56.2	41.7	44.9
MSMEG	MSMEG	K.LGDALYAAQC#VSRPPGS									
_3564	3564	A	2	155.7	189.3	517.8	593.5	342.9	351.1	528.7	498.6
		K.LGDALYAAQC*VSRPPGS									
		A	2	103.9	120.4	737.6	826.5	218.6	220.6	752.7	709.1
		K.LGDALYAAQC*VSRPPGS									
		A	3	40.5	43.1	164.7	187.7	81.7	89.1	161.6	169.6
		K.LLNEQLTSELTAINQYFLH									
		SK.M	3	255.1	246.5	1402.8	1382.7	615.9	692.4	1476.8	1472.1
		K.M#QDNWGFTELAEHTR.A	2	0.2	0.1	5.1	6.4	0.2	0.3	3.1	2.6
		K.M#QDNWGFTELAEHTR.A	3	51.2	46.7	240.3	230.1	83.7	77.9	146.8	138.5
		K.M*QDNWGFTELAEHTR.A	3	36.2	36.7	192.5	175.8	79.5	70.8	146.8	138.5
		K.MQDNWGFTELAEHTR.A	3	36.0	36.4	194.4	175.8	79.3	82.5	182.6	182.7
		R.ILLLDGLPNYQR.L	2	154.5	170.7	912.5	973.9	307.2	289.7	922.4	871.3
		R.ILLLDGLPNYQR.L	3	0.0	0.0	5.6	8.6	0.0	0.0	0.9	5.3
		R.LLEQILADEETHIDYLETQL									
		QLMDK.L	3	3.7	4.7	15.0	18.9	12.9	16.2	15.1	21.1
MSMEG	MSMEG										
_3569	3569	R.TDALANIALLR.R	2	11.9	11.6	4.4	3.4	6.8	6.8	4.9	6.1
MSMEG	MSMEG										
_3574	3574	K.AWDAFDPVDLAASLTR.A	2	103.5	94.1	98.8	98.1	67.7	63.3	107.2	105.0
		R.GPLNFYSLYR.A	2	56.4	65.7	5.8	10.7	116.0	110.7	1.3	5.4
MSMEG	MSMEG	R.EALDDGDEPFGSVLVDHT									
_3575	3576	GTTLFEDR.N	3	71.1	74.8	90.3	94.1	74.6	64.4	95.5	92.4
MSMEG	MSMEG	K.WETFLTQELPAWLEANR.									
_3580	3581	G	2	261.3	224.5	4.5	5.2	173.0	149.5	2.4	8.1

		R.NDPMVNINQLVANNT.R.L	2	60.4	65.8	9.3	5.5	33.2	41.6	6.2	3.5
		R.VQFQGGGPHAVYLLDGL									
		R.A	3	152.0	150.9	21.7	19.4	94.6	99.8	20.5	22.5
MSMEG	MSMEG										
_3595	3599	R.LADRPGGWVGLAR.L	3	12.0	7.9	9.4	5.3	7.2	8.9	9.2	10.2
MSMEG	MSMEG	R.AIGDDDLTPEILTDFVTAL									
_3596	3600	HK.A	3	17.2	19.4	29.1	31.4	13.6	16.6	29.3	29.7
		R.AMTDVLAAFDDAAR.E	2	9.3	8.6	6.9	8.5	8.0	7.3	6.1	6.8
		R.GVSSIVLDPNNDLSR.L	2	16.9	19.7	18.6	20.6	10.4	14.2	14.3	18.3
		R.HC#LEHDTVEELTR.L	3	2.6	1.5	1.9	1.4	0.9	1.8	0.6	1.5
MSMEG	MSMEG	R.TGVPIVGIDGIEDGLNAVK.									
_3598	3602	S	2	110.4	96.2	173.8	176.1	147.3	130.4	167.4	157.8
MSMEG	MSMEG										
_3609	3614	R.INVAPGSSVSQVADAVK.I	2	27.6	29.3	41.3	41.0	28.9	26.5	79.9	88.4
MSMEG	MSMEG	K.FTDANKPAGQIWAGVVG									
_3618	3624	QPVPAGTPR.G	3	607.4	575.5	788.1	784.8	379.0	399.9	599.0	724.3
		K.TVAEGAEPNDTSVLLGR.									
		L	2	512.0	521.4	520.7	552.6	345.8	384.8	419.7	516.1
MSMEG	MSMEG	K.AALSDWTAGQADFFGTR.									
_3619	3625	G	2	248.8	249.9	51.7	58.1	196.5	210.1	48.5	46.3
		R.LALFLSTPAAR.H	2	75.7	81.1	38.4	44.8	63.6	73.7	79.0	80.9
MSMEG	MSMEG										
_3620	3626	K.AITTLDVVSR.G	2	9.0	10.4	0.9	1.6	4.0	5.7	0.4	0.4
		K.LDEALQIILPMLK.G	2	229.0	218.4	238.9	211.0	78.1	72.1	100.9	86.0
		R.FRDIPLMIGGSGEK.K	3	101.1	105.9	38.6	37.8	48.9	56.7	15.7	19.6
		R.HFDHLNVIAGFDELAR.K	3	154.1	154.5	115.0	118.9	48.2	51.3	58.6	52.0
		R.HFDHLNVIAGFDELAR.K	4	27.9	25.2	2.7	1.3	5.5	5.6	0.0	1.1
		R.LALQIPNFSYGTGVEELFP									
		TVIAQAK.E	3	629.4	723.2	538.9	657.0	246.7	347.0	347.8	478.7
		R.PGDITAIGEALKPLISG	2	49.3	43.4	32.2	39.8	6.2	6.7	24.1	18.5
		R.VQLGTLVTGNTYR.N	2	747.2	762.9	358.7	391.2	552.3	491.8	249.3	258.6
MSMEG	MSMEG										
_3621	3627	K.DLAEQSGVELDR.A	2	25.6	26.5	31.6	30.4	21.6	30.9	35.5	40.9
		R.TRIEEELEEIAAAVQDTEK.A	3	21.5	19.9	7.0	6.5	35.6	27.1	9.3	14.7
MSMEG	MSMEG	R.AERPTALISLTEDPTAGPV									
_3623	3628	LDWVR.E	3	223.3	239.4	328.9	344.4	391.1	310.8	434.5	418.4

MSMEG	MSMEG										
_3625	3631	K.GNTVSADSMWEQLR.G	2	135.6	138.6	160.8	158.7	136.3	121.0	79.8	70.0
		K.LADLVLWEPAFFGVR.P	2	23.0	28.1	94.1	119.4	6.7	14.0	37.2	55.8
		R.M#LES LDSWPMNIVLLGK.									
		G	2	12.4	17.8	18.2	21.3	4.3	14.9	2.3	6.0
		R.MLES LDSWPMNIVLLGK.									
		G	2	96.2	66.4	72.1	90.5	43.1	63.3	34.6	65.6
		R.SGGPELAGDEAVFGGK.									
		V	2	75.2	55.1	226.5	184.2	53.8	41.7	153.4	103.2
		R.SNYAALFGPTTGDR.I	2	33.7	43.1	141.2	150.1	13.3	17.8	73.5	67.9
MSMEG	MSMEG										
_3627	3633	R.LLISYAAELAR.R	2	4.2	5.5	10.1	9.3	8.6	7.5	16.9	16.5
MSMEG	MSMEG	K.GFDSEIGLNYTELGPDGG									
_3628	3634	R.A	2	86.5	92.3	66.7	64.1	63.5	73.0	58.5	64.1
		R.AIGSGTVTAVSTPIHR.G	2	31.2	21.9	22.8	14.9	25.8	27.2	22.2	21.7
MSMEG	MSMEG	K.ATVGLASGALGATPSDAA									
_3632	3638	DFIEAVR.R	2	141.4	148.7	183.3	204.8	162.1	130.1	176.3	169.3
		K.ATVGLASGALGATPSDAA									
		DFIEAVR.R	3	229.4	202.8	272.2	256.5	267.7	223.7	350.6	309.3
		K.SALDLGVPVTGIAEAVFAR									
		.A	2	776.4	717.0	1110.7	1052.8	741.0	650.4	1052.0	932.6
		K.SALDLGVPVTGIAEAVFAR									
		.A	3	36.4	44.8	24.7	34.3	40.5	44.0	32.5	34.8
		K.TGKPLVDVIVDEAEQK.G	2	167.2	199.6	667.2	798.3	195.2	224.1	473.3	551.5
		K.TGKPLVDVIVDEAEQK.G	3	152.9	123.1	138.6	126.2	181.7	147.9	174.9	151.0
		R.GDLDSFLVEITAK.V	2	73.7	60.6	77.2	70.1	102.3	74.8	105.6	90.6
		R.IKDAYDAEPDLPTLLAAPY									
		FR.D	3	208.4	186.8	286.0	262.6	391.1	305.1	589.2	488.4
		R.LPAALIQGLR.D	2	44.0	33.6	91.7	76.8	73.7	71.8	79.5	66.4
		R.SETIAEFIDALEKPR.K	2	316.1	309.0	440.6	438.5	292.6	285.6	438.4	399.1
MSMEG	MSMEG	K.VVLGVQSAAGFAEGHPLP									
_3634	3639	AGW	2	120.3	122.2	68.1	73.3	83.6	82.9	58.7	66.6
		R.DIALSDFVTAPVGTDPRE	2	251.4	227.2	224.9	211.3	178.7	183.9	298.9	248.4
		R.DLIEAGASIVK.V	2	56.1	43.9	30.8	25.3	43.1	29.1	46.3	49.8

MSMEG _3640	MSMEG 3646	R.GGVEDLLDHITSGVR.S	3	60.5	50.4	22.6	21.0	35.3	33.9	34.1	29.0
		R.RGGIVVLPQDLPIAVSET									
		VDFVK.S	3	202.3	190.7	127.4	146.7	170.7	151.9	214.2	185.8
		K.GMWAMTDLADMVEQK.									
		I	2	73.1	73.6	39.2	46.0	25.3	34.2	14.3	21.5
		K.IDDGALEVALGDDK.V	2	359.8	343.0	196.2	184.9	215.9	202.5	189.5	193.2
		K.TPDGEGELTLPGR.S	2	51.9	40.3	19.5	11.9	26.9	25.8	10.9	10.0
		K.VLHDFITNEALPGTGVPD									
		DSFWSGVDK.V	3	1086.0	1293.6	468.5	535.2	588.2	918.6	339.3	551.6
		K.VPDIHDVALM*EDR.A	2	24.8	18.6	34.1	30.6	14.1	8.6	43.1	50.2
		K.VPDIHDVALM*EDR.A	3	62.6	41.1	45.5	30.2	40.6	20.5	28.4	22.5
		K.VPDIHDVALMEDR.A	2	187.9	203.1	177.3	180.2	133.6	136.3	167.6	146.3
		K.VPDIHDVALMEDR.A	3	388.5	357.3	210.6	190.0	249.9	234.1	178.6	171.4
		R.GFLDEVVPLAEGSWSEAT									
		GLK.I	2	394.4	425.3	197.1	209.6	264.1	335.5	187.3	259.7
		R.GFLDEVVPLAEGSWSEAT									
		GLK.I	3	305.6	391.1	125.2	154.2	207.2	274.4	130.3	171.6
		R.HGVITEEDVK.T	2	0.4	0.2	10.6	7.8	0.1	0.2	7.9	6.7
		R.ISSQLLANWLR.H	2	420.1	394.4	163.7	161.9	413.1	300.0	240.4	189.6
		R.RDELQAQIDK.W	2	2.0	1.2	0.0	0.0	0.7	1.2	0.1	0.1
		R.SHVLEPVPDPVAYK.Q	2	134.5	90.5	71.2	47.0	112.8	38.6	80.2	25.7
MSMEG _3642	MSMEG 3648	R.TGDEIHTSMEAGPM*VR.K	3	1.7	1.3	0.2	0.2	0.7	0.7	0.2	0.3
		R.TGDEIHTSMEAGPMVR.K	2	47.4	32.2	102.3	73.2	21.6	14.2	88.5	50.9
		R.TGDEIHTSMEAGPMVR.K	3	42.8	35.5	13.4	13.1	16.7	19.4	6.9	7.5
		R.VEDVLGLPANTLK.V	2	799.6	848.0	421.5	415.4	766.9	591.5	611.4	452.0
		R.VVFINTGFLDR.T	2	797.1	815.7	441.0	410.7	711.5	532.6	601.9	413.3
		K.ALPTGILDALDAAGR.A	2	229.4	205.9	195.0	173.8	658.4	474.4	325.6	227.2
		K.FFDTVLVR.V	2	148.0	137.2	106.5	89.0	334.3	241.2	181.4	150.3
		K.LNAAAEMEPITWTEFSR.Q	2	349.0	323.1	99.0	87.7	432.4	376.7	75.1	80.7
		K.TFC#IPHGGGGPGVGPVA									
		VR.A	2	11.5	15.0	17.6	31.9	35.4	55.2	8.7	64.2

		K.TFC#IPHGGGGPGVGPVA									
		VR.A	3	97.7	89.9	61.8	72.4	200.3	236.8	69.3	105.7
		R.AATLTAIASANYVAR.R	2	87.6	79.1	368.3	388.7	208.3	206.1	302.4	311.8
		R.APGLAELPPAATEEEALA									
		ELR.A	2	209.1	216.1	202.6	170.3	428.8	443.4	270.3	190.8
		R.APGLAELPPAATEEEALA									
		ELR.A	3	16.8	17.1	73.0	57.6	22.9	29.7	66.5	65.1
		R.ARPLGIEIVTADLSK.G	2	126.1	134.3	100.0	113.1	330.9	279.5	136.0	119.5
		R.ARPLGIEIVTADLSK.G	3	110.3	100.1	62.6	58.6	304.4	238.4	96.0	74.4
		R.GAPHTADC#LLVADWNR									
		PYTR.E	4	30.2	30.2	20.5	19.6	95.4	107.3	25.7	22.9
		R.LVGVSVSDSGSPAYR.L	2	162.8	129.1	137.9	115.3	282.1	211.1	135.9	105.6
		R.NILENPAWYTAYTPYQPEI									
		SQGR.L	3	67.7	82.7	98.5	103.1	107.6	152.6	39.9	75.7
		R.RVHAHADAIASALGDAVV									
		HDK.F	3	5.2	13.1	18.4	19.5	7.8	48.6	5.0	21.2
		R.RVHAHADAIASALGDAVV									
		HDK.F	4	30.5	34.0	13.4	18.3	43.8	96.1	4.8	24.7
		R.VSGGEWPVDDNPLR.G	2	514.4	510.2	624.2	597.4	858.4	813.9	724.8	675.2
		R.VHAHADAIASALGDAVVH									
		DK.F	4	89.5	77.3	41.8	41.1	156.3	181.2	33.8	47.8
MSMEG	MSMEG	R.EPVDSAVLANGDEVQIGK.									
_3647	3653	F	2	346.5	394.7	403.5	412.7	206.6	250.2	236.4	282.3
		R.FLLDQPTTSAGR.H	2	9.2	0.0	1.4	0.0	6.8	8.2	0.3	1.0
		R.HPDSIFLDDVTVSR.R	2	389.7	422.2	581.1	594.9	379.0	356.7	926.6	922.6
		R.HPDSIFLDDVTVSR.R	3	140.9	143.8	192.3	175.6	148.5	145.1	194.7	180.8
MSMEG	MSMEG	R.VEAGTLDEALGGLLDAEG									
_3648	3654	YR.A	2	680.1	824.6	832.2	961.3	611.1	681.4	793.3	796.3
		R.VEAGTLDEALGGLLDAEG									
		YR.A	3	72.1	53.8	81.7	63.2	63.2	67.5	68.1	74.3
MSMEG	MSMEG										
_3654	3660	K.LEDLAGASDITQFLAIAR.E	2	63.4	66.0	75.5	82.8	72.1	62.0	94.0	101.5
		K.LGVSPIPPNTPNIR.K	2	97.3	97.1	93.6	84.2	96.9	89.7	122.2	128.4
		K.TGQPVLVGTHDVAESEEL									
		HEK.L	3	73.4	69.3	84.2	86.1	58.3	66.7	109.2	126.9
		K.TGQPVLVGTHDVAESEEL									
		HEK.L	4	103.5	99.7	70.5	76.3	69.2	86.5	73.1	92.4

		K.TLAGAIAAAGYALGGR.R	2	47.3	48.2	81.0	73.6	52.8	48.1	98.2	70.0
		R.TTGLRPFDVQLLAALR.M	3	21.8	22.4	21.7	24.0	19.0	25.7	23.0	41.7
		R.VHVITINDYLAR.R	3	16.6	12.2	75.0	62.5	15.2	12.9	86.4	65.3
MSMEG	MSMEG	R.VPLSGPDGRPLLEEVD									
_3673	3679	DVR.A	3	16.1	20.8	47.0	56.6	26.9	20.0	50.7	49.2
MSMEG	MSMEG										
_3710	3716	R.GPPLPSTVGALER.K	2	14.1	0.0	4.2	0.0	0.9	2.1	1.1	1.4
MSMEG	MSMEG	R.VRLEKVFDC*GDPLLLNR.									
_3715	3722	F	2	29.7	29.2	64.0	69.8	21.4	22.6	49.4	50.5
MSMEG	MSMEG	K.AGVELDDGPAHVDDFAVV									
_3740	3746	DTVPGK.T	3	82.3	99.5	79.2	91.2	93.0	94.9	77.4	91.5
		R.LLAAVDFPVQELVR.T	2	48.4	48.2	84.9	80.3	65.9	59.5	87.9	85.1
MSMEG	MSMEG										
_3745	3751	R.VLVDLDSTPGFSDESVR.V	2	66.4	73.5	47.1	54.0	35.7	23.7	27.5	6.0
MSMEG	MSMEG										
_3746	3752	K.HLFVTGGVVSSLGK.G	2	47.9	48.4	99.1	108.3	53.3	57.5	70.2	98.7
		K.VLHREELDAYVVR.R	3	13.6	16.7	16.4	18.0	25.4	25.2	19.0	25.5
		K.YIDLSDAYLSVAEALR.A	2	132.3	124.9	139.1	141.1	170.1	141.4	174.7	139.3
		R.DVDWTEWDDLLR.R	2	25.7	39.5	29.7	43.7	27.6	37.0	25.1	34.9
		R.DVDWTEWDDLLRRVHEP									
		QETVR.I	3	17.7	19.5	621.2	638.6	10.6	9.4	775.7	720.6
		R.NLSGSANVTGQVYSSVI									
		AK.E	2	77.4	77.9	306.2	254.2	84.0	88.3	236.7	263.6
		R.RGEYLGDTVQVIPHITDEI									
		K.S	3	109.3	138.0	126.0	146.4	137.7	146.6	141.4	173.8
		R.RGEYLGDTVQVIPHITDEI									
		K.S	4	24.2	20.6	14.7	13.0	28.8	29.2	12.3	16.2
		R.SIGITPDALILR.C	2	86.2	78.1	759.3	768.2	108.9	86.4	690.9	539.6
		R.SVGITEANSAEFDPK.T	2	114.3	92.0	113.2	87.7	123.6	96.6	117.3	86.2
MSMEG	MSMEG										
_3754	3760	R.SPEAEALTGEDADELR.I	2	60.5	61.5	55.1	42.9	41.6	51.3	20.5	29.3
MSMEG	MSMEG										
_3758	3764	R.GELADLDESTLSAALR.E	2	62.4	75.2	133.0	133.6	55.8	54.5	186.7	175.4
		R.TVAEGGVYVNNAR.V	2	13.8	10.2	10.8	9.9	7.1	5.9	7.9	6.1
MSMEG	MSMEG										
_3767	3773	R.AAPQADVYEYLIR.A	2	33.7	41.8	116.9	110.8	34.5	40.6	117.9	113.0



MSMEG _3770	MSMEG 3776	R.AGIDPWVIDFGEPDKVEG										
		GMER.T	3	3.3	4.1	13.1	12.4	3.8	3.3	7.3	9.1	
		R.GPVFATTISDAAGR.L	2	11.0	12.4	58.4	62.4	12.1	12.3	45.0	43.8	
		R.GVFAPADTWVSTEYLFR.										
		R	2	62.9	69.6	64.2	72.7	25.7	43.8	38.5	68.4	
			R.IDIPGWLAR.T	2	14.0	13.0	10.6	9.9	19.9	13.7	23.1	15.4
			R.TLADHVVALSEAITVR.E	3	2.4	3.5	11.9	13.5	2.7	2.6	8.4	7.3
			K.AIAFAEENAIPIVTK.R	2	1988.1	2071.0	357.4	370.8	1836.9	1954.9	369.7	398.9
			K.GVPVSIDGRPVSVLQAIEE									
			LNR.R	3	226.4	221.9	136.0	142.4	154.6	140.8	124.2	108.9
			R.ALESFVAHTQEHVSGEIR.									
			L	3	174.9	222.3	66.7	145.0	137.3	110.7	68.4	85.0
			R.AVETGFLEHLWNAPTK.D	2	128.4	115.5	72.7	60.0	105.2	117.1	103.5	102.4
			R.FEVGFASLAPDLQVLAPV									
			R.D	2	314.6	297.6	162.0	167.1	276.0	264.9	194.0	192.3
			R.PVSVLQAIEELNR.R	2	65.7	49.5	20.9	19.0	32.7	24.4	18.7	15.9
		R.SPFSIDQNVWGR.A	2	122.3	114.1	70.6	81.0	121.0	116.7	63.5	89.7	
MSMEG _3773	MSMEG 3779	K.TLSHGIEELGHPLVDK.V	3	35.9	18.2	12.2	10.9	27.2	31.7	21.4	27.5	
MSMEG _3775	MSMEG 3781	K.AAPVQWSQQVLTGTLNR.										
		A	2	378.5	472.6	86.1	97.0	426.6	437.4	102.3	105.6	
		K.TALFGSDANWGR.V	2	27.0	21.3	13.2	14.3	13.5	19.7	7.3	9.0	
		R.TTDLSHAYVEENSAYSS	2	49.9	56.9	15.8	13.7	32.3	38.7	11.1	14.5	
		R.VLAAVGIAPVTLDPQR.I	2	132.9	148.8	203.6	220.3	80.5	89.7	180.7	195.6	
MSMEG _3776	MSMEG 3782	K.VDLLGAEVIGSAR.A	2	19.0	20.7	86.1	96.1	8.9	6.2	62.6	111.9	
MSMEG _3777	MSMEG 3783	R.AAGVEFTFR.A	2	35.7	10.5	12.2	15.1	77.7	20.6	7.9	4.6	
		R.AGAPDWDVTPEELEQTFI										
		R.I	2	138.9	136.2	128.0	121.2	138.5	161.4	141.0	167.3	
		R.DGAGELLEDVR.L	2	25.2	16.9	32.7	15.7	33.5	9.7	20.3	15.1	
		R.EPAGPWGPGRPTEAADA										
		FEAVR.V	3	356.9	370.7	287.9	314.6	376.2	386.2	372.9	390.3	

		R.FGLRPVTGIDPAAVSPW									
		WMQR.R	3	193.3	284.1	52.3	73.1	147.0	278.2	84.6	106.4
		R.GAADVALFGIQQVVQPTD									
		ATK.A	2	90.7	91.6	110.8	104.9	110.8	107.5	121.3	147.1
		R.IGHEVEEIIITAGPVSGPLT									
		VGR.V	3	204.5	252.5	197.1	246.1	218.3	240.6	277.0	263.8
		R.LEGLEIIPSVLPTAPAGR.G	2	236.0	225.7	390.7	396.7	296.3	242.9	389.2	381.5
		R.LFDVYTGPQIGEGR.K	2	298.3	288.9	345.2	338.6	243.9	238.3	377.9	403.9
		R.RPTDEEIAALDASLPR.Q	2	64.8	66.0	48.4	50.6	61.1	92.0	65.0	95.1
		R.RPTDEEIAALDASLPR.Q	3	84.9	82.4	59.6	72.9	106.1	117.8	84.6	118.6
		R.SVDPAISVAALDR.C	2	279.3	243.7	121.7	118.7	401.6	257.8	175.9	117.6
		R.TTQVLNPLESDRPHLATT									
		LLPGLLEALSR.N	4	165.5	203.1	182.4	224.8	197.1	206.2	228.8	258.3
		R.VIEIEELTEFK.K	2	73.7	75.2	74.9	77.4	108.1	78.6	134.1	90.0
MSMEG	MSMEG										
_3778	3784	R.DLPVYIISIGR.T	2	33.4	36.9	18.2	21.0	22.2	28.4	25.5	8.1
MSMEG	MSMEG										
_3791	3797	K.AKEQQLHSLTYAYR.D	3	13.5	5.5	5.9	1.5	20.3	16.3	8.6	5.8
		K.EQQLHSLTYAYR.D	2	8.0	5.6	2.4	1.6	9.6	9.0	3.6	1.9
		K.NLAELAVSDPAAFTALVDV									
		AR.A	2	502.9	564.9	321.6	356.4	446.0	494.3	305.6	308.9
		K.NLAELAVSDPAAFTALVDV									
		AR.A	3	283.4	222.8	184.8	143.2	240.7	278.5	155.3	171.1
		R.AALPEDVNAPSGEAA	2	94.5	86.0	81.3	73.7	90.5	119.4	83.5	95.3
MSMEG	MSMEG										
_3793	3799	R.LGADVAEYGFVETSAK.Q	2	126.6	127.8	335.2	348.7	127.5	115.3	308.9	322.4
		R.LIGPGGEQVGIVR.I	2	187.2	152.1	186.8	148.9	133.7	167.7	153.4	185.5
		R.VAADADLDLVEVAPNARP									
		PVC#K.I	3	269.5	300.1	1921.2	2215.5	401.4	381.5	2035.8	2162.6
		R.VAADADLDLVEVAPNARP									
		PVC*K.I	3	269.5	299.7	1919.6	2208.6	401.4	381.5	2025.2	2162.6
MSMEG	MSMEG	K.EIDVAFPLGVLTSTGVSG									
_3808	3814	SGK.S	2	72.7	65.3	36.0	33.8	80.4	71.3	29.9	39.9
		K.HDIEVVVDR.L	2	3.9	2.9	0.4	0.3	2.7	3.9	0.1	0.6
		R.STVGTITEVYDYLR.L	2	96.4	102.6	95.4	88.3	107.5	83.0	102.1	73.8
		R.VDGVVYPLTDPPK.L	2	32.6	26.5	299.8	257.5	24.5	20.1	337.5	329.9

MSMEG	MSMEG	K.ASVGPMDDNNC#YLVTC#R									
_3810	3815	.S	2	43.5	42.2	40.9	43.7	52.7	64.3	46.9	50.9
		K.ASVGPMDDNNC*YLVTC*R.									
		S	2	42.4	41.6	40.8	43.6	52.7	64.3	46.9	50.9
		R.TVVYPGHGDDTTLGAERP									
		SLAEWR.E	3	68.3	90.6	68.3	64.4	125.3	142.3	69.7	78.9
MSMEG	MSMEG	K.AAGATDIEERPVGAPVD									
_3811	3816	ALVELADEVK.A	3	465.3	462.2	480.4	475.9	245.7	273.8	500.7	521.2
		K.AAGATDIEERPVGAPVD									
		ALVELADEVK.A	4	101.2	70.5	82.6	49.4	41.4	47.7	64.8	69.6
		K.ADLLVVGNVGLSTIAGR.L	2	227.8	369.7	217.1	335.6	109.4	116.3	218.2	207.8
		K.ADLLVVGNVGLSTIAGR.L	3	70.5	43.7	52.4	29.7	36.7	36.2	59.4	50.3
		K.LIIATAYFPQSEDSR.A	2	2020.0	2651.7	2231.4	2786.6	961.8	1038.3	2079.5	2186.3
		K.LIIATAYFPQSEDSR.A	3	121.9	69.3	86.3	49.6	47.9	55.6	71.4	76.7
		K.M#AGNAPIYAILR.E	2	527.9	526.5	413.3	408.0	225.8	225.5	354.3	351.7
		K.MAGNAPIYAILR.E	2	443.3	492.6	508.0	504.2	242.0	220.4	561.8	468.3
		K.TDVLIVHTS	2	4.8	5.0	2.1	1.3	1.2	1.0	0.8	1.5
		R.PVVGAPVDALVELADEVK.									
		A	2	459.0	899.7	422.1	797.2	156.8	144.4	298.6	262.6
		R.PVVGAPVDALVELADEVK.									
		A	3	209.2	159.8	145.0	107.9	59.8	62.0	88.7	88.6
MSMEG	MSMEG	K.TLAAQLANELR.E	2	6.5	8.0	34.8	30.4	13.0	11.0	61.4	39.2
_3816	3820										
MSMEG	MSMEG	R.IAAQATVEER.R	2	10.0	7.8	7.1	5.4	7.7	6.0	6.7	5.0
_3831	3837										
MSMEG	MSMEG	K.FAAAEAEAAANAPVSNSS									
_3833	3838	R.S	2	76.8	54.7	41.8	28.6	76.8	69.4	33.6	32.4
		K.FAAAEAEAAANAPVSNSS									
		R.S	3	14.7	13.3	12.8	12.3	3.3	5.4	2.6	5.1
		K.GGLILDIGLR.G	2	194.1	142.3	110.2	74.8	217.3	165.8	117.6	67.2
		K.HDVDPNEVSVSGDEVEAL									
		VLTK.E	2	135.9	120.8	145.0	127.6	66.5	70.1	81.1	76.9
		K.HDVDPNEVSVSGDEVEAL									
		VLTK.E	3	1059.0	1165.5	940.7	1028.7	1281.8	972.2	1002.7	784.0
		K.VDRDEVLLDIGYK.T	2	485.5	508.4	623.2	626.3	519.7	563.4	545.1	610.5

		K.VDRDEVLLDIGYK.T	3	318.4	272.2	236.4	187.0	294.9	264.5	188.9	166.0
		K.YFNDGDIVEGTIVK.V	2	1861.4	1811.7	1681.5	1660.3	1860.8	1755.7	1532.3	1546.1
		R.AWGTIEELKEKDEAVK.G	2	57.1	53.0	202.8	213.7	125.4	162.0	187.6	402.1
		R.AWGTIEELKEKDEAVK.G	3	148.3	121.3	451.3	403.9	337.6	341.0	552.7	560.4
		R.GFLPASLVEM*R.R	2	155.7	144.2	84.9	75.8	131.6	125.0	45.8	39.5
		R.GFLPASLVEMR.R	2	643.6	583.8	464.4	409.7	426.8	350.2	295.7	229.2
		R.HVEVPDQVVQVGDDAM*VK.V	3	107.0	118.7	145.8	171.4	46.5	47.5	94.4	129.2
		R.HVEVPDQVVQVGDDAMVK.V	2	629.5	651.3	489.8	490.9	334.1	379.0	281.2	374.2
		R.HVEVPDQVVQVGDDAMVK.V	3	553.4	482.2	604.3	530.8	253.3	234.1	251.8	263.7
		R.SEESGGTLASDAQLAALR.E	2	1313.8	1289.1	983.4	971.4	1225.6	1069.0	980.3	922.6
		R.VEEGIEGLVHISELSER.H	2	480.9	404.8	367.4	311.9	564.1	515.0	323.7	310.1
		R.VEEGIEGLVHISELSER.H	3	688.0	603.8	498.8	465.3	774.2	638.9	458.7	381.9
MSMEG	MSMEG	K.AADDTPTLMLLDGNSLAF									
_3839	3843	R.A	2	37.6	46.7	34.1	33.7	34.2	37.9	35.7	49.8
		K.TGYTTDADALQSLFEK.T	2	85.8	85.6	90.9	92.0	107.7	79.2	127.8	107.4
		K.VTVDGLLNSVASDGR.I	2	130.2	161.7	76.9	94.6	119.5	113.3	83.0	81.0
		K.YGLTPQQYPDFAALR.G	2	194.3	178.3	234.2	175.4	179.5	150.0	270.3	159.4
		R.AALNAPIQGSAAIIK.V	2	175.5	166.2	212.6	218.9	168.9	184.3	203.3	229.9
		R.AC#AVLDLADALDQELAR.I	3	16.0	21.3	9.4	13.0	22.5	17.9	20.6	15.5
		R.AC*AVLDLADALDQELAR.I	2	98.6	92.6	46.2	45.3	127.3	96.4	77.8	54.0
		R.AFSVPIDEVTPELR.R	2	141.9	146.7	484.4	573.4	152.0	132.1	552.2	524.6
		R.AFYALPAENFK.T	2	54.1	44.0	48.9	38.4	59.1	47.6	58.3	54.8
		R.DAGLIEAFNTGEDLHSFV									
		ASR.A	3	117.9	105.4	102.7	85.5	148.2	84.2	151.5	92.0
		R.LFDDLEFR.V	2	42.6	37.0	20.3	17.4	44.7	42.9	35.9	24.6
		R.LSSTEPNLQNIPIR.T	2	203.3	205.1	169.3	180.7	187.4	215.1	208.9	224.7
		R.SFTLDDLAVR.Y	2	46.7	36.4	22.8	25.6	51.7	36.8	38.0	29.7

MSMEG	MSMEG										
_3859	3862	K.AGLGAAYLAGFDWGLR.R	2	16.9	19.6	33.8	35.6	15.6	15.1	19.4	16.7
MSMEG	MSMEG										
_3863	3866	K.SEAVEAHAEILDK.S	3	3.4	0.0	5.3	0.0	4.1	3.5	4.7	4.1
		K.YILLTTFTK.D	2	9.0	9.1	14.0	14.1	11.8	11.6	22.5	20.2
MSMEG	MSMEG										
_3864	3867	R.ALDGGFIPSGPSGSPLR.G	2	55.5	52.2	20.3	18.2	34.8	38.6	18.1	20.8
		R.GGQDAEWLTEEQLAR.N	2	24.3	22.8	0.8	2.0	13.1	15.3	1.4	1.4
		R.IGNAVGLDTPASAVALLR.									
		A	2	52.4	47.5	85.6	99.2	35.2	33.5	84.1	80.6
		R.LAGTEC#EIDQVLR.A	2	19.2	21.1	2.6	2.9	11.5	12.9	1.3	3.4
		R.LVDGELEELLAGADIIVVR									
		.I	2	9.9	9.4	7.5	6.0	6.7	6.8	2.0	3.8
		R.LVDGELEELLAGADIIVVR									
		.I	3	6.4	7.0	0.3	0.5	4.1	4.4	0.5	0.7
MSMEG	MSMEG										
_3872	3875	R.LGGAVLAIGNAPTALFR.L	2	20.1	21.7	50.8	51.4	35.2	37.3	58.1	61.3
MSMEG	MSMEG										
_3881	3884	R.LTALVLPADGDPTIVVPR.L	2	148.5	84.2	166.2	112.7	126.0	126.6	194.0	196.1
		R.YALLQQAQQAATAVVRP									
		GVTAEQVDAAR.D	3	156.1	149.1	178.0	185.3	121.4	121.6	185.4	188.1
MSMEG	MSMEG	R.PIGPAGAVQKPQDVNLR.									
3892	3892	D	3	22.1	19.6	7.5	8.0	8.9	11.4	1.7	3.9
MSMEG	MSMEG	R.TTVAGYADSPSDEAFSR.									
_3889	3893	M	2	17.6	19.2	4.6	7.0	4.8	6.7	0.4	2.4
MSMEG	MSMEG										
_3895	3899	K.LYSQVSDADSALK.V	2	23.8	20.0	15.4	11.6	7.0	9.0	17.1	13.6
		K.VAVEALYDAADDDSATGG									
		PDLVR.G	3	338.8	348.4	273.9	269.9	179.1	188.3	269.4	270.6
		R.GIYPTAVTIGAEGAEVPE									
		TR.I	2	204.1	243.9	126.9	138.7	129.3	133.2	101.6	135.9
		R.GNLGAALQGFVALPLLVG									
		YDLDDPHPEGAGR.I	3	121.7	124.7	97.1	105.1	48.5	56.7	66.8	78.7
		R.LYAVELEHYEK.L	2	251.3	192.1	158.8	102.2	180.9	167.5	178.4	171.5
MSMEG	MSMEG	K.AHVGALLDSVDSAVELVE									
_3897	3901	QLTN	2	28.2	30.6	41.2	59.7	19.7	27.8	22.9	39.0

		R.VGIGPSGDEPGFQLSQR.									
		A	2	198.5	201.3	262.4	263.4	194.6	203.9	239.3	269.6
MSMEG	MSMEG	K.AEVEDLVLEEVPDVSYNDI									
_3902	3906	GGLGR.Q	3	339.9	425.5	89.6	129.0	152.0	212.2	59.3	94.8
		K.ASEGTPVIVFFDEMDSIFR									
		.T	2	17.1	24.6	9.2	14.8	0.0	14.7	0.0	7.3
		K.DFNSGAMIQNVVDR.A	2	338.3	332.5	151.7	150.8	302.1	307.9	110.3	115.9
		K.DLPDEPTDYFDDSRPR.K	2	97.6	88.5	25.6	37.8	76.4	94.8	12.8	32.5
		K.IERPDAEAAQDIFSK.Y	2	62.9	65.6	76.7	72.9	40.7	49.7	75.3	75.9
		K.IKIERPDAEAAQDIFSK.Y	2	20.5	24.1	0.9	1.7	22.5	31.5	1.4	2.2
		K.IKIERPDAEAAQDIFSK.Y	3	132.5	132.6	65.3	79.9	125.6	128.6	80.9	85.9
		K.IKIERPDAEAAQDIFSK.Y	4	57.4	51.8	17.2	14.3	63.5	76.5	18.9	17.8
		K.YLTEDLPVHADDLTEFNG									
		DR.A	3	386.4	430.7	252.5	250.8	341.5	331.9	199.1	204.6
		R.DAVELPFLHK.D	2	91.9	75.9	30.5	26.2	104.8	84.1	31.0	30.6
		R.EQLENAVGPQSGLR.S	2	9.7	9.1	27.2	25.8	6.9	9.4	18.4	26.6
		R.IVWLAEPLVAAK.D	2	333.8	320.5	179.7	166.2	400.2	295.1	203.8	160.1
MSMEG	MSMEG										
_3906	3910	R.GIIAFDDVIGLPEGSVVK.S	2	54.9	46.7	84.4	86.2	88.4	85.6	100.3	93.6
		R.HYTMVLNHGGEFHTHR.G	4	5.0	4.2	4.6	3.7	6.3	8.1	4.0	5.5
MSMEG	MSMEG	R.ILELLARFTDDAVAADRI									
_3918	3923	R.L	3	6.7	6.9	75.7	77.1	10.6	16.7	64.2	81.0
MSMEG	MSMEG										
_3932	3937	R.SVTLPPGADEDAIK.A	2	168.0	149.7	3.9	3.7	10.8	13.7	3.5	4.6
MSMEG	MSMEG										
_3945	3950	K.ALEFAFDAASR.R	2	30.4	28.2	0.3	0.3	3.4	2.2	0.7	0.2
		K.ASAIATTAPVVVGVDGSP									
		ASEK.A	2	130.3	131.1	2.5	3.2	27.8	34.2	0.9	2.5
		R.GGFAGLLLGSVSTSVAEA									
		AERPVVVVR.G	4	31.0	34.6	0.1	0.3	2.9	3.6	0.0	0.0
		R.GVLVGVDGSEPSTA									
		AAVE									
		WAAK.E	2	88.5	89.3	30.0	29.2	18.8	22.5	37.8	45.9
		R.LLGSVTAGLIR.H	2	93.5	94.5	0.5	0.2	22.8	21.7	0.6	0.5
MSMEG	MSMEG	K.VVADC#LGETHGLTVQTEI									
_3950	3957	R.K	3	300.8	257.2	11.7	6.2	94.2	96.1	9.2	11.4

		R.GGFTGMLLGSVSSR.V	2	88.0	89.5	5.6	6.6	18.1	18.4	5.2	7.8
		R.LPVLLGIDGSPASEVATSH									
		AFDEASR.R	3	968.8	1006.7	104.4	100.2	334.3	341.3	101.6	98.9
		R.LPVLLGIDGSPASEVATSH									
		AFDEASRR.G	4	30.1	49.1	20.4	15.6	23.9	30.9	22.2	12.9
		R.VLLGSTSTSLHYASGPV									
		VVVHGDDQAAHDSR.L	5	333.4	348.2	10.6	15.8	102.3	97.3	7.8	12.0
MSMEG	MSMEG										
_3962	3970	K.ASGDTPVLFDSGIR.T	2	140.6	149.1	189.9	146.9	478.6	514.7	378.8	405.7
		K.HAGDTPAYFQLYYPEDR.									
		D	2	46.6	75.9	423.9	566.9	366.5	417.5	294.8	384.8
		R.DLSVELWGK.T	2	4.2	5.0	93.3	84.7	153.5	144.9	89.5	87.1
		R.DLTISNFPFLR.G	2	150.7	153.7	729.0	676.4	786.3	844.0	711.1	735.4
		R.GLC*LTNYVTDPVFQK.K	2	106.5	98.9	808.2	842.6	776.4	687.6	912.2	886.0
		R.SLLAEADLIMAVDGYR.N	2	21.1	25.1	163.9	154.7	99.2	95.9	174.5	162.2
		R.TGVPYITSTLAVSSLEDIR.									
		K	2	44.5	46.1	299.2	293.6	240.1	205.0	250.3	222.0
		R.TGVPYITSTLAVSSLEDIR									
		K.H	2	6.4	4.6	245.2	200.6	94.0	94.9	363.2	114.6
MSMEG	MSMEG										
_3980	3987	R.SLIDYLTEFAYASVK.V	2	10.7	12.9	13.7	10.5	8.0	10.4	8.5	8.5
MSMEG	MSMEG										
_4042	4047	R.EDEVTAEGVSR.T	2	2.7	1.9	1.3	0.9	3.9	2.4	2.0	1.1
		R.LQSEGLVQLVR.H	2	104.1	102.6	148.7	142.1	137.0	114.5	129.3	154.0
MSMEG	MSMEG	K.LVSDAAQARAAAESLGYP									
_4075	4082	VVVK.A	3	1.8	2.1	46.5	29.2	10.8	12.1	64.3	61.0
MSMEG	MSMEG										
_4125	4132	R.AEWSSELFQLK.L	2	28.5	27.3	16.1	12.0	39.2	34.0	19.9	18.9
MSMEG	MSMEG										
_4180	4185	K.GALSESAAEILAEAGYR.R	2	75.8	87.4	52.2	57.2	66.9	72.2	50.0	61.3
		R.IATSFPNLVR.K	2	48.5	50.0	47.4	43.8	44.4	44.1	48.8	46.8
MSMEG	MSMEG										
_4185	4189	K.AAIFAIETLFEER.G	2	6.8	5.2	1.2	2.2	25.0	13.7	4.9	3.3
		K.AVAYLLPYIEAEK.K	2	92.9	81.8	419.6	214.3	63.0	59.8	86.7	75.5
		K.ETGLADYIGAFVATAGLG									
		SAEK.I	2	10.4	11.0	2.2	3.3	14.8	13.3	2.4	2.6

MSMEG _4188	MSMEG 4192	K.ETGLADYIGAFVAVTAGLG									
		SAEK.I	3	2.4	3.2	0.7	1.7	3.8	4.1	0.7	1.2
		R.EFENYDLSEL.R.Q	2	66.8	66.9	13.7	18.8	60.1	56.9	12.5	12.7
		R.EGMDIPLLIGGATTSR.A	2	38.2	36.4	11.6	10.4	33.5	35.4	5.4	9.7
		R.LSGLEPLNIDEDSLFVNIG									
		ER.T	3	5.7	10.1	21.6	21.4	5.2	9.8	5.8	6.4
		R.NVSYDQLAEAYLEAAR.G	2	49.1	44.1	13.4	10.9	48.3	48.5	11.3	11.0
		R.TPIDWDGYTPPVPAQGLG									
		IR.E	2	30.6	25.9	2.3	4.2	27.3	32.0	2.2	5.2
		R.WPVIISGTITDASGR.T	2	19.9	23.1	17.5	27.4	29.4	32.3	11.0	22.5
		K.AAVEQFANALR.L	2	23.4	12.5	57.4	39.0	19.0	22.8	47.1	59.4
		K.ADLSTFGEMLSK.L	2	28.1	32.1	15.5	20.5	25.9	27.7	17.3	18.2
		K.LMLVDVDADALK.A	2	30.9	33.3	51.0	59.5	32.8	28.8	27.6	35.1
		R.SATALPEAPDATDVIAR.V	2	248.6	269.5	111.2	130.9	181.1	191.1	120.1	128.0
		R.VLPPHDYVAATDAIAEVVE									
		MVEK.L	3	118.8	127.4	72.1	76.2	65.4	72.0	41.6	56.3
		K.AVLADALGVHLDGFQR.I	3	28.9	30.6	17.4	14.8	17.3	11.9	5.4	7.7
		R.LTEVDYGSWTGR.K	2	71.0	60.2	89.9	63.6	49.5	52.4	79.2	83.0
MSMEG _4199	MSMEG 4204	K.LDLPENATPAYLGFNLFG									
		HAIAR.A	3	97.1	92.8	83.5	74.3	82.9	82.7	89.5	88.6
		R.YYIAVHAVDVEK.L	2	48.2	52.6	121.4	135.6	32.6	28.4	88.4	113.1
MSMEG _4205	MSMEG 4210	R.YYIAVHAVDVEK.L	3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
		R.AC*IKLGVADRDELAR.M	2	60.5	64.0	90.9	100.8	35.6	37.5	71.3	81.1
		-.MIVVGYSADPFGR.A	2	0.4	0.4	73.1	71.9	0.2	0.9	83.1	93.8
MSMEG _4207	MSMEG 4213	R.DTGLLVINATAGDAYVDA									
		R.F	2	18.3	23.7	103.2	103.4	7.2	12.1	113.6	108.0
		R.LLLEC*PKPVLAVKPHGF	3	11.6	10.0	181.7	169.4	22.0	20.0	206.0	186.6
		R.SGEVHDVEAHLQDSGVP									
		FEIR.Q	3	9.8	11.4	662.7	737.9	3.0	9.8	616.9	594.5



MSMEG	MSMEG	R.GTAFGFPPFGALPAGGAEL									
_4208	4214	PTFLSYITEK.R	3	36.9	39.0	83.3	129.4	6.2	29.1	18.7	77.7
MSMEG	MSMEG	K.IAAGTTGLGEFVDQIEAGQ									
_4210	4216	VR.V	2	18.2	22.3	524.4	552.0	32.9	56.2	471.1	466.3
		K.IAAGTTGLGEFVDQIEAGQ									
		VR.V	3	7.9	6.9	358.8	381.1	5.1	1.8	311.5	321.2
		K.MVEEQEGILVPGDSPFR.T	3	41.8	42.2	26.3	35.9	38.8	38.6	14.1	16.7
		K.NGWSDAFTTGPEFEQFL									
		K.D	2	8.0	7.6	146.2	163.7	6.7	6.0	88.2	114.1
		K.VSIGGGSSPGGPDHLFPM									
		ETAR.A	3	11.4	19.0	909.5	1033.2	14.8	24.9	839.1	857.6
		R.DAMVAALTELHDTDEWK.									
		E	2	26.0	22.6	174.9	185.0	22.8	22.9	78.6	106.2
		R.DAMVAALTELHDTDEWK.									
		E	3	0.7	0.4	206.3	203.3	0.7	0.3	137.6	128.5
		R.DAMVAALTELHDTDEWK									
		EAMVK.N	3	97.0	114.1	102.5	105.5	90.9	90.2	173.3	186.1
		R.IEVFNVIGAGGTVAMAR.L	2	11.7	16.7	287.9	242.1	10.4	9.0	295.2	279.4
		R.M#MVPNSPGGGYDLTAR.									
		T	2	9.9	11.8	125.8	131.1	4.8	5.5	84.0	99.4
		R.MM#VPNSPGGGYDLTAR.									
		T	2	9.8	11.8	124.1	130.1	4.8	5.4	82.0	98.3
		R.MMVPNSPGGGYDLTAR.T	2	36.8	40.3	603.8	576.1	48.2	50.1	536.7	552.2
		R.TIDDLVAAWK.A	2	0.3	0.1	318.5	214.3	0.7	0.6	297.1	289.8
		R.TVNYITYDGGGDLLTALLG									
		K.K	2	34.9	42.1	222.6	216.0	8.6	17.6	212.6	199.6
		R.VPGVDAPTLTEAGIDMTF									
		TNWR.G	2	2.8	2.6	175.0	197.6	1.7	5.5	141.2	157.0
		R.VPGVDAPTLTEAGIDMTF									
		TNWR.G	3	49.4	51.7	119.7	128.9	51.1	58.8	78.1	92.6
MSMEG	MSMEG										
_4217	4223	K.TYLESQLEELGQR.G	2	354.1	363.4	568.7	573.9	344.1	323.1	541.3	510.1
		R.AQAEAMVSDAR.Q	2	5.7	3.7	7.7	4.9	1.8	1.1	1.4	0.7

		R.GSAAPVDSSANSASGF									
		GQFNR.G	2	201.5	135.5	316.9	196.2	260.9	256.2	317.0	368.3
		R.GSAAPVDSSANSASGF									
		GQFNR.G	3	101.2	84.3	172.9	125.0	100.1	141.9	141.4	228.9
		R.GYNEDEVDAFLDLVENEL									
		TR.L	2	82.0	97.9	122.7	163.9	24.3	43.5	38.3	67.8
		R.GYNEDEVDAFLDLVENEL									
		TR.L	3	33.7	49.1	53.6	77.9	11.4	22.6	15.5	34.3
		R.LIEENADLR.Q	2	10.5	8.1	11.0	9.4	6.8	5.7	6.8	5.5
MSMEG	MSMEG										
_4222	4228	K.AAEDAKDDIEELLR.G	2	58.8	64.8	221.8	228.0	56.5	54.4	253.9	273.6
		R.KAAEDAKDDIEELLR.G	3	11.3	8.4	12.6	12.4	13.8	12.6	24.7	19.1
		R.LLQMGDAAVSLMDAFR.S	2	106.2	104.2	95.6	91.2	39.4	32.4	41.9	45.3
MSMEG	MSMEG										
_4237	4241	R.MLDQIESALYAEDPK.F	2	27.3	28.2	12.6	15.6	14.5	19.6	12.1	16.6
MSMEG	MSMEG										
_4240	4244	R.DALDVLAAANVHPQAK.A	3	39.6	33.2	17.9	17.2	36.9	41.8	12.1	11.9
		R.PLQLGAAAAADRPDVQEL									
		FHR.I	4	98.9	89.6	79.8	62.8	84.8	81.8	66.7	64.8
		R.SVIEPADAVAGPDVLR.L	2	320.3	355.3	360.4	381.8	227.7	209.4	320.0	327.2
		R.TVLLAEALELADASDPAAA									
		ALLR.R	2	82.8	78.6	75.7	74.1	55.2	75.5	44.3	70.5
		R.TVLLAEALELADASDPAAA									
		ALLR.R	3	60.3	62.3	47.0	63.6	59.3	62.0	53.3	53.0
MSMEG	MSMEG										
_4244	4247	K.LGPTTTPELAVEYVER.L	2	364.5	351.8	262.4	271.1	327.3	331.6	276.4	284.2
MSMEG	MSMEG										
_4251	4254	R.TSVTWSLVSSSLLR.S	2	16.6	20.7	22.2	28.1	16.9	11.6	28.3	21.4
MSMEG	MSMEG										
_4254	4256	K.GC*QLTHSNLLHEIR.G	3	108.2	93.6	161.2	109.4	57.9	53.4	113.9	73.6
		K.SSDPATLIYTS GTTGQPK.									
		G	2	190.8	161.2	149.1	138.9	89.0	94.2	102.0	117.7
		K.VTLGFTSDIK.N	2	23.4	18.2	26.8	11.3	15.8	12.0	15.9	8.2
		R.AALGGEC#HAAISGGAPL									
		GER.L	3	98.6	84.9	107.0	108.0	82.8	79.6	67.3	53.7

		R.AALGGEC*HAAISGGAPL GER.L	3	98.6	84.9	107.0	108.0	82.8	79.6	67.3	53.7
		R.ILPVDFTEDTGELTPTLK.V	2	570.0	588.6	280.4	274.5	353.1	389.0	180.4	177.7
		R.ILVFLPLAHVLAR.A	3	8.5	4.6	6.9	3.5	16.8	8.1	18.1	4.8
		R.SAALGLIAEGVQPGDR.V	2	187.0	169.4	352.0	332.1	175.5	194.1	376.6	424.0
MSMEG	MSMEG	R.AASSLSGGADTLEALGVR									
_4258	4262	.I	2	276.2	245.9	189.6	213.4	207.8	187.7	280.4	206.8
		R.AVEAIDSGAAEQLLAR.W	2	326.4	335.4	212.7	212.4	278.3	258.7	218.7	245.9
MSMEG	MSMEG	R.LTFDPAAFGFK.R	2	92.4	82.1	66.9	60.0	69.3	60.9	80.4	72.3
_4262	4265	K.AVLWTSGWTPR.F	2	103.6	94.8	21.1	10.7	66.5	76.8	8.2	12.9
		K.TVAANLTDALLEGSTLK.R	2	395.8	361.7	242.4	238.5	307.2	308.6	191.6	205.1
		K.VC#SHLGC#PSSLYEQQT YR.I	3	113.4	69.9	104.1	22.1	200.5	240.7	219.8	125.0
		K.VCSHLGCPSSLYEQQTYR .I	3	112.3	71.1	100.6	23.9	197.3	239.9	214.8	124.9
MSMEG	MSMEG	R.ILC*PC*HQSQFDALEFAK. P	3	182.9	185.1	74.1	94.1	149.7	176.2	55.9	80.8
_4263	4266	R.SDREVLEHGVETGIIK.R	3	43.7	44.5	45.3	41.4	52.7	48.2	83.7	73.0
		R.SDREVLEHGVETGIIK.R	4	4.0	0.2	0.0	0.2	16.7	13.2	0.4	0.7
MSMEG	MSMEG	K.IETLGTSSSEIPVLVLPAGK. R	2	98.6	103.3	26.7	30.9	41.7	40.9	44.4	53.2
_4268	4271										
MSMEG	MSMEG	R.EPLSLRPFDYLP.R.P	3	25.7	25.8	8.3	6.1	21.1	16.2	4.5	5.9
_4269	4272	R.LGLDLGIDQR.A	2	28.1	30.3	10.0	14.6	22.9	18.3	16.6	13.5
		R.VPFLDPEVFAVASR.L	2	104.4	96.3	161.7	156.7	112.1	74.3	221.8	145.9
		R.YDEITAALDSVAK.H	2	56.6	71.4	58.1	60.5	62.6	54.1	122.0	115.2
MSMEG	MSMEG	K.FSEQLLADHLQK.V	2	73.9	56.2	43.2	51.8	36.2	37.1	23.9	42.6
_4270	4273	K.FSEQLLADHLQK.V	3	144.9	115.3	16.5	15.8	125.6	110.8	22.1	16.6
		K.LGLAFAADPSQQLAR.L	2	1083.1	1129.9	681.7	710.1	1417.2	1408.9	679.4	669.4
		K.VSLSFLVDDLVIHR.G	3	42.8	38.9	5.8	4.2	15.5	15.8	0.7	1.5

		R.DGTFVHVDVVPETHKEDP									
		TGIGDAFR.A	4	167.0	149.0	212.7	204.1	187.1	172.6	189.6	213.1
MSMEG _4272	MSMEG 4275	R.M*SAPYVQGATIDFVDTIE									
		K.Q	2	26.3	26.0	1.1	1.9	11.4	11.0	0.4	0.6
		R.MSAPYVQGATIDFVDTIEK									
		.Q	2	33.7	33.7	2.8	5.3	20.7	19.0	5.6	4.2
		R.TLDGDLTAIEFGGVTLTVD									
		R.M	2	57.1	61.8	3.7	11.8	41.6	48.1	4.5	6.5
		R.YNLFFDDR.T	2	58.0	56.2	7.3	6.8	38.7	39.6	3.3	4.3
MSMEG _4273	MSMEG 4276	K.NNDDDKNVASDAADSAV									
		DEQNGPAAEDRPR.T	4	13.7	17.2	7.8	10.0	13.1	17.2	6.7	10.2
MSMEG _4276	MSMEG 4280	K.GGIKPVS VWLSHEYVR.A	3	94.6	98.6	159.6	141.2	51.7	58.2	136.0	167.2
		R.LAIPELPEEVFIESLR.Q	2	505.0	445.9	494.7	459.0	303.1	293.9	419.2	379.7
		R.LAIPELPEEVFIESLR.Q	3	40.5	42.9	38.5	49.6	26.5	24.9	44.7	31.9
		R.LVTPELSGSLLPGITR.D	2	460.9	414.1	481.3	452.7	373.3	350.0	469.6	433.7
		R.RLAIPELPEEVFIESLR.Q	3	14.6	13.8	11.9	8.7	32.9	27.2	35.5	23.7
		R.YLLIASPAGAYFK.G	2	78.1	66.7	137.0	146.4	65.9	41.8	79.8	195.0
MSMEG _4278	MSMEG 4281	K.GPGAAAYVNSALTNDLGK									
		.I	2	269.4	260.1	288.7	295.7	126.4	114.1	132.4	140.2
		R.AGVVFDALVA AVR.A	2	75.1	62.2	30.3	26.7	37.1	32.8	23.2	25.2
		R.STVG LFDVSHLGK.A	2	109.7	92.5	170.4	169.2	73.5	71.6	147.5	175.0
		R.VGVTTSGTFSPTLK.V	2	265.5	242.7	211.5	235.9	123.1	121.6	189.4	214.5
MSMEG _4281	MSMEG 4283	K.GITFDTGGISIK.P	2	82.0	77.7	190.4	137.2	55.8	59.5	94.1	109.3
		K.GPGLTAITVLAHDTK.A	2	303.4	237.9	140.4	137.6	138.1	141.9	276.8	285.9
		K.GPGLTAITVLAHDTK.A	3	395.6	269.5	123.0	71.1	205.3	184.6	206.7	159.8
		K.LLTPAPFFDATVVTAIESG									
		LR.A	2	596.9	640.4	237.9	239.1	168.9	255.4	181.8	277.4
		K.LLTPAPFFDATVVTAIESG									
		LR.A	3	333.1	379.9	134.8	159.5	138.3	158.4	143.8	190.8
		K.LSQDVGENGWPMPLPEE									
		LRDDLK.S	3	447.8	423.8	122.6	127.1	163.3	139.4	56.8	64.9
		R.DFVNTPPSHLFPDEFK.R	2	531.6	617.9	153.7	177.4	208.0	225.3	160.8	185.0
		R.FAGMLVAGTYLR.E	2	124.9	103.9	16.6	13.6	22.4	32.1	14.8	24.2
		R.GVDIATAVATAR.D	2	59.0	42.2	17.8	17.2	15.8	12.1	111.9	130.9

MSMEG_4283	MSMEG_4286	R.LILADAIVR.A	2	62.1	41.9	30.8	23.8	28.7	20.5	15.8	12.2
		R.LVVDPALPVGSVLAVGLGK.D	2	1705.9	1623.2	699.8	653.4	678.4	581.7	707.7	608.2
		R.LVVDPALPVGSVLAVGLGK.D	3	146.0	152.3	28.7	28.5	63.3	49.5	39.9	32.3
		K.AEPAPAASSDGSPYVTPLVR.K	2	1581.2	1581.6	2298.1	2277.0	1669.5	1927.3	2454.4	2972.1
		K.AEPAPAASSDGSPYVTPLVR.K	3	258.3	364.5	481.3	567.4	262.4	370.8	580.1	638.3
		K.IGDAGAAAEPKPEPKPEPK.A	3	0.2	0.2	0.1	0.1	0.0	0.0	0.0	0.0
		K.IGDAGAAAEPKPEPKPEPK.A	4	1.3	1.4	0.9	1.1	1.0	1.7	0.7	1.8
		K.IHPNVNASYNEDTK.E	2	2.0	0.7	2.3	0.7	3.0	2.1	4.3	2.9
		K.IHPNVNASYNEDTK.E	3	9.4	5.8	11.5	7.4	8.3	8.8	11.2	11.3
		K.LAAENGIDLSTVK.G	2	138.7	112.2	275.3	251.1	126.3	98.8	282.0	197.7
		K.QAPAAPAAAAAPAAAAATAPALAHLR.G	3	474.5	467.4	662.5	642.0	588.8	741.4	935.7	1100.7
		R.EGVNLTFLPFIR.A	2	70.1	76.1	99.7	110.8	368.3	312.1	525.8	484.0
		R.ESLQATAQLTQTHEVDM#TK.I	3	245.0	231.8	358.2	310.7	203.5	185.2	305.0	264.4
		R.ESLQATAQLTQTHEVDM*TK.I	3	242.9	230.0	357.4	309.6	200.7	183.5	302.5	263.7
		R.ESLQATAQLTQTHEVDMTK.I	2	87.2	80.8	95.4	81.8	71.2	108.8	103.0	138.1
		R.ESLQATAQLTQTHEVDMTK.I	3	838.1	813.0	1122.8	1173.7	705.7	846.3	924.5	1261.3
		R.KLAAENGIDLSTVK.G	2	29.6	27.6	305.0	267.2	55.1	37.6	443.2	326.9
		R.LEEGAFEADLGL	2	7.0	10.6	15.0	19.4	21.7	6.4	27.5	18.1
		R.RLEEGAFEADLGL	2	366.4	370.9	791.3	779.0	536.1	402.8	1207.5	903.3
		R.SVC#YLPLTYDHR.L	2	453.1	416.6	592.0	513.4	449.3	477.5	702.7	679.3
R.SVC*YLPLTYDHR.L	2	452.9	416.6	542.7	466.7	449.3	477.5	694.9	679.3		
R.VIVDEYGNESIGVR.S	2	499.8	461.7	803.9	724.1	633.7	580.4	1056.6	957.3		
MSMEG_4287	MSMEG_4290	R.VIGRPGVIFVGEGAPNR.V	3	47.5	43.4	29.1	17.6	72.9	75.7	31.3	38.1
MSMEG_4288	MSMEG_4292	R.LGLPEDGPGSIAR.T	2	13.7	15.4	6.3	7.0	14.6	20.8	2.6	7.6

MSMEG	MSMEG	K.DGQPLFHDESGYAGLSDI									
_4290	4293	AR.H	2	546.6	628.0	2076.3	2438.5	429.4	496.6	2056.0	2296.7
		K.DGQPLFHDESGYAGLSDI									
		AR.H	3	1281.9	1288.9	5231.3	5510.4	978.5	980.5	4446.5	4487.0
		K.FNTLLAAADDVLLFK.Y	2	452.3	449.3	1924.0	1900.7	475.5	406.0	2028.8	1721.5
		K.FNTLLAAADDVLLFK.Y	3	138.1	179.5	490.6	602.8	193.3	175.4	726.5	687.2
		K.GGYFPVAPYDHYVDLR.D	2	883.4	975.3	2947.7	3292.6	731.6	766.4	2940.5	3067.4
		K.LIKDENVEYVDIR.F	2	474.2	478.9	1675.7	1727.2	505.2	452.1	2068.2	1901.2
		K.LIKDENVEYVDIR.F	3	719.0	736.2	2386.3	2504.4	737.7	693.8	2747.0	2595.3
		K.PLFGDNGSGMHAHQSLW									
		K.D	2	44.5	56.8	142.1	178.2	15.5	22.3	117.4	128.8
		K.PLFGDNGSGMHAHQSLW									
		K.D	3	191.2	167.8	475.9	439.1	83.1	106.4	287.3	373.5
		K.PLFGDNGSGMHAHQSLW									
		K.D	4	196.2	193.9	716.2	671.5	137.8	140.5	639.7	616.5
		K.TLNM#NFFVHDPFTR.E	3	70.7	75.3	154.3	148.7	39.0	42.9	143.3	147.6
		K.TLNMNFFVHDPFTR.E	2	1121.5	1090.0	834.2	844.4	271.1	271.1	712.9	639.6
		K.TLNMNFFVHDPFTR.E	3	30.6	22.5	10.8	12.7	1.9	0.7	16.4	16.5
		R.DQM#ATNLQNAGFTLER.									
		G	2	235.5	265.1	404.4	418.8	141.1	180.1	444.6	426.3
		R.DQM*ATNLQNAGFTLER.									
		G	2	432.4	462.7	1274.3	1222.9	284.5	334.5	981.3	1012.6
		R.DQMATNLQNAGFTLER.G	2	1008.4	1006.7	3346.9	3269.1	601.7	574.9	2193.4	2155.9
		R.DQMATNLQNAGFTLER.G	3	36.6	40.0	133.7	123.7	14.8	18.4	81.1	100.3
		R.GFQSIHESDMMLLPDPNT									
		AR.I	2	96.1	124.0	308.6	368.5	6.1	12.2	66.7	105.0
		R.GFQSIHESDMMLLPDPNT									
		AR.I	3	499.0	456.6	1837.3	1755.9	180.9	188.1	876.4	863.9
		R.GHHEVGTAGQAEINYK.F	2	25.9	14.3	86.3	51.6	26.2	16.9	106.5	72.8
		R.GHHEVGTAGQAEINYK.F	3	202.0	157.4	565.5	466.3	166.5	163.9	531.0	556.8
		R.LVPGYEAPINLVYSQR.N	2	2293.8	2357.9	8525.9	8595.4	1951.0	2008.7	8551.6	8802.9
		R.LVPGYEAPINLVYSQR.N	3	507.3	484.9	1640.8	1647.5	491.0	477.3	1921.8	1841.6

		R.PHPYEFSLYYDV	2	225.2	235.0	1300.0	1506.7	183.1	186.7	1365.2	1307.1
MSMEG	MSMEG	R.RPSWNAAPGSVAEPLV									
_4291	4294	TEFTEALR.R	3	29.1	12.0	48.0	16.2	21.8	23.9	37.2	39.8
MSMEG	MSMEG										
_4293	4296	R.APEVIQMYADGPSGPK.L	2	16.8	27.8	84.5	100.6	16.3	22.5	84.2	92.7
MSMEG	MSMEG	K.SFIAGILEHANEISAVTNQ									
_4294	4297	WVNSYK.R	3	97.1	128.8	249.4	314.1	55.3	103.5	176.0	275.1
		R.LWFTDVLGYLK.S	2	122.2	115.8	254.0	253.4	166.6	151.1	344.6	314.9
		R.VFESDTVARPDPSTFQVL									
		PWK.T	3	195.0	182.6	433.7	406.0	320.8	306.8	679.3	659.4
		R.YADALSMADNVMTFR.Y	2	49.9	48.0	127.5	124.9	16.4	15.6	30.5	26.8
MSMEG	MSMEG	K.GAPHALVIGDLPGFSYED									
_4298	4301	GPSQALATATR.F	3	1834.9	1352.4	109.8	140.5	8312.1	8667.8	75.0	104.6
		K.GAPHALVIGDLPGFSYED									
		GPSQALATATR.F	4	171.1	157.3	100.7	74.7	632.4	642.3	176.9	115.3
		K.WAM*LTC#YDYSSAR.V	2	19.5	22.5	2.4	1.9	91.3	108.6	4.6	2.5
		K.WAMLTC#YDYSSAR.V	2	236.4	268.4	6.5	6.8	721.8	815.2	17.3	15.4
		R.AATQFADDVAAGVFPAEE									
		HSY	2	1209.1	1289.8	1.2	1.2	4244.8	4475.2	2.5	1.0
		R.AATQFADDVAAGVFPAEE									
		HSY	3	1516.7	1630.8	27.8	31.7	5285.7	5456.9	91.9	47.5
		R.FGDVGGELHR.A	2	1.6	1.8	1.2	0.4	7.3	5.8	1.5	1.0
		R.RFGDVGGELHR.A	3	15.4	13.1	0.1	0.0	25.7	21.3	0.0	0.0
		R.VADQIATLSR.A	2	6.9	4.6	2.2	1.6	29.9	38.1	2.0	2.3
MSMEG	MSMEG										
_4299	4302	K.VGLSPDGSASYLPR.L	2	160.7	169.6	47.2	45.6	129.8	138.6	47.7	46.3
		R.ITLNRPDAAANGMNDTMTR									
		.E	3	50.5	52.0	16.4	18.9	28.7	37.2	6.6	14.3
MSMEG	MSMEG	K.ELGASDVPTFAAAPNFAY									
_4301	4304	ELAAHR.G	3	205.3	213.9	163.1	183.9	215.4	206.1	118.7	135.8
		K.GYWGRPHETEVSFHNK.L	4	12.3	11.7	6.8	7.5	8.8	11.7	2.2	4.7
		R.LPQGSHAAGAPDGAAWF									
		R.T	3	127.3	117.3	17.6	20.4	112.3	110.3	8.9	13.7
MSMEG	MSMEG	R.ALASAPGAPSDTPEPAQP									
_4302	4305	TDALHR.A	3	124.6	127.3	182.0	190.6	94.1	111.1	183.4	206.3

MSMEG	MSMEG										
_4306	4311	R.DALVNAIDQLVELYEK.Q	2	26.0	31.2	25.0	24.9	30.6	35.1	29.6	31.0
		R.LAALGIALEDLDAQVAK.Y	2	28.1	26.5	40.4	43.8	46.8	41.6	43.5	43.8
MSMEG	MSMEG										
_4313	4318	R.ALIGADPVLDER.T	2	247.7	233.0	208.0	210.2	225.5	214.8	227.2	209.4
		R.DLAVSGPWYR.A	2	74.2	81.4	59.5	64.7	57.3	69.3	64.8	66.7
		R.LDELGIAHGGIVDAPYGS									
		GLSFR.D	3	538.8	583.9	449.8	474.6	443.9	463.4	464.9	444.1
		R.TDAGFHHIVWALPGGTLF									
		GIHQHDK.R	4	47.2	0.0	30.1	0.0	27.4	31.6	21.6	27.6
		R.VGLDHVSFGVGSR.D	2	45.1	43.2	54.0	57.1	28.2	30.3	29.4	44.9
		R.VGLDHVSFGVGSR.D	3	147.4	149.2	81.5	80.3	117.0	127.4	79.2	85.0
MSMEG	MSMEG										
_4320	4325	K.VWTAALQALR.A	2	19.3	0.0	97.0	0.0	18.4	21.3	55.5	57.9
		R.DYGVFNEDAGYPNR.G	2	31.4	33.5	30.8	37.0	22.5	23.7	13.6	21.1
MSMEG	MSMEG	R.LMDAITPLAEDGVIWVLT									
_4321	4326	K.T	2	36.8	43.2	60.9	73.2	29.7	35.8	62.1	74.1
MSMEG	MSMEG										
_4323	4328	K.ALVADM#SDQEIWNLK.R	2	25.3	22.9	239.9	210.2	10.1	8.2	324.4	245.0
		K.ALVADM#SDQEIWNLK.R	2	150.7	138.7	248.5	230.7	109.4	93.3	267.3	213.3
		K.ALVADM#SDQEIWNLK.R									
		K.ALVADM#SDQEIWNLK.R.G	3	26.3	26.7	38.2	36.5	60.2	47.1	69.4	63.1
		K.DTSDQHVVWAF LGDGEMD									
		EPESR.G	3	370.2	399.6	215.8	227.8	312.3	299.7	131.2	186.2
		K.IIQELESFFR.G	2	368.3	360.7	604.2	545.9	368.3	285.3	770.7	554.5
		K.SAQILASGVAM*PEALR.A	2	392.5	411.8	516.6	513.6	330.8	344.8	538.0	536.1
		K.SAQILASGVAMPEALR.A	2	521.2	541.3	644.0	634.1	486.4	500.5	657.2	638.8
		K.SHPGGGDHVF IQGHASP									
		GIYAR.A	3	33.8	27.1	78.2	70.8	35.0	45.6	72.5	87.1
		K.SHPGGGDHVF IQGHASP									
		GIYAR.A	4	150.7	156.1	187.0	191.0	120.9	174.4	188.7	264.9
		R.AVPEQIRPWVPGTYVTLG									
		TDGFGFSDTRPAAR.R	4	407.6	455.4	689.4	731.3	276.4	444.9	671.5	977.0
		R.EWDVLLHADR.D	2	81.0	78.1	94.2	88.2	60.4	51.8	84.9	78.9



		R.IDDVSAAGVSYADTGSA	2	55.2	82.0	111.6	170.7	31.8	50.9	88.6	138.5
		R.LTTDQLDGFR.Q	2	21.3	19.4	33.2	27.9	14.0	10.8	22.0	22.0
		R.TFGMDSWFPSLK.I	2	150.3	159.3	205.8	214.3	101.7	106.7	197.3	202.1
		R.TGDGLWAAADQMAR.G	2	528.1	539.1	496.0	509.6	484.3	461.1	348.3	347.8
		R.VPVSDAQLEEDPYLPPYY									
		HPGPEAPEIR.Y	3	702.3	747.0	1029.1	1104.4	523.2	564.5	879.5	1083.4
		R.YFNTDAESVVVAVLQGLA									
		R.D	2	80.9	95.8	103.7	113.5	45.8	83.4	87.2	128.0
		R.YFNTDAESVVVAVLQGLA									
		R.D	3	73.5	96.9	119.9	161.4	55.5	68.9	120.0	145.6
MSMEG	MSMEG										
_4325	4330	R.LEALDLVPANR.N	2	206.3	215.5	97.9	95.2	245.1	225.4	78.1	66.2
		R.NAAGQIVAAGAVAALDK.L	2	321.0	328.7	381.2	396.0	338.8	320.6	546.9	500.5
		R.NAAGQIVAAGAVAALDK.L	3	31.3	33.9	11.4	11.4	47.0	39.0	6.6	7.5
		R.WDLC#TATLR.D	2	30.8	35.7	14.6	13.0	28.0	30.2	5.3	9.6
MSMEG	MSMEG										
_4326	4331	K.IPDEDLAGLR.T	2	184.7	155.3	195.0	173.4	202.7	249.3	249.2	286.4
		K.LEEENPEAAAAALR.E	2	96.6	86.5	117.2	102.8	104.5	122.1	141.7	147.8
		R.TVGDVVAYIQK.L	2	727.1	824.0	814.6	950.7	731.2	746.7	976.0	936.2
		R.TVGDVVAYIQK.L	3	0.0	0.0	17.4	14.8	0.0	0.0	25.1	20.2
MSMEG	MSMEG	K.GALGHSVGAVGAVESILT									
_4328	4334	VLALR.D	3	6.0	8.8	9.1	10.9	0.3	0.8	0.2	0.7
		R.AIELAGLKPTDIDHVNAHA									
		TGTNVGDVAESK.A	4	688.6	872.7	590.3	602.1	667.3	669.0	663.2	638.9
		R.IGGHLLEEFDSLTR.V	2	134.2	127.3	135.2	141.1	68.4	88.5	128.7	148.4
		R.IGGHLLEEFDSLTR.V	3	64.5	48.1	46.8	33.0	42.9	57.3	47.6	55.9
		R.NLNNLDPEIDLDDVVAGEP									
		R.Q	2	183.8	192.9	235.9	272.2	151.8	144.7	204.2	225.3
		R.TLTDPFVEEYNLPVR.I	2	740.1	710.1	836.4	788.0	711.9	684.2	871.1	847.8
MSMEG	MSMEG										
_4329	4335	K.WAPSIVVGLGR.L	2	59.9	46.6	17.6	15.2	69.6	62.3	45.4	44.0
		R.AYDVHPLVHALLDEGVPPF									
		EEFQAK.W	3	175.7	159.2	134.4	127.8	198.4	204.0	180.4	214.6
		R.EALHEQLAVEHEK.I	2	2.6	1.1	0.7	0.4	3.2	1.7	1.7	0.3
		R.LSTFFDDGGSVELLHER.D	2	102.4	107.3	260.5	242.4	207.1	167.4	189.9	233.5

MSMEG	MSMEG	R.GVNVAVHYNSASTEADAD									
_4330	4336	K.T	3	3.7	3.4	7.5	5.4	6.3	4.9	8.0	5.3
MSMEG	MSMEG	K.LLGGADAAGFGVTSTVSD									
_4337	4343	LAR.F	2	87.8	85.4	59.8	58.2	69.6	76.0	78.9	82.8
		R.YLTEAVFEPLGMSTSK.L	2	233.5	251.2	90.5	91.2	222.5	231.4	100.7	107.2
MSMEG	MSMEG										
_4340	4346	K.LEM*PLIDFFSR.G	2	102.6	99.7	62.3	59.9	73.5	70.4	65.1	64.6
		K.LEMPLIDFFSR.G	2	296.2	276.4	332.3	302.3	210.5	166.5	349.6	271.3
		K.MTLTDGTELTPLGIGAFADK.T	2	321.1	332.9	308.2	300.4	187.6	173.6	282.2	271.3
		R.DFPTLISLYLQGR.L	2	301.6	267.4	297.2	280.8	227.9	188.7	348.1	294.5
		R.GRPHLC#FDTFNATQK.M	3	28.5	20.9	14.1	7.4	44.9	32.0	82.7	55.2
		R.GRPHLC*FDTFNATQK.M	3	25.5	18.0	14.1	7.4	44.6	30.8	81.3	54.9
		R.IGLDGIEDAFHK.M	2	191.0	195.6	169.7	169.7	137.0	136.2	153.0	137.1
		R.IGLDGIEDAFHK.M	3	279.1	233.4	197.9	152.7	208.4	189.2	247.1	197.2
MSMEG	MSMEG										
_4342	4347	R.SYSDFPTILDSIK.N	2	184.7	235.7	189.5	190.2	99.3	98.2	268.0	237.7
MSMEG	MSMEG										
_4358	4364	K.TALVTGASAGLGA AVAK.L	2	28.3	34.3	48.5	113.3	28.6	37.6	54.3	53.1
MSMEG	MSMEG	R.TVVSAAVDDGDAEGVDA									
_4362	4368	THHVK.R	3	33.7	40.5	59.9	60.5	31.2	31.6	46.8	50.5
		R.TVVSAAVDDGDAEGVDA									
		THHVK.R	4	26.4	25.8	39.3	38.7	28.1	26.8	45.4	42.0
MSMEG	MSMEG	K.FGYSPEQAYLLLGA APIEG									
_4367	4372	R.L	2	152.6	168.5	548.1	591.2	130.7	134.6	610.7	601.0
		R.HIPGVEFTGIVHPGLMGT									
		APSAGLLAK.W	3	258.2	208.3	543.7	511.9	79.5	96.6	244.0	275.2
		R.VPPLALPPEPQDAILGGLT									
		GDAFTK.A	2	107.2	131.4	404.9	451.6	38.4	79.0	326.5	415.9
MSMEG	MSMEG	R.IKPGTVLTLWTEDAYGGR.									
_4381	4385	I	3	18.2	19.8	58.4	67.4	6.3	7.0	31.9	53.3
MSMEG	MSMEG										
_4396	4399	K.ALGFPPNNVASIPPLAK.H	2	212.3	203.5	498.0	438.2	277.2	276.7	841.7	932.1
		K.ALQTA FVGTDLP GTLIR.Q	2	454.0	474.4	221.2	231.4	482.0	507.6	135.6	150.0
		K.NFTSFNWIGFSVFR.D	2	25.7	22.1	5.6	5.3	15.1	19.7	5.0	3.4

		R.DHGLLPVIGDATGAAHPD									
		HER.A	3	119.0	122.6	243.3	254.6	125.5	135.6	133.1	135.4
		R.ELVEPGDNELFEK.A	2	399.7	395.3	18.8	22.2	433.9	437.6	10.4	15.8
		R.PAAFLSVSQSNSLYR.P	2	76.2	87.2	121.5	123.5	34.4	37.9	84.4	85.6
		R.PAAFLSVSQSNSLYRPGG									
		VQYAEGHAFR.G	4	270.0	308.4	13.4	20.1	356.7	376.9	23.9	37.8
MSMEG	MSMEG	K.AAYAEPVPLPGVPDAI									
_4401	4404	R.D	3	157.1	165.3	76.3	91.2	114.0	113.4	77.0	87.7
		R.ALLAPADDAALQVIVEDFR									
		.A	2	118.6	129.7	102.0	109.7	82.8	89.5	78.0	88.3
		R.ALLAPADDAALQVIVEDFR									
		.A	3	46.2	45.0	17.4	16.7	31.4	30.0	15.0	13.1
		R.VLEQTVVAHGGTPSEADI									
		AK.W	2	25.2	23.8	14.1	13.0	20.6	18.3	14.2	12.1
		R.VLEQTVVAHGGTPSEADI									
		AK.W	3	505.6	503.0	348.6	369.0	332.9	368.4	303.4	324.9
MSMEG	MSMEG										
_4454	4449	R.RPELFEGIHFAQK.Q	3	24.5	28.7	0.1	1.0	1.3	3.3	0.9	0.2
MSMEG	MSMEG										
_4463	4458	R.FNESPLDLLR.R	2	14.6	17.7	3.6	5.8	7.9	8.7	3.4	6.9
		R.YTQPTGSVEVNAK.R	2	7.1	4.8	9.5	7.9	2.6	2.1	5.0	4.0
MSMEG	MSMEG										
_4471	4466	K.LLADVAEHPLPEEN	2	38.4	45.4	73.8	83.8	28.9	34.0	58.0	59.5
MSMEG	MSMEG	K.AGVQWGLFGGAIENLGTE									
_4474	4469	R.H	2	58.9	65.0	51.4	71.7	55.2	58.5	58.6	84.3
		K.ELLTAYADDIK.G	2	107.6	97.2	66.5	60.8	92.6	68.8	100.5	65.8
		K.SYALQFAQNELVAK.C	2	260.1	253.2	260.7	261.0	212.3	194.8	297.0	264.2
		R.ADTDVFTTFEGDNHVLQ									
		LVAK.E	3	170.6	170.8	181.1	181.1	151.7	125.3	234.5	189.9
		R.ENLSNEVFRPHYTPNTAIA									
		R.A	3	70.5	74.4	44.6	51.4	73.0	73.7	57.6	74.0
		R.FFTMLGTLIR.G	2	31.2	34.0	43.6	50.4	22.3	19.5	53.6	46.8
		R.TAAQTIIQTILDTR.Q	2	270.7	216.1	323.8	264.5	270.5	167.0	466.5	309.8
		R.VTVGGSA AAAAR.V	2	7.6	5.3	5.2	3.3	4.5	3.5	4.5	3.8
		R.YADVSPGVYSSPIENPG									
		R.R	2	134.8	142.7	135.0	132.6	58.5	85.4	90.6	117.7

MSMEG	MSMEG										
_4475	4470	K.LPAPHGGSQWVQVR.D	3	11.8	8.5	15.9	13.0	6.0	8.4	12.5	16.3
MSMEG	MSMEG										
_4476	4471	K.AVLYQLQESVDTDK.L	2	19.2	0.0	15.7	0.0	15.6	17.0	8.6	5.6
MSMEG	MSMEG	K.FGFQGNPWGELEGVANR									
_4485	4480	.T	2	321.2	307.9	266.2	276.6	283.4	226.3	302.9	278.1
		K.HSGVDLSFYDQAADTR.Y	2	87.7	89.4	46.3	52.2	45.5	44.6	29.2	31.1
		K.SAWDYGPLGVELK.E	2	189.9	214.0	125.3	147.3	153.8	140.4	86.0	113.3
		R.GLVYQSGEIYGGTK.S	2	95.4	115.6	78.5	107.1	55.3	56.8	59.3	65.1
		R.YVPYVIEPAAGLTR.S	2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
MSMEG	MSMEG	K.TISNLTEHGEAHDHAGTP									
_4486	4481	APALPSR.D	4	17.7	17.8	8.4	9.0	22.2	19.4	8.3	8.4
		R.DVLETAGELLR.A	2	8.1	8.7	2.7	2.9	8.9	10.0	8.1	8.4
MSMEG	MSMEG										
_4487	4482	R.AAIADLLNETEGFR.S	2	453.1	513.7	37.8	43.3	392.8	402.7	36.7	35.0
MSMEG	MSMEG										
_4489	4484	R.YNFPAAGLTDDALR.T	2	28.4	33.5	58.8	56.4	35.5	35.8	63.9	56.6
MSMEG	MSMEG										
_4490	4485	R.ADIPDVDLFIR.T	2	27.4	27.6	30.0	24.1	25.7	21.7	10.2	8.7
MSMEG	MSMEG	K.RPLIDGPAPEPVTRPIDHV									
_4527	4520	GVQK.L	3	60.1	56.9	19.0	15.1	20.3	28.3	18.0	20.9
		K.RPLIDGPAPEPVTRPIDHV									
		GVQK.L	4	138.8	146.1	12.4	19.0	45.7	64.0	2.6	8.6
		K.VLSSELGDYIER.V	2	140.0	162.2	204.4	201.5	74.1	67.1	102.4	102.0
		R.AGLDALGLPSTPSHWR.R	3	63.5	61.2	4.3	2.0	53.2	44.7	1.3	2.3
MSMEG	MSMEG										
_4528	4521	K.GYSAWVTGIR.R	2	34.6	32.2	2.5	5.0	16.0	20.1	3.1	1.9
		R.GAAELADASAEELLR.W	2	135.5	160.2	57.7	53.3	106.9	103.2	63.3	71.0
MSMEG	MSMEG										
_4533	4526	K.GIPFGSVVSLVVR.Q	2	271.2	254.4	191.0	173.2	218.7	192.9	144.8	105.9
		K.IENPVAVVNTTSHSEAANA									
		LK.N	3	953.3	1101.5	805.0	869.8	726.1	845.1	690.5	891.4
		K.IWAEAGFRPVDPAVAAEF									
		AADFPAPK.L	3	163.8	200.0	50.4	58.8	91.2	114.5	34.1	45.2
		K.PADIVNFSVEPDVTR.L	2	210.7	205.9	153.9	163.1	199.5	176.2	81.1	97.0

MSMEG _4535	MSMEG 4528	K.WNLLAPYAAK.S	2	48.5	50.6	42.0	28.1	43.3	43.4	84.6	62.3
		R.AVVDGKPADIVNFSVEPD									
		VTR.L	3	462.4	478.9	311.2	339.8	549.1	376.0	366.7	332.7
		R.PVDPAVAAEFAADFPAPE									
		K.L	2	33.6	38.9	16.5	27.3	37.6	45.8	2.1	5.8
		R.PVDPAVAAEFAADFPAPE									
		K.L	3	26.0	22.6	19.5	27.5	9.6	12.5	2.2	12.4
		K.ASDGPLTVTAPVPYAAGP									
		TLR.N	2	17.0	21.3	39.9	47.6	25.3	38.5	53.8	107.4
		K.GLTYSPTGALLAAPTSLP									
		ETPQGER.N	2	66.0	88.1	96.4	130.7	29.4	59.5	46.9	95.3
		K.GLTYSPTGALLAAPTSLP									
		ETPQGER.N	3	240.4	290.2	379.0	424.5	151.7	200.8	293.7	348.0
		R.ATVLAIADELTEDGLVLR.Y	2	231.9	226.6	401.8	371.2	268.4	229.0	501.0	425.5
		R.DALVMGPWHDIDTR.S	2	85.5	83.5	137.1	142.5	58.8	75.4	107.8	140.9
		R.DALVMGPWHDIDTR.S	3	71.9	65.8	77.1	71.2	73.4	80.0	67.8	67.6
		R.DSTFALWGLYTLGLDR.E	2	28.2	35.2	48.6	61.0	25.3	38.3	46.8	75.8
		R.EADFFSFIADVSGANNG									
		ER.H	2	91.0	91.2	156.2	153.8	75.1	84.7	141.7	161.0
		R.HLGNFPQAFTHLALINAVV									
		HVIR.A	4	14.5	20.3	20.0	29.7	8.2	12.7	16.1	21.9
		R.LGPYGVSVPAAR.R	2	153.2	99.9	220.0	153.3	152.7	63.4	260.5	105.4
		R.LLSFASPLHLYAEEIEPR.T	2	43.7	40.9	61.2	61.8	43.7	33.5	70.4	50.1
		R.LLSFASPLHLYAEEIEPR.T	3	237.0	271.6	434.2	427.2	236.5	181.3	480.0	356.5
		R.LTEGDNVFWALWSK.H	2	55.3	57.7	147.5	150.8	73.1	52.3	175.0	133.3
		R.SLVEEELHHLSGYDNSR.P	3	63.9	69.9	102.0	110.6	40.7	28.6	69.6	57.2
		R.SLVEEELHHLSGYDNSRP									
		VR.I	4	60.9	53.1	63.6	80.9	70.3	90.1	91.4	123.7
		R.TPMDWDAEHILLR.T	2	127.2	130.7	202.8	183.3	105.4	90.9	253.9	174.4
		R.TPMDWDAEHILLR.T	3	58.2	54.8	182.1	173.8	56.0	42.7	212.9	155.6
		R.VSATWEYSGPAYGEAIAR									
		.A	2	214.1	209.7	396.4	382.8	159.6	199.9	313.5	365.5

		R.YGDDALDASLLAVLTR.F	2	79.7	72.7	134.0	121.6	82.9	91.1	161.1	162.1
MSMEG	MSMEG	R.SEPDSMVVAATAGEATK.									
_4553	4547	H	2	18.6	21.8	10.2	12.8	10.9	15.8	5.1	4.8
		R.TDTPALSPVAANLEAVA									
		EK.L	2	78.3	83.4	88.1	89.3	85.4	84.7	80.8	75.3
MSMEG	MSMEG	R.SELEFLQPGALLESLETR.									
_4569	4566	L	2	12.7	13.6	49.3	51.7	8.1	6.5	33.2	35.2
MSMEG	MSMEG	R.VALPENSLVVNSSQGGGS									
_4570	4567	K.D	2	100.0	102.4	163.6	181.3	99.2	153.1	95.1	224.3
MSMEG	MSMEG										
_4571	4568	K.SALALALNKL	2	138.4	131.5	43.9	45.1	279.5	262.8	97.2	96.9
MSMEG	MSMEG										
_4617	4609	K.VGPYALQDFSLFQVLR.F	2	103.5	136.7	146.4	148.3	91.7	111.1	146.6	157.4
		K.VYDVTFENVQAGLR.T	2	200.4	160.9	113.9	121.1	239.4	120.4	143.3	130.7
		R.FPFVPSNYER.L	2	56.6	50.2	59.2	57.6	55.0	44.6	77.2	50.4
		R.IEFQLDPPTGDIGLLR.E	2	60.1	56.2	1508.5	1547.3	46.6	36.2	1044.4	1311.4
MSMEG	MSMEG										
_4624	4616	K.TVNIVPVARPEA	2	131.6	100.3	48.8	39.1	138.3	171.6	49.3	65.8
		R.GGDDTLFALAPGAVEFGA									
		K.R	2	750.5	802.9	331.1	345.9	669.3	718.3	337.2	323.2
		R.GGDDTLFALAPGAVEFGA									
		K.R	3	49.3	38.7	11.6	6.4	46.9	52.7	11.4	16.8
		R.GTHFHPGVNVGR.G	3	1.0	0.5	0.1	0.1	1.1	0.8	0.2	0.1
MSMEG	MSMEG	K.LDSEPGASVSLPVALVVD									
_4625	4617	GANVTSK.A	2	331.9	394.8	243.4	273.9	426.2	413.5	225.0	224.0
		K.LDSEPGASVSLPVALVVD									
		GANVTSK.A	3	537.5	399.8	424.4	324.5	624.8	779.6	374.0	466.3
		K.VAVTAEVLEHTK.G	2	61.9	58.2	45.9	44.2	80.9	67.2	46.8	41.3
		K.VAVTAEVLEHTK.G	3	163.0	147.6	93.4	82.2	221.4	193.3	97.0	78.6
MSMEG	MSMEG										
_4626	4618	K.AGAVALYEEPDLVK.V	2	77.9	76.8	72.2	66.4	57.8	50.9	70.4	73.8
		K.VWLPSGGTLVIDR.T	2	28.2	26.7	15.0	13.4	22.3	22.7	19.3	19.4
		K.YEPAGPDAPDVFAVHR.I	2	4.9	6.4	35.7	35.7	7.7	6.3	34.6	36.3
		R.EVVPDAGVIIR.T	2	63.3	61.7	19.1	21.8	51.5	49.0	21.1	19.4

		R.KIEQALKPGDYVVVQVSK. D	3	18.1	25.2	21.1	23.4	17.6	21.6	14.2	15.7
		R.LGTGLVEAFSTAC#THC# GGR.G	3	25.8	27.8	15.6	18.8	32.9	27.2	19.0	16.3
		R.RRPILSEAEFLAR.R	3	34.0	31.6	6.5	9.4	33.2	34.9	3.6	9.1
		R.VLDALAEFDGR.Q	2	16.6	17.7	6.9	14.4	12.1	13.0	3.1	6.6
		R.YLVYVPGASSTGISR.K	2	77.9	76.3	69.7	74.7	57.7	55.0	86.9	82.9
MSMEG	MSMEG										
_4627	4619	K.GLTAALELK.N	2	174.6	169.5	92.8	87.9	164.0	157.8	112.1	102.9
		R.GDFALITQDNLVHGSDSP ESAAR.E	3	918.3	931.0	526.7	523.3	769.6	812.4	620.2	568.4
		R.KGLTLAALELK.N	2	25.1	39.7	9.6	15.5	21.2	22.9	13.6	12.6
MSMEG	MSMEG										
_4630	4622	K.LLHPVMPFVTETLWK.T	3	13.9	19.5	7.7	12.9	11.3	13.4	6.7	10.0
		K.VTPAHDPNDFEIGMR.H	3	62.7	38.7	28.3	14.5	46.4	19.7	28.6	6.8
		K.YEDVEGELVSFR.Y	2	166.6	161.7	144.1	166.8	156.4	132.9	170.0	165.7
		R.AEVDSAFDNYEFNR.A	2	724.9	711.6	127.2	145.8	676.7	663.1	138.2	173.6
		R.LFDAGLIYQAER.L	2	239.2	226.8	277.1	248.2	218.1	189.1	340.0	273.0
		R.LSLQWWVK.V	2	30.6	28.8	16.4	15.4	37.5	28.4	27.9	22.3
		R.LVNWSPVLETAISDLEVK. Y	2	207.2	241.0	266.1	301.7	165.9	207.0	283.4	366.5
		R.LVNWSPVLETAISDLEVK. Y	3	99.6	119.8	90.1	106.0	81.7	87.2	103.1	114.3
		R.TTAVLAAVLDTLLK.L	2	102.4	102.4	89.9	90.9	119.6	85.0	152.7	102.5
		R.TTAVLAAVLDTLLK.L	3	6.9	6.4	3.1	2.0	6.7	6.5	3.6	3.5
		R.YGSMNDDEPHIVVATTR. V	2	36.2	34.5	24.6	29.1	16.8	37.4	10.3	47.3
		R.YGSMNDDEPHIVVATTR. V	3	155.2	159.1	72.3	79.1	66.5	78.6	63.1	67.3
MSMEG	MSMEG	K.AIIHKPVEPGPAAEGEPT PY	3	0.3	0.0	309.1	0.0	0.0	0.1	297.9	321.0
MSMEG	MSMEG	K.TAEVSADDIVVHDAQIDDP AYAFALSR.L	3	251.3	252.4	90.3	93.7	357.4	342.4	65.8	78.1
_4645	4636	R.APTIATGLALAR.P	2	9.7	8.2	60.6	53.4	12.7	13.7	63.4	65.4
		R.LINLTHGEPITFGADGEYA VVK.S	3	395.3	373.6	188.9	171.6	518.0	496.4	156.9	150.2

MSMEG	MSMEG	R.WC#PGC#GDYVILNTIR.N	2	81.4	84.8	16.3	15.2	99.5	103.6	15.5	11.4
_4646	4637	K.TEQADLLQALFGR.N	2	174.9	160.7	78.2	68.3	367.4	271.0	117.5	81.6
		K.TEQADLLQALFGR.N	3	1.6	3.8	0.0	0.0	14.9	9.0	0.1	0.5
		K.VVVPEMNLGQLALLLR.G	2	242.4	268.3	119.8	124.0	520.5	531.9	165.3	170.3
		K.VVVPEMNLGQLALLLR.G	3	23.0	27.4	5.8	6.6	47.6	51.5	8.9	10.3
		R.ELEASEAFIR.E	2	25.4	20.9	8.7	6.1	19.5	33.7	1.3	15.9
		R.FLVQVQSVTK.V	2	187.2	172.7	85.5	83.6	340.2	253.4	103.3	76.0
		R.FTSEAALFGNDLATQPNY									
		PAEIR.A	3	133.6	175.6	57.5	80.9	220.1	231.0	47.6	65.0
		R.GGLIIANSDEFTK.R	2	173.8	185.5	167.5	175.2	185.3	201.7	113.9	143.6
		R.HLNPFPANLGEVLAR.Y	2	136.3	149.0	68.2	93.9	201.1	229.7	72.2	74.5
		R.HLNPFPANLGEVLAR.Y	3	101.9	91.2	21.7	19.5	183.4	169.1	28.1	20.6
		R.IGGLESANGSGNISYEPK.									
		N	2	239.1	240.4	111.5	107.4	296.5	353.3	91.5	109.6
		R.KPEIAEANVLALK.A	2	180.6	154.0	129.1	110.3	311.8	239.8	134.9	115.3
		R.KPEIAEANVLALK.A	3	126.3	102.7	46.0	28.1	222.6	151.6	47.4	32.9
		R.LAAATVEGEANEESAVGA									
		NA	2	40.9	43.7	5.2	8.8	47.5	67.6	12.4	9.8
		R.SPSDC*FDIAVEAAR.I	2	155.8	155.2	29.6	29.6	240.2	197.4	34.3	26.4
MSMEG	MSMEG										
_4647	4638	R.TDFPAETLAALVER.G	2	18.5	17.2	13.1	15.6	22.2	17.2	24.5	13.9
MSMEG	MSMEG										
_4664	4654	R.LPVLLLPAETFATR.V	2	13.2	10.9	61.0	67.5	27.0	18.9	90.5	51.4
MSMEG	MSMEG	K.APDAFLDALDAHFGITSPR									
_4668	4658	.K	3	8.0	18.8	0.8	1.6	15.4	19.9	0.9	0.8
MSMEG	MSMEG										
_4672	4662	K.EYGIIDTVLQYR.K	2	796.1	793.6	691.0	640.6	707.9	688.9	671.7	602.3
		R.ADIQTVCLGQAASAAAV									
		LLAAGTPGK.R	3	179.9	163.0	94.4	86.8	94.8	113.4	54.7	61.5
		R.ADIQTVCLGQAASAAAV									
		LLAAGTPGKR.L	3	79.0	83.2	41.0	46.4	98.5	91.3	52.9	50.1
		R.ADIQTVCLGQAASAAAVL									
		LAAGTPGK.R	3	179.9	163.0	94.4	86.8	93.0	113.1	54.4	61.5



		R.VLIHQPALSGVIQQQFSDL									
		EIQAAEIER.M	3	760.7	799.6	368.6	378.6	512.1	617.2	296.8	316.7
		R.YILPSFIEHSSFGVK.E	2	281.0	257.9	313.0	301.1	308.5	292.3	345.9	326.0
MSMEG	MSMEG										
_4673	4663	R.GTGQGLNLVDSVYER.L	2	1947.6	2143.2	1891.5	1992.4	1846.0	1819.3	1966.4	1892.7
		R.IIFLGSQVDDDIANR.L	2	1690.9	1762.6	1701.7	1680.5	1467.7	1446.0	1725.0	1695.8
		R.IIFLGSQVDDDIANR.L	3	160.2	130.7	130.6	98.0	147.3	133.5	101.6	97.3
		R.ILM*HQPLGGVTGSAADIA									
		IQAEQFAVIK.K	3	496.1	474.5	684.9	645.4	389.7	374.0	669.6	635.6
		R.ILM*HQPLGGVTGSAADIA									
		IQAEQFAVIK.K	4	18.8	14.0	10.4	7.4	10.4	10.5	3.7	4.7
		R.ILMHQPLGGVTGSAADIAI									
		QAEQFAVIK.K	3	706.5	687.5	825.9	784.5	507.2	492.6	750.7	721.1
		R.LC#AQILLLSAEDPTK.D	2	212.8	207.3	204.2	208.6	113.9	110.0	106.0	106.8
		R.LC*AQILLLSAEDPTK.D	2	208.3	206.7	204.2	208.6	112.3	106.6	106.0	106.8
		R.LNAEFTGQPIER.I	2	164.6	146.2	127.0	115.2	149.5	169.6	122.5	134.1
MSMEG	MSMEG										
_4674	4664	K.AIEALLEQTEVPLPEK.I	2	604.4	575.3	543.2	546.3	585.2	468.6	549.2	502.5
		K.FAEQLAEQGSSR.E	2	7.3	4.7	8.8	4.0	1.6	2.3	1.3	4.5
		K.ITVDPIEVTDEEVDAELQS									
		LR.A	2	247.1	232.4	214.8	210.3	128.9	144.9	182.5	203.0
		K.ITVDPIEVTDEEVDAELQS									
		LR.A	3	196.0	255.0	181.3	242.6	103.0	116.5	147.7	172.0
		K.IVQAQIDEVVHNAIHGLDH									
		DEEK.F	4	154.0	150.2	99.4	105.9	42.2	45.7	48.8	46.9
		K.LEIQVSQNDLTER.L	2	85.2	84.1	196.3	185.1	34.3	32.4	120.0	120.3
		K.TQLLLMDAVADKLEIQVSQ									
		NDLTER.L	3	236.7	238.6	214.7	198.8	157.2	133.5	177.1	165.3
		R.ELPEPDDEFAQLASEYDTI									
		EELR.N	3	95.6	157.3	89.0	137.6	23.3	57.0	29.9	75.5
		R.INVEVPFTELEPDFDR.A	2	849.1	851.5	703.7	682.4	809.8	761.0	709.5	653.8
		R.YSEAVSTSDLKPLGQPEIE									
		ITK.L	3	1629.6	1791.6	899.5	918.6	1028.6	1139.1	635.8	616.3
MSMEG	MSMEG										
_4679	4669	K.DVDLPWTQDITFSGK.V	2	4.1	6.4	2.4	5.5	7.9	10.6	5.6	2.5
MSMEG	MSMEG	K.GLSEGGIPIGAALFSADGE									
_4687	4676	LLGSGHNR.R	3	66.5	70.7	107.7	114.0	53.9	60.6	74.7	72.8

		R.RVQDGDPSIHAETDAFR.A	3	4.2	3.3	3.7	1.2	6.4	5.2	5.4	5.6
		R.TFSGGHEWLADNGVSVTLLDDER.C	3	79.0	81.7	189.1	188.0	91.2	95.9	184.5	175.4
		R.VQDGDPSIHAETDAFR.A	3	12.8	0.0	24.6	0.0	13.7	16.5	18.2	24.0
MSMEG	MSMEG										
_4688	4677	R.DLPEEYQEMMK.K	2	59.5	69.9	29.4	44.3	48.3	37.2	40.2	33.5
MSMEG	MSMEG	R.AAEAGSDHQLAYVNALTT									
_4690	4679	SVLSAR.H	3	590.2	577.2	403.4	377.8	591.2	523.1	545.6	455.3
		R.ADFDVDSSGAFTR.F	2	303.3	249.9	198.6	158.4	279.3	225.3	259.0	196.9
		R.DHAFANATFGDLLGALEK.A	2	164.7	177.8	126.2	134.4	172.1	177.5	163.7	155.7
		R.DHAFANATFGDLLGALEK.A	3	146.2	162.1	97.8	110.8	170.5	125.1	147.9	103.5
		R.DLSGWGQQWLK.T	2	118.4	120.3	61.4	68.6	124.0	103.5	84.4	90.1
		R.FVDPVDDEVYLYSQFETA									
		DAK.R	3	210.9	233.7	146.4	167.3	180.5	190.4	166.1	189.8
		R.GQLILVNDDDLTYC*SLR.L	2	183.4	156.4	95.0	103.0	187.4	166.9	108.2	90.9
		R.HTTLLADLLDKDPGSLGL									
		EGLVVDTDLR.W	3	31.9	39.8	26.8	41.6	31.8	41.9	30.5	49.3
		R.HTTLLADLLDKDPGSLGL									
		EGLVVDTDLR.W	4	89.4	106.6	59.3	66.7	78.6	102.8	64.0	93.4
		R.IADIADPLPR.T	2	67.2	47.8	98.5	79.5	85.0	30.0	138.9	136.8
		R.LAVGIYDDVDGK.L	2	173.5	127.1	89.8	73.2	163.2	112.2	108.9	77.7
		R.LDPDSLSTVVTR.I	2	515.4	481.9	566.0	548.4	471.0	429.6	551.1	540.1
		R.MFAC#FDQPDLK.A	2	48.9	48.7	17.9	26.2	56.7	55.8	51.6	52.5
		R.SGEIDADGPETPFIDAEAQ									
		R.D	2	282.4	271.1	142.2	146.0	204.6	245.3	147.4	174.8
		R.SGEIDADGPETPFIDAEAQ									
		R.D	3	61.5	72.5	26.7	30.7	49.3	51.9	20.3	32.1
		R.TLAWSAAWEMTR.D	2	116.8	113.1	58.2	63.9	99.6	82.8	86.5	61.5
MSMEG	MSMEG										
_4692	4681	K.EGNLIDGLISAVR.V	2	71.7	71.3	27.2	29.5	70.3	67.5	26.4	24.6
		R.FAVYIGPLGADTAATAR.E	2	275.0	275.2	102.3	102.9	312.0	314.6	106.2	100.2

		R.GIESAAPLGVSAAAASFKE	2	273.9	282.6	207.2	212.5	275.1	286.3	182.7	181.0
		R.ISAVTEPGELSVHYPFPTMDLVVLDDALK.Y	3	41.6	52.2	21.2	26.7	31.1	44.8	15.3	23.2
MSMEG	MSMEG	K.MSDPWTHAPILWAAEEP									
_4693	4682	R.E	3	35.0	35.6	6.3	7.5	30.5	33.6	7.1	5.7
MSMEG	MSMEG	R.SVNAAPDSKPSVIGETQL									
_4698	4687	AAVHIEQQR.L	4	169.2	162.7	191.6	250.6	138.0	140.2	158.1	175.7
MSMEG	MSMEG	K.APVDLLWNGGIGITYIK.A	2	10.7	12.1	16.3	14.9	14.3	15.4	21.4	23.6
_4699	4688	K.ATGAVVTPPEVVR.R	2	0.4	0.7	18.0	12.8	0.3	0.5	15.7	11.0
		K.GTATFSDIANEVAK.S	2	52.0	49.2	41.6	40.0	53.3	44.9	51.8	45.7
		K.ISPHPSIPHAPDAEAQR.D	3	8.1	5.5	5.0	3.5	5.1	5.8	4.6	5.8
		K.ISPHPSIPHAPDAEAQR.D	4	13.3	9.7	9.9	7.7	6.5	9.5	7.1	9.9
		K.LALKDDVLASDLPDQEVF									
		ASR.L	3	60.4	58.8	69.8	64.0	56.4	66.7	102.5	85.8
		K.VIGEGGNLGVLTALGR.I	2	68.2	72.8	125.8	152.4	70.7	75.2	124.5	140.5
		R.AFANLIEATLR.T	2	22.2	19.4	17.4	15.9	26.8	22.8	31.9	26.0
		R.FADAVTAIWHGR.V	3	10.1	9.7	5.1	3.9	7.9	9.1	5.2	7.2
		R.GPQADAPGVTSTGPLAVA									
		AHDDLVSDDLVAAHYR.L	4	55.3	53.1	88.7	85.3	67.7	68.4	118.5	130.4
		R.INTDALDNSAGVDC#SDH									
		EVNIK.I	3	17.2	19.9	17.4	20.6	19.3	20.6	31.4	33.7
		R.ITEDVGVPVDAVR.S	2	40.8	40.7	46.4	49.1	51.7	44.5	71.7	61.2
		R.LEMQDILVR.E	2	15.4	15.0	7.6	6.9	13.9	13.4	12.2	10.3
		R.LFISGLLDVTDNVDK.A	2	14.0	11.6	23.5	25.2	18.5	18.3	36.3	49.5
		R.LPEGTAADSVDTSENES									
		R.I	2	29.6	32.3	20.1	24.6	33.3	30.2	37.5	32.9
		R.LPEGTAADSVDTSENES									
		R.I	3	9.8	14.6	9.3	14.1	7.7	12.0	11.0	16.6
		R.LPYYPTR.L	2	11.3	11.0	9.4	12.7	11.7	12.7	13.2	19.6
		R.LVPGILAEAR.Q	2	18.4	16.6	8.3	6.8	20.0	20.3	13.8	14.9
		R.TALGLDADVEELTPPALIK.									
		A	2	20.3	19.1	21.5	24.3	26.6	23.5	44.1	37.3

MSMEG _4700	MSMEG 4689	R.YGAYPYIVVVR.E	2	16.5	18.0	8.1	8.8	20.0	24.5	23.8	22.1
		K.DLSFTLPR.N	2	102.5	76.1	106.9	65.9	72.9	51.1	124.5	90.0
		K.TVWQVVSDGLDYIEVGQ									
		NEIPSR.A	3	76.1	105.9	72.7	101.8	19.5	39.6	36.2	70.0
		K.VILDDVTLNFLPGAK.I	2	316.5	300.6	458.5	447.5	248.3	157.1	567.6	380.2
		R.AYPYEGNYSTYLEK.K	2	289.7	293.3	384.4	368.9	164.1	185.2	335.0	349.7
		R.KLDFEEIQIPTPPR.L	2	78.4	95.7	245.6	341.4	41.2	49.4	255.6	301.7
		R.KLDFEEIQIPTPPR.L	3	152.6	133.7	228.2	190.3	100.2	82.0	239.8	200.4
		R.LDRYEEMVAEAEK.T	2	55.2	44.8	49.0	49.3	23.8	29.0	41.8	49.9
		R.LDRYEEMVAEAEK.T	3	38.7	30.8	40.7	40.4	13.4	17.2	36.5	37.9
		R.LGSVVVEVEHLDK.G	3	159.9	141.6	183.7	153.8	108.6	93.9	205.3	161.2
		R.LNLALTLK.E	2	51.4	37.2	39.0	22.4	42.3	20.9	59.6	30.3
MSMEG _4709	MSMEG 4698	R.NGIVGVIGPNGVGK.T	2	12.1	12.9	79.2	85.3	7.5	5.8	91.4	56.5
		K.LGIHPGGGATWMLQR.A	3	18.0	24.1	26.8	24.3	12.5	17.1	43.1	33.6
		R.HGLALTVADDPLAAAR.E	2	55.1	61.1	149.0	134.3	44.8	74.2	185.1	232.8
		R.HGLALTVADDPLAAAR.E	3	20.2	17.2	24.2	24.3	13.7	12.4	27.1	23.7
		R.SAVEAAEADPDVHAVVVT									
		GAGK.A	2	12.7	12.7	19.3	25.1	5.9	4.3	11.4	23.1
		R.SAVEAAEADPDVHAVVVT									
		GAGK.A	3	183.6	181.6	244.2	254.5	136.9	140.6	253.8	239.2
		K.SRPGEGILTFHAHTGR.N	3	15.8	17.2	22.2	20.1	14.1	19.4	7.1	16.2
		R.LQVEHPVTELVTGIDLVEQ									
		QIR.I	3	11.0	14.7	26.7	35.6	17.7	22.5	31.0	35.6
		R.LQVEHPVTELVTGIDLVEQ									
MSMEG _4714	MSMEG 4704	K.SRPGEGILTFHAHTGR.N	3	15.8	17.2	22.2	20.1	14.1	19.4	7.1	16.2
		R.LQVEHPVTELVTGIDLVEQ									
		QIR.I	3	11.0	14.7	26.7	35.6	17.7	22.5	31.0	35.6
		R.LQVEHPVTELVTGIDLVEQ									
		K.AFANTFSESLR.G	2	45.9	27.4	36.3	22.4	34.3	35.6	45.5	48.5
		R.AVVTGASQNIGEALATEL									
		AAR.G	2	62.4	72.2	71.5	72.4	48.8	52.5	67.3	76.8
		R.AVVTGASQNIGEALATEL									
MSMEG _4716	MSMEG 4706	AAR.G	3	124.1	132.1	127.0	143.3	109.0	106.1	150.6	126.7
		R.LIPDFLWIDTEYTAK.L	2	84.2	96.3	131.0	148.1	57.8	68.0	114.5	136.6
		R.TELPDPSEQSLVER.L	2	226.4	235.8	268.7	279.2	205.6	208.4	302.3	322.1
		R.YGVTVEVR.A	2	49.9	26.1	11.4	8.5	99.5	79.9	13.3	9.8
		R.YGVTVEVR.A									
		R.YGVTVEVR.A									
MSMEG _4722	MSMEG 4713	K.AFANTFSESLR.G	2	45.9	27.4	36.3	22.4	34.3	35.6	45.5	48.5
		R.AVVTGASQNIGEALATEL									
		AAR.G	2	62.4	72.2	71.5	72.4	48.8	52.5	67.3	76.8
		R.AVVTGASQNIGEALATEL									
		AAR.G	3	124.1	132.1	127.0	143.3	109.0	106.1	150.6	126.7
		R.LIPDFLWIDTEYTAK.L	2	84.2	96.3	131.0	148.1	57.8	68.0	114.5	136.6
MSMEG _4722	MSMEG 4713	R.TELPDPSEQSLVER.L	2	226.4	235.8	268.7	279.2	205.6	208.4	302.3	322.1
		R.YGVTVEVR.A	2	49.9	26.1	11.4	8.5	99.5	79.9	13.3	9.8

MSMEG	MSMEG										
_4724	4715	R.STVDLATAEEMVLDYIR.G	2	24.1	27.8	33.3	33.4	18.6	20.0	28.7	31.7
MSMEG	MSMEG										
_4727	4717	R.GPAIDLGDLAYTLAR.R	2	4.5	4.2	122.7	114.0	7.4	6.1	154.9	164.3
		R.LIAEQVGLLLR.R	2	0.7	1.0	0.0	0.0	3.0	2.8	0.1	0.1
MSMEG	MSMEG										
_4742	4734	K.AALDEILHSWR.S	2	21.7	23.7	22.0	29.7	38.2	31.7	21.5	26.4
		K.LWVEQGALPAR.M	2	95.6	78.8	194.1	145.1	127.4	134.2	146.0	154.6
		K.TLADSIGGHAFELDVEDP									
		AAITR.V	3	155.2	159.5	262.1	264.6	212.9	190.7	281.5	263.8
		R.LADNGVVLIASSHDVGRP									
		R.A	4	72.0	70.3	98.0	99.9	111.8	107.5	111.6	101.1
		R.LLVVGASSGIGHAVAESA									
		AK.R	2	60.7	57.1	187.8	183.7	78.2	78.7	154.4	146.5
		R.LLVVGASSGIGHAVAESA									
		AK.R	3	225.2	213.5	373.3	332.0	254.7	260.0	378.9	384.3
		R.VGVGPTEDTEILR.G	2	113.8	85.9	205.2	166.4	95.0	121.4	133.3	172.1
MSMEG	MSMEG										
_4752	4742	R.LALTVDLSLAER.A	2	220.0	228.2	229.0	249.5	209.0	205.9	229.1	217.2
MSMEG	MSMEG										
_4753	4743	K.EGLTFPLLSDPDR.S	2	137.9	126.9	173.9	173.3	106.1	106.4	178.2	169.9
		K.IAVAQYNVR.A	2	3.5	0.0	2.8	0.0	2.0	2.5	2.8	3.3
		K.VIVYFYPAASTPGC#TK.Q	2	380.9	440.4	573.1	641.2	239.7	247.6	492.7	461.8
		K.VIVYFYPAASTPGC*TK.Q	2	379.9	437.9	561.1	636.8	239.3	246.5	476.5	454.7
		R.DKEGLTFPLLSDPDR.S	2	107.6	106.4	132.3	129.2	82.4	69.9	134.5	107.5
		R.DKEGLTFPLLSDPDR.S	3	147.9	128.7	148.1	131.6	102.2	105.4	136.5	143.0
		R.DNLAELNDAGLDVVGISP									
		DKPEK.L	2	64.6	61.6	71.7	67.7	26.2	33.9	70.2	54.0
		R.DNLAELNDAGLDVVGISP									
		DKPEK.L	3	1193.7	1281.6	1195.4	1323.8	895.6	989.8	1197.6	1185.1
		R.KVIVYFYPAASTPGC#TK.									
		Q	2	35.7	37.2	49.5	58.7	32.5	29.4	58.0	49.6
		R.KVIVYFYPAASTPGC*TK.									
		Q	2	35.7	37.2	49.5	58.7	32.5	29.4	58.0	49.6

		R.LQAGDTAPAFSLPDADGN									
		TVSLSDYR.G	2	73.8	93.5	97.2	120.1	39.6	46.1	74.1	79.5
		R.LQAGDTAPAFSLPDADGN									
		TVSLSDYR.G	3	443.9	509.2	490.6	545.5	290.0	342.8	354.0	456.4
		R.SVLTAWGAYGEK.T	2	250.8	241.1	336.0	320.5	186.8	184.4	330.0	313.1
MSMEG	MSMEG										
_4755	4745	K.AATAEALLLDALGR	2	59.4	49.3	107.4	90.3	44.3	42.9	147.5	110.2
		K.PAVTVIGIDTTPIGK.S	2	121.6	124.4	124.9	139.0	63.1	62.5	96.9	133.9
MSMEG	MSMEG	K.AGWYDTETGELVPEC#EI									
_4757	4747	VER.Y	2	43.3	42.4	46.3	49.3	60.5	65.7	49.6	57.0
		K.AGWYDTETGELVPEC*EI									
		VER.Y	2	43.3	42.4	46.3	49.3	60.5	65.7	49.5	56.9
		K.AREEM*SGAADESDDDEAP									
		AGTIR.A	3	3.7	1.6	2.5	1.0	3.3	2.9	1.1	1.4
		K.AREEMSGAADESDDDEAP									
		AGTIR.A	3	90.6	63.2	88.5	63.1	65.9	75.7	55.3	60.4
		K.DAQTPPTLLFPFAAPR.V	2	193.3	173.0	172.9	145.1	367.3	302.6	286.6	215.0
		K.DAQTPPTLLFPFAAPR.V	3	13.4	12.0	7.0	6.4	21.9	25.7	7.6	12.8
		K.DFVAEISER.T	2	11.6	7.7	4.2	1.8	2.6	4.1	0.1	0.4
		K.DVELLALAQLIGAAGTLVA									
		R.R	3	5.8	6.2	3.5	3.9	14.3	10.3	6.8	5.3
		K.ELTESILVR.Q	2	24.0	21.1	18.4	14.3	30.4	27.6	13.5	14.0
		K.GGAAVFQM*MGLC#QILR.									
		D	2	5.0	6.4	1.2	2.3	12.1	10.4	1.6	1.9
		K.GGAAVFQMMGLC#QILR.									
		D	2	25.4	23.0	14.3	12.7	41.6	33.4	28.1	20.3
		K.GGAAVFQMMGLC*QILR.									
		D	2	23.4	21.3	14.2	12.7	40.6	32.4	28.1	20.3
		K.GSIAASVVGQLLDGGATVI									
		ATTSR.L	2	35.7	38.0	45.9	44.2	21.4	37.4	16.9	31.7
		K.GSIAASVVGQLLDGGATVI									
		ATTSR.L	3	97.4	100.1	108.5	116.0	111.1	103.9	115.5	92.5
		K.GSIAASVVGQLLDGGATVI									
		ATTSR.L	4	4.4	5.2	2.3	2.0	6.0	4.9	2.2	1.3
		K.HDTSTLANDPNETELHER.									
		I	3	0.7	0.7	0.3	0.3	1.3	1.1	0.3	0.4
		K.HVTVEFALGTR.E	2	14.8	13.6	152.2	149.0	23.1	20.5	119.9	118.0

K.IVAAAAANAGHWAELAGGG QVTEQIFNDR.I	3	287.9	271.0	294.9	281.7	364.6	416.6	340.2	343.4
K.IVAAAAANAGHWAELAGGG QVTEQIFNDR.I	4	59.1	55.3	60.5	63.5	81.8	86.2	58.9	67.9
K.LPEYSHSTVEVLNSER.D	2	65.6	51.3	58.3	46.3	116.8	78.2	94.1	53.5
K.LPEYSHSTVEVLNSER.D	3	298.7	312.5	299.3	312.7	338.6	368.3	282.6	292.4
K.LVEWVGTEQTESLGPQSI HLK.D	3	473.0	495.2	609.0	601.7	403.1	448.7	450.3	479.1
K.LWLAEEGDIDAQWEQLS QR.F	3	10.5	9.9	3.6	3.4	20.0	26.3	7.7	12.3
K.M*GLPVLAVVGYAQSFAD GVHTSIPAPGLGALGAAR.G	4	25.3	33.5	20.1	27.2	7.2	19.2	7.9	15.0
K.PVNFVPVIDKDVR.R	3	12.9	10.3	6.9	6.3	7.3	9.8	7.2	8.4
K.PYFGDVAEM*TYLQWLR. R	2	7.5	7.6	4.1	3.4	13.5	11.9	4.2	4.1
K.PYFGDVAEMTYLQWLR.R	2	28.8	39.1	4.1	3.9	35.3	38.6	12.9	9.5
K.QLTSAAVSVPGVLLTQIAA VR.A	2	6.8	5.4	3.6	2.9	20.3	14.6	12.1	7.1
K.QLTSAAVSVPGVLLTQIAA VR.A	3	23.8	25.6	14.9	13.9	46.9	42.3	30.7	23.3
K.RPDSPWLDITWR.D	2	33.6	30.2	21.4	18.3	54.8	52.2	32.5	27.1
K.RPDSPWLDITWR.D	3	40.2	36.0	23.3	19.9	49.4	57.0	23.2	25.9
K.SAPTVAGLATNTLK.L	2	431.8	412.4	670.7	656.7	459.0	461.3	639.9	587.7
K.TLGKPVNFVPVIDK.D	2	22.4	20.3	16.0	16.2	26.6	19.2	16.3	9.0
K.TLGKPVNFVPVIDKDVR.R	3	88.5	78.7	57.6	50.6	166.7	138.9	99.5	80.3
K.TVYAFPGQGIQHK.G	2	24.7	8.4	4.6	4.5	16.9	10.4	5.5	5.0
K.TWELGPGWAK.H	2	117.0	110.4	93.2	91.5	127.1	142.2	84.3	95.0
K.VDLTGGLGDIK.I	2	197.8	186.4	181.2	168.1	227.9	221.3	180.4	166.3
K.VIDGAVAAVAAR.R	2	5.6	4.9	3.5	3.9	4.1	3.4	2.5	4.4
K.VLLWAVQR.L	2	182.4	162.0	148.7	128.8	218.1	224.6	160.3	153.5
K.VTGPDGVLASAAR.L	2	9.2	10.3	7.6	8.6	13.2	13.2	10.7	11.3

K.VVDNTATVTVDWDPER.V	2	130.6	122.2	105.2	109.4	173.6	180.9	125.3	131.2
R.AAALLAGLEGPIVHGMWL									
SAAAQHVVVTATDGKPVPPA									
K.L	4	56.6	64.2	44.6	42.5	77.2	74.0	52.5	48.5
R.AAALLAGLEGPIVHGMWL									
SAAAQHVVVTATDGKPVPPA									
K.L	5	58.4	58.6	46.0	47.7	73.5	77.7	46.7	48.5
R.AFVQFDPEHTVAR.P	2	63.1	46.6	43.5	34.6	73.7	42.3	37.2	22.4
R.AFVQFDPEHTVAR.P	3	108.7	97.7	69.3	70.1	79.1	84.0	39.5	41.9
R.AFVQFDPEHTVARPLPDS									
SDWEVTR.K	3	52.4	43.3	38.7	33.5	135.3	97.8	93.5	58.5
R.AFVQFDPEHTVARPLPDS									
SDWEVTR.K	4	139.6	153.8	453.3	457.4	225.6	283.6	354.9	392.9
R.AGGHHSWEDLDDLLLAT									
YSEL.R.S	4	4.7	4.9	1.9	1.8	7.7	8.9	2.7	3.7
R.AIQFNTLFLDPYLWK.L	2	55.5	66.4	59.1	61.6	83.4	109.4	62.1	80.4
R.APGNPLFIVSQK.T	2	231.1	212.3	228.2	200.3	296.3	271.2	241.8	208.8
R.AVLAIAAGVEGPENLPK.V	2	309.9	298.4	293.1	285.5	409.9	387.4	330.3	297.6
R.AVLAIAAGVEGPENLPK.V	3	58.7	55.3	61.2	58.6	67.3	73.4	54.5	60.3
R.DASGPLAVVLDAPDVLWA									
GR.M	2	87.6	64.4	82.9	62.2	95.3	76.9	69.2	58.6
R.DASGPLAVVLDAPDVLWA									
GR.M	3	20.8	22.7	11.0	14.0	17.7	26.8	7.4	15.2
R.DEIIAAMAQTAK.P	2	58.1	52.9	43.4	37.1	62.0	55.8	38.5	35.3
R.DLVPAEPLDEVLYDTW									
R.N	2	102.5	112.3	97.1	105.0	82.5	129.1	59.2	98.0
R.DLVPAEPLDEVLYDTW									
R.N	3	27.6	36.8	23.1	34.8	18.4	43.0	8.9	30.4
R.DVTVGAPVDMRPFVVS									
GDHNPIHTDR.A	3	24.7	25.3	2.0	1.0	45.7	34.6	12.9	6.4
R.EEMSGAADESDEAPAG									
TIR.A	2	4.5	2.6	2.7	1.3	1.1	1.8	0.3	0.4
R.EFVDDGAIDPDHASPLL									
SVFLDK.D	3	53.1	53.7	43.4	45.1	35.6	41.1	30.2	30.2



R.ETLGFSVLHVVR.D	2	48.8	38.9	122.6	104.0	130.2	96.4	152.8	102.2
R.FEGTGHVVATQANWWQ									
GK.A	2	22.9	19.7	13.0	11.3	42.3	38.9	23.2	19.9
R.FEGTGHVVATQANWWQ									
GK.A	3	208.6	204.2	219.9	202.6	190.2	258.0	180.8	193.4
R.FELYC#TQIAEK.E	2	53.4	49.0	48.7	44.4	43.2	39.3	32.1	31.5
R.FELYC#TQIAEKKEEAER.K	3	69.5	67.2	79.3	65.6	75.3	86.4	72.4	70.5
R.FELYC#TQIAEKKEEAERK.									
N	4	12.5	13.4	5.6	11.8	35.2	40.5	22.0	25.7
R.FEQAAVDEVLGAGAEPVE									
VLSR.R	2	55.1	51.4	48.3	48.7	48.0	51.3	33.0	32.4
R.FEQAAVDEVLGAGAEPVE									
VLSR.R	3	150.3	166.7	131.0	136.7	112.0	145.7	75.4	99.7
R.FLGM*VKPGDQVDFR.V	2	9.9	9.2	23.9	24.4	26.3	13.4	32.6	27.3
R.FLGMVKPGDQVDFR.V	2	67.5	60.8	56.8	33.9	95.1	71.8	71.4	45.5
R.FTLTDVVR.S	2	5.1	6.4	2.4	1.9	6.8	9.3	0.3	0.9
R.GGAVFAPVFDPVQVEVG									
FHTPR.L	3	225.3	200.5	215.5	173.0	284.7	256.6	225.7	184.7
R.GGDLGGLHAGALASAAD									
VDK.V	2	78.7	76.3	24.0	22.5	83.0	66.7	32.1	20.2
R.GGDLGGLHAGALASAAD									
VDK.V	3	129.2	126.7	111.8	112.3	101.8	107.9	83.3	77.1
R.GGDLGGLHAGALASAAD									
VDKVIDGAVAAVAAR.R	3	30.8	31.8	30.5	38.7	58.2	58.7	36.3	39.4
R.GGDLGGLHAGALASAAD									
VDKVIDGAVAAVAAR.R	4	72.9	73.4	71.7	69.7	147.6	160.3	118.7	121.3
R.GGDLGGLHAGALASAAD									
VDKVIDGAVAAVAAR.R	5	15.9	10.5	1.1	0.7	7.2	16.1	2.0	2.9
R.GISVSLPSAGGASGGVVD									
SAALGEFAEK.V	3	130.1	144.5	109.1	126.5	107.3	158.7	70.3	109.5
R.GITVLGDRPPM#VSVTNA									
DPER.I	3	99.4	102.0	80.0	77.6	105.2	109.7	69.0	70.1
R.GITVLGDRPPM*VSVTNA									
DPER.I	3	99.0	101.1	73.6	74.6	104.8	106.2	68.2	69.3
R.GITVLGDRPPMVSVTNAD									
PER.I	3	243.4	232.7	197.9	197.2	260.5	257.7	180.4	180.5

R.GLGIGIVPAATR.G	2	217.3	242.8	216.7	230.3	377.3	331.7	336.8	262.9
R.GSQYAIAGTVAGLEALEE									
EIER.R	2	67.5	61.7	62.2	56.0	74.4	81.5	55.2	62.1
R.GSQYAIAGTVAGLEALEE									
EIER.R	3	76.9	95.8	59.1	69.5	78.0	122.1	52.9	80.4
R.IAAEVPTKPVIVHIEGGR.A	2	13.4	12.0	3.1	3.3	51.5	23.6	21.6	8.3
R.IAAEVPTKPVIVHIEGGR.A	3	189.9	174.4	112.9	113.4	314.9	257.7	182.0	141.0
R.IAAEVPTKPVIVHIEGGR.A	4	262.8	252.4	259.2	235.6	363.5	369.0	286.3	279.8
R.IAAPTEWQVR.E	2	175.2	161.4	132.1	115.4	182.0	195.3	116.6	121.0
R.IAELETLLPEGR.A	2	287.4	247.3	277.5	235.3	331.1	375.9	291.5	293.1
R.IDQIEALDSIESITDGASSR									
.R	2	45.8	40.7	6.5	5.4	90.7	77.0	3.0	5.6
R.IGSELM*AATAR.L	2	4.7	5.1	1.0	1.2	4.7	4.2	0.4	1.0
R.IGSELMMAATAR.L	2	102.3	91.7	101.3	94.2	110.3	100.8	102.8	95.8
R.IYELLEEFSSDVR.T	2	192.0	170.5	166.4	151.0	312.2	248.1	251.9	176.8
R.IYELLEEFSSDVR.T	3	13.1	13.2	5.4	6.3	18.2	21.6	3.6	8.2
R.LAAIRPSQIDLDDADVK.D	2	14.2	11.6	6.3	8.4	17.9	12.4	8.3	4.5
R.LAAIRPSQIDLDDADVK.D	3	85.7	91.0	80.1	83.0	62.4	63.9	50.6	53.9
R.LAAIRPSQIDLDDADVKDF									
VAEISER.T	3	28.9	34.0	127.2	118.6	72.3	65.4	97.2	105.9
R.LAAIRPSQIDLDDADVKDF									
VAEISER.T	4	87.0	104.0	82.4	93.1	184.4	157.3	128.3	117.9
R.LEVADDQHVVLSVPLSGT									
WIEIR.F	3	7.9	9.9	8.1	8.6	23.6	16.5	11.2	10.1
R.LGFLEAQGGGTILLAR.G	2	125.0	108.3	92.0	74.9	189.1	141.8	118.1	86.0
R.LHPQDFGPIETLFDADAD									
GER.L	3	293.3	270.5	297.1	273.0	348.7	354.5	299.3	296.0
R.LHVVLPGSPNR.G	2	3.4	2.9	4.6	4.8	6.8	5.0	4.7	6.0
R.LLAELPKPAEFTVTAK.A	2	32.9	25.0	27.1	19.3	110.1	75.6	83.2	49.7
R.LLAELPKPAEFTVTAK.A	3	190.1	166.0	177.9	157.1	284.7	332.6	218.3	247.4

R.LLDEVAGDADAVAER.R	2	405.4	412.7	395.7	398.1	547.9	522.9	431.6	394.5
R.LLDEVAGDADAVAER.R	3	54.5	55.2	42.6	41.9	56.8	70.1	37.8	42.3
R.LLEDPEAAITALLQR.Y	2	167.2	173.4	142.9	137.0	268.9	241.3	203.4	165.0
R.LLEDPEAAITALLQR.Y	3	122.9	129.4	91.5	97.9	178.5	173.5	114.8	103.1
R.LSDGIEIVGR.W	2	6.7	6.7	4.2	4.2	12.9	11.8	6.1	4.5
R.NAADGALLATLEER.F	2	273.5	252.9	282.5	259.9	384.8	358.1	330.3	301.7
R.NAADGALLATLEER.F	3	23.8	26.6	15.2	15.5	26.7	37.4	12.0	17.4
R.NLFTVGAVPEVAR.P	2	240.7	241.7	322.2	274.6	341.1	286.9	346.0	263.2
R.NLFTVGAVPEVARPWSSY									
APTVVK.L	3	6.1	6.6	8.0	12.8	31.1	40.6	26.3	36.6
R.PFAVVSGDHNPIHTDR.A	3	7.7	6.4	8.6	14.6	5.7	5.0	7.7	14.4
R.PFAVVSGDHNPIHTDR.A	4	20.1	18.5	9.3	8.7	11.5	14.2	3.7	4.8
R.PFTLDRDFIQEIR.D	3	51.7	46.3	34.9	31.8	89.9	92.7	49.6	53.7
R.PIGFEPLQWVR.A	2	16.3	15.7	14.3	17.7	16.9	14.3	9.4	9.2
R.PLPDSSDWEVTR.K	2	167.5	184.1	156.4	174.1	120.5	125.2	90.2	85.8
R.PSQIDLDDADVKDFVAEIS									
ER.T	3	16.2	22.3	14.2	18.6	18.0	18.6	8.5	11.2
R.PWSSYAPTVVK.L	2	172.3	167.2	179.2	166.3	160.4	168.2	137.3	139.1
R.QVDWVDEITELHEAGAR.									
W	2	21.7	16.5	19.7	18.5	28.9	22.8	16.2	13.8
R.QVDWVDEITELHEAGAR.									
W	3	21.7	16.7	16.0	11.3	44.1	41.0	28.4	25.3
R.RDASGPLAVVLDAPDVLW									
AGR.M	3	34.8	33.2	38.4	33.7	56.9	47.5	46.4	37.6
R.RDEIIAAMAQTAK.P	2	33.4	25.3	16.2	14.5	52.8	40.0	14.5	13.0
R.RDEIIAAMAQTAK.P	3	34.7	24.8	18.6	9.8	39.6	37.7	10.5	12.1
R.RGISVSLPSAGGASGGVV									
DSAAALGEFAEK.V	3	139.1	130.9	114.9	104.6	233.9	218.4	159.9	151.8
R.RYVELAIGDGNSTADTK.R	2	4.3	4.1	4.6	3.7	9.1	6.7	8.1	6.7
R.RYVELAIGDGNSTADTK.R	3	29.5	26.6	21.7	19.4	30.3	39.1	17.1	23.4
R.SFILVPGIDVPPFHSSVLR.V	2	28.9	27.7	17.1	16.4	70.4	46.8	39.9	23.3
R.SFILVPGIDVPPFHSSVLR.V	3	112.3	129.2	85.9	104.3	165.9	156.1	124.2	101.4

R.SGGAPIVEVDDAATAM#R. A	2	46.7	41.1	93.0	81.4	52.6	45.0	54.9	53.8
R.SGGAPIVEVDDAATAM*R. A	2	46.7	41.1	80.7	72.8	52.6	45.0	50.8	49.8
R.SGGAPIVEVDDAATAMR. A	2	309.5	245.8	246.1	201.3	292.0	259.6	220.0	186.4
R.SGGAPIVEVDDAATAMR. A	3	20.4	23.7	5.4	10.0	18.1	27.3	1.9	9.8
R.SLAQLGVGADDIAVISK.H	2	373.0	361.0	487.8	487.9	503.1	444.4	484.5	495.6
R.SLDC#VDDDELATSGHFVW VR.E	3	42.1	36.1	58.2	54.5	75.7	68.3	57.4	58.0
R.SNITIC#VGGGIGTPER.S	2	39.5	35.6	11.9	14.0	55.2	58.5	21.3	21.8
R.SPILLAGM#TPTTVDAK.I	2	95.3	96.3	94.6	97.8	115.4	102.4	88.7	76.9
R.SPILLAGM*TPTTVDAK.I	2	267.5	274.7	521.4	521.7	299.7	226.3	569.8	466.5
R.SPILLAGMTPTTVDAK.I	2	477.8	484.1	830.4	836.5	546.8	479.9	891.6	779.7
R.SQLGADIHEIDNAASR.C	2	99.2	93.8	63.2	51.2	135.8	115.2	79.5	61.4
R.SQLGADIHEIDNAASR.C	3	176.0	191.5	129.8	136.6	219.5	235.1	140.7	130.8
R.SVVITGTPEQLSR.F	2	174.3	159.7	148.9	139.8	129.0	163.1	96.7	113.2
R.TADGNAADTAHALVDR.L	2	1.4	1.1	1.1	0.7	3.6	2.3	1.4	0.4
R.TADGNAADTAHALVDR.L	3	9.5	9.0	5.0	4.8	10.7	11.5	3.7	4.7
R.TGEFLEIVNFNLR.G	2	37.2	38.7	1163.2	1260.7	99.7	68.3	349.7	274.7
R.TVLPPVLSIR.N	2	226.0	197.7	203.7	176.7	324.6	274.5	247.9	202.9
R.TYKPFPGPVLSDAINDQLR. T	2	14.3	15.1	28.1	25.1	38.3	28.9	33.7	22.7
R.TYKPFPGPVLSDAINDQLR. T	3	306.2	281.9	241.6	235.3	363.4	422.2	271.7	274.2
R.VADHTGVTATFGAPLAPT LTVVPDALVGR.C	3	444.3	353.5	370.6	286.5	424.7	359.5	324.9	239.4
R.VDEPVGELLDR.F	2	134.4	124.1	209.4	212.8	105.9	107.8	150.0	128.9
R.VGIDVGAEVLEVSAR.I	2	152.4	161.5	225.2	227.4	220.4	213.3	272.3	255.5
R.VGIDVGAEVLEVSAR.I	3	5.7	8.2	1.2	1.4	6.9	12.9	0.7	2.1
R.VSLAHALIGWTK.G	2	48.8	39.8	45.3	36.0	89.6	70.5	65.2	46.0
R.VSLAHALIGWTK.G	3	72.5	63.2	44.2	40.7	106.7	115.0	61.5	64.5
R.WAETVGLDVELAK.E	2	14.7	13.1	27.8	78.9	50.5	44.9	88.5	133.0

		R.WIETQDLLFIEEAAGGLGV									
		ER.F	3	2.2	2.2	1.1	1.3	15.1	15.4	8.2	11.3
		R.WILDLGPGDILTR.L	2	113.3	119.2	99.4	109.2	268.8	231.7	197.6	178.4
		R.YEADQVC#VIPGTAAVAGI									
		TR.V	2	73.5	72.1	68.7	61.7	105.5	102.7	92.7	73.2
		R.YEADQVC#VIPGTAAVAGI									
		TR.V	3	53.9	50.0	63.2	61.0	51.7	71.0	47.9	64.4
		R.YEADQVC*VIPGTAAVAGI									
		TR.V	2	73.5	72.1	68.7	61.7	105.5	102.7	92.7	73.2
		R.YPDAETVVLHPADVPFFV									
		ELC#K.T	3	137.7	148.1	109.1	123.3	193.1	209.5	139.0	146.2
		R.YPDAETVVLHPADVPFFV									
		ELC*K.T	3	137.7	148.1	109.1	123.3	193.1	209.5	139.0	146.2
		R.YVELAIGDGNSTADTK.R	2	86.9	68.2	81.8	56.5	72.9	78.1	58.7	56.3
MSMEG	MSMEG										
_4847	4835	K.HELLLALFEDALSR.S	3	11.5	11.3	10.3	8.1	5.6	4.8	4.8	4.6
		K.RPLFTDFAPR.L	3	10.1	3.3	5.3	0.2	8.5	7.1	4.2	1.7
		K.VAIQLLFESSRPDPAAK.R	3	37.9	37.7	41.9	36.5	24.1	20.5	17.0	23.8
MSMEG	MSMEG										
_4888	4874	R.HGIVLSLQFETDDDR.N	3	0.1	0.1	1.7	1.4	1.2	2.0	0.7	1.1
MSMEG	MSMEG										
_4891	4876	K.DFTFVC#PTEIAAFGK.L	2	867.3	840.2	54.4	41.2	358.7	367.0	19.9	20.6
		K.VLGVSVSDNEFVHFQWR.A	3	412.2	411.4	3.1	2.2	161.1	172.7	1.1	1.3
		R.ATFIVDPNNEVQFVSVTA									
		GSVGR.N	2	387.9	369.0	4.1	4.7	266.8	245.4	4.2	2.8
		R.ATFIVDPNNEVQFVSVTA									
		GSVGR.N	3	763.4	729.1	24.4	24.6	536.2	511.2	28.9	29.0
		R.ELTAAC#GVLNADGVADR									
		.A	2	1039.7	1268.7	23.4	32.6	617.3	598.1	9.8	21.7
		R.ELTAAC#GVLNADGVADR									
		.A	3	59.8	64.9	2.5	2.2	18.2	28.0	1.9	3.3
		R.VLDALQSDELC#AC#NWK									
		.K	2	1487.5	1614.8	71.2	73.0	847.6	849.0	66.3	78.1
		R.VLDALQSDELC#AC#NWK									
		.K	3	28.6	23.6	0.7	0.0	15.2	16.7	0.4	0.5

MSMEG	MSMEG	K.GSGQGWLTAEYAMLPA										
_4901	4886	THDR.S	3	38.7	50.3	62.5	74.4	28.7	30.9	36.7	40.7	
		R.EALDAPYPGVLPEGPAPK.										
		K	2	134.6	151.1	179.7	214.7	203.2	207.5	204.2	253.0	
MSMEG	MSMEG	R.FSVGSFDAVR.R	2	25.8	25.6	6.8	11.1	17.6	23.7	2.5	2.8	
_4905	4890											
		R.IIFSPAEGGSNTAVATAK.E	2	120.6	117.1	68.7	66.9	92.0	102.0	30.3	38.3	
MSMEG	MSMEG	K.EVITDLENNYSGISER.I	2	57.2	70.2	25.7	25.3	55.5	59.0	23.6	29.7	
_4906	4891	R.FVNIYVNDEDVR.F	2	54.0	62.4	31.7	32.3	51.5	59.9	26.6	33.8	
MSMEG	MSMEG	R.GFLDADTLDYLAGYR.F	2	30.3	26.1	61.3	42.3	35.2	35.7	87.0	66.9	
_4911	4896											
MSMEG	MSMEG	R.VTETGEVAVYPVAPQAR.										
_4914	4899	P	2	24.2	26.5	15.0	10.5	26.0	31.2	13.7	14.6	
MSMEG	MSMEG	K.RLDELAADHSFLDR.L	3	174.4	153.7	114.0	105.2	119.5	117.1	86.9	112.5	
_4915	4900	K.SALNGGLNLSIR.D	2	97.4	84.7	205.8	173.6	88.6	75.7	163.0	154.2	
		K.SASDLGLPLIAVGLYYR.S	2	41.2	42.0	98.2	101.6	76.0	68.1	147.3	145.4	
		R.AFTEIEGLPAPEVFMNE										
		GHAGFLGAER.I	4	119.0	130.3	180.0	169.7	129.0	135.1	183.6	200.4	
		R.DDLEAAALYDLLENAP										
		K.F	2	152.0	171.3	117.4	124.2	165.6	208.4	128.5	166.6	
		R.ELIGGELAESALESSEVWE										
		R.L	2	78.3	78.6	135.5	136.4	99.0	95.4	173.6	163.3	
		R.IKQEILAGIGGVR.A	2	38.8	36.2	57.8	47.2	66.2	50.8	122.6	80.6	
		R.IKQEILAGIGGVR.A	3	53.5	38.2	43.6	33.7	82.9	62.2	89.2	69.7	
		R.IPLLLLDSDIPENEHDLR.G	3	244.1	252.0	364.1	394.0	342.1	268.7	582.9	406.5	
		R.LDELAADHSFLDR.L	2	22.0	20.9	87.7	72.8	24.6	22.4	75.3	67.7	
		R.LDELAADLDNYLTR.P	2	36.3	46.7	57.1	69.5	25.9	28.0	29.6	33.0	
		R.LLLDPDRPVQLIVAGK.S	2	60.5	51.4	185.0	148.6	103.1	70.6	233.9	147.6	
		R.LLTAADGDPVLIELALPEG										
		R.D	2	83.4	98.4	134.7	161.2	128.5	131.5	196.9	205.9	
		R.LQQVEPGHLWWIR.S	2	41.0	29.0	109.4	106.7	45.0	31.9	145.8	127.4	
		R.LQQVEPGHLWWIR.S	3	77.0	75.3	98.6	100.3	92.7	93.5	140.6	135.1	

		R.NDGDPVALLGSVSPK.R	2	92.8	107.5	209.0	222.7	139.1	141.8	288.5	288.5
		R.PLWYQQQLDTGVAMPK.									
		G	2	44.4	41.5	101.2	106.5	23.0	30.6	43.7	88.6
		R.RDDLEAAAALYDLLENAVA									
		PK.F	3	41.0	44.3	79.2	88.5	54.9	56.6	192.8	115.2
		R.SSTVFTTHTPVPAGIDR.F	3	96.3	101.3	173.0	153.0	72.4	90.3	155.2	152.4
MSMEG	MSMEG										
_4916	4901	K.FHHLNDNDALLAYSK.F	3	25.1	28.1	2.9	3.4	39.3	43.1	4.9	5.0
		K.NEDPDILFLSEAFTR.P	2	17.1	17.9	11.7	9.9	16.7	13.8	8.5	8.4
MSMEG	MSMEG	R.LEIDYPGVGDAVVTHTTA									
_4918	4902	DAYR.F	3	164.2	157.3	235.9	246.6	129.2	146.2	234.1	256.8
		R.LLAGEHHDPHPSVLGAHEY									
		PGHTVIR.A	4	48.6	52.8	35.5	41.0	32.3	55.2	27.0	52.2
		R.SSNQLTDAHLRPDPSTDIH									
		R.L	4	31.6	21.1	42.9	29.0	19.1	11.5	40.0	25.2
MSMEG	MSMEG	K.LSGSGEAEQVDPALAAQA									
_4917	4903	R.A	2	29.8	26.1	12.8	12.0	13.5	18.0	4.2	6.6
		K.LSGSGEAEQVDPALAAQA									
		R.A	3	31.1	20.3	36.6	21.1	23.4	26.7	30.7	34.8
MSMEG	MSMEG										
_4920	4905	K.DFSGTDLGAIAIR.A	2	702.2	658.4	750.1	700.5	1129.9	1047.3	806.3	751.5
		K.DGVFADEVVPVSIPQR.K	2	1991.6	1942.6	2052.7	1953.9	2667.4	2781.0	2269.7	2299.2
		K.DGVFADEVVPVSIPQR.K	3	45.1	41.1	23.1	28.6	51.9	60.2	18.8	17.2
		K.GDPIEFAEDEGIR.A	2	550.6	525.9	835.5	991.2	832.2	847.9	624.8	654.0
		K.M#C*LSGIDAIALADQLIR.A	2	174.3	164.2	139.7	148.8	126.0	124.6	83.3	86.0
		K.M*C#LSGIDAIALADQLIR.A	2	205.7	205.7	171.7	181.4	163.7	173.7	120.5	127.3
		K.MC#LSGIDAIALADQLIR.A	2	800.4	840.8	473.1	449.3	921.3	983.3	562.3	517.8
		K.MC#LSGIDAIALADQLIR.A	3	41.5	54.1	34.2	42.4	89.4	82.4	48.4	49.2
		K.MC*LSGIDAIALADQLIR.A	2	800.4	840.8	470.6	448.2	921.3	983.3	559.4	516.5

		K.MC*LSGIDAIALADQLIR.A	3	41.5	53.9	34.2	42.4	89.4	82.4	48.4	49.2
		K.VNVNGGAIAIGHPIGMSG									
		AR.I	2	256.4	301.5	289.9	328.7	243.3	225.8	241.3	291.1
		K.VNVNGGAIAIGHPIGMSG									
		AR.I	3	802.9	852.2	872.0	826.9	771.4	589.8	604.3	500.4
		K.YGDATLVDHLAYDGLHDV									
		FTDQPMGALTEQR.N	4	516.4	541.6	514.8	563.3	446.1	408.6	313.7	284.6
		R.AGEFDVIVAGGQESM*SQ									
		APHLLPK.S	3	400.9	418.7	478.4	515.3	528.9	539.9	477.1	435.1
		R.AGEFDVIVAGGQESMSQ									
		APHLLPK.S	3	1817.2	1688.5	1677.6	1620.3	1624.3	1506.8	1096.2	990.9
		R.AGEFDVIVAGGQESMSQ									
		APHLLPK.S	4	67.7	66.6	41.4	35.5	37.5	44.1	4.7	12.2
		R.ANTTAESLAGLKPAFR.K	2	605.6	388.0	696.9	531.5	1029.4	960.9	772.6	774.9
		R.ANTTAESLAGLKPAFR.K	3	1183.0	757.6	853.7	512.0	2144.8	2123.3	1172.1	1160.2
		R.GSGYAVAALC#GAGGQG									
		DALVLR.R	2	314.0	320.3	279.2	274.5	359.5	328.5	236.7	198.1
		R.GSGYAVAALC*GAGGQG									
		DALVLR.R	2	314.0	320.3	266.6	268.3	359.5	328.5	230.2	185.0
		R.IALHAAELAR.R	2	273.9	286.5	162.8	186.2	314.7	281.8	106.8	115.2
		R.KGDPIEFAEDEGIR.A	2	489.9	387.2	526.4	462.0	659.9	719.0	554.7	589.0
		R.KGDPIEFAEDEGIR.A	3	248.1	145.3	102.4	40.0	342.1	326.0	156.7	157.8
		R.QAAVAAGIPWDVAALSIN									
		K.M	2	195.2	183.1	189.9	197.9	366.8	317.7	231.7	235.3
MSMEG	MSMEG										
_4921	4906	K.DAGGVLIELVEPSPEEH	2	127.7	154.0	14.8	24.8	176.5	183.9	13.3	18.0
		K.GSAQIQLLAPIDEK.S	2	194.3	214.4	433.0	484.9	261.7	266.3	403.7	444.5
		R.GPGLQQLAYR.T	2	2.5	2.1	6.1	6.2	3.4	5.6	6.6	7.7
		R.PALASALVTAIDHVGIAVP									
		DLDAAAK.W	3	273.0	319.2	82.4	92.0	297.8	338.9	58.7	65.0
		R.PALASALVTAIDHVGIAVP									
		DLDAAAK.W	4	79.7	51.7	14.6	9.9	93.3	93.5	13.3	12.8
MSMEG	MSMEG	R.AGAGLVLAGLVADGETEV									
_4932	4917	HDVFHIDR.G	4	56.9	50.4	11.6	11.8	46.3	61.0	9.2	10.4
		R.GIPQLSSAPVWSSDIR.A	2	205.3	216.5	273.6	245.7	184.4	196.8	199.1	208.7



		R.GYPLFVENLVSLGAEIER.V	2	67.2	66.0	13.4	10.7	78.9	78.4	5.2	9.9
		R.LSGEVAVGGAK.N	2	4.9	3.6	0.1	0.0	5.0	3.7	0.0	0.0
MSMEG	MSMEG										
_4934	4918	R.LSDLLFILSR.V	2	63.6	62.1	33.7	40.6	49.1	46.4	22.3	23.2
		R.SAWIAVNEFGDSVSVLPA									
		K.Y	2	127.2	124.9	61.1	65.1	81.9	94.7	39.6	48.7
		R.VANPEGDVLWKPGANQ	2	230.7	236.5	153.0	152.1	225.7	232.6	160.9	170.1
MSMEG	MSMEG										
_4935	4920	R.ELWSGPATFVFTR.T	2	62.7	63.3	108.7	105.8	239.6	216.5	146.9	123.8
		R.HIPLVAQLVDDAMVR.V	3	7.9	6.5	10.7	11.0	25.6	25.2	9.0	9.5
		R.IAVDGGFLSVTEETVR.I	2	125.8	125.8	103.8	104.5	258.4	248.3	102.4	90.2
		R.ILVENAQFESEIDADAAKE									
		DAASDDER.T	3	64.8	73.1	82.5	104.6	270.0	259.6	121.2	121.0
MSMEG	MSMEG										
_4936	4921	K.DTALVFGQMDEPPGTR.M	2	246.8	252.3	323.0	300.2	339.2	393.0	136.1	149.3
		K.GEFDHLPEQAFFLIGGLD									
		DLAK.K	2	13.6	20.1	30.9	44.1	55.5	78.7	29.4	40.4
		K.GEFDHLPEQAFFLIGGLD									
		DLAK.K	3	254.0	286.7	529.7	609.3	968.0	1054.0	657.0	727.6
		K.GHVFNALGDC#LDDPGY									
		GK.D	3	35.2	33.3	74.9	65.0	100.1	124.1	58.8	64.7
		K.GIFPAVDPLASSSTILDPAI									
		VGDEHYR.V	3	482.2	517.8	947.7	997.1	1618.7	1798.3	1078.4	1183.7
		K.IALFGGAGVGK.T	2	12.6	12.0	22.3	21.4	114.9	91.3	32.6	17.8
		K.TLTLEVAQHLGDSLVR.C	2	174.3	171.0	730.3	804.7	676.0	622.8	830.1	866.2
		K.TLTLEVAQHLGDSLVR.C	3	166.4	144.9	266.9	237.8	654.7	594.2	300.9	296.2
		K.TVLIQEMINR.I	2	52.2	61.8	104.7	90.9	245.3	249.0	124.2	189.2
		K.VVDLLTPYVR.G	2	120.2	97.8	244.8	193.4	716.4	624.4	384.0	372.6
		R.DEQGQDVLLFIDNIFR.F	2	217.1	233.8	326.7	344.7	442.4	656.4	283.9	418.6
		R.DEQGQDVLLFIDNIFR.F	3	12.1	12.0	8.9	14.1	32.6	44.6	11.7	19.8
		R.EGNDLWVELADANVLK.D	2	196.7	183.8	327.7	294.6	593.0	515.2	336.0	291.2
		R.FTQAGSEVSTLLGR.M	2	537.1	510.8	2106.2	2252.6	1979.5	1976.7	2010.4	2107.6
		R.GVEVTDTGASISVPVGDG									
		VK.G	2	419.4	492.2	917.0	1025.3	1703.3	1603.3	942.3	1001.3
		R.ITGPVVDVEFPR.G	2	394.6	407.1	763.5	773.0	1306.6	1277.7	1110.8	1102.2

		R.NFGGTSVFAGVGER.T	2	188.3	164.1	315.2	239.8	811.6	657.0	502.7	390.2
		R.VALSALTMAEFFR.D	2	123.9	113.1	301.4	350.6	430.6	371.8	285.3	217.5
		R.YKDLQDIIAILGIDELSEED									
		KQLVNR.A	3	23.6	33.6	81.9	89.5	128.5	180.4	75.7	117.4
MSMEG	MSMEG	R.AAPMEVEYVGEVETGPR.									
_4937	4922	T	2	7.8	13.0	16.1	17.7	44.1	47.2	3.4	4.6
		R.AEELFSLLR.D	2	2.9	3.7	15.1	14.4	21.5	23.4	19.7	20.6
		R.PYAAEITNMLTELAGASAL									
		DHPLLVER.K	3	28.5	36.3	34.4	38.1	29.0	40.8	7.2	12.7
		R.RAEELFSLLR.D	2	26.1	34.5	46.5	54.9	46.4	45.0	63.3	58.4
		R.TLYSFEPDPETLFDALLPR									
		.Y	2	17.9	25.1	30.8	36.7	48.4	66.4	10.2	17.0
		R.VYAALLEAAASESASR.R	2	28.0	26.6	55.0	63.8	108.7	104.1	71.9	100.9
MSMEG	MSMEG	K.SAEQVAAAQADYEKEM*A									
_4940	4926	EAR.A	3	2.0	3.8	3.8	8.2	15.6	19.5	20.2	17.8
		R.AQASGEVAQTLTQADQQ									
		LSAQGDQVR.S	3	90.2	111.0	78.2	93.2	218.5	224.3	63.3	65.9
MSMEG	MSMEG	R.LQALAEQAEADASADR.									
_4950	4935	A	2	16.6	18.1	2.5	2.4	7.4	14.7	1.5	0.5
MSMEG	MSMEG	K.TGIHPEYVDTTVQC#GC#									
_4951	4936	GHSFTTR.S	3	174.5	198.0	98.3	118.3	214.3	201.0	117.3	115.3
		K.TGIHPEYVDTTVQC#GC#									
		GHSFTTR.S	4	344.3	386.3	163.8	192.4	335.0	377.8	146.9	177.8
		K.TGIHPEYVDTTVQC*GC*G									
		HSFTTR.S	3	174.5	198.0	98.3	118.3	214.3	201.0	117.3	115.3
MSMEG	MSMEG										
_4955	4941	R.AAAMPASAEYLAILR.R	2	46.7	49.8	45.8	42.5	56.2	56.4	63.6	66.4
MSMEG	MSMEG										
_4956	4942	K.AAVHQPWPGLIEAYR.D	3	154.9	132.7	48.6	58.3	101.3	112.1	27.7	53.7
		R.IGSPASWNSAVEAQQQS									
		DGR.F	2	134.4	76.8	73.0	45.0	85.7	102.1	58.2	78.8
		R.IGSPASWNSAVEAQQQS									
		DGR.F	3	120.7	91.1	46.3	30.2	93.9	114.0	27.9	52.5
		R.LPIGDDWTTVTLLGGTP									
		LIHAK.R	3	176.5	198.9	171.8	175.6	98.5	81.0	109.4	109.9

MSMEG	MSMEG										
_4957	4943	K.LPIAPIGFIPTR.Y	2	99.9	84.7	81.1	70.9	109.6	94.9	116.3	86.4
		R.EGITTVSAEDFASAR.A	2	199.2	184.3	279.5	258.3	200.9	195.7	348.4	321.3
MSMEG	MSMEG										
_4958	4944	K.FGTPLFVIDEDDFR.T	2	133.6	121.8	436.9	440.2	144.2	119.5	413.9	425.5
		R.PAVVAVADGQAR.L	2	10.7	9.7	6.5	5.3	8.3	6.6	3.8	2.2
MSMEG	MSMEG	K.GEPTPEDGYAGDYIVDIA									
_4959	4945	QQVIAK.A	3	87.6	76.7	151.0	128.9	113.2	105.8	221.7	168.4
		R.AGTVITLDDLVEAIGVDAA									
		R.Y	2	112.9	112.2	141.7	143.5	96.7	101.4	101.2	134.6
		R.AGTVITLDDLVEAIGVDAA									
		R.Y	3	48.2	51.6	33.0	37.5	56.3	52.3	48.0	37.8
MSMEG	MSMEG										
_4971	4957	R.AALQNPEFTETVVTR.A	2	33.2	41.9	97.7	96.8	11.1	13.3	149.6	153.0
MSMEG	MSMEG										
_4974	4960	K.AQGIPAQFLVDILSDLR.T	2	5.4	4.9	5.3	3.9	6.1	7.5	8.4	9.5
		R.PADAISIADVLR.C	2	9.8	11.3	12.1	13.0	10.4	12.6	13.0	11.7
MSMEG	MSMEG										
_4976	4962	K.NFPNSFVQTDLQQR.L	2	270.3	300.0	232.6	299.5	327.2	351.0	212.1	242.1
		R.EEIGAIVESVAPR.G	2	172.5	188.5	327.6	347.4	192.6	211.5	267.3	295.6
		R.GAFNLGFAPTVVAAATAT									
		R.S	2	599.1	70.5	415.7	181.9	583.6	625.1	361.6	376.3
		R.GVM*ELEGVQAALDATAE									
		LLDR.A	3	37.3	33.1	52.8	51.4	47.0	48.7	42.0	41.3
		R.GVMELEGVQAALDATAEL									
		LDR.A	2	7.3	0.0	7.4	0.0	8.1	10.9	4.2	6.9
		R.GVMELEGVQAALDATAEL									
		LDR.A	3	44.2	39.3	60.5	57.8	56.6	59.7	49.6	49.0
		R.LADSALVLIDC#QNTYTR.									
		G	2	34.6	39.3	21.5	22.8	44.6	46.6	17.3	16.5
		R.LADSALVLIDC*QNTYTR.									
		G	2	34.6	39.3	21.3	22.5	44.6	46.6	17.3	16.5
		R.TAGIPIIIHQHDSGPGSPY									
		DVR.E	3	99.5	115.2	69.2	86.1	132.7	127.0	72.2	59.2
		R.TAGIPIIIHQHDSGPGSPY									
		DVR.E	4	154.0	163.7	96.9	103.2	184.4	196.8	83.9	88.4

MSMEG	MSMEG	R.AGEITHFTGIDSPYQRPK.									
_4978	4965	H	4	9.1	10.2	4.8	3.9	3.9	9.5	1.2	3.9
MSMEG	MSMEG										
_4985	4972	K.HVAVVAC#MDAR.L	2	2.2	1.8	1.1	1.0	1.2	0.7	0.9	0.3
		K.TFSGPLPLPPSK.H	2	128.9	146.3	74.2	101.4	63.9	73.5	44.2	52.1
		R.AIQGETGIKPEWAAESFT									
		DLEEDVR.Q	3	1191.6	1279.8	948.0	989.3	946.2	975.6	890.5	837.0
		R.GFIFDVATGK.L	2	230.5	214.0	178.2	156.0	191.1	195.3	176.9	163.0
		R.ILGLGDGEAHVIR.N	2	166.0	189.2	133.7	131.3	144.9	134.7	139.8	109.8
		R.ILGLGDGEAHVIR.N	3	503.1	0.0	308.6	0.0	470.1	450.1	305.4	265.2
MSMEG	MSMEG										
_4997	4983	K.HLAHDVAVMYK.G	3	1.4	0.2	2.3	0.8	0.1	0.0	0.6	0.6
MSMEG	MSMEG										
_5006	4992	K.FPTSAIAVLR.F	2	3.9	0.0	3.0	0.0	4.4	5.2	2.8	2.6
MSMEG	MSMEG										
_5005	4993	R.FWYEQGSLDNER.Q	2	41.8	48.8	32.0	33.4	29.4	35.7	27.7	31.1
		R.WQAANPAGLVDITR.F	2	112.2	120.5	77.0	80.4	85.7	95.3	72.2	66.1
MSMEG	MSMEG										
_5022	5007	K.ADLTFASLPYR.I	2	3.4	3.5	8.7	10.5	9.2	9.3	14.7	10.2
		R.AWTLLTTLQELK.G	2	1.9	1.5	27.7	28.1	18.3	12.4	53.1	33.9
		R.VDAWLADFESALAAAR.D	2	5.7	6.3	27.5	31.8	16.3	13.6	44.5	31.7
MSMEG	MSMEG	K.GSLLLEDVGVPLPALADLV									
_5037	5024	SGVEK.I	3	118.4	150.3	46.1	61.0	87.1	113.0	46.7	63.8
MSMEG	MSMEG										
_5042	5030	K.LIEAELPSVEDVNAQR.V	2	102.7	108.5	99.6	111.0	78.7	88.9	105.8	149.5
		K.TAAFAIPILSK.I	2	29.3	27.8	18.5	18.8	25.6	18.8	24.4	22.8
		K.VGPGHIVGAIANEGGLHR.									
		N	4	62.1	43.6	25.4	22.3	47.9	50.9	38.7	46.5
		K.YLHDPVEVTVK.A	3	6.4	3.0	1.5	0.0	2.5	1.3	2.2	0.9
		R.DSISDSLAPGIDLFR.R	2	46.2	46.7	34.2	39.5	24.2	26.7	37.8	30.8
		R.ELALQVAEAFGR.Y	2	38.7	37.0	160.4	156.4	36.0	39.9	175.6	159.0
		R.ESNVPLADIAAALAVQTR.									
		N	2	30.8	42.3	25.8	36.5	21.6	28.6	31.6	43.1
		R.ISHVINYDIPHDTESYVHR.									
		I	4	39.0	45.2	29.8	35.0	18.0	34.1	15.0	40.3
		R.ISHVINYDIPHDTESYVHR.									
		I	5	28.7	28.2	19.2	15.6	15.6	28.4	16.1	32.6

		R.LDYSLVELPEK.L	2	22.3	19.6	18.5	16.1	3.0	10.6	3.4	7.7
		R.YGSHLPQVNVLPYGGSS									
		YTVQLSGLR.R	3	75.4	86.4	66.2	70.2	49.0	66.8	60.5	84.7
MSMEG	MSMEG	K.NLPATVEGANGLSDDPGT									
_5048	5036	AAK.V	2	8.3	12.6	16.4	23.2	3.9	4.5	9.0	17.1
MSMEG	MSMEG										
_5049	5037	K.DGIQRPLIVFTPK.S	2	91.1	75.0	93.8	88.6	125.3	89.5	151.6	108.1
		K.DGIQRPLIVFTPK.S	3	139.7	125.7	127.1	118.6	130.3	138.1	131.9	129.4
		K.DVVIDM#LC*YR.R	2	8.9	7.6	19.2	22.8	4.5	5.2	20.0	21.7
		K.DVVIDM*LC#YR.R	2	8.8	7.7	18.7	22.8	4.4	5.2	19.3	20.4
		K.DVVIDMLC#YR.R	2	56.8	54.4	55.0	54.7	52.4	44.3	54.7	47.9
		K.DVVIDMLC*YR.R	2	56.7	54.3	55.0	54.7	52.4	44.1	54.7	47.7
		K.HEIEPSESVEADQQIPSK.L	2	5.5	3.7	4.7	2.6	3.8	2.2	2.9	1.3
		K.HEIEPSESVEADQQIPSK.L	3	104.2	86.8	128.4	91.2	38.0	42.9	45.4	48.6
		K.ISFTHLLGYAIVQAVK.K	2	40.6	37.2	51.2	50.0	45.0	32.2	54.8	41.9
		K.ISFTHLLGYAIVQAVK.K	3	94.1	91.5	87.8	86.6	84.7	78.6	85.3	74.7
		K.IYYELAAR.K	2	2.9	3.2	1.1	1.0	3.1	2.2	0.8	1.2
		K.LNAAEAFETFLQTK.Y	2	292.6	244.2	325.1	273.6	305.4	223.3	380.8	261.6
		K.LNAAEAFETFLQTK.Y	3	33.3	38.5	39.2	42.9	32.5	35.4	40.5	40.9
		K.LRDILSVLR.D	2	0.5	0.1	0.1	1.0	3.4	3.4	1.1	1.8
		K.LTAEDFSGVTISLTNPGTL									
		GTVHSVPR.L	3	425.6	389.5	442.8	399.1	396.9	348.7	451.1	405.0
		K.M*IGAPIFHVNGDDPEAC#									
		AWVAR.L	3	43.5	39.9	39.3	34.3	11.3	19.6	10.7	18.5
		K.MIGAPIFHVNGDDPEAC#A									
		WVAR.L	3	43.5	39.9	39.3	34.3	36.4	43.1	36.3	43.7
		K.MIGAPIFHVNGDDPEAC*A									
		WVAR.L	3	43.5	39.9	39.3	34.3	36.4	43.1	36.3	43.7
		K.NM#NASLEVPTATSVR.A	2	42.9	36.9	42.7	39.3	21.4	22.6	40.0	37.8
		K.NM*NASLEVPTATSVR.A	2	88.2	110.6	72.0	78.2	85.3	131.7	83.7	98.6
		K.NMNASLEVPTATSVR.A	2	304.9	326.9	331.7	322.8	288.4	308.0	326.2	300.2
		K.PTAITPAHTNLGLAIDLQG									
		K.D	3	51.9	43.9	36.4	35.4	27.6	27.6	14.0	19.0

K.PYSQIFSEFEGNLNPSQA HGSGDV.K.Y	3	158.2	143.8	145.1	125.3	112.6	114.3	103.1	89.7
K.TGEEFTPLQLLATNPDGT PTGGK.F	2	139.8	124.0	152.7	132.1	129.9	108.7	145.5	126.3
K.TGEEFTPLQLLATNPDGT PTGGK.F	3	205.9	211.1	225.9	223.9	119.8	172.1	143.7	198.6
K.VHAVEQQEILDATFG	2	628.3	600.7	885.8	780.6	491.6	420.5	879.0	677.1
K.WGQLSDVVLPLPHGHEG QGPDHTSGR.I	4	67.5	54.5	72.9	53.4	88.5	87.7	111.0	92.1
K.WGQLSDVVLPLPHGHEG QGPDHTSGR.I	5	42.3	37.2	34.0	29.6	56.0	60.9	54.4	53.2
R.ELEKHEIEPSESVEADQQI PSK.L	3	133.8	125.7	135.1	123.0	201.4	153.2	237.5	163.5
R.ELEKHEIEPSESVEADQQI PSK.L	4	247.1	279.1	224.3	249.2	227.1	300.1	217.4	278.2
R.FGQFIAAYEDIVR.R	2	377.8	327.8	404.8	326.4	400.2	314.6	489.1	311.0
R.GHLMADIDPLR.L	2	33.4	30.6	141.8	145.3	32.8	29.8	108.1	93.2
R.GHLMADIDPLR.L	3	58.3	42.8	38.2	25.9	43.3	43.2	27.8	28.6
R.GHNEGDDPSMTQPYMYD VIDTK.R	3	55.6	58.3	61.7	64.4	31.6	38.5	30.2	42.6
R.HFAVVDGKPTAITPAHTNL GLAIDLQ GK.D	4	242.4	228.3	232.6	254.7	168.6	188.4	198.4	258.7
R.HFAVVDGKPTAITPAHTNL GLAIDLQ GK.D	5	28.1	28.5	26.7	24.1	14.5	20.1	15.3	25.0
R.HVGVEYTHILEPEQQR.W	2	21.9	17.3	19.5	13.4	32.6	19.6	31.9	18.9
R.HVGVEYTHILEPEQQR.W	3	404.2	422.1	529.7	520.2	271.0	290.7	407.0	447.4
R.HVGVEYTHILEPEQQR.W	4	107.0	100.2	103.9	93.0	88.0	89.2	89.0	85.4
R.IEQLAPLPR.R	2	8.6	8.2	2.3	4.3	9.6	9.0	3.1	3.8
R.IGDAHLALPEGFTVHPR.V	3	87.6	78.2	81.3	72.3	93.7	82.3	95.4	77.1
R.IGDAHLALPEGFTVHPR.V	4	216.8	208.5	207.3	195.5	197.0	216.0	206.2	218.6
R.IIQGAESGDFLR.T	2	298.9	257.8	280.6	244.7	176.4	185.6	173.6	183.0

		R.KTGEEFTPLQLLATNPDG									
		TPTGGK.F	3	120.3	115.2	129.3	110.3	124.3	121.8	139.7	127.6
		R.LNVLANIVGK.P	2	66.7	64.1	55.8	54.2	48.8	51.2	41.6	37.8
		R.LNVLANIVGKPYSQIFSEF									
		EGNLNPSQAHGSGDVK.Y	4	66.5	80.9	61.3	69.3	48.0	72.7	52.4	72.5
		R.RLAETLDRYPNVK.E	3	2.5	2.0	4.4	4.1	2.2	2.7	3.8	5.0
		R.SHPDLDVNSHGLTLWDL									
		DR.E	3	138.8	132.9	191.4	172.1	112.7	118.2	139.8	138.7
		R.SVLEEMMYTDGEGDR.N	2	93.0	79.7	96.3	80.7	30.6	40.8	32.2	41.3
		R.TIHQLLLDDDDFFDEIFR.E	2	4.0	4.1	3.0	3.0	7.8	3.8	5.8	4.3
		R.TIHQLLLDDDDFFDEIFR.E	3	49.8	46.2	38.7	42.5	54.9	41.8	52.4	45.1
		R.TTTAAPVTPPTPAPAPAP									
		EPK.A	2	254.1	227.3	333.9	292.4	258.1	216.1	363.3	302.7
		R.TTTAAPVTPPTPAPAPAP									
		EPK.A	3	143.3	176.5	208.6	239.4	93.7	155.8	153.0	231.4
		R.VIELIAAYR.N	2	162.2	158.1	171.1	168.5	152.3	156.6	179.3	180.9
MSMEG	MSMEG										
_5053	5041	R.EAFLLYADAVK.E	2	14.6	10.7	21.8	20.6	16.4	16.0	24.2	23.3
MSMEG	MSMEG										
_5055	5043	R.ALSIAYTPGVAQVSR.A	2	493.4	478.2	890.1	836.6	415.8	413.7	985.0	891.1
		R.LRPTFGAVNLEDISAPR.C	3	235.7	220.5	193.9	181.6	192.7	197.8	56.6	69.3
		R.SDFPNQINNVLAFPGVFR.									
		G	2	271.6	251.7	166.9	154.2	233.9	219.6	163.2	163.5
		R.TPQVVIEDSEIFAAHEGGK									
		.L	3	130.9	115.0	22.7	21.0	113.0	122.9	13.5	22.6
MSMEG	MSMEG										
_5058	5046	K.ILDLSSELLDR.K	2	37.3	34.8	65.4	73.5	87.7	75.9	86.5	74.3
		K.LSIFDAATGLNLTR.D	2	46.4	48.1	73.9	78.3	77.4	69.2	138.4	112.1
MSMEG	MSMEG										
_5062	5050	R.GWPIGSYPTYAEAQR.A	2	48.0	55.4	90.6	100.4	56.8	66.0	81.0	77.3
MSMEG	MSMEG	K.TLPADQVFLDLEDAVAAD									
_5064	5052	AK.A	2	82.7	91.8	62.6	63.6	35.6	40.9	30.5	34.2
		R.IGIEPQIEDALGLTNVEAIA									
		AGPR.V	3	40.1	43.5	42.8	52.2	52.2	53.0	32.5	33.1

		R.VQALVLGPGDMAASLR.M	2	34.4	41.4	29.9	29.2	40.4	43.5	32.1	29.4
MSMEG	MSMEG	R.ADDIGAGAVTPAVGALLS									
_5073	5061	VLAR.L	2	20.4	20.6	50.3	54.4	13.5	15.2	34.5	37.3
		R.ADDIGAGAVTPAVGALLS									
		VLAR.L	3	11.1	10.2	24.5	22.7	6.2	5.9	15.4	13.9
		R.LTPVLIPLGDGLLAAYRD	2	0.8	1.0	100.1	113.2	0.4	0.5	96.3	117.7
MSMEG	MSMEG	K.VSSFQPFDDGYTDSSATEK									
_5086	5074	.K	2	55.9	55.5	114.9	104.1	18.3	23.6	73.0	76.4
		R.ALAFGLGLR.L	2	46.6	40.9	26.9	24.4	39.7	25.5	28.0	21.4
		R.LATTAPTTNPASASAVLAK									
		.D	2	237.9	208.6	259.0	222.0	202.0	238.6	193.5	223.1
		R.LPGFLMDAPVILR.G	2	21.9	26.5	22.8	37.5	17.3	16.4	30.3	26.9
		R.NSVGLLDLALR.L	2	16.5	17.2	16.1	12.1	10.5	7.8	27.8	11.1
MSMEG	MSMEG										
_5104	5090	R.GAVAVYGIDKFPR.M	2	40.3	38.1	115.7	84.6	34.6	32.7	29.8	21.7
		R.LTGDDVPADLAALTGK.D	2	191.2	193.3	170.5	179.2	65.6	69.4	119.2	137.9
		R.LTGDDVPADLAALTGKDE									
		DRDVEVVAVR.T	4	438.6	456.1	98.7	98.3	304.4	294.2	79.4	77.0
		R.NSLSGAVEVVK.R	2	41.3	27.7	41.3	35.9	18.2	14.3	46.9	46.0
		R.TTIADLNDKPADTHDVWL									
		R.L	3	405.1	441.7	282.4	360.4	190.1	235.9	436.2	385.0
MSMEG	MSMEG										
_5117	5103	R.GVDDFEYQMLYNIR.D	2	47.7	46.5	40.3	27.0	66.5	60.6	56.2	37.7
MSMEG	MSMEG										
_5119	5104	K.DFVLAHSSAHPDVLR.T	3	0.6	0.3	226.9	214.1	0.2	1.2	132.4	140.9
		K.MGDDFLSATEALR.Y	2	6.5	10.2	116.7	147.6	5.0	7.9	106.4	121.4
		K.SAYQAEIDAPC*ELIDFWR.									
		F	2	22.2	26.2	56.3	58.8	20.9	25.5	21.5	30.7
		K.YGLTGAVIADDR.T	2	2.3	2.2	149.5	121.9	3.9	3.4	81.4	72.8
		R.AADLLSGPWR.E	2	0.3	0.4	100.4	64.9	0.5	1.3	61.2	31.5
		R.TAVQQALDGLR.Y	2	30.7	23.6	115.3	71.4	43.4	37.7	93.0	47.9
		R.YGDVADLTNYGGAVIDDR									
		.A	2	19.3	16.2	151.0	153.7	23.9	14.7	93.3	77.9
MSMEG	MSMEG	R.AGFVAGDPAVVAELLAVR.									
_5121	5107	K	2	111.5	110.3	114.5	115.2	119.8	105.4	123.4	127.6



		R.DALAAGSSSPGYPTTAGT PELR.E	2	56.4	88.0	36.6	53.9	38.2	53.0	15.3	38.1
		R.GILVAPGEFYGPAGDR.Y	2	135.4	115.7	78.4	84.6	97.5	108.9	74.1	68.7
MSMEG	MSMEG	K.AC#IEEC#PVDC#IYEGAR.	2								
_5122	5108	M	2	99.0	102.4	141.0	138.2	106.3	116.9	158.2	150.3
		K.AC*IEEC*PVDC*IYEGAR.	2	99.0	102.4	141.0	138.2	106.3	116.9	158.2	150.3
		M	2	99.0	102.4	141.0	138.2	106.3	116.9	158.2	150.3
MSMEG	MSMEG	R.IAELTAALQSLGLR.G	2	37.5	40.0	48.4	68.6	29.9	27.5	42.2	41.6
_5129	5117	R.LLFVHAHPDDETLTTGGTI	2								
		AHYVAR.S	4	72.1	91.0	102.0	114.8	41.1	45.1	87.4	87.0
		R.YAQLAVDHADQLGGYR.I	2	90.8	71.1	24.0	19.6	53.1	58.0	26.6	25.0
		R.YAQLAVDHADQLGGYR.I	3	160.9	131.5	120.3	101.0	107.4	123.1	114.1	138.0
MSMEG	MSMEG	K.ALDLPTLYASGR.A	2	22.0	22.2	62.8	73.1	18.0	17.1	65.7	66.6
_5132	5120	K.HIPPPSGDPEAPLQALVTN	2								
		LDASAFLGR.L	3	85.9	106.7	207.3	248.5	43.6	74.9	141.0	234.4
		K.ITELLVTEGVER.T	2	66.1	69.9	203.7	172.8	41.1	42.6	145.4	132.0
		R.VVDIGKPDABEVQGR.G	2	13.5	13.4	83.2	79.0	6.9	10.5	80.1	68.8
		R.VVDIGKPDABEVQGR.G	3	77.7	77.4	187.9	156.6	46.8	63.7	147.4	153.7
MSMEG	MSMEG	K.NQVVAFEADELDPDLR.T	2	113.0	122.4	0.6	2.5	19.8	20.4	2.2	0.9
_5136	5121										
		R.LVFTEDALPAVQPVNFR.L	2	150.9	182.2	3.6	4.4	27.2	29.9	2.7	1.6
MSMEG	MSMEG	K.FPTFLDGIDAVR.R	2	9.8	10.6	31.6	29.6	15.7	17.1	36.8	34.9
_5150	5135	R.DAAALPLTTITAWETLFR	2								
MSMEG	MSMEG	.F	2	84.6	99.2	46.0	58.2	17.0	29.1	31.6	60.0
_5164	5148	R.LLADAADLVDR.G	2	17.0	4.7	947.0	913.8	2.4	3.0	397.7	444.7
MSMEG	MSMEG	R.AQTFQVSITEPR.A	2	139.0	184.4	459.9	676.4	96.1	116.1	353.2	434.9
_5170	5154	R.NISGEHPDWDEFER.Q	2	15.2	18.3	16.0	20.8	8.0	3.2	17.3	10.4

MSMEG	MSMEG	K.DAVAVVTGGASGLGLATT									
_5183	5166	K.R	2	183.4	193.7	194.1	194.0	142.2	148.6	237.3	244.7
		K.FVATDVTDEAGVTEALNV									
		AESLGPVR.I	3	203.3	224.1	195.2	201.1	132.0	143.9	182.8	198.0
		K.GGVVGMTLPIAR.D	2	90.8	85.5	153.2	145.1	86.0	67.7	204.8	162.0
		K.NGPFPLDGFR.K	2	57.6	55.0	39.1	42.1	33.8	39.3	36.6	41.4
		K.TPLLGSLPPEAQK.S	2	290.6	281.3	460.2	443.1	227.3	229.0	458.6	421.6
		R.LLDAGAQVVVIDLK.G	2	83.8	83.7	194.8	189.4	23.3	29.0	271.8	307.3
		R.VVTIAPGLFK.T	2	159.0	156.2	164.5	163.8	124.7	123.8	167.8	178.9
MSMEG	MSMEG	K.GLGLDGADLPAQNDISR.									
_5184	5167	W	2	64.6	71.5	438.2	638.3	41.7	45.7	258.5	260.2
MSMEG	MSMEG										
_5191	5175	K.AYVHLIDLHR.Q	2	8.1	6.1	8.9	9.8	4.2	3.9	9.4	6.6
		K.AYVHLIDLHR.Q	3	76.1	68.7	32.9	27.1	54.9	53.3	28.7	27.0
		R.ASVWYGATLR.A	2	39.3	35.3	20.2	13.2	20.9	27.3	18.1	21.5
MSMEG	MSMEG	K.SGVHGPALSLHNDVVGPY									
_5197	5179	FK.E	3	35.4	39.6	25.0	39.1	38.0	46.8	34.9	54.5
		R.FNAIIDEEIAK.S	2	35.7	30.2	42.3	65.7	61.0	51.1	26.8	27.7
MSMEG	MSMEG	R.NAINSSVSQAVGDALAEA									
_5198	5180	QNDPEVR.A	3	37.3	41.3	35.5	33.5	68.7	75.1	42.5	57.8
		R.VAYGAEEGTVPAEQPSW									
		K.R	2	33.3	42.1	16.6	24.5	48.9	61.0	10.9	20.8
MSMEG	MSMEG	K.AAAAQDSGAFSDQIVGIK.									
_5199	5181	T	2	242.1	229.0	201.2	162.5	280.2	287.8	181.2	169.6
		R.TAVLSAGWPETVPGVTV									
		DR.Q	2	193.2	206.5	204.9	221.5	238.8	244.0	193.9	265.1
MSMEG	MSMEG										
_5211	5192	K.NFLVTQGDETVGVLK.I	2	87.7	83.3	127.2	125.9	82.9	73.2	118.8	116.1
		R.FNYASVVEFSER.L	2	62.0	64.3	35.3	38.4	62.2	64.5	46.9	39.0
		R.GYLRPSTVAELGALAGR.V	2	23.7	25.6	36.8	27.3	22.7	35.6	23.3	50.5
		R.GYLRPSTVAELGALAGR.V	3	53.9	49.6	63.1	55.8	54.0	47.7	80.2	86.4
		R.LASLLPDPLDTVFLVNSGS									
		EASDLALR.L	3	44.4	62.6	39.0	54.5	25.7	57.6	29.2	63.4
		R.PLFGLPALATDSTDADLV									
		AR.R	2	124.0	123.6	157.6	146.6	120.1	123.9	159.6	154.2

		R.YADEAVAQIQELAAAGR.A	2	104.1	82.9	88.9	102.9	112.0	85.5	123.0	99.2
MSMEG	MSMEG										
_5215	5199	R.GLGYEIASAFGR.S	2	3.4	2.7	2.2	3.7	2.9	3.6	2.3	1.5
MSMEG	MSMEG	R.FALYSTGTPDSAEESEPAA									
_5225	5209	R.S	2	149.9	143.0	260.0	273.0	235.7	320.3	276.5	305.7
		R.LLVGAAVTTLEEAR.K	2	59.7	57.0	459.5	446.8	326.8	294.3	521.5	471.2
		R.LTSLSIGDLEALLAYEEAG									
		R.A	2	26.7	35.7	114.1	122.7	75.3	103.7	98.2	122.9
		R.LTSLSIGDLEALLAYEEAG									
		R.A	3	8.1	6.6	40.4	39.5	37.5	36.6	40.1	38.8
MSMEG	MSMEG										
_5239	5224	K.GMPNAISVLAVAER.G	2	201.8	195.1	246.6	259.0	72.9	78.3	164.8	164.4
		K.IAAGPDVADFIDITSPIAANI									
		QR.I	2	332.8	356.6	339.7	358.8	235.3	227.6	275.0	309.0
		K.IAAGPDVADFIDITSPIAANI									
		QR.I	3	349.0	361.3	314.9	327.5	284.3	275.9	344.9	349.0
		R.GAMFDPSAVFYMNK.I	2	135.4	115.6	127.9	114.4	17.7	19.9	21.1	18.0
MSMEG	MSMEG	K.DLGLLDPEKADAIIAAAGEI									
_5240	5225	AEGK.H	2	118.7	129.7	111.6	153.2	104.9	113.3	116.8	147.8
		K.DLGLLDPEKADAIIAAAGEI									
		AEGK.H	3	944.8	898.1	1053.2	1013.3	1106.9	1053.0	1465.8	1299.3
		K.VVEVLVNETGLAELR.T	2	109.2	104.5	443.9	484.3	99.8	97.8	482.9	469.9
		R.AVENFPISFR.G	2	357.1	259.5	300.7	226.2	446.0	383.7	454.2	418.5
		R.DGLVEASGALR.T	2	80.3	63.7	71.8	61.6	77.8	58.0	60.4	49.6
		R.ELAESSPSIVTPLNSAIGY									
		EEAAK.V	2	317.7	357.9	332.2	388.0	286.9	289.5	355.4	383.6
		R.HLIPALEVLHASLAAK.A	3	427.3	292.2	404.8	282.4	325.4	355.1	381.8	446.1
		R.LGELAIGGTAVGTGLNAP									
		EGFGAK.V	2	492.7	536.8	415.2	455.9	591.2	566.1	546.7	550.8
		R.NLLESFTLLSNVSR.L	2	436.2	442.3	535.1	522.5	512.6	422.4	819.2	711.9
		R.TAVDSFEAQAAR.D	2	35.3	36.4	40.9	48.3	16.6	15.1	15.8	17.9
		R.THLMDAVPVTLGQEFGG									
		YAR.Q	3	387.4	343.1	320.5	281.7	219.0	215.8	234.0	227.0
MSMEG	MSMEG	R.IVTTVDNTSHIFPINFVVQN									
_5243	5228	R.T	3	263.5	274.0	15.7	17.8	61.2	71.8	19.4	17.8

MSMEG	MSMEG										
_5244	5229	R.VLLDLLGEGLTNK.Q	2	6.6	0.0	8.7	0.0	1.2	0.9	2.0	2.7
MSMEG	MSMEG										
_5245	5230	R.ALATAEVAIR.Q	2	32.2	26.2	1.3	0.7	2.3	2.8	0.2	0.3
		R.GGIGSVASAVLR.S	2	162.9	159.0	3.1	2.8	25.7	25.5	13.4	13.6
		R.ILVEFDGRPSASTALQTG									
		VDEAR.L	3	342.1	370.1	37.3	47.5	48.3	55.4	17.4	23.1
MSMEG	MSMEG	K.VLLEC#TMSGLATC#PVT									
_5246	5231	HVTELHTSR.D	4	226.2	214.0	3.6	4.0	10.3	9.7	16.0	11.0
		R.IGLAPALDEVPPPTPR.R	2	816.7	840.6	250.1	250.1	105.8	113.3	253.6	272.9
		R.LGDGPVHMDTLGEDVRE									
		EVAEAAAALTESLR.L	4	69.8	75.8	4.7	5.8	4.3	8.2	4.1	7.0
		R.RPVDAFLEVRPR.S	3	34.5	29.8	3.6	4.7	1.6	2.2	4.4	2.3
		R.VALAAAGWDTEVQR.F	2	789.2	794.2	267.5	197.3	145.9	165.0	579.6	563.9
MSMEG	MSMEG										
_5248	5233	K.SITDALEILLITK.D	2	58.4	47.6	16.2	17.2	40.4	33.4	20.0	18.5
		R.AAGLDVIGADIAPYQDK.V	2	337.7	359.8	114.8	128.6	280.0	293.9	142.2	152.8
		R.IATDEERHEEFFSNLVSIV									
		LDK.H	3	81.3	58.4	19.3	14.5	67.1	70.0	26.4	26.6
		R.ITAWGLAGEASLK.D	2	80.7	87.3	57.6	71.0	69.8	61.4	38.9	56.6
		R.NLQAQITEPVLASLMGR.I	2	148.2	166.5	106.5	107.0	109.3	114.5	117.1	124.3
		R.NLQAQITEPVLASLMGR.I	3	189.1	219.8	78.6	82.1	159.5	213.4	75.5	90.9
MSMEG	MSMEG										
_5249	5234	K.HINDLSEADWETLR.N	2	316.9	353.5	233.1	279.4	257.8	277.6	219.5	218.0
		K.HINDLSEADWETLR.N	3	136.0	118.8	60.3	53.2	120.9	117.4	69.7	64.8
		R.EFKPLVLVAGYSAYPR.R	3	54.4	52.2	29.1	32.9	54.6	51.9	41.4	47.7
		R.FYAGC#QNVDTVESVAAE									
		HAR.E	3	848.5	970.2	1157.8	1245.4	896.3	907.1	1285.7	1294.4
		R.FYAGC*QNVDTVESVAAE									
		HAR.E	3	848.5	970.2	1157.4	1245.4	896.3	907.1	1285.1	1294.4
		R.GGMVLATEEYAPAVDK.G	2	462.5	447.0	759.9	733.5	226.3	243.6	804.0	913.2

		R.NSIPADPNGAWYTSGVR. L	2	309.0	357.6	291.8	377.0	254.1	258.4	212.0	292.5
		R.SYGTNPETGFLDYDAVAA AAR.E	2	374.2	371.8	237.7	270.8	334.2	330.0	284.6	302.2
		R.VHAASSELLSANPLYPGL TL	2	364.4	360.0	325.9	335.8	333.3	311.0	396.3	367.0
MSMEG	MSMEG										
_5252	5236	K.LDLLEVEEVYLPLAR.L	2	54.6	55.5	56.5	59.9	26.2	29.6	16.1	25.7
		R.IEDIEQWYISR.F	2	24.7	26.6	20.1	18.7	35.4	32.5	21.5	32.4
MSMEG	MSMEG	R.YLDTVAGGSAADIAALYA DDATVEDPVGSGEVHIGR.Q	3	70.4	88.8	64.2	82.7	65.4	85.1	54.9	62.5
MSMEG	MSMEG	K.AELDQLIANRPVIAAEINDR .R	3	297.4	355.6	215.1	244.1	312.7	332.0	193.2	197.2
		K.LEVYSPNSPLGGALLDAK. V	2	123.9	125.2	118.4	117.0	105.2	109.7	98.3	89.2
MSMEG	MSMEG	K.VFTHWGISHTPAALSDLD SVR.S	3	190.6	197.0	145.4	136.7	206.2	155.3	155.5	179.8
_5265	5251	K.VLVDNTFASPALQQPLLL GADIVLHSTTK.Y	3	792.6	663.9	555.2	487.3	513.8	558.1	572.7	605.3
		R.AVLRPGDHVVIPDDAYGG TFR.L	3	387.2	382.8	246.9	270.6	274.3	280.6	257.2	253.8
		R.AVLRPGDHVVIPDDAYGG TFR.L	4	387.1	343.0	169.3	155.7	286.4	285.2	145.4	176.4
MSMEG	MSMEG	K.ITHFVAGVGTGGTITGTG R.Y	3	127.7	116.6	108.0	101.9	106.0	111.1	119.9	113.4
_5270	5255	K.LADAVAHEHMSPLPLIGA GELVSTAAK.T	3	437.0	404.9	345.7	326.6	305.1	255.1	251.6	241.0
		K.SGALPDLVHTHPSETVR.D	4	13.3	10.4	10.4	14.6	4.3	6.5	4.1	4.1
		R.ELLSAVFEGR.A	2	63.3	41.9	54.1	38.5	52.1	54.0	38.1	57.7
MSMEG	MSMEG										
_5273	5258	K.AGEGHAFISAGVETVSR.F	2	413.5	384.6	290.0	281.8	348.8	321.3	333.9	330.8
		K.AGEGHAFISAGVETVSR.F	3	627.9	514.2	453.2	393.7	502.0	417.0	464.9	427.3
		K.GSLVEMRPDDLAAQMVK. A	2	258.4	266.1	186.6	217.9	40.8	42.2	43.1	46.4

		R.AVAVQLGYDFLPGTTVNR									
		.Y	2	1250.5	1242.7	1422.8	1401.5	1115.8	1045.3	1413.5	1455.9
		R.EITPVTLPDGTVVSK.D	2	2184.3	2184.0	2873.9	3045.1	1553.8	1706.4	2680.3	2906.8
		R.ITATLLNNLQTHDK.T	2	192.9	167.7	267.0	290.4	215.0	197.4	293.5	229.0
		R.ITATLLNNLQTHDK.T	3	181.1	157.0	124.3	109.9	237.0	152.2	219.3	132.9
		R.IVSTGVSGLSPEIMGLGPI									
		EAVK.K	2	727.2	728.0	586.1	596.3	286.5	274.6	273.2	275.0
		R.IVSTGVSGLSPEIMGLGPI									
		EAVKK.A	3	214.9	192.8	200.8	188.1	185.3	184.6	206.7	200.1
MSMEG	MSMEG										
_5274	5259	R.LAAETLGVPTSPYR.F	2	117.5	114.3	328.1	359.6	150.2	136.3	339.7	360.9
MSMEG	MSMEG										
_5285	5270	R.IGEIAAQTQTVPEsvR.R	2	161.4	164.7	22.7	23.1	39.2	46.7	14.4	17.1
MSMEG	MSMEG	K.GVDESDVLQDAIAVAADY									
_5358	5339	NR.T	2	124.9	138.9	76.7	78.2	77.7	77.2	82.1	71.7
		K.GVDESDVLQDAIAVAADY									
		NR.T	3	67.4	74.2	19.9	21.3	56.8	54.7	35.2	34.4
MSMEG	MSMEG										
_5359	5340	K.ADAAGLVVAAR.I	2	0.1	0.0	2.4	0.0	0.0	0.1	3.0	2.1
		K.HLDAPLVWC*VAALLGQH									
		PLSAEQAEK.V	3	2.5	0.0	38.9	0.0	4.1	3.1	42.5	41.0
		K.HLDAPLVWC*VAALLGQH									
		PLSAEQAEK.V	4	0.3	0.4	36.1	33.5	0.5	0.6	34.8	38.3
		R.FHEALNVYGPALK.E	2	4.4	4.7	327.2	403.7	6.2	6.4	386.3	342.9
		R.FHEALNVYGPALK.E	3	4.6	6.2	124.8	130.5	9.0	7.3	137.5	124.5
		R.GIDPALQSDPTIYR.F	2	33.3	37.4	456.3	497.8	37.0	41.7	471.9	436.8
		R.NGLSWADIak.H	2	5.1	4.2	64.6	64.3	3.9	5.6	48.2	56.2
MSMEG	MSMEG										
_5397	5377	R.EVIDILGLR.K	2	7.9	6.2	35.9	21.3	7.5	5.2	43.1	20.4
MSMEG	MSMEG	R.ALfESSITDPATFWADAA									
_5404	5383	K.A	2	72.6	78.1	42.9	46.5	24.5	31.5	44.7	49.5
		R.GDQAALIYDSPVTGTK.R	2	85.8	77.1	51.6	69.5	30.0	29.3	45.3	86.4
		R.GIADGKDEPVPSTIEDPSV									
		LDDLK.S	3	101.0	107.3	51.4	65.1	38.8	48.3	38.6	62.8
MSMEG	MSMEG	R.LGQGVDATGQFAPEALA									
_5413	5393	R.T	2	22.9	27.1	294.8	325.0	26.0	26.3	171.6	186.4

## MSMEG MSMEG

_5415	5395	K.AAAESAGLPLFR.Y	2	37.5	38.6	73.6	84.3	46.3	48.9	76.3	89.4
		K.AALDLISSAIEATGLK.L	2	1929.3	1638.3	2002.6	1797.6	1555.6	1344.0	1924.2	2015.5
		K.AALDLISSAIEATGLK.L	3	127.0	150.5	87.8	111.0	132.8	114.5	117.0	116.4
		K.AVEAVLDEIAPQVIGLSAD									
		DQR.L	2	374.3	436.3	256.8	293.1	193.5	265.1	171.4	255.7
		K.AVEAVLDEIAPQVIGLSAD									
		DQR.L	3	807.8	723.4	646.4	605.8	712.7	595.3	855.8	755.3
		K.LGSDVALALDVAATEFYTE									
		GSGYAFEK.E	3	84.8	92.2	69.3	78.2	28.7	43.7	36.7	40.6
		K.NQGLATGLGDEGGFAPD									
		VAGTK.A	2	1227.9	1364.3	1038.8	1041.3	813.5	815.0	1168.5	1116.4
		K.VNQIGTLTETLDAVSLAHN									
		SGYR.T	3	2712.1	2479.4	2108.9	1957.8	2099.6	1926.6	2511.8	2277.6
		R.AAVPSGASTGEHEAVELR									
		.D	2	75.7	48.7	55.6	38.0	72.3	49.4	74.5	52.6
		R.GNPTVEVEVALTDGTFAR									
		.A	2	337.9	299.0	338.7	333.4	210.2	213.6	394.5	405.3
		R.IQLVGDDLFTVTPER.L	2	1882.1	1783.1	1891.5	1811.8	1725.9	1573.0	2529.7	2217.1
		R.LVDQALLDLGTPDK.S	2	1829.6	1778.9	1371.6	1427.5	1380.2	1273.0	1445.0	1443.2
		R.SGETEDTTIADLAVAVGS									
		GQIK.T	2	430.5	434.8	366.7	407.0	331.5	286.4	393.7	375.7
		R.SGETEDTTIADLAVAVGS									
		GQIK.T	3	249.9	221.3	240.4	222.9	156.1	134.2	264.0	224.7
MSMEG	MSMEG										
_5419	5399	K.ITGEEDIFSHTDLWDFR.A	3	179.6	159.4	83.3	75.5	66.8	57.5	133.9	99.1
		K.SNQITVEASDTEC#K.L	2	35.6	27.5	19.1	14.7	9.0	8.3	13.0	12.3
		K.SNQITVEASDTEC*K.L	2	35.6	27.5	19.1	14.7	9.0	8.3	13.0	12.3
		R.ANVEGSQTAVASVR.P	2	18.1	15.9	13.7	11.3	1.4	1.3	9.4	8.0
		R.ANVEGSQTAVASVRPILD									
		ER.D	3	264.3	250.7	72.4	71.6	62.3	52.7	54.3	38.9
		R.FADVEALLEK.Y	2	259.2	216.6	62.0	62.6	95.4	101.4	86.4	80.1
		R.IEPVAESFPDDLDPRI	2	423.5	435.5	145.4	171.9	152.9	154.3	155.3	149.3
MSMEG	MSMEG	R.AHVATGGYAAVVTPGIGT									
_5423	5404	AHR.V	3	15.4	11.6	8.1	8.5	10.6	9.0	17.9	11.6
		R.EFGITEIGAVSASTVR.L	2	29.8	23.4	60.5	47.2	19.7	16.8	59.8	50.8

MSMEG _5424 MSMEG _5427	MSMEG 5405 MSMEG 5408	R.GYAYFLYPPNKPLTETAY										
		DR.L	3	49.9	54.2	12.9	17.8	26.1	28.2	12.9	13.0	
		R.LAAAADDDAVASVVDELID										
		R.Y	2	34.5	34.4	12.1	12.2	22.7	23.2	9.5	12.1	
		R.LARPDDETLGAPLR.V	2	17.6	14.4	10.7	12.1	11.7	11.9	7.7	10.0	
		R.LATIAQNNELGAGM*AVA										
		M*K.D	3	2.6	2.3	30.7	14.7	0.5	0.5	21.7	14.1	
		R.LSPMVLPSAQLR.L	2	28.4	31.8	28.0	43.2	17.0	20.6	33.8	48.8	
		R.SIPEVPVQTVVAVPC#R.E	2	20.8	19.6	49.7	57.6	14.4	13.1	32.9	42.1	
		R.TLEMSLAGIR.E	2	10.7	11.0	13.3	13.2	5.9	6.9	7.8	9.4	
		R.VALALLTYVEEHTDGFR.I	3	7.6	6.6	27.0	27.1	2.1	2.5	25.1	34.1	
		K.DVIIAATHGVLSDPAPQR.L	2	76.9	81.5	41.3	41.2	44.8	50.4	12.8	16.3	
		K.DVIIAATHGVLSDPAPQR.L	3	164.2	227.5	119.9	132.0	131.1	141.0	58.9	58.0	
		K.ELDVAVTAQTAR.D	2	96.3	89.6	138.1	149.1	81.4	74.2	79.6	78.7	
		K.RFPQLTVLSIAPLLANTIR.										
		A	3	70.3	69.6	38.9	37.4	73.6	58.7	24.8	25.6	
		R.DFANGEIFVR.F	2	38.8	34.9	5.9	4.4	22.6	25.1	0.7	1.0	
		R.EVIVTNTLPITEDK.R	2	377.1	443.8	84.1	115.2	399.5	407.9	65.4	81.2	
		R.EVIVTNTLPITEDKR.F	2	19.2	14.9	7.6	11.9	19.1	13.6	5.3	8.5	
		MSMEG _5431	MSMEG 5412	R.FPQLTVLSIAPLLANTIR.A	2	49.1	49.8	21.4	22.3	36.3	39.2	9.4
R.FPQLTVLSIAPLLANTIR.A	3			25.6	26.8	8.9	8.8	18.5	18.9	1.7	3.0	
R.ITAILPFYYPYAR.Q	2			170.5	171.4	104.3	100.9	142.0	142.8	64.6	63.4	
K.VPAVLYGHGTDPPQHLELN												
AR.D	3			769.2	805.7	676.1	674.6	825.7	962.2	627.5	708.7	
K.VPAVLYGHGTDPPQHLELN												
MSMEG _5435	MSMEG 5415	AR.D	4	1056.0	982.1	746.8	693.7	1412.5	1348.2	872.8	818.9	
		R.NIQHADLLVVQR.G	3	52.6	40.0	22.3	16.2	80.2	65.7	28.7	18.7	
		K.AVIIEPFLVATPVLEEK.G	2	134.2	140.2	39.4	38.6	163.1	171.8	80.0	69.2	
		R.IEHQVAHEVVSEVDVRPR.										
		N	4	327.1	284.8	177.4	170.0	307.0	395.8	134.5	218.1	



		R.IEHQVAHEVVSEVDVRP.R									
		N	5	26.3	16.5	0.0	0.2	41.2	47.4	0.5	0.5
		R.LASLGPLLNDLEAR.V	2	78.0	73.1	25.3	33.2	111.2	74.1	20.2	13.7
		R.NVVVLGPGSIPK.T	2	46.3	41.8	67.4	54.3	58.0	34.4	54.3	54.3
		R.RIEHQVAHEVVSEVDVRP									
		R.N	3	38.0	25.9	317.5	378.9	68.2	64.7	30.8	42.1
		R.RIEHQVAHEVVSEVDVRP									
		R.N	4	277.9	275.4	61.6	79.3	335.1	425.7	64.1	80.8
		R.RIEHQVAHEVVSEVDVRP									
		R.N	5	174.2	163.5	15.9	17.6	252.2	293.5	7.8	19.6
MSMEG	MSMEG										
_5438	5418	R.VTAVEIDPLLAR.Q	2	182.5	162.2	527.8	496.8	219.1	198.8	451.0	444.7
MSMEG	MSMEG										
_5441	5421	R.VNADLANELGNLAQR.S	2	87.1	87.9	88.3	72.4	87.9	76.1	68.2	69.5
MSMEG	MSMEG	K.ELLPVVDTPGIELVAAEAA									
_5471	5450	EAGAER.L	3	168.6	169.3	151.7	147.0	172.3	207.7	211.6	200.2
		K.GMVEKPRPEDAPSHFAAA									
		GR.Y	4	2.4	1.6	2.3	1.3	2.0	2.0	1.2	1.6
MSMEG	MSMEG	R.FDAVQAFSDDALTTC#PK.									
_5479	5458	C	2	43.2	46.5	0.4	0.6	31.9	30.8	0.0	1.1
MSMEG	MSMEG										
_5485	5465	R.ASGLAAGIVDAGLSR.G	2	138.6	147.7	156.9	171.0	151.0	158.9	171.1	163.0
		R.ELLGISEALR.A	2	135.7	139.9	134.5	126.8	163.5	155.8	145.5	129.0
		R.GLAGISGSTLVVNIAGSR.									
		A	2	178.8	196.4	402.2	409.4	178.2	179.5	458.2	412.4
MSMEG	MSMEG										
_5486	5466	R.VIGSADALVAAVR.S	2	29.2	19.7	26.8	14.2	11.2	13.0	14.9	21.4
MSMEG	MSMEG	R.VAGLDAGADDYLPKPFAL									
_5488	5468	EELLAR.M	3	45.8	52.3	90.7	88.3	37.2	39.2	112.3	116.7
MSMEG	MSMEG										
_5489	5469	K.AEAPGLVTVSVAGQQR.K	2	499.5	512.7	205.8	208.7	475.2	531.0	227.4	243.2
		K.AEAPGLVTVSVAGQQR.K	3	51.3	48.8	24.0	20.3	44.4	53.1	28.7	35.5
MSMEG	MSMEG										
_5512	5490	K.DVVAALPDLPDAIAHR.L	3	60.4	50.5	68.8	67.4	36.4	41.0	68.1	70.9
		K.LATPDTSVADLVGDIDPIK.									
		V	2	122.7	124.7	189.6	182.9	91.3	87.6	208.5	201.2

MSMEG _5515	MSMEG 5493	R.DVWPGILGFEDTVIPQLE									
		R.A	2	106.8	126.1	70.1	84.1	62.0	78.9	48.7	69.7
		R.GIVAVNELPDLAER.I	2	111.9	103.3	105.1	106.5	89.1	91.2	156.7	143.4
		R.SLGDPETIAYGLIPR.A	2	76.6	74.2	56.8	55.5	43.1	42.2	62.9	61.8
		R.VVDLGTVIDVLR.G	2	55.9	51.0	53.5	50.6	43.2	34.6	61.0	52.9
		K.HANPC#GIAISSTSVADAH									
		R.K	3	25.9	27.9	19.9	20.8	23.4	22.4	21.7	25.8
		K.HANPC*GIAISSTSVADAH									
MSMEG _5520	MSMEG 5498	R.K	3	41.9	38.5	33.1	27.9	35.8	30.9	25.7	30.6
		K.TLEDLVFAWR.A	2	26.3	28.7	17.5	21.2	19.4	20.5	21.1	27.2
		R.GLHQAGVAIVSTGSTAK.T	3	26.7	21.7	24.0	23.2	18.9	18.7	22.0	23.3
		K.LLQDIWAAAGR.E	2	41.6	41.2	10.7	11.9	72.6	69.5	14.8	18.7
		K.PVQAHIPVLVGAAGNEK.N	3	128.0	112.3	43.6	45.0	153.7	143.8	17.5	23.0
		R.TLDPWVSLGTAAAVTSR. V	2	61.3	56.6	68.6	61.6	97.8	89.5	53.6	62.1
		K.AGTQIVGGVNAR.K	2	8.4	5.9	10.7	7.2	17.8	10.8	13.5	9.4
		K.ANVTKPVVGYVAGFTAPE GK.T	2	444.1	470.9	472.3	485.5	740.7	745.8	531.8	515.3
MSMEG _5524	MSMEG 5502	K.KDKDGNDIELPVFGSVAEAI K.E	2	227.5	213.7	217.4	197.1	361.6	326.6	209.4	200.0
		K.KDKDGNDIELPVFGSVAEAI K.E	3	711.1	668.4	674.1	668.7	1147.4	1067.7	699.4	680.1
		K.ETGADVSIASFVPPAFSK.D	2	1178.8	1243.5	1314.0	1364.1	1720.8	1669.2	1297.8	1237.6
		K.SGTLTYQM#MYELR.D	2	58.1	67.0	510.0	660.3	89.0	85.4	289.7	398.4
		K.SGTLTYQM*MYELR.D	2	57.8	65.4	265.2	219.5	89.0	85.4	289.7	237.2
		K.SGTLTYQMM*YELR.D	2	58.3	66.7	265.2	219.5	92.5	87.4	383.1	237.2
		K.SGTLTYQMMYELR.D	2	243.3	210.4	265.2	219.5	479.0	338.7	383.1	237.2
		K.TM*GHAGAIVSGSSGTAA AK.K	3	14.5	4.7	18.9	8.0	23.9	15.3	15.8	9.8
		K.TMGHAGAIVSGSSGTAAA K.K	2	1.7	0.8	0.9	0.3	5.1	2.1	1.9	0.6

MSMEG _5525	MSMEG 5503	K.TMGHAGAIVSGSSGTAAA									
		K.K	3	14.5	10.8	18.9	13.9	23.9	15.3	15.8	9.8
		K.VIVMIGEIGGDAEER.A	2	130.1	134.0	93.2	107.6	181.8	170.5	71.7	68.0
		K.VIVQGITGGEGTK.H	2	11.1	10.3	4.5	3.8	20.4	19.9	2.3	4.8
		R.IIGPNC#PGIITPGEALVGIT									
		PNNITGK.G	3	267.0	211.1	322.0	284.5	600.0	654.3	470.0	529.3
		K.EDATLVEVNPLVR.T	2	2176.5	1973.4	2051.5	2005.9	2448.3	2594.8	2248.8	2272.1
		K.LWEVFK.E	2	41.0	19.5	6.7	6.2	84.5	87.9	32.0	33.1
		K.TIAEEIGRPVMVK.A	2	5.0	5.2	293.2	289.1	23.3	25.5	223.6	296.8
		K.VTLDENAGFR.Q	2	383.6	285.9	357.4	282.9	373.7	321.9	330.8	286.5
		K.YAATPDDAFTHANNILGLD									
		IK.G	2	470.3	512.4	365.7	402.4	526.2	500.6	369.8	352.8
		K.YAATPDDAFTHANNILGLD									
		IK.G	3	2257.2	2135.8	1733.9	1642.0	2512.2	2498.2	1939.9	1812.3
		R.ILAEANHPLVIQAETM#DA									
		GADK.A	3	425.0	437.6	354.5	376.1	455.9	416.8	311.5	313.3
		R.ILAEANHPLVIQAETM*DA									
		GADK.A	3	481.4	500.1	397.7	434.0	564.2	532.8	397.2	402.7
		R.ILAEANHPLVIQAETMDAG									
		ADK.A	3	2364.7	2309.6	2245.4	2242.0	1473.7	1388.9	1292.7	1231.2
R.SIAEQGHLPAEVLDAAAVT											
IQK.L	2	657.7	737.3	607.2	669.3	659.1	659.0	580.9	586.8		
R.SIAEQGHLPAEVLDAAAVT											
IQK.L	3	2703.8	2436.5	2663.4	2432.5	3224.1	2943.5	3125.7	2720.4		
R.SIAEQGHLPAEVLDAAAVT											
IQK.L	4	85.6	74.2	47.1	37.6	124.1	108.8	43.4	45.0		
R.TPDDQILALDGK.V	2	202.3	218.5	201.1	207.2	199.4	189.2	165.6	166.6		
MSMEG _5534	MSMEG 5512	R.GKLDEELGDLVEAVLER.T	3	4.0	4.2	0.1	0.0	8.2	9.5	0.2	0.1
MSMEG _5538	MSMEG 5516	K.GEVAYGAEFFR.W	2	96.2	64.2	66.5	56.1	61.8	54.3	51.8	50.0
		K.GLDPSSTLGPLINSK.Q	2	306.2	319.5	202.2	233.0	161.0	162.3	203.3	238.2
		R.EGGIEGIEEYLDTK.Y	2	150.3	133.8	54.4	46.3	105.6	91.3	90.5	73.2
		R.GVISDPAAPFGGIK.E	2	258.1	253.2	129.5	102.0	234.9	147.2	196.9	126.8
		R.IEDLISSVPTGLWIGGEER. E	2	212.6	213.8	123.5	131.4	143.8	162.3	88.7	130.4

		R.VAETIQSGMVGINR.G	2	103.9	82.2	99.1	70.1	144.0	88.4	63.5	55.3
MSMEG	MSMEG	K.LVVDGQDVVADVHDLDR									
_5541	5517	.M	3	487.6	470.5	342.4	333.6	433.8	362.9	343.3	311.8
		K.TFSTLETLTNATAAR.R	2	603.4	582.3	426.5	416.2	392.1	369.3	444.8	389.0
		R.FVSNVDPADLVAK.L	2	600.1	605.9	350.0	364.6	540.5	498.0	540.2	471.6
		R.HYADAGISAR.F	2	10.4	4.4	5.7	2.2	2.9	2.7	1.6	1.8
		R.TDLLVDLAR.A	2	102.6	92.3	36.7	44.5	69.5	54.0	27.9	29.0
MSMEG	MSMEG										
_5553	5530	K.IYATDVDEDALTEAR.A	2	60.8	55.7	153.4	138.6	71.0	74.1	110.1	115.2
MSMEG	MSMEG										
5534	5534	K.GVTDVIVGFR.I	2	38.6	40.0	46.4	49.3	28.9	26.7	34.5	32.9
		R.IPYIEGQDTEPLDKK.I	3	73.5	79.9	21.9	23.4	43.5	52.5	10.7	18.2
MSMEG	MSMEG										
_5592	5572	R.EEFEAAELPFPSAR.E	2	46.6	60.2	113.8	139.9	55.0	60.2	145.3	160.6
		R.FLGHLTDEQLLR.H	2	23.2	36.0	58.5	73.7	9.7	27.6	52.8	66.1
		R.FLGHLTDEQLLR.H	3	3.4	4.0	27.7	24.4	4.2	4.9	31.0	35.5
MSMEG	MSMEG	R.DLDGNLVGSSSYLNVDT									
_5612	5590	NR.R	2	6.0	9.0	45.8	53.3	6.4	13.3	24.5	39.5
		R.RLEIGHTWYTAAAR.G	3	132.1	122.2	38.6	41.1	214.5	213.5	34.7	48.6
MSMEG	MSMEG	R.SELTVNQTSPLAGYSGPR									
_5615	5592	.S	2	34.2	44.1	58.4	67.9	25.4	33.1	46.4	51.5
MSMEG	MSMEG										
_5634	5613	R.YHEWLSIHR.A	3	23.6	15.5	20.6	13.0	18.2	19.0	10.6	12.9
MSMEG	MSMEG										
_5639	5618	K.LDAETALQTGMANR.I	2	268.4	255.3	184.0	170.3	216.4	203.1	163.1	168.1
		K.LDAETALQTGMANR.I	3	17.8	20.8	7.8	5.6	16.1	15.9	4.5	3.6
		K.WAAEIAGFAPLALQHAK.R	2	65.8	53.4	126.5	127.2	48.9	53.8	71.0	86.6
		K.WAAEIAGFAPLALQHAK.R	3	101.4	97.1	87.3	84.8	76.6	76.0	57.6	63.9
		K.YGLALDNWSIR.R	2	148.3	145.8	90.1	92.3	127.9	119.4	73.3	74.3
		R.DGNVLTLELQRP.R	2	132.5	119.9	61.2	54.3	118.0	109.5	93.2	91.8
		R.NALNC#ELVDSL.R	2	215.2	226.5	115.2	116.2	198.0	197.2	112.5	104.2
		R.NALNC*ELVDSL.R	2	208.0	199.1	112.2	102.4	183.2	188.2	102.4	98.5
		R.VLNDDGAYEEPWPAHK.E	2	45.6	45.2	20.7	11.5	37.4	45.2	7.9	14.9

		R.VLNDDGAYEEPWPAHK.E	3	128.8	134.0	75.9	80.0	90.6	105.1	55.3	68.0
		R.VVVPEAYFQFPVAK.Y	2	609.4	649.6	559.9	568.7	549.4	545.0	508.7	501.4
		R.VVVPEAYFQFPVAK.Y	3	38.4	38.9	22.6	20.5	19.6	26.8	48.9	34.1
MSMEG	MSMEG	K.AYVALAEGWEPNADTAK.									
_5650	5630	A	2	2.0	3.1	22.2	38.4	4.8	5.7	5.4	10.4
MSMEG	MSMEG	K.REFDLLAVLAEHKTAVLSR									
_5662	5641	.A	4	5.2	3.7	0.9	0.6	0.2	0.2	0.7	0.7
		R.EFDLLAVLAEHK.T	2	70.6	81.3	31.8	30.1	67.7	72.9	26.3	24.8
		R.LSGFDVSTAVDGAEALR.									
		S	2	80.5	83.0	134.0	139.5	74.6	73.6	135.1	124.7
		R.VAGLEAGADDYLVKPFVL									
		AELVAR.V	3	50.7	49.1	207.3	192.2	61.3	68.7	288.8	294.6
		R.VLVVDDDPDVLASLER.G	2	236.7	266.5	321.1	345.5	229.2	254.9	312.2	317.3
MSMEG	MSMEG										
_5664	5643	R.GESIEFPLR.G	2	70.4	60.2	13.8	12.6	47.6	49.4	10.0	11.4
		R.GLIQGWQDGIPGM*R.V	2	143.6	115.8	119.6	104.9	112.8	122.1	131.0	124.8
		R.GLIQGWQDGIPGMR.V	2	98.7	115.8	96.0	104.9	90.6	97.9	113.1	105.1
		R.KLIIPPEQAYGPAGGGHR.									
		L	3	7.5	8.2	22.4	16.2	6.7	6.1	25.7	30.4
		R.KLIIPPEQAYGPAGGGHR.									
		L	4	12.3	0.0	0.3	0.0	8.6	10.3	0.4	0.3
MSMEG	MSMEG	K.KSEGQPFLYPDNSLSLVE									
_5672	5650	NFLR.M	3	118.5	123.6	100.6	101.0	148.3	126.6	198.5	165.8
		K.LGGDDELDDIAK.Q	2	812.2	601.5	616.1	499.1	817.3	729.0	866.8	794.1
		K.LPTIAAYAYK.K	2	70.6	54.9	57.1	45.8	133.3	135.6	113.1	118.7
		K.LYPNVDDYYTGVYIR.A	2	891.1	878.3	962.1	974.5	573.8	560.4	726.9	762.0
		K.SAITYIDGDAGILR.Y	2	1101.3	1095.5	1329.6	1354.8	970.1	836.1	1479.3	1233.7
		K.SAITYIDGDAGILR.Y	3	41.1	40.0	5.0	1.0	36.6	40.3	15.7	7.0
		K.SEGQPFLYPDNSLSLVEN									
		FLR.M	2	764.8	878.1	715.6	786.7	471.5	550.7	593.4	684.3
		K.SEGQPFLYPDNSLSLVEN									
		FLR.M	3	498.9	563.1	507.1	575.9	300.1	397.7	376.3	519.3
		K.TGYTTYDGGFVNTASTK.									
		S	2	586.8	491.9	354.7	299.5	476.4	476.7	365.9	341.8

		K.YPGGELDLEIVHATEGAD									
		GIALGSLLAK.T	3	2241.5	2336.6	1359.6	1306.0	1015.1	1099.0	1204.8	1276.0
		R.KLYPNVDYYTGVIYR.A	2	103.7	122.5	193.8	228.3	121.0	138.2	218.4	246.9
		R.KLYPNVDYYTGVIYR.A	3	48.5	42.2	81.6	86.2	68.1	72.7	130.0	139.1
		R.LPGWIAHWR.E	2	75.4	53.4	52.1	50.3	38.0	43.6	26.1	43.5
		R.M#TFGFPAEPYEVDPEIV									
		R.A	2	333.3	374.5	233.5	265.2	141.0	140.2	106.1	118.3
		R.MTFGFPAEPYEVDPEIVR.									
		A	2	823.0	847.1	798.4	826.5	571.1	530.9	690.9	708.9
MSMEG	MSMEG										
_5675	5653	K.SVDPDGITFYTNYSK.G	2	93.7	103.3	18.5	26.6	95.1	77.7	19.4	23.2
		R.IAPEVVFEFWQGR.E	2	132.4	150.2	103.5	121.0	91.0	104.0	115.2	121.4
MSMEG	MSMEG										
_5676	5654	K.VTFADVWGLLDGR.F	2	47.8	48.3	62.5	62.0	30.7	34.3	50.5	55.5
		R.VIASTGADAAAALSGAVG									
		AMSGPLHGGAPAR.V	3	153.0	138.1	197.0	164.4	53.5	43.9	82.4	70.0
MSMEG	MSMEG	K.AFGGTPVTIHLTVTDVDAK									
_5680	5658	.F	2	107.4	95.0	78.7	69.6	78.9	80.3	79.7	66.0
		K.AFGGTPVTIHLTVTDVDAK									
		.F	3	235.2	197.1	273.3	246.0	172.9	201.1	248.7	252.9
		K.AVEAGAEVVM#ELADQF									
		WGDR.Y	2	16.4	0.0	11.7	0.0	6.8	9.5	4.5	9.1
		K.AVEAGAEVVM*ELADQFW									
		GDR.Y	2	16.4	23.9	11.7	20.8	6.8	9.5	4.5	9.1
		R.DPFGHQWSM*GQPVR.E	3	16.0	10.1	8.9	3.1	9.2	14.2	6.4	12.0
		R.DPFGHQWSMGQPVR.E	2	43.6	45.6	24.6	27.2	65.8	50.7	19.6	13.5
		R.DPFGHQWSMGQPVR.E	3	51.6	60.7	47.8	53.3	28.8	30.0	33.0	32.4
		R.EVSPEEIAEAMK.S	2	98.7	92.4	110.9	103.2	64.0	55.6	81.2	73.2
MSMEG	MSMEG	K.NFAGDGGLWLAVMSPAA									
_5684	5662	LAR.I	2	163.0	165.7	122.9	131.5	80.8	91.8	112.7	118.0
		K.NPFIDEPIVVK.T	2	268.5	206.7	245.9	203.6	209.9	190.6	256.1	270.0
		K.VRPEQLTALAAAGDLFGT									
		SHR.Q	3	434.1	363.5	313.2	216.8	472.8	357.6	335.8	285.1
		K.VRPEQLTALAAAGDLFGT									
		SHR.Q	4	323.3	218.4	194.7	125.0	245.8	235.0	219.4	205.7

		R.WVPDFLSLPIAVENSLK.N	2	394.8	407.0	358.1	356.8	273.9	294.3	310.5	364.9
		R.WVPDFLSLPIAVENSLK.N	3	83.2	93.7	42.2	47.9	51.6	54.8	39.7	36.6
MSMEG	MSMEG										
_5690	5667	K.TIGPLRPGALTVDNLNR.R	3	77.7	83.1	129.5	136.5	86.2	89.8	108.4	117.8
		K.TVWAYELEPTETGTR.V	2	130.2	151.3	149.1	165.7	121.5	142.1	132.7	134.1
		R.VWSLISDLR.R	2	41.2	39.8	46.4	52.8	45.7	46.8	42.6	45.0
MSMEG	MSMEG										
_5694	5670	K.YPVQLSVPSAIGR.A	2	26.8	0.0	98.4	0.0	13.5	15.9	159.6	132.1
MSMEG	MSMEG										
_5696	5672	K.GFGFLSQEDGEDVYVR.S	2	173.0	181.3	136.9	136.9	188.7	198.1	143.4	139.4
		R.SSALPAGVEALK.S	2	5.2	5.4	72.0	82.9	8.4	11.2	39.8	51.5
MSMEG	MSMEG										
_5701	5677	K.IGDAALVAAVAADHR.R	3	23.6	26.0	28.8	28.9	22.0	22.3	27.9	24.8
MSMEG	MSMEG										
_5702	5678	R.AVLDYEVPLADAIR.R	2	60.7	68.9	95.6	100.4	28.8	32.0	100.3	100.4
		R.TGPLIVEWLAK.R	2	22.4	22.2	14.4	14.4	11.2	11.3	13.1	11.9
		R.TLIVNLPSPGGVK.D	2	34.0	32.3	20.4	18.8	15.3	15.4	17.6	14.6
MSMEG	MSMEG	R.TAVAAGTLLTRPDVVALIA									
_5703	5679	SGGLPK.G	3	105.3	0.0	89.6	0.0	42.8	72.2	43.7	74.9
MSMEG	MSMEG										
_5706	5682	R.YPVPQPLLVDIVDTMAR.Y	2	51.2	52.9	39.0	39.1	35.2	34.6	25.3	34.3
MSMEG	MSMEG	K.LANSEASWEGSPGDLLVI									
_5707	5683	PR.T	2	118.7	136.5	142.0	166.8	121.6	122.3	149.4	150.3
		K.LANSEASWEGSPGDLLVI									
		PR.T	3	47.5	0.0	55.6	0.0	43.0	53.5	58.6	61.0
MSMEG	MSMEG	K.HYQADGAIVSPTPLQEDGI									
_5715	5691	PLWIAGGGEK.V	3	649.8	675.3	837.8	836.3	335.4	328.8	719.0	659.7
		K.YAQYTNFTSEPEAFR.R	2	979.8	1032.5	874.4	857.4	442.2	483.3	645.0	620.7
		R.DLGC*EYAILYFPEAAYDR.									
		S	2	115.2	135.7	112.4	120.7	43.1	56.7	57.6	89.6
		R.FGLFIPQGWR.L	2	121.2	119.4	72.5	56.5	52.0	52.3	29.0	34.6
		R.LDLVDIPTDR.H	2	363.4	280.9	356.6	256.5	229.2	220.4	339.4	348.2
		R.SANFNAVIGESEK.D	2	149.8	132.0	222.5	204.1	66.0	52.8	146.1	120.8
MSMEG	MSMEG	K.AAEATGATYEPHPAEAVV									
_5720	5695	NK.M	3	7.9	6.0	4.1	2.8	5.7	5.1	2.3	2.8

		K.AFMEVLSQGTR.F	2	33.5	24.9	60.9	55.5	39.2	13.1	55.9	46.0
		K.ALEVGLVDQLVSSVDELV									
		PAAK.A	2	210.3	206.0	96.6	90.0	188.8	264.5	86.3	107.5
		K.ALEVGLVDQLVSSVDELV									
		PAAK.A	3	94.9	121.8	44.3	53.0	91.9	118.2	30.8	49.3
		K.ANPETVAVQPWDR.K	2	88.7	60.3	14.2	6.3	93.7	46.7	20.9	8.3
		K.GVVIGLPEVTLGLLPGGG									
		GVAR.T	2	215.6	211.5	97.1	89.5	286.5	286.5	117.7	109.9
		K.GVVIGLPEVTLGLLPGGG									
		GVAR.T	3	32.0	41.3	2.0	7.6	53.1	47.9	9.8	9.1
		K.MPGGTPSSPALASILPSFP									
		ALLR.K	3	60.7	86.2	46.4	57.1	72.4	106.1	82.1	67.0
		K.MPLVEIIK.G	2	60.5	51.7	32.5	26.1	114.3	63.2	36.6	19.0
		K.RQEDFIGIHFFSPVDK.M	3	46.7	47.6	18.8	15.8	57.8	71.6	11.6	17.4
		K.VDIPLQDMIDR.M	2	133.6	122.5	50.1	52.0	171.1	125.2	55.5	41.4
		K.VGPENAAESFAEVEFIK.A	2	323.5	295.9	120.9	117.0	457.1	365.3	159.8	132.2
		K.VGPENAAESFAEVEFIK.A	3	19.9	24.4	1.6	2.1	30.5	29.1	3.3	2.2
		R.AGFEVVLK.D	2	7.5	7.1	1.1	0.0	16.8	11.6	0.8	0.3
		R.KAAEATGATYEPHPAEAV									
		VNK.M	3	3.2	3.0	0.8	0.6	3.6	3.7	0.9	2.2
		R.LAAEKDSITGVVITSAC.K	2	9.4	6.8	1.1	1.2	39.9	36.5	3.5	6.4
		R.LAAEKDSITGVVITSAC.K	3	26.3	27.5	6.9	5.4	74.3	65.8	10.5	11.2
		R.MLFAEALETQK.C	2	111.9	103.1	45.5	48.3	190.6	156.6	76.4	61.9
		R.VFDYTLAIGK.T	2	170.2	168.6	62.2	52.0	229.6	199.6	62.7	57.9
		R.YFVSLVTGQTAK.N	2	301.6	261.0	168.7	153.3	419.6	273.8	205.0	143.8
MSMEG	MSMEG	R.GGALNEIKPVNLVVGLIDE									
_5721	5696	LR.V	3	232.1	246.4	120.8	128.4	230.9	206.4	105.8	105.7
		R.IGFVPQGIGADLIATIEGFS									
		R.E	3	17.4	21.8	4.5	4.5	21.2	24.9	5.5	6.8
		R.TATLVANLPETTGGVQLN									
		R.F	2	184.5	205.8	65.3	85.2	182.9	191.5	64.3	84.8
MSMEG	MSMEG	K.ALILNSPHNPTGAVASDAE									
_5725	5700	LR.A	3	316.8	324.3	218.1	254.7	198.7	189.8	276.2	317.3
		R.GFAIDVDALR.A	2	14.2	14.7	1.9	2.8	0.8	6.4	0.0	1.6



MSMEG	MSMEG										
_5727	5702	R.FLVDVADVSEVR.L	2	51.6	48.0	98.6	98.2	36.1	36.4	89.7	73.2
MSMEG	MSMEG	R.VTAMVPVVLSDDAETAR.									
_5732	5707	R	2	45.9	53.2	59.3	76.5	21.2	29.1	47.9	59.8
MSMEG	MSMEG										
_5733	5708	K.LGAPLHILHALPTLGR.N	3	54.7	53.3	3.6	2.4	18.3	17.7	0.9	1.5
		K.LGAPLHILHALPTLGR.N	4	70.4	70.1	0.4	0.5	35.7	31.2	1.2	0.5
MSMEG	MSMEG	R.RPGGLTLPAENVDLLHR.									
_5734	5709	G	3	91.4	74.7	77.3	47.4	54.6	43.9	32.7	32.4
		R.STLIDVDGVAQAAPAPR.F	2	272.3	260.1	166.7	201.7	151.3	155.7	117.0	167.9
MSMEG	MSMEG										
_5739	5713	R.FDTLTYAQVWSR.V	2	30.2	24.9	20.9	19.3	17.6	12.9	13.6	12.7
		R.FLTQLWLER.L	2	16.6	14.2	28.1	23.1	1.7	2.0	20.8	15.9
		R.LAPILAEVEPR.I	2	27.6	25.7	0.3	0.6	0.3	0.1	0.2	0.0
		R.RFETALTALPEKR.R	3	4.3	4.9	0.1	0.3	0.0	0.0	0.0	0.0
		R.RPSFTTVHGADATEIR.A	3	15.4	12.5	0.2	0.2	1.7	6.2	0.2	0.2
		R.VVAGDIGDPNLGLTPEIW									
		HR.L	3	60.9	59.0	3.0	3.7	1.3	3.8	4.2	5.8
MSMEG	MSMEG										
_5773	5743	K.NYYALGGQDWDPEQSK.L	2	206.6	219.8	2.4	4.5	149.7	144.5	1.9	1.8
MSMEG	MSMEG	R.ATQSLLQADLVLAEQVISD									
_5776	5747	HEK.M	3	145.2	135.8	192.5	177.1	118.2	100.9	192.8	154.0
		R.TVVSAIQIADVD.R.M	2	50.7	51.4	60.6	71.0	28.2	26.6	45.3	60.1
		R.VIFQVTGNYPDGDKVTTQ									
		Q	2	99.8	139.1	117.7	155.7	49.3	70.1	137.1	184.7
MSMEG	MSMEG										
_5784	5755	K.LGPEYEALIGTVR.N	2	56.2	62.7	187.1	200.9	80.5	83.9	208.3	219.3
		R.AQLLQEVWGYDFFGGTR.									
		T	2	20.8	23.3	56.0	64.9	17.6	21.7	35.9	51.5
MSMEG	MSMEG	K.ILAPAHLPQEQSQRPGRHIP									
_5789	5759	GAINVPWSK.A	4	2602.6	2734.6	1393.7	1448.8	2671.8	2822.8	1472.4	1501.6
		K.LYAEAGLDGEK.E	2	24.5	19.4	8.3	5.9	17.3	11.3	2.4	2.0
		K.LYAEAGLDGEKETIAYC#R									
		.I	2	160.3	148.0	32.2	38.1	174.2	157.6	37.0	40.4
		K.LYAEAGLDGEKETIAYC#R									
		.I	3	827.7	852.1	328.2	364.2	882.5	919.7	290.1	355.3

		K.LYAEAGLDGEKETIAYC*R. I	2	159.6	147.1	32.1	37.8	172.2	156.6	36.7	40.2
		K.LYAEAGLDGEKETIAYC*R. I	3	827.7	852.1	328.2	364.2	882.5	919.7	290.1	355.3
		K.TVFVEVDEDT SAYDTGHI EGAVK.L	3	335.3	371.7	59.4	69.5	300.9	302.4	24.3	34.8
		R.AFRDEVIAAIGTK.N	2	889.3	784.6	508.0	449.6	947.3	909.3	512.1	501.8
		R.AFRDEVIAAIGTK.N	3	555.0	474.9	153.2	129.7	659.3	597.8	169.2	152.7
		R.DEVIAAIGTK.N	2	22.8	14.2	5.7	3.6	8.9	3.8	1.0	1.9
		R.DFVDAQQFSK.L	2	68.5	57.6	36.6	33.2	46.7	53.7	34.5	38.1
		R.PGHIPGAINVPWSK.A	3	202.3	188.3	30.8	29.1	133.7	114.0	4.0	5.1
		R.SDVLVSTDWAESNLK.A	2	2216.4	2320.6	1018.3	1095.3	1955.1	1670.6	881.8	772.3
		R.SSHTWFLVQELLGHK.N	2	40.6	46.4	83.5	84.4	47.9	43.1	69.9	66.1
		R.SSHTWFLVQELLGHK.N	3	739.0	627.7	273.9	239.0	568.3	569.3	214.6	220.4
		R.SSHTWFLVQELLGHK.N	4	232.2	200.8	71.6	55.2	233.6	194.6	69.6	59.0
MSMEG	MSMEG	R.ALSSAGNGNVT VAPTGA GIHEVDVK.V	3	1529.1	1770.0	290.2	334.9	1246.5	1308.1	354.2	347.6
_5790	5760	R.FFAAPGTWTVR.A	2	463.1	471.3	53.4	54.5	401.7	395.0	73.1	66.9
		R.VVDGSGQAVGGAFVR.L	2	112.8	107.0	10.9	10.3	94.1	89.1	12.6	12.0
MSMEG	MSMEG	R.NIPVFDDLPLPADTANLR. D	2	75.0	74.2	80.8	100.6	66.0	74.3	78.9	89.5
_5792	5762										
		R.PLNQSSWELVTDALAR.S	2	49.2	52.7	60.6	57.5	38.5	39.7	33.8	29.2
MSMEG	MSMEG	R.EGGGPPTAFATIGALADR. V	2	55.1	54.9	50.6	44.4	49.6	49.5	42.6	46.2
_5795	5764	R.GDGVFETLLVR.D	2	15.0	10.8	1.9	0.9	16.8	19.4	1.8	1.1
MSMEG	MSMEG	R.GGLGGFAGLFALK.R	2	32.5	34.5	21.1	20.4	27.4	22.6	25.3	18.5
_5798	5766	R.TLGEELLEPTLIYAK.D	2	118.6	106.7	580.5	527.8	118.8	99.1	650.4	590.8
MSMEG	MSMEG	R.HLQQHLPVRMSAKHWR. R	2	308.8	303.3	4.5	9.5	336.9	326.2	1.1	4.0
_5804	5771										
MSMEG	MSMEG	K.KLPSVQVGDPFMEK.V	2	52.2	51.4	149.5	107.5	30.6	37.5	176.3	77.6
_5824	5789	K.KLPSVQVGDPFMEK.V	3	50.8	37.7	17.5	11.8	32.7	29.3	16.4	15.0
		K.LLAEVLTAASR.D	2	352.3	326.5	194.9	168.7	317.1	266.4	232.6	190.6
		K.LPRPTTGDELKETLLK.L	3	85.3	87.2	32.8	33.4	96.5	129.7	61.0	71.1

		K.LPSVQVGDPFMEK.V	2	124.3	133.6	142.0	140.7	98.7	94.6	165.5	171.8
		K.VESHNHPSYVEPYQGAAT									
		GVGGIVR.D	3	305.0	305.6	195.2	200.5	186.7	263.9	154.2	213.6
		K.VESHNHPSYVEPYQGAAT									
		GVGGIVR.D	4	337.9	346.3	196.2	201.9	222.5	272.8	169.1	193.9
		R.AANMTPAEVLSSSESQER.									
		M	2	273.1	279.0	156.0	147.6	186.2	208.9	124.2	176.7
		R.AANMTPAEVLSSSESQER.									
		M	3	47.7	47.3	6.4	16.4	37.4	30.8	3.0	11.7
		R.DGLISAHDLAEGGLIQAV									
		VESALAGETGC#R.V	3	71.5	94.2	39.6	49.5	33.3	77.4	27.6	61.6
		R.GIAVSTDASGR.Y	2	0.7	0.3	0.3	0.1	0.2	0.4	0.1	0.2
		R.TVAHEGPVYERPVERPEC									
		#QDALIADTSAK.L	4	331.2	353.5	353.7	378.7	217.7	354.0	264.7	436.4
		R.VIIPEGADPFVFLFSESSG									
		R.V	2	342.7	419.8	229.1	275.1	223.3	331.8	210.4	307.7
		R.VIIPEGADPFVFLFSESSG									
		R.V	3	168.3	213.6	69.0	110.7	195.2	174.9	68.2	107.9
		R.YTQLDPYTGAQLALAEAY									
		R.N	2	306.4	288.3	166.1	160.9	268.4	244.9	201.0	163.4
		R.YTQLDPYTGAQLALAEAY									
		R.N	3	72.6	103.6	44.5	63.9	69.4	51.1	52.0	39.6
MSMEG	MSMEG										
_5830	5795	R.EIPDVIAQALSELR.L	2	112.0	114.4	188.5	186.7	156.6	140.3	221.0	206.8
		R.EIPDVIAQALSELR.L	3	12.2	9.9	7.8	7.2	15.9	17.2	6.1	8.4
		R.LAGVDGPYSVLLSAETYT									
		K.V	2	172.5	172.7	247.9	244.1	225.8	225.3	300.1	295.3
		R.VVDVSGPNGPTTASVSTG									
		HLLDVSPPGDGVIAHLR.D	4	295.8	321.9	449.8	440.3	352.2	365.3	435.6	453.2
MSMEG	MSMEG										
_5831	5796	K.FAPVMGSVVEAANK.G	2	356.0	392.8	220.3	254.6	292.8	269.5	259.9	260.0
		R.VGVITFPGLDDIDAAR.A	2	99.2	106.1	41.8	47.2	86.8	101.7	48.5	52.5
		R.YETGADLLIPLK.S	2	235.4	232.8	185.8	185.2	168.9	163.1	179.7	160.1
		R.YVASESVLDELEGEDR.V	2	345.4	369.0	177.3	171.7	245.2	259.2	160.7	168.7

MSMEG	MSMEG										
_5832	5797	K.AEILDPQGQAIVGALGR.L	2	136.9	179.8	233.6	303.6	94.0	107.7	228.0	250.6
MSMEG	MSMEG										
_5834	5800	R.AAVPIHQGIIAPDAR.G	3	21.5	16.1	22.5	17.7	9.9	14.6	16.2	19.4
MSMEG	MSMEG										
_5835	5801	R.VPDQLISGVPAAHVDGR.M	3	16.3	13.0	5.3	7.8	54.9	53.1	20.5	25.1
MSMEG	MSMEG										
_5837	5803	K.FLLAADGTVVNR.F	2	203.1	230.1	208.1	238.1	116.9	126.5	163.0	163.1
		R.HPLYAALTETPDAGGEAG									
		DIQWNFEK.F	3	236.0	269.6	130.6	143.9	126.8	140.1	98.3	105.0
MSMEG	MSMEG										
_5839	5806	K.KNTFTDFIAVAR.H	3	5.0	3.2	0.0	0.0	5.8	3.9	1.5	0.9
		K.KNTFTDFIAVAR.H	2	33.4	31.6	17.3	17.3	42.3	30.4	30.4	25.9
		R.DLVEYSVEHAVVGGEDR.									
		F	2	40.4	48.6	14.0	15.3	35.2	51.0	8.5	21.5
		R.FLILHNDGAENFTLVDA PV									
		SDPNDFR.T	3	146.9	151.0	131.5	147.9	116.4	137.6	93.7	142.0
		R.YGDATDPQAEFTSVWGR.									
		R	2	205.0	206.7	95.4	101.1	208.0	190.4	100.1	108.4
MSMEG	MSMEG										
_5841	5807	-.MRPALSDYQHLASGK.V	3	9.4	9.9	8.2	4.4	6.4	9.8	6.0	6.2
		K.VIELVGAELANQLR.D	2	121.9	137.0	103.0	101.1	115.6	129.1	87.8	86.5
		K.VIELVGAELANQLR.D	3	16.5	16.6	7.6	9.4	13.6	14.3	2.9	3.2
		R.ALVVRRRLDM#LPVECVAR.									
		G	2	0.1	0.0	126.4	132.0	0.0	0.2	163.1	158.1
		R.DGTVVLADEVFTPDSSR.									
		Y	2	84.4	97.0	60.6	84.3	78.9	83.3	39.8	51.6
		R.IDDEHLLFVASDR.I	3	54.5	55.3	43.5	39.8	43.1	39.8	34.2	38.8
		R.ISAYDYILDSQIPDK.G	2	156.2	163.0	213.4	229.2	114.1	119.3	147.2	155.8
MSMEG	MSMEG										
_5847	5813	K.ARIEEFNALAGHEHVHK.G	2	12.6	10.6	202.8	188.9	5.8	13.1	195.1	198.5
		R.DLTENVEQLQIR.Q	2	202.1	189.3	626.8	672.1	193.1	205.7	981.4	819.5
		R.FASAAEETLVALTR.L	2	263.6	223.9	77.3	79.6	142.5	125.3	127.6	99.5
		R.VLENVDLESIAAR.E	2	171.4	156.8	305.1	305.9	203.2	190.0	319.5	462.9
MSMEG	MSMEG										
_5852	5818	R.FGDPETQAVLALLESPLG									
		QLLR.A	2	11.3	16.9	6.1	13.0	1.6	3.8	1.2	4.3

MSMEG _5871	MSMEG 5835	R.FGDPETQAVLALLESPLG									
		QLLR.A	3	54.5	57.0	23.1	29.9	0.0	30.7	0.0	19.0
		R.FGPPAGQAAWVVK.D	2	303.3	176.2	261.7	127.8	213.5	226.4	276.6	274.2
		R.IGADLVVIGPEVPLVLGVA									
		DAVR.E	3	79.1	69.2	76.0	82.0	43.6	54.0	75.7	85.1
		R.TATSEVVVDNPGHLDAALD									
		R.F	2	172.5	146.7	113.3	77.9	129.7	151.4	97.8	107.6
		R.TATSEVVVDNPGHLDAALD									
		R.F	3	424.6	425.2	295.3	254.2	411.4	396.7	430.2	429.0
		R.VGDPIHGADADGVLHAGT									
		AR.R	3	55.2	46.3	31.0	33.4	37.2	44.3	43.4	42.4
		R.VGDPIHGADADGVLHAGT									
		AR.R	4	107.1	83.3	62.4	52.0	81.9	82.8	88.2	83.4
		R.VLSVVG TGADLSAAR.E	2	230.2	145.5	280.0	276.2	214.1	182.8	309.2	309.6
		R.AELDNWQDIEPAVFAR.V	2	287.1	311.4	276.6	288.3	332.3	351.6	315.7	290.4
		R.AELDNWQDIEPAVFAR.V	3	17.4	8.7	11.3	6.7	20.3	22.2	11.5	13.5
		R.NLSDFGFANVDR.N	2	133.8	134.2	115.0	117.2	176.8	141.2	144.7	110.0
		R.NLSDFGFANVDRNPSPES									
		LDEAQAK.I	3	47.1	56.9	32.3	36.3	122.8	135.8	99.4	102.5
R.SGLIAGLEVPHLHVHVFP											
AR.N	3	26.7	37.4	49.2	51.3	28.4	30.5	75.8	70.5		
R.SGLIAGLEVPHLHVHVFP											
AR.N	4	45.9	44.9	27.0	28.9	52.1	51.7	33.5	32.3		
R.VMEVSQ LIGK.A	2	76.9	70.3	92.8	89.8	71.6	75.6	80.0	78.7		
MSMEG _5872	MSMEG 5837	K.AGEPVSLSPTEFTLLR.Y	2	389.0	377.4	164.1	168.7	171.4	167.5	133.4	143.6
		R.EVRPDAVILDVMMPGMD									
		GFGLLR.R	3	16.6	17.2	2.4	3.2	2.6	4.2	1.9	2.4
MSMEG _5873	MSMEG 5838	R.LLAEGGLD TLTPDGPLL									
		K.L	2	39.6	34.0	34.0	36.1	22.4	28.5	29.1	34.3
MSMEG _5884	MSMEG 5848	K.VAALAEQGATAAESVR.D	2	46.4	36.6	47.4	38.8	25.0	25.6	34.1	37.7
		R.TFVVGDEPSAASLVK.I	2	190.5	181.0	170.6	180.9	159.1	158.1	135.0	137.6
		R.VPLPVGSLLR.D	2	21.4	22.3	28.5	28.0	6.7	7.1	7.9	8.0

MSMEG	MSMEG											
_5892	5854	K.VGAFFISIDSAELDGK.A	2	60.2	69.4	77.4	98.2	78.3	80.0	129.9	123.1	
		R.SPGGLVTALEPLLR.K	2	30.1	28.9	61.3	54.0	25.4	22.4	27.3	33.6	
MSMEG	MSMEG											
_5893	5856	R.VFGYDYQTVER.S	2	68.6	82.5	23.4	21.2	70.3	73.4	16.6	15.5	
MSMEG	MSMEG											
_5925	5884	K.GFLQDVEIWK.H	2	35.5	31.6	4.7	2.6	20.5	32.5	5.0	5.2	
MSMEG	MSMEG	R.NAGLGPTVIVSPLLALMR.										
_5935	5893	N	2	21.1	21.4	29.4	30.1	23.9	28.2	28.5	35.1	
MSMEG	MSMEG											
_5937	5895	K.IAFLMLPGVGTK.E	2	34.3	31.2	13.2	13.1	21.8	20.2	6.0	6.7	
		R.FGAGAGNAPVEALIGVFD										
		K.I	2	366.1	329.3	246.7	211.9	387.0	354.8	195.9	182.2	
MSMEG	MSMEG											
_5939	5896	K.AIIVLNPAEPPMIMR.D	2	62.0	67.0	60.3	63.9	85.5	87.1	52.3	62.0	
		K.LGLETSAGVDWLLAQSE										
		KPDLVFEATSAYVHR.D	4	44.7	52.6	26.2	29.1	22.3	34.1	9.7	14.3	
		R.AIDLTPAAVGPVPPANL										
		R.D	2	72.2	68.4	21.2	25.5	96.4	106.0	34.4	43.5	
MSMEG	MSMEG	R.AIDAPAGSDFVADFAGLG										
_5940	5897	SVHLR.F	3	39.4	37.4	45.1	36.4	85.8	67.8	66.0	40.4	
		R.SDAVLGNPVTAVAWLAR.										
		K	2	119.1	128.8	250.1	276.1	214.9	198.7	278.1	300.2	
MSMEG	MSMEG											
_5943	5899	K.AAVIVSETTVTDPSGK.V	2	30.7	25.0	21.0	11.2	39.1	34.5	7.4	21.3	
		K.AIVDNLLDGDVSR.V	2	63.6	66.0	139.5	129.6	112.8	109.9	178.1	127.2	
		K.VLHASEAVSVPGIPTSGT										
		AK.S	3	125.8	153.2	219.5	248.3	196.2	246.7	189.0	233.1	
MSMEG	MSMEG											
_6008	5965	K.LFATMLNTLER.T	2	13.1	20.8	43.2	50.9	11.4	13.3	13.0	22.5	
		R.NAWLAAGYPEEVPGVTV										
		DR.Q	2	110.6	140.9	104.3	93.1	85.1	113.4	162.0	164.0	
MSMEG	MSMEG											
_6024	5983	K.GIMHGHGGVLIEHLK.A	3	18.4	23.1	10.5	12.7	27.0	31.2	11.2	18.7	
		R.HVPDEIIAAPGVPHTR.T	3	38.3	28.2	27.7	19.6	19.0	16.0	15.7	16.1	
		R.LGQLEPTVLVTADGYHFA										
		GK.T	3	51.6	55.1	33.5	37.5	25.4	32.8	16.0	35.5	

MSMEG	MSMEG										
_6073	6035	R.VTESVQIAADR.G	2	19.1	16.1	13.9	12.1	9.8	9.0	7.6	8.2
MSMEG	MSMEG	R.GEGLAAIATALVAAEPVG									
_6075	6037	DAK	2	5.8	0.0	21.4	0.0	5.4	4.4	12.0	15.9
MSMEG	MSMEG										
_6076	6038	K.ITTPLDLVLAEAVLAR.G	2	32.8	32.2	80.8	75.2	28.5	28.0	89.7	112.5
		K.ITTPLDLVLAEAVLAR.G	3	8.0	7.0	13.8	12.3	6.2	6.1	11.7	12.5
MSMEG	MSMEG										
_6077	6039	K.AETILDEVLAAS	2	30.6	26.1	1.9	1.7	18.5	20.7	0.5	0.2
MSMEG	MSMEG										
_6082	6044	K.ATLSALDEGEVPSGFVR.D	2	42.9	54.6	235.7	263.5	85.5	85.8	252.1	225.6
		K.VPLIVVLGHDSC*GAVK.A	3	149.4	147.2	30.5	34.0	174.0	166.1	26.0	35.4
		R.STAIAQGLAAGTQAIVGTT									
		YHLADGR.V	3	71.0	80.1	232.3	258.5	123.5	126.0	257.8	238.8
		R.TAGHVIDNAVLGSIEYAVT									
		VLK.V	3	28.4	25.4	113.9	103.1	36.0	39.5	78.8	74.7
MSMEG	MSMEG										
_6086	6049	K.INAIEVPPNAGPELEK.R	2	216.7	237.9	238.7	258.7	167.5	166.0	282.7	252.0
		K.INAIEVPPNAGPELEKR.F	3	38.2	44.9	34.3	40.5	61.2	62.3	90.6	87.0
		R.AHAVDNQPGFLGFQLLR.									
		P	3	33.1	32.5	22.5	20.8	19.5	18.0	15.4	19.6
		R.AHAVDNQPGFLGFQLLRP									
		VK.G	3	212.7	282.4	159.9	209.1	243.6	214.9	260.2	247.6
MSMEG	MSMEG										
_6091	6054	K.AHQEIYNSLLQVLEDGR.L	2	54.4	67.2	212.9	232.5	58.9	72.6	246.1	335.7
		K.AHQEIYNSLLQVLEDGR.L	3	105.3	116.2	142.7	164.3	112.6	128.7	172.2	202.3
		K.AVGLGFSQGGSENNYER.									
		M	2	146.9	101.0	151.7	103.0	133.4	118.3	132.2	111.8
		K.HFRPEFLNR.I	3	122.1	45.8	144.8	47.6	99.2	31.9	125.0	35.0
		K.NTVLIFTSNLGTSDISK.A	2	174.4	167.6	277.7	262.0	223.3	186.1	368.5	286.7
		K.RAETAEPDLAGAGAAGAP									
		TAGTE	2	61.3	37.0	98.2	62.7	54.3	33.3	93.4	58.8
		K.RPSGSFIFAGPSGVGK.T	2	196.1	179.8	251.3	230.4	178.7	161.3	275.2	264.4

		K.RPSGSFIFAGPSGVGK.T	3	158.9	119.3	164.7	119.0	184.8	134.8	203.7	141.6
		K.SLESLGISLEGVR.S	2	167.5	165.1	261.4	265.2	216.9	177.8	359.6	351.3
		K.TAVVEGLAQAIVHGEVPE									
		TLK.D	3	226.8	202.2	453.9	409.4	195.9	154.0	552.9	495.9
		K.TAVVEGLAQAIVHGEVPE									
		TLKDK.Q	3	89.5	96.1	123.9	122.5	184.5	161.1	236.1	220.0
		K.TAVVEGLAQAIVHGEVPE									
		TLKDK.Q	4	40.5	37.9	52.7	42.1	90.9	82.1	133.0	116.9
		R.EALQLGHNYIGTEHILLGLI									
		R.E	3	67.6	68.5	120.9	136.7	97.6	86.1	157.1	148.2
		R.GELQTIGATTLDEYR.K	2	126.8	130.1	221.0	184.6	96.4	119.8	245.6	196.8
		R.GELQTIGATTLDEYRK.Y	2	240.1	183.7	240.5	227.1	416.1	265.6	390.3	359.5
		R.GELQTIGATTLDEYRK.Y	3	134.1	121.7	196.2	167.5	187.4	169.9	299.4	266.6
		R.GGESGNPSTSLVLDQFG									
		R.N	2	308.0	288.5	406.7	378.4	286.4	296.5	451.9	436.1
		R.LFGAPPGYVGYEEGGQL									
		TEK.V	2	191.4	182.2	237.6	235.6	212.2	214.8	346.0	311.2
		R.M*LNHNHYIGTEHILLGLIHE									
		GEGVAAK.S	4	49.4	56.3	67.2	96.4	24.9	21.2	49.4	80.3
		R.MLNHNHYIGTEHILLGLIHE									
		GEGVAAK.S	4	49.4	86.3	67.2	96.4	26.4	133.5	49.4	153.4
		R.RKPFVVLFDIEK.A	3	0.6	1.5	15.0	14.8	9.3	18.7	20.8	31.2
		R.RVVVLAQEEAR.M	3	3.0	1.7	2.2	1.4	3.3	4.1	2.7	4.3
		R.SQVEEIIGQQQAPSGHI									
		PFTPR.A	3	633.3	664.3	1064.5	1050.7	603.2	714.5	1063.6	1261.0
		R.VSITDSAMVAAATLADR.Y	2	152.5	160.8	205.5	242.9	185.3	162.5	339.1	252.5
		R.VVVLAQEEAR.M	2	2.1	1.3	1.9	1.4	1.2	2.4	1.2	2.6
MSMEG	MSMEG										
_6092	6056	R.GRIPADVIDAFHAAT	2	34.9	42.7	25.0	31.8	53.0	52.2	46.8	54.3
		R.GRIPADVIDAFHAAT	3	63.3	56.7	12.5	11.7	106.6	102.6	38.0	35.2
		R.IPADVIDAFHAAT	2	457.0	349.3	221.7	233.2	342.3	374.5	239.3	226.0
MSMEG	MSMEG	R.AHPDLAADTATGQIVGVS									
_6094	6057	GR.V	2	42.4	53.7	37.7	41.7	10.2	22.8	13.6	29.8
		R.AHPDLAADTATGQIVGVS									
		GR.V	3	220.0	230.3	269.6	281.5	87.2	103.6	158.2	225.6



MSMEG _6096	MSMEG 6059	R.DFPVETTPLTR.A	2	69.2	54.9	102.0	91.5	18.4	18.3	62.7	63.8
		R.ELIQEVADEAIGTR.Q	2	47.6	35.9	29.7	24.1	60.0	58.1	52.1	45.2
		R.GFLEVETPMLQTLAGGAA									
		AR.P	2	52.9	57.6	66.9	58.3	9.9	23.0	23.8	29.7
		K.GEFLGGAIAPGVQVSSDA									
MSMEG _6097	MSMEG 6060	AAAR.S	2	75.4	75.1	41.3	49.5	103.2	93.0	42.8	57.5
		K.FSAGELNVYSAPADVAAV									
		TR.A	2	868.3	866.9	1192.1	1122.8	2767.7	2758.3	1440.6	1443.0
MSMEG _6105	MSMEG 6068	R.AVLDEVPALVDYLQVR.D	2	121.5	137.8	195.3	185.5	120.3	117.5	194.6	173.1
		K.YPTGYGVTLFNALQDK.G	2	98.7	94.7	38.1	42.5	126.4	97.5	58.6	66.6
		R.AAEELVFREPTTGAVSDIE									
		QATK.I	3	36.0	35.2	52.5	46.6	74.9	94.1	62.2	53.6
		R.AELEAIFGDVK.K	2	57.4	62.2	68.3	67.0	39.9	38.3	72.1	57.3
MSMEG _6110	MSMEG 6073	R.DVLDILAGELLEK.E	2	184.7	188.3	24.1	28.9	287.7	253.9	32.4	29.6
		R.GYKPVDTTVALAQIR.G	2	18.7	25.6	213.7	214.7	31.8	35.0	89.8	114.9
		K.GAVMFVTDLAR.S	2	6.9	6.9	1.9	2.6	3.7	5.8	1.0	1.4
		R.DLPFIGLLDPK.V	2	14.6	15.9	25.6	25.6	17.4	18.4	19.0	18.2
		R.DNLGDDDLLLVTVLK.G	2	7.3	9.0	67.8	67.9	4.3	10.4	22.0	39.6
MSMEG _6114	MSMEG 6077	K.LLC#VPAGDPR.W	2	5.6	6.3	5.0	5.9	4.6	5.7	3.4	3.3
		K.M#TDEAGGDDKLLC*VPA									
		GDPR.W	3	40.9	49.7	39.2	48.5	54.9	56.7	44.0	51.3
		K.M*TDEAGGDDKLLC#VPA									
		GDPR.W	3	43.1	0.0	40.8	0.0	57.6	59.8	45.4	53.3
MSMEG _6127	MSMEG 6090	K.MTDEAGGDDKLLC*VPAG									
		DPR.W	3	21.8	0.0	18.1	0.0	40.3	41.5	27.0	31.8
		R.AEAEAEELQR.S	2	0.6	0.3	0.2	0.1	0.6	0.3	0.2	0.0
		R.WDHIQDVGDISQFELDAIK									
		.H	3	302.3	289.8	307.6	277.2	267.2	304.2	278.6	292.7
MSMEG _6128	MSMEG 6092	R.LVVVADGPATSR.P	2	1.0	1.2	7.0	7.5	0.8	0.9	8.8	7.5
		R.LVVVADGPATSRPLK.L	3	6.9	0.0	5.3	0.0	11.5	15.7	11.2	15.1
		R.AIDILLVEDDPGDELITR.E	2	16.4	18.1	29.7	36.5	35.6	39.4	30.4	31.4

MSMEG MSMEG

_6142	6105	R.AENLHSAENSDKFEFVK.A	3	75.8	57.5	46.4	37.5	44.8	46.8	6.3	17.0
		R.DYVFVDDVVDVAFVR.A	2	90.8	62.1	44.7	35.9	57.0	52.9	24.7	25.6
		R.ELHTAIAGAVGAPDEPEF									
		HPPR.L	3	109.1	98.4	20.5	29.3	55.3	52.2	10.0	11.9
		R.EVLGWQPQVALAEGIAK.									
		T	2	315.4	307.9	277.2	284.8	204.3	208.6	261.9	259.2
		R.FNVGTGVETSTR.E	2	4.8	3.5	0.8	0.7	4.1	2.6	0.2	0.3
		R.LLADGHGVVGLDDLSSGR									
		.A	2	42.9	41.3	5.6	11.2	21.9	20.7	2.0	11.3
		R.LLADGHGVVGLDDLSSGR									
		.A	3	120.0	127.0	54.0	65.3	80.6	84.7	30.3	34.6
		R.SVDDPPFDATVNVVGTVR									
		.L	2	158.1	175.3	9.5	10.5	92.3	113.1	7.2	4.7
		R.TLVTGAAGFIGSTLVDR.L	2	201.2	202.0	283.4	273.5	148.6	153.2	275.5	261.9
		R.TLVTGAAGFIGSTLVDR.L	3	43.0	41.3	6.6	7.3	23.6	25.4	1.4	1.4

MSMEG MSMEG

_6157	6120	K.IAGYLGSNYVVESSR.G	2	66.3	63.3	39.1	44.9	51.7	47.9	27.7	33.0
		K.NAQEAHEAIRPAGDVFQT									
		PGQLHSALDTDEF.R.L	4	139.5	148.3	115.0	127.5	156.3	184.3	125.5	147.4
		R.ANLKEDLTPDELTPELAER									
		.L	3	98.1	97.4	37.9	37.4	30.7	32.0	27.4	33.4
		R.FGPYVTDGETNASLR.K	2	119.2	119.9	156.7	152.1	130.0	129.4	155.0	168.0
		R.GAQLAVTSVEQKPYTR.R	3	4.5	3.7	8.4	7.0	2.7	4.0	2.0	4.3
		R.IGGSASSGEQVVFNASGR									
		.T	2	27.8	28.7	40.0	35.7	27.7	32.4	57.9	84.5
		R.LGVNVVDQNFEPLYIVSPE									
		K.K	2	8.9	11.6	13.1	16.0	1.2	3.1	3.8	3.3
		R.LYELIWQR.T	2	17.2	17.2	90.1	86.0	26.0	23.1	87.4	82.9
		R.LYGYEVSPVLWK.K	2	93.2	94.6	176.8	194.5	144.9	102.2	180.8	192.9
		R.MVFHEITEPAIR.N	3	2.7	2.6	6.5	5.4	4.9	6.8	4.7	7.9
		R.SLATEDQIFTITLDEALK.I	2	38.0	40.3	59.9	72.0	51.8	49.7	54.8	63.7
		R.SMDLETVTLEDALK.L	2	46.7	29.5	25.1	23.5	52.0	30.1	23.4	19.2

		R.VVGVDPTTNEEITAQNGR.									
		Y	2	5.9	5.0	16.2	14.3	3.2	4.5	7.1	9.2
MSMEG	MSMEG	R.TLEENQKVEFEVGQSPK.									
_6159	6122	G	3	10.7	15.0	7.9	10.0	33.5	38.3	31.9	35.4
MSMEG	MSMEG										
_6179	6139	K.AANALTDLGLVAGDR.V	2	246.8	231.5	1082.1	1028.6	412.7	388.6	1239.4	1192.3
		K.ASAHGGPENMIEELR.A	2	83.4	82.8	552.1	559.2	86.0	93.1	629.5	671.5
		K.ASAHGGPENMIEELR.A	3	61.2	53.5	140.5	105.5	90.9	79.0	153.6	121.9
		K.LGHQIPASHDLSSLR.L	3	62.0	29.6	115.0	53.5	87.6	29.2	92.3	31.9
		K.LGHQIPASHDLSSLR.L	4	76.9	27.9	133.3	47.5	101.6	34.6	104.9	35.6
		K.LVITSDGQYR.R	2	2.8	1.8	4.1	1.9	3.2	5.4	1.4	3.8
		K.YGVTIYYTAPTLIR.T	2	142.0	160.0	322.5	337.9	241.5	239.2	344.6	342.7
		R.EIHIVPELPK.T	2	45.4	33.3	84.1	62.6	102.5	63.7	92.2	50.2
		R.ELGDTSTLVDPSVFEAIR.									
		A	2	200.2	197.6	441.7	398.1	336.6	282.4	474.3	388.3
		R.FAEQGWYFAGDGAR.Y	2	264.7	354.6	277.3	292.2	237.7	378.9	256.7	295.5
		R.LLGSVGEPINPEAWR.W	2	539.7	561.5	756.6	752.7	660.0	631.8	761.5	697.7
		R.LSWQTPFTDVLWDSDAP									
		FAK.W	2	57.2	70.8	93.8	108.5	55.4	112.2	57.2	124.7
		R.SITYAELKDEVC#K.A	2	76.7	81.5	225.9	227.1	106.6	110.1	216.6	219.9
		R.SITYAELKDEVC*K.A	2	76.7	81.5	225.6	227.1	106.6	106.9	216.6	219.2
		R.VAIHWEGEPVGDAR.S	2	60.1	40.8	134.8	79.4	105.4	63.6	90.0	53.6
		R.YDSDGHIWVLGR.I	3	131.3	131.4	60.5	50.5	92.6	94.9	56.7	46.9
MSMEG	MSMEG										
_6189	6148	R.AGIFQGVEPTAVAALTK.Q	2	791.1	816.6	1359.0	1373.8	1027.5	855.3	1413.2	1340.0
		R.AWIADRPEIAEQLLR.V	2	207.6	201.8	386.7	365.9	180.2	184.5	341.7	345.5
		R.AWIADRPEIAEQLLR.V	3	317.3	330.2	497.9	485.4	272.6	292.1	461.2	443.0
		R.TNNNLADLIFTDVPGR.V	2	1637.6	1785.1	1135.0	1116.9	1707.9	1615.3	1191.0	1056.0
		R.TNNNLADLIFTDVPGR.V	3	49.5	46.8	39.3	34.9	37.8	41.8	30.3	34.5
		R.VTHDLTQEEIAQLVGASR.									
		E	2	160.2	154.9	281.4	287.1	159.0	153.6	279.9	299.2
		R.VTHDLTQEEIAQLVGASR.									
		E	3	470.7	456.9	653.2	661.3	418.1	424.5	612.8	631.0
MSMEG	MSMEG										
_6191	6150	K.VGAEVSAEEAK.E	2	4.9	2.4	3.0	1.8	2.9	1.9	3.4	2.0

		K.VVGFVASAPGFGGQPGV									
		VNGASELFGEIFGDAGAHA									
		R.S	3	40.2	58.0	24.9	33.7	18.3	33.1	15.0	25.1
		K.VVGFVASAPGFGGQPGV									
		VNGASELFGEIFGDAGAHA									
		R.S	4	33.9	43.1	22.0	25.7	16.7	23.2	11.3	18.8
		R.VC#GLNALAAVHALVGIDS									
		VVK.V	3	183.4	130.3	119.9	82.1	146.1	119.0	127.9	95.6
		R.VC*GLNALAAVHALVGIDS									
		VVK.V	3	183.4	130.3	119.9	82.1	146.1	119.0	127.9	95.6
MSMEG	MSMEG										
_6195	6153	R.GTQFVVVSAAEPDALR.E	2	150.2	144.7	192.5	208.7	151.8	162.0	206.0	226.5
MSMEG	MSMEG										
_6207	6167	R.FAEDYLVEPLGEGR.A	2	25.1	24.7	56.0	57.3	14.9	19.5	43.8	50.7
		R.FALEPADEAFFGSAPHVF									
		TYR.K	2	0.7	0.4	4.2	3.8	0.3	0.6	1.6	2.8
		R.FALEPADEAFFGSAPHVF									
		TYR.K	3	20.1	20.9	50.4	54.9	26.5	22.2	68.2	57.0
		R.PAFAVPFK.A	2	8.8	7.7	18.2	14.9	8.9	10.0	18.4	17.8
		R.YSFYVDHASVPSLR.R	2	6.6	0.0	14.0	0.0	10.4	9.3	8.9	10.8
		R.YSFYVDHASVPSLR.R	3	11.8	0.0	28.9	0.0	13.2	11.3	26.5	25.8
MSMEG	MSMEG	R.LTTPIDGSGLSVDAVADQI									
_6210	6170	R.S	2	2.5	3.9	110.0	124.1	18.0	22.7	99.6	109.6
MSMEG	MSMEG	R.FATLLQEFGGANGELK.									
_6213	6172	A	2	11.3	14.5	93.9	110.0	6.7	12.2	109.7	118.2
MSMEG	MSMEG										
_6215	6174	K.SGGAPEVELAPEDIK.I	2	143.6	135.4	178.9	153.0	166.0	158.7	139.3	161.8
MSMEG	MSMEG										
_6229	6190	R.ATLESIC#YQSR.D	2	12.0	8.9	11.8	4.8	31.6	42.8	2.3	9.4
		R.HQLEHEQILPR.A	3	7.6	5.7	10.7	8.9	41.3	36.5	19.8	20.8
		R.PYYNAIVWQDTR.T	2	246.9	247.1	352.0	375.8	557.8	577.5	324.1	354.9
		R.TDSIAAALDR.D	2	10.5	4.1	24.3	15.9	27.5	26.2	65.7	59.0
MSMEG	MSMEG										
_6242	6203	R.LAQDVGIPDNFSQVR.V	2	449.0	424.8	60.3	73.4	476.7	443.2	109.3	106.8
MSMEG	MSMEG										
_6243	6204	R.FAYEHDDSGNWFR.S	2	7.4	6.7	10.1	12.2	24.0	10.1	11.8	11.7

MSMEG	MSMEG										
_6256	6217	K.ILGIPELLVSGTC#VR.V	2	206.3	166.7	249.8	217.5	149.5	165.6	189.8	215.1
		K.ILGIPELLVSGTC*VR.V	2	196.1	156.3	234.4	205.3	126.6	145.4	168.5	188.8
		K.LVDVPTPLAAAGIDDC*LV									
		GR.I	2	143.7	144.2	174.6	185.5	150.7	133.1	214.3	205.4
		R.AVIDGVEQLVHDGSALQY									
		PAPNK.Y	3	410.0	380.4	492.5	458.7	438.8	412.7	494.0	493.7
		R.KDPDVPLVVSEVNFDR.D	2	167.5	197.0	86.7	118.3	121.3	114.2	51.5	68.3
		R.KDPDVPLVVSEVNFDR.D	3	58.4	67.4	51.5	47.6	57.0	61.0	28.7	45.1
		R.KGAALNTIQIAELLAADL	2	123.0	114.8	265.2	254.2	134.4	120.0	267.1	258.8
MSMEG	MSMEG	K.AVSALHEAFGLGGDDEAV									
_6257	6218	VYAGTGR	3	178.9	181.1	208.5	199.8	146.2	137.1	193.1	181.3
		K.SEIGFSQVLYDDHIGK.V	2	69.1	82.0	82.3	90.1	47.7	48.1	74.0	71.1
		K.VTVVGLPDVPGYAAK.V	2	680.3	745.1	955.7	1093.8	559.7	557.0	931.0	914.8
MSMEG	MSMEG										
_6271	6231	K.IATDAAELVLEEAK.K	2	231.6	234.9	168.5	173.4	202.5	217.0	160.3	170.6
		R.GTGVAAGELGYQAGADR.									
		I	2	29.8	26.6	9.1	7.2	16.0	15.5	3.5	6.5
		R.GVDPQIDFSNIDEIR.R	2	102.5	139.7	22.5	23.0	47.4	163.9	13.0	35.0
		R.HPYGGDLVYTAFSGSHQ									
		DAINK.G	3	40.3	38.1	5.4	9.5	34.0	34.3	8.3	12.5
MSMEG	MSMEG										
_6280	6240	K.GSGEVSVQIDPK.V	2	2.5	0.0	20.8	0.0	2.5	1.9	22.1	27.2
		K.VVDPDDVETLQDLIVGALS									
		DASK.Q	2	22.0	33.8	30.0	46.6	20.3	24.9	31.6	38.2
		K.VVDPDDVETLQDLIVGALS									
		DASK.Q	3	40.5	35.7	62.4	54.5	37.4	46.7	66.3	79.1
MSMEG	MSMEG										
_6282	6242	K.ATVDVAGHTVIEK.D	2	28.3	26.9	31.1	30.2	22.2	17.2	34.8	24.1
		K.DANSSLVSNWTVAPAGT									
		GSSVNLK.T	2	116.4	149.4	110.7	132.6	72.0	77.2	92.1	97.1
		K.ILSSHYSQVLEGGQGA									
		GT VATWK.L	3	549.1	602.4	530.8	572.2	343.4	376.3	462.0	467.0
		R.IQDEVLENLKK.H	3	6.4	4.5	2.4	1.2	5.0	6.3	3.0	3.6
		R.RIQDEVLENLKK.K	2	19.8	25.2	1833.9	2223.9	7.6	13.6	2012.1	1921.3

		R.RIQDEVLENLKK.H	3	64.4	74.5	48.5	56.3	68.1	66.6	76.8	69.8
MSMEG	MSMEG	K.GLDVSGLTGVIGVDPDAR.									
_6283	6243	T	2	32.0	25.0	37.6	34.8	71.0	55.3	23.2	23.2
MSMEG	MSMEG										
_6284	6244	K.AIAQEGLTDLAEVR.H	2	365.5	364.7	384.9	436.5	352.5	362.4	431.0	461.2
		R.GTTYLATAPGDLGLAR.A	2	229.6	220.3	241.3	262.1	175.7	173.5	248.7	263.5
		R.IITEAQDVGLEVIHEENLR.									
		N	3	435.0	382.6	397.3	316.6	455.9	356.4	532.7	447.8
		R.SIGIEHLKPIAPPPQEALPR									
		.W	4	111.0	109.7	53.3	66.2	103.1	103.7	85.7	84.9
MSMEG	MSMEG	R.LDMSIPAGEASSGVAPAE									
_6285	6245	PAK.Q	2	75.4	86.7	14.6	23.1	59.9	96.1	10.6	31.4
		R.LLLPSAADTESALLQR.I	2	109.1	102.4	159.2	160.5	117.2	89.8	161.4	162.0
		R.RDPEEVALELLQNELGAR.									
		R	3	7.7	9.2	6.4	8.3	15.9	11.0	14.7	15.1
MSMEG	MSMEG										
_6286	6246	K.DAGIAVTEAGSAFPYR.K	2	184.2	178.9	111.5	117.5	145.7	146.1	125.1	141.9
		K.FALVAEILED.R.L	2	31.6	31.5	16.4	14.7	32.9	30.8	26.0	24.8
		R.NYGGVQGLPELR.A	2	68.4	31.8	19.0	10.6	79.7	79.5	88.6	85.5
MSMEG	MSMEG	K.DTADADEIDKDAADEDEA									
_6288	6249	GEGEDATER.A	3	10.5	13.8	6.9	11.1	1.8	12.4	0.1	9.5
MSMEG	MSMEG										
_6309	6269	K.TVLQNITEGP IVAQGR.P	2	43.8	44.4	251.4	233.3	60.0	56.1	255.6	195.2
MSMEG	MSMEG	K.VPFFDAGSVISTDGV DGIH									
_6317	6277	FTEANNR.D	3	574.1	636.8	359.4	367.2	366.2	396.1	269.4	282.5
		R.DLGVALAEQVR.S	2	64.5	59.0	94.8	97.3	70.0	64.7	79.6	90.5
MSMEG	MSMEG	R.SSEQTVDDAWPAVL TWR									
_6329	6290	.A	2	22.3	23.1	34.9	42.9	44.1	45.0	37.3	36.9
		R.TDSVSLPVAYVR.L	2	7.4	11.1	3.6	5.2	11.9	9.7	4.8	3.0
MSMEG	MSMEG										
_6337	6297	R.IDNTVLDAEDATVVR.A	2	45.8	58.6	340.7	332.4	42.3	54.3	231.1	251.7
MSMEG	MSMEG										
_6351	6314	R.DHTHDL DAMLAAITDR.T	2	63.3	77.5	18.0	21.5	64.3	99.7	4.4	7.2
		R.SFEIYPLQVR.T	2	241.6	208.0	79.7	86.0	223.7	171.6	95.5	79.6
		R.VGYAVADPEIVTALGK.V	2	634.5	624.8	430.7	457.2	480.6	465.4	392.0	370.9
		R.VTIGAPHENDAFLDFAQR.									
		W	3	203.7	181.8	168.7	158.3	165.1	146.3	148.6	153.9

MSMEG	MSMEG										
_6352	6315	R.DGEIPDAELDAFWALLR.P	2	21.3	26.2	13.5	18.8	14.1	21.8	9.1	15.0
		R.GEVTASM*VYDGRPVHDH									
		FK.V	3	2.8	2.6	1.5	1.2	2.9	2.3	0.8	1.0
		R.HLYFYLER.I	2	63.0	65.9	30.9	38.7	47.6	53.9	31.2	31.1
MSMEG	MSMEG										
_6353	6316	K.DHVAQVTLIGPGK.G	2	9.6	5.3	124.6	120.9	4.7	4.3	89.3	97.3
		K.DLAEAVTAMFEK.R	2	43.3	46.6	35.3	37.0	38.7	38.0	27.7	36.6
		K.IGLVNDVYDDAEASLAAA									
		HATAAEIAANPPLTVAGVK.D	4	142.4	178.5	131.1	162.1	62.5	109.9	56.8	105.5
		K.LAIVADVGLAR.L	2	105.0	108.1	94.4	94.5	105.6	105.4	80.1	90.7
		K.MQGAITAVADC#R.T	2	6.6	4.4	3.7	3.4	7.2	5.3	4.9	3.3
		R.LPLILSDGHLR.E	2	40.3	41.5	24.7	20.8	39.6	36.5	20.2	25.2
		R.LPLILSDGHLR.E	3	138.6	123.9	71.8	65.6	169.1	141.5	97.4	76.5
		R.YVAAWNSAFLPSK.D	2	187.0	210.4	198.8	229.1	216.8	216.6	232.2	245.6
MSMEG	MSMEG	R.GTFEPPGVGVGQAFVD									
_6354	6317	ALR.G	2	5.1	3.7	53.8	48.8	6.1	5.2	61.3	52.2
MSMEG	MSMEG	K.LTHEVGGLVVVDHSAAAP									
_6363	6325	YR.L	3	179.5	175.4	67.3	120.4	116.8	116.4	48.5	81.7
		R.LDDEANIAPWLR.A	2	57.3	56.9	24.1	25.6	41.4	46.5	18.7	13.9
		R.LFDYLQTSR.S	2	24.2	22.5	51.8	60.3	17.2	15.2	31.2	28.8
MSMEG	MSMEG										
_6365	6327	R.LTLPFTDDNVPSDAELR.I	2	115.9	124.3	108.2	123.7	123.0	126.3	137.8	142.9
MSMEG	MSMEG										
_6384	6346	K.AAGFDVTVPFTPGR.G	2	151.2	150.7	245.3	251.2	400.5	349.6	255.7	271.9
		K.ELIADSGLTVSQLVSTAW									
		K.A	2	3.6	6.2	5.5	8.4	16.2	14.2	6.2	7.6
		K.NPDVINPLDEDFDYR.S	2	145.4	161.9	146.5	136.7	325.5	357.2	137.8	141.6
		R.ANLLGLSAPEMTTLVGGL									
		R.V	2	70.0	75.1	85.2	88.0	193.8	180.4	85.6	77.2
		R.FAPLNSWPDNASLDK.A	2	645.1	622.9	242.2	255.2	757.5	745.0	259.6	242.3
		R.GDATQEETDVDSFAYLEP									
		K.A	2	34.0	31.7	28.2	35.7	107.7	90.8	31.4	28.1
		R.SAVQNLDVDALR.A	2	188.1	189.3	253.2	250.3	311.3	188.2	528.0	289.5
		R.VDLVFASNSQLR.A	2	53.2	67.0	81.0	107.3	171.2	168.6	95.2	97.3
		R.WLDHPEELAEFEK.A	2	53.5	61.8	26.8	29.2	57.8	65.1	24.7	27.9

MSMEG _6385	MSMEG 6347	R.WLDHPEELAEFAK.A	3	11.1	9.9	7.5	6.9	50.9	50.9	7.2	11.9
		K.AGLDGFYLGLEALR.E	2	109.1	107.3	132.2	120.2	92.9	87.0	115.6	93.7
		K.ELVWAPGAFR.Y	2	94.8	93.5	71.9	69.5	66.8	67.9	80.4	72.7
MSMEG _6391	MSMEG 6353	R.IVLAVMPGDPGR.D	2	163.7	152.7	176.0	158.8	114.3	153.6	115.6	177.9
		K.DVTGEDVTFDELGGADE									
		QAK.R	2	65.6	73.4	68.5	75.8	40.4	48.0	17.7	19.8
		K.TPGDPNALYGDGVVTGR.									
		G	2	382.7	317.5	467.4	429.4	360.0	308.3	419.7	402.5
		K.TTAELLAELR.E	2	70.7	54.5	154.5	128.8	119.6	112.1	272.8	244.7
		R.DQGYMFITGPDVIK.D	2	244.3	237.1	267.9	258.4	148.5	146.8	116.5	108.3
		R.FFNAIVEADVPK.V	2	367.5	317.3	528.4	512.2	409.3	368.5	607.8	545.3
		R.GLVPEISLIFGK.C	2	90.6	89.7	69.2	76.1	107.5	98.7	70.3	60.7
		R.GYIDAVIQPHETR.L	3	16.7	6.5	35.3	14.6	13.3	3.0	14.7	7.1
MSMEG _6392	MSMEG 6354	R.IFDDGDVFEIAEQR.G	2	411.0	388.1	415.8	426.6	486.6	411.0	402.7	314.3
		R.INALLDPGSFIEIGALAK.T	2	550.9	530.6	605.3	573.8	653.1	536.6	599.5	539.8
		R.IQDAVTSLAWYAE LGR.R	2	181.9	180.9	373.6	369.9	206.2	192.0	293.1	246.2
		R.VDGHVPGVIANQPMVLSG									
		AIDNEASDK.A	3	749.8	752.5	403.0	394.8	596.5	630.8	185.0	209.9
		K.EGSNAVPLFVFHPAGGST									
		VVYEPLMK.R	3	83.9	72.0	158.5	141.7	93.1	79.4	139.2	113.3
		K.ESGVQIPGGIIEHQR.T	2	35.2	31.8	154.1	144.9	61.3	41.1	160.6	113.6
		K.GASHTQQM*DPLLGE LAA									
		ELQGIEPK.P	3	90.9	98.2	179.1	191.8	95.5	105.6	150.1	155.7
		K.GASHTQQMDPLLGE LAAE									
		LQGIEPK.P	3	90.9	98.2	179.1	191.8	95.5	105.6	153.3	158.7
		K.GFDSEFFALSK.M	2	52.2	45.4	95.7	83.6	72.5	62.0	105.0	79.3
		K.LPPSINYAGPNPYIDFEK.E	2	39.8	39.4	72.6	69.0	35.4	32.9	34.2	34.3
		K.PAAVVGQSLGEAAA SYFA									
		GGLSLADATR.T	3	104.3	117.9	197.0	217.1	106.8	130.3	140.8	164.8
		K.PLTTGYFSTVHEGT FIR.P	3	18.5	15.3	42.0	38.0	9.1	12.7	19.5	22.9
		K.PLTTGYFSTVHEGT FIRPG									
		SAPIHDVDYWK.K	4	43.6	39.5	105.7	92.5	54.1	54.7	112.7	123.0



K.PLTTGYFSTVHEGTFIRPG									
SAPIHDVDYWK.K	5	66.2	57.8	99.7	100.2	53.2	75.2	56.6	95.2
K.RLPADVVPYGLER.V	2	9.0	8.3	26.0	22.6	17.1	14.0	27.1	21.0
K.RLPADVVPYGLER.V	3	12.8	12.3	18.5	17.0	23.3	22.7	24.0	24.3
K.SNLGHLESAAGAASLAK.									
M	2	32.6	27.4	95.8	82.4	59.0	36.5	114.7	74.4
K.SNLGHLESAAGAASLAK.									
M	3	78.7	74.6	127.4	122.9	88.2	87.5	115.7	108.8
K.SPGGIFNELPTVSEETAK.									
K	2	83.3	80.0	183.4	163.8	90.9	82.6	145.1	130.3
K.SPGGIFNELPTVSEETAKK									
.M	3	32.7	37.9	48.3	53.8	39.4	45.2	63.5	55.6
K.TAEEIAAEQSELLGGASTV									
AELEAK.L	3	81.0	79.6	180.8	179.0	81.6	103.5	158.6	174.1
K.TIEGLATIVR.E									
K.VLTQEAVTEALGADVPPR.	2	66.7	60.0	114.9	103.0	81.0	78.3	115.4	101.3
D	2	19.9	19.9	41.3	48.5	23.5	30.8	26.6	42.5
K.VLTQEAVTEALGADVPPR.									
D	3	29.3	32.4	64.0	60.7	29.4	39.9	39.1	54.5
R.AEGTITVEDVLGAK.T									
R.DANLYNVEELIR.Y	2	105.9	81.6	200.7	167.9	107.3	88.9	158.1	124.7
R.DGDQILAVIAGSAVNHDG	2	99.7	87.7	185.9	165.9	128.3	123.1	177.3	161.9
R.S	2	10.9	9.1	28.9	22.3	22.5	16.8	31.1	24.6
R.DGDQILAVIAGSAVNHDG									
R.S	3	31.4	27.9	63.2	53.1	44.8	46.1	64.0	57.9
R.DVDYIEAHGTGTILGDPIE									
ADALGR.I	3	88.4	83.4	176.2	148.3	97.8	113.7	149.4	147.5
R.DVEDIAIVGVATR.F									
R.EQLEEGVVDGFVR.T	2	44.1	47.7	80.1	91.2	38.3	42.9	45.4	59.1
R.EVLAGDLVEPEPEPEPEA	2	139.3	136.1	158.6	158.3	124.5	118.4	161.2	142.9
KPEK.S	3	239.5	246.8	494.3	511.7	285.3	276.4	462.0	428.9
R.FPGDLNTPDEMWEALLE									
GK.D	2	16.6	19.1	34.8	34.3	13.1	24.4	15.5	29.2
R.FVGLIDTVLPGEPIDQSK.E									
R.GPSVAVDTAC#SSSLVAT	2	159.5	142.5	346.0	306.1	205.5	186.6	363.5	300.4
HQGVQALR.A	3	41.8	39.4	149.4	133.4	39.4	31.6	172.8	136.2

		R.GPSVAVDTAC*SSSLVAT									
		HQGVQALR.A	3	41.8	39.4	141.6	132.3	39.4	31.6	170.4	136.2
		R.HPGGATVQVHAR.V	3	0.5	0.2	0.5	0.2	0.5	0.4	0.3	0.2
		R.HSVYFTQGIR.N	2	6.0	4.1	9.2	5.3	6.3	4.5	5.4	3.4
		R.HVWEFVPR.G	2	37.0	30.3	59.4	51.7	42.5	41.4	55.9	53.0
		R.LMALVEYSADEIK.T	2	276.0	261.6	159.7	144.7	125.7	142.0	125.7	138.1
		R.LPADVPVYGler.V	2	85.0	86.1	227.4	224.7	68.3	88.2	163.5	188.8
		R.M#ALELTWEALEHAR.I	3	8.5	6.4	11.9	12.0	6.5	7.2	5.4	5.4
		R.M*ALELTWEALEHAR.I	3	2.0	1.4	2.9	2.7	6.5	6.8	5.4	5.4
		R.MALELTWEALEHAR.I	2	3.4	5.3	7.2	5.8	9.9	9.5	8.7	4.6
		R.MALELTWEALEHAR.I	3	2.0	1.4	2.9	2.7	8.5	6.8	10.7	8.3
		R.NEVFAEWINK.V	2	48.1	45.2	83.0	72.1	52.8	47.0	62.4	57.6
		R.PGSAPIHDVDYWK.K	3	11.0	12.5	19.7	21.1	5.4	7.7	7.5	11.1
		R.RDGDQILAVIAGSAVNHD									
		GR.S	3	12.6	10.3	22.5	19.8	19.4	24.2	30.1	24.7
		R.RDGDQILAVIAGSAVNHD									
		GR.S	4	3.4	3.2	3.1	2.2	5.4	5.7	2.6	2.8
		R.SNGLLAPNPDAQAEVLR.									
		K	2	50.3	52.7	178.4	141.8	45.0	43.9	105.9	69.4
		R.TFNVEIPAIPYEELEK.L	2	24.2	24.2	61.3	64.8	16.2	20.9	34.0	50.0
		R.TFNVEIPAIPYEELEKLDD									
		EGQVK.Y	3	103.9	123.1	158.8	199.5	125.3	153.9	150.9	206.2
		R.TRDVEDIAIVGVATR.F	3	7.4	5.9	9.6	10.6	14.3	14.1	15.0	14.9
		R.VEESFTLVYDAIVAR.A	2	8.1	8.3	13.0	18.9	24.6	19.5	33.7	24.1
		R.VEYDFDLPPIQLTAVR.D	2	27.0	22.9	47.0	38.2	32.6	28.0	39.0	30.6
		R.VSYFYDFR.G	2	57.4	48.4	90.3	84.0	47.3	46.8	75.5	73.0
		R.VTFATWAIVTGK.S	2	26.5	21.8	56.6	42.1	44.9	37.4	69.8	50.0
		R.YAIEHRDEVEQIAESQK.G	2	0.6	0.3	1.4	1.3	6.3	2.8	7.8	3.6
		R.YAIEHRDEVEQIAESQK.G	3	59.9	66.6	148.8	131.4	124.5	127.2	192.1	177.3
		R.YHDDAIVFEPAYATR.K	2	20.2	19.7	57.1	53.1	32.9	30.5	64.3	52.5
MSMEG	MSMEG	K.AIKPSYGLAEATLFVSTTP									
_6393	6355	SAEPPK.I	3	793.4	737.7	1438.7	1283.5	971.3	1016.3	1470.6	1460.1
		K.AVLNGSEPISAATVR.R	2	386.1	309.8	698.0	527.5	431.4	295.5	643.4	409.1
		K.EGDTGGTISVAPNFAFDH									
		AAAR.G	3	430.8	410.1	788.9	739.0	477.6	503.0	603.0	631.4

		K.FPDGSSIVAHVER.W	2	212.1	190.2	226.8	250.5	236.8	229.1	187.4	183.9
		K.FPDGSSIVAHVER.W	3	344.7	307.1	538.9	477.6	346.4	342.9	440.3	447.5
		K.LDIGPITDDIR.A	2	323.0	302.5	523.7	497.8	439.9	360.8	599.8	486.7
		K.RDPDDTSEQLVIVAER.A	2	200.9	189.3	148.6	163.8	169.2	228.5	106.8	224.2
		K.RDPDDTSEQLVIVAER.A	3	202.9	196.9	254.9	235.4	242.2	246.8	267.7	274.8
		R.DLTWAQFSAR.N	2	102.7	94.6	140.9	125.6	187.4	157.9	203.6	173.0
		R.DVLLTAAGAIPR.T	2	466.1	403.8	770.0	650.8	661.4	520.2	851.3	683.3
		R.DVLLTAAGAIPR.T	3	0.4	0.2	17.3	12.0	0.7	0.0	17.0	15.1
		R.FNEAFGPF GFPPK.A	2	22.6	19.3	28.3	24.1	43.0	19.6	33.6	18.4
		R.GVPKPGSPPLDLSNVK.A	2	219.2	200.2	501.1	469.9	277.7	285.9	434.1	480.6
		R.IAVPLFDPSEPGHVGR.L	2	164.8	154.0	231.3	212.7	231.6	231.3	289.8	249.9
		R.IAVPLFDPSEPGHVGR.L	3	15.2	12.4	9.8	8.2	14.9	17.4	5.4	9.0
		R.IPTGVQITHLNLATNVVQVI									
		EALEGEEGDR.G	3	188.8	261.4	267.8	353.0	95.4	283.3	107.6	306.5
		R.KEGDTGGTISVAPNFAFD									
		HAAAR.G	3	200.7	215.6	215.3	239.4	177.1	254.8	182.0	265.7
		R.KEGDTGGTISVAPNFAFD									
		HAAAR.G	4	172.0	151.4	219.8	168.1	211.4	213.2	223.5	195.4
		R.LHAVLDNC#HPSAILTTTE									
		AAEGVR.K	3	286.9	293.6	445.5	449.0	289.8	352.1	366.0	440.5
		R.LHAVLDNC#HPSAILTTTE									
		AAEGVR.K	4	332.2	294.6	593.4	494.7	328.7	365.3	471.7	465.6
		R.LHAVLDNC*HPSAILTTTE									
		AAEGVR.K	4	328.2	292.7	591.3	494.3	324.2	363.0	471.0	465.2
		R.NHYPQDLEYS AQEASK.A	2	29.0	11.1	34.9	7.5	20.1	15.8	12.3	9.5
		R.NHYPQDLEYS AQEASK.A	3	104.0	60.1	118.9	68.1	73.1	58.6	74.2	46.3
		R.TGDYGAFYDGDLYITGR.V	2	230.8	208.8	300.3	257.7	309.0	230.4	359.5	255.7
		R.TGYVAAFSVPANQLPDEV									
		FENAHSGIK.R	3	414.9	434.3	612.3	626.6	651.1	648.7	764.5	785.6
		R.TNPSHAEGATDDATWVR.									
		T	3	3.6	3.6	4.2	3.2	2.7	4.7	1.2	3.6
MSMEG	MSMEG	K.ADDMWGSTNDPNNAWK.									
_6398	6360	A	2	158.9	169.2	51.2	56.8	260.1	322.6	37.8	51.7

		K.ANDPTENVATIANNNGTR.I	2	5.1	3.7	0.9	0.5	10.5	12.6	0.4	1.9
		K.WETFLTQELPAWLAANR.									
		D	2	260.3	276.0	107.3	106.6	340.0	367.5	69.5	76.4
		K.WETFLTQELPAWLAANR.									
		D	3	56.0	64.2	21.6	25.5	70.6	85.9	18.5	22.7
		R.PGLPVEYLEVPSAAM*GR.									
		D	2	185.8	207.7	18.9	33.3	134.5	239.7	28.8	37.8
		R.PGLPVEYLEVPSAAMGR.									
		D	2	285.4	287.8	73.8	78.7	341.0	358.7	28.8	37.8
		R.VEFQSGGPGAPALYLLDG									
		M*R.A	2	88.0	84.7	79.4	79.8	97.9	94.4	73.2	67.9
		R.VEFQSGGPGAPALYLLDG									
		MR.A	2	411.7	426.1	158.6	170.8	885.0	864.0	171.5	170.5
		R.VEFQSGGPGAPALYLLDG									
		MR.A	3	69.3	79.2	13.4	14.5	150.6	135.2	15.0	17.6
MSMEG	MSMEG										
_6399	6361	R.AVYLLDGLR.A	2	4.1	2.3	4.4	4.1	9.5	15.1	7.0	5.5
		R.ELPAWLAANR.N	2	22.1	27.1	25.2	39.9	63.8	54.4	30.7	32.9
MSMEG	MSMEG										
_6402	6364	R.ERPSHPDIAVNVGTPSR.L	3	5.8	3.7	3.5	2.2	4.2	4.3	2.4	2.5
		R.GEDAVLVAVQAALAGR.P	2	32.2	33.1	29.5	29.9	23.1	21.4	24.2	24.0
		R.GEDAVLVAVQAALAGR.P	3	5.4	2.5	1.3	0.8	2.5	2.6	0.4	1.0
		R.GEDAVLVAVQAALAGRPG									
		VLTGAR.A	3	14.4	3.8	13.8	4.7	15.0	13.8	16.3	15.6
		R.LVLGVHYPTDVVTGVVVG									
		ALVGK.A	3	61.8	54.6	44.4	40.0	50.7	48.8	32.7	32.1
MSMEG	MSMEG										
_6403	6365	K.IAIPVSKPAIAVNLR.G	3	37.8	37.0	15.5	11.4	58.8	61.8	30.2	35.8
		R.LSIHNQPNLGGSGGYSR.									
		V	3	9.2	6.8	2.8	1.9	7.8	6.9	1.5	2.1
		R.SHDPETHVRPQINVATQD									
		AR.W	3	19.5	4.5	14.9	3.0	18.6	3.7	14.5	2.7
		R.SHDPETHVRPQINVATQD									
		AR.W	4	83.6	31.5	55.0	19.4	51.8	22.5	32.9	13.9

		R.VHSAGWYAPVPAPGR.A	3	46.9	24.3	19.4	22.5	44.0	16.3	31.8	27.9
MSMEG	MSMEG										
_6404	6366	R.AANPDAPVVYTGPLDR.Y	2	132.1	75.7	36.4	15.4	185.7	192.3	121.9	154.5
		R.ALIAEQASEIDTK.D	2	160.2	154.0	186.1	182.4	119.6	104.6	201.3	212.4
		R.LDTDWFDVR.D	2	38.3	39.9	8.7	7.8	19.2	27.6	4.5	12.2
		R.RPHIGGNAYSEPEPETGIE									
		VHK.Y	3	15.2	3.4	9.7	3.1	48.9	31.2	63.4	37.9
		R.RPHIGGNAYSEPEPETGIE									
		VHK.Y	4	60.2	39.0	57.4	42.1	131.9	127.2	200.5	184.8
		R.YFNDTYEGLPVEGYTK.W	2	132.0	150.0	69.6	94.5	95.5	100.6	78.8	87.9
MSMEG	MSMEG										
_6408	6371	R.AGELVGVYPEATISR.S	2	110.5	136.2	219.3	283.1	166.5	162.3	228.4	262.4
MSMEG	MSMEG	K.VPIFIAVGEPIAPTLPAPEL									
_6409	6372	TALLHSR.M	3	71.5	73.6	834.4	873.0	56.7	81.7	1192.1	1196.5
MSMEG	MSMEG										
_6410	6373	K.DAVVLLPDYPVPDLR.R	2	146.6	139.4	170.9	159.1	182.1	159.2	179.8	164.4
		R.VGGYNEYLYTFFK.C	2	85.6	81.5	42.5	34.7	109.5	95.0	81.0	75.1
		R.YGFEIPAALVR.T	2	31.7	28.8	36.4	80.9	32.8	34.2	12.2	13.0
MSMEG	MSMEG										
_6412	6375	K.GIFPWWYAPGR.D	2	27.8	28.2	27.0	24.3	33.7	32.4	16.4	23.5
		K.GIFPWWYAPGRDDFLGEFP									
		LSSESIK.L	3	39.5	39.2	31.7	39.5	45.0	59.1	36.9	56.0
		K.GSDDTPLEDVGALMVAS									
		GHPEVVLIGIGATR.Y	3	115.7	128.0	132.3	130.8	91.6	114.7	89.8	110.3
		R.DDFLGEFPLSSESIK.L	2	170.3	163.8	172.0	172.9	166.9	169.4	141.4	155.1
		R.YTPLGESTYLKPGDEAIVR									
		.V	2	38.3	37.3	34.2	31.5	61.3	51.2	44.5	30.8
		R.YTPLGESTYLKPGDEAIVR									
		.V	3	305.4	291.4	354.4	361.5	420.6	395.1	433.1	401.5
MSMEG	MSMEG										
_6413	6376	R.GEDPALVDALLAADTAR.R	2	128.7	119.4	23.5	26.6	130.4	130.1	17.8	16.8
MSMEG	MSMEG	R.FVLVGLPGTPPPATGADR									
_6418	6381	.T	2	81.2	85.1	66.5	68.8	116.8	110.4	57.4	59.3
		R.LDEATTWLEGLR.A	2	13.6	18.7	22.2	20.4	17.8	25.6	10.8	21.4

MSMEG	MSMEG										
_6422	6385	R.AGSNLFHIEDFVAR.E	2	16.5	19.9	10.7	22.5	40.1	38.1	16.8	15.3
		R.AGSNLFHIEDFVAR.E	3	12.1	11.5	1.0	1.0	55.2	56.0	2.9	1.2
		R.DALALDQER.T	2	29.8	39.9	406.4	437.5	71.8	75.9	432.4	428.2
MSMEG	MSMEG	K.ADISAVPTTFDQSVLLDV									
_6425	6388	R.E	2	31.5	37.7	76.0	56.7	25.0	27.2	46.9	63.3
MSMEG	MSMEG										
_6427	6390	K.AFWNVVNWDDVQNR.F	2	4535.0	5364.1	2386.5	2610.6	2992.6	3672.6	1784.3	2144.9
		K.AFWNVVNWDDVQNR.F	3	400.2	441.3	219.8	223.9	292.2	293.8	172.2	177.2
		K.NLAFHLGGHINHSIWWK.									
		N	3	332.4	272.6	231.7	211.9	247.2	223.8	158.5	176.9
		K.NLSPNGGDKPTGELAAAI									
		DDQFGSFDK.F	3	6059.2	6722.4	2557.8	3034.8	3237.5	3942.4	1836.6	2229.5
		R.ANGDHAAIFLNEK.N	3	33.3	29.8	8.1	5.8	33.2	22.2	6.1	4.2
MSMEG	MSMEG										
_6431	6392	K.ELTWLANMR.D	2	18.8	19.5	5.5	6.2	19.6	18.4	6.6	7.1
		K.SEGITM#SAPYLSQLR.S	2	234.1	211.3	70.2	71.3	245.9	229.8	68.9	63.1
		K.SEGITM*SAPYLSQLR.S	2	120.1	123.6	70.2	71.3	102.4	106.5	68.9	63.1
		K.SEGITMSAPYLSQLR.S	2	120.1	123.6	91.8	92.3	102.4	106.5	73.4	76.2
		R.GPHTSAEVIAALK.S	2	27.3	20.4	17.2	14.6	30.7	21.1	19.3	12.2
		R.GPHTSAEVIAALK.S	3	71.3	56.1	41.5	37.0	72.4	63.3	44.1	36.5
		R.IKPAYFTDDEYYEK.L	2	146.5	160.7	104.8	112.5	139.4	135.6	108.1	92.3
		R.IKPAYFTDDEYYEK.L	3	241.9	274.3	173.6	201.8	200.6	239.2	148.7	170.0
		R.TNPSAATM*AALANFFR.I	2	42.6	42.9	27.8	30.7	36.0	33.8	18.2	18.6
		R.TNPSAATMAALANFFR.I	2	61.9	67.9	27.8	30.7	80.0	74.0	41.6	35.4
		R.TNPSAATMAALANFFR.I	3	6.6	5.1	1.4	1.1	7.4	8.0	2.3	2.0
		R.TVGLSPEAQQDLVQK.A	2	403.4	325.7	291.6	232.8	443.2	500.6	336.9	377.9
		R.TVGLSPEAQQDLVQK.A	3	13.2	11.4	3.8	1.9	12.2	18.5	1.6	5.0
MSMEG	MSMEG										
_6434	6397	R.LLAPVLVPVVYR.A	2	95.1	87.2	459.3	482.6	80.9	93.5	241.1	281.4
		R.LTDLAAAVTAAENMPSAR.									
		R	2	284.0	280.6	56.2	55.7	242.6	251.4	30.4	49.6
MSMEG	MSMEG										
_6439	6402	K.IMFAGPVTTVR.C	2	265.0	270.3	221.8	219.4	247.4	196.2	260.6	191.8
		R.ATADLVDEIYPDVR.S	2	311.1	316.8	165.8	159.5	196.9	226.5	141.0	153.1

MSMEG	MSMEG										
_6440	6403	R.ANIGGTWDLFK.Y	2	30.7	22.2	8.4	5.8	6.7	5.3	0.7	1.8
MSMEG	MSMEG	K.FLADEPIELLDGEGSAVIK.									
_6452	6415	R	2	363.0	326.0	355.1	315.9	371.4	335.9	429.0	390.4
		K.FLADEPIELLDGEGSAVIK.									
		R	3	128.1	112.0	86.1	72.0	170.7	128.2	130.2	108.5
		K.LLAAGEGIAPLSSEQAAVR									
		.L	2	757.5	722.1	691.5	677.2	728.4	669.8	745.7	727.2
		R.FAGPNLVVGNTILLK.H	2	217.1	200.9	235.4	199.2	269.9	234.9	354.0	330.2
		R.FIVNESIYDDFLAK.F	2	226.4	202.8	165.8	157.1	243.4	202.6	209.7	165.3
		R.VAAVSLTGSR.A	2	13.6	10.9	12.2	10.3	11.5	9.3	10.4	6.5
MSMEG	MSMEG										
_6454	6416	K.EITLSAHVR.L	2	11.0	8.0	0.4	0.1	2.6	1.4	0.5	0.2
		K.GLLTQETTTFDGK.F	2	977.8	653.1	108.1	67.9	150.8	167.2	77.0	110.9
		K.TSPQNTTWADM*LAIWK.									
		A	2	50.6	46.8	10.4	19.7	10.1	9.7	11.9	14.4
		K.TSPQNTTWADM*LAIWK.A	2	612.4	599.6	81.9	78.9	101.5	107.0	90.8	83.6
		K.TSPQNTTWADM*LAIWK.A	3	19.2	20.5	0.1	0.0	0.5	0.2	0.1	0.0
		K.YADHWNFVGGTPEEFAR.									
		K	2	248.3	268.1	5.6	6.7	36.6	41.4	9.0	12.0
		K.YADHWNFVGGTPEEFAR.									
		K	3	489.3	539.1	55.6	64.4	70.4	84.8	58.0	77.8
		R.FDRFEEAC#EVLK.G	2	368.4	306.2	32.8	20.3	63.4	60.5	34.7	27.9
		R.FDRFEEAC#EVLK.G	3	400.8	354.0	40.0	36.9	78.8	56.9	53.9	40.2
		R.FDRFEEAC*EVLK.G	3	400.8	354.0	40.0	36.0	78.8	56.9	53.9	40.2
		R.VGVLVTGIHYR.H	2	35.8	26.3	0.8	3.2	0.3	2.1	13.6	11.7
		R.VGVLVTGIHYR.H	3	144.0	107.3	4.2	0.7	15.8	16.9	4.7	2.3
MSMEG	MSMEG										
_6457	6419	R.LVLPGDLNGSRYVSEL.R.E	2	8.9	14.5	37.5	44.9	42.9	52.0	37.4	53.1
MSMEG	MSMEG	K.VAVVGSGPAGLAAAQQLT									
_6458	6420	R.A	2	115.3	124.9	73.6	81.6	129.0	125.8	9.2	14.2
MSMEG	MSMEG	K.AHADVVLI SGHDGGTGAS									
_6459	6421	PLTSLK.H	3	56.4	55.1	29.5	24.9	78.1	73.8	18.5	18.9
		K.AITALVNLEHR.G	2	5.3	6.1	107.8	153.8	12.6	5.7	53.1	119.7
		K.IAEAEGLEVLGWR.E	2	36.5	32.9	17.9	14.4	57.4	56.9	19.6	23.4

		K.LVSENGVGTVAAGVSK.A	2	27.6	26.5	14.5	16.1	27.5	28.6	18.5	20.7
		K.VGLVVEAGDAR.E	2	2.4	2.3	0.6	0.8	3.7	3.9	0.2	0.3
		R.EGEYHLFNPDTVFK.L	2	29.2	21.4	13.5	7.9	21.8	18.8	3.6	2.5
		R.EGHRPPVPIEEVEPASEIV									
		K.R	3	45.1	47.1	47.5	45.7	69.6	63.2	58.6	53.1
		R.ELMAQLGFR.T	2	2.6	2.8	2.7	2.0	5.8	7.2	1.8	0.9
		R.ETVYFPSLSGQTFVYK.G	2	92.1	70.3	62.0	80.9	108.3	82.8	75.2	112.8
		R.EVPTDDSSLGALAR.D	2	49.9	50.4	24.4	25.1	66.3	65.4	31.3	30.1
		R.FDEVLELLHLGGR.S	2	11.7	14.1	4.6	4.1	22.2	18.4	3.1	6.3
		R.FGVTSHYLANC#TDIQUIK.									
		M	3	17.6	17.2	10.8	9.1	18.4	24.0	8.2	12.1
		R.GAQGAEPNTGDGAGILIQ									
		VPDAFLR.A	3	16.9	18.0	8.5	8.4	19.5	25.0	7.6	14.4
		R.GILASHVDATDSAVGQR.I	3	19.1	15.7	5.5	8.9	14.1	19.4	4.4	6.6
		R.ILADWDNELK.H	2	34.7	34.6	16.6	19.4	46.2	51.7	13.9	13.8
		R.IVVQVDGQLK.T	2	16.7	14.2	1.1	0.2	20.7	20.4	0.5	0.8
		R.TGAEALGSMGTDTPIAVL									
		SAR.P	2	34.7	39.5	273.9	213.6	47.0	40.8	297.7	243.8
		R.TVNEMVGQVGALDTTK.A	2	33.2	34.9	18.2	18.5	50.6	44.8	24.0	23.5
		R.VC#HLDTC#PVG VATQNP									
		LLR.Q	3	60.8	58.5	14.7	19.2	83.0	89.4	11.8	15.7
MSMEG	MSMEG										
_6464	6424	R.LAVEVAESGGATK.T	2	1.3	1.4	4.7	3.2	3.9	2.9	5.7	4.4
MSMEG	MSMEG	K.LEDLDLVSQDLLIAHAGEL									
_6467	6427	EK.F	3	108.1	106.8	255.7	235.2	62.7	63.2	259.6	226.8
MSMEG	MSMEG	K.ALNEAVDEVI AVADAEGID									
_6471	6431	AGAVK.G	3	84.6	80.7	30.9	25.1	59.1	45.0	57.7	36.0
MSMEG	MSMEG	R.NHPGHAEAVEIVYDPAQT									
_6477	6437	DYR.A	3	44.5	48.9	6.6	10.7	30.4	31.3	2.9	5.4
MSMEG	MSMEG										
_6502	6463	R.VIASVQVQQ	2	7.2	5.1	10.5	7.9	7.7	4.3	14.6	8.8
		R.VNSDAADELHVHSNPEHN									
		FPIEPR.S	3	125.1	122.5	231.5	220.4	130.4	113.3	260.4	228.5



		R.VNSDAADELHVHSNPEHN									
		FPIEPR.S	4	135.5	156.4	45.4	53.7	140.9	172.1	34.0	41.6
		R.VNSDAADELHVHSNPEHN									
		FPIEPR.S	5	86.5	0.0	17.5	0.0	115.5	121.7	17.7	18.1
MSMEG	MSMEG	R.LTAGVAPESTTAAVDQLR.									
_6506	6467	S	2	39.3	44.9	288.7	309.1	29.9	30.7	430.3	313.7
MSMEG	MSMEG	K.AYPLGATYDGSGTNFALF									
_6507	6469	SEVAER.V	3	56.0	67.9	30.6	47.8	25.8	28.9	21.1	35.0
		K.GLSNYWGYNTIGFLAPDS									
		K.Y	2	80.4	80.1	51.3	65.0	44.8	47.8	47.4	57.9
		K.GLTQTHPDIPDNIR.G	2	97.5	73.0	157.0	165.4	70.6	49.9	120.6	115.1
		R.ITGSADLYEQTGR.R	2	37.8	28.0	28.0	20.7	16.3	17.9	21.3	24.8
		R.LATFFELVQQDPVVSQVK.									
		L	2	179.5	181.9	153.9	161.3	105.3	103.6	182.2	165.7
		R.LATFFELVQQDPVVSQVK.									
		L	3	33.3	48.2	16.5	34.4	35.8	30.3	20.8	29.8
		R.NFITLLLSQGVPMALHG									
		DELGR.T	3	110.8	131.6	119.0	135.7	53.5	71.8	99.2	129.4
		R.VELC#LFDDDDGGGLR.E	2	39.0	50.7	16.6	27.1	12.1	15.4	13.0	30.8
		R.VTETGLEIWR.G	2	143.7	131.0	191.2	170.8	103.9	92.4	204.4	143.2
MSMEG	MSMEG	R.VPADQLVGEENQGWTYA									
_6511	6473	K.F	2	185.1	194.2	136.8	138.7	143.6	153.9	101.3	106.3
MSMEG	MSMEG	R.ISAGLAAEALGAMEEALR.									
_6512	6474	L	2	163.8	141.1	125.0	109.0	87.0	88.4	71.0	70.4
		R.ISAGLAAEALGAMEEALR.									
		L	3	27.1	31.6	13.8	16.8	18.3	15.1	12.3	7.1
		R.LAPEPVLHGALAPGAIIE									
		R.G	3	200.0	177.7	199.3	177.5	170.7	160.1	170.3	176.5
		R.LTAIEHTLGSAQDQLR.T	2	99.1	104.1	182.4	184.1	76.7	87.1	134.7	137.2
		R.LTAIEHTLGSAQDQLR.T	3	144.6	147.3	408.2	359.0	134.1	111.6	437.2	413.9
MSMEG	MSMEG	R.FFSHQPDNLNYDNPAVQEA									
_6515	6477	MLDVLR.F	3	50.3	72.7	58.3	96.5	19.1	42.7	33.5	94.0
MSMEG	MSMEG										
_6520	6479	R.DLGIEPVKDV	2	10.8	11.0	12.2	10.4	4.0	8.6	11.7	14.4
		R.GVPFAALVTYR.D	2	71.5	37.6	75.6	44.6	80.3	83.6	78.8	76.0

		R.VTAAGAVVSGVIPMVDR. G	2	48.0	61.1	217.4	216.4	46.6	54.0	182.8	200.6
MSMEG	MSMEG	K.AAFADLPVVHGPVTNPTP EQTEAATK.Y	3	103.0	109.7	374.6	390.2	178.1	167.1	350.4	406.2
MSMEG	MSMEG	R.GDFPLNTAGGQLGFGQA GLAGGMHHVCDATR.Q	3	3.7	0.0	6.0	0.0	1.6	1.5	5.1	5.7
MSMEG	MSMEG	R.DITDALLSALNR.R	2	71.9	65.6	44.2	44.8	57.6	52.1	77.6	53.0
_6565	6527	R.NAAIDNVANLLGTSR.T	2	306.3	333.0	297.3	314.7	237.7	235.0	300.9	283.1
		R.SEMASYFPAVPMVVR.A	2	179.8	177.4	164.0	160.1	176.7	179.0	137.9	151.4
		R.TSDVGASGDGSGAPAAD LDEEIR.A	2	119.1	139.6	97.3	111.8	84.3	98.9	79.1	96.9
		R.TSDVGASGDGSGAPAAD LDEEIR.A	3	59.0	68.1	46.8	54.8	28.5	33.3	23.9	37.5
MSMEG	MSMEG	R.VEWVLAHPTGITEIQEGTL TVGGDR.I	3	66.4	66.7	49.4	52.2	29.2	31.0	33.9	35.4
_6574	6535										
MSMEG	MSMEG	R.LPIEPISQASAAQR.A	2	3.7	4.4	5.9	6.5	1.8	2.7	3.2	5.0
_6587	6549										
MSMEG	MSMEG	K.TTEHRPEILLSFGFVPK.M	3	82.5	77.6	38.5	41.8	56.3	59.6	46.8	42.9
_6596	6557	K.VLAIAAETGIEGR.I	2	78.5	81.1	42.8	60.0	67.4	89.8	25.5	26.8
		R.GLC#TQVTSFLGEEALR.E	2	108.1	115.7	59.2	56.9	129.0	126.3	37.7	39.0
		R.GLC*TQVTSFLGEEALR.E	2	107.5	114.9	58.3	56.9	129.0	119.8	37.7	37.8
		R.LTALSGAGFDGISFVGVP R.T	2	332.8	356.7	79.2	74.0	222.1	305.7	43.4	48.4
MSMEG	MSMEG	R.GAHFC#LGASLARVEGR. V	2	235.3	286.3	35.2	46.3	177.9	164.1	42.8	45.9
_6622	6584										
MSMEG	MSMEG	K.EIEATGGAIK.G	2	6.1	5.1	8.6	7.9	8.8	5.9	11.3	8.0
_6630	6591	K.FYETLGFSK.F	2	3.8	3.3	4.2	5.3	7.0	6.0	10.8	9.3
		K.M#VVLSTENLDESIK.F	2	37.5	44.0	55.2	61.3	34.3	38.3	52.1	49.2
		K.MVVLSTENLDESIK.F	2	221.2	0.0	177.7	0.0	215.0	232.4	232.3	205.6
		R.AVVYDNTGNGLVFYSPLK. R	2	29.4	35.8	59.0	64.7	28.2	26.1	50.3	42.3

MSMEG	MSMEG										
_6636	6597	K.AIWNVVNWQDVQVR.F	2	562.2	593.3	504.3	523.8	439.7	423.2	376.4	362.1
		K.AIWNVVNWQDVQVR.F	3	89.7	82.3	55.3	48.3	61.5	61.9	31.4	32.6
		K.NLSPHGGDKPTGDLAAAI									
		DDQFGSFDNFR.A	3	257.4	273.5	210.8	218.8	222.7	220.1	178.6	174.0
		K.NLSPHGGDKPTGDLAAAI									
		DDQFGSFDNFR.A	4	829.6	822.0	652.9	604.9	682.5	687.4	530.2	526.9
MSMEG	MSMEG										
_6638	6600	K.AVGGAVAPISR.L	2	0.1	0.1	0.0	0.0	0.6	1.0	0.0	0.0
		K.GM*LTGPVTILAWSFVR.D	2	37.2	46.5	15.3	26.9	55.2	77.9	13.1	21.4
		K.GMLTGPVTILAWSFVR.D	2	45.2	69.8	15.3	26.9	87.3	127.0	13.1	21.4
		K.GMLTGPVTILAWSFVR.D	3	0.9	4.2	0.0	0.0	4.8	11.4	0.0	0.0
		K.LQEDLGLDVLVHGEPER.									
		N	2	98.8	89.9	27.8	22.1	240.9	194.0	17.4	14.8
		K.LQEDLGLDVLVHGEPER.									
		N	3	303.7	284.3	78.2	70.5	695.2	497.8	95.2	63.2
		K.RPALFVASYFGELTDALPA									
		LAR.T	3	217.5	296.9	166.3	228.4	347.7	515.8	106.6	197.9
		K.VTEVVALAR.G	2	1.9	1.7	0.0	0.0	8.8	8.8	0.1	0.0
		K.WFDTNYHYIVPELGPDTS									
		FALHPAK.V	4	8.5	8.1	5.8	6.7	18.9	23.1	5.3	5.5
		R.ALGIPARPVVGPITFLAL									
		SK.A	3	325.0	322.7	93.1	90.0	1249.5	1171.4	213.8	188.0
		R.DDQPLADTAAQVALAIR.D	2	196.1	161.8	56.0	53.2	397.2	196.7	72.9	51.8
		R.DDQPLADTAAQVALAIR.D	3	40.6	37.7	0.5	1.0	65.6	48.7	0.8	0.7
		R.EAIGEIAASNDIAAAR.K	2	638.5	593.7	243.5	220.0	1263.1	1290.5	285.4	270.4
		R.GGTYDGTDIAPLEM*TK.W	2	48.4	42.3	50.4	39.3	87.2	68.8	40.8	32.5
		R.GGTYDGTDIAPLEM*TK.W	2	543.2	540.3	233.8	228.0	973.0	1021.0	233.1	224.4
		R.LGLPPLPTTTIGSYPTSA									
		IR.V	2	493.2	558.2	134.2	156.2	1045.4	1135.6	139.8	172.6

		R.LGLPPLPTTTIGSYPQTSA									
		IR.V	3	300.3	414.9	120.5	138.0	589.5	734.7	251.7	128.8
		R.LWVNPDC#GLK.T	2	10.7	7.9	3.8	5.3	12.4	14.9	1.3	4.2
		R.SHMEVLDDLNAAGFGNG									
		VGPGVYDIHSPR.V	4	273.1	319.3	123.0	141.1	460.6	548.3	117.9	121.3
		R.SWLAFGFEK.V	2	159.2	149.9	38.4	35.4	409.8	328.8	64.4	44.5
		R.TPVEAIGVDLVAGTAAAV									
		AAVPELTTK.T	2	39.3	43.8	6.3	9.7	68.9	114.6	3.7	16.7
		R.TPVEAIGVDLVAGTAAAV									
		AAVPELTTK.T	3	687.0	874.3	253.5	305.6	1573.6	1623.5	328.8	387.4
		R.VPTTEEMATALR.N	2	268.0	217.5	106.7	76.1	562.3	296.6	122.6	68.3
MSMEG	MSMEG										
_6733	6692	R.VTPATATSTEDDVLYLR.H	2	82.1	87.0	92.6	97.4	78.6	97.0	95.6	112.9
MSMEG	MSMEG										
_6740	6701	K.SMAGLIDLVR.S	2	10.4	10.8	1.0	0.1	0.3	1.4	0.1	0.0
		R.LEGVILDPVYEGK.S	2	183.2	212.1	311.2	385.9	156.7	167.0	301.2	305.5
		R.YPLTFGPSPIHPLER.L	3	49.9	58.3	29.9	24.6	10.6	17.4	39.6	30.7
MSMEG	MSMEG										
_6741	6702	R.LVDIAGQIIESR.-	2	36.9	43.1	56.3	65.9	32.2	38.9	66.3	83.8
MSMEG	MSMEG										
_6743	6704	K.SFYQTVFGFDVLR.E	2	40.0	39.7	35.8	38.0	53.1	49.8	36.6	31.5
MSMEG	MSMEG	K.AGWDMWPGPYGQLGSR.									
_6746	6707	A	2	183.2	181.1	120.7	132.1	57.7	78.0	41.8	52.9
		R.ATARPTFDDDLVTDQVR.									
		E	2	147.1	163.5	53.3	60.5	97.2	118.8	91.1	72.5
		R.ATARPTFDDDLVTDQVR.									
		E	3	315.9	256.8	375.2	303.2	230.9	215.4	431.0	358.3
		R.AYVLASLDESLDR.M	2	180.8	165.4	246.3	200.6	152.9	130.8	301.9	266.4
		R.GITHFDLANNYGPPYGSA									
		EENFGR.M	3	381.0	376.9	413.6	414.8	244.7	260.4	407.4	414.0
		R.IDPVTPLEETIGALDTAVR.									
		A	2	509.3	483.6	533.8	501.2	335.4	318.0	557.1	528.3
		R.IDPVTPLEETIGALDTAVR.									
		A	3	188.9	200.4	205.8	215.7	155.5	136.6	245.9	223.2
		R.LGTPLVIHQPSYSLLNR.W	2	75.5	93.8	55.2	86.6	30.1	33.7	50.7	71.4

		R.LGTPLVIHQPSYSLLNR.W	3	226.0	216.5	253.2	263.7	134.9	136.2	282.9	259.4
		R.PTFDDDLVTDQVR.E	2	173.8	182.3	152.1	156.5	107.5	112.5	151.6	154.1
MSMEG	MSMEG	R.GDLVNYAGVAGDANPLH									
_6754	6715	WDENIAK.L	3	160.5	162.2	98.3	94.4	132.4	145.8	61.4	82.3
		R.LSQPAVVPAEGTEIEYSG									
		R.I	2	230.1	240.2	99.1	136.3	163.2	176.5	80.4	94.0
MSMEG	MSMEG	R.TAGLLPAIAAELDDEILLAR									
_6756	6717	.C	2	24.8	20.2	51.0	46.8	30.3	28.4	47.0	43.2
MSMEG	MSMEG										
_6759	6720	K.IQWILENVPGVR.E	2	924.9	900.1	2431.6	2345.9	3642.6	3208.6	2918.5	2753.7
		K.IQWILENVPGVR.E	3	27.2	19.5	29.7	22.7	160.1	147.0	28.9	34.2
		K.LQPSDLAALGVTNQR.E	2	2156.1	2218.6	3735.5	3781.1	7395.5	7365.3	4468.6	4460.5
		K.LQPSDLAALGVTNQR.E	3	142.2	138.2	186.7	172.2	646.0	612.5	259.0	250.4
		K.NTYGTGNFLLLNTGTPV									
		R.S	2	1248.6	1298.1	2063.3	2062.3	3895.4	3932.4	2192.6	2288.3
		R.DQM*HVIDSAAESESAR.									
		L	3	736.8	581.6	1304.8	1052.2	1553.8	1488.4	892.7	919.0
		R.DQMHVIDSAAESESAR.L	2	682.4	635.0	1219.4	1181.9	1343.5	1475.1	774.4	845.3
		R.DQMHVIDSAAESESAR.L	3	757.0	600.9	1327.7	1073.0	1584.9	1518.1	899.4	931.1
		R.DVAEAM*EADSGVHLDVL									
		K.V	2	172.1	214.0	298.5	301.5	239.8	234.2	232.0	218.0
		R.DVAEAMEADSGVHLDVLK									
		.V	2	420.5	403.5	298.5	301.5	678.9	570.0	232.0	218.0
		R.DVAEAMEADSGVHLDVLK									
		.V	3	71.1	73.5	123.8	122.9	330.5	232.4	104.2	79.7
		R.FMIFDHAGNEVAR.H	2	251.8	214.5	750.3	654.4	586.8	568.3	1347.4	1397.0
		R.LGDDAPVYALEGSIAVTG									
		SAVQWLR.D	3	64.7	57.5	97.9	101.3	227.9	230.3	96.9	114.8
		R.LVDDNGGVYFVPAFSGLF									
		APYWR.S	2	70.7	85.7	107.6	143.1	103.9	222.6	40.2	111.8
		R.LVDDNGGVYFVPAFSGLF									
		APYWR.S	3	75.4	101.6	84.3	127.6	102.3	210.3	28.7	94.1
		R.PGWVEHNPVEIWER.S	2	620.6	604.5	704.1	713.7	1505.2	1518.0	782.9	774.6
		R.PGWVEHNPVEIWER.S	3	710.7	665.9	909.2	847.7	2198.1	2413.3	881.9	1043.2

MSMEG _6761	MSMEG 6721	R.SM*LPQIRPSSDPAGYGT									
		TTSSR.P	3	121.0	97.4	293.0	259.8	425.3	483.1	327.8	354.5
		R.SMLPQIRPSSDPAGYGTT									
		TSSR.P	3	623.9	647.1	1039.1	1108.5	1339.7	1269.3	787.9	802.2
		R.SSSAVQSALNAAK.L	2	18.7	16.3	26.4	27.8	32.8	40.2	14.9	21.4
		R.TGRPYYYNAIVWQDTR.T	2	610.2	724.4	502.3	434.9	966.3	1112.2	571.2	622.8
		R.TGRPYYYNAIVWQDTR.T	3	478.7	462.6	318.5	216.9	929.5	992.4	443.0	496.3
		R.EHAVASPVPGTLVIAGGK.									
		Y	2	41.2	54.2	31.3	42.1	129.0	144.7	25.5	37.8
		R.EHAVASPVPGTLVIAGGK.									
Y	3	30.5	27.1	0.2	3.9	119.6	113.3	0.0	2.0		
		R.EVADLIAPVLGWSQTDIA									
		R.E	2	26.7	29.4	7.6	9.5	52.1	48.0	1.0	6.2
		R.TAEDTGLAVTTVAHLLGR.									
		Y	3	17.2	18.0	0.6	1.4	45.2	34.5	0.3	0.0
MSMEG _6760	MSMEG 6722	R.VPLLGDAGYPAAWNAR.R	2	226.5	237.4	135.6	141.1	362.6	401.7	92.9	116.5
		R.IWQIYADPR.Q	2	78.4	76.9	22.0	17.6	36.1	43.3	17.1	19.4
MSMEG _6776	MSMEG 6737	R.WLRAAGVDTTGAYSGMK									
		.Y	2	81.7	61.5	181.3	117.4	71.2	62.4	77.3	74.0
MSMEG _6787	MSMEG 6749	K.EWLGLEFDPQSASAAK.V	2	23.2	21.0	195.3	205.7	16.4	18.9	250.9	257.2
		K.IVIGGDNAGFNYK.E	2	13.5	0.0	49.5	0.0	10.7	13.5	55.5	37.4
MSMEG _6816	MSMEG 6779	K.FGEIC*RPDWIPEGTR.V	3	0.5	0.3	117.9	101.0	0.1	0.1	152.4	129.1
		K.LAYEYATTQPAAIR.Q	2	46.7	40.5	359.1	339.5	38.6	66.3	301.5	273.2
		K.SLFVYNSNPVSQGPAQEK									
		.T	2	141.6	181.9	530.3	542.7	53.2	99.0	411.2	483.7
		R.AITC*LPALVGAWR.H	2	2.2	1.5	121.9	123.9	2.9	1.4	149.3	120.3
		R.DDLFTVVSEHFITDTAK.F	2	8.1	8.4	223.7	218.5	3.3	5.1	189.9	158.1
		R.DDLFTVVSEHFITDTAK.F	3	0.2	0.0	69.7	61.8	0.0	0.1	83.7	46.5
		R.EMLIDFHDWDAPALAGIT									
		YEK.L	3	7.5	3.5	102.2	146.4	3.4	3.4	78.2	96.1
		R.GSFQGPAAYETGLIPGLV									
MANVGHWQGK.T	3	2.4	2.0	279.5	226.7	0.9	2.3	226.7	320.3		
		R.ITWDEALAEIK.T	2	0.2	0.1	186.3	165.3	0.0	0.3	242.9	171.0

MSMEG _6822	MSMEG 6786	R.VEEITGIPADDVR.K	2	0.4	0.3	222.9	167.4	0.0	0.3	183.8	84.4
		K.LFIADDDLLQSESGK.T	2	63.4	59.3	123.0	131.5	48.5	56.1	122.6	121.8
		R.FGIPDGLSGEAVAVK.Q	2	75.4	88.5	330.1	389.7	94.7	95.9	386.5	382.0
MSMEG _6854	MSMEG 6817	R.YLMAISSLDPTSAGAAR.E	2	450.8	570.4	313.5	345.6	359.3	522.9	236.0	296.0
		R.KIDQAFIGSCANGQLDDL									
		R.I	2	71.5	80.5	1.6	1.5	44.1	60.9	0.7	1.1
MSMEG _6875	MSMEG 6839	R.KIDQAFIGSCANGQLDDL									
		R.I	3	62.4	74.6	0.0	0.5	49.0	59.6	0.1	0.2
		R.AAFDAAIAQPGAVEPVK.V	2	71.0	71.4	102.1	115.8	30.0	32.6	70.0	112.0
MSMEG _6894	MSMEG 6855	K.LFGSVTAADV VNAIK.K	2	660.7	842.1	475.0	620.1	619.3	655.5	465.4	453.3
		K.LFGSVTAADV VNAIK.K	3	123.9	72.6	55.8	31.2	112.6	120.4	52.2	54.5
		K.LFGSVTAADV VNAIKK.A	2	23.8	21.9	5.0	7.4	36.9	33.8	12.8	4.7
		K.LFGSVTAADV VNAIKK.A	3	46.6	42.2	27.2	22.0	81.6	78.5	45.9	41.1
		K.LILTA EVEHLGAAGDTVEV									
		K.D	2	202.6	219.2	121.7	123.3	191.7	179.9	119.8	105.4
		K.LILTA EVEHLGAAGDTVEV									
		K.D	3	988.5	1136.7	655.6	738.3	1000.8	1067.5	753.3	649.3
		K.TALEGLGDVTL SVNAAGD									
		TGK.L	2	250.1	222.2	133.6	105.2	237.7	238.3	129.4	120.7
		K.TALEGLGDVTL SVNAAGD									
		TGK.L	3	58.3	0.0	27.6	0.0	92.0	80.0	47.3	33.8
MSMEG _6896	MSMEG 6857	K.DDPWGSAPASGSFSGAD									
		DEPPF	2	59.5	78.0	23.1	34.2	33.8	52.9	6.9	18.5
		R.EAAENVAESLTR.G	2	21.4	22.1	13.2	13.7	18.2	22.8	7.0	15.2
		R.FTPSGAAVANFTVASTPR.									
		M	2	800.0	840.1	478.2	501.6	766.0	812.5	575.6	569.7
		R.FTPSGAAVANFTVASTPR.									
		M	3	377.3	430.2	89.1	84.1	251.4	328.0	85.2	79.2
		R.TVVEVEVDEIGPSLR.Y	2	291.3	310.4	200.8	207.3	223.7	241.6	165.8	172.7
MSMEG _6897	MSMEG 6858	K.DGGTVDKVDIWGR.R	3	3.2	0.5	1.7	0.7	9.9	9.8	2.7	4.7
		K.HAEGIYAVIDVK.A	2	33.6	31.8	13.2	14.9	41.7	32.9	19.3	15.5
		K.HAEGIYAVIDVK.A	3	13.5	10.5	9.0	5.2	18.8	15.2	7.9	7.9

		R.TVAPSLETFLNVIR.K	2	351.7	315.9	320.6	283.9	395.5	399.5	367.5	332.6
		R.TVAPSLETFLNVIR.K	3	28.1	17.3	16.7	9.1	28.2	29.9	16.2	16.8
MSMEG	MSMEG	K.IAKDRGIGGPIEAASAYLM									
_6904	6866	#K.S	3	3.5	6.6	6.6	3.8	2.4	1.4	8.5	4.6
		K.KFEDAGVPIVGDDIK.S	2	418.2	454.3	248.7	283.3	441.6	443.1	259.2	273.4
		K.KFEDAGVPIVGDDIK.S	3	199.2	189.7	7.1	7.8	236.0	221.7	74.2	82.9
		K.LEVWDSPNSAGVIIDAVR.									
		A	2	381.0	381.4	253.8	267.8	446.9	480.1	177.0	272.1
		K.NVHIGPSDHVAWLDDR.K	2	161.1	175.8	24.7	19.4	126.1	130.0	14.7	32.8
		K.NVHIGPSDHVAWLDDR.K	3	143.7	122.9	3.2	4.2	116.6	125.9	0.1	3.9
		K.NVHIGPSDHVAWLDDR.K	4	84.4	57.4	0.8	0.0	66.2	65.2	0.0	0.5
		K.NVHIGPSDHVAWLDDR.K									
		W	4	13.7	1.0	0.3	0.0	145.7	131.4	0.5	0.0
		K.TQAVTSNLSGALAGK.V	2	153.1	135.3	98.2	116.3	161.6	148.1	53.4	75.9
		K.YYADTIEVSDAEPVDVVK.									
		V	2	725.9	766.7	122.0	165.0	993.3	994.1	163.9	207.6
		R.AFGDVPLNLEYK.L	2	434.9	400.5	125.3	111.4	503.9	491.4	162.4	193.6
		R.GIGGPIEAASAYLMK.S	2	256.4	228.0	39.5	38.3	160.9	132.8	48.7	43.4
MSMEG	MSMEG										
_6907	6868	R.LDDLAAALPR.I	2	80.4	65.3	104.3	87.5	66.9	73.5	118.6	96.7
		R.LILGIGSGWK.Q	2	83.2	82.9	87.4	87.8	58.0	54.4	90.8	79.7
MSMEG	MSMEG										
_6913	6872	K.LSDEDLATLAR.A	2	11.2	0.0	12.9	0.0	11.1	12.1	9.2	9.9
MSMEG	MSMEG	K.FFWPGPDGEIEVNQEF GK									
_6917	6875	.I	2	162.8	145.0	133.3	112.2	133.9	128.9	146.4	135.7
		K.FFWPGPDGEIEVNQEF GK									
		.I	3	13.6	14.7	2.7	4.8	2.6	3.8	0.8	3.4
		K.NSVSPDEIC#DNYGADTL									
		R.V	2	14.1	15.2	26.2	26.7	7.7	7.3	20.5	20.8
		K.NSVSPDEIC*DNYGADTLR									
		.V	2	14.1	15.2	26.2	26.7	7.7	7.3	20.5	20.8
		K.TGVFLGAYATNPADGK.Q	2	284.9	285.8	207.4	219.5	264.3	262.2	254.3	235.3
		K.VLYDLGYVSSR.E	2	163.3	169.2	134.5	145.5	109.6	119.2	137.2	138.0



		R.AAIEPLVLM*VAPLAPHLA									
		EELWK.R	3	49.5	58.4	32.7	42.5	43.4	63.8	39.4	64.9
		R.AAIEPLVLMVAPLAPHLAE									
		ELWK.R	3	51.1	59.0	32.9	42.5	45.6	65.3	45.4	68.2
		R.DTNVMPQWAGSSWYEL									
		R.Y	2	13.5	13.3	13.1	14.9	3.1	6.2	5.1	8.8
		R.GTFNVANPVGSLAPTDGS									
		DVPADK.M	2	36.9	40.1	34.8	37.4	20.0	23.0	34.4	34.3
		R.GTFNVANPVGSLAPTDGS									
		DVPADK.M	3	48.1	65.4	39.9	66.4	12.1	27.1	13.3	41.0
		R.GTYVPAAEVIER.D	2	308.9	13.3	291.8	266.9	186.2	198.3	193.6	202.5
		R.ISELVEEFESGK.R	2	27.6	28.2	27.7	32.7	8.1	11.6	12.0	17.2
		R.ISELVEEFESGKR.T	3	14.6	15.4	15.3	13.5	9.1	9.3	13.4	13.8
		R.LLEDLDVLDWPEK.V	2	184.3	209.2	198.9	209.3	136.7	147.9	233.5	216.9
		R.NVLHALGFDAFGLPAEQY									
		AVQTGTHPR.T	3	139.6	167.7	613.1	715.6	112.5	138.7	432.3	740.8
		R.NVLHALGFDAFGLPAEQY									
		AVQTGTHPR.T	4	102.9	99.5	123.5	111.8	49.2	51.6	98.4	94.0
		R.VYEMSMGPLEASRPWAT									
		K.D	3	21.4	24.0	24.9	24.7	5.2	8.9	11.2	13.9
		R.YNADLAGQIER.A	2	4.7	4.1	5.2	4.0	1.6	1.8	2.3	3.2
		R.YWGEPFPIVYDADGR.A	2	61.0	60.0	70.2	67.1	32.0	40.0	46.3	54.4
MSMEG	MSMEG	R.KHEPDGGVSFHHHEVVG									
_6926	6882	AK.M	4	0.7	0.6	1.8	1.4	1.2	1.2	0.3	0.4
MSMEG	MSMEG	R.SAPDLLNLLQQATAIADR.									
_6929	6886	T	2	16.0	13.3	42.5	46.3	16.8	16.9	33.2	43.7
MSMEG	MSMEG										
_6933	6889	K.ITFLTNTTEITQIEGDPK.V	2	241.4	263.0	88.1	91.7	241.4	241.1	57.5	60.2
		R.AVILAMGAAAR.H	2	15.5	10.5	16.4	14.1	16.5	11.2	14.7	14.7
		R.MEDVDAVQLEGPVK.T	2	160.5	160.1	125.6	112.8	148.7	171.8	47.4	56.3
MSMEG	MSMEG										
_6934	6890	K.M*VAPVLEEIAAEK.G	2	33.0	27.8	78.3	64.2	12.6	17.2	55.1	61.7
		K.MVAPVLEEIAAEK.G	2	38.4	35.1	78.3	64.2	29.6	31.3	55.1	61.7
		R.DFQVVSIPTM#ILFK.D	2	33.1	0.0	28.2	0.0	15.7	20.6	21.0	20.1
		R.DFQVVSIPTMILFK.D	2	42.2	40.3	49.7	47.3	35.3	33.0	52.6	49.8
MSMEG	MSMEG										
6941	6896	K.IVHDAVAAIDGVR.S	2	29.1	15.0	20.6	11.5	25.3	19.8	29.3	23.9

		R.EELAPMTPFER.K	2	82.6	90.7	39.5	45.6	68.7	72.8	36.3	42.6
		R.KGEVLDALQELTR.L	2	224.1	224.5	198.6	190.8	242.1	239.3	238.5	250.7
		R.KGEVLDALQELTR.L	3	62.1	57.4	18.2	14.7	61.2	54.3	18.3	18.0
		R.KIVHDAVA AIDGVR.S	2	32.6	35.9	8.9	10.2	55.7	49.9	22.5	19.5
		R.KIVHDAVA AIDGVR.S	3	86.8	82.8	22.1	24.4	99.3	113.1	37.2	37.3
MSMEG	MSMEG	K.YFSRPEPDTSSDDSNV									
_6947	6901	LNR.R	3	25.6	27.9	91.4	96.6	7.7	13.6	31.0	42.3
		R.LDVPDDVLELIASSIER.N	2	6.4	10.5	16.8	27.3	0.9	5.5	2.7	8.6