

SUPPORTING INFORMATION

Ubiquitin conjugation probed by inflammation in MDSC extracellular vesicles

Katherine R. Adams^{1*}, Sitara Chauhan^{1*}, Divya B. Patel², Virginia K. Clements³, Yan Wang⁴, Steven M. Jay², Nathan J. Edwards⁵, Suzanne Ostrand-Rosenberg³, and Catherine Fenselau^{1**}

¹ Department of Chemistry and Biochemistry, University of Maryland, College Park, Maryland 20742, United States

² Fischell Department of Bioengineering, University of Maryland 20742, United States

³ Department of Biological Sciences, University of Maryland, Baltimore County, Baltimore, Maryland 21250, United States

⁴ Proteomic Core Facility, College of Mathematics and Natural Sciences, University of Maryland, College Park, Maryland, 20742, United States

⁵ Department of Biochemistry and Molecular & Cellular Biology, Georgetown University Medical Center, Washington DC 20057, United States

*These authors contributed equally

** To whom communications should be addressed

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Table S1- Proteins identified in Conventional (CON) and Inflammatory (INF) exosomes.

Protein	CON Spectral Counts	CON Distinct Peptides	CON Unshared Peptides	CON Protein Coverage %	INF Spectral Counts	INF Distinct Peptides	INF Unshared Peptides	INF Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description
<u>A0</u> <u>A0</u> <u>75</u> <u>B6</u> <u>D5</u>	2	2	2	29.57	0	0	0		2	2	2	3.3	29.57	Protein Igkv19-93
<u>A0</u> <u>A0</u> <u>87</u> <u>W</u> <u>R5</u> <u>0</u>	841	76	76	46.52	1055	96	96	53.81	1896	102	102	0	55.03	Fibronectin
<u>A0</u> <u>A0</u> <u>A6</u> <u>YY</u> <u>E5</u>	11	2	2	28.57	8	2	2	28.57	19	2	2	3.3	28.57	Protein Igkv4-78
<u>A2</u> <u>A5</u> <u>13</u>	51	11	3	20.14	92	12	4	27.27	143	15	4	0.66	27.27	Keratin, type I cytoskeletal 10
<u>A2</u> <u>AF</u> <u>Q2</u>	11	5	5	38.75	24	5	5	39.48	35	6	6	0.47	47.97	3-hydroxyacyl-CoA dehydrogenase type-2
<u>A2</u> <u>AG</u> <u>H6</u>	1	1	1	0.68	3	2	2	1.19	4	2	2	3.3	1.19	Mediator of RNA polymerase II transcription subunit 12
<u>A2</u> <u>AI</u> <u>V8</u>	6	2	2	5.41	5	2	2	7.65	11	3	3	1.19	9.51	Caspase recruitment domain-containing protein 9
<u>A2</u> <u>AI</u> <u>W4</u>	3	1	1	6.09	2	2	2	11.47	5	2	2	3.3	11.47	Protein phosphatase 1 regulatory subunit
<u>A2</u> <u>AK</u> <u>G8</u>	0	0	0		2	2	2	2.06	2	2	2	3.3	2.06	Focadhesin
<u>A2</u> <u>AN</u> <u>08</u>	5	3	3	1.35	2	2	2	0.83	7	5	5	0.47	2.18	E3 ubiquitin-protein ligase UBR4
<u>A2</u> <u>AQ</u> <u>07</u>	38	9	6	29.05	71	14	10	44.35	109	14	10	0	44.35	Tubulin beta-1 chain
<u>A2</u> <u>AQ</u> <u>A9</u>	3	2	2	0.49	0	0	0		3	2	2	3.3	0.49	Protein Neb
<u>A2</u> <u>AS</u> <u>S6</u>	4	3	3	0.12	1	1	1	0.05	5	4	4	0.66	0.17	Titin
<u>A2</u> <u>RT</u> <u>H5</u>	4	1	1	5.42	4	2	2	9.04	8	2	2	3.3	9.04	Leucine carboxyl methyltransferase 1
<u>A6</u> <u>ZI4</u> <u>4</u>	464	23	23	61.96	632	34	34	68.9	1096	35	35	0	71.53	Fructose-bisphosphate aldolase
<u>B1</u> <u>AT</u> <u>Y1</u>	1425	40	1	86.27	1618	48	2	84.31	3043	53	3	1.19	95.42	Actin, cytoplasmic 2
<u>B1</u> <u>AU</u> <u>Y2</u>	24	6	6	11.23	26	6	6	10.91	50	8	8	0	13.98	Protein Arhgap4

<u>B1</u> <u>AY</u> <u>13</u>	2	2	2	1.15	0	0	0		2	2	2	3.3	1.15	Ubiquitin carboxyl-terminal hydrolase 24
<u>B2</u> <u>RP</u> <u>V6</u>	0	0	0		8	4	4	4.88	8	4	4	0.6 6	4.88	Multimerin-1
<u>B2</u> <u>RQ</u> <u>C6</u>	21	5	5	3.37	14	6	6	4.22	35	7	7	0	4.81	CAD protein
<u>B2</u> <u>RU</u> <u>P2</u>	1	1	1	2.03	7	2	2	4.33	8	2	2	3.3	4.33	Protein unc-13 homolog D
<u>B2</u> <u>RV</u> <u>77</u>	66	5	5	53.61	53	5	5	53.61	119	6	6	0.4 7	53.6 1	MCG130182, isoform CRA a
<u>B2</u> <u>RX</u> <u>R6</u>	27	6	6	7.85	16	4	4	6.14	43	7	7	0	9.47	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B
<u>B5</u> <u>TH</u> <u>E2</u>	11	2	2	1.59	60	11	11	7.83	71	11	11	0	7.83	Maltase-glucoamylase
<u>B9</u> <u>EJ5</u> <u>4</u>	3	2	2	1.59	7	4	4	3.04	10	5	5	0.4 7	3.59	MCG21756, isoform CRA b
<u>D3</u> <u>Y</u> <u>W4</u> <u>8</u>	199	16	14	42.32	199	21	12	75.52	398	23	14	0	75.5 2	Calpain small subunit 1 (Fragment)
<u>D3</u> <u>Z6</u> <u>Q9</u>	24	5	5	14.93	47	5	5	17.18	71	6	6	0.4 7	17.1 8	Bridging integrator 2
<u>D4</u> <u>AF</u> <u>X7</u>	21	9	9	6.98	13	9	9	6.98	34	13	13	0	9.96	Protein Dnajc13
<u>E0</u> <u>CX</u> <u>C2</u>	2	2	2	3.76	0	0	0		2	2	2	3.3	3.76	Protein Gm28043
<u>E0</u> <u>CY</u> <u>M8</u>	1	1	1	4.29	4	2	2	9.94	5	3	3	1.1 9	9.94	Tyrosine-protein phosphatase non-receptor type substrate 1
<u>E9</u> <u>PV</u> <u>24</u>	86	12	12	24.33	98	14	14	29.4	184	14	14	0	29.4	Fibrinogen alpha chain
<u>E9</u> <u>PV</u> <u>60</u>	4	3	3	1.62	4	2	2	1.16	8	4	4	0.6 6	2.35	Protein Wdfy4
<u>E9</u> <u>PV</u> <u>A8</u>	3	2	2	1.61	6	4	4	2.62	9	5	5	0.4 7	3.14	Protein Gcn111
<u>E9</u> <u>PY</u> <u>K3</u>	9	3	3	2.34	0	0	0		9	3	3	1.1 9	2.34	Protein Parp4
<u>E9</u> <u>PZ</u> <u>F0</u>	52	8	3	43.82	118	12	5	52.81	170	12	5	0.4 7	52.8 1	Nucleoside diphosphate kinase
<u>E9</u> <u>Q0</u> <u>70</u>	36	6	6	30.28	26	7	7	38.17	62	9	9	0	39.1 2	Uncharacterized protein
<u>E9</u> <u>Q0</u> <u>F0</u>	1	1	1	1.12	8	2	2	1.31	9	2	2	3.3	1.31	Protein Krt78
<u>E9</u> <u>Q1</u> <u>Z6</u>	1	1	1	2.5	4	2	2	4.41	5	2	2	3.3	4.41	Protein Gm14548
<u>E9</u> <u>Q3</u> <u>97</u>	217	42	41	28.5	179	51	51	34.77	396	59	58	0	39.7 8	Spectrin beta chain, erythrocytic

<u>E9</u> <u>Q3</u> <u>X0</u>	465	32	32	59.43	334	35	35	65.29	799	38	38	0	67.5 9	Major vault protein
<u>E9</u> <u>Q5</u> <u>K8</u>	291	26	26	33.33	375	39	39	46.36	666	40	40	0	47.4 7	Integrin alpha-M
<u>F8</u> <u>VP</u> <u>N2</u>	8	1	1	0.36	10	2	2	0.97	18	2	2	3.3	0.97	Protein Tex15
<u>F8</u> <u>VP</u> <u>N4</u>	8	3	3	2.02	5	2	2	2.28	13	4	4	0.6 6	3.52	Protein Agl
<u>F8</u> <u>WI</u> <u>35</u>	1202	22	1	59.26	1306	27	2	60	250 8	27	2	3.3	60	Histone H3
<u>G3</u> <u>X8</u> <u>U3</u>	0	0	0		3	2	2	10.36	3	2	2	3.3	10.3 6	MCG6895
<u>G3</u> <u>X9</u> <u>72</u>	11	3	3	4.38	28	5	5	9.12	39	6	6	0.4 7	10.4 9	Protein Sec24c
<u>G3</u> <u>X9</u> <u>G4</u>	48	9	9	22.07	79	15	15	30	127	15	15	0	30	Dynamin-2
<u>G5</u> <u>E8</u> <u>R2</u>	30	5	2	14.52	37	9	5	35.89	67	10	6	0.4 7	40.7 3	Tropomyosin 1, alpha, isoform CRA_k
<u>O0</u> <u>855</u> <u>3</u>	10	2	2	7.52	25	5	5	18.01	35	5	5	0.4 7	18.0 1	Dihydropyrimidinase- related protein 2
<u>O0</u> <u>858</u> <u>2</u>	3	2	2	5.24	9	3	3	8.08	12	4	4	0.6 6	10.1 8	GTP-binding protein 1
<u>O0</u> <u>858</u> <u>3</u>	9	4	4	27.45	30	4	4	21.96	39	5	5	0.4 7	27.8 4	THO complex subunit 4
<u>O0</u> <u>858</u> <u>5</u>	34	3	3	20	25	4	4	16.6	59	5	5	0.4 7	24.2 6	Clathrin light chain A
<u>O0</u> <u>866</u> <u>3</u>	10	2	2	7.74	7	2	2	7.95	17	3	3	1.1 9	7.95	Methionine aminopeptidase 2
<u>O0</u> <u>869</u> <u>1</u>	6	2	2	8.76	0	0	0		6	2	2	3.3	8.76	Arginase-2, mitochondrial
<u>O0</u> <u>869</u> <u>2</u>	401	17	17	69.46	586	25	25	71.86	987	25	25	0	71.8 6	Neutrophilic granule protein
<u>O0</u> <u>870</u> <u>2</u>	57	11	11	66.52	102	12	12	69.64	159	12	12	0	69.6 4	Peroxisredoxin-6
<u>O0</u> <u>873</u> <u>8</u>	2	1	1	3.99	16	3	3	13.41	18	3	3	1.1 9	13.4 1	Caspase-6
<u>O0</u> <u>873</u> <u>9</u>	38	10	10	21.15	66	12	12	26.37	104	14	14	0	31.3 3	AMP deaminase 3
<u>O0</u> <u>874</u> <u>0</u>	15	2	2	38.46	6	1	1	25.64	21	2	2	3.3	38.4 6	DNA-directed RNA polymerase II subunit RPB11
<u>O0</u> <u>874</u> <u>2</u>	0	0	0		7	3	3	12.87	7	3	3	1.1 9	12.8 7	Platelet glycoprotein V
<u>O0</u> <u>874</u> <u>9</u>	22	6	6	23.97	79	6	6	23.97	101	6	6	0.4 7	23.9 7	Dihydrolipoyl dehydrogenase, mitochondrial
<u>O0</u> <u>875</u> <u>9</u>	0	0	0		2	2	2	3.79	2	2	2	3.3	3.79	Ubiquitin-protein ligase E3A

<u>O0</u> <u>878</u> <u>8</u>	16	8	8	8.59	7	2	2	2.26	23	8	8	0	8.59	Dynactin subunit 1
<u>O0</u> <u>879</u> <u>5</u>	0	0	0		3	2	2	4.22	3	2	2	3.3	4.22	Glucosidase 2 subunit beta
<u>O0</u> <u>879</u> <u>7</u>	14	2	2	8.82	6	1	1	3.74	20	2	2	3.3	8.82	Protein Serpinb9
<u>O0</u> <u>880</u> <u>8</u>	25	8	8	11.79	51	8	8	12.19	76	9	9	0	13.3 9	Protein diaphanous homolog 1
<u>O0</u> <u>881</u> <u>0</u>	139	16	16	26.57	98	19	19	31.82	237	22	22	0	36.9 7	116 kDa U5 small nuclear ribonucleoprotein component
<u>O0</u> <u>899</u> <u>2</u>	66	8	8	58.53	117	9	9	58.53	183	9	9	0	58.5 3	Syntenin-1
<u>O0</u> <u>904</u> <u>3</u>	2	2	2	7.4	7	1	1	5.25	9	2	2	3.3	7.4	Napsin-A
<u>O0</u> <u>906</u> <u>1</u>	144	9	9	54.58	176	13	13	58.75	320	13	13	0	58.7 5	Proteasome subunit beta type-1
<u>O0</u> <u>910</u> <u>6</u>	37	6	6	21.99	58	8	8	25.31	95	9	9	0	28.8 4	Histone deacetylase 1
<u>O0</u> <u>915</u> <u>9</u>	14	6	6	10.46	77	14	14	25.27	91	14	14	0	25.2 7	Lysosomal alpha-mannosidase
<u>O0</u> <u>917</u> <u>2</u>	10	2	2	11.31	12	2	2	11.31	22	2	2	3.3	11.3 1	Glutamate--cysteine ligase regulatory subunit
<u>O3</u> <u>512</u> <u>2</u>	0	0	0		4	2	2	10.37	4	2	2	3.3	10.3 7	Prohibitin-2
<u>O3</u> <u>522</u> <u>6</u>	4	3	3	11.97	0	0	0		4	3	3	1.1 9	11.9 7	26S proteasome non-ATPase regulatory subunit 4
<u>O3</u> <u>528</u> <u>6</u>	32	9	9	15.85	42	7	7	13.08	74	10	10	0	17.1 1	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
<u>O3</u> <u>529</u> <u>5</u>	2	2	2	16.05	7	3	3	15.74	9	4	4	0.6 6	22.2 2	Transcriptional activator protein Pur-beta
<u>O3</u> <u>534</u> <u>3</u>	11	3	3	9.98	21	4	4	15.55	32	4	4	0.6 6	15.5 5	Importin subunit alpha-3
<u>O3</u> <u>535</u> <u>0</u>	42	10	10	15.99	75	15	15	24.26	117	15	15	0	24.2 6	Calpain-1 catalytic subunit
<u>O3</u> <u>559</u> <u>3</u>	61	6	6	41.29	64	8	8	48.39	125	8	8	0	48.3 9	26S proteasome non-ATPase regulatory subunit 14
<u>O3</u> <u>563</u> <u>8</u>	13	8	8	11.45	12	3	3	3.74	25	8	8	0	11.4 5	Cohesin subunit SA-2
<u>O3</u> <u>563</u> <u>9</u>	102	14	14	47.99	117	21	21	63.16	219	21	21	0	63.1 6	Annexin A3
<u>O3</u> <u>564</u> <u>3</u>	123	16	9	28.21	115	19	10	34.57	238	21	11	0	35.9 5	AP-1 complex subunit beta-1
<u>O3</u> <u>574</u> <u>4</u>	246	16	11	56.78	166	18	13	62.31	412	19	14	0	62.3 1	Chitinase-like protein 3

<u>O3</u> <u>584</u> <u>1</u>	13	4	4	15.08	48	4	4	15.08	61	4	4	0.6 6	15.0 8	Apoptosis inhibitor 5
<u>O3</u> <u>586</u> <u>4</u>	5	4	4	25.15	11	5	5	21.86	16	7	7	0	36.8 3	COP9 signalosome complex subunit 5
<u>O3</u> <u>593</u> <u>0</u>	26	3	3	9.13	26	3	3	9.13	52	3	3	1.1 9	9.13	Platelet glycoprotein Ib alpha chain
<u>O3</u> <u>595</u> <u>5</u>	27	3	3	18.68	22	2	2	14.65	49	3	3	1.1 9	18.6 8	Proteasome subunit beta type-10
<u>O5</u> <u>477</u> <u>4</u>	11	4	4	5.84	6	3	3	4.09	17	5	5	0.4 7	7.17	AP-3 complex subunit delta-1
<u>O5</u> <u>482</u> <u>4</u>	7	4	4	5.14	21	3	3	4.01	28	4	4	0.6 6	5.14	Pro-interleukin-16
<u>O5</u> <u>487</u> <u>9</u>	11	2	1	6	31	5	4	19.5	42	5	4	0.6 6	19.5	High mobility group protein B3
<u>O5</u> <u>489</u> <u>0</u>	1	1	1	1.78	10	3	3	6.1	11	3	3	1.1 9	6.1	Integrin beta-3
<u>O5</u> <u>496</u> <u>2</u>	227	4	4	42.7	77	4	4	42.7	304	4	4	0.6 6	42.7	Barrier-to-autointegration factor
<u>O5</u> <u>501</u> <u>3</u>	0	0	0		4	2	2	15	4	2	2	3.3	15	Trafficking protein particle complex subunit 3
<u>O5</u> <u>502</u> <u>9</u>	50	10	10	16.8	28	8	8	14.14	78	11	11	0	18.2 3	Coatomer subunit beta'
<u>O5</u> <u>509</u> <u>8</u>	2	2	2	3.31	7	2	2	4.14	9	4	4	0.6 6	7.45	Serine/threonine-protein kinase 10
<u>O5</u> <u>510</u> <u>6</u>	14	3	3	6.28	14	1	1	2.82	28	3	3	1.1 9	6.28	Striatin
<u>O5</u> <u>513</u> <u>1</u>	8	3	3	11.24	20	4	4	15.14	28	4	4	0.6 6	15.1 4	Septin-7
<u>O5</u> <u>522</u> <u>2</u>	46	5	5	16.15	37	8	8	25	83	8	8	0	25	Integrin-linked protein kinase
<u>O5</u> <u>523</u> <u>4</u>	22	4	4	21.97	37	9	9	44.32	59	9	9	0	44.3 2	Proteasome subunit beta type-5
<u>O7</u> <u>013</u> <u>3</u>	54	14	14	14.2	57	15	15	16.45	111	18	18	0	19.0 6	ATP-dependent RNA helicase A
<u>O7</u> <u>013</u> <u>8</u>	66	11	11	26.88	108	18	18	39.78	174	19	19	0	43.2 3	Neutrophil collagenase
<u>O7</u> <u>014</u> <u>5</u>	132	13	13	34.1	134	16	16	37.33	266	19	19	0	40	Neutrophil cytosol factor 2
<u>O7</u> <u>019</u> <u>4</u>	14	6	6	16.79	28	8	8	25.91	42	9	9	0	26.0 9	Eukaryotic translation initiation factor 3 subunit D
<u>O7</u> <u>025</u> <u>1</u>	14	2	2	12.44	20	3	3	26.67	34	3	3	1.1 9	26.6 7	Elongation factor 1-beta
<u>O7</u> <u>031</u> <u>0</u>	10	4	4	15.93	22	4	4	15.93	32	4	4	0.6 6	15.9 3	Glycylpeptide N-tetradecanoyltransferase 1
<u>O7</u> <u>032</u> <u>5</u>	4	1	1	7.11	2	2	2	13.2	6	2	2	3.3	13.2	Phospholipid hydroperoxide

														glutathione peroxidase, mitochondrial
<u>O7</u> <u>043</u> <u>5</u>	90	7	7	27.84	71	7	7	28.63	161	8	8	0	33.3 3	Proteasome subunit alpha type-3
<u>O7</u> <u>049</u> <u>7</u>	1	1	1	8.92	5	2	2	15.61	6	2	2	3.3	15.6 1	Ficolin-2
<u>O7</u> <u>056</u> <u>6</u>	0	0	0		3	2	2	3.46	3	2	2	3.3	3.46	Protein diaphanous homolog 2
<u>O7</u> <u>059</u> <u>1</u>	4	2	2	16.88	17	2	2	16.88	21	2	2	3.3	16.8 8	Prefoldin subunit 2
<u>O8</u> <u>830</u> <u>7</u>	29	10	10	6.55	141	17	17	11.29	170	17	17	0	11.2 9	Sortilin-related receptor
<u>O8</u> <u>834</u> <u>2</u>	98	15	15	48.35	200	21	21	61.72	298	22	22	0	61.7 2	WD repeat-containing protein 1
<u>O8</u> <u>845</u> <u>6</u>	247	20	18	38.66	255	27	18	68.03	502	29	20	0	68.0 3	Calpain small subunit 1
<u>O8</u> <u>848</u> <u>7</u>	14	3	3	12.09	25	3	3	10.62	39	4	4	0.6 6	16.0 1	Cytoplasmic dynein 1 intermediate chain 2
<u>O8</u> <u>854</u> <u>3</u>	10	2	2	7.33	11	2	2	7.33	21	2	2	3.3	7.33	COP9 signalosome complex subunit 3
<u>O8</u> <u>854</u> <u>4</u>	26	8	8	31.28	44	8	8	31.28	70	8	8	0	31.2 8	COP9 signalosome complex subunit 4
<u>O8</u> <u>854</u> <u>5</u>	2	2	2	12.65	8	4	4	26.23	10	6	6	0.4 7	38.8 9	COP9 signalosome complex subunit 6
<u>O8</u> <u>856</u> <u>9</u>	89	9	9	31.44	121	15	13	44.76	210	18	16	0	56.3 7	Heterogeneous nuclear ribonucleoproteins A2/B1
<u>O8</u> <u>859</u> <u>3</u>	54	6	6	46.15	140	8	8	50	194	8	8	0	50	Peptidoglycan recognition protein 1
<u>O8</u> <u>868</u> <u>5</u>	109	14	14	45.48	77	11	11	40.05	186	16	16	0	47.7 4	26S protease regulatory subunit 6A
<u>O8</u> <u>869</u> <u>6</u>	3	2	2	12.13	4	2	2	12.13	7	2	2	3.3	12.1 3	ATP-dependent Clp protease proteolytic subunit, mitochondrial
<u>O8</u> <u>871</u> <u>2</u>	1	1	1	4.54	3	2	2	6.35	4	3	3	1.1 9	10.8 8	C-terminal-binding protein 1
<u>O8</u> <u>878</u> <u>3</u>	1	1	1	0.46	14	4	4	2.61	15	4	4	0.6 6	2.61	Coagulation factor V
<u>O8</u> <u>884</u> <u>2</u>	3	2	2	5.46	4	2	2	5.46	7	2	2	3.3	5.46	FYVE, RhoGEF and PH domain-containing protein 3
<u>O8</u> <u>884</u> <u>4</u>	55	10	10	32.85	111	16	15	50.24	166	16	15	0	50.2 4	Isocitrate dehydrogenase [NADP] cytoplasmic
<u>O8</u> <u>887</u> <u>9</u>	0	0	0		8	2	2	2.32	8	2	2	3.3	2.32	Apoptotic protease-activating factor 1
<u>O8</u> <u>895</u> <u>8</u>	12	4	4	18.69	9	2	2	8.3	21	4	4	0.6 6	18.6 9	Glucosamine-6-phosphate isomerase 1
<u>O8</u> <u>896</u> <u>8</u>	7	1	1	3.49	28	5	5	25.81	35	5	5	0.4 7	25.8 1	Transcobalamin-2

<u>O8</u> <u>905</u> <u>1</u>	0	0	0		8	2	2	8.65	8	2	2	3.3	8.65	Integral membrane protein 2B
<u>O8</u> <u>905</u> <u>3</u>	375	22	22	47.94	376	30	30	49.67	751	31	31	0	49.67	Coronin-1A
<u>O8</u> <u>907</u> <u>9</u>	18	5	5	23.7	13	4	4	19.81	31	6	6	0.47	24.03	Coatomer subunit epsilon
<u>O8</u> <u>908</u> <u>6</u>	39	2	2	32.68	26	2	2	32.68	65	2	2	3.3	32.68	RNA-binding protein 3
<u>P0</u> <u>049</u> <u>3</u>	20	3	3	16.51	28	6	6	41.28	48	6	6	0.47	41.28	Hypoxanthine-guanine phosphoribosyltransferase
<u>P0</u> <u>092</u> <u>0</u>	10	2	2	11.15	34	5	5	30	44	5	5	0.47	30	Carbonic anhydrase 2
<u>P0</u> <u>102</u> <u>7</u>	315	44	44	40.23	819	76	75	63.68	1134	76	75	0	63.68	Complement C3
<u>P0</u> <u>132</u> <u>5</u>	27	3	3	17.59	46	5	5	25.93	73	5	5	0.47	25.93	Insulin-1
<u>P0</u> <u>164</u> <u>3</u>	6	2	2	31.48	0	0	0		6	2	2	3.3	31.48	Ig kappa chain V-V region MOPC 173
<u>P0</u> <u>178</u> <u>7</u>	16	4	4	42.28	3	1	1	13.01	19	4	4	0.66	42.28	Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3
<u>P0</u> <u>183</u> <u>7</u>	20	4	4	63.21	19	2	2	50	39	4	4	0.66	63.21	Ig kappa chain C region
<u>P0</u> <u>187</u> <u>2</u>	94	10	10	35.24	94	13	13	39.43	188	13	13	0	39.43	Ig mu chain C region
<u>P0</u> <u>188</u> <u>7</u>	0	0	0		9	2	2	22.69	9	2	2	3.3	22.69	Beta-2-microglobulin
<u>P0</u> <u>190</u> <u>0</u>	1	1	1	3.56	5	3	3	10.68	6	3	3	1.19	10.68	H-2 class I histocompatibility antigen, D-D alpha chain
<u>P0</u> <u>194</u> <u>2</u>	974	17	17	83.8	488	33	33	83.8	1462	34	34	0	83.8	Hemoglobin subunit alpha
<u>P0</u> <u>208</u> <u>8</u>	812	27	15	95.24	545	35	20	95.24	1357	36	21	0	95.24	Hemoglobin subunit beta-1
<u>P0</u> <u>208</u> <u>9</u>	423	19	7	85.71	305	26	11	91.16	728	26	11	0	91.16	Hemoglobin subunit beta-2
<u>P0</u> <u>253</u> <u>5</u>	111	15	7	19.82	147	14	6	26.84	258	18	7	0	26.84	Keratin, type I cytoskeletal 10
<u>P0</u> <u>395</u> <u>8</u>	0	0	0		3	2	2	8.52	3	2	2	3.3	8.52	Adenosine deaminase
<u>P0</u> <u>410</u> <u>4</u>	19	2	1	3.77	22	3	2	13.19	41	3	2	3.3	13.19	Keratin, type II cytoskeletal 1
<u>P0</u> <u>420</u> <u>2</u>	0	0	0		16	2	2	8.21	16	2	2	3.3	8.21	Transforming growth factor beta-1
<u>P0</u> <u>424</u> <u>7</u>	10	2	2	12.99	20	2	2	12.99	30	2	2	3.3	12.99	Myoglobin

P0 491 9	148	14	14	23.57	154	17	17	25.62	302	19	19	0	27.0 2	Band 3 anion transport protein
P0 520 1	23	5	5	23.24	25	5	5	23.24	48	5	5	0.4 7	23.2 4	Aspartate aminotransferase, cytoplasmic
P0 520 2	37	4	4	14.88	49	8	8	30	86	8	8	0	30	Aspartate aminotransferase, mitochondrial
P0 578 4	2	1	1	4.96	2	2	2	7.33	4	2	2	3.3	7.33	Keratin, type I cytoskeletal 18
P0 615 1	451	21	20	58.43	368	29	28	69.88	819	30	29	0	70.7 8	L-lactate dehydrogenase A chain
P0 674 5	702	29	29	61.47	703	39	39	69.71	140 5	39	39	0	69.7 1	Glucose-6-phosphate isomerase
P0 680 0	32	4	4	4.57	44	6	6	8.21	76	6	6	0.4 7	8.21	Receptor-type tyrosine-protein phosphatase C
P0 690 9	0	0	0		5	3	3	3.81	5	3	3	1.1 9	3.81	Complement factor H
P0 735 6	230	14	14	56.05	144	19	19	59.88	374	19	19	0	59.8 8	Annexin A2
P0 772 4	162	16	16	32.24	153	19	19	41.45	315	21	21	0	42.7 6	Serum albumin
P0 774 2	23	4	4	9.85	51	8	8	19.95	74	8	8	0	19.9 5	Ribonucleoside-diphosphate reductase large subunit
P0 775 9	29	4	4	17.7	15	5	5	23.68	44	6	6	0.4 7	27.5 1	Serine protease inhibitor A3K
P0 790 1	127	25	17	42.97	225	30	22	48.29	352	32	23	0	50.0 7	Heat shock protein HSP 90-alpha
P0 800 3	10	6	6	14.11	109	17	17	36.05	119	17	17	0	36.0 5	Protein disulfide-isomerase A4
P0 803 0	86	8	8	61.11	83	10	10	61.11	169	10	10	0	61.1 1	Adenine phosphoribosyltransferase
P0 803 2	392	54	53	35.53	421	82	81	49.23	813	87	86	0	52.5 5	Spectrin alpha chain, erythrocytic 1
P0 807 1	2113	54	54	64.07	2321	90	90	75.53	443 4	93	93	0	76.1	Lactotransferrin
P0 810 3	3	3	2	8.02	16	6	5	19.66	19	7	6	0.4 7	23.2 8	Tyrosine-protein kinase HCK
P0 811 3	11	5	4	8.85	72	13	11	21.07	83	14	12	0	23.0 7	Endoplasmic
P0 822 6	19	5	5	32.15	39	6	6	38.26	58	6	6	0.4 7	38.2 6	Apolipoprotein E
P0 822 8	2	2	2	15.58	30	4	4	32.47	32	4	4	0.6 6	32.4 7	Superoxide dismutase [Cu-Zn]
P0 824 9	43	6	6	25.74	70	8	8	35.8	113	9	9	0	39.3 5	Malate dehydrogenase, mitochondrial
P0 860 7	6	3	3	8.74	12	5	5	13.22	18	5	5	0.4 7	13.2 2	C4b-binding protein

<u>P0</u> <u>875</u> <u>2</u>	26	6	6	20.56	50	9	9	30.42	76	9	9	0	30.4 2	Guanine nucleotide-binding protein G(i) subunit alpha-2
<u>P0</u> <u>877</u> <u>5</u>	8	5	5	4.67	2	1	1	1.07	10	5	5	0.4 7	4.67	DNA-directed RNA polymerase II subunit RPB1
<u>P0</u> <u>890</u> <u>5</u>	40	3	3	33.11	36	5	5	37.84	76	5	5	0.4 7	37.8 4	Lysozyme C-2
<u>P0</u> <u>910</u> <u>3</u>	84	13	13	38.9	210	21	21	48.92	294	21	21	0	48.9 2	Protein disulfide-isomerase
<u>P0</u> <u>940</u> <u>5</u>	108	14	14	23.06	152	16	16	22.63	260	17	17	0	25.4 6	Nucleolin
<u>P0</u> <u>941</u> <u>1</u>	151	16	16	49.4	219	21	21	53.48	370	22	22	0	55.4	Phosphoglycerate kinase 1
<u>P0</u> <u>952</u> <u>8</u>	62	11	11	66.48	168	15	15	68.68	230	15	15	0	68.6 8	Ferritin heavy chain
<u>P0</u> <u>954</u> <u>2</u>	23	1	1	7.84	27	3	3	12.25	50	3	3	1.1 9	12.2 5	Myosin light chain 3
<u>P0</u> <u>958</u> <u>1</u>	0	0	0		3	2	2	3.68	3	2	2	3.3	3.68	Macrophage colony-stimulating factor 1 receptor
<u>P0</u> <u>960</u> <u>2</u>	38	3	3	30	111	9	9	52.22	149	9	9	0	52.2 2	Non-histone chromosomal protein HMG-17
<u>P0</u> <u>C0</u> <u>S6</u>	1844	22	19	56.25	1807	29	25	58.59	365 1	29	25	0	58.5 9	Histone H2A.Z
<u>P0</u> <u>CG</u> <u>50</u>	175	8	8	8.99	273	18	18	10.49	448	18	18	0	10.4 9	Polyubiquitin-C
<u>P1</u> <u>010</u> <u>7</u>	687	24	24	61.56	368	31	31	64.45	105 5	31	31	0	64.4 5	Annexin A1
<u>P1</u> <u>012</u> <u>6</u>	466	19	19	48.05	308	27	27	49.57	774	27	27	0	49.5 7	Elongation factor 1-alpha 1
<u>P1</u> <u>051</u> <u>8</u>	69	9	9	43.64	76	7	7	38.48	145	9	9	0	43.6 4	Delta-aminolevulinic acid dehydratase
<u>P1</u> <u>063</u> <u>9</u>	0	0	0		21	3	3	31.43	21	3	3	1.1 9	31.4 3	Thioredoxin
<u>P1</u> <u>064</u> <u>9</u>	73	8	8	40.37	78	8	8	37.61	151	11	11	0	51.3 8	Glutathione S-transferase Mu 1
<u>P1</u> <u>071</u> <u>1</u>	4	2	2	13.62	15	2	2	13.62	19	2	2	3.3	13.6 2	Transcription elongation factor A protein 1
<u>P1</u> <u>081</u> <u>0</u>	13	3	3	13.39	9	3	3	13.39	22	3	3	1.1 9	13.3 9	Monocyte differentiation antigen CD14
<u>P1</u> <u>085</u> <u>2</u>	1	1	1	3.23	14	4	4	17.87	15	4	4	0.6 6	17.8 7	4F2 cell-surface antigen heavy chain
<u>P1</u> <u>085</u> <u>4</u>	1932	27	8	65.87	1525	31	7	65.87	345 7	33	8	0	65.8 7	Histone H2B type 1-M
<u>P1</u> <u>103</u> <u>1</u>	18	4	4	19.69	62	5	5	37.8	80	6	6	0.4 7	37.8	Activated RNA polymerase II transcriptional coactivator p15

<u>P1</u> <u>124</u> <u>7</u>	383	28	28	41.92	521	47	47	52.09	904	47	47	0	52.0 9	Myeloperoxidase
<u>P1</u> <u>135</u> <u>2</u>	55	9	9	56.72	92	9	9	53.73	147	10	10	0	61.1 9	Glutathione peroxidase 1
<u>P1</u> <u>149</u> <u>9</u>	91	21	12	45.03	243	28	18	50.41	334	29	18	0	52.0 7	Heat shock protein HSP 90-beta
<u>P1</u> <u>167</u> <u>2</u>	64	8	8	51	155	7	7	51	219	8	8	0	51	Neutrophil gelatinase- associated lipocalin
<u>P1</u> <u>183</u> <u>5</u>	62	11	11	21.79	156	19	19	35.02	218	19	19	0	35.0 2	Integrin beta-2
<u>P1</u> <u>198</u> <u>3</u>	83	11	10	29.32	91	16	15	44.06	174	17	16	0	46.0 4	T-complex protein 1 subunit alpha
<u>P1</u> <u>224</u> <u>6</u>	3	1	1	8.93	12	2	2	14.29	15	2	2	3.3	14.2 9	Serum amyloid P- component
<u>P1</u> <u>226</u> <u>5</u>	0	0	0		23	8	8	20.22	23	8	8	0	20.2 2	Beta-glucuronidase
<u>P1</u> <u>238</u> <u>2</u>	8	3	2	6.92	13	5	4	9.36	21	6	5	0.4 7	11.5 4	ATP-dependent 6- phosphofructokinase, liver type
<u>P1</u> <u>278</u> <u>7</u>	13	2	2	30.82	30	5	5	51.37	43	5	5	0.4 7	51.3 7	Cytochrome c oxidase subunit 5A, mitochondrial
<u>P1</u> <u>281</u> <u>5</u>	4	1	1	15.71	22	7	7	56.54	26	7	7	0	56.5 4	Programmed cell death protein 6
<u>P1</u> <u>302</u> <u>0</u>	121	20	20	45	242	25	25	47.95	363	28	28	0	53.4 6	Gelsolin
<u>P1</u> <u>343</u> <u>9</u>	3	1	1	2.91	6	2	2	6.44	9	2	2	3.3	6.44	Uridine 5'- monophosphate synthase
<u>P1</u> <u>360</u> <u>9</u>	0	0	0		6	2	2	18.42	6	2	2	3.3	18.4 2	Serglycin
<u>P1</u> <u>386</u> <u>4</u>	3	2	2	2.35	3	3	3	3.77	6	4	4	0.6 6	4.88	DNA (cytosine-5)- methyltransferase 1
<u>P1</u> <u>406</u> <u>9</u>	712	13	13	67.42	691	20	20	80.9	140 3	20	20	0	80.9	Protein S100-A6
<u>P1</u> <u>413</u> <u>1</u>	48	6	6	30.82	16	4	4	30.14	64	6	6	0.4 7	30.8 2	40S ribosomal protein S16
<u>P1</u> <u>414</u> <u>8</u>	11	2	2	11.48	3	2	2	11.11	14	3	3	1.1 9	15.5 6	60S ribosomal protein L7
<u>P1</u> <u>415</u> <u>2</u>	18	6	6	23.35	36	6	6	26.35	54	7	7	0	27.8 4	Malate dehydrogenase, cytoplasmic
<u>P1</u> <u>420</u> <u>6</u>	62	8	8	45.08	63	11	11	52.2	125	12	12	0	58.6 4	40S ribosomal protein SA
<u>P1</u> <u>421</u> <u>1</u>	33	8	8	39.42	95	13	13	46.15	128	13	13	0	46.1 5	Calreticulin
<u>P1</u> <u>423</u> <u>4</u>	17	6	5	18.76	20	5	4	17.99	37	7	6	0.4 7	25.1 5	Tyrosine-protein kinase Fgr
<u>P1</u> <u>468</u> <u>5</u>	43	9	9	31.89	62	11	11	36.23	105	11	11	0	36.2 3	26S proteasome non- ATPase regulatory subunit 3

<u>P1</u> <u>473</u> <u>3</u>	70	10	10	27.55	89	12	12	31.12	159	12	12	0	31.1 2	Lamin-B1
<u>P1</u> <u>482</u> <u>4</u>	4	2	2	4.61	33	10	10	22.29	37	10	10	0	22.2 9	Annexin A6
<u>P1</u> <u>510</u> <u>5</u>	3	2	2	9.65	0	0	0		3	2	2	3.3	9.65	Glutamine synthetase
<u>P1</u> <u>553</u> <u>2</u>	48	6	1	57.89	97	10	3	73.68	145	10	3	1.1 9	73.6 8	Nucleoside diphosphate kinase A
<u>P1</u> <u>586</u> <u>4</u>	566	18	3	44.34	421	25	10	46.23	987	27	10	0	50.4 7	Histone H1.2
<u>P1</u> <u>611</u> <u>0</u>	70	8	8	39.39	97	10	10	40.91	167	10	10	0	40.9 1	Galectin-3
<u>P1</u> <u>612</u> <u>5</u>	26	4	3	17.07	12	5	4	17.96	38	5	4	0.6 6	17.9 6	L-lactate dehydrogenase B chain
<u>P1</u> <u>654</u> <u>6</u>	238	56	55	35.56	330	51	50	34.83	568	70	69	0	43.8 9	Spectrin alpha chain, non-erythrocytic 1
<u>P1</u> <u>685</u> <u>8</u>	1273	33	31	65.17	800	39	37	66.97	207 3	42	40	0	66.9 7	Glyceraldehyde-3-phosphate dehydrogenase
<u>P1</u> <u>687</u> <u>9</u>	9	2	2	4.26	10	3	3	6.08	19	3	3	1.1 9	6.08	Tyrosine-protein kinase Fes/Fps
<u>P1</u> <u>709</u> <u>5</u>	1	1	1	14.95	15	4	4	23.36	16	4	4	0.6 6	23.3 6	High mobility group protein HMG-I/HMG-Y
<u>P1</u> <u>718</u> <u>2</u>	920	26	19	66.36	659	47	35	70.05	157 9	48	35	0	70.0 5	Alpha-enolase
<u>P1</u> <u>722</u> <u>5</u>	34	5	5	21.06	81	11	10	38.9	115	11	10	0	38.9	Polypyrimidine tract-binding protein 1
<u>P1</u> <u>742</u> <u>6</u>	24	6	3	9.62	36	9	6	15.15	60	10	6	0.4 7	16.1 7	AP-2 complex subunit alpha-1
<u>P1</u> <u>742</u> <u>7</u>	58	13	10	24.95	56	17	14	30.38	114	21	17	0	36.2 5	AP-2 complex subunit alpha-2
<u>P1</u> <u>743</u> <u>3</u>	24	1	1	3.68	15	2	2	8.46	39	2	2	3.3	8.46	Transcription factor PU.1
<u>P1</u> <u>771</u> <u>0</u>	16	5	3	7.49	18	7	5	9.45	34	7	5	0.4 7	9.45	Hexokinase-1
<u>P1</u> <u>774</u> <u>2</u>	176	11	11	66.46	186	14	14	70.73	362	14	14	0	70.7 3	Peptidyl-prolyl cis-trans isomerase A
<u>P1</u> <u>775</u> <u>1</u>	38	7	7	39.46	104	10	10	48.16	142	10	10	0	48.1 6	Triosephosphate isomerase
<u>P1</u> <u>787</u> <u>9</u>	96	6	1	12.46	97	8	2	14.95	193	9	2	3.3	17.2 9	Heat shock 70 kDa protein 1B
<u>P1</u> <u>791</u> <u>8</u>	0	0	0		6	2	2	10.34	6	2	2	3.3	10.3 4	Proliferating cell nuclear antigen
<u>P1</u> <u>824</u> <u>2</u>	4	3	3	11.46	45	6	6	23.17	49	7	7	0	25.6 1	Cathepsin D
<u>P1</u> <u>865</u> <u>3</u>	32	9	7	18.09	18	5	3	9.39	50	9	7	0	18.0 9	Ribosomal protein S6 kinase alpha-1

P1 865 4	14	4	2	8.24	10	3	1	5.54	24	4	2	3.3	8.24	Ribosomal protein S6 kinase alpha-3
P1 876 0	82	9	8	50.6	132	20	18	62.65	214	20	18	0	62.6 5	Cofilin-1
P1 909 6	141	35	35	22.48	154	30	30	21.17	295	43	43	0	27.5 2	Fatty acid synthase
P1 915 7	3	1	1	7.62	5	3	3	20.48	8	3	3	1.1 9	20.4 8	Glutathione S- transferase P 1
P1 997 3	47	6	6	31.21	52	8	8	39.39	99	9	9	0	39.3 9	Lymphocyte-specific protein 1
P2 002 9	189	22	19	40.76	286	32	28	52.52	475	32	28	0	52.5 2	78 kDa glucose- regulated protein
P2 006 0	5	1	1	1.87	24	5	5	17.72	29	5	5	0.4 7	17.7 2	Beta-hexosaminidase subunit beta
P2 006 5	3	1	1	26	17	2	2	38	20	2	2	3.3	38	Thymosin beta-4
P2 010 8	1	1	1	5.84	2	2	2	8.95	3	3	3	1.1 9	14.7 9	Thioredoxin-dependent peroxide reductase, mitochondrial
P2 015 2	126	20	20	50.43	191	26	26	54.08	317	27	27	0	56.4 4	Vimentin
P2 110 7	73	8	2	21.4	81	9	2	25.96	154	9	2	3.3	25.9 6	Tropomyosin alpha-3 chain
P2 110 7-2	113	12	6	34.68	136	14	7	41.13	249	14	7	0	41.1 3	Isoform 2 of Tropomyosin alpha-3 chain
P2 155 0	162	8	1	24.19	128	14	2	27.65	290	15	2	3.3	29.2 6	Beta-enolase
P2 268 2	0	0	0		3	2	2	2.96	3	2	2	3.3	2.96	E3 ubiquitin-protein ligase CBL
P2 275 2	7123	57	1	70.77	5961	67	2	73.08	130 84	70	2	3.3	73.0 8	Histone H2A type 1
P2 289 2	37	9	9	19.1	78	11	11	21.29	115	11	11	0	21.2 9	AP-1 complex subunit gamma-1
P2 311 6	94	22	22	23.51	95	18	18	20.31	189	24	24	0	25.2 2	Eukaryotic translation initiation factor 3 subunit A
P2 324 9	1	1	1	1.59	5	3	3	5.38	6	3	3	1.1 9	5.38	Putative helicase MOV- 10
P2 349 2	59	6	6	30.45	76	10	10	53.63	135	11	11	0	57.4 4	Purine nucleoside phosphorylase
P2 406 3	10	4	4	5.76	31	12	12	16.6	41	12	12	0	16.6	Integrin alpha-L
P2 427 0	176	16	16	41.37	218	20	20	40.8	394	21	21	0	46.3	Catalase
P2 436 9	29	8	8	37.5	52	8	8	38.89	81	9	9	0	38.8 9	Peptidyl-prolyl cis-trans isomerase B
P2 452 7	87	12	12	31.26	111	16	16	34.53	198	17	17	0	36.1 7	Leukotriene A-4 hydrolase

<u>P2</u> <u>454</u> <u>7</u>	22	6	6	21.6	9	5	5	17.12	31	7	7	0	24.5 1	Inosine-5'- monophosphate dehydrogenase 2
<u>P2</u> <u>520</u> <u>6</u>	23	4	4	9.24	12	6	6	14.04	35	6	6	0.4 7	14.0 4	DNA replication licensing factor MCM3
<u>P2</u> <u>544</u> <u>4</u>	8	4	4	16.04	6	2	2	8.87	14	5	5	0.4 7	21.1 6	40S ribosomal protein S2
<u>P2</u> <u>591</u> <u>1-2</u>	50	9	8	24.64	78	15	14	44.4	128	16	15	0	47.2 5	Isoform 2 of Tyrosine- protein kinase Lyn
<u>P2</u> <u>597</u> <u>6</u>	0	0	0		3	2	2	3.92	3	2	2	3.3	3.92	Nucleolar transcription factor 1
<u>P2</u> <u>603</u> <u>9</u>	838	74	74	45.93	812	80	80	50.26	165 0	87	87	0	52.5 8	Talin-1
<u>P2</u> <u>604</u> <u>0</u>	133	14	6	29.69	204	19	8	32.42	337	20	8	0	33.7 9	Ezrin
<u>P2</u> <u>604</u> <u>1</u>	421	29	21	55.81	558	42	29	61.53	979	43	29	0	62.9 1	Moesin
<u>P2</u> <u>604</u> <u>3</u>	99	13	5	27.1	176	22	9	37.74	275	23	9	0	39.1 1	Radixin
<u>P2</u> <u>636</u> <u>9</u>	32	5	5	17.89	59	7	7	25.05	91	7	7	0	25.0 5	Splicing factor U2AF 65 kDa subunit
<u>P2</u> <u>644</u> <u>3</u>	93	16	16	42.83	157	19	19	45.7	250	19	19	0	45.7	Glutamate dehydrogenase 1, mitochondrial
<u>P2</u> <u>645</u> <u>0</u>	5	3	3	7.6	8	5	4	12.85	13	5	4	0.6 6	12.8 5	Phosphatidylinositol 3- kinase regulatory subunit alpha
<u>P2</u> <u>651</u> <u>6</u>	68	10	10	59.5	68	8	8	52.96	136	10	10	0	59.5	26S proteasome non- ATPase regulatory subunit 7
<u>P2</u> <u>663</u> <u>8</u>	9	5	5	19.14	11	4	4	13.67	20	5	5	0.4 7	19.1 4	Serine--tRNA ligase, cytoplasmic
<u>P2</u> <u>700</u> <u>5</u>	2356	29	29	94.38	2551	52	52	94.38	490 7	52	52	0	94.3 8	Protein S100-A8
<u>P2</u> <u>704</u> <u>8</u>	28	2	2	9.96	31	3	3	12.55	59	3	3	1.1 9	12.5 5	Small nuclear ribonucleoprotein- associated protein B
<u>P2</u> <u>761</u> <u>2</u>	8	4	4	8.06	19	6	6	13.73	27	8	8	0	17.3 8	Phospholipase A-2- activating protein
<u>P2</u> <u>766</u> <u>1</u>	7393	68	14	60.14	6150	77	15	67.13	135 43	82	17	0	68.5 3	Histone H2AX
<u>P2</u> <u>777</u> <u>3</u>	164	23	23	48.51	362	30	30	57.23	526	31	31	0	59.4 1	Protein disulfide- isomerase A3
<u>P2</u> <u>787</u> <u>0</u>	39	10	10	17.04	47	10	10	17.63	86	13	13	0	20.7 1	Proto-oncogene vav
<u>P2</u> <u>806</u> <u>3</u>	72	9	9	40.94	84	9	9	40.94	156	9	9	0	40.9 4	Proteasome subunit beta type-8
<u>P2</u> <u>807</u> <u>6</u>	32	5	5	32.88	50	4	4	24.66	82	6	6	0.4 7	37.4 4	Proteasome subunit beta type-9
<u>P2</u> <u>827</u> <u>1</u>	2	2	2	3.37	1	1	1	2.14	3	3	3	1.1 9	5.51	Cytoplasmic aconitate hydratase

<u>P2</u> <u>829</u> <u>3</u>	73	7	7	29.89	119	13	13	58.62	192	13	13	0	58.6 2	Cathepsin G
<u>P2</u> <u>835</u> <u>2</u>	20	5	5	31.55	27	5	5	33.12	47	7	7	0	43.5 3	DNA-(apurinic or apyrimidinic site) lyase
<u>P2</u> <u>865</u> <u>0</u>	77	8	8	24.73	62	8	8	25.82	139	10	10	0	31.2 9	Adenylosuccinate synthetase isozyme 1
<u>P2</u> <u>865</u> <u>6</u>	14	4	4	14.58	32	6	6	14.58	46	6	6	0.4 7	14.5 8	Nucleosome assembly protein 1-like 1
<u>P2</u> <u>865</u> <u>8</u>	1	1	1	2.32	10	3	3	8	11	3	3	1.1 9	8	Ataxin-10
<u>P2</u> <u>866</u> <u>5</u>	1	1	1	0.88	12	4	3	5.56	13	5	4	0.6 6	6.44	Murinoglobulin-1
<u>P2</u> <u>886</u> <u>7</u>	6	2	2	4.15	9	5	5	14.09	15	6	6	0.4 7	16.4 7	Protein kinase C delta type
<u>P2</u> <u>934</u> <u>1</u>	18	8	8	16.67	66	10	10	21.7	84	12	12	0	23.4 3	Polyadenylate-binding protein 1
<u>P2</u> <u>935</u> <u>1</u>	109	14	14	33.45	167	21	21	47.06	276	22	22	0	48.4	Tyrosine-protein phosphatase non- receptor type 6
<u>P2</u> <u>939</u> <u>1</u>	126	10	10	53.01	154	10	10	53.01	280	10	10	0	53.0 1	Ferritin light chain 1
<u>P2</u> <u>941</u> <u>6</u>	0	0	0		6	4	4	11.36	6	4	4	0.6 6	11.3 6	Beta-hexosaminidase subunit alpha
<u>P2</u> <u>969</u> <u>9</u>	3	1	1	8.41	2	2	2	15.36	5	2	2	3.3	15.3 6	Alpha-2-HS- glycoprotein
<u>P2</u> <u>975</u> <u>8</u>	3	3	3	14.58	9	4	4	24.15	12	5	5	0.4 7	27.5 6	Ornithine aminotransferase, mitochondrial
<u>P3</u> <u>041</u> <u>6</u>	0	0	0		13	4	4	13.97	13	4	4	0.6 6	13.9 7	Peptidyl-prolyl cis-trans isomerase FKBP4
<u>P3</u> <u>068</u> <u>1</u>	174	13	10	46.67	171	13	9	37.14	345	17	12	0	50.9 5	High mobility group protein B2
<u>P3</u> <u>123</u> <u>0</u>	10	3	3	16.45	22	4	4	21.94	32	4	4	0.6 6	21.9 4	Aminoacyl tRNA synthase complex- interacting multifunctional protein 1
<u>P3</u> <u>132</u> <u>4</u>	5	3	3	9.38	6	1	1	4.09	11	3	3	1.1 9	9.38	cAMP-dependent protein kinase type II- beta regulatory subunit
<u>P3</u> <u>172</u> <u>5</u>	5666	37	37	83.19	5233	61	61	83.19	108 99	61	61	0	83.1 9	Protein S100-A9
<u>P3</u> <u>193</u> <u>8</u>	7	4	4	18.83	25	5	5	26.46	32	7	7	0	33.0 8	Dual specificity mitogen-activated protein kinase kinase 1
<u>P3</u> <u>206</u> <u>7</u>	12	3	3	9.88	17	4	4	12.77	29	5	5	0.4 7	15.9	Lupus La protein homolog
<u>P3</u> <u>292</u> <u>1</u>	11	3	3	10.81	14	3	3	11.02	25	4	4	0.6 6	11.6 4	Tryptophan--tRNA ligase, cytoplasmic
<u>P3</u> <u>488</u> <u>4</u>	39	3	3	35.65	34	3	3	35.65	73	3	3	1.1 9	35.6 5	Macrophage migration inhibitory factor

<u>P3</u> <u>517</u> <u>4</u>	38	5	5	40.78	30	4	4	38.83	68	5	5	0.4 7	40.7 8	Stefin-2
<u>P3</u> <u>527</u> <u>8</u>	11	3	2	20.37	11	5	3	31.94	22	5	3	1.1 9	31.9 4	Ras-related protein Rab-5C
<u>P3</u> <u>544</u> <u>1</u>	223	29	29	29.23	293	32	32	31.79	516	33	33	0	31.7 9	Thrombospondin-1
<u>P3</u> <u>550</u> <u>5</u>	16	4	4	15.99	36	9	9	35.56	52	9	9	0	35.5 6	Fumarylacetoacetase
<u>P3</u> <u>556</u> <u>4</u>	9	2	2	4.4	16	3	3	6.43	25	3	3	1.1 9	6.43	Calnexin
<u>P3</u> <u>558</u> <u>5</u>	25	6	6	22.93	33	6	6	21.75	58	7	7	0	26.9 5	AP-1 complex subunit mu-1
<u>P3</u> <u>570</u> <u>0</u>	37	5	5	28.14	47	9	9	50.75	84	9	9	0	50.7 5	Peroxiredoxin-1
<u>P3</u> <u>582</u> <u>1</u>	0	0	0		6	2	2	5.56	6	2	2	3.3	5.56	Tyrosine-protein phosphatase non- receptor type 1
<u>P3</u> <u>597</u> <u>9</u>	14	2	2	18.79	4	2	2	18.79	18	2	2	3.3	18.7 9	60S ribosomal protein L12
<u>P3</u> <u>598</u> <u>0</u>	8	2	2	12.77	16	3	3	19.68	24	3	3	1.1 9	19.6 8	60S ribosomal protein L18
<u>P3</u> <u>599</u> <u>1</u>	3	2	2	4.4	10	3	3	6.53	13	3	3	1.1 9	6.53	Tyrosine-protein kinase BTK
<u>P3</u> <u>699</u> <u>3</u>	0	0	0		10	2	2	7.69	10	2	2	3.3	7.69	Protein phosphatase 1B
<u>P3</u> <u>806</u> <u>0</u>	9	3	3	19.69	10	4	4	24	19	4	4	0.6 6	24	Hydroxymethylglutaryl -CoA lyase, mitochondrial
<u>P3</u> <u>864</u> <u>7</u>	24	9	8	19.29	14	5	5	10.46	38	10	9	0	21.0 6	Stress-70 protein, mitochondrial
<u>P3</u> <u>965</u> <u>5</u>	14	4	4	10.56	26	5	5	12.97	40	6	6	0.4 7	14.6 3	Arachidonate 12- lipxygenase, 12S-type
<u>P4</u> <u>012</u> <u>4</u>	876	26	26	59.28	662	27	27	57.81	153 8	31	31	0	61.8 1	Adenylyl cyclase- associated protein 1
<u>P4</u> <u>014</u> <u>2</u>	821	36	36	62.44	883	57	57	70.47	170 4	60	60	0	70.4 7	Transketolase
<u>P4</u> <u>023</u> <u>7</u>	0	0	0		3	2	2	8.65	3	2	2	3.3	8.65	CD82 antigen
<u>P4</u> <u>033</u> <u>6</u>	11	4	3	16.82	7	3	2	12.84	18	4	3	1.1 9	16.8 2	Vacuolar protein sorting-associated protein 26A
<u>P4</u> <u>124</u> <u>1</u>	21	6	6	17.11	10	3	3	9.78	31	6	6	0.4 7	17.1 1	Tyrosine-protein kinase CSK
<u>P4</u> <u>124</u> <u>5</u>	274	21	21	39.04	310	32	32	54.66	584	32	32	0	54.6 6	Matrix metalloproteinase-9
<u>P4</u> <u>222</u> <u>5</u>	16	6	6	10.55	38	7	7	14.29	54	8	8	0	15.6 2	Signal transducer and activator of transcription 1
<u>P4</u> <u>222</u> <u>7</u>	37	6	6	15.71	56	8	8	20.91	93	9	9	0	23.2 5	Signal transducer and activator of transcription 3

<u>P4</u> <u>222</u> <u>8</u>	6	2	2	3.2	0	0	0		6	2	2	3.3	3.2	Signal transducer and activator of transcription 4
<u>P4</u> <u>266</u> <u>9</u>	129	7	7	36.14	132	10	10	37.38	261	11	11	0	37.38	Transcriptional activator protein Pur-alpha
<u>P4</u> <u>293</u> <u>2</u>	12	4	4	9.12	26	11	11	25.91	38	12	12	0	28.83	T-complex protein 1 subunit theta
<u>P4</u> <u>327</u> <u>4</u>	510	18	6	37.9	397	19	6	33.79	907	20	6	0.47	37.9	Histone H1.4
<u>P4</u> <u>327</u> <u>5</u>	226	11	8	30.52	170	16	11	30.99	396	16	11	0	30.99	Histone H1.1
<u>P4</u> <u>327</u> <u>6</u>	185	14	10	30.94	224	16	12	30.94	409	16	12	0	30.94	Histone H1.5
<u>P4</u> <u>327</u> <u>7</u>	565	18	2	41.63	403	20	4	37.56	968	22	4	0.66	41.63	Histone H1.3
<u>P4</u> <u>343</u> <u>0</u>	0	0	0		20	3	3	9.72	20	3	3	1.19	9.72	Mast cell protease 8
<u>P4</u> <u>537</u> <u>6</u>	3	1	1	4.43	4	2	2	13.92	7	2	2	3.3	13.92	Aldose reductase
<u>P4</u> <u>559</u> <u>1</u>	9	2	1	16.87	34	4	2	16.87	43	4	2	3.3	16.87	Cofilin-2
<u>P4</u> <u>595</u> <u>2</u>	18	3	3	14.01	10	2	2	10.45	28	3	3	1.19	14.01	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial
<u>P4</u> <u>606</u> <u>1</u>	4	2	2	2.04	3	2	2	2.04	7	2	2	3.3	2.04	Ran GTPase-activating protein 1
<u>P4</u> <u>606</u> <u>2</u>	0	0	0		6	2	2	3.47	6	2	2	3.3	3.47	Signal-induced proliferation-associated protein 1
<u>P4</u> <u>646</u> <u>0</u>	13	2	2	3.49	3	1	1	1.88	16	2	2	3.3	3.49	Vesicle-fusing ATPase
<u>P4</u> <u>646</u> <u>7</u>	25	8	8	28.6	56	8	8	30.86	81	9	9	0	33.56	Vacuolar protein sorting-associated protein 4B
<u>P4</u> <u>647</u> <u>1</u>	51	11	11	32.56	50	8	8	22.17	101	13	13	0	35.57	26S protease regulatory subunit 7
<u>P4</u> <u>663</u> <u>8</u>	5	2	2	9.63	5	2	2	9.63	10	2	2	3.3	9.63	Ras-related protein Rab-11B
<u>P4</u> <u>666</u> <u>4</u>	3	2	2	4.82	6	3	3	10.96	9	4	4	0.66	13.38	Adenylosuccinate synthetase isozyme 2
<u>P4</u> <u>773</u> <u>8</u>	394	25	25	64.74	302	28	28	73.99	696	32	32	0	74.95	Aldehyde dehydrogenase, mitochondrial
<u>P4</u> <u>775</u> <u>4</u>	46	6	4	33.22	66	7	5	42.31	112	7	5	0.47	42.31	F-actin-capping protein subunit alpha-2
<u>P4</u> <u>775</u> <u>7-2</u>	79	11	11	56.99	121	14	14	67.65	200	14	14	0	67.65	Isoform 2 of F-actin-capping protein subunit beta
<u>P4</u> <u>779</u> <u>1</u>	121	12	12	45.8	224	18	18	57.6	345	18	18	0	57.6	Glutathione reductase, mitochondrial

<u>P4</u> <u>780</u> <u>2</u>	0	0	0		5	2	2	8.56	5	2	2	3.3	8.56	Dual specificity mitogen-activated protein kinase kinase 4
<u>P4</u> <u>781</u> <u>1</u>	10	2	2	12.22	30	5	5	21.67	40	5	5	0.4 7	21.6 7	Mitogen-activated protein kinase 14
<u>P4</u> <u>785</u> <u>6</u>	3	2	2	4.45	5	2	2	4.3	8	3	3	1.1 9	6.46	Glutamine--fructose-6- phosphate aminotransferase [isomerizing] 1
<u>P4</u> <u>791</u> <u>1</u>	40	6	6	20.95	38	5	5	16.55	78	7	7	0	20.9 5	60S ribosomal protein L6
<u>P4</u> <u>794</u> <u>1</u>	3	2	2	9.57	5	2	2	13.2	8	4	4	0.6 6	22.7 7	Crk-like protein
<u>P4</u> <u>795</u> <u>5</u>	31	1	1	14.04	17	2	2	35.09	48	2	2	3.3	35.0 9	60S acidic ribosomal protein P1
<u>P4</u> <u>796</u> <u>2</u>	6	3	3	15.15	31	7	7	29.29	37	7	7	0	29.2 9	60S ribosomal protein L5
<u>P4</u> <u>796</u> <u>8</u>	3	1	1	5.61	13	2	2	10.89	16	2	2	3.3	10.8 9	Ribose-5-phosphate isomerase
<u>P4</u> <u>802</u> <u>5</u>	92	14	14	38.16	93	17	17	48.01	185	20	20	0	53.7 4	Tyrosine-protein kinase SYK
<u>P4</u> <u>803</u> <u>6</u>	46	6	6	22.26	36	8	8	32.92	82	9	9	0	37.9 3	Annexin A5
<u>P4</u> <u>819</u> <u>3</u>	8	2	2	5.01	9	2	2	3.96	17	3	3	1.1 9	6.88	Protein 4.1
<u>P4</u> <u>931</u> <u>2</u>	47	6	5	27.5	95	11	8	35.94	142	11	8	0	35.9 4	Heterogeneous nuclear ribonucleoprotein A1
<u>P4</u> <u>971</u> <u>7</u>	13	5	5	9.63	10	3	3	4.52	23	6	6	0.4 7	10.4 4	DNA replication licensing factor MCM4
<u>P4</u> <u>971</u> <u>8</u>	3	2	2	3.68	1	1	1	2.05	4	2	2	3.3	3.68	DNA replication licensing factor MCM5
<u>P4</u> <u>972</u> <u>2</u>	208	9	9	38.89	198	11	11	60.26	406	12	12	0	60.2 6	Proteasome subunit alpha type-2
<u>P4</u> <u>996</u> <u>2</u>	0	0	0		2	2	2	25.58	2	2	2	3.3	25.5 8	Signal recognition particle 9 kDa protein
<u>P5</u> <u>024</u> <u>7</u>	45	7	7	25.69	51	8	8	30.32	96	9	9	0	32.8 7	Adenosylhomocysteina se
<u>P5</u> <u>039</u> <u>6</u>	42	10	6	38.93	87	11	7	34	129	12	8	0	39.3 7	Rab GDP dissociation inhibitor alpha
<u>P5</u> <u>043</u> <u>1</u>	9	2	1	5.44	13	3	2	9.83	22	4	3	1.1 9	12.3 4	Serine hydroxymethyltransfera se, cytosolic
<u>P5</u> <u>051</u> <u>6</u>	89	10	10	26.9	113	17	17	44.89	202	18	18	0	47.6 5	V-type proton ATPase catalytic subunit A
<u>P5</u> <u>051</u> <u>8</u>	31	3	3	20.8	31	3	3	20.8	62	3	3	1.1 9	20.8	V-type proton ATPase subunit E 1
<u>P5</u> <u>054</u> <u>3</u>	23	3	3	27.55	32	4	4	27.55	55	4	4	0.6 6	27.5 5	Protein S100-A11

<u>P5</u> <u>054</u> 4	0	0	0		2	2	2	4.88	2	2	2	3.3	4.88	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial
<u>P5</u> <u>058</u> 0	53	10	10	32.99	111	19	19	47.97	164	19	19	0	47.97	Proliferation-associated protein 2G4
<u>P5</u> <u>112</u> 5	4	2	2	4.95	10	3	3	9.14	14	4	4	0.66	11.93	Calpastatin
<u>P5</u> <u>115</u> 0	10	2	2	12.08	9	2	2	12.08	19	2	2	3.3	12.08	Ras-related protein Rab-7a
<u>P5</u> <u>117</u> 4	53	10	10	24.65	117	13	13	33.95	170	14	14	0	33.95	Long-chain specific acyl-CoA dehydrogenase, mitochondrial
<u>P5</u> <u>143</u> 7	55	3	3	19.65	51	3	3	19.65	106	3	3	1.19	19.65	Cathelin-related antimicrobial peptide
<u>P5</u> <u>166</u> 0	1	1	1	3.13	2	2	2	4.9	3	2	2	3.3	4.9	Peroxisomal multifunctional enzyme type 2
<u>P5</u> <u>185</u> 9	3	1	1	6.75	10	2	2	7.17	13	2	2	3.3	7.17	Hepatoma-derived growth factor
<u>P5</u> <u>186</u> 3	0	0	0		10	2	2	11.4	10	2	2	3.3	11.4	V-type proton ATPase subunit d 1
<u>P5</u> <u>219</u> 6	0	0	0		4	2	2	10.44	4	2	2	3.3	10.44	Thiosulfate sulfurtransferase
<u>P5</u> <u>248</u> 0	1639	43	43	65.35	749	57	57	69.3	2388	60	60	0	69.3	Pyruvate kinase PKM
<u>P5</u> <u>262</u> 4	1	1	1	7.07	34	8	8	46.3	35	8	8	0	46.3	Uridine phosphorylase 1
<u>P5</u> <u>302</u> 6	14	5	5	18.89	29	5	5	22.58	43	6	6	0.47	22.58	60S ribosomal protein L10a
<u>P5</u> <u>407</u> 1	30	6	6	19.69	51	10	9	29.42	81	10	9	0	29.42	Isocitrate dehydrogenase [NADP], mitochondrial
<u>P5</u> <u>477</u> 5	87	12	12	44.5	90	12	12	45.69	177	14	14	0	47.85	26S protease regulatory subunit 6B
<u>P5</u> <u>482</u> 2	4	1	1	1.86	9	2	2	6.82	13	2	2	3.3	6.82	Adenylosuccinate lyase
<u>P5</u> <u>482</u> 3	36	8	8	24.43	75	14	14	43.48	111	15	15	0	47.62	Probable ATP-dependent RNA helicase DDX6
<u>P5</u> <u>492</u> 3	8	2	2	13.26	8	2	2	12.71	16	3	3	1.19	18.78	[Protein ADP-ribosylarginine] hydrolase
<u>P5</u> <u>498</u> 7	1	1	1	6.35	10	2	2	10.45	11	2	2	3.3	10.45	Cis-aconitate decarboxylase
<u>P5</u> <u>525</u> 8	7	3	2	17.87	19	3	2	17.87	26	3	2	3.3	17.87	Ras-related protein Rab-8A
<u>P5</u> <u>526</u> 4	0	0	0		5	3	3	13.02	5	3	3	1.19	13.02	Adenosine kinase
<u>P5</u> <u>639</u> 9	27	9	9	20.16	27	6	6	13.4	54	10	10	0	22.38	Ubiquitin carboxyl-terminal hydrolase 5

<u>P5</u> <u>648</u> <u>0</u>	40	10	10	37.43	87	16	16	52.36	127	16	16	0	52.3 6	ATP synthase subunit beta, mitochondrial
<u>P5</u> <u>695</u> <u>9</u>	23	6	6	13.32	17	2	2	8.88	40	6	6	0.4 7	13.3 2	RNA-binding protein FUS
<u>P5</u> <u>775</u> <u>9</u>	0	0	0		4	3	3	18.7	4	3	3	1.1 9	18.7	Endoplasmic reticulum resident protein 29
<u>P5</u> <u>777</u> <u>6</u>	22	3	3	17.08	23	5	5	21.71	45	5	5	0.4 7	21.7 1	Elongation factor 1- delta
<u>P5</u> <u>778</u> <u>0</u>	491	37	20	55.7	576	43	26	62.94	106 7	47	28	0	65.6 8	Alpha-actinin-4
<u>P5</u> <u>778</u> <u>4</u>	44	5	5	37.25	62	6	6	38.43	106	7	7	0	43.9 2	U2 small nuclear ribonucleoprotein A'
<u>P5</u> <u>805</u> <u>8</u>	30	6	6	19.36	33	7	7	19.59	63	7	7	0	19.5 9	NAD kinase
<u>P5</u> <u>825</u> <u>2</u>	325	30	30	47.44	401	35	35	52.1	726	37	37	0	54.7 8	Elongation factor 2
<u>P5</u> <u>838</u> <u>9</u>	2	1	1	8.98	13	3	3	23.22	15	3	3	1.1 9	23.2 2	Serine/threonine-protein phosphatase 2A activator
<u>P5</u> <u>877</u> <u>4-2</u>	17	3	0	5.28	23	6	2	26.06	40	6	2	3.3	26.0 6	Isoform 2 of Tropomyosin beta chain
<u>P5</u> <u>932</u> <u>5</u>	3	1	1	3.5	9	3	3	5.59	12	3	3	1.1 9	5.59	Eukaryotic translation initiation factor 5
<u>P5</u> <u>999</u> <u>9</u>	94	9	9	65.48	128	12	12	67.86	222	12	12	0	67.8 6	Actin-related protein 2/3 complex subunit 4
<u>P6</u> <u>012</u> <u>2</u>	76	12	12	41.67	33	7	7	21.49	109	14	14	0	44.7 4	RuvB-like 1
<u>P6</u> <u>022</u> <u>9</u>	72	10	10	31.24	100	14	14	39.33	172	14	14	0	39.3 3	Eukaryotic translation initiation factor 3 subunit E
<u>P6</u> <u>033</u> <u>5</u>	25	4	2	18.82	42	4	2	17.13	67	5	3	1.1 9	23.6	Poly(rC)-binding protein 1
<u>P6</u> <u>071</u> <u>0</u>	7224	105	30	91.73	6124	152	48	97.07	133 48	158	49	0	97.0 7	Actin, cytoplasmic 1
<u>P6</u> <u>076</u> <u>6</u>	52	4	4	31.94	84	10	9	68.59	136	10	9	0	68.5 9	Cell division control protein 42 homolog
<u>P6</u> <u>084</u> <u>3</u>	161	16	15	51.72	221	22	21	63.55	382	24	23	0	66.7 5	Eukaryotic initiation factor 4A-I
<u>P6</u> <u>086</u> <u>7</u>	22	3	3	22.69	20	2	2	19.33	42	3	3	1.1 9	22.6 9	40S ribosomal protein S20
<u>P6</u> <u>102</u> <u>1</u>	6	1	0	5.12	7	4	2	25.58	13	4	2	3.3	25.5 8	Ras-related protein Rab-5B
<u>P6</u> <u>102</u> <u>7</u>	3	2	1	11	10	3	2	18.5	13	3	2	3.3	18.5	Ras-related protein Rab-10
<u>P6</u> <u>108</u> <u>9</u>	3	2	2	16.45	6	1	1	9.87	9	2	2	3.3	16.4 5	Ubiquitin-conjugating enzyme E2 N
<u>P6</u> <u>116</u> <u>1</u>	285	17	17	48.73	446	20	20	48.73	731	20	20	0	48.7 3	Actin-related protein 2

P6 116 4	35	9	5	38.83	35	7	3	35.11	70	10	6	0.4 7	43.6 2	Alpha-centractin
P6 120 2	14	7	7	24.15	16	5	5	14.45	30	8	8	0	26.4 1	COP9 signalosome complex subunit 2
P6 122 2	1	1	1	2.67	12	5	5	13.19	13	6	6	0.4 7	15.8 6	ATP-binding cassette sub-family E member 1
P6 129 0	5	2	2	9.45	11	3	3	14.17	16	3	3	1.1 9	14.1 7	Proteasome activator complex subunit 3
P6 132 7	4	2	2	20.55	3	1	1	13.7	7	2	2	3.3	20.5 5	Protein mago nashi homolog
P6 135 8	6	1	1	5.88	4	2	2	15.44	10	3	3	1.1 9	21.3 2	60S ribosomal protein L27
P6 175 9	5	3	3	22.45	9	2	2	22.45	14	3	3	1.1 9	22.4 5	Prefoldin subunit 3
P6 196 7	8	3	3	20.25	16	3	3	20.25	24	3	3	1.1 9	20.2 5	AP-1 complex subunit sigma-1A
P6 197 9	50	9	9	30.02	71	11	11	27.65	121	13	13	0	34.1 3	Heterogeneous nuclear ribonucleoprotein K
P6 198 2	43	6	4	28.34	84	9	6	50.61	127	10	7	0	50.6 1	14-3-3 protein gamma
P6 208 2	42	6	6	38.66	20	4	4	32.99	62	6	6	0.4 7	38.6 6	40S ribosomal protein S7
P6 213 7	70	7	3	24.55	64	10	4	32.42	134	10	4	0.6 6	32.4 2	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit
P6 214 1	64	6	2	19.57	60	9	3	27.22	124	9	3	1.1 9	27.2 2	Serine/threonine-protein phosphatase PP1-beta catalytic subunit
P6 219 2	57	7	7	23.18	22	8	8	25.68	79	9	9	0	30.6 8	26S protease regulatory subunit 4
P6 219 6	37	8	8	28.82	37	5	5	19.95	74	9	9	0	32.0 2	26S protease regulatory subunit 8
P6 224 2	28	3	3	18.75	13	4	4	24.04	41	4	4	0.6 6	24.0 4	40S ribosomal protein S8
P6 224 5	0	0	0		12	2	2	16.92	12	2	2	3.3	16.9 2	40S ribosomal protein S15a
P6 225 9	99	8	6	35.29	118	12	10	57.65	217	13	11	0	62.7 5	14-3-3 protein epsilon
P6 226 4	13	2	2	16.56	4	1	1	8.61	17	2	2	3.3	16.5 6	40S ribosomal protein S14
P6 227 0	23	6	6	32.89	14	4	4	24.34	37	7	7	0	38.8 2	40S ribosomal protein S18
P6 230 5	11	2	2	25	25	3	3	25	36	3	3	1.1 9	25	Small nuclear ribonucleoprotein E
P6 230 7	7	2	2	55.81	35	4	4	72.09	42	4	4	0.6 6	72.0 9	Small nuclear ribonucleoprotein F
P6 230 9	11	2	2	17.11	29	3	3	26.32	40	3	3	1.1 9	26.3 2	Small nuclear ribonucleoprotein G

<u>P6</u> <u>231</u> <u>5</u>	54	4	4	45.38	65	5	5	54.62	119	5	5	0.4 7	54.6 2	Small nuclear ribonucleoprotein Sm D1
<u>P6</u> <u>231</u> <u>7</u>	16	4	4	31.36	51	6	6	47.46	67	6	6	0.4 7	47.4 6	Small nuclear ribonucleoprotein Sm D2
<u>P6</u> <u>232</u> <u>0</u>	26	3	3	31.75	35	3	3	31.75	61	3	3	1.1 9	31.7 5	Small nuclear ribonucleoprotein Sm D3
<u>P6</u> <u>233</u> <u>4</u>	50	7	7	28.79	43	5	5	18.25	93	7	7	0	28.7 9	26S protease regulatory subunit 10B
<u>P6</u> <u>248</u> <u>2</u>	21	6	6	31.61	27	4	4	22.89	48	6	6	0.4 7	31.6 1	Voltage-gated potassium channel subunit beta-2
<u>P6</u> <u>270</u> <u>2</u>	34	7	7	27	18	3	3	15.21	52	7	7	0	27	40S ribosomal protein S4, X isoform
<u>P6</u> <u>274</u> <u>6</u>	29	3	1	20.92	27	6	3	47.96	56	7	3	1.1 9	47.9 6	Rho-related GTP- binding protein RhoB
<u>P6</u> <u>274</u> <u>8</u>	6	3	3	18.65	10	2	2	13.47	16	3	3	1.1 9	18.6 5	Hippocalcin-like protein 1
<u>P6</u> <u>275</u> <u>4</u>	25	2	2	10.84	7	1	1	6.02	32	2	2	3.3	10.8 4	40S ribosomal protein S6
<u>P6</u> <u>280</u> <u>6</u>	5901	34	34	60.19	4521	44	44	62.14	104 22	44	44	0	62.1 4	Histone H4
<u>P6</u> <u>281</u> <u>4</u>	86	10	10	37.57	150	17	17	50.49	236	17	17	0	50.4 9	V-type proton ATPase subunit B, brain isoform
<u>P6</u> <u>282</u> <u>1</u>	4	2	1	13.66	12	4	3	30.73	16	4	3	1.1 9	30.7 3	Ras-related protein Rab-1A
<u>P6</u> <u>282</u> <u>7</u>	89	10	10	53.7	117	15	15	59.26	206	15	15	0	59.2 6	GTP-binding nuclear protein Ran
<u>P6</u> <u>283</u> <u>0</u>	5	3	3	33.57	10	2	2	25	15	3	3	1.1 9	33.5 7	60S ribosomal protein L23
<u>P6</u> <u>284</u> <u>3</u>	34	3	3	28.28	12	3	3	28.28	46	3	3	1.1 9	28.2 8	40S ribosomal protein S15
<u>P6</u> <u>285</u> <u>5</u>	2	1	1	7.83	4	2	2	20.87	6	2	2	3.3	20.8 7	40S ribosomal protein S26
<u>P6</u> <u>288</u> <u>0</u>	13	2	2	10	18	4	4	18.82	31	4	4	0.6 6	18.8 2	Guanine nucleotide- binding protein G(I)/G(S)/G(T) subunit beta-2
<u>P6</u> <u>288</u> <u>9</u>	2	2	2	24.35	7	2	2	24.35	9	2	2	3.3	24.3 5	60S ribosomal protein L30
<u>P6</u> <u>289</u> <u>7</u>	7	2	2	11.43	31	4	4	26.67	38	4	4	0.6 6	26.6 7	Cytochrome c, somatic
<u>P6</u> <u>290</u> <u>8</u>	61	7	7	31.69	44	5	5	26.34	105	7	7	0	31.6 9	40S ribosomal protein S3
<u>P6</u> <u>296</u> <u>0</u>	14	5	5	28.26	23	5	5	31.37	37	7	7	0	41.3	Nuclease-sensitive element-binding protein 1
<u>P6</u> <u>296</u> <u>2</u>	54	5	5	45.71	61	8	8	65	115	8	8	0	65	Profilin-1

<u>P6</u> <u>299</u> <u>6</u>	11	2	2	10.42	20	3	3	12.85	31	3	3	1.1 9	12.8 5	Transformer-2 protein homolog beta
<u>P6</u> <u>300</u> <u>1</u>	38	5	1	25.52	48	8	2	36.46	86	8	2	3.3	36.4 6	Ras-related C3 botulinum toxin substrate 1
<u>P6</u> <u>300</u> <u>5</u>	26	8	8	26.59	60	11	11	28.54	86	12	12	0	32.4 4	Platelet-activating factor acetylhydrolase IB subunit alpha
<u>P6</u> <u>301</u> <u>7</u>	419	30	25	59.91	533	47	39	73.37	952	47	39	0	73.3 7	Heat shock cognate 71 kDa protein
<u>P6</u> <u>302</u> <u>8</u>	1	1	1	27.33	9	2	2	35.47	10	2	2	3.3	35.4 7	Translationally- controlled tumor protein
<u>P6</u> <u>308</u> <u>5</u>	18	4	2	20.39	40	8	5	27.37	58	10	7	0	37.7 1	Mitogen-activated protein kinase 1
<u>P6</u> <u>310</u> <u>1</u>	183	11	9	52.24	152	16	13	62.45	335	16	13	0	62.4 5	14-3-3 protein zeta/delta
<u>P6</u> <u>315</u> <u>8</u>	100	9	6	31.63	176	13	9	40	276	14	9	0	44.1 9	High mobility group protein B1
<u>P6</u> <u>324</u> <u>2</u>	39	6	6	55.84	109	7	7	70.78	148	8	8	0	71.4 3	Eukaryotic translation initiation factor 5A-1
<u>P6</u> <u>327</u> <u>6</u>	14	2	2	32.59	5	2	2	32.59	19	2	2	3.3	32.5 9	40S ribosomal protein S17
<u>P6</u> <u>328</u> <u>0</u>	1	1	1	8.23	3	2	2	27.85	4	2	2	3.3	27.8 5	SUMO-conjugating enzyme UBC9
<u>P6</u> <u>332</u> <u>5</u>	20	3	3	20	4	1	1	5.45	24	3	3	1.1 9	20	40S ribosomal protein S10
<u>P6</u> <u>332</u> <u>8</u>	11	3	2	9.21	10	3	2	11.32	21	5	4	0.6 6	18.6 2	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform
<u>P6</u> <u>333</u> <u>0</u>	24	6	6	39.16	40	6	6	31.72	64	7	7	0	43.6 9	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform
<u>P6</u> <u>777</u> <u>8</u>	7	2	2	13.24	21	5	5	28.68	28	5	5	0.4 7	28.6 8	Prohibitin
<u>P6</u> <u>787</u> <u>1</u>	5	2	2	15.81	12	2	2	15.81	17	2	2	3.3	15.8 1	Casein kinase II subunit beta
<u>P6</u> <u>803</u> <u>3</u>	3336	53	12	65.52	2701	82	22	74.27	603 7	84	22	0	74.2 7	Actin, alpha cardiac muscle 1
<u>P6</u> <u>803</u> <u>7</u>	7	3	3	40.26	32	3	3	40.26	39	3	3	1.1 9	40.2 6	Ubiquitin-conjugating enzyme E2 L3
<u>P6</u> <u>804</u> <u>0</u>	47	7	7	35.96	71	10	10	45.74	118	11	11	0	50.7 9	Guanine nucleotide- binding protein subunit beta-2-like 1
<u>P6</u> <u>825</u> <u>4</u>	57	10	8	38.78	98	12	9	46.94	155	13	10	0	46.9 4	14-3-3 protein theta
<u>P6</u> <u>836</u> <u>8</u>	176	14	6	51.79	176	19	7	59.82	352	20	7	0	63.6 2	Tubulin alpha-4A chain
<u>P6</u> <u>836</u> <u>9</u>	170	14	6	51.44	194	21	9	59.42	364	22	9	0	63.1 9	Tubulin alpha-1A chain

<u>P6</u> <u>843</u> <u>3</u>	1556	23	2	66.91	1760	32	6	67.65	331 6	32	6	0.4 7	67.6 5	Histone H3.1
<u>P6</u> <u>851</u> <u>0</u>	31	5	3	26.83	40	6	4	27.24	71	7	5	0.4 7	32.9 3	14-3-3 protein eta
<u>P7</u> <u>016</u> <u>8</u>	114	17	17	29.11	179	26	26	43.15	293	27	27	0	44.1 8	Importin subunit beta-1
<u>P7</u> <u>019</u> <u>5</u>	57	7	7	28.16	104	15	15	58.48	161	15	15	0	58.4 8	Proteasome subunit beta type-7
<u>P7</u> <u>026</u> <u>8</u>	10	2	2	5.29	16	4	4	7.29	26	4	4	0.6 6	7.29	Serine/threonine-protein kinase N1
<u>P7</u> <u>029</u> <u>0</u>	2	2	2	8.58	12	6	6	13.73	14	6	6	0.4 7	13.7 3	55 kDa erythrocyte membrane protein
<u>P7</u> <u>029</u> <u>6</u>	3	1	1	13.9	6	2	2	20.86	9	2	2	3.3	20.8 6	Phosphatidylethanolami ne-binding protein 1
<u>P7</u> <u>031</u> <u>5</u>	3	3	3	10	1	1	1	5.77	4	4	4	0.6 6	15.7 7	Wiskott-Aldrich syndrome protein homolog
<u>P7</u> <u>033</u> <u>3</u>	24	4	3	13.36	18	3	2	9.58	42	4	3	1.1 9	13.3 6	Heterogeneous nuclear ribonucleoprotein H2
<u>P7</u> <u>037</u> <u>2</u>	17	4	4	16.26	11	3	3	12.88	28	4	4	0.6 6	16.2 6	ELAV-like protein 1
<u>P7</u> <u>039</u> <u>8</u>	35	10	10	6.49	20	7	7	4.73	55	13	13	0	9.14	Probable ubiquitin carboxyl-terminal hydrolase FAF-X
<u>P7</u> <u>040</u> <u>4</u>	2	1	1	7.89	5	2	2	13.74	7	2	2	3.3	13.7 4	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial
<u>P7</u> <u>044</u> <u>1</u>	4	2	2	7.04	10	2	2	7.04	14	3	3	1.1 9	10.1 4	Na(+)/H(+) exchange regulatory cofactor NHE-RF1
<u>P7</u> <u>046</u> <u>0</u>	50	7	7	25.6	57	9	9	35.2	107	10	10	0	37.8 7	Vasodilator-stimulated phosphoprotein
<u>P7</u> <u>067</u> <u>0</u>	21	4	4	1.92	46	4	4	1.92	67	4	4	0.6 6	1.92	Nascent polypeptide- associated complex subunit alpha, muscle- specific form
<u>P7</u> <u>067</u> <u>7</u>	5	2	2	9.03	8	2	2	12.64	13	4	4	0.6 6	21.6 6	Caspase-3
<u>P7</u> <u>069</u> <u>8</u>	3	2	2	5.41	9	4	4	11.51	12	4	4	0.6 6	11.5 1	CTP synthase 1
<u>P8</u> <u>031</u> <u>3</u>	22	7	7	20.4	27	7	7	23.35	49	9	9	0	27.7 6	T-complex protein 1 subunit eta
<u>P8</u> <u>031</u> <u>4</u>	103	12	12	40.19	95	10	10	34.58	198	12	12	0	40.1 9	T-complex protein 1 subunit beta
<u>P8</u> <u>031</u> <u>5</u>	56	9	8	27.83	54	8	7	25.05	110	10	9	0	30.9 8	T-complex protein 1 subunit delta
<u>P8</u> <u>031</u> <u>6</u>	72	7	7	27.36	61	7	7	27.54	133	9	9	0	34.9 4	T-complex protein 1 subunit epsilon
<u>P8</u> <u>031</u> <u>7</u>	31	5	5	15.63	34	6	6	21.47	65	8	8	0	23.5 4	T-complex protein 1 subunit zeta

P8 031 8	98	16	16	35.6	94	17	17	42.57	192	20	20	0	44.7 7	T-complex protein 1 subunit gamma
P8 219 8	119	14	14	39.24	320	24	24	58.27	439	25	25	0	59.5 9	Transforming growth factor-beta-induced protein ig-h3
P8 394 0	5	2	2	28.57	13	1	1	17.86	18	2	2	3.3	28.5 7	Transcription elongation factor B polypeptide 1
P8 407 8	49	7	2	46.96	66	8	3	49.72	115	8	3	1.1 9	49.7 2	ADP-ribosylation factor 1
P8 408 4	27	5	0	34.44	58	9	4	60.56	85	9	4	0.6 6	60.5 6	ADP-ribosylation factor 5
P8 408 9	0	0	0		6	2	2	40.38	6	2	2	3.3	40.3 8	Enhancer of rudimentary homolog
P8 409 1	16	5	5	20.69	37	7	7	27.59	53	9	9	0	33.7 9	AP-2 complex subunit mu
P8 409 6	29	2	2	18.85	33	7	6	36.65	62	7	6	0.4 7	36.6 5	Rho-related GTP- binding protein RhoG
P8 422 8	2587	37	13	67.65	3258	49	18	68.38	584 5	50	19	0	68.3 8	Histone H3.2
P8 424 4	1851	29	6	59.56	2078	37	8	60.29	392 9	37	8	0	60.2 9	Histone H3.3
P9 731 0	3	2	2	4.31	15	5	5	8.41	18	5	5	0.4 7	8.41	DNA replication licensing factor MCM2
P9 731 1	8	3	3	4.87	9	1	1	1.46	17	3	3	1.1 9	4.87	DNA replication licensing factor MCM6
P9 731 3	9	1	1	0.46	28	2	2	0.68	37	2	2	3.3	0.68	DNA-dependent protein kinase catalytic subunit
P9 735 2	26	4	4	41.84	14	3	3	33.67	40	4	4	0.6 6	41.8 4	Protein S100-A13
P9 736 9	156	16	16	52.51	134	18	18	45.13	290	21	21	0	54.8 7	Neutrophil cytosol factor 4
P9 737 1	6	1	1	7.63	31	3	3	18.07	37	3	3	1.1 9	18.0 7	Proteasome activator complex subunit 1
P9 737 2	11	4	4	26.78	32	3	3	20.92	43	4	4	0.6 6	26.7 8	Proteasome activator complex subunit 2
P9 738 4	121	11	11	25.25	172	16	16	31.41	293	16	16	0	31.4 1	Annexin A11
P9 742 5	1	1	1	12.18	9	2	2	19.87	10	2	2	3.3	19.8 7	Eosinophil cationic protein 2
P9 745 0	3	1	1	17.59	5	3	3	34.26	8	3	3	1.1 9	34.2 6	ATP synthase-coupling factor 6, mitochondrial
P9 749 6	12	3	2	4.17	4	1	1	1.72	16	3	2	3.3	4.17	SWI/SNF complex subunit SMARCC1
P9 780 7	25	7	7	24.06	47	7	7	26.43	72	9	9	0	32.1 5	Fumarate hydratase, mitochondrial
P9 781 4	7	2	2	7.95	6	2	2	7.95	13	2	2	3.3	7.95	Proline-serine-threonine phosphatase-interacting protein 1

<u>P9</u> <u>782</u> <u>2</u>	4	2	2	12.69	2	1	1	5.38	6	2	2	3.3	12.6 9	Acidic leucine-rich nuclear phosphoprotein 32 family member E
<u>P9</u> <u>782</u> <u>3</u>	13	2	2	10.43	10	2	2	10.43	23	2	2	3.3	10.4 3	Acyl-protein thioesterase 1
<u>P9</u> <u>902</u> <u>4</u>	232	21	4	65.32	277	28	5	69.37	509	28	5	0.4 7	69.3 7	Tubulin beta-5 chain
<u>P9</u> <u>902</u> <u>6</u>	136	6	6	41.67	138	10	10	55.68	274	10	10	0	55.6 8	Proteasome subunit beta type-4
<u>P9</u> <u>902</u> <u>7</u>	95	8	8	85.22	75	5	5	69.57	170	8	8	0	85.2 2	60S acidic ribosomal protein P2
<u>P9</u> <u>902</u> <u>9</u>	41	8	8	48.57	51	8	8	49.05	92	9	9	0	49.0 5	Peroxisomal oxidase, mitochondrial
<u>Q0</u> <u>051</u> <u>9</u>	268	23	23	25.84	254	29	29	34.46	522	29	29	0	34.4 6	Xanthine dehydrogenase/oxidase
<u>Q0</u> <u>061</u> <u>2</u>	416	28	28	63.11	474	45	45	74.37	890	46	46	0	74.3 7	Glucose-6-phosphate 1- dehydrogenase X
<u>Q0</u> <u>0PI</u> <u>9</u>	1	1	1	2.28	5	2	2	5.37	6	3	3	1.1 9	7.65	Heterogeneous nuclear ribonucleoprotein U- like protein 2
<u>Q0</u> <u>132</u> <u>0</u>	1	1	1	0.98	5	4	3	3.66	6	4	3	1.1 9	3.66	DNA topoisomerase 2- alpha
<u>Q0</u> <u>140</u> <u>5</u>	16	7	5	17.25	12	5	4	12.68	28	8	6	0.4 7	18.9 5	Protein transport protein Sec23A
<u>Q0</u> <u>173</u> <u>0</u>	15	4	4	27.08	34	4	4	30.69	49	5	5	0.4 7	33.2 1	Ras suppressor protein 1
<u>Q0</u> <u>185</u> <u>3</u>	774	43	43	62.28	806	54	54	71.96	158 0	54	54	0	71.9 6	Transitional endoplasmic reticulum ATPase
<u>Q0</u> <u>205</u> <u>3</u>	286	32	32	43.1	395	47	47	54.44	681	48	48	0	54.4 4	Ubiquitin-like modifier- activating enzyme 1
<u>Q0</u> <u>235</u> <u>7</u>	20	10	10	9.56	49	16	16	14.23	69	18	18	0	16.3 3	Ankyrin-1
<u>Q0</u> <u>326</u> <u>5</u>	24	6	6	15.01	25	10	10	27.49	49	11	11	0	29.2 9	ATP synthase subunit alpha, mitochondrial
<u>Q0</u> <u>475</u> <u>0</u>	62	14	14	20.34	194	25	25	32.07	256	25	25	0	32.0 7	DNA topoisomerase 1
<u>Q0</u> <u>514</u> <u>4</u>	95	11	7	41.67	111	13	7	53.12	206	15	9	0	55.7 3	Ras-related C3 botulinum toxin substrate 2
<u>Q0</u> <u>613</u> <u>8</u>	0	0	0		6	2	2	7.04	6	2	2	3.3	7.04	Calcium-binding protein 39
<u>Q0</u> <u>707</u> <u>6</u>	37	5	5	15.98	80	8	8	23.33	117	8	8	0	23.3 3	Annexin A7
<u>Q0</u> <u>741</u> <u>7</u>	10	2	2	10.44	5	2	2	10.44	15	2	2	3.3	10.4 4	Short-chain specific acyl-CoA dehydrogenase, mitochondrial
<u>Q0</u> <u>779</u> <u>7</u>	4	1	1	3.12	16	4	4	13.17	20	4	4	0.6 6	13.1 7	Galectin-3-binding protein

<u>Q0</u> <u>894</u> <u>3</u>	3	2	2	3.67	0	0	0		3	2	2	3.3	3.67	FACT complex subunit SSRP1
<u>Q0</u> <u>901</u> <u>4</u>	71	16	16	48.72	98	17	17	52.82	169	21	21	0	59.74	Neutrophil cytosol factor 1
<u>Q0</u> <u>9P</u> <u>K2</u>	97	8	8	48.67	118	9	9	58.11	215	9	9	0	58.11	Retroviral-like aspartic protease 1
<u>Q1</u> <u>101</u> <u>1</u>	80	20	20	31.63	138	25	25	40.33	218	27	27	0	41.52	Puromycin-sensitive aminopeptidase
<u>Q1</u> <u>4C</u> <u>H1</u>	0	0	0		2	2	2	4.87	2	2	2	3.3	4.87	Molybdenum cofactor sulfurase
<u>Q3</u> <u>TB</u> <u>D2</u>	21	7	7	12.99	26	8	8	14.07	47	10	10	0	17.92	Minor histocompatibility protein HA-1
<u>Q3</u> <u>TE</u> <u>A8</u> <u>-2</u>	71	14	14	32.53	33	9	9	24.03	104	16	16	0	36.41	Isoform 2 of Heterochromatin protein 1-binding protein 3
<u>Q3</u> <u>TH</u> <u>E2</u>	114	12	3	79.65	144	14	3	79.65	258	14	3	1.19	79.65	Myosin regulatory light chain 12B
<u>Q3</u> <u>TH</u> <u>K7</u>	7	2	2	5.63	12	2	2	5.34	19	3	3	1.19	8.23	GMP synthase [glutamine-hydrolyzing]
<u>Q3</u> <u>TR</u> <u>M8</u>	193	20	18	34.27	262	26	24	40.46	455	27	25	0	42.52	Hexokinase-3
<u>Q3</u> <u>T</u> <u>W9</u> <u>6</u>	11	3	3	7.89	12	4	4	11.44	23	4	4	0.66	11.44	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1
<u>Q3</u> <u>T</u> <u>W</u> <u>W8</u>	0	0	0		2	2	2	5.31	2	2	2	3.3	5.31	Serine/arginine-rich splicing factor 6
<u>Q3</u> <u>TX</u> <u>S7</u>	127	20	20	34.1	125	17	17	32.21	252	24	24	0	40.29	26S proteasome non-ATPase regulatory subunit 1
<u>Q3</u> <u>U0</u> <u>V1</u>	8	3	3	6.02	6	2	2	3.61	14	3	3	1.19	6.02	Far upstream element-binding protein 2
<u>Q3</u> <u>U1</u> <u>J4</u>	25	7	7	11.84	28	7	7	10.09	53	11	11	0	17.28	DNA damage-binding protein 1
<u>Q3</u> <u>U2</u> <u>G2</u>	55	11	11	20.78	90	18	18	34.32	145	21	21	0	38.6	Heat shock 70 kDa protein 4
<u>Q3</u> <u>U3</u> <u>90</u>	2	2	2	6.14	1	1	1	3.58	3	2	2	3.3	6.14	Protein Sirpb1b
<u>Q3</u> <u>U7</u> <u>R1</u>	9	2	2	2.47	32	6	6	10.35	41	6	6	0.47	10.35	Extended synaptotagmin-1
<u>Q3</u> <u>U8</u> <u>98</u>	11	1	1	35.09	12	2	2	71.93	23	2	2	3.3	71.93	Myeloma-overexpressed gene 2 protein homolog
<u>Q3</u> <u>UA</u> <u>06</u>	0	0	0		3	2	2	6.02	3	2	2	3.3	6.02	Pachytene checkpoint protein 2 homolog
<u>Q3</u> <u>UD</u> <u>E2</u>	3	1	1	1.56	2	2	2	3.6	5	2	2	3.3	3.6	Tubulin--tyrosine ligase-like protein 12
<u>Q3</u> <u>UH</u> <u>H2</u>	0	0	0		2	2	2	4.21	2	2	2	3.3	4.21	Solute carrier family 22 member 23

<u>Q3</u> <u>UJ</u> <u>B0</u>	9	6	6	10.59	16	3	3	3.87	25	7	7	0	11.3 9	Protein Sf3b2
<u>Q3</u> <u>UK</u> <u>J7</u>	0	0	0		3	2	2	4.87	3	2	2	3.3	4.87	WD40 repeat-containing protein SMU1
<u>Q3</u> <u>UK</u> <u>W2</u>	263	8	8	60.41	254	13	13	63.96	517	14	14	0	64.9 7	Calmodulin
<u>Q3</u> <u>U</u> <u>M4</u> <u>5</u>	5	3	3	10.8	8	2	2	10.53	13	4	4	0.6 6	16.3 4	Protein phosphatase 1 regulatory subunit 7
<u>Q3</u> <u>U</u> <u>M</u> <u>W7</u>	3	1	1	4.95	17	3	3	14.32	20	3	3	1.1 9	14.3 2	MAP kinase-activated protein kinase 3
<u>Q3</u> <u>UN</u> <u>D0</u>	25	9	9	41.06	30	7	7	24.86	55	11	11	0	51.4	Src kinase-associated phosphoprotein 2
<u>Q3</u> <u>UP</u> <u>87</u>	48	6	6	35.85	120	12	12	43.4	168	14	14	0	55.0 9	Neutrophil elastase
<u>Q3</u> <u>UP</u> <u>L0</u>	0	0	0		12	4	4	5.69	12	4	4	0.6 6	5.69	Protein transport protein Sec31A
<u>Q3</u> <u>UQ</u> <u>44</u>	41	6	4	5.27	15	5	4	4.57	56	7	5	0.4 7	6.22	Ras GTPase-activating-like protein IQGAP2
<u>Q3</u> <u>U</u> <u>W5</u> <u>3</u>	19	6	6	11.34	57	8	8	16.63	76	10	10	0	19.0 1	Protein Niban
<u>Q3</u> <u>UY</u> <u>V9</u>	15	6	6	10.76	24	8	8	14.3	39	9	9	0	15.1 9	Nuclear cap-binding protein subunit 1
<u>Q3</u> <u>UZ</u> <u>39</u>	6	5	5	10.29	26	6	6	13.31	32	9	9	0	14.8 1	Leucine-rich repeat flightless-interacting protein 1
<u>Q3</u> <u>UZ</u> <u>A1</u>	2	2	2	11.17	0	0	0		2	2	2	3.3	11.1 7	CapZ-interacting protein
<u>Q3</u> <u>UZ</u> <u>Z4</u>	91	12	12	28.32	95	10	10	25.74	186	14	14	0	31.8 8	Olfactomedin-4
<u>Q3</u> <u>V1</u> <u>G4</u>	12	1	1	2.55	21	4	4	8.45	33	4	4	0.6 6	8.45	Olfactomedin-like protein 2B
<u>Q3</u> <u>V1</u> <u>L4</u>	61	11	11	30.54	94	10	10	28.39	155	12	12	0	32.3 2	Cytosolic purine 5'-nucleotidase
<u>Q3</u> <u>V3</u> <u>R1</u>	7	3	3	4.71	9	3	3	4.61	16	4	4	0.6 6	6.14	Monofunctional C1-tetrahydrofolate synthase, mitochondrial
<u>Q4</u> <u>97J</u> <u>0</u>	12	3	3	37.11	10	2	2	24.74	22	3	3	1.1 9	37.1 1	MCG130175, isoform CRA b
<u>Q4</u> <u>LD</u> <u>D4</u>	2	2	2	2.07	8	3	3	4.55	10	4	4	0.6 6	5.58	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1
<u>Q4</u> <u>QR</u> <u>L3</u>	7	4	4	4.93	7	5	5	4.73	14	7	7	0	7.56	Coiled-coil domain-containing protein 88B
<u>Q4</u> <u>VA</u> <u>A7</u>	0	0	0		4	2	2	4.53	4	2	2	3.3	4.53	Sorting nexin-33

<u>Q5</u> <u>01J</u> <u>6</u>	26	5	1	9.08	36	7	3	13.23	62	7	3	1.1 9	13.2 3	Probable ATP-dependent RNA helicase DDX17
<u>Q5</u> <u>2K</u> <u>18</u>	6	2	2	5.07	5	1	1	2.96	11	2	2	3.3	5.07	Serine/arginine repetitive matrix protein 1
<u>Q5</u> <u>71</u> <u>E4</u>	2	1	1	2.31	22	3	3	10.19	24	3	3	1.1 9	10.1 9	N-acetylgalactosamine-6-sulfatase
<u>Q5</u> <u>711</u> <u>9</u>	76	7	7	12.84	59	8	8	14.46	135	8	8	0	14.4 6	Aldehyde dehydrogenase family 16 member A1
<u>Q5</u> <u>FW</u> <u>K3</u>	4	2	2	8.2	12	2	2	10.02	16	3	3	1.1 9	14.1 2	Rho GTPase-activating protein 1
<u>Q5</u> <u>RK</u> <u>N9</u>	97	12	10	61.89	115	11	9	61.54	212	13	11	0	61.8 9	Capping protein (Actin filament) muscle Z-line, alpha 1
<u>Q5</u> <u>SQ</u> <u>X6</u>	29	10	4	11.01	21	6	3	6.07	50	12	6	0.4 7	13.1 7	Cytoplasmic FMR1-interacting protein 2
<u>Q5</u> <u>SS</u> <u>L4</u>	2	2	2	4.66	15	4	4	8.73	17	4	4	0.6 6	8.73	Active breakpoint cluster region-related protein
<u>Q5</u> <u>SS</u> <u>W2</u>	9	2	2	2.17	7	2	2	2.17	16	2	2	3.3	2.17	Proteasome activator complex subunit 4
<u>Q5</u> <u>SU</u> <u>A5</u>	3	2	2	2.15	3	1	1	1.07	6	2	2	3.3	2.15	Unconventional myosin-Ig
<u>Q5</u> <u>SU</u> <u>R0</u>	36	10	10	14.66	47	11	11	16.01	83	15	15	0	21.0 2	Phosphoribosylformylglycinamidine synthase
<u>Q5</u> <u>XG</u> <u>71</u>	0	0	0		2	2	2	1	2	2	2	3.3	1	Small subunit processome component 20 homolog
<u>Q5</u> <u>XJ</u> <u>Y5</u>	4	2	2	4.5	3	1	1	2.15	7	2	2	3.3	4.5	Coatomer subunit delta
<u>Q6</u> <u>059</u> <u>7</u>	0	0	0		4	3	3	7.14	4	3	3	1.1 9	7.14	2-oxoglutarate dehydrogenase, mitochondrial
<u>Q6</u> <u>060</u> <u>5-2</u>	195	10	10	76.16	184	14	14	76.82	379	14	14	0	76.8 2	Isoform Smooth muscle of Myosin light polypeptide 6
<u>Q6</u> <u>063</u> <u>1</u>	8	2	2	18.89	33	3	3	22.12	41	3	3	1.1 9	22.1 2	Growth factor receptor-bound protein 2
<u>Q6</u> <u>066</u> <u>8</u>	66	8	8	25.63	60	8	8	25.92	126	10	10	0	25.9 2	Heterogeneous nuclear ribonucleoprotein D0
<u>Q6</u> <u>067</u> <u>5</u>	0	0	0		2	2	2	1.03	2	2	2	3.3	1.03	Laminin subunit alpha-2
<u>Q6</u> <u>069</u> <u>2</u>	57	4	4	34.45	96	9	9	65.55	153	9	9	0	65.5 5	Proteasome subunit beta type-6
<u>Q6</u> <u>071</u> <u>0</u>	197	20	20	47.53	234	27	27	53.11	431	27	27	0	53.1 1	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1
<u>Q6</u> <u>073</u> <u>7</u>	36	7	7	29.41	27	6	6	26.34	63	7	7	0	29.4 1	Casein kinase II subunit alpha
<u>Q6</u> <u>074</u> <u>9</u>	4	2	2	7.67	11	2	2	7.67	15	2	2	3.3	7.67	KH domain-containing, RNA-binding, signal transduction-associated protein 1

<u>Q6</u> <u>086</u> <u>4</u>	15	4	4	10.68	46	7	7	19.15	61	7	7	0	19.1 5	Stress-induced-phosphoprotein 1
<u>Q6</u> <u>086</u> <u>5</u>	3	1	1	1.7	21	4	4	13.15	24	4	4	0.6 6	13.1 5	Caprin-1
<u>Q6</u> <u>096</u> <u>3</u>	16	5	5	20.91	68	10	10	37.73	84	11	11	0	37.7 3	Platelet-activating factor acetylhydrolase
<u>Q6</u> <u>096</u> <u>7</u>	0	0	0		2	2	2	4.81	2	2	2	3.3	4.81	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1
<u>Q6</u> <u>097</u> <u>2</u>	39	8	5	34.82	47	7	3	25.65	86	9	5	0.4 7	36.7 1	Histone-binding protein RBBP4
<u>Q6</u> <u>097</u> <u>3</u>	14	5	2	15.76	21	5	1	14.82	35	6	2	3.3	17.6 5	Histone-binding protein RBBP7
<u>Q6</u> <u>102</u> <u>4</u>	7	2	2	4.1	26	5	5	12.12	33	5	5	0.4 7	12.1 2	Asparagine synthetase [glutamine-hydrolyzing]
<u>Q6</u> <u>103</u> <u>3</u>	16	5	5	9.52	32	9	9	20.78	48	11	11	0	22.9 4	Lamina-associated polypeptide 2, isoforms alpha/zeta
<u>Q6</u> <u>103</u> <u>5</u>	33	9	9	29.27	107	14	14	39.49	140	14	14	0	39.4 9	Histidine--tRNA ligase, cytoplasmic
<u>Q6</u> <u>108</u> <u>1</u>	10	1	1	5.54	14	2	2	10.03	24	2	2	3.3	10.0 3	Hsp90 co-chaperone Cdc37
<u>Q6</u> <u>109</u> <u>3</u>	0	0	0		3	2	2	8.6	3	2	2	3.3	8.6	Cytochrome b-245 heavy chain
<u>Q6</u> <u>109</u> <u>6</u>	49	8	8	31.5	101	9	9	31.5	150	9	9	0	31.5	Myeloblastin
<u>Q6</u> <u>114</u> <u>7</u>	0	0	0		32	10	10	16.31	32	10	10	0	16.3 1	Ceruloplasmin
<u>Q6</u> <u>116</u> <u>6</u>	12	4	4	29.1	14	4	4	27.61	26	6	6	0.4 7	42.1 6	Microtubule-associated protein RP/EB family member 1
<u>Q6</u> <u>117</u> <u>1</u>	35	5	5	26.77	39	8	8	61.11	74	8	8	0	61.1 1	Peroxisredoxin-2
<u>Q6</u> <u>118</u> <u>7</u>	0	0	0		9	2	2	11.76	9	2	2	3.3	11.7 6	Tumor susceptibility gene 101 protein
<u>Q6</u> <u>120</u> <u>6</u>	0	0	0		4	2	2	18.78	4	2	2	3.3	18.7 8	Platelet-activating factor acetylhydrolase IB subunit beta
<u>Q6</u> <u>120</u> <u>7</u>	2	1	1	2.69	5	2	2	4.67	7	2	2	3.3	4.67	Prosaposin
<u>Q6</u> <u>121</u> <u>0-5</u>	52	14	14	23.39	52	9	9	15.53	104	16	16	0	26.4 6	Isoform 5 of Rho guanine nucleotide exchange factor 1
<u>Q6</u> <u>123</u> <u>3</u>	771	41	41	79.27	784	52	52	84.37	155 5	54	54	0	84.3 7	Plastin-2
<u>Q6</u> <u>136</u> <u>2</u>	27	5	5	19.02	64	7	7	30.59	91	7	7	0	30.5 9	Chitinase-3-like protein 1
<u>Q6</u> <u>140</u> <u>0</u>	0	0	0		8	2	2	19.62	8	2	2	3.3	19.6 2	Carcinoembryonic antigen-related cell adhesion molecule 10

Q6 141 9	5	2	2	6.41	4	1	1	3.99	9	2	2	3.3	6.41	Cytidine monophosphate-N- acetylneuraminic acid hydroxylase
Q6 154 5	9	2	2	4.43	17	3	3	7.18	26	3	3	1.1 9	7.18	RNA-binding protein EWS
Q6 155 0	2	2	2	6.77	0	0	0		2	2	2	3.3	6.77	Double-strand-break repair protein rad21 homolog
Q6 159 8	146	20	16	53.71	225	26	22	62.25	371	26	22	0	62.2 5	Rab GDP dissociation inhibitor beta
Q6 159 9	61	6	6	48.5	109	9	9	53	170	10	10	0	53	Rho GDP-dissociation inhibitor 2
Q6 163 5	0	0	0		6	4	4	13.33	6	4	4	0.6 6	13.3 3	GTP-binding protein
Q6 164 6	176	12	12	42.65	239	17	17	56.77	415	17	17	0	56.7 7	Haptoglobin
Q6 165 5	0	0	0		5	2	2	7.74	5	2	2	3.3	7.74	ATP-dependent RNA helicase DDX19A
Q6 165 6	33	6	2	11.89	35	7	3	15.15	68	7	3	1.1 9	15.1 5	Probable ATP- dependent RNA helicase DDX5
Q6 168 6	2	2	2	13.61	2	1	1	6.81	4	3	3	1.1 9	20.4 2	Chromobox protein homolog 5
Q6 175 3	8	2	2	3.94	33	6	6	14.63	41	6	6	0.4 7	14.6 3	D-3-phosphoglycerate dehydrogenase
Q6 176 8	10	3	3	4.36	11	3	3	4.47	21	4	4	0.6 6	5.82	Kinesin-1 heavy chain
Q6 179 2	3	2	2	10.65	6	2	2	10.65	9	2	2	3.3	10.6 5	LIM and SH3 domain protein 1
Q6 180 5	2	2	2	9.77	13	3	3	12.06	15	3	3	1.1 9	12.0 6	Lipopolysaccharide- binding protein
Q6 183 8	3	1	1	1.07	77	25	24	27.49	80	25	24	0	27.4 9	Alpha-2-macroglobulin
Q6 188 1	16	4	4	8.48	10	4	4	8.9	26	6	6	0.4 7	13.3 5	DNA replication licensing factor MCM7
Q6 193 7	112	6	6	26.03	116	7	7	26.03	228	7	7	0	26.0 3	Nucleophosmin
Q6 199 0	30	3	1	12.15	36	4	2	16.57	66	4	2	3.3	16.5 7	Poly(rC)-binding protein 2
Q6 209 3	9	2	2	11.31	27	2	2	11.31	36	2	2	3.3	11.3 1	Serine/arginine-rich splicing factor 2
Q6 216 7	31	6	5	12.08	26	7	6	14.65	57	8	7	0	16.4 7	ATP-dependent RNA helicase DDX3X
Q6 217 8	0	0	0		6	2	2	5.13	6	2	2	3.3	5.13	Semaphorin-4A
Q6 220 3	4	2	2	8.84	0	0	0		4	2	2	3.3	8.84	Splicing factor 3A subunit 2

Q6 226 1	128	32	31	22.77	145	26	26	17.77	273	38	37	0	26.6 6	Spectrin beta chain, non-erythrocytic 1
Q6 231 8	13	5	5	10.67	9	3	3	6.35	22	6	6	0.4 7	12.8 3	Transcription intermediary factor 1- beta
Q6 234 8	14	3	3	22.37	18	3	3	22.37	32	3	3	1.1 9	22.3 7	Translin
Q6 237 6	13	5	5	17.41	30	6	6	16.74	43	8	8	0	21.8 8	U1 small nuclear ribonucleoprotein 70 kDa
Q6 238 3	0	0	0		3	3	3	3.59	3	3	3	1.1 9	3.59	Transcription elongation factor SPT6
Q6 239 3	6	2	2	22.32	11	3	3	22.32	17	3	3	1.1 9	22.3 2	Tumor protein D52
Q6 241 8	24	6	6	22.94	22	6	6	22.02	46	7	7	0	25.2 3	Drebrin-like protein
Q6 242 2	19	4	4	29.77	59	7	7	37.21	78	7	7	0	37.2 1	Osteoclast-stimulating factor 1
Q6 243 1	0	0	0		7	2	2	4.66	7	2	2	3.3	4.66	AT-rich interactive domain-containing protein 3A
Q6 246 5	17	7	7	23.4	35	8	8	24.63	52	10	10	0	26.8 5	Synaptic vesicle membrane protein VAT-1 homolog
Q6 252 3	5	2	2	4.96	13	5	5	13.83	18	5	5	0.4 7	13.8 3	Zyxin
Q6 381 0	1	1	1	17.06	17	5	5	52.35	18	5	5	0.4 7	52.3 5	Calcineurin subunit B type 1
Q6 382 9	9	2	2	16.92	9	1	1	10.77	18	2	2	3.3	16.9 2	COMM domain- containing protein 3
Q6 384 4	48	9	7	34.47	72	9	6	33.68	120	10	7	0	36.5 8	Mitogen-activated protein kinase 3
Q6 391 8	0	0	0		3	2	2	5.98	3	2	2	3.3	5.98	Serum deprivation- response protein
Q6 401 2	8	2	2	9.94	16	3	3	13.78	24	3	3	1.1 9	13.7 8	RNA-binding protein Raly
Q6 415 2	5	3	3	33.82	25	4	4	33.82	30	4	4	0.6 6	33.8 2	Transcription factor BTF3
Q6 427 7	0	0	0		5	2	2	7.07	5	2	2	3.3	7.07	ADP-ribosyl cyclase/cyclic ADP- ribose hydrolase 2
Q6 432 4	17	5	5	11.8	45	6	6	15.51	62	7	7	0	18.2 1	Syntaxin-binding protein 2
Q6 443 3	0	0	0		2	2	2	21.57	2	2	2	3.3	21.5 7	10 kDa heat shock protein, mitochondrial
Q6 444 2	2	1	1	4.48	9	2	2	9.24	11	2	2	3.3	9.24	Sorbitol dehydrogenase
Q6 445 5	0	0	0		2	2	2	2.67	2	2	2	3.3	2.67	Receptor-type tyrosine- protein phosphatase eta
Q6 451 1	12	5	5	3.35	20	6	5	4.34	32	8	7	0	5.46	DNA topoisomerase 2- beta

<u>Q6</u> <u>451</u> <u>4</u>	21	6	6	8.95	52	16	16	19.18	73	17	17	0	19.9 7	Tripeptidyl-peptidase 2
<u>Q6</u> <u>467</u> <u>4</u>	2	1	1	4.3	9	4	4	18.21	11	5	5	0.4 7	18.2 1	Spermidine synthase
<u>Q6</u> <u>472</u> <u>7</u>	231	31	31	43.43	359	37	37	47.75	590	38	38	0	48.7 8	Vinculin
<u>Q6</u> <u>473</u> <u>7</u>	2	2	2	4.36	8	3	3	5.64	10	4	4	0.6 6	8.12	Trifunctional purine biosynthetic protein adenosine-3
<u>Q6</u> <u>8F</u> <u>D5</u>	539	51	51	44.06	459	59	59	50.15	998	63	63	0	51.7	Clathrin heavy chain 1
<u>Q6</u> <u>9Z</u> <u>K0</u>	4	3	3	4.12	6	2	2	2.55	10	5	5	0.4 7	6.67	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein
<u>Q6</u> <u>A0</u> <u>26</u>	5	3	3	4.73	3	1	1	1.05	8	3	3	1.1 9	4.73	Sister chromatid cohesion protein PDS5 homolog A
<u>Q6</u> <u>A0</u> <u>68</u>	4	3	3	6.11	0	0	0		4	3	3	1.1 9	6.11	Cell division cycle 5-like protein
<u>Q6</u> <u>A4</u> <u>J8</u>	36	10	10	15.59	56	14	14	19.49	92	17	17	0	23.7 5	Ubiquitin carboxyl-terminal hydrolase 7
<u>Q6</u> <u>BC</u> <u>L1</u>	2	2	2	4.3	1	1	1	1.93	3	3	3	1.1 9	6.22	PML-RARA-regulated adapter molecule 1
<u>Q6</u> <u>DT</u> <u>Y7</u>	7	4	4	10.45	11	3	3	7.25	18	4	4	0.6 6	10.4 5	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4
<u>Q6</u> <u>GS</u> <u>S7</u>	7241	50	16	70.77	5950	60	22	73.08	131 91	63	22	0	73.0 8	Histone H2A type 2-A
<u>Q6</u> <u>IR</u> <u>U2</u>	8	3	3	13.31	35	9	8	40.32	43	9	8	0	40.3 2	Tropomyosin alpha-4 chain
<u>Q6</u> <u>NS</u> <u>R8</u>	1	1	1	5.15	4	3	3	8.97	5	4	4	0.6 6	14.1 2	Probable aminopeptidase NPEPL1
<u>Q6</u> <u>NX</u> <u>H9</u>	15	1	0	2.23	22	3	2	6.49	37	3	2	3.3	6.49	Keratin, type II cytoskeletal 73
<u>Q6</u> <u>P0</u> <u>69</u>	33	6	6	33.84	94	11	10	48.48	127	12	11	0	48.4 8	Sorcin
<u>Q6</u> <u>P1</u> <u>B1</u>	5	3	3	9.63	21	4	4	13.96	26	5	5	0.4 7	15.4 1	Xaa-Pro aminopeptidase 1
<u>Q6</u> <u>P2</u> <u>B1</u>	9	5	5	9.86	22	6	6	15.93	31	8	8	0	18.9 6	Transportin-3
<u>Q6</u> <u>P4</u> <u>T2</u>	136	28	28	20.08	108	23	23	17.09	244	33	33	0	23.7 8	U5 small nuclear ribonucleoprotein 200 kDa helicase
<u>Q6</u> <u>P5</u> <u>E4</u>	97	19	19	23.28	200	31	31	33.66	297	32	32	0	34.6 2	UDP-glucose:glycoprotein glucosyltransferase 1
<u>Q6</u> <u>P5</u> <u>F9</u>	63	14	14	20.07	144	19	19	27.64	207	20	20	0	28.7 6	Exportin-1
<u>Q6</u> <u>P8</u> <u>K8</u>	0	0	0		3	2	2	5.24	3	2	2	3.3	5.24	Carboxypeptidase A4

<u>Q6</u> <u>PA</u> <u>V2</u>	1	1	1	2.18	4	2	2	3.5	5	2	2	3.3	3.5	Probable E3 ubiquitin-protein ligase HERC4
<u>Q6</u> <u>PD</u> <u>O3</u>	19	7	7	17.9	43	9	9	25.72	62	11	11	0	30.45	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform
<u>Q6</u> <u>PD</u> <u>G5</u>	17	2	1	2.72	5	2	2	3.3	22	3	2	3.3	4.29	SWI/SNF complex subunit SMARCC2
<u>Q6</u> <u>PD</u> <u>I5</u>	12	4	4	4.51	16	6	6	6.96	28	8	8	0	9.02	Proteasome-associated protein ECM29 homolog
<u>Q6</u> <u>PD</u> <u>M2</u>	15	4	4	23.79	24	4	4	23.79	39	4	4	0.66	23.79	Serine/arginine-rich splicing factor 1
<u>Q6</u> <u>PD</u> <u>Q2</u>	24	10	10	8.83	39	7	7	7	63	11	11	0	10.08	Chromodomain-helicase-DNA-binding protein 4
<u>Q6</u> <u>PE</u> <u>O1</u>	4	2	2	10.89	4	1	1	3.07	8	2	2	3.3	10.89	U5 small nuclear ribonucleoprotein 40 kDa protein
<u>Q6</u> <u>PE</u> <u>B6</u>	5	2	2	23.11	4	2	2	23.11	9	2	2	3.3	23.11	MOB-like protein phocein
<u>Q6</u> <u>PH</u> <u>U5</u>	0	0	0		5	2	2	2.91	5	2	2	3.3	2.91	Sortilin
<u>Q6</u> <u>Q8</u> <u>99</u>	3	2	2	5.08	7	3	3	6.26	10	4	4	0.66	8.42	Probable ATP-dependent RNA helicase DDX58
<u>Q6</u> <u>QI</u> <u>O6</u>	1	1	1	0.47	2	2	2	0.53	3	2	2	3.3	0.53	Rapamycin-insensitive companion of mTOR
<u>Q6</u> <u>UR</u> <u>W6</u>	40	6	2	3.6	47	8	2	4.05	87	8	2	3.3	4.05	Myosin-14
<u>Q6</u> <u>W</u> <u>VG3</u>	41	5	5	20.8	44	6	6	24.16	85	7	7	0	30.58	BTB/POZ domain-containing protein KCTD12
<u>Q6</u> <u>ZQ</u> <u>38</u>	65	11	11	15.04	51	9	9	13.17	116	12	12	0	16.59	Cullin-associated NEDD8-dissociated protein 1
<u>Q6</u> <u>ZQ</u> <u>A0</u>	40	10	10	5.87	31	9	9	6.13	71	13	13	0	8.28	Neurobeachin-like protein 2
<u>Q6</u> <u>ZQ</u> <u>K5</u>	10	3	3	6.49	7	4	4	8.83	17	5	5	0.47	11.3	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2
<u>Q6</u> <u>Z</u> <u>W</u> <u>M4</u>	2	1	1	16.67	12	2	2	41.67	14	2	2	3.3	41.67	U6 snRNA-associated Sm-like protein LSM8
<u>Q6</u> <u>Z</u> <u>W</u> <u>N5</u>	12	3	3	12.37	4	1	1	4.12	16	3	3	1.19	12.37	40S ribosomal protein S9
<u>Q6</u> <u>Z</u> <u>W</u> <u>Q0</u>	2	2	2	0.42	2	1	1	0.25	4	3	3	1.19	0.67	Nesprin-2
<u>Q6</u> <u>Z</u> <u>W</u> <u>Q9</u>	100	11	3	63.95	136	14	4	79.65	236	15	5	0.47	79.65	MCG5400
<u>Q6</u> <u>Z</u> <u>Z</u>	100	36	36	6.81	56	19	19	3.47	156	42	42	0	7.83	Nesprin-1

<u>W</u> <u>R6</u>														
<u>Q6</u> <u>Z</u> <u>W</u> <u>X6</u>	8	1	1	3.81	12	4	4	19.37	20	4	4	0.6 6	19.3 7	Eukaryotic translation initiation factor 2 subunit 1
<u>Q7</u> <u>6M</u> <u>Z3</u>	145	15	13	38.71	153	18	16	44.82	298	20	17	0	48.5 6	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
<u>Q7</u> <u>8P</u> <u>Y7</u>	23	8	8	17.03	52	13	13	22.53	75	15	15	0	23.9 6	Staphylococcal nuclease domain- containing protein 1
<u>Q7</u> <u>8Z</u> <u>A7</u>	19	4	4	15.2	26	4	4	15.2	45	4	4	0.6 6	15.2	Nucleosome assembly protein 1-like 4
<u>Q7</u> <u>92</u> <u>Z1</u>	17	2	2	18.7	16	3	3	23.17	33	3	3	1.1 9	23.1 7	MCG140784
<u>Q7</u> <u>M6</u> <u>Y3</u>	3	1	1	3.03	6	3	3	6.82	9	3	3	1.1 9	6.82	Phosphatidylinositol- binding clathrin assembly protein
<u>Q7</u> <u>TM</u> <u>B8</u>	26	8	2	7.58	18	5	2	4.79	44	8	2	3.3	7.58	Cytoplasmic FMR1- interacting protein 1
<u>Q7</u> <u>TM</u> <u>K9</u>	7	3	3	6.74	6	2	2	4.65	13	3	3	1.1 9	6.74	Heterogeneous nuclear ribonucleoprotein Q
<u>Q7</u> <u>TM</u> <u>M9</u>	188	16	1	48.31	234	23	2	58.43	422	23	2	3.3	58.4 3	Tubulin beta-2A chain
<u>Q7</u> <u>TN</u> <u>G5</u>	11	3	3	8.17	18	4	4	11.25	29	4	4	0.6 6	11.2 5	Echinoderm microtubule-associated protein-like 2
<u>Q7</u> <u>TN</u> <u>P2</u>	40	3	1	8.49	30	4	2	11.98	70	5	2	3.3	13.9 8	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform
<u>Q7</u> <u>TN</u> <u>V0</u>	24	5	5	16.32	39	5	5	16.32	63	5	5	0.4 7	16.3 2	Protein DEK
<u>Q7</u> <u>TP</u> <u>D0</u>	4	2	2	4.13	1	1	1	1.63	5	2	2	3.3	4.13	Integrator complex subunit 3
<u>Q7</u> <u>TP</u> <u>R4</u>	572	43	26	59.42	654	55	38	76.01	122 6	57	38	0	76.0 1	Alpha-actinin-1
<u>Q7</u> <u>TP</u> <u>V4</u>	3	2	2	2.98	19	6	6	6.92	22	7	7	0	8.41	Myb-binding protein 1A
<u>Q7</u> <u>TQ</u> <u>I3</u>	16	2	2	11.07	17	5	5	19.56	33	5	5	0.4 7	19.5 6	Ubiquitin thioesterase OTUB1
<u>Q7</u> <u>TSI</u> <u>3</u>	7	5	4	12.5	8	5	4	12.97	15	6	5	0.4 7	15.6 5	Serine/threonine-protein phosphatase 6 regulatory subunit 1
<u>Q7</u> <u>TS</u> <u>V4</u>	5	1	1	2.9	11	2	2	4.84	16	2	2	3.3	4.84	Phosphoglucosylase-2
<u>Q8</u> <u>0U</u> <u>G5</u>	10	4	4	8.4	1	1	1	3.09	11	4	4	0.6 6	8.4	Septin-9
<u>Q8</u> <u>0U</u> <u>M3</u>	14	1	1	3.24	14	3	3	7.4	28	3	3	1.1 9	7.4	N-alpha- acetyltransferase 15, NatA auxiliary subunit
<u>Q8</u> <u>0U</u> <u>R4</u>	0	0	0		25	3	3	12.89	25	3	3	1.1 9	12.8 9	Mast cell protease-11

<u>Q8</u> <u>0W</u> <u>S3</u>	2	1	1	3.5	5	2	2	7.01	7	2	2	3.3	7.01	rRNA/tRNA 2'-O-methyltransferase fibrillar-like protein 1
<u>Q8</u> <u>0X</u> <u>41</u>	12	5	5	17.05	33	6	6	19.09	45	6	6	0.4 7	19.0 9	Serine/threonine-protein kinase VRK1
<u>Q8</u> <u>0X</u> <u>90</u>	39	6	4	3.61	16	4	2	2.34	55	7	5	0.4 7	4.38	Filamin-B
<u>Q8</u> <u>10</u> <u>B6</u>	14	5	5	7.53	6	2	2	4.45	20	6	6	0.4 7	10.0 9	Rabankyrin-5
<u>Q8</u> <u>BF</u> <u>Q4</u>	4	2	2	10.22	10	2	2	10.86	14	3	3	1.1 9	14.7	WD repeat-containing protein 82
<u>Q8</u> <u>BF</u> <u>Y6</u>	5	1	1	11.27	34	4	4	24.73	39	4	4	0.6 6	24.7 3	Peflin
<u>Q8</u> <u>BF</u> <u>Y9</u>	5	3	3	3.9	22	8	8	14.03	27	10	10	0	16.4 8	Transportin-1
<u>Q8</u> <u>BF</u> <u>Z3</u>	2606	47	7	53.72	2125	73	12	63.03	473 1	75	12	0	63.0 3	Beta-actin-like protein 2
<u>Q8</u> <u>BG</u> <u>05</u>	59	8	7	26.39	61	10	8	28.5	120	11	9	0	29.8 2	Heterogeneous nuclear ribonucleoprotein A3
<u>Q8</u> <u>BG</u> <u>32</u>	47	9	9	30.57	55	9	9	32.94	102	10	10	0	35.7 8	26S proteasome non-ATPase regulatory subunit 11
<u>Q8</u> <u>BG</u> <u>48</u>	2	2	2	7.8	0	0	0		2	2	2	3.3	7.8	Serine/threonine-protein kinase 17B
<u>Q8</u> <u>BG</u> <u>A3</u>	2	2	2	3.5	0	0	0		2	2	2	3.3	3.5	Leucine-rich repeat transmembrane neuronal protein 2
<u>Q8</u> <u>BG</u> <u>Q7</u>	18	6	6	11.98	34	9	9	17.46	52	10	10	0	19.2 1	Alanine--tRNA ligase, cytoplasmic
<u>Q8</u> <u>BH</u> <u>43</u>	9	2	2	6.44	3	1	1	3.82	12	2	2	3.3	6.44	Wiskott-Aldrich syndrome protein family member 2
<u>Q8</u> <u>BH</u> <u>59</u>	0	0	0		2	2	2	7.24	2	2	2	3.3	7.24	Calcium-binding mitochondrial carrier protein Aralar1
<u>Q8</u> <u>BH</u> <u>61</u>	81	13	13	25	35	9	9	19.54	116	13	13	0	25	Coagulation factor XIII A chain
<u>Q8</u> <u>BH</u> <u>69</u>	5	2	2	11.22	8	3	3	17.09	13	4	4	0.6 6	22.9 6	Selenide, water dikinase 1
<u>Q8</u> <u>BH</u> <u>D7</u>	39	6	6	30.02	32	3	2	12.43	71	7	6	0.4 7	31.5 5	Polypyrimidine tract-binding protein 3
<u>Q8</u> <u>BH</u> <u>G1</u>	18	9	9	12.92	40	9	9	14.9	58	12	12	0	17.3 1	Nardilysin
<u>Q8</u> <u>BH</u> <u>N3</u>	39	9	9	16.84	65	19	19	28.39	104	21	21	0	33.5 8	Neutral alpha-glucosidase AB
<u>Q8</u> <u>BI</u> <u>Q5</u>	2	2	2	7.07	0	0	0		2	2	2	3.3	7.07	Cleavage stimulation factor subunit 2
<u>Q8</u> <u>BJ</u> <u>S4</u>	8	4	4	7.25	25	5	5	8.48	33	6	6	0.4 7	10.4	SUN domain-containing protein 2
<u>Q8</u> <u>BJ</u> <u>Y1</u>	25	9	9	32.54	26	5	5	13.89	51	10	10	0	33.3 3	26S proteasome non-ATPase regulatory subunit 5

<u>Q8</u> <u>BK</u> <u>67</u>	8	2	2	9.62	28	6	6	17.88	36	7	7	0	23.8 5	Protein RCC2
<u>Q8</u> <u>BK</u> <u>C5</u>	91	18	18	25.71	160	25	25	34.37	251	27	27	0	38.0 1	Importin-5
<u>Q8</u> <u>BL</u> <u>97</u>	18	3	3	11.24	38	4	4	15.73	56	4	4	0.6 6	15.7 3	Serine/arginine-rich splicing factor 7
<u>Q8</u> <u>B</u> <u>MJ</u> <u>2</u>	11	3	3	4.07	9	3	3	4.41	20	4	4	0.6 6	5.18	Leucine--tRNA ligase, cytoplasmic
<u>Q8</u> <u>B</u> <u>M</u> <u>K4</u>	2	2	2	6.26	0	0	0		2	2	2	3.3	6.26	Cytoskeleton-associated protein 4
<u>Q8</u> <u>B</u> <u>ML</u> <u>9</u>	6	3	3	7.61	4	3	3	7.1	10	4	4	0.6 6	9.16	Glutamyl-tRNA synthetase
<u>Q8</u> <u>B</u> <u>MS</u> <u>1</u>	3	3	3	8.78	5	4	4	11.27	8	5	5	0.4 7	13.5	Trifunctional enzyme subunit alpha, mitochondrial
<u>Q8</u> <u>BN</u> <u>D5</u>	2	2	2	3.61	56	6	6	11.63	58	6	6	0.4 7	11.6 3	Sulfhydryl oxidase 1
<u>Q8</u> <u>BP</u> <u>47</u>	33	8	8	18.07	62	10	10	24.69	95	10	10	0	24.6 9	Asparagine--tRNA ligase, cytoplasmic
<u>Q8</u> <u>BP</u> <u>U7</u>	47	11	11	30.67	34	6	6	22.7	81	11	11	0	30.6 7	Engulfment and cell motility protein 1
<u>Q8</u> <u>BR</u> <u>F7</u>	0	0	0		4	3	3	8.92	4	3	3	1.1 9	8.92	Sec1 family domain- containing protein 1
<u>Q8</u> <u>BT</u> <u>60</u>	10	3	3	7.32	45	10	9	25.52	55	10	9	0	25.5 2	Copine-3
<u>Q8</u> <u>BT</u> <u>M8</u>	876	77	75	45.26	885	101	99	51.91	176 1	105	103	0	53	Filamin-A
<u>Q8</u> <u>BT</u> <u>Z7</u>	10	5	5	21.11	18	3	3	12.22	28	5	5	0.4 7	21.1 1	Mannose-1-phosphate guanylttransferase beta
<u>Q8</u> <u>BU</u> <u>30</u>	15	7	7	9.83	12	3	3	4.04	27	7	7	0	9.83	Isoleucine--tRNA ligase, cytoplasmic
<u>Q8</u> <u>BU</u> <u>V3</u>	3	1	1	2.21	4	3	3	9.62	7	3	3	1.1 9	9.62	Gephyrin
<u>Q8</u> <u>BV</u> <u>13</u>	9	1	1	6.82	8	2	2	11.74	17	2	2	3.3	11.7 4	COP9 signalosome complex subunit 7b
<u>Q8</u> <u>BV</u> <u>E3</u>	11	3	3	12.42	10	4	4	15.32	21	5	5	0.4 7	19.6 7	V-type proton ATPase subunit H
<u>Q8</u> <u>BV</u> <u>G4</u>	7	3	3	6.15	9	4	4	7.08	16	4	4	0.6 6	7.08	Dipeptidyl peptidase 9
<u>Q8</u> <u>B</u> <u>W</u> <u>T1</u>	24	8	8	40.55	49	8	8	38.79	73	9	9	0	43.8 3	3-ketoacyl-CoA thiolase, mitochondrial
<u>Q8</u> <u>B</u> <u>W</u> <u>U5</u>	0	0	0		5	2	2	11.34	5	2	2	3.3	11.3 4	Probable tRNA N6- adenosine threonylcarbamoyltrans ferase

<u>Q8</u> <u>B</u> <u>W</u> <u>Y3</u>	4	1	1	2.75	13	5	5	17.39	17	5	5	0.4 7	17.3 9	Eukaryotic peptide chain release factor subunit 1
<u>Q8</u> <u>BY</u> <u>71</u>	1	1	1	4.33	11	3	3	11.78	12	3	3	1.1 9	11.7 8	Histone acetyltransferase type B catalytic subunit
<u>Q8</u> <u>BY</u> <u>A0</u>	2	1	1	1.84	2	2	2	3.6	4	3	3	1.1 9	5.43	Tubulin-specific chaperone D
<u>Q8</u> <u>BY</u> <u>C6</u>	1	1	1	0.89	3	3	3	3.56	4	3	3	1.1 9	3.56	Serine/threonine-protein kinase TAO3
<u>Q8</u> <u>BZ</u> <u>05</u>	2	2	2	1.23	5	1	1	0.59	7	2	2	3.3	1.23	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 2
<u>Q8</u> <u>C0</u> <u>C7</u>	11	2	2	8.66	18	3	3	9.45	29	4	4	0.6 6	15.3 5	Phenylalanine--tRNA ligase alpha subunit
<u>Q8</u> <u>C0</u> <u>E2</u>	21	7	6	30.65	40	8	7	29.46	61	10	9	0	39.5 8	Vacuolar protein sorting-associated protein 26B
<u>Q8</u> <u>C0</u> <u>I1</u>	0	0	0		5	2	2	5.27	5	2	2	3.3	5.27	Alkylldihydroxyacetone phosphate synthase, peroxisomal
<u>Q8</u> <u>C0</u> <u>L9</u>	5	3	3	8	0	0	0		5	3	3	1.1 9	8	Glycerophosphocholine phosphodiesterase GPCPD1
<u>Q8</u> <u>C0</u> <u>P5</u>	2	2	2	4.2	2	1	1	2.1	4	2	2	3.3	4.2	Coronin-2A
<u>Q8</u> <u>C1</u> <u>47</u>	28	11	11	8.57	37	11	11	8.95	65	15	15	0	12.2 9	Dedicator of cytokinesis protein 8
<u>Q8</u> <u>C1</u> <u>66</u>	6	2	2	5.41	20	4	3	8.77	26	4	3	1.1 9	8.77	Copine-1
<u>Q8</u> <u>C1</u> <u>A5</u>	3	2	2	5.09	5	2	2	6.4	8	3	3	1.1 9	9.17	Thimet oligopeptidase
<u>Q8</u> <u>C1</u> <u>B7</u>	7	3	1	8.58	16	4	2	13.23	23	5	2	3.3	15.5 5	Septin-11
<u>Q8</u> <u>C2</u> <u>K1</u>	9	2	2	4.92	1	1	1	1.75	10	2	2	3.3	4.92	Differentially expressed in FDCP 6
<u>Q8</u> <u>C3</u> <u>J5</u>	27	11	11	7.49	16	8	8	7.88	43	15	15	0	12.5 3	Dedicator of cytokinesis protein 2
<u>Q8</u> <u>C7</u> <u>R4</u>	1	1	1	1.42	2	2	2	2.75	3	2	2	3.3	2.75	Ubiquitin-like modifier-activating enzyme 6
<u>Q8</u> <u>CA</u> <u>Q8</u>	0	0	0		6	2	2	5.15	6	2	2	3.3	5.15	MICOS complex subunit Mic60
<u>Q8</u> <u>CC</u> <u>86</u>	8	2	2	7.62	31	6	6	20.45	39	6	6	0.4 7	20.4 5	Nicotinate phosphoribosyltransferase
<u>Q8</u> <u>CC</u> <u>K0</u>	167	7	3	14.78	168	14	6	14.78	335	14	6	0.4 7	14.7 8	Core histone macro-H2A.2
<u>Q8</u> <u>CD</u> <u>N6</u>	21	4	4	19.38	15	3	3	20.76	36	5	5	0.4 7	27.3 4	Thioredoxin-like protein 1
<u>Q8</u> <u>CF</u> <u>I7</u>	6	3	3	4	0	0	0		6	3	3	1.1 9	4	DNA-directed RNA polymerase II subunit RPB2

<u>Q8</u> <u>CF</u> <u>Q3</u>	3	2	2	2.43	1	1	1	1.28	4	2	2	3.3	2.43	Intron-binding protein aquarius
<u>Q8</u> <u>CG</u> <u>29</u>	53	7	7	10.38	46	10	10	15.94	99	10	10	0	15.9 4	Myosin IF
<u>Q8</u> <u>CG</u> <u>47</u>	1	1	1	1.32	4	2	2	2.18	5	3	3	1.1 9	3.5	Structural maintenance of chromosomes protein 4
<u>Q8</u> <u>CG</u> <u>C7</u>	38	13	13	14.22	50	13	13	14.48	88	16	16	0	18.0 6	Bifunctional glutamate/proline-- tRNA ligase
<u>Q8</u> <u>CG</u> <u>K3</u>	11	3	3	8.64	6	4	4	8.75	17	4	4	0.6 6	8.75	Lon protease homolog, mitochondrial
<u>Q8</u> <u>CG</u> <u>P0</u>	1700	21	2	56.35	1434	27	3	56.35	313 4	28	3	1.1 9	56.3 5	Histone H2B type 3-B
<u>Q8</u> <u>CG</u> <u>P4</u>	2635	21	1	56.59	1931	29	5	60.47	456 6	32	5	0.4 7	60.4 7	Histone H2A
<u>Q8</u> <u>CG</u> <u>Y8</u>	1	1	1	1.91	4	2	2	2.87	5	2	2	3.3	2.87	UDP-N- acetylglucosamine-- peptide N- acetylglucosaminyltrans ferase 110 kDa subunit
<u>Q8</u> <u>CH</u> <u>P8</u>	2	2	2	9.66	6	2	2	9.66	8	2	2	3.3	9.66	Phosphoglycolate phosphatase
<u>Q8</u> <u>CI</u> <u>4</u>	53	10	5	14.47	85	16	8	18.74	138	16	8	0	18.7 4	Glycogen phosphorylase, brain form
<u>Q8</u> <u>CI</u> <u>E6</u>	65	15	15	19.85	26	9	9	12.5	91	15	15	0	19.8 5	Coatomer subunit alpha
<u>Q8</u> <u>CI</u> <u>H5</u>	114	21	21	26.8	157	29	28	33.91	271	30	29	0	34.6 2	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2
<u>Q8</u> <u>CI</u> <u>N4</u>	18	5	5	20.23	28	5	5	15.65	46	8	8	0	27.2 9	Serine/threonine-protein kinase PAK 2
<u>Q8</u> <u>CI</u> <u>Z8</u>	27	10	10	6.15	95	18	18	10.81	122	18	18	0	10.8 1	von Willebrand factor
<u>Q8</u> <u>CJ</u> <u>G0</u>	7	4	4	6.4	11	4	4	7.09	18	6	6	0.4 7	10.1 2	Protein argonaute-2
<u>Q8</u> <u>JZ</u> <u>Q9</u>	78	15	15	28.39	57	12	12	26.53	135	18	18	0	36.3 6	Eukaryotic translation initiation factor 3 subunit B
<u>Q8</u> <u>JZ</u> <u>V7</u>	6	2	2	6.85	0	0	0		6	2	2	3.3	6.85	Putative N- acetylglucosamine-6- phosphate deacetylase
<u>Q8</u> <u>K0</u> <u>E8</u>	74	8	8	24.74	139	13	13	35.14	213	13	13	0	35.1 4	Fibrinogen beta chain
<u>Q8</u> <u>K1</u> <u>B8</u>	140	23	23	47.67	167	28	28	56.54	307	30	30	0	58.2	Fermitin family homolog 3
<u>Q8</u> <u>K1</u> <u>M6</u>	5	4	4	10.51	19	4	4	10.11	24	5	5	0.4 7	12.8	Dynamin-1-like protein
<u>Q8</u> <u>K1</u> <u>X4</u>	42	8	8	13.49	29	4	4	8.38	71	8	8	0	13.4 9	NCK associated protein 1 like
<u>Q8</u> <u>K2</u> <u>H4</u>	2	2	2	4.05	0	0	0		2	2	2	3.3	4.05	Arf-GAP with coiled- coil, ANK repeat and

														PH domain-containing protein 1
<u>Q8</u> <u>K2</u> <u>J0</u>	3	1	1	4.33	2	2	2	5.73	5	2	2	3.3	5.73	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-3
<u>Q8</u> <u>K2</u> <u>Q0</u>	11	2	2	16.67	4	2	2	16.67	15	2	2	3.3	16.67	COMM domain-containing protein 9
<u>Q8</u> <u>K2</u> <u>T1</u>	0	0	0		4	2	2	7.77	4	2	2	3.3	7.77	NmrA-like family domain-containing protein 1
<u>Q8</u> <u>K2</u> <u>Z4</u>	9	3	3	4.31	12	4	4	5.82	21	5	5	0.47	7.26	Condensin complex subunit 1
<u>Q8</u> <u>K4</u> <u>I1</u>	6	2	2	3.57	7	2	2	3.57	13	2	2	3.3	3.57	Presequence protease, mitochondrial
<u>Q8</u> <u>K4</u> <u>Z6</u>	32	3	3	31.62	39	5	5	32.48	71	5	5	0.47	32.48	Myeloid cysteine-rich protein
<u>Q8</u> <u>K4</u> <u>82</u>	21	5	5	7.91	95	13	13	18.25	116	13	13		18.25	EMILIN-2
<u>Q8</u> <u>K4</u> <u>I3</u>	3	2	2	5.58	2	1	1	1.43	5	3	3	1.19		Rho guanine nucleotide exchange factor 6
<u>Q8</u> <u>K4</u> <u>Z5</u>	21	4	4	8.6	5	2	2	3.54	26	4	4	0.66	8.6	Splicing factor 3A subunit 1
<u>Q8</u> <u>QZ</u> <u>W8</u>	20	3	3	10.36	6	2	2	7.4	26	3	3	1.19	10.36	Protein Arhgap9
<u>Q8</u> <u>QZ</u> <u>Y1</u>	63	12	12	31.74	84	17	17	40.78	147	17	17		40.78	Eukaryotic translation initiation factor 3 subunit L
<u>Q8</u> <u>QZ</u> <u>Y6</u>	0	0	0		4	2	2	10.37	4	2	2	3.3	10.37	Tetraspanin-14
<u>Q8</u> <u>QZ</u> <u>Y9</u>	37	4	4	18.4	43	6	6	27.36	80	6	6	0.47	27.36	Splicing factor 3B subunit 4
<u>Q8</u> <u>R0</u> <u>01</u>	4	2	2	9.82	0	0	0		4	2	2	3.3	9.82	Microtubule-associated protein RP/EB family member 2
<u>Q8</u> <u>R0</u> <u>10</u>	7	3	3	21.88	7	4	4	33.12	14	4	4	0.66	33.12	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2
<u>Q8</u> <u>R0</u> <u>16</u>	58	8	8	35.82	84	10	10	42.2	142	10	10	0	42.2	Bleomycin hydrolase
<u>Q8</u> <u>R0</u> <u>81</u>	159	7	7	23.21	101	9	9	31.23	260	10	10		33.62	Heterogeneous nuclear ribonucleoprotein L
<u>Q8</u> <u>R0</u> <u>J7</u>	1	1	1	6.32	5	3	3	21.75	6	3	3	1.19	21.75	Vacuolar protein sorting-associated protein 37B
<u>Q8</u> <u>R1</u> <u>46</u>	28	9	9	22.68	57	11	11	26.91	85	12	12	0	28.42	Acylamino-acid-releasing enzyme
<u>Q8</u> <u>R1</u> <u>80</u>	7	3	3	9.27	31	6	6	16.16	38	6	6	0.47	16.16	ERO1-like protein alpha
<u>Q8</u> <u>R1</u> <u>B4</u>	30	8	8	12.4	55	11	11	15.92	85	13	13	0	16.9	Eukaryotic translation initiation factor 3 subunit C

<u>Q8</u> <u>R1</u> <u>Q8</u>	29	7	7	22.94	9	2	2	7.65	38	7	7	0	22.9 4	Cytoplasmic dynein 1 light intermediate chain 1
<u>Q8</u> <u>R1</u> <u>S0</u>	4	2	2	2.1	4	2	2	2.1	8	2	2	3.3	2.1	Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial
<u>Q8</u> <u>R2</u> <u>H9</u>	7	2	2	12.73	6	1	1	7.87	13	2	2	3.3	12.7 3	Phosphoethanolamine/p hosphocholine phosphatase
<u>Q8</u> <u>R2</u> <u>S8</u>	65	9	9	13.1	116	13	13	22.64	181	14	14	0	24.1 1	CD177 antigen
<u>Q8</u> <u>R4</u> <u>K2</u>	2	2	2	6.75	3	1	1	3.7	5	2	2	3.3	6.75	Interleukin-1 receptor- associated kinase 4
<u>Q8</u> <u>R5</u> <u>A3</u>	12	4	4	12.09	2	2	2	4.78	14	5	5	0.4 7	13.4 3	Amyloid beta A4 precursor protein- binding family B member 1-interacting protein
<u>Q8</u> <u>R5</u> <u>C5</u>	22	5	1	21.01	17	6	2	28.46	39	6	2	3.3	28.4 6	Beta-centractin
<u>Q8</u> <u>R5</u> <u>H1</u>	3	2	2	4.59	1	1	1	3.26	4	3	3	1.1 9	7.85	Ubiquitin carboxyl- terminal hydrolase 15
<u>Q8</u> <u>R5</u> <u>L1</u>	27	3	3	27.24	47	5	5	32.26	74	5	5	0.4 7	32.2 6	Complement component 1 Q subcomponent-binding protein, mitochondrial
<u>Q8</u> <u>VB</u> <u>V3</u>	6	2	2	11.26	4	2	2	11.26	10	2	2	3.3	11.2 6	Exosome complex component RRP4
<u>Q8</u> <u>VB</u> <u>V7</u>	6	2	2	17.22	16	4	4	30.14	22	4	4	0.6 6	30.1 4	COP9 signalosome complex subunit 8
<u>Q8</u> <u>VC</u> <u>03</u>	6	3	3	5.02	0	0	0		6	3	3	1.1 9	5.02	Echinoderm microtubule-associated protein-like 3
<u>Q8</u> <u>VC</u> <u>30</u>	2	2	2	6.57	2	1	1	2.94	4	2	2	3.3	6.57	Bifunctional ATP- dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)
<u>Q8</u> <u>VC</u> <u>88</u>	29	6	6	39.55	62	10	9	57.27	91	10	9	0	57.2 7	Grancalcin
<u>Q8</u> <u>VC</u> <u>I0</u>	12	2	2	5.82	25	5	5	16.18	37	5	5	0.4 7	16.1 8	Phospholipase B-like 1
<u>Q8</u> <u>VC</u> <u>M7</u>	92	8	8	27.29	130	13	13	43.58	222	13	13	0	43.5 8	Fibrinogen gamma chain
<u>Q8</u> <u>VC</u> <u>T3</u>	5	3	3	9.54	30	9	9	25.23	35	10	10	0	25.3 8	Aminopeptidase B
<u>Q8</u> <u>VD</u> <u>D5</u>	1002	72	68	43.62	1063	104	98	53.11	206 5	108	102	0	54.1 8	Myosin-9
<u>Q8</u> <u>VD</u> <u>L4</u>	5	1	1	3.02	30	4	4	15.32	35	4	4	0.6 6	15.3 2	ADP-dependent glucokinase
<u>Q8</u> <u>VD</u> <u>M4</u>	213	25	25	45.48	250	29	29	49.56	463	30	30	0	49.5 6	26S proteasome non- ATPase regulatory subunit 2
<u>Q8</u> <u>VD</u> <u>M6</u>	21	4	4	7.22	17	2	2	3.96	38	4	4	0.6 6	7.22	Heterogeneous nuclear ribonucleoprotein U- like protein 1

<u>Q8</u> <u>VD</u> <u>P3</u>	2	1	1	1.43	3	2	2	2.58	5	2	2	3.3	2.58	Protein-methionine sulfoxide oxidase MICAL1
<u>Q8</u> <u>VD</u> <u>P4</u>	18	4	4	8.46	12	2	2	3.58	30	4	4	0.6 6	8.46	Cell cycle and apoptosis regulator protein 2
<u>Q8</u> <u>VD</u> <u>W0</u>	40	8	3	21.55	58	7	3	18.74	98	8	3	1.1 9	21.5 5	ATP-dependent RNA helicase DDX39A
<u>Q8</u> <u>VE</u> <u>37</u>	23	3	3	9.98	11	4	4	14.01	34	4	4	0.6 6	14.0 1	Regulator of chromosome condensation
<u>Q8</u> <u>VE</u> <u>K3</u>	41	7	7	18.38	33	6	6	13.38	74	8	8	0	19.3 8	Heterogeneous nuclear ribonucleoprotein U
<u>Q8</u> <u>VI</u> <u>93</u>	2	1	1	1.32	2	2	2	3.51	4	2	2	3.3	3.51	2'-5'-oligoadenylate synthase 3
<u>Q8</u> <u>VI</u> <u>6</u>	9	6	6	11.3	14	7	7	14.59	23	9	9	0	17.6	Splicing factor, proline- and glutamine-rich
<u>Q9</u> <u>IV</u> <u>12</u>	6	3	3	8.92	33	5	5	20.21	39	5	5	0.4 7	20.2 1	Cytosolic acyl coenzyme A thioester hydrolase
<u>Q9</u> <u>IV</u> <u>41</u>	12	4	3	32.56	22	5	4	39.53	34	5	4	0.6 6	39.5 3	Ras-related protein Rab-14
<u>Q9</u> <u>IV</u> <u>55</u>	7	2	2	13.73	13	2	2	13.73	20	2	2	3.3	13.7 3	40S ribosomal protein S5
<u>Q9</u> <u>IV</u> <u>89</u>	1	1	1	2.19	5	3	3	7.41	6	3	3	1.1 9	7.41	Protein Ppp2r5d
<u>Q9</u> <u>IV</u> <u>92</u>	139	21	21	30.06	191	23	23	32.72	330	25	25	0	34.9 2	ATP-citrate synthase
<u>Q9</u> <u>IV</u> <u>A7</u>	3	2	2	8.59	1	1	1	2.6	4	3	3	1.1 9	11.2	Isocitrate dehydrogenase [NAD] subunit, mitochondrial
<u>Q9</u> <u>IV</u> <u>C3</u>	37	7	6	20.44	56	8	7	28.95	93	11	10	0	35.2 8	Eukaryotic initiation factor 4A-III
<u>Q9</u> <u>IV</u> <u>H6</u>	11	2	2	16.84	9	3	3	16.16	20	4	4	0.6 6	26.6	Protein MEMO1
<u>Q9</u> <u>IV</u> <u>I7</u>	20	6	6	22.15	39	8	8	30.26	59	8	8	0	30.2 6	Ribonuclease inhibitor
<u>Q9</u> <u>IV</u> <u>W3</u>	5	1	1	20.43	20	4	4	46.24	25	4	4	0.6 6	46.2 4	SH3 domain-binding glutamic acid-rich-like protein 3
<u>Q9</u> <u>IV</u> <u>89</u>	5	3	3	3.46	3	2	2	2.31	8	4	4	0.6 6	4.72	Alpha-mannosidase 2C1
<u>Q9</u> <u>IV</u> <u>K2</u>	20	4	4	19.6	40	10	10	50	60	10	10	0	50	Eukaryotic translation initiation factor 3 subunit H
<u>Q9</u> <u>IV</u> <u>Q3</u>	6	3	3	6.82	13	4	4	11.36	19	5	5	0.4 7	13.4 5	Tyrosine--tRNA ligase, cytoplasmic
<u>Q9</u> <u>IX</u> <u>72</u>	9	3	3	6.74	59	13	13	34.13	68	13	13	0	34.1 3	Hemopexin
<u>Q9</u> <u>IX</u> <u>L1</u>	25	5	5	15.79	40	5	5	17.84	65	6	6	0.4 7	20.7 6	Leucine-rich HEV glycoprotein
<u>Q9</u> <u>IX</u> <u>E6</u>	10	4	4	9.32	30	6	6	13.74	40	6	6	0.4 7	13.7 4	Importin-9

<u>Q9</u> <u>1Y</u> <u>10</u>	12	2	2	6.25	14	5	5	20.47	26	5	5	0.4 7	20.4 7	Argininosuccinate lyase
<u>Q9</u> <u>1Y</u> <u>14</u>	24	7	7	29.76	26	4	4	13.66	50	8	8	0	32.9 3	Beta-arrestin-2
<u>Q9</u> <u>1Y</u> <u>P3</u>	30	8	8	37.74	32	10	10	44.65	62	11	11	0	49.6 9	Deoxyribose-phosphate aldolase
<u>Q9</u> <u>1Y</u> <u>Q5</u>	0	0	0		2	2	2	5.59	2	2	2	3.3	5.59	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
<u>Q9</u> <u>1Y</u> <u>R9</u>	35	4	4	27.66	66	8	8	42.55	101	8	8	0	42.5 5	Prostaglandin reductase 1
<u>Q9</u> <u>1Z</u> <u>50</u>	21	4	4	21.05	25	5	5	23.95	46	5	5	0.4 7	23.9 5	Flap endonuclease 1
<u>Q9</u> <u>1Z</u> <u>98</u>	103	6	1	22.39	80	7	2	24.38	183	7	2	3.3	24.3 8	Chitinase-like protein 4
<u>Q9</u> <u>1Z</u> <u>5</u>	39	11	11	33.66	60	15	15	42.91	99	16	16	0	44.6 9	UTP--glucose-1-phosphate uridylyltransferase
<u>Q9</u> <u>1Z</u> <u>R2</u>	5	2	2	11.07	6	2	2	11.07	11	2	2	3.3	11.0 7	Sorting nexin-18
<u>Q9</u> <u>1Z</u> <u>W3</u>	7	3	3	3.52	7	2	2	2.57	14	3	3	1.1 9	3.52	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5
<u>Q9</u> <u>20</u> <u>B9</u>	14	4	4	6.02	12	2	2	4.11	26	5	5	0.4 7	7.64	FACT complex subunit SPT16
<u>Q9</u> <u>20</u> <u>E5</u>	9	3	3	14.45	76	11	11	60.06	85	11	11	0	60.0 6	Farnesyl pyrophosphate synthase
<u>Q9</u> <u>21</u> <u>F2</u>	21	4	4	15.94	21	5	5	21.26	42	5	5	0.4 7	21.2 6	TAR DNA-binding protein 43
<u>Q9</u> <u>21</u> <u>F4</u>	7	2	2	5.25	5	2	2	5.25	12	2	2	3.3	5.25	Heterogeneous nuclear ribonucleoprotein L-like
<u>Q9</u> <u>21</u> <u>G6</u>	4	1	1	2.5	10	2	2	5.44	14	2	2	3.3	5.44	Leucine-rich repeat and calponin homology domain-containing protein 4
<u>Q9</u> <u>21</u> <u>H8</u>	0	0	0		8	3	3	14.86	8	3	3	1.1 9	14.8 6	3-ketoacyl-CoA thiolase A, peroxisomal
<u>Q9</u> <u>21I</u> <u>1</u>	94	14	14	23.82	125	22	22	35.44	219	24	24	0	36.4 4	Serotransferrin
<u>Q9</u> <u>21I</u> <u>2</u>	0	0	0		4	2	2	6.85	4	2	2	3.3	6.85	Kelch domain-containing protein 4
<u>Q9</u> <u>21</u> <u>M3</u>	122	25	25	29.99	173	27	27	38.46	295	31	31	0	42.0 7	Splicing factor 3B subunit 3
<u>Q9</u> <u>21</u> <u>M7</u>	32	7	7	39.51	44	6	6	34.88	76	7	7	0	39.5 1	Protein FAM49B
<u>Q9</u> <u>22</u> <u>B2</u>	37	9	9	26.95	39	10	10	24.95	76	13	13	0	35.3 3	Aspartate--tRNA ligase, cytoplasmic

<u>Q922D4</u>	7	4	3	8.29	20	5	4	10.66	27	6	5	0.47	12.2	Serine/threonine-protein phosphatase 6 regulatory subunit 3
<u>Q922D8</u>	12	5	5	6.95	20	5	5	7.06	32	6	6	0.47	8.24	C-1-tetrahydrofolate synthase, cytoplasmic
<u>Q922F4</u>	87	9	1	24.83	87	14	2	32.44	174	14	2	3.3	32.44	Tubulin beta-6 chain
<u>Q922H4</u>	9	3	3	12.86	9	3	3	12.86	18	3	3	1.19	12.86	Mannose-1-phosphate guanylttransferase alpha
<u>Q922P9</u>	6	2	2	6.59	2	1	1	3.48	8	2	2	3.3	6.59	Putative oxidoreductase GLYR1
<u>Q922R8</u>	29	5	5	17.5	55	9	9	28.41	84	9	9	0	28.41	Protein disulfide-isomerase A6
<u>Q922S4</u>	28	11	11	22.27	46	9	9	19.21	74	12	12	0	23.36	cGMP-dependent 3',5'-cyclic phosphodiesterase
<u>Q923D4</u>	10	2	2	32.56	7	3	3	43.02	17	3	3	1.19	43.02	Splicing factor 3B subunit 5
<u>Q923T9</u>	6	3	3	8.88	2	1	1	1.7	8	3	3	1.19	8.88	Calcium/calmodulin-dependent protein kinase type II subunit gamma
<u>Q924B0</u>	15	4	4	20.94	16	4	4	20.94	31	5	5	0.47	24.91	Inositol (Myo)-1(Or 4)-monophosphatase 1
<u>Q924K8</u>	2	1	1	2.88	5	2	2	4.74	7	3	3	1.19	7.61	Metastasis-associated protein MTA3
<u>Q93092</u>	48	7	7	23.74	92	13	13	31.75	140	13	13	0	31.75	Transaldolase
<u>Q99020</u>	24	4	4	15.09	55	7	7	27.72	79	7	7	0	27.72	Heterogeneous nuclear ribonucleoprotein A/B
<u>Q99109</u>	2	2	2	6.14	0	0	0		2	2	2	3.3	6.14	Methylosome protein 50
<u>Q99177</u>	3	2	2	9.19	1	1	1	3.9	4	3	3	1.19	13.09	N-acetylneuraminic acid synthase (Sialic acid synthase)
<u>Q99199</u>	4	2	2	7.41	6	4	4	15.49	10	4	4	0.66	15.49	3-mercaptopyruvate sulfurtransferase
<u>Q991B2</u>	0	0	0		5	2	2	7.93	5	2	2	3.3	7.93	Stomatin-like protein 2, mitochondrial
<u>Q991F5</u>	0	0	0		3	2	2	9.23	3	2	2	3.3	9.23	Diphosphomevalonate decarboxylase
<u>Q991F8</u>	1	1	1	3.22	3	3	3	6.06	4	3	3	1.19	6.06	PC4 and SFRS1-interacting protein
<u>Q991I4</u>	59	10	10	32.9	60	11	11	32.39	119	13	13	0	41.39	26S proteasome non-ATPase regulatory subunit 6
<u>Q991I6</u>	45	6	6	50.54	54	8	8	49.46	99	9	9	0	57.61	Ras-related protein Rap-1b
<u>Q991X4</u>	84	9	9	38.5	77	10	10	43.58	161	10	10	0	43.58	Eukaryotic translation initiation factor 3 subunit M

Q9 9J Y9	490	22	22	65.31	422	26	26	72.25	912	27	27	0	72.4 9	Actin-related protein 3
Q9 9K 48	17	3	3	11.84	35	4	4	13.74	52	4	4	0.6 6	13.7 4	Non-POU domain- containing octamer- binding protein
Q9 9K 85	0	0	0		9	4	4	17.03	9	4	4	0.6 6	17.0 3	Phosphoserine aminotransferase
Q9 9K E1	54	7	7	22.07	72	10	10	29.88	126	11	11	0	31.5 8	NAD-dependent malic enzyme, mitochondrial
Q9 9K H8	6	2	2	5.34	10	4	4	12.3	16	4	4	0.6 6	12.3	Serine/threonine-protein kinase 24
Q9 9K J0	41	7	7	14.36	36	7	7	14.1	77	9	9	0	18.0 8	Aconitate hydratase, mitochondrial
Q9 9K J8	38	8	8	33.08	19	4	4	15.17	57	8	8	0	33.0 8	Dynactin subunit 2
Q9 9K K7	19	4	4	10.84	30	6	6	17.75	49	6	6	0.4 7	17.7 5	Dipeptidyl peptidase 3
Q9 9K P6	23	6	6	25.79	27	6	6	28.17	50	7	7	0	35.1 2	Pre-mRNA-processing factor 19
Q9 9K Q4	0	0	0		24	4	4	12.63	24	4	4	0.6 6	12.6 3	Nicotinamide phosphoribosyltransfera se
Q9 9K V1	1	1	1	4.47	15	4	4	17.88	16	4	4	0.6 6	17.8 8	DnaJ homolog subfamily B member 11
Q9 9L 45	13	5	5	22.66	9	4	4	19.94	22	6	6	0.4 7	29.3 1	Eukaryotic translation initiation factor 2 subunit 2
Q9 9L B4	53	7	7	26.07	93	8	8	29.51	146	8	8	0	29.5 1	Capping protein (Actin filament), gelsolin-like
Q9 9L C5	11	4	4	23.42	10	4	4	23.12	21	5	5	0.4 7	28.2 3	Electron transfer flavoprotein subunit alpha, mitochondrial
Q9 9L D4	12	3	3	15.29	14	2	2	11.89	26	3	3	1.1 9	15.2 9	COP9 signalosome complex subunit 1
Q9 9L I7	0	0	0		3	2	2	4.04	3	2	2	3.3	4.04	Cleavage stimulation factor subunit 3
Q9 9L T0	18	2	2	36.36	21	2	2	36.36	39	2	2	3.3	36.3 6	Protein dpy-30 homolog
Q9 9L X0	2	1	1	10.05	21	2	2	24.34	23	2	2	3.3	24.3 4	Protein deglycase DJ-1
Q9 9M K8	3	1	1	3.34	10	5	5	14.08	13	5	5	0.4 7	14.0 8	Beta-adrenergic receptor kinase 1
Q9 9M N1	1	1	1	3.7	32	7	7	22.18	33	7	7	0	22.1 8	Lysine--tRNA ligase
Q9 9M R6	6	2	2	4.46	1	1	1	2.97	7	2	2	3.3	4.46	Serrate RNA effector molecule homolog
Q9 9N B9	81	12	12	16.72	78	13	13	18.56	159	16	16	0	22.3 2	Splicing factor 3B subunit 1
Q9 9P 58	4	2	2	10.09	4	2	2	10.09	8	2	2	3.3	10.0 9	Ras-related protein Rab-27B

<u>Q9</u> <u>9P</u> <u>T1</u>	24	3	3	23.04	50	5	5	29.9	74	5	5	0.4 7	29.9	Rho GDP-dissociation inhibitor 1
<u>Q9</u> <u>9P</u> <u>V0</u>	83	17	17	13.15	73	16	16	11.61	156	23	23	0	16.2 7	Pre-mRNA-processing-splicing factor 8
<u>Q9</u> <u>CP</u> <u>N9</u>	12	1	1	4.45	11	2	2	4.86	23	2	2	3.3	4.86	Protein 2210010C04Rik
<u>Q9</u> <u>CP</u> <u>R4</u>	7	2	2	16.3	8	2	2	16.3	15	2	2	3.3	16.3	60S ribosomal protein L17
<u>Q9</u> <u>CP</u> <u>W4</u>	100	8	8	61.59	92	9	9	62.25	192	9	9	0	62.2 5	Actin-related protein 2/3 complex subunit 5
<u>Q9</u> <u>CP</u> <u>X6</u>	0	0	0		2	2	2	7.32	2	2	2	3.3	7.32	Ubiquitin-like-conjugating enzyme ATG3
<u>Q9</u> <u>CP</u> <u>Y7</u>	3	2	2	6.55	6	3	3	10.6	9	3	3	1.1 9	10.6	Cytosol aminopeptidase
<u>Q9</u> <u>CQ</u> <u>19</u>	60	10	3	62.21	98	12	3	68.02	158	14	5	0.4 7	68.0 2	Myosin regulatory light polypeptide 9
<u>Q9</u> <u>CQ</u> <u>80</u>	0	0	0		3	2	2	30.11	3	2	2	3.3	30.1 1	Vacuolar protein-sorting-associated protein 25
<u>Q9</u> <u>CQ</u> <u>C6</u>	0	0	0		7	2	2	12.65	7	2	2	3.3	12.6 5	Basic leucine zipper and W2 domain-containing protein 1
<u>Q9</u> <u>CQ</u> <u>E1</u>	6	1	1	9.31	16	3	3	23.48	22	3	3	1.1 9	23.4 8	Protein NipSnap homolog 3B
<u>Q9</u> <u>CQ</u> <u>E8</u>	5	3	3	19.26	20	3	3	20.49	25	4	4	0.6 6	25.8 2	UPF0568 protein C14orf166 homolog
<u>Q9</u> <u>CQ</u> <u>I6</u>	19	3	3	35.92	29	3	3	35.92	48	3	3	1.1 9	35.9 2	Coactosin-like protein
<u>Q9</u> <u>CQ</u> <u>I7</u>	12	3	3	20	5	2	2	12	17	3	3	1.1 9	20	U2 small nuclear ribonucleoprotein B''
<u>Q9</u> <u>CQ</u> <u>M9</u>	3	2	2	7.42	5	2	2	7.42	8	2	2	3.3	7.42	Glutaredoxin-3
<u>Q9</u> <u>CQ</u> <u>R6</u>	15	4	4	19.34	21	5	5	28.2	36	5	5	0.4 7	28.2	Serine/threonine-protein phosphatase 6 catalytic subunit
<u>Q9</u> <u>CQ</u> <u>V8</u>	58	8	6	41.46	133	12	8	53.25	191	12	8	0	53.2 5	14-3-3 protein beta/alpha
<u>Q9</u> <u>CQ</u> <u>W9</u>	0	0	0		11	2	2	20.44	11	2	2	3.3	20.4 4	Interferon-induced transmembrane protein 3
<u>Q9</u> <u>CR</u> <u>16</u>	1	1	1	2.43	9	4	4	11.62	10	4	4	0.6 6	11.6 2	Peptidyl-prolyl cis-trans isomerase D
<u>Q9</u> <u>CR</u> <u>51</u>	9	2	2	23.73	13	2	2	26.27	22	3	3	1.1 9	26.2 7	V-type proton ATPase subunit G 1
<u>Q9</u> <u>CR</u> <u>57</u>	28	3	3	17.05	14	2	2	11.52	42	3	3	1.1 9	17.0 5	60S ribosomal protein L14
<u>Q9</u> <u>CR</u> <u>86</u>	1	1	1	24.32	4	2	2	35.14	5	2	2	3.3	35.1 4	Calcium-regulated heat stable protein 1
<u>Q9</u> <u>CR</u> <u>A5</u>	4	1	1	4.36	16	2	2	12.42	20	2	2	3.3	12.4 2	Golgi phosphoprotein 3

<u>Q9</u> <u>CS</u> <u>42</u>	7	1	1	5.35	12	2	2	10.06	19	2	2	3.3	10.0 6	Ribose-phosphate pyrophosphokinase 2
<u>Q9</u> <u>CS</u> <u>N1</u>	0	0	0		4	2	2	6.34	4	2	2	3.3	6.34	SNW domain- containing protein 1
<u>Q9</u> <u>CU</u> <u>62</u>	28	6	6	7.62	15	4	4	4.3	43	7	7	0	8.68	Structural maintenance of chromosomes protein 1A
<u>Q9</u> <u>CV</u> <u>B6</u>	400	25	25	74.67	391	31	31	80	791	32	32	0	80	Actin-related protein 2/3 complex subunit 2
<u>Q9</u> <u>C</u> <u>W0</u> <u>3</u>	32	13	13	15.78	20	7	7	9.12	52	13	13	0	15.7 8	Structural maintenance of chromosomes protein 3
<u>Q9</u> <u>C</u> <u>WJ</u> <u>9</u>	31	12	12	33.11	83	20	20	52.36	114	20	20	0	52.3 6	Bifunctional purine biosynthesis protein PURH
<u>Q9</u> <u>CX</u> <u>56</u>	8	3	3	15.3	6	2	2	13.03	14	3	3	1.1 9	15.3	26S proteasome non- ATPase regulatory subunit 8
<u>Q9</u> <u>CX</u> <u>W3</u>	0	0	0		5	2	2	13.1	5	2	2	3.3	13.1	Calcyclin-binding protein
<u>Q9</u> <u>CX</u> <u>W4</u>	18	2	2	12.92	12	2	2	12.92	30	2	2	3.3	12.9 2	60S ribosomal protein L11
<u>Q9</u> <u>CX</u> <u>Y6</u>	5	3	3	16.15	13	5	5	24.87	18	6	6	0.4 7	31.5 4	Interleukin enhancer- binding factor 2
<u>Q9</u> <u>CY</u> <u>50</u>	0	0	0		4	2	2	18.53	4	2	2	3.3	18.5 3	Translocon-associated protein subunit alpha
<u>Q9</u> <u>CY</u> <u>58</u>	6	1	1	3.93	14	2	2	7.86	20	2	2	3.3	7.86	Plasminogen activator inhibitor 1 RNA- binding protein
<u>Q9</u> <u>CY</u> <u>L5</u>	6	4	4	45.45	18	5	5	45.45	24	5	5	0.4 7	45.4 5	Golgi-associated plant pathogenesis-related protein 1
<u>Q9</u> <u>CZ</u> <u>13</u>	1	1	1	4.38	8	3	3	15.62	9	3	3	1.1 9	15.6 2	Cytochrome b-c1 complex subunit 1, mitochondrial
<u>Q9</u> <u>CZ</u> <u>30</u>	15	2	2	7.32	15	3	3	11.62	30	4	4	0.6 6	15.1 5	Obg-like ATPase 1
<u>Q9</u> <u>CZ</u> <u>44</u>	23	5	5	22.97	51	7	7	30.27	74	8	8	0	33.5 1	NSFL1 cofactor p47
<u>Q9</u> <u>CZ</u> <u>D3</u>	10	3	3	8.37	16	6	6	13.17	26	6	6	0.4 7	13.1 7	Glycine--tRNA ligase
<u>Q9</u> <u>CZ</u> <u>M2</u>	11	2	2	12.25	14	2	2	5.88	25	3	3	1.1 9	12.7 5	60S ribosomal protein L15
<u>Q9</u> <u>CZ</u> <u>N7</u>	20	5	4	19.84	31	7	6	24.01	51	8	7	0	27.5 8	Serine hydroxymethyltransfera se
<u>Q9</u> <u>CZ</u> <u>U3</u>	5	2	2	3.08	4	1	1	1.92	9	2	2	3.3	3.08	Superkiller viralicidic activity 2-like 2
<u>Q9</u> <u>CZ</u> <u>U6</u>	45	9	9	36.85	93	12	12	41.59	138	13	13	0	43.9 7	Citrate synthase, mitochondrial
<u>Q9</u> <u>CZ</u> <u>X8</u>	6	2	2	13.79	0	0	0		6	2	2	3.3	13.7 9	40S ribosomal protein S19

<u>Q9</u> <u>D0</u> <u>20</u>	5	2	2	7.55	10	6	6	30.21	15	6	6	0.4 7	30.2 1	Cytosolic 5'- nucleotidase 3A
<u>Q9</u> <u>D0</u> <u>51</u>	13	3	3	13.37	10	2	2	8.36	23	4	4	0.6 6	17.2 7	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial
<u>Q9</u> <u>D0</u> <u>71</u>	3	2	2	4.95	2	1	1	2.23	5	2	2	3.3	4.95	MMS19 nucleotide excision repair protein homolog
<u>Q9</u> <u>D0</u> <u>E1</u>	42	6	6	14.13	24	5	5	10.7	66	8	8	0	17.0 1	Heterogeneous nuclear ribonucleoprotein M
<u>Q9</u> <u>D0</u> <u>F9</u>	3	1	1	2.85	2	2	2	5.52	5	3	3	1.1 9	8.36	Phosphoglucumutase-1
<u>Q9</u> <u>D0</u> <u>I9</u>	15	4	4	9.39	26	9	9	20.3	41	10	10	0	23.3 3	Arginine--tRNA ligase, cytoplasmic
<u>Q9</u> <u>D0</u> <u>R2</u>	20	9	9	16.62	70	14	14	25.9	90	14	14	0	25.9	Threonine--tRNA ligase, cytoplasmic
<u>Q9</u> <u>D1</u> <u>54</u>	201	19	19	57.52	208	19	19	56.46	409	21	21	0	62.5 3	Leukocyte elastase inhibitor A
<u>Q9</u> <u>D1</u> <u>A2</u>	4	3	3	9.26	20	4	4	11.37	24	4	4	0.6 6	11.3 7	Cytosolic non-specific dipeptidase
<u>Q9</u> <u>D1</u> <u>K2</u>	0	0	0		6	3	3	40.34	6	3	3	1.1 9	40.3 4	V-type proton ATPase subunit F
<u>Q9</u> <u>D1</u> <u>Q6</u>	11	4	4	19.46	43	5	5	23.15	54	5	5	0.4 7	23.1 5	Endoplasmic reticulum resident protein 44
<u>Q9</u> <u>D2</u> <u>V7</u>	55	10	10	23.32	57	12	12	26.46	112	14	14	0	32.4 3	Coronin-7
<u>Q9</u> <u>D5</u> <u>54</u>	24	6	6	18.36	27	6	6	20.76	51	7	7	0	24.5 5	Splicing factor 3A subunit 3
<u>Q9</u> <u>D6</u> <u>62</u>	11	5	3	13.95	22	6	5	16.82	33	7	5	0.4 7	18.6 4	Protein transport protein Sec23B
<u>Q9</u> <u>D6</u> <u>F9</u>	177	18	4	55.86	225	21	4	57.88	402	21	4	0.6 6	57.8 8	Tubulin beta-4A chain
<u>Q9</u> <u>D6</u> <u>J6</u>	1	1	1	4.03	4	2	2	12.1	5	2	2	3.3	12.1	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial
<u>Q9</u> <u>D6</u> <u>R2</u>	11	4	4	14.75	40	5	5	21.04	51	5	5	0.4 7	21.0 4	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial
<u>Q9</u> <u>D6</u> <u>Y7</u>	1	1	1	6.87	4	2	2	14.16	5	3	3	1.1 9	21.0 3	Mitochondrial peptide methionine sulfoxide reductase
<u>Q9</u> <u>D6</u> <u>Z1</u>	11	4	4	12.41	10	3	3	9.14	21	4	4	0.6 6	12.4 1	Nucleolar protein 56
<u>Q9</u> <u>D7</u> <u>M1</u>	25	6	6	36.84	13	3	3	29.39	38	7	7	0	47.3 7	Glucose-induced degradation protein 8 homolog
<u>Q9</u> <u>D8</u> <u>19</u>	10	3	3	15.57	27	3	3	15.57	37	3	3	1.1 9	15.5 7	Inorganic pyrophosphatase
<u>Q9</u> <u>D8</u> <u>83</u>	1	1	1	7.53	12	2	2	12.97	13	2	2	3.3	12.9 7	Splicing factor U2AF 35 kDa subunit

<u>Q9</u> <u>D8</u> <u>B3</u>	0	0	0		5	2	2	13.39	5	2	2	3.3	13.3 9	Charged multivesicular body protein 4b
<u>Q9</u> <u>D8</u> <u>E6</u>	7	2	2	7.16	1	1	1	2.86	8	2	2	3.3	7.16	60S ribosomal protein L4
<u>Q9</u> <u>D8</u> <u>N0</u>	39	11	11	39.59	95	12	12	41.19	134	13	13	0	44.1 6	Elongation factor 1- gamma
<u>Q9</u> <u>D8</u> <u>W5</u>	62	9	9	28.29	28	7	7	17.98	90	11	11	0	30.2 6	26S proteasome non- ATPase regulatory subunit 12
<u>Q9</u> <u>D8</u> <u>Y7</u>	2	2	2	21.74	4	3	3	26.63	6	4	4	0.6 6	40.7 6	Tumor necrosis factor alpha-induced protein 8-like protein 2
<u>Q9</u> <u>D9</u> <u>O6</u>	30	10	10	24.64	27	6	6	12.03	57	12	12	0	27.9 4	Ubiquitin-like modifier- activating enzyme ATG7
<u>Q9</u> <u>D9</u> <u>64</u>	4	2	2	7.09	15	5	5	20.33	19	5	5	0.4 7	20.3 3	Glycine amidinotransferase, mitochondrial
<u>Q9</u> <u>DB</u> <u>O5</u>	1	1	1	5.08	4	2	2	9.49	5	2	2	3.3	9.49	Alpha-soluble NSF attachment protein
<u>Q9</u> <u>DB</u> <u>C7</u>	2	1	1	3.15	4	2	2	9.45	6	2	2	3.3	9.45	cAMP-dependent protein kinase type I- alpha regulatory subunit
<u>Q9</u> <u>DB</u> <u>G3</u>	125	19	12	28.5	182	26	17	41.62	307	28	18	0	43.0 1	AP-2 complex subunit beta
<u>Q9</u> <u>DB</u> <u>G5</u>	4	1	1	4.35	7	2	2	8.47	11	2	2	3.3	8.47	Perilipin-3
<u>Q9</u> <u>DB</u> <u>G6</u>	4	2	2	8.56	18	7	7	24.25	22	7	7	0	24.2 5	Dolichyl- diphosphooligosacchari de--protein glycosyltransferase subunit 2
<u>Q9</u> <u>DB</u> <u>J1</u>	56	11	11	59.06	133	16	16	69.29	189	16	16	0	69.2 9	Phosphoglycerate mutase 1
<u>Q9</u> <u>DB</u> <u>K7</u>	3	2	2	2.97	9	5	5	8.39	12	5	5	0.4 7	8.39	MCG18845, isoform CRA d
<u>Q9</u> <u>DB</u> <u>R7</u>	5	3	3	5.25	1	1	1	2.14	6	3	3	1.1 9	5.25	Protein phosphatase 1 regulatory subunit 12A
<u>Q9</u> <u>DB</u> <u>T5</u>	24	7	7	11.78	43	7	7	12.41	67	9	9	0	15.2 9	AMP deaminase 2
<u>Q9</u> <u>DB</u> <u>Z5</u>	9	4	4	24.31	29	4	4	26.61	38	5	5	0.4 7	31.6 5	Eukaryotic translation initiation factor 3 subunit K
<u>Q9</u> <u>DC</u> <u>C4</u>	5	2	2	10.95	2	1	1	4.01	7	2	2	3.3	10.9 5	Pyrroline-5-carboxylate reductase 3
<u>Q9</u> <u>DC</u> <u>C5</u>	19	5	5	39.34	27	5	5	39.34	46	5	5	0.4 7	39.3 4	Cbx3 protein
<u>Q9</u> <u>DC</u> <u>D0</u>	513	21	21	57.14	471	38	38	66.87	984	39	39	0	66.8 7	6-phosphogluconate dehydrogenase, decarboxylating
<u>Q9</u> <u>DC</u> <u>H4</u>	91	7	7	35.18	79	6	6	31.02	170	7	7	0	35.1 8	Eukaryotic translation initiation factor 3 subunit F
<u>Q9</u> <u>DC</u> <u>L9</u>	6	1	1	3.29	10	4	4	19.29	16	4	4	0.6 6	19.2 9	Multifunctional protein ADE2

<u>Q9</u> <u>DC</u> <u>X2</u>	0	0	0		5	2	2	21.74	5	2	2	3.3	21.7 4	ATP synthase subunit d, mitochondrial
<u>Q9</u> <u>EP</u> <u>K7</u>	6	2	2	2.48	7	2	2	3.31	13	3	3	1.1 9	4.78	Exportin-7
<u>Q9</u> <u>EP</u> <u>L8</u>	27	7	7	9.92	66	8	8	12.24	93	9	9	0	13.7 8	Importin-7
<u>Q9</u> <u>EP</u> <u>L9</u>	1	1	1	1.86	6	2	2	3.43	7	2	2	3.3	3.43	Peroxisomal acyl- coenzyme A oxidase 3
<u>Q9</u> <u>EQ</u> <u>G9</u>	6	3	3	9.78	4	3	3	11.22	10	4	4	0.6 6	14.2 6	Collagen type IV alpha- 3-binding protein
<u>Q9</u> <u>EQ</u> <u>H3</u>	107	19	19	36.56	150	19	19	31.78	257	23	23	0	40.3 3	Vacuolar protein sorting-associated protein 35
<u>Q9</u> <u>EQ</u> <u>I5</u>	5	2	2	20.35	17	2	2	20.35	22	2	2	3.3	20.3 5	Chemokine (C-X-C motif) ligand 7, isoform CRA b
<u>Q9</u> <u>EQ</u> <u>U5</u>	40	6	6	33.91	68	9	9	34.95	108	9	9	0	34.9 5	Protein SET
<u>Q9</u> <u>ER</u> <u>72</u>	14	4	4	8.9	42	9	9	18.53	56	9	9	0	18.5 3	Cysteine--tRNA ligase, cytoplasmic
<u>Q9</u> <u>ER</u> <u>D8</u>	11	5	5	21.75	35	5	5	23.26	46	6	6	0.4 7	27.1 9	Gamma-parvin
<u>Q9</u> <u>ER</u> <u>F3</u>	31	2	2	13.44	16	3	3	22.95	47	3	3	1.1 9	22.9 5	WD repeat-containing protein 61
<u>Q9</u> <u>ER</u> <u>K4</u>	110	8	8	13.7	87	12	12	21.11	197	13	13	0	22.4 5	Exportin-2
<u>Q9</u> <u>ER</u> <u>L7</u>	8	2	2	16.9	15	4	4	23.94	23	4	4	0.6 6	23.9 4	Glia maturation factor gamma
<u>Q9</u> <u>ES</u> <u>46</u>	2	1	1	3.84	5	2	2	8.77	7	2	2	3.3	8.77	Beta-parvin
<u>Q9</u> <u>ES</u> <u>52</u>	13	5	5	6.13	11	3	3	4.2	24	5	5	0.4 7	6.13	Phosphatidylinositol 3,4,5-trisphosphate 5- phosphatase 1
<u>Q9</u> <u>ES</u> <u>P1</u>	7	2	2	19.91	7	2	2	19.91	14	2	2	3.3	19.9 1	Stromal cell-derived factor 2-like protein 1
<u>Q9</u> <u>ES</u> <u>T5</u>	2	1	1	6.99	3	2	2	10.66	5	2	2	3.3	10.6 6	Acidic leucine-rich nuclear phosphoprotein 32 family member B
<u>Q9</u> <u>ES</u> <u>X5</u>	16	4	4	12.57	18	3	3	11	34	4	4	0.6 6	12.5 7	H/ACA ribonucleoprotein complex subunit 4
<u>Q9</u> <u>ET</u> <u>01</u>	1083	50	45	60.94	985	79	71	70.12	206 8	79	71	0	70.1 2	Glycogen phosphorylase, liver form
<u>Q9</u> <u>JHI</u> <u>5</u>	0	0	0		4	2	2	10.85	4	2	2	3.3	10.8 5	Isovaleryl-CoA dehydrogenase, mitochondrial
<u>Q9</u> <u>JHI</u> <u>0</u>	10	3	3	16.19	13	3	3	17.61	23	4	4	0.6 6	21.5 9	Tropomodulin-3
<u>Q9</u> <u>JH</u> <u>K5</u>	31	6	6	28	88	9	9	42.57	119	10	10	0	42.5 7	Pleckstrin
<u>Q9</u> <u>JH</u> <u>R7</u>	2	2	2	2.94	2	2	2	2.55	4	3	3	1.1 9	4.02	Insulin-degrading enzyme

<u>Q9</u> <u>JH</u> <u>U4</u>	184	46	46	16.21	109	28	28	9.88	293	50	50	0	17.3 1	Cytoplasmic dynein 1 heavy chain 1
<u>Q9</u> <u>JII</u> <u>0</u>	8	2	0	5.84	11	4	2	11.47	19	5	2	3.3	14.0 8	Serine/threonine-protein kinase 3
<u>Q9</u> <u>JII</u> <u>1</u>	16	4	2	12.11	17	4	2	12.32	33	6	3	1.1 9	18.2 8	Serine/threonine-protein kinase 4
<u>Q9</u> <u>JIA</u> <u>7</u>	0	0	0		3	2	2	6	3	2	2	3.3	6	Sphingosine kinase 2
<u>Q9</u> <u>JIF</u> <u>0</u>	17	4	4	14.56	21	4	4	14.56	38	4	4	0.6 6	14.5 6	Protein arginine N-methyltransferase 1
<u>Q9</u> <u>JIF</u> <u>7</u>	32	9	9	16.37	46	10	10	18.15	78	14	14	0	25.7 1	Coatmer subunit beta
<u>Q9</u> <u>JIG</u> <u>7</u>	4	2	2	5.42	3	2	2	4.78	7	3	3	1.1 9	6.86	Coiled-coil domain-containing protein 22
<u>Q9</u> <u>JII</u> <u>5</u>	8	2	2	7.64	9	1	1	3.94	17	2	2	3.3	7.64	DAZ-associated protein 1
<u>Q9</u> <u>JIY</u> <u>5</u>	4	2	2	6.11	6	2	2	9.61	10	3	3	1.1 9	12.8 8	Serine protease HTRA2, mitochondrial
<u>Q9</u> <u>JJ2</u> <u>8</u>	54	13	13	19.04	102	14	14	19.51	156	17	17	0	23.4 5	Protein flightless-1 homolog
<u>Q9</u> <u>JJU</u> <u>8</u>	5	2	2	27.19	1	1	1	11.4	6	2	2	3.3	27.1 9	SH3 domain-binding glutamic acid-rich-like protein
<u>Q9</u> <u>JK</u> <u>C8</u>	1	1	1	4.78	2	2	2	9.81	3	2	2	3.3	9.81	AP-3 complex subunit mu-1
<u>Q9</u> <u>JK</u> <u>F1</u>	720	70	68	53.41	784	80	79	57.75	150 4	88	86	0	59.9 9	Ras GTPase-activating-like protein IQGAP1
<u>Q9</u> <u>JK</u> <u>R6</u>	14	6	6	11.61	50	10	10	20.32	64	10	10	0	20.3 2	Hypoxia up-regulated protein 1
<u>Q9</u> <u>JL2</u> <u>6</u>	61	10	10	16.73	38	8	8	12.25	99	12	12	0	20.0 2	Formin-like protein 1
<u>Q9</u> <u>JLI</u> <u>8</u>	5	3	3	4.37	1	1	1	1.25	6	3	3	1.1 9	4.37	Squamous cell carcinoma antigen recognized by T-cells 3
<u>Q9</u> <u>JLJ</u> <u>2</u>	5	3	3	7.49	34	6	6	14.57	39	7	7	0	17.6 1	4-trimethylaminobutyraldehyde dehydrogenase
<u>Q9</u> <u>JL</u> <u>Q2</u>	3	2	2	6.07	5	1	1	2.54	8	2	2	3.3	6.07	ARF GTPase-activating protein GIT2
<u>Q9</u> <u>JL</u> <u>V5</u>	2	2	2	3.78	1	1	1	2.47	3	2	2	3.3	3.78	Cullin-3
<u>Q9</u> <u>JL</u> <u>V6</u>	99	15	15	50.57	120	19	19	52.68	219	19	19	0	52.6 8	Bifunctional polynucleotide phosphatase/kinase
<u>Q9</u> <u>JM</u> <u>14</u>	12	1	1	10.5	3	2	2	23	15	2	2	3.3	23	5'(3')-deoxyribonucleotidase, cytosolic type
<u>Q9</u> <u>JM</u> <u>76</u>	153	8	8	47.19	131	11	11	53.93	284	11	11	0	53.9 3	Actin-related protein 2/3 complex subunit 3
<u>Q9</u> <u>JM</u> <u>A1</u>	10	3	3	10.75	25	6	6	19.88	35	6	6	0.4 7	19.8 8	Ubiquitin carboxyl-terminal hydrolase 14

<u>Q9</u> <u>JM</u> <u>H6</u>	41	8	8	24.47	109	8	8	23.33	150	9	9	0	26.1	Thioredoxin reductase 1, cytoplasmic
<u>Q9</u> <u>JM</u> <u>H9</u>	8	4	4	3.8	8	3	3	3.07	16	4	4	0.6 6	3.8	Unconventional myosin-XVIIIa
<u>Q9</u> <u>QU</u> <u>G9</u>	1	1	1	2.8	4	2	2	6.74	5	2	2	3.3	6.74	RAS guanyl-releasing protein 2
<u>Q9</u> <u>QU</u> <u>H0</u>	24	2	2	38.32	34	3	3	38.32	58	3	3	1.1 9	38.3 2	Glutaredoxin-1
<u>Q9</u> <u>QU</u> <u>I0</u>	50	5	3	34.2	50	9	6	60.62	100	10	6	0.4 7	60.6 2	Transforming protein RhoA
<u>Q9</u> <u>QU</u> <u>M0</u>	58	11	11	19.07	133	22	22	38.72	191	22	22	0	38.7 2	Integrin alpha-IIb
<u>Q9</u> <u>QU</u> <u>M9</u>	117	10	10	46.75	99	13	13	52.85	216	13	13	0	52.8 5	Proteasome subunit alpha type-6
<u>Q9</u> <u>QU</u> <u>R6</u>	18	6	6	14.37	24	8	8	17.75	42	10	10	0	21.6 9	Prolyl endopeptidase
<u>Q9</u> <u>Q</u> <u>W</u> <u>R8</u>	0	0	0		2	2	2	7.47	2	2	2	3.3	7.47	Alpha-N-acetylgalactosaminidase
<u>Q9</u> <u>QX</u> <u>K3</u>	30	5	3	10.68	27	4	2	7.35	57	5	3	1.1 9	10.6 8	Coatomer subunit gamma-2
<u>Q9</u> <u>QX</u> <u>S1</u>	54	20	20	7.21	71	19	19	6.82	125	29	29	0	10.3 2	Plectin
<u>Q9</u> <u>QX</u> <u>Z0</u>	0	0	0		2	2	2	0.33	2	2	2	3.3	0.33	Microtubule-actin cross-linking factor 1
<u>Q9</u> <u>QY</u> <u>B5</u>	8	4	4	7.93	4	3	3	4.96	12	5	5	0.4 7	9.49	Gamma-adducin
<u>Q9</u> <u>QY</u> <u>C0</u>	26	3	3	6.67	15	3	3	5.58	41	4	4	0.6 6	8.03	Alpha-adducin
<u>Q9</u> <u>QZ</u> <u>88</u>	1	1	1	12.64	10	2	2	18.13	11	2	2	3.3	18.1 3	Vacuolar protein sorting-associated protein 29
<u>Q9</u> <u>QZ</u> <u>D9</u>	7	3	3	19.69	22	6	6	30.15	29	6	6	0.4 7	30.1 5	Eukaryotic translation initiation factor 3 subunit I
<u>Q9</u> <u>QZ</u> <u>E5</u>	45	8	6	15.22	61	11	9	23.57	106	11	9	0	23.5 7	Coatomer subunit gamma-1
<u>Q9</u> <u>QZ</u> <u>K7</u>	8	2	2	5.86	6	2	2	5.86	14	2	2	3.3	5.86	Docking protein 3
<u>Q9</u> <u>QZ</u> <u>Q8</u>	4822	42	26	65.05	3924	49	29	64.52	874 6	54	34	0	65.5 9	Core histone macro-H2A.1
<u>Q9</u> <u>R0</u> <u>62</u>	140	10	10	40.84	380	19	19	69.67	520	19	19	0	69.6 7	Glycogenin-1
<u>Q9</u> <u>R0</u> <u>N0</u>	19	4	4	19.13	15	3	3	14.29	34	4	4	0.6 6	19.1 3	Galactokinase
<u>Q9</u> <u>R0</u> <u>P3</u>	36	4	4	19.5	71	5	5	40.78	107	7	7	0	44.3 3	S-formylglutathione hydrolase

<u>Q9</u> <u>R0</u> <u>P5</u>	65	8	8	55.15	77	8	8	55.15	142	8	8	0	55.1 5	Dextrin
<u>Q9</u> <u>R0</u> <u>Q7</u>	2	2	2	18.12	8	2	2	18.12	10	2	2	3.3	18.1 2	Prostaglandin E synthase 3
<u>Q9</u> <u>R1</u> <u>I1</u>	191	20	20	50.66	223	23	23	72.69	414	26	26	0	72.6 9	Guanine deaminase
<u>Q9</u> <u>R1</u> <u>I2</u>	19	2	2	6.22	1	1	1	3.11	20	3	3	1.1 9	9.33	Sulfide:quinone oxidoreductase, mitochondrial
<u>Q9</u> <u>R1</u> <u>90</u>	9	2	2	4.94	17	4	4	7.63	26	4	4	0.6 6	7.63	Metastasis-associated protein MTA2
<u>Q9</u> <u>R1</u> <u>P0</u>	37	6	6	32.95	106	9	9	57.47	143	10	10	0	60.9 2	Proteasome subunit alpha type-4
<u>Q9</u> <u>R1</u> <u>P1</u>	66	7	7	40.49	65	7	7	40.49	131	7	7	0	40.4 9	Proteasome subunit beta type-3
<u>Q9</u> <u>R1</u> <u>P3</u>	89	8	8	55.22	143	12	12	75.62	232	13	13	0	79.6	Proteasome subunit beta type-2
<u>Q9</u> <u>R1</u> <u>P4</u>	64	11	11	50.57	101	13	13	53.61	165	14	14	0	53.9 9	Proteasome subunit alpha type-1
<u>Q9</u> <u>R1</u> <u>T2</u>	5	2	2	13.71	10	3	3	9.43	15	4	4	0.6 6	17.4 3	SUMO-activating enzyme subunit 1
<u>Q9</u> <u>R1</u> <u>T4</u>	16	6	4	22.81	8	3	1	11.29	24	7	4	0.6 6	25.3 5	Septin-6
<u>Q9</u> <u>R2</u> <u>S7</u>	2	2	2	18.95	0	0	0		2	2	2	3.3	18.9 5	Heme-binding protein 1
<u>Q9</u> <u>W</u> <u>TM</u> <u>5</u>	70	10	10	28.29	47	12	12	33.69	117	12	12	0	33.6 9	RuvB-like 2
<u>Q9</u> <u>W</u> <u>TX</u> <u>5</u>	14	4	4	44.79	26	3	3	27.61	40	4	4	0.6 6	44.7 9	S-phase kinase- associated protein 1
<u>Q9</u> <u>W</u> <u>TX</u> <u>6</u>	3	3	3	6.19	8	3	3	5.93	11	5	5	0.4 7	10.5 7	Cullin-1
<u>Q9</u> <u>W</u> <u>U0</u> <u>0</u>	4	1	1	7.75	13	2	2	10.14	17	2	2	3.3	10.1 4	Nuclear respiratory factor 1
<u>Q9</u> <u>W</u> <u>U2</u> <u>8</u>	4	1	1	11.69	25	3	3	33.77	29	3	3	1.1 9	33.7 7	Prefoldin subunit 5
<u>Q9</u> <u>W</u> <u>U7</u> <u>8</u>	105	12	12	25.43	115	15	15	31.07	220	17	17	0	32.4 5	Programmed cell death 6-interacting protein
<u>Q9</u> <u>W</u> <u>UA</u> <u>2</u>	10	5	5	9.17	8	3	3	8.32	18	6	6	0.4 7	13.9 2	Phenylalanine--tRNA ligase beta subunit
<u>Q9</u> <u>W</u> <u>UA</u> <u>3</u>	6	2	1	5.1	12	3	2	7.27	18	3	2	3.3	7.27	ATP-dependent 6- phosphofructokinase, platelet type

<u>Q9</u> <u>W</u> <u>U</u> <u>M3</u>	13	4	4	19.21	29	6	6	21.49	42	6	6	0.4 7	21.4 9	Coronin-1B
<u>Q9</u> <u>W</u> <u>U</u> <u>M4</u>	18	4	4	16.03	42	6	6	20.89	60	6	6	0.4 7	20.8 9	Coronin-1C
<u>Q9</u> <u>W</u> <u>UP</u> <u>7</u>	8	3	3	12.46	2	1	1	4.26	10	3	3	1.1 9	12.4 6	Ubiquitin carboxyl-terminal hydrolase isozyme L5
<u>Q9</u> <u>W</u> <u>V3</u> <u>2</u>	141	9	9	32.8	153	13	13	41.94	294	13	13	0	41.9 4	Actin-related protein 2/3 complex subunit 1B
<u>Q9</u> <u>W</u> <u>VA</u> <u>3</u>	11	3	3	11.96	15	5	5	23.62	26	6	6	0.4 7	25.7 7	Mitotic checkpoint protein BUB3
<u>Q9</u> <u>W</u> <u>VA</u> <u>4</u>	34	5	5	29.65	58	9	9	56.78	92	9	9	0	56.7 8	Transgelin-2
<u>Q9</u> <u>W</u> <u>VG</u> <u>5</u>	4	2	2	7.6	38	8	8	22	42	8	8	0	22	Endothelial lipase
<u>Q9</u> <u>W</u> <u>VJ</u> <u>2</u>	42	7	7	34.84	73	11	11	47.87	115	12	12	0	51.0 6	26S proteasome non-ATPase regulatory subunit 13
<u>Q9</u> <u>W</u> <u>VK</u> <u>4</u>	77	19	19	48.5	106	22	22	58.43	183	24	24	0	60.6 7	EH domain-containing protein 1
<u>Q9</u> <u>W</u> <u>VQ</u> <u>5</u>	0	0	0		10	3	3	19.09	10	3	3	1.1 9	19.0 9	Methylthioribulose-1-phosphate dehydratase
<u>Q9</u> <u>Z0</u> <u>E6</u>	1	1	1	2.55	2	2	2	5.77	3	2	2	3.3	5.77	Interferon-induced guanylate-binding protein 2
<u>Q9</u> <u>Z0</u> <u>H4</u>	3	2	2	9.84	1	1	1	7.09	4	2	2	3.3	9.84	CUGBP Elav-like family member 2
<u>Q9</u> <u>Z0I</u> <u>7</u>	0	0	0		16	3	3	13.06	16	3	3	1.1 9	13.0 6	Protein Slfn1
<u>Q9</u> <u>Z0</u> <u>M6</u>	7	3	3	6.85	14	4	4	8.07	21	4	4	0.6 6	8.07	CD97 antigen
<u>Q9</u> <u>Z0</u> <u>N1</u>	23	5	5	20.55	37	6	6	26.27	60	7	7	0	29.6 6	Eukaryotic translation initiation factor 2 subunit 3, X-linked
<u>Q9</u> <u>Z0</u> <u>P5</u>	20	6	6	31.23	56	7	7	38.11	76	7	7	0	38.1 1	Twinfilin-2
<u>Q9</u> <u>Z1</u> <u>10</u>	5	2	2	3.77	6	1	1	1.51	11	2	2	3.3	3.77	Delta-1-pyrroline-5-carboxylate synthase
<u>Q9</u> <u>Z1</u> <u>26</u>	6	1	1	8.57	26	4	4	46.67	32	4	4	0.6 6	46.6 7	Platelet factor 4
<u>Q9</u> <u>Z1</u> <u>83</u>	256	20	20	44.74	109	16	16	37.09	365	22	22	0	49.8 5	Protein-arginine deiminase type-4

<u>Q9</u> <u>Z1</u> <u>B7</u>	0	0	0		6	3	3	13.93	6	3	3	1.1 9	13.9 3	Mitogen-activated protein kinase 13
<u>Q9</u> <u>Z1</u> <u>D1</u>	13	4	4	16.88	9	3	3	16.88	22	4	4	0.6 6	16.8 8	Eukaryotic translation initiation factor 3 subunit G
<u>Q9</u> <u>Z1</u> <u>E4</u>	49	10	10	23.04	46	11	11	24.53	95	14	14	0	30.4 9	Glycogen [starch] synthase, muscle
<u>Q9</u> <u>Z1</u> <u>F9</u>	9	4	4	11.91	25	5	5	16.14	34	5	5	0.4 7	16.1 4	SUMO-activating enzyme subunit 2
<u>Q9</u> <u>Z1</u> <u>G3</u>	5	1	1	4.19	13	4	4	22.77	18	4	4	0.6 6	22.7 7	V-type proton ATPase subunit C 1
<u>Q9</u> <u>Z1</u> <u>N5</u>	51	8	3	26.87	79	10	6	35.28	130	11	6	0.4 7	38.0 8	Spliceosome RNA helicase Ddx39b
<u>Q9</u> <u>Z1</u> <u>Q5</u>	84	9	9	55.6	119	16	16	70.95	203	16	16	0	70.9 5	Chloride intracellular channel protein 1
<u>Q9</u> <u>Z1</u> <u>Q9</u>	54	9	9	13.7	71	13	13	19.64	125	13	13	0	19.6 4	Valine--tRNA ligase
<u>Q9</u> <u>Z1</u> <u>R9</u>	34	2	2	9.76	23	1	1	8.13	57	2	2	3.3	9.76	MCG124046
<u>Q9</u> <u>Z1</u> <u>T1</u>	1	1	1	1.18	6	2	2	2.35	7	2	2	3.3	2.35	AP-3 complex subunit beta-1
<u>Q9</u> <u>Z1</u> <u>Z2</u>	6	3	3	13.71	8	3	3	13.43	14	4	4	0.6 6	18	Serine-threonine kinase receptor-associated protein
<u>Q9</u> <u>Z2</u> <u>04</u>	5	2	2	3.83	8	3	3	10.54	13	4	4	0.6 6	10.5 4	Heterogeneous nuclear ribonucleoproteins C1/C2
<u>Q9</u> <u>Z2</u> <u>D6</u>	8	2	2	8.06	13	2	2	8.06	21	2	2	3.3	8.06	Methyl-CpG-binding protein 2
<u>Q9</u> <u>Z2</u> <u>9</u>	1	1	1	5.62	4	2	2	9.5	5	2	2	3.3	9.5	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial
<u>Q9</u> <u>Z2</u> <u>L7</u>	5	1	1	3.17	11	2	2	8.14	16	2	2	3.3	8.14	Cytokine receptor-like factor 3
<u>Q9</u> <u>Z2</u> <u>N8</u>	3	3	3	14.69	3	1	1	6.99	6	3	3	1.1 9	14.6 9	Actin-like protein 6A
<u>Q9</u> <u>Z2</u> <u>U0</u>	84	8	8	39.11	120	10	10	47.18	204	10	10	0	47.1 8	Proteasome subunit alpha type-7
<u>Q9</u> <u>Z2</u> <u>U1</u>	105	10	10	45.23	149	10	10	45.23	254	10	10	0	45.2 3	Proteasome subunit alpha type-5
<u>Q9</u> <u>Z2</u> <u>W0</u>	79	6	6	23.26	83	11	11	37	162	11	11	0	37	Aspartyl aminopeptidase
<u>Q9</u> <u>Z2</u> <u>X1</u>	47	4	3	16.87	30	6	5	24.58	77	6	5	0.4 7	24.5 8	Heterogeneous nuclear ribonucleoprotein F
<u>V9</u> <u>GX</u> <u>06</u>	81	3	1	19.67	39	5	3	27.32	120	5	3	1.1 9	27.3 2	Protein Gm11214 (Fragment)

Table S2- GG modified peptides identified from conventional (CON) and inflammatory (INF) exosomal proteins

Protein	Sample	GG modified Peptide	Mods	m/z	MW	Min FDR
A0A087WR50	CON	GPMKEINLSPDSSSVIVSGLMVATK	M3:+15.995,M21:+15.995,K25:+114.043	135 3.68 9	270 5.36 2	0.05 668 8
A0A087WR50	CON	GHCVTDSGVVSVGMQWLKSQGNK	C3:+45.988,M15:+15.995,K19:+114.043	137 8.63 4	275 5.25 2	0.04 144 1
A0A087WR50	CON	EKPYQGWMMVDCTCLGEGNGR	E1:- 18.011,K2:+114.043,M8:+15.995,M9:+15.995, C12:+45.988,C14:+45.988	129 7.50 7	259 2.99 9	0.06 267 1
A0A087WR50	INF	NTYKVGDTYERPK	K4:+114.043	842. 918 7	168 3.82 2	0.06 231 8
A0A087WR50	INF	FGFCPMAAHEEICTTNEGVMYRIGDQWDK	C4:+45.988,C13:+45.988,K29:+114.043	118 5.49 8	355 3.47	0.08 392 4
A0A0A6YYE5	CON	QIVLTQSPAIMSASPGKV	Q1:-17.027,K18:+114.043	685. 026 4	205 2.05 6	0.04 197 7
A2A513	CON	GSSGGGYGGSSGGAGGHGGSSGGGYGGSSSSGG QGGSGGFK	K43:+114.043	115 1.80 4	345 2.38 7	0.03 690 6
A2A513	CON	GGGGSYGGSSGGSHGGSSGGGYGGSSSSGGAGG HGGSSGGGYGGSSSGGQGGSGGFK	K60:+114.043	118 2.97 6	472 7.87 4	0.08 621 5

A2A51 3	CO N	GGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K39:+114.043	105 5.76 8	316 4.28	0.06 772 5
A2A51 3	CO N	GSSGGGGSYGGSSGGGSYGGSSGGGSHGGSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K73:+114.043	143 2.32	572 5.24 7	0.01 236 9
A2A51 3	CO N	GGSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K44:+114.043	117 0.81 1	350 9.40 9	0.04 116 7
A2A51 3	CO N	GGSSGGGGSYGGSSGGGSYGGSSGGGSHGGSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K74:+114.043	144 6.57 5	578 2.26 9	0.01 077 7
A2A51 3	CO N	SSGGGGSYGGSSGGGSYGGSSGGGSHGGSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K72:+114.043	141 8.06 4	566 8.22 6	0.03 207 1
A2A51 3	CO N	YGGSSSGGSHGGSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K55:+114.043	147 1.92 6	441 2.75 6	0.06 024 7
A2A51 3	CO N	GGGGSYGGSSGGGSYGGSSGGGSHGGSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K70:+114.043	137 4.54 8	549 4.16 2	0.04 881
A2A51 3	CO N	SGGGGSYGGSSGGGSYGGSSGGGSHGGSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K71:+114.043	139 6.30 6	558 1.19 4	0.03 755 2
A2A51 3	CO N	GSFGGGSYGGGFGGGFGGDGGSLSGNEK K30:+114.043	904. 064 2	270 9.16 9	0.08 145 7
A2A51 3	CO N	GYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K38:+114.043	103 6.76 1	310 7.25 9	0.07 286 9
A2A51 3	CO N	SSGGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K42:+114.043	113 2.79 6	339 5.36 6	0.09 141
A2A51 3	CO N	GGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K36:+114.043	144 4.59 5	288 7.17 4	0.03 349 6
A2A51 3	CO N	SSGGQGGSGGFKSSGGGDQSSK K12:+114.043	677. 298 9	202 8.87 3	0.04 800 5
A2A51 3	CO N	GSYGGGFGGGFGGDGGSLSGNEK K25:+114.043	115 3.01	230 4.00 4	0.06 337 3
A2A51 3	CO N	GGGSYGGSSGGGSYGGSSGGGSHGGSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K69:+114.043	136 0.29 3	543 7.14	0.09 067 8
A2A51 3	CO N	GGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K40:+114.043	107 4.77 5	322 1.30 2	0.08 816 7
A2A51 3	CO N	HGGSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K45:+114.043	121 6.49 7	364 6.46 7	0.09 067 8
A2A51 3	INF	GSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K43:+114.043	115 1.80 4	345 2.38 7	0.03 378 2
A2A51 3	INF	GGGGSYGGSSGGGSHGGSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K60:+114.043	118 2.97 6	472 7.87 4	0.08 392 4
A2A51 3	INF	GGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K39:+114.043	792. 077 8	316 4.28	0.07 630 8
A2A51 3	INF	GSSGGGGSYGGSSGGGSYGGSSGGGSHGGSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK K73:+114.043	143 2.32	572 5.24 7	0.00 929 7

A2A51 3	INF	GGSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSSG GQGGSGGFK	K44:+114.043	117 0.81 1	350 9.40 9	0.04 116 7
A2A51 3	INF	GGSSGGGGSYGGSSGGGGSYGGSSGGGSHGGSSG GGYGGSSSGGAGGHGGSSGGGYGGSSSSGGQGGG GGFK	K74:+114.043	144 6.57 5	578 2.26 9	0.01 695 5
A2A51 3	INF	SSGGGGSYGGSSGGGGSYGGSSGGGSHGGSSGGGY GGSSSSGGAGGHGGSSGGGYGGSSSSGGQGGSGGF K	K72:+114.043	141 8.06 4	566 8.22 6	0.03 157 8
A2A51 3	INF	YGGSSGGGSHGGSSGGGYGGSSSGGAGGHGGSS GGGYGGSSSGGQGGSGGFK	K55:+114.043	147 1.92 6	441 2.75 6	0.03 666 5
A2A51 3	INF	GGGGSYGGSSGGGGSYGGSSGGGSHGGSSGGGYG GGSSSGGAGGHGGSSGGGYGGSSSSGGQGGSGGFK	K70:+114.043	137 4.54 8	549 4.16 2	0.05 294
A2A51 3	INF	SGGGSHGGSSGGGYGGSSSGGAGGHGGSSGGGYG GGSSSGGQGGSGGFK	K50:+114.043	133 1.54	399 1.59 6	0.07 896 1
A2A51 3	INF	SGGGGSYGGSSGGGGSYGGSSGGGSHGGSSGGGY GGSSSGGAGGHGGSSGGGYGGSSSSGGQGGSGGF K	K71:+114.043	139 6.30 6	558 1.19 4	0.03 282 5
A2A51 3	INF	GSFGGGSYGGGFGGGFGGDGGSLLSGNEK	K30:+114.043	904. 064 2	270 9.16 9	0.09 764 2
A2A51 3	INF	GYGGSSSGGAGGHGGSSGGGYGGSSSSGGQGGSG GFK	K38:+114.043	103 6.76 1	310 7.25 9	0.08 994 9
A2A51 3	INF	SSGGGYGGSSSGGAGGHGGSSGGGYGGSSSSGGQ GGSGGFK	K42:+114.043	113 2.79 6	339 5.36 6	0.09 141
A2A51 3	INF	GGSSSGGAGGHGGSSGGGYGGSSSSGGQGGSGGF K	K36:+114.043	144 4.59 5	288 7.17 4	0.06 772 5
A2A51 3	INF	HGGSSGGGYGGSSSGGAGGHGGSSGGGYGGSSSS GGQGGSGGFK	K45:+114.043	121 6.49 7	364 6.46 7	0.09 259 4
A2A51 3	INF	GGGSYGGSSGGGSHGGSSGGGYGGSSSSGAGGH GGSSGGGYGGSSSGGQGGSGGFK	K59:+114.043	116 8.72 1	467 0.85 2	0.09 141
A2A51 3	INF	YGGSSSGGAGGHGGSSGGGYGGSSSGGQGGSGG FK	K37:+114.043	763. 567 1	305 0.23 7	0.08 392 4
A2A51 3	INF	GYGGSSSGGQGGSGGFKSSGGGDQSSK	K28:+114.043	627. 771 4	250 7.05 5	0.04 401 7
A2A51 3	INF	GGSYGGSSGGGGSYGGSSGGGSHGGSSGGGYGGG SSSGGAGGHGGSSGGGYGGSSSGGQGGSGGFK	K68:+114.043	134 6.03 8	538 0.11 9	0.08 515 8
A2AF Q2	CO N	GLVAVVTGGASGLLATAK	K19:+114.043	439. 755 1	175 4.98 9	0.08 109
A2AF Q2	CO N	GVIINTASVAAFEGQVVGQAAYSASKGGIV	K25:+114.043	960. 502	287 8.48 3	0.04 910 9
A2AG H6	CO N	ISSNFSSIIAEK	K12:+114.043	705. 367 7	140 8.72	0.09 344 7
A2AG H6	INF	QSSLELQLMIK	K11:+114.043	702. 382 3	140 2.74 9	0.00 190 4
A2AG H6	INF	LDQWTMRQSSLELQLMIK	K18:+114.043	116 7.60 1	233 3.18 7	0.07 090 1

A2AG H6	INF	VNDIAILCAELTYGCK	C8:+45.988,C15:+45.988,K16:+114.043	644. 63	193 0.86 7	0.06 536 7
A2AK G8	CO N	SWIKVVLTEGAPTMLCLAALHGLVALVGSVDVDMQLK	K4:+114.043,M14:+15.995,C16:+45.988	135 2.04 7	405 3.11 8	0.04 938 8
A2AK G8	CO N	CVCTSAFSAGIIEAAEAEDIMSK	C1:+28.961,C3:+45.988,M21:+15.995,K23:+114.043	851. 023 1	255 0.04 6	0.09 764 2
A2AK G8	CO N	GAPTMLCLAALHGLVALVGSVDVDMQLK	C7:+45.988,M25:+15.995,K28:+114.043	100 0.18	299 7.51 6	0.06 632 8
A2AK G8	INF	NDLELYISIAK	K11:+114.043	696. 872 7	139 1.73	0.02 172 5
A2AK G8	INF	PSSQSAASLLGLWVMPPLIHGLSLNIKK	M15:+15.995,K28:+114.043	102 9.90 6	308 6.69 5	0.07 963 6
A2AK G8	INF	FVENLMVEVFKTASQPCHEMCLSLQGLSQAMK	K11:+114.043,C17:+45.988,M21:+15.995,C22:+45.988,K34:+114.043	102 6.47 4	410 1.86 3	0.04 315 4
A2AK G8	INF	ECTKPDQATPAALVLQGLHALCQAEVVCIR	C2:+45.988,K4:+114.043,C22:+45.988,C28:+45.988	114 3.88 2	342 8.62 1	0.06 300 9
A2AK G8	INF	VVMKPIATVGESYQYPPANLAALLS	K4:+114.043	916. 154 9	274 5.44 1	0.00 965 4
A2AN 08	CO N	PVETFSEFLDAAGLLSEITDPESFLK	K26:+114.043	990. 494 3	296 8.45 9	0.02 566 2
A2AN 08	CO N	ETFSEFLDAAGLLSEITDPESFLKDLLNSVP	E1:-18.011,K24:+114.043	874. 187 4	349 2.71 8	0.04 197 7
A2AN 08	CO N	DVTFLEFNEEGKNIIVIMSSAGYMYTQLMEEASSAQ	K11:+114.043,M23:+15.995,M28:+15.995	135 4.96 1	406 1.85 9	0.06 123 4
A2AN 08	CO N	ANTKPGGFTIEISNNSSTMVMTGMR	K4:+114.043,M21:+15.995	138 7.65	277 3.28 3	0.03 993 5
A2AN 08	CO N	KLSLFIGASVDPAGV	K1:+114.043	794. 441 2	158 6.86 7	0.05 076 6
A2AN 08	INF	MTTGTESETKAFMAVCIETAK	M1:+15.995,K10:+114.043,M13:+15.995,C16:+45.988,K21:+114.043	127 8.06 1	255 4.10 7	0.05 734
A2AN 08	INF	LLLFIGSKEK	C6:+45.988,K9:+114.043,K11:+114.043	762. 9	152 3.78 4	0.03 071
A2AN 08	INF	EQSSPDQVSAATK	E1:-18.011,K14:+114.043	786. 387	157 0.75 8	0.08 582
A2AN 08	INF	TTVKPYCNEIHAQAQLWLK	K4:+114.043,C7:+45.988,K19:+114.043	125 9.12 3	251 6.23 1	0.06 465 9
A2AN 08	INF	LCQWSEVMNHPGLVCCVQQTGTGVPLVVMVKPGTFLI QEIKTLPK	C2:+45.988,M8:+15.995,C15:+45.988,C16:+45.988,K30:+114.043,K45:+114.043	133 0.16 3	531 6.62 1	0.05 322 5
A2AN 08	INF	GHQGFGLSVILANHAIKLLASLFQDLQ	K18:+114.043	103 5.24	310 2.69 8	0.03 583 3
A2AQ 07	INF	ESESCDCLQGFQIVHSLGGGTGSGMGTLMLMNK	C5:+45.988,C7:+45.988,K32:+114.043	866. 379 3	346 1.48 6	0.04 423

A2AQ A9	CO N	DPKMMWSMHVAK	M4:+15.995,M5:+15.995,M8:+15.995,K12:+114.043	811. 860 5	162 1.70 5	0.03 403 7
A2AQ A9	CO N	IGWIPIGSLDQEKVK	K13:+114.043,K15:+114.043	956. 021	191 0.02 6	0.04 776 4
A2AQ A9	CO N	KGLTEQQTQFTSLPDPPEVEFAK	K1:+114.043	135 2.67 7	270 3.33 9	0.05 231 3
A2AQ A9	CO N	TPADMLSVTAAKDAQANITNTNYK	K24:+114.043	132 6.65 1	265 1.28 6	0.05 633 6
A2AQ A9	CO N	GYILPPDAVPFVHAHHSSDVQSELK	K25:+114.043	142 9.21 8	285 6.42	0.04 667 3
A2AQ A9	CO N	INIPADMVSVVAAKEGQNLVSD	K14:+114.043	596. 809 1	238 3.20 5	0.02 643
A2AQ A9	CO N	GTGIPTTVTPEIERVK	K16:+114.043	604. 667 4	181 0.97 9	0.05 322 5
A2AQ A9	CO N	KGYDLPVDAISVQLAK	K1:+114.043,K16:+114.043	487. 015 7	194 4.03 2	0.05 668 8
A2AQ A9	CO N	KLWSNYLYTDNAR	K1:+114.043	586. 625 6	175 6.85 3	0.03 736 3
A2AQ A9	CO N	KGYDLKPDIAIAIK	K6:+114.043	773. 436	154 4.85 6	0.04 012 7
A2AQ A9	CO N	NQEMVNIQIKYK	K9:+114.043,K11:+114.043	811. 902	162 1.78 8	0.06 502 7
A2AQ A9	CO N	DALANYPNFTSVEDPPEIVLAKINSVNQSDVK	K32:+114.043	120 1.27 3	360 0.79 5	0.07 125 9
A2AQ A9	CO N	HIMPDTDPDILAKANLINTSDK	K22:+114.043	126 7.66 8	253 3.32 1	0.00 158 6
A2AQ A9	CO N	EWMKGIGWVPIGSLEVVK	E1:-18.011,M3:+15.995,K4:+114.043	107 0.56 7	213 9.11 8	0.06 738 7
A2AQ A9	INF	KLWSNYLYTDNAR	K1:+114.043	586. 625 6	175 6.85 3	0.05 025 6
A2AQ A9	INF	YSTLMDSMNMLVLAQNNAK	M8:+15.995,M10:+15.995,K18:+114.043	108 8.98 8	217 5.96	0.09 973 2
A2AQ A9	INF	IHTYNMLPDAMSFELAKNMMQIQSDNQYK	M6:+15.995,M19:+15.995,K29:+114.043	902. 664 1	360 6.62 5	0.03 132 7
A2AQ A9	INF	EATELQSIVKYK	[0:-18.011,K10:+114.043	752. 904 3	150 3.79 3	0.06 901 4
A2AQ A9	INF	ENFSSVLYKENVGK	K9:+114.043,K14:+114.043	921. 455 6	184 0.89 6	0.04 694 9
A2AQ A9	INF	VYELQSENMYK	M9:+15.995,K11:+114.043	767. 348 7	153 2.68 2	0.08 207 5
A2ASS 6	CO N	TEIVSTDYTTTLTVK	K15:+114.043	595. 975 9	178 4.90 4	0.00 091 7

A2ASS 6	CO N	EGNYSVVVENSDBGK	K14:+114.043	537. 581 8	160 9.72 2	0.09 180 3
A2ASS 6	CO N	AVNKIGGGYEYELK	K4:+114.043,K14:+114.043	859. 957 8	171 7.9	0.08 956 6
A2ASS 6	CO N	DGIEVHAGDKYR	K10:+114.043	737. 358 2	147 2.70 1	0.08 741 6
A2ASS 6	CO N	YIPVMSGENK	M5:+15.995,K10:+114.043	634. 303 6	126 6.59 2	0.08 582
A2ASS 6	CO N	AIAWKPPKNGGSPHGYHVEMCPVGTEK	C23:+45.988,K29:+114.043	109 0.20 4	326 7.58 8	0.08 075 6
A2ASS 6	CO N	EEVSWSKVESQLK	K13:+114.043	831. 920 9	166 1.82 6	0.05 668 8
A2ASS 6	CO N	PSDIAQITSTPTSSMLTVKYATR	M15:+15.995,K19:+114.043	866. 774 7	259 7.30 1	0.07 350 6
A2ASS 6	INF	TEIVSTDYTTTLTVK	K15:+114.043	595. 975 9	178 4.90 4	0.04 144 1
A2ASS 6	INF	ILMASADTLK	K10:+114.043	588. 818 8	117 5.62 2	0.08 956 6
A2ASS 6	INF	VDVLDVPGPGIPFLSDNLTNDSCK	C24:+45.988,K25:+114.043	694. 340 5	277 3.33 1	0.07 672 7
A2ASS 6	INF	LYNCQLDMTGEISFQAANAK	C4:+45.988,K20:+114.043	793. 026 2	237 6.05 5	0.08 892 1
A2ASS 6	INF	VTAENEYGIGLPARTADPIK	K20:+114.043	743. 722 4	222 8.14 4	0.09 973 2
A2ASS 6	INF	VWTLVDANVQTLSCVKLK	C14:+45.988,K15:+114.043,K18:+114.043	114 6.09 9	229 0.18 2	0.09 462 2
A2ASS 6	INF	VLWYKDEVEIQESSK	K15:+114.043	983. 992	196 5.96 8	0.09 764 2
A2ASS 6	INF	VTREPPSFIK	K11:+114.043	467. 601 9	139 9.78 2	0.03 455 1
A2ASS 6	INF	ETEEIAASMVVVATAK	K16:+114.043	881. 948 8	176 1.88 2	0.00 709
A2ASS 6	INF	EKLEAPDIDLLELR	K2:+114.043	941. 992	188 1.96 8	0.09 067 8
A2ASS 6	INF	KVEPPPPPK	K1:+114.043	551. 817	110 1.61 8	0.02 721 5
A2ASS 6	INF	MTLVENTATLTVLK	K14:+114.043	412. 730 6	164 6.89 1	0.01 389 1
A2ASS 6	INF	VTETFDGEVSLAWEEPLTDGGSK	K23:+114.043	646. 054 5	258 0.18 7	0.06 337 3
A2ASS 6	INF	ENSVGEVSSSTFLTVQEQK	K19:+114.043	109 2.02 7	218 2.03 9	0.07 419 6

A2ASS 6	INF	DIENQTVLK	K9:+114.043	587. 309 7	117 2.60 4	0.08 892 1
A2ASS 6	INF	QLKPGDNFR	K3:+114.043	594. 810 2	118 7.60 5	0.08 278 5
A6ZI4 4	CO N	CVLKIGEHTPSALAIMENANVL	C1:+28.961,K4:+114.043,M16:+15.995	828. 076 7	248 1.20 7	0.05 928
B1ATY 1	CO N	KEITALAPSTMK	K1:+114.043	702. 382 3	140 2.74 9	0.01 731 6
B1ATY 1	CO N	EEEIAALVIDNGSGMCK	M15:+15.995,C16:+45.988,K17:+114.043	977. 932 1	195 3.84 9	0.01 601 4
B1ATY 1	INF	KEITALAPSTMK	K1:+114.043	702. 382 3	140 2.74 9	0.01 389 1
B1ATY 1	INF	KDLYANTVLSGGTTMYPGIADR	K1:+114.043	122 9.10 8	245 6.20 1	0.00 091 7
B1ATY 1	INF	DLYANTVLSGGTTMYPGIADRMQK	M14:+15.995,K24:+114.043	136 6.65 5	273 1.29 5	0.07 031 5
B1AU Y2	CO N	CMAPPSASCLGDGQLESFIGEPELEKTGT	C1:+45.988,M2:+15.995,C9:+45.988,K27:+114.043	109 0.15 7	326 7.44 8	0.06 337 3
B1AU Y2	INF	CMAPPSASCLGDGQLESFIGEPELELK	C1:+45.988,M2:+15.995,C9:+45.988,K27:+114.043	100 3.78 5	300 8.33 2	0.05 264 8
B1AU Y2	INF	QTSQMQLGLSLEEALDPPGDKAK	Q1:- 17.027,M5:+15.995,K24:+114.043,K26:+114.043	147 0.69 9	293 9.38 2	0.07 090 1
B1AY1 3	CO N	EMLGSSLIK	K9:+114.043	546. 292 5	109 0.56 9	0.01 090 8
B1AY1 3	CO N	QEKSPLGVVMALVCNVFDMLYQLANLEPR	Q1:- 17.027,K3:+114.043,M10:+15.995,C14:+45.988,M19:+15.995	119 4.57 7	358 0.70 7	0.08 515 8
B1AY1 3	CO N	VFGEGNMFAISPSTFQK	M7:+15.995,K18:+114.043	523. 007 5	208 7.99 9	0.04 857 5
B1AY1 3	INF	EMLGSSLIK	K9:+114.043	546. 292 5	109 0.56 9	0.07 192 7
B1AY1 3	INF	QSSTVIENIHTIIAAAVK	Q1:-17.027,K19:+114.043	516. 534 2	206 2.10 5	0.01 483 8
B2RQ C6	CO N	SSENAGTLGAVAGSAAGLK	K19:+114.043	592. 303 1	177 3.88 6	0.06 337 3
B2RQ C6	CO N	GAVAGSAAGLKLYLNETFSELR	K11:+114.043	119 1.12 7	238 0.23 9	0.04 256 6
B2RQ C6	CO N	LFLGASSENAGTLGAVAGSAAGLK	K24:+114.043	759. 401 4	227 5.18 1	0.05 410 2
B2RQ C6	CO N	LLTFGGQTALNCGVELTKAGVLAR	C12:+45.988,K18:+114.043	648. 847	259 1.35 7	0.07 125 9
B2RQ C6	INF	GEVAGFGESRCEAYLK	C11:+45.988,K16:+114.043	625. 951	187 4.82 9	0.05 264 8

B2RQ C6	INF	ILGSGGLSIGQAGEFDYSGSQAIAK	K24:+114.043	823. 747 3	246 8.21 8	0.04 959 9
B2RV7 7	CO N	VEYKSQVVAGQNYFIK	K16:+114.043	994. 018 4	198 6.02 1	0.03 639
B2RXR 6	CO N	DAKGQTPLMLAVAYGHIDAVSLLEK	K3:+114.043	956. 516 6	286 6.52 6	0.06 088 5
B2RXR 6	INF	NKMILGNAHDNSEELER	K2:+114.043,M3:+15.995	105 0.49 3	209 8.97	0.07 090 1
B2RXR 6	INF	GYTPLHAAASNGQISVVKHL	K18:+114.043	726. 387 5	217 6.13 9	0.03 583 3
B2RXR 6	INF	LSSGFEIDTPDTFGRTCLHAAAAGGNVECIK	C17:+45.988,C29:+45.988,K31:+114.043	112 9.51 5	338 5.52 1	0.07 254 2
B5THE 2	CO N	GLLITPVLDQGAKEVK	K14:+114.043	898. 020 4	179 4.02 5	0.02 432 6
B5THE 2	INF	SLKFDGLWIDMNEPSSFVNGAVPSGCSDAT	K3:+114.043,M11:+15.995,C26:+45.988	110 7.49	331 9.44 8	0.07 155 3
B5THE 2	INF	GQKLVILDPAISNNSFSSNPYGPYDR	K3:+114.043	770. 643 1	307 8.54 1	0.09 676 7
B9EJ5 4	CO N	PPVLKAELLK	K5:+114.043	407. 924 2	122 0.74 9	0.04 530 6
B9EJ5 4	CO N	FTDELMEQGLTYKVLTLQSQIDVNNEFE	K13:+114.043	113 5.22 6	340 2.65 4	0.09 501 2
B9EJ5 4	CO N	YKPPGFSLMYHLLNESPMLLELALSLEEGLVK	M9:+15.995,K31:+114.043	121 6.96 2	364 7.86 2	0.09 141
B9EJ5 4	CO N	GLGIIIIYLLKQSATDFFSYDSDHR	K10:+114.043	146 1.24 6	292 0.47 6	0.08 816 7
B9EJ5 4	CO N	WTPVVVILGLLQCSIPPVLKAELLK	C13:+45.988,K25:+114.043	144 5.34	288 8.66 4	0.08 621 5
B9EJ5 4	INF	LPGLGIIIIYLLKQSATDFF	K12:+114.043	111 2.12 5	222 2.23 5	0.06 901 4
B9EJ5 4	INF	LALCEHPQWTPVVVILGLLQCSIPPVLKAELLK	C4:+45.988,C21:+45.988,K33:+114.043	127 6.36 8	382 6.07 9	0.04 372 4
B9EJ5 4	INF	QGLTYKVLTLQSQIDVNNEFEK	K6:+114.043,K22:+114.043	139 0.72 7	277 9.43 9	0.07 319
B9EJ5 4	INF	EEIIAYKPPGFSLMYHLLNESPMLLELALSLEEGLVK	E1:-18.011,M23:+15.995,K36:+114.043	139 6.05 5	418 5.14 2	0.05 698 3
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGG	K9:+114.043	123 4.95 2	370 1.83 3	0.04 559 7
D3YW 48	CO N	LKGGGGGGGGGGGLGGGLGNVLGGLISGAAGGGGGG GGGMGLGGGGGGGTAMR	K2:+114.043	136 0.99 9	407 9.97 3	0.01 060 4
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLGGGGGGG	K9:+114.043	144 9.37 7	434 5.10 8	0.01 006 6

D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGG	K9:+114.043	117 7.93 1	353 0.76 9	0.07 782 3
D3YW 48	CO N	FLKGGGGGGGGGLGGGLGNVLGGLISGAAGGGGG GGGGMGLGGGGGGGTAMR	K3:+114.043	141 0.02 1	422 7.04 1	0.03 329 7
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLGG	K9:+114.043	137 3.34 9	411 7.02 2	0.09 380 1
D3YW 48	CO N	KGGGGGGGGGLGGGLGNVLGGLISGAAGGGGGGG GGMGLGGGGGGGTAMR	K1:+114.043	132 3.30 4	396 6.88 9	0.01 996 1
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMG	K9:+114.043	129 7.64	388 9.89 5	0.01 653 5
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLGGGG	K9:+114.043	141 1.36 3	423 1.06 5	0.00 943 1
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGG	M1:+15.995,K9:+114.043	901. 954 1	360 3.78 5	0.08 244 9
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISG MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISG	M1:+15.995,K9:+114.043	102 1.86 1	306 2.56 1	0.04 285 7
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLGGGGG	K9:+114.043	143 0.37	428 8.08 7	0.02 660 9
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLGGGGGGG	M1:+15.995,K9:+114.043	111 9.79 4	447 5.14 6	0.08 515 8
D3YW 48	CO N	FLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAAG GGGGGGGGGM	K8:+114.043,M45:+15.995	124 0.28 4	371 7.82 8	0.06 568
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGM	K9:+114.043,M46:+15.995	128 3.96 4	384 8.86 9	0.05 803 7
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLG	K9:+114.043	135 4.34 1	406 0.00 1	0.04 315 4
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLGGG	K9:+114.043,M46:+15.995	139 7.68 7	419 0.03 9	0.02 115 4
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGG	K9:+114.043	115 8.92 4	347 3.74 7	0.07 060 6
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLGGGGGGGT	K9:+114.043,M46:+15.995	114 5.05 6	457 6.19 4	0.07 823 6
D3YW 48	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGA MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGA	M1:+15.995,K9:+114.043	104 5.54	313 3.59 8	0.07 823 6
D3YW 48	CO N	FLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAAG GGGGGGGGGMGLGG	K8:+114.043	132 9.66 8	398 5.98 2	0.03 455 1
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGG	K9:+114.043	123 4.95 2	370 1.83 3	0.04 285 7
D3YW 48	INF	LKGGGGGGGGGLGGGLGNVLGGLISGAAGGGGGGG GGGMGLGGGGGGGTAMR	K2:+114.043	136 0.99 9	407 9.97 3	0.00 943 1
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLGGGGGGG	M1:+15.995,K9:+114.043,M46:+15.995	146 0.04 1	437 7.09 8	0.01 472 9

D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLGGGGGGG	K9:+114.043	146 8.38 4	440 2.13	0.01 601 4
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGG	M1:+15.995,K9:+114.043	118 3.26 2	354 6.76 4	0.06 568
D3YW 48	INF	FLKGGGGGGGGGLGGGLGNVLGGLISGAAGGGGG GGGGMGLGGGGGGGGTAMR	K3:+114.043	141 0.02 1	422 7.04 1	0.05 197 5
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLGG	K9:+114.043,M46:+15.995	137 8.68	413 3.01 7	0.03 947 5
D3YW 48	INF	KGGGGGGGGGLGGGLGNVLGGLISGAAGGGGGGG GGMGLGGGGGGGGTAMR	K1:+114.043	132 3.30 4	396 6.88 9	0.02 016 7
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLGGGG	K9:+114.043	141 1.36 3	423 1.06 5	0.00 943 1
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGG	M1:+15.995,K9:+114.043	122 1.27 7	366 0.80 7	0.07 672 7
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGG	M1:+15.995,K9:+114.043	120 2.27	360 3.78 5	0.03 252 1
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISG	M1:+15.995,K9:+114.043	102 1.86 1	306 2.56 1	0.01 814 4
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLGGGGG	K9:+114.043,M46:+15.995	143 5.70 2	430 4.08 2	0.00 547 6
D3YW 48	INF	FLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAAG GGGGGGGGGM	K8:+114.043,M45:+15.995	124 0.28 4	371 7.82 8	0.05 962 2
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGM	K9:+114.043	127 8.63 2	383 2.87 4	0.08 741 6
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLG	K9:+114.043,M46:+15.995	135 9.67 3	407 5.99 6	0.06 159 8
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGG	M1:+15.995,K9:+114.043	116 4.25 5	348 9.74 2	0.03 609 6
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGLGGGGGGT	K9:+114.043,M46:+15.995	114 5.05 6	457 6.19 4	0.07 492 7
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGA	K9:+114.043	104 0.20 9	311 7.60 3	0.08 892 1
D3YW 48	INF	FLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAAG GGGGGGGGMGLGGGGG	K8:+114.043,M45:+15.995	139 2.02 2	417 3.04 1	0.03 282 5
D3YW 48	INF	FLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAAG GGGGGGGGMMLGG	K8:+114.043,M45:+15.995	133 5	400 1.97 7	0.03 947 5
D3YW 48	INF	KLFVQLAGDDMEVSATELMNILNK	M19:+15.995,K24:+114.043	703. 108 8	280 8.40 4	0.04 910 9
D3YW 48	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGMGL	M1:+15.995,K9:+114.043,M46:+15.995	134 5.99 8	403 4.96 9	0.09 883 5
D3YW 48	INF	VNSFLKGGGGGGGGGLGGGLGNVLGGLISGAAGG GGGGGGGMMLGGGGGGGGTAMR	K6:+114.043,M43:+15.995	113 6.80 3	454 3.17 9	0.05 322 5

D3YW 48	INF	FLVNSFLKGGGGGGGGGLGGGLGNVLGGGLISGAAG GGGGGGGGMGL	K8:+114.043,M45:+15.995	129 6.98 6	388 7.93 4	0.06 871 7
D3YW 48	INF	FLVNSFLKGGGGGGGGGGGLGGGLGNVLGGGLISGAAG GGGGGGGGMGLGGG	K8:+114.043	134 8.67 6	404 3.00 3	0.03 666 5
D3Z6 Q9	CO N	HEDLKAIVGNNDLLWEDYEK	K5:+114.043	132 2.63	264 3.24 5	0.06 772 5
D3Z6 Q9	INF	SAQSPGRGQTGK	K12:+114.043	429. 885 4	128 6.63 3	0.02 959
D4AFX 7	CO N	LFQHPSMAIVK	M7:+15.995,K11:+114.043	700. 872	139 9.72 8	0.04 959 9
D4AFX 7	CO N	EVPKEFAASLLDYIGSQAQYLHTFMAITHAAK	K4:+114.043,M25:+15.995,K32:+114.043	126 5.63 4	379 3.87 8	0.06 632 8
D4AFX 7	INF	LAVASATETLKMLN	K11:+114.043	788. 424 7	157 4.83 4	0.06 568
D4AFX 7	INF	MAIVKGAGLVMK	K5:+114.043,K12:+114.043	723. 402 6	144 4.79	0.03 609 6
D4AFX 7	INF	QLLLTFDPILVEK	K13:+114.043	821. 974 9	164 1.93 4	0.06 536 7
D4AFX 7	INF	ISYSGVLHAVTQDGLFSENK	K20:+114.043	760. 382 1	227 8.12 3	0.04 256 6
D4AFX 7	INF	KYSTDESITSLAEFVVQK	K1:+114.043	108 0.04 8	215 8.07 9	0.04 938 8
E9PV6 0	CO N	VSQKVP MVIVQGHLVSEGILL	K4:+114.043,M7:+15.995	118 8.67	237 5.32 5	0.05 111 3
E9PV6 0	CO N	ELTYVMLSTVTVTLQGSVRNAVVLK	K25:+114.043	949. 872 5	284 6.59 4	0.06 969 8
E9PV6 0	INF	TRWDSSSDMK	M9:+15.995,K10:+114.043	671. 788 8	134 1.56 2	0.05 346 2
E9PV6 0	INF	IFNMCSKDR	C5:+45.988,K7:+114.043	637. 278 6	127 2.54 2	0.06 502 7
E9PV6 0	INF	TVMSALYSSLNK	K12:+114.043	714. 364 1	142 6.71 3	0.02 499 4
E9PVA 8	CO N	GAAYGLAGLVK	K11:+114.043	567. 319 9	113 2.62 4	0.06 841
E9PVA 8	CO N	GEHVPGFCLPKR	C8:+45.988,K11:+114.043	500. 580 4	149 8.71 8	0.05 6
E9PVA 8	CO N	ILPVLREGVLTSPEQK	K17:+114.043	650. 706	194 9.09 5	0.05 171 8
E9PVA 8	INF	QCLLLLLEVGGSHK	C2:+45.988,K14:+114.043	835. 442 5	166 8.86 9	0.05 231 3
E9PVA 8	INF	TKAGSVELLGAMAYCAPK	K2:+114.043,C15:+45.988	657. 323 6	196 8.94 7	0.09 102 3

E9PVA 8	INF	VTPGLKASLLDPVPEVR	K6:+114.043	953. 044 4	190 4.07 3	0.02 759 2
E9PVA 8	INF	EQSSVDRSGAAQGLAEVMAGLGVEK	M18:+15.995,K25:+114.043	131 0.13 8	261 8.26 1	0.04 881
E9PVA 8	INF	LTIIAQKMSVLSGIGSLSHHVSGPSGQVLNGCVAEL	K7:+114.043,C33:+45.988	128 8.00 6	386 0.99 5	0.03 378 2
E9PVA 8	INF	EMMAALTDAIQDK	M3:+15.995,K13:+114.043	783. 861 2	156 5.70 7	0.02 457 3
E9PVA 8	INF	ETASEDDNFGTAQSNKAITALGVDR	E1:-18.011,K16:+114.043	705. 591 9	281 8.33 7	0.04 509 1
E9PYK 3	CO N	TDSKMATEFIMSAAPSMGNTDFWK	M5:+15.995,M11:+15.995,M17:+15.995,K24:+ 114.043	141 4.61 5	282 7.21 4	0.06 632 8
E9PYK 3	INF	AGTQFSLSPIGFIPPKLGPPK	K16:+114.043	756. 091 9	226 5.25 2	0.07 385 3
E9PYK 3	INF	APEMGVLHQSPFCSPKPPSAPPLVTNVLCSEA	M4:+15.995,C13:+45.988,K17:+114.043,C30:+ 45.988	120 8.23 5	362 1.68 1	0.05 463 2
E9PYK 3	INF	APEMGVLHQSPFCSPKPPSAPPLVTNVLCSEAPQ	M4:+15.995,C13:+45.988,K17:+114.043,C30:+ 45.988	128 3.27 2	384 6.79 2	0.03 690 6
E9PYK 3	INF	LLVVCDDVALGK	C5:+45.988,K11:+114.043	645. 352 1	128 8.68 9	0.03 736 3
E9PZF 0	CO N	LVKYMNSGPVVAMVWEGLVVVK	K3:+114.043,M13:+15.995,K22:+114.043	133 9.19 6	267 6.37 7	0.06 231 8
E9Q07 0	CO N	PAAAAATTAAPAAAAAPAK	K18:+114.043	536. 290 3	160 5.84 8	0.05 410 2
E9Q07 0	INF	SAFAAAAPAAAATTAAPAAAAAPAK	K25:+114.043	109 8.57 5	219 5.13 4	0.08 145 7
E9Q07 0	INF	ADPSAFAAAAPAAAATTAAPAAAAAPAKAEAK	K28:+114.043	960. 161 9	287 7.46 2	0.06 666 4
E9Q07 0	INF	PSAFAAAAPAAAATTAAPAAAAAPAK	K26:+114.043	765. 069 9	229 2.18 6	0.04 959 9
E9Q1Z 6	CO N	CYSYDRNRPYVWSPSESVELLVSGNLQKPTI	C1:+45.988,K29:+114.043	128 6.62 6	385 6.85 6	0.07 963 6
E9Q1Z 6	INF	KPSLLTHQGHILDPGM	K1:+114.043,M16:+15.995	937. 483 7	187 2.95 2	0.06 231 8
E9Q39 7	CO N	LENMYHLFQLK	K11:+114.043	775. 395 8	154 8.77 6	0.08 244 9
E9Q39 7	CO N	EADIAIQGDK	E1:-18.011,K10:+114.043	578. 286	115 4.55 6	0.05 562 4
E9Q39 7	CO N	FFWEMDEAESWIEK	K13:+114.043,K15:+114.043	110 1.99 4	220 1.97 3	0.07 457 6
E9Q39 7	INF	KWIGAMEDQLR	K1:+114.043	730. 869 9	145 9.72 4	0.06 432 4

E9Q39 7	INF	LQDALQGQELSLGEASKLQAFLLQDLDDFK	K17:+114.043,K29:+114.043	115 0.24 6	344 7.71 6	0.05 836 2
E9Q39 7	INF	PDLIDFDK	K8:+114.043	538. 767 1	107 5.51 9	0.05 562 4
E9Q39 7	INF	DEPPKDEEGAIVMLK	K5:+114.043	892. 940 9	178 3.86 6	0.05 346 2
E9Q3X 0	CO N	AVIGSTYMLTQDEVLWEKELPSGVEELLNLG	M8:+15.995,K18:+114.043	891. 701 7	356 2.77 5	0.04 256 6
E9Q3X 0	INF	ELEAMSMAVESTGNAKAEASR	M5:+15.995,M7:+15.995,K16:+114.043	122 9.04 8	245 6.08 7	0.06 738 7
E9Q3X 0	INF	GPGTIRDLAVAGPEMQVK	K18:+114.043	489. 011 6	195 2.01 5	0.07 896 1
E9Q5K 8	CO N	RTQVFGLMQK	M8:+15.995,K10:+114.043	669. 354	133 6.69 2	0.03 229 7
E9Q5K 8	CO N	GGTSVVVAAPQEA	K14:+114.043	714. 378 6	142 6.74 2	0.07 457 6
E9Q5K 8	INF	RTQVFGLMQK	M8:+15.995,K10:+114.043	669. 354	133 6.69 2	0.05 025 6
F8VPN 2	INF	LSYPDISCVGEILDQAK	C8:+45.988,K17:+114.043	100 5.98	200 9.94 4	0.00 254 6
F8WI3 5	CO N	FQSAAGALQASEAYLVGLFEDTNLCAIHAK	C26:+45.988,K31:+114.043	113 7.89 6	341 0.66 4	0.04 938 8
F8WI3 5	INF	FQSAAGALQASEAYLVGLFEDTNLCAIHAK	C26:+45.988,K31:+114.043	113 7.89 6	341 0.66 4	0.00 912 6
G3X8 U3	INF	ILLEKFGGSFLNCVQK	C13:+45.988,K16:+114.043	652. 674 9	195 5.00 1	0.09 588 5
G3X97 2	INF	QLVSSMDVAETNVFFYPRLPLTK	K24:+114.043	144 1.76	288 1.50 5	0.04 509 1
G3X97 2	INF	EKTLFQPQT	K2:+114.043	603. 312 2	120 4.60 9	0.05 231 3
O0858 2	CO N	KEHLGLALALNPVFVVVTK	K1:+114.043	754. 451 4	226 0.33 1	0.04 800 5
O0858 2	CO N	GQTASFALKK	K9:+114.043,K10:+114.043	639. 844 3	127 7.67 3	0.07 090 1
O0858 3	CO N	DKMDMSLDDIHK	M3:+15.995,M5:+15.995,K12:+114.043	785. 361	156 8.70 6	0.03 207 1
O0869 2	INF	KETECTSTQER	K1:+114.043,C5:+45.988	736. 311 9	147 0.60 8	0.01 178 6
O0870 9	CO N	LSIDSVEDHLAWSK	K14:+114.043	571. 953 5	171 2.83 7	0.00 53
O0870 9	INF	LSIDSVEDHLAWSK	K14:+114.043	571. 953 5	171 2.83 7	0.00 53

O0873 9	INF	EFLHKGLHVSLSDDPMQ	E1:-18.011,K5:+114.043	107 5.52 1	214 9.02 6	0.07 672 7
O0873 9	INF	MIRSQSLSLQMPTQQDWK	M11:+15.995,K18:+114.043	769. 712 8	230 6.11 5	0.05 463 2
O0874 9	CO N	QTKIPNIYAIGDVVAGPMLAHK	K3:+114.043,M18:+15.995,K22:+114.043	860. 792 2	257 9.35 3	0.09 922 2
O0874 9	INF	EFLGHVGGIGIDMEISK	[0:-18.011,K17:+114.043	633. 321 1	189 6.94	0.03 349 6
O0875 9	INF	MIAMENPADLK	M1:+15.995,K11:+114.043	681. 823 8	136 1.63 2	0.03 639
O0878 8	CO N	RPKPTRPASTGVAGPSSSLGPSGSASAGELSSSEPSTPA QTPLA	K3:+114.043	141 6.37 8	424 6.11	0.07 286 9
O0878 8	INF	DQLDETVNVEPLTK	K14:+114.043	572. 288 5	171 3.84 2	0.08 312 1
O0878 8	INF	QAQEKFDLSENCSE	Q1:-17.027,K5:+114.043,C12:+45.988	963. 901 9	192 5.78 8	0.08 145 7
O0878 8	INF	AAAAAQLIAPLAENEGLPVALEELAFK	K28:+114.043	145 3.28 8	290 4.56	0.05 374 6
O0879 7	CO N	ENNLTFEKLTAWMEADFMK	K8:+114.043,M13:+15.995	816. 712 4	244 7.11 4	0.00 539 6
O0880 8	CO N	EAVLTESMIQNLIK	M8:+15.995,K14:+114.043	859. 953 9	171 7.89 2	0.02 185 9
O0880 8	CO N	KSEGVPTILE	K1:+114.043	593. 819 9	118 5.62 4	0.04 996 1
O0880 8	CO N	AMDPAVPNMMIDAAKLLSAL	M2:+15.995,M9:+15.995,M10:+15.995,K15:+1 14.043	111 7.54 8	223 3.08	0.04 197 7
O0880 8	INF	DLSQDCFWTKVK	C6:+45.988,K10:+114.043,K12:+114.043	872. 395 8	174 2.77 6	0.04 750 8
O0880 8	INF	CLKAFMNNK	C1:+45.988,M6:+15.995,K9:+114.043	622. 783 6	124 3.55 2	0.09 344 7
O0881 0	CO N	NKITMIAEPLEK	K2:+114.043,M5:+15.995,K12:+114.043	815. 927 7	162 9.84	0.05 6
O0906 1	CO N	HSNNKAMTTGAIAAM	K5:+114.043,M7:+15.995	549. 924 7	164 6.75 1	0.06 195 4
O0906 1	INF	CYKLTDK	C1:+45.988,K3:+114.043,K7:+114.043	572. 760 6	114 3.50 6	0.04 144 1
O0906 1	INF	DVYTGDAIRICIVTK	C11:+45.988,K15:+114.043	609. 643 5	182 5.90 7	0.04 644 6
O0910 6	CO N	DGLFEFCQLSTGGSVASAVKLNK	C7:+45.988,K20:+114.043,K23:+114.043	132 3.13 9	264 4.26 3	0.04 530 6
O0910 6	CO N	GLFEFCQLSTGGSVASAVKLNK	C6:+45.988,K19:+114.043	120 8.60 4	241 5.19 3	0.05 866 5

O0910 6	INF	DGIDDESIEAIFKPVMSKVME	K13:+114.043,M16:+15.995	126 7.07 8	253 2.14	0.02 566 2
O0915 9	INF	ATFDSGTGLLMKIENLEQNLSPVSGFFWYNASVGD E	K12:+114.043	143 1.35 5	429 1.04 2	0.05 410 2
O0915 9	INF	RASDSLEPPAADLFTGVLPNNYNPPK	K26:+114.043	144 9.22 6	289 6.43 6	0.05 767 9
O3522 6	INF	MRIIAFVGSPVEDNEK	M1:+15.995,K16:+114.043	967. 986 3	193 3.95 7	0.02 784 1
O3535 0	INF	FOLDKSGSMSAYEMR	K5:+114.043,M14:+15.995	933. 904 1	186 5.79 3	0.04 401 7
O3559 3	CO N	AVEEEDKMTPEQLAIK	K7:+114.043,K16:+114.043	515. 506 3	205 7.99 4	0.04 173 1
O3559 3	CO N	TAEQVYISSALLKMLK	K17:+114.043	101 1.56 9	202 1.12 3	0.06 267 1
O3559 3	CO N	VIDVFAMPQSGTGVSEAVDPVFQAKMLDMLK	M27:+15.995,M30:+15.995,K32:+114.043	119 0.26 3	356 7.76 7	0.05 463 2
O3559 3	INF	EMLELAKNYNK	K7:+114.043,K11:+114.043	790. 891 1	157 9.76 7	0.04 315 4
O3563 8	CO N	DYPLTMAGPQWK	K12:+114.043	760. 864 3	151 9.71 3	0.03 834 3
O3563 8	INF	SAHRPVAVAAGEFLYK	K16:+114.043	915. 487	182 8.95 8	0.03 993 5
O3563 9	CO N	KGDLSGHFEHVMVALVTAPALFDAQ	K1:+114.043	138 4.21 6	276 6.41 6	0.06 632 8
O3563 9	INF	GDLSGHFEHVMVALVTAPALFDAQ	K24:+114.043	132 0.16 9	263 8.32 1	0.07 861 1
O3564 3	CO N	DLDDYYATLLKK	K10:+114.043	486. 261 5	145 5.76 1	0.08 109
O3564 3	INF	MDRQMFLATWK	M1:+15.995,K11:+114.043	778. 871 7	155 5.72 8	0.07 705 1
O3564 3	INF	MEPLNNLQVAVKNNIDV	M1:+15.995,K12:+114.043	681. 018 2	204 0.03 1	0.07 286 9
O3574 4	CO N	SGYKIPELSQSLDYIQVMTY	K4:+114.043,M18:+15.995	123 3.09 9	246 4.18 3	0.05 836 2
O3584 1	CO N	ADATEQVGQHKDAYQVILDGVK	K11:+114.043	833. 754 5	249 8.24	0.06 536 7
O3586 4	CO N	ISALALLKMVMHAR	K8:+114.043,M9:+15.995,M11:+15.995	567. 317	169 8.92 8	0.06 871 7
O3586 4	INF	GYKPPDEGPSEYQTIPLNKIE	K3:+114.043	124 5.11 4	248 8.21 2	0.06 369 3
O3595 5	INF	MLKQAVEPTGGFSFENCQR	M1:+15.995,K3:+114.043,C17:+45.988	115 9.52 2	231 7.02 9	0.09 225

O5477 4	CO N	VDGKCSDATLLSSLEEMK	K4:+114.043,C5:+45.988,K19:+114.043	115 7.04 3	231 2.07	0.04 996 1
O5477 4	CO N	KQVAPLENGAAAAEEEEIPPMSSYCLAESPYIK	M22:+15.995,C26:+45.988,K35:+114.043	132 7.29 4	397 8.85 8	0.06 901 4
O5477 4	INF	VEHIPVVQIDLSVPLKVPGMPSDQYVK	K16:+114.043,K28:+114.043	837. 444 5	334 5.74 7	0.04 173 1
O5477 4	INF	VTYDIQASLQK	K11:+114.043	460. 577 6	137 8.70 9	0.09 259 4
O5477 4	INF	DISWAAFNIEVMSASKFTFK	M13:+15.995,K17:+114.043,K21:+114.043	132 5.15 5	264 8.29 5	0.03 666 5
O5482 4	CO N	GQAKGLGFSIVGGK	K4:+114.043	716. 899 5	143 1.78 3	0.06 502 7
O5482 4	CO N	SVISNIVLMKGQAK	M9:+15.995,K14:+114.043	809. 453 9	161 6.89 2	0.03 132 7
O5482 4	INF	EAVAQAVEGVKF	K11:+114.043	681. 357 2	136 0.69 9	0.04 173 1
O5482 4	INF	DEILQLAGTAVQGLTRFEAWNVIK	K24:+114.043	139 3.74 6	278 5.47 6	0.05 668 8
O5482 4	INF	SSTDSAASASAASDISVESK	K20:+114.043	992. 951 3	198 3.88 7	0.05 767 9
O5487 9	INF	KNPEVPVNFAEFSK	K1:+114.043	860. 439 2	171 8.86 3	0.04 448 1
O5489 0	INF	PESIEFPVSEAIQLEARPLSSKSGSSAQITQVSPQR	K22:+114.043	100 7.02	402 4.05	0.05 928
O5489 0	INF	KPVGFKDSLTVQVTFDCDCACQAFAPSSPR	K6:+114.043,C17:+45.988,C19:+45.988,C21:+45.988	900. 150 3	359 6.57 4	0.06 401 4
O5489 0	INF	DILVLLSVMGAILLIGLATLLIWK	M10:+15.995,K25:+114.043	140 4.35 8	280 6.70 1	0.06 267 1
O5496 2	INF	DFVAEPMGEKPVGSLAGIGDVLSKR	M7:+15.995,K24:+114.043	676. 351 5	270 1.37 5	0.05 895 8
O5510 6	CO N	KSTSLDVEPIYTF	K1:+114.043	807. 407 1	161 2.79 9	0.08 851 8
O5510 6	INF	NLQKTAPAK	K4:+114.043	542. 809 7	108 3.60 4	0.09 501 2
O5513 1	INF	MEQVFEMKVK	M7:+15.995,K10:+114.043	699. 842	139 7.66 8	0.04 256 6
O5513 1	INF	SGHGLKPLDIEFMK	M13:+15.995,K14:+114.043	851. 435 7	170 0.85 6	0.04 530 6
O5522 2	CO N	GMKVALEGLRPTIPPGISPHVCK	K3:+114.043,C22:+45.988,K23:+114.043	133 7.70 4	267 3.39 2	0.04 012 7
O5522 2	INF	LEKMQDK	K3:+114.043	503. 255 9	100 4.49 6	0.04 776 4
O5522 2	INF	ICNKYGEMPVDK	C2:+45.988,K12:+114.043	778. 849 6	155 5.68 4	0.06 901 4

O7013 3	CO N	FIAEMTIYIKQLGR	K10:+114.043	898. 990 6	179 5.96 6	0.05 498 6
O7013 3	INF	INEVKSEEVPAVGI	K5:+114.043	799. 425 8	159 6.83 6	0.03 947 5
O7014 5	CO N	LWNEGVLAAADKK	K11:+114.043,K12:+114.043	524. 611 3	157 0.81	0.06 337 3
O7049 7	INF	VLDLEGYKQLTILQGCPGLPGAAGPK	K8:+114.043,C16:+45.988,K26:+114.043	145 6.75 5	291 1.49 4	0.04 229 4
O8830 7	CO N	LFWKSLALK	K9:+114.043	610. 364 1	121 8.71 3	0.06 088 5
O8830 7	INF	GGKYHIIVQLGNMSK	K3:+114.043,M13:+15.995,K15:+114.043	630. 328 7	188 7.96 3	0.08 926 9
O8830 7	INF	YTWGDHGGIIMAI AQMETNELK	M17:+15.995,K23:+114.043	133 3.12 3	266 4.23 1	0.05 6
O8830 7	INF	GQVSLNDSHNQMVVHWAGEK	K20:+114.043	117 5.55 4	234 9.09 2	0.07 060 6
O8830 7	INF	CDGHQDCQDQGQDEANCPHSTLTCTSTREFK	[0:- 17.027,C1:+45.988,C7:+45.988,C16:+45.988,C 24:+45.988,K30:+114.043	902. 578	360 6.28 1	0.06 088 5
O8834 2	CO N	CLAWSPDNEHFASGGMDMMVYVWTLSDPETKVK	C1:+28.961,K33:+114.043	129 6.56 8	388 6.68 1	0.05 803 7
O8845 6	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLG	K9:+114.043,M47:+15.995	137 8.68	413 3.01 7	0.06 432 4
O8845 6	CO N	MFLVNSFLKGGGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGGG	K9:+114.043	143 0.37	428 8.08 7	0.01 456 9
O8845 6	CO N	MFLVNSFLKGGGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGG	K9:+114.043,M47:+15.995	139 7.68 7	419 0.03 9	0.00 807 4
O8845 6	CO N	MFLVNSFLKGGGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGGGG	K9:+114.043	144 9.37 7	434 5.10 8	0.00 461 1
O8845 6	CO N	MFLVNSFLKGGGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGG	K9:+114.043	125 3.95 9	375 8.85 5	0.06 969 8
O8845 6	CO N	MFLVNSFLKGGGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGM	K9:+114.043	129 7.64	388 9.89 5	0.03 026 5
O8845 6	CO N	LKGGGGGGGGGGGLGGGLGNVLGGLISGAAGGGGGG GGGGMGLGGGGGGGTAMR	K2:+114.043	138 0.00 6	413 6.99 4	0.01 456 9
O8845 6	CO N	MFLVNSFLKGGGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGGGGGG	K9:+114.043	111 5.79 6	445 9.15 1	0.05 668 8
O8845 6	CO N	MFLVNSFLKGGGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGGGGGG	K9:+114.043	146 8.38 4	440 2.13	0.01 204 1
O8845 6	CO N	MFLVNSFLKGGGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGL	K9:+114.043,M47:+15.995	135 9.67 3	407 5.99 6	0.03 533 2
O8845 6	CO N	MFLVNSFLKGGGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGG	K9:+114.043,M47:+15.995	141 6.69 5	424 7.06	0.00 162 6

O8845 6	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGGGGGGGG	K9:+114.043	113 0.05 1	451 6.17 2	0.06 841
O8845 6	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGGGGGGGGT	M1:+15.995,K9:+114.043	115 9.31 2	463 3.21 5	0.09 462 2
O8845 6	CO N	KGGGGGGGGGGGLGGGLGNVLGGLISGAAGGGGGGG GGGMGLGGGGGGGGTAMR	K1:+114.043	134 2.31 1	402 3.91	0.02 457 3
O8845 6	CO N	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMG	K9:+114.043,M47:+15.995	132 1.97 8	396 2.91 2	0.01 731 6
O8845 6	CO N	SFLKGGGGGGGGGLGGGLGNVLGGLISGAAGGGGG GGGGGGMGLGGGGGGGGTAMR	K4:+114.043,M42:+15.995,M55:+15.995	146 8.70 3	440 3.08 5	0.07 060 6
O8845 6	CO N	FLKGGGGGGGGGGGLGGGLGNVLGGLISGAAGGGGG GGGGMGLGGGGGGGGTAMR	K3:+114.043	142 9.02 9	428 4.06 3	0.03 282 5
O8845 6	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLG	K9:+114.043,M47:+15.995	137 8.68	413 3.01 7	0.03 182 7
O8845 6	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGGGG	K9:+114.043	143 0.37	428 8.08 7	0.01 406 1
O8845 6	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGG	K9:+114.043,M47:+15.995	139 7.68 7	419 0.03 9	0.01 799 1
O8845 6	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGGGGG	K9:+114.043,M47:+15.995	145 4.70 9	436 1.10 3	0.00 604 2
O8845 6	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGG	K9:+114.043	125 3.95 9	375 8.85 5	0.06 841
O8845 6	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGM	M1:+15.995,K9:+114.043	130 2.97 1	390 5.89	0.04 724 1
O8845 6	INF	LKGGGGGGGGGGGLGGGLGNVLGGLISGAAGGGGGGG GGGMGLGGGGGGGGTAMR	K2:+114.043	138 0.00 6	413 6.99 4	0.01 977
O8845 6	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGGGGGGG	K9:+114.043,M47:+15.995	111 9.79 4	447 5.14 6	0.05 294
O8845 6	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGGGGGGG	K9:+114.043	146 8.38 4	440 2.13	0.01 373 6
O8845 6	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGL	K9:+114.043,M47:+15.995	135 9.67 3	407 5.99 6	0.03 010 1
O8845 6	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGGG	K9:+114.043	141 1.36 3	423 1.06 5	0.00 592 4
O8845 6	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGGGGGGGG	K9:+114.043	113 0.05 1	451 6.17 2	0.05 962 2
O8845 6	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMGLGGGGGGGGT	M1:+15.995,K9:+114.043,M47:+15.995	116 3.31	464 9.21	0.04 800 5
O8845 6	INF	KGGGGGGGGGGGLGGGLGNVLGGLISGAAGGGGGGG GGGMGLGGGGGGGGTAMR	K1:+114.043	134 2.31 1	402 3.91	0.02 643
O8845 6	INF	MFLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAA GGGGGGGGGGMG	K9:+114.043	131 6.64 7	394 6.91 7	0.04 372 4

O8845 6	INF	SFLKGGGGGGGGGLGGGLGNVLGGLISGAAGGGG GGGGGGMGLGGGGGGGTAMR	K4:+114.043,M42:+15.995,M55:+15.995	146 8.70 3	440 3.08 5	0.08 312 1
O8845 6	INF	FLKGGGGGGGGGLGGGLGNVLGGLISGAAGGGG GGGGGGMGLGGGGGGGTAMR	K3:+114.043	142 9.02 9	428 4.06 3	0.00 981
O8845 6	INF	FLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAAG GGGGGGGGGMGLG	K8:+114.043	132 9.66 8	398 5.98 2	0.06 401 4
O8845 6	INF	FLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAAG GGGGGGGGGMGLGG	K8:+114.043	134 8.67 6	404 3.00 3	0.01 601 4
O8845 6	INF	FLVNSFLKGGGGGGGGGLGGGLGNVLGGLISGAAG GGGGGGGGGMGLGGGGG	K8:+114.043,M46:+15.995	141 1.02 9	423 0.06 3	0.06 536 7
O8848 7	CO N	QSKAVAVTSMSPVGDVNNFVVGSEEGSVYTACR	[0:-17.027,K3:+114.043,C33:+45.988	920. 427 8	367 7.68	0.07 090 1
O8854 3	CO N	FYEQAITPAMAVSHIMLESYKK	K22:+114.043,K23:+114.043	144 3.71 2	288 5.40 9	0.07 031 5
O8854 3	INF	LSAQGQMTQLCELINKSGELLAK	M7:+15.995,C11:+45.988,K16:+114.043	884. 445 6	265 0.31 3	0.04 644 6
O8854 3	INF	LKAMDQEITVNPQFVQK	K17:+114.043	701. 702 2	210 2.08 3	0.07 598 5
O8854 3	INF	QAIDKMQMNTNQLTSVHA	Q1:-17.027,K5:+114.043,M6:+15.995	107 1.99 9	214 1.98 3	0.06 632 8
O8854 3	INF	HFLCYYYYGGMIYTGLKNFER	C4:+45.988,K17:+114.043	139 9.63 3	279 7.24 9	0.06 465 9
O8854 4	INF	SASKLYNNITFEELGALLEIPAAK	K4:+114.043,K24:+114.043	940. 831 4	281 9.47 1	0.04 828 8
O8854 5	CO N	QVCEIIESPLFLKLN	C3:+45.988,K13:+114.043	953. 495	190 4.97 4	0.01 426 1
O8854 5	CO N	NHEILREAYALCHCLPVLSTDK	C12:+45.988,C14:+45.988,K22:+114.043	136 6.14 6	273 0.27 6	0.03 993 5
O8856 9	INF	FVGGIKEDTEHHLR	K6:+114.043	940. 966 7	187 9.91 8	0.00 091 7
O8868 5	INF	ATFLKLAGP	K5:+114.043	516. 298 4	103 0.58 1	0.04 589 2
O8868 5	INF	GVLMYGPPGTGKTLLA	K12:+114.043	844. 956 2	168 7.89 7	0.06 701 2
O8878 3	CO N	KVSTVTLVSATSTTANMTMSPEGR	K1:+114.043,M17:+15.995	130 0.13 9	259 8.26 3	0.07 350 6
O8878 3	INF	QKTSSPDLGQVPLSLDDNQK	Q1:-17.027,K2:+114.043	113 4.06 1	226 6.10 7	0.06 772 5
O8878 3	INF	EQDKPKTIK	[0:-18.011,K9:+114.043	591. 827 8	118 1.64	0.04 996 1
O8884 4	INF	FMDKLGENLK	K4:+114.043,K10:+114.043	711. 856 5	142 1.69 7	0.04 423

O8884 4	INF	DIFQEYDKK	K9:+114.043	706. 857	141 1.69 8	0.07 741 6
O8895 8	CO N	KVPTMALTVGVGTVM DAK	M15:+15.995,K18:+114.043	974. 516 3	194 7.01 7	0.03 378 2
O8895 8	CO N	HIDIHPENTHILDGNAADLQAECDAFEKIQ	C23:+45.988,K29:+114.043	912. 419 5	364 5.64 7	0.06 841
O8907 9	INF	EALDKDSGHPETLINLIVLSQHLGKPPEVTNR	K5:+114.043	121 2.31 2	363 3.91 2	0.06 088 5
P0049 3	CO N	MQTL LSLVK	K9:+114.043	573. 831 7	114 5.64 8	0.04 910 9
P0049 3	CO N	EMGGHHIVALCVLK	C11:+45.988,K14:+114.043	833. 915 6	166 5.81 6	0.09 547 1
P0049 3	INF	NDQSTGDIK	K9:+114.043	546. 252 4	109 0.48 9	0.06 432 4
P0092 0	CO N	QDNAVLKGGPLSDSYR	Q1:-17.027,K7:+114.043	908. 945 2	181 5.87 5	0.06 088 5
P0092 0	INF	DIDTATAQHDPALQPLLISYDK	K22:+114.043	635. 572 9	253 8.26	0.04 092 9
P0102 7	CO N	NVDGTA FVIFGVQDGD KK	K18:+114.043	675. 341 5	202 3.00 1	0.04 667 3
P0102 7	CO N	EPEKN GISTK	E1:-18.011,K4:+114.043	599. 807 1	119 7.59 9	0.02 934 5
P0102 7	CO N	VSIRPAPETAKK	K11:+114.043,K12:+114.043	762. 928 9	152 3.84 2	0.06 738 7
P0102 7	INF	NVDGTA FVIFGVQDGD KK	K17:+114.043	675. 341 5	202 3.00 1	0.08 816 7
P0102 7	INF	VVIEDGVGD AVLTRK	K15:+114.043	842. 965 6	168 3.91 6	0.03 876 9
P0102 7	INF	AGEYIEASYMNLQRPYTVAIAGYALALMNKLEEPYL	M10:+15.995,K30:+114.043	139 9.36 3	419 5.06 5	0.04 530 6
P0102 7	INF	VKAAVFNHFISDGVK	K15:+114.043	582. 649 8	174 4.92 6	0.06 432 4
P0102 7	INF	KGICVADPYEIR	K1:+114.043,C4:+45.988	762. 371 6	152 2.72 8	0.04 448 1
P0102 7	INF	RPYTVAIAGYALALMNKLEEPYLGK	M15:+15.995,K25:+114.043	145 6.27 4	291 0.53 2	0.05 322 5
P0102 7	INF	SYMNLQRPYTVAIAGYALALMNKLEEPYLGK	M21:+15.995,K23:+114.043,K31:+114.043	125 4.64	376 0.89 6	0.04 959 9
P0102 7	INF	LKHLIVTPAGCGEQNMIGMTPTVI AVHYLDQ	K2:+114.043,C11:+45.988,M16:+15.995,M19: +15.995	118 1.24 9	354 0.72 4	0.04 828 8
P0102 7	INF	QSKIWDVVEK	K10:+114.043	673. 359 7	134 4.70 4	0.04 475 4

P0187 2	CO N	ICEATNFTP KPITVSWLK	C2:+45.988,K10:+114.043	110 4.56 4	220 7.11 2	0.07 419 6
P0187 2	INF	GQLLPQEKYVTSAPMPEPGAPGYF	K8:+114.043	141 9.69 5	283 7.37 4	0.03 455 1
P0194 2	CO N	MVLSGEDKSNIK	K8:+114.043,K12:+114.043	774. 888 5	154 7.76 1	0.06 666 4
P0194 2	INF	PHFDVSHGSAQVK	K13:+114.043	508. 252	152 1.73 3	0.06 937 5
P0208 8	INF	YFDSFGDLSSASAIMGNAKVK	K21:+114.043	774. 707 8	232 1.1	0.04 229 4
P0208 9	INF	VHLTDAEKSAVSLWAK	K8:+114.043,C13:+45.988,K17:+114.043	106 6.51 8	213 1.01 9	0.04 857 5
P0410 4	CO N	FLEQQNQVLQTKWELLQQVDTTTR	K12:+114.043	102 0.86 4	305 9.56 8	0.09 724 8
P0410 4	CO N	SISKSVAGGGGSCGGFGGGSYGGGGFGGGSYGGGG FGGGSFGGGGF	K4:+114.043,C14:+45.988	135 0.9	404 9.67 6	0.08 109
P0410 4	INF	SISKSVAGGGGSCGGFGGGSYGGGGFGGGSYGGGG FGGGSFGGGGF	K4:+114.043,C14:+45.988	135 0.9	404 9.67 6	0.04 938 8
P0410 4	INF	SKSVAGGGGSCGGFGGGSYGGGGFGGGSYGGGGF GGGSFGGGGFGGSGFGGGLGGGGFGSGGGFGGGR	K2:+114.043,C12:+45.988	144 1.10 8	576 0.40 1	0.05 463 2
P0491 9	CO N	VVMKPKPQGPVPNTALFSLVLMAGTFLAMTLR	M3:+15.995,K4:+114.043,K6:+114.043,M22:+ 15.995,M30:+15.995	127 3.02 5	381 6.05 1	0.05 698 3
P0491 9	CO N	KEAVPLEDLVLPEPVGFLVLLGPEAPHVDYTLGR	K1:+114.043	134 6.73 7	403 7.18 8	0.00 147 3
P0491 9	INF	KEAVPLEDLVLPEPVGFLVLLGPEAPHVDYTLGR	K1:+114.043	134 6.73 7	403 7.18 8	0.00 091 7
P0491 9	INF	ANFLEKPVLG FVRLK	K15:+114.043	923. 041 5	184 4.06 7	0.05 264 8
P0491 9	INF	EDLGNLEGVKPAVLTR	E1:-18.011,K10:+114.043	903. 989 4	180 5.96 3	0.07 218 1
P0491 9	INF	IPPDSETTLVLVGRANFLEKPV LGF	K20:+114.043	141 3.77 4	282 5.53 3	0.04 800 5
P0491 9	INF	SHAEDLGNLEGVKPAVLTRSGGASEPLLPHQPSL	K13:+114.043	119 7.62 4	358 9.84 9	0.04 315 4
P0491 9	INF	VPNTALFSLVLMAGTFLAMTLRK	M20:+15.995,K24:+114.043	913. 176 9	273 6.50 7	0.05 962 2
P0491 9	INF	FGMPWLSATTVRSVTHANAL TVMGK	M3:+15.995,M23:+15.995,K25:+114.043	141 1.21	282 0.40 5	0.08 109
P0491 9	INF	KASGPGAAAQIQEVK	K15:+114.043	784. 923 7	156 7.83 2	0.05 322 5
P0491 9	INF	AEGGSEGPSTSGTLKIPPDSETTLVLVGR	K15:+114.043	990. 507 5	296 8.49 9	0.04 012 7

P0520 1	CO N	INMCGLTTKN	M3:+15.995,C4:+45.988,K9:+114.043	635. 783 8	126 9.55 2	0.07 823 6
P0520 1	INF	IGMFSFTGLNPKQVEYLVNEK	K12:+114.043	126 4.64 7	252 7.27 8	0.04 959 9
P0615 1	CO N	TLKDQLIVNLLK	K3:+114.043	756. 462	151 0.90 8	0.00 539 6
P0615 1	CO N	AIGLSVADLAESIMK	K15:+114.043	816. 437 8	163 0.86	0.06 056 1
P0615 1	INF	TLKDQLIVNLLK	K3:+114.043	756. 462	151 0.90 8	0.01 030 5
P0615 1	INF	KGYTSWAIGLSVADLAESIMK	K1:+114.043	117 7.60 7	235 3.19 9	0.00 091 7
P0615 1	INF	VHPISTMIKGLYGINE	M7:+15.995,K9:+114.043	634. 665 1	190 0.97 2	0.06 600 8
P0674 5	CO N	SITDIINIGIGGSDLGPLMVTEALKPYS	M19:+15.995,K25:+114.043	100 2.19	300 3.54 8	0.00 091 7
P0674 5	CO N	HFEQLLSGAHWMDQHFLK	K18:+114.043	116 9.56 3	233 7.11 1	0.06 568
P0674 5	INF	SITDIINIGIGGSDLGPLMVTEALKPYS	M19:+15.995,K25:+114.043	100 2.19	300 3.54 8	0.00 091 7
P0680 0	CO N	IEFHNEVDGGKQDANCVRPDGPLNK	K11:+114.043,C16:+45.988	971. 452 6	291 1.33 4	0.06 502 7
P0680 0	CO N	PESASKPHGYVLCYK	K6:+114.043,C13:+45.988,K15:+114.043	976. 954	195 1.89 2	0.07 125 9
P0680 0	CO N	EAQYILIHQALVEYNQFGETEVLNSELHSLHNMK	E1:-18.011,C30:+45.988,K35:+114.043	141 5.00 7	424 1.99 7	0.04 256 6
P0680 0	CO N	DPPSTTIATTTKQTCAAMFGNITVNYTYESSNQTFK	K12:+114.043,C15:+45.988,M18:+15.995,K36: +114.043	140 7.97 4	422 0.89 8	0.06 195 4
P0680 0	INF	QFGETEVLNSELHSLHNMK	C15:+45.988,K20:+114.043	826. 040 6	247 5.09 8	0.07 155 3
P0680 0	INF	VCAQYWGEKGQTYGDMEVEMK	C2:+45.988,K10:+114.043,M16:+15.995,M20: +15.995,K21:+114.043	137 9.56 7	275 7.11 9	0.06 810 4
P0680 0	INF	GASLTLTPSTLGLASTDPPSTTIATTTK	K29:+114.043	973. 512 2	291 7.51 3	0.06 600 8
P0680 0	INF	KQDANCVRPDGPLNK	C6:+45.988,K15:+114.043	605. 626 7	181 3.85 7	0.06 666 4
P0735 6	CO N	SALSGHLETVILGLLTPAQYDASE	K16:+114.043	136 4.21 4	272 6.41 3	0.05 139 9
P0772 4	CO N	GLVLIAFSQYLQKCSYDEHAK	C14:+45.988,K21:+114.043	858. 423 1	257 2.24 6	0.00 954
P0772 4	INF	GLVLIAFSQYLQKCSYDEHAK	C14:+45.988,K21:+114.043	858. 423 1	257 2.24 6	0.01 633 4

P0772 4	INF	EAKDVFLGTFLYEYSR	K3:+114.043	102 6.50 8	205 1	0.08 621 5
P0772 4	INF	ADDRAELAK	K9:+114.043	551. 778 6	110 1.54 2	0.07 218 1
P0772 4	INF	QEPERNECFLQHK	C8:+45.988,K13:+114.043	909. 407 2	181 6.79 9	0.05 767 9
P0772 4	INF	CAEANPPACYGTVLAEFQPLVEEPK	C1:+45.988,C9:+45.988,K25:+114.043	144 1.64 8	288 1.28	0.03 993 5
P0774 2	INF	KNQIIACNGSIQSIPEIPDDLK	C7:+45.988,K22:+114.043	639. 826	255 5.27 3	0.03 428 2
P0775 9	INF	DVAETGTEAAAATGVIGGIRK	K21:+114.043	105 1.04 8	210 0.08 1	0.05 866 5
P0790 1	INF	EVIYMIEPIDEYCVQLKEFEGK	M5:+15.995,C13:+45.988,K18:+114.043	993. 799 7	297 8.37 6	0.06 300 9
P0790 1	INF	KHSQFIGYPITLFVEK	K16:+114.043	101 1.04 7	202 0.07 8	0.05 264 8
P0800 3	CO N	PIAVAKIDATSASMLASK	M14:+15.995,K18:+114.043	635. 344	190 3.00 9	0.06 568
P0800 3	CO N	LKPVIKSQ	K2:+114.043,K6:+114.043	570. 841	113 9.66 6	0.06 088 5
P0803 2	CO N	ELLEATAQKGT	K9:+114.043	637. 833 5	127 3.65 1	0.07 385 3
P0803 2	INF	SEIAELKDQLVAGEHSQAK	K7:+114.043	108 4.05 4	216 6.09 2	0.02 959
P0807 1	CO N	KDFELLCLDDTR	K1:+114.043,C7:+45.988	543. 254	162 6.73 9	0.00 308 3
P0807 1	CO N	ADAMTLDGGTMFDAGKPPY	M11:+15.995,K16:+114.043	696. 640 4	208 6.89 8	0.00 728 6
P0807 1	INF	LRPVAAEVYGTKEQPR	K12:+114.043	482. 764 7	192 7.02 8	0.03 809
P0807 1	INF	KDFELLCLDDTR	K1:+114.043,C7:+45.988	814. 377 1	162 6.73 9	0.00 091 7
P0807 1	INF	KDSTVLQNTDGK	K1:+114.043	710. 357 9	141 8.7	0.06 056 1
P0807 1	INF	KQCSSSPLEACAFLTQ	K1:+114.043,C3:+45.988,C12:+45.988	101 6.45 5	203 0.89 4	0.01 472 9
P0807 1	INF	DKEEAIWELLR	K2:+114.043	758. 394 3	151 4.77 3	0.02 934 5
P0810 3	CO N	MKPGSMSVEAFLAEANLMK	K2:+114.043,M18:+15.995	109 2.52 9	218 3.04 3	0.00 641
P0810 3	INF	MKPGSMSVEAFLAEANLMKSLQHDK	M6:+15.995,K19:+114.043	144 6.70 7	289 1.39 8	0.06 871 7

P0811 3	CO N	GTIAKSGTSEFLNK	K14:+114.043	783. 910 3	156 5.80 5	0.06 632 8
P0811 3	CO N	EEKEESDDEAAVEEEEEK	K3:+114.043,K19:+114.043	124 1	247 9.98 4	0.03 974 7
P0811 3	CO N	DISTNYYASQKK	K12:+114.043	511. 251 6	153 0.73 2	0.04 071 8
P0811 3	CO N	FLVADKVIVTSK	K6:+114.043,K12:+114.043	774. 443 8	154 6.87 2	0.05 668 8
P0811 3	INF	SGTSEFLNK	K9:+114.043	548. 767 7	109 5.52	0.05 322 5
P0822 6	CO N	ELTALMEDTMTEVK	K14:+114.043	862. 908 3	172 3.80 1	0.01 695 5
P0824 9	INF	TSAQNNAKVAVLGASGGIGQPLSLLK	K8:+114.043,K27:+114.043	141 8.28 9	283 4.56 2	0.03 509 5
P0860 7	CO N	MMVYCKPSGEWEISVCAKK	C5:+45.988,C17:+45.988,K19:+114.043	621. 275 3	248 1.07	0.08 145 7
P0860 7	CO N	IECQGNGNWSSLPTCEFDCLPPAIVNGYYTSMVYSKI TLVTYECDK	C3:+45.988,C15:+45.988,C19:+45.988,M33:+1 5.995,C45:+45.988,K47:+114.043	139 6.09 6	558 0.35 3	0.07 492 7
P0860 7	INF	VSGPTLFQMTFTAALWVAVFGKCGPPPAIPNALP	M9:+15.995,K22:+114.043,C23:+45.988	919. 470 4	367 3.85	0.06 937 5
P0877 5	CO N	QNGAAHVIAEDVK	K14:+114.043	768. 892 4	153 5.76 9	0.05 6
P0877 5	CO N	HFGHIELAKPVFHVGLVKTMK	K9:+114.043,K19:+114.043,M21:+15.995,K22: +114.043	144 7.26 9	289 2.52 2	0.08 701
P0877 5	CO N	CKYGMEIPTNIPGLGAAGPTGMFFGSAP	C1:+28.961,K2:+114.043,M22:+15.995	981. 778 2	294 2.31 1	0.09 300 5
P0877 5	CO N	NMLTDMTLQIEQISKVYMHLPTQDNK	M6:+15.995,K27:+114.043	109 3.53 4	327 7.57 8	0.06 300 9
P0877 5	INF	GIEQISKVYMHLPTQDNK	M10:+15.995,K18:+114.043	111 6.06	223 0.10 5	0.04 197 7
P0877 5	INF	LMEAAAHGESDPMKGVSENI MLGQLAPAGTGCFDLL LDAEK	M2:+15.995,M13:+15.995,C32:+45.988,K41:+ 114.043	147 4.68 7	442 1.03 6	0.04 959 9
P0877 5	INF	VVVENGELIMGILCKK	C14:+45.988,K15:+114.043,K16:+114.043	673. 686 7	201 8.03 7	0.06 810 4
P0910 3	CO N	GADALEEEDNVVLKK	K15:+114.043	928. 984 2	185 5.95 3	0.09 676 7
P0940 5	CO N	AMEDGEIDGNKVTLDWAKPK	M2:+15.995,K11:+114.043	117 4.06 6	234 6.11 6	0.05 866 5
P0940 5	CO N	ESKTLVLSNLSYSATK	K16:+114.043	927. 994 6	185 3.97 4	0.04 401 7
P0940 5	CO N	KATTTPAK	K8:+114.043	466. 264 6	930. 513 5	0.07 254 2

P09405	INF	DEFEPPIVKGVPKAK	K12:+114.043,K15:+114.043	941. 507 7	188 1	0.04 509 1
P09411	CON	TGQATVASGIPAGWMGLDCGTESSK	M15:+15.995,C19:+45.988,K25:+114.043	867. 386 4	259 9.13 6	0.04 857 5
P09411	CON	QLINNMLDKVNEMIIGGGMAFTFLK	K9:+114.043	971. 168	291 0.48 1	0.07 672 7
P09411	CON	KVLNNMEIGTSLYDEEGAK	M6:+15.995,K19:+114.043	112 1.03 9	224 0.06 3	0.04 448 1
P09411	CON	EMIIGGGMAFTFLKVLNNMEIGTSLYDEEGAK	E1:- 18.011,M2:+15.995,K14:+114.043,M19:+15.995	120 2.91 1	360 5.70 9	0.03 207 1
P09411	INF	TGQATVASGIPAGWMGLDCGTESSK	M15:+15.995,C19:+45.988,K25:+114.043	867. 386 4	259 9.13 6	0.00 222 2
P09411	INF	EMIIGGGMAFTFLKVLNNMEIGTSLYDEEGAK	E1:- 18.011,M8:+15.995,K14:+114.043,M19:+15.995	120 2.91 1	360 5.70 9	0.08 780 5
P09411	INF	VNEMIIGGGMAFTFLK	M4:+15.995,K16:+114.043	929. 466 1	185 6.91 7	0.08 515 8
P09528	CON	MGAPEAGMAEYLFDKHTLGHGDE	K15:+114.043	129 5.57 1	258 9.12 6	0.06 159 8
P09528	CON	ATDKNDPHLCDFIETYYLSEQVK	K4:+114.043,C10:+45.988	963. 774 5	288 8.3	0.00 573 5
P09528	INF	KMGAPEAGMAEYLFDK	K1:+114.043,K16:+114.043	993. 459	198 4.90 2	0.06 632 8
P09528	INF	ATDKNDPHLCDFIETYYLSEQVK	K4:+114.043,C10:+45.988	963. 774 5	288 8.3	0.00 091 7
P09528	INF	MGAPEAGMAEYLFDKHT	M8:+15.995,K15:+114.043	500. 224 3	199 6.86 6	0.04 509 1
P09602	INF	SAKPAPPKPEPKPK	K3:+114.043	793. 457 2	158 4.89 9	0.02 185 9
POC056	CON	SAAILEYLTAEVLELAGNASK	K21:+114.043	759. 737 8	227 6.19	0.01 116 2
POC056	INF	SAAILEYLTAEVLELAGNASK	K21:+114.043	113 9.10 3	227 6.19	0.01 546 3
POC056	INF	AAILEYLTAEVLELAGNASK	K20:+114.043	730. 727 1	218 9.15 8	0.06 810 4
POC056	INF	SAAILEYLTAEVLELAGNASKDLK	K21:+114.043,K24:+114.043	687. 617 6	274 6.43 9	0.01 300 4
POCG50	CON	IQDKEGIPPDQQR	K4:+114.043	819. 416 3	163 6.81 7	0.09 764 2
POCG50	CON	LIFAGKQLEDGR	K6:+114.043	730. 897	145 9.77 8	0.00 091 7
POCG50	CON	TLSDYNIQKESTLHLVLR	K9:+114.043	112 2.60 3	224 3.19 1	0.00 222 2

P0CG5 0	CO N	TLTGKTITLEVEPSDTIENVK	K5:+114.043	120 1.63 7	240 1.25 9	0.00 091 7
P0CG5 0	CO N	QDKEGIPPDQQR	K3:+114.043	762. 874 3	152 3.73 3	0.01 960 2
P0CG5 0	INF	IQDKEGIPPDQQR	K4:+114.043	819. 416 3	163 6.81 7	0.00 878 8
P0CG5 0	INF	LIFAGKQLEDGR	K6:+114.043	730. 897	145 9.77 8	0.00 091 7
P0CG5 0	INF	TLSDYNIQKESTLHLVLR	K9:+114.043	112 2.60 3	224 3.19 1	0.00 091 7
P0CG5 0	INF	TLTGKTITLEVEPSDTIENVK	K5:+114.043	120 1.63 7	240 1.25 9	0.00 091 7
P0CG5 0	INF	QDKEGIPPDQQR	K3:+114.043	762. 874 3	152 3.73 3	0.00 091 7
P0CG5 0	INF	MQIFVKTLTGK	K6:+114.043	690. 39	137 8.76 4	0.06 123 4
P1012 6	CO N	AFVPISGWNGDNMLEPSANMPWFKGWK	M20:+15.995,K27:+114.043	107 0.50 4	320 8.49	0.05 6
P1012 6	INF	IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK	M21:+15.995,K32:+114.043	123 3.24 2	369 6.70 2	0.01 518 7
P1012 6	INF	NMITGTSQADCAVLIVAAGVGEFEAGISKNG	C11:+45.988,K29:+114.043	106 1.84 3	318 2.50 5	0.06 195 4
P1063 9	CO N	LVVVDFSATWCGPCKMIK	C11:+45.988,C14:+45.988,K15:+114.043,K18:+114.043	115 9.03 8	231 6.06	0.09 840 5
P1063 9	INF	MIKPFHSLCDKYSNVVFLEVDVDDCQDVAA	M1:+15.995,K3:+114.043,C10:+45.988,C26:+45.988	125 7.22 9	376 8.66 5	0.05 498 6
P1064 9	CO N	IDGSHKITQSNAILR	K6:+114.043	883. 979 6	176 5.94 4	0.06 088 5
P1085 2	CO N	FSYGDELGLQGALPGQPAK	K19:+114.043	103 1.51 6	206 1.01 7	0.08 036 3
P1085 4	CO N	PDTGISSKAMGIMNSFVNDIFER	K8:+114.043	132 2.13 1	264 2.24 7	0.06 056 1
P1085 4	INF	KQVHPDTGISSK	K1:+114.043	470. 916 6	140 9.72 6	0.07 896 1
P1103 1	CO N	KPGETSRALASSK	K13:+114.043	723. 389 5	144 4.76 3	0.07 630 8
P1124 7	INF	VVLSCMEEAKQLVDR	C5:+45.988,M6:+15.995,K10:+114.043	632. 639 6	189 4.89 6	0.06 810 4
P1124 7	INF	FCGLPQPSTVGELGTVLKNLELAR	C2:+45.988,K18:+114.043	901. 472 3	270 1.39 3	0.03 903 5
P1135 2	CO N	NDIAWNFEKFLVGPDPGVPV	K9:+114.043	111 6.06 1	223 0.10 6	0.02 399 7

P1183 5	INF	TEIIPKSAVGELSDDSSNVVQLIK	K24:+114.043	132 8.70 6	265 5.39 7	0.07 492 7
P1183 5	INF	KLTEIIPK	K1:+114.043	528. 327 2	105 4.63 9	0.04 372 4
P1198 3	INF	FGPVGLDKMLVDDIGDVTITNDGATILK	K28:+114.043	101 1.19 4	303 0.55 8	0.09 547 1
P1198 3	INF	LATGANVILTTGGIDDMYLK	K20:+114.043	109 0.56 8	217 9.12 3	0.04 617 3
P1198 3	INF	ESMLINGYALNCVVGSQGMMPK	E1:- 18.011,M3:+15.995,C12:+45.988,M19:+15.99 5,K21:+114.043	119 3.03 9	238 4.06 3	0.07 933 9
P1226 5	INF	ELKALDGLWHFR	K3:+114.043	799. 926 1	159 7.83 7	0.08 075 6
P1226 5	INF	HPAVVMWSVANEPSSALKPAAYYFKTLITHTK	M6:+15.995,K32:+114.043	122 9.97 2	368 6.89 2	0.03 509 5
P1238 2	CO N	MGIYVGAKVFLIYEGYGLVEGGENIK	M1:+15.995,K27:+114.043	102 6.85 5	307 7.54 2	0.04 996 1
P1238 2	CO N	AGKAIGVLTSGGDAQGMNAVR	K3:+114.043	720. 039 8	215 7.09 6	0.04 012 7
P1238 2	INF	SGAGKAIGVLTSGGDAQGMNAVR	K5:+114.043,M19:+15.995	773. 389 3	231 7.14 5	0.07 896 1
P1302 0	CO N	SGRAQVHVSEEGGEPEAMLQVLGPKPALPEGTEDTAK	K37:+114.043	131 0.31 7	392 7.92 7	0.07 385 3
P1302 0	INF	EGSNKVPVDPATYQQFYGGDSYIILYNR	K5:+114.043	113 4.20 9	339 9.60 5	0.00 091 7
P1343 9	CO N	EGEINPGQTCLVIEDVVTSGASVLETVEVLQKEGLK	C10:+45.988,K32:+114.043	131 5.33 5	394 2.98 1	0.03 403 7
P1343 9	INF	EGEINPGQTCLVIEDVVTSGASVLETVEVLQKEGLK	C10:+45.988,K32:+114.043	131 5.33 5	394 2.98 1	0.03 809
P1343 9	INF	KFADIGNTVK	K10:+114.043	402. 888 1	120 5.64 1	0.04 694 9
P1406 9	CO N	KDQEVNFQEYVAFLGALALIYNEALK	K1:+114.043	103 4.20 5	309 9.59 2	0.00 091 7
P1406 9	CO N	CPLDQAIGLLVAIFHK	C1:+45.988,K16:+114.043	949. 505 7	189 6.99 6	0.03 903 5
P1406 9	CO N	NKDQEVNFQEYVAFLGALALIY	K2:+114.043	133 0.17 4	265 8.33 3	0.04 475 4
P1406 9	INF	KDQEVNFQEYVAFLGALALIYNEALK	K1:+114.043	103 4.20 5	309 9.59 2	0.00 091 7
P1406 9	INF	CPLDQAIGLLVAIFHK	C1:+45.988,K16:+114.043	949. 505 7	189 6.99 6	0.03 282 5
P1414 8	INF	LSSPRGGMK	K9:+114.043	523. 774 8	104 5.53 4	0.05 076 6

P1415 2	CO N	EIAFKDLDDVAVLVGSMR	E1:-18.011,K5:+114.043	686. 035 1	205 5.08 2	0.00 380 6
P1415 2	CO N	PMMGVLDGVLMEQLQDCALPLLQDVIATDK	M2:+15.995,M3:+15.995,M11:+15.995,C16:+4 5.988,K29:+114.043	111 2.86 9	333 5.58 4	0.04 042 1
P1421 1	CO N	KDPDAAKPEDWDER	K1:+114.043	893. 406 1	178 4.79 7	0.07 350 6
P1421 1	INF	KDPDAAKPEDWDER	K1:+114.043	893. 406 1	178 4.79 7	0.00 357 3
P1423 4	CO N	LKPGTMSPKAFLEEAQIMK	M6:+15.995,K9:+114.043,M18:+15.995,K19:+ 114.043	119 0.10 7	237 8.19 8	0.05 928
P1473 3	CO N	EQLLDVKLALDMEISAYR	E1:-18.011,K7:+114.043	110 2.07 5	220 2.13 5	0.05 346 2
P1473 3	CO N	VVAANAGVTASPTDLIWKQNSWGTGEDVK	K31:+114.043	857. 423 8	342 5.66 4	0.04 173 1
P1473 3	INF	VFKTTIPEEEEEEEPIGVAVEEER	K3:+114.043	790. 873 3	315 9.46 2	0.04 256 6
P1482 4	CO N	FPEFDANQDAEALYTAMK	K18:+114.043	725. 662	217 3.96 3	0.06 632 8
P1482 4	INF	DAFVAIVQSVKNK	K11:+114.043,K13:+114.043	823. 947 3	164 5.87 9	0.04 996 1
P1510 5	CO N	PIPGNWNAGAGCHTNFSTKAMR	C11:+45.988,K18:+114.043	807. 033 9	241 8.07 8	0.04 776 4
P1510 5	INF	ATSASSHLNK	K10:+114.043	565. 284	112 8.55 2	0.04 509 1
P1510 5	INF	GIKQMYMSLPQGEK	K3:+114.043,K14:+114.043	919. 451	183 6.88 6	0.06 568
P1510 5	INF	CHTNFSTKAMR	C1:+28.961,K8:+114.043,M10:+15.995	727. 802 8	145 3.59 9	0.04 910 9
P1586 4	CO N	KALAAAGYDVEK	K12:+114.043	675. 357 2	134 8.69 9	0.00 091 7
P1586 4	CO N	ALAAAGYDVEK	K11:+114.043	611. 309 7	122 0.60 4	0.00 091 7
P1586 4	INF	KALAAAGYDVEK	K12:+114.043	675. 357 2	134 8.69 9	0.00 091 7
P1586 4	INF	ALAAAGYDVEK	K11:+114.043	611. 309 7	122 0.60 4	0.00 091 7
P1612 5	INF	GYTNWAIGLSVADLIESMLK	K20:+114.043	765. 728 4	229 4.16 2	0.09 032
P1612 5	INF	IGLSVADLIESMLKNLSR	K14:+114.043	103 7.07 3	207 2.13 7	0.07 192 7
P1612 5	INF	LIASVADDEAAVPNNKITVVGVGQVGMACAISIL	K16:+114.043,M27:+15.995,C29:+45.988	117 2.27 1	351 3.78 9	0.06 231 8

P1654 6	CO N	EPMVARK	M3:+15.995,K7:+114.043	480. 750 8	959. 486	0.03 639
P1654 6	CO N	KHALLEADVAAHQDR	K1:+114.043	894. 461 6	178 6.90 8	0.08 437 5
P1654 6	CO N	AFLNEDLGDSLDSVEALLK	K20:+114.043	113 8.58 7	227 5.15 8	0.03 051 5
P1654 6	CO N	DINKVAEDLESEGLMAEEVQAVQQQEVYGAM	K4:+114.043,M15:+15.995	118 5.21 6	355 2.62 4	0.03 809
P1654 6	INF	EPMVARK	M3:+15.995,K7:+114.043	480. 750 8	959. 486	0.04 776 4
P1654 6	INF	EEKITALDEFATK	K3:+114.043	804. 91	160 7.80 4	0.03 736 3
P1685 8	CO N	VINGKPITIFQERDPTNIK	K5:+114.043	114 9.13 5	229 6.25 4	0.00 190 4
P1685 8	CO N	VINGKPITIFQER	K5:+114.043	814. 960 1	162 7.90 5	0.00 190 4
P1685 8	CO N	IVEGLMTTVHAITATQK	K17:+114.043	964. 020 1	192 6.02 5	0.06 701 2
P1685 8	INF	VINGKPITIFQERDPTNIK	K5:+114.043	114 9.13 5	229 6.25 4	0.00 123 3
P1687 9	INF	VKTLLQMVGDAAAGMEYLESK	K21:+114.043	118 4.59 9	236 7.18 1	0.03 132 7
P1687 9	INF	QMLQEAIQGLQIALCSQDKLQAQQELLQSK	M2:+15.995,C15:+45.988,K19:+114.043	118 7.26 9	355 8.78 5	0.03 924 8
P1718 2	CO N	EVILPVPAFNVINGGSHAGNKLAMQEFMILPVGASSFR	E1:- 18.011,K21:+114.043,M24:+15.995,M28:+15. 995	138 0.37 9	413 8.11 3	0.04 423
P1718 2	CO N	GIQVVGDDLTVTNPKR	K15:+114.043	913. 492 5	182 4.96 9	0.06 901 4
P1718 2	INF	IGAEVYHNLKNVIK	K10:+114.043	856. 478 7	171 0.94 2	0.05 436 4
P1722 5	CO N	SLFSSNGGVVKGFK	K14:+114.043	770. 910 1	153 9.80 5	0.06 969 8
P1722 5	CO N	MDGIVPDIAVGTK	M1:+15.995,K13:+114.043	723. 369 5	144 4.72 3	0.06 432 4
P1742 6	CO N	VHLLNDQHMGVVTAASLITCLCK	C21:+45.988,C23:+45.988,K24:+114.043	138 6.18 1	277 0.34 7	0.08 473 4
P1742 6	CO N	FINLFPETKATI	K9:+114.043	754. 411 9	150 6.80 8	0.06 159 8
P1742 6	INF	MGEAFAADIPRILVAGDSMDSVK	M19:+15.995,K23:+114.043	126 2.11 5	252 2.21 5	0.02 522 7
P1742 6	INF	FHLCSVATRALLSTYIK	C4:+45.988,K18:+114.043	109 8.58 8	219 5.16	0.04 724 1

P1742 7	CO N	TTLAQKNPEEFK	K6:+114.043	760. 391 7	151 8.76 8	0.07 090 1
P1742 7	CO N	MGLALHCIANVGSREMAEAFAGEIPK	C7:+45.988,M16:+15.995,K26:+114.043	964. 461 2	289 0.36	0.04 938 8
P1742 7	INF	TTLAQKNPEEFK	K6:+114.043	760. 391 7	151 8.76 8	0.09 764 2
P1742 7	INF	FENQLLQJGLKSEFR	K11:+114.043	968. 518 5	193 5.02 1	0.06 969 8
P1743 3	INF	LEVSDGEADGLEPGPGLHGETGSKK	K25:+114.043	135 3.66 5	270 5.31 4	0.05 294
P1771 0	CO N	SQLFDHVAECLGDFMEKR	C10:+45.988,M15:+15.995,K17:+114.043	115 1.00 9	230 0.00 3	0.07 254 2
P1771 0	INF	EGVQNAKEI	E1:-18.011,K7:+114.043	542. 275 4	108 2.53 5	0.05 111 3
P1771 0	INF	YNPTASVK	K8:+114.043	497. 254 2	992. 492 8	0.08 145 7
P1787 9	CO N	AKNTAIGIDLGTTYSCVGVFQHGK	K2:+114.043,C16:+45.988	132 0.65	263 9.28 4	0.03 157 8
P1787 9	CO N	NTAIGIDLGTTYSCVGVFQHGKVEIIANDQG	C14:+45.988,K22:+114.043	112 7.54 7	337 9.61 8	0.03 639
P1787 9	INF	NTAIGIDLGTTYSCVGVFQHGKVEIIANDQG	C14:+45.988,K22:+114.043	112 7.54 7	337 9.61 8	0.01 663 3
P1787 9	INF	LESYAFNMKSAVEDEGLK	M8:+15.995,K18:+114.043	721. 009 4	216 0.00 5	0.05 668 8
P1824 2	INF	KFDGILGMGYPHISVNNVLPVFDNLMQQK	M26:+15.995,K29:+114.043	113 5.57 6	340 3.70 6	0.05 111 3
P1824 2	INF	VFVAAKFDGILGMGYPHISVNNVLPVFDNLMQQK	M13:+15.995,K34:+114.043	129 8.00 3	389 0.98 5	0.05 836 2
P1865 3	CO N	KGAMAATYSALNSSKPTQLKPIESSILAQR	K1:+114.043,K15:+114.043	872. 465 3	348 5.83	0.06 701 2
P1865 3	CO N	GAMAATYSALNSSKPTQLKPI	M3:+15.995,K14:+114.043,K20:+114.043	124 5.63 7	248 9.25 9	0.06 701 2
P1865 3	INF	AGSEKADPSQFELL	K5:+114.043	803. 391 9	160 4.76 8	0.04 694 9
P1865 3	INF	TPCYTANFVAPEVLKR	C3:+45.988,K15:+114.043	984. 987 8	196 7.96	0.05 895 8
P1876 0	CO N	IILEEGKEILVGDVGQTVDDPYTTFVK	K7:+114.043	103 1.54	309 1.59 7	0.00 091 7
P1876 0	INF	IILEEGKEILVGDVGQTVDDPYTTFVK	K7:+114.043	103 1.54	309 1.59 7	0.00 091 7
P1876 0	INF	LEEGKEILVGDVGQTVDDPYTTFVK	K5:+114.043	143 3.72 2	286 5.42 8	0.00 992

P18760	INF	EDLVFIFWAPENAPLK	K16:+114.043	100 2.01 8	200 2.02	0.03 182 7
P19096	CON	ALALDNMVAALK	K12:+114.043	448. 583 8	134 2.72 8	0.04 996 1
P19096	INF	MLENQTPELFQDVNPKP	K17:+114.043	715. 693 6	214 4.05 7	0.05 231 3
P19096	INF	DLFLNQPHAVLSSFVLAEEK	K20:+114.043	118 5.64 5	236 9.27 4	0.06 465 9
P19096	INF	AAVNEFVEQLKQEGVFAK	K18:+114.043	106 1.05 3	212 0.09	0.07 254 2
P19096	INF	LALQNAYQAIRSGECPAALVGGINLLKPNTSVQFMK	C15:+45.988,M36:+15.995,K37:+114.043	136 9.05 2	410 4.13 3	0.05 668 8
P19096	INF	SNLSNTSHAPKLDPGSPQLQQVLK	K11:+114.043,K24:+114.043	139 4.71 5	278 7.41 5	0.08 109
P19096	INF	IQVLVSTSNVSSLEGARALIAEATK	K25:+114.043	891. 159 6	267 0.45 5	0.02 784 1
P20029	CON	LYGSGGPPPTGEEDTSEKDE	K18:+114.043	108 9.97	217 7.92 4	0.00 126 5
P20029	CON	AVQAGVLSGDQDGTDLVLLDVCPLTLGIETVGGVMTK	C22:+45.988,K37:+114.043	128 2.31 8	384 3.93 1	0.03 755 2
P20029	INF	LYGSGGPPPTGEEDTSEKDE	K18:+114.043	108 9.97	217 7.92 4	0.00 126 5
P20029	INF	DVGTVVGIDLGTTYSVGVFK	C16:+45.988,K21:+114.043	114 5.55 9	228 9.10 2	0.05 562 4
P20029	INF	TLGIETVGGVMTKLIPR	K13:+114.043	633. 696 5	189 8.06 6	0.07 192 7
P20060	INF	LESFYIKK	K7:+114.043	571. 316 8	114 0.61 8	0.07 218 1
P20060	INF	PAILSAPWYLDLISYGQDWK	K20:+114.043	817. 418 4	244 9.23 2	0.04 559 7
P21550	CON	HIADLAGNPDVLPVPAFNVINGGSHAGNKL	K30:+114.043	107 8.90 6	323 3.69 5	0.06 300 9
P22682	INF	KSSGAGGGGSGGSGAGGLIGLMK	K1:+114.043,K23:+114.043	523. 512 2	209 0.01 8	0.06 701 2
P22752	CON	NDEELNKLGR	K7:+114.043	707. 868 4	141 3.72 1	0.00 091 7
P22752	CON	VTIAQGGVLPNIQAVLLPKK	K19:+114.043	108 7.15 8	217 2.29 9	0.00 091 7
P22752	CON	VTIAQGGVLPNIQAVLLPK	K19:+114.043	102 3.11	204 4.20 5	0.02 522 7
P22752	INF	NDEELNKLGR	K7:+114.043	707. 868 4	141 3.72 1	0.02 934 5

P2275 2	INF	VTIAQGGVLPNIQAVLLPKK	K19:+114.043	108 7.15 8	217 2.29 9	0.00 091 7
P2275 2	INF	VTIAQGGVLPNIQAVLLPK	K19:+114.043	102 3.11	204 4.20 5	0.06 536 7
P2275 2	INF	TIAQGGVLPNIQAVLLPKK	K19:+114.043	692. 084 8	207 3.23 1	0.07 782 3
P2289 2	INF	PFLLDGLSSQPLFNDIAPGIPSITAYSKNGLK	K28:+114.043	116 3.28 8	348 6.84	0.04 559 7
P2311 6	INF	QLDSAISMELWQEAFK	K16:+114.043	100 5.48 6	200 8.95 6	0.08 075 6
P2406 3	CO N	EMLHVYVLSGIGGLVLLFLALYKVGFFK	M2:+15.995,K31:+114.043	121 0.69 1	362 9.05	0.03 552 7
P2406 3	INF	FNMESSSGISADLSKGHAVVGAVGAK	M3:+15.995,K16:+114.043	138 1.69 3	276 1.37 1	0.02 986 6
P2406 3	INF	MPVSCEELTEGSSLLTKLK	C5:+45.988,K20:+114.043	776. 050 1	232 5.12 7	0.02 851 6
P2406 3	INF	MELSSSGISADLSKGHAVVGAVGAK	K25:+114.043	829. 095 9	248 4.26 4	0.06 937 5
P2427 0	CO N	HMNGYGSHTFK	M2:+15.995,K11:+114.043	704. 807 4	140 7.59 9	0.03 157 8
P2427 0	INF	PQTHLKDPMVWDFWLSRPESLHQVSFLFSR	K6:+114.043	100 7.74 5	402 6.94 8	0.00 53
P2436 9	CO N	NMKVLFAAALIVGSVVFLLPGPSVANDK	M2:+15.995,K3:+114.043,K29:+114.043	107 6.60 1	322 6.77 9	0.06 432 4
P2436 9	INF	DVIIVDSGKIEVEKPFIAK	K14:+114.043,K20:+114.043	600. 585 5	239 8.31 1	0.08 701
P2436 9	INF	SMANAGKDTNGSQFFITTVK	K20:+114.043	111 6.04 2	223 0.06 9	0.07 782 3
P2452 7	CO N	DKSLSNVIAHEISHSWTGNLVTNK	K2:+114.043,K24:+114.043	720. 367 1	287 7.43 7	0.07 192 7
P2454 7	CO N	EDLVVAPAGVTLKEAN	E1:-18.011,K13:+114.043	574. 640 9	172 0.89 9	0.03 876 9
P2454 7	INF	AQGVSGAVQDK	K11:+114.043	587. 297 1	117 2.57 9	0.04 800 5
P2520 6	INF	DHQTITIQEMPEKAPA	M10:+15.995,K13:+114.043	646. 979 6	193 7.91 5	0.05 895 8
P2544 4	CO N	IKSLEEIYLSPIK	K2:+114.043	954. 048 6	190 6.08 2	0.07 861 1
P2544 4	INF	IGDYNGHVGLGVKCSK	K13:+114.043,C14:+45.988,K16:+114.043	960. 957 1	191 9.89 9	0.06 969 8
P2591 1-2	CO N	IITEFMAKGSLLDFLK	M6:+15.995,K8:+114.043	978. 529 8	195 5.04 4	0.08 621 5

P2591 1-2	INF	ESETLKGSFS	E1:-18.011,K6:+114.043	590. 778	117 9.54	0.03 780 3
P2591 1-2	INF	KWTAPEAINFGCFTIK	K1:+114.043,C12:+45.988,K16:+114.043	105 0.50 6	209 8.99 7	0.05 346 2
P2597 6	INF	SQEDMLTLLECMK	C11:+45.988,M12:+15.995,K13:+114.043	572. 915 9	171 5.72 4	0.06 369 3
P2597 6	INF	VAFKDFSGDMCK	M10:+15.995,C11:+45.988,K12:+114.043	762. 320 7	152 2.62 6	0.09 501 2
P2603 9	CO N	GDYQDGYYSVQTTEGEQIAQLIAGYIDIILKK	K31:+114.043	123 6.28 8	370 5.84 1	0.05 633 6
P2603 9	CO N	DYTAVGCAVTTISSNLTEMSRGVK	C7:+45.988,K24:+114.043	133 2.12 8	266 2.24 2	0.05 962 2
P2603 9	CO N	KAIHAVTVQEMVTK	K1:+114.043	766. 429 8	153 0.84 4	0.06 056 1
P2603 9	CO N	PLTLAAVGAASKTSLHPQQMALDQTK	K12:+114.043	726. 896 3	290 3.55 4	0.04 343 2
P2603 9	CO N	ALHYGRECANGYLELLDHVLLTLQKPNPDLK	C8:+45.988,K25:+114.043,K31:+114.043	126 9.98 2	380 6.92 4	0.08 621 5
P2603 9	CO N	SKVTVDMLMTICAR	K2:+114.043,C12:+45.988	865. 409 5	172 8.80 3	0.02 759 2
P2603 9	CO N	TIMVDDSKTVDMLMTICAR	K8:+114.043,M13:+15.995,C18:+45.988	121 0.55 4	241 9.09 3	0.06 568 3
P2603 9	CO N	ELGHGCSALVTKAGALQCSPSDVYTK	E1:- 18.011,C6:+45.988,K12:+114.043,C18:+45.988	941. 769 9	282 2.28 6	0.03 974 7
P2603 9	INF	ISATKAAAGK	K10:+114.043	516. 296 4	103 0.57 7	0.03 010 1
P2603 9	INF	QYFEPLTLAAVGAASKTSLHPQQMALDQTK	Q1:-17.027,K16:+114.043,M24:+15.995	868. 446 5	346 9.75 5	0.07 003 4
P2603 9	INF	VQSAKEVANSTANLVK	K5:+114.043,K16:+114.043	944. 000 7	188 5.98 6	0.04 197 7
P2603 9	INF	DVVKLGAASLGAEDPETQVVLINAVK	K4:+114.043	917. 503 2	274 9.48 6	0.05 526 5
P2603 9	INF	VLGEAMTGISQNAKNGNLPEFGDAIAT	M6:+15.995,K14:+114.043	950. 131 5	284 7.37 1	0.04 530 6
P2603 9	INF	QLITMCTQQAPGQK	C6:+45.988,K14:+114.043	853. 905 5	170 5.79 5	0.04 559 7
P2603 9	INF	MVEAAKGAAHPDSEEQQQR	K6:+114.043	113 4.02 8	226 6.04 7	0.08 816 7
P2603 9	INF	ELLENPVQPINDMSYFGCLDSVMENSKVLGEAM	E1:-18.011,C18:+45.988,K27:+114.043	954. 434 5	381 3.70 7	0.05 346 2
P2603 9	INF	ATQTIAAAQHAASAPK	K16:+114.043	825. 932 1	164 9.84 9	0.06 195 4

P2604 0	CO N	EKEQMLR	K2:+114.043,M5:+15.995	532. 264 3	106 2.51 3	0.06 337 3
P2604 0	INF	YPEDVAELIQDITQK	K16:+114.043	100 2.99 2	200 3.96 9	0.01 943 7
P2604 0	INF	DSAMLEYLKIAQDLEMYGINY	K9:+114.043,M16:+15.995	130 5.60 9	260 9.20 3	0.02 603
P2604 3	CO N	FTAKIALLEEAK	K12:+114.043	724. 411 9	144 6.80 8	0.04 042 1
P2636 9	CO N	DSATGLSKGYAFCEYVDINVTDQAIAGLNGM	K8:+114.043,C13:+45.988	112 8.51 3	338 2.51 6	0.04 197 7
P2636 9	INF	YGLVKSIEIPRPVDGVEVPGCGK	C21:+45.988,K23:+114.043	128 6.66 7	257 1.31 9	0.05 962 2
P2644 3	CO N	ALASLMTYKCAVVDVPFGGAK	K9:+114.043,C10:+45.988,K21:+114.043	604. 552 8	241 4.18	0.05 962 2
P2644 3	CO N	VIPDLYLNAGGVTVSYFEWLK	K21:+114.043	124 9.65 2	249 7.28 9	0.04 315 4
P2644 3	CO N	TGRGVFHGIENFINEASYMSILGMTPGFGDK	M19:+15.995,M24:+15.995,K31:+114.043	116 4.55 1	349 0.62 9	0.04 644 6
P2645 0	CO N	EEYTRTSQEIQMK	K13:+114.043	878. 912 7	175 5.81	0.06 465 9
P2663 8	INF	EFMPPGLQELIPVK	M3:+15.995,K15:+114.043	937. 990 3	187 3.96 5	0.04 285 7
P2700 5	CO N	ALSNLIDVYHNYSNIQGNHHALYK	K24:+114.043	144 9.71 8	289 7.42 1	0.03 533 2
P2700 5	CO N	KMVTTECPQFVQNNIENLFR	K1:+114.043,C7:+45.988	134 2.65 4	268 3.29 2	0.00 091 7
P2700 5	CO N	ELDINSDNAINFEEFLAMVIK	M18:+15.995,K21:+114.043	852. 416 6	255 4.22 6	0.05 668 8
P2700 5	INF	ALSNLIDVYHNYSNIQGNHHALYK	K24:+114.043	144 9.71 8	289 7.42 1	0.05 866 5
P2700 5	INF	KMVTTECPQFVQNNIENLFR	K1:+114.043,C7:+45.988	134 2.65 4	268 3.29 2	0.00 091 7
P2700 5	INF	ELDINSDNAINFEEFLAMVIK	M18:+15.995,K21:+114.043	852. 416 6	255 4.22 6	0.00 747 5
P2700 5	INF	ELDINSDNAINFEEFLAMVIKGVASHK	K21:+114.043	805. 160 9	321 6.61 3	0.04 694 9
P2700 5	INF	ELDINSDNAINFEEFLAMVIKGV	K21:+114.043	932. 137 7	279 3.39	0.03 329 7
P2700 5	INF	MPSELEKALSNLIDVYHNYSNIQGNHHALYK	K7:+114.043	928. 960 4	371 1.81	0.05 562 4
P2761 2	CO N	GKPANQLLALR	K2:+114.043	647. 883 7	129 3.75 2	0.01 601 4

P2761 2	INF	SHLINLLNPKGKPANQLLALR	K10:+114.043	808. 812	242 3.41 3	0.05 294
P2761 2	INF	DDSNAIQLAKSLGVDSQIK	K19:+114.043	529. 778	211 5.08 1	0.04 012 7
P2761 2	INF	CMMTLQGHTAAVWAVKI	C1:+45.988,M3:+15.995,K16:+114.043	101 8.48 4	203 4.95 2	0.05 025 6
P2766 1	CO N	LLGGVTIAQGGVLPNIQAVLLPKK	K23:+114.043	838. 511 3	251 2.51 1	0.00 091 7
P2766 1	CO N	DEELNKLGGVTIAQGGVLPNIQAVLLPK	K6:+114.043	103 8.59 1	311 2.75	0.00 091 7
P2766 1	CO N	LGGVTIAQGGVLPNIQAVLLPK	K22:+114.043	113 6.67 4	227 1.33 2	0.06 123 4
P2766 1	INF	LLGGVTIAQGGVLPNIQAVLLPKK	K23:+114.043	838. 511 3	251 2.51 1	0.00 091 7
P2766 1	INF	DEELNKLGGVTIAQGGVLPNIQAVLLPK	K6:+114.043	103 8.59 1	311 2.75	0.00 091 7
P2777 3	INF	FDGNLKR	K6:+114.043	482. 254 5	962. 493 4	0.04 750 8
P2787 0	INF	TPPKMTEYDK	K4:+114.043,K10:+114.043	719. 338 2	143 6.66 1	0.03 229 7
P2807 6	CO N	VILGDELPK	K9:+114.043	549. 314 2	109 6.61 3	0.02 759 2
P2807 6	INF	VILGDELPK	K9:+114.043	549. 314 2	109 6.61 3	0.08 003 2
P2829 3	CO N	LVCSNVAQGIVSYGSNNGNPPAVFTK	C3:+45.988,K26:+114.043	139 8.67 7	279 5.33 7	0.05 139 9
P2829 3	CO N	SNNGNPPAVFTKIQSFMPIK	M17:+15.995,K21:+114.043	836. 090 3	250 5.24 8	0.04 667 3
P2865 0	CO N	AVSFIGNGVVIHPLGLFEEAEKNEK	K22:+114.043,K25:+114.043	975. 842 3	292 4.50 3	0.06 231 8
P2865 6	CO N	PDEEDEVSEELKEK	K14:+114.043	597. 271 2	178 8.79	0.04 229 4
P2865 6	INF	TVTKTVSNDSE	K4:+114.043	656. 823 2	131 1.63 1	0.07 060 6
P2865 6	INF	PTEEECEWKPDDEDEVSEELK	C6:+45.988,K21:+114.043	135 5.55 5	270 9.09 5	0.04 828 8
P2866 5	CO N	PAPSPEDLTLSMSTIMWLTK	M16:+15.995,K20:+114.043	117 4.58	234 7.14 4	0.04 475 4
P2866 5	CO N	IMQWRDIK	M2:+15.995,K8:+114.043	610. 316 8	121 8.61 8	0.08 473 4
P2866 5	CO N	YITMALLESSLATHPVVSKALSCLESSWK	K20:+114.043,C24:+45.988,K30:+114.043	117 9.26	353 4.75 7	0.03 876 9

P2866 5	CO N	PETWVWDIVTVNSTGLAEVEMTVPDTITEWK	K31:+114.043	915. 950 5	365 9.77 1	0.08 075 6
P2866 5	INF	LSSVPLQAFKPFVEVSLPYSVVRGEAFMLK	K32:+114.043	123 3.67 3	369 7.99 5	0.08 312 1
P2866 5	INF	KYFPETWVWDIVTVNSTGLAEVEMTVPDTI	K1:+114.043	889. 441	355 3.73 3	0.04 229 4
P2866 5	INF	PEEPPRK	K7:+114.043	483. 754 4	965. 493 1	0.05 322 5
P2866 5	INF	TVVKVLIVEPEGIK	K4:+114.043	819. 496	163 6.97 6	0.03 609 6
P2866 5	INF	LVMAQGSIIQTGNHTHQVEPGEAPVK	M3:+15.995,K26:+114.043	143 6.22 5	287 0.43 5	0.06 937 5
P2934 1	CO N	KITGMILLEIDNSELLHMLESPELR	K1:+114.043,M17:+15.995	750. 386 6	299 7.51 5	0.04 071 8
P2934 1	CO N	DEAVAVLQAHQAK	K13:+114.043	747. 389 5	149 2.76 3	0.04 617 3
P2934 1	INF	LFPLIQAMHPSLAGKI	M8:+15.995,K15:+114.043	933. 519 5	186 5.02 3	0.04 938 8
P2935 1	INF	VIDMLMESISTKGLDCDIDIQK	K12:+114.043,C16:+45.988,K22:+114.043	914. 434 3	274 0.28	0.05 803 7
P2941 6	CO N	KGFTDFK	K1:+114.043,K7:+114.043	535. 767 5	106 9.51 9	0.05 171 8
P2969 9	CO N	ETLHSPKVGQPGAAGPVSPMCPGR	E1:-18.011,K7:+114.043,C21:+45.988	125 8.10 4	251 4.19 3	0.08 207 5
P2975 8	INF	MNTGVEAGETACK	M1:+15.995,C12:+45.988,K13:+114.043	743. 802 9	148 5.59	0.05 197 5
P2975 8	INF	LEVLEENLAENADK	K15:+114.043	915. 442 4	182 8.86 9	0.04 644 6
P3068 1	CO N	IKIEHPGLSIGDTAK	K2:+114.043,K15:+114.043	903. 989 7	180 5.96 4	0.03 282 5
P3068 1	CO N	KIEHPGLSIGDTAK	K1:+114.043	790. 426 1	157 8.83 7	0.00 091 7
P3068 1	INF	IKIEHPGLSIGDTAK	K2:+114.043,K15:+114.043	903. 989 7	180 5.96 4	0.08 741 6
P3068 1	INF	KIEHPGLSIGDTAK	K1:+114.043	790. 426 1	157 8.83 7	0.02 643
P3123 0	INF	KIWEQIQPDLHTNAECVATYK	C16:+45.988,K21:+114.043	883. 093 6	264 6.25 7	0.04 423
P3132 4	CO N	FIVESGEVK	K9:+114.043	561. 296 1	112 0.57 7	0.00 981
P3172 5	CO N	QMVEAQLATFMK	M11:+15.995,K12:+114.043	763. 871 3	152 5.72 7	0.00 091 7

P3172 5	CO N	RNEALINDIMEDLDTNQDNQLSFEECMMLMAK	C26:+45.988,K32:+114.043	131 2.24 2	393 3.70 3	0.00 112 9
P3172 5	CO N	NEALINDIMEDLDTNQDNQLSFEECMMLMAK	C25:+45.988,M26:+15.995,K31:+114.043	126 5.54	379 3.59 6	0.00 254 6
P3172 5	CO N	EFRQMVEAQLATFMK	M14:+15.995,K15:+114.043	979. 977 4	195 7.93 9	0.00 582 4
P3172 5	CO N	EALINDIMEDLDTNQDNQLSFEECMMLMAK	C24:+45.988,M28:+15.995,K30:+114.043	920. 896 2	367 9.55 3	0.09 805 6
P3172 5	CO N	NEALINDIMEDLDTNQDNQLSFEECMMLMAKL	C25:+45.988,M29:+15.995,K31:+114.043	130 3.23 5	390 6.68	0.02 316 6
P3172 5	INF	QMVEAQLATFMK	M11:+15.995,K12:+114.043	763. 871 3	152 5.72 7	0.00 821 1
P3172 5	INF	RNEALINDIMEDLDTNQDNQLSFEECMMLMAK	C26:+45.988,K32:+114.043	131 2.24 2	393 3.70 3	0.00 263 3
P3172 5	INF	NEALINDIMEDLDTNQDNQLSFEECMMLMAK	C25:+45.988,M26:+15.995,K31:+114.043	126 5.54	379 3.59 6	0.00 622 3
P3172 5	INF	NEALINDIMEDLDTNQDNQLSFEECMMLMAKLI	C25:+45.988,M26:+15.995,M27:+15.995,K31: +114.043	100 9.94 8	403 5.76	0.09 724 8
P3172 5	INF	EFRQMVEAQLATFMK	M14:+15.995,K15:+114.043	979. 977 4	195 7.93 9	0.00 14
P3172 5	INF	NEALINDIMEDLDTNQDNQLSFEECMMLMAKL	C25:+45.988,M26:+15.995,K31:+114.043	130 3.23 5	390 6.68	0.00 841 4
P3172 5	INF	NKAPSQMER	K2:+114.043,M7:+15.995	595. 783 4	118 9.55 1	0.09 724 8
P3172 5	INF	IFACHEKLHENNPR	C4:+45.988,K7:+114.043	934. 438 9	186 6.86 2	0.06 871 7
P3172 5	INF	NEALINDIMEDLDTNQDNQLSFEECMMLMAKLIFACH	C25:+45.988,M26:+15.995,M27:+15.995,M29: +15.995,K31:+114.043,C36:+45.988	113 9.98 7	455 5.91 6	0.03 993 5
P3206 7	INF	IKLDEGWVPLETMK	K2:+114.043,K15:+114.043	100 0.53	199 9.04 5	0.03 666 5
P3527 8	CO N	AGRGAARPNGPAAGNK	K17:+114.043	409. 716 6	163 4.83 5	0.05 294
P3544 1	CO N	FQMIPLDPK	K9:+114.043	601. 816 1	120 1.61 7	0.04 229 4
P3544 1	CO N	SQNDPNWVVRHQGK	K14:+114.043	889. 938 2	177 7.86 1	0.06 772 5
P3544 1	INF	RNPCTDGTHDCNK	C4:+45.988,C11:+45.988,K13:+114.043	833. 813 9	166 5.61 2	0.07 031 5
P3544 1	INF	NKGCSSSTNVLLTDNNVVGSSPAIR	K2:+114.043,C4:+45.988	974. 147 2	291 9.41 8	0.07 492 7
P3544 1	INF	CKPRNPCTDGTHDCNK	C1:+45.988,K2:+114.043,C7:+45.988,C14:+45. 988,K16:+114.043	107 7.90 8	215 3.8	0.05 866 5

P35505	CO N	RPMGQMRPDNSKPPVYGACRLDMELEMAFFV	M3:+15.995,K12:+114.043,C19:+45.988,M24: +15.995,M28:+15.995	130 2.93 6	390 5.78 6	0.06 536 7
P35564	CO N	KQSNAMEYK	K1:+114.043	606. 788 1	121 1.56 1	0.07 598 5
P35564	CO N	KAADGAAEPGVVLQ	K1:+114.043	480. 588 4	143 8.74 2	0.04 617 3
P35564	CO N	QMLEAAEERPWLWVVYILTVALPVFLVILFCCSGK	Q1:- 17.027,M2:+15.995,C31:+45.988,C32:+45.988 ,K35:+114.043	141 4.71 8	424 1.13	0.06 901 4
P35585	CO N	FELMSYRLNTHVKPLIWIESVIEK	K13:+114.043	102 0.55 2	305 8.63 1	0.06 300 9
P35585	CO N	GDVDMSEVEHFMPILEKEEGMLSPILA	M12:+15.995,K18:+114.043	113 6.19 1	340 5.54 9	0.05 139 9
P35585	CO N	LNTHVKPLIWIESVIEKHSHSR	K6:+114.043	136 9.24 9	273 6.48 2	0.04 589 2
P35700	INF	EYFSKQK	K5:+114.043	522. 262	104 2.50 8	0.03 903 5
P35979	CO N	ELSGTIKEILGTAQSVGC	E1:-18.011,K7:+114.043,C18:+45.988	974. 479 8	194 6.94 4	0.05 767 9
P35979	INF	KEILGTAQSVGCNVDGR	K1:+114.043,C12:+45.988	636. 309 1	190 5.90 4	0.06 369 3
P38060	CO N	LIDMLSEAGLPVIEATSFVSPK	M4:+15.995,K22:+114.043	816. 43	244 6.26 7	0.09 676 7
P38647	CO N	KDSETGENIR	K1:+114.043	631. 802 8	126 1.59	0.04 589 2
P38647	INF	MAGDNKLLGQFTLIGIPPAPR	M1:+15.995,K6:+114.043	117 0.13 1	233 8.24 7	0.05 866 5
P39655	INF	GILSLPEGTARLAGDNALDVFQK	K23:+114.043	833. 778 8	249 8.31 3	0.06 600 8
P39655	INF	LPSGMEELQAQLEKELK	M5:+15.995,K14:+114.043	103 7.03 1	207 2.04 6	0.03 455 1
P40124	CO N	KEPALLELEGK	K1:+114.043	670. 875 2	133 9.73 5	0.07 090 1
P40124	CO N	KPQTSPSPKATKK	K1:+114.043,K13:+114.043,K14:+114.043	919. 000 6	183 5.98 6	0.07 630 8
P40142	CO N	GEVSEGSVWEAMAFAGIYKLDNLVAIFDINR	K19:+114.043	117 6.92 1	352 7.74	0.05 139 9
P40142	CO N	TVIGAGVTLHEALAAESLKK	K20:+114.043,K21:+114.043	769. 761	230 6.26	0.04 071 8
P40142	INF	GEVSEGSVWEAMAFAGIYKLDNLVAIFDINR	K19:+114.043	117 6.92 1	352 7.74	0.07 672 7
P40142	INF	GPSQMALEDLAMFRSVPMTSTFYPSDGVATEK	M5:+15.995,M12:+15.995,K32:+114.043	120 3.23 1	360 6.66 8	0.06 401 4

P4124 1	CO N	CIKNATAQAFLAEASVMTQLR	C1:+45.988,K3:+114.043	847. 747 4	254 0.21 9	0.05 053 6
P4124 1	CO N	LGVIVEEKGGLYIVTEYMAK	K8:+114.043,M18:+15.995,K20:+114.043	614. 824 6	245 5.26 7	0.05 803 7
P4124 1	INF	ATAQAFLAEASVMTQLRHSNLVQLLGIVIVEEK	K32:+114.043	119 4.31 1	357 9.90 8	0.04 116 7
P4124 5	CO N	LMLQKQLSLPQTGELDSQTLK	M2:+15.995,K21:+114.043	125 1.16 8	250 0.32 1	0.07 125 9
P4124 5	INF	YTEHNGEGKPCVFPFIFEGR	K10:+114.043,C12:+45.988	848. 72	254 3.13 7	0.04 116 7
P4124 5	INF	CTTDGRNDGTPWCSTTADYDK	C1:+45.988,C13:+45.988,K21:+114.043	628. 992 9	251 1.94 1	0.05 346 2
P4124 5	INF	YSYLEGFPLNKDDIDGIQYLYGR	K11:+114.043	142 7.19 1	285 2.36 6	0.05 803 7
P4222 5	CO N	KMFLMLDNK	K1:+114.043,M2:+15.995,K9:+114.043	692. 342 2	138 2.66 9	0.06 056 1
P4222 5	CO N	FNILGHTKVMNMEESTNGSLA	K9:+114.043,M13:+15.995	842. 065 6	252 3.17 4	0.08 956 6
P4222 5	CO N	NDLLCLWNDGCIMGFISKER	C5:+45.988,C11:+45.988,M13:+15.995,K18:+114.043	850. 376 1	254 8.10 5	0.04 589 2
P4222 5	INF	NILGHTKVMNMEESTNGSLAAELR	K8:+114.043,M12:+15.995	949. 464 5	284 5.37	0.06 810 4
P4222 5	INF	KVMAAENIPENPLK	M3:+15.995,K14:+114.043	842. 441	168 2.86 6	0.01 653 5
P4222 5	INF	KELSAVTFPDIIR	K1:+114.043	534. 967 1	160 1.87 8	0.08 312 1
P4222 7	CO N	ESNNGSLSAEFKHLTLR	E1:-18.011,K12:+114.043	100 0.00 4	199 7.99 2	0.08 109
P4222 8	CO N	QPCMPHPQRPMVLK	C3:+45.988,M4:+15.995,K15:+114.043	969. 962 8	193 7.91	0.09 840 5
P4222 8	INF	QPCMPHPQRPMVLK	C3:+45.988,M4:+15.995,K15:+114.043	969. 962 8	193 7.91	0.08 851 8
P4266 9	CO N	GSLGHPGSGSGSGGGGGGGGGGGGGGGGGGGGAPGG LQHETQELASKR	K45:+114.043	129 1.59 3	387 1.75 7	0.00 325 1
P4266 9	CO N	GSGGSLGHPGSGSGSGGGGGGGGGGGGGGGGGGGGA PGGLQHETQELASKR	K48:+114.043	135 8.61 8	407 2.83 2	0.04 285 7
P4266 9	CO N	GGSLGHPGSGSGSGGGGGGGGGGGGGGGGGGGGAPG GLQHETQELASKR	K46:+114.043	131 0.60 1	392 8.77 8	0.01 006 6
P4266 9	CO N	GSEQGGAALGSGGSLGHPGSGSGSGGGGGGGGGGGGG GSGGGGGGAPGGLQHETQELASKR	K57:+114.043	121 1.80 5	484 3.18 8	0.02 566 2
P4266 9	CO N	SLGHPGSGSGSGGGGGGGGGGGGGGGGGGGGAPGGL QHETQELASKR	K44:+114.043	127 2.58 6	381 4.73 5	0.03 716 4

P4266 9	CO N	SLGHPGSGSGSGGGGGGGGGGGSGGGGGAPGGL QHETQELASK	K44:+114.043	915. 666 3	365 8.63 4	0.09 883 5
P4266 9	CO N	SGGSLGHPGSGSGSGGGGGGGGGGGSGGGGGAP GGLQHETQELASKR	K47:+114.043	133 9.61 1	401 5.81	0.01 060 4
P4266 9	CO N	LGHPGSGSGSGGGGGGGGGGGSGGGGGAPGGLQ HETQELASKR	K43:+114.043	124 3.57 6	372 7.70 3	0.00 418 8
P4266 9	CO N	HPGSGSGSGGGGGGGGGGGSGGGGGAPGGLQHE TQELASK	K41:+114.043	113 4.84	340 1.49 7	0.05 668 8
P4266 9	CO N	GGAALGSGGSLGHPGSGSGSGGGGGGGGGGGSGG GGGAPGGLQHETQELASK	K53:+114.043	142 9.65 2	428 5.93 2	0.04 667 3
P4266 9	CO N	ALGSGGSLGHPGSGSGSGGGGGGGGGGGSGGGGG GAPGGLQHETQELASKR	K50:+114.043	141 9.99 2	425 6.95 3	0.08 207 5
P4266 9	CO N	GHPGSGSGSGGGGGGGGGGGSGGGGGAPGGLQH ETQELASKR	K42:+114.043	120 5.88 1	361 4.61 9	0.03 132 7
P4266 9	CO N	HPGSGSGSGGGGGGGGGGGSGGGGGAPGGLQHE TQELASKR	K41:+114.043	890. 407 2	355 7.59 8	0.06 300 9
P4266 9	CO N	LGSGLGHPGSGSGSGGGGGGGGGGGSGGGGG APGGLQHETQELASKR	K49:+114.043	139 6.31 3	418 5.91 6	0.02 759 2
P4266 9	CO N	PGSGSGSGGGGGGGGGGGSGGGGGAPGGLQHET QELASKR	K40:+114.043	114 1.18 7	342 0.53 9	0.03 993 5
P4266 9	CO N	GSGSGGGGGGGGGGGGGSGGGGGAPGGLQHETQEL ASK	K37:+114.043	100 8.78 5	302 3.33 1	0.04 285 7
P4266 9	INF	GSLGHPGSGSGSGGGGGGGGGGGSGGGGGAPGG LQHETQELASKR	K45:+114.043	129 1.59 3	387 1.75 7	0.00 345 4
P4266 9	INF	GSGGSLGHPGSGSGSGGGGGGGGGGGSGGGGGGA PGGLQHETQELASKR	K48:+114.043	135 8.61 8	407 2.83 2	0.04 509 1
P4266 9	INF	GGSLGHPGSGSGSGGGGGGGGGGGSGGGGGAPG GLQHETQELASKR	K46:+114.043	131 0.60 1	392 8.77 8	0.01 663 3
P4266 9	INF	SLGHPGSGSGSGGGGGGGGGGGSGGGGGAPGGL QHETQELASKR	K44:+114.043	127 2.58 6	381 4.73 5	0.05 6 6
P4266 9	INF	SLGHPGSGSGSGGGGGGGGGGGSGGGGGAPGGL QHETQELASK	K44:+114.043	122 0.55 3	365 8.63 4	0.05 836 2
P4266 9	INF	SGGSLGHPGSGSGSGGGGGGGGGGGSGGGGGAP GGLQHETQELASKR	K47:+114.043	133 9.61 1	401 5.81	0.02 034 6
P4266 9	INF	LGHPGSGSGSGGGGGGGGGGGSGGGGGAPGGLQ HETQELASKR	K43:+114.043	124 3.57 6	372 7.70 3	0.00 547 6
P4266 9	INF	HPGSGSGSGGGGGGGGGGGSGGGGGAPGGLQHE TQELASK	K41:+114.043	113 4.84	340 1.49 7	0.04 423
P4266 9	INF	ALGSGGSLGHPGSGSGSGGGGGGGGGGGSGGGGG GAPGGLQHETQELASKR	K50:+114.043	141 9.99 2	425 6.95 3	0.08 994 9
P4266 9	INF	GHPGSGSGSGGGGGGGGGGGSGGGGGAPGGLQH ETQELASKR	K42:+114.043	120 5.88 1	361 4.61 9	0.04 229 4

P4266 9	INF	HPGSGSGSGGGGGGGGGGGGGGGGGGGGAPGGLQHE TQELASKR	K41:+114.043	118 6.87 4	355 7.59 8	0.07 782 3
P4266 9	INF	LGSGGSLGHPGSGSGSGGGGGGGGGGGGGGGGGGG APGGLQHETQELASKR	K49:+114.043	139 6.31 3	418 5.91 6	0.03 639
P4266 9	INF	RDSGSEQGGAALGSGGSLGHPGSGSGSGGGGGGGGG GGGGSGGGGGGAPGGLQHETQELASK	K60:+114.043	126 2.31 9	504 5.24 7	0.08 003 2
P4266 9	INF	SEQGGAALGSGGSLGHPGSGSGSGGGGGGGGGGGGG SGGGGGGAPGGLQHETQELASKR	K56:+114.043	119 7.54 9	478 6.16 6	0.08 437 5
P4266 9	INF	GGGGGGGGGGSGGGGGGAPGGLQHETQELASK	K30:+114.043	855. 727 8	256 4.16	0.05 436 4
P4293 2	CO N	VCKILGSGIYSSSVLHGMVFK	C2:+45.988,K3:+114.043	795. 743 1	238 4.20 6	0.07 319
P4293 2	INF	EENLMDAQVKAIAGTGANVIVTGGK	E1:-18.011,K25:+114.043	129 1.66 6	258 1.31 7	0.06 159 8
P4293 2	INF	LATNAAVTVLRVDQIIMAKPAGGPKPPS	M17:+15.995,K19:+114.043	982. 546 8	294 4.61 7	0.05 171 8
P4293 2	INF	MLEASILDYLGK	K13:+114.043	523. 273 3	156 6.79 6	0.03 854 5
P4327 5	CO N	SLAAAGYDVEK	K11:+114.043	619. 307 2	123 6.59 9	0.00 203 7
P4327 5	CO N	KKPAGPSVSEL	K1:+114.043	613. 841 2	122 5.66 7	0.04 910 9
P4327 5	CO N	AGPSVSELIVQAVSSSKER	K17:+114.043	102 9.54 5	205 7.07 5	0.06 568
P4327 6	CO N	ALAAGGYDVEK	K11:+114.043	604. 301 9	120 6.58 8	0.00 091 7
P4327 6	CO N	KALAAGGYDVEK	K12:+114.043	668. 349 3	133 4.68 3	0.03 329 7
P4327 6	CO N	ETAAPAPVEKSPAK	K10:+114.043	755. 399 6	150 8.78 4	0.04 750 8
P4327 6	INF	ALAAGGYDVEK	K11:+114.043	604. 301 9	120 6.58 8	0.00 112 9
P4327 6	INF	KPKVTKPK	K1:+114.043,K6:+114.043	577. 356 8	115 2.69 8	0.04 229 4
P4559 1	CO N	KEDLVFIFWAPESAPLK	K17:+114.043	105 2.56	210 3.10 4	0.00 091 7
P4559 1	INF	KEDLVFIFWAPESAPLK	K17:+114.043	105 2.56	210 3.10 4	0.00 091 7
P4559 1	INF	EDLVFIFWAPESAPLK	K16:+114.043	988. 512 4	197 5.00 9	0.00 755 9
P4595 2	INF	QIFGGYGFNTEYPVEKLMR	Q1:-17.027,K16:+114.043,M18:+15.995	591. 285 2	236 1.11	0.05 294

P4595 2	INF	NTYYASIAKAFAGDIANQLATD	K9:+114.043	121 6.59 1	243 1.16 6	0.07 218 1
P4606 1	CO N	VLDAIDALMK	K10:+114.043	601. 826 7	120 1.63 8	0.00 470 5
P4606 1	INF	VLDAIDALMK	K10:+114.043	601. 826 7	120 1.63 8	0.00 503 4
P4646 0	CO N	TALAAKIAEESNFPFIK	K6:+114.043,K17:+114.043	103 9.55	207 7.08 5	0.01 300 4
P4646 7	CO N	KLQNQLQGAIVIERPN	K1:+114.043	968. 042 7	193 4.07	0.01 533 6
P4646 7	INF	KLQNQLQGAIVIERPN	K1:+114.043	968. 042 7	193 4.07	0.05 076 6
P4647 1	CO N	FVNLGIEPPKGVLLFGPPGTGK	K10:+114.043	117 6.16	235 0.30 5	0.05 668 8
P4666 4	INF	ELQIPVKWIGVGK	K13:+114.043	790. 962 1	157 9.90 9	0.06 969 8
P4773 8	CO N	TYLAALETLDNGKPYVISYLDLDMVL	K13:+114.043,M25:+15.995	105 3.87 8	315 8.61	0.04 197 7
P4773 8	INF	LLMQAWKLGPALATGNVVMK	M3:+15.995,K7:+114.043,K21:+114.043	124 2.67 8	248 3.33 9	0.07 192 7
P4780 9	INF	GGGGSGGGGGTGPPIGPPASGHPAVSSMQGK	M28:+15.995,K31:+114.043	901. 756 7	270 2.24 7	0.07 218 1
P4781 1	CO N	EFNDVYLVTHLMGADLNNIVKCQK	C22:+45.988,K24:+114.043	146 2.71	292 3.40 3	0.06 600 8
P4781 1	CO N	LSRPFQSIIHAKR	K12:+114.043	556. 322 1	166 5.94 3	0.05 139 9
P4795 5	INF	SLICNVGAGGPAPAAGAAPAGGAAPSTAAAPAEK	C4:+45.988,K35:+114.043	104 5.17 4	313 2.49 7	0.04 828 8
P4795 5	INF	IGSLICNVGAGGPAPAAGAAPAGGAAPSTAAAPAEK K	C6:+45.988,K37:+114.043,K38:+114.043	118 2.58 8	354 4.74 1	0.06 465 9
P4795 5	INF	EDKINALIK	K3:+114.043,K9:+114.043	636. 351 9	127 0.68 8	0.07 254 2
P4796 2	CO N	KHIMGQNVADY	K1:+114.043	695. 333 2	138 8.65 1	0.05 025 6
P4796 8	INF	VKQENLDLICPTSF	K2:+114.043,C10:+45.988	627. 315 2	187 8.92 2	0.06 159 8
P4796 8	INF	NLIKGGGGCLTQEK	K4:+114.043,C9:+45.988	789. 393	157 6.77	0.06 701 2
P4802 5	CO N	EANDPALKDELLAEANVMQQLDNPYIVR	K8:+114.043	109 5.21 4	328 2.61 9	0.00 091 7
P4819 3	CO N	TSAPAIQSQVTEGPGAPIKK	K20:+114.043,K21:+114.043	114 0.10 4	227 8.19 2	0.06 841

P4819 3	CO N	EEGEGATNSGQQETQLEEFASQAAAAEGSDQGEQKLK	E1:-18.011,K34:+114.043	126 7.90 3	380 0.68 4	0.08 207 5
P4819 3	INF	LNLLEEDYFGLALWDSATSK	K20:+114.043	600. 550 1	239 8.16 9	0.03 109 4
P4971 7	CO N	SGKGSSAVGLTAYVMK	K3:+114.043	557. 291 3	166 8.85 1	0.05 767 9
P4972 2	INF	VAGGAPSVGIK	K11:+114.043	535. 304 2	106 8.59 3	0.05 231 3
P4972 2	INF	QIEYALAAVAGGAPSVGIKAANGVVLATEK	K30:+114.043	994. 880 7	298 1.61 9	0.03 974 7
P4972 2	INF	KLVQIEYALAAVAGGAPSVGIK	K1:+114.043,K22:+114.043	119 2.17 1	238 2.32 7	0.07 003 4
P5024 7	CO N	FDNLYGCRESLIDGIK	C7:+45.988,K16:+114.043	668. 317 5	200 1.92 9	0.08 392 4
P5024 7	INF	EYLCWIEQTLHFQDGPLNMILDDGGDLTNLIHTK	E1:-18.011,C5:+45.988,K34:+114.043	136 2.32 6	408 3.95 3	0.04 617 3
P5024 7	INF	GCRESLIDGIK	C2:+45.988,K11:+114.043	675. 829 6	134 9.64 4	0.05 436 4
P5039 6	CO N	YLDQPCLETINRIK	C6:+45.988,K14:+114.043	933. 466 7	186 4.91 8	0.08 185 4
P5039 6	INF	LSAIYGGTYMLNK	K13:+114.043	515. 598	154 3.77 1	0.04 530 6
P5043 1	CO N	GGTEFIDELEMLCQK	M11:+15.995,C13:+45.988,K15:+114.043	630. 276 4	188 7.80 6	0.06 568
P5043 1	CO N	ELESLSINSAVFPGLQGGPHNHAIAGVAVALKQAMTTE FK	E1:-18.011,M34:+15.995,K39:+114.043	138 6.72	415 7.13 7	0.06 502 7
P5043 1	CO N	ELTLQIQSHMATKATLK	M10:+15.995,K13:+114.043	102 2.04 9	204 2.08 3	0.03 947 5
P5043 1	INF	KIADDNGAYLMADMMAHISGLVAAGVVPSP	K1:+114.043,M14:+15.995	100 5.16 4	301 2.46 9	0.04 617 3
P5051 6	INF	FLQQNGYTPYDRFCPFYK	C14:+45.988,K18:+114.043	816. 370 4	244 6.08 8	0.05 562 4
P5051 8	CO N	QDFPLVKAQVQK	K7:+114.043	729. 409 7	145 6.80 4	0.03 282 5
P5051 8	CO N	IQMSNLMNQARLK	K13:+114.043	554. 292 8	165 9.85 5	0.04 071 8
P5058 0	CO N	VLRSLVEASSSGVSVLSLCEK	C19:+45.988,K21:+114.043	116 2.10 4	232 2.19 3	0.05 734
P5058 0	INF	LCEKGDAMIMEETGK	C2:+45.988,K4:+114.043	605. 598 5	181 3.77 2	0.06 123 4
P5058 0	INF	VKPGNQNTQVTEAWNK	K2:+114.043	964. 485 2	192 6.95 5	0.00 112 9

P50580	INF	HLCAEAAALRLVKPGNQNTQVTEAWNK	C3:+45.988,K12:+114.043,K26:+114.043	792.1481	3164.561	0.05928
P51125	CON	KTEEVSKPK	K7:+114.043,K9:+114.043	637.3416	1272.668	0.084734
P51125	CON	VVLDPMYSTYLEALGIK	K17:+114.043	1013.532	2025.049	0.043154
P51125	INF	DKELDDALDESLGQRPPDPDENK	K2:+114.043,K26:+114.043	1047.149	3138.423	0.060247
P51125	INF	EQKPFPTASPVQSTPSKPSDK	K3:+114.043	790.7366	2369.186	0.092594
P51125	INF	VLDPMYSTYLEALGIK	K16:+114.043	643.0014	1925.981	0.053225
P51125	INF	PANISSELEFEDAK	K13:+114.043	767.8734	1533.731	0.050536
P51125	INF	DKDGKPLLPEPEE	K2:+114.043	527.5988	1579.773	0.020167
P51150	INF	KVIILGDSGVGK	K1:+114.043	650.3857	1298.756	0.064324
P51174	CON	QGLLGINIAEKHGG	K11:+114.043	760.9132	1519.811	0.047241
P51174	INF	PANALLGEENKGFYYLMQELPQER	K11:+114.043	975.4803	2923.418	0.002432
P51660	INF	DLKFVYEGSADFSCLPFGVIVAQK	K3:+114.043,C14:+45.988	724.3586	2893.403	0.072181
P52480	CON	AGKPVICATQMLESMIKKPRP	K3:+114.043,C7:+45.988,M15:+15.995,K18:+114.043	1294.663	2587.311	0.068104
P52480	CON	EGSDVANAVLDGADCIMLSGETAK	E1:-18.011,C15:+45.988,K24:+114.043	836.707	7.098	0.04423
P52480	INF	KGVNLPAAVDLPVASEK	K1:+114.043	627.0148	1878.021	0.036906
P52624	INF	YAMYKAGPVLVSVSHGMGIPSIGIMLHELK	M16:+15.995,M24:+15.995,K30:+114.043	1120.251	3357.729	0.031827
P54071	CON	WACKNYDGDVQSDILAQGFGLMTSVLVC PDGK	C3:+45.988,K4:+114.043,C31:+45.988	1298.595	3892.761	0.044754
P54071	CON	EVYNFPAGGVGMGMYNTDESISGFAHSCFQYSIQK	M14:+15.995,C28:+45.988,K35:+114.043	1003.434	4009.706	0.075985
P54071	INF	QTVESGAMTKDLAGCIHGLSNVK	K10:+114.043,C15:+45.988	1260.107	2518.198	0.035332
P54775	CON	HSNALVDVLPPEADSSIMMLTSDQKP	M18:+15.995,K25:+114.043	1463.203	2924.39	0.070606
P54775	INF	ELLKPNASVALHKHSNALVDVLPPEADSSIM	E1:-18.011,K13:+114.043,M31:+15.995	1136.593	3406.755	0.052313

P5477 5	INF	EAVELPLTHFELYK	K14:+114.043	901. 970 4	180 1.92 5	0.06 738 7
P5477 5	INF	LELLNQMDGFDQNVNVKIMATNR	K17:+114.043,M20:+15.995	144 6.72 1	289 1.42 7	0.04 229 4
P5477 5	INF	IMMLTSDQKPDVVMYADIGGMDIQK	M2:+15.995,M3:+15.995,M13:+15.995,M20:+ 15.995,K24:+114.043	143 9.65 3	287 7.29 1	0.04 372 4
P5482 3	CO N	GIDIQAVNVVINFDPKLA	K17:+114.043	729. 732 3	218 6.17 4	0.07 254 2
P5482 3	CO N	FMNSHLQPYEINLME	M2:+15.995,K8:+114.043	106 2.49 9	212 2.98 2	0.05 866 5
P5482 3	CO N	GPGGGGTQPQPQLNQLK	K17:+114.043	597. 643 5	178 9.90 7	0.07 492 7
P5482 3	INF	QKVHCLNTLFSR	[0:-17.027,K2:+114.043,C5:+45.988	794. 890 3	158 7.76 5	0.05 231 3
P5482 3	INF	DDTVHVVIATPGRILDIK	K19:+114.043	109 5.11 9	218 8.22 2	0.03 455 1
P5482 3	INF	CTDLFTRGIDIQAVNVVINFDPK	C1:+28.961,K24:+114.043	956. 807 3	286 7.39 9	0.05 197 5
P5498 7	INF	IPKFSGLDLLAFNVGIEVQGR	K3:+114.043	834. 136 1	249 9.38 5	0.05 025 6
P5526 4	INF	VAQWLIQEPHK	K11:+114.043	731. 894 3	146 1.77 3	0.06 432 4
P5639 9	CO N	QLFAFISHMGTSTMCGHYVCHIK	Q1:- 17.027,M9:+15.995,C15:+45.988,C20:+45.988 ,K23:+114.043	140 8.60 1	281 5.18 7	0.07 060 6
P5639 9	CO N	SKPALESGDGEQVPEQKEVQDGIAPR	K2:+114.043	960. 144 6	287 7.41 1	0.06 502 7
P5639 9	CO N	KLDVSIEMPEELDI	K1:+114.043,M8:+15.995	880. 935 4	175 9.85 5	0.03 229 7
P5639 9	INF	KLDVSIEMPEELDI	K1:+114.043,M8:+15.995	880. 935 4	175 9.85 5	0.04 401 7
P5639 9	INF	AVDWIFSHIDDLAEAAAMDISEGRSAAESISESPVGP K	M18:+15.995,K39:+114.043	106 2.00 4	424 3.98 6	0.04 938 8
P5648 0	CO N	DYAAQASAAPK	K11:+114.043	402. 863 7	120 5.56 8	0.04 173 1
P5775 9	CO N	FDTQYPYGEKQDEFK	K10:+114.043	100 4.95	200 7.88 5	0.03 207 1
P5775 9	INF	FDTQYPYGEKQDEFK	K10:+114.043	100 4.95	200 7.88 5	0.05 025 6
P5778 0	INF	DYETATLSDIKALIR	K11:+114.043	911. 981 5	182 1.94 7	0.05 463 2
P5778 4	INF	SLVELGDLPLASLKSILTYLSILR	K15:+114.043	910. 848 3	272 9.52 2	0.04 857 5

P5825 2	CO N	IISTYGESESGPMGNIMIDPVLGTVGFGSGLHGWAFTL K	K39:+114.043	137 5.01 6	412 2.02 3	0.07 350 6
P5825 2	CO N	FKVFDAIMNFR	K2:+114.043	751. 385 2	150 0.75 5	0.06 159 8
P5825 2	INF	EGIPALDNFLDK	K12:+114.043	723. 367 7	144 4.72	0.02 478 7
P5999 9	INF	LVDFVIHFMEIDKEISEM	K14:+114.043,M19:+15.995	818. 724 3	245 3.15	0.09 141
P6012 2	INF	EACGVIVELIK	C3:+45.988,K11:+114.043	667. 347	133 2.67 8	0.06 056 1
P6012 2	INF	IQDVTLHDLVDVANARPQGGQDILSMMGQLMKPK	M25:+15.995,K33:+114.043	125 0.63 1	374 8.87	0.07 630 8
P6012 2	INF	KEIIQDVTLHDLVDVANARPQGGQDILSMMGQLMKPK	K1:+114.043,M28:+15.995,M29:+15.995,K36: +114.043	141 7.38 4	424 9.13	0.04 343 2
P6012 2	INF	ANARPQGGQDILSMMGQLMKPK	M19:+15.995,K22:+114.043	834. 419 5	250 0.23 5	0.07 286 9
P6022 9	CO N	QLQAETEPIVK	K11:+114.043	685. 370 3	136 8.72 5	0.06 632 8
P6033 5	CO N	NQVARQQSHFAMMHGGTGFGAGIDSSSPEVK	M12:+15.995,M13:+15.995,K30:+114.043	110 7.51 1	331 9.51	0.04 959 9
P6033 5	CO N	QQSHFAMMHGGTGFGAGIDSSSPEVKG	K25:+114.043	926. 418 9	277 6.23 3	0.05 734
P6033 5	INF	TLTGPTNAIFK	K11:+114.043	638. 849	127 5.68 2	0.04 372 4
P6071 0	CO N	FEQEMATAASSSSLEKSYELPDGQVITIGNER	K16:+114.043	120 1.23 7	360 0.68 9	0.02 499 4
P6071 0	CO N	HQGVMMVGMGQKDSY	M5:+15.995,K11:+114.043	833. 869 8	166 5.72 4	0.08 109
P6071 0	CO N	KLCYVALDFEQEMATAASSSSLEK	K1:+114.043,C3:+45.988	139 1.14 3	278 0.27 1	0.09 380 1
P6071 0	CO N	SSLEKSYELPDGQVITIGNER	K5:+114.043	122 5.11 4	244 8.21 3	0.08 956 6
P6071 0	INF	KLCYVALDFEQEMATAASSSSLEK	K1:+114.043,C3:+45.988,M13:+15.995	933. 096 5	279 6.26 6	0.00 738 5
P6076 6	CO N	DVFLVCFSVVSPSSFENVKEK	C6:+45.988,K19:+114.043,K21:+114.043	131 7.63 3	263 3.25 1	0.04 857 5
P6084 3	INF	EMLSRGFK	M2:+15.995,K8:+114.043	549. 274 6	109 6.53 4	0.06 401 4
P6116 4	INF	QIPKYCFPNYVGRPK	[0:-17.027,C6:+45.988,K15:+114.043	976. 979 6	195 1.94 4	0.04 694 9
P6116 4	INF	NGSGVIKAGFAGDQIPK	K7:+114.043,K17:+114.043	943. 990 2	188 5.96 5	0.06 369 3

P6120 2	INF	LVLANMLMK	M6:+15.995,K9:+114.043	581. 820 4	116 1.62 5	0.05 734
P6122 2	CO N	CPFGALSIVNLPNLEK	[0:-17.027,C1:+45.988,K17:+114.043	648. 990 6	194 3.94 8	0.05 231 3
P6122 2	INF	VFKVAETANEEVK	K14:+114.043	853. 934	170 5.85 2	0.04 042 1
P6122 2	INF	MLAGRLKPDEGGEVPLNVSYKPQK	K25:+114.043	142 0.26 1	283 8.50 6	0.07 782 3
P6175 9	CO N	QTEILKYMQK	M9:+15.995,K11:+114.043	762. 908 8	152 3.80 2	0.08 515 8
P6197 9	CO N	PQGGSGYDYSYAGGRGSYDGLGGPIITTQVTIPK	K34:+114.043	118 2.91	354 5.70 6	0.06 267 1
P6198 2	INF	NLLSVAYK	K8:+114.043	511. 288	102 0.56	0.03 854 5
P6208 2	CO N	VKPNGEKPDEFESGISQALLELEMNSDLK	K2:+114.043	111 1.21 7	333 0.62 9	0.00 285 9
P6208 2	INF	VKPNGEKPDEFESGISQALLELEMNSDLK	K2:+114.043	111 1.21 7	333 0.62 9	0.00 158 6
P6213 7	CO N	TFTDCFNCLPIAAIVDEKIFCCHGGLSPDLQS	C5:+45.988,C8:+45.988,K18:+114.043,C21:+45.988,C22:+45.988	125 2.53 5	375 4.58 1	0.05 866 5
P6219 2	CO N	LDNQIQEIKESVELPLTHPEYYEEMGIKPPK	K9:+114.043,M25:+15.995,K28:+114.043,K31:+114.043	134 2.66 6	402 4.97 3	0.06 159 8
P6219 2	CO N	IQEIKESVELPLTHPEYYEEMGIKPPK	M21:+15.995,K24:+114.043,K27:+114.043	114 7.91 4	344 0.71 8	0.06 231 8
P6219 6	CO N	VDPLVSLMMVEK	M8:+15.995,K12:+114.043	497. 591 9	148 9.75 2	0.04 173 1
P6219 6	INF	VDPLVSLMMVEK	M8:+15.995,K12:+114.043	497. 591 9	148 9.75 2	0.05 668 8
P6219 6	INF	DPLVSLMMVEKVPDSTYEMIGGLDK	M8:+15.995,K11:+114.043	966. 471 5	289 6.39 1	0.04 475 4
P6225 9	CO N	TSDMQGDGEEQNK	K13:+114.043	776. 813 2	155 1.61 1	0.06 401 4
P6231 5	CO N	KNGTQVHGTITGVDVSMNTHLK	K1:+114.043,M17:+15.995	823. 084	246 6.22 9	0.07 350 6
P6231 5	INF	KNGTQVHGTITGVDVSMNTHLK	K1:+114.043,M17:+15.995	823. 084	246 6.22 9	0.04 910 9
P6232 0	CO N	QGSAGARGK	K9:+114.043	466. 239 4	930. 463 2	0.08 473 4
P6233 4	CO N	ENDLKALQSVGQJVGEVLK	K19:+114.043	107 7.59 2	215 3.16 9	0.03 924 8
P6248 2	CO N	LLGASNAEQLMENIGAIQVLPK	M11:+15.995,K22:+114.043	610. 578 8	243 8.28 4	0.05 197 5

P6248 2	INF	AEVVLGNIKK	K10:+114.043	649. 396 1	129 6.77 7	0.09 344 7
P6274 6	INF	HFCPNVPILVANK	C3:+45.988,K14:+114.043	575. 638	172 3.89 1	0.00 091 7
P6274 8	INF	FLKDCPTGHLTVDEFK	K3:+114.043,C5:+45.988	100 5.47 7	200 8.93 9	0.01 060 4
P6280 6	CO N	DNIQGITKPAIR	K8:+114.043	720. 402 4	143 8.78 9	0.03 378 2
P6280 6	CO N	KTVTAMDVVYALK	K1:+114.043	776. 924 4	155 1.83 3	0.00 091 7
P6280 6	CO N	TVTAMDVVYALK	K12:+114.043	712. 876 9	142 3.73 8	0.04 144 1
P6280 6	INF	DNIQGITKPAIR	K8:+114.043	720. 402 4	143 8.78 9	0.00 091 7
P6280 6	INF	KTVTAMDVVYALK	K1:+114.043	776. 924 4	155 1.83 3	0.00 225 8
P6280 6	INF	TVTAMDVVYALK	K12:+114.043	712. 876 9	142 3.73 8	0.03 109 4
P6282 1	INF	VEQSFMTMAAEIKK	K14:+114.043	863. 929 3	172 5.84 3	0.05 767 9
P6284 3	INF	DMIILPEMVGSMGVYNGKTFNQVE	M8:+15.995,M12:+15.995,K19:+114.043	145 9.19 3	291 6.37 1	0.04 256 6
P6290 8	CO N	KPEPPAMPQPVPTA	K1:+114.043	787. 406 3	157 2.79 7	0.00 225 8
P6290 8	CO N	KPLPDHVSIVEPKDEIL	K1:+114.043	102 2.06	204 2.10 5	0.04 617 3
P6290 8	INF	KPEPPAMPQPVPTA	K1:+114.043	787. 406 3	157 2.79 7	0.00 292 7
P6290 8	INF	IVEPKDEILPTTPISEQK	K5:+114.043,K18:+114.043	113 3.10 3	226 4.19	0.07 963 6
P6296 0	CO N	DTKPGSTGSGAGSGGPGGLTSAAPAGGDKK	K29:+114.043,K30:+114.043	138 6.16 4	277 0.31 2	0.04 857 5
P6296 0	CO N	DTKPGSTGSGAGSGGPGGLTSAAPAGGDK	K29:+114.043	843. 732 5	252 8.17 4	0.03 736 3
P6296 0	CO N	ETQQPPAAPAAALSAADTKPGSTGSGAGSGGPGGLTSAAPAGGDKK	K45:+114.043	137 8.01 1	413 1.01 1	0.07 823 6
P6296 0	CO N	PAAPAAALSAADTKPGSTGSGAGSGGPGGLTSAAPAGGDKK	K40:+114.043	118 3.59 1	354 7.75	0.01 564 8
P6296 0	CO N	PPAAPAAALSAADTKPGSTGSGAGSGGPGGLTSAAPAGGDKK	K15:+114.043,K41:+114.043	125 3.95 7	375 8.84 6	0.07 090 1
P6296 0	CO N	ADTKPGSTGSGAGSGGPGGLTSAAPAGGDK	K4:+114.043	130 0.61 3	259 9.21 1	0.08 278 5

P6296 0	CO N	APAAALSAADTKPGSTGSGAGSGGPGGLTSAAPAGG DKK	K12:+114.043	845. 922 9	337 9.66	0.09 724 8
P6296 0	CO N	AAPAAALSAADTKPGSTGSGAGSGGPGGLTSAAPAG GDKK	K13:+114.043,K39:+114.043	118 9.25 5	356 4.74 1	0.02 917 6
P6296 0	CO N	QPPAAPAAALSAADTKPGSTGSGAGSGGPGGLTSAAP AGGDKK	K16:+114.043	944. 223 2	377 2.86 2	0.08 109
P6296 0	CO N	LSAADTKPGSTGSGAGSGGPGGLTSAAPAGGDK	K7:+114.043,K33:+114.043	747. 109 6	298 4.40 7	0.03 690 6
P6296 0	CO N	SAADTKPGSTGSGAGSGGPGGLTSAAPAGGDK	K6:+114.043	137 9.64 8	275 7.28	0.07 896 1
P6296 0	CO N	QPPAAPAAALSAADTKPGSTGSGAGSGGPGGLTSA APAGGDKK	Q1:-17.027,K17:+114.043,K43:+114.043	100 0.49 2	399 7.93 6	0.02 499 4
P6296 0	CO N	AADTKPGSTGSGAGSGGPGGLTSAAPAGGDK	K5:+114.043	133 6.13 2	267 0.24 8	0.08 515 8
P6296 0	CO N	ADTKPGSTGSGAGSGGPGGLTSAAPAGGDKK	K30:+114.043,K31:+114.043	142 1.68 2	284 1.34 9	0.04 724 1
P6296 0	INF	DTKPGSTGSGAGSGGPGGLTSAAPAGGDKK	K29:+114.043,K30:+114.043	138 6.16 4	277 0.31 2	0.05 053 6
P6296 0	INF	DTKPGSTGSGAGSGGPGGLTSAAPAGGDK	K29:+114.043	126 5.09 5	252 8.17 4	0.09 180 3
P6296 0	INF	ETQPPAAPAAALSAADTKPGSTGSGAGSGGPGGLTS AAPAGGDKK	K19:+114.043,K45:+114.043,K46:+114.043	145 4.04	435 9.09 7	0.03 282 5
P6296 0	INF	PAAPAAALSAADTKPGSTGSGAGSGGPGGLTSAAPAG GDKK	K40:+114.043	118 3.59 1	354 7.75	0.02 201 2
P6296 0	INF	PPAAPAAALSAADTKPGSTGSGAGSGGPGGLTSAAPA GGDKK	K15:+114.043,K41:+114.043	125 3.95 7	375 8.84 6	0.05 410 2
P6296 0	INF	ADTKPGSTGSGAGSGGPGGLTSAAPAGGDK	K30:+114.043	130 0.61 3	259 9.21 1	0.09 380 1
P6296 0	INF	APAAALSAADTKPGSTGSGAGSGGPGGLTSAAPAGG DKK	K12:+114.043	112 7.56 1	337 9.66	0.06 369 3
P6296 0	INF	AAPAAALSAADTKPGSTGSGAGSGGPGGLTSAAPAG GDKK	K13:+114.043,K39:+114.043	118 9.25 5	356 4.74 1	0.04 938 8
P6296 0	INF	QPPAAPAAALSAADTKPGSTGSGAGSGGPGGLTSAAP AGGDKK	K16:+114.043	944. 223 2	377 2.86 2	0.08 657 5
P6296 0	INF	SAADTKPGSTGSGAGSGGPGGLTSAAPAGGDK	K32:+114.043	137 9.64 8	275 7.28	0.08 582
P6296 0	INF	QPPAAPAAALSAADTKPGSTGSGAGSGGPGGLTSA APAGGDKK	Q1:-17.027,K43:+114.043,K44:+114.043	100 0.49 2	399 7.93 6	0.09 588 5
P6296 0	INF	AADTKPGSTGSGAGSGGPGGLTSAAPAGGDK	K5:+114.043	133 6.13 2	267 0.24 8	0.03 109 4
P6296 0	INF	ADTKPGSTGSGAGSGGPGGLTSAAPAGGDKK	K30:+114.043	910. 109 8	272 7.30 6	0.06 337 3

P6296 0	INF	QPPAAPAAALSAADTKPGSTGSGAGSGGPGGLTSAAP AGGDK	K16:+114.043,K42:+114.043	125 3.94 4	375 8.81	0.03 207 1
P6296 0	INF	QQPPAAPAAALSAADTKPGSTGSGAGSGGPGGLTSA APAGGDK	K43:+114.043	125 8.61 6	377 2.82 5	0.05 962 2
P6296 0	INF	PGSTGSGAGSGGPGGLTSAAPAGGDK	K26:+114.043	729. 009 3	218 4.00 4	0.07 564 5
P6296 0	INF	KPGSTGSGAGSGGPGGLTSAAPAGGDKK	K27:+114.043,K28:+114.043	127 8.12 6	255 4.23 7	0.04 959 9
P6296 2	INF	KEGVHGGLINK	K1:+114.043	633. 352 2	126 4.68 9	0.06 056 1
P6300 1	INF	VDGKPVNLGLWDTAGQEDYDR	K4:+114.043	821. 391 5	246 1.15 1	0.06 937 5
P6300 5	INF	NEAKEEFTSGGPLGQK	K4:+114.043	903. 437 4	180 4.85 9	0.00 331 6
P6301 7	CO N	TKLYQSAGGMPGGMPGGFPGGGAPPSGGASSGPTIE EVD	K2:+114.043,M10:+15.995	123 5.89 9	370 4.67 2	0.05 436 4
P6301 7	CO N	NVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDT	K27:+114.043	890. 203 4	355 6.78 3	0.03 974 7
P6301 7	INF	TKLYQSAGGMPGGMPGGFPGGGAPPSGGASSGPTIE EVD	K2:+114.043,M10:+15.995	123 5.89 9	370 4.67 2	0.03 207 1
P6301 7	INF	LSGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIK	K5:+114.043	128 5.03 5	385 2.08 1	0.00 091 7
P6301 7	INF	DKSQIHDIVLVGGSTR	K2:+114.043	919. 990 1	183 7.96 5	0.00 129
P6301 7	INF	LLQDFFNGKELNK	K9:+114.043,K13:+114.043	598. 644 8	179 2.91 1	0.02 301 1
P6308 5	INF	GKHYLDQLNHILGILGSPSQEDLNCIINLK	K2:+114.043,C25:+45.988	877. 204 3	350 4.78 6	0.03 736 3
P6310 1	CO N	LEKFLIPNASQPESK	K3:+114.043	907. 986 5	181 3.95 7	0.04 694 9
P6310 1	INF	EAFEISK	K7:+114.043	469. 235 5	936. 455 3	0.07 782 3
P6315 8	CO N	KGEHPGLSIGDVAK	K1:+114.043	761. 405 2	152 0.79 5	0.02 586 4
P6315 8	INF	KGEHPGLSIGDVAK	K1:+114.043	761. 405 2	152 0.79 5	0.00 345 4
P6324 2	INF	YDCGEEILITVLSAMTEEA A VAIKAM	C3:+45.988,K24:+114.043,M26:+15.995	983. 132 4	294 6.37 4	0.02 682 7
P6324 2	INF	KVHLVGIDIFTGK	K1:+114.043	514. 300 3	153 9.87 7	0.03 132 7
P6327 6	INF	CEEIAIIPSKK	C1:+45.988,K10:+114.043	695. 857 8	138 9.7	0.04 372 4

P6327 6	INF	LSNLQVTQPTVGMNFK	M13:+15.995,K16:+114.043	953. 988 8	190 5.96 2	0.05 803 7
P6332 8	INF	KSQTTGFPSLITIFSAPNYLDV	K1:+114.043	125 7.15	251 2.28 5	0.04 343 2
P6332 8	INF	TPTGMLPSGVLSGGKQTLQSATVEAIEADEAIK	M5:+15.995,K15:+114.043,K33:+114.043	886. 702 2	354 2.77 8	0.04 116 7
P6803 3	CO N	YPIEHGIITNWDDMEK	K16:+114.043	103 7.98 1	207 3.94 7	0.00 091 7
P6803 3	CO N	FENEMATAASSSSLEKSYELPDGQVITIGNER	M5:+15.995,K16:+114.043	120 1.89 7	360 2.66 8	0.03 051 5
P6803 3	CO N	EKMTQIMFETFNVPAMYVAIQAVLSLYAS	K2:+114.043,M3:+15.995,M7:+15.995,M16:+15.995	115 3.23	345 6.66 6	0.05 076 6
P6803 3	INF	KYPIEHGIITNWDDMEK	K1:+114.043	110 2.02 9	220 2.04 2	0.00 091 7
P6803 3	INF	YPIEHGIITNWDDMEK	K16:+114.043	103 7.98 1	207 3.94 7	0.00 091 7
P6803 3	INF	LKYPIEHGIITNWDDMEK	K18:+114.043	115 8.57 1	231 5.12 6	0.04 509 1
P6803 3	INF	DFENEMATAASSSSLEKSYELPDGQVITIGNER	K17:+114.043	123 4.90 8	370 1.7	0.03 182 7
P6803 3	INF	GMESAGIHETTYNSIMKCDIDIR	M2:+15.995,M16:+15.995,K17:+114.043,C18:+45.988	138 8.60 7	277 5.19 8	0.06 738 7
P6825 4	CO N	YEILNNPELACTLAK	C11:+45.988,K15:+114.043	617. 971 5	185 0.89 1	0.06 024 7
P6836 9	CO N	ELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGA GK	C4:+45.988,K39:+114.043	143 6.96 5	430 7.87 3	0.08 075 6
P6843 3	CO N	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	C13:+45.988,C27:+45.988,K32:+114.043	122 6.89 8	367 7.67	0.00 254 6
P6843 3	CO N	FQSSAVMALQEACEAYLVGLFEDTNLCAIHA KR	C13:+45.988,C27:+45.988,K32:+114.043	127 8.93 2	383 3.77 1	0.01 331 2
P6843 3	INF	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	C13:+45.988,C27:+45.988,K32:+114.043	122 6.89 8	367 7.67	0.00 786 1
P6851 0	INF	YDDMASAMKAVTELNE	M4:+15.995,M8:+15.995,K9:+114.043	967. 412	193 2.80 8	0.04 401 7
P7016 8	CO N	CDEEMDLAIEASEAAEQGRPPEHTSKFYAK	C1:+28.961,M5:+15.995,K26:+114.043,K30:+114.043	907. 143 9	362 4.54 4	0.03 780 3
P7016 8	CO N	QDENDDDDWNPCAAAGVC	Q1:- 17.027,C13:+45.988,K14:+114.043,C19:+45.988	114 9.88 8	229 7.76 1	0.07 419 6
P7016 8	CO N	MFQSTAGSGGVQEDALMAVSTLVEVLGGFLKYMEA	M1:+15.995,K32:+114.043	129 9.28 7	389 4.83 7	0.06 502 7
P7016 8	INF	CDEEMDLAIEASEAAEQGRPPEHTSKFYAK	C1:+28.961,M5:+15.995,K26:+114.043,K30:+114.043	907. 143 9	362 4.54 4	0.06 337 3

P7016 8	INF	LKPLVIQAMPTLIELMK	K2:+114.043,M9:+15.995,M16:+15.995	695. 400 7	208 3.17 9	0.05 866 5
P7016 8	INF	QVARVAAGLQIK	K12:+114.043	684. 410 1	136 6.80 5	0.05 139 9
P7016 8	INF	HRSVKPQILSVFGDIALAIGGEFK	K5:+114.043	134 8.74 8	269 5.48 1	0.06 901 4
P7016 8	INF	QSTAGSGGVQEDALMAVSTLVEVLGGEFLK	Q1:-17.027,M15:+15.995,K30:+114.043	103 6.18	310 5.51 7	0.07 319
P7016 8	INF	PDGHQNNLRSSAYESLMEIVK	K21:+114.043	125 1.60 6	250 1.19 7	0.06 738 7
P7016 8	INF	DCYPAVQK	C2:+45.988,K8:+114.043	542. 234 2	108 2.45 3	0.04 071 8
P7019 5	CO N	FNDLGSGSNIDLCVISK	C13:+45.988,K17:+114.043	647. 973 6	194 0.89 8	0.09 501 2
P7019 5	INF	LVSEIAAGIFNDLGSGSNIDLCVISK	C23:+45.988,K27:+114.043	956. 149 7	286 5.42 6	0.04 750 8
P7026 8	CO N	GDIVARDEVESLMCEK	C14:+45.988,K16:+114.043	977. 440 1	195 2.86 5	0.03 736 3
P7026 8	CO N	LPSTCSLSPTHESTTSPELPSETQETPGPLCSPLRK	C6:+45.988,C34:+45.988,K39:+114.043	141 5.65 4	424 3.93 9	0.08 994 9
P7026 8	CO N	VAGLEKQLAIELK	K13:+114.043	763. 451 6	152 4.88 8	0.04 197 7
P7026 8	INF	KLNLGADSDSSSQK	K1:+114.043,K14:+114.043	839. 406 1	167 6.79 7	0.05 197 5
P7026 8	INF	LLLTAQQMLQDSKTK	K13:+114.043,K15:+114.043	973. 523	194 5.03	0.03 182 7
P7026 8	INF	AVATGTFSNPASPGAEIRHTGDISMEK	K27:+114.043	715. 349 4	285 7.36 7	0.03 809
P7026 8	INF	GEAENATEVSTVLKLDNTVVGQTAWKPCGPNAWD	K26:+114.043,C28:+45.988	125 4.25 8	375 9.75 1	0.05 498 6
P7029 0	CO N	VFIAPTQGTQTEALQQLQKDSEAIR	K20:+114.043	100 1.18	300 0.51 5	0.08 207 5
P7029 0	INF	QFEKITEEPMGITLK	M10:+15.995,K15:+114.043	631. 993	189 2.95 6	0.04 315 4
P7031 5	CO N	GGGGGQPLRPPVGSNK	K17:+114.043	845. 953 4	168 9.89 1	0.08 278 5
P7031 5	INF	GGGGGGGGGGGGGQPLRPPVGSNKGR	K25:+114.043	787. 402 9	235 9.18 5	0.06 738 7
P7031 5	INF	GGGGGGGGGGGGGGGQPLRPPVGSNKGR	K28:+114.043	633. 570 3	253 0.25	0.04 667 3
P7031 5	INF	LPPPPPPCRGGGGGGGGGGGGGGGGGQPLRPPV GSNK	C8:+45.988,K39:+114.043	114 4.89 8	343 1.66 9	0.04 724 1

P7033 3	CO N	GEADVEFATHEDAVAAMAKDK	K19:+114.043	116 0.03 2	231 8.04 9	0.04 256 6
P7033 3	INF	KLMTMQRPGPYDR	K1:+114.043	569. 620 9	170 5.83 9	0.04 828 8
P7039 8	CO N	DLLHCHSKTVR	C6:+45.988,K9:+114.043	791. 403 8	158 0.79 2	0.07 192 7
P7039 8	CO N	EQVCCEALEVMTLCFALIPTALDALS	C4:+45.988,C5:+45.988,M11:+15.995,C14:+45.988,K27:+114.043	106 0.48 3	317 8.42 7	0.06 088 5
P7039 8	INF	TGQRAQENYEGGEEVSPQTK	K21:+114.043	121 0.06	241 8.10 5	0.07 782 3
P7039 8	INF	FFKAVNCR	K3:+114.043,C7:+45.988	572. 773 9	114 3.53 2	0.08 473 4
P7039 8	INF	NLEIFRLK	K8:+114.043	573. 835 7	114 5.65 6	0.05 562 4
P7039 8	INF	EVLLEAAIDLSK	K12:+114.043	707. 893 6	141 3.77 2	0.04 092 9
P7039 8	INF	GDEPDLDPDINK	K12:+114.043	721. 326 3	144 0.63 7	0.02 316 6
P7039 8	INF	LYLTEVVYALLMPAGAPLTDDSSDFQFHLKSGGLPLVLSMLTR	M12:+15.995,K31:+114.043	123 9.89 5	495 5.54 9	0.04 724 1
P7040 4	INF	RHTVTMIPGDGIGPELMLHVK	K21:+114.043	805. 759 9	241 4.25 6	0.05 498 6
P7046 0	CO N	PPPAPPLPTAQGPNSGGSGAPGLAAAIAGAK	K31:+114.043	140 2.73 9	280 3.46 2	0.08 003 2
P7046 0	CO N	QGPNSGGSGAPGLAAAIAGAK	K21:+114.043	933. 477 4	186 4.93 9	0.03 947 5
P7046 0	INF	GAGAAPPPAPPLPTAQGPNSGGSGAPGLAAAIAGAKLR	K36:+114.043	113 4.27 5	339 9.80 1	0.04 229 4
P7046 0	INF	GHGAGAAPPPAPPLPTAQGPNSGGSGAPGLAAAIAGAKLR	K38:+114.043	119 8.96 8	359 3.88 2	0.04 372 4
P7046 0	INF	PSSGVSGAGHGAGAAPPPAPPLPTAQGPNSGGSGAPGLAAAIAGAK	K46:+114.043	132 3.33 9	396 6.99 4	0.08 185 4
P7067 0	CO N	PAPKPAGTPAPAPSAK	K16:+114.043	524. 623 4	157 0.84 7	0.06 231 8
P7067 0	CO N	EMLAAPAPESALAITAPIQKSPGANSNSASSPK	E1:- 18.011,M2:+15.995,K20:+114.043,K33:+114.043	114 4.90 7	343 1.69 9	0.06 231 8
P7067 0	CO N	VPVSPLPATEGLKNLPISALVNVGAPVSPAQAGLPTR	K13:+114.043	937. 031 3	374 4.09 4	0.08 621 5
P7067 0	CO N	GGEFPQILVNMPAPKPAGTPAPAPSAKQPVLK	M12:+15.995,K16:+114.043,K33:+114.043	118 3.96 8	354 8.88 2	0.05 668 8
P7067 0	INF	EAPATLPPSPTKSPK	K12:+114.043	817. 941 6	163 3.86 8	0.06 465 9

P7067 0	INF	EAPATLPPSPTK	K12:+114.043	441. 570 4	132 1.68 8	0.03 903 5
P7067 0	INF	VSSKDPASPVTSLVVPAHK	K20:+114.043	105 2.57 4	210 3.13 2	0.05 053 6
P7067 0	INF	ASVAPKPAPAASLTAPSPVAPLPPK	K6:+114.043,K26:+114.043	133 8.75 8	267 5.50 1	0.06 300 9
P7067 0	INF	SKVLMSSPPK	K2:+114.043,M5:+15.995	602. 324 3	120 2.63 3	0.05 463 2
P7067 0	INF	EGVTAVPLEIPPCSKK	C13:+45.988,K15:+114.043	914. 471 5	182 6.92 7	0.03 834 3
P7067 0	INF	AAAAEIDEEPVS	K13:+114.043	722. 352 3	144 2.68 9	0.04 401 7
P7067 0	INF	LEVSLPEAGLAVQGPKGSLNK	K22:+114.043	592. 827 8	236 7.28 5	0.08 437 5
P7067 0	INF	ILVNMPPAPKAGTPAPAPSAKQPVK	M5:+15.995,K9:+114.043	681. 637 9	272 2.52 1	0.04 559 7
P7067 0	INF	LPHVPPTSPPK	K11:+114.043	428. 575 6	128 2.70 3	0.07 350 6
P7067 0	INF	VSDACSTGTTTPQASEKLPSK	C5:+45.988,K17:+114.043	113 4.52 8	226 7.04 1	0.06 738 7
P7067 0	INF	PEDAVTILAGSPLSPKK	K17:+114.043	613. 007 6	183 5.99 9	0.06 267 1
P7067 0	INF	KSPAAPAAASASLSPATAAPQTAPK	K1:+114.043	594. 818 9	237 5.24 5	0.06 536 7
P7067 0	INF	GSKETPTTSPPEGVTAAPLEIPSSK	K3:+114.043	135 4.70 4	270 7.39 2	0.05 928
P7067 0	INF	TNELCSPGSSNVAGTSLSPK	C5:+45.988,K21:+114.043	110 3.51	220 5.00 5	0.07 963 6
P7067 0	INF	VPPEAVSASVAPKPAPA	K13:+114.043	851. 462 7	170 0.91	0.04 530 6
P7067 0	INF	PKPAGTPAPAPSAK	K14:+114.043	702. 386 3	140 2.75 7	0.06 772 5
P7069 8	CO N	ISGIGKGVIASSVGTLK	K6:+114.043	907. 541 5	181 3.06 7	0.06 337 3
P8031 3	CO N	AKSQDAEVDGTTSVTLAAEFLK	K2:+114.043,K24:+114.043	134 0.17 8	267 8.34	0.08 312 1
P8031 3	INF	MLDELLQLKMIGIK	M1:+15.995,K9:+114.043,M10:+15.995,K14:+114.043	635. 678 3	190 4.01 1	0.04 530 6
P8031 3	INF	DAVMMMLDELLQLKMIGIK	M4:+15.995,M5:+15.995,K13:+114.043,M14:+15.995	111 2.07 6	222 2.13 6	0.04 530 6
P8031 4	CO N	TVYGGGCSEMLMAHAVTQLANRTPGK	C7:+45.988,M10:+15.995,K26:+114.043	956. 780 8	286 7.31 9	0.01 663 3

P8031 4	INF	DAALMVTNDGATILKN	K15:+114.043	880. 946 6	175 9.87 8	0.02 898 8
P8031 5	CO N	IGLIQFCLSAPKTDMDNQIVVSDYAQMD	C7:+45.988,K12:+114.043,M15:+15.995,M27: +15.995	110 3.17 2	330 6.49 2	0.05 322 5
P8031 5	INF	LGGTIDDCELVEGLVLTQKV	C8:+45.988,K19:+114.043	113 1.57 2	226 1.12 9	0.03 924 8
P8031 5	INF	TADMLGSAELAEVSLNGSGK	K21:+114.043	109 7.02 1	219 2.02 7	0.03 583 3
P8031 5	INF	KGDVTITNDGATILK	K1:+114.043,K15:+114.043	887. 471 3	177 2.92 7	0.05 498 6
P8031 6	CO N	MMVDKDGDVTITNDGATILSMMDVD	M2:+15.995,K5:+114.043,M22:+15.995	945. 080 3	283 2.21 8	0.04 559 7
P8031 6	INF	DKMLVIEK	M3:+15.995,K8:+114.043	553. 300 3	110 4.58 5	0.05 025 6
P8031 6	INF	NDGATILSMMDVDHQIAK	M9:+15.995,M10:+15.995,K18:+114.043	105 2.98 6	210 3.95 7	0.06 432 4
P8031 6	INF	DGDVTITNDGATILSMMDVDHQIAKLMVE	K25:+114.043,M27:+15.995	108 8.18 1	326 1.52	0.08 185 4
P8031 7	CO N	GFVVINQKGIDPFSLDALAK	K8:+114.043	112 3.61 3	224 5.21 1	0.09 032
P8031 7	INF	QADLYISEGLHPRIITEGFEEAK	K23:+114.043	133 6.68 8	267 1.36 1	0.04 750 8
P8031 8	CO N	ELREDDVGTGAGLLEIK	K17:+114.043	965. 000 4	192 7.98 5	0.05 962 2
P8219 8	CO N	ALLMRLTLALALSVGPAGTLGPAK	M4:+15.995,K26:+114.043	883. 523 1	264 7.54 6	0.03 993 5
P8219 8	CO N	MLTPPMGTVMMDVLKGDN	K14:+114.043	966. 965 6	193 1.91 6	0.05 264 8
P8219 8	CO N	NVSVNKEPVAETDIMATNGVVYAINTVLQPPANRPQ ER	K7:+114.043	108 7.81 5	434 7.22 8	0.01 763 7
P8219 8	INF	NVSVNKEPVAETDIMATNGVVYAINTVLQPPANRPQ ER	K7:+114.043	145 0.08 4	434 7.22 8	0.03 736 3
P8219 8	INF	ETLGGTTLEVGCSDGK	C12:+45.988,K16:+114.043	863. 885 4	172 5.75 5	0.05 025 6
P8219 8	INF	TLGGTTLEVGCSDGK	C11:+45.988,K15:+114.043	799. 364 2	159 6.71 3	0.05 668 8
P8407 8	CO N	MVGLDAAGKTILYK	M1:+15.995,K15:+114.043	570. 975 3	170 9.90 2	0.08 312 1
P8407 8	CO N	LKLGEIVTTIPTIGFNVETVEYK	K2:+114.043	893. 493 8	267 7.45 8	0.04 776 4
P8407 8	INF	PNAMNAAEITDK	M4:+15.995,K12:+114.043	702. 825 4	140 3.63 5	0.05 231 3

P8409 1	INF	NSETGALKTFTITQQGIK	K17:+114.043	975. 518 7	194 9.02 2	0.06 432 4
P8409 1	INF	LYKMCDVMAAYFGK	C5:+45.988,K14:+114.043	600. 605 1	179 8.79 2	0.03 207 1
P8409 6	CO N	KEQGQAPITPQQGQALAK	K1:+114.043	100 4.03 5	200 6.05 5	0.01 030 5
P8409 6	INF	KEQGQAPITPQQGQALAK	K1:+114.043	100 4.03 5	200 6.05 5	0.00 091 7
P8422 8	CO N	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	C27:+45.988,K32:+114.043	120 6.24 3	361 5.70 5	0.00 091 7
P8422 8	CO N	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAKR	C27:+45.988,K32:+114.043	125 8.27 7	377 1.80 6	0.07 419 6
P8422 8	CO N	QSSAVMALQEASEAYLVGLFEDTNLCAIHAK	C26:+45.988,K31:+114.043	115 7.22	346 8.63 7	0.01 472 9
P8422 8	INF	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	C27:+45.988,K32:+114.043	120 6.24 3	361 5.70 5	0.00 091 7
P8422 8	INF	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAKR	C27:+45.988,K32:+114.043	125 8.27 7	377 1.80 6	0.00 091 7
P8424 4	CO N	FQSAAGALQEASEAYLVGLFEDTNLCAIHAK	C27:+45.988,K32:+114.043	885. 934 5	353 9.70 7	0.01 763 7
P8424 4	INF	FQSAAGALQEASEAYLVGLFEDTNLCAIHAK	C27:+45.988,K32:+114.043	118 0.91	353 9.70 7	0.00 091 7
P8424 4	INF	FQSAAGALQEASEAYLVGLFEDTNLCAIHAKR	C27:+45.988,K32:+114.043	123 2.94 4	369 5.80 8	0.01 583 1
P9731 0	CO N	DNNDLLLFIKQLVAE	K11:+114.043	986. 541 7	197 1.06 8	0.03 903 5
P9731 0	CO N	EAMEQQSISISK	E1:-18.011,K12:+114.043	723. 848 6	144 5.68 2	0.07 861 1
P9731 3	CO N	IPCWQFIGWISHMMALLDK	C3:+45.988,M13:+15.995,K19:+114.043	617. 047	246 4.15 7	0.01 044 7
P9731 3	CO N	DLPPWMKFLHDK	K12:+114.043	820. 916 9	163 9.81 8	0.05 993 8
P9731 3	CO N	LMDEFKIGELFNK	K13:+114.043	566. 624 3	169 6.85	0.02 172 5
P9731 3	INF	IPCWQFIGWISHMMALLDK	C3:+45.988,M13:+15.995,K19:+114.043	617. 047	246 4.15 7	0.06 502 7
P9731 3	INF	IMEFTTTLLIASPEDCK	M2:+15.995,C16:+45.988,K17:+114.043	104 4.48 9	208 6.96 3	0.02 457 3
P9736 9	CO N	NKDWLEGTSQGATGIFPGSFVK	K2:+114.043	122 7.10 9	245 2.20 2	0.00 091 7
P9736 9	INF	NKDWLEGTSQGATGIFPGSFVK	K2:+114.043	122 7.10 9	245 2.20 2	0.00 112 9

P9736 9	INF	LKDFPEDEDTTNWLR	K2:+114.043	996. 969 1	199 1.92 3	0.00 091 7
P9737 1	INF	LKAPLDIPVPDPVK	K2:+114.043	404. 741 4	161 4.93 5	0.05 866 5
P9737 1	INF	LDIPVPDPVKEK	K10:+114.043	732. 409 4	146 2.80 3	0.05 264 8
P9749 6	CO N	YQVPFQSQGNPVMSTVAFLASVVDPRVASAAK	K34:+114.043	902. 216 5	360 4.83 5	0.05 264 8
P9749 6	CO N	EEVPLELVEAHVKK	K13:+114.043,K14:+114.043	616. 667 5	184 6.97 9	0.06 901 4
P9749 6	CO N	NDVDAEIEDAPIPEKPWKVHVK	K18:+114.043,K22:+114.043	919. 800 2	275 6.37 7	0.05 410 2
P9749 6	INF	EEVPLELVEAHVK	K13:+114.043	803. 428 3	160 4.84 1	0.06 337 3
P9780 7	CO N	SGLGELILPENEPGSSIMPGKVNPTQCEAMTMVAAQ	M18:+15.995,K21:+114.043,C27:+45.988	129 2.60 5	387 4.79 2	0.05 410 2
P9780 7	CO N	AIELGYLTAEQFDEWVKPKDMLGPK	K17:+114.043,K19:+114.043,M21:+15.995,K25:+114.043	809. 904 4	323 5.58 6	0.03 809
P9780 7	CO N	VAAQVMGNHVAVTVGGSNGHFELNVFKPMMIK	M6:+15.995,M29:+15.995,K32:+114.043	117 6.92 4	352 7.74 8	0.07 350 6
P9782 2	CO N	ELSDNIISGGLEVLAEK	K17:+114.043	634. 334 1	189 9.97 9	0.03 666 5
P9782 2	INF	DDEDEAGSEVGESEEEVGLSYLMK	M23:+15.995,K24:+114.043	906. 380 6	271 6.11 8	0.05 928
P9782 3	CO N	ISVLQCHGDCDPLVPLMFGSLTVERLK	C6:+45.988,C10:+45.988,M17:+15.995,K27:+114.043	106 4.85 2	319 1.53 2	0.05 436 4
P9782 3	INF	GLGDTGHGWAEAFAGIKSPHIK	K22:+114.043	788. 401 8	236 2.18 2	0.05 633 6
P9902 4	CO N	IMNTFSVVPSPKVSDTVVE	M2:+15.995,K12:+114.043	727. 037 1	217 8.08 8	0.03 716 4
P9902 4	INF	PDNFVFGQSGAGNNWAK	K17:+114.043	961. 943 2	192 1.87 1	0.05 197 5
P9902 6	CO N	LGASGDYADFQYLKQVLGQMVIDEELLGDGHSYSPR	K14:+114.043,M20:+15.995	136 7.98 9	410 0.94 3	0.07 705 1
P9902 7	CO N	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEK	K33:+114.043	963. 497	288 7.46 8	0.05 139 9
P9902 7	CO N	PAGGAVAVSAAPGSAAPAAGSAPAAAEKK	K29:+114.043,K30:+114.043	138 0.7	275 9.38 4	0.05 111 3
P9902 7	CO N	GGAVAVSAAPGSAAPAAGSAPAAAEKK	K28:+114.043	826. 758 2	247 7.25 1	0.03 349 6
P9902 7	CO N	SAAPGSAAPAAGSAPAAAEKK	K22:+114.043	101 2.50 6	202 2.99 7	0.06 568

P9902 7	CO N	YVASYLLAALGGNSSPSAKD	K19:+114.043	104 9.52 7	209 7.03 8	0.04 256 6
P9902 7	INF	PAGGAVAVSAAPGSAAPAAGSAPAAEEKK	K29:+114.043,K30:+114.043	138 0.7	275 9.38 4	0.02 259 3
P9902 7	INF	GGAVAVSAAPGSAAPAAGSAPAAEEKK	K28:+114.043	826. 758 2	247 7.25 1	0.05 111 3
P9902 7	INF	AGGAVAVSAAPGSAAPAAGSAPAAEEKK	K28:+114.043	606. 056 1	242 0.19 3	0.07 254 2
P9902 7	INF	IAQGVGKLASVPAGGAVAVSAAPGSAAPAAGSAPAA AEEK	K7:+114.043	886. 221 2	354 0.85 4	0.06 632 8
P9902 7	INF	VAVSAAPGSAAPAAGSAPAAEEKK	K25:+114.043	765. 064 8	229 2.17 1	0.05 111 3
P9902 7	INF	NIEDVIAQGVGKLASVPAGGAVAVSAAPGSAAPAAGS APAAEEKK	K45:+114.043	137 1.38 1	411 1.11 9	0.04 617 3
P9902 7	INF	AGGAVAVSAAPGSAAPAAGSAPAAEEKK	K28:+114.043,K29:+114.043	133 2.17 3	266 2.33 1	0.09 141
P9902 7	INF	AVAVSAAPGSAAPAAGSAPAAEEKK	K25:+114.043,K26:+114.043	123 9.63 3	247 7.25 1	0.09 922 2
P9902 9	INF	LLADPTGAFGKA	K11:+114.043	637. 841 2	127 3.66 7	0.03 854 5
P9902 9	INF	AHQAEKGVR	K7:+114.043	555. 294 7	110 8.57 4	0.08 621 5
Q0051 9	CO N	KPEPTVEEIEAFQGNLCR	K1:+114.043,C18:+45.988	116 7.54 7	233 3.07 8	0.00 651 3
Q0051 9	INF	KPEPTVEEIEAFQGNLCR	K1:+114.043,C18:+45.988	116 7.54 7	233 3.07 8	0.00 091 7
Q0051 9	INF	TFAKDGGCCGGSGNNP	K4:+114.043,C8:+45.988,C9:+45.988	423. 408 1	168 9.60 1	0.04 959 9
Q0051 9	INF	DPPANVQLFQEVPKGQSEEDMVGRMPHLLADMQ ASGE	K14:+114.043,M26:+15.995,M33:+15.995	141 7.98 5	425 0.93 1	0.09 141
Q0051 9	INF	FKPGTTEVQELSLCFGMADRTVSALK	K2:+114.043,C14:+45.988,M18:+15.995	766. 125 9	306 0.47 2	0.05 633 6
Q0051 9	INF	TETSTNTVPNTSPTAASASADLNGQAIYEACQTILKR	C31:+45.988,K36:+114.043	132 8.96 9	398 3.88 4	0.07 823 6
Q0061 2	INF	EKPQPIPVYVYGSR	K2:+114.043	549. 955	164 6.84 2	0.07 003 4
Q0061 2	INF	DVMQNHLLQMLCLVAMEKPATTGSDDVRDE	C12:+45.988,M16:+15.995,K18:+114.043	117 9.20 5	353 4.59 3	0.00 539 6
Q00PI 9	CO N	SDTPAEATAGSGGVNGGEEHDNGKGEEDGPEER	K24:+114.043	112 3.80 4	336 8.39	0.09 344 7
Q00PI 9	INF	CDYMDEVTYGELEK	[0:-17.027,C1:+45.988,K14:+114.043	919. 352 4	183 6.68 9	0.06 701 2

Q00PI 9	INF	DEAGVGGAGPGGACK	C14:+45.988,K15:+114.043	703. 296 1	140 4.57 7	0.02 898 8
Q0132 0	CO N	MSVVDLESDVK	M1:+15.995,K11:+114.043	676. 324 7	135 0.63 4	0.08 582
Q0140 5	CO N	IMMFIGGPATQGPGMVVGDELK	M15:+15.995,K22:+114.043	118 9.58 2	237 7.14 8	0.04 644 6
Q0140 5	CO N	GPQMPLIFLYVVDTCIEDEDLQALKESMQMSL	C15:+45.988,K25:+114.043,M28:+15.995	127 8.26 8	383 1.77 9	0.03 993 5
Q0140 5	INF	IMMFIGGPATQGPGMVVGDELK	M2:+15.995,M3:+15.995,M15:+15.995,K22:+114.043	603. 292 3	240 9.13 8	0.02 986 6
Q0140 5	INF	AATTGHVIDIYACALDQTGLLEMKCCPNLTGGYMV	C13:+45.988,K24:+114.043,C25:+45.988,C26:+45.988	130 8.91 6	392 3.72 4	0.06 231 8
Q0140 5	INF	ECTFPNTGARIMMFIGGPATQGPGMVVGDELK	C2:+45.988,M13:+15.995,K32:+114.043	116 7.54 3	349 9.60 7	0.03 609 6
Q0140 5	INF	CALDQTGLLEMKCCPNLTGGYVMGDSFNSTSLFK	C1:+45.988,C13:+45.988,C14:+45.988,K34:+114.043	131 3.89 8	393 8.66 9	0.07 705 1
Q0140 5	INF	FLLSKVNPSQTHN	K5:+114.043	799. 918 5	159 7.82 1	0.05 346 2
Q0173 0	CO N	NLDLTGQKQVFK	K8:+114.043,K12:+114.043	540. 290 3	161 7.84 8	0.06 841
Q0185 3	CO N	SGADSKGDDLSTAILK	K6:+114.043	846. 426 5	169 0.83 7	0.01 016 9
Q0185 3	CO N	HPALFKAIGVKPPR	K11:+114.043	548. 995 3	164 3.96 2	0.04 285 7
Q0185 3	CO N	DGGGAADRVINQILTEMDGMSTK	M20:+15.995,K23:+114.043	837. 060 7	250 8.15 9	0.06 738 7
Q0185 3	INF	SGADSKGDDLSTAILK	K6:+114.043	846. 426 5	169 0.83 7	0.00 414 1
Q0185 3	INF	KMDLIDLEDETIDAEVMNSLAVTMDDFR	K1:+114.043,M17:+15.995	112 0.51 6	335 8.52 6	0.00 292 7
Q0185 3	INF	AFEEAEK	K7:+114.043	469. 217 3	936. 418 9	0.04 910 9
Q0185 3	INF	QIKEMVELPLR	K3:+114.043,M5:+15.995	743. 408 9	148 4.80 2	0.07 060 6
Q0205 3	CO N	KNGSEADIDESLYSR	K1:+114.043	899. 416 7	179 6.81 8	0.00 477 2
Q0205 3	CO N	FMPIMQWLYFDALECLPEDKEALTEEK	C15:+45.988,K20:+114.043,K27:+114.043	118 8.54 7	356 2.61 7	0.06 024 7
Q0205 3	CO N	IGCELLKNFAMIGLCGEGGEVVVTDMDTIEK	C3:+45.988,M11:+15.995,C16:+45.988,K32:+114.043	118 8.54 8	356 2.62	0.03 092 9
Q0205 3	INF	FEVQGLQPNGEEMTLK	M13:+15.995,K16:+114.043	975. 467 9	194 8.92	0.06 666 4

Q0205 3	INF	KNGSEADIDESLYSR	K1:+114.043	899. 416 7	179 6.81 8	0.00 14
Q0205 3	INF	YFLVGAGAIGCELLK	C11:+45.988,K15:+114.043	857. 439 5	171 2.86 3	0.00 728 6
Q0205 3	INF	QKYFLVGAGAIGCELLK	K2:+114.043,C13:+45.988	493. 262	196 9.01 7	0.06 901 4
Q0205 3	INF	FLVGAGAIGCELLK	C10:+45.988,K14:+114.043	775. 907 8	154 9.8	0.00 517 8
Q0205 3	INF	DPKPGSNCSPAQSALSEVSSVPTNGMAK	C8:+45.988,M26:+15.995,K28:+114.043	146 8.16 6	293 4.31 6	0.06 432 4
Q0326 5	CO N	FNDGTDEKK	K8:+114.043,K9:+114.043	641. 289 5	128 0.56 3	0.04 372 4
Q0326 5	INF	EPMQTGIK	M3:+15.995,K8:+114.043	517. 253 4	103 2.49 1	0.02 220 9
Q0326 5	INF	EPMQTGIKAVDSLPIG	E1:-18.011,M3:+15.995,K8:+114.043	933. 985 5	186 5.95 5	0.04 372 4
Q0475 0	CO N	KDEPEDDGYFAPPK	K1:+114.043	861. 386 9	172 0.75 8	0.03 716 4
Q0475 0	CO N	DEPEDDGYFAPPKEDIK	K13:+114.043,K17:+114.043	109 6.98 5	219 1.95 5	0.03 974 7
Q0475 0	INF	VPSPPPGHKWK	K11:+114.043	672. 365 1	134 2.71 5	0.08 392 4
Q0707 6	INF	KAMQGAGTQER	K1:+114.043	645. 815 2	128 9.61 5	0.02 185 9
Q0741 7	CO N	ENLLGEPGMGFKIAMQT	M9:+15.995,K12:+114.043	983. 474 7	196 4.93 4	0.05 463 2
Q0779 7	INF	QLYTYGYGSVARYNSYQSFQTPQHPSFLFK	K30:+114.043	123 1.25 9	369 0.75 3	0.03 924 8
Q0901 4	INF	PYVTIKAYAAVEEDEMSLSEGEAIEVIHK	K6:+114.043	111 2.55	333 4.62 8	0.06 024 7
Q1101 1	CO N	NAATEDLWESLESASGKPIAAVMNTWT	K17:+114.043,M23:+15.995	100 8.14 2	302 1.40 3	0.00 291 5
Q1101 1	INF	ILMDKPEMSVVLK	M8:+15.995,K13:+114.043	816. 939 2	163 1.86 3	0.07 530 6
Q1101 1	INF	VTLSFPSTLQTGTGLK	K17:+114.043	622. 339 2	186 3.99 4	0.07 963 6
Q1101 1	INF	WESLESASGKPIAAVMNTWTK	K21:+114.043	121 0.6	241 9.18 4	0.06 738 7
Q1101 1	INF	KNAATEDLWESLESASGKPIAAVMNTWTK	K1:+114.043,M24:+15.995	109 3.53 9	327 7.59 3	0.05 6
Q1101 1	INF	DEPAIKATFDISLVVPK	K6:+114.043,K17:+114.043	691. 041 1	207 0.1	0.04 996 1

Q14C H1	CO N	KVAAAMSVTSIP	K1:+114.043,M6:+15.995	652. 848 2	130 3.68 1	0.05 633 6
Q3TB D2	INF	EEQQTGPGAGTAASKALDK	E1:-18.011,K20:+114.043	671. 327 9	201 0.96	0.03 947 5
Q3TB D2	INF	QQGTGPGAGTAASKALDK	Q1:-17.027,K14:+114.043,K18:+114.043	934. 958 9	186 7.90 2	0.09 840 5
Q3TB D2	INF	EDTKVTALR	K4:+114.043	573. 809 9	114 5.60 4	0.03 834 3
Q3TE A8-2	CO N	AEGEEKEPEEQENETPPATSSEAEQPK	K7:+114.043	102 8.78 5	308 3.33 3	0.00 604 2
Q3TE A8-2	CO N	SGEKPLLGSLMEYAILSAI	K4:+114.043	108 2.07 2	216 2.12 9	0.00 929 7
Q3TE A8-2	INF	SGEKPLLGSLMEYAILSAI	K4:+114.043	108 2.07 2	216 2.12 9	0.01 191 3
Q3TE A8-2	INF	EKPLLGSLMEYAILSIAIAMNEPK	K2:+114.043,M10:+15.995	926. 147 4	277 5.41 9	0.04 694 9
Q3TE A8-2	INF	EENNNKSAEEPK	K12:+114.043	751. 840 1	150 1.66 5	0.06 568
Q3TE A8-2	INF	DMSQGELIHPKALPLIVGAQLIHADK	K26:+114.043	145 4.79	290 7.56 4	0.07 630 8
Q3TH E2	CO N	INFTMFLTMFGEKLNGTDPEDVIR	M9:+15.995,K13:+114.043	145 9.70 7	291 7.39 9	0.04 857 5
Q3TH E2	INF	EDLHDMLASLGKNPTDAYLDAMMNEAPGPINFTMF	K12:+114.043,M23:+15.995	133 3.93 6	399 8.78 4	0.07 419 6
Q3TH K7	INF	MALCNGDSKPENAGGDLKDGSHHYEGAVVIL	C4:+45.988,K9:+114.043	111 9.84 9	335 6.52 3	0.07 705 1
Q3TR M8	CO N	QIQASLLCSMEQALKGQDSPAPSVR	C8:+45.988,K15:+114.043	140 9.18 9	281 6.36 2	0.05 410 2
Q3TR M8	INF	LSEFLDAYPVENQGLK	K16:+114.043	968. 986 7	193 5.95 8	0.03 378 2
Q3TW 96	CO N	KVPYVDEEGNLVKPLR	K13:+114.043	985. 539 5	196 9.06 3	0.07 319
Q3TW W8	INF	AGEVTYADAHK	K11:+114.043	638. 302 4	127 4.58 9	0.00 799 1
Q3TXS 7	CO N	LYQDDAVTGEAAGLALGLVMLGSK	K24:+114.043	836. 100 7	250 5.27 9	0.07 823 6
Q3TXS 7	INF	DSDPMETEEKTASA	K10:+114.043	406. 922 1	162 3.65 7	0.05 264 8
Q3U1J 4	CO N	GDFILVGDLMRSVLLLAYKPMEGNFEEIAR	K19:+114.043,M21:+15.995	117 6.27 5	352 5.8	0.06 701 2
Q3U1J 4	INF	SVLLLAYKPMEGNFEEI	K8:+114.043	689. 687 6	206 6.03 9	0.05 139 9

Q3U2 G2	CO N	KEDQYEHLDAAADVTK	K1:+114.043	938. 440 2	187 4.86 5	0.00 091 7
Q3U2 G2	INF	KEDQYEHLDAAADVTK	K1:+114.043	938. 440 2	187 4.86 5	0.00 091 7
Q3U2 G2	INF	AESEEMETSQAGSK	M6:+15.995,K14:+114.043	807. 334	161 2.65 2	0.05 962 2
Q3U2 G2	INF	AEQNGPVDGQGDNPGSQAAEHGADTAVPSDGDKK	K33:+114.043,K34:+114.043	887. 644 8	354 6.54 8	0.07 782 3
Q3U2 G2	INF	GPVDGQGDNPGSQAAEHGADTAVPSDGDGK	K29:+114.043	143 2.12 2	286 2.22 9	0.03 583 3
Q3U3 90	CO N	ILLLIAATVIYMHK	K14:+114.043	571. 676 5	171 2.00 6	0.02 350 7
Q3U3 90	CO N	EVPFTLIVNK	K10:+114.043	637. 361 7	127 2.70 8	0.00 408 3
Q3U3 90	INF	ILLLIAATVIYMHK	M12:+15.995,K14:+114.043	577. 008 1	172 8.00 1	0.00 747 5
Q3U3 90	INF	EVPFTLIVNK	K10:+114.043	637. 361 7	127 2.70 8	0.02 499 4
Q3UA 06	INF	QDLIDDKEALVFVLIDEVESLTAAR	K7:+114.043	972. 845 4	291 5.51 3	0.00 112 9
Q3UA 06	INF	HLLDYVMTTVLFSDK	K15:+114.043	948. 482 8	189 4.95 5	0.09 883 5
Q3UH H2	CO N	LASLLQLGLLNLIGK	K15:+114.043	840. 525 1	167 9.03 5	0.01 270 6
Q3UH H2	CO N	QHPDSELQLKLAVGMSDSVK	Q1:- 17.027,K10:+114.043,M15:+15.995,K20:+114.043	803. 729 1	240 8.16 4	0.07 155 3
Q3UH H2	INF	LASLLQLGLLNLIGK	K15:+114.043	840. 525 1	167 9.03 5	0.00 477 2
Q3UJB 0	CO N	GEDGDKAAPPPMSAQLSGIPMPPPMGLPPLQPPPP	K6:+114.043,M21:+15.995	928. 711 5	371 0.81 5	0.07 192 7
Q3UJB 0	INF	LTIHGDLYEGKEFETR	K12:+114.043	729. 024 1	218 4.04 9	0.06 123 4
Q3UJB 0	INF	QLVARPDVVMHDVTAQDPKLLVHLK	M11:+15.995,K26:+114.043	102 7.88 9	308 0.64 4	0.03 736 3
Q3UM W7	CO N	ETAGEKGSVPPPGALGGSALGGAPAGVR	E1:-18.011,K6:+114.043	922. 823	276 5.44 6	0.06 738 7
Q3UN D0	CO N	EELPEEEEDTASVKMDEQGK	K14:+114.043,K20:+114.043	126 1.04 8	252 0.08 1	0.07 319
Q3UN D0	INF	TVFYYYGSDKDK	K10:+114.043	800. 370 5	159 8.72 5	0.06 300 9
Q3UP L0	CO N	KMPENFMPPVPITSPIMNPSG	K1:+114.043,M2:+15.995,M17:+15.995	810. 722 2	242 9.14 3	0.06 536 7

Q3UP L0	INF	MDSKGDVSGVLIAGGENGNII	M1:+15.995,K4:+114.043	108 8.53 2	217 5.04 8	0.06 465 9
Q3UP L0	INF	ACWTKAQDGGSSPLSLQDLIEK	C2:+45.988,K21:+114.043	122 5.58 9	244 9.16 2	0.06 502 7
Q3UQ 44	CO N	FLGVEMEKVQLNIQDLLQM	M6:+15.995,K8:+114.043	118 9.60 9	237 7.20 2	0.04 448 1
Q3UQ 44	CO N	MPAFSKIGGILANELSVDEAALHAAVIAINEAIEK	M1:+15.995,K35:+114.043	124 5.99 3	373 4.95 5	0.06 024 7
Q3UQ 44	CO N	LFKTALEEEIK	K3:+114.043,K11:+114.043	774. 917 6	154 7.82	0.09 380 1
Q3UQ 44	CO N	AWVNQLETQTGEASKLP	K15:+114.043	497. 254 2	198 4.98 5	0.05 526 5
Q3UQ 44	CO N	IGGILANELSVDEAALHAAVIAINEAIEKG	K29:+114.043	103 9.22 7	311 4.65 6	0.05 374 6
Q3UQ 44	CO N	EKSDLLNELLESIGEVPVTVESFLGEGAVDPNDPNK	E1:-18.011,K35:+114.043	128 4.30 1	384 9.87 9	0.06 568
Q3UQ 44	INF	IGGILANELSVDEAALHAAVIAINEAIEKG	K29:+114.043	103 9.22 7	311 4.65 6	0.00 719
Q3UQ 44	INF	ELLESIGEVPVTVESFLGEGAVDPNDPNK	E1:-18.011,K28:+114.043	101 7.83 2	305 0.47 2	0.09 300 5
Q3UW 53	CO N	FEDNMALPSESVSSTDLK	K19:+114.043	109 9.02 1	219 6.02 6	0.09 724 8
Q3UW 53	CO N	NGTPVPQENIKEEESK	K11:+114.043,K16:+114.043	676. 328	202 5.96	0.06 401 4
Q3UW 53	INF	KEQPGVPGSLAISASSCPSGDGQVSDHSAGGPLTV ENTAGP	K1:+114.043,C17:+45.988	139 3.31 9	417 6.93 3	0.07 254 2
Q3UW 53	INF	LFEDNMALPSESVSSTDLK	M6:+15.995,K20:+114.043	776. 042 7	232 5.10 5	0.06 810 4
Q3UZ 39	CO N	TVEDQVGTVASGPAKQSK	K15:+114.043	958. 490 2	191 4.96 5	0.08 437 5
Q3UZ 39	INF	LNALKSAGEGTLGK	K5:+114.043,K14:+114.043	793. 929 1	158 5.84 3	0.02 350 7
Q3UZ Z4	CO N	KNFVGSTHIIDMLE	K1:+114.043	859. 433 1	171 6.85 1	0.03 666 5
Q3UZ Z4	CO N	PSVSNAFMVCGVLYATRTLNTK	M8:+15.995,C10:+45.988,K22:+114.043	637. 815	254 7.22 9	0.02 154 9
Q3UZ Z4	CO N	EIRNMTLLVEK	K11:+114.043	730. 401 1	145 8.78 7	0.06 632 8
Q3UZ Z4	INF	PSVSNAFMVCGVLYATRTLNTK	M8:+15.995,C10:+45.988,K22:+114.043	637. 815	254 7.22 9	0.07 385 3
Q3UZ Z4	INF	YANVNWQDIDLAVDEQALWAIYATEASTGNIVISKLN DTTLEVISTWVTK	K35:+114.043	142 4.97 2	569 5.85 7	0.07 457 6

Q3V1L 4	INF	IKCFGFDMDYTLAVYK	C3:+45.988,K16:+114.043	691. 988 2	207 2.94 1	0.03 010 1
Q3V3 R1	CO N	FVVTEAGFGADIGMEKFFNIK	M14:+15.995,K16:+114.043,K21:+114.043	855. 421 8	256 3.24 2	0.06 738 7
Q3V3 R1	INF	QPSQGPTFGVGGAAGGGYAQVIPM	Q1:-17.027,K11:+114.043,M25:+15.995	124 4.6	248 7.18 5	0.04 800 5
Q4LD D4	CO N	PMDELPGGPTPITPVIK	M2:+15.995,K17:+114.043	946. 495 9	189 0.97 6	0.07 319
Q4LD D4	INF	FSFSADSELEKEQWLEAMQGAIAEALSTSEVAER	K11:+114.043	129 1.94 3	387 2.80 5	0.03 282 5
Q4LD D4	INF	TPTSTAAPDPVLPPLPAKR	K18:+114.043	102 2.06 6	204 2.11 6	0.04 724 1
Q4LD D4	INF	FILNSSCLRLYK	C7:+45.988,K12:+114.043	404. 963 3	161 5.82 2	0.06 738 7
Q4QR L3	CO N	EMQGQELHRK	E1:-18.011,K10:+114.043	676. 330 8	135 0.64 6	0.05 526 5
Q4QR L3	CO N	RNNATLVAEK	K10:+114.043	615. 334	122 8.65 2	0.08 244 9
Q4QR L3	CO N	QKFLQEENQ	K2:+114.043	703. 339 5	140 4.66 3	0.05 498 6
Q4QR L3	INF	LVEKIMD	K4:+114.043,M6:+15.995	489. 252 8	976. 490 1	0.05 374 6
Q501J 6	CO N	EANQAINPKMLQLVDHR	K9:+114.043,M11:+15.995	105 4.04	210 6.06 4	0.04 694 9
Q501J 6	INF	FAQPPGATNMIGYMGQTAYQYPPPPPPPPSRK	M14:+15.995,K33:+114.043	122 8.59 8	368 2.77	0.06 841
Q571E 4	INF	IMDLFTTSLSLAGLKPPSDRVIDGLDLLPTMLK	M2:+15.995,K15:+114.043	926. 003 6	369 9.98 3	0.03 109 4
Q571I 9	CO N	FKAWSQLPGAAR	K2:+114.043	723. 386 6	144 4.75 8	0.03 509 5
Q571I 9	INF	APCQDPITGENLASCLQAEAEIAAAVEAAKIAFK	C3:+45.988,C15:+45.988,K31:+114.043	125 5.59 4	376 3.75 7	0.05 668 8
Q5FW K3	CO N	YNMGLPVDFDQYNELHLPVILK	M3:+15.995,K23:+114.043	940. 474 5	281 8.4	0.08 207 5
Q5RK N9	INF	QLVSHKDVQDSVTVSNEIQTTK	Q1:-17.027,K22:+114.043	851. 764 9	255 2.27 1	0.05 562 4
Q5SQ X6	CO N	EVIPGYEELLADIVNCVDYYENKMYLTPSEK	E1:- 18.011,C17:+45.988,K24:+114.043,M25:+15.9 95	130 3.61 6	390 7.82 5	0.02 874 5
Q5SQ X6	INF	FDLDFCFYHLLK	C7:+45.988,K12:+114.043	860. 897 4	171 9.77 9	0.06 123 4
Q5SQ X6	INF	FDLALRGLQLLSK	K13:+114.043	794. 465	158 6.91 4	0.04 857 5

Q5SQ X6	INF	EKFAFVEVIAMIK	M11:+15.995,K13:+114.043	552. 301 2	165 3.88	0.04 694 9
Q5SQ X6	INF	YMKSVETDSSTVEHVR	M2:+15.995,K3:+114.043	999. 465 9	199 6.91 6	0.07 823 6
Q5SQ X6	INF	NDHSAYK	K7:+114.043	474. 712 7	947. 409 8	0.06 369 3
Q5SSL 4	CO N	KDILLMLSDMDINAIAGTLK	K20:+114.043	763. 745 2	228 8.21 2	0.04 315 4
Q5SSL 4	INF	PVLTIQIETIFYKIQDIYEIHK	K14:+114.043,K23:+114.043	765. 916 1	305 9.63 3	0.04 448 1
Q5SSL 4	INF	EEIYNQLEALLPMKPLKATATTSQPVLTIQQIET	K16:+114.043,K19:+114.043	142 2.77	426 5.28 7	0.02 743 3
Q5SS W2	CO N	LLKYLEPK	K3:+114.043,K8:+114.043	616. 356 5	123 0.69 7	0.09 344 7
Q5SS W2	INF	FLQPELIK	K8:+114.043	551. 319 3	110 0.62 3	0.05 895 8
Q5SU R0	CO N	EAMVAVMAALGVAVDGGK	M3:+15.995,M7:+15.995,K18:+114.043	612. 306 7	183 3.89 7	0.03 755 2
Q5SU R0	CO N	SGNWMWAAKLPGEAALADACEAMVAVMAALGV AVDGGK	M5:+15.995,K9:+114.043,C21:+45.988,M28:+ 15.995	132 7.62 1	397 9.84	0.05 171 8
Q5SU R0	CO N	ALGVAVDGGKDSLSMAAR	K10:+114.043	611. 316 4	183 0.92 6	0.05 526 5
Q5SU R0	INF	AAKLPGEAALADACEAMVAVMAALGVAVDGGK	K3:+114.043,C15:+45.988,M18:+15.995,M22: +15.995,K33:+114.043	111 1.87	333 2.58 8	0.02 547 6
Q5SU R0	INF	LPGEAALADACEAMVAVMAALGVAVDGGKD	C12:+45.988,M19:+15.995,K30:+114.043	101 6.81	304 7.40 8	0.05 895 8
Q5XG 71	INF	KPGHPEYDILTNVFAVLSAK	K1:+114.043,K20:+114.043	121 4.13 8	242 6.26	0.09 922 2
Q6059 7	CO N	ISSTDKLGFGYGLHESDLK	K19:+114.043	747. 034 6	223 8.08 1	0.04 667 3
Q6060 5-2	CO N	KDQGTIEDYVEGLR	K1:+114.043	893. 916 3	178 5.81 7	0.00 091 7
Q6060 5-2	INF	KDQGTIEDYVEGLR	K1:+114.043	893. 916 3	178 5.81 7	0.00 091 7
Q6066 8	CO N	GSAGEQEGAMVAAAAQGPAAGSGSGGGGSAAG GTEGGSAAEAGAK	M10:+15.995,K47:+114.043	132 1.58 2	396 1.72 2	0.03 924 8
Q6066 8	CO N	EQEGAMVAAAAQGPAAGSGSGGGGSAAGGTEG GSAEAGAK	E1:-18.011,K43:+114.043	121 9.54 2	365 5.60 4	0.09 141
Q6066 8	CO N	AGEQEGAMVAAAAQGPAAGSGSGGGGSAAGGT EGGSAEAGAK	M8:+15.995,K45:+114.043	955. 424 9	381 7.66 8	0.04 372 4
Q6066 8	CO N	GEQEGAMVAAAAQGPAAGSGSGGGGSAAGGTE GGSAEAGAK	K44:+114.043	124 4.55 3	373 0.63 6	0.04 750 8

Q6066 8	CO N	MVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAK	K38:+114.043	105 4.14 5	315 9.41 2	0.01 342 8
Q6066 8	CO N	EGAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAK	E1:-18.011,K41:+114.043	113 3.84 2	339 8.50 3	0.05 025 6
Q6066 8	CO N	AMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAK	K39:+114.043	107 7.82 4	323 0.44 9	0.03 307 9
Q6066 8	CO N	MVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAKIDASK	K38:+114.043	919. 429 7	367 3.68 7	0.05 139 9
Q6066 8	CO N	GAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAK	K40:+114.043	109 6.83 1	328 7.47 1	0.04 092 9
Q6066 8	CO N	AMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAKIDASK	K39:+114.043	124 9.24 9	374 4.72 5	0.05 993 8
Q6066 8	CO N	GEQEGAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAKIDASK	K44:+114.043	141 5.97 8	424 4.91 1	0.06 841
Q6066 8	CO N	EGAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAKIDASK	E1:-18.011,K41:+114.043,K46:+114.043	134 3.28 1	402 6.82 1	0.01 163 2
Q6066 8	CO N	GAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAKIDASK	K40:+114.043	951. 444 3	380 1.74 6	0.05 231 3
Q6066 8	CO N	VGGSAGEQEGAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAK	K49:+114.043	136 8.28	410 1.81 7	0.05 562 4
Q6066 8	CO N	EQEGAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAKIDASK	E1:-18.011,K43:+114.043,K48:+114.043	142 8.98 2	428 3.92 2	0.06 267 1
Q6066 8	CO N	SAGEQEGAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAKIDASK	K46:+114.043,K51:+114.043	113 0.26 4	451 7.02 3	0.05 6
Q6066 8	CO N	QEGAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAKIDASK	K42:+114.043	135 3.95 7	405 8.84 7	0.00 943 1
Q6066 8	CO N	SAGEQEGAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAK	K46:+114.043	129 7.24 3	388 8.70 5	0.05 053 6
Q6066 8	CO N	VAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAKIDASK	K37:+114.043	118 1.89	354 2.64 7	0.05 346 2
Q6066 8	CO N	AAAGSGSGGGGSAAGGTEGGSAAEAE GAK	K28:+114.043	765. 002 8	229 1.98 5	0.07 003 4
Q6066 8	CO N	QGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAKIDASK	K32:+114.043,K37:+114.043	819. 376 1	327 3.47 3	0.07 933 9
Q6066 8	CO N	AGEQEGAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAKIDASK	K45:+114.043,K50:+114.043	147 7.67 2	442 9.99 1	0.06 871 7
Q6066 8	CO N	GGSAGEQEGAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAK	K48:+114.043	100 1.69 5	400 2.74 8	0.06 159 8
Q6066 8	CO N	AVGGSAGEQEGAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAK	M13:+15.995,K50:+114.043	139 7.29 1	418 8.84 9	0.09 225
Q6066 8	CO N	AAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAE GAKIDASK	K35:+114.043,K40:+114.043	116 3.20 3	348 6.58 4	0.03 639

Q6066 8	CO N	GSGGGGSAAGGTEGGSAAEAGAK	K23:+114.043	968. 417 9	193 4.82	0.08 892 1
Q6066 8	CO N	SEEQFGDGAATAAVGGSAGEQEGAMVAAAQ GPAAAAGSGGGGSAAGGTEGGSAAEAGAK	M29:+15.995,K66:+114.043	140 6.62 1	562 2.45 5	0.05 025 6
Q6066 8	CO N	AAGSGSGGGGSAAGGTEGGSAAEAGAK	K27:+114.043	111 1.48 2	222 0.94 8	0.01 695 5
Q6066 8	CO N	AAAGSGSGGGGSAAGGTEGGSAAEAGAKIDASK	K28:+114.043,K33:+114.043	146 1.15 9	292 0.30 3	0.04 959 9
Q6066 8	CO N	AAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAGAKID ASK	K39:+114.043	110 1.50 9	330 1.50 4	0.07 254 2
Q6066 8	CO N	SGSGGGGSAAGGTEGGSAAEAGAK	K24:+114.043	674. 958 6	202 1.85 2	0.02 499 4
Q6066 8	INF	GSAGEQEGAMVAAAQGPAAAAGSGSGGGGSAAG GTEGGSAAEAGAK	K47:+114.043	131 6.25	394 5.72 7	0.03 307 9
Q6066 8	INF	EQEGAMVAAAQGPAAAAGSGSGGGGSAAGGTEG GSAAEAGAK	E1:-18.011,K43:+114.043	121 9.54 2	365 5.60 4	0.05 633 6
Q6066 8	INF	AGEQEGAMVAAAQGPAAAAGSGSGGGGSAAGGT EGGSAAEAGAK	K45:+114.043	126 8.23 2	380 1.67 3	0.09 423
Q6066 8	INF	GEQEGAMVAAAQGPAAAAGSGSGGGGSAAGGTE GGSAAEAGAK	K44:+114.043	124 4.55 3	373 0.63 6	0.05 928
Q6066 8	INF	MVAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAE GAK	K38:+114.043	105 4.14 5	315 9.41 2	0.02 201 2
Q6066 8	INF	EGAMVAAAQGPAAAAGSGSGGGGSAAGGTEGGS AAEAGAK	E1:-18.011,K41:+114.043	113 3.84 2	339 8.50 3	0.03 455 1
Q6066 8	INF	AMVAAAQGPAAAAGSGSGGGGSAAGGTEGGSAA EAGAK	K39:+114.043	107 7.82 4	323 0.44 9	0.04 071 8
Q6066 8	INF	MVAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAE GAKIDASK	K38:+114.043,K43:+114.043	126 3.58 5	378 7.73	0.02 115 4
Q6066 8	INF	GAMVAAAQGPAAAAGSGSGGGGSAAGGTEGGS AAEAGAK	K40:+114.043	109 6.83 1	328 7.47 1	0.04 116 7
Q6066 8	INF	AMVAAAQGPAAAAGSGSGGGGSAAGGTEGGSAA EAGAKIDASK	K39:+114.043	124 9.24 9	374 4.72 5	0.06 632 8
Q6066 8	INF	GEQEGAMVAAAQGPAAAAGSGSGGGGSAAGGTE GGSAAEAGAKIDASK	K44:+114.043	141 5.97 8	424 4.91 1	0.05 633 6
Q6066 8	INF	EGAMVAAAQGPAAAAGSGSGGGGSAAGGTEGGS AAEAGAKIDASK	E1:-18.011,K41:+114.043,K46:+114.043	134 3.28 1	402 6.82 1	0.01 977
Q6066 8	INF	GAMVAAAQGPAAAAGSGSGGGGSAAGGTEGGS AAEAGAKIDASK	K40:+114.043	126 8.25 6	380 1.74 6	0.07 155 3
Q6066 8	INF	VGGSAGEQEGAMVAAAQGPAAAAGSGSGGGGSA AGGTEGGSAAEAGAK	K49:+114.043	136 8.28	410 1.81 7	0.06 267 1
Q6066 8	INF	EQEGAMVAAAQGPAAAAGSGSGGGGSAAGGTEG GSAAEAGAKIDASK	E1:-18.011,K43:+114.043,K48:+114.043	107 1.98 8	428 3.92 2	0.08 553 1

Q6066 8	INF	SAGEQEGAMVAAAAQGPAAAAGSGSGGGGSAAGG TEGGSAAEAGAKIDASK	K46:+114.043	146 8.66 8	440 2.98	0.06 666 4
Q6066 8	INF	QEGAMVAAAAQGPAAAAGSGSGGGGSAAGGTEGG SAEAGAKIDASK	K42:+114.043	135 3.95 7	405 8.84 7	0.00 799 1
Q6066 8	INF	SAGEQEGAMVAAAAQGPAAAAGSGSGGGGSAAGG TEGGSAAEAGAK	K46:+114.043	129 7.24 3	388 8.70 5	0.05 410 2
Q6066 8	INF	VAAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAG AKIDASK	K37:+114.043	118 1.89	354 2.64 7	0.02 185 9
Q6066 8	INF	AAAGSGSGGGGSAAGGTEGGSAAEAGAK	K28:+114.043	114 7	229 1.98 5	0.08 312 1
Q6066 8	INF	GSAGEQEGAMVAAAAQGPAAAAGSGSGGGGSAAG GTEGGSAAEAGAKIDASK	M10:+15.995,K47:+114.043,K52:+114.043	114 8.51 8	459 0.04	0.07 564 5
Q6066 8	INF	QGPAAAAGSGSGGGGSAAGGTEGGSAAEAGAKIDAS K	K37:+114.043	105 4.15 1	315 9.43	0.07 896 1
Q6066 8	INF	AGEQEGAMVAAAAQGPAAAAGSGSGGGGSAAGGT EGGSAAEAGAKIDASK	K45:+114.043,K50:+114.043	147 7.67 2	442 9.99 1	0.05 633 6
Q6066 8	INF	GGSSAGEQEGAMVAAAAQGPAAAAGSGSGGGGSA GGTEGGSAAEAGAK	K48:+114.043	100 1.69 5	400 2.74 8	0.01 116 2
Q6066 8	INF	AVGGSAGEQEGAMVAAAAQGPAAAAGSGSGGGGS AAGGTEGGSAAEAGAK	M13:+15.995,K50:+114.043	139 7.29 1	418 8.84 9	0.06 536 7
Q6066 8	INF	AAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAGAKI DASK	K35:+114.043,K40:+114.043	116 3.20 3	348 6.58 4	0.02 622 9
Q6066 8	INF	GSGGGSAAGGTEGGSAAEAGAK	K23:+114.043	968. 417 9	193 4.82	0.09 225
Q6066 8	INF	GGSSAGEQEGAMVAAAAQGPAAAAGSGSGGGGSA GGTEGGSAAEAGAKIDASK	K53:+114.043	113 0.26 4	451 7.02 3	0.07 782 3
Q6066 8	INF	AAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAGAKID ASK	K34:+114.043,K39:+114.043	113 9.52 4	341 5.54 7	0.07 090 1
Q6066 8	INF	AAAAQGPAAAAGSGSGGGGSAAGGTEGGSAAEAGA KIDASK	K36:+114.043,K41:+114.043	118 6.88 2	355 7.62 2	0.09 724 8
Q6066 8	INF	PAAAAGSGSGGGGSAAGGTEGGSAAEAGAKIDASK	K35:+114.043	992. 457 8	297 4.35	0.08 582
Q6067 5	INF	DTMDKLSAITNDTAAK	M3:+15.995,K5:+114.043	608. 960 2	182 3.85 7	0.00 912 6
Q6067 5	INF	SQKMDGMGIEMIDEK	K15:+114.043	913. 410 6	182 4.80 6	0.04 644 6
Q6067 5	INF	EVYLEPSEEHIEVSLKEEAFTIHGTNLP	K17:+114.043	115 1.89 5	345 2.66 2	0.05 410 2
Q6067 5	INF	QEGILYVDDASSQTISPKK	K18:+114.043,K19:+114.043	769. 720 9	230 6.13 9	0.07 705 1
Q6069 2	CO N	GMTKDECLQFTANALALAMER	M2:+15.995,K4:+114.043,C7:+45.988	830. 381 9	248 8.12 2	0.01 204 1

Q6069 2	INF	GMTKDECLQFTANALALAMER	M2:+15.995,K4:+114.043,C7:+45.988	830. 381 9	248 8.12 2	0.00 091 7
Q6071 0	INF	LVMKNYGLVPE	K4:+114.043	688. 866 3	137 5.71 7	0.01 016 9
Q6074 9	CO N	TPLLPPSATAAVKMEPENK	K13:+114.043,M14:+15.995	708. 705 6	212 3.09 3	0.05 410 2
Q6074 9	INF	PLLPPSATAAVKMEPENK	K12:+114.043,K18:+114.043	106 1.05 5	212 0.09 4	0.04 996 1
Q6086 5	CO N	SKSSGPPPPSGSSGSEAAAGAAAPASQHPATGTGAVQ TEAMK	K2:+114.043,K42:+114.043	134 0.29 9	401 7.87 2	0.07 705 1
Q6086 5	CO N	SEAAAGAAAPASQHPATGTGAVQTEAMK	K28:+114.043	899. 096 7	269 4.26 7	0.06 024 7
Q6086 5	INF	SKSSGPPPPSGSSGSEAAAGAAAPASQHPATGTGAVQ TEAMK	K2:+114.043,K42:+114.043	134 0.29 9	401 7.87 2	0.06 969 8
Q6096 3	INF	DTVWIPNKEYFLGLSIFLGTSPVGNILHLLYGLTTPAS WNSPLR	K8:+114.043	130 4.44 8	521 3.75 9	0.08 851 8
Q6097 2	CO N	DKEAAFDDAVEER	K2:+114.043	804. 861	160 7.70 6	0.00 091 7
Q6097 2	INF	DKEAAFDDAVEER	K2:+114.043	804. 861	160 7.70 6	0.00 171 5
Q6097 2	INF	VEDVSWHLLHESLFGSVADDQKLMIWDR	K22:+114.043	118 0.91 3	353 9.71 4	0.04 071 8
Q6097 2	INF	LKLHSFESHK	K2:+114.043,K10:+114.043	727. 381 6	145 2.74 8	0.08 553 1
Q6102 4	CO N	LLSGGLDSSLVAASLLK	K17:+114.043	586. 672 3	175 6.99 4	0.02 316 6
Q6102 4	CO N	VDDEMMSAASQKFPFNTPK	K12:+114.043,K19:+114.043	118 6.03 9	237 0.06 2	0.05 374 6
Q6103 3	CO N	EDKDDLDTLSNEELLDQLVR	K3:+114.043	901. 438 8	270 1.29 3	0.05 322 5
Q6103 3	CO N	KSELVANNVTLPAGEQR	K1:+114.043	970. 514	193 9.01 2	0.07 963 6
Q6103 3	CO N	LKSELVANNVTLPAGEQ	K2:+114.043	949. 005 5	189 5.99 5	0.05 231 3
Q6103 3	INF	EDKDDLDTLSNEELLDQLVR	K3:+114.043	135 1.65 4	270 1.29 3	0.00 091 7
Q6109 3	CO N	EVVMLVGAGIGVTPFASILK	E1:-18.011,K20:+114.043	104 9.09 3	209 6.17	0.05 866 5
Q6109 3	INF	FSYEVVMLVGAGIGVTPFASILKSVWYK	M7:+15.995,K23:+114.043,K28:+114.043	110 2.58 1	330 4.72 1	0.07 896 1
Q6114 7	INF	MHAINGKMFQNLQGLTMHVK	M1:+15.995,K20:+114.043	117 9.08 8	235 6.16	0.09 423

Q6114 7	INF	LFPTVFDENESLLDDNIRMFTTAPDQVDK	M20:+15.995,K30:+114.043	904. 190 2	361 2.73	0.07 782 3
Q6114 7	INF	EDEDFQESNKMHSNMNGFMYGNQPGNLMCLGESI	K10:+114.043,M27:+15.995,C28:+45.988	131 0.19 5	392 7.56 2	0.08 437 5
Q6116 6	CO N	TAVAPSLVAPALSKPK	K16:+114.043	555. 330 1	166 2.96 7	0.05 6
Q6116 6	CO N	YDPVAARQGQETAVAPSLVAPALSKPK	K27:+114.043	960. 186 1	287 7.53 5	0.08 036 3
Q6120 6	INF	CKPLHELMQLLEETPEEK	C1:+45.988,M9:+15.995,K19:+114.043	819. 401 2	245 5.18	0.07 192 7
Q6120 7	CO N	VVDSYLPVILDMIK	M12:+15.995,K14:+114.043	578. 983 6	173 3.92 8	0.06 536 7
Q6120 7	INF	LVLYLEHNLEKNSTK	K11:+114.043,K15:+114.043	677. 029 2	202 8.06 4	0.03 716 4
Q6120 7	INF	EVMDPGFVCSKIGVCPSAYK	C9:+45.988,K11:+114.043,C15:+45.988,K20:+114.043	613. 273 2	244 9.06 2	0.05 498 6
Q6120 7	INF	YVDQYSEVCVQMLMHMQDQQPK	C9:+45.988,K22:+114.043	954. 079 9	285 9.21 6	0.08 036 3
Q6120 7	INF	EMMDPYEQNLVQAHNVILCQTCQFVMNK	C19:+45.988,C22:+45.988,M26:+15.995,K28:+114.043	118 3.51 5	354 7.52	0.05 993 8
Q6120 7	INF	YQKQCDDFVAEYEPILLEILVEVMDPGFVCSK	K3:+114.043,C5:+45.988,M24:+15.995,C30:+45.988	131 4.94	394 1.79 5	0.04 828 8
Q6120 7	INF	EVVDSYLPVILDMIKGEMSNPGEVCSALNLCQSLQ	E1:- 18.011,M13:+15.995,K15:+114.043,M18:+15.995,C25:+45.988,C31:+45.988	133 8.95	401 3.82 7	0.05 463 2
Q6120 7	INF	EALEQPAPAIVSALLKEPTPPK	K22:+114.043	805. 116 6	241 2.32 6	0.06 337 3
Q6121 0-5	CO N	LDLTHLRQSSDPMLSEFK	K18:+114.043	111 6.06	223 0.10 5	0.06 123 4
Q6121 0-5	INF	VLSLKQILLSTEEDSGAGP	K5:+114.043	103 6.05	207 0.08 5	0.08 003 2
Q6123 3	INF	HVIPMNPNTDDLFAVGDGIVLCKMINLSVPDTID	C23:+45.988,K24:+114.043	131 4.30 4	393 9.88 8	0.00 698 4
Q6136 2	INF	MLSTWEWNDESNDYKLNK	K15:+114.043,K18:+114.043	125 1.05 6	250 0.09 7	0.02 959
Q6154 5	CO N	FNKPGGPMDEGPDLDLGLPIDDESDNSAIYVQGLN DNVTLDDLADFFK	K3:+114.043	138 1.39 1	552 1.53 1	0.05 668 8
Q6159 8	CO N	LSAIYGGTYMLNKPIEEIIVQNG	M10:+15.995,K13:+114.043	885. 123 5	265 2.34 7	0.00 698 4
Q6159 8	CO N	YMDFKVIEGSFVYK	K5:+114.043	920. 453 5	183 8.89 1	0.05 139 9
Q6159 8	INF	LSAIYGGTYMLNKPIEEIIVQNG	M10:+15.995,K13:+114.043	885. 123 5	265 2.34 7	0.00 112 9

Q6159 8	INF	YKVPSTEAEALASSLMGLFEK	K2:+114.043	795. 738 9	238 4.19 3	0.00 091 7
Q6159 9	CO N	DAQPQLEEADDDLD SKLNYK	K16:+114.043,K20:+114.043	126 8.07 8	253 4.14 1	0.05 111 3
Q6159 9	INF	LNYPKPPQK	K9:+114.043	599. 833 1	119 7.65 1	0.04 197 7
Q6164 6	CO N	KDWVQETMAK	K10:+114.043	675. 330 1	134 8.64 5	0.05 526 5
Q6164 6	INF	ATDLKDWVQETMAK	K14:+114.043	875. 428	174 8.84	0.00 091 7
Q6164 6	INF	TAKNLFNLHSETASAK	K16:+114.043	462. 242 3	184 4.93 8	0.05 463 2
Q6164 6	INF	HSETASAKDITPTLTLYVGK	K20:+114.043	112 3.58 7	224 5.15 9	0.07 564 5
Q6164 6	INF	VQRIIGGSMDAK	K12:+114.043	694. 869 9	138 7.72 4	0.07 630 8
Q6165 5	INF	SFEELRLKPQLQGVYAMGFNR	K8:+114.043,M18:+15.995	136 3.70 8	272 5.40 1	0.00 237 5
Q6165 6	CO N	STKTGTAYTFFTPNNIK	K17:+114.043	100 3.00 5	200 3.99 5	0.05 498 6
Q6175 3	CO N	GTELNGKTLGILGLGR	K7:+114.043	571. 660 5	171 1.95 8	0.05 836 2
Q6175 3	CO N	QLLSYQTSMTVSDGEPWHVMGLSSLLPSLETWK	Q1:-17.027,K32:+114.043	123 9.60 4	371 5.79	0.06 024 7
Q6175 3	CO N	AMGTLMHAWAGSPKGTIQVVTQGTSLK	K14:+114.043	144 2.74 5	288 3.47 4	0.05 562 4
Q6175 3	INF	VTADVINA AEKLQVVGR	K11:+114.043	949. 029 3	189 6.04 3	0.09 180 3
Q6175 3	INF	MQSFGMKTVGYDPIISPEVAASFGVQQLPLE	M1:+15.995,K7:+114.043	115 7.23 9	346 8.69 5	0.07 350 6
Q6176 8	INF	SAEVDSDDTGGSAAQKQK	K16:+114.043,K18:+114.043	101 1.45 5	202 0.89 4	0.03 329 7
Q6183 8	CO N	TVQGAFFGVVYK	K13:+114.043	763. 904 3	152 5.79 3	0.06 088 5
Q6183 8	INF	ALLAYAFALAGNKAK	K13:+114.043,K15:+114.043	583. 993 6	174 8.95 7	0.04 448 1
Q6183 8	INF	LTNQTLGFSAVEQDIPVKNLK	K19:+114.043,K22:+114.043	673. 359 7	268 9.40 8	0.05 294
Q6183 8	INF	NYQHSDGSYSTFGNHGGGNTPGNTWLTAFVLK	K32:+114.043	886. 159 9	354 0.60 8	0.03 482
Q6183 8	INF	EPALGIYKVVVQK	K8:+114.043,K13:+114.043	557. 986 4	167 0.93 6	0.06 300 9

Q6216 7	INF	DFLDEYIFLAVGRVGSTSENITQK	K24:+114.043	704. 858 5	281 5.40 3	0.03 552 7
Q6220 3	CO N	GRPGYKVTK	K6:+114.043	560. 317 7	111 8.62	0.06 024 7
Q6220 3	INF	LTLHNNEGSYLAHTQGKK	K17:+114.043	709. 031 6	212 4.07 1	0.08 926 9
Q6226 1	CO N	LWKFFWEMAE	K3:+114.043,M8:+15.995	758. 850 7	151 5.68 6	0.09 102 3
Q6226 1	CO N	QALQDTLALYK	K11:+114.043	689. 372 8	137 6.73	0.05 562 4
Q6226 1	CO N	EMPTTLEGAEAAIK	K14:+114.043	787. 890 7	157 3.76 6	0.03 974 7
Q6226 1	CO N	SRTQTAIASEDMPNTLTEAEK	K21:+114.043	803. 052 3	240 6.13 3	0.05 668 8
Q6226 1	INF	VLAHTEMPTTLEGAEAAIKK	M7:+15.995,K19:+114.043	112 0.58 4	223 9.15 2	0.07 286 9
Q6226 1	INF	MAGTMETSEMVNGAAEQRTSSK	M10:+15.995,K22:+114.043	122 3.53 6	244 5.05 7	0.04 644 6
Q6226 1	INF	LSDGNEYLFQAKDDEEMNTWQAISSAISK	K12:+114.043,M17:+15.995	934. 680 2	373 4.69	0.05 053 6
Q6226 1	INF	ETWLSENQRLVSQDNFGFDLPAVEAATK	[0:-18.011,K28:+114.043	108 7.86 6	326 0.57 3	0.05 836 2
Q6231 8	CO N	MAASAAATAAASAATAASAASGSPGSGEGSAGGEKR PAASSAAAAASAA	K35:+114.043	135 0.30 1	404 7.87 9	0.09 883 5
Q6231 8	CO N	MAASAAATAAASAATAASAASGSPGSGEGSAGGEKR PA	K35:+114.043	109 7.51 5	328 9.52 3	0.04 559 7
Q6231 8	CO N	MAASAAATAAASAATAASAASGSPGSGEGSAGGEKR P	K35:+114.043	107 3.83 6	321 8.48 6	0.03 428 2
Q6231 8	CO N	MAASAAATAAASAATAASAASGSPGSGEGSAGGEKR PAASSAAAAASA	K35:+114.043	995. 218 2	397 6.84 2	0.05 139 9
Q6231 8	CO N	MAASAAATAAASAATAASAASGSPGSGEGSAGGEKR PAASS	M1:+15.995,K35:+114.043	118 4.54 8	355 0.61 9	0.05 993 8
Q6231 8	CO N	AASAAATAAASAATAASAASGSPGSGEGSAGGEKRPA ASSAAAAASAASSP	K34:+114.043	142 0.67 2	425 8.99 2	0.02 898 8
Q6231 8	CO N	AGQAGTVPPGAPGAPPLPGMAIVK	K24:+114.043	756. 744 4	226 7.21	0.02 622 9
Q6231 8	INF	MAASAAATAAASAATAASAASGSPGSGEGSAGGEKR PA	K35:+114.043	109 7.51 5	328 9.52 3	0.04 197 7
Q6231 8	INF	MAASAAATAAASAATAASAASGSPGSGEGSAGGEKR P	K35:+114.043	107 3.83 6	321 8.48 6	0.08 352 7
Q6231 8	INF	MAASAAATAAASAATAASAASGSPGSGEGSAGGEKR PAASSAAAAASAAA	K35:+114.043	137 3.98	411 8.91 6	0.08 207 5

Q6231 8	INF	MAASAAATAAASAATAASAASGSPGSGEGSAGGEKR PAASS	M1:+15.995,K35:+114.043	118 4.54 8	355 0.61 9	0.05 171 8
Q6231 8	INF	ERGAAAAAGQAGTVPPGAPGAPPLPGMAIVK	K32:+114.043	989. 194 6	296 4.56	0.07 090 1
Q6231 8	INF	MAASAAATAAASAATAASAASGSPGSGEGSAGGEKR PAAS	K35:+114.043	115 0.20 5	344 7.59 2	0.07 741 6
Q6231 8	INF	CLGPATPAAANNSSGDGGSAGDGAMVDCPVCK	C1:+28.961,C27:+45.988,C30:+45.988,K31:+11 4.043	101 4.39 5	304 0.16 3	0.05 836 2
Q6231 8	INF	LSPPYSSPQEFQDVGGRMFK	K20:+114.043	600. 293 4	239 7.14 2	0.07 090 1
Q6231 8	INF	AAGQAGTVPPGAPGAPPLPGMAIVK	M21:+15.995,K25:+114.043	785. 755 1	235 4.24 2	0.04 401 7
Q6231 8	INF	PAAANNSSGDGGSAGDGAMVDCPVCK	C21:+45.988,C24:+45.988,K25:+114.043	823. 990 9	246 8.94 9	0.03 307 9
Q6231 8	INF	MAASAAATAAASAATAASAASGSPGSGEGSAGGEKR PAASSA	M1:+15.995,K35:+114.043	906. 421 9	362 1.65 6	0.08 582
Q6237 6	INF	GGGDMAEPSEAGDGAPDDGPPGELGPEGPDGPEEK	K35:+114.043	113 5.47 1	340 3.39 1	0.06 568
Q6237 6	INF	EAGDGAPDDGPPGELGPEGPDGPEEK	E1:-18.011,K26:+114.043	647. 028 6	258 4.08 3	0.07 090 1
Q6239 3	CO N	QNIAKGWQDVTATNAYK	K17:+114.043	506. 257	202 0.99 7	0.05 734
Q6239 3	INF	LSQAGQKASAAFSSVGSVITK	K7:+114.043	107 6.07 4	215 0.13 3	0.07 060 6
Q6239 3	INF	SKVGGAKPAGGDFGEVLNSTANATSTMTT	K2:+114.043,M27:+15.995	145 0.19 1	289 8.36 7	0.05 866 5
Q6241 8	CO N	VKDPNSGLPK	K10:+114.043	584. 820 2	116 7.62 5	0.08 621 5
Q6242 2	INF	AESIDNPLHEAAKR	K13:+114.043	832. 921 7	166 3.82 8	0.06 300 9
Q6246 5	INF	MDPLGGSDTAK	M1:+15.995,K11:+114.043	611. 275	122 0.53 4	0.07 060 6
Q6246 5	INF	IVMDPLGGSDTAKGYHLLKPMGK	M3:+15.995,K13:+114.043,K19:+114.043,M21 :+15.995,K23:+114.043	934. 802 6	280 1.38 4	0.07 319
Q6246 5	INF	ENVTVFGTASASK	K13:+114.043	475. 572 6	142 3.69 4	0.00 719
Q6252 3	CO N	PFVVPKSTKPAPGGTAPLPPWK	K5:+114.043,K9:+114.043	124 9.68 2	249 7.34 8	0.04 116 7
Q6252 3	INF	FAPVVAPKPK	K8:+114.043,K10:+114.043	641. 369 9	128 0.72 4	0.09 423
Q6381 0	INF	YDMDKDGYISNGELFQVLK	K5:+114.043	117 5.05 8	234 8.1	0.03 583 3

Q63810	INF	ISFEFCAVVGGLDIHKK	C7:+45.988,K17:+114.043,K18:+114.043	113 3.55 4	226 5.09 3	0.06 300 9
Q63829	INF	AAATCILEAGKHQVDK	C5:+45.988,K11:+114.043,K16:+114.043	964. 970 2	192 7.92 5	0.05 562 4
Q64012	INF	LDINMAGEPKPNRPKGLK	K15:+114.043,K18:+114.043	736. 064 1	220 5.16 9	0.06 231 8
Q64012	INF	KGDSSSGGGGGSSGGGSSNVG	K1:+114.043	913. 381 4	182 4.74 7	0.08 185 4
Q64324	CON	ELNKYSTHLHLA	K4:+114.043	770. 399 9	153 8.78 4	0.07 419 6
Q64511	CON	KDIVALMTR	K1:+114.043,M7:+15.995	588. 824 5	117 5.63 3	0.00 345 4
Q64511	CON	EVKVAQLAGSVAEMSAYHH	K3:+114.043,M14:+15.995	107 9.02 4	215 6.03 2	0.06 465 9
Q64511	CON	NMTCIKVSIDPESNIISIWN	C4:+45.988,K6:+114.043	121 9.08 2	243 6.14 9	0.04 530 6
Q64511	INF	KDIVALMTR	K1:+114.043,M7:+15.995	588. 824 5	117 5.63 3	0.01 389 1
Q64511	INF	DEEFSGTAEGTGEETLTPSAPVNGPKPK	K28:+114.043	106 2.18 1	318 3.52 1	0.03 736 3
Q64511	INF	GEETLTPSAPVNGPKPK	K13:+114.043,K18:+114.043	693. 368	207 7.08 1	0.08 185 4
Q64514	CON	VLDTGVDPGAPGMQVTTDGKPK	M13:+15.995,K20:+114.043	771. 718 5	231 2.13 2	0.06 123 4
Q64514	INF	GVLI AVLDTGVDPGAPGMQVTTDGKP	M18:+15.995,K25:+114.043	880. 118 5	263 7.33 2	0.00 651 3
Q64727	CON	TDELAPPKPPLPEGEVPPRPPPPPEEKDEEFPEQK	K8:+114.043	100 7.50 5	402 5.99	0.07 564 5
Q64727	CON	KAQM QEAMTQEVSDVFSDTTPIK	K1:+114.043,M4:+15.995	939. 109 6	281 4.30 5	0.06 632 8
Q64727	CON	EVENSEDPKF	K9:+114.043	654. 291 7	130 6.56 8	0.06 231 8
Q64727	CON	VPPRPPPPPEEKDEEFPEQK	K12:+114.043	819. 408 5	245 5.20 2	0.04 475 4
Q64727	INF	ETVQTTEDQILKR	K12:+114.043	837. 937	167 3.85 8	0.04 530 6
Q64727	INF	TDELAPPKPPLPEGEVPPRPPPPPEEKDEEFPEQK	K8:+114.043	100 7.50 5	402 5.99	0.01 342 8
Q64727	INF	NPGNQAAEYHFETMKNQWIDNVE	K15:+114.043	142 5.13 3	284 8.25 1	0.06 401 4
Q64727	INF	CKVAMANIQPQMLVAGATSIAR	C1:+45.988,K2:+114.043,M12:+15.995	122 5.11 3	244 8.21 1	0.04 724 1

Q6473 7	INF	MLNIHPSLLPSFK	K13:+114.043	805. 940 4	160 9.86 5	0.01 483 8
Q68F D5	CO N	KLHIEVGTPPTGNQPFQK	K1:+114.043,K19:+114.043	576. 064 8	230 0.22 8	0.06 772 5
Q68F D5	CO N	AHMGMFTELAILYSKFQPK	K15:+114.043,K17:+114.043	128 4.65 9	256 7.30 3	0.04 776 4
Q68F D5	CO N	YEEYDNAITMMNHPTDAWKEGQFK	M11:+15.995,K25:+114.043	105 4.47 1	316 0.39 1	0.05 053 6
Q68F D5	CO N	EATAGIIGVNRK	K12:+114.043	671. 876 1	134 1.73 7	0.08 994 9
Q68F D5	CO N	LDVDCSEDEVIKNLILVVR	C5:+45.988,K11:+114.043	735. 054 2	220 2.13 9	0.03 780 3
Q68F D5	CO N	DFAMPYFIQVMKEYLTK	K12:+114.043	111 9.55 3	223 7.09 6	0.05 374 6
Q68F D5	INF	WISLNTVALVTDNAVYHWSMEGESQPVK	K28:+114.043	822. 905 8	328 7.59 2	0.09 588 5
Q68F D5	INF	LDNSVFSEHRNLQNLILTAIK	K22:+114.043	132 6.72 8	265 1.44 5	0.08 207 5
Q69ZK 0	CO N	PPCVFAVGRGSEAVAAGLCAGQCILK	C3:+45.988,C19:+45.988,C23:+45.988,K26:+114.043	923. 766 9	276 8.27 7	0.03 993 5
Q69ZK 0	INF	QMEKLEALEQLQSHIEGWEGSNLTDICTELL	K4:+114.043,C27:+45.988	127 7.61 5	382 9.82 2	0.05 866 5
Q69ZK 0	INF	EEAVALGVGLCNGFMHHVLEKSEFK	E1:- 18.011,C11:+45.988,M16:+15.995,K22:+114.043,K26:+114.043	104 4.15 7	312 9.44 7	0.04 042 1
Q6A0 26	CO N	VLLLTGKPKPTGVLGTVNKPLSATGRKP	K19:+114.043	986. 261 1	295 5.76 6	0.07 741 6
Q6A0 26	CO N	ISVTPVKNIDTVK	K7:+114.043,K13:+114.043	821. 462 7	164 0.91 8	0.06 159 8
Q6A0 26	INF	FASHCLMNHPDLAK	C5:+45.988,M7:+15.995,K14:+114.043	880. 39	175 8.76 4	0.05 993 8
Q6A0 26	INF	SADGKIAYPPGVK	K5:+114.043	708. 878 3	141 5.74 1	0.07 630 8
Q6A0 26	INF	VLLLTGKPKPTGVLGTVNKPL	K7:+114.043	113 0.19 4	225 8.37 3	0.05 076 6
Q6A0 26	INF	LFSVINSHNTKVQMHMLDLMSSIIMEGDGVTQELLD SILINLIPAHK	K12:+114.043,M21:+15.995	137 3.20 5	548 8.78 7	0.08 003 2
Q6A0 68	CO N	AAVMKYGK	K5:+114.043	491. 263 5	980. 511 4	0.07 896 1
Q6A0 68	INF	AQDALVQEMEUVKQGMESHGELSSEA	M9:+15.995,K13:+114.043	701. 577 8	280 2.28 8	0.06 632 8
Q6A4J 8	CO N	TFRIEIEPLDQVDIDK	K16:+114.043	102 3.03 2	204 4.04 8	0.08 515 8

Q6DT Y7	INF	TFFVESICVDPEVVAANIVQVKGSP	C8:+45.988,K22:+114.043	146 1.24 4	292 0.47 2	0.07 782 3
Q6DT Y7	INF	PTLIVMVGLPARGK	K14:+114.043	783. 464	156 4.91 2	0.04 343 2
Q6NS R8	CO N	AEGRLVLADGVSYACK	C15:+45.988,K16:+114.043	906. 443 3	181 0.87 1	0.03 876 9
Q6NS R8	CO N	DMATLTGAQGIATGK	K15:+114.043	774. 888 5	154 7.76 1	0.06 536 7
Q6P2 B1	CO N	FAVRCSVGK	C5:+45.988,K8:+114.043	520. 263 1	103 8.51 1	0.00 559 2
Q6P2 B1	CO N	CEKPLASAAAKAIHNICSVC	C1:+28.961,K3:+114.043,C17:+45.988,C20:+45.988	121 0.54 6	241 9.07 7	0.08 956 6
Q6P2 B1	CO N	CLGSWFNLGVLSNFMANNKLLALLFEVLQQ	C1:+45.988,M16:+15.995,K20:+114.043	919. 211 5	367 2.81 5	0.06 810 4
Q6P2 B1	INF	RTEIIEDLAFYSSTVVSLLMTCVEK	C22:+45.988,K25:+114.043	100 3.16 6	300 6.47 6	0.02 784 1
Q6P4T 2	CO N	IRLIQACVDVLSSNGWLSPALAAMELAQMVTQAMWSK	C7:+45.988,M24:+15.995,M34:+15.995,K37:+114.043	140 8.69 8	422 3.07 1	0.05 463 2
Q6P4T 2	CO N	ALAAMELAQMVTQAMWSKDSYLK	M5:+15.995,M10:+15.995,K23:+114.043	136 6.65 9	273 1.30 2	0.06 088 5
Q6P4T 2	CO N	HLSHDHSELVEQTLSDLEQSK	K21:+114.043	841. 417 7	252 1.23	0.04 996 1
Q6P4T 2	INF	GYTLLSEGIDEMVGIIYKPK	M12:+15.995,K20:+114.043	117 8.60 9	235 5.20 3	0.04 530 6
Q6P4T 2	INF	RPVPLEQTYVGITEKK	K15:+114.043	986. 547 3	197 1.07 9	0.06 871 7
Q6P4T 2	INF	LNAEIVLGNVQNAKDAVNWLGYAYLYIR	K14:+114.043	109 8.91 4	329 3.72	0.06 772 5
Q6P4T 2	INF	VDSEVILHHEYFLLKAK	K15:+114.043	107 8.08 2	215 4.14 7	0.04 589 2
Q6P4T 2	INF	LDLVHTAALMLDK	K13:+114.043	777. 422	155 2.82 8	0.07 350 6
Q6P5E 4	CO N	KVDALLSAQPK	K1:+114.043	642. 370 1	128 2.72 5	0.04 750 8
Q6P5E 4	CO N	SHDGTDSPPDANDVVVILNFKSK	K22:+114.043,K24:+114.043	933. 118 3	279 6.33 2	0.09 764 2
Q6P5F 9	CO N	EPEVLSTMAIIVNKLGGHITAEIPQ	E1:-18.011,K14:+114.043	919. 493 6	275 5.45 7	0.05 264 8
Q6P5F 9	CO N	ISTPLNPGNPVNNQMFIQDYVANLLKSAFPHLQDA	K26:+114.043	996. 005 1	397 9.98 9	0.06 969 8
Q6P5F 9	INF	EFMKDTSINLYK	[0:-18.011,K13:+114.043	567. 271 8	169 8.79 2	0.07 218 1

Q6PA V2	INF	KPEQVVALDAQNIV	K1:+114.043	819. 447 1	163 6.87 9	0.07 457 6
Q6PD 03	INF	SPSPAPVACAAISASEK	C10:+45.988,K18:+114.043	921. 940 6	184 1.86 6	0.07 385 3
Q6PD 03	INF	NEYILSLIEENIDKILPIMFASLYK	K25:+114.043	102 8.55 1	308 2.63	0.06 810 4
Q6PD G5	CO N	DIGEGNLSTAAAAALAAAVK	K21:+114.043	667. 020 6	199 8.03 8	0.01 889 6
Q6PD G5	CO N	IPASEIEASVEDAPTPEKPR	K18:+114.043	750. 713 7	224 9.11 8	0.07 564 5
Q6PD G5	CO N	LPIKCFDFK	K4:+114.043,C5:+45.988,K10:+114.043	749. 384	149 6.75 2	0.07 741 6
Q6PD G5	INF	IGEGNLSTAAAAALAAAVKAK	K22:+114.043	104 2.07 9	208 2.14 3	0.07 218 1
Q6PDI 5	CO N	VVSTVSGIELK	K11:+114.043	623. 356 6	124 4.69 8	0.05 734
Q6PDI 5	CO N	MWTEVWQENVPGSFGIRLYLQELITITQK	K30:+114.043	121 7.62 8	364 9.86	0.05 053 6
Q6PDI 5	CO N	ELCSLASDLSQPDLVYKF	C3:+45.988,K17:+114.043	730. 015 5	218 7.02 3	0.09 676 7
Q6PDI 5	CO N	SQGSSNSGGGSGIPQPPPGMSFYAAK	K27:+114.043	133 4.10 9	266 6.20 3	0.09 423
Q6PDI 5	INF	QSAFVSVLSENDELSDQDVASKGLGLVYELGNEQDQQE LVSTLVETLMTGK	K21:+114.043	137 8.93 5	551 1.70 9	0.06 401 4
Q6PDI 5	INF	MEGKPPQPPQDSLMLHLLIPTLFHMKYPAESSK	M1:+15.995,M23:+15.995,K24:+114.043	124 3.28 1	372 6.82 1	0.06 600 8
Q6PD M2	INF	VVVSGLPPSGSWQDLKDH	K16:+114.043	101 8.01 6	203 4.01 7	0.04 173 1
Q6PD Q2	CO N	ATATAPEDDKAPAEPPEGEEK	K10:+114.043	113 4.02	226 6.02 4	0.08 741 6
Q6PD Q2	INF	AHRIGQNK	K8:+114.043	519. 284 1	103 6.55 3	0.07 705 1
Q6PD Q2	INF	AAAVAVVESMTATEVAPPPPPVEVPIRK	K29:+114.043	760. 669 7	303 8.64 8	0.06 123 4
Q6Q8 99	CO N	FQAFLDALYHAGYCGLCEAIESWDFQKIEK	C14:+45.988,C17:+45.988,K27:+114.043	123 4.55 8	370 0.65 1	0.03 993 5
Q6Q8 99	INF	IMNESILRLQTWDEMK	K16:+114.043	531. 017 7	212 0.04	0.09 764 2
Q6UR W6	INF	QRYEILTPNAIPK	[0:-17.027,K13:+114.043	820. 444 1	163 8.87 3	0.09 724 8
Q6UR W6	INF	INFDIAGYIVGANIETYLLEK	K21:+114.043	618. 327 6	246 9.27 9	0.01 258 3

Q6WV G3	INF	EQAFDKLSESGFHMVACSSTGTCAFASSTDQSEDK	K6:+114.043,M14:+15.995,C17:+45.988,C23:+45.988	130 8.53 3	392 2.57 4	0.07 419 6
Q6WV G3	INF	LSESGFHMVACSSTGTCAFASSTDQSEDKIWTS	C11:+45.988,C17:+45.988,K29:+114.043	122 6.17 2	367 5.49 4	0.07 492 7
Q6ZQ 38	CO N	KTVIGELPPASSGSALAANVCK	K1:+114.043,C21:+45.988,K22:+114.043	119 4.10 7	238 6.19 9	0.06 465 9
Q6ZQ 38	CO N	SESDMHVSQMAISFLTTLAK	K20:+114.043	115 5.55 9	230 9.10 3	0.04 116 7
Q6ZQ 38	CO N	PPLISESDMHVSQMAISFLTTLAK	M14:+15.995,K24:+114.043	137 3.69 4	274 5.37 2	0.05 322 5
Q6ZQ 38	CO N	KEVYPHVSTIINICK	K1:+114.043,C14:+45.988,K16:+114.043	106 6.05 6	213 0.09 7	0.07 319
Q6ZQ 38	INF	TRHEMLPEFYK	K11:+114.043	782. 883	156 3.75	0.03 071
Q6ZQ 38	INF	DTPLTMLQSQVPNIVKALHK	M6:+15.995,K16:+114.043	118 2.14 2	236 2.26 8	0.06 337 3
Q6ZQ 38	INF	LKAADIDQE	K2:+114.043	558. 780 8	111 5.54 6	0.05 197 5
Q6ZQ 38	INF	LKTVIGELPPASSGSALAANVCK	K2:+114.043,C22:+45.988,K23:+114.043	125 0.64 9	249 9.28 3	0.07 564 5
Q6ZQ 38	INF	VKANSVK	K2:+114.043	430. 254	858. 492 4	0.07 031 5
Q6ZQ A0	CO N	LESPADVK	K8:+114.043	486. 754	971. 492 4	0.05 698 3
Q6ZQ A0	CO N	LLQDFLCAEGHGNQELWSEK	C7:+45.988,K20:+114.043	826. 379 6	247 6.11 5	0.08 075 6
Q6ZQ A0	INF	MTPTEETSLPLAVTKEAK	K15:+114.043,K18:+114.043	544. 281 2	217 3.09 4	0.05 803 7
Q6ZQ K5	CO N	FCFEVVSPTKSCML	C2:+45.988,K10:+114.043,C12:+45.988,M13:+15.995	906. 879 4	181 1.74 3	0.07 125 9
Q6ZQ K5	INF	LVVDAAK	K7:+114.043	415. 243 1	828. 470 6	0.07 782 3
Q6ZW Q0	CO N	TEPPSASWSFLGK	K13:+114.043	760. 873 2	151 9.73 1	0.02 478 7
Q6ZW Q0	CO N	KEDLLVDLK	K9:+114.043	593. 838 1	118 5.66 1	0.07 350 6
Q6ZW Q9	INF	LASMGKNPTDEYLDAMMNEAPGPINFTMFLTMFGEK	K6:+114.043,M28:+15.995,K36:+114.043	141 9.31 1	425 4.90 8	0.08 109
Q6ZW R6	CO N	WISLMESVILK	M5:+15.995,K11:+114.043	724. 895 1	144 7.77 5	0.02 432 6
Q6ZW R6	CO N	LMEWAEQQPNIVEALK	K17:+114.043	107 1.53 1	214 1.04 6	0.08 515 8
Q6ZW R6	CO N	EIEDKPVATSNIQELQAQISLHEE	K5:+114.043	945. 805 6	283 4.39 3	0.08 582

Q6ZW R6	CO N	LEVSERTAAPSSSGVLYTVAK	K22:+114.043	121 3.63 2	242 5.24 9	0.03 583 3
Q6ZW R6	CO N	TWLAHMESELAKEPIVDSCN	K12:+114.043,C19:+45.988	823. 041 8	246 6.10 2	0.03 109 4
Q6ZW R6	CO N	MLFDEVQFK	M1:+15.995,K9:+114.043	643. 808 5	128 5.60 1	0.04 530 6
Q6ZW R6	CO N	QFDELLFSFSVWIK	K14:+114.043	936. 980 7	187 1.94 6	0.06 502 7
Q6ZW R6	CO N	ALENLKIQMK	K6:+114.043,M9:+15.995	659. 364	131 6.71 2	0.06 123 4
Q6ZW R6	CO N	ALQDLVDLLDTGQEKMTGDQK	M16:+15.995,K21:+114.043	122 4.6	244 7.18 5	0.04 144 1
Q6ZW R6	CO N	LQDLVDLLDTGQEKMTGDQK	K14:+114.043,M15:+15.995	118 9.08 2	237 6.14 8	0.05 463 2
Q6ZW R6	CO N	ICSSAAETKVLQEHMDLCQAVESLSSTVTMFSAS	C2:+45.988,K10:+114.043,C19:+45.988,M31:+ 15.995	133 0.25 4	398 7.73 9	0.07 419 6
Q6ZW R6	CO N	MLSQSEHAK	M1:+15.995,K9:+114.043	580. 772 5	115 9.52 9	0.04 589 2
Q6ZW R6	CO N	EVKLNLAIGK	K3:+114.043	599. 861 9	119 7.70 8	0.04 881
Q6ZW R6	INF	MLFDEVQFK	M1:+15.995,K9:+114.043	643. 808 5	128 5.60 1	0.00 613
Q6ZW R6	INF	LNTMLFKGELLSSLLTEEK	K7:+114.043,K19:+114.043	119 7.63 3	239 3.25 1	0.05 734
Q6ZW R6	INF	DIYVKAEGSVEEAENVMK	K18:+114.043	709. 009 3	212 4.00 5	0.08 036 3
Q6ZW R6	INF	WESLHQEFSKQK	K11:+114.043	577. 953 7	173 0.83 8	0.06 369 3
Q6ZW R6	INF	ELEINIAQNMVMQVK	E1:-18.011,M10:+15.995,K15:+114.043	624. 650 4	187 0.92 8	0.07 125 9
Q6ZW R6	INF	AKHATMLLTVTEVEGLAEG	K2:+114.043,M6:+15.995	105 0.53 6	209 9.05 7	0.04 343 2
Q6ZW R6	INF	VVDYETFAK	K9:+114.043	593. 293 5	118 4.57 1	0.03 455 1
Q6ZW R6	INF	LLDPEDVDVDKPEKSIMTYVAQFLTQYPDIHGAG	K11:+114.043	134 5.31 8	0.06 403 2.93	369 3
Q6ZW R6	INF	DMWESLLSAAIRCK	C13:+45.988,K14:+114.043	594. 95	178 1.82 7	0.06 841
Q6ZW R6	INF	MEMKLGESLEPSR	K4:+114.043	810. 890 2	161 9.76 5	0.07 896 1
Q6ZW R6	INF	KLALALQEEMYA	K1:+114.043	747. 387 6	0.03 149 2.76	609 6

Q76M Z3	CO N	MVADKFTELQK	M1:+15.995,K5:+114.043	720. 364 2	143 8.71 3	0.06 901 4
Q76M Z3	CO N	SALASVIMGLSPILGKDN	K16:+114.043	100 1.03 8	200 0.06 1	0.04 229 4
Q78PY 7	CO N	EVEVEVESMDKAGNFIGWLHMDGA	K11:+114.043	138 9.13 1	277 6.24 7	0.07 457 6
Q78PY 7	INF	VMQVLNADAIVVK	K13:+114.043	757. 424 5	151 2.83 3	0.08 185 4
Q792Z 1	CO N	LLFLALVGA AVFPVDDDKIVGGYTCR	K20:+114.043,C27:+45.988	103 3.52 8	309 7.56 2	0.04 256 6
Q792Z 1	INF	LLFLALVGA AVFPVDDDKIVGGYTCR	K20:+114.043,C27:+45.988	103 3.52 8	309 7.56 2	0.05 076 6
Q7TM B8	CO N	LTSVVELDGLLEINRMTHK	M16:+15.995,K19:+114.043	766. 742 8	229 7.20 5	0.06 465 9
Q7TM B8	CO N	SECKNQGATIHLP	C3:+45.988,K4:+114.043	779. 361 7	155 6.70 8	0.07 861 1
Q7TM B8	CO N	HILETKEASMMMEYVLYSLDLYNDSAHYALTK	M11:+15.995,K31:+114.043	126 0.27 1	377 7.79 1	0.07 630 8
Q7TM B8	INF	FAYYKVMAGSLLLDK	K15:+114.043	916. 985	183 1.95 4	0.03 482
Q7TM B8	INF	YLMDGVSNIYKLDK	K12:+114.043,K16:+114.043	102 3.00 5	204 3.99 4	0.06 159 8
Q7TN G5	INF	VLCVTFLEGGDVVTGDSGGNLYVWGK	C3:+45.988,K26:+114.043	949. 123 3	284 4.34 7	0.05 633 6
Q7TN G5	INF	ADGTDINAVARSHDGK	K16:+114.043	870. 917 2	173 9.81 9	0.06 901 4
Q7TN G5	INF	DYEILYWDPTCK	C12:+45.988,K13:+114.043	902. 900 4	180 3.78 5	0.03 716 4
Q7TN P2	INF	SALASVIMGLSTVLGKENT	K16:+114.043	100 3.03 6	200 4.05 6	0.05 076 6
Q7TP R4	INF	QYEKSIVNYKPK	K10:+114.043	537. 623 3	160 9.84 6	0.08 701
Q7TP V4	CO N	EFLDFFWDIAKPDQETR	[0:-18.011,K11:+114.043	112 7.03 5	225 2.05 3	0.05 633 6
Q7TP V4	CO N	AGNALGGVDNEEEELGDEAMMALDQNLASLFK	M21:+15.995,K33:+114.043	120 4.21 1	360 9.60 9	0.06 841
Q7TP V4	CO N	EEELGDEAMMALDQNLASLFKEQK	M9:+15.995,M10:+15.995,K21:+114.043	144 3.16 3	288 4.31 1	0.06 337 3
Q7TP V4	INF	AGNALGGVDNEEEELGDEAMMALDQNLASLFK	M21:+15.995,K33:+114.043	120 4.21 1	360 9.60 9	0.05 197 5
Q7TP V4	INF	QAWDQMMSTLKE	K11:+114.043	791. 356	158 0.69 6	0.06 937 5

Q80U G5	CO N	ESTASAAGPSRFLK	K15:+114.043	531. 606 3	159 1.79 6	0.04 644 6
Q80U G5	INF	MVVGQSGLGKSTLINTLFK	K19:+114.043	703. 058 1	210 6.15 1	0.06 088 5
Q80U G5	INF	KIPEGSAPATDAAPK	K1:+114.043	833. 444 5	166 4.87 3	0.06 465 9
Q80X9 0	CO N	SNMLLIGVHGPTTPCEEVSMKHVGK	C15:+45.988,K21:+114.043	942. 125 9	282 3.35 4	0.09 805 6
Q80X9 0	INF	ILAQDGEGQPIDIQMK	M15:+15.995,K16:+114.043	629. 316 2	188 4.92 5	0.08 036 3
Q810 B6	CO N	LHMAIAYNHPDVVSVILEQK	M3:+15.995,K20:+114.043	120 4.12 6	240 6.23 7	0.03 639
Q810 B6	CO N	ALVNAATAGAQETPLHLVALYSPK	K24:+114.043	850. 462 8	254 8.36 5	0.05 346 2
Q810 B6	CO N	ALQLAIKHQLPLVVDICTR	K7:+114.043,C18:+45.988	788. 108 7	236 1.30 3	0.09 724 8
Q810 B6	CO N	PVPKESPVLMSSADSIYLTPLHMAIAYNHPDVVSVILEQK	K4:+114.043	115 8.60 3	463 0.38 2	0.05 053 6
Q810 B6	INF	VMSEMAQIAEALLQAGANPNMQDSK	M2:+15.995,K25:+114.043	138 9.14 9	277 6.28 3	0.04 800 5
Q810 B6	INF	GADMSVPDEKGNPPLWLALASNLEDIASTL	K10:+114.043	108 0.20 3	323 7.58 6	0.04 996 1
Q8BF Q4	INF	NPKFMTFASACSNMAFWLPTIDD	K3:+114.043,M5:+15.995,C11:+45.988,M14:+15.995	140 0.1	279 8.18 5	0.06 231 8
Q8BF Q4	INF	GGYANSKAVTLEASFTPDSQFIMIGSEDGK	K30:+114.043	809. 387 5	323 3.51 9	0.03 755 2
Q8BFY 9	CO N	YLAYILDTLVFAFSKYQHK	K15:+114.043,K19:+114.043	127 4.66 6	254 7.31 6	0.06 536 7
Q8BFY 9	CO N	QSSFALLGDLTKACFQHVKPCIADFMPIGTNLNPEFI	Q1:- 17.027,K12:+114.043,C14:+45.988,C21:+45.988,M26:+15.995	146 2.03 8	438 3.09 1	0.04 776 4
Q8BFY 9	INF	KCSAAALDVLANVYR	K1:+114.043,C2:+45.988	877. 440 5	175 2.86 5	0.09 840 5
Q8BFZ 3	INF	VAPDEHPILLTEAPLNPKIN	K18:+114.043	114 8.12 1	229 4.22 7	0.00 091 7
Q8BFZ 3	INF	EKMTQIMFEAFNTPAMYVA	E1:- 18.011,K2:+114.043,M3:+15.995,M7:+15.995,M16:+15.995	118 3.52 9	236 5.04 3	0.08 553 1
Q8BFZ 3	INF	FANTVLSGGSTMYPGIADRMQK	M12:+15.995,K22:+114.043	619. 301 1	247 3.17 3	0.05 294
Q8BFZ 3	INF	DELTALVVDNGSGMCK	C15:+45.988,K16:+114.043	906. 403	181 0.79	0.04 644 6
Q8BG 05	INF	KPGAHLTVKK	K9:+114.043	596. 862 2	119 1.70 9	0.05 111 3

Q8BG 32	INF	SIDILHSIVK	K10:+114.043	619. 859 4	123 7.70 3	0.03 403 7
Q8BG Q7	CO N	QVSGLMGKGGGK	M6:+15.995,K9:+114.043	682. 336	136 2.65 6	0.05 734
Q8BG Q7	CO N	VQREIADLGEALATAVIPQWQK	K22:+114.043	638. 347 9	254 9.36	0.05 866 5
Q8BG Q7	INF	NPNQPLVILEMESGASAKALNEALK	M11:+15.995,K25:+114.043	923. 148 6	276 6.42 2	0.04 644 6
Q8BG Q7	INF	LEMESGASAKALNEALK	K10:+114.043	938. 478 2	187 4.94 1	0.05 895 8
Q8BH 59	CO N	INLLTAGALAGVPAASLVTPADVIK	K25:+114.043	830. 483 3	248 8.42 7	0.04 644 6
Q8BH 61	CO N	PASVQAVKHGHVCFQFDAPFVFAEVNSDLVYITAK	C13:+45.988,K35:+114.043	133 2.32 6	399 3.95 5	0.07 254 2
Q8BH 61	CO N	YTILAYLSGNITFYTGVSCK	K19:+114.043,K20:+114.043	823. 101	246 6.28	0.04 750 8
Q8BH 61	INF	GAAMVGSDMVVTVEFTNPLK	M9:+15.995,K20:+114.043	109 8.53 8	219 5.06	0.04 475 4
Q8BH 69	CO N	CANVLSLDYAMGVTECDNMLMLLGVSNNKMTDR	C1:+28.961,C16:+45.988,K28:+114.043	123 2.87 3	369 5.59 7	0.06 337 3
Q8BH D7	CO N	TLLPGQSPVLRRIIENLFYPTLEVLHQIFSK	K32:+114.043	126 4.72 1	379 1.13 9	0.04 343 2
Q8BH D7	INF	SNIPPSVTMDDLKNLFTEAGCSVK	M9:+15.995,C21:+45.988,K24:+114.043	137 1.64 4	274 1.27 1	0.04 401 7
Q8BH D7	INF	QNIFPPSATLHLSNIPPSVTMDDLK	K25:+114.043	142 5.22 9	284 8.44 3	0.05 410 2
Q8BH G1	CO N	LQNGLQALLISDLSNVEGK	K19:+114.043	709. 387 1	212 5.13 8	0.00 954
Q8BH G1	CO N	MVFMGSLKYPDENGDFDAFLK	M1:+15.995,K20:+114.043	813. 717 4	243 8.12 9	0.08 621 5
Q8BH G1	CO N	PNNGLPKPNFSLTDPFDTPAFNK	K24:+114.043	928. 124 8	278 1.35 1	0.09 380 1
Q8BH G1	INF	LQNGLQALLISDLSNVEGK	K19:+114.043	709. 387 1	212 5.13 8	0.02 457 3
Q8BH G1	INF	WSMIDKYQALMDGL	K6:+114.043	892. 921 5	178 3.82 7	0.07 782 3
Q8BJS 4	CO N	LTAESKASEDFFGSSSGYSEDDLAGYTDSDQHSSGSR	K6:+114.043	136 4.57 6	409 0.70 6	0.08 816 7
Q8BJS 4	INF	SQDDNDGGSSSGASSVAGSQGTVFKD	K26:+114.043	133 1.06 1	266 0.10 7	0.05 436 4
Q8BJS 4	INF	QDDNDGGSSSGASSVAGSQGTVFKDSPLR	Q1:-17.027,K25:+114.043	100 4.11 4	300 9.31 8	0.04 315 4

Q8BJS 4	INF	SSGASSVAGSQGTVFKDSPLR	K16:+114.043	107 6.53 6	215 1.05 6	0.05 053 6
Q8BJY 1	CO N	ISLTQAGLEALFESNLLDDLKNVMK	K21:+114.043,M24:+15.995,K25:+114.043	100 2.85 4	300 5.53 8	0.07 530 6
Q8BJY 1	CO N	IGVAVDTVGILGSSVEGK	K18:+114.043	907. 997 1	181 3.97 9	0.06 056 1
Q8BJY 1	INF	QDPTMIGVAVDTVGILGSSVEGK	Q1:-17.027,M5:+15.995,K23:+114.043	796. 065 5	238 5.17 3	0.03 780 3
Q8BK 67	INF	VPSPAQIMYNGQPITKMACGAEFSSMLMDCK	M8:+15.995,M17:+15.995,C19:+45.988,M25:+ 15.995,M27:+15.995,C29:+45.988,K30:+114.0 43	883. 629 3	353 0.48 6	0.07 319
Q8BK 67	INF	NGQPITKMACGAEFSSMLMDCK	K7:+114.043,M8:+15.995,C10:+45.988,M16:+ 15.995,C20:+45.988	629. 009 4	251 2.00 7	0.05 264 8
Q8BK C5	CO N	ACQMLVCYAK	C2:+45.988,C7:+45.988,K10:+114.043	445. 851 8	133 4.53 2	0.00 091 7
Q8BK C5	CO N	IMKFKPDCVNVEEVLPHWLSWLPLHE	M2:+15.995,K3:+114.043,C8:+45.988	111 2.55 3	333 4.63 5	0.03 349 6
Q8BK C5	CO N	EKFMQDASDVMQLLK	M4:+15.995,M11:+15.995,K16:+114.043	102 1.50 1	204 0.98 6	0.04 617 3
Q8BK C5	CO N	EFQQYLPVVMGPLMKTASIKPEVALLDTQDMENM	M10:+15.995,K20:+114.043,M31:+15.995	133 8.31 9	401 1.93 4	0.03 780 3
Q8BK C5	INF	ACQMLVCYAK	C2:+45.988,C7:+45.988,K10:+114.043	445. 851 8	133 4.53 2	0.00 123 3
Q8BK C5	INF	EFQQYLPVVMGPLMKTASIKPEVALLDTQDMENM	K20:+114.043,M31:+15.995	133 2.98 8	399 5.93 9	0.06 901 4
Q8BK C5	INF	FMQDASDVMQLLKTQTFNDME	M9:+15.995,K14:+114.043,M22:+15.995	717. 320 5	286 5.25 1	0.07 630 8
Q8BK C5	INF	LPVVMGPLMKTASIKPEVALLDTQDMENMSDDDGW EFVNLGDQQSFGIK	M5:+15.995,K15:+114.043	138 5.66 6	553 8.63 4	0.07 530 6
Q8BM L9	CO N	LVMEDGKMDPV	K7:+114.043,M8:+15.995	455. 213 2	136 2.61 6	0.06 123 4
Q8BM L9	INF	MDPVAYRVK	M1:+15.995,K9:+114.043	604. 808 8	120 7.60 2	0.06 432 4
Q8BM S1	CO N	GLYPAPLKIIDAVK	K14:+114.043	806. 477 6	161 0.94	0.04 644 6
Q8BM S1	CO N	QQLAILGAGLMGAGIAQVSVDK	Q1:-17.027,K22:+114.043	111 9.10 2	223 6.18 8	0.09 225
Q8BM S1	CO N	RLPAKPEVSSDEDVQYR	K5:+114.043	105 2.02 7	210 2.03 9	0.05 410 2
Q8BM S1	INF	VLKEVESVTPEHCIFASNTSALPINQIAAVSK	K3:+114.043,C13:+45.988,K32:+114.043	122 3.95 9	366 8.85 5	0.05 633 6
Q8BM S1	INF	IIDAVKAGLEQGS DAGYLAESQK	K6:+114.043,K23:+114.043	864. 437	259 0.28 8	0.04 042 1

Q8BM S1	INF	LEKSPKPVVAAISGSLGGGLELAIAC	K3:+114.043,C16:+45.988,C27:+45.988	930. 474 5	278 8.4	0.04 589 2
Q8BP 47	CO N	EGNDATGDGTKEKPFK	[0:-18.011,K13:+114.043	597. 283 6	178 8.82 7	0.05 374 6
Q8BP U7	CO N	ERIQSSSMDAK	M8:+15.995,K11:+114.043	691. 323	138 0.63	0.09 380 1
Q8BP U7	CO N	FVELMDHGIVSWDTFSVAFIKK	K21:+114.043,K22:+114.043	139 9.20 5	279 6.39 5	0.07 155 3
Q8BP U7	INF	PSSLDQFK	K8:+114.043	518. 259 5	103 4.50 3	0.07 060 6
Q8BR F7	INF	LKSIMGLEGEDEGAISMLSDNT	K2:+114.043	121 2.56 8	242 3.12	0.07 492 7
Q8BR F7	INF	HVKNSTGEPVWK	K3:+114.043	499. 260 5	149 4.75 8	0.04 828 8
Q8BT6 0	CO N	QQQTASQYFVLLIITDGVITDLDETRQAIVNAAK	K34:+114.043	970. 014 5	387 6.02 7	0.06 536 7
Q8BT6 0	INF	QAIVNAAKLPMSIIIVGVGGADFSAMEFLDGDG	Q1:-17.027,K8:+114.043	113 5.23 6	340 2.68 4	0.04 229 4
Q8BT6 0	INF	PMWKPFIKISLNSLCYGDMDK	M2:+15.995,K7:+114.043,C14:+45.988,M18:+ 15.995	855. 727	256 4.15 8	0.03 092 9
Q8BT M8	CO N	NLKILGLIWLILHYSIMPMWDEEEDEEAK	K3:+114.043,M20:+15.995	132 0.66 6	395 8.97 4	0.04 071 8
Q8BT M8	CO N	GVPASLPVEFTIDAKDAGEGLLAVQITDPEGKPK	K32:+114.043	894. 975 9	357 5.87 2	0.04 285 7
Q8BT M8	CO N	TDPEGKPKK	K8:+114.043	557. 299 1	111 2.58 3	0.03 947 5
Q8BT M8	CO N	TVITVDTKAAGK	K12:+114.043	659. 372 8	131 6.73	0.06 195 4
Q8BT M8	CO N	RNGHVGISFVPK	K12:+114.043	712. 892	142 3.76 8	0.05 767 9
Q8BT M8	CO N	TVSSLQESGLK	K11:+114.043	631. 833 5	126 1.65 1	0.05 346 2
Q8BT M8	CO N	EAVAPTKPSK	E1:-18.011,K7:+114.043	562. 309 3	112 2.60 3	0.05 053 6
Q8BT M8	CO N	RVHGPGIQSGTTNKPKN	K17:+114.043	953. 006 7	190 3.99 8	0.07 963 6
Q8BT M8	CO N	EDLEDGTCRVTYCPTGPNYIINIK	E1:- 18.011,C8:+45.988,C13:+45.988,K25:+114.043	101 1.11 6	303 0.32 3	0.05 498 6
Q8BT M8	INF	ATFTVNTKDAGEGGLSLAIEGPSK	K8:+114.043	826. 422 7	247 6.24 5	0.04 857 5
Q8BT M8	INF	AEVYIQDHGDGTHITYIPLCPGAYTVTIK	C21:+45.988,K30:+114.043	114 6.22 4	343 5.64 8	0.06 195 4

Q8BT M8	INF	EGGIVGKSADFVVEAIGDDVGTLGFSVEGPSQAK	K34:+114.043	115 0.57 4	344 8.7	0.04 343 2
Q8BTZ 7	CO N	EGQLYAMELQGFWM DIGQPKDFLTGMCLFL	M14:+15.995,K20:+114.043,C27:+45.988	915. 171	6.65 3	0.05 436 4
Q8BU 30	CO N	GSELEITLTKGSCVPGPA	K10:+114.043,C13:+45.988	959. 966 8	191 7.91 8	0.03 609 6
Q8BU 30	INF	IFATIKAPLPYPVPTSDNILIQEQTLK	K10:+114.043	112 7.63 3	337 9.87 6	0.05 633 6
Q8BU 30	INF	GVKVM PFSTACGTPLSNFES	K3:+114.043,C11:+45.988	111 6.51 1	223 1.00 6	0.07 218 1
Q8BV E3	CO N	MTHISKEQTVQYILTMVDDMLQENHQR	K6:+114.043,M20:+15.995	114 0.21 2	341 7.61 2	0.03 947 5
Q8BV E3	CO N	TKLLEVSDDPQVLAVAAHDVGEYVR	K2:+114.043	946. 826 5	283 7.45 6	0.06 056 1
Q8BV E3	INF	ILTKLLEVSDDPQVLAVAAHDVGE	K4:+114.043	132 3.70 3	264 5.39 1	0.04 959 9
Q8BV G4	CO N	ENSLLYSEIPKK	K11:+114.043	767. 909 8	153 3.80 4	0.04 071 8
Q8BV G4	INF	LSGPDDDDLHKQ	K11:+114.043	718. 344 8	143 4.67 4	0.04 800 5
Q8BW T1	INF	DGTVTAGNASGVSDGAGAVIIASEDAVK	K28:+114.043	662. 327 3	264 5.27 8	0.05 6
Q8BW T1	INF	GLSLKMDMLIDVNEAFAPQFLSVQK	K25:+114.043	964. 832 5	289 1.47 4	0.05 668 8
Q8BY7 1	INF	GTLHTYTVPSQTGGETFTFQIHK	K24:+114.043	926. 468 5	277 6.38 2	0.07 385 3
Q8BY7 1	INF	PPGFCTNTNDFLSLEK	C5:+45.988,K17:+114.043	685. 989 3	205 4.94 4	0.07 286 9
Q8BY A0	CO N	PKVATWR	K2:+114.043	486. 275 3	970. 534 9	0.06 195 4
Q8BY A0	CO N	SVFIAGFQEYTKPMIDHLVSMKINHWDGAIR	K12:+114.043,M14:+15.995,M21:+15.995	125 0.62 4	374 8.85	0.06 600 8
Q8BY A0	INF	MDGMLQALAQIFK	M1:+15.995,M4:+15.995,K13:+114.043	537. 934 4	161 0.78	0.04 315 4
Q8BZ0 5	CO N	KMKPPTSWGLTVYSE	K1:+114.043	919. 461 8	183 6.90 8	0.04 092 9
Q8C0 C7	INF	EMLLPMGLPENVSIAWGLSLERPTMIK	M2:+15.995,M6:+15.995,M26:+15.995,K28:+114.043	109 6.23 5	328 5.68 1	0.03 639
Q8C0 C7	INF	VFRPEMLLPMGLPENVSIAWGLSLERPTMIK	M30:+15.995,K32:+114.043	125 2.00 2	375 2.98 2	0.05 463 2
Q8C0 P5	CO N	VLFLGSLKK	K8:+114.043	559. 850 8	111 7.68 6	0.01 925 7

Q8C1 47	CO N	FEIEIEPLFASIALYDVKER	K18:+114.043	124 8.65 5	249 5.29 5	0.04 530 6
Q8C1 47	CO N	LLEQAAELFSTGGLYETVNEVYK	K23:+114.043	134 4.67 4	268 7.33 3	0.05 928
Q8C1 47	CO N	QVTMALASLVGK	K12:+114.043	666. 371 8	133 0.72 8	0.06 024 7
Q8C1 47	INF	VKIAALYLPLVGIILDALPQLY	K2:+114.043	837. 505 3	250 9.49 2	0.04 401 7
Q8C2 K1	CO N	LQEALQLEVkar	K10:+114.043	756. 431 2	151 0.84 7	0.07 896 1
Q8C3J 5	CO N	KPVPDQIINFYK	K1:+114.043	525. 956 4	157 4.84 6	0.00 142 7
Q8C3J 5	INF	GKMWEEAISLCK	C11:+45.988,K12:+114.043	777. 86	155 3.70 4	0.04 750 8
Q8CA Q8	CO N	MIVDLDNVVK	K10:+114.043	630. 337 4	125 8.65 9	0.02 660 9
Q8CD N6	CO N	KQHLENDPGSNEDADIPK	K1:+114.043	106 0.99 6	211 9.97 7	0.05 836 2
Q8CD N6	CO N	DIPKGYMDLMPFINK	M7:+15.995,K15:+114.043	637. 983 5	191 0.92 7	0.05 139 9
Q8CG 29	CO N	EAINRAMQKPQEEYSIGVLDIYGFEIFQK	E1:-18.011,K9:+114.043	878. 943 9	351 1.74 4	0.05 139 9
Q8CG 47	CO N	QRLNEFMAGFYVITNK	M7:+15.995,K16:+114.043	103 1.01 5	206 0.01 5	0.08 075 6
Q8CG C7	CO N	EDIDAAVKQLLTLK	K14:+114.043	835. 970 4	166 9.92 5	0.01 178 6
Q8CG C7	CO N	SKSQSGSLSSGGAGEGQGPk	K20:+114.043	945. 451 6	188 8.88 8	0.08 312 1
Q8CG C7	INF	EDIDAAVKQLLTLK	K14:+114.043	835. 970 4	166 9.92 5	0.01 103 7
Q8CG C7	INF	CLTVNAGNPPLEALLAVEHVKGdVSISVEEGK	C1:+28.961,K21:+114.043,K32:+114.043	887. 196 3	354 4.75 4	0.03 947 5
Q8CG C7	INF	DSSKSQSGSLSSGGAGEGQGPk	K22:+114.043	104 6.48 1	209 0.94 7	0.09 259 4
Q8CG C7	INF	AQYKSLTGIEYKPVsATGAEDK	K22:+114.043	123 5.62 7	246 9.23 9	0.06 871 7
Q8CG C7	INF	AKIDMSSNNGCMR	K2:+114.043,C11:+45.988,M12:+15.995	801. 828 9	160 1.64 2	0.06 502 7
Q8CG K3	CO N	DENLDLARAQAVLEEDHYGMEDVK	M20:+15.995,K24:+114.043	144 5.66 2	288 9.30 9	0.06 369 3
Q8CG K3	INF	LYKALSLK	K9:+114.043	581. 863 9	116 1.71 2	0.05 633 6

Q8CG K3	INF	QDPENDFLVTSHIHLHVPEGATPK	K24:+114.043	932. 463 6	279 4.36 8	0.04 256 6
Q8CG K3	INF	KEVLMVEVENVAHEDFQVTEEVK	K1:+114.043,M5:+15.995	141 6.19 3	283 0.37	0.06 056 1
Q8CG Y8	CO N	IIFSPVAPK	K9:+114.043	543. 321 9	108 4.62 8	0.07 125 9
Q8CH P8	INF	LDTDILLGSTCSLKTILTLTGVSSELDVK	C11:+45.988,K14:+114.043,K29:+114.043	110 3.91 1	330 8.71	0.05 803 7
Q8CI9 4	CO N	TVMIGGKAAPGYHMA	M3:+15.995,K7:+114.043,M14:+15.995	550. 597 9	164 8.77	0.06 502 7
Q8CI9 4	CO N	VIPAADLSQQJSTAGTEASGTGNMKFMLNGALTIGTM DG	K25:+114.043,M27:+15.995	133 3.64 4	399 7.90 7	0.04 667 3
Q8CI9 4	INF	AAPGYHMAKMIK	K9:+114.043,M10:+15.995	780. 905 5	155 9.79 5	0.09 764 2
Q8CIE 6	CO N	FLYLITGNLEK	K11:+114.043	712. 893 4	142 3.77 1	0.06 632 8
Q8CIE 6	INF	CYQLTTVGKFEEAVEK	C1:+45.988,K9:+114.043,K16:+114.043	707	211 7.97 7	0.05 111 3
Q8CIE 6	INF	LSPGAVESDVRGITGVDLFGTTDAVVK	K27:+114.043	939. 826 4	281 6.45 6	0.05 264 8
Q8CIH 5	CO N	VLGDMLLTKPTEASADQLPSPSQLR	M5:+15.995,K9:+114.043	933. 152 1	279 6.43 3	0.01 270 6
Q8CIH 5	CO N	TADKIEGFIDI	K4:+114.043	668. 343 7	133 4.67 2	0.04 724 1
Q8CIH 5	INF	EYDSNKF	K6:+114.043,K8:+114.043	629. 789 2	125 7.56 3	0.05 322 5
Q8CIH 5	INF	KTTVVNDNGLSPVWAPTQEK	K20:+114.043	766. 729 5	229 7.16 5	0.02 898 8
Q8CIN 4	CO N	MSSTIFSTGGKDPLSANHSLK	K11:+114.043	764. 715	229 1.12 2	0.07 630 8
Q8CIN 4	INF	NKIISIFSGTE	K2:+114.043	661. 851 7	132 1.68 8	0.06 600 8
Q8CIN 4	INF	EPPLYNENPLRALYLIATNGTPELQNPEK	K29:+114.043	113 6.92	340 7.73 6	0.05 562 4
Q8CIZ 8	CO N	VEDLSTMATLGNSFFHKLCSGFSGVCVDEDGNEK	M7:+15.995,K17:+114.043,C19:+45.988,C26:+ 45.988	128 6.88 6	385 7.63 6	0.04 343 2
Q8CIZ 8	INF	CHPLVDPESFVALCEKILCTCAT	C1:+28.961,C14:+45.988,K16:+114.043,C19:+4 5.988,C21:+45.988	138 7.07 3	277 2.13	0.03 071
Q8CJG 0	CO N	KPPPRPDFGTTGR	K1:+114.043	770. 405 5	153 8.79 5	0.06 871 7
Q8CJG 0	CO N	KNLYTAMPL	K1:+114.043	582. 808 3	116 3.60 1	0.05 767 9

Q8CJG 0	CO N	SLWKMMMLNIDVSATAFYK	K4:+114.043	111 6.56 4	223 1.11 2	0.07 861 1
Q8CJG 0	INF	MPIQGQPCFCK	M1:+15.995,C8:+45.988,C10:+45.988,K11:+114.043	737. 295 3	147 2.57 5	0.03 780 3
Q8JZQ 9	CO N	KMAQELYMK	K1:+114.043,K9:+114.043	685. 334 4	136 8.65 3	0.09 462 2
Q8JZQ 9	INF	YETPSMGLLDKK	K12:+114.043	748. 377 2	149 4.73 9	0.05 374 6
Q8JZV 7	INF	HTLGQQEVEVDGLIAYIAGTKTLGGSIA PMDVC	K21:+114.043,C33:+45.988	887. 438	354 5.72 1	0.08 036 3
Q8K0E 8	INF	IAELNNNIQSVSDTSSVTFQYLTLKDMWK	K26:+114.043,K30:+114.043	122 9.61 8	368 5.83	0.07 419 6
Q8K1 B8	CO N	QWLLQTHWTLDK	K12:+114.043	841. 936 7	168 1.85 8	0.04 285 7
Q8K1 B8	INF	YEQARWDLLTEEIDCTEEEMMVFAALQYHINK	C15:+45.988,M20:+15.995,K32:+114.043	136 5.61 5	409 3.82 1	0.08 278 5
Q8K1 B8	INF	LTLGSDVGELASGDLGLDDLDAA LNNLEVKL	K30:+114.043	108 5.56	325 3.65 7	0.08 994 9
Q8K1 X4	CO N	LEICAEQRNLNEQLLPK	C4:+45.988,K17:+114.043	543. 529 8	217 0.08 8	0.03 071
Q8K1 X4	CO N	ENMDILVQIRSNFSKPELMASLLPQLTGAENVLK	K15:+114.043,M19:+15.995,K34:+114.043	134 8.37	404 2.08 7	0.06 465 9
Q8K1 X4	INF	ENMDILVQIRSNFSKPELMASLLPQLTGAENVLK	M3:+15.995,K34:+114.043	131 0.35 6	392 8.04 4	0.03 282 5
Q8K2T 1	INF	SFLLDLPMGDVPMDGMSVSDLGPVVL SLLK	K30:+114.043	108 7.22 7	325 8.65 9	0.04 828 8
Q8K2Z 4	INF	EEEPFHTIMK	K10:+114.043	687. 822 1	137 3.62 9	0.06 502 7
Q8K2Z 4	INF	IIQMLQHFEHLPVVLVTAVSLWATDYGMK	K29:+114.043	115 1.26 9	345 0.78 3	0.03 809
Q8K41 1	CO N	PSGPSGA AHVSGSQIVRK	K18:+114.043	924. 987 9	184 7.96	0.05 993 8
Q8K41 1	CO N	ALKVSDIEPSMPFTK	K3:+114.043,K15:+114.043	945. 985 7	188 9.95 6	0.07 598 5
Q8K41 1	INF	PNSIETLQSFGKAVDWAK	K18:+114.043	702. 360 8	210 4.05 9	0.04 401 7
Q8K41 1	INF	GGDPLCIPELTWEQLK	C6:+45.988,K16:+114.043	979. 971 9	195 7.92 8	0.04 423
Q8K41 1	INF	EAYFSVGLQGIAEKD	E1:-18.011,K14:+114.043	861. 920 6	172 1.82 6	0.04 959 9
Q8K41 1	INF	STHGLAILGPENSK	K14:+114.043	769. 402 6	153 6.79	0.05 463 2

Q8K48 2	INF	NELYQAYVDSKIDALR	K11:+114.043	100 6.50 8	201 1.00 1	0.01 850 5
Q8K48 2	INF	GVDGQMGQGPIHSSEGYAGAPGYKSPVTTTPG	M6:+15.995,K25:+114.043	110 9.51 8	332 5.53 1	0.03 666 5
Q8K4I 3	INF	KSLVDTVYALK	K1:+114.043	450. 926 3	134 9.75 6	0.00 414 1
Q8K4Z 5	CO N	PPAAPPIMAPRPPPMIVPTAFVPAPPVAPVPAPAPMP PVHPPPPMEDEPPSKK	M15:+15.995,K52:+114.043,K53:+114.043	141 6.74 2	566 2.93 7	0.05 562 4
Q8QZ W8	CO N	EGKLDLDSAEWDDIHVVTGALK	K22:+114.043	126 3.13	252 4.24 5	0.06 901 4
Q8QZ W8	INF	SAEWDDIHVVTGALK	K15:+114.043	877. 939 6	175 3.86 4	0.05 197 5
Q8QZ Y1	CO N	NLVWTSGISALDGEFQSASEVDFYIDKDMIHI	K27:+114.043	123 8.92 6	371 3.75 6	0.08 003 2
Q8QZ Y1	CO N	QQTYQVPIPEVIK	K12:+114.043	780. 425 6	155 8.83 6	0.09 102 3
Q8QZ Y9	CO N	GFVEFLSEEDADYAIKIMNMIK	K16:+114.043,K22:+114.043	139 6.17	279 0.32 5	0.04 448 1
Q8R0 10	INF	QSRHEYQLGFTLIWK	K15:+114.043	101 0.52 4	201 9.03 3	0.03 132 7
Q8R0 16	CO N	VQYLLMNPTNDGGQWDMMLVNIVEK	M6:+15.995,K24:+114.043	969. 805 9	290 6.39 4	0.06 738 7
Q8R0 16	INF	NYHKIGPITPLQFYK	K15:+114.043	967. 020 7	193 2.02 6	0.06 369 3
Q8R0 81	CO N	LKTENAGDQHGGGGGGSGAAGGGGGGENY	K2:+114.043	130 2.05 9	260 2.10 3	0.03 252 1
Q8R0 81	CO N	KTENAGDQHGGGGGGSGAAGGGGGGENYDDPHK	K1:+114.043	102 8.10 1	308 1.27 9	0.05 436 4
Q8R0 81	INF	LKTENAGDQHGGGGGGSGAAGGGGGGENY	K2:+114.043	130 2.05 9	260 2.10 3	0.05 993 8
Q8R0 81	INF	KTENAGDQHGGGGGGSGAAGGGGGGENYDDPHK	K1:+114.043	102 8.10 1	308 1.27 9	0.07 741 6
Q8R0 81	INF	TENAGDQHGGGGGGSGAAGGGGGGENYDDPHKT	K32:+114.043	101 9.08 5	305 4.23 2	0.06 841
Q8R0 81	INF	LKTENAGDQHGGGGGGSGAAGGGGGGENYDDPHK	K2:+114.043	106 5.79 6	319 4.36 3	0.06 337 3
Q8R0 81	INF	AKASLNGADIYSGCCTLK	C14:+45.988,C15:+45.988,K18:+114.043	674. 304 2	201 9.88 9	0.06 231 8
Q8R1 46	CO N	QFLEVWEKNR	K8:+114.043	488. 253 3	146 1.73 7	0.05 668 8
Q8R1 46	INF	PSNSPDKSQVPMVMPHGGPHSSFTAWMLFPAML CK	K7:+114.043,M15:+15.995,M29:+15.995,M34: +15.995,C36:+45.988	140 6.98 6	421 7.93 3	0.06 024 7

Q8R1 46	INF	FPAMLCKMGFAVLLVNYR	M4:+15.995,C6:+45.988,K7:+114.043,M8:+15.995	113 3.05 7	226 4.09 8	0.06 969 8
Q8R1 46	INF	GDQFVFYEDWGETMVSKSIPVLCVLDIESGNISVL	M14:+15.995,K17:+114.043,C23:+45.988	135 5.97 8	406 4.91	0.04 448 1
Q8R1 46	INF	NSPDKSQVPMVVMPHGGPHSSFVTAWMLFPAMLCK	K5:+114.043,M27:+15.995,C34:+45.988,K35:+114.043	137 2.97 5	411 5.90 2	0.05 734
Q8R1 46	INF	QTGSVTSLTAGGSAGSWK	Q1:-17.027,K18:+114.043	896. 429 4	179 0.84 3	0.05 294
Q8R1 80	CO N	DCAVKPCHSDEVP	C2:+45.988,K5:+114.043,C7:+45.988	803. 312 7	160 4.61	0.04 828 8
Q8R1 80	INF	ENTFYNWLEGLCVEK	[0:-18.011,C12:+45.988,K15:+114.043	993. 940 3	198 5.86 5	0.09 102 3
Q8R1 B4	CO N	ESHITNYKQNPEQSADEDAEK	K21:+114.043	637. 536 7	254 6.11 6	0.06 231 8
Q8R1 B4	INF	DFESHITNYKQNPEQSADEDAE	K10:+114.043	134 1.06 6	268 0.11 6	0.03 583 3
Q8R1 B4	INF	AKGTEITHAVVIK	K2:+114.043,K13:+114.043	797. 949 8	159 3.88 4	0.09 883 5
Q8R1 Q8	CO N	KTGSPGGPGVGGSPGGGAAGASPSLPPSAK	K1:+114.043,K30:+114.043	134 4.67 1	268 7.32 6	0.03 010 1
Q8R1 Q8	CO N	TGSPGGPGVGGSPGGGAAGASPSLPPSAKK	K29:+114.043,K30:+114.043	134 4.67 1	268 7.32 6	0.05 374 6
Q8R1 Q8	INF	KTGSPGGPGVGGSPGGGAAGASPSLPPSAK	K1:+114.043,K30:+114.043	134 4.67 1	268 7.32 6	0.01 191 3
Q8R1 Q8	INF	TGSPGGPGVGGSPGGGAAGASPSLPPSAKK	K29:+114.043,K30:+114.043	134 4.67 1	268 7.32 6	0.04 959 9
Q8R1 Q8	INF	GSPGGPGVGGSPGGGAAGASPSLPPSAKK	K28:+114.043,K29:+114.043	129 4.14 7	258 6.27 9	0.04 372 4
Q8R1 Q8	INF	KTGSPGGPGVGGSPGGGAAGASPSL	K1:+114.043	104 7.51 5	209 3.01 4	0.05 767 9
Q8R1 Q8	INF	KTGSPGGPGVGGSPGGGAAGASPSLP	K1:+114.043	731. 03	219 0.06 7	0.05 294
Q8R2 H9	CO N	AVYETIPLSPMGMDLLQFIKQG	K21:+114.043	128 1.66 8	256 1.32	0.04 828 8
Q8R2S 8	CO N	FSRLPGMLVASYTK	K14:+114.043	842. 448 5	168 2.88 1	0.04 694 9
Q8R4 K2	INF	GAMVEISTEELK	M3:+15.995,K12:+114.043	718. 851 1	143 5.68 7	0.09 588 5
Q8R5 A3	CO N	LSQEITKSSLPPK	K7:+114.043	819. 957 3	163 7.89 9	0.09 634 5
Q8R5 A3	CO N	LASRWTNLGTVGTPMPAQPTVSGLK	K27:+114.043	957. 499 7	286 9.47 6	0.02 399 7

Q8R5 A3	INF	LASRWTNLGTVGTPMPAQPSTVSSGLK	K27:+114.043	957. 499 7	286 9.47 6	0.01 564 8
Q8R5 C5	INF	IKISAPQER	K2:+114.043	578. 328 2	115 4.64 1	0.09 634 5
Q8R5 H1	CO N	QNVYPGPIDNSGLLKDGDAQSLK	Q1:-17.027,K15:+114.043,K23:+114.043	880. 768 6	263 9.28 2	0.09 547 1
Q8R5 H1	INF	VVEQGMFVKHCK	M6:+15.995,C11:+45.988,K12:+114.043	790. 873 5	157 9.73 1	0.05 294
Q8R5 H1	INF	NEDGTWPRGPSTPK	K14:+114.043	828. 392 8	165 4.77	0.08 701
Q8R5 H1	INF	YPGPIDNSGLLKDGDAQSLK	K20:+114.043	734. 706 6	220 1.09 6	0.07 630 8
Q8VB V7	CO N	AAFVGLPVEEAVK	K13:+114.043	722. 396 3	144 2.77 7	0.04 144 1
Q8VCI 0	CO N	RVANMMAEGGK	M5:+15.995,K11:+114.043	647. 306 1	129 2.59 7	0.07 031 5
Q8VC M7	CO N	ELIKAIQVYYNPDQPPKPGM	K4:+114.043,K17:+114.043	843. 765 6	252 8.27 3	0.07 031 5
Q8VC M7	INF	FFTSHNGMQFSTWDNDNDKF	M8:+15.995,K19:+114.043	128 4.53	256 7.04 5	0.04 857 5
Q8VC M7	INF	AIQVYYNPDQPPKPGMIDSATQ	K13:+114.043,M16:+15.995	128 2.11 1	256 2.20 6	0.05 6
Q8VC T3	CO N	GVDSIPGFEFDRWLNTPGWPPYLPDLSPGDSLMLK	K34:+114.043	130 6.63 4	391 6.87 7	0.09 634 5
Q8VC T3	CO N	GYCFVSYLAHLVGDQDQFDKFLK	C3:+45.988,K23:+114.043	951. 784 7	285 2.33 1	0.09 380 1
Q8VC T3	INF	GVDSIPGFEFDRWLNTPGWPPYLPDLSPGDSLMLK	K34:+114.043	130 6.63 4	391 6.87 7	0.04 589 2
Q8VD D5	CO N	KDLEGLSQR	K1:+114.043	580. 307 5	115 8.59 9	0.06 231 8
Q8VD D5	CO N	LHAQVTDMKK	M8:+15.995,K9:+114.043,K10:+114.043	707. 859 6	141 3.70 4	0.03 252 1
Q8VD D5	CO N	KHEAMITDLEER	K1:+114.043	793. 386 1	158 4.75 7	0.00 091 7
Q8VD D5	CO N	NMDPLNDNIATLLHQSSDKFVSELWK	M2:+15.995,K26:+114.043	104 9.18 1	314 4.51 9	0.04 910 9
Q8VD D5	CO N	CQYLQAEKK	C1:+45.988,K8:+114.043,K9:+114.043	692. 821 8	138 3.62 8	0.06 738 7
Q8VD D5	CO N	EMDLKDLEAHIDTANK	K16:+114.043	978. 970 8	195 5.92 6	0.06 701 2
Q8VD D5	CO N	VDYKADEWLMLK	K11:+114.043	756. 364 1	151 0.71 3	0.06 123 4

Q8VD D5	INF	KHEAMITDLEER	K1:+114.043	793. 386 1	158 4.75 7	0.00 091 7
Q8VD D5	INF	VIQYLAHVASSHKSK	K15:+114.043	594. 660 6	178 0.95 8	0.02 759 2
Q8VD D5	INF	EEDQIIMEDQNCKLAK	C12:+45.988,K16:+114.043	103 3.96 4	206 5.91 2	0.07 031 5
Q8VD D5	INF	DRIIGLDQVAGMSETALPGAFK	K22:+114.043	120 2.12 1	240 2.22 6	0.05 053 6
Q8VD L4	CO N	VVISGVKLLQALGLSPGSGK	K20:+114.043	101 9.10 8	203 6.19 9	0.06 502 7
Q8VD L4	INF	HSSLSSWDGVPDVGMSDILFWILKEHGR	M15:+15.995,K25:+114.043	113 3.22 7	339 6.65 6	0.05 698 3
Q8VD L4	INF	FAANTDLKVLLCGPIGP	K8:+114.043,C12:+45.988	944. 987 3	188 7.95 9	0.07 672 7
Q8VD M4	CO N	LMLNDMELVEDIFTCKDVVVQK	M6:+15.995,C16:+45.988,K17:+114.043,K23:+114.043	987. 136 2	295 8.38 5	0.04 173 1
Q8VD M4	CO N	TPVQSQQPSATTPSGADEKSSGK	K19:+114.043,K23:+114.043	125 8.59 7	251 5.17 9	0.09 501 2
Q8VD M4	INF	KDHGMLSAASLGMILLWDVDGGLTQIDK	K1:+114.043	793. 156 5	316 8.59 5	0.08 582
Q8VD M4	INF	MNLASSFVNGFVNAAFQDKLLTDDGNK	K20:+114.043,K28:+114.043	801. 137 8	320 0.52	0.03 809
Q8VD M6	CO N	GTAQPPPPGLQPHPEPGGYSGPDGHYVMDNITRQN QFYETPVIK	K44:+114.043	122 6.09	490 0.33	0.07 385 3
Q8VD M6	INF	YNILGTNAIMDKMR	K12:+114.043,M13:+15.995	885. 437 9	176 8.86	0.01 044 7
Q8VD P3	CO N	KNSLVTEEAELMITVQELDLEEK	M12:+15.995,K23:+114.043	139 6.2	279 0.38 5	0.08 185 4
Q8VD P4	CO N	AAYNPGQAVPWNAVQVQTL	K15:+114.043	107 1.06 1	214 0.10 7	0.04 857 5
Q8VD P4	INF	QPLLKSPAPLLHVAALGQK	K5:+114.043	731. 435 9	219 1.28 4	0.03 974 7
Q8VD W0	CO N	SGMGKTAVFVLATLQ	K5:+114.043	818. 940 5	163 5.86 5	0.03 552 7
Q8VD W0	CO N	FGTKGLAVTFVSDENDAK	K18:+114.043	504. 004 1	201 1.98 5	0.04 828 8
Q8VD W0	INF	PSEVQHECIPQAILGMDVLCQAK	C8:+45.988,M16:+15.995,C20:+45.988,K23:+114.043	911. 085	273 0.23 1	0.03 809
Q8VE K3	CO N	SSLTMESFAFLWAGGRASYGVSK	K23:+114.043	856. 085 2	256 5.23 2	0.07 286 9
Q8VE K3	INF	LNTLLQRAPQCLGK	C11:+45.988,K14:+114.043	572. 308 5	171 3.90 2	0.05 231 3

Q8VIJ 6	CO N	KMPGGPKPGGGPGMGAPGGHPPHR	K1:+114.043,K22:+114.043	134 2.67 5	268 3.33 4	0.03 924 8
Q8VIJ 6	CO N	GGKMPGGPKPGGGPGMGAPGGHPPH	K3:+114.043	126 4.62 4	252 7.23 3	0.07 741 6
Q8VIJ 6	CO N	GGKMPGGPKPGGGPGMGAPGGHPPHR	K24:+114.043	134 2.67 5	268 3.33 4	0.04 042 1
Q8VIJ 6	CO N	GSGGQKFPLGGGGIGYEANPGVPPATMSGMMG SDMR	K6:+114.043,M29:+15.995,M33:+15.995,M34: +15.995	968. 684 6	387 0.70 7	0.07 031 5
Q8VIJ 6	CO N	GKMPGGPKPGGGPGMGAPGGHPPHR	K23:+114.043	876. 445 2	262 6.31 2	0.08 926 9
Q8VIJ 6	CO N	PSTAPGPPPPSTPSSGVSTTPQTGGPPPPAGGAGP GPKPGPGPGGPKGGK	K49:+114.043,K52:+114.043	118 8.60 1	475 0.37 4	0.04 694 9
Q8VIJ 6	CO N	MGGGGTMNMGDPYSGGQKFPLGGGGIGYEAN	M1:+15.995,M7:+15.995,K19:+114.043	111 2.14 5	333 3.41 3	0.03 736 3
Q8VIJ 6	INF	KMPGGPKPGGGPGMGAPGGHPPHR	K1:+114.043,K7:+114.043,K22:+114.043	933. 466 7	279 7.37 7	0.02 054 3
Q8VIJ 6	INF	GGKMPGGPKPGGGPGMGAPGGHPPH	K24:+114.043	843. 418 7	252 7.23 3	0.09 724 8
Q8VIJ 6	INF	GGKMPGGPKPGGGPGMGAPGGHPPHR	K3:+114.043	134 2.67 5	268 3.33 4	0.03 207 1
Q8VIJ 6	INF	GKMPGGPKPGGGPGMGAPGGHPPHR	K2:+114.043,K23:+114.043	137 1.18 5	274 0.35 5	0.03 071
Q8VIJ 6	INF	PSTAPGPPPPSTPSSGVSTTPQTGGPPPPAGGAGP GPKPGPGPGGPKGGK	K49:+114.043,K52:+114.043	118 8.60 1	475 0.37 4	0.08 207 5
Q8VIJ 6	INF	GGKMPGGPKPGGGPGMGAPGGHPK	K3:+114.043,M4:+15.995,K24:+114.043	116 4.06 1	232 6.10 6	0.04 617 3
Q8VIJ 6	INF	AGPGPKPGPGGPK	K15:+114.043	692. 870 8	138 3.72 6	0.06 123 4
Q8VIJ 6	INF	GGKMPGGPKPGGGPGMGAPGGH	K3:+114.043,M16:+15.995	663. 312 9	198 6.91 5	0.05 6
Q8VIJ 6	INF	PGGGPGMGAPGGHPPHRGGGEPR	M7:+15.995,K15:+114.043	122 2.59 2	244 3.16 8	0.04 617 3
Q91V 12	INF	IMRPDDANVAGNVHGGTILKMIEE	M2:+15.995,K20:+114.043	135 5.66 9	270 9.32 2	0.03 455 1
Q91V 12	INF	TMKLMDEVAGIVAAR	M2:+15.995,K3:+114.043,M5:+15.995	875. 945 6	174 9.87 6	0.04 401 7
Q91V 41	CO N	FGTRIEVSGQK	K12:+114.043	724. 897	144 7.77 8	0.04 800 5
Q91V 55	CO N	MTEWEAATPAVAETPDILF	K18:+114.043	116 7.57	233 3.12 5	0.02 334 2
Q91V 92	CO N	IIGPATVGGIKPGCFKIGNTGGMLDNILASK	K11:+114.043,C14:+45.988,M23:+15.995	107 3.56 3	321 7.66 7	0.07 125 9

Q91V 92	CO N	SEQTGKELLYK	K6:+114.043	705. 367 7	140 8.72	0.03 876 9
Q91V 92	CO N	YILDLAAKVDATADYICK	C17:+45.988,K18:+114.043	107 3.53 2	214 5.04 9	0.06 088 5
Q91V 92	CO N	GVTIIGPATVGGIKPGCFKIGNTGGMLDNILAS	C17:+45.988,K19:+114.043,M26:+15.995	837. 685 1	334 6.70 9	0.04 559 7
Q91V 92	CO N	ATMFSSEVQFGHAGACANQASETAVAK	M3:+15.995,C16:+45.988,K27:+114.043	963. 758 9	288 8.25 3	0.06 502 7
Q91V 92	INF	SEVQFGHAGACANQASETAVAKNQALK	C11:+45.988,K22:+114.043	964. 124 5	288 9.35	0.02 547 6
Q91V C3	CO N	EEDMTKVEFETSEEVDVTPFTDT	E1:-18.011,M4:+15.995,K6:+114.043	930. 732 7	278 9.17 5	0.06 159 8
Q91V H6	CO N	EASHAGSWYTASGPQLNAQLEGWLSQVQSTKR	K31:+114.043	120 1.25 3	360 0.73 5	0.07 598 5
Q91V H6	INF	HPIGVLLNAITELQK	K15:+114.043	440. 757 6	175 8.99 9	0.06 901 4
Q91V H6	INF	KTGMFER	K1:+114.043,M4:+15.995	499. 740 4	997. 465 3	0.03 509 5
Q91VI 7	CO N	TNELGDGGVGLVLQGLQNPTCKIQK	C21:+45.988,K25:+114.043	914. 802 6	274 1.38 4	0.07 060 6
Q91W K2	CO N	ITFEHMFEEVPIVIKNSHLINVLMWEELEK	M6:+15.995,K15:+114.043	122 3.63 4	366 7.87 8	0.08 994 9
Q91W K2	INF	ITFEHMFEEVPIVIKNSHLINVLMWEELEK	M6:+15.995,K15:+114.043	122 3.63 4	366 7.87 8	0.03 552 7
Q91YE 6	INF	GALAIRQLASVILK	K14:+114.043	522. 995 1	156 5.96 2	0.06 195 4
Q91YE 6	INF	AVEIFTTCAHMICNMEELEK	C8:+45.988,C13:+45.988,M15:+15.995,K20:+114.043	845. 357 7	253 3.05	0.06 871 7
Q91YI 4	CO N	GGDVSVELPFVLMHPKPHDITLPRPQSAPR	K16:+114.043	118 1.28 8	354 0.84 1	0.07 705 1
Q91YI 4	CO N	GGDVSVELPFVLMHPKP	K16:+114.043	968. 504	193 4.99 2	0.06 401 4
Q91YI 4	INF	CPVAQLEQDDQVSPSTFCKVYT	C1:+28.961,C19:+45.988,K20:+114.043	912. 055 5	273 3.14 3	0.05 346 2
Q91YP 3	CO N	LVAMMAGSDFIK	M4:+15.995,K12:+114.043	706. 849 9	141 1.68 4	0.09 225
Q91YR 9	CO N	LPLSLALGTVGMPGLTAYFGLLDICGVKGGETVMVSAAAGAV	M12:+15.995,C25:+45.988,K28:+114.043	139 9.38 9	419 5.14 5	0.07 598 5
Q91YR 9	CO N	KLPLSLALGTVGMPGLTAYFGLLDICGVK	C26:+45.988,K29:+114.043	777. 673 7	310 6.66 4	0.07 031 5
Q91YR 9	INF	ICGVKGGETVMVSAAAGAVGSVVGQIAK	C2:+45.988,K28:+114.043	680. 604 6	271 8.38 7	0.07 031 5

Q91Z5 0	CO N	AEAEKQLQQAQEAGMEEVEK	M15:+15.995,K21:+114.043	835. 719 1	250 4.13 4	0.05 668 8
Q91Z5 0	CO N	TIRMMENGIKPVYVFDGKPP	M4:+15.995,K10:+114.043,K18:+114.043	126 8.63 9	253 5.26 2	0.06 159 8
Q91ZJ 5	CO N	DLYLNLHLMNPPNGK	M9:+15.995,K15:+114.043	934. 970 4	186 7.92 5	0.05 993 8
Q91Z W3	CO N	MSSAVEPPPPPPESAPSKPSAAGAGSSSGNKGGP GGAAPAA	K19:+114.043	995. 724 2	397 8.86 5	0.03 378 2
Q91Z W3	CO N	PSAAGAGSSSGNK	K14:+114.043	631. 292 6	126 0.57	0.07 419 6
Q91Z W3	INF	ADVEKSLPPK	K10:+114.043	599. 327 9	119 6.64	0.03 509 5
Q920 B9	CO N	VQFHLKNFDMVIVYK	K15:+114.043	665. 689 4	199 4.04 5	0.07 598 5
Q920 B9	INF	KAASITSEVFNK	K1:+114.043,K12:+114.043	761. 897 2	152 1.77 9	0.05 436 4
Q920 B9	INF	TKGNENANGAPAITLLVR	K2:+114.043	977. 029 8	195 2.04 4	0.05 836 2
Q921F 2	CO N	VQKTSDLIVGLPWK	K3:+114.043,K15:+114.043	963. 047	192 4.07 8	0.04 559 7
Q921F 2	INF	DLKTGHSK	K3:+114.043,K8:+114.043	557. 286 6	111 2.55 8	0.05 993 8
Q921 H8	CO N	CGVESMSLSGMGNPGNISSRLLESEK	C1:+28.961,M6:+15.995,K26:+114.043	711. 069	284 0.24 5	0.08 109
Q921I 1	INF	MRLTVGALLACAALGLCLAVPDK	C11:+45.988,C17:+45.988,K23:+114.043	125 3.14 9	250 4.28 2	0.07 823 6
Q921I 1	INF	LKQEDFELLCPDGTR	K2:+114.043,C10:+45.988	962. 451 3	192 2.88 7	0.00 091 7
Q921I 1	INF	AVLTSQETLFGSDCTGNFCLFKS	C15:+45.988,C20:+45.988,K23:+114.043	136 6.09 8	273 0.18	0.07 003 4
Q921 M3	CO N	TEQGDIFKITLETDEDMVTEIR	K8:+114.043,M17:+15.995	679. 077 8	271 2.28	0.03 974 7
Q921 M3	CO N	PVEEVPAAIAPFQGRVLIGVGK	K22:+114.043	787. 781 7	236 0.32 2	0.03 924 8
Q921 M3	CO N	KEMSADVVCN	K1:+114.043,C9:+45.988	636. 758 9	127 1.50 2	0.06 701 2
Q921 M3	INF	LTISSPLEAHKANTLVYHVGVVDVGFENPMFA	K11:+114.043	119 0.60 9	356 8.80 3	0.03 974 7
Q921 M7	CO N	MSLFYAEATPMLKTLSDA	M1:+15.995,K13:+114.043	530. 508 2	211 8.00 1	0.04 644 6
Q922 B2	INF	EMAFNYHYHEVVEEADTLVQIFKGLQER	E1:-18.011,K24:+114.043	120 2.25 6	360 3.74 5	0.04 724 1

Q922 D4	CO N	SILISRKPEQIVDFLK	K7:+114.043	100 0.58 1	199 9.14 7	0.04 285 7
Q922 D4	CO N	EAPGSMAMEASSDGEEDAESTDKVTETVMNGGMK	E1:-18.011,M8:+15.995,K34:+114.043	901. 623 7	360 2.46 4	0.03 780 3
Q922 D4	CO N	QPEAPGSMAMEASSDGEEDAESTDKVTETVMNGGM K	Q1:-17.027,M35:+15.995,K36:+114.043	127 7.19 4	382 8.55 9	0.06 432 4
Q922 D4	INF	EAPGSMAMEASSDGEEDAESTDKVTETVMNGGMK	E1:-18.011,M8:+15.995,K34:+114.043	120 1.82 9	360 2.46 4	0.03 809
Q922 D4	INF	FVDLIKHIGTSAIMDLLR	K7:+114.043	794. 791 3	238 1.35 1	0.06 337 3
Q922 D8	CO N	PTPLGEGKSTTTIGLVQALGAHLR	K8:+114.043	633. 604 5	253 0.38 7	0.06 088 5
Q922 D8	CO N	GEPISCEDLVSGALTVMKDAIKP	C6:+45.988,K24:+114.043	901. 785 6	270 2.33 3	0.04 372 4
Q922 D8	CO N	AIKPNLMQTLGTPVVFHAGPFANIAHGNSIIADRIAL K	K3:+114.043	108 2.33 5	432 5.31 1	0.05 866 5
Q922 D8	CO N	PNLMQTLGTPVVFHAGPFANIAHGNSIIADRIALK	K37:+114.043	133 8.70 6	401 3.09 5	0.06 871 7
Q922 D8	INF	KVVGDVAYDEAK	K12:+114.043	704. 359 9	140 6.70 4	0.05 463 2
Q922 D8	INF	GDILVVATGQPEMVKGWIKPGAVVI	M13:+15.995,K15:+114.043,K20:+114.043	147 5.79	294 9.56 4	0.05 139 9
Q922 D8	INF	ALKMHGGGPTVTAGLPLPK	K3:+114.043,M4:+15.995,K19:+114.043	523. 036 6	208 8.11 5	0.04 372 4
Q922 D8	INF	MVVASSK	K7:+114.043	418. 221 3	834. 427	0.07 672 7
Q922 D8	INF	FHELTQTDKALFNR	K9:+114.043	917. 466 3	183 2.91 7	0.05 6
Q922P 9	CO N	TIPESSTVKGMMAGPMAAFK	M16:+15.995,K20:+114.043	109 2.52 9	218 3.04 3	0.05 526 5
Q922P 9	CO N	PAEVVSTCDITFACVSDPK	C8:+45.988,C14:+45.988,K19:+114.043	109 4.47 6	218 6.93 6	0.04 343 2
Q922P 9	CO N	LGLGLMGSGIVSNLLK	M6:+15.995,K16:+114.043	567. 991	170 0.95	0.04 229 4
Q922P 9	INF	TSFFLGEVGNAAKMMLIVNMVQGSF	K13:+114.043,M14:+15.995	941. 129 5	282 0.36 5	0.09 032
Q922P 9	INF	LGLMGSGIVSNLLKMGHTVTVWNR	M4:+15.995,K14:+114.043,M15:+15.995	136 5.21 6	272 8.41 6	0.06 369 3
Q922 R8	CO N	VNQVLASRYGIK	K12:+114.043	731. 412 8	146 0.81	0.06 337 3
Q922 R8	CO N	TGEAIVDAALSALRQLVK	K18:+114.043	985. 058	196 8.1	0.07 741 6

Q922S 4	INF	ILQLCGELFDLATSLLQK	C5:+45.988,K19:+114.043	760. 726	227 9.15 4	0.01 060 4
Q924 B0	CO N	NEMDVMIKSSPADLVTVDQ	M3:+15.995,M6:+15.995,K8:+114.043	117 0.04 1	233 8.06 7	0.08 657 5
Q9309 2	INF	AIDKLFVLFGAEILK	K4:+114.043	597. 685 9	179 0.03 4	0.00 091 7
Q9902 0	CO N	GEAPVEPSAAAAAPAASAGSGGGTTTAPSGNQNGAE GDQINASK	K44:+114.043	133 6.95 2	400 7.83 3	0.06 231 8
Q9902 0	INF	GEAPVEPSAAAAAPAASAGSGGGTTTAPSGNQNGAE GDQINASK	K44:+114.043	133 6.95 2	400 7.83 3	0.09 676 7
Q99J7 7	CO N	FQKSELEFK	K3:+114.043,K9:+114.043	692. 349 4	138 2.68 3	0.05 231 3
Q99J7 7	INF	FQKSELEFK	K3:+114.043,K9:+114.043	692. 349 4	138 2.68 3	0.09 547 1
Q99JF 5	INF	ILVVSADKK	K8:+114.043	543. 830 1	108 5.64 5	0.00 365 5
Q99JI 4	CO N	DKVNEIVETNRPDSK	K2:+114.043	929. 469 2	185 6.92 3	0.03 903 5
Q99JI 4	INF	SLDWQMDVDLLSKMK	M6:+15.995,K13:+114.043,M14:+15.995,K15: +114.043	103 4.98 8	206 7.96 1	0.05 734
Q99JX 4	INF	QNMAKMR	Q1:-17.027,M3:+15.995,K5:+114.043	496. 226 4	990. 437 2	0.04 667 3
Q99JY 9	INF	KPKPIDVQVITHHMQR	K1:+114.043	102 1.06	204 0.10 5	0.00 291 5
Q99KE 1	CO N	CIDVGTDNMALLKDPFYMGLYQK	C1:+28.961,K13:+114.043,M18:+15.995	139 7.63 4	279 3.25 2	0.06 568
Q99KE 1	INF	ANIAIKLAELYANK	K15:+114.043	904. 999 5	180 7.98 3	0.06 231 8
Q99K H8	CO N	VGTPFWMAPEVIKQSAYDSK	M7:+15.995,K13:+114.043,K20:+114.043	124 9.60 5	249 7.19 5	0.04 828 8
Q99K H8	INF	VLFLIPKNNPPTLEGNYSK	K19:+114.043	112 9.61 3	225 7.21 1	0.03 252 1
Q99KI 0	CO N	QIILENYAYPGVLLIGTDSHTPNGGGLGGICIGVGGA VDVMAGIPWELKCPK	C31:+45.988,K51:+114.043,C52:+45.988,K54:+ 114.043	144 3.21 2	576 8.81 8	0.04 116 7
Q99KI 0	INF	QIILENYAYPGVLLIGTDSHTPNGGGLGGICIGVGGA VDVMAGIPWELKCPK	C31:+45.988,K51:+114.043,C52:+45.988,K54:+ 114.043	144 3.21 2	576 8.81 8	0.05 436 4
Q99KI 0	INF	IHQIILENYAYPGVLLIGTDSHTPNGGGLGGICIGVGGA DAVDVMAGIPWELK	C33:+45.988,M45:+15.995,K53:+114.043	138 7.7	554 6.76 8	0.07 385 3
Q99KI 0	INF	GTDSHTPNGGGLGGICIGVGGA DAVDVMAGIPWELK CPK	C16:+45.988,C37:+45.988,K39:+114.043	131 9.28 1	395 4.82	0.04 828 8
Q99K K7	CO N	QLLKELPWPLAFEK	K14:+114.043	913. 514 7	182 5.01 4	0.03 252 1

Q99K K7	INF	EGVTTFYSGDCTMEDAKLAQDFLDSQNLSAY	C11:+45.988,K17:+114.043	119 3.84 7	357 8.51 7	0.03 378 2
Q99K P6	CO N	LTTGVAFGHHAK	K12:+114.043	451. 574 4	135 1.7	0.04 256 6
Q99K P6	CO N	PSSQPSVVGAGPEMDLGELVGMTPEIIQK	M14:+15.995,K29:+114.043	103 2.84 6	309 5.51 6	0.05 025 6
Q99K P6	CO N	PSSQPSVVGAGPEMDLGELVGMTPEIIQKLQDK	M22:+15.995,K33:+114.043	119 4.26 8	357 9.78	0.06 701 2
Q99K P6	CO N	FSENGYLLATAADDSSVK	K18:+114.043	102 6.46 4	205 0.91 2	0.03 132 7
Q99K P6	CO N	GAGEPMDLGELVGMTPEIIQK	M6:+15.995,K21:+114.043	115 8.06 7	231 4.11 9	0.06 937 5
Q99K Q4	CO N	HIVTQFSSVPVSVSDSYDIYNACEKIWGEDLR	C24:+45.988,K26:+114.043	130 6.29	391 5.84 5	0.07 530 6
Q99K Q4	CO N	LIIRPDSGNPLDTVLK	K16:+114.043	467. 018 3	186 4.04 2	0.03 455 1
Q99K V1	INF	YDTYGEGLK	K10:+114.043	644. 788 8	128 7.56 2	0.05 231 3
Q99LB 4	CO N	AQVEITDGEPAEMIQVLGPKPAL	M15:+15.995,K22:+114.043	138 9.71 6	277 7.41 6	0.06 159 8
Q99LB 4	CO N	EMIQVLGPKPALKEGNPEEDITADQTNAQAAALYK	K9:+114.043,K13:+114.043	132 8.00 1	398 0.97 9	0.06 432 4
Q99LB 4	INF	AQVEITDGEPAEMIQVLGPKPAL	M15:+15.995,K22:+114.043	138 9.71 6	277 7.41 6	0.06 701 2
Q99LC 5	CO N	TSGGSASSEKAPSSSSVGISEWLDQK	K10:+114.043	134 8.63 6	269 5.25 7	0.06 568
Q99L D4	INF	SSFKLFELEPQVR	K4:+114.043	903. 991 6	180 5.96 8	0.05 294
Q99LI 7	CO N	TRHHVYVTAALMEYYCSK	M12:+15.995,C16:+45.988,K18:+114.043	117 4.53 5	234 7.05 5	0.08 473 4
Q99LI 7	CO N	EAQNQPIDK	[0:-18.011,K9:+114.043	569. 778 3	113 7.54 1	0.05 498 6
Q99LI 7	INF	LMKVLHIDLWK	M2:+15.995,K11:+114.043	763. 432 2	152 4.84 9	0.04 644 6
Q99LI 7	INF	KIGMEIMSYQIWVDYINFLK	K1:+114.043,M4:+15.995	656. 084 6	262 0.30 7	0.06 195 4
Q99LI 7	INF	GCVNPMINIEQLWRDYNK	C2:+45.988,K18:+114.043	117 7.04 9	235 2.08 2	0.04 144 1
Q99LX 0	CO N	FALAIVEALVGKDMANQVK	K12:+114.043,M14:+15.995	107 4.08 1	214 6.14 6	0.06 056 1
Q99LX 0	INF	VVVLPGGNLGAQNLSESPMVKEILK	K25:+114.043	135 3.74 7	270 5.47 9	0.05 197 5

Q99M K8	CO N	DLKPANILLDEHGHV	K3:+114.043	595. 648 4	178 3.92 2	0.07 630 8
Q99M K8	CO N	PANILLDEHGHVRISDLGLACDFSK	C21:+45.988,K25:+114.043	960. 809 9	287 9.40 6	0.04 315 4
Q99M K8	CO N	ILLPEPSIRSVMQK	K14:+114.043	575. 663	172 3.96 6	0.02 805 7
Q99M K8	INF	GEVNAADAFDIGSFDEEDTKGIK	K23:+114.043	127 1.58 3	254 1.15 1	0.05 111 3
Q99M N1	CO N	KETAATTETPESTEASPS	K1:+114.043	975. 942 9	194 9.87	0.03 403 7
Q99M N1	INF	SFLDELGFLEIETPMMNIIIPGGAVAKPFITY	M16:+15.995,K26:+114.043	886. 700 8	354 2.77 2	0.05 374 6
Q99N B9	CO N	MVMETIEKIMGNLGAAD	M1:+15.995,K8:+114.043,M10:+15.995	656. 974 6	196 7.9	0.03 455 1
Q99N B9	INF	ISNLAKAAGLATMISTMRPDIDNMDEYVR	K6:+114.043,M13:+15.995,M17:+15.995,M24: +15.995	112 0.20 8	335 7.60 1	0.07 155 3
Q99N B9	INF	TVNTFGYIAKAIGPHDVLATLLNNLK	K10:+114.043	966. 534 8	289 6.58 1	0.07 090 1
Q99P V0	CO N	MLNLLIHRK	M1:+15.995,K9:+114.043	634. 369 4	126 6.72 3	0.03 834 3
Q99P V0	INF	TILQHLSEAWRCWK	C12:+45.988,K14:+114.043	965. 975 1	192 9.93 5	0.06 024 7
Q99P V0	INF	GMLSMGHVLIPOQSDLRWSK	M2:+15.995,M5:+15.995,K19:+114.043	115 1.07 8	230 0.14 1	0.05 322 5
Q99P V0	INF	CWKANIPWK	C1:+45.988,K3:+114.043,K9:+114.043	710. 337 4	141 8.65 9	0.03 947 5
Q9CPY 7	INF	EMLNISGPPLK	K11:+114.043	656. 850 7	131 1.68 6	0.06 195 4
Q9CQ 19	INF	HDMLASLGKNPTDEYLEGMMNEAPGINFTMFLTMF GEK	K9:+114.043	112 3.51 8	449 0.04	0.00 681 3
Q9CQ C6	INF	CIQGLTETGTDLEAVAK	C1:+28.961,K18:+114.043	100 2.98 5	200 3.95 4	0.05 6
Q9CQ C6	INF	AAQEDLETMQAFAQVFNKLIR	M9:+15.995,K18:+114.043	127 7.14 3	255 2.26 9	0.05 993 8
Q9CQ C6	INF	SWINEKDINAVAASLR	K6:+114.043	950. 998	189 9.98	0.04 012 7
Q9CQI 7	INF	QGFPFYGKPMR	Q1:-17.027,K8:+114.043	712. 843	142 3.67	0.07 218 1
Q9CQ M9	INF	VLTKNASVMLFMK	K13:+114.043	798. 436 6	159 4.85 8	0.06 666 4
Q9CQ R6	INF	TKVFDMLTVAALIDEQILCVHGGGLSPDIK	M6:+15.995,C19:+45.988,K29:+114.043	110 1.56 7	330 1.67 6	0.06 123 4

Q9CQ V8	INF	AIAELDTLNEESYKDSTLIMQLLR	K14:+114.043	960. 827 4	287 9.45 9	0.04 012 7
Q9CS4 2	INF	EDVYIIQSGCGEINDNLMELLIMINACK	C10:+45.988,M23:+15.995,C27:+45.988,K28:+ 114.043	112 1.84 3	336 2.50 4	0.06 300 9
Q9CS N1	INF	KLAPAQYIR	K1:+114.043	587. 341 1	117 2.66 7	0.07 492 7
Q9CV B6	CO N	IIETLALK	K9:+114.043	572. 335 2	114 2.65 5	0.01 258 3
Q9CW 03	INF	ILMEFNK	M3:+15.995,K7:+114.043	512. 760 8	102 3.50 6	0.04 776 4
Q9CW 03	INF	EQLSAERQEQIK	E1:-18.011,K12:+114.043	777. 897 5	155 3.77 9	0.04 667 3
Q9CW J9	INF	YGMNPHQTPAQLYTLKPKLPITVLNGAPGFINLCDALN A	M3:+15.995,K16:+114.043,C34:+45.988	145 7.41	436 9.20 7	0.05 803 7
Q9CX 56	CO N	KMAATAATVNGSTTVSSSGPAATSVGILQAAAG	K1:+114.043,M2:+15.995	102 6.85 1	307 7.53	0.05 498 6
Q9CX 56	CO N	SSGPAATSVGILQAAAGMYEQLK	K23:+114.043	118 2.59 7	236 3.17 9	0.07 125 9
Q9CX 56	CO N	TAATVNGSTTVSSSGPAATSVGILQAAAGMYEQLK	M30:+15.995,K35:+114.043	868. 183 9	346 8.70 4	0.05 264 8
Q9CX 56	INF	AATAATVNGSTTVSSSGPAATSVGILQAAAGMYEQLK	M32:+15.995,K37:+114.043	120 4.60 1	361 0.77 9	0.06 465 9
Q9CY5 0	CO N	IQKVEMGTSSQNDVDMSWIPQETLNQINK	K3:+114.043,M16:+15.995	866. 667 7	346 2.64	0.09 259 4
Q9CY5 0	INF	QKVEMGTSSQNDVDMSWIPQETLNQINK	Q1:- 17.027,K2:+114.043,M5:+15.995,K28:+114.04 3	114 9.86 5	344 6.57 2	0.03 071
Q9CZ3 0	CO N	PEYDIMCK	M6:+15.995,C7:+45.988,K8:+114.043	587. 733 2	117 3.45 1	0.09 676 7
Q9CZ D3	CO N	KVPLVAEKPLK	K1:+114.043	668. 422 1	133 4.82 9	0.07 530 6
Q9CZ N7	CO N	EVRAHLLADMAHISGLVAAK	E1:-18.011,K20:+114.043	109 9.59 7	219 7.17 9	0.05 111 3
Q9CZ U3	INF	VIPNEENVVIYYK	K13:+114.043	847. 444	169 2.87 2	0.02 316 6
Q9CZ U6	INF	LLTAATRLLGAK	K12:+114.043	671. 414 8	134 0.81 4	0.05 322 5
Q9D0 20	CO N	EESLEVNSILQK	K13:+114.043	801. 423 2	160 0.83 1	0.07 672 7
Q9D0 20	CO N	IVLVKEESLEVNSILQK	K18:+114.043	107 7.62 3	215 3.23 1	0.03 736 3
Q9D0 20	INF	LLGDSQGDRLRMADGVANVEHILK	M11:+15.995,K23:+114.043	129 1.15 6	258 0.29 7	0.06 123 4

Q9D0 51	CO N	DIIFAVKK	K8:+114.043	524. 314	104 6.61 2	0.03 282 5
Q9D0 51	INF	RPMDIEAIEASVMK	K14:+114.043	852. 426 9	170 2.83 8	0.00 091 7
Q9D0 51	INF	NNPVVMLENELMYGVAFELPAEAQSKDFLIPIGK	K26:+114.043	129 7.66 2	388 9.96 4	0.07 896 1
Q9D0 71	CO N	LPKLAEEELHK	K3:+114.043	646. 372 6	129 0.73	0.04 042 1
Q9D0 E1	CO N	LGPGGQPIDANHLSKGIGMGNLGPAGMGMEGIGFGI NK	M27:+15.995,K38:+114.043	126 4.95 9	379 1.85 5	0.06 738 7
Q9D0 E1	CO N	AMQKVMATTGGMGMPGGPGMINIPPSILNNPNIP N	M2:+15.995,K4:+114.043,M21:+15.995	124 1.93 2	372 2.77 1	0.02 743 3
Q9D0 E1	CO N	AMQKVMATTGGMGMPGGPGMINIPPSILN	K4:+114.043,M12:+15.995,M14:+15.995,M21: +15.995	103 0.82 4	308 9.44 8	0.05 463 2
Q9D0 E1	CO N	EEESGAPCVPSGNGAPGPK	C8:+45.988,K19:+114.043	971. 917 8	194 1.82	0.07 090 1
Q9D0 E1	CO N	QQLPHGLGGIGMGLPGGQPIDANHLSK	M12:+15.995,K28:+114.043	720. 620 5	287 8.45 1	0.07 782 3
Q9D0 E1	CO N	ANHLSKGIGMGNLGPAGMGMEGIGFGINK	M18:+15.995,M20:+15.995,K29:+114.043	744. 364 3	297 3.42 6	0.04 229 4
Q9D0 E1	INF	ANHLSKGIGMGNLGPAGMGMEGIGFGINK	K6:+114.043,M10:+15.995,M20:+15.995	992. 149 9	297 3.42 6	0.04 315 4
Q9D0 E1	INF	GIGMGNLGPAGMGMEGIGFGINKIGGMEGPFGGG MENMG	M4:+15.995,M12:+15.995,M14:+15.995,K23: + 114.043,M27:+15.995,M35:+15.995,M38:+15. 995	130 3.89 5	390 8.66 1	0.02 701 1
Q9D0 E1	INF	GSGMNMGRINEILSNALK	M6:+15.995,K18:+114.043	101 8.00 7	203 3.99 9	0.07 286 9
Q9D0 E1	INF	AMQKVMATTGGMGMPGGPGMINIPPSILNNPN	K4:+114.043,M12:+15.995,M14:+15.995	850. 655 7	339 8.59 2	0.05 171 8
Q9D0I 9	INF	KVTLVTHVFGFVVLGEDK	K1:+114.043	100 6.56 3	201 1.11	0.04 475 4
Q9D0I 9	INF	VLRLNHVGDWGTQFGMLIAHLQDK	M16:+15.995,K24:+114.043	960. 164 8	287 7.47 1	0.06 337 3
Q9D0I 9	INF	KIVFVPGCSVPLTIVK	K1:+114.043,C8:+45.988,K16:+114.043	658. 702 7	197 3.08 5	0.06 159 8
Q9D0 R2	CO N	ETLLEMFKYNK	M6:+15.995,K11:+114.043	773. 385 1	154 4.75 5	0.04 724 1
Q9D0 R2	CO N	LEEGGVSSNDFSLETLC	C18:+45.988,K19:+114.043	725. 658 2	217 3.95 1	0.05 374 6
Q9D1 54	CO N	CKVLEMPYQGGEELSMVILLPK	C1:+28.961,M6:+15.995,K21:+114.043	125 4.12 5	250 6.23 4	0.05 197 5
Q9D1 54	INF	MPYQGGELSMVILLPK	M1:+15.995,M10:+15.995,K16:+114.043	961. 492 4	192 0.96 9	0.05 197 5

Q9D1 A2	CO N	EGGSIPVTLTFQEATGKNVMLLPVGSADDGAHSQN	K17:+114.043,M20:+15.995	918. 447 4	366 9.75 8	0.07 385 3
Q9D1 A2	CO N	GKILIPGINDAVAPVTDE	K2:+114.043	968. 523 5	193 5.03 1	0.04 144 1
Q9D1 A2	INF	PVTDEEHALYDHIDFDMEEFAKDVGAETLLHSCK	M17:+15.995,K22:+114.043,C33:+45.988,K34: +114.043	139 8.95 1	419 3.83	0.03 809
Q9D1 Q6	CO N	EITFENGEEELTEEGLPFLILFHMK	E1:-18.011,K24:+114.043	146 6.72 6	293 1.43 6	0.06 502 7
Q9D1 Q6	INF	EITFENGEEELTEEGLPFLILFHMK	E1:-18.011,K24:+114.043	146 6.72 6	293 1.43 6	0.02 350 7
Q9D2 V7	CO N	VAVPLLSSGGQVAVLELQKP	K19:+114.043	707. 076 1	211 8.20 5	0.07 419 6
Q9D6 62	INF	PLACLLTPLKERPDLPVQYEPVLCSPRTCK	C4:+45.988,C25:+45.988,C30:+45.988,K31:+11 4.043	124 3.62 3	372 7.84 6	0.06 871 7
Q9D6 62	INF	HKIDMNLTDLLGELQR	K2:+114.043	100 5.52 6	200 9.03 6	0.07 933 9
Q9D6 R2	CO N	IFESVHGTAPDIAGK	K15:+114.043	828. 423 6	165 4.83 2	0.05 928
Q9D6 R2	CO N	NGVAIFESVHGTAPDIAGK	K19:+114.043	666. 341 6	199 6.00 1	0.04 509 1
Q9D6 R2	INF	VHGTAPDIAGK	K11:+114.043	590. 31	117 8.60 4	0.07 090 1
Q9D6 R2	INF	NIGANGVAIFESVHGTAPDIAGKDMANPTALLSAVM MLR	K23:+114.043,M37:+15.995	139 9.38 2	419 5.12 3	0.04 776 4
Q9D6 Z1	INF	LSACKAQLGLGHSYSR	C4:+45.988,K5:+114.043	925. 954 3	184 9.89 3	0.08 437 5
Q9D6 Z1	INF	SDLEEMATSSAK	K12:+114.043	461. 542 2	138 1.60 3	0.04 910 9
Q9D8 19	CO N	CDPDAAKAIVDALPPPCESACSLPTDV	C1:+28.961,K7:+114.043,C17:+45.988,C21:+45 .988	146 7.11 5	293 2.21 4	0.06 195 4
Q9D8 19	CO N	AIPQTWEDPGHSDKHTGCCGDNDPIDVCEIGSK	C18:+45.988,C19:+45.988,C28:+45.988,K33:+1 14.043	125 9.51 3	377 5.51 5	0.07 564 5
Q9D8 19	INF	AIPQTWEDPGHSDKHTGCCGDNDPIDVCEIGSK	C18:+45.988,C19:+45.988,C28:+45.988,K33:+1 14.043	125 9.51 3	377 5.51 5	0.07 530 6
Q9D8 B3	CO N	EQELTAAKK	K8:+114.043	566. 304 4	113 0.59 3	0.08 701
Q9D8 B3	CO N	VDELMQDIADQQELAEIESTAISKPVGFGEFDEDELM	M5:+15.995,K24:+114.043	146 7.66 5	439 9.97 2	0.05 803 7
Q9D8 B3	INF	LFGAGGGK	K8:+114.043	410. 719 8	819. 424	0.03 482
Q9D8 E6	CO N	EKVVPEK	E1:-18.011,K2:+114.043	462. 761 4	923. 507 3	0.04 881

Q9D9 06	CO N	LLNKFLLLTADLK	K4:+114.043,K14:+114.043	939. 049	187 6.08 2	0.06 432 4
Q9D9 06	CO N	LQFAPFNSALDVGFWHELTQK	K21:+114.043	128 1.64 3	256 1.27	0.05 895 8
Q9D9 06	INF	LLLEQSANEIWEAIKSGAALENPMLLNK	K15:+114.043,M24:+15.995,K28:+114.043	111 3.91 4	333 8.71 8	0.05 803 7
Q9D9 64	INF	MFEKLGISTIK	K4:+114.043,K11:+114.043	747. 903 5	149 3.79 1	0.03 755 2
Q9DB 05	CO N	LCHFCIDMLNAKLAVQK	C2:+45.988,C5:+45.988,K12:+114.043,K17:+114.043	113 4.03 6	226 6.05 6	0.01 178 6
Q9DB G3	CO N	PLMPNQSIDVSLPLNTLGPVMK	K22:+114.043	123 9.65 9	247 7.30 2	0.05 346 2
Q9DB G3	INF	LSTGIGMAPGGYVAPK	M7:+15.995,K16:+114.043	550. 284 2	164 7.82 9	0.05 928
Q9DB G3	INF	QVFLATWKDIPNE	K8:+114.043	837. 928 5	167 3.84 1	0.05 498 6
Q9DB G6	INF	EDQVIQLMNTIFSK	K14:+114.043	593. 970 3	177 8.88 7	0.09 501 2
Q9DBJ 1	CO N	LKPIKPMQFLGDEETVR	K2:+114.043	105 8.06 8	211 4.11 9	0.00 091 7
Q9DBJ 1	INF	LKPIKPMQFLGDEETVR	K2:+114.043	105 8.06 8	211 4.11 9	0.00 091 7
Q9DBJ 1	INF	LKPIKPMQFLGDEETVRK	K2:+114.043	561. 561 4	224 2.21 4	0.00 254 6
Q9DBJ 1	INF	ERHYGGLTGLNK	K12:+114.043	729. 876 6	145 7.73 8	0.09 922 2
Q9DB K7	CO N	YLRGGVVTEVK	K11:+114.043	667. 875 5	133 3.73 5	0.06 401 4
Q9DB K7	CO N	KGTEESLDEALLR	K1:+114.043	568. 620 3	170 2.83 7	0.00 158 6
Q9DB K7	INF	KGTEESLDEALLR	K1:+114.043	568. 620 3	170 2.83 7	0.00 237 5
Q9DB K7	INF	PMAAIMGGVAAQEVKKAISR	K16:+114.043	106 4.07 5	212 6.13 4	0.08 437 5
Q9DB T5	INF	KAPVLQYLYYLAQIGIAMSPNSLFLSYH	K1:+114.043	121 0.30 1	362 7.88	0.09 259 4
Q9DC D0	INF	GSQVSGGEEGARYGPSLMPGGNK	K23:+114.043	113 9.53	227 7.04 4	0.03 974 7
Q9DC H4	INF	IGVDLIMKTCFSPN	M7:+15.995,K8:+114.043,C10:+45.988	857. 404 8	171 2.79 4	0.04 448 1
Q9DC L9	CO N	KDDANNDPQWSEEQLIAAK	K1:+114.043,K19:+114.043	600. 782 6	239 9.09 9	0.09 225

Q9DC L9	INF	KAEYEGDGIPTVFVSVAGR	K1:+114.043	105 5.03 5	210 8.05 4	0.00 091 7
Q9EPK 7	CO N	LYGDDALENALQTFIKLLLSIPHSDDLDPK	K16:+114.043,K31:+114.043	124 8.65 6	374 2.94 6	0.03 974 7
Q9EPL 8	CO N	PELPWWK	K7:+114.043	535. 277 5	106 8.53 9	0.04 996 1
Q9EPL 8	INF	NEFAEVFLKAFVGVQQVLLK	K21:+114.043	822. 125 4	246 3.35 3	0.04 589 2
Q9EPL 9	CO N	FNSGELLFWDGQDVHFK	K19:+114.043	119 0.09 3	237 8.17	0.07 218 1
Q9EPL 9	INF	LEAYPGILGQK	K11:+114.043	434. 907 1	130 1.69 8	0.00 418 8
Q9EQ G9	CO N	MVSLVSGASGYSATSTSSFCK	K21:+114.043	110 5.04 4	220 8.07 3	0.04 857 5
Q9EQ G9	INF	GSMVSLVSGASGYSATSTSSFCK	M3:+15.995,K22:+114.043	561. 014 5	224 0.02 7	0.04 694 9
Q9EQ G9	INF	DGDFLHNTNGNK	K12:+114.043	723. 324 4	144 4.63 3	0.07 286 9
Q9EQ H3	INF	NKLMDALK	K8:+114.043	523. 787 3	104 5.55 9	0.02 660 9
Q9EQ U5	INF	YRIDFYFDENPYFENK	K16:+114.043	113 7.51 1	227 3.00 7	0.04 012 7
Q9ER D8	CO N	KYLSPNSK	K1:+114.043,K8:+114.043	582. 804 6	116 3.59 4	0.04 559 7
Q9ER D8	INF	KYLSPNSK	K1:+114.043,K8:+114.043	582. 804 6	116 3.59 4	0.04 092 9
Q9ERF 3	CO N	LAFSPDSQYLATGTHMGKVNIFGVESGK	M16:+15.995,K28:+114.043	771. 883 4	308 3.50 2	0.05 698 3
Q9ERF 3	INF	QMKSIDAGPVDWTLAFSPDSQYLATGTH	Q1:-17.027,M2:+15.995,K3:+114.043	107 4.16 8	321 9.48 2	0.07 419 6
Q9ERF 3	INF	QMKSIDAGPVDWTLAFSPDSQ	K3:+114.043	123 9.58 4	247 7.15 3	0.07 630 8
Q9ER K4	CO N	VMSLLLETHKNDIPSSYMALFPHLLQPVLWER	M2:+15.995,K10:+114.043,M18:+15.995	130 8.67 8	392 3.01 2	0.06 300 9
Q9ER K4	INF	PGSSENEYIMKAIMR	K11:+114.043,M14:+15.995	928. 438 1	185 4.86 1	0.04 144 1
Q9ERL 7	CO N	ETNNAIIMKVDK	M9:+15.995,K13:+114.043	788. 904 2	157 5.79 3	0.03 854 5
Q9ERL 7	INF	MVVLEDELQNISPEELK	K17:+114.043	105 0.53 1	209 9.04 6	0.05 346 2
Q9ES4 6	CO N	VHNVAFAFELMLDGGGLKKPK	K18:+114.043	116 4.63 1	232 7.24 6	0.05 895 8

Q9ES5 2	CO N	ILQLIKSQK	K6:+114.043	592. 872 3	118 3.72 9	0.07 060 6
Q9ES5 2	CO N	VPACGVSSLNEMINPNYIGMPFGQPLHGKSTLSPD	C4:+45.988,K30:+114.043	129 6.61 3	388 6.81 5	0.07 782 3
Q9ES5 2	CO N	LDQLIDFYKK	K9:+114.043,K10:+114.043	755. 899 2	150 9.78 3	0.06 810 4
Q9ESP 1	INF	LLLALSVRSGGASK	K14:+114.043	495. 963 6	148 4.86 8	0.01 780 7
Q9ESX 5	CO N	EIGDYIRTGFINDKPSNPSSHEVVAWIR	K15:+114.043	114 3.25 2	342 6.73 2	0.06 231 8
Q9ETO 1	CO N	KVIPATDLSEQISTAGTEASGTGNMK	M25:+15.995,K26:+114.043	684. 839 9	273 5.32 9	0.03 182 7
Q9ETO 1	CO N	KQEYFVVAATLQDVIR	K1:+114.043	997. 539 5	199 3.06 3	0.06 701 2
Q9ETO 1	INF	KQEYFVVAATLQDVIR	K1:+114.043	997. 539 5	199 3.06 3	0.00 091 7
Q9JHJ 0	INF	VELEMAKMLEENTNILK	M5:+15.995,K7:+114.043,M8:+15.995	717. 694 5	215 0.06	0.04 617 3
Q9JH U4	CO N	EFGPVVIDYGK	K11:+114.043	669. 341	133 6.66 6	0.00 398 3
Q9JH U4	CO N	LERMNTLLANGEVPGLFEGDEYATLMTQCK	M4:+15.995,M26:+15.995,C29:+45.988,K30:+114.043	884. 661 4	353 4.61 4	0.05 463 2
Q9JH U4	CO N	IPWSALKTLMAQSIYGGR	K7:+114.043	702. 710 9	210 5.10 9	0.05 526 5
Q9JH U4	CO N	MQMLEDEDDLAYAEOTEK	K18:+114.043	113 7.00 2	227 1.98 8	0.04 116 7
Q9JH U4	CO N	GVQDKLVQTPLTDR	K5:+114.043	561. 972 9	168 2.89 5	0.06 088 5
Q9JH U4	CO N	QINHGLMMVGPSPSGKSMWR	Q1:-17.027,K16:+114.043	781. 038 5	234 0.09 2	0.05 895 8
Q9JH U4	CO N	FEKVMVACFEVFTWDDEYEK	K3:+114.043,C8:+45.988	140 2.10 9	280 2.20 2	0.04 229 4
Q9JH U4	INF	KSVLVSAGNVK	K1:+114.043	405. 907 3	121 4.69 8	0.03 071
Q9JH U4	INF	DKAEVDMDDAPQVSHKPGGEPK	K2:+114.043,M7:+15.995	861. 066 6	258 0.17 6	0.06 738 7
Q9JH U4	INF	QEMYLYTDGEEVGGMWVEK	Q1:-17.027,M3:+15.995,M16:+15.995,K20:+114.043	613. 26	244 9.00 9	0.07 933 9
Q9JH U4	INF	NPLMKDFPLNDLLSATELDK	M4:+15.995,K5:+114.043,K20:+114.043	125 9.62 9	251 7.24 2	0.06 369 3
Q9JH U4	INF	KWLVLFCDEINLPDMDK	C7:+45.988,K17:+114.043	112 0.03 4	223 8.05 3	0.04 475 4

Q9JH U4	INF	GWENHVEGQKLK	K10:+114.043,K12:+114.043	826. 911 2	165 1.80 7	0.04 667 3
Q9JI 0	CO N	QPILDAMDAKK	K10:+114.043	672. 353 6	134 2.69 2	0.03 403 7
Q9JI 0	INF	QPILDAMDAKK	K10:+114.043	672. 353 6	134 2.69 2	0.00 14
Q9JI 1	CO N	GTMVINTEDEEEEGTMK	M3:+15.995,M16:+15.995,K17:+114.043	102 9.92 8	205 7.84 1	0.03 974 7
Q9JIF 0	INF	FVATLANGMSLQPPLEEVSCGQAESSEKPAEDMTSK	C20:+45.988,M34:+15.995,K37:+114.043	135 7.94 9	407 0.82 2	0.06 568
Q9JIF 0	INF	MAAAEAANCIMENFVATLANGMSLQPPLEEVSCGQAESSEKPAEDMTSKDY	C9:+45.988,M11:+15.995,C33:+45.988,K41:+114.043,M47:+15.995,K50:+114.043	146 2.12 5	584 4.46 9	0.05 231 3
Q9JIF 7	CO N	KEAELEPLMPAIR	K1:+114.043	862. 474 8	172 2.93 4	0.04 071 8
Q9JIF 7	CO N	LKLVEKPSPLTLAPHDFANIK	K21:+114.043	122 3.19 7	244 4.37 9	0.05 346 2
Q9JIF 7	INF	FDNLRMLIVEK	K11:+114.043	746. 403 6	149 0.79 2	0.08 244 9
Q9JIF 7	INF	KLVEKPSPLTLAPHDFANIK	K5:+114.043,K20:+114.043	122 3.67 7	244 5.33 8	0.04 800 5
Q9JIY 5	INF	VNLDGEVIGVNTMKVTAGISFAIPSDR	M13:+15.995,K14:+114.043	978. 506 7	293 2.49 7	0.07 492 7
Q9JJ 28	CO N	QVINEGEEPENFFWVGIGAQKPYDDDAEYM	K21:+114.043,M30:+15.995	120 7.53 2	361 9.57 3	0.00 408 3
Q9JJ 28	CO N	DYTRNAEAVLQGQGLSGK	K18:+114.043	674. 340 3	201 9.99 7	0.05 053 6
Q9JJ 28	INF	ENPSLVMPPK	E1:-18.011,K10:+114.043	604. 311	120 6.60 6	0.06 701 2
Q9JJ 28	INF	CIQINTDSSLNSEFCILK	[0:- 17.027,C1:+45.988,C16:+45.988,K20:+114.043	826. 379 4	247 6.11 5	0.07 492 7
Q9JJ 28	INF	FYEADCYIVLKTFLDDSGSLNWEIYYWIGGEAT	C6:+45.988,K11:+114.043	101 1.21 2	404 0.81 7	0.03 252 1
Q9JK 8	CO N	LQSGAPKPEENPNLNQFK	K19:+114.043	111 9.58	223 7.14 4	0.04 938 8
Q9JK 8	INF	LQSGAPKPEENPNLNQFK	K19:+114.043	111 9.58	223 7.14 4	0.03 736 3
Q9JKF 1	CO N	MLQHAASNKMFLGDNAHLSIINEYLSQSYQK	K31:+114.043	917. 202	366 4.77 7	0.05 928
Q9JKF 1	CO N	KEQLSDMMINK	K1:+114.043	791. 375 9	158 0.73 6	0.00 091 7
Q9JKF 1	CO N	LENDLNLMDIKIGLLVK	K17:+114.043	102 8.08	205 4.14 5	0.08 145 7

Q9JKF 1	CO N	EHHERILAIGLINEALDEGDAQK	K22:+114.043	637. 831	254 7.29 3	0.03 282 5
Q9JKR 6	CO N	FLGDSAAGMAIKNP	K12:+114.043,K15:+114.043	874. 444	174 6.87 2	0.04 828 8
Q9JKR 6	CO N	LLALSDTLAVMSVDLGSESMKVAIVKPGVPMEIVLNK	M11:+15.995,M20:+15.995,K26:+114.043,M3 1:+15.995	134 4.05 6	402 9.14 5	0.05 633 6
Q9JKR 6	CO N	LKTVLSANADHMAQIEGLMDD	K2:+114.043,M12:+15.995	120 1.57 1	240 1.12 6	0.07 741 6
Q9JL2 6	CO N	NFPDTAQLLMPQLNAAASMSIKSSDK	M10:+15.995,M21:+15.995,K28:+114.043	105 0.86 6	314 9.57 4	0.06 056 1
Q9JL2 6	INF	MGNAAGSAEQPAGPTASPPKQPAVVK	M1:+15.995,K26:+114.043	648. 074 2	258 8.26 5	0.06 568
Q9JL2 6	INF	LNCMNLPPDKVQLLSQYDNEK	C3:+45.988,M4:+15.995,K21:+114.043	131 9.62	263 7.22 4	0.06 337 3
Q9JLJ 2	INF	CWKSAPALACGNAMIFKPSFPTVPSALLAEIYTK	C1:+45.988,C10:+45.988,M14:+15.995,K17:+1 14.043	132 0.99 2	395 9.95 3	0.04 938 8
Q9JLJ 2	INF	TCYINNYNVSPVELPFGGYKK	C2:+45.988,K20:+114.043	856. 075 7	256 5.20 4	0.04 423
Q9JLQ 2	INF	QILQAELLAVYGADPGTQDSSGK	K23:+114.043	825. 750 8	247 4.22 9	0.06 024 7
Q9JLV 6	CO N	LLVFTASGVKPPQK	K14:+114.043	520. 303 8	155 7.88 8	0.03 609 6
Q9JM 14	INF	GFLANEQYGALRPDLAEKVASVYESPGFFLNLEP	K18:+114.043	128 5.98	385 4.91 6	0.08 075 6
Q9JM 76	INF	EMYTLGITNFPIPGEPGFPLNAIYAKPASK	M2:+15.995,K26:+114.043,K30:+114.043	870. 943 7	347 9.74 4	0.04 750 8
Q9JM A1	CO N	VNQQPANANDKNSPPK	K15:+114.043	882. 935 4	176 3.85 5	0.09 141
Q9JM A1	CO N	DLFDSMDK	M6:+15.995,K8:+114.043	550. 732 5	109 9.44 9	0.07 090 1
Q9JM A1	INF	DLFDSMDK	M6:+15.995,K8:+114.043	550. 732 5	109 9.44 9	0.02 478 7
Q9JM A1	INF	ALYIKSSK	K8:+114.043	512. 295 9	102 2.57 6	0.09 462 2
Q9JM H6	INF	FDLIIGGGSGGLAAAK	K17:+114.043	837. 465 2	167 2.91 5	0.05 322 5
Q9QU M0	CO N	TGAVFLCPWKANGGK	C7:+45.988,K15:+114.043	854. 919 2	170 7.82 3	0.09 922 2
Q9QU M0	INF	TGAVFLCPWKANGGK	C7:+45.988,K15:+114.043	854. 919 2	170 7.82 3	0.05 767 9
Q9QU M9	CO N	PKLLDSSTVTHLFK	K3:+114.043	454. 497 2	181 3.95 7	0.03 854 5

Q9QU M9	INF	PDKLLDSSTVTHLFK	K3:+114.043	454. 497 2	181 3.95 7	0.05 025 6
Q9QU M9	INF	FKPSEIEVGVTVENPK	K2:+114.043	993. 531 3	198 5.04 7	0.03 229 7
Q9QU R6	CO N	NVKLPEADDIQYPSMLLLTADHDDR	K3:+114.043	995. 154 3	298 2.43 9	0.04 996 1
Q9QU R6	INF	NILQLHDLTTGALLK	K15:+114.043	588. 672 5	176 2.99 4	0.03 639
Q9QX K3	INF	ILKPNFAAAWEEVGDAFEKEETFALSSTK	K19:+114.043,K29:+114.043	115 2.90 4	345 5.68 9	0.05 463 2
Q9QX K3	INF	LENEAVRAAAVSALAK	K16:+114.043	863. 976 5	172 5.93 7	0.02 259 3
Q9QX K3	INF	DKVSSVASSALVSSLHMMK	K2:+114.043,M18:+15.995	703. 022 8	210 6.04 5	0.05 562 4
Q9QX K3	INF	QMALNATYIFNGLTVSIPGMEKAL	Q1:-17.027,K22:+114.043	134 0.18	267 8.34 4	0.03 876 9
Q9QX S1	INF	IRPGTAFELLEQAATGYVIDPIK	K24:+114.043	896. 485 5	268 6.43 3	0.05 436 4
Q9QX S1	INF	ELLQQQKELAQEQAR	K7:+114.043	963. 506 2	192 4.99 7	0.05 866 5
Q9QX Z0	CO N	MLEEEGLDLLGLK	K14:+114.043	837. 935 1	167 3.85 5	0.06 369 3
Q9QX Z0	INF	KVEVYQQQIEMEK	K1:+114.043,M11:+15.995	891. 441 2	178 0.86 7	0.00 943 1
Q9QX Z0	INF	GDSGSGSKTEQSVALLEQK	K19:+114.043	101 8.00 1	203 3.98 7	0.08 075 6
Q9QX Z0	INF	MGVLGPLSIDPNMLK	M1:+15.995,K15:+114.043	857. 947 6	171 3.88	0.09 102 3
Q9QY B5	CO N	FTHGVAMSGGGGVNMASHQKWK	M15:+15.995,K20:+114.043	120 9.06 6	241 6.11 7	0.05 264 8
Q9QY B5	CO N	YKAFTHGVAMSGGGGVNMASHQK	K2:+114.043,M10:+15.995,K23:+114.043	860. 401 4	257 8.18 1	0.03 854 5
Q9QY B5	CO N	AFHYIFNVQMACEIQVQAVAGAGGVDNLLVLDLQKY K	M10:+15.995,C12:+45.988,K35:+114.043	141 4.71 2	424 1.11 2	0.07 963 6
Q9QY B5	INF	KGHNPSGLLALQQIADY	K1:+114.043	970. 005 8	193 7.99 6	0.07 125 9
Q9QY C0	CO N	CIVHIHTPAGAAVSAMKCGLLPISPEALS	C1:+45.988,M16:+15.995,K17:+114.043,C18:+ 45.988	107 4.53 9	322 0.59 5	0.05 895 8
Q9QY C0	CO N	EQNLQDIKTAGPQSQVLCGVMM	K8:+114.043,C18:+45.988,M21:+15.995	128 3.59 3	256 5.17	0.02 934 5
Q9QZ 88	CO N	GDFDENLNYPEQKVVTVGQFK	K13:+114.043,K21:+114.043	885. 761 6	265 4.26 1	0.05 734

Q9QZ E5	INF	ILYLINQGEHLGTTEATEAFFAMTKLFQSNDP	M23:+15.995,K25:+114.043	124 3.94 2	372 8.80 3	0.06 465 9
Q9QZ E5	INF	AGAVSALAKFGAQNEEMLP	K9:+114.043,M17:+15.995	101 7.50 2	203 2.98 9	0.04 092 9
Q9QZ E5	INF	IVKFLGMHPCER	K3:+114.043,C10:+45.988	795. 391 8	158 8.76 8	0.04 285 7
Q9QZ Q8	INF	LEVAGAAISAGHGLPAK	K17:+114.043	838. 460 5	167 4.90 5	0.09 423
Q9R0 P3	CO N	AVYLPPQAESGKCPALYWLSGLTCTEQNFISK	K12:+114.043,C13:+45.988,C24:+45.988,K32:+ 114.043	127 8.93 9	383 3.79 3	0.05 734
Q9R1 12	INF	ITMYLMKADMMMPFLYWNMML	K7:+114.043,M11:+15.995,M18:+15.995,M19: +15.995	135 3.10 5	270 4.19 5	0.05 526 5
Q9R1 90	INF	KPNPNQIISVGSKPGMNGAGFQKGLTCESCHTTQSAQ WYAWGPPNMQCR	M16:+15.995,K23:+114.043,C27:+45.988,C30: +45.988,C48:+45.988	139 4.12 3	557 2.45 9	0.04 509 1
Q9R1 90	INF	ANGRPLASGIRSSSQPAK	K19:+114.043	991. 530 5	198 1.04 5	0.05 866 5
Q9R1 P0	INF	QDYKEGEMTLK	K4:+114.043	728. 343 4	145 4.67 1	0.05 993 8
Q9R1 P1	CO N	EPNMDPEHLFETISQAMLNAVDRDAVSGMGVIVHVI EK	M4:+15.995,M29:+15.995,K38:+114.043	144 6.7	433 7.07 7	0.04 173 1
Q9R1 P1	INF	AVSGMGVIVHVIEK	M5:+15.995,K14:+114.043	784. 927 5	156 7.83 9	0.08 036 3
Q9R1T 2	CO N	SIKFFTGDVFGYHGYTFANLGEHEFVEEK	K3:+114.043	116 1.55	348 1.62 6	0.08 582
Q9R1T 2	INF	VLIVGMKGLGAEIAK	M6:+15.995,K15:+114.043	543. 652 2	162 7.93 3	0.02 743 3
Q9R1T 4	CO N	KAAAELLQSQGSQAG	K1:+114.043	786. 903	157 1.79	0.04 694 9
Q9R1T 4	INF	AAAELLQSQGSQAGGSQTLK	K20:+114.043	103 0.02 5	205 8.03 4	0.04 617 3
Q9R2 57	CO N	GMTVPVSFALFPNEDGSLQK	M2:+15.995,K20:+114.043	113 4.05 5	226 6.09 4	0.07 598 5
Q9WT M5	CO N	EEGKAEIIPGVLFIDEVHMLDIESFSFLNR	E1:-18.011,K4:+114.043	118 1.93 3	354 2.77 5	0.04 042 1
Q9WT X6	INF	FLQQNPVTEYMKK	K13:+114.043	870. 443 5	173 8.87 1	0.02 154 9
Q9WU 00	INF	VTAHLAAAGPVGMAAAAVATGKK	K23:+114.043	750. 079 7	224 7.21 6	0.06 632 8
Q9WU 78	CO N	PPPAYQSSPAAGHAAAPPTAPRTMPPAKPQPPARPP PPVLPANR	K29:+114.043	115 9.11 5	463 2.42 9	0.05 803 7
Q9WU 78	INF	DLDPIGKATLVKPTPVNVPSQK	K23:+114.043	633. 362	252 9.41 7	0.04 530 6

Q9WU A2	CO N	AQGASDVVLYK	K11:+114.043	632. 830 8	126 3.64 6	0.05 111 3
Q9WU A2	CO N	EDAAIAYGYNNIQMTLPK	E1:-18.011,K18:+114.043	105 4.51	210 7.00 4	0.04 589 2
Q9WU A2	CO N	DRIMQLLDVPPGEESGGYMIK	M19:+15.995,K21:+114.043	123 9.60 4	247 7.19 3	0.06 871 7
Q9WU A2	INF	IHACDIVEDAAIAYGYNNIQMTLPKTYTIANQFPLNK	C4:+45.988,M21:+15.995,K37:+114.043	144 4.03 8	432 9.09 1	0.06 666 4
Q9WU A2	INF	IFVGGQSIGKLGVLHPDVITK	K10:+114.043,K21:+114.043	120 3.67 9	240 5.34 3	0.03 229 7
Q9WU A2	INF	NIFIECTGTDFTK	C6:+45.988,K13:+114.043	824. 871 6	164 7.72 8	0.06 088 5
Q9WU A3	CO N	EEPFDIGDLQSNVHLTEKMK	K19:+114.043,M20:+15.995	128 0.12 4	255 8.23 2	0.05 767 9
Q9WU A3	CO N	EIGWADVGGWVGQGSILGTR	K21:+114.043	787. 065	235 8.17 2	0.03 780 3
Q9WU A3	CO N	MVMVPATVSNNVPGSDFSIGADTALNTITDTCRIK	C32:+45.988,K36:+114.043	130 5.28 7	391 2.83 7	0.07 492 7
Q9WU A3	CO N	EKHEAFCVPMVMVPATVSNNVPGSDFSIGADTALNTI T	E1:-18.011,K2:+114.043,C7:+45.988	102 6.98 5	410 3.91	0.08 956 6
Q9WU A3	INF	QMHSHSINALLIIGGFEAYLGLLELAAAREK	M2:+15.995,K31:+114.043	116 5.95 3	349 4.83 5	0.05 668 8
Q9WU A3	INF	AMEWISAKLK	K8:+114.043,K10:+114.043	702. 869 4	140 3.72 3	0.07 419 6
Q9WU M3	INF	GGGAFMVLPNKTGR	K12:+114.043	816. 438 5	163 0.86 1	0.04 724 1
Q9WU M4	INF	WQIPENGLTSLTEPVVILEGHSK	K24:+114.043	138 7.74	277 3.46 5	0.05 498 6
Q9WV G5	CO N	EFSLGNVHLIGYSLGAHVAGYAGNFVKGTVGR	K27:+114.043	113 5.58 9	340 3.74 3	0.08 956 6
Q9WV K4	CO N	ADVDDKGLLDDEEFALANHLIK	K5:+114.043	852. 426 2	255 4.25 5	0.00 112 9
Q9WV K4	CO N	QEESLMPSQAVKGGAFDGTMNGP	Q1:-17.027,K12:+114.043,M20:+15.995	822. 030 4	246 3.06 8	0.05 734
Q9WV K4	INF	ADVDDKGLLDDEEFALANHLIK	K5:+114.043	852. 426 2	255 4.25 5	0.00 091 7
Q9WV K4	INF	FHEFHSPALEDADFNDKPMVLLVGQYSTG	K17:+114.043,M19:+15.995	113 2.19 5	339 3.56 1	0.01 716 8
Q9WV Q5	INF	AAVMATLLFPGQEFKITHQEM	M4:+15.995,K15:+114.043,M21:+15.995	627. 812 6	250 7.21 9	0.02 566 2
Q9WV Q5	INF	IQPEDMFVCDINEQDISGPPASKK	M6:+15.995,C9:+45.988,K23:+114.043	141 9.14 4	283 6.27 2	0.07 963 6

Q9Z0E 6	CO N	QKQLLAEQENIIAAK	K15:+114.043	906. 005 3	180 9.99 5	0.00 430 9
Q9Z0E 6	INF	QKQLLAEQENIIAAK	K15:+114.043	906. 005 3	180 9.99 5	0.00 775 7
Q9Z0 M6	CO N	SSGQHQCCHNSTVCKNTVGSYK	C7:+45.988,C13:+45.988,K14:+114.043	618. 514 1	247 0.02 5	0.03 854 5
Q9Z0 M6	CO N	ELDWAVTAGAKISENGSSVAGILSSPNMEK	K11:+114.043,M28:+15.995,K30:+114.043	110 2.53 7	330 4.58 8	0.07 286 9
Q9Z0 M6	CO N	EDVDECSSGQHQCCHNSTVCKNTVGSYK	E1:- 18.011,C6:+45.988,C13:+45.988,C19:+45.988, K20:+114.043	106 3.74 7	318 8.21 9	0.09 840 5
Q9Z0 M6	INF	SCVCKPGFSSEK	C2:+45.988,C4:+45.988,K12:+114.043	739. 301 6	147 6.58 8	0.05 264 8
Q9Z0 N1	CO N	FAEHNDLQYAAPGGLIGVGTKIDPTLCR	K21:+114.043,C27:+45.988	779. 888 4	311 5.52 2	0.05 139 9
Q9Z0 N1	INF	EVDDLKGGVAGGSILK	K16:+114.043	557. 969 1	167 0.88 4	0.03 666 5
Q9Z0 N1	INF	AVMDAALLIAGNESCPQPQTSEHLAAIEIMK	M3:+15.995,C16:+45.988,M31:+15.995,K32:+ 114.043	889. 935	355 5.70 9	0.04 071 8
Q9Z11 0	CO N	EMMLVTSGAVAFGKQR	M2:+15.995,K14:+114.043	618. 978 8	185 3.91 3	0.03 780 3
Q9Z1B 7	INF	QDINKTAWELPK	K5:+114.043	519. 607 6	155 5.8	0.08 392 4
Q9Z1F 9	INF	AEKGDGAELIWDK	K3:+114.043	515. 923 5	154 4.74 7	0.05 6
Q9Z1 N5	INF	NVKVAVFFGGLSIK	K14:+114.043	796. 962 1	159 1.90 9	0.04 644 6
Q9Z1 N5	INF	DYEDDEVETAAGADGTEAPAKK	K21:+114.043	119 8.52 3	239 5.03	0.03 207 1
Q9Z1 N5	INF	LDYEDDEVETAAGADGTEAPAK	K22:+114.043	119 1.01 7	238 0.01 9	0.05 803 7
Q9Z1 Q5	CO N	NLLPKLHIVQVCK	C13:+45.988,K14:+114.043	588. 672 9	176 2.99 5	0.02 934 5
Q9Z1 Q9	CO N	SYADTELIPACGATLPALGLRGPQDPQAALGALGK	C12:+45.988,K37:+114.043	931. 726 9	372 2.87 6	0.06 401 4
Q9Z1 Q9	CO N	QGLYDQLLNSNLDPSEVEK	Q1:-17.027,K19:+114.043	753. 697 8	225 8.07	0.03 533 2
Q9Z1 Q9	INF	ATLPALGLRGPQDPQAALGALGK	K24:+114.043	796. 112 1	238 5.31 3	0.08 278 5
Q9Z1 Q9	INF	APASLCVTPYPEPSECSWKDPE	C6:+45.988,C16:+45.988,K19:+114.043	130 6.54 5	261 1.07 5	0.05 962 2
Q9Z1Z 2	CO N	ITPYGYFLISACKDGKPMRLR	C12:+45.988,K13:+114.043,K16:+114.043	127 4.13 2	254 6.24 9	0.04 694 9

Q9Z1Z 2	INF	PMLRQGDTGDWIGTFLGHK	M2:+15.995,K19:+114.043	753. 704 6	225 8.09	0.01 016 9
Q9Z2 D6	INF	KPGSVVAAAAAEAK	K14:+114.043	692. 383 7	138 2.75 2	0.05 498 6
Q9Z2 N8	CO N	FSSWIGGSILASLGTFFQQMWISKQEYEEGGK	M19:+15.995,K23:+114.043	899. 436 3	359 3.71 4	0.05 171 8
Q9Z2 U1	CO N	LNATNIELATVQPGQNFHMFTEEELEVIK	K22:+114.043,K30:+114.043	122 4.61 8	367 0.83	0.00 091 7
Q9Z2 U1	CO N	LLFGGVDEK	K9:+114.043	546. 290 8	109 0.56 6	0.08 036 3
Q9Z2 U1	CO N	SIEKIVEIDAHIGCAMSGLIADAK	C14:+45.988,K24:+114.043	661. 834 6	264 3.30 7	0.03 809
Q9Z2 U1	INF	LNATNIELATVQPGQNFHMFTEEELEVIK	K22:+114.043,K30:+114.043	122 4.61 8	367 0.83	0.00 179 9
Q9Z2 U1	INF	DPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQ CDAR	M5:+15.995,K21:+114.043,C37:+45.988	147 6.02 3	442 5.04 4	0.05 734
Q9Z2 U1	INF	TAIGIQTSEGVCLAVEK	C12:+45.988,K17:+114.043	939. 969 3	187 7.92 3	0.05 294
Q9Z2 W0	INF	PKSFMISADMAHAVHPNYSKD	K2:+114.043,M5:+15.995,M10:+15.995,K21:+ 114.043	130 3.59 2	260 5.16 9	0.05 6
V9GX 06	CO N	TCYLEKPAMYDYIKK	C2:+45.988,K6:+114.043,K15:+114.043	107 0.5	213 8.98 4	0.07 741 6

Table S3- Proteasome subunits identified and ratios of spectral counts calculated

Accession	Protein Name	Spectral Counts INF(-gg*)	Spectral Counts CON (-gg*)
Q3TXS7	26S proteasome non-ATPase regulatory subunit 1	152(29)	175(26)
Q8BG32	26S proteasome non-ATPase regulatory subunit 11	64(1)	54(0)
Q9D8W5	26S proteasome non-ATPase regulatory subunit 12	35(0)	70(0)
Q9WVJ2	26S proteasome non-ATPase regulatory subunit 13	88(0)	63(0)
O35593	26S proteasome non-ATPase regulatory subunit 14	76(1)	81(3)
Q8VDM4	26S proteasome non-ATPase regulatory subunit 2	326(40)	271(38)
P14685	26S proteasome non-ATPase regulatory subunit 3	87	65
O35226	26S proteasome non-ATPase regulatory subunit 4	2(1)	7
Q8BJY1	26S proteasome non-ATPase regulatory subunit 5	28(2)	37(2)
Q99JI4	26S proteasome non-ATPase regulatory subunit 6	80(1)	80(1)
P26516	26S proteasome non-ATPase regulatory subunit 7	75	93
Q9CX56	26S proteasome non-ATPase regulatory subunit 8	7(1)	12(3)
P46471	26S protease regulatory subunit 7	63	72(1)
P62192	26S protease regulatory subunit 4	29	65(2)
P62334	26S protease regulatory subunit 10B	53	58(1)
O88685	26S protease regulatory subunit 6A	139(2)	88
P62196	26S protease regulatory subunit 8	36(2)	47(1)
Q9R1P4	Proteasome subunit alpha type-1	121	79
P49722	Proteasome subunit alpha type-2	230(3)	264
O70435	Proteasome subunit alpha type-3	78	98
Q9R1P0	Proteasome subunit alpha type-4	136(2)	46
Q9Z2U1	Proteasome subunit alpha type-5	179(3)	139(3)
Q9QUM9	Proteasome subunit alpha type-6	121(2)	168(3)
Q9Z2U0	Proteasome subunit alpha type-7	143	103
O09061	Proteasome subunit beta type-1	202(2)	162(1)
Q9R1P3	Proteasome subunit beta type-2	163	100
Q9R1P1	Proteasome subunit beta type-3	94(1)	83(1)
P99026	Proteasome subunit beta type-4	164	175(1)
<i>O55234</i>	<i>Proteasome subunit beta type-5</i>	48	27
<i>Q60692</i>	<i>Proteasome subunit beta type-6</i>	127(1)	103(1)
<i>P70195</i>	<i>Proteasome subunit beta type-7</i>	140(1)	81(1)
<i>O35955</i>	<i>Proteasome subunit beta type-10</i>	26(1)	31
<i>P28063</i>	<i>Proteasome subunit beta type-8</i>	98	77
<i>P28076</i>	<i>Proteasome subunit beta type-9</i>	60(1)	64(1)

† Italics indicate the subunit belongs uniquely to the immunoproteasome.

* Entries in parenthesis indicate the number of GG-tagged peptides identified

Table S4- Truncated proteoforms identified in MDSC-derived exosomes using top-down mass spectrometry.

Protein Accessions	Protein Name	Expected Mass (Da)	Observed Mass (Da)
P0CG50	Polyubiquitin-C	8,559	2853.45838
P0CG50	Polyubiquitin-C	8,559	3426.67838
P0CG50	Polyubiquitin-C	8,559	3426.69958
P27005	Protein S100-A8	10,295	3338.64788
P60710	Actin, cytoplasmic 1	41,737	5994.40498
P60710	Actin, cytoplasmic 1	41,737	5994.40638
P60710	Actin, cytoplasmic 1	41,737	6097.47508
P60710	Actin, cytoplasmic 1	41,737	6845.31728
P60710	Actin, cytoplasmic 1 (Da)	41,737	6845.36118
P60710	Actin, cytoplasmic 1	41,737	6958.42988
P60710	Actin, cytoplasmic 1	41,737	6958.43708
P60710	Actin, cytoplasmic 1	41,737	6958.44028
P60710	Actin, cytoplasmic 1	41,737	6974.44178
P60710	Actin, cytoplasmic 1	41,737	6974.44328
P60710	Actin, cytoplasmic 1	41,737	6990.41968
P60710	Actin, cytoplasmic 1	41,737	6990.43668
Q91Z25	Actin-related protein 2/3 complex subunit 1B	41,498	6456.23578
Q91Z25	Actin-related protein 2/3 complex subunit 1B	41,498	6584.32228
Q91Z25	Actin-related protein 2/3 complex subunit 1B	41,498	6584.32808
Q91VB8	Alpha globin 1	15,112	5130.76458
Q91VB8	Alpha globin 1	15,112	6402.45148
Q91VB8	Alpha globin 1	15,112	6402.47218
Q91VB8	Alpha globin 1	15,112	8574.32888
Q91VB8	Alpha globin 1	15,112	8574.33008
Q91VB8	Alpha globin 1	15,112	8574.33428
Q91VB8	Alpha globin 1	15,112	9846.05408
Q497J0	CDNA sequence BC100530	10,959	5482.10538
Q497J0	CDNA sequence BC100530	10,959	5893.37278
Q497J0	CDNA sequence BC100530	10,959	10863.49548
Q497J0	CDNA sequence BC100530	10,959	10863.50538
Q497J0	CDNA sequence BC100530	10,959	10863.53438
Q497J0	CDNA sequence BC100530	10,959	10863.54028
Q497J0	CDNA sequence BC100530	10,959	10863.54548
Q497J0	CDNA sequence BC100530	10,959	10863.56128
Q497J0	CDNA sequence BC100530	10,959	10939.46658
Q497J0	CDNA sequence BC100530	10,959	10939.50708
Q497J0	CDNA sequence BC100530	10,959	10955.47888

G3UYK8	Coronin	43,261	5018.61218
G3UYK8	Coronin	43,261	4846.52298
D3Z510	Fructose-bisphosphate aldolase A	14,177	6399.35828
D3Z510	Fructose-bisphosphate aldolase A	14,177	8546.52148
D3Z510	Fructose-bisphosphate aldolase A	14,177	8546.56008
D3Z510	Fructose-bisphosphate aldolase A	14,177	8693.61298
D3Z510	Fructose-bisphosphate aldolase A	14,177	8693.64508
P62827	GTP-binding nuclear protein Ran	24,423	3084.38738
P62827	GTP-binding nuclear protein Ran	24,423	3085.38168
P62827	GTP-binding nuclear protein Ran	24,423	3102.41068
Q61646	Haptoglobin	38,752	9462.53098
Q61646	Haptoglobin	38,752	9478.52528
P01942	Hemoglobin subunit alpha	15,085	5130.76458
P01942	Hemoglobin subunit alpha	15,085	6402.45148
P01942	Hemoglobin subunit alpha	15,085	6402.47218
P01942	Hemoglobin subunit alpha	15,085	6873.69618
P01942	Hemoglobin subunit alpha	15,085	8560.34168
P01942	Hemoglobin subunit alpha	15,085	8560.34298
P01942	Hemoglobin subunit alpha	15,085	8560.34868
P01942	Hemoglobin subunit alpha	15,085	9846.05408
P01942	Hemoglobin subunit alpha	15,085	10289.25308
P01942	Hemoglobin subunit alpha	15,085	10289.25538
P01942	Hemoglobin subunit alpha	15,085	10289.25928
P01942	Hemoglobin subunit alpha	15,085	10303.28988
P02088	Hemoglobin subunit beta-1	15,840	3336.72928
P02088	Hemoglobin subunit beta-1	15,840	6526.44448
P02088	Hemoglobin subunit beta-1	15,840	6597.48128
P02088	Hemoglobin subunit beta-1	15,840	7460.85888
P02088	Hemoglobin subunit beta-1	15,840	7460.90928
P02088	Hemoglobin subunit beta-1	15,840	7607.93448
P02088	Hemoglobin subunit beta-1	15,840	7607.93478
P02088	Hemoglobin subunit beta-1	15,840	7607.94348
P02088	Hemoglobin subunit beta-1	15,840	8109.21948
P02088	Hemoglobin subunit beta-1	15,840	8109.22808
P02088	Hemoglobin subunit beta-1	15,840	8109.24748
P02089	Hemoglobin subunit beta-2	15,878	3475.82358
P02089	Hemoglobin subunit beta-2	15,878	6466.45188
P02089	Hemoglobin subunit beta-2	15,878	6957.43348
P02089	Hemoglobin subunit beta-2	15,878	8081.29658
P02089	Hemoglobin subunit beta-2	15,878	8081.31298
F8WIX8	Histone H2A	13,607	7891.53558
P22752	Histone H2A type 1-B	14,135	7919.54598

Q8CGP6	Histone H2A type 1-H	13,950	7734.44208
P27661	Histone H2AX	15,143	8960.05768
P27661	Histone H2AX	15,143	8960.04798
P70696	Histone H2B type 1-A	14,237	6511.53128
P70696	Histone H2B type 1-A	14,237	6541.56558
P70696	Histone H2B type 1-A	14,237	6640.60268
P70696	Histone H2B type 1-A	14,237	6988.74528
P70696	Histone H2B type 1-A	14,237	9388.06808
P70696	Histone H2B type 1-A	14,237	9404.00798
Q64475	Histone H2B type 1-B	13,952	6541.55338
Q64475	Histone H2B type 1-B	13,952	6640.59568
Q64475	Histone H2B type 1-B	13,952	6640.60058
Q64475	Histone H2B type 1-B	13,952	6640.60268
Q64475	Histone H2B type 1-B	13,952	6874.70168
Q64475	Histone H2B type 1-B	13,952	6988.74528
Q64475	Histone H2B type 1-B	13,952	6988.75198
Q64475	Histone H2B type 1-B	13,952	9109.91838
Q64475	Histone H2B type 1-B	13,952	9109.92928
Q64475	Histone H2B type 1-B	13,952	9372.03028
Q64475	Histone H2B type 1-B	13,952	9372.05648
Q64475	Histone H2B type 1-B	13,952	9388.02148
Q64475	Histone H2B type 1-B	13,952	9388.06808
Q64475	Histone H2B type 1-B	13,952	9404.04168
Q6ZWY9	Histone H2B type 1-C/E/G	13,906	6511.52718
Q6ZWY9	Histone H2B type 1-C/E/G	13,906	6511.53128
Q6ZWY9	Histone H2B type 1-C/E/G	13,906	6610.60128
Q6ZWY9	Histone H2B type 1-C/E/G	13,906	6610.60658
Q6ZWY9	Histone H2B type 1-C/E/G	13,906	6844.69548
Q6ZWY9	Histone H2B type 1-C/E/G	13,906	6958.73018
Q6ZWY9	Histone H2B type 1-C/E/G	13,906	9079.82558
Q6ZWY9	Histone H2B type 1-C/E/G	13,906	9079.88568
Q6ZWY9	Histone H2B type 1-C/E/G	13,906	9342.05328
Q6ZWY9	Histone H2B type 1-C/E/G	13,906	9373.99308
P10853	Histone H2B type 1-F/J/L	13,936	6541.55338
P10853	Histone H2B type 1-F/J/L	13,936	6640.59568
P10853	Histone H2B type 1-F/J/L	13,936	6640.60268
P10853	Histone H2B type 1-F/J/L	13,936	6874.70168
P10853	Histone H2B type 1-F/J/L	13,936	6988.74528
P10853	Histone H2B type 1-F/J/L	13,936	6988.75198
P10853	Histone H2B type 1-F/J/L	13,936	9372.03028
P10853	Histone H2B type 1-F/J/L	13,936	9372.05648
P10853	Histone H2B type 1-F/J/L	13,936	9372.99078
P10853	Histone H2B type 1-F/J/L	13,936	9388.02148

P10853	Histone H2B type 1-F/J/L	13,936	9388.06808
P10853	Histone H2B type 1-F/J/L	13,936	9404.04168
Q64478	Histone H2B type 1-H	13,920	6511.52718
Q64478	Histone H2B type 1-H	13,920	6511.53128
Q64478	Histone H2B type 1-H	13,920	6610.60128
Q64478	Histone H2B type 1-H	13,920	6610.60658
Q64478	Histone H2B type 1-H	13,920	6844.69548
Q64478	Histone H2B type 1-H	13,920	6958.73018
Q64478	Histone H2B type 1-H	13,920	9079.82558
Q64478	Histone H2B type 1-H	13,920	9079.88568
Q64478	Histone H2B type 1-H	13,920	9342.01538
Q64478	Histone H2B type 1-H	13,920	9342.04278
Q64478	Histone H2B type 1-H	13,920	9342.05328
Q8CGP2-1	Histone H2B type 1-K	13,920	6541.55338
Q8CGP1	Histone H2B type 1-K	13,920	6624.60298
Q8CGP1	Histone H2B type 1-K	13,920	6624.61018
Q8CGP1	Histone H2B type 1-K	13,920	6624.63428
Q8CGP2-1	Histone H2B type 1-K	13,920	6640.59568
Q8CGP2-1	Histone H2B type 1-K	13,920	6640.60268
Q8CGP2-1	Histone H2B type 1-K	13,920	6874.70168
Q8CGP2-1	Histone H2B type 1-K	13,920	6988.74528
Q8CGP2-1	Histone H2B type 1-K	13,920	6988.75198
Q8CGP2-1	Histone H2B type 1-K	13,920	9372.02748
Q8CGP2-1	Histone H2B type 1-K	13,920	9372.03028
Q8CGP2-1	Histone H2B type 1-K	13,920	9372.05648
Q8CGP2-1	Histone H2B type 1-K	13,920	9388.02148
Q8CGP2-1	Histone H2B type 1-K	13,920	9388.06808
Q8CGP2-1	Histone H2B type 1-K	13,920	9404.04168
P10854	Histone H2B type 1-M	13,936	6511.52718
P10854	Histone H2B type 1-M	13,936	6511.53128
P10854	Histone H2B type 1-M	13,936	6610.59758
P10854	Histone H2B type 1-M	13,936	6610.60128
P10854	Histone H2B type 1-M	13,936	6610.60658
P10854	Histone H2B type 1-M	13,936	6844.69548
P10854	Histone H2B type 1-M	13,936	6958.73018
P10854	Histone H2B type 1-M	13,936	8257.75018
P10854	Histone H2B type 1-M	13,936	9079.82558
P10854	Histone H2B type 1-M	13,936	9079.88568
P10854	Histone H2B type 1-M	13,936	9342.02608
P10854	Histone H2B type 1-M	13,936	9342.04278
Q64525	Histone H2B type 2-B	13,920	6511.52718
Q64525	Histone H2B type 2-B	13,920	6511.53128
Q64525	Histone H2B type 2-B	13,920	6610.60128

Q64525	Histone H2B type 2-B	13,920	6610.60658
Q64525	Histone H2B type 2-B	13,920	6844.69548
Q64525	Histone H2B type 2-B	13,920	6958.73018
Q64525	Histone H2B type 2-B	13,920	9079.82558
Q64525	Histone H2B type 2-B	13,920	9079.88568
Q64525	Histone H2B type 2-B	13,920	9342.01538
Q64525	Histone H2B type 2-B	13,920	9342.04278
Q64525	Histone H2B type 2-B	13,920	9342.05328
Q9D2U9	Histone H2B type 3-A	13,994	9372.01988
Q9D2U9	Histone H2B type 3-A	13,994	9373.99608
O08692	Neutrophilic granule protein	19,332	989.66988
O08692	Neutrophilic granule protein	19,332	3677.96818
O08692	Neutrophilic granule protein	19,332	6918.38278
O08692	Neutrophilic granule protein	19,332	7552.94348
O08692	Neutrophilic granule protein	19,332	7552.94468
O08692	Neutrophilic granule protein	19,332	14818.90698
O08692	Neutrophilic granule protein	19,332	14819.94918
O08692	Neutrophilic granule protein	19,332	14820.94838
O08692	Neutrophilic granule protein	19,332	14820.95058
O08692	Neutrophilic granule protein	19,332	14832.93578
O08692	Neutrophilic granule protein	19,332	14835.97618
O08692	Neutrophilic granule protein	19,332	14836.00808
O08692	Neutrophilic granule protein	19,332	14836.02428
O08692	Neutrophilic granule protein	19,332	14836.94118
O08692	Neutrophilic granule protein	19,332	14850.94208
O08692	Neutrophilic granule protein	19,332	14851.96348
P52480	Pyruvate kinase PKM	57,845	7649.78618