

Spot ID	70nM MG132 / C	Protein Name	UniProt Accession	Sequence Coverage	Total Ion Score
179	1,56	Aconitate hydratase	ACON	31%	123
180	1,19	Aconitate hydratase	ACON	28%	89
181	2,40	Aconitate hydratase	ACON	31%	209
552	0,89	Actin	ACTG	64%	370
648	1,20	Actin	ACTG	53%	371
662	2,57	Actin	ACTG	52%	394
719	1,30	Actin	ACTG	60%	334
723	0,68	Actin	ACTG	58%	421
726	0,78	Actin	ACTG	67%	365
733	0,84	Actin	ACTG	65%	536
757	0,62	Actin	ACTG	53%	382
780	1,19	Actin	ACTG	29%	136
273	1,49	Apoptosis-inducing factor 1	AIFM1	30%	33
676	1,71	Fructose-bisphosphate aldolase A	ALDOA	47%	156
836	1,24	Fructose-bisphosphate aldolase A	ALDOA	54%	84
837	1,18	Fructose-bisphosphate aldolase A	ALDOA	54%	169
781	0,00	Annexin A2	ANXA2	54%	219
820	1,85	Annexin A2	ANXA2	58%	273
903	1,34	Annexin A2	ANXA2	66%	262
947	0,62	Annexin A2	ANXA2	63%	246
1272	0,39	Actin-related protein 2/3 complex subunit 5	ARPC5	54%	60
1370	0,30	Actin-related protein 2/3 complex subunit 5	ARPC5	45%	58
524	1,35	ATP synthase subunit alpha	ATPA	57%	298
579	0,83	ATP synthase subunit alpha	ATPA	58%	304
553	0,83	ATP synthase subunit beta	ATPB	54%	482
566	0,76	ATP synthase subunit beta	ATPB	60%	528
129	1,36	C-1-tetrahydrofolate synthase	C1TC	36%	106
130	2,43	C-1-tetrahydrofolate synthase	C1TC	34%	95
131	2,93	C-1-tetrahydrofolate synthase	C1TC	38%	131
352	1,51	60 kDa heat shock protein	CH60	51%	287
393	1,12	60 kDa heat shock protein	CH60	51%	287
439	0,74	60 kDa heat shock protein	CH60	40%	73

445	0,83	60 kDa heat shock protein	CH60	52%	278
448	1,20	60 kDa heat shock protein	CH60	50%	304
449	1,50	60 kDa heat shock protein	CH60	56%	414
748	0,78	Citrate synthase	CISY	30%	259
1151	0,68	Chloride intracellular channel protein 1	CLIC1	50%	196
1347	1,45	Cofilin-1	COF1	36%	53
1230	1,52	Cofilin-2	COF2	32%	37
331	1,45	Coronin-1B	COR1B	16%	53
1027	1,65	Cysteine-rich protein 2	CRIP2	31%	74
401	1,39	UPF0027 protein C22orf28	CV028	39%	81
467	1,24	UPF0027 protein C22orf28	CV028	38%	103
241	2,52	Probable ATP-dependent RNA helicase DDX17	DDX17	28%	43
370	1,38	Probable ATP-dependent RNA helicase DDX5	DDX5	39%	68
380	1,41	Probable ATP-dependent RNA helicase DDX5	DDX5	38%	87
526	1,29	Glutamate dehydrogenase 1	DHE3	34%	160
527	1,23	Glutamate dehydrogenase 1	DHE3	40%	180
535	1,86	Glutamate dehydrogenase 1	DHE3	27%	49
394	1,10	Dihydropyrimidinase-related protein 2	DPYL2	40%	152
346	1,35	Trifunctional enzyme subunit alpha	ECHA	51%	192
556	1,57	Elongation factor 1-alpha 1	EF1A1	31%	83
602	0,23	Elongation factor 1-alpha 1	EF1A1	33%	131
609	1,70	Elongation factor 1-alpha 1	EF1A1	32%	75
614	0,77	Elongation factor 1-alpha 1	EF1A1	31%	91
620	0,68	Elongation factor 1-alpha 1	EF1A1	30%	115
776	1,59	Elongation factor 1-alpha 1	EF1A1	26%	91
1011	0,63	Elongation factor 1-beta	EF1B	16%	43
905	1,83	Elongation factor 1-delta	EF1D	48%	205
1011	0,63	Elongation factor 1-delta	EF1D	45%	193
164	1,82	Elongation factor 2	EF2	24%	116
165	2,26	Elongation factor 2	EF2	28%	120
699	1,49	Elongation factor Tu	EFTU	44%	161
741	1,27	Elongation factor Tu	EFTU	50%	163
780	1,19	Elongation factor Tu	EFTU	46%	102

780	1,19	Eukaryotic translation initiation factor 3 subunit I	EIF3I	31%	34
990	1,44	ELAV-like protein 1	ELAV1	67%	130
657	0,89	Alpha-enolase	ENOA	44%	34
208	0,69	Endoplasmin	ENPL	28%	123
211	0,70	Endoplasmin	ENPL	29%	115
525	1,15	Fascin	FSCN1	47%	73
73	1,37	Far upstream element-binding protein 1	FUBP1	47%	136
237	1,85	Far upstream element-binding protein 2	FUBP1	50%	196
295	1,32	Far upstream element-binding protein 3	FUBP1	47%	109
297	1,49	Far upstream element-binding protein 4	FUBP1	50%	196
677	1,19	Fumarate hydratase	FUMH	33%	215
824	1,62	Glyceraldehyde-3-phosphate dehydrogenase	G3P	50%	300
854	1,55	Glyceraldehyde-3-phosphate dehydrogenase	G3P	51%	284
905	1,83	Glyceraldehyde-3-phosphate dehydrogenase	G3P	50%	192
34	1,24	Neutral alpha-glucosidase AB	GANAB	35%	82
96	1,67	Neutral alpha-glucosidase AB	GANAB	44%	68
947	0,62	Guanine nucleotide-binding protein subunit beta-2-like 1	GBLP	48%	161
1110	0,60	Rho GDP-dissociation inhibitor 1	GDIR1	46%	155
262	1,56	Stress-70 protein	GRP75	52%	434
286	0,84	Stress-70 protein	GRP75	27%	108
301	1,42	Stress-70 protein	GRP75	45%	234
180	1,19	78 kDa glucose-regulated protein	GRP78	34%	61
211	0,70	79 kDa glucose-regulated protein	GRP78	52%	453
244	0,69	80 kDa glucose-regulated protein	GRP78	57%	540
537	1,64	Glutathione reductase	GSHR	25%	103
1421	0,27	Histone H2B type 1-M	H2B1M	75%	106
1117	1,32	High mobility group protein B1	HMGB1	36%	66
1225	0,72	High mobility group protein B1	HMGB1	36%	113
1198	0,86	High mobility group protein B2	HMGB2	38%	49
473	1,25	Heterogeneous nuclear ribonucleoprotein H	HNRH1	51%	215
507	1,56	Heterogeneous nuclear ribonucleoprotein H	HNRH1	30%	32
562	1,41	Heterogeneous nuclear ribonucleoprotein H	HNRH1	53%	435
565	1,02	Heterogeneous nuclear ribonucleoprotein H	HNRH1	41%	123

1302	0,35	Heterogeneous nuclear ribonucleoprotein H	HNRH1	27%	158
563	1,29	Heterogeneous nuclear ribonucleoprotein H2	HNRH2	25%	159
754	1,26	Heterogeneous nuclear ribonucleoprotein H3	HNRH3	54%	228
854	1,55	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRPC	26%	185
657	0,89	Heterogeneous nuclear ribonucleoprotein D0	HNRPD	25%	44
683	1,11	Heterogeneous nuclear ribonucleoprotein D1	HNRPD	21%	54
780	1,19	Heterogeneous nuclear ribonucleoprotein D2	HNRPD	12%	38
646	1,50	Heterogeneous nuclear ribonucleoprotein F	HNRPF	48%	247
772	1,89	Heterogeneous nuclear ribonucleoprotein G	HNRPG	63%	214
301	1,42	Heterogeneous nuclear ribonucleoprotein K	HNRPK	44%	87
359	1,30	Heterogeneous nuclear ribonucleoprotein K	HNRPK	53%	137
360	1,35	Heterogeneous nuclear ribonucleoprotein K	HNRPK	52%	129
362	1,26	Heterogeneous nuclear ribonucleoprotein K	HNRPK	23%	40
368	1,42	Heterogeneous nuclear ribonucleoprotein K	HNRPK	55%	168
347	1,26	Heterogeneous nuclear ribonucleoprotein L	HNRPL	33%	176
353	1,43	Heterogeneous nuclear ribonucleoprotein L	HNRPL	37%	229
262	1,56	Heterogeneous nuclear ribonucleoprotein M	HNRPM	48%	50
371	1,48	Heat shock 70 kDa protein 1	HSP71	27%	31
271	1,65	Heat shock cognate 71 kDa	HSP7C	46%	431
1215	0,72	Heat shock protein beta-1	HSPB1	68%	331
875	1,21	Isocitrate dehydrogenase [NAD] subunit alpha	IDH3A	20%	49
364	1,87	Insulin-like growth factor 2 mRNA-binding protein 2	IF2B2	48%	67
1366	0,51	Eukaryotic translation initiation factor 5A-1	IF5A1	56%	108
157	1,40	Mitochondrial inner membrane protein	IMMT	26%	66
219	1,24	Mitochondrial inner membrane protein	IMMT	29%	67
378	1,43	Pyruvate kinase isozymes M1/M2	KPYM	62%	346
417	0,77	Pyruvate kinase isozymes M1/M2	KPYM	49%	113
434	1,30	Pyruvate kinase isozymes M1/M2	KPYM	50%	120
459	1,54	Pyruvate kinase isozymes M1/M2	KPYM	53%	90
1001	0,83	L-lactate dehydrogenase A	LDHA	35%	48
1294	1,52	Galectin-1	LEG1	76%	60
1441	2,20	Galectin-1	LEG1	51%	138
258	1,79	Lamin-A/C	LMNA	43%	61

277	1,92	Lamin-A/C	LMNA	33%	35
280	2,22	Lamin-A/C	LMNA	27%	51
281	2,89	Lamin-A/C	LMNA	46%	145
289	2,16	Lamin-A/C	LMNA	38%	136
290	1,91	Lamin-A/C	LMNA	37%	57
394	1,10	Lamin-A/C	LMNA	37%	51
395	1,36	Lamin-A/C	LMNA	42%	106
418	0,68	Lamin-A/C	LMNA	36%	263
419	0,90	Lamin-A/C	LMNA	38%	124
429	1,41	Lamin-A/C	LMNA	31%	80
338	1,58	Lamin-B2	LMNB2	44%	105
385	1,51	Lamin-B2	LMNB2	22%	33
1122	0,70	Microtubule-associated protein RP/EB family member 1	MARE1	42%	101
192	1,46	DNA replication licensing factor MCM7	MCM7	42%	79
976	1,18	Malate dehydrogenase	MDHM	50%	373
1402	0,42	Myosin regulatory light chain MRLC2	MRLC2	40%	83
1259	0,71	Nucleoside diphosphate kinase B	NDKB	51%	71
1410	0,50	Nucleoside diphosphate kinase B	NDKB	53%	66
1296	3,44	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	NDUB9	43%	101
565	1,02	Dihydrolipoyllysine-residue succinyltransferase component	ODO2	39%	31
1027	1,65	Pyrroline-5-carboxylate reductase 1	P5CR1	53%	31
277	1,92	Polyadenylate-binding protein 1	PABP1	52%	254
311	1,40	Polyadenylate-binding protein 1	PABP1	44%	311
449	1,50	Polyadenylate-binding protein 1	PABP1	26%	99
495	0,58	Polyadenylate-binding protein 1	PABP1	35%	222
508	1,39	Plasminogen activator inhibitor 1 RNA-binding protein	PAIRB	26%	57
683	1,11	Poly(rC)-binding protein 1	PCBP1	42%	37
759	1,28	Poly(rC)-binding protein 1	PCBP1	32%	144
156	1,27	Programmed cell death 6-interacting protein	PDC6I	19%	68
398	1,41	Protein disulfide-isomerase	PDIA1	63%	119
448	1,20	Protein disulfide-isomerase	PDIA1	55%	149
462	1,48	Protein disulfide-isomerase A3	PDIA3	52%	120
462	1,48	Protein disulfide-isomerase A3	PDIA3	42%	191

1222	0,79	Phosphoglycerate mutase 1	PGAM1	39%	52
780	1,19	Phosphoglycerate kinase 1	PGK1	38%	70
1009	1,28	Prohibitin-2	PHB	83%	351
1134	0,62	Prohibitin-2	PHB	53%	36
984	1,93	Prohibitin-2	PHB2	84%	191
988	1,39	Prohibitin-2	PHB2	80%	167
186	1,66	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	PLOD3	32%	115
301	1,42	Peptidyl-prolyl cis-trans isomerase A	PPIA	45%	221
1314	0,55	Peptidyl-prolyl cis-trans isomerase A	PPIA	68%	96
1378	0,67	Peptidyl-prolyl cis-trans isomerase A	PPIA	36%	60
1380	1,92	Peptidyl-prolyl cis-trans isomerase A	PPIA	47%	95
1382	1,49	Peptidyl-prolyl cis-trans isomerase A	PPIA	69%	91
1383	1,80	Peptidyl-prolyl cis-trans isomerase A	PPIA	43%	84
1229	1,43	Peptidyl-prolyl cis-trans isomerase B	PPIB	59%	124
1334	1,70	Peptidyl-prolyl cis-trans isomerase B	PPIB	56%	129
1167	0,64	Peroxiredoxin-1	PRDX1	57%	277
1294	1,52	Peroxiredoxin-2	PRDX1	37%	288
1298	0,46	Peroxiredoxin-3	PRDX1	51%	248
499	1,16	Pre-mRNA-processing factor 19	PRP19	32%	307
709	1,32	26S protease regulatory subunit 8	PRS8	49%	81
1342	0,68	Proteasome subunit alpha type-2	PSMA2	50%	76
1201	0,71	Proteasome subunit alpha type-7	PSMA7	54%	235
429	1,41	Polypyrimidine tract-binding protein 1	PTBP1	30%	212
429	1,41	Polypyrimidine tract-binding protein 2	PTBP1	30%	212
477	1,29	Polypyrimidine tract-binding protein 3	PTBP1	45%	415
691	1,32	Cytochrome b-c1 complex subunit 2	QCR2	48%	183
1077	0,73	Putative heterogeneous nuclear ribonucleoprotein A1-like protein	RA1L3	38%	20
220	1,36	Radixin	RADI	8%	86
1305	1,46	GTP-binding nuclear protein Ran	RAN	42%	56
539	1,41	Histone-binding protein RBBP4	RBBP4	16%	122
1259	0,71	Putative RNA-binding protein 3	RBM3	38%	51
1410	0,50	Putative RNA-binding protein 3	RBM3	36%	41
437	1,99	Protein RCC2	RCC2	33%	21

1222	0,79	60S ribosomal protein L12	RL12	49%	188
1349	0,67	60S ribosomal protein L13	RL12	49%	200
928	0,91	60S acidic ribosomal protein	RLA0	41%	311
880	1,59	Heterogeneous nuclear ribonucleoprotein A1	ROA1	51%	136
896	1,79	Heterogeneous nuclear ribonucleoprotein A1	ROA1	34%	91
903	1,34	Heterogeneous nuclear ribonucleoprotein A1	ROA1	55%	125
935	1,37	Heterogeneous nuclear ribonucleoprotein A1	ROA1	48%	191
967	1,44	Heterogeneous nuclear ribonucleoprotein A1	ROA1	25%	42
971	1,51	Heterogeneous nuclear ribonucleoprotein A1	ROA1	36%	77
990	1,44	Heterogeneous nuclear ribonucleoprotein A1	ROA1	45%	96
991	1,45	Heterogeneous nuclear ribonucleoprotein A1	ROA1	52%	153
998	1,73	Heterogeneous nuclear ribonucleoprotein A1	ROA1	33%	29
1014	1,65	Heterogeneous nuclear ribonucleoprotein A1	ROA1	41%	39
1091	0,68	Heterogeneous nuclear ribonucleoprotein A1	ROA1	43%	140
804	1,28	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2	69%	282
872	1,54	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2	71%	420
882	1,63	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2	73%	266
926	1,62	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2	66%	235
935	1,37	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2	73%	163
950	1,32	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2	54%	73
1295	1,46	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2	26%	33
741	1,27	Heterogeneous nuclear ribonucleoprotein A3	ROA3	37%	137
801	1,55	Heterogeneous nuclear ribonucleoprotein A3	ROA3	45%	79
869	1,51	Heterogeneous nuclear ribonucleoprotein A3	ROA3	29%	27
818	1,52	Heterogeneous nuclear ribonucleoprotein A/B	ROAA	25%	130
727	0,64	Syntenin-1	SDCB1	26%	60
1035	1,34	Syntenin-1	SDCB1	38%	68
801	1,55	Septin-2	SEP2	59%	112
566	0,76	Serpin H1	SERPH	42%	162
673	1,35	Serpin H2	SERPH	40%	375
777	1,63	Serpin H3	SERPH	48%	249
96	1,67	Splicing factor, proline- and glutamine-rich	SFPQ	40%	127
107	1,74	Splicing factor, proline- and glutamine-rich	SFPQ	48%	267

110	1,70	Splicing factor, proline- and glutamine-rich	SFPQ	48%	174
116	2,13	Splicing factor, proline- and glutamine-rich	SFPQ	48%	267
118	2,06	Splicing factor, proline- and glutamine-rich	SFPQ	46%	202
691	1,32	Stomatin-like protein 2	STML2	46%	69
1376	0,64	Stathmin	STMN1	30%	95
1388	0,62	Small ubiquitin-related modifier 2	SUMO2	37%	110
486	1,32	T-complex protein 1 subunit eta	TCPH	32%	84
1077	0,73	Translationally-controlled tumor protein	TCTP	42%	23
1091	0,68	Translationally-controlled tumor protein	TCTP	29%	37
1279	0,37	Translationally-controlled tumor protein	TCTP	56%	220
141	2,00	Transitional endoplasmic reticulum ATPase	TERA	41%	124
142	1,50	Transitional endoplasmic reticulum ATPase	TERA	34%	19
748	0,78	Acetyl-CoA acetyltransferase	THIL	37%	100
779	1,35	Acetyl-CoA acetyltransferase	THIL	33%	85
262	1,56	Transketolase	TKT	27%	27
271	1,65	Transketolase	TKT	25%	44
322	1,41	Transketolase	TKT	43%	242
29	1,51	Nucleoprotein TPR	TPR	12%	38
588	1,38	Thioredoxin domain-containing protein 5	TXND5	24%	32
592	1,58	Thioredoxin domain-containing protein 6	TXND5	28%	91
804	1,28	Ubiquitin fusion degradation protein 1 homolog	UFD1	33%	31
903	1,34	Voltage-dependent anion-selective channel protein 1	VDAC1	62%	142
757	0,62	Voltage-dependent anion-selective channel protein 2	VDAC2	55%	259
439	0,74	Vimentin OS	VIME	62%	70
448	1,20	Vimentin OS	VIME	67%	384
448	1,20	Vimentin OS	VIME	47%	60
502	1,52	Vimentin OS	VIME	77%	428
553	0,83	Vimentin OS	VIME	54%	195
598	0,89	Vimentin OS	VIME	51%	296
73	1,37	Vinculin	VINC	33%	102
302	1,27	WD repeat-containing protein 1	WDR1	38%	441

Protein Score	pI	MW [kDa]	Peptide Count
220	7,36	85,4	21
185	7,36	85,4	20
332	7,36	85,4	21
552	5,31	41,8	23
530	5,31	41,8	21
530	5,31	41,8	19
453	5,31	41,8	18
587	5,31	41,8	22
540	5,31	41,8	23
724	5,31	41,8	24
512	5,31	41,8	19
174	5,31	41,8	9
115	9,04	66,9	17
247	8,3	39,4	14
181	8,3	39,4	15
279	8,3	39,4	16
371	7,57	38,6	22
463	7,57	38,6	25
498	7,57	38,6	29
459	7,57	38,6	27
111	5,47	16,3	7
138	5,47	16,3	7
579	9,16	59,7	34
569	9,16	59,7	33
638	5,26	56,5	23
752	5,26	56,5	28
369	6,89	101,5	35
305	6,89	101,5	30
354	6,89	101,5	37
465	5,7	61,0	27
465	5,7	61,0	27
163	5,7	61,0	18

442	5,7	61,0	26
77	5,26	56,5	15
611	5,7	61,0	28
377	8,45	51,7	19
302	5,09	26,9	14
98	8,22	18,5	5
68	8,48	26,1	9
85	5,61	54,2	8
98	9,01	22,5	4
189	6,77	55,2	20
180	6,77	55,2	15
119	8,82	72,3	21
233	9,06	69,1	31
259	9,06	69,1	27
282	7,66	61,4	14
354	7,66	61,4	18
107	7,66	61,4	11
247	5,95	62,3	18
445	9,16	82,9	37
159	9,1	50,1	15
222	9,1	50,1	17
165	9,1	50,1	16
168	9,1	50,1	15
190	9,1	50,1	15
140	9,1	50,1	12
71	4,5	24,7	4
313	4,9	31,1	15
71	4,5	24,7	4
207	6,41	95,3	22
224	6,41	95,3	25
292	7,26	49,5	21
348	7,26	49,5	26
174	5,31	41,8	9

174	5,31	41,8	9
324	9,23	36,1	23
138	7,01	47,1	17
239	4,76	92,4	24
205	4,76	92,4	23
226	6,84	54,5	23
299	7,18	67,5	25
372	7,18	67,5	27
265	7,18	67,5	25
372	7,18	67,5	27
297	8,85	54,6	15
424	8,57	36,0	17
418	8,57	36,0	18
313	4,9	31,1	15
264	5,74	106,8	32
337	5,74	106,8	39
459	7,57	38,6	27
253	5,02	23,2	13
677	5,87	73,6	33
198	5,87	73,6	19
381	5,87	73,6	25
185	7,36	85,4	20
205	4,76	92,4	23
821	5,07	72,3	36
197	8,74	56,2	11
238	10,31	14,0	13
102	5,62	24,9	9
156	5,62	24,9	10
93	7,62	24,0	10
372	5,89	49,2	23
71	5,89	49,2	10
587	5,89	49,2	23
198	5,89	49,2	15

221	5,89	49,2	15
189	5,89	49,2	8
345	6,37	36,9	15
418	8,57	36,0	18
138	7,01	47,1	17
108	7,62	38,4	8
174	5,31	41,8	9
385	5,38	45,6	20
395	10,06	42,3	25
381	5,87	73,6	25
319	5,39	50,9	25
296	5,39	50,9	24
71	5,39	50,9	9
360	5,39	50,9	26
298	6,65	60,1	21
361	6,65	60,1	22
677	5,87	73,6	33
107	5,48	70,0	17
685	5,37	70,9	33
437	5,98	22,8	13
88	6,47	39,6	10
206	8,22	61,8	23
156	5,08	16,8	7
211	6,08	83,6	21
174	6,08	83,6	21
626	7,96	57,9	35
208	9,06	69,1	31
283	7,96	57,9	25
78	8,27	51,8	12
163	8,44	36,7	14
146	5,34	14,7	10
210	5,34	14,7	9
226	6,57	74,1	30

145	6,57	74,1	24
158	6,57	74,1	18
359	6,57	74,1	35
281	6,57	74,1	28
195	6,57	74,1	26
247	5,95	62,3	18
312	6,57	74,1	34
420	6,57	74,1	30
243	6,57	74,1	26
218	6,57	74,1	22
252	5,29	67,6	27
78	5,29	67,6	12
143	5,02	30,0	8
204	6,08	81,3	26
473	8,92	35,5	15
120	4,71	19,8	7
57	6,19	28,1	9
113	8,52	17,3	8
147	8,58	21,8	8
198	5,89	49,2	15
98	9,01	22,5	4
145	6,57	74,1	24
476	9,52	70,6	29
611	5,7	61,0	28
352	9,52	70,6	24
134	8,66	44,9	11
108	7,62	38,4	8
184	6,66	37,5	9
112	6,13	96,0	14
341	4,76	57,1	29
77	5,26	56,5	15
289	5,98	56,7	26
289	5,98	56,7	26

112	6,67	28,8	10
174	5,31	41,8	9
570	5,57	29,8	23
58	5,45	28,8	10
491	9,83	33,3	30
395	9,83	33,3	25
267	5,69	84,7	19
381	5,87	73,6	25
177	7,68	18,0	11
97	7,68	18,0	5
128	7,68	18,0	5
183	7,68	18,0	12
131	7,68	18,0	5
237	9,33	22,7	15
266	9,33	22,7	15
456	8,27	22,1	19
146	5,34	14,7	10
373	8,27	22,1	15
392	6,14	55,1	16
181	7,11	45,6	18
142	6,92	25,9	10
328	8,6	27,9	13
218	6,57	74,1	22
218	6,57	74,1	22
552	9,22	57,2	21
312	8,74	48,4	17
102	9,23	34,2	11
114	6,03	68,5	6
126	7,01	24,4	11
136	4,74	47,6	5
57	6,19	28,1	9
113	8,52	17,3	8
76	7,66	61,4	11

112	6,67	28,8	10
255	9,48	17,8	9
414	5,71	34,3	15
263	9,26	38,8	18
151	9,26	38,8	11
498	7,57	38,6	29
309	9,26	38,8	17
77	9,26	38,8	8
79	9,23	34,2	9
324	9,23	36,1	23
292	9,26	38,8	19
69	9,26	38,8	9
144	9,26	38,8	16
236	9,26	38,8	15
501	8,97	37,4	24
653	8,97	37,4	25
516	8,97	37,4	26
442	8,97	37,4	23
309	9,26	38,8	17
244	8,97	37,4	20
87	8,97	37,4	10
348	7,26	49,5	26
170	9,1	39,6	15
102	9,1	39,6	10
170	8,22	36,2	9
446	5,31	41,8	24
152	7,05	32,4	13
170	9,1	39,6	15
752	5,26	56,5	28
475	8,75	46,4	15
382	8,75	46,4	20
337	5,74	106,8	39
461	9,45	76,1	32

339	9,45	76,1	30
461	9,45	76,1	32
359	9,45	76,1	29
312	8,74	48,4	17
154	5,76	17,3	6
134	5,32	10,9	4
164	7,55	59,3	17
102	9,23	34,2	11
236	9,26	38,8	15
287	4,84	19,6	10
244	5,14	89,3	25
100	5,14	89,3	20
377	8,45	51,7	19
127	8,98	45,2	10
677	5,87	73,6	33
685	5,37	70,9	33
399	7,58	67,8	23
72	5,01	265,4	23
60	5,63	47,6	8
132	5,63	47,6	10
501	8,97	37,4	24
498	7,57	38,6	29
512	5,31	41,8	19
163	5,7	61,0	18
77	5,26	56,5	15
77	5,26	56,5	15
741	5,06	53,6	35
638	5,26	56,5	23
424	5,06	53,6	20
299	7,18	67,5	25
565	6,17	66,2	22