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Supplemental Material to:

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De novo post-pollen mitosis II tobacco pollen tube transcriptome

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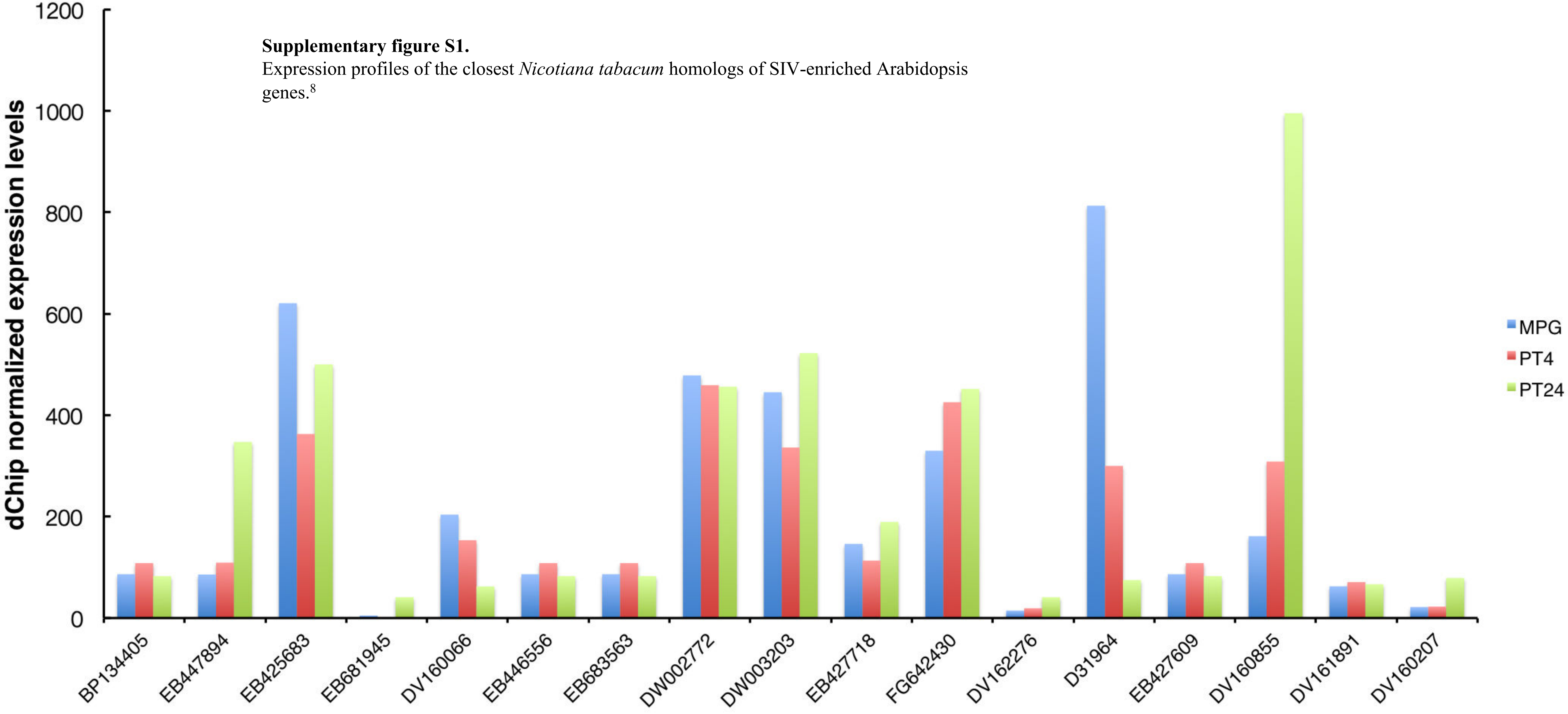
Supplementary figure S1.
Expression profiles of the closest *Nicotiana tabacum* homologs of SIV-enriched Arabidopsis genes.[8]



Supplementary Table S1.

Mean normalized expression of tobacco PT24-expressed probe sets with associated detection calls computed from two biological replicates with expression levels "well above background".

Line	Row	Col	Start	Sequence	ProbeUID	ProbeName	GeneName
12	1	12	697	TTTTGGATATGTTGCGACATTTGTGAAATGTGGTTTCATGGCAAGTGTGTGAAGATC	3	A_95_P225077	EB681313
13	1	13	258	TTGCCTCTGGAACTCTATAAAGTTGATAGTATCAATAGCATGTGATAAGCATTTGAAT	5	A_95_P129702	EB429667
15	1	15	507	GAGATTATAGATCAAGGTCACCGGTAAGATCCCGTCGTTATTCAGGCTATGAAGATG	9	A_95_P026506	TA19895_4097
20	1	20	381	ATCATCGCTAATATAGGTTCAAAATCTTTCTGTTCAGGCTTTAAACAACGCAACAGTT	19	A_95_P005006	EH666078
21	1	21	485	TCCTTGAATTGTATGGAATTTTATGTGCAAGAATGTCAGCATTTCGGCTGTTATAGTTT	21	A_95_P124072	DW003919
22	1	22	742	TTGAGACCAGCTTTGCCTCTCTTGACTTCGTTTATGATGTTGAATCCCATTTCATTGCT	23	A_95_P025461	EB440074
25	1	25	827	GGGAAAGAAAAGGCTGCTATGATCTGGATGTTCCCTAGAACAAGTAATATGAATTAT	29	A_95_P014051	EB450974
33	1	33	486	ATTGCATTGAGGATCATTAGGGTAGTTTCTGACAGTATTCTATCCAGTTTGATATTCT	45	A_95_P024291	DW001674
34	1	34	839	GCCCTGGTGTTGCAAACTTTTTTGAACTGATGATGATGAAAATATTTGTTGCTCCTTTT	47	A_95_P126092	EB425321
35	1	35	678	AGTGATAGACAAAGCAGAAGTGGTACAAGTCAGATGTCAAGCAATGCTCTAGTTTCT	49	A_95_P272641	EB451681
47	1	47	396	GGAAATGTTGGAGCGGGTACAGAATCAACAACTGCTACAAGCGAATGGATGCTTGT	73	A_95_P283178	AM817961
48	1	48	753	GTCTTATTTCTTGACAATGGACAATGAAGTTATGCTTGTTTTCAGCGAATGTTACAAC	75	A_95_P014466	DW000079
52	1	52	174	TACCAGTCAGCTCGTACTGTAATTTCCCCAAAAAATGTAAGAGAAATTATCTTTCTTT	83	A_95_P222367	TA22018_4097
53	1	53	568	GGAGTTATATCAATATCATCACCAAACCTTCATATGGTACAGTATTCTCCTATCTTTGC	85	A_95_P043826	BP130717
56	1	56	588	ATTTGTGACTAGTTTGTAATTTAGGGAGCATTGGCATCTCAAACTCTTTATGTTTGCT	91	A_95_P125232	DW005032
58	1	58	841	CAGAAAAGCTGTAGAAAAGAAGCATCGGGGAAAACTGGAAAATATGCACTGCTATC	95	A_95_P000936	EB425859
59	1	59	1320	TCCTCCTGAGGTATGTCACAGGATTTGGCTAATAAAAGCTTGAGAAACTTCGTCTTTG	97	A_95_P177682	TA12046_4097
62	1	62	403	GGTGCCAAATGATGGACCCTCTGGTCTCTTCTTTTATAGAAAGGAGGTCACCTCTTTT	103	A_95_P255989	AM798722
64	1	64	1192	GTATATCCCATTCGCTTGAGTCATGTTTATAGCAATGTGTCCTTTTGATATCTCTTCCTT	107	A_95_P210412	TA19391_4097
68	1	68	516	CCTGCATTTCTTTGACCATTGTGTGGTGTATAAAAGGCATTTGGAAATGTATCACTAA	115	A_95_P066855	BP136709
96	2	11	874	TTGGAGGAAATGCCAACGAATTACGGAGGGTTTAGAGAAAAAGTGCAAGGATTGG	2	A_95_P118807	TA16218_4097
99	2	14	410	GATTCCTTAACTTGGATAGTAGATTCAGGTGCATCTGATCATATGACTTCCAATAAAG	8	A_95_P073690	BP526277
103	2	18	426	TTTCTTACGAATTAGTGTACTCGTTAATGTATCCCTAATAAGATAGGGGTAAGATCTA	16	A_95_P213177	AM807618
108	2	23	246	TGGATCTGACTGCCAGTGTAACCCTGCACTTGTTCTAAATGATCACATTTAATCTTTTT	26	A_95_P104772	CV017163
109	2	24	863	TAGCACCTGATATGCTCGCATCTAGCTGACTGTTTAAATTATACTGTTGTTTATGTCA	28	A_95_P198842	TA16866_4097
110	2	25	705	ATTGAACTTGTTGCTCCAAATGGAAGTGCAGAATTATCTATTACTAGAACCTATGCAT	30	A_95_P232269	EH622574
114	2	29	1055	CCACTACTGAAACTTAATCACCATTTGGATTAATCTTGCTTAACAGCAAAGTTTCTCTG	38	A_95_P202097	TA17562_4097
120	2	35	685	GAGTCCGAGTCTAAGTTGTTGAAAGCAAATGAACTGAATGAAGTAAGTGAAGAGCG	50	A_95_P118297	DV161317
123	2	38	811	GGTTCTGCTACAGGTGTCTATAAGACACTGGTGAAGTATTTAGTTGGAGTGCCACAA	56	A_95_P138262	EB442001
125	2	40	283	TGTATTTTCTTTTCTCTTATTAATAAAAAACTAGCCCTAGGCGCTTGCCTAGCGGATTG	60	A_95_P147422	EB451836
127	2	42	1177	GAATTCAAGTGATTGCATCATCGATACTTGATGCATTTTCCATGTTATCTTTGCCATTG	64	A_95_P007661	TA15553_4097
129	2	44	721	CATCCCCAAATATGCAGTTCAATTTATTGATGAGACTACTGGACATATAAGACAGTTT	68	A_95_P204437	EB683003
130	2	45	736	CTTTTCTTTGAATCCTCCCTATGTAATGAGATTCTATATATGACATGCTTGAGTGGTG	70	A_95_P134077	EB435899

131	2	46	525	CTCGGTCGAATTTTGGGGTCAAAATTTTGTAACTGACTACTAGTTTTGTTCTTATCAA	72	A_95_P162367	EH621296
134	2	49	752	ATTAGCTAATACTGTGTCCATGCACCGGTTCCAAAACAGCACGAGGATGTGTACTGG	78	A_95_P228639	DW000441
136	2	51	754	CAACCTACAATGTGATGATCAGGTTTATTGCCTCCATCCAGGTGCAGAAGTTAAAAT	82	A_95_P160222	EH618902
138	2	53	711	ATTCAAACAAAAGTCCCCAACCAGTAACTGAAATGTGCCATTCTCAGGAGAGAAAGA	86	A_95_P145577	EB449328
142	2	57	530	TCCCATATTTGGTGTAAACATTCTTATCCTTCACAGTATCAGGCATCAAGGAGGCTCA	94	A_95_P056696	BP134024
145	2	60	819	GGCCGAGTGTGAATATGCAAAAAGATATTAACGCATGATGCATAAATAGTTTAACCT	100	A_95_P018191	EB425016
150	2	65	1406	GGAGATCTATGTATAATTCTTCATTGAGTACTCCTATTATGATGGAAATGTTCTTGCT	110	A_95_P016916	TA12069_4097
151	2	66	1537	GATATGCCTCCATTTGTACATCCTCTATTTCTATATATCATCATATTGTGGAACTTCTC	112	A_95_P177617	TA12022_4097
182	3	12	1523	AATTTAAGTCTGCTATACTGTTTCTCTATGCAATGCCTCAAGTACCAGTACTGACTGA	132	A_95_P025616	TA15544_4097
187	3	17	558	GATGATATTGGAATCTTCATGACCACCAATTTTCTGTTTAGTGAAGCTACTTTATGGA	142	A_95_P243467	FG643614
191	3	21	686	ACTTGAGCTGCTCTTGAAGGCATGTGAAGCTGTCAAACTCAAACCTTATGCCAGAAA	150	A_95_P019511	TA17507_4097
193	3	23	1630	TTGAAAGCGATAGATGTGGACAGTTTGGAGAAAACTTCTGGTGCCAAGCATGCCGA	154	A_95_P148717	TA14441_4097
194	3	24	661	GACCATGCGCTTTTTAACAGTTTGATTCTGAACCATATGTTTGTCCTGCATTACGAAG	156	A_95_P068340	BP137106
205	3	35	771	GCAGCAATCCTCCATAAACAGCTTTCATATCCATGACATTCCTTACTGAAGACCAGG	178	A_95_P228484	FG171716
208	3	38	630	TTGAAACCACTCATCGTACCAATCTTGAGCGAAGGAGAATGAGATGCTTATGGAATC	184	A_95_P284553	FG642068
210	3	40	434	GTTTCGAATTTTCTGGTCAAGCTTTGTCTGCTATCCATTTTTTGTACATTTGGACAGAA	188	A_95_P094548	EH619915
214	3	44	760	ACTGGCCATCCTGTGTTTGAGACAGCATATGGCAAGATTGCTGTTAATATATGTTAC	196	A_95_P269866	EB427498
218	3	48	462	GAAGTGGTACCAATTGCAGTTCTTGCACTTACATACTATCATGCTGCTGACGTTTCTT	204	A_95_P192517	FS407121
219	3	49	1259	GTACTGCTTGCTACTTGATACTTGAAATTATATACCCATATATATTTGACGTTACTCGG	206	A_95_P025021	TA13312_4097
221	3	51	748	ATAATAAACAGAAAAGTTTGGCTGGTAGCCTCTCCATGTTTGTTCTCGGTTTCCTGGT	210	A_95_P118202	DW003261
223	3	53	715	TTTGTAATGTGTGGCCTAAGCTGCATTGCCGATGCTGCTAGCCATGAAAATAATTTTG	214	A_95_P253374	FG150164
224	3	54	362	TCCAAAGGTCAATCCATGAACCGATTTCATAATTATGATCCCCGTTGGTTTCGCAGGG	216	A_95_P157867	EH615898
225	3	55	441	TCTCACTTTTACATGGGTTACACTAGATCAAAGTATACTTTTCTTAGCTTAGCTGTACT	218	A_95_P192677	DV162205
238	3	68	221	TCACTGAAAAGATTGAGAATATAAATGACCAGTATTGGACATTGCGGGCAGATCCG	244	A_95_P154422	EG649585
241	3	71	691	TTGCCTTCTCTTCTTTCTTCCCTGAATTTTTGAGACCAGTAATTGATCCAATTGCAACA	250	A_95_P162122	EH620925
244	3	74	290	TCAAAAGAGTCAATTAACCATTATGTTGCCCACCCCTGCAATTCATCTCGCAACGATA	256	A_95_P101548	CN498857
271	4	16	665	CGAGGCCATTTTGCCACATGTAATTTCATTTTGATGTTATGTTGGTTTGTAATATATG	141	A_95_P126012	EB425210
272	4	17	637	CCAGATATGATAGAGCTAGGGGAGTTGAAATAGGGAACAAGGACATCAAGCTGAG	143	A_95_P054976	BP133575
274	4	19	379	ATTCTTGTAAGCATTGATTGTTTCGAGAGGAATGGTCATTGCTCAGGAATAGATAAT	147	A_95_P030076	TA18497_4097
278	4	23	404	TATATGTGTGCTTCTGATCCTAAGGAAGATCCTCCCAAAACAATTCCAGGGAGTGAG	155	A_95_P080025	BP527906
280	4	25	1010	TGAGTGAAGATGAGTCCTGTTTCAGTGATCTATGATCAGAAAAGGAACTTAGCAGCT	159	A_95_P029391	TA16965_4097
282	4	27	758	CTTAGCTGGTTCTGTGCTATGCCATCATTTCTCATAAATTTTTGGTCACTTGCATCCCG	163	A_95_P218832	TA21262_4097
285	4	30	1364	GATTCTTTAAGATAGCCTGGTGTAATTCTTTGATCAGTTCTAATGAACTATCCTTTGCC	169	A_95_P013036	TA12793_4097
286	4	31	486	TTGGAGTGCAAAACTAAAAACTTTATAAAGTTGATCCACTTGGTTGGATATCTTCCC	171	A_95_P220127	TA21544_4097

287	4	32	576	GATGTGATTTGAGTCTAGAAGTATGTTGTTTGAGGTTTTCTGTCATTCCCTATTTCAA	173	A_95_P112927	EH618900
288	4	33	165	ACTATTGTTGGTTCTCTTGCATTCAAGCCCTCAATTTGCAGCAGTTTCATTATTTCACC	175	A_95_P110357	CV019698
292	4	37	92	GTGGAAGAAGTTCCTAAAGTTATGATGATTGATGCCAACACTTTTGTAGAATGATGTT	183	A_95_P130427	EB430486
293	4	38	339	TAATCTCAGAGATGCTTTGGAACGTGGTTATTCAATGGATAATTTGCTAATTCTCAGG	185	A_95_P223257	TA22210_4097
295	4	40	438	ATGGTTAAAGAGAAAGCGAAAGGCCATCTGTAATAGAGCTTGAAGTGGCTGCAATT	189	A_95_P090918	BP531140
298	4	43	905	GCCATGATAACTGTAGAAATTGATCCTAATGATATTTATTGTACCAGAAGAGGACCCT	195	A_95_P212702	TA19892_4097
299	4	44	679	CCTAGATAGCCAATGAGATTGAAAATGTCGGTTAATGACTTCTGGTTAATATCACTCA	197	A_95_P223042	TA22163_4097
300	4	45	823	TTGGGGGTTGCAATGGTCTGAAAATCGTTGCACCTTTTCAGATCATGTGCGTATTATA	199	A_95_P120347	DW000191
307	4	52	603	GGCTCGTAGCCTTGATGTTTCTATTTTTGCATGACCAGTGGAGTTTAGACCTTATATTT	213	A_95_P122427	DW002401
318	4	63	1063	AAGATGAGCCTACAGAGGGAGCTCCGGAATTCTTTCTGCTTCAGTTTTACCTGGTAAT	235	A_95_P198057	TA16697_4097
322	4	67	351	GAGATAGACTGGAATGGCAGTTTTATGCACTAGCTTGAATTCAAAATGGATTCAGAT	243	A_95_P026121	BP530829
326	4	71	1489	CTGGTTTGACCAAGAGGACGAAGCTCGGGGTAATTTTTATTTGTATATATAATTCAA	251	A_95_P202027	TA17545_4097
327	4	72	689	GTGATGGTTTAGTTGGATTATACAGGGGGTTTGTTCCCAATGCGCTGAAAACTCTCC	253	A_95_P213537	TA20069_4097
328	4	73	1264	GAACTATTCTTGGCTTTTTGTGTTCCACCCGAAGCCCTATGAACCTGCATTTTGAAAA	255	A_95_P249317	U91924
329	4	74	337	CTGATGTAGTGAATTTGGTGTTGTAATTTTAAATCCGGATGAACATGTACTCATGCTT	257	A_95_P030896	EB444971
354	5	14	855	TCTCAAAACTGAACAGTCATATCTATTTGTGAAAGAGAGTGGCTTTTCAGAAAAGTC	271	A_95_P131332	TA14146_4097
355	5	15	1082	CACTTGAGAGGTTTCTGCTCGAGATTTTAGTCCGATTAAAAGCATCAATTTTTGAAGA	273	A_95_P182887	TA13330_4097
358	5	18	694	TTTGGCAATGAAGTTAATGGAAGAGCGAATAGCTCATCCAGATAAGTATACTGATGA	279	A_95_P141182	FG143459
361	5	21	591	CGGAATAGGTTTCTGCTAAATGATGTTAATGTTCTTGATCTAGAGACAATGACTTGG	285	A_95_P070695	FG159775
364	5	24	591	TTGAAACAGAGTCAGTTGCTATCTTGTTTATGTTTTGCTCTGCATATGGGACCTAATGT	291	A_95_P160137	EH618785
366	5	26	2415	ATGAACTGTTGTGGCTCTGTTGAAGTGTTTGTTCATGCACGGATGCACCCATTTACTTT	295	A_95_P180402	TA12734_4097
372	5	32	537	GTATATATTCATAGCATTTTCAAATGCAGAGGGAGAGCGCATGGTGTCTACTGTCTA	307	A_95_P036008	BP128618
374	5	34	805	CTCTGTTTCTGCATTATAAGAGAGTTTTCTGGCTTGAGATGCCGCTCCAGATGAAACG	311	A_95_P179912	TA12615_4097
378	5	38	564	TGTGTTTTGGTGTAGAACTTTCTCAGTTCTGGCTATGTAGTTGAATCAAGTGCATTTT	319	A_95_P001071	FG641470
383	5	43	810	CTGTGACACTACAGTTGGGAAATATGTAATGATGTTTGTCTAGGTTCGAGTTAATTTC	329	A_95_P178007	EB438099
384	5	44	282	TACACTCTGATGTAATGGATGACAATATCCACATTGGAACCACTGTTCCGTCGCTTCT	331	A_95_P063155	BP135702
385	5	45	296	TCAAATCTCACAGGAATGTGTTTGTTGATTGACTTATTGTAGAAGGTCACTCCATCTC	333	A_95_P131862	EB432289
386	5	46	420	TTTGTCAGTGTACGAGTCACAATTAAGTTGCCAGAAAGAGCTGGAACAGTTATCGAA	335	A_95_P262716	AM791244
392	5	52	624	ATGTCTGTATTTGGTACTGTTGCAGCCTGGTGGATGATCACGATCAGTCATGTTTGTA	347	A_95_P057061	BP134118
393	5	53	299	TTCCTTAGACACCAATGATACTGGCAGTTGAATGTGATTTTTGTATGAGAAAAATCTT	349	A_95_P142467	EB445919
394	5	54	1480	CCCCATGTATCTGTTATCAACCCTGTGTGCTAAGGGTTTATTTACTGAATCTAATATAT	351	A_95_P199102	TA16920_4097
396	5	56	755	GCTCAAGGACAACAAAGGATTTATGTAATAGGTTCCTGTGTTATTTCATGTCAACTTC	355	A_95_P011226	X95752
397	5	57	845	CTGTAGATGGACATGTACCAAGTAATAACTGTTAAGTTTCTGTAAATACACCTCTCTT	357	A_95_P214572	TA20290_4097
398	5	58	565	CATTACTCAAGTGCATGTGTAGAGGAGATTTTTGGCACGCAATTGTGTGGTTTCTCC	359	A_95_P164247	EH623377

400	5	60	860	ACTGGTGCTCAAGGCATGGATCAGTACTTACCATTTGTTCAATGCTTAAGCGCAATCC	363	A_95_P284493	EB443060
402	5	62	1131	CTATGTTCAGCTCTTGTTATTATAAGGGTTTTTATTGCACGAATCTTCAATCTTCTCAG	367	A_95_P024491	TA17600_4097
403	5	63	452	GATCCGTTTGGGCTCTGTTGCTATTTAGGTTGAACCACAATTGTTTTGTATTATATTG	369	A_95_P132142	EB432597
406	5	66	368	TACATTGTAAACCTATGTTTGGAAAAGAATTATTGGCGTTTGAGGAAGTGGGAGTCC	375	A_95_P090493	BP530974
407	5	67	531	GACGACTTAAATATGTTAGATGCAAGACGGAAAGAAAATTTCATGGATGAGGTAGC	377	A_95_P133477	FG139569
412	5	72	496	TGATTGTATCTCTTGAAAATATGAACTTTGATGTTTTGGTCTCTGTGCGTGCACGCCC	387	A_95_P183512	TA13476_4097
414	5	74	791	GGTGTATGTTTTTCGATTCCTACCAACGTTATGACGACCTAATAATTATGATTAGGTG	391	A_95_P000206	TA11706_4097
415	5	75	514	CTTGGAGAGAGTATGCATGTTTATTAAGTTGTAGGTGTCACAGAAGTGTAAATTAAT	393	A_95_P039876	BP129677
434	6	9	739	TGAGATATATAAACTCCCTCTTCAAAGAGTATTTCTTATTGGGATTCTTGCCCTATTCC	262	A_95_P117007	DV159791
435	6	10	762	CCGCATTACGTAATGTATGTACGTTAACCTTCTGTTATGTCCTTAAGAAGTGAAATTT	264	A_95_P120062	DV999782
437	6	12	2082	CCTAGTGTAACTTGTGACAATATGACTATCTCAACTTTCTTGTAAGTTTCACCTGTCTT	268	A_95_P238964	AY183721
438	6	13	800	AGCAGGCTAATGATTGATAGGCTTTTTAGTGAGGTATTACTTTCTTCCCAATTTGGTA	270	A_95_P190597	EB425670
441	6	16	776	CTGAACAGCGATTGTTCATATGATCGTATGATCTCCCCATTCTGATCCTTTTATCAAAT	276	A_95_P204707	TA18121_4097
443	6	18	609	TTTTACTTGAGCCTGTTTCAAAAGATAATGAGGTTGGCATATTGGAGCTTGTTTTGAC	280	A_95_P027936	TA15225_4097
445	6	20	672	AAATTTGCGCAGTTGATGTACTGGGTTTTATCCTAAAAATAGTGCATCTCGTTCCTTT	284	A_95_P235244	FG640658
453	6	28	894	CCATTTTAGACGCTATTCCAAACTATGATAGTAGTATATGACATTTTTGTTGACGTGG	300	A_95_P009751	TA13415_4097
455	6	30	694	ATGTTGTACAGTTGTACGTTGAGCCACTACTAATTTCAATCCATATTCAACCCCCCTCC	304	A_95_P021026	TA15945_4097
458	6	33	1836	GGTTTCTATGTTGTGTATTTGAGTACAGCTTGTTAGGTTGATGAACTGTACTCATTCA	310	A_95_P011666	TA12667_4097
464	6	39	1365	GAGTGGGTAAGGAGTTGATTGTTGGGTCATCTTATTCTTTTATTTCTCTATTTGACTTT	322	A_95_P029081	TA12248_4097
470	6	45	883	CGTTTGTTTGGAGATGATGCCCTTGGAGCTATGAATATAGAGATGGTTGAAATTGCT	334	A_95_P292013	EB425986
471	6	46	919	GGTATTTATGTAATTCGTGTGTTGGTTCCGTGTTTCAATTGTTCAGCTCTTTTCATTCT	336	A_95_P012161	TA13321_4097
472	6	47	929	CTGTGGCTCAAGTTCCATTATTACTTGAGGTTGCAGGCAATTGGTAAAGTTTCCGATT	338	A_95_P026821	TA11780_4097
473	6	48	345	ATCTCTGATAGGCATTTCACAGCTGCTCTATTGCAAGGGAAATAATAAATTGCTATGA	340	A_95_P029066	BP533408
479	6	54	839	TGCATTCTGAACTTAGTTTAAACCTTACATTGCTGGAGTGACAGATGAGCTAACTCAA	352	A_95_P148987	EB678617
480	6	55	829	TCATCTGTTAAAGCAGCTTACATATGTGTCTCGACTGTACTCATATCGGTCTCCTGAG	354	A_95_P269216	FG161667
486	6	61	170	ATTACTAAAGGCGGCAAGACCTCCCCGAAGTCTCCAAAATCTGATGATGAAGAAGA	366	A_95_P034299	AJ718371
490	6	65	682	ATGGTTGGAGTACCAAGGATTCTTTTTGTTCGTGCACAAGTTATACCAGGATTGAAA	374	A_95_P193562	DW002831
492	6	67	1109	TGACTGTTGGTTTTGGATGTAGAGTTTGCTTTCTTCTTGATATGAGTATGTGAATTCT	378	A_95_P188352	TA14551_4097
494	6	69	1608	ACACTGTCCAGTAGCAGTTTGTCTTACATATATGATGTGTCAACTGAATGCCACAAAA	382	A_95_P012441	TA13731_4097
496	6	71	254	AATGAAGAAAGTGTGCCTGTTGAGAATCTGCCCCTGGAGTCTAAGCTTCAGCAAAA	386	A_95_P104927	CV017226
500	6	75	540	TCACTGTTGTGAGGAATACTTTCAGATTAGCTTATCAATTTGAAGAAAGCATGTTGCT	394	A_95_P027046	TA15610_4097
523	7	13	1197	ATTTGCACTCACTATTTGGTCCACCGTATTCATGTGGCTCTTGTCCTAATTAATGTCAC	408	A_95_P189027	TA14703_4097
529	7	19	862	GGCATTGTTTTGGAGGTTGTAACACATGTTGTGCAGCTTGTTTGGCTGTTCTCTGTTT	420	A_95_P012681	TC41934
540	7	30	171	TACAGTACTTTTTTGTTGGTGATTAACTGATTAATAACACCACTTGCCCCAGTTCTTGT	442	A_95_P029356	TA22188_4097

542	7	32	488	TGCAGTTCCATTCACTTGGATTGAGAGTGATCCTAAACTGATTGCAAATCCACATATG	446	A_95_P263316	AM840768
543	7	33	378	AAGAATAACACACAGGTGCTCATCAACTGTAGGAACAACAGGAAACTTCTCGGTCGT	448	A_95_P111177	DW000043
545	7	35	731	GGTACTTCTTTTAAATGGTTATGTCTCTGATGATCCTTTTGCTGATCAAACTATAGGC	452	A_95_P192357	TA15434_4097
547	7	37	684	AATTAAATTAGACAATCACTGATTTGATTTTCAGTCCCAGTGGTCTGACTTCATATGC	456	A_95_P316418	FG189056
548	7	38	733	ATGGCTTAATCCTGTAATATGTTGGTCATCGCTCAAGCTTCTGCTAGAGGAACCAAA	458	A_95_P269376	DW005181
552	7	42	379	TAGACTTTATTTTTCAAGTTTCCCGGCTCAAATAATGTTGGCGGTCGCCAATCGGCGG	466	A_95_P006151	TA14767_4097
563	7	53	843	AATACAATCTGCATCAGCATTATATGGAGCAGCGAGAATACAGTTCTTCGATCAGCT	488	A_95_P236059	FG174267
569	7	59	533	AACGGCTATTCATCAACCACTCAACATTATGTGTTTTCTGGCCATAATTCGGAGTTTG	500	A_95_P021241	FG137478
570	7	60	287	ACAAAGTCATGCCTTCACCAAATATGAGGCTCTTCAAGCCAAAACATGGGCGACAAC	502	A_95_P047526	BP131680
572	7	62	565	ATTGCTGTTGACGCTGCTAAGAACCTTCTTGCCTTTTTCATATGAAGAAAGGGTTGG	506	A_95_P301823	FG635691
578	7	68	1105	TTTTCAAGAATTCACTCCACCCTGCCTGCTGAGATGACTGAAGTTTCAGGCATCCGAA	518	A_95_P178437	TA12252_4097
580	7	70	846	CAAAAAGACCAATTACAACAATGGAAACGCAACCGCCGTGCCTTGGCATATTCTACT	522	A_95_P118982	DV162047
587	7	77	697	AGACACCTGAGTCATGGGCTCCAAATGCAGCTAATATGATACTGAATCTAACTGCAG	536	A_95_P294083	EB439461
588	7	78	583	ATGCTTTGCCAATGAAATGGACCAATAGAAATGCTGGCAATATTTATTTCGTGACTTG	538	A_95_P203937	TA17960_4097
603	8	8	511	AGAATATTTAGGCATTCAACAAGTGGTTTTTGGTGGTCGTCGGATGGGTGATTGGG	399	A_95_P029891	DV160581
605	8	10	763	GCTTTTTTACTGTCGGTTTAAAAACAAAACCCGGGGGGCGCCATCAGAAAATCAAGT	403	A_95_P266681	EH665604
606	8	11	741	GCTGGTTTCTGTAAACCCCTTCTTGTTTTACTGAAATAGAGATCTAATTTAAATGGCC	405	A_95_P119547	DV998889
609	8	14	516	GATGGACCATGTAATTTTGTTTGGCGTTTGTCATACCTTGAGATAATATACAGGGAAT	411	A_95_P200232	DW003491
610	8	15	467	TTCCGCACATTTTGAACTCTCCCAATGTTGAGTTCTATGCCTTTAGAATGAGCATTGG	413	A_95_P096708	BP533729
612	8	17	344	GTTGGCCATCATATATTGCAGTGGATATGGTCATTCGATATTGAGATATTGTAAATCT	417	A_95_P092793	BP531974
617	8	22	893	TGCTCAGCGTGGATAGCCAATGGCAGTTGGAAATCCAAGTTAAAGAGTTGACTGTTC	427	A_95_P217637	TA20976_4097
618	8	23	782	TAGCAGGCATTTGACTCAGTTCTCCTTTCTAATAATCTCTCCTTCCATTTCTTAAATGG	429	A_95_P287598	EB678998
621	8	26	224	TTTGTGTGCTGCACGCAGCGTCTGTTTTCAGCATTTGACATTCTTTATAAGGTTCCTTT	435	A_95_P140772	EB444610
625	8	30	483	CCTTTGTATCATGTATATGCCAGGAGAATATAGTTAACATTATTGAGAAAGAGGCAT	443	A_95_P131192	EB431321
627	8	32	418	ACTTTTTGATTACCCGAGTCGTTATCAGACTAGTGTGCCTGTGTAATTCCTATATTTTT	447	A_95_P132312	FS424443
629	8	34	645	TATGTTGCTCAGTATGAGTTTTTGGCATTCTGTTTTCACAGAACTTCTATGTTGAATGT	451	A_95_P285878	FG643752
630	8	35	810	CCGAAAAAGAAGCAAGGAGTACATTGTCTAAACTCTCTTTAGTGGAGTCTGCGGTAA	453	A_95_P294983	EB443347
634	8	39	797	TGGAGCGGACAAGCGGATCATTGGATTTGATTTGCTAGCTCAAAGAGCAGAATACA	461	A_95_P150432	EB680511
635	8	40	243	GTCTGCTGAAATCAAATATTTGCACTTTTGCCCAGTTAAATGGAGAAAAAGAGATTA	463	A_95_P028261	TA13558_4097
638	8	43	966	ATATAATATAGATGAATGCATGTGCAGACTAGTGAGCTTGGTCTAATGAGGGCTTGT	469	A_95_P008131	TA12822_4097
639	8	44	779	TTAGGAATTTATTCCATCGCCAGTCGTCTGTCCCTCTTGCTGATCTAAGTTCAACTCTT	471	A_95_P116552	DV159312
641	8	46	854	CTCTTGCCATTTGATTCAGTCGGTACTTTATTGGTGTAACATGACATTTGTGATTGTA	475	A_95_P027581	TA16249_4097
642	8	47	1425	CAAGCTACGAAAGCAAATTCCAAGTGTTGTAGAGTCACTATGATGTAATAAACATGT	477	A_95_P009856	U60057
645	8	50	980	GACAAATGTTTTTCCACTCATGCAATGATGCCGAACTTGAGACAGATTGCCAAGTACT	483	A_95_P287388	TC56180

647	8	52	821	TAAAAGCTCGGGTGAACTTGTTGGGACATTGCTGACATTCTGGGACGTGAATTGTGT	487	A_95_P293178	FG156161
657	8	62	477	GAATGTCTGAACAATTGGTTACAAATAAACAAGGTCTGTCCAATGTGTAGCACTGAG	507	A_95_P090863	BP531123
659	8	64	816	ATAGAAACCGCAAAGCTTCTGGCCTTGAAGGAAGGTTTACTTGTGGGCATATCATCT	511	A_95_P125592	AM087458
661	8	66	1455	ATCACTGGAGACTTGTCAACAACAGTTATCAGGCACTAAATGAAGGAAAGCCTGTAA	515	A_95_P089993	TA16258_4097
666	8	71	410	CAATTGGAAGATGGACGAACCCTCGCTGATTAAACATTCAAGAAGGAGTCAACCATG	525	A_95_P112762	CV020825
668	8	73	1367	TGAGATGGTAGGTGTGGGCTGTAAACGAGTCAAATGATAGATTGCTATTGGAACCAT	529	A_95_P193557	TA15698_4097
671	8	76	471	GAAAGGGCAAATTGGTTTCTGACATCCACTGGTTATGTCAGTGGACCAAATCCCTTA	535	A_95_P088108	BP529962
700	9	20	296	CAAGGGCAGATGTCGTACATACTATGTAATATTTGAACTGGTTATTTAGGCACTCCTG	563	A_95_P104447	CV017016
703	9	23	502	GGTGGAAACTTATATGTCCTTTCTTTTTCCCATGAATTTGGCATGAACATTTCTTCTCC	569	A_95_P101113	BQ843168
711	9	31	343	ATTTGGGGTAGGGGTTAGTGGAAAGCTTCTTTGGAACAGATGTAGGGGTTAACAGA	585	A_95_P108917	CV019063
713	9	33	1095	TTCAAGACTGCATTGTGTGTATAATGTCATTTCTGTTAATATAGAGGGCCATTTGGAA	589	A_95_P211412	TA19604_4097
714	9	34	781	AAATACCATATCAATGATCTGGTTCGACAGTTGGAGATCGGAAATGTTTCCGATCCAT	591	A_95_P190682	TA15068_4097
715	9	35	112	CTCAACATTGCATGTTATGTTCCCAGTTGTGAATTGATAACGGCATAATTTTCTTCCAG	593	A_95_P095883	BP533375
718	9	38	704	GCAGTTAACAAAACTGTTGCATTTGTGAGTTTGTAACTCTCTAATGGCAAAGCAAATG	599	A_95_P136152	EB439783
719	9	39	615	AAACTCTGGTGGGGCTCCACAAGGAATTCCACGAAAGGTGGTATTTTGATCTTCTCTA	601	A_95_P004866	EH665108
720	9	40	244	CGTTATGCCACAGAGAAAGTGACCAGAGAAGAATTACGAAAGTCACTTGAGGATGA	603	A_95_P215557	FG160952
721	9	41	94	CCACCAATATCTCTCGTCGACTGAAACAACATAATGGTGAAATAAAAAGCCGGGGCA	605	A_95_P155127	EG649912
723	9	43	370	GCCCGGTCGTATTTTTTCTATTCCATTTTGTAAGTGATACCTTTGAAAGGTTACTCACA	609	A_95_P110982	CV019994
725	9	45	782	AGACCTTGAAGTTGCTGGAGCATCAAAGTTGGATGTGGCTTTGGTAACCACTGTAAT	613	A_95_P289258	DV158360
734	9	54	278	TAACGTTCCCATTGTGGAGAAGAGACTGATACCAAATTCCTGTTGACCTTCGTCAGTG	631	A_95_P204607	TA18101_4097
735	9	55	176	CTAGGTGGGCACTTGTTGTATTGTTAAAAAGTAGATAAAAGAAATGTACCAGTTTACT	633	A_95_P127152	EB426613
737	9	57	813	GATCTTAGAAATAGCTGTGATCTGATCCCATTCCCTAGCTCCATTCTCATGTGTTCCCA	637	A_95_P224767	FG143180
738	9	58	1438	GTCCTGTTTCTAATGTGTTGGATATCTTGAGCCTTAGAAGATAAAAGATGCACACTAT	639	A_95_P028136	TA12404_4097
739	9	59	704	ATTTGGTTCAAAATGGCTGCTTGTAATTCCCCCCGCCACCCCTGTTGCGTTTATCTTAT	641	A_95_P029256	TA19404_4097
742	9	62	737	CCAATTTTTCACATCCTCACTTGGGATTTTGATTATTCCGAATTCCAAAGTAGAATGG	646	A_95_P021886	DV159766
743	9	63	631	TTGGCCACACATCTGCTATTTCTGAAGCAACTGGAAGCCAGAGGACTGCATCATTTA	648	A_95_P149587	FG164564
744	9	64	425	ATCCGAATCCGGACAATGATATTGGGTTCACGTATTTTGATTTGGATGATGACCACCA	650	A_95_P096373	BP533597
747	9	67	460	AAGGGTCTGTGTCTTGCTTGTTTGAAACTATCGTATTACTTGTTAGCTGCTAAAAATA	656	A_95_P214197	TA20209_4097
753	9	73	844	TTGATTTATGGAGATGCTGACCGGCAGCCACTGTGATCATTTATAGTCGTTCATCTTA	668	A_95_P012311	TA14276_4097
759	9	79	650	CCTTGAACAGTTGAGAACAGTCCTCGTAGTTGGAGATAAATAATCCTAATCTGTTGAA	680	A_95_P187542	TA14369_4097
772	10	7	449	GCATTACTGGTGTAAGGCTATATGCCCAATTCTACAAAAAGACTACTTTTAGATTTCG	540	A_95_P016491	BP534995
774	10	9	607	GGCATCATGTGCAATAGAGTTGATGTAGCAGTGACTAAGTTCATCTTTAATCATGTAT	544	A_95_P025711	EB438078
779	10	14	808	TAATTGTACCAATGCATATCTGATGAAACAATGAAGACGTAAAACGCAGATTGTTCCT	552	A_95_P195802	TA16197_4097
794	10	29	690	TATTCTGTACGAATACATGGAACTTTTGCACCGTCTCTGTATATAAGCGATTGCTTTCC	582	A_95_P218072	TA21091_4097

796	10	31	846	CAGTAATGTGTGTATATTGTGACAAGGTGATGAATGAGTGTTTTAAGTTGAGATCCG	586	A_95_P016951	EB427980
798	10	33	824	GAAATTTTAGTACCGAAGTCCCTGATTTCACACTGCCAAGAAAAGCGTCTAGCGAGG	590	A_95_P032686	AF043554
802	10	37	681	TTGGTGGCGGCACTTTCTGGGGCCTAAGGAAAACTTTTGACTAAATGCAAAGTTTGA	598	A_95_P296403	FG175896
807	10	42	5987	TGAAAATTCCATTCAGAGTGGGGTTCTTCCTATGGATGAGAAGGCACTTTCAGGTCT	608	A_95_P238744	AB080692
808	10	43	477	CTAGAGTTGCAGCCTTTTGGAAAGATACTATTCCCTCCGTTTCAATTTATGTGAACCC	610	A_95_P144007	FG635525
810	10	45	1384	TGGTCTTGAACTCCTTTTTACTGTGCAATCAAATGGGAAGACTATCTCAAACTTTGGT	614	A_95_P177482	TA11987_4097
818	10	53	785	ACACTTCAATGGAAGTTTACTTTGTTTGCCAGTTTACCTAAGCCTTTCTCTAGTTTTTC	630	A_95_P109167	TA12316_4097
823	10	58	774	ATGAGGAGGTAATGTAAGTCTGGCTTCGTAATGTTCTTATGTACGATAAAGATTTAG	640	A_95_P148322	EB677604
825	10	60	639	ATATTGCTCAGCTGACGAGTAGATGGAACACTATTCCGTTGGCATTAGAACACTTGG	643	A_95_P130682	EB446106
832	10	67	739	CAGGATGAACACAAAAGCAATACATCACATCCGTGTTCAACATTTAAGGTTCTTTAA	657	A_95_P228154	DW004594
835	10	70	344	GCTTTTCTGCTTTTTAATTGTTACCAGTTACTGGCCTTTTATTGAATGCCCTTAGTAAG	663	A_95_P108952	CV019083
837	10	72	606	CCCAGTTTGGGGTTCGCAATTCAGATAACAGTTCTTTTTGGGATATGATATGGGGCT	667	A_95_P215512	EH614410
838	10	73	213	GGCTTTATGGAAGGATAGTTTGGCTAGCACTAGTAGCTGTTAGCTGTCACCTGGATA	669	A_95_P114462	CV021612
839	10	74	817	ATGTTCCCGCAGTTTTGTCATAATGTTTTTTGCTGGCTTAAGTCTCATGGCTGTAAGA	671	A_95_P224082	EB443143
840	10	75	742	ATCAACTTGCGTGAGGCGACCAAAGTTTATTATGTGCACTGGTGGTAATGGTGCAG	673	A_95_P019801	FG167577
858	11	8	539	TTAACCATATGTGTGCCTGGAATAGGTTGACCCGACTAATTCAGATTTGCGTCGTAG	685	A_95_P305688	FG645575
859	11	9	885	GGGTAAAACAAGTTCATAAATCTGGTGGTTACCAGTCTAGGGGATATGGGTATGAT	687	A_95_P191507	DW000640
863	11	13	599	GCTAATGATCCTGGTTGAGTTGAAAGTTCTCTTATTAAATCCTCTTTTAGCAGTTTTG	695	A_95_P013096	TA13412_4097
866	11	16	977	ATTTATTTTTCTGGCTTGGCTAGGTGGGATAGCCGAGCCATTCCCTTTTCTTTCGGAT	701	A_95_P220802	TA21687_4097
876	11	26	794	CATCTTTTACTCTTTGGATGACATCTAAATGCATATCCCTCGTCTGAGCTGGATCCTG	721	A_95_P024736	TC65556
881	11	31	571	AAAGAGTATCACGGTCTTTTCTGAGTGATACTGGTATTATGCTCTTTTTCCATAATGT	731	A_95_P152802	EB683143
883	11	33	549	TAATACCTCAAGTTTTCACTTTGGCTTTTTGGCCATGGAATTGCATGTTTATCAACGTT	735	A_95_P210377	TA19384_4097
884	11	34	712	CATTATATCATCATATTCAGCTTCCAAAGTTGACGTTCAGCCTCTCTAATCGCAAAAG	737	A_95_P303113	FG173678
885	11	35	488	ATGCTCAACTAGTGGAACAATTGAATAAATCACGACATTATCAATGATGTCAAAGGT	739	A_95_P019281	TA13065_4097
886	11	36	750	ACAGTTGGAGACCAAGATGCCTCTCTAGAATCCCCTCCATTCCATTACCTTGATCATG	741	A_95_P145932	EB449699
889	11	39	462	TAGACCTTGGAGTCCGTTTTATATATTTTAGTTTGATGGGTAGGTCGAGGCCATGTCC	747	A_95_P090308	BP530896
906	11	56	537	GATTACGTGGAATTTCACCAAAGTACTTGGTTGATAAGGACGGGAAAGTAATCCGC	781	A_95_P113662	CV021245
908	11	58	324	ACAATTGTAATCGCCCCTGGCCAAACAACAAATGTTATAGTAACTGCTGATCAGAGT	785	A_95_P147147	U45243
912	11	62	163	TTATCGTTTGCTGCATTGCATTGACAAGCTCCTGTAATATATGAATGTTCGTTTTGGT	793	A_95_P108157	TA12282_4097
914	11	64	798	AATACTTTTTGCTGTCTTCTTCGTGTTGAATGCTCTCATCTGGGAAGAGCATTCTTCTG	797	A_95_P016706	EB682133
917	11	67	535	ATTACGATCTTCACTTCTCACAGTTCAGCTTAGAAAGCTTGGACAGAGCGGAGGAGC	803	A_95_P084410	BP529010
920	11	70	820	TCACGGATAAAAGTTAGAAACATTGTGTGTGGGCCAGGCCATGGTATAAGCATTGG	809	A_95_P204087	EB680983
924	11	74	618	GCTTCCAACTCTAATGTACATGCTTATAATCTGTTTAATCTCACTGCCTTGGTTTGGTC	817	A_95_P211417	TA19605_4097
925	11	75	617	AGATTGCAGAACTGAAACAAATCTCTATGAAGCCTGATGTCGTTGAGGTGTGGGAT	819	A_95_P137887	FG141586

944	12	9	713	GTGCTTAGCTTCCTTTGATTTGTAACGCTTGTTATGTAATCGACAGCTAATCATCTATG	688	A_95_P185322	FG638902
946	12	11	581	TTTCCCTTGGCTTGTGGACGGTATAGCATGTGCATTACCGAAATAGAGGCAGGATTT	692	A_95_P189007	TA14699_4097
950	12	15	859	ACCTTGTTGACGTGAGTCACACCATCACTACAATCTTCACAGCTATTTTATTCGTTCTA	700	A_95_P292753	EB428347
954	12	19	454	CTCAAGAGGTCATTATTCTTTTGTAGCTAAGGGTCTCTTTGGCTTGAAACTACATGAA	708	A_95_P071565	BP525734
956	12	21	1439	GGTTTCAGAAAACATTTAGAAACAGATCACAGACTCAGTTTAACGTTCAGTGTTTAGT	712	A_95_P017931	TA15520_4097
957	12	22	1263	GCTCTACCTTTTTTCCGTCAAAGGACGAATACTTTTACTCATTAAACAAAGTGTTGTTT	714	A_95_P196147	TA16276_4097
959	12	24	574	TGTTGTTCTGAGGTTGAGATGGCATATTATTCACGAAAATGCATCTTACATGTAGCCT	718	A_95_P186897	TA14226_4097
962	12	27	1195	CCGCCAGCATGCTGATTAATTATTAGTACGTCTTTTCTACCTCAAATTATGTCTATGAA	724	A_95_P033041	AF248538
965	12	30	757	TTTTGATGATTTTGATCCTCGAGGGACTTCAAGTACTAAGCCTTCCACCGAAAAATCT	730	A_95_P152307	EB682651
968	12	33	688	TCAATACTACGACCAATCTGGTAATTACCACCAGAGGAACCATTTTAATAACTATAGG	736	A_95_P263761	FG194966
974	12	39	820	GGTGCTTGTGCTGATGTAGAACACTCATTATGTGAATAAATAAGGTGGTATAGAAGT	748	A_95_P017451	TA16621_4097
975	12	40	105	GCTTTCTAAACTCTAAATCTTAGAAGCTCATGATTTGTACTACCAGCCCTTGGAAAATT	750	A_95_P242962	BP136210
977	12	42	505	ACACCGAGTCAAAACCATCTTTTGCATGGAATTCTTTTTCTTGGCCATGCCTTGGGGA	754	A_95_P261866	BP535041
980	12	45	0	AATGTTATTCCTGGCTATTCTGGTGCACGCCATTCCTGATGTTAGGCAAACTTCAGAG	760	A_95_P018896	A_95_P018896
981	12	46	747	TGCATGCTTCATTCGCGTCATTGGTAGTGAGCTTGTTCAGAAAATTTGTTTGGTGAGG	762	A_95_P161222	EH619974
987	12	52	1384	CACTGTTATTAGGTCCTAATTTTCATGTTATGACAGGACGTTGCAGTAATGCAATTTAT	774	A_95_P186867	TA14220_4097
993	12	58	866	GTGGTTAAAAGCTGTCGATATGTAGTTGGTCAATGGTGCTGTTATATATGTCACCTCC	786	A_95_P235814	EB438108
995	12	60	741	ACTCGAAATGCTGTATACAATCTGCAATGGCCTCCACATGGAGGAAAGCTACTTGTT	790	A_95_P311933	FG182336
1001	12	66	333	GATTTCGAGTGTCCATGCGGGGTTTCGTTCGAAGCTTCTGTTTGATTTAGCTGCTGAA	802	A_95_P255334	FS390767
1010	12	75	687	TTGTTGGATGTTCTACTGGGATGCTGAGATATTAAGACTTTGTTACCTCTGTTGGATG	820	A_95_P291363	EB443533
1011	12	76	847	TCACATCCGGTTGTGACGCCACTTGTAAGACGAAAGTGCTTACTATAATAGCAGTAT	822	A_95_P230634	FG153736
1013	12	78	230	AAAGTGTATAATTGGTTCAAGTGAAGCAGATGGTATGCATCAGTTTTGTTTCATTGT	826	A_95_P103572	CV016582
1014	12	79	701	AACCACACGTGGTCAAGTTGAGCTTTTATCAATATTAAATCTTGCACACCAAATTCTA	828	A_95_P218477	DV158252
1032	13	12	589	CTGTCCTCCCTTGGATTTTTGTTTGCGCTCATCATTTTTAATAATTTAGCTGTTCAAGC	840	A_95_P018666	TA15222_4097
1034	13	14	1846	GTTAGTCCATTTTTTAATTATTTTCTTGGCTATAGATTGGTTGGCAGCTGTAATTCCCC	844	A_95_P101338	AB063573
1037	13	17	1460	GGAGACTTGTCAACAACAGTTATCAGGCACTAAATGAAGGAAGGCCTGTAATGTCCT	850	A_95_P196067	TA16258_4097
1041	13	21	525	TTATCTTATAGATATCTGAAAGTTGGAGCTACAGTCCCCTGAATGATACTGAGGAGG	858	A_95_P083975	BP528901
1046	13	26	456	ACCAGCTCGGCTGTACTTAATCACTACTGTAAAACTTGATATGAAAGTCATTACTTCC	868	A_95_P003151	TA15228_4097
1047	13	27	1049	CACGTATACTTCGTGGGGAAATTTTTTGATGTATTGAATAGAGAAAATGCAGCTCTAT	870	A_95_P012456	TA14712_4097
1051	13	31	801	GATGTTCTACATTCTCAAATTCCGCGAGTTGGCAAAATCTGTTCCTCTGGCAATTGAT	878	A_95_P254744	FG645377
1059	13	39	798	CTATTCTCCAGTGTTTGAAGTTCTCAAAAAGCACTCCGTGACAGTAAAGTTTATCTGC	894	A_95_P136062	EB439624
1060	13	40	507	GCCACTGTACTCGTAATTTTCATGAATTAACAATATGTTTGCTTTTTCAACTCAGTCGC	896	A_95_P199682	EB428431
1062	13	42	490	CCCTCAGGTAGCTAGTGCGACAGCAACATTTGTGATGATGTTCTCATCATCTTTATCA	900	A_95_P155647	EG650179
1064	13	44	526	ACTGTTGTTGCAGCCTTGTTGGCCTAGGTCATATATATATGTCGTGTTGGACTCTTTA	904	A_95_P308353	FG642098

1065	13	45	420	AGTTTCAAGCACTGATATAGTCGGTCGAATGCTTCTTTGTGTGAGAGAAAGGTCCAC	906	A_95_P058821	BP134571
1069	13	49	748	CCGAAAGATTTGGATTCTGACACTGGAACAGGATAGAGTCTGTCTGGCATATTTTAA	914	A_95_P164787	EH624095
1071	13	51	518	TCATGCTTCTGTTTCTTATTCCATCTAGAAAGGTCCAACAGGCTTTGATTTGATATTCA	918	A_95_P073150	BP526144
1072	13	52	648	GGTACGTTCGAATAATAAAAAGAAGTTCTCTTTCTAATCCTATTTAGATTCTGTCGGG	920	A_95_P016546	EB432718
1078	13	58	233	CAGTTGGAAGTTTTGATTGTAGTTCATTTTGATGGCTTTGACAATTGAAATGCTACTC	932	A_95_P000781	FS383363
1081	13	61	232	GCAGCCTCTACATGGAAGAAGTGCATGTAAAGCTGGGGGAAGAATTATGGTTTAGC	938	A_95_P128062	DV159197
1087	13	67	758	TCTTGCTGGCTTCATGAATTTAATAGTTAGCAATAGGTATGCCCTCTTGTTCTTTTTC	950	A_95_P015131	EB425115
1088	13	68	563	GTTGGTTGCATCAGCACTGTAATGCAGTTCTCTCTTTCTTATGCTAATGATAAATGGA	952	A_95_P124112	EB437086
1089	13	69	0	ATGAGCGCCTGATACTATCACTGGGGACATAGTTTTATCTGCACAGAAGAACATCCA	954	A_95_P259776	A_95_P259776
1091	13	71	802	CTCGTGCATTCAATTAACACAACGACGGTCAAGCAAATGGTTATTGGTTCAACTGCA	958	A_95_P233494	EB426692
1093	13	73	511	GCAAAAGGTGAATTCACGTGAGCACCAGCTTAGCTAGCAAAGGCTAAATCTGGGAT	962	A_95_P293318	FG638280
1094	13	74	291	CTTCCTCAGTAGTCAGTTTTGCAGTTCATTTTCCAGGCTCTCTTGTAAATAGTATATA	964	A_95_P213932	TA20153_4097
1099	13	79	1282	ATGTTTGTTTGTACCTAAGAAGTCATGCTCTGACCATCATGTACTAGGAATACCTTTT	974	A_95_P204147	TA18002_4097
1111	14	6	432	CGAGAGTTATAGTAGCTACTAGCTAATGAGAGTTGAGATGGAGTTGGAATAGTACT	829	A_95_P023241	TA14334_4097
1112	14	7	747	TCTTTTTGTAACTGTCCAGTGGTGTTAATGAAATGAATTGTTTGTGTTCTTGCTCCCGA	831	A_95_P220582	DV160025
1119	14	14	395	CATTTAAGTGGGGCGCTTAGAAGTCATGGATGTGGATTGAAGTCATTGGTTGCTTTG	845	A_95_P133602	TA13380_4097
1122	14	17	237	GGATTAATGATTCTTTTCTTATGGGTGGCTGGTTTGGAAGGAAATGTGTTGTTACAG	851	A_95_P142142	EB445689
1126	14	21	303	TTTGTGTGTTCATTTGGTTGGGTCAACCGGATTTCGTCACCGGAGAGCCTTCATTAT	859	A_95_P100553	BP535423
1127	14	22	492	AAAGAAAAGAATCCCTGATTGGTCTTACTGCAATGCGTCTTGCTCTGCAGCTTATATC	861	A_95_P147742	EB643431
1129	14	24	798	AGCTTCTGTAACTCAGGGGAACTTCTCTCTCTCTTCGAATGTGTCTACATCTCTTACAT	865	A_95_P292893	FG159469
1131	14	26	757	AGAATAAACGCTATTTAAGAACATGCTGTAACTCAGCGGCCATCCATTTATCCAAACT	869	A_95_P123482	TA13385_4097
1133	14	28	397	CTTCCTAAACCTTGCCTTTGATGGTTTCACCAATGCTACTCAGGATTCAATTTCAGCAA	873	A_95_P147318	EB451668
1143	14	38	567	TGCACATTGTGTTTGTAAATATTGGACCCTAGGATGGGTATAGAATGGCTTAATAGT	893	A_95_P035258	BP128420
1150	14	45	828	AGATCTGATGCTACAAAAACAGTCTGCTCAGAAGCTGACTCTGCTAAAGCTTTGACT	907	A_95_P231484	FG168673
1154	14	49	579	TACAGAGTGTCCTTGCCTCCATTCATCCAGTCCCTGTCTTCTAATCTATTACGCAGATG	915	A_95_P211622	TA19656_4097
1166	14	61	785	TAGTAGCTTTGGAGGCCTATGATCCATGATGCTTAAACTCGTGAAGAAACTCCAGCC	939	A_95_P222877	DV160855
1168	14	63	830	TTATTTTTCAGTAAGGCTACCGCTTGTGGGTGACAAACACGTCTGCAAGTCATGGCT	943	A_95_P190282	DW000482
1169	14	64	579	CCCCAGACCCTACTGCTAGAATTATACTGGGTTGTTGTTATTGTATATGTTTGAGGAA	945	A_95_P133892	EB435588
1171	14	66	596	TTTCCTGATTCTTCTCCGACTCGGCTTGATTATTCAGTCGTGACTCTATGGAGCTGTTG	949	A_95_P261386	BP131950
1177	14	72	250	GCGGTCTCCCAAATTCAGAGATTTATTTTCTGTTTCTTTTGCTTTGCTGCTACTAATTG	961	A_95_P210012	EH622576
1179	14	74	755	GTTTTATGGTTGTAAGAGAAGATGAGAGGAGATCTGATCTCTGCTTTTGAATAATAA	965	A_95_P005176	TA13310_4097
1182	14	77	727	CCAGGAAAATGTTCTTTTGTGATGAATGCCCCTATGCTTATGTTTGATATTATGTACT	971	A_95_P185927	TA14019_4097
1183	14	78	777	ATTGGATCAGTTGAGGGAAGTCAATTCTCAACTTGAAAGAGATGTCGAGCGTCTCCG	973	A_95_P150662	EB680800
1196	15	6	550	GAGCCCTTTCCGTCTCTGTTTCTCTTGCTATCTTGTGGTTTATTTTGGCTAATACCATA	979	A_95_P161672	EH620337

1197	15	7	179	CTACAAGCATACACATCTTTAAGGTGCTCAAGCAAGTACATCCAAATATTGGGATCTC	981	A_95_P107987	CV018625
1198	15	8	374	GTAGTTGCTAATAACTTGCCCTGGAGATAATCTAATAATAGGAGTGATTTCCCTTATT	983	A_95_P072015	BP525847
1200	15	10	659	GTCAGGAAGGAGTGGTTTGAATATGAATTGTTTGTAAATGTTATCAAAAAGAGCAC	987	A_95_P273261	EB683099
1201	15	11	735	GGCTATATTGTTCTTAGTGGTGCATCCATATAACATGTTTCTGAATCTTTAAGCTTCCT	989	A_95_P015766	TA12645_4097
1207	15	17	761	ATGCCAATTCCTACAGTTCTTGCCACATTCCAGACATGTTTTTCAACACCTAAAAATCA	1001	A_95_P145362	EB449049
1209	15	19	931	TGACCCGCGACAAGGATTCATTTACTTTATCTTTGAAAATAATGATGGCACTGGTGCT	1005	A_95_P287008	EB680567
1213	15	23	568	GAAGTTCTCGGGTTTATACTTTATATATGAGGGACATGTATGTCTACCAGAATGTTTA	1013	A_95_P181402	TA12971_4097
1217	15	27	739	GATTTCATCTTCCTCGTTACCACCTACTGCTTTACAAGATGAAAAGATGAGAAAATCT	1021	A_95_P295748	EB447898
1220	15	30	506	ATTTTGAAAGGAAGTTTTGACTGATGTCGAATCTGAGTAACAAATTCTCCTGAGTTGT	1027	A_95_P020906	TA18706_4097
1221	15	31	793	GTGGTATTATAGAGATGAAATAGATGCTAGACATTTCTGCTCAGTGTGCATGCTGCG	1029	A_95_P230794	FG142267
1231	15	41	104	ATCACTGGACAAAATATGTTGAAAACCGAATTGCTGAGCTTGACGGAATTAGCGTGA	1049	A_95_P104922	CV017224
1233	15	43	214	TGAATCAAGAGTAGTCCAAAAGAACCATTTTTCCAGGACAAGTAAATCAGAATGATT	1053	A_95_P222417	TA22028_4097
1234	15	44	800	CAAAGTTGATTGCCCGCAATAAAATAATAGTGCTACTCCAAGATGAGAATGTTAAAA	1055	A_95_P224272	EB451426
1236	15	46	634	GATGGACTTTTTCATTGCCTCTTAGCTGTTTCGCTTGTTTCTTGTATACCATAATTGGT	1059	A_95_P203992	EB437103
1238	15	48	1711	GTGCAAACTCGATAGAAGTAAGATTTTCGTCGGTATAGGAGAAATATATCTGCATGT	1063	A_95_P020731	AJ001770
1240	15	50	337	ATATCCCTGCTAAATGGTAGAAAATCCAGTTCATGATTTTATAAAGGATCGGTCTAGT	1067	A_95_P027626	BP532334
1243	15	53	742	ATAGTGTCATGGATTCTATATATCCTCTTGCAATGAATACATCATTCAATGTCTGGGC	1073	A_95_P228739	FG641655
1247	15	57	780	TCGCAGCTAAATTTGAGCTTGACCAGAAGCTGTTCCTTCTCCTAAGGAAGGTTTGATG	1081	A_95_P236759	EB438902
1251	15	61	874	GTAGCGTTTGTTTCTTACTAGTCCGGTCGCCTTAGGTTATTATTGATATTAACTATTAA	1089	A_95_P237649	D63951
1252	15	62	955	CGGGCAATGGAGATGATTATATTCATCAAATCCTTTTAGATGTCTCCATGCTTTCTATT	1091	A_95_P019756	TA15277_4097
1254	15	64	769	ACTTCCTCTTTGGAACTTGTGAAGTATGTAGCAATAGGTGACAAAAGTGCTCCTGAA	1095	A_95_P183097	TA13379_4097
1263	15	73	785	ACTTTTCTAGTCTCTTAAAGTAGCACGCCGTGCGTTTCTGGGGACACTAGGTTAATTG	1113	A_95_P135997	EB439557
1265	15	75	836	GGTGCCATTCACACATTCCTGTACATAGAAACTCTAATTTTGAATGTAGATAAAACTG	1117	A_95_P026471	EB424860
1266	15	76	758	CCCTGCATATGGTTGAGATGTAAAATTGGATAGCGGAATATACTTAAAGATAATTGT	1119	A_95_P226524	TA16197_4097
1283	16	8	769	GCTTACTGTCTTTCATTGTATACCAGAGACATACTGAGTTATGCAAATGAAAAGATTC	984	A_95_P011941	DV158664
1284	16	9	873	CACGTTGCAATGGTCAGTTGTTTGATATGACCTTAATTCCTCTCGTACTGTTATTTTGA	986	A_95_P297143	FG158759
1296	16	21	1116	TACTCTCAATCTGGATATACTTCTCCTTGCATAGCTTGTAAGCTCCCATTCTCCTCAAA	1010	A_95_P012986	TA13713_4097
1307	16	32	736	TTCTAAGGTTGGTGTCCAGAATGCGCTCCTCTGCATGTTGTTTACAGATCAATGTCAG	1032	A_95_P215462	EB441710
1308	16	33	834	CTTCGGCTAATTAGCTTTAGTGACCTCATAGCGTTACATTATTCTTTTGAGGCATAAAT	1034	A_95_P009306	TA15339_4097
1309	16	34	428	GCCAGTGAGAGTGTTCTCACCAACTATATTGTCCAGTTCAATAAATTCAAATTTTCATT	1036	A_95_P097368	EH620951
1310	16	35	874	ACTTCTGTCATGTTCAGCTTTCCCATGGTTTACTGGACTTGCTTAACACATGTTTATGG	1038	A_95_P267136	EB451747
1311	16	36	780	ACTTTGACAGGAAAAACTATCACCTTGGAGGTTGAGAGTTCGGACACAATTGATAAC	1040	A_95_P009637	EB451553
1316	16	41	261	GAGGAAGCAATTGATACACAACCAGTTGTTCACTTAGAAAGTTACTGAGTTATATTG	1050	A_95_P221132	AM807541
1318	16	43	474	GACTGCCCGTATGTGGTGAGTTATCTCTTTTCCTACAAAAAACACAAGAAAAAACAC	1054	A_95_P097913	BP534257

1321	16	46	897	CTCTATATATAGAGACATGTTTGGGGAATTGCTATTTGTTACATCGACAATCGTAATG	1060	A_95_P178282	TA12203_4097
1330	16	55	779	TGATGCTGAGCTTAACTATGGATCCAAGAACTGAACACTTTCCAGGGCAGAATATCCA	1078	A_95_P158732	EH616597
1333	16	58	834	TGGTGACCTTGGATTGTTTTGAATAGTTACTGAATATTTTGTTCTTTATCCAAGTCCG	1084	A_95_P026426	DV159019
1337	16	62	354	GATTTGCCTCCAGATGCTAGGCCTCTGCTAGTTTTTCTAAACAAGAAAAGTGGAGCT	1092	A_95_P085270	BP529235
1339	16	64	687	TGGGATTAGGAGTTAGAGGGGGAGATTCATTTGTTAGGTAGGTTTAGACATGATTGT	1096	A_95_P193372	TA15655_4097
1350	16	75	1590	GCTGTTGCACAGTTCTGGAAACTAGTAGTTCTATTTCATTCTTACCTTTAATTTAGATC	1118	A_95_P190337	TA14994_4097
1356	16	81	1155	CAAAAGAAGAAAAGATTAGCAGTATCTGAGGAACTCTGATCCTCTTCGTGCGCAGCG	1130	A_95_P248977	Z99173
1366	17	6	759	GTCTGCATATTGTGCTTTGGCTATTGTGTTTTTATTGCCTTTTCTTTATTATAGGAGCGA	1134	A_95_P117527	DV160448
1367	17	7	779	GTTCTATGTGTTCTGTCAAGGTTGGTTTTGTCAGTTTGTTGTCGTGATTTTGTTATAGT	1136	A_95_P148532	EB447962
1371	17	11	637	GCTGATCATTTCGTTTGACCGTTGCTTTACAATTGTGAAAAAACTGTCTGCAAGTTCTT	1144	A_95_P187902	X83731
1373	17	13	0	GTAATTATCGTTGGCGCCGAACAACATTACCTTTTCGTGGTCAGTGAAGTGGCAATT	1148	A_95_P316223	A_95_P316223
1375	17	15	2685	TTGTACACATGTTGTTTCTATAGTTACTCGATTAGCTCAGGCACTTGGTGAATCAAAAA	1152	A_95_P251837	AJ344534
1376	17	16	235	GGTACCTTAGTTATATAAACGGAAAACTGTAAAAGCTACTATGAGGTTGATAGATGG	1154	A_95_P089203	BP530396
1380	17	20	553	AATGGCTGTGGAAGCACAAACGTATTTTCTTTTTCTGGATGTATCAGATAGTGGGTGT	1162	A_95_P205437	TA18288_4097
1387	17	27	0	CATTAGCCTACTGAATATCCAAATGTAGTCTATTAGTGAAACAAATGTCTGTACTGTA	1176	A_95_P029521	A_95_P029521
1393	17	33	0	AGTAGCTTTGGGTTTGGTGGTCGTCTTGGCAGTACATATTCAATCTTATTAAGCAAAA	1188	A_95_P015856	A_95_P015856
1395	17	35	375	TTAGCTGCAAAAGTCACCTGCAATTGTTTGGGCTGACACACCTAGGTATTGGAGATG	1192	A_95_P163957	EB424810
1396	17	36	800	GTACAATTGTCTATACCTTTGTCAAGTTGAAGAAAAAGAGAGTTTCTACCATTGCTGA	1194	A_95_P272451	EB450147
1402	17	42	600	AAATACTCATATCTTTGATGTTGTGGGAAGGGACAGTGGTGGTCCTAGAAAAGGAAA	1206	A_95_P208787	DV161692
1404	17	44	455	GACATTGATTGAATAAACCTGGATATTGAGTTTAGTATATCCACAGCCATTTGTAAGT	1210	A_95_P075645	BP526781
1411	17	51	496	TGGGGGTTGTAGAGACAATTCTTGTGAACTTAAATTTTATGGTGCAATGCATTTTTCA	1223	A_95_P143562	EB446820
1416	17	56	767	CATTAAGCATACTGGAAGGTCAATTCCTTTAAGGCAAGGTAGGACTCATAACGGGA	1233	A_95_P195332	TA16092_4097
1421	17	61	986	CTTGCTTTCTTGGTGTTTTGTGTCGCTTTTATCTTTCTAAAAGACCTGTTTTGCTACTGG	1243	A_95_P185087	TA13839_4097
1422	17	62	810	CTCTATCCCATAAACGTGTATCTCTTGCAATGTTCCATGATTAATGGTAAGAGTTTCT	1245	A_95_P020111	EB437080
1427	17	67	1625	CCTTCTAAGCTAAGGTTGTAAATGTTTTTGGCTTCTTGTAGTTCTTTATCATGTGCTAT	1255	A_95_P187747	TA14415_4097
1430	17	70	628	AGGTTCGAAAGATTGATGCTGCAAAGCCTGTTGGAGAAGTATTTGAAGCAGTTAAA	1260	A_95_P058081	TA13632_4097
1431	17	71	952	TCCGTTGTTTCAAATAAACATGTCTGTTGTGTGTATTTCTTGCCCCACGGAGAATTGT	1262	A_95_P177252	TA11924_4097
1435	17	75	656	CGAGCACATTACAAATGATGAGGTCTTATCGTGCTACCGTGGAACCAAATTATTCCTA	1270	A_95_P040596	DQ156499
1455	18	10	724	TTTTGCAGCTATTTATTATAGACCAAGATACATCTACTGCTAATTATGTCCCCTTCTTG	1143	A_95_P117032	DV159832
1456	18	11	782	ACCTGCGTTACCAGCTGTTGAATGGATTTGACAGAGCTGTAATTAGTTACTTTGATGT	1145	A_95_P030656	EB441893
1457	18	12	960	CCGGTTACAGGTTTCCCTGTCGAAAAATTATAAGCTGACAAGTTAATTTTTACATGTA	1147	A_95_P222862	TA22124_4097
1460	18	15	298	GGCCGAAGTCCCTTTTCCATGTTATTTGTTTGTTTATCTTGTATCAGACAAACATGATA	1153	A_95_P272056	EB447213
1464	18	19	252	AGAAGGCTGACGAGTTGAAATCTAAAGGCGTGGACGAAATTCTCTGGCATTAGCGTT	1161	A_95_P111412	FG163565
1477	18	32	239	ATGATCCGTGAATGGCCACGCTATGTGAATGTTCCTTTTCCTATTGCTAAGGCTATTG	1187	A_95_P162257	EH621191

1480	18	35	409	AAACACGGTTTAATGAATGTGACATCTGCTCATAGCAGCAGCAGAGGTATTACCTCA	1193	A_95_P155047	FG624180
1482	18	37	860	ATGGTGGAGCGCTTAAGAACTTTGAGCGCAAAGTCAAAAGGACAGTTCATTGCAGT	1197	A_95_P119137	DV162210
1483	18	38	799	TTTACGCTCTTGTCAGACTATGATTCTTGTAGTAGTGGTTACCTTGAAGGTTAAGTTC	1199	A_95_P185217	TA13865_4097
1495	18	50	1574	CTTCTGCTGCTATGAAAGTTCAAACATTGCTTGTTTGTGTGAAATCGCTTTATCTTTTG	1222	A_95_P177047	TA11865_4097
1496	18	51	587	GGCGGTTTTCATGCTCGTGCTTAATAAGTTGTAACTTGTATCATGACATTAACAATTT	1224	A_95_P015446	TA13395_4097
1497	18	52	915	GGGTAGCTGCTACCTTTTCAGAATGTGATAGTGTGCTTTTCTTGTACTACATGGGGCT	1226	A_95_P228949	EB424767
1500	18	55	429	CTCTGTTCAGTTTCTTTCTCAATGTGGGCTATGTTTTGTTGGTGATATGCAAGATATGT	1232	A_95_P112117	CV020527
1508	18	63	244	ATACAGTCTTTATCTGATTTGAGAGAGGGACCTAATAATGTTGTCTAAGGGTGAACA	1248	A_95_P115457	DV157676
1511	18	66	824	GCCTGTGGGGAAATTATGCGGCGGATGAATTCTGGATATGCTGTGACTTATGTGAA	1254	A_95_P148747	EB678220
1512	18	67	194	TCTTTTCCCCATAGGATAAAAGGCTTCCATTTGAGTATGAGAAGCTGCATTTCATTCT	1256	A_95_P092228	BP531705
1513	18	68	801	GTTGATGTTATATTTTGGTTGTCACAGAACCAATATGGCCAATCCAGGGATTTTTTGG	1258	A_95_P244182	DV159141
1524	18	79	511	TCCCTGTTGGTATGGTTTTGGTTTAGGAATCATTATGGATTTACTGCTATCTGAGAAA	1279	A_95_P161502	EH619999
1536	19	6	534	TAAGGTGGATCAGGAAGGTGCTGGCATATGTGTAGTAGGTGCTTAATGTTCTCATTT	1287	A_95_P099593	BP534984
1540	19	10	201	AATTTGTTCAGTCCCAGCTTATATTGGCGGGCCTAACCATTGTCACTCACATACTAAA	1295	A_95_P142792	EB448450
1543	19	13	894	TGCCGGATGATATTTTGGTGCAAATATATGTGGTGGGCTTAATTTACAGTGTGTAGT	1301	A_95_P017981	TC50995
1550	19	20	838	ATTTCTTTGGGCCGAATCTTCATGCCTCTTCTGGATCTAATGCTTCTTCATCAGCAGCA	1315	A_95_P126742	EB426082
1553	19	23	765	CAGCTGACCCACTATACTCTTGGTTCCTTCAATAGAAAACAACAAATCATTTATACAT	1321	A_95_P179122	TA12432_4097
1566	19	36	491	TCAATGCTAAAGAATTTTGGTGAGTAAACCAGATACCAGTTGATGGTCAAATTCGAT	1347	A_95_P123572	DW003446
1575	19	45	378	TAGTAGGATTTTCGGATTTTTCACTATGGCTCTCGCTATTGCTACTCGTTGCTTTTGCC	1365	A_95_P237209	TC72133
1579	19	49	659	AAGAAGTTAGCGAAGCAGCACAAAGTTGATATAAACGAAGTGACTGGGACTGGGG	1373	A_95_P021456	TA16973_4097
1580	19	50	512	TGATTATGCTTGGGTTGATGCAAATGAGAAAAAACGCCGGATGAAAGCCCAGAAGG	1375	A_95_P046926	BP131524
1588	19	58	832	AGGTAATAGTCTTACAACCCATCTCGACCCGCTCGGGTGCTCGACATTCTTTTCATAT	1391	A_95_P252894	FG158368
1589	19	59	766	TAATGATAGGGACAAAGTTTGATGACTTTGTGAAATTGCCATTGGATCTGCAGTGGA	1393	A_95_P269676	EB425968
1590	19	60	852	ATTTCATGTGCATGCAAACAAGCGATTGTCGATTCTGTGATGGTGTCAGCAGCAGCA	1395	A_95_P311493	FG143338
1593	19	63	506	ATGAAGGGTTTGGATTTGGTTAACACCGGTGGTCTCTGAATTAGATTCTGTAGATCA	1401	A_95_P218522	TA21194_4097
1596	19	66	748	ACTTTAATAATACTTTGAAGCGGCATACACTTGTCTTACGGAAAAGAGATATAATGC	1407	A_95_P252699	EB425907
1597	19	67	185	CGTAAACGCATCGTGGTGGCATCTGTATTTTTCATTGTCTTTCATCATATTGTAAAATT	1409	A_95_P031131	CV018094
1599	19	69	537	CGTGACAGTTATCGTACTTGTTATGTCCGTGCCAGAGATGCTATCCACAATAAGTTCT	1413	A_95_P103187	CV016386
1600	19	70	821	AAAGGGAGTCGATGAGTTTCATTCTGTGTTCACTGTCAGTGGGAGAAGAGATGTCT	1415	A_95_P310308	FG166065
1601	19	71	301	TTATCCCAACTTAATGTGGTCTGTGCCTCTGTCTTCTCAGTATCAGTGGCTTCCTAGAG	1417	A_95_P046951	BP131533
1602	19	72	760	CGACCCGAATATATGCGGACAAAAGTTCTCAACTTTTTGGGATCTTAATTTCTCCATG	1419	A_95_P293828	EB679766
1603	19	73	782	TACAGATGTTTCCACCAACAGTGAACTGGGATACATCACTGGTCTACTAGAGACCGA	1421	A_95_P231349	FG144474
1607	19	77	666	TATGAGAATGACTGGGATGTCGTTAAAAGAGGTTGGGATGCTCAAGTTCTTGGTGA	1429	A_95_P136632	X70651
1608	19	78	847	CCTCTTGTAATTACCGGCATTCTGCAATGCAATCTAGTTTTCCATTCGTAATCATATTA	1431	A_95_P124602	DV162646

1609	19	79	842	AGTATATGTGCTGACGCTCAGACTCTTGACAGAGCAAGTATAGCTGTCTCAGCAAGC	1433	A_95_P235359	FG157246
1612	19	82	681	AGGCCGGTTGCTGTACGCTCCCTTTTAGCATTCCTTTTAGCAATTTCTGGGAGCAAAA	1439	A_95_P265546	BP531034
1620	20	5	201	GAGTGCTAGTTATGTGAACTCTCCTTCAATTTGTACTTGTCTCCATATATTGTGTGTAA	1286	A_95_P028816	TA22261_4097
1621	20	6	256	CTGTGTCATATTGGTGATTTGTACCTTGACCGGATTACATTCTTTAGATTTCTTACTTG	1288	A_95_P074425	BP526468
1625	20	10	319	CTTCCAAAACGTTTGTTGAGCAAAGTAGTTCCCGTTTTCCAATTTGGCGTTATTGGCC	1296	A_95_P126567	BP530134
1627	20	12	830	CAAGATTAAATTGATACAACTTCTAGCCTGTTTGGCCAAGCCTTTTTCTTGGCCAGAA	1300	A_95_P013401	TA13459_4097
1629	20	14	745	CGCTGCATAATATGTACATTGGCTCTATTCATAATTTCATATTGTATTGAGTTGATGG	1304	A_95_P013051	TA15815_4097
1630	20	15	707	GCTGACGACGTTAACACTATACGTTGTGGAATATGAATTCACTACTTGATCTGATGTT	1306	A_95_P013171	TA13802_4097
1631	20	16	849	TCTTGGCCACAAATGCAAGCATTGTAATTCATATAACACCCGCATGATTGGTACTGG	1308	A_95_P015471	EB432321
1632	20	17	1452	TTTTAGCATGGGATGTAGCATTACTAATAGGAGTTCTTGAATGCAATGGAATAAGGG	1310	A_95_P176692	TA11722_4097
1634	20	19	736	GTGAGAATATTTTCTGAATGCGGCAAATTAGTGATTATTGGTTGTAATTGCTGGAGTT	1314	A_95_P267571	DV160713
1639	20	24	1133	GACTTTGGGAGGTATCTTTACCAGGCTGATCAACAGGAATACCACCATACCTACAAA	1324	A_95_P187002	TA14248_4097
1643	20	28	783	CAAGGAGTTACAGGCTTCGGAAGGAACATTAGTGGACTATTCAAGCATGCAATCACT	1332	A_95_P150762	AM746200
1645	20	30	2611	GGTGTTTCGGGCTATTGCCTATTTATTGTAAGAATTCTGTATTGAACATAAGCAATGA	1336	A_95_P250567	AB120519
1649	20	34	838	AAAGAAGTTGGGATGGATTTGGGGTCATTGCTGAATTTTGACAGATGTGGTCATCGT	1344	A_95_P230919	EB426067
1651	20	36	833	CTGGGAATTTGTAATTTGGATCTACCTACTTGGGAGTTTAGTTAGTAATTTGTTATGG	1348	A_95_P187082	EB452066
1654	20	39	426	CTGCTCAAGTACAACGTACTGAACGAAGACGCGAAAGATAACATAAGAAATACTAC	1354	A_95_P086663	BP529596
1657	20	42	654	TACTCTCTTCCTTATTGTGACTGTTGGACGCTATAGCTATTCTATGAACTCGTTGTTTT	1360	A_95_P124737	TA14667_4097
1658	20	43	762	CTTACAGCAGGACTTCTATTTACCAGTCAAAGGAAAAGCCATAGGCAACGCCAGAAA	1362	A_95_P146502	EB450560
1663	20	48	1048	TTCCATACTTTGAACCTTCATCTGAATGATTTAATCAATCGTCCAAGTCTTTACTGTCGT	1372	A_95_P189327	TA14765_4097
1664	20	49	578	ACTTTTTGATTGATCCACGAGTTTCCTATTTAGTCTAGCAAAGCGCATGTTGAGGACTT	1374	A_95_P046336	BP131370
1665	20	50	232	CCAGACGATAATAATTGTTATACTGAACTTGGTATCTCTTAAGACTTGGTAAAGACTG	1376	A_95_P100593	BP535445
1668	20	53	865	TAACCATATGGTCTATGATTATTGCACAGACACTGCTAGGTTCCCTGTTGCTCCGGTT	1382	A_95_P248747	EB451610
1675	20	60	103	GAGATTGCAGGGTGAGAAATTTTCATGTTTTGAAGTGGTTGTCAATGATTTATCAACT	1396	A_95_P164537	EH623777
1676	20	61	613	AGCATATGTTTAATGCACGACATGTTATTAAACTTGCAGTCTGAATGGCTGTTGTTTTT	1398	A_95_P162847	EH621855
1686	20	71	716	CAGTAATTGCTTTCTCAACTTTTGGAAAGGCTTAGAATAGTTTCTACAAATCCTTTCC	1418	A_95_P273066	EB681278
1688	20	73	430	TTTTAGGAGTCTTTATGTTGTGCCCTGGAAGAAACCTCTTTTACACTAGTGTAATGCTT	1422	A_95_P120937	FG621759
1690	20	75	620	TGGCAAAAGCTGGTGAGAGAAGGAAGGATAAATTTATGTAGTTCTACTTTTGATGG	1426	A_95_P291608	DW004941
1693	20	78	274	GTCATGTTTGATCAAGTCAACTTGTAGGATGTAGGACACTGGAAATGTTAATTTGAC	1432	A_95_P106777	CV018053
1695	20	80	991	TGAACAAGGTTGGTGGTTTTCTGCAGAGAATGGATCTGGCTCGCAAGTATGCTTTTG	1436	A_95_P179227	TA12454_4097
1706	21	6	812	ATGGGGGTTTAAGTCTTTGAATAAGAAGTTTGTGTTTTGCTCCCGGCTCGCGAAAACT	1445	A_95_P013261	TA13424_4097
1710	21	10	257	TTGCTCCTTCACTTGCCTCCTCCGTTGAGTTCCGTAAAAAACTCTTAAAGGTCCCTGTTT	1453	A_95_P156737	EH614763
1711	21	11	824	ATTTGGCTCATTTGCCCCTTCAGCTGGTACCGATATCTACTTCAACTCTGATGTTGGA	1455	A_95_P251017	AY286010
1712	21	12	316	TGTGTGCATCCTTTCTGTACTTCAACAGGCTCTAATGTACTTCTTTATACTAAGAAAG	1457	A_95_P108027	CV018637

1714	21	14	1125	TGTGAGAAGGTTTGTGTTTTTTGCCACTCCTGTTTTGATGTAAAGAATTACCCATGGA	1461	A_95_P198282 TA16745_4097
1715	21	15	840	ATGTATATTGCACGCTTCTGCTCAAAGTTGTGTCATGGAGCATGGCAGGTACACAGT	1463	A_95_P311048 FG157628
1717	21	17	732	TGGGGGTGCGGTTGGGGTGATCTCTGCATTGATGGTTGTTGAAATCAATAATGTGA	1467	A_95_P194747 DW000246
1718	21	18	444	TGGGGCCTTATCTTTACTTGGTGTTTGCGATCATTCTCAAATACAGGAGTTCCTCCTTA	1469	A_95_P086155 BP529465
1721	21	21	366	GCACGGTTATGGAAGTTGCAAAGGAGGTACATTTGTTATGCAATTGGTGGTTTCTTA	1475	A_95_P052831 BP133024
1724	21	24	830	ATTCATTTTTGATATCATATTCGCTGAAGAGATGGCTTGATGTCCTTCTCGCATGGAT	1481	A_95_P296388 EB451875
1733	21	33	953	CAGGAGCTAATTGTGTGATACATAACAGTGTTGTTACTTACTAGTATTCTTCTGTTAC	1499	A_95_P197782 TA16639_4097
1734	21	34	568	CCAAGGAAGTTACGAAGATAAGCAATTATGGCATATCCGTCTGACTGAACTGCACTG	1501	A_95_P134237 DV159211
1735	21	35	555	CGTTGTACTAAAATGTTGTCAACGTCCCGCAAGTAGTTTAAGGCATCAATATGATTAT	1503	A_95_P065490 BP136345
1737	21	37	479	GCTGGTGTTAGTCTATCATCTCTCTTTTTGTATGATACTGTTTGAGTGTCTGGGACATT	1507	A_95_P116377 EB678172
1738	21	38	694	AGAGGGCTACGCTAGGTAGGTGCTAGTTTTTCTGTTTTGTTTTTGTCACTGACAGATA	1509	A_95_P146202 EB450178
1739	21	39	895	CAGCGTCAGATTTTCTGCCTTCATTTGAGACTGCTTAGAATTGTTAGAATATACAACA	1511	A_95_P183797 DV157991
1741	21	41	798	AATGCCCACTGACTGCGTACAAGCAATAAATGTACCTCTACGTCTTTACAACAATAAC	1515	A_95_P116252 DV158875
1744	21	44	495	CCTAAGGGATGACTGGAACAATTTTTCCAGGCCCCCTTTTGTCTCCTAAACATCCAGT	1520	A_95_P208992 TA19092_4097
1745	21	45	487	TAAGCTGCCAATCAGTAATGAGTTCATTTGTGTGTATGTTGTGCTTGCAATTAACTCA	1522	A_95_P274063 AM812698
1748	21	48	855	TGAGCCTGTCCAGAACTAATCTCCTCCTCTTGTCTTTCACTTGCTGTTCAATTGTAACG	1528	A_95_P008501 EB438265
1754	21	54	696	ATGGCAAGGCCGAGCTATACATTTCATGATTTCACCAATATATCCTCATGAATCTGTT	1540	A_95_P132852 EB433640
1755	21	55	759	CTGTTTCTGCACACACTACGTAAATGTCTTACATGTTCATAGATTTTATTGGTTCTTGT	1542	A_95_P191267 TA15195_4097
1757	21	57	491	GTGTCGTTTTGCTAAACAGAAAACCACGATATTGTCGTGAATTTGCGTCTAAATGATA	1546	A_95_P247577 FG640440
1765	21	65	614	CAGCGAACAACCTTCAGCTGTCTGTAATTCCAATTCAGACATAGATTTTGTTAGTAAT	1562	A_95_P203967 TA17966_4097
1770	21	70	826	TGAAAGAAATAAAAAATGGCCGCCTTGCTATGGTTGCCTGGTTAGGCTTTTATGTCC	1572	A_95_P217102 EB429719
1772	21	72	1728	CTTCTGCATAAATGTGTTATCATAAGGAAGGATTTGCCAAGATTATGTGGCAGCTTTA	1576	A_95_P105667 TA12833_4097
1773	21	73	409	TGACCATATCTAAGGTACTGTTGGTACATCTGGTTCTCTGGTTGAAAAGATTCCAAAT	1578	A_95_P102667 CV016132
1775	21	75	799	ATGAGGGAAAGTGCATCTTGGACATGGTATTATAAAGTATTTTTGTATTCTAGACGG	1582	A_95_P224422 EB449164
1795	22	10	740	AACCATAGATTTGTGGATGGGGAAACTGTTGTAGTTTGGAAACTTTGGTTCGTTCAC	1454	A_95_P147367 EB451746
1801	22	16	495	TTGCTGCCCTACTGTCACTTGCTTATTGTACTATGAATAATTCTTCTTTTGGGTTGACT	1466	A_95_P190847 FS417555
1803	22	18	452	TGTTTAGCTGATCGTTCCTGTAATTAGGTACATAAACGCTTGCCTAAAATATTCCGTT	1470	A_95_P143682 EB446921
1807	22	22	457	TATACAAGTTCCTCCCTCGTAACAGGGCACATCTTTGCATATACTATTTGTCAGTTGTT	1478	A_95_P184262 TA13652_4097
1810	22	25	787	AGGATGATGTGTTGATTGAACTTTCTTCTGGATATGTAGTTTGCTATTTTCAACCTCG	1484	A_95_P018891 TA15828_4097
1812	22	27	967	GGGATATGATAGAATCCAAACGAATCCAATCCCTGCAAAAATATTTACTTTGGTTGA	1488	A_95_P216792 TA20781_4097
1816	22	31	828	CCAAGACACCACTTTTCATTGCGATGTCAGCATTTGATTATTATCAGATCAAAACTAC	1496	A_95_P291938 EB425600
1817	22	32	757	ACTCCTGGAAGCTAAACGGATGGAAGAAGAGAATGAAAGAAAACGCATAATAGCAT	1498	A_95_P016556 FG135238
1818	22	33	766	AAATGGTTGAAAGTTGGAGGCTACATATTTTTCAGAGAGTCATGCTTCCATCAATCA	1500	A_95_P235519 EB441159
1822	22	37	711	GCTGCTAGAATAGTTCTCTGTTCTGTATTTTTGTGTGCAGTATTGCTGTGTATATTAG	1508	A_95_P265721 DW005248

1825	22	40	652	TGTGTCTGATTTGAGAACCATGGGTTCGTACAGCTAAGTGCATCTGTATGGTAGGCA	1514	A_95_P284768	BP132833
1826	22	41	657	GCGGGTTTGGACCTGTTGCTTTAACTATGTAACAATGTATCTGTATGCTATAAATTAA	1516	A_95_P306593	FG638062
1828	22	43	0	ATAGGATTCGAGACACAGCAGAGCAGTGAAAGAACAAGCAGTTGCACTAACCGAGT	1519	A_95_P292743	A_95_P292743
1829	22	44	813	GCAAAGCAAAAGCTAAAGTTGAAGGCAATATCTTTGGGGATTGTAATATCTTTATTG	1521	A_95_P258226	DV999323
1831	22	46	792	AGATTCTCTGGGCTATGCTGCTTTGACACTCAAGTATGCAAATATCATCATACTTATA	1525	A_95_P127147	EB426607
1832	22	47	1230	TCCAAATGTTTGCCAAATTTGTTGGACAATGAAAGAAATGCAGAAGAATGGATCTTG	1527	A_95_P185567	TA13943_4097
1837	22	52	572	GTCGGTCTATGTTCAGTGTACGAGCGATCATTTTGGTCTTATAGGCCCGTATGTCATA	1537	A_95_P268847	EB683229
1838	22	53	720	TGCACATATTTGACATTCTTTGTTAATCACCTTTCTGGGAGGAACAATGCTTCAGTTA	1539	A_95_P140782	EB444622
1843	22	58	1036	GTTTGTCCTCTGCTTCAGCATCCATGATAAAGAAATATCAGGATTTTCCTTTTGTATTG	1549	A_95_P031851	AB017693
1846	22	61	624	GGAGATTCAGAGCTGGAATTATGTGATATATTGTATGGTGCTAGTTTTCTAGATTGT	1555	A_95_P200022	EB680907
1847	22	62	1481	CCGAAATTTATTTCTGATGTACCCGGACACAAACAACTTCTTTTGTCATTGTGTTCATT	1557	A_95_P026906	TA11920_4097
1852	22	67	641	TGGTTTTGTTCATGCTATTTCTAGGTTGACCTGTTGTTATCAATGCTACTGGAATTTG	1567	A_95_P016481	EH616635
1855	22	70	886	AAAGACTAGCTATCTCTCGGAGCTCAAGTCTGGCAAAGAGGTCATTGTGGTTGATCA	1573	A_95_P267806	EB680163
1856	22	71	868	CCGGGATTTAGATGCTTGCTCTGCTGAATAAATTTGTTGTTGTGTTCTTAATAATGCA	1575	A_95_P010046	DV162733
1860	22	75	386	CCCATTCTTACCACAAGCTTTTAATAATATGGCCGTGATCTGTCATTACGTGCGACTA	1583	A_95_P178507	TA12267_4097
1864	22	79	826	AGAGGTTCTCTTTGTTTTGAGCGCAAAAATTGACATGGCAGTTGTACTTCTCCCTCTA	1590	A_95_P247167	EB425325
1865	22	80	719	CCATTGTTTGAAGCTAATATGGTCTGTTCTGTTGTTGCCTTACCGGAAATCCGGTCCT	1592	A_95_P136702	EB440471
1866	22	81	881	AGCAGATGTTGTCACAGCCTTGTCTTACCTTGCTGCACAAAGATTTGACAGTGATAG	1594	A_95_P230109	EB426242
1867	22	82	254	TATGCACCCTTTAGCTTAGATGTATTTGTATGCCTGTTTAAGTCGTTACAACTTCCAAA	1596	A_95_P110177	CV019613
1875	23	5	634	TCAAGTCCAATGATATCATTAAGACGCTTTGTTCCCATAATTTGAATATGTAGCTCCT	1600	A_95_P284288	EB430965
1877	23	7	839	CTTGATAGAATCTCCCCTCCACTGAGCATATGTCGTTACTTCTATGTAGTCTCTTCTAT	1604	A_95_P224477	FG148796
1879	23	9	584	CCTGTATTTGTACTTCTGATTCTTGTGTTGTATCATAATGTACTAGTCAATGGACTCCA	1608	A_95_P211872	TA19710_4097
1881	23	11	363	GGTTGTCTGAAAGGAGCATATATATTAAAATTTGAACCCTTGTAGTCATGTTTGTCCC	1612	A_95_P204082	TA17989_4097
1884	23	14	299	GTAAGCTTGCCATTGACAATCTTGTACGGTTAATTAGATTTTTGAATCCGTACAAGAT	1618	A_95_P004281	FS432984
1887	23	17	609	ACCTATAACTGTGTATAGTTCAAGAAAATCAAATGCCAGGATCTTCTGGCAACTGAT	1624	A_95_P095078	FG641869
1888	23	18	425	GCTCCGGTTCGTCGGTCTTCTTTTGTTTTGATCCAGTTTTCTTCTCAACCATTAAGGTT	1626	A_95_P037273	BP128961
1889	23	19	609	CCGAAAAGAGGTCAAATAATGTATTGTGATGTGGCTACAGAACTTTTTTCTCTTACAA	1628	A_95_P262381	FG643390
1897	23	27	119	ACTTTTGTATGATTTTGTCCTGGATCTAATCTCCACCTAGTTGATTTCTTTGACCCGAT	1644	A_95_P212787	FS391062
1899	23	29	2235	CATTGTTCCTTTTTTGTTTCAATAAAGTGGCAATTTAGTTTGTCGTTGAGGTCGTCTGT	1648	A_95_P129997	AB110952
1903	23	33	375	GAGCTCCTACATTTGCAGTGATAAGAGGAAGAGAATTATGGAGATGTCTTTTGAAG	1656	A_95_P092523	BP531842
1904	23	34	774	TTGTGTTCACATGTTCTTGATGTTGTATTCTTGGGGTTTGTTATGCGAAATTGGCAGG	1658	A_95_P014281	EB680757
1906	23	36	958	GTTAGTCCCGGTCATTGATGTGATTTTTATTAATGAAGCTATGAAGTACTAGTTCTTC	1662	A_95_P180877	TA12846_4097
1910	23	40	464	AACCCTCTGTGAAACAGCATAGTCTATAAACTGCTGATGTCAAAAATGCTTTTGTACT	1670	A_95_P304723	AM799542
1911	23	41	842	ATGAACCCTCATTAGATAACTGTTTTATTTCAACTAGCTATGATCCCACAACTCACTTT	1672	A_95_P225048	EB446006

1923	23	53	384	ATTCCGTTTTCCAGTTGAATGGGTTGGGTTTCGATCCCAATTCGGGTTCTCCTTGTGT	1696	A_95_P085140	BP529205
1931	23	61	814	ATAGGCAGGTAACACGTGGAAGGAAACGACATGATTTAAGGTCCCCCAGTCATGAT	1712	A_95_P261351	EB445678
1933	23	63	294	GGTGCTGGTGGATATCTGGAATTAGAGTTTTTAAATATTTCATCTCACTTCAGCTAAA	1716	A_95_P106967	DW003761
1934	23	64	770	ACCACTGGTGTTGAACAAGTTTCAGAATTTGCATCTAATGTTTAGTTCAACTGTTTGG	1718	A_95_P005171	TA11929_4097
1935	23	65	551	GTTGAATCTGAGTAACAATTCTCCTGAGTTGTCTTTCAATCTTATTCTCTATGGACTTT	1720	A_95_P001281	TA16836_4097
1936	23	66	573	CCTTGAAAATTGAGAGTGGTACAATTGTGCCGTAGACGCGGAAAAGAAACAATAAG	1722	A_95_P222027	TA21943_4097
1939	23	69	383	GTATGTGTTATCATGATCCTGAACTTAAATGAAATGGGCTTTAACTAACTCTATAACC	1728	A_95_P114737	TA12197_4097
1942	23	72	1207	ATCCAAGTTGTATTGATTCCCTATCACTAGGACAGTCACTGCTGTCAACTTCTATTGC	1733	A_95_P183867	TA13554_4097
1943	23	73	440	AAGATGACAAGATTATAGCAGTATGTGCTGATGATCCCGAGTTCCGCCACTACTCAG	1735	A_95_P147052	EB425859
1944	23	74	821	GTGTATTGTTGTGGCCCTTTTGCTTCTGCAAAAATGTGTTATCATAAGGAAGGATTTT	1737	A_95_P018206	TA12832_4097
1946	23	76	820	CTCTTCCAGCTCCCGTGCTTTGGTGCTCTTTATATCTTTTGCAGTGTATGTTAGCATCA	1741	A_95_P285678	FG141850
1953	23	83	776	GTAGTGTAGAGTCTGTGAAGTGAGGATATATCAAGTTGCTATGTTGGCTTGAAAATA	1755	A_95_P116242	DV158853
1959	24	4	413	ACATCCCATGAGTGCTTGCTTCTTCCTTATGAACAAGCACTTACAAGGGAGGATTCAA	1599	A_95_P181177	EB679951
1960	24	5	343	GGGGGACCACCCTCTAGTAGGAGATATGGCATAATGAAAAATAGAATAGAGGAATT	1601	A_95_P129167	EB428907
1963	24	8	455	GTTTTCTAACGATATCCATTACAGGAATTGTTTGTACTTCTTCTATCCCTCCCTTCCTG	1607	A_95_P089858	BP530689
1966	24	11	279	GTAGCCATTATTAACAAGTCACTCTTGCATTCTAATTGTAGGAGGGAAGTACAATAA	1613	A_95_P154072	EB684240
1975	24	20	1992	TTGGACTTAAAATTGTGCCCGATTTCCTGTTGCTGCTTAATGAATTTGTTGATCCTTTC	1631	A_95_P016431	TA13483_4097
1976	24	21	389	GGTCGCCCTGTTTCTAGTGTGTTGGATATCTTGAGCCTTACAAGATAAAAAATGTACT	1633	A_95_P159807	EH618284
1981	24	26	1556	CATGCTGATGCTGCAGTTCACTTGAAGATGACAATAAGATGTTTGTTAGTATTTGGTT	1643	A_95_P012346	TA13959_4097
1982	24	27	422	TCACATTAGTGGTCTTGTTGCTGCTCAGGAAGCTGCGGATCCGTTTGAATATTGTGA	1645	A_95_P004841	DV160254
1983	24	28	844	TATTTTGGTTGTGCGAAGTTATTATCTAGCATTTCCATTTTGCCTGAGCAGCTCTGTG	1647	A_95_P010726	EB449682
1984	24	29	639	AGCCAAAAAGTATGTCCAAATTTGCATACATCCATATTCCCCTGTACGCAAGAAGCTA	1649	A_95_P067730	BP136949
1987	24	32	690	GAACGTCTAATGATAGATCATTGCGGTCTCTACTGGACCAGTTCCTCTTTTTAGTCAG	1655	A_95_P134182	EB436164
1989	24	34	788	GACCTACTGGCAAGATGCCTCCCAACGGGTCTTTGTTAAATGAATAGCTTTTGTTTGC	1659	A_95_P289688	DV160487
2001	24	46	765	CTGTTCTTGTCTCGGAGCACATTGTAATCTTTAAGGAATTGTTCATAGTCCTACAAAA	1683	A_95_P293438	EB435226
2002	24	47	434	TATGCGACCAAGAACTAATCCCATATATAGTCACTACCCCTTGAACGAGCCCCGTGTT	1685	A_95_P050266	BP132354
2003	24	48	849	TGCGAGTTTGTACGATCATCCGACATGATCAGAATAATAATAAGGTTGGGGGTCCGC	1687	A_95_P293188	FG155602
2004	24	49	760	ATTTTGCAACGTGCAAAACCATTGAGTCAAATACCCCTTGTCGGGCCACTGTTTACTC	1689	A_95_P013546	EB677742
2011	24	56	391	TTTCATGGGAATCTCGTTTCATATCTTCGGCTGTTTTTCATGTGTAGCTGTAATTCAAA	1703	A_95_P133402	EB434846
2012	24	57	726	CTTGTATTTGTCAATTTGAATAAAAGAGAATCTGTATCCATCACAGCAAGCTAGAGG	1705	A_95_P124872	DW004680
2013	24	58	806	CTTTTTCCTGCTGTCTGGCTCAAATCACAATCTTTATAGAATGCATATAAGGAAATAG	1707	A_95_P013136	TA13402_4097
2015	24	60	375	GTACTAGTTGGTTTGATTGTGACCTTTCATCAATAAAATGATGAAGAAGCTTCATTGA	1711	A_95_P090638	BP531039
2016	24	61	608	GTATTGGTTCGACAGGTCAAAGAGATGCTCCAGGAAAGGTATTTAAAGGGAGAAAG	1713	A_95_P148262	FG138767
2019	24	64	583	GTAGTGGCTGAAATAGTCTAGTATGAGACAGAAGTAGTTGGTTCTTGAATGTAAAT	1719	A_95_P212312	TA19806_4097

2022	24	67	1106	CTGATCGGATGTCCCTTTCATAAATATTTTCTGTCTGTTTATCTTGCTTTTGGATTGCG	1725	A_95_P194612	TA15934_4097
2027	24	72	1040	TTTCCTGATGAGTCACCGAGGGACTGAGTTTGTTCAGACATTGGCATCAGAATTTCA	1734	A_95_P161942	TA14378_4097
2034	24	79	1136	GCGGGCTGGTAGGGAAAAATGACTTTTCTAACAGAAATTATTTCATTAGTGTATACA	1748	A_95_P193757	TA15739_4097
2036	24	81	124	ATGAATAAAACATTTATAGGGCGTTCTTCAGAGCTTGAATGGTTAAGTCCTTTTTTGT	1752	A_95_P134657	EB437242
2037	24	82	668	CTCGACAGTGGGACTCCTGCTTATATTGCTCCGGAGGTTTTTCTAAAGAAAGAGTTAT	1754	A_95_P157827	EH615857
2043	25	3	962	CTTTGTGGGTGGTTTGTATTTGCGCCCAATATAGAGAATCGTATTTTAACTTTCAGTT	1756	A_95_P001921	AB029614
2045	25	5	179	TGGCCGCCATTCTCGTTAAATTTGCGTCGGTGTTTCTTACATTTGGTATGTCAATGGT	1760	A_95_P112832	CV020871
2052	25	12	1735	GCATGTGCCTAAAAGTTTTGCTCGTTAGAGTTATTTTAGCCTTGGTAAATGATTTGTA	1774	A_95_P003346	Y13465
2053	25	13	815	ACTTCGATTATGTCTGTTATGTGTTGTTCTGATTCACCTGGTATTCTATCCGATATTTC	1776	A_95_P135867	DV160063
2055	25	15	599	TGAATTGCTGCCAACGCAAACTAAACAATTTGAATTATGCTACTCCCATCTCTCTTTTT	1780	A_95_P043741	BP130693
2061	25	21	1124	GGAGGTGGAGGTGCAACTTTTTCTGTTTCTTTTCTTTTCCTTTTTTGTTGTATTGAATG	1791	A_95_P027921	TA15259_4097
2062	25	22	630	GCTATCGCTGTTATCGATTCGGTATTATGAGAAGATGAACTTCAAAGCTAATAAATC	1793	A_95_P003801	TA20677_4097
2064	25	24	729	GATGTTCTTTTTCCTTATGCTCGTGATAATGTGGGGAGACATTTGGATGCAACATATG	1797	A_95_P207742	DW000809
2067	25	27	91	TTCTCCCGCAAATCCAACAGTATTTAGTAGAAGCTTGAATGGATAATATGCTTAATTG	1803	A_95_P103242	CV016417
2068	25	28	501	GCTAAGGATTATTGCTGCCATTTTAATGGAGGTTTTCATTAGCAGAAAAGCTTAGTTT	1805	A_95_P269511	AM789132
2070	25	30	528	TTTTCTTCTGCTAACCAGAATCTGTACAGAGACCACCTTATCTCTTTATGTTACAGATG	1808	A_95_P074455	BP526474
2073	25	33	468	GATGAAGCTTGGTGGTTAGTCCTTTGTAATACTTCGGCAAGTGAACTGTATGCTCTG	1814	A_95_P073815	BP526307
2080	25	40	1311	CACAGGTCTCAAGTATGTGTGCAGGGATATTTAACTAAATACAAACGTTTTCTTTGCA	1828	A_95_P021576	TA15994_4097
2081	25	41	1310	GGAGAAACTTGTTTCATAAACAGCAGCTAGATATTGTTCAACATCTTTTACTGTGATG	1830	A_95_P198507	TA16791_4097
2084	25	44	1023	AGCAAAGAATTTCCTTATGGCTGGTGGTATGGTATTGTAGGCCACTTGGAAACATGT	1836	A_95_P216182	TA20649_4097
2086	25	46	956	GTGATGGAGAATCCTTCTTTAAGTGAGATGGATAATTGAGATTCATCTGTTGTACTAT	1840	A_95_P287948	TA15643_4097
2087	25	47	532	TCCAGGATTAAGTGGAATTTCACCAAAGTACTTGGTTGAATAAGGACGGAAAAGTA	1842	A_95_P020017	CV021245
2092	25	52	789	TATAACATTCCAAAAAGATTTGCCTTGCACTGCTGTGTGACTGGTGTGCCTCCTGCAC	1852	A_95_P310938	TC50163
2093	25	53	365	GGGCTGGGCATATATCGGGTAAAACCGATAAACCGGACCGTTAATTGTTTAATGGG	1854	A_95_P040811	BP129930
2095	25	55	154	CTTGCTTCCTTTCAATTTCGATTTTGGTGTTCCAAAAATGGAGATTCAGTTGATGTAT	1858	A_95_P091208	BP531254
2102	25	62	854	ATTCTCTGTGAGTGCGAGTGGTTTGGTTCTAAATTTTGAAGGCATGATTGCAAGTTG	1872	A_95_P162127	TA11944_4097
2107	25	67	781	TCTCAAGATCGTGTATGGTCTGGGTCTCCATTTTCTTTTGTATTTGCTGCTGTGTTTTT	1882	A_95_P217947	EH621825
2110	25	70	375	GCTGCTCTGGTCCTCTTTTTGTTGCTCCTTGAGCTATTAAACTATTATGGAGTATCATA	1888	A_95_P092738	BP531949
2111	25	71	125	TGACTTGTATAGTCATCAGTTGGCTAGCGACGGATTAAGTGTTTTTGTGGATCTTTAC	1890	A_95_P119677	DV999151
2116	25	76	771	TACGCCTATATTCCACCAACTCAGTGGCAACAACAGCAGTAGCAGCAGAGATCTAAT	1900	A_95_P264966	EB449034
2120	25	80	910	ATATGAAATCACAAACCGTGGAAAATTTAGTTGTAGTGCTGATACTGAAATTATGGT	1908	A_95_P200727	TA17269_4097
2129	26	4	134	AACTGGGTTAACTTCCTTTGGCCCAAGGTTAATTTGACAGACTTTCTTTTAATTTAACT	1759	A_95_P141937	EB445540
2137	26	12	876	AGCTACCACTGCCTGAATACCCTGGTTGCTCGTTTCTTCATTTCCTTGCTCTTCAAGTA	1775	A_95_P258653	TA12129_4097
2144	26	19	402	GTACATGCACAGAAATGTAAGGTCACTTATGCTTCAACTCTGAATATAATAACACTGT	1789	A_95_P008531	EB431801

2146	26	21	622	CTTCAATTGCGATAATAGGCAGGGAGATTACTATGTCTGCAGTTCGAGAATGGGCA	1792	A_95_P127127	FG144509
2147	26	22	764	GTCTGATGCTTGGGTATGAGTTTTTGACATAAACAATCACAAAATGAGTTGTAGTTT	1794	A_95_P204952	EB445412
2151	26	26	343	TCAACCGTGTTTAGTGGTGAGAATGGGTATTTAAGTTACTTCAATGTTACTCTTTCTC	1802	A_95_P019386	EH620340
2152	26	27	607	TTGGCAAGAACACTGTTTTTCTAGTTTTGACTCTTGAGCAAATATTGGCTTCCTTTATC	1804	A_95_P182252	TA13168_4097
2155	26	30	690	CCCCCCTCTTTCGAAACATAAAATTCCAAAATCCTTTAAGAATTTCAGAACTTGACTTG	1809	A_95_P088473	BP530081
2156	26	31	1221	AGTATGTTCTGAGTGGTAATCTTTTGTGAATTATAAAGTAAAACCTGGGTTTAGGTT	1811	A_95_P018561	TA14557_4097
2160	26	35	277	TACAGCTGAACAGGAAAGTCTTGTCAGAATTGTCGATGCACGAACCATACAGCTTC	1819	A_95_P102157	FG640658
2161	26	36	486	ACTGCTCCGACAGCTAGTAGAACTAGAAGACAATTCTAATTTTTATGGAGGAATGAG	1821	A_95_P307938	FG640175
2162	26	37	500	ACACTGTAATGCTGCTGAAGTATTTATTTCTTGTATGAGATTCTTGTTTGGAGTGTTG	1823	A_95_P287943	BP530879
2168	26	43	141	GGAGCTATATGGATGTGATTGTGAATTAAGACTGGTTCGCATTGAATCTATTAGTAG	1835	A_95_P112332	CV020626
2169	26	44	1168	TAATTGCATTGTGTATCTGCTTCAGGGAAAAAGAACGAACTAGATCAATAATTTCTG	1837	A_95_P011461	AB036735
2172	26	47	145	GTGAAGGATTTAGGGAACCTTATGTATTTAATTGACTCCTTAAGAGCTGAATATGAG	1843	A_95_P147652	EB452169
2175	26	50	856	AGATTGAAGAACTTCCAGAAGTTGAACGTGCTTTTGTCCATCTTGATTATGAGTGTG	1849	A_95_P228929	EB424649
2180	26	55	407	GCCTGAAAAGAACCTTGGGGAATTTTCTACGTCATCCAAATTATGTGGTTTCAAATAT	1859	A_95_P018086	FG623230
2181	26	56	422	GTATGAAAGGAAGCTGATTTGGGCTGTAACACGAACTTATCAATATATATCTCCTCTT	1861	A_95_P000051	FG625247
2185	26	60	380	TCAACAGGCATTTTCCAACAGGGGAACAGCCCAAGCTAAATCTCTTGATGCAGCTAT	1869	A_95_P236074	BP134550
2187	26	62	781	TTGAGGTTCATAATGCCATTTCTTTGCCAACCAATTTGGGTGTAATTTCAGTCAAGTG	1873	A_95_P012871	TA18107_4097
2188	26	63	334	TGTTGTAGGGATGTCTTTTGAAACCTGTACCTTTACAGAAAAGAGAAAGAAAAAGTC	1875	A_95_P134582	EB437145
2191	26	66	821	ATGTTATGATTCTGGTTATGTTTGAGGAGGAAGCTTTTATTAGAGTAACTTGGTGTT	1881	A_95_P198832	EB424739
2193	26	68	615	ACTCTGATAGAATAATGGATGTGAGATGTTATCTCCTGCGAGCATAAGATCTCTTGT	1885	A_95_P019186	TA19579_4097
2197	26	72	583	GAGCTTGGTGGGTCCTTGAGAGTTGTGGATTCTGCATTATCTGTTAACGCATAACAA	1893	A_95_P046781	BP131484
2202	26	77	768	GGAGCTCGTATTGCACTTTGTGGGATGATATCCGAGTACAACAAGGTTTGGACAGA	1903	A_95_P295973	EB449118
2206	26	81	712	GTTCATGTGCTTTCTGGCATTCTGAGGTAATTCATTTGGTTTTCATCTAAAGACTGTAT	1911	A_95_P196962	TA16457_4097
2217	27	7	108	CTCAGCGGGCTATGTTATATATGAATAGTGGACCATTAAGACCATTTTATACAGGAT	1925	A_95_P142752	EB446162
2221	27	11	771	GTTCAAAAAGCCCATCCATCTCTTTCAACTGAAGATGGTTCGTGGTTTCTGTATATTTT	1933	A_95_P254174	EB449045
2222	27	12	449	TGTCCTGTTTAACTTCTGGTCTTCTGCACGCTCAATATTGCTATAACACTTGTTAATTT	1935	A_95_P152562	EB682890
2228	27	18	679	GTACAAAATTCAAGGTTGTTCACCTAAACTAGTCGAGGCATTTTTTGATTACAGATG	1947	A_95_P286458	FG640556
2229	27	19	159	GTAACTTAATTCTCACTCCATCACAAGGCTCTTTCCGAAATACCAAAAAATCGTATTT	1949	A_95_P097413	BP534033
2235	27	25	745	TATAGCAGCATTTTGGACCTTAACTTTGAGATTCATATGATTCGCACATCGGTACCAG	1960	A_95_P145987	EB449801
2238	27	28	411	TTGGGGGACTGTGAACTGGCTTGTTTTGTGTAGACCTGATGCCTCTGTTAATTTAAAT	1966	A_95_P242207	AM803627
2245	27	35	1052	CGCAGTTTCTAGCGCTGTGTCAATGATCTTTGCTCTCCAGTTTTATAAATAAATCTTTT	1979	A_95_P192222	TA15405_4097
2247	27	37	246	GTCGCTCTTCAGAGCTGTATCAAGGCAAATCCTAACGCATTTTCAAAGGACATCCTAG	1983	A_95_P069290	BP530854
2248	27	38	796	GATCCTGTATGAATGCTAAATGCCTCGTACATCAAGCTGCCCTTTTAATCTATAAAAT	1985	A_95_P028561	X97945
2249	27	39	652	AACTGCTGTTACGCTGAATAGCTGAACTGTGGAGTAATACTAATGTTTCTGGCTTTA	1987	A_95_P266306	FG636446

2255	27	45	3121	GGTTTACTTCACCAAAATGAACTGTAATCTCATTGTTGGCTCAATGGAATATCAAGTT	1999	A_95_P239934	X59016
2257	27	47	42	TATGTTGTGGATTAAACTTTTGTTGAGATTTCTAAGTGTTAATCTGCAATGGGGTACG	2003	A_95_P031561	EB445604
2264	27	54	60	TTGGGTGCACATTTATGTGACCCAAATCCGAATCTCAACGGAGTCGAAATGTGTCAA	2017	A_95_P097838	BP534219
2265	27	55	785	GTTGTTGTAAACTTGTAACTTTAATCGGTGCTTACGATTGCACCGTGTTATATCATTG	2019	A_95_P133977	EB435692
2266	27	56	689	TACAACAAAGCAGAAGTCTGAGCACAGAGGTTTGGCATCTAGACCTCCAGTTAGTTG	2021	A_95_P314558	FG173217
2268	27	58	128	AGATGGATGTGCCGTCGCCTGCATAGACGTATTGCAGATAACTCATGCAGCTATATC	2025	A_95_P155942	EG650334
2269	27	59	135	ACATTACATAGCATTGATGTTTTGCGTATCCTGGCCCGGGTTATTTCGACTTCCAAAA	2027	A_95_P255909	EH617005
2274	27	64	844	GTTGGAACCTTTTGAAAGTGAGTATTCTGTAGCTTTTTTGCTCGTGTAAGCAAAATAT	2037	A_95_P020786	TA14532_4097
2278	27	68	795	CATGTCTGCATTGCGTTCATTCAAGCGCCGAGTTGCATATTCAAATGTTGGCTATGAC	2045	A_95_P079970	EB424877
2280	27	70	807	CAAATTATCATATATCAAAAGCCGACGCCCTCAGAAAGAGAAAAAGAGGAGATAGA	2049	A_95_P227919	EH622808
2289	27	79	1195	AAGAGATCCTGTTCAAGTGAGGAGAATGGCTTCGCGGAAAGAGGAGATTTATCAAG	2066	A_95_P184667	TA13745_4097
2290	27	80	666	CTCGAGCGGATGATAGGGTTCATTTAAGTTTCCTATTCAGGATTTTAACATTCAGAC	2068	A_95_P014241	TA12817_4097
2291	27	81	440	AACGGTGTTGGCCAAAATGGAGAAGATCCTTGGTGTTAAACTTAGAGGTAAAATTC	2070	A_95_P025311	FG642155
2299	28	4	1334	GAGATACTATGTATATGTAATTGGCATTTTCATTTTCTTGCTTCGGCAAGTTTGCAAC	1920	A_95_P214117	TA20193_4097
2303	28	8	784	GCTGTGTCAGTTAAGGTTTTCCTTTTAGAATTTAATCACAGACTTGACATACTCTATTG	1928	A_95_P003146	TA16403_4097
2304	28	9	782	TATGCAGGCAGACACAGTAAATGTGCTTCGTAGTACTACTTTATATATCCATGTTAAA	1930	A_95_P271191	EB440232
2305	28	10	1370	GACTGTCTGTCTGTGGTTGTATTTGTTCTTCATATACCAATACCAATCTTTTCTCCATC	1932	A_95_P011211	TA16016_4097
2309	28	14	946	TTGGATGGTTTGATAGCCATGTTGTTGTATTCCAAATTGATATTCCACTAATGGTATT	1940	A_95_P025901	TA17914_4097
2317	28	22	778	GAGAACTAAAGGCAATCTGAAGGAAAACATGCTAAATTTTGGGCAACATGTGCAAA	1955	A_95_P192692	TA15508_4097
2318	28	23	663	AGGTTGGAGCCGTTGCATAGACTTGTGGCATATCTTTCAGTCAACATCCTTGTCGAAT	1957	A_95_P146287	EB450281
2320	28	25	632	TCCATTTCTTCTCCGATGATGCTTGCCTGGAGTGCAGCGAGCTTGTATTCTGAGTATA	1961	A_95_P066415	BP136598
2323	28	28	371	TGTACTTTTGATTCGACATGCTGTAACTGTCGCTGGATGCTCCCTTATACTGAAATAT	1967	A_95_P127787	EB427357
2338	28	43	775	TCCGTTCCTTTGGTCATGTCAGCCGAGTGTATGTTGCCATTGATCAAAAGACTGGAAT	1996	A_95_P234779	EB450504
2344	28	49	1090	GCTGCACCCATGTAATGATGATTCAAGATTTTGAATGCATTTCTACTCATAGATAAAG	2008	A_95_P177967	TA12113_4097
2346	28	51	495	AAACAACGATAGCGTGCAAATACTACTAGAATTGAATGAAATGCCATATCATCGGAA	2012	A_95_P285363	FS418967
2357	28	62	492	CACAATCCAAATCTGTGATATTCCCTATCATTGCTCCTTTTGTATTGCTATAGCCAATT	2034	A_95_P009516	BP128540
2360	28	65	773	TAGGCTGGGGGGATAGTCATGCAGTTCATGCTGTTTAGAGCACTTCTAATATATACC	2040	A_95_P229355	EB450123
2361	28	66	836	GATATATGGCATCTCTTTGCACGGACGCAAATTTGATGGTCACACAACATTTTTTGAG	2042	A_95_P217027	TA20838_4097
2367	28	72	19	ACAACCCAACTGGTATTGATCCCACAATTGAACAATGGGAAAAGATTGCTGATGTAA	2054	A_95_P127937	AB126259
2371	28	76	720	ATTAGTTCACAAAAACAAAATAAAAAGCCGGCCGGGGGTATCCAATGCCTATGTGC	2061	A_95_P232624	BP530798
2373	28	78	934	GCAGCTCGAAATTCACATTACATGTACAATAAAAATGACAATACATTGCACTGCCCTC	2065	A_95_P183007	TA13355_4097
2375	28	80	122	ATTTATCAGGGAGAACTGTCAACTTATGATACTTATGACGCGGTCTTCGTGTTTCAGT	2069	A_95_P034529	AJ718931
2384	29	4	662	AGTCACTGCCAGAATGGTAGTTTATATATTCTATGTAGTAGCACGAAAAAAGATGCT	2079	A_95_P207337	TA18718_4097
2385	29	5	238	ATGTTCTATTGGAGTGTAGCGTTGGGGTTGTTCTAGGTTAGCAATGGAAAGTAAAGT	2081	A_95_P138812	EB442551

2394	29	14	601	GATTTGATTGGCTGGTACAAGACATTGCATCACGGATCTATATGCTTGATTGAGTAA	2098	A_95_P292993 FG644433
2397	29	17	650	ATATATGCCTCAGGACATTCTGGATTAGACGAAAATCTGCCAATATCCTGATGAGGC	2104	A_95_P062085 BP135422
2401	29	21	1070	TTTTGCCCTTTGGATGGACAATGGACAGTATTACACCATCTTTTATGGTTGTGGTTCTT	2112	A_95_P010656 TA13680_4097
2404	29	24	409	TTCTGCTTTGGTTAGTTAATGGTCATACTTTTGCGTATTTTGGCTTGTTTATCAAGCAC	2118	A_95_P141007 EB444809
2407	29	27	786	CAATGAAAGAAATGCAGAAGAATGGATCTTGGGTAACCAGATTACTTTGATTGTTGC	2124	A_95_P010986 DV999391
2410	29	30	1021	CGGATGTCATATCTATAGTGAATTGTTTGAGTCATTATAAATGATTGGTTGGTCTCTA	2130	A_95_P012886 TA15273_4097
2413	29	33	866	GAGTTTCCCGAATGTTTTAGTGATTTTTCTGATATCTGATAGATTTGGAGGTTACTGG	2136	A_95_P192398 TA15443_4097
2414	29	34	490	TGGGTGGAGGCATCAGTTCGTTTATCGGAGGGCGAATGAACATGATTTTGTATTAAC	2138	A_95_P083005 BP528649
2415	29	35	669	GGAAAAGAAGTAGTGAGGTTTATCTTGGTTGATTTACTTGTCCCATCTTTTTGATTCC	2140	A_95_P005026 FG167674
2416	29	36	99	AGTTTGACCACTCGACCTCCCATAGTGGTAAAATTAGAGTTTATGGTTTGATTTGTTG	2142	A_95_P129542 EB429512
2422	29	42	454	AAGTAACAGATAGTCATGAAGGCATTCCCCCTTTGTTCTATTAAAGCTGTACTAATTA	2154	A_95_P023261 BP531380
2426	29	46	662	TAGCTTGAACCAGATGAGCTGCTTTCCAGTTTTTGAATCAAACTAATGTTCGAAGATG	2162	A_95_P015941 EB444306
2428	29	48	1525	GTGGTGTGATAGTGTGATTTGATTTTGGAGTGTGAAACTTTTGTATGGTTGATGATG	2166	A_95_P008451 Z37978
2441	29	61	619	ACAGTGTAAGCTTAAAGTATACAGAGCCAGAACTCTGGTCTCTCTCTCTTAAGAGAT	2192	A_95_P039586 BP129590
2444	29	64	394	TTCCATTGTTTAATTGCCTCTGATTTATTGTTGTAGGAGTCTTAGTTGGAGAAAGGTT	2198	A_95_P198017 TA16687_4097
2455	29	75	775	AAGCCTATCTTTATTGCATCTGGAGTTGGCACTGATCTTCTTTTGATGTAATGTTTTCT	2220	A_95_P117737 DV160682
2457	29	77	832	CATGAATTATCAACCCCCAAGAAGAAAGTCCACAAGAAAAGAAAAGAGCAAAATGA	2224	A_95_P289278 DV158497
2460	29	80	156	CTGTTGCACATGTCTCAGCTGCGAAACTATTGGCTCAAGCATTGAGTTGGCATCATAT	2230	A_95_P233934 AJ718943
2462	29	82	511	TGTAAAGAGTAGTAGATGGATCAATCACTTGCATATTCCTTTTTGCAAGTACCTGATT	2234	A_95_P283093 AM834279
2463	29	83	813	ATGAGAGATGGGATCCGAAAGCAGTACTAAAGTAGAGCATCGTATCAGTACGTGGT	2236	A_95_P312698 FG160619
2470	30	5	650	GGATTTTATGCTTTTTACGTGCTTGATGTAGTCATTAGATTTCATGGTCCTGCTCTTTT	2082	A_95_P192917 TA15559_4097
2471	30	6	553	GGGATAGCTAAAGGGGTTTTTTCTGAGACTCTGAATTTTGTTGCAGTATTTAGTGAT	2084	A_95_P017496 TA13353_4097
2473	30	8	561	TCTGTCCATAGATCGCTGCTGTATTAAATGCGGATTGGCTTGTGTATAATATAACAGT	2088	A_95_P309303 FG645534
2476	30	11	701	ACTGTTCGTTGATGAACTAACTTCTGATCCTTTCTAACACCTAAGTTTTTCTTCCTTAA	2093	A_95_P136082 DV162727
2477	30	12	1623	GAGGTTCTCTGACATTTTTAAAGACCTCAATAGCTTTGCTAATATAGTGGGCACTTTG	2095	A_95_P023801 TA14230_4097
2483	30	18	550	ATCCTGGAAGTTAGAGAAGTGAATTTGTATGATGCCGTTGTTCTTTGTTTTGCTTTTG	2107	A_95_P017441 DW005086
2486	30	21	821	TATAGCAGCTTATACTGCAGCTTGTAGTAGCAGCTTACACGGCAGCTTGTAATAGCA	2113	A_95_P128092 EB427637
2492	30	27	564	CTAATGGTGTTAATGTCTTCGTTACTTTCTATGTTTAACCCCCTAACCATCCCTGCCAA	2125	A_95_P161947 EH620535
2494	30	29	1478	AAGCCATCTTCCATGTGGAGTGTATTGTTTGAGAATTGCAATTTACTGAAGCTTTTAC	2129	A_95_P182927 TA13338_4097
2504	30	39	1025	GATGTCCCTTTTTCTCCCCTATCTTTTGGGTTGACATAAACCTTATGTGCATTTATTGA	2149	A_95_P223262 TA22211_4097
2509	30	44	419	CTAAGGACTCTATGAAGCAGACGATTTCTACTATGTTAGGCTTGCTCCCCTCCGATCA	2159	A_95_P158727 EH616596
2512	30	47	875	ATAAATTGACACGCCGCTGTGAAGTGACTGCAATTCTTATCTTATACGGTCTACCTAG	2165	A_95_P069635 EB682391
2513	30	48	841	GTCTTATTGAGAAACTAAGTCTGTTTTTCCTTGATCGCTTCCTTGTCCTTTGATGTTAA	2167	A_95_P248247 EB424783
2514	30	49	782	GCGTTATTATACCTTGGGCGCGCCATTAATCTTGGAGTTTATTTCTTTGTTCTTTTTA	2169	A_95_P218122 EB426328

2515	30	50	771	CTGTTTCGAGTTTGGTATTTTGTTTGCTTGGACAGTTGGAATCCTAGCTATAAATAAC	2171	A_95_P258663	FG163600
2517	30	52	1590	CTTTTGATTACTTGTTCTCTCAGTCTCAGACTTGCTGTTGTTGGAGTTATTGAATTTGA	2175	A_95_P181207	TA12924_4097
2518	30	53	845	AAAGCTGAGCATCCCACATGACATGCCTATTATCGATTATGACTTGGCTGTCTCATCA	2177	A_95_P291028	FG153536
2524	30	59	613	CTTCACTGGTGCTTTAACTCAGCTTCCAGCTCATCGATAATCTACGTCAATAAGAAAA	2189	A_95_P158977	EH616867
2527	30	62	781	TCACTTGGCTATAAGGTCAAGAAGAGCCTCAAGAATCATGTATCTTCGTGGGGGATG	2195	A_95_P217412	DW001948
2528	30	63	915	CGCCCTACCAGAAAGTTATGTCAAAATTGTTTTACGGTGAATTGCTCTATACTACGTT	2197	A_95_P133467	EB430421
2532	30	67	1284	CCTATTTGGACTGCTTGTCTGTGTTATACGTTTAGATAGTTTCAACTTATTGTGTGTGG	2205	A_95_P230619	GQ260131
2534	30	69	1089	TGATGCAGACAGTGACAATAGCGGGGATGATAATGATGATAGTGGCATATCGCTAG	2209	A_95_P200792	TA17283_4097
2540	30	75	351	CACCTACGAAAGGTTGTTTGTGAGCATAACCCAAGGTATACACTTTGTAAATTTCCTT	2221	A_95_P095893	BP533380
2541	30	76	329	GTTATCGGTATGCCTTGACAAAGAGATGTATTATGTCAATGCCTCTGAACACTATGGT	2223	A_95_P132677	EB433261
2542	30	77	1643	GAGGATAGAAATAGGATTATGGATGCTCCTGACCATGTACACTTAAAACATATCTGT	2225	A_95_P019581	TA12715_4097
2553	31	3	239	GGGGATTAACCTTTGTATAAATGAGACTCTCTCTTAGTTTGCTCCATATAAGTTTCCAT	2241	A_95_P154742	EG649742
2555	31	5	443	ATGGCCCACACTTCGAAATGTAAACTAAGTTGTAAAGAGATTTCTTGGGAATAAAGC	2244	A_95_P003001	FS414230
2559	31	9	111	TCCACCACCTTTTGACTGGAGATCTTTGGCTTAAACTTGTGCTGTATGAGGTTGTACT	2252	A_95_P143382	EB446710
2563	31	13	795	CTCGGCATGACATTTAGTTCATTAAGATGTTAGGTGTGGTTATTCTGTATGTTGAATT	2259	A_95_P204227	DV160192
2575	31	25	709	TAAAGTCGAATGATCACTAGCAGATATTTTCACTAAGTCTCTTACTGGTTCTCGTATT	2283	A_95_P164597	EH623846
2578	31	28	738	GTGGGGATTAGGCCTTTGAAAATATACAATTCACGACAATTCAGAAAGAACTGCTCT	2289	A_95_P145302	EB448935
2580	31	30	266	GGCTCAGAACTCAACACTCTTGAACACGTTTAAGTTTCTAGGATTATACATGTATATC	2293	A_95_P134732	EB437461
2582	31	32	636	AGAAGAATGGGAAGGAAATCATCCATGGAAACCTTGGGACCGTGAAAAGGATTTG	2297	A_95_P204982	EB677299
2587	31	37	1139	AATGGAGATTCAACTTTCTTGATCAGTCGATTGAAACCATTCGTGCAATGTTATGGAC	2307	A_95_P028306	TA17377_4097
2589	31	39	408	TATTGGGGTGGTTTCTCAGATTTTGGGGGGTGAACAGAAAAGATAGGGGAAAAATT	2311	A_95_P099223	FG202927
2591	31	41	874	AGATTTGCTCTTCTTTTAACCTGGTGTTGCGTAATAAATGTTAATGCTTGAGCTCTAGT	2315	A_95_P008781	EB426350
2592	31	42	854	AACAGCTGCTCTTGATCAAACTGCCACCCAAGTTGTTGATTGCATCAGTGGGAAATG	2317	A_95_P231184	EB426728
2595	31	45	467	ATGACGCTAGCCTAGGGATGTAAAGTAACGAGGTTTATACTGAGAGGTCTATGGAA	2323	A_95_P106667	CV017998
2596	31	46	636	GGTTACCTTGGAATTGCAGAAGACCTGGATAAACTAGATTTTGAGACGAAGAAACG	2325	A_95_P295568	FG637271
2610	31	60	308	GGACAAGAAAGGAAAGGGAACCTCATCTTTTCTAAAATTGCCTGTGATGCAAAATTT	2353	A_95_P106592	EB102901
2611	31	61	949	ACATGTGGTGCAACTTTGCTTATGAAGAGAGCTAATCTAGATTCAATCTTACACGTTT	2355	A_95_P025501	TA17447_4097
2612	31	62	424	AAATTGAAAAAGAAAGCTTGGGTTCTTCCCAAACCGATTCCACGCTTGTCCAGGTCCT	2357	A_95_P280003	AM838454
2613	31	63	513	GTTGCTAAGGTCTGGATATTGTAATTCCTCGTTATACAATCAAGTAAAACAGACCATT	2359	A_95_P000741	TA12963_4097
2616	31	66	1067	AAAGGATTTTGACTCTTGTGGATCTACTGAATTGTTTAGTCATTGCTAGCACGGTTTTT	2365	A_95_P179272	TA12465_4097
2620	31	70	613	TGCCAGTTTTGGCGGTTGTATAATCTACTGATCCTACAGAAGTGGAAAGATTCTTTTG	2373	A_95_P151302	FG635179
2621	31	71	935	GCTGCCTATCTTAAGGTTTCAATTTGTCAACGCATTTGATGTATGATGTGACTTCTTCA	2375	A_95_P002256	TA11934_4097
2623	31	73	716	ATTCAGAATCCGACCACTCACAGGAGTCTGATCAAGGATATGAACCTTCAGATGTAG	2379	A_95_P242932	EB426614
2633	31	83	312	TCAAGGGCTTTATTTCTTAAATGTCCATAGCTGGAACTACAGTGGCATCTTCGATCAA	2399	A_95_P070640	BP192688

2640	32	5	630	TCTTTCATCTGGGTGCTTACATATTCATCAAGTCTGTCGGTCAAACGAGTCAGACTTC	2245	A_95_P063525	BP135803
2643	32	8	225	CTAGTCAAGAAAAGTCTTCCCAAGATGTGGGATCACATTTTTGAACTGTACTCATTTA	2251	A_95_P158982	EH616875
2648	32	13	787	TGCTGTCTTCTGGAGCAGATACTAATAATGTTGGGGATAAGGTGCTATTTTGACTGA	2260	A_95_P186577	DV158612
2649	32	14	784	GGTTTTCCATGCGTTACCATAGACCAATTTTCAGTAGTATAATGTCTTCTCCCATTTTT	2262	A_95_P307768	FG155283
2651	32	16	730	GGCATTGTCTTGTGCTGTGATCTAGATGTTCTTAATAATGTGATGGAACTTGATATAT	2266	A_95_P012661	EB683906
2655	32	20	281	TCATGTCCATGCATGGAGGGGTTTTATCTGAAGTTATGAAATAGACATTTGCTCAGC	2274	A_95_P134747	EB437498
2657	32	22	243	GCCCTGATCGAATTCTTCAAACATGGGAAACCAAGAAAATAATAACAGTTTCTGAAG	2278	A_95_P137077	EB429767
2671	32	36	819	CGAAGATTGTTTTACCACAGGAATTAGCGAACCTTGGAAATGCATGAAAGAGAATTA	2306	A_95_P205782	TA18364_4097
2675	32	40	415	CAAAATCTGATCTTCACCGTTCAAATCAAAGAACAGGATATTGAGAATCTCCGGTCC	2314	A_95_P038751	BP129361
2684	32	49	415	TTTGAGTGGAACAGTGAAGGAGATAAGGGCACGTGTGTATCAGTTGGTTGTACGGA	2332	A_95_P108087	CV018663
2686	32	51	197	CCTGCAGTTTATCTATCAATGTTCTATTTCTTCAATAATCCAAGATCCACTATTGTGGG	2336	A_95_P080425	BP528000
2691	32	56	510	AGCTCCTGCTCGAGTTCAGGATCTAGTCTCTATTATGCAGAAAGAAGTTTGCGTTGT	2346	A_95_P085100	BP529196
2693	32	58	905	TGGACCTCCTTGTGGAATTCTGTTAATAATATGAGTTAATTGGTACTCTGTATCAAGG	2350	A_95_P015741	TA13590_4097
2694	32	59	886	GGTTTGAGTGTTATTGTACTGTAAACGTTTCGTTTTTTGAGGAAGAAATCTCCCATTT	2352	A_95_P032191	TA12181_4097
2697	32	62	140	CTAGTGTCTGAGATTACGAACTTGTGAGTAATTTACACTAGCGTTGTTTAATCAATCA	2358	A_95_P091948	BP531574
2705	32	70	378	TGCAAAAGCTGAACCCTTACACTGGACATCTCTCGAATATATGAGAGAGGCTGCTGT	2374	A_95_P014441	TA13869_4097
2711	32	76	181	CGCACTCCATCAGTTCATAGCCAAGGAAATGTTCAGATGGAAGCAACAATATGTTAA	2386	A_95_P003821	TA21758_4097
2712	32	77	831	AGCTTTATGGAAAGCTGCCTTTCCTGAGGAAGAACTTCGTGGTTTAATATCTGAACA	2388	A_95_P146222	EB682547
2715	32	80	797	GTACCTGATCAAGAAGACATAGTTGGAAGGAGACACATTGATTCATTAGGTGGGTG	2394	A_95_P210962	DV159002
2722	33	2	0	CAAGGATGTTGGAGATGCATTTTGCATTCCATAATCGTTTGTCTAAAACAAAACCAC	2404	A_95_P023906	A_95_P023906
2723	33	3	840	CTTGCAGTGTAAAGGGCATTGTAAAAGTCCTTGTTGAATCTTGATATACTATTAATCC	2406	A_95_P124617	DW004404
2724	33	4	788	TTGATAACTATGGGGAAGACGATTTGGAGGGTGAGGATGACATTGATGATGATACC	2408	A_95_P229609	DV160165
2728	33	8	540	AGCAACTGTGCTTCTCTACGATGCTCCTATAAATCTTCTTGTTACATTTGAGGTTGCTT	2416	A_95_P143952	EB447159
2729	33	9	648	GGATTTGAGGATAATTTTGGAGAAAGTGTCAGTTTTATTGGCATTGTTAGGATTTGG	2418	A_95_P190657	EB678112
2731	33	11	883	AAGGATATCATCGCAGAGATACAAACAGAAAATGGTGAGGAGTGGTGGACGTATG	2422	A_95_P229389	EB442871
2732	33	12	862	ATTTTCTCAACCCCACCTCCAGCGAACGCTACGAAACAACTTGTCTCGTTTGAGAAAG	2424	A_95_P212852	EB449778
2744	33	24	658	TTCCAATTACTTTTGTCGATAGAGTATTTGGAAGTTCCAAGTCTGGGAGGATCTGAA	2448	A_95_P050931	DV159747
2745	33	25	609	ACTGCCCGAACTTGGCTAATTTTTGACGTTACGTGAAATCTTTAACTTGGAGTATTCT	2450	A_95_P189012	EH617488
2748	33	28	150	TAAACGCAGGCACTGGACGTAGAACCACGCTAGGATTATAAGGTGAAAGATTGGTG	2456	A_95_P105072	CV017286
2749	33	29	1205	CAACAGTCCATCTAGAATGTAGGTTAACATTTAACCTAGGAGAAAACCTTTTAGCAC	2458	A_95_P204187	TA18012_4097
2750	33	30	554	ATTAGACTATGTTGGTGCGGAAATCAGCATGTCAACTAATGCATCTTCCTTTATAGTA	2460	A_95_P231944	FG637879
2751	33	31	735	GCTAGCTCGTGACATGAACCTACTTTATCTGGTGTTTATTATTGAATTGTGTATTTCTT	2462	A_95_P010296	DV999846
2759	33	39	727	GCAGAGCTTGTTCCATATTTGCTTTGATCTCTGTACATTATATTTCCTGATAAGATGTA	2478	A_95_P024386	EB428278
2763	33	43	1520	CTTTGGTTGTTCTTCAGTTGCTGCATTTTAGACATTCCAGTACTAGTTTATACTTTGAT	2486	A_95_P009281	AB052822

2764	33	44	794	GAGACGCAATCTTTGTTGTTGCTTAGATTGAGTATTGTTTCTCTCTTCTTTGTTTCACT	2488	A_95_P255459	EH615240
2766	33	46	149	TAATAGCAGCCTCTTCTGGTGCCATGAAAGCTGACGAAGTTGCCAAGATAGCTTTGA	2492	A_95_P033919	AJ717913
2767	33	47	795	ATCTTGTTGGCAAGGTACACGGTACTTCTTTTGATGTTTTTGTGACTTGTGATGTCTCT	2494	A_95_P127992	EB427565
2771	33	51	1539	GTGGGAGTAGCTATTTGATATGACCAGAATTGTGTATTTATGAAGTCACTTCTGTTTT	2502	A_95_P133687	U35111
2772	33	52	527	GGAAATTGTAGCCTTTTGTTTCTCTTGAGCTTCATGTCTTTTCTAATGTACCTTACTAG	2504	A_95_P141602	EB445283
2776	33	56	822	ACCACCTGCTAATGCTTCCCTTTTGGGAGAGAGAATGAAGCTCTGCAGAGACTAGAA	2512	A_95_P225772	FG135892
2780	33	60	777	GATATGTGCAATGCTCCTTGTCTGCTTGTTTGTGTATGACATATTTTGGGTTTTCTATT	2520	A_95_P014326	DV161576
2784	33	64	1485	TGATCTGAAGGATCAATTTTCTGTAATTGATGTGGATAAGAATGGTGTCATCAGTCT	2528	A_95_P028096	AY971376
2785	33	65	901	TTCTGAGCATGCGTGGCTCTTCAAGTTGATGCAACCTATGAAGGCAATCCTTCAAGT	2530	A_95_P011106	EB680133
2790	33	70	858	GACCTGAAAGAAAAAGCAAAATTCAATTTGTTTTCTCCGTTCCTGGATTACTTTCCTCT	2540	A_95_P013661	DV999924
2794	33	74	1142	ATATCTCTACTTCAGAACACAACCATCTTTTCCCGAGTAGAAGTGAAGAGACTGTTTC	2548	A_95_P198307	TA16750_4097
2797	33	77	474	CTTACCACTGTTAATGTGGCGATTTGATAAGTGATTGGTTGCTTAATCACAGTTGATA	2554	A_95_P197802	TA16644_4097
2801	33	81	2001	GGTTGTATATTGTGACAAAGTCCTCTTTACCCTTTTTCACCCATTGATTAACATTGTTT	2562	A_95_P023196	X71057
2802	33	82	861	AGAAGCTTGCTATATGCTGCTGCTGTCGAAGCTTTTGTGTGACATAGTATTTTTCCTT	2564	A_95_P218817	EB450082
2803	33	83	513	AACACGCGTTGTTCAAGAATCAATATCATCTTGATTTTGACCAGTTTGGTTATGTTGC	2566	A_95_P231789	FG644307
2809	34	4	458	TTTAATAATAAGGATGGCTTCTCAGGACGTTGGGTTGCGTTTGGTATACTTTATAGG	2409	A_95_P116502	DV159262
2814	34	9	136	TATGGTAAGAGAGATAATTTTACCTCCCAGGCCCACCCCGAAGCCAGAAGATCTATG	2419	A_95_P055326	BP133672
2821	34	16	497	CTCTCAGAAGTTCTGCCTCCACGTTCTGCCAGTGATTCTAATTTCTATCATAGTATGTA	2433	A_95_P226509	EG650211
2823	34	18	475	GCAAAATGGCATTGATCTAAGCACAGTTGATGTCAGTTATGTTTTTCTTTCTCTCATT	2437	A_95_P158112	EH616189
2825	34	20	492	ATTTATTCATGCTTTCTGTCGAATAAGCCCATTGAAGAAGACGGAGCATGTGAAAAT	2441	A_95_P139872	EB443794
2828	34	23	173	AGGCATCTGTATTGATGGATTGTGTCATTCACTTCCTGCTCGCACCATTGAATTGGAA	2447	A_95_P110277	CV019661
2831	34	26	545	TTATCATTACTGTTGTAGTTTAGAGCAGAACCTTGGTTTCTGGGTGTACTTTGTTAGA	2453	A_95_P044446	BP130882
2835	34	30	622	CTCTTGATTCTTTTATCATTGTGGAAACAAGAAAATCCCCCAAATTCTCTGAGGTAGG	2461	A_95_P143482	EB446772
2839	34	34	784	TGGTGAGCTTTCTCCCTCTTGACTTGAGAAAAGAGAGCAGCATACAGTACATCTTAT	2469	A_95_P116257	DV158876
2840	34	35	759	AAATATGTATTGCCATTATTCTTTCATTTCATCTCCCTCCCAAATACTGGGCAACCCCG	2471	A_95_P097853	BP534229
2841	34	36	486	TTACAATAAAACAGTGAACTTCACTTTCTTGCTAAGACTTGGAATAAGCTTGTTGCTT	2473	A_95_P053156	BP133101
2843	34	38	467	TCTTCGATACCTGCTGGAAACACGTTAACATTTCATTCATCATCTATAATGTCCGCAG	2477	A_95_P091918	BP531557
2846	34	41	0	CTCTGTTTCCACCTCCAGTAAAGCAGAAGCCTCAGAAGGCAAAGAAAAATTGGAGA	2483	A_95_P013166	A_95_P013166
2847	34	42	1123	ACAGTTGGGTGCGCCTGCGATGTGCATGTTTTCTTTGGTTAGGATGTAGTTGCAATT	2485	A_95_P192832	TA15541_4097
2849	34	44	1101	CATAAACTGAGCCATTTTAAACATGTGGGACATTCATCAACAAATAAAACAGCCTTG	2489	A_95_P194202	TA15842_4097
2850	34	45	475	ATTTTCGTAAAAGAACGGACAAGTTGGTAAAGTGTCATAAATTAATCCTCCCCAGTCT	2491	A_95_P131472	EB431765
2856	34	51	262	CTCTTCGTCATATTGAACCACAAGTTTGCTTCTTTACTTTACTATGTATTGAGCTGTAT	2503	A_95_P154437	EG649591
2858	34	53	503	GGCATTCTTTTGTCTGCAGATGTGAAACATGTGATATATACATACCTCTTTGGTCTAG	2507	A_95_P026251	TA21745_4097
2859	34	54	556	AGGCAATGTTTAGTCTTGCATTCGTGAGCCAGTTGACTATGGGTCCTACTATATTATA	2509	A_95_P125127	DW004935

2865	34	60	837	GTGAACTTTCAGGGAATGTGATTGATATTTGTCCAGTTGGAGCCCTTACCTCAAAAC	2521	A_95_P129057	EB428820
2868	34	63	756	GAGCTATGTCTAGGTAAAAAGGATTTCTTTCATCTGAGAGGAACTCTCATGTCTTGTT	2527	A_95_P123182	DV160610
2874	34	69	356	ATGCTTTTGACCCAATAATTATGTTTGTTTCATAGCCTCTCTTAGGTAAGTAGGATTT	2539	A_95_P192187	TA15398_4097
2876	34	71	770	AATGGAGCTGGAGTTGTGCCTTATGAACTGTTGAAACCATTTTCTGGACCTGGTGTT	2543	A_95_P150967	EB681141
2877	34	72	28	CCTGCTTTGTTGCTTTGCAAATAGCAGGCTGTATTTCTGATATTAATTGAATGTGTAG	2545	A_95_P012376	EB442968
2879	34	74	890	TCTCAAGAATAATGACAGATGCATCTATGAAAGACTTGGCGTCTGCTGGCACTCCTG	2549	A_95_P289158	DV157868
2883	34	78	159	AAGCAGATTATGACAAGGAGTGCAAGATATGCACACGACCCTTCACAGTGTTCAGAT	2557	A_95_P167646	EH664239
2887	34	82	755	TGTTGTTGTGATTCTTACCTTTAAAAAGAAACTTGTTCCCGTCACCATCTGAAGTAGC	2565	A_95_P017636	AF422802
2895	35	5	491	GAGGGAACCATATTCAGAAGGGTTGGTAACTCAAATGGGCATTATATATTAGTTAGT	2577	A_95_P308568	FG642847
2897	35	7	628	GCTGTGGGCAGTAACATGAATTGCTAATTCATCTAGAGTGCTAATTCTTGAATTGAA	2581	A_95_P140142	EB444092
2900	35	10	367	GTATAAGCTTCATGGCCTTGGTCAGGAGTTCAAGTGTGAGATATGTGGGAACCATA	2587	A_95_P175012	EH665986
2901	35	11	203	TTCCCTTTCACATCTAAGTGGAAACAGTTGTTCATCTAAGTATACATCCTCGGTTTTGC	2589	A_95_P095818	BP533357
2910	35	20	1294	GATGACACATTGTTGTACTGCTAGTAGACATAAAAAGTATTCAATGCTGCAAGGAAA	2607	A_95_P010631	AB004307
2913	35	23	490	GCCGAGCTTCTTCAGTTCTAAGAAGAGACACAAAAAATGAAGCTTCAAAGAGGTGA	2612	A_95_P071375	BP525688
2917	35	27	204	CGAAGAGACGAGAGGAGTTTTGACAGATATTTTGGGAGAATGTGATTCGTGATGCT	2620	A_95_P110737	FG632373
2918	35	28	600	GCAACTTCAGGTTTGACTTTCAATTTTTCTCCCATGTAACTCTGTTTTCTCAAGCTGTT	2622	A_95_P019236	BP530353
2920	35	30	570	CCTTAGGTGAATTTTATTCCCCCTAATGTTTTTGAAGAAACTCTTCTGAGAAGTAGAA	2626	A_95_P195567	TA16145_4097
2922	35	32	845	GACAGGGTGATACTGGTTGTTGGATTTATTATTTTCTCCTTGGCTGTTCTTTATGTGG	2629	A_95_P290318	DV162653
2923	35	33	779	CATCTCTTTACATGTACAGCCAACTCGATATCGACTATATGACCTAGTATACAATAAC	2631	A_95_P267336	DV159801
2930	35	40	874	TAAATGTTCATTTCTCAAACTCAGAGAAGCATTGAGGAGAAAAAGACAGGCTGGGC	2645	A_95_P206427	EB438827
2931	35	41	606	GAATGGTGACTGTGATACTCCATAACTTGCGGTACCAAGCAATAATCGGACCTATGC	2647	A_95_P246802	EB435034
2934	35	44	216	TTGTAAGGACGCTTGTCAGTAAGGACTAAGGATTTTAATCCCAGATGGTTTATGCAA	2653	A_95_P176252	T18337
2941	35	51	767	CAGCAATAATAGTGTAGAACCGAGGATGACAGTGTAGAATGGGTGGGAGATGAGA	2667	A_95_P310283	FG135791
2942	35	52	610	GTGGTATGACAGTAATAAAGATGGTAGAGATCTAAGAGTGGTTTTTCTTTCCCTTTG	2669	A_95_P259406	EB436297
2949	35	59	475	TGGATGTTACTGGTGATAATGGGACTGCAAGTTTCTCTTTTTCAAAAAAGGCCATTC	2683	A_95_P159877	EH618406
2952	35	62	813	TTGATAGGCTTTTTAGTGAGGTATTACTTTCTTCCCAATTTGGTATCTGGCATTGCTTT	2689	A_95_P232974	EB425670
2957	35	67	566	GAAAGGATGTAGAATATATCTGTACAGTGAGTGGAGTTCTGGCAAAAGTTAACTTAT	2699	A_95_P053861	BP133296
2960	35	70	386	TTCCTAGCCCTGATTATCATGCCTATTTTGAATTTTCTCCAATTCCAGAATACAGATTT	2705	A_95_P065565	BP136366
2962	35	72	658	GAAAATAACGTTTAACTTATTCTGCACCCCCACCCAAATTTTTCCAAGCCAACCTTTT	2709	A_95_P296603	FG638025
2965	35	75	125	GGCGAACTGCTGCCATCATCCATGAATTGAAGAATGAGATCGTAATTCAGAATGACA	2714	A_95_P114977	CV507105
2968	35	78	445	ACCTCCTGTATTTGGATTCTGAATTGTGCATTTCATGGTTATTTTTCATTCAAACCAGT	2720	A_95_P181737	TA13051_4097
2977	36	2	221	TTAGCTTACCATTTTCTGTGAACCTGCAGCTTTTGAAGGTTTATGTTTCTCATTAGAGT	2572	A_95_P196597	FG626013
2981	36	6	732	CATGCAATTCAGTATGAATTTGCTTGTAGATGCATGATTTCATCTCCTGCCATGAAAT	2580	A_95_P016821	EB681829
2984	36	9	593	CACCGGATATTTGGGGCTGTGTAGTTTCATTTTTATTTGACTTCCGCATATATTTTGTT	2586	A_95_P201752	TA17490_4097

2999	36	24	0	GAGCTCCCTGCTCCTTTCTTTGCTTTTATTAGGGATAATTTCGCAATGTATTATTGCTG	2615	A_95_P265926	A_95_P265926
3011	36	36	435	ATATCTGGAAGACTCATTATTTGACAAAACTTTCAATAAACCACTGCGTTCATTGAGC	2638	A_95_P104552	CV017065
3020	36	45	576	CAGCGTTAATGAGTATGTAACGAGTTCCCCATATAAGTGATGCCCGTATTATTGTTTT	2656	A_95_P028016	EB443690
3022	36	47	320	ATATGCTAAAACAAAGTCAGATTGTATTGCTAAGGCAGAGGGGACCTATGACAAGA	2660	A_95_P200922	FG644997
3024	36	49	126	CTCTGGACATTCGGGTTATTACTTGGTACAAGTTAATAACACTTATGCTCTCTCTTATT	2664	A_95_P033259	AJ344589
3025	36	50	705	TCTGAAAAGTATAGTGATTGATGGAGATACAACTGTACCCGTTTACACGATTCTTGA	2666	A_95_P127812	EB427384
3026	36	51	110	TGGTTGTGGAGGTTCTGTACTAGCTTCAACTCCGGAATTTTTTGCGGCTTGCCATACA	2668	A_95_P242202	AJ719161
3028	36	53	290	CTTTAATCGTTTCCTTTTCGTTCTTTTTTCTTAGTGGGATGGAGTCTGCTATTTGAGCG	2672	A_95_P077050	AM783661
3033	36	58	731	TCCTTGCAAGGGAGAGGAAGCTCATCAAAAAGAATAATTTTGATATTCAGAGGTTTG	2682	A_95_P126797	EB426152
3038	36	63	814	GGGATGACAAAAGGGAATTAATTGGAACTTGGAACTGTTAGACCTTAATAGGTTGTT	2692	A_95_P100978	TA12699_4097
3046	36	71	425	ATCAGTGTCAATGGACGATTGGATCTGGAGAGGGTTCAAGTAGTTTTGACCAAAAC	2708	A_95_P052446	BP132926
3048	36	73	710	AAATTTAAACCACAGATAAGTGAATTTGTTTATCAAGGTGAAGAACCCGTTTCTGGT	2711	A_95_P150902	EB681052
3057	36	82	370	TACTTTAGATAACGTGTTTATGCAAAGCATGTCCTGTTTTCTATTGACCTTGAACATC	2729	A_95_P040221	BP129769
3058	36	83	1077	TGATCTTATATGAGATGCTAGAAGGTGATCCACCATTATCCCACTATGAACCATATGA	2731	A_95_P008056	TA15653_4097
3059	36	84	1122	TTAGGTCTAGTTTGGGATAATTCATTGTTGATGGGGATGGATTTAGACACTGTTAATT	2733	A_95_P017346	TA14303_4097
3062	37	2	325	GGTTTTTTGCCCTTTGGGAAGCTATAGACAATCGGGTTTTAAATTTAATCCAGAAAAA	2736	A_95_P113562	CV021194
3071	37	11	623	GCGGCATCAAGCATGTATTGTGCGATTATTGTTGCTTCTATATGTTTATTTTCCTCTGG	2753	A_95_P090088	TA16335_4097
3072	37	12	294	TGCATCCCACTCGGCTCTTCTAGTTAAGCAACATAAGTTTCATGTTTTCTTAAAATACT	2755	A_95_P157992	EH616031
3073	37	13	586	CAGTTGCTTTCTTGCCCAATTTAAGCAAAATGTAATGTTTTTGTGCCTGGAAGATAAA	2757	A_95_P280808	FG635057
3074	37	14	141	TGGCCTTAAGATCAGCTGCCTCATTCCCTGTTTCAAGGAAGCAAAACCTTGACATCAC	2759	A_95_P105292	EB438050
3077	37	17	1075	TAGGAGCACATTGTCTCCTGAACTTTTGGAGCAAATATTTCGTGATTGTTTGGGTGCT	2765	A_95_P190027	TA14917_4097
3079	37	19	449	CATGAAGGACTGCTTTGTAATTAATTTGTTCGAGTGTTATTTGTGTGGCCTGTATATG	2769	A_95_P033439	AJ632746
3082	37	22	342	AGCCACGTGTCTAGTTTGTTATGAAGTTGATTCTGCCTATATTTATATTCCTTGTACTC	2775	A_95_P133192	EB434485
3088	37	28	682	TTTCGAAGTATGTAGAAGACCATAGTTGCTCTGCTGATGTGCTTCAGCCTGACCAACA	2787	A_95_P138707	EB442425
3091	37	31	1319	GGAGCATGGTCTTTCTTGATTTACTATATATGCAGGTCCTCTTTAGGGATATTATATG	2793	A_95_P250337	AB041514
3095	37	35	905	CATATTGTTTGAATTGTAGCGAACCACACTGGATTTTGAGAACATCTGTTGTTGTTTA	2801	A_95_P253654	DV161692
3099	37	39	496	GTATCAATGGTTTCGGTTTCTCATCTTAGATTTGGGAGCTGAGATTTAGTGTATTTTA	2809	A_95_P153677	EB683895
3101	37	41	1366	GAAGGGGATGGTTTAATGCTTCAGCTGTATTTATCAGTTGTTTGAGAAGATCTATAT	2813	A_95_P011416	TA12493_4097
3102	37	42	1379	CTCTGAATGTTTTCTTTGCAGTGGTGGTGTATTGGATATTTAATGGCTGTTTGCAGCC	2815	A_95_P002656	TA16132_4097
3111	37	51	330	ATATCTCCGATCTCGATTACGGCGTCTCAAATGAGGATATCAAGGAGCTCTTCTCCAA	2833	A_95_P102547	CV016069
3112	37	52	413	TTTGGGCATTCTGAATCTTGTACTGAGTTTTGAGTTTGAAATGAGTTCATAAACACTC	2835	A_95_P187742	FG125349
3116	37	56	578	GGACCTACTGGTTGCTACTTTGATCATACTGGTAGTAGCCGAAGTTTAAGATCCTGTT	2843	A_95_P102327	EB681115
3118	37	58	450	ATGGTCTTTTGAACTTTTTGTGCATTCCAATCTACTCCAGGAATGGAGTCTGAAAAAA	2847	A_95_P156602	EH614327
3120	37	60	847	ATAGGGTTGGAAGAGTTCGAGAAGCACTCAAATACTACTCCATAGAGTCGACAGCT	2851	A_95_P242602	EB427401

3124	37	64	271	TTTCAGTTAAACGCTTTAGTTCTCTTTACTTATGTTGATGGCTTCTGATCTTCTGGCAA	2859	A_95_P183927	TA13571_4097
3130	37	70	540	CTTCTTTATGTTGGTAAAACTGCTGGTTACCATAGCAGGACTCAGGAAGAAATTCAT	2871	A_95_P051126	DV161248
3136	37	76	503	AGGTTCAAGCATTCGATTCCAGTTTGGCATACTGGATGGGAAGCTTTAGCGTGTTAT	2883	A_95_P088268	BP530000
3144	37	84	2532	CACCTGAATTTTCTTGTGCTTTTTCAGTTTAATTGCAGATGCAAGCTGAAAATTTAAC	2899	A_95_P182947	TA13342_4097
3145	37	85	131	TTAGAACAGGCAAAGGATGCATTGGCCAATCTTGAAGTTCCGGTGGGTTGCGTTATT	2901	A_95_P158182	EH616253
3146	38	1	882	CAGTATATGCTCACTACTTTTTGGCTTATATAAATGAAGGGACACTCTGCCTTCTAAA	2735	A_95_P008396	AB079024
3153	38	8	2218	CCATGTAAGATTGACAAAATGTGTACGCTTTCTTATCTCTATAGTTGGCTCATATCAT	2749	A_95_P237724	AB004797
3155	38	10	290	CTCCGCTCCTGCGACTAAGAATTCTCAACTATATGTTTGTACATAAAATGCATAATGA	2752	A_95_P155337	EG650018
3157	38	12	670	AAGAAGAGCAGGAAACATCATGTAGGCACTGCGGTATTAGTTCGAAATCCACTCCTA	2756	A_95_P028876	TA15643_4097
3159	38	14	753	TGACTATAATTAAGGTTGGTTGGGTGCTTTCGCTAGTGCACAGCCTTGCTTTTACTCA	2760	A_95_P198702	TA16835_4097
3160	38	15	1229	CATCTTTGATGGCTTTAAGATAGCGTGATCGATTTTGCATTGTCAATGTCTAGTTATT	2762	A_95_P176842	TA11803_4097
3161	38	16	663	TAGGCATATCAGTCACGAATGAGAGATCTGTGAATATGTTGCTATTATATTTACGCA	2764	A_95_P153427	EB449788
3165	38	20	481	CATAATGCGATCCGTAGTGACAGCAAATGCTTCTCTCTTTATTGATGTTTGAATTGTA	2772	A_95_P035358	BP128453
3166	38	21	572	TTAATTGACACAGGAGTCAAACGGCTATGCAAGTGCTGAATGCATTCCATTATTTCTA	2774	A_95_P234179	FG645147
3168	38	23	729	CAGAAAATTCAGTGCTCCGAAGCAAGCTCTTGGAACATGATAATCTTGTAAGATACA	2778	A_95_P302058	FG194027
3169	38	24	261	CATCTAGCTTCGACCCTCCAAATGTTTTAGAAAAGCGTGGGTTGTTTGTCACTTGCAG	2780	A_95_P071340	FG642353
3170	38	25	765	GATGCTCAAGGATAATATTGGAATGTATGCCCAAGTTTACCCAGCAAATTCATTTTGG	2782	A_95_P164742	EH624051
3173	38	28	127	ATACTGTCAAGCAAAATTTAATTCTACCACATAGGTGGGTGCGGCAGCATTTCGCAC	2788	A_95_P113257	CV021079
3180	38	35	900	TTGGAAGATTTACCGAGCAAACTAAGGGGTCTTGTGAGAAATGCGAAGAAAGTGGA	2802	A_95_P145807	EU342421
3183	38	38	895	TCGGTGTGATTGTAGCTGACAATTGTAGCTGTTTGACACAAAATAGAGTGACTAAGA	2808	A_95_P186237	TA14082_4097
3189	38	44	988	GGTTTTCCATTGGGACTGCATGTTGGGTAAGTTGTCATCGTCTATTGGGACTGGAAA	2820	A_95_P193942	TA15779_4097
3190	38	45	583	AATACAGCTTAAGGATGCTTTCCACACAATTGAAGTGCAAGGACTGCTTCAGCACAC	2822	A_95_P254834	EH617724
3191	38	46	787	GGGAAGCAAGTTTAGGTGGTAATGTAAACTTCTTATTATGGATTAATTCGGCTTTAG	2824	A_95_P211407	DV157963
3194	38	49	683	ATTTATTCATCCAATATGGGATGGTGAAAATTATCCCCAGTCAATGTTTCCCGCTCTG	2830	A_95_P242822	FG636021
3195	38	50	623	CATTCATGATTTGTGTTGTTAGCCAGGGGCTTATTAAATTATAGCTCCATTTGTCAAAT	2832	A_95_P062030	BP135410
3196	38	51	703	TTGGCTGAGGTGGATTTAAAATTTAAACGTACGTCCAACCTTTATATTCTCACTACAA	2834	A_95_P178707	TA12325_4097
3198	38	53	774	ATGGAAGCCTATTGCCGGCCTCTGTGATATCTGTTTACTGTGCTTATGTTTGCTACACT	2838	A_95_P253969	FG125331
3203	38	58	364	TAAGATTAGTTAACTGTCAAGGCATTGCTGTAGAAGACCAGGCTCCCGGAATTCACC	2848	A_95_P115712	FG644328
3212	38	67	406	TAATGTTGGAAAGCTATTGAGTATTCCTTTAATTTATTTATGGGGAGCCAGTGGCTGT	2866	A_95_P132482	EB432975
3223	38	78	702	AGCTGCTGACAATGGAAGACATTCTCTGTACATAATTCAATTTAGCAAGTATTTCGTT	2888	A_95_P117907	DV160875
3228	38	83	850	GATTTGTTTGGCCAATATCATGGGAGGATTTACCAGTCTTTTCTTTCCGGGGTGAATT	2898	A_95_P180712	TA12811_4097
3232	39	2	603	GAAACTAATTCCGAGGCGATAACAGGCTATGTCAGGGGTCGTGATGTCCATTTCATA	2904	A_95_P004746	FG176614
3233	39	3	588	TTCACTGAGAGGCTTCCTTTCTTGCCTCTTATGTTGATAAGCATATACTGTGCCTTCGG	2906	A_95_P236189	BP133167
3237	39	7	531	GATGTTTTGCATAAGCTAACATTGATTTATAAATTGGTCAATGGATGCCCCATTTTGT	2914	A_95_P029381	DW003030

3238	39	8	184	GAAATCCATAGGCTTTCAGTTGTTTAGCAGCATGGATATAGATCTTCGGCTGCCTTCT	2916	A_95_P127507	EB427025
3240	39	10	82	CGCCTTTTTCTGTATTTTCTGGGGTTGTTTGATTGACCATATTACATATAATCTCAGTA	2919	A_95_P013211	EB446083
3241	39	11	1382	ATAGCATCCACCACCTGTAATTGGTGACTCATTAGTTTGCAGGGAATAAGAGTTTAAT	2921	A_95_P123412	X96727
3242	39	12	765	TGACACAAGAACTCCATAACATAAGTAGAGCTCCCAGGTATCTCCGGTGATTGACTGT	2923	A_95_P147237	EB451503
3243	39	13	806	GCCTGAATGTTGGTTATTATTGTACTTACTATGCGTCCAAGTTGTAATTCTAAGGAAA	2925	A_95_P010341	TA13001_4097
3244	39	14	304	TAGGTCAAAGGGGGTCTGTAAAGTACCTTTGCTTATGCCTTATGTCAAATTTAATGTA	2927	A_95_P084360	BP528997
3247	39	17	732	ACAATCAGTGATGGAAGGATATTCTCAAAGGATATGGGGATCGCTTGGCATAAAAC	2933	A_95_P162097	EH620870
3248	39	18	232	CTTCGATTTTAGTTGTTGTTGTATCCTAGTCTACGACTAAATCTGTCCTCAGCTTTATGT	2935	A_95_P027856	EB442502
3251	39	21	461	CTGGCCATGTTATTCATGTAACCGTAAATTCCGAAGGTTGATACAATTTGTTAAATCT	2941	A_95_P005591	TA14421_4097
3262	39	32	930	ATTGAATTGTGACGATTAGTCTAAAATGATCCAGCAAGCAATTGTTGGGATTTCCTTT	2963	A_95_P222892	TA22130_4097
3263	39	33	722	ACTGGGCAGGCATTGCTTAGTTTTTGTATGAGATGTTTGTTAGTAAATGGAAAAATG	2965	A_95_P012556	TA13220_4097
3277	39	47	1454	AAATGCTATCTGGCGTTATATTCCTTAATTCCAGTTGGCAAGTTCTAGAAATTCAGTG	2991	A_95_P192007	TA15360_4097
3282	39	52	409	GAAAGAGAGTGGAAAGTCATCCATTCTTAAGGACGTAAAGCCATGGGATGATGAAA	3001	A_95_P103947	CV016769
3283	39	53	549	AGAGAACTAATATTTCGGGAGATACTAGAGTACCATCCTCAGCTTCTGAAGGACTAC	3003	A_95_P164402	FG151562
3285	39	55	1307	GGAAAAAGAACGAACTAGATCAATAATTTTCTGGCCAGTCTATGTTTTTGTTCCCTTC	3007	A_95_P180357	TA12723_4097
3287	39	57	578	TGAGTGAATGATAACGTTTATCTAAGTAAAGGGACTTTTTTGGGGGATAGCTTTGTTT	3011	A_95_P161392	EH620136
3288	39	58	578	TTGCTGGCTGTGAGAATTTTGCATCAAGAATACAGAACTAGTATCTGTTTCTACTGTTT	3013	A_95_P179042	TA12415_4097
3290	39	60	955	CTTCTCCTTTTTCAGGCTTGTAGATTACTGTCTTGATTCATATAAGAGAAGAGCTTGT	3017	A_95_P176187	L29271
3293	39	63	826	GTCTGATGATGAGTGACTTGTTGACGATGAAGTTTATTTTGTTGTCTGTGGGTCAGCT	3023	A_95_P126482	EB425800
3296	39	66	921	CGCTGTTCACCTTTTTGTTGTTAAGATGTGCATTTTCATATAGAAATCAAAGAAAGCA	3029	A_95_P016346	TA13728_4097
3298	39	68	566	TTGGAATACTTGTTGAAGGTAGCAAAAGGGTTTGTTGTCGGTTCAAATCAACCTTTA	3033	A_95_P068170	BP137067
3299	39	69	795	ACTAAAGACAGCTTTGGAAATGCTAAGACTAGCATGCACCCTCGAAGAAAGTTTGCC	3035	A_95_P299388	FG172777
3302	39	72	635	ATATCTGAACTTGATTTATTGTACTTTGTATGAGTTGCACAGTGGCCATTTGTAGTGC	3041	A_95_P270277	EB445989
3304	39	74	622	GGCGGTGGTGACTGCGTACATGCTATTGATTTGATTTTTACTCTGGTTATTGTTTATT	3045	A_95_P181307	EB683516
3309	39	79	664	AGATTCAAAAGCCGATGCTTGGAGAGCTCTTTGGACTGTCTGTCTACACAAGATATTT	3055	A_95_P275003	FG192759
3315	39	85	293	TTCCACCCAAAACATCAACAGCAATGGTAGCATATGCCTTGACATTTTGAAGGAACA	3067	A_95_P114207	FG636798
3316	40	1	377	CCATTCAAGTTCTGTCCTAATTTGGAGAAGGAAAAAGTTGAGTATTCTAGCCAATGGT	2903	A_95_P131752	EB432143
3320	40	5	668	GCAGTAGAGATTGATATAAAGTAGATTATGAGCTCTCCTATGACCTATCTATCTTGCT	2911	A_95_P232314	FG641881
3330	40	15	538	ACCAAATAGATGGGTTTTTTACCCATGCAGTGACTTCCCTTTTCGTTTATACTGAAATT	2930	A_95_P057036	BP134112
3341	40	26	839	ACAGACATAGACCGCATCCAAACCAAGATTAATTCTTCTGCTAATACCCTTGCCACTA	2952	A_95_P309753	FG172772
3344	40	29	410	CGTTCCTAATTCCATACCCTGTAGAATTTTAGTAAACTCTGTAGTAGCTCATGACTTGT	2958	A_95_P092528	BP531845
3345	40	30	648	GTTTGGAGAGGAACCTTGGCATGGATCCAAGTGACCCAATTATTCCGTTTGTTCTTTT	2960	A_95_P214587	FG136377
3348	40	33	763	CGGTGTTTTTAGCAGAATAAAGGGGCGCTTAATGTTTGCTTCGAAGGAGCTGATGTC	2966	A_95_P180542	TA12769_4097
3356	40	41	728	GATCTATGCAAGAAGAAAGGAGCGTGAATATTTTGCTACCAGTCCGGACTATGGGC	2980	A_95_P297028	EB680938

3358	40	43	481	GCTTGGATTTCTCATTGTTAATGCATTGAAGATGCTTTGCCTACCAGTGAAGGTCCCT	2984	A_95_P275138	AM804984
3361	40	46	863	GAACTACTTGCCATTTGTACAGCTGAAACAGTTTGAGCACTGCTGCTCATGATGCATT	2990	A_95_P253574	FG177904
3364	40	49	834	TTTCAGAGATAACAGAGGAGAATGTAAAGCAACACGGTGAGAAACTTGGTGAAGCC	2996	A_95_P220837	EB424748
3366	40	51	796	GGATATGACTCCGTGGTGCCCTTCCCGTGAAGATTAATTCAATGAATAAAATAATTA	3000	A_95_P146457	EB450511
3369	40	54	701	TGTAGATTCTCCCAAAGGAGGATTAAGAGATTCCACTTTTTATAGCTGAGATCTTTTT	3006	A_95_P029031	TA17801_4097
3373	40	58	300	CTTCTATTATGCTTAGAGGCTCTCTAGACAGGTTGTGGGTGGTGTTTGATGTTGGGA	3014	A_95_P160977	EH619674
3374	40	59	803	ATTTGCTGAAGCAGCTTAATAAAACCAATGACCCTACATTCACCCCGTTCTACAGCTG	3016	A_95_P188467	TA14577_4097
3375	40	60	647	GAGGTTGCTTCAGAATTGAAGAAGTTTCACTTGTCCTGCAAAAGTTGATATTATCAGT	3018	A_95_P210502	TA19411_4097
3377	40	62	960	AGGGTTACATTTTACTCGGTTTGACAGACGCTATGGGATCAGTATAACTAAAACAAAT	3022	A_95_P129452	TA18724_4097
3378	40	63	788	ATAACTGGTCTTAACTCTTACCCAACCATTGCATTTCTGTTTGTAAAGTTTACAGAAAG	3024	A_95_P017336	EB425231
3386	40	71	0	TCCAACCCTCCCCCGAATTCGAGCGTCAACTGCATCTCTATTTGAGATTTATGAAAAG	3040	A_95_P285233	A_95_P285233
3388	40	73	1696	GACATGTATAATGAGTTATATACTTTTTTCAGGTGACGTCTTTCCGTTCTACTTGACAT	3044	A_95_P198987	TA16896_4097
3389	40	74	420	ATATGTACAAGACCGATAAAAGCAAGTATGAAGCCACTGCTCGGAGCTGGACTCAA	3046	A_95_P106047	EH619487
3392	40	77	831	TTAAAGCAATAAAGGAGAGATCCAGTACACCTAAAGCGCCTCGTGATCCGCGTTTAC	3052	A_95_P030566	EB680520
3400	40	85	261	CACTTGTTTCTGGTGCTATTGGATCATGTTCAGTATTGTTTGCTAAGTCTCTTTCAAAC	3068	A_95_P242547	DQ460173
3402	41	2	706	TCACTGTCCAAATGGTGAAAATTCCCCAAATTGGTTGGGACATTAGGCTATGCCTTA	3071	A_95_P054096	BP133353
3407	41	7	635	CATGAAATGTAATTGGTCGTTGCAACAAATCACCTATATACGTTCTAGTACTATCTAC	3081	A_95_P000966	FG638726
3411	41	11	1035	TGGCAAACAGACGAGACTCACGGATTTTGGAACTTTCTGCATTTCTTTTCCAATGTAA	3089	A_95_P026766	TA18491_4097
3412	41	12	719	AGCTCGTTTTCAACTGATTCTTGATTTTGTTCTTTCTTACGGCGTAAATTCAGTTGTCT	3091	A_95_P032906	AF197568
3416	41	16	314	TGCATCAAACTGGAGGCACAATTCTTTAGAGTCTTCTTTGCTGTATCTGTGAGACCTA	3099	A_95_P106167	FG640961
3419	41	19	520	CTCTTAAGGATACGATATCTCAGAAAGATGAGGAGATTGAGAAACTGCAGTGATCA	3105	A_95_P085145	BP529206
3420	41	20	783	ATTGTTGCTACCTGCTAATCTCGTCTGCATGAAAAGCTCTGTTTCTGCATTATAAAGAT	3107	A_95_P013776	TA12614_4097
3426	41	26	742	GTTTGTAGTTCTGTTAATTGCTAAATTTGTGTAGTTTAGCTCTCTGCATTGACAAGTA	3119	A_95_P012371	TA15245_4097
3428	41	28	1601	ATAACGTTATTTCATGTTTCTTGCATCCTATCTCGGGATGGAAAACTCATAATGTTGCT	3123	A_95_P041432	TA13097_4097
3434	41	34	436	GTATTTGGACCATTATATCTGAGAGTCCATTCAAGGGCCAGCTACTTGGTCTTACTTA	3135	A_95_P203573	FG643084
3435	41	35	142	TATTAGGATTGCGATAAGCTGATTTTTTGTCCTAGCTCCGGCGCTCGATCTTGGCAAC	3137	A_95_P058386	BP134463
3440	41	40	356	TGACCTGCTTTGACAGGCCAGAATGAATTTTCTTCATCAGTTTAAGTGTGTCATTTAA	3147	A_95_P180847	EH618138
3441	41	41	667	CCTGGTGTGGTTGCCTCATATATTTGATACTTACAAAGTCTTTGCAATGAATGCATTCT	3149	A_95_P287823	EH620884
3442	41	42	648	CACTCAGAAGTTACATCGCCCGATCGCTCTTAAAGATCTACTTATTGCTAGCACTCCA	3151	A_95_P300273	FG637378
3444	41	44	460	TCCAATCATTTGTACCTGTAAATGTGCACCAGATGTTATAAACTTGGTAGTGTCATAC	3155	A_95_P154022	EB684183
3447	41	47	715	CTTATTATTCTCGGAAAGCTTCAAGTTGGATTGTGGAAAGATTCTTGTCCAGATTATA	3161	A_95_P239139	AJ344536
3452	41	52	297	ATTGTCTAATTATTTTTTCCTTTTCTTGGTTTTAGTCGAGATGATGAGTTGCCACCTTG	3171	A_95_P124562	TA20094_4097
3454	41	54	346	ACCGATTTCAGAACTTTGTAGATACTCTGCCTGCTTCTCTATTGCTCTTGTTTGACAGA	3175	A_95_P090453	BP530961
3455	41	55	756	CGGTTCATCCCTGTTACTACATTTTCCTTTCCAATCAAAAACCATAAGCGTTTTATTTA	3177	A_95_P020621	TA21510_4097

3459	41	59	529	TTAGCACAGTTGAAGAACTTAGATTTTGCTTTAAAAACTTGCTTGAGGCTGACATTG	3185	A_95_P018611 TA15760_4097
3460	41	60	630	GTGGGATAGCTTTGTTGAGTTTATCTATATTGAGACTTCTTTTCGTGCAAGGTTTTGGT	3187	A_95_P116172 DV158743
3464	41	64	374	GGGCTGTGTTAAGATGAGTTTGTTTTACATGTGTTATGTGGTGATATAATTGTTGTG	3195	A_95_P143207 EB446547
3470	41	70	734	GAAATCCAGTTTCTACGTTCAAAGTAACATTGCCGGTCTTGTACTTTTTCTAGAGCTT	3207	A_95_P163042 EH622055
3477	41	77	816	CTTGTGGACTTGTCCTGCAAAATCCTTACAGCTAGATGTATCTTCTTTTTTCTTGATTA	3220	A_95_P001106 EB443952
3478	41	78	505	ACAAATGAAAAGTCTTACCTTCTTGATAACAATGCTCAAGATCATCTTCCTGTTAGTGT	3222	A_95_P082985 BP528645
3480	41	80	519	ATCAGTGTACTTTGACCTTGACCTTGACCTATAGTAGTGAGTAGGCAAATTTTACCAT	3226	A_95_P083640 BP528812
3482	41	82	923	ATGGTGCCCAGTCTCTAGTAAGGCCTCGTATGCGCTCATATATGTGAATTTCAATAGA	3230	A_95_P195007 TA16025_4097
3486	42	1	290	CCAGTTTGAGTTCAGAAGAATATTTGTAATGTATGTAAAACTTGTGCAAAATCGGAG	3070	A_95_P094163 BP532589
3491	42	6	807	ACACATGACCAAGCTCTGCAGTACTTGTGGAATTGCAAATATAACTCGTTGCAGTCA	3080	A_95_P289118 DV157762
3496	42	11	856	ATAATGAGTGGGTTCTTGCTACAGCATCATCAGATAGTACTGTCGGTCTGTTCGACAT	3090	A_95_P269961 EB428345
3497	42	12	379	CATGGTGGGTTGCAGTGCTCTTCTTGTATCGTGTCAATATTATAATACTAACCACAAT	3092	A_95_P075800 BP526819
3499	42	14	1523	AAACACTATCTGCTTTAGAGCGTCATGAAGAATCTTCTTCTTCTTTGTCCAGATATCCT	3096	A_95_P196582 TA16370_4097
3501	42	16	705	CAATACTGCGCACTACCACATTTTGAAATACTGTTATTGAGGCTATCACAATTGTTGT	3100	A_95_P204557 DV158965
3506	42	21	454	GAATACATAGCAGAGGTTTGTGTATTAGCCAGCCTATTCATCCCATTTATTATTATGT	3110	A_95_P161212 TA17504_4097
3507	42	22	805	CGGTTTGAACCTGCGTTTAGAGGTCAATATTGAGGATTTGCTGATTATAAACATGTTT	3112	A_95_P258601 DV162530
3508	42	23	1411	ATTGTCTGACTTTGATTTACAATGCTTGTCTGGACGCTGTTGATAAGCATGTAAAATA	3114	A_95_P003836 TA12877_4097
3509	42	24	643	TGCCATGGACTGTTGAAATTTGTACTCAAATCAGATCTCTTAGGGCTGTTAATTGATG	3116	A_95_P293768 FG635385
3513	42	28	223	GTGCTTAGCATGTTGTAAATAGACAAGAATGTCAAATTCTATCAGTGCAAAGCAATC	3124	A_95_P139082 EB442786
3521	42	36	768	AATTACTTTGAGATCTGGTTAGAGCACTGGAGATGTCTTGCAGATGTGGATTCCCAG	3140	A_95_P228304 FG167556
3528	42	43	186	TCCATCAGTTCATAGCCCAGGAAATGTTCAGATGGAAGCAACAATATGTTAAATATTT	3154	A_95_P002331 TA21758_4097
3529	42	44	0	ATCAACCTTATCAAATATGGGGTACTCGGCCTTGAAGCGAGTGCAAACCATGTTCTG	3156	A_95_P241639 A_95_P241639
3532	42	47	687	GGTTGTTTTCCATGTCTGCACTTCACTACATTACCCTTCCTATTTAAATGAAAGTAGTA	3162	A_95_P213172 TA19992_4097
3539	42	54	406	TATTCCCTGATCCATTGGCGGTCCCTGACGTATCGACTAATTCGGCGTCAATATAGTT	3176	A_95_P271746 AM791353
3540	42	55	685	GGAGATATGTTTAGCAAAAACAGTGAAATGCATATTTGCTATCCCTTGGTCCTAGTTA	3178	A_95_P291668 DW005231
3544	42	59	581	CTACCACAGATAGTGATTCTACTTAGTATACTTGACGTGCTATGTAATGTCAAAGTGC	3186	A_95_P211287 TA19577_4097
3549	42	64	856	TTTATTTTGCACTTTCATGTGGCTTCATGTGGGAGCTCATTTGCAGCTCGTCTATGGC	3196	A_95_P259031 FG138736
3553	42	68	619	ACTAATGCACGGGTTGCTTGGTTCAGTATCATGTCTTTGGGAGTCTGCATTGTAGCAT	3204	A_95_P301358 FG634200
3558	42	73	806	GTACGGTGCAGCTCCCTGTATATGAGTAAATTTTTGTATAGTTTTAGATAGCTGATTC	3214	A_95_P122492 DW002464
3573	43	3	516	ACTTCAGATACTCAACTCGAGGCCCATAGGATATCCTTACAGCAGCAGATTGAGATT	3242	A_95_P032151 BP128511
3577	43	7	523	AAAGCTTCACCCTTAAGGGGTTTTGTGCATGGAGATGTGAAGCCAGAAAAACTTTTT	3249	A_95_P162267 EH621204
3580	43	10	648	AATGGTTTTGAAATTCTGCTGGATGGGTTCTAAGTGGTAAGCATTTTAACCATTGGG	3255	A_95_P016101 TC50020
3581	43	11	780	TTTCCCTGTTGACTTTGCCTTCTTTGATGAGCAGTACCCCCATTTCTTTGATAAGGAGT	3257	A_95_P312538 FG150405
3583	43	13	240	TTGGTTACCTGTCTGACATGCTACTTTCCCTAACTTTCCCAATTTGCATGACTAGTTGG	3261	A_95_P029806 CV019868

3589	43	19	370	TGTTAGGATTGTAAAGGCATTCGTTGACAACCTTATCGAAGATCCAGCATCACTTGCT	3273	A_95_P091603	BP531431
3600	43	30	708	ACTTAGATGGTCCTTTTTCAGGGCTCGTCCTTCTCAGATTCTATAAATCTTTTGGGTCT	3294	A_95_P068405	BP137120
3602	43	32	675	AGGATCGTCCAAGGATTTGTCCTAGAGACGCGAGAAAAATCATGCTTCATGCTTTTG	3298	A_95_P223732	EB684141
3603	43	33	385	TTAGGTGTTCCACCCGCAAGCCCTATGAACCTGCATTTTGAATTCTTGTGTCAAATAA	3300	A_95_P110667	CV019842
3604	43	34	1476	CATATGATAGGCAAGCTTGGATGCTTTGCTTTCAAATTTGCCATCATTTCTCTACATTT	3302	A_95_P013611	TA15009_4097
3606	43	36	412	TACCCATTGCAGATGCACCTCCTGAAGATGAAGCTGCCTTTGCAACATTTAAAGGCAT	3306	A_95_P041136	BP130016
3608	43	38	352	TCTGTGGTTGTGTAATGTGAGTCTGTATTGAAAAAGATTGAAGCTAGTATTGGAGGT	3310	A_95_P141797	EB445426
3609	43	39	1018	CCTTCATAAATGGAAGGGGAGGTCCATTTGTTGGCTATAGTTTATATTTTTACCTTAG	3312	A_95_P032746	AF068724
3613	43	43	297	AATCTACACCTGGGGACTCTTGGTCAGAGACTGAAGAAATAGACCGAGCTATTGCAA	3320	A_95_P136607	TA16023_4097
3614	43	44	446	AAGGGTTGAAGAAGTTCAAGTATTTGTTGTGATATTCATGGTACACTAACGGGTCTG	3322	A_95_P282703	AM833244
3617	43	47	462	CAGAATAGTTGTTATGGCAGGGCAGGAAGCTCCCACAATTACCAAGGACAAGAAGG	3328	A_95_P086968	BP529679
3618	43	48	557	CCATGAATTGCAGAAGCATGGGGAAGATTTGAACTTGCAAAACACAAAAACAACAA	3330	A_95_P141442	EB445170
3619	43	49	720	AGTTGGACCATTTTCAAAGACCCAAAATTACACCATTTAACAACCTCCCCTGTTTTAG	3332	A_95_P127852	EB427399
3628	43	58	777	AGCATTGGCTGAAAATGAAGACATTGATGACATATTGCCATCGCCAGAGCTACCAAC	3350	A_95_P145697	EB449444
3629	43	59	784	GTTTGGACTTAGTTGAACACGTTAAGATATAATGCAAACTTGATTCTTGTGTAGAGA	3352	A_95_P236304	EB449505
3631	43	61	824	GTTATACCTTTTTAAAATTTCTATGGGGGTCTGGATGGGGGAGAAGGGTGTTCACTG	3356	A_95_P073290	BP526179
3632	43	62	824	TCTGCATGTTGACGCATAACCTGTAATTTACATCTAAATTTAAATGCCTGTTAGTGCTT	3358	A_95_P011791	TA17964_4097
3633	43	63	443	ACTTCTTTCAGTCTCAGATCATGTACTTGCCAATGTGGATGCCATGACGTTATAAAAT	3360	A_95_P092448	FG638854
3635	43	65	561	TCAAATGGTTCGTGAGCTTATTCAGAGCGTTACAGCAAAATCTGCGGCACCCATGAT	3364	A_95_P117717	FG163875
3637	43	67	1670	CTGTTCGAAGGGAGAAAACATGGATAGCATTTTATACGATATTGCCTTTCTCTTTTGT	3368	A_95_P015786	TA13905_4097
3644	43	74	443	AGCACGAAGGTGATGCCGTGTCATGATATGTAAATGTTAATGCACGAAAGTGATGT	3382	A_95_P148002	EB643514
3651	43	81	399	ATTACTCTGACTGTCGATTTTGATTGGAAATCTGTTGTAGCTGCTAAGGACTGGACCA	3396	A_95_P125612	FS416721
3652	43	82	412	GTTGGTACAGTTCCAGATTATGGACCCAAGCAAGCTCTGTTTATTTGGTTATTAAATG	3398	A_95_P131102	FG638602
3656	44	1	1338	AGAATATATGCAAAACCTGTGCCCGGAACGACTGCAGAAGAGATTGCTTGTGGATT	3239	A_95_P021111	TA14936_4097
3657	44	2	401	CGAGGCCTCGACTGTTTCAGTTTGGAATTCTTATTTATTATTTGTTCCATCGAATATCT	3241	A_95_P270606	EB433468
3661	44	6	843	GACTTGTTAATGTTGGCGCTACCTTTGTTTCCATCTATGCTGTTGACAAGCTTGGAAG	3248	A_95_P227589	EB428791
3664	44	9	777	CTTTAATGAAGCTATTATAGAGGAACGGGAGCAGGGAATACAAGAAGTACAACAAC	3254	A_95_P145382	EB449091
3665	44	10	11	GAATGTGGAGGAATTGACATTGAAGAAACTGGGACAAGGTTAAGACTATTTTCGTG	3256	A_95_P161087	EB426400
3666	44	11	659	AGATCCAATTTTGTGGAAAGGATCTTCTGTACCTATACTCTAGATATGTTGGCCTAGA	3258	A_95_P300303	FG636488
3667	44	12	541	TCTCGATCGGAAAAGAATCAAGAGAAAAAGAAAGAATCGGAATTGATCGATAGATT	3260	A_95_P026466	TA17335_4097
3670	44	15	608	GGTTGTCTTGTTGATTTCTCTTCCATCGATTATATAATAAGCCTTGTTTGTAATGCAGT	3266	A_95_P243307	DV999315
3671	44	16	880	TGAGTTTGACAGTGGCCTTTCCAGGGTGTTGCTTTGGAAATGGCTTAAATTCACATGT	3268	A_95_P246472	EB679910
3674	44	19	926	CACTTGTGTGATGATTCCTTGAATTTGCATCTACTATGTGTTGTTAAAATGTAACCGA	3274	A_95_P007861	U64924
3678	44	23	1607	GAGCTCAAGCTTTTTCTGCTCATCAGATTTGTGTTGTAGCAAATTGTCTTGTAAAATG	3281	A_95_P180902	TA12853_4097

3679	44	24	315	CCCAATTGCTGATATTCCATAAAATTGGTAATTAGACCTTTATTTGTTATGGTGCGCT	3283	A_95_P032631	AB293952
3681	44	26	1993	GGAGTCGTATATTGTTACTAATTCTTTTGTAGGATTTGACATTCAAGATGCTGTGACA	3287	A_95_P189352	X97913
3682	44	27	571	CTTTCGTCGGCTCCTGTGCTTTGACGTTTTAACTGCATTTACTACCTTTTTATGGTTTT	3289	A_95_P123062	DW002976
3685	44	30	241	GGCAGACTAGCTCCTTCGTCTCACATGATTTACATTTTCGTCATATTAACTACTGATGT	3295	A_95_P142222	EB445748
3686	44	31	567	TCCGATCCAATTTATCGTAATCGATTAGTTTACATGTAGGTTACCGTATTCTGAAACA	3297	A_95_P236404	BP132634
3692	44	37	412	CTTGGACCTCTAATGTGCCTGAGAATCAGCCTCTACTAATTTTGATATTTCTTTCAGAA	3309	A_95_P273756	EH620104
3693	44	38	782	TCAATGTCAAAAGAGAATCCTGATTTGCATGATCAACACATGTATCCTAATGAGGAA	3311	A_95_P219107	EB442007
3698	44	43	575	GATATTGTTAACAGGGAGTCGAACTTTGAAATCAGGATTATGGGGGAAAATTCCCA	3321	A_95_P200772	DV159471
3702	44	47	418	GGACTTGTTCCTTTCCAATATAATGACTTGTATTGTGGTGCCTTTCCCTATCAATAATT	3329	A_95_P000291	EH616159
3703	44	48	824	AACGGTAGAGAAATGAAGCCTAACGTGTTGGTTCGTGCCGATAGTTGTATTCCTACA	3331	A_95_P233559	EB426457
3705	44	50	532	GGAGAACCTCCAATTGCATCTCCAACGTTTGAGCATTTACAGTTTAATCAACCACCAC	3335	A_95_P051501	BP132663
3707	44	52	468	TTCATACTAATGGATTCCATCTGTTTTGAATCATACACCCTTAGTTTAGAGGCCACTAT	3339	A_95_P095248	BP533100
3708	44	53	789	TATTTATTCTTTCGCACACATTCGTCGATTCGTTGTGAATTCTAAAGTTATAGTCGCTA	3341	A_95_P115902	DV158330
3711	44	56	821	GTAACAGGCACTCAAATGTTTTATTCCCTGAGGTTGTAACATCATTGAAGCAGCTGA	3347	A_95_P009266	TA18912_4097
3720	44	65	930	TTGATGCTGGCGCCTTGAGTAACTTTTCCAGGTCTTGAGGCTTACTGGAAATATCTTA	3365	A_95_P026486	TA14276_4097
3724	44	69	898	GTAGGTTATTAGAAATGTGGTGTTAGGGCATCTCCAACCTTTACCCCATTTTGGTACA	3373	A_95_P236999	DV999529
3727	44	72	452	TTTGGCTGTGGATTGCTGGATGTATTTTCTCTTTTCTGAGTGAGTCTTCTTCTTCTCAA	3379	A_95_P306783	FG636230
3728	44	73	664	GCGGTGAACTTCCACTATAAACTAAGGTTTTGTAAATGCAGATATGGAATCTATAGA	3381	A_95_P003966	FG640581
3733	44	78	124	GTGGATCAGTTAGATAGTAGGTTTACAGTGGATACTAATTTGACCCTTTCATTTTGAT	3391	A_95_P141857	EB445475
3739	44	84	486	ATTACTAAGTTGTGGTTTGGCTGCTGAGATTTGAAATCAAACCCTGTGCATGGCTGTT	3403	A_95_P121947	DW002019
3741	45	1	403	GATTATTCCTTATTTCCAGTGCTACTCATGGGAAATCCCGATTGGTTATGTTGGCTGG	3406	A_95_P096568	BP533679
3742	45	2	2340	GCGGTATTACCAGTGTTCTTATCGCCATTCATCTTCTGTTTCTTAGTTTTACCTGTAAT	3408	A_95_P217582	AY220483
3743	45	3	359	GCTTGGCGAGAATTCTTTAAGGTCCATTTCTAACTGTACTCTTCAATGTTTTTGTATGA	3410	A_95_P093868	BP532453
3745	45	5	1944	TGCATGGCCAGTTACAAAGTGAAGCTTACTACACCAGCGGGAACAGTTGAGTTTGAT	3414	A_95_P114352	AF223573
3748	45	8	1462	TTTGTACCTTAAAATTGGAAGGGTGTATTTATTCCATAATCTATCGATTCTTGCTGCT	3420	A_95_P195537	TA16139_4097
3749	45	9	198	GTTCAGGATATTTTAAAGAAGGCGGAGGTTTTTAAGGAACTTCGTCCTAATCAATCC	3422	A_95_P007101	TC72713
3761	45	21	762	GTTCTGGTCTGGGGGTTTGGTCATTTTTACATTTTTATTATCTCTACTTTGATGAAGGT	3446	A_95_P012736	EB440145
3762	45	22	305	AAAGCAGCAGTCAGGCGATTCTTTCTAGAATTGTCACACCCATATTTTGGGAGTCTTT	3448	A_95_P038111	BP129180
3770	45	30	376	GACTCATGGATTAGCTTCATATGTTGCTGGTCAAATTGATCGCACTATGAGTTGGAA	3464	A_95_P111112	CV020059
3772	45	32	570	CCAGGTGCAATATTGGCTTTTCTATGTAAATGAAGTTGTAGTGTAATGTAGCCTTTTG	3468	A_95_P132927	EB433720
3776	45	36	79	ATTGTTGAGATGATACTCTTTCCCGTTGTGAATGAGGCATGTCGTGTTTTGGAAGAC	3475	A_95_P088913	BP530270
3779	45	39	460	GTACGGATGAAGATATTTACTATTAGGTTTTCAGCGCAAGTATATTGATCTCATGCAA	3481	A_95_P097890	BP534246
3781	45	41	1899	CATTTAGAGATAGCAACGCTTTTCTCAATTGGAAATACAATGTGTAGTCCTTTAGACG	3485	A_95_P176887	AB009881
3783	45	43	863	CTCCCTAATGGTTTACAGAATTTGCGTGTCTATAATTTAAAGTGCTTGTTGGTAAAGG	3489	A_95_P029171	TA13947_4097

3785	45	45	2302	CTGTGAAATATTTACATCAACAAGGTGGAGAGACCATTAGAGTTGGTTGCTCCGACC	3493	A_95_P022741	TA11868_4097
3786	45	46	861	TAATATATCGTGCTATTGTCTTGTGAAATGTACTGTTTGGTCCATTATGCATTAAGCCT	3495	A_95_P120117	DV999850
3789	45	49	615	CTGCTGTTGCTAAGTGAATGAACAAATCTACTTTTGGGATATTGCTTGTTACATCCTT	3501	A_95_P178982	FG146455
3802	45	62	338	GTAGAGTTTTCTACTGATGTTTTGGTAAAAGTATTGGAGCTTGAATTTCCGCAGATAT	3526	A_95_P189437	TA14789_4097
3806	45	66	374	ATGGTAATGGAAAGAAGAGTGCCCAGTGATACATTCTTTCGATTGTGCGGTAGGAT	3534	A_95_P090883	BP531131
3810	45	70	677	GGCTACTTAAAGTGGAAAGTTGATTGAGCTTTCCTCTTAGTTTTTGGGTATTTTTCAA	3542	A_95_P206662	TA18566_4097
3812	45	72	693	GCAATAGCAATAGCAATAGCACAGCAACAGAAACACCAAAAACTTAGTAGGTGTTT	3546	A_95_P302828	FG638481
3816	45	76	473	GGTTGAAGTGTTGGCTTATGTTTTTTCTGCGACATTGATTTCTCTGGCGTTTGTTGTA	3554	A_95_P094123	BP532576
3818	45	78	1263	CACCCCCCAAAACCTCCTCCATAAAGGAAAATAGAAGAAACAGTGAATTTTAATATAT	3558	A_95_P203917	TA17956_4097
3820	45	80	488	TGGTCAGATCAGAAGTTTTATCCATGTCAGCACGGATGAGGTTTATGGGGAGACTG	3562	A_95_P035093	BP128355
3821	45	81	1074	CCTTTATGGATCAAATCTTGTTCTTTTGGTTCTAAATGTGCTTTACTGTGACCAGGTTT	3564	A_95_P113422	TA13535_4097
3824	45	84	748	CCTGAAGGCTATTTGGTGTGTTGAATCTTGGTTCTTTCAAACATTTTTATGTCTACCTA	3570	A_95_P162612	EH621581
3825	45	85	446	CATGCCTCTGTCGAAGGACTAGTCTTCCTTTTTTCTTTTGATTGTTTTACTGTAAGAGA	3571	A_95_P139727	EB443613
3832	46	7	338	TTGTAGAATACATATTGTACTAACTGTAGTGTACCCACTTTTTTGGGCAAAACTTATG	3419	A_95_P130642	EB430687
3838	46	13	0	CAAAATCACTAGCTGTGTTTACCCTGAAAACTTTCAAGTGCCCGTGACCGCACATACA	3431	A_95_P296703	A_95_P296703
3846	46	21	389	CTGTGCGAACAGGCAACACATTCTTGGGTTCACTATTGTGGGTTGATTATGCTCGTTT	3447	A_95_P135882	EB439426
3849	46	24	775	GATTTCGCGTTACATATGCCTTTCTCTTTCCGACAAGAGTGAATTTGCTTCCCTTCTGA	3453	A_95_P226389	EB683342
3853	46	28	356	AGCGCCTAAGCGGGCAAGAATTGTATGTAAGGTTTACTTTTTTGCCTATTATCTGGAA	3461	A_95_P104282	CV016923
3854	46	29	836	TGCACTGACTACATTATATCACTAGATGCAGATGAAATGTCAAAGGGAGGTGGAACT	3463	A_95_P127742	TA17459_4097
3858	46	33	891	CCTTTTATGGTTTGAACGTGTATGCTTACTAAGTTGTCTGCCTGTGAAACAAAATGTA	3470	A_95_P199402	EB426061
3865	46	40	427	AATGGATCAATCACGCAAAAGTTGAAAATCACAAACAGCCAACGTGGCAAGAAATC	3484	A_95_P075850	BP526833
3867	46	42	874	TTCATATGGCTGATGGTCAAAGCAAGAGCTTCTTTTATCCTTTTAGCGGGGTCACTGA	3488	A_95_P289128	DV157784
3871	46	46	800	ACAAGAACTACGACTTTGGTAGATGCCCACGAGTTTTATTGCAGTGGACAGCCTTGT	3496	A_95_P189872	DV160053
3872	46	47	768	CTGCTGGTGAATCTTTTAGTTTTCTTGAAGATGCTATTTTACAGTGTTGGATGGATTA	3498	A_95_P029541	EB424800
3874	46	49	589	AGTTGGTAACCACTATATACATTTTCATCTGGGGTATAATGTCAAATGAGGAAAGGT	3502	A_95_P017491	EB430176
3875	46	50	1229	TAAATTGAAGGCGGTAATTCTGGGCCAGCAAATAGCAGAGATTCAGGATTCCGGTA	3504	A_95_P239389	AY220480
3881	46	56	809	GTTGAAGCTACATAACAATTTTCCAGTCATCGAAAAGCATCACATTGTTAAATAAGGA	3515	A_95_P178452	TA12256_4097
3887	46	62	741	TTGAAGAGAAGTTTGGGATTGTTTTTAAGAAGAAACTGCCTCTGGTGGCTATACCTA	3527	A_95_P128392	EB428093
3892	46	67	621	TAAGTAGAGGACTTTTGGGGGATAGCTTAGTTGAGTTTATCTATATTAGGACTTCTTT	3537	A_95_P108177	DV158042
3902	46	77	699	AGATATGCTGCAATTATGCAGTCGCATAACTCACATTCGAACCGCATAATTGCCCTGC	3557	A_95_P260236	FG640213
3905	46	80	1558	GCTTTACCTTGATGTGTGTGATATCTGGCTATTGTTTTGAAGTCTTGCACATATTTGAT	3563	A_95_P197042	TA16476_4097
3906	46	81	222	GTAGGAGATGGAATGCATGCCAATACACTCAAGTCTATTTGTTTTTCAGTAATTGAAA	3565	A_95_P006476	TA19814_4097
3907	46	82	377	GCTTTGTAAATTCTAATCTTAGAAGCTCGTGATTTGTACTACCACTCCTTGGAAAATG	3567	A_95_P099803	BP535071
3910	46	85	549	CGCCTAGCGTTGTCCTTGTCTGTAAACAGTAGCTTTAGTACATGAATTAGCGTTATTT	3572	A_95_P001631	EH623842

3912	47	2	1096	GTGTGTTGCACACTATGTAATAGTCTCTTGCTTATTAAGAACCTTGCATGTTAAAAAT	3575	A_95_P198197	TA16726_4097
3914	47	4	831	TATATGTCTTCACATCTTAGTCCTTCTGGAGGAGAGGCGGGGGTAACAATTTTGGTC	3579	A_95_P026856	TA18162_4097
3917	47	7	855	TTGGATTCCTCCTTATTGTCATGCTTCTCCTTGTCATCGTTTGTGCTGAGGTGTCTCTT	3585	A_95_P244727	EB428396
3919	47	9	842	CTTCTTTAAAGATGTTAGCAGTGATTGCAATAGCATTCAAGGTGCCAATTTCTTCTCA	3589	A_95_P005066	DV157707
3920	47	10	688	TGCTGACTGTTGGTTTTGGATGTAGAGTTTGATCTCTTCTTGATATGAGTATGTGAAT	3591	A_95_P018991	TA14550_4097
3923	47	13	331	TAGTGTATCCTTTGGGAACTTCTTGAAAGTCCATCATGTACAGAATCTAGAGTTATAT	3597	A_95_P090523	BP530987
3927	47	17	159	TGGTCAGTCTGTTACCTTGTTAAATGGAACACATATATCTCTTAGTTGAAGAATAGTT	3605	A_95_P134187	EB436165
3929	47	19	92	ATGCAATGAGCTCCATGAGAAGCAGGGAATGAAAGAATGTCCTTCTTGTAGGAGCC	3609	A_95_P034199	AJ718275
3930	47	20	489	GTACGCTCACATTTTGTTTTGATTCCATTGACGGTGATGTAAAGTCGAGAATAACTAA	3611	A_95_P209162	FG636399
3931	47	21	875	ATCCCTGCACTTTTCATGGGCATTGCCATTGCAAGTTTCTTTTTCGGTACACCACTCTA	3613	A_95_P243132	DW000541
3935	47	25	831	CTTGTTTAGAAAAAAATTGCTAAATGAGAAGCTGCTTATGAATGCAGAGAGGATAGG	3621	A_95_P205097	DV157876
3937	47	27	416	TGTGGTATTCGTAGAATGGCATGTATAATTTGGTACTGTATATTTAGACGATAAGCA	3625	A_95_P221212	TA21773_4097
3938	47	28	540	CAATAGCTTCTCACCGTTTTCTGCTATGTTGTACTAAAACATTCCGATTATATTGCATT	3627	A_95_P024236	TA17414_4097
3942	47	32	304	TTTAATGCTCTCTACCTTGTTTCAGTATTCTACTATTGATACAAATATCTGGACATGGC	3635	A_95_P196417	TA16334_4097
3944	47	34	611	TTGCGTTTCGTCGTGAACTTTTGTCATTGACCTATTGGTTGATTATATATAATGGAAT	3639	A_95_P001951	TA14124_4097
3946	47	36	675	TCAATGTCCTGTTTGTGGAATAGCGAAAAAAGCAGCATTGAGGGTTTGATTGACCAT	3643	A_95_P215117	BP131006
3947	47	37	783	TGGTTACTGCCAGCCTCACTTTTAGCATTATCTGTATCACTGTGGATGACGAGAGTTA	3645	A_95_P125677	EB424755
3953	47	43	556	CAAGTGGAACTGTCTCTCTGCAGGTATTCTTTTTGAGGGGTAAATAAATAACTATCAA	3657	A_95_P133747	EB435398
3954	47	44	525	GTTTTTTGCTGCAGTTATCTGCAATGAGAATGGAGAGTTATGAGTTTACTTACTGTAT	3659	A_95_P039981	BP129699
3957	47	47	766	CTGTTCATTGTTGGGGTTTTGTTGAACCATGTCTACGGAGACTGTAACTTTTTATTTAT	3665	A_95_P000026	EB439159
3958	47	48	485	TTGAAGAAAGAGGCAACGGAGAGGTCATTCCTCCCTCCTTTGACAATTTGAAGGAG	3667	A_95_P062710	BP135584
3961	47	51	748	GCCAATGTACACTTTAACCCCTGGAAAGACATACAGGTTCAGGTTTTGCAACGTTGG	3673	A_95_P013121	EB426854
3962	47	52	630	ACAAAATGGCTTCGAGTCAACTCAGCTTTATGCTGTTTCAATGGTTAGTTTTTACAAT	3675	A_95_P284293	FG190566
3963	47	53	897	CTCTGCTCGTATATTACTTGTAAGTAGTGTTAAAGTTTCCAATGTTTTGATGGTGTCA	3677	A_95_P244642	EB424839
3965	47	55	172	CTAATTGAAGGATATATGTGGAATTTATAACTGAACGCGCAATGCGTCTTGGATTTC	3681	A_95_P144397	EB447769
3966	47	56	567	TGTGGGACGGCATGAAAAGGGTGCTGCATTTTTATTTTATTTTTGCATATGGTGTAT	3683	A_95_P024521	BP535201
3970	47	60	769	GAAGGTACAGATGATTCCTAGTTAGTAGGCTTCTTTATTCTTTTGTAGACTTCTTTAG	3691	A_95_P014591	EB451434
3972	47	62	776	TTTTGGGAAGACAAAGGAAATGGTTTGTACTCTGAGGCCACCTGCTGAACTGGTGA	3695	A_95_P236939	EB450672
3974	47	64	260	GAAAGAGTTAACTACCTGTATTCTGTCCAAAAATGAAGAAATGATGAAGTCATTCTC	3699	A_95_P130982	EB431109
3975	47	65	699	AACACAGCAACACCCCAAGTTCGAAAAGGATTTTGTGTCTTGATCGATTCGTTGACC	3701	A_95_P304378	FG173393
3977	47	67	1262	AGCTAAGCCCATGCTATCTTTGGTAGAAGAGAAGCTTTGGACAAGTTATTGTTATTTT	3705	A_95_P012656	TA12420_4097
3979	47	69	975	CGTACTGTGGATGATCTTTTGTGACCTTTGAACTTATAATGGATTAATGTTGGCTTTA	3709	A_95_P198452	TA16780_4097
3985	47	75	639	TCATTGGGATCTTTGATAAATTACAAATGTGGATCAGTTGAGACTAATGTTTGAGTCT	3720	A_95_P181822	TA13069_4097
3987	47	77	252	GTAGGTCTCAATTTACTGTTGCAGCACATTTCTTGTATCTTTTGACAAGAAAGATGAT	3724	A_95_P079765	BP527843

3988	47	78	716	AAGGCGGCTGCTTTTATTAAGGAAAGCAAAGGCCTTTTGATGGTGTTCGGAAAAAG	3726	A_95_P163697	EH622802
3998	48	3	254	TCGTTTGTAAATTTTATGGAATCAGCTTCAGTGTTAGATTTAAACTTTGCCATCTCGCT	3578	A_95_P133832	EB435523
3999	48	4	416	GTGCTGTATGATGCCACACTTCCAATGTATACTTTTGGTAAAAAGGTTTGTGGTTATT	3580	A_95_P212222	TA19787_4097
4000	48	5	1273	CTAGGTTAATTGTGATAGACACTATTAAACTTGGTGCTGCATTAGTCCCTTTTGCTTT	3582	A_95_P185452	TA13915_4097
4001	48	6	188	GACGTAGGCTCGGCCACTCTTTATTGTGGAACTGAAATTAAGAGTATGTCCTCATGCT	3584	A_95_P134482	EB436850
4004	48	9	235	CAGCTATCTTATGGCTTGTGGGTTCTAACACTTGATAATGCACATTGAAATAAAGTTT	3590	A_95_P134387	EB436630
4013	48	18	240	CCTTTATGGATCTCCTCGTCCGATAGACAGGTCTATGTAGTTGGCTGGTATTTGCAAT	3608	A_95_P109047	CV019124
4017	48	22	1091	AGGGGAATTGTATGTTATGCCGATGCTTCTGCTTCTGCAGAGAAATCTAATTGCTTCT	3616	A_95_P010911	TA14600_4097
4021	48	26	971	CCATTTGTTGCCTACTCAGGTTCTTTCTTATCTAGGACCAGTAATTTATCAAATGTACA	3624	A_95_P015751	TA13441_4097
4023	48	28	1076	TGTCAATGGTATGAATTGCGAATGGACCACTGTTTTCTTAGTGAAATTTGATTTCGTT	3628	A_95_P016966	TA17738_4097
4024	48	29	454	CTTCAGGTGCTTGTCTTTCTATAATTGTTGAATTAACATGTCTTTCCACATTGATTGCA	3630	A_95_P006436	DW004769
4026	48	31	718	TGACGACGTTAACAGTATACGTAGTGGAATCTGAATTCACTACTTGATCTGTTGTTAA	3634	A_95_P013591	EH618959
4030	48	35	145	AACCGTTTTGGTTGAAAGCTAGTTCCTTTTCCATCTGCATTTGCTCTTGGTTATAAAAA	3642	A_95_P100088	BP535209
4031	48	36	543	GAGCAAGTCTTAGTGCTCATTCGTGGTTGACCTATTTTATGTAAGCAGTTTAAAATGC	3644	A_95_P125242	DW005039
4032	48	37	554	GCGGACAAAGATTGGTTGTATCACCATTATGAGTTCAGTATCTCCTTATATTATCCAA	3646	A_95_P245537	TA13261_4097
4033	48	38	1174	GTTGGTTGATGCAAAAGTATTCTTATGGTTACTCTCTCCACATAGCAATAGATTTTGT	3648	A_95_P186302	TA14095_4097
4034	48	39	1352	TTGGTCAATCCCTCTGTGCTTCACGGGATTCTTTCATCTGGAGAGGACTATATGTTGA	3650	A_95_P220372	TA21593_4097
4035	48	40	717	TACTGTGGGATCAAAGTTTTGCCGGTTGCGTTTGAATTAATACATTGAATGAGTACTT	3652	A_95_P013321	TA13046_4097
4038	48	43	731	TTCAACATATGTTGGGGGGCTAATATCACCACAGTCTTCTGGCTGTGCTCTTGTTTGA	3658	A_95_P192827	DW000248
4039	48	44	110	ATTTAAGCATCTAGGTGTCCCTCTGGACAGAATTTTACTATGGTGCAATGGCAATCCT	3660	A_95_P132897	EB433713
4046	48	51	724	GTAGCAGTCGGGAGTTTGGAGGAGAATTTCATTAGCATTACTACTATAATTGTTTGA	3674	A_95_P207167	TA18681_4097
4048	48	53	393	AACCAACAGTCTTCAAGGAGCCATTTTGTCTTCACTCTGAGAATTTCGGGTGTGAATG	3678	A_95_P032411	NP916877
4051	48	56	1709	GATACCGATAGGGGGTCTTTATAATTATCAGAAGCTTTTCTTCTGAAACACTTGAATC	3684	A_95_P022886	TA16036_4097
4053	48	58	735	CTAGACAATAAGTGTTGGATATGAAAGAATTCGCCGCCATTGCTTTACCATCTTAAAA	3688	A_95_P215007	TA20389_4097
4054	48	59	708	AGTAGGCCATGGCTTTGATCCATGCTCAAGCATGAAATGGCATCAACATGCTTGATC	3690	A_95_P315583	FG180841
4061	48	66	1003	GGTTGTATGAATTTGGTTTAGATACTTGTGTAACTTGTACAGCAGCGAAGAGAAAAT	3704	A_95_P202712	TA17693_4097
4062	48	67	676	ACAAAAATTTCAGTACGCTACCCTGTGCATACGTGAAAAATCCAGGAATGTCTCTTTT	3706	A_95_P157562	EH615609
4067	48	72	518	AGTCCTAGGGGATGTATGTTTCTTTTCCCTTTTTCAGAAACAGAATATTATGACCTCT	3715	A_95_P088688	BP530178
4068	48	73	332	GGACATTTTCTTGGATTAATACATCACTTAGACCAAAGATTGGCTTCGGTGGTATTAC	3717	A_95_P216622	TA20746_4097
4070	48	75	306	TATGGGAGATTATCCTGAACGTATTCTCTATAGCTAGAATGCTTGACTTTCTTGAGAG	3721	A_95_P176272	U26255
4071	48	76	532	TTGGGTTGTGTTACTGTTGCACCCCGCAATATTACGTCAATATTACATCCTGCAGTAT	3723	A_95_P149367	EB679206
4077	48	82	722	GCTCATGTAAATTATGAACTCTGGTATTTGATTTGCTTAGAATGTGGTAGTTGCTTTT	3735	A_95_P124002	TA13071_4097
4083	49	3	541	GGAACTGCAACCACTCCTGTTGTGAAGAAAGTCATAAGACTTGATGTTCCTGTAGAG	3745	A_95_P079705	FG148784
4084	49	4	93	GTGCTGGTTTAGGAAAGGGATTGTTTTGTACTCATTTCTGTTTAGCAAGAGTACAGA	3747	A_95_P032981	AF211726

4085	49	5	750	GGTGGTGTTTAATGAAAAATTCAGCTACGGATTTCCCTTTGTTGGTAGTATTTTACAC	3749	A_95_P000656	EB683570
4087	49	7	866	GTCGCCATGAGGATTCTAGTTGAGAATATTAGTAATGCAAAAGTTTTGTTGTTGTGG	3753	A_95_P179057	TA12418_4097
4089	49	9	439	GATGTTGGAGATAGCCTTCAGGCCTGATAACTATCAATGAATGTTAGTTGAATGTTA	3757	A_95_P299473	FG641450
4097	49	17	789	GGAGCTGGTAGTGGAAGTGGTGCTGGACCAAAGATTGAAGAAGTGGATTAATAGT	3773	A_95_P231164	EB429028
4102	49	22	423	TGTCATATCTTCATATTGGTGTCGGGTGTGAGGGATGAAGCTGTCTTTTCTGTGAAG	3783	A_95_P067030	BP136752
4104	49	24	697	TGATTGTTTCATAACTGAGGCCGGAGAACCTGAAGCTGCAGGCCAAAAATCTCCTTT	3787	A_95_P137317	EB441048
4106	49	26	629	AGATATCCATATGGAGGAATAATTCTGAGGCCTGGATTTATCTATGGGACCGTCGTG	3791	A_95_P061650	BP135314
4115	49	35	815	CTTTCCCGGCAGCATGGCATATACTGTCCTTTATGATATGTTTAGATTCTTTTTTGTTC	3809	A_95_P233129	EB678181
4122	49	42	215	CTACTGATTTATGTACCTCAGGCAAGAACTATCAATCTTATTTTGTAGAATGCACCGT	3823	A_95_P141447	EB445171
4127	49	47	865	TGTAGGTGGTTATACTCTTTGAATTATGCCCCTGATTTGACGGGGGAACTAAAGGTG	3833	A_95_P227399	EB426308
4128	49	48	515	TTGGAAAGTTGATAAGTCCATCAGGAAAATCTGGCAGATGGTTCCTGCCTGCATCTT	3835	A_95_P279383	AM784351
4129	49	49	596	AGTTGGGGTTAGCTGTATGAATCATACTTTAATTTCTTTTATGTTGGGCGATAATAAC	3837	A_95_P001201	EB446750
4133	49	53	398	AATTCTTTGATTCAATCAAAAGCCACACCAGCAGTGTGCTGCATTAATGTTTGTTGTA	3845	A_95_P193062	TA15590_4097
4135	49	55	133	TGGGCTTATTCAATTGAGCAAACTATTTTCTTGGTTGAGTTTGGAGGTGGAGGGGTG	3849	A_95_P040401	BP129821
4136	49	56	444	TCCCCTCTTCCAGCCTGCTATCAGATTTTGTAAACTTTCCTGTTGAATTCAAGATTACA	3851	A_95_P003061	TA12899_4097
4145	49	65	340	GCGTTTAAGTCATGGTGGAAACCTTCCTTCACTTTCAATGTTTCAGCTACTAGAGATC	3869	A_95_P070340	BP192601
4146	49	66	831	GAAATTGCTGCAAAAGCAGGATCTGACCTTGGATTTAGATGGTTAAAAAGACTTGA	3871	A_95_P018901	EB428306
4147	49	67	251	CAACGGGAAGTTGCAGGCCCGTTTTTGCTTTGTAAAAAATTCTCCCAAGTTATTTATA	3873	A_95_P100003	BP535166
4148	49	68	196	TATTAGATTGTGTCCATTGCCAAGTTTTGCTGGCTAATTTGACCAGTTTGTTCTATCTA	3875	A_95_P105717	CV017582
4149	49	69	829	CATCTTTATTATCCAAAACATCCACTTGACTGTGCTCATGCTGAGCTTGGATAGACGT	3877	A_95_P310423	FG142191
4154	49	74	783	AAGAAAGTCTACTTCAGGAACCCCTATCAGCAGTACTAGACTTCTGCGCTCGAAGTC	3886	A_95_P220982	TA21724_4097
4159	49	79	870	CTTGCTCAACCGGCTGGCATGAATTTAGTTCAATATGTTATCGAGAATCAAACAGCT	3896	A_95_P245677	EB438409
4160	49	80	356	ACAGTGAAAATGGGTAACACAAGTTACTCAAAGATTGCGGGGATTGGTGACATTTG	3898	A_95_P155937	EG650332
4164	49	84	657	CAACTCAATTAGTCTGTTTTGTGCGCATTCATTCAATATAGGAAGAACGATCAGATTT	3906	A_95_P291233	FG187663
4170	50	5	678	TCACCAGCTCTTCAATAAGTTTGCAGTTTGGCGTTGTTTTAAAAATAGTTGATGATAT	3750	A_95_P204162	EB427763
4183	50	18	451	GTGTATGAAAGCTGTCACGTTGGGTTACCAGTACAAGGGAAACATTATCCCTGTATG	3776	A_95_P023916	BP135073
4184	50	19	800	AGAGGAAAAATCTGCTTCTGCCCCTCATGTATCATCATCTGCTATTGAAGCTGATGG	3778	A_95_P191332	DW000704
4188	50	23	663	TAAAAGTTATGGATTCAAACGCAGATTAGTAGTGCTACCCGCCCCTGCTTCCTCTTGT	3786	A_95_P124332	DW004189
4193	50	28	1002	TGCAATGCTGTTGTACCTACTATCATGTGCTTCAAATAAAATGCTCTGTGATAATACA	3796	A_95_P008626	TA14741_4097
4201	50	36	438	ATACTGAAAATACCTTATTATGCCTATGTTGTACATGGAGCTCTGTTTCTTGTGGTTA	3812	A_95_P043416	BP130610
4206	50	41	1030	TTCTTGTATAGAGTTGGTATATGGCGGCTCTCCCTTTTCCTCCTTTGCATCTTTGTTTT	3822	A_95_P134072	TA14095_4097
4207	50	42	0	GAGAGTGCATGAGCTGATCCACATTTGTAAAGGGCTACACCAGAAAGTGCTGTCAG	3824	A_95_P251662	A_95_P251662
4209	50	44	505	CATGTTTTTGCCATGGGTTTCTTTCTGAATTGTGGTGGTTGTGCTTTGTTTTCAGATAA	3828	A_95_P004331	TA12804_4097
4212	50	47	1836	TTATGTTATTAGAGTATGCGGTTCTGGACCTTGTGATATAGTTAGCTTGTGCTTTCTT	3834	A_95_P032771	AF116915

4219	50	54	998	CAGCAGTGGACGTTTTGGATAAGTAAAAACAGTAGACATTAGCAGATAAATTAGCA	3848	A_95_P027371	TA11967_4097
4221	50	56	779	AAGAGCTGAGTGAAGGAGAAGCAAGAGTATTAATGGCATATGGTTGGGTACCTAAC	3852	A_95_P149467	EB679315
4223	50	58	742	TGAACCTCTTTGTCGGACAAACTTCTGCACTGGTTTATGATGATGATTTCCGTGTTTTT	3856	A_95_P292153	EB426676
4226	50	61	710	AGATTCTTCTTTGTGAAATGAGGCCTTGTTCCCTCTCTGAGCTTTATCTTGATCGTCAT	3862	A_95_P316283	FG199960
4230	50	65	882	GGAGAGAACAAATTCCTCCTTTTTAAGCCGAAACGGAATTGGCTTATATACTTAAGT	3870	A_95_P011346	TA17203_4097
4231	50	66	367	GTGTGGCTAAGATGTCGCTTAATAACTGGAAAGTCACTCTTCCTTTAGTCATAGTAGC	3872	A_95_P037971	BP129145
4233	50	68	990	AATGATGAAAAGTTTCCTGTTCGTGAAACATCAGCGAGAGCATTAGGATTGCTTCTA	3876	A_95_P206012	TA18414_4097
4237	50	72	789	TTGTCAGAGAGATGGAGTTATCATGAATGATGAGACTGTGCATCAGTTGTGTAGCA	3883	A_95_P229214	FG158067
4238	50	73	783	CAGCTTGTTGAATGTTGTAATTCGAGCACTAAATAAATCTCCTATGGGGATATTGAA	3885	A_95_P116182	EB446238
4239	50	74	1674	CAAGGTGGCCCAGAAGTTTTGTTTGTTATGTTGCTTAAGATACTTAATTCGGAACTTA	3887	A_95_P002321	U04632
4240	50	75	193	CTTTCCAAAAGGGTTTAATGCCTTCTCCTCAGACACCAGCAAAGATTATGCACAAAGC	3889	A_95_P211082	TA19534_4097
4245	50	80	820	CGAATCTCACTTGCCTCTCGTTGAATAATCTCCGAATGTTACATTTATAAGTCAAGTTT	3899	A_95_P020091	TA15046_4097
4246	50	81	313	TTCTACATGAATCCAAAAGAGAAGAGGCGATTTTGCACCGTCTTTAAAAATGCCAAA	3901	A_95_P087723	BP529866
4258	51	8	358	TATTTATGCGCACTTGGTTGTGGTCGTTGTGGTCACTGAGATGCTTGCTCTAATTTAA	3924	A_95_P213247	FS403828
4263	51	13	709	CAGCAAAAAATCCTCCTAGGAATTGGTGGGGGACATTACGTACCACGGCATATGGA	3934	A_95_P295693	EB448394
4264	51	14	397	CCGCTGTTGGTGGATCTAAAGACTAGTACCTTTAATCTGAATATTGGTTCTATACCTT	3936	A_95_P153862	DW003761
4268	51	18	914	GGGAATGCATTGCAATATAGTTGGCTCATAAGCTTTTGATAGTAGTGTTTCATCTTTT	3944	A_95_P009236	TA13141_4097
4277	51	27	864	CTTGTTAAGGAGCCAGTTCCGAGTGGATAGTGCTGGGTTTTTGTTGTATTCTATTCC	3960	A_95_P218527	TA21195_4097
4284	51	34	232	ACTCATTTTGGGGATTAACCTTTGTATAAATGAGACTCTCTCTATAGTTTGCTACCTTA	3973	A_95_P102287	CV015956
4285	51	35	580	ATTTGAATCGCTCAAAAAGCGGAAAGATACGGGGAGCTTCACTGTTCAAGATTTTGA	3975	A_95_P287163	FG641271
4286	51	36	604	GCTGAGACTGAATTGGGCTTGCCTCAATGACTTTCTTCCTTCTCATATTATGTAACAG	3977	A_95_P267441	DV160207
4292	51	42	597	ACCCTCAATGAGTCTGGCTTCATTCGTCTCATTTAGCAATGTGAGAGTCTGGCTTTAA	3989	A_95_P038906	BP129401
4293	51	43	252	ATTGCTGCTGTATTTGTTGCTGTTTGCACCGGAATTGCTAACTGGTATTTTTCAACCAT	3991	A_95_P096138	BP533490
4294	51	44	231	GCCTTATTTGCTTCTCCATAGGTCCAAATTGTTTGTAAAATAACTACCACGTTTACAG	3993	A_95_P164202	EH623346
4299	51	49	375	ATTTGTCTCAGGAGGATTTCTTGGAAGTCAAGCTCGGAGAAAAAAGTCATCTTCGTC	4003	A_95_P220667	EH664450
4303	51	53	654	TGACATAGCAGATTGTAACATGAGTATTAATGCTAGAGAAGAATGATGGGGCTTGG	4011	A_95_P121627	DW001741
4307	51	57	474	ATTTGGAGGGGCAAGTAGACATGCCTTTGTAGGTTTAAGGACTTTTTCCTTAATATTT	4019	A_95_P174682	EH665907
4311	51	61	682	GCATTTTTGTCAAAGTTTGAGTGTTCTCAAATGCCGCATCCTCTGTTAGAGAATATCA	4026	A_95_P059141	BP134661
4312	51	62	450	AAAGCCTCTCAAATTCAGAAATTTTGAGCTTTTGTGGAGCATGGCAAGTGATGGTTT	4028	A_95_P139917	EB443828
4317	51	67	118	TCTAATGTTCATTTAGGCTAAATAGAAGCCACAATGCATAAAATGCACTAACCCCATT	4038	A_95_P241890	AJ718724
4318	51	68	1377	GGCCATGAAATGTACAAGAACATATGCCCTTGATTTGCAATAAATTGTGGAATTTGT	4040	A_95_P210177	TA19343_4097
4319	51	69	817	ATCGAGAGGATTTACTGTTCTTGATTAATTTTTGTTATTCTTGTGCTGTCCCTTTCCAG	4042	A_95_P009681	EB439113
4326	51	76	524	GAAAATATGTATCAGTAAATATAGGGCCCATTCAAAGTTGTTACTAGATGAGCAGGG	4056	A_95_P103407	CV016487
4327	51	77	252	ACCATACATTTAGAGGTATCGCTTTCAATTGAGAAATAGCAATGAGACTGTTCCTGT	4058	A_95_P103967	CV016776

4333	51	83	338	GGCAACATGACCAATAATAAGCTGAAGTTATGGCCCTCAAATTTGTAATTCAATGGT	4070	A_95_P077100	BP527165
4334	51	84	831	ATGGAGGATATTGAGCAACGTTTATACCTGATTTGCTTTGGATATATAGATGTCTGG	4072	A_95_P124277	EB435434
4336	52	1	252	GCTACTTAGTTTGGAACTCTTTGTTACCCCATGTCTTATAATAAGCTGTCTCCTCTCAT	3911	A_95_P102872	CV016242
4341	52	6	137	CTTGAGGTTACGATTTATGAACATCTGTTATGTCAGTAATTGTTACTTATTGCTGTCTC	3921	A_95_P154337	EG649523
4344	52	9	81	GTGGGATTATACTGGATTGTTGTTGTTGTTGTTGTAGTCTGTTGAATTTTGGCTA	3927	A_95_P103902	CV016740
4346	52	11	701	ATTGCAGTGATGAGGGCTCATGATGGTCGAGGTCCACAAACAATGCTTTCGAGTTGT	3931	A_95_P116972	DV159737
4347	52	12	850	CTGGCTTTGTCAATGCCATCAAATCTTCATGAAAAAAGGTTGTTTCTTTGTGCTTCATT	3933	A_95_P229324	EB430351
4353	52	18	21	GGTCATTGAGTTGATTATCTGTCTGAACTACATGGAATCCTTGCTGGAAATTCATTAT	3945	A_95_P013511	EB437780
4355	52	20	517	ACCTAGGCCTAGCGTTCATGTTCTGTTTTTCTTATGTATTTGTGGATTATATTATGTCC	3948	A_95_P023291	FG645383
4361	52	26	139	CTGCTTAGGATTTAAAGGGTATTCTGGTCAATTCAGTTAGATGGAACATAGTGATTG	3959	A_95_P120947	DW000919
4365	52	30	853	TTTTTGGTTGTCCTGCTATTCTAATATCTTGAGTACATAGTTTGTCTTCCACAACACTA	3967	A_95_P018736	DW000151
4370	52	35	780	TGCTGTAACTCAGCGGCCATCCATTTATCCAAACTTCTAGTCGATAAATCCAGATTAT	3976	A_95_P011331	TA13385_4097
4371	52	36	725	AGCACGATCTGCTGAGCAGCAGTTAGACTAATGAGCAGACGACTTTATCTGCATTTG	3978	A_95_P161107	EH619832
4372	52	37	1659	TATACCAAGTGGGAGAAAGGAAGGCAAGTGTAGATCTGTGAAGTGGGGTTGTAAT	3980	A_95_P012771	TA12291_4097
4374	52	39	202	AATTTGTTTGAATGATGTGTGGTATGTATGCCCAGAGTTCGGTTTGCATTATATGGA	3984	A_95_P111257	CV020125
4377	52	42	465	TTTGTGAACACTTTCAACTTAGTCATTGGCTACTCTTTGGGAAAGTGGATTATTCTGA	3990	A_95_P190097	FG635177
4378	52	43	846	TGTATACATTCGCCTCATCTAGATGCATGGATGCTGATAGACATGAGTGTCGTGACG	3992	A_95_P250377	FG161363
4382	52	47	176	TTACAACAATAACAACAACAAACCCAGTTTGATCCCAACAGGTGGGGTATGGGGAG	4000	A_95_P142267	EB445777
4383	52	48	733	AAGGAGCAGTATAAGCTCATGTTTGATGTCAGTTAGTTTTCCACAATTGTCTGGATG	4002	A_95_P308088	FG640803
4385	52	50	766	TTACTTGGAGTCATCGGAATCTCAAGCTTTACTAGAGTTGCTCGCCAACAGCCAGTT	4006	A_95_P230214	EB679403
4389	52	54	514	TTGGCCAAGCTTTTGAGAGTCTAAAAGTACTTTTTGGAAAATTAAAGGTGTGTGGCC	4014	A_95_P188012	FS401498
4390	52	55	1849	GCGAGTTGCCTTCTTAACTCTGCGACCATGTTTGTCAATATTTAATCCTACCTCCTCAT	4016	A_95_P196752	Y13466
4392	52	57	310	GTGATATTCTTTGAGTGCCTCTTTGGTTTACTGTTGTGTTCCTTTTTGTGCAACAAATT	4020	A_95_P143052	EB446421
4396	52	61	274	TTATTTTTTGATTTTTGATGTAATAACATGACCGTGGACCGGAATCTCGACGGAACG	4027	A_95_P089158	BP530370
4397	52	62	593	CTCAGCAAAGGAGTTAAAAGAGAACGCTCCAAACTGTTTGCAGCTCAAGTTTCGGA	4029	A_95_P024241	TA19175_4097
4399	52	64	594	ATGGGCAAGAAAGTAAAGACCATGTCAAAAACATATGGAATACAATTCCGACCTGC	4033	A_95_P024906	TA14548_4097
4404	52	69	315	ACGGATAATGGTAGGCATGATTTGATCATGTATTTCATACTCTTGTATTCTTAAGGAG	4043	A_95_P110842	CV019936
4405	52	70	510	CAATGCCTTTTATATTTGATACGGTCTGGGACTTGATAAAACTGGCAGATTATCTGAC	4045	A_95_P103252	TA14564_4097
4406	52	71	832	ATTTGCTTCGAGGCTTGAGAGGAGTTATTTGGGCATTTGCATGAGTCTGAGAGCATT	4047	A_95_P300083	FG137250
4408	52	73	780	GCTGGAGTGGAGACTTAAGGTCTTCTATTATAATTCATTCATTGTACAATGCATTAAC	4051	A_95_P268141	DV999608
4412	52	77	1031	ATGTGTCATCTTTTGCCTGACATGAACTATTGTGCCAATTGTGATTTCTGGCCTACTAC	4059	A_95_P009066	TA12228_4097
4414	52	79	269	GCATGTGCAGTTTGGTTGCACCTCCTCTGGCATATGACTATTTATCAATAATCATTGC	4063	A_95_P095158	BP533050
4416	52	81	429	GGCCTATGATCTGTATCTAGTAATTTAACTCTGTTGACACTCTGTACAGGATATTCTTT	4067	A_95_P273821	FG644588
4417	52	82	317	TGTTTGGCTACTCTGTGTTGTTGCTGTCTCTTGGAGGAGTGCTGTAGATGCTTCTAAT	4069	A_95_P106922	CV018125

4418	52	83	560	GGCCCTCTATAGATACCAAATGGGATTTCTGGTGTTTTGAAGTCTCTTGCATGGATAT	4071	A_95_P264826	TC66144
4422	53	2	300	CCCAGGTTTTGTATCTTTAATCATTTCTATGTGGTGAACGATCTATCATCTTAGAGCAA	4078	A_95_P141397	EB445132
4425	53	5	784	CAAACAGAGGAAGTCATCTTTGACCATTTGCATTCAACTGCATTCCAGTACTCACCTT	4084	A_95_P016786	EB444467
4426	53	6	538	GTGTGCATATGCTTATCGTCAGCTTCCCTTGTTTATTTTACATTTCATAAGACGAATTT	4086	A_95_P014951	BP128466
4429	53	9	747	TTAGCCTGATCGGTTACTGTATGTGCTATGTGATTTGTCCGCGATCTCGTTGTTTTTGC	4092	A_95_P286033	FG176065
4430	53	10	894	TCTGTTGATTTTAGTAATTGTGCTTGTGATGAAGTATTATTGTGTAGGTTAGTCTGCC	4094	A_95_P251562	EB679203
4436	53	16	412	CAAACCCCTAATGTAGTGATACCCCTTCCCCTTTTATGAAATTCATAAAGTCATACTAT	4106	A_95_P073185	BP526154
4442	53	22	342	GGCCAGTTGTTATTTCAGGTTTCAGTACTGAAACCGTTGGAATGGGATAATGTTTTTT	4117	A_95_P008541	TA14036_4097
4443	53	23	704	CTTGGAGATTATACTGTGTAATGCTTACTCTCAAACTCTTCGTTTACACAGTAATGATT	4119	A_95_P124902	DW004697
4444	53	24	618	GTGCAATCTCTTTCAACAACGGAAGTGCTTAAGGTGTTCCATGATTATCTGTCAAAGA	4121	A_95_P085075	FG639353
4447	53	27	1193	GCAGATGTTAATCTATTGGTCTTTTTGGTTTGACGTTAATCCAGAGTTGTGTTAAATT	4127	A_95_P236339	AF098635
4449	53	29	756	TGAAGTTCTGTTGCCCTCAGCTGTTGGTTGTGTTTCTGTGAATGAACTTTTTTAGCCTT	4131	A_95_P019311	EB678616
4451	53	31	764	ACCTGTGCTCAAGTCATACGCTTCATTGGTGAGATTTTTGTTCAGCGAAAGGATGTCA	4135	A_95_P162782	EH621767
4452	53	32	1124	GCTGCTTTGTTCAACTTTCCATGTTGATTGCATTTGCTTGCAACTATGCCTAAACTTTT	4137	A_95_P198637	TA16822_4097
4453	53	33	352	GTTGCTAGTTGCAATGATGAAGTTTTAGCTCCAAAATCAACCTGAATATATTGTTCTG	4139	A_95_P209917	TA19290_4097
4460	53	40	732	GGGACATAGTCATTATAATGTGAAAATTATGCATTGTCTGCCGATTTGTCAATTCAGC	4153	A_95_P163187	EH622159
4463	53	43	320	GTTTTGGGTGCAGGTACCCTTCCTTTCGGTACTCTTTTCATCGAGTTCTTCTTCATCAT	4159	A_95_P094710	BP532841
4466	53	46	365	CCCTTTAACAAACTCTCTTCATGGCAATTTGCCCCTGCTAAAGTAAATGTTTGCACATC	4165	A_95_P078505	BP527532
4467	53	47	519	ATGGTCACCAGATTTTGAGTGTGATTGCAGATTGCCTTTCGATGGCTAGGAGTAACT	4167	A_95_P115872	DV158291
4472	53	52	596	CCCACCCCCAACAACCAATTTAACTTTTATACAGGTATAGTATCTGTTAATAAAGTAA	4176	A_95_P200652	EB444504
4473	53	53	727	AATTGAACACTGGCTTTAACTGTGGTTGTAACTTCAGTCTCTTCTAATATTCTTCCTTC	4178	A_95_P020041	TA21816_4097
4474	53	54	478	AGGTTGATGATGTCATTCTCCCTTACATATTCAAGGAATAGTAATAGCTAGGTCCCCA	4180	A_95_P105207	CV017355
4477	53	57	608	GACGCTGATATATTTACCTTTCCTTCAAAATACGAAGTTCGACAGGAAGTAAATTGTG	4186	A_95_P146392	TA18636_4097
4482	53	62	1376	GTAATGCAAAAGTTTTGTTGTTGTGGTTCAAAGGCATGATCACTACGTGAGAGTTGA	4195	A_95_P016956	TA12419_4097
4487	53	67	830	AATCAAAGACACACCACAAGACTGTGAGGTGAAGTCTACGAGTCAGCTAGCAGCAA	4205	A_95_P200317	EB438594
4498	53	78	689	GTATTTTGTTAGGGATCTTGGTGATGAGATTGAAAATGTCGGTTAATGACACTTCTG	4227	A_95_P241709	FG636765
4501	53	81	488	GCATAGAAGCCATGAAGGTTCTACAACATATAAAGACTTTGCCAAAGGTGGAGGGA	4232	A_95_P084250	BP528970
4505	53	85	54	GCCTTGAATATGCTTTACACGACTTGTAGATCAATTGTGCGTTTGTTATAGTTACATT	4240	A_95_P131842	EB432260
4508	54	3	636	ACAACTCAGTAAAATTTACCTGGTGGGATTTGGGGAGGGTAGAGTGTGCAGATCTG	4081	A_95_P223677	BP129613
4512	54	7	1217	TTAAGATTCTTGAGACATACTGGTTGGAGGAAGATGACGAGACAATGCCACCTGGT	4089	A_95_P203867	TA17945_4097
4513	54	8	476	CTCTTTCTTATTTCAAGGTATGACACTAACAGAATAGGGAGTCTCGACCAGCGAGCA	4091	A_95_P059705	BP134806
4514	54	9	293	CTGTTTTCCTCATCTCAAAAAGTGAACCGTTTAATTAGGTGCCAAACATCCTTGCAGA	4093	A_95_P107632	FS416927
4515	54	10	531	ATTACTTGTGTGGTTGTATGACAGCCTGGTGATGCCTTTTCTGTAATCATTCATCCTAA	4095	A_95_P122127	DW002161
4516	54	11	572	GCTTATTGAACTGGCTTCGACTTATGCTTTATGAAAACATGAATATTGAGTGATGATT	4097	A_95_P275143	FG641096

4519	54	14	1089	TATATCTAACCTTCACGAGATGCGGTTGGAAAACACAAGCAAAGCGGTCAAATCTGC	4103	A_95_P196512	TA16355_4097
4527	54	22	857	TAGCACGGACGATGGGTTTAGAGACTAATTAAGAGATTCCTGATACCATTAATGCAC	4118	A_95_P012071	EB447706
4534	54	29	112	CTTGGCTGGCTTCTATTGTTCTCTGTTTCTCATATATCATGAATGTACCAAGTTCTAAT	4132	A_95_P212317	TA19807_4097
4542	54	37	549	ATAGGAACTGCACCACTGAATTCTCCTTTTATGTTATGGAAAAGATACCACTACTCAT	4148	A_95_P307373	FG638314
4543	54	38	705	GAGTACTTTGCTTCTTTAGTGCTAGTGCTTCTCTAGATAATATACTGGAGCAATAAAT	4150	A_95_P291048	EB449388
4546	54	41	811	GTCTCTTGCATTTGTAGCATACTATTCATGTATAGTAGAGATCAAATGGTAGGATGG	4156	A_95_P254529	FG163907
4549	54	44	248	CTGTCCTTTATAGCTGAAATTAATGTTTTATTCCTGTCTGGCATCTGTGTGTTCTTGAT	4162	A_95_P160647	EH619317
4550	54	45	247	TTTTGTGATCGCATTCGCAGGTGAAGGCGAACCTTGCGTTTTGTTGCCAAAATAAATT	4164	A_95_P145612	EB449372
4553	54	48	889	AATATACTTTAGGAGGTACAATATATGGCTGCATTCAAAACGGGACATGCACAGCAA	4170	A_95_P011426	EB424698
4554	54	49	295	GGGGTCCTAGTAGAGTCAGTTCAACCTGGGGATTTCGTTTTATTGTTAGTTTTATTGA	4172	A_95_P141407	EB445138
4555	54	50	874	CTAAAGCCTACGATGGCTGACTTTACTCTCCAGTTAAATTATTCGTCTAGTCAATGGC	4174	A_95_P228174	EU880279
4558	54	53	486	ACAAAAAGGTTGAATCTGGATGCTGTTGGTGTTGAGCTTGACAAGATGCAAGCCGT	4179	A_95_P207697	FG159329
4561	54	56	1080	TTATCTTGTGGATGTAGAATTCAGCGTGGCAAGAGTCGTCTCTTGTATTTTCTTTTTC	4185	A_95_P018011	TA17173_4097
4573	54	68	235	TATTAAGTATAGGGTGACCTTTGTATCTTTGTTGGACAACAAACTTCCCTCTGTTTAA	4208	A_95_P100868	BQ842877
4574	54	69	1578	GCCCATGTATCTTGTATTAATTGTTACAAGCTCGTGTATTCTTGAACGTTTGTCTAAGT	4210	A_95_P181327	TA12952_4097
4576	54	71	746	AAGGCCTTAGGTGATAGGTCTCCTTGTATTCCTTATCAAAAAATAGGTCCTTTGTATC	4214	A_95_P260881	EB681914
4578	54	73	0	TTTCTGATCCACATCACTCTGCATCAGAGCAGCTAGTGTAGACTGAAAGCATGCAAC	4218	A_95_P267256	A_95_P267256
4580	54	75	1326	GGTCTGATGAGTGTACCTGATTATTTACACTTACATGTGGCTTTATAAATCATGATGA	4222	A_95_P007531	AJ271748
4584	54	79	254	CATTTAGCAGTGATAGCAGTCCAATAAACCATAAGCTCTGCTTGCAGGCCAAAAAGG	4229	A_95_P062115	BP135430
4585	54	80	564	CAAAGCCTTGATGAGCTCATTAACACAGTAAGGCGCAGTTAGAGTTCGATCAGCAAA	4231	A_95_P056896	BP134073
4588	54	83	643	ACTGTTGGACGCTGTAGCTATTCTATAAACTCGTTGTTTTAGAGTTTTGTTCAATCAA	4237	A_95_P125037	FG144478
4589	54	84	750	GCTCATCTATTCTGAGTTCCAACATTTTCATGATTTGTTATTCATTCTGAGAGTAGTGC	4239	A_95_P003736	EB438934
4591	55	1	504	TAGTAGCTCTAGACCAATTGTTTATAGTCCTAGTTCAAAATCGTCAGTCGATGAGATA	4242	A_95_P053476	BP133188
4592	55	2	90	GTGAAGGATTTCTCGCATTTTGAAAATAGGAGCGGAGAAAATGTACGGAGAGAAAG	4244	A_95_P241185	AJ718186
4593	55	3	756	GGATAGCAGCATCCCCACTGCACAAAAATAATACTTAATTCTATGTAAAATGTAAAA	4246	A_95_P240905	EB681754
4596	55	6	353	ATTTAACCGCTGTTGGTGGATCTAAAGACTCAGTACCTTTAATCTGAATATTGGTTCC	4252	A_95_P037826	BP129104
4598	55	8	658	CTCTGGAGGGTCTTCTGTTAAGGAAAGGAATCATCAAAGAGAACAAGGAAGAAGAA	4256	A_95_P114947	EB677239
4599	55	9	358	TATGATGATGCTGTACAAGGTATATCGGTCACCAAACGTCTAACAGCTACGGAAGAG	4258	A_95_P048961	BP132047
4607	55	17	147	CAACAAACTCGGTGGTCTTTTGAGGCAGAGCATTTCTAGGAAATGCAGTCAAGTGCA	4273	A_95_P112482	DV158042
4609	55	19	812	CTGTATCCGAACATTCCGAATCATTGTGAAGTATAGAATGAAATCTCTATGAAAAGG	4277	A_95_P268466	DV159080
4613	55	23	434	TAAAATTCCCGTCGTAAGGGCTAATGTGTGACCCTATTGAAGTGATACGAAATTACT	4285	A_95_P099148	BP534811
4618	55	28	44	CACAAAGCTTTGGCACTGATTGAGTTGTGCATACACCAGTGTTGTATAATATCATTAT	4295	A_95_P132687	EB433279
4621	55	31	255	AGGGGTGTTTTATATGTACTTCTGTACAACTCTTCACGTTTTGTGTTTCAAGATCTTTG	4300	A_95_P110957	CV019980
4626	55	36	499	CCAGGAAGAGTATCCTGAAATAGTTGCAGAACAGCTTTACAGGTTTCTGCAAGAGAA	4310	A_95_P034464	TA17755_4097

4628	55	38	707	TAAAATGGAAAGGTAATCTCTTGGAGTTCTTCCCTTCAGCAAAGCGGACACCTGAAG	4314	A_95_P216417	FG145536
4633	55	43	699	TGAGCATCTAGGTCACCTAAGATTGTATGGACATGGGGTTACCAAGACTTCCTTAAA	4323	A_95_P271831	EB445661
4639	55	49	212	CACAGGCAAAAGCTACTTAGTTTTTCTAAGAATTTTGATTGGATTTGTACACGAAGG	4335	A_95_P132977	EB433894
4640	55	50	522	TTTGATATTGCTAGTGCAAAATTGTCACTCCTGACTAGTAGTTTTCTTGAGATTGAGT	4337	A_95_P123207	DW003077
4643	55	53	873	AAGCGAATGGTATTGGATTTTCAAATACAAGTGAGACTGACAGTGGGAGGCAATAT	4342	A_95_P273141	EB681892
4658	55	68	527	CTAGTGCCACTGATTACTTAATTGCTTCTGGTGGTAGTCCATATTGCAATGGGGAAT	4372	A_95_P040521	BP129852
4659	55	69	925	ATGATTTTGTTGATGCTGTAATGGCGTGCGTGCCTATGCAATGTCCTGTCCATGCATG	4374	A_95_P247182	EB438044
4660	55	70	673	TTTTTTGTATTCATCATCCACTGATCTGAGCCCTCAAAGATTCGACCCTCCTATCTGAT	4376	A_95_P299883	FG640616
4662	55	72	830	TGCAATATGTGCTTTGGCCTGAATGTGGTTGGCAGTCTGTGTCCTTGACAGATTTGA	4380	A_95_P215172	DV159554
4664	55	74	749	TCAAATTATCTCCTGAGGTGAAAACTTCCTTTGTTTATCAATTGGTTTGCCTTTGTCTG	4384	A_95_P013146	DV160860
4666	55	76	819	TTGTTATGAATGCTATGACACAAGCGATGAACATGGCCGAAGAACAGACTAGCGGA	4388	A_95_P260801	EB438781
4668	55	78	467	CCATATACTAAGGTCTATGCTCTCCATCTGCTCCCTATTGACTGAACCAAATCCAGAT	4391	A_95_P106137	CV017770
4682	56	7	894	TAAACTATAAAGACATGCCTCATTGTGCTGCACTTTTCCATAGCTATGCGTTAATCTT	4255	A_95_P008096	EB677862
4689	56	14	90	ATTCTCAGTGGTGATCATTGCGATCTTTGGTTGAAACAGCTAAAAGAACGGCTTTAA	4268	A_95_P152277	EB682620
4690	56	15	0	CTAAACTTTTGGTAATGGTATAATTATCGCTTGGATGTCAAAAAACTGGAAGAATTC	4270	A_95_P025376	A_95_P025376
4692	56	17	454	CTAGTTGCTTTATTGTCTTTTTGAAACATTTGTGCACTCTGAATCTTGTACTAAGTTCG	4274	A_95_P024626	TA14413_4097
4694	56	19	862	GTCTTATCGATGCTGTTGCTGCTTCCACTAACATTACCATATCCAATTGCCACTTCACT	4278	A_95_P013181	EB428794
4696	56	21	697	GTCGCCTTTTGTTGTACTACTGAATCTTGATAGTTAATGCAACGAGAACAAGATAATT	4282	A_95_P132812	EB433568
4708	56	33	93	CCGTTTCAATTTACGAGAAAATATTTCCTTTTTAGTCGGGGCTAAAAAGAATGAGCC	4305	A_95_P115267	DR109313
4715	56	40	0	CGGTAATGTCTGTGTTCATCTTTCTTCTTCTTCTCTCTTGGGTTTGGCTATTCTTCGAG	4318	A_95_P235174	A_95_P235174
4718	56	43	863	AATGAATTGTTGGGGTTTACTTGAATCAAATTCGAGATCATACATAACAGCTCCCAA	4324	A_95_P187177	EB448119
4721	56	46	769	GAATGTTCGTTCTGGTTTAAAAATGCAAGTAACTTTCTGTACGAAGGGAATTGGTTT	4330	A_95_P012381	TA12284_4097
4723	56	48	0	ATTGATCTGAGCTATGCTGTAGCTTCAGTTGGACTTTGGGAGAGACTTTCTGGGATC	4334	A_95_P312453	A_95_P312453
4725	56	50	818	ATTACCCTGTGCCGCCGCATCAGCTGATTTATTCTGTTTATCCAACTACTTTTGTTTTT	4338	A_95_P000346	Z56282
4733	56	58	805	AACAGATTAAGGATCTGAAGTGCCCGCGTGATTCTACTTCTGGTTATGAGTTTAGAG	4353	A_95_P272626	EB451564
4744	56	69	1120	CATGGCCTTCAAAGGTTTATTTTGGAACTGTTCGGCATATCTAATCCTTGTTATGAAT	4375	A_95_P195337	TA16094_4097
4745	56	70	823	ATAATAGGGCTTGGTGAGGCTGAAGAGGATAGAATTGGTTTGTTGCATACCCTGGC	4377	A_95_P009206	DW000005
4746	56	71	1370	GCTTTGTGCCACTTGTACGAATGGTTGAATTATGAATATGATTTATCTCTTGAAAGCT	4379	A_95_P002281	TA14949_4097
4751	56	76	903	ACCTCAGCACTAACGATTCTGTTCAGCTTATAGTTGTACATTTTTCACATATCCCATTT	4389	A_95_P288238	EB424835
4755	56	80	848	AAGTATCTGCAGAGATCTAGATGCTGATCTGATGAAGTATCATTCAAAGCATGCAGA	4396	A_95_P285973	FG138693
4761	57	1	289	GAAAAGATGGGAAGAGAAGATTCCTGTGATGCTAAAGAGTCATGCTATCAAAGAG	4407	A_95_P146957	EB451143
4766	57	6	677	GGTATCATCCCAAATTAGTTGGGGAAGACGATATGCGTCAATCTGATGATTTGAGTG	4417	A_95_P219622	TA21434_4097
4772	57	12	233	ATGAATGAGGGATGTTAGGGGAATTTTGGGTTTGGTTTCTAAATTTCCCTGGGAATT	4428	A_95_P031251	BP532474
4773	57	13	317	GGGAAATAAGGAAAATGCTTGGTTTATTTACCTGAATAGGTTTCCATATTGGCTTTCT	4430	A_95_P156377	TA18129_4097

4775	57	15	708	CTATAAGGCGTCTTCTCTTGTTGAGGTTCAGTCACTGTTAGAAAGTCATTTCGAGCTG	4434	A_95_P078240	EB680119
4787	57	27	131	TAGTGGTCGCGTGCCAAGTGTGTATTGTTGAGTTACCTTATTGCACTATCACAAACGA	4457	A_95_P112842	CV020875
4789	57	29	1094	TCCTTAGTGAGCAGCACATTCTTTAATTTGTCTGTGTTAGACATGTTCAGTGTTGACCT	4461	A_95_P091368	TA16297_4097
4790	57	30	1165	GATCCAAGAAGCTCTTTTGCCTAGCCTTATGAGTAATTTTATGTTTCCTTCTGTGTTTTT	4463	A_95_P007856	D17526
4803	57	43	253	GAGGTTTTCTTGTCTCTGTAGTATGTTTTCTAAATTTTCGATTTGACATAGTGAACTGG	4488	A_95_P130232	EB430269
4807	57	47	851	TTCCTGTAAATCAATTTAATTCCATTGAGGACGCAAAATGGCACTATTGCTTGTGCAT	4496	A_95_P011876	TA12111_4097
4812	57	52	428	TGGGATAGCTTATCTTTGGATATTTCACTTGGCTTCATGGTTTTGATCTCCTTTTCTGTT	4504	A_95_P181082	TA12894_4097
4816	57	56	489	ACCGCAATAAGGAAACCTAATTTAGCTCGTTGTACTTTGTATTGCATTGGATGTTTAT	4511	A_95_P146997	EB451231
4818	57	58	175	TTATGTGTTCACCAATGGGTTTCGTTCATGCTTCCGCAGCTTTTCAACCAGGCAACAT	4515	A_95_P102737	CV016169
4824	57	64	652	TCAAGGAGATAGATAGCTGAGGTCTGATCAACCAATATAGTCCTGGGAAACGTCTAC	4527	A_95_P287178	FG642291
4826	57	66	438	GCTTGCAGGCTGCAGCATTTCTACATTTTGTTTTGTCCATTTCTTATTTATGATGTCCTA	4531	A_95_P039296	BP129511
4835	57	75	101	ATACTAAAGAAGAAGAAGAGAGAAGGAGCTCTGATGGGATCTTTGCTGAACTAACT	4548	A_95_P077845	FG136330
4843	57	83	555	CAAGTGGAGAAACAAGTTCAGTTGGATTCTACAACTCCTACTGTAGATGAACAAGGC	4564	A_95_P125152	DW004953
4850	58	5	716	GATTTGTCAGGAGCTGTGCGCCGTCCTTCTGAGCTAATTTCTGGAAAATTTGATGGA	4416	A_95_P128692	DV161230
4855	58	10	694	AAATTTCACCATTCCTCTCTCTTATAGCGGCGAGTATAAGCTTCCTACCTTGTCCGACT	4425	A_95_P259066	EB440322
4859	58	14	794	ACGAAAGGATAACTGGAAGGGCTGAATATTAACTTGAGCATAAGAGTAATGCTTTTA	4433	A_95_P245942	DW005092
4875	58	30	666	TTTTCTATGCATCTTGAGTTTTGAGTAAATGTAATATTCCAGCGAACGACTTCCCCTTC	4464	A_95_P193282	TA15637_4097
4878	58	33	550	AATTAGTTCAGTGAAGCAAATTTGGTTTTTACATCTTGAATGAAAAGAGCACGATTG	4470	A_95_P021611	DW002468
4882	58	37	568	CGGAAAAGAGACGTTTATTTATGAACATGACAAATGGTGAATAAGACAGTAATTGA	4477	A_95_P302308	FG641357
4888	58	43	551	AATTTTGGAAGGTCACTTTTAAGTATGCGCCGTGATCAGGTGCATTCGATGGAATCT	4489	A_95_P145172	EB448736
4889	58	44	1006	TTGCTCTTTGGATGGATAATGGACAGTATTGCACCATCTTTTATGGCTTTTGTTCTCCG	4491	A_95_P184372	TA13681_4097
4896	58	51	534	GCTTGACAGAACTCCAGAAAAATGAGAGATTAGGTTTCAAAAATTTCTATGCTGGAT	4503	A_95_P280973	FG635775
4899	58	54	818	CGTTAGTTGAAATGTATTTCCAACTTTGGCTCATGGGTGTTATGTGAAGGAATGATAA	4508	A_95_P107782	DV999956
4902	58	57	899	ATTTTGCAGAGGGAAATGCACTACCTACAAGCTAACTCTTTTTTGCATGATTTATTTCT	4514	A_95_P224172	DV162682
4905	58	60	599	GCACTTTGTAGGAAGGAACTTTTGTGTAGTGAAACTTGTCATGGAAATTGTAATCTTT	4520	A_95_P143412	FG175871
4907	58	62	240	GTATTTTTGATAGCGCCAGACTTTGGCATTTGACTGTGGTGCATACTGGTCTTAAAAA	4524	A_95_P127447	EB426991
4908	58	63	211	GTGTTGCAGTATGACATTGAGTTGAATCTTAGTATGTTGTACACTTGAAATATAAAG	4526	A_95_P097043	BP533860
4909	58	64	0	TGTGCGTAGCTTCTTACATATCTTGTTGCTGCATGTCAGCTGTATGCTAACTGCAGTAT	4528	A_95_P269151	A_95_P269151
4911	58	66	271	TACTGTTAAGAAGGGTACGCCAGATCTTAAGAAGACGGTTATGCCAGCGTGTCATTG	4532	A_95_P113056	CV020981
4919	58	74	524	CAGTTTGTGCTGCCTGATTAACGTAGAAATTAAATGACATGTAGCGGCTGCTATTAGT	4547	A_95_P000861	EH624123
4923	58	78	786	AATAACACTACTCTATATCGCTGTTCAATGTCTATTGGTCTTTCTTGCTTGCATTTTCA	4555	A_95_P135562	EB439058
4929	58	84	693	AGATACAAAAGAGTTTGATTGAGTTGCACCAAGTGTTTCTTGATATGGCTGTTATGGT	4567	A_95_P303668	FG192050
4932	59	2	852	TTACTATGCAGATGTTGCAAGGTTCTCTCAAGGAATTCCTCCTGAATGCAAGCGTTCG	4572	A_95_P146262	EB450248
4933	59	3	678	CTCCTGAAACAAGACTCAAGTACTCGCAGAGATAACAAAGTTTCGGTGGGCATCATC	4574	A_95_P067455	TA18559_4097

4935	59	5	294	CCCTTGCAATTGTTAAGATAACTCTCTTGTGATATCCACAATAATGTGTGTGTTTACTG	4578	A_95_P102557	TA11636_4097
4937	59	7	829	GACGTTCCTGTTTATATCTTATGTATCAAGGAATATCCACAGTGGAATATAGGCTTTA	4582	A_95_P130397	EB430442
4944	59	14	699	TTTACCTTTTCTCATGTAAAACATGAAAAGTTGGTTAAAGCTGACTAGCTGAGATTGG	4596	A_95_P014766	TA15482_4097
4950	59	20	1187	GTATACTGTTTTTGATTCGGATATTTCTGTTGGTGTTGAGGTATCTTTGCTCTTCAGTT	4608	A_95_P023361	TA15533_4097
4953	59	23	630	TCTATCTTGGAGCGTGTCTCAATCTTGGTCAGCATCTAAACAGCTCCAGTCAATTGCA	4614	A_95_P128632	DV160797
4954	59	24	231	GTAGATGAGGACGTCCATTGTGGTTCAAGAATTTTGTCACCTTGTTTTGTTTGTAAAA	4616	A_95_P000981	EH624474
4956	59	26	402	TCACCATTTGATCTGTGAAACTGAAGAAGCTGTTTTACGTCTTTCCTCTGCAATTAGTT	4620	A_95_P005896	FG638066
4958	59	28	861	TCGAGCATGTGTTCATGTGTGACTGATAAATGATCTTGGGGCTATGCAAGTTATGTCA	4624	A_95_P295243	FG143459
4959	59	29	935	TTTGTCAAAACTCCAGACTATGACTTCCAATTCTGAGTTACTCATTCTCTTCTGCTCTAA	4626	A_95_P009726	TA12569_4097
4962	59	32	771	TCCAAGTGGAAGTTGATTGGATTAAAGCCTTGCGGATGCAGTAAGCAAAAGGGGAA	4632	A_95_P296828	EB680052
4964	59	34	807	CAGTTTTTGAGGGGGAAGTTACTACTGAAGAAGCAGAGAGTTTTATTAGCTCCGTTCT	4636	A_95_P212182	EB444636
4977	59	47	727	AAGGAGCTATGCTCGTGGTCCAAGATAGGAGCTTCTTATGTCCTATGAATTCCTAGAT	4662	A_95_P126407	TA17269_4097
4979	59	49	394	TACTCCTCCACCAAATCCTTCTGGATGTGCTCGCAGTGAGCCTTACAATTATTTTGGAA	4666	A_95_P073220	BP526163
4980	59	50	259	GTATATCTGCTAGCGTCCGCAGACCTCAAAATCCCCTTCTATCCTTATTATGTTGTTTC	4668	A_95_P093018	BP532102
4982	59	52	2083	GTCGGTTTGGTACGGTTTTGAAAGACTTCGATTTGCTATTTTCGGTTTTAAAAAGGTT	4672	A_95_P213547	AJ244024
4984	59	54	838	GCTGCATATACCTATTGGATTAGAGGTTTTGTGGCATGTAAAGCTTTTGTCTCAAGGA	4676	A_95_P241490	FG172752
4987	59	57	344	TATGTGCTGATCACAATGTTAACCTGATCACAGTTCCTAGTGCCAAGACACTCGGCGA	4682	A_95_P107207	DV159293
4990	59	60	224	CTTTTGTGCGTAAGGGCGTGGCCATCAATGAAATGAGCTCGTCTTCTTTCTTGGTTAA	4688	A_95_P204232	TA18022_4097
4994	59	64	829	AGGTTGAGTACTGTATATGGTGCTTGGTCAAATGAAATTTGAAGCTTTTGCTATACTG	4696	A_95_P204167	TA18008_4097
4995	59	65	804	ACTCGAGCGAAAATGATTCCATGAGAAAGAAAGTCTCTCACAAGGACAAGAAGTTTA	4698	A_95_P291833	EB425003
5000	59	70	305	CTGATGTATGCATGATCTCCAAGTTCTTTGAGAATTCTGAGTTGCAACGTCTTGGTTTT	4707	A_95_P144977	EB448528
5001	59	71	301	GGGATTCACGGTGGGTCGCATGTGCCTTTACATTAATTTAATCATATTTCTTCTCTGCA	4709	A_95_P134152	EB436081
5004	59	74	851	TCTATAATGATTCAGACTCGGAGCCTAAAGTCATCAGGAATGTCCCGAGAGTGTTGC	4715	A_95_P228689	DV999980
5005	59	75	828	GCTGGCCATTTTGGAGGAATCTGTAAATAGAGAGGGCTTTGATATGGAATTGAATAT	4717	A_95_P121687	DW001798
5006	59	76	417	ATCCCTTTAAAAAGCTTGTAATGTCGCTGTAATTGGCAAATCTCTCTAATGCTATTTG	4719	A_95_P025076	TA17794_4097
5007	59	77	207	CAAAGGAATGGAAAGAAAAGCTCGACAACAGTTCAAGGACTGAGGAAACAATTCAG	4721	A_95_P093283	TA12804_4097
5008	59	78	846	CTGAAATACTTGCAATGACAAATCTTATAGCAGCATATCAACGAAATGAGATCTTGGA	4723	A_95_P235219	DV162035
5009	59	79	378	TTTCGCAACTGGTTCGCGGTCTTCGCTTCGAAATTGTTGCTGGTTTTCTTGGACAGATT	4725	A_95_P158782	EH616659
5011	59	81	859	ATCTTGAGCCTGTTGACATCGCACTTTTTCAATTTCGGGTGTATCATGTATGACAAATT	4729	A_95_P236014	DV161341
5015	59	85	592	TTTGATGCTATCATGTATGTGTGTGTTTTGGTAGTGGATTTGGCTATTTATATAGCGCA	4737	A_95_P000258	EB441762
5019	60	4	565	CTTCGCGTAATTGGGATAGTTTTCTGATTGACAAAAGGAAGGAAAGCTAGAAATGTG	4577	A_95_P220707	TA21664_4097
5020	60	5	290	GCATTTCTTAATTGCTGCTGAAATAATTCGCTTGTTTAGATTTTACTCGCTGGTGATCA	4579	A_95_P028736	TA19500_4097
5021	60	6	596	TGGAGCAAGTGAACTTGGTTCTTGATACACTGTTGGGTCAAATAATTTATGCTGAAAT	4581	A_95_P178372	TA12231_4097
5026	60	11	353	AACTACTTTTTGAGCCTCATGTTGTGGGACTGATTCTTGTCGGCGCTTTATCAAATTAA	4591	A_95_P076675	BP527049

5027	60	12	454	CTAGTAGAGTCAAATCCTTCGTTTGAGGTCCCTTCTTCCGTTTGTTTTTCTTCTAGATT	4593	A_95_P074875	BP526583
5029	60	14	352	CTAACTTGCCACCTAAGTCTATGGGATCTAAAGGGTTTAGGGGTTTTTACATTGTTAC	4597	A_95_P107812	CV018541
5030	60	15	1092	CTGGAATTAGGTGTAGCTATATCACAAGCTCATGTTTCTACGATCTTAATCTGTATTT	4599	A_95_P022591	TC60690
5034	60	19	821	TCACCACAATGCGAGATCAAGGTGGAAGTATTTCGAAGTGGAGTACTACTACGTGG	4607	A_95_P188652	TA14618_4097
5036	60	21	112	TGATTCAGATTGATGGAGTGAACACTAATGAGTGAAGTGGATTGGTCACCTCGGCA	4611	A_95_P102652	CV016125
5037	60	22	457	TTGTGATCAGGTATTTTGGAGGAATTAAACTTGGCACTGGCGGTCTAGTTAGAGCTT	4613	A_95_P067385	FG196569
5047	60	32	449	CCAAAATTACTATGAACAAAGCTCTGTGTTAGCGGAACCTTCCTTGGAGCATCCTCTT	4633	A_95_P057666	BP134274
5049	60	34	740	TGTGTCTCCTCCTTTGGCAAAGTGCCATTAATTGGCAACAGATTTGCTATTGACTTTT	4637	A_95_P261566	FG641293
5053	60	38	530	ATGCCATCCAATACCTGTTTCCAGTTGCTCATAGAACATGTGAAAAAGAGATTTAAAT	4645	A_95_P021021	EB682892
5054	60	39	906	GCGTAAGACCAATGGTGTAGACCTATGTTTTGGATTAACTTGTGTACAATCTGAAAT	4647	A_95_P000806	TA13182_4097
5055	60	40	297	CTGGCCTTTGGGGATGTCCAATTGTGATAGTTTACCTTTCTTTATTGTATACAGTTCAT	4649	A_95_P003931	EB445315
5058	60	43	504	TGTCGTGGTTTTGACTGTACTGTTTTCATTTAGTTGATGGGACCATTTACCATTTTATG	4655	A_95_P188067	FG639309
5063	60	48	155	GCTTAAAGTTGTTTTTGACTTCTGGCTCCTTGAAGTTATGGAATTTCTCTGAGTTGCT	4665	A_95_P163322	EH622333
5064	60	49	901	AATTAGTGTCCCTCGCACTAATTGCATATCTGCAAGCCATTTAAAAACTGACGTCAAG	4667	A_95_P210882	TA19490_4097
5066	60	51	823	GATTCAGGATGTTCTTGAAACAAGAAAAGCAGGCTGTAATCTTCGCAAAGTTATTGA	4671	A_95_P186102	TA14054_4097
5068	60	53	522	TCCATGCCTGTGTGGATCTTCCAATTGCAGGGGACGTCTTTACTAAATTCTCTGATGC	4675	A_95_P302453	FG636848
5071	60	56	1025	AACATCAAGTTCCCCAGCAAGCTTACTTCTGAGCAGAAAGCTGGCATTAAGCGATAC	4681	A_95_P220592	TA21641_4097
5075	60	60	216	GAAGGTATTTGGCATCAGCTTCATTTGAGAGCTCTTCATTCATCATATGGGATGTTGC	4689	A_95_P138667	EH664831
5078	60	63	302	TGCTGATGTAACAGCTGATACTGTGATCTTATAATATATGCAGTATGCACTGTCGTTC	4695	A_95_P121922	DW002001
5081	60	66	863	TCATAAGAACTCAAACATGGCTGGCATGATTCTGAGATACTCCAACGTGATTGGTTC	4700	A_95_P294363	EB440991
5083	60	68	297	TGTCTGTCCACTTGCAACCTACCTTGTAATTCTGTGTACCATTATAAATTGAAAGAGA	4704	A_95_P159762	EH618208
5088	60	73	242	TCTTAGAATGCTGGGATCGTGAGAGGAAAGAACATGGTGGCTATTAAAATTGTTCG	4714	A_95_P172001	FG152454
5089	60	74	465	GCTTAGAGATTTTCTCACTAGAAAAACTGAGGCTGGATGTTACCTTTGGCTATGTAAA	4716	A_95_P005471	CV018427
5094	60	79	618	TACGTTTACGAAGAGAGAAATACAGTTTTTGATTTATTTAAAGAGTTGCTTGTGCCGT	4726	A_95_P136017	EB439579
5095	60	80	1030	TAACATTAATGTTGGCCGCTTGGTGCAGCATCCTTAATAAAAATGCCTTCTCAGCTCG	4728	A_95_P198122	TA16711_4097
5097	60	82	749	TCCGTGCTCGTATATTGTCCTGTTTGTTGAAGATTCTCTTAATTCGCGAGCTATTCATT	4732	A_95_P220292	TA21577_4097
5111	61	11	353	TTTCGAAATCACTGTTGCTGGTTGCCCGAATATGCTGTTTTTATTTCTTGATGTACTTG	4758	A_95_P093913	BP532471
5113	61	13	157	AGGTAGATGTCATGTTTCGCAGACCTTGTCTCTCCTTCCCTATCCTCTTGTTTATTTTAT	4761	A_95_P077710	BP527321
5118	61	18	504	CCTGAGATTTTGAGTTGATCTGATACTTACTTTCAAGATTGAAGATTTTGGTTACTTG	4770	A_95_P019221	TA11958_4097
5125	61	25	677	CTGCTTTGAGGAAGCCATAAATTCTTTACCTTAGTCGGTGTTGTATATACAGGCATTT	4784	A_95_P122997	DW002883
5126	61	26	625	CTAGGGACCTGTATTCGAGCATTGCAAATCATTGTTAAGTTTGAGTATAGAATGAAA	4786	A_95_P153567	EB683815
5128	61	28	705	TGATTATCAATGGAAAGAGCGGGAAAGGCGACGGTAAGGATGAGCCAATGTACAC	4790	A_95_P227754	EB426854
5132	61	32	848	AGGGGGAATCCGAAGATGAGGAGTGATTTTATGTTTGGTTGGATTATTGTTTAGTTG	4798	A_95_P293993	EB439039
5133	61	33	228	GTCCTATGTTTCGGAAATGAACAGGACTGAGGGATCCTTCTTTACTTCCAGTGATATT	4800	A_95_P055936	BP133833

5136	61	36	401	GTTCGATGTGAATCCCTTGAATTATGAATGGTATAAAGTAGAAAGCCCTAAGGTTTT	4806	A_95_P006316	TA15490_4097
5137	61	37	639	TGTGCCTGTAGCTTTGGATATTTTGGCTGATATACTTCAGAATTCCAAGTTTGAAGAG	4808	A_95_P139017	EB442727
5139	61	39	560	TGAAACTATTATCTCACTTGACAGCCGCCAACACGAGTGACTTATGGTCAGTTTGAAC	4812	A_95_P143777	FG634181
5148	61	48	636	GACTACTATTTGTGAATTTTTGCTCCCTTTCTTTTGGCATGCTATCGTGTTGATTTCAA	4829	A_95_P219647	TA21439_4097
5150	61	50	685	CCCTGGAAGTTTGCTTAATTTGCTCATATGCGCAGAATTAATACTGAATATAACCTTG	4833	A_95_P120432	DW000345
5154	61	54	160	CTCTTTCCAGGTACACCGAAATGGTTGATGATGTCATTAGGTCTCAAGCTGAGAGAT	4841	A_95_P195597	TA16151_4097
5157	61	57	631	TCGCTCGTATGCATTTGTAGTGTACCATTGTAATTTAGTTTGTACACAATGCATACTTA	4847	A_95_P305538	FG636265
5159	61	59	493	CAAACGTATCGAAAAGAAAGCATCATGTATAGCAGTGATTCTTATACAGTTCTTGTTT	4851	A_95_P031101	EB431808
5164	61	64	885	ATCTAAAGATCTGATCAAGCGCATGGCTTCTTTCATCCAACGCAAGTGATTACAATTC	4861	A_95_P183507	EB429241
5166	61	66	2429	GCCAAAGCTGTGTGATATGTTTTAGCATCCTATATGCAATGGCTTAAGAATAAAGTG	4865	A_95_P188932	TA14682_4097
5167	61	67	969	CTGATATCCCCCTCCATCTCAACCTTGTAAACATCTTTAATGTATGTGAATATATGTAC	4867	A_95_P123017	TA15096_4097
5170	61	70	625	AAGGTTGAACATGCCCCTCTTGTAACAATTTGATTTGCTGTTTGTTTGCAAGAATCTA	4873	A_95_P258256	FG636798
5171	61	71	1215	TTGGTATTTCATGATTTCCTGTCTCATATATTATGCAGCTGTTACTGGTGCTGTTACTT	4875	A_95_P183167	TA13397_4097
5182	61	82	744	TTCTTGAGCACTTCTTGGAAGAGCAATTTCCCAAGTTGTATGCAGAAAGGAAAAGCG	4896	A_95_P222677	EB443066
5186	62	1	490	GAATGGATTGCTAGTGCAGTATATACCATGGTGGAGAAGGTACAATGATAAGTTAG	4740	A_95_P046941	DW003630
5188	62	3	290	TATCAAGCACCCTTCACTATTTCGGATAGTATTTATGGTTCTACCTTTTTCTTAGCAAC	4744	A_95_P147877	EB643481
5189	62	4	800	AGAAGAGACAGTCCCAGCTAGTTTTAGAAAATGAAGACATGAGCACCTGGTACACC	4746	A_95_P125872	EB424994
5192	62	7	693	GAGATGTCACTTATGCTCATCTCACGATTTGTTCAACTTTGAATTTTGGGTAAATGAA	4751	A_95_P151147	EB681377
5196	62	11	857	ATATTTCTTTGGTAGAAAAACTAGTTCGTGCGTCGGATTTTGCAGGGAATACTTAGA	4759	A_95_P248842	DW004634
5199	62	14	449	GCTAGGGGTTGTCTATCAAGCTTGATTTTGGAGGTCAGATGCATTGAAGGATTGCAG	4764	A_95_P054221	BP133380
5204	62	19	738	AATGAGTTGCATCTGTGTGGAGATGCAGCAGCTGTTCCTCTTGTTCAGGAAATCCTC	4773	A_95_P128892	EB428617
5205	62	20	638	AACATTATAAATTAGTTGCCATATGGGATTGAGCTGACACATGTGGCTGGCTGCTAG	4775	A_95_P221732	TA21882_4097
5208	62	23	661	GGATGTTATGTAAAGCTAGCCCTTTCTAAATGTAGTAGTTGATTTTCTGGCAATCATA	4781	A_95_P020866	DW003321
5220	62	35	1105	CTAAATGTGCTTTGCTGTGACCAGGTTTGGTTTTAATAAGGATTCATGCCAGTTTGGT	4805	A_95_P026241	TA13535_4097
5223	62	38	795	TTGTGGCGTGGACTAGGTTACTTTGTGATTCAGACTTCAGCTTTCATGAGGCTCACTT	4811	A_95_P018591	EB449715
5230	62	45	429	TGCAAAGTGGAGGCTAATTTGTTATAAAACGTCTTTGCAGATTCCCTCCTCTAAACTT	4825	A_95_P079405	BP527753
5233	62	48	707	CGTTTTCTGTGACAATGAGCTTGCATGTGTATATTATGTAAGGCTGGTATATGTTTCT	4830	A_95_P232529	EB430886
5235	62	50	0	TTGACACTTTGATATCAACCCGAAGATCTGATTCGATGTGTTGCCATCGTGCTCACGC	4834	A_95_P284853	A_95_P284853
5238	62	53	742	TAAAACATTGACTGAAATGAGGAAAAGGAGTGGGGTTGGGGGTTTTGAATTCATGC	4840	A_95_P128452	EB428150
5241	62	56	157	TTTTTCTTTATTGCCAACACAGTAACTTTATTGGTACTGAACATGGCATTACCTTTGGG	4846	A_95_P034434	AJ718741
5248	62	63	976	GGATCTACCAACTCGGAGGTTTATTTACTGTCATTCGTTATAGAGAATGATGTTAATT	4860	A_95_P008611	TA14267_4097
5250	62	65	157	AGTCCTTTAGGTAGTGTCAGAGTCTATCATGTCTTTCATTATCGTATTTCCCTTTGTAT	4864	A_95_P097743	BP534179
5253	62	68	372	GGTATTGTATGTCGTACCTACAGAAGTTGTGCTGAATTAATGAAGATAAAGCTTTAT	4870	A_95_P220312	TA21581_4097
5256	62	71	457	CTGCTCTCGTCAAGTTCCTTTGTAACTTGTGCTTACACAATTAAAATGTAGTACATTA	4876	A_95_P105172	CV017334

5257	62	72	373	AACTTGCTGAGATCAAGCATGCTCGTCTTGCTATAGGTTGACCTTCTTGGGCTTTGAT	4878	A_95_P107127	CV018219
5266	62	81	358	AATGGAAATCTGCTCTCCCAAATATCCGTCCATTTTACGCTGTTAAATGCACCCCTGA	4895	A_95_P160357	Y10472
5268	62	83	232	AACTCATAGTTGTCCCTTGATAGAGGCTCCTTCTCTCCTTTCAATTATTCTGTTTCTTGA	4899	A_95_P099023	BP534733
5271	63	1	313	TTGCAAAGGCTAAGGAGGCATTAGATAGGAAAAAACGCAATGCAGAAAAGGCCCA	4904	A_95_P157822	EH615856
5272	63	2	771	GAGAAGAGTATGAACATATTCTGCTTCAGATAATCAAAACAATAACAATGGAGGAG	4906	A_95_P126957	EB426356
5274	63	4	763	ATGGAATGGTGAACTTCAAAGAATTCCTTTTTGCTTTTACTCATTGGGTAGGGATCGA	4910	A_95_P236489	FG194427
5275	63	5	753	TTACTGTATGTAAGCATACACCGTCGTGTATTGACGAAAGAATAGATGCAATCTATAT	4912	A_95_P234994	DV158042
5280	63	10	837	CAGTCTCCGGTGTGACCTCTTGTAGCTGACTTGTAATTTATGCAAAGCTGCTCGTTTT	4922	A_95_P224647	EB447622
5282	63	12	315	TCACTCTGTGACTGTAGACATGTGATTTTTTGACCCTCCCAAGATTTTTTATATTTTAG	4926	A_95_P089958	BP530737
5283	63	13	760	CAAAGCTTGACTGTGACTTCCTCCATTTACTTTGCCGTCTTTCTCATTTGGGCCTTCTTT	4928	A_95_P116192	DV158776
5284	63	14	739	TCAGAATTGCATTAGAATCCGTCTTCAATGCTATCCACCCTGCTGCGCTGAAGTATAC	4930	A_95_P267786	DV161891
5292	63	22	522	CCAGCTTTTTATTTGGTGGAGGTCAAGAAGTCCAATGGAGATGCATTGGAATATCAG	4946	A_95_P043516	BP130636
5297	63	27	788	CAGATGGGCATTTGATCATTGAAGCTATTAGTACATCTTATTGTTTAGTGAGTGAGC	4956	A_95_P126507	EB425820
5300	63	30	555	ATACTGTTTACCCATTTCTCTATGTTCGAGAGTACTATCCTCTGAGGAGACCATATTG	4962	A_95_P042601	BP130400
5301	63	31	722	GGGCTGCCATTTATGTGACTTTGTATGTGATGTTTGTATTATATGTATATTGTGACAG	4964	A_95_P017061	TA13746_4097
5303	63	33	2531	GCATAGGTCTTTGCTCATCATAATTTCCCTATTTCTTTTTTGCCGTTAGAGTTGAACTA	4968	A_95_P033166	AJ294474
5304	63	34	809	CCCACGTGGCAAGATCTAATTGCTTTTCTATCCAAAATTCAACCTTCAATTTGTAATTG	4970	A_95_P178392	DV999089
5310	63	40	704	ATGCTCCGTTCCTCGTAAATATATACCCTTTTCTTAGTCTTCACGAGAACAAAAATTTC	4982	A_95_P315618	FG196991
5312	63	42	599	GTGGACTGTTCTTAAAGGCCATGTCTACAATATAACACCATACATGAAGTTTCACCCA	4986	A_95_P303688	FG644381
5321	63	51	499	AGCAATTTGAAAACCCTGCAAAACCAAAGGTACACTATGAGACCACTGGTCTGAGAT	5004	A_95_P035323	AM087458
5324	63	54	296	ATTCCCAGAGCTGGCAGATTTATATGTAAAGGGCTCTTCAGCTCCCCTTATTAAGAAC	5010	A_95_P113202	CV021049
5325	63	55	420	ATCTCGAGGCCTAGTGGTGCTAGTTCATTCTTCTACGGCTTCTTCTGATAAAAACTGG	5012	A_95_P072540	BP525991
5327	63	57	994	CGATTTGCTTAGGTTTGAAGGGCATGTTACTGATCTGTTTCTGACCTTAGTTCCTTTTT	5015	A_95_P201082	TA17348_4097
5328	63	58	827	TTCACTGTTTGGTCAGTACTTCTGTCTCATTTGAGCATTTCAGCTGGGATGGCACCGT	5017	A_95_P292323	FG148939
5333	63	63	116	CGCAATGCTTGTATGAGAGACTATGAGCAGGCAAATCATATTTTCTTTCTCAAAATAC	5027	A_95_P110807	CV019919
5334	63	64	291	GAACATAAACATTATGTGCAATGAACCTAGAACAGACGGTTTCGCTGTCTCAATCGA	5029	A_95_P218017	TA21076_4097
5339	63	69	397	ATGCCACCTGAAGTTGCAAATGCACTTGAGAAGAATAAGCAGTTGCTGCTTAGTCAG	5039	A_95_P085255	BP529232
5342	63	72	123	AGATATGTAACTGTTCTACGCAAGGATTATTTAGACGTAAAACTAGGAAGTGTTGAA	5045	A_95_P106472	CV017916
5344	63	74	800	AGCGATTAGTTTCTGCTGCTAAAGATGGTGATCTCCAGAGCCAGCTTACTGGAGTTA	5049	A_95_P298158	FG145187
5345	63	75	563	CAGATGAAGCATCTCAATGCTCGTGAAAAGAGATACATTGGCTTCATTCTTTACAAG	5051	A_95_P125917	EB425045
5346	63	76	664	TAATGTGAATCTGGGCAGAGAAGTAAGCTCAGCAGACCATGAGATAGTGTTGCCTTT	5053	A_95_P203837	TA17939_4097
5355	63	85	928	TGATTGACCTCAAGAGGGCTTGGAGCAAGCTAAAGCTGAGCAAAACAAGAAACTTT	5071	A_95_P008971	TA16183_4097
5356	64	1	893	AGTGGTCTGGTTGTGAGATTACCCTTTGCTTCTCTTTTTGATACCCTTGGCATGTGCTT	4905	A_95_P212072	DV159330
5368	64	13	666	ATGCACGTAGTTTCCCCTCTCACTTTTCCCTACGCTTATGTGTTCACTGATGCAAATTT	4929	A_95_P205187	EB441986

5369	64	14	556	AAACAGAGATACCTTCATTGCTGATCTCGCCGTGAGATTGTCACGGGACAAATCTAG	4931	A_95_P163142	EH622112
5372	64	17	488	TCAGTTCAAGCTGAAAGTGAGGTGCAAAATGTGGGTGATAATAATGTAGAAAACAC	4937	A_95_P024466	DW004047
5378	64	23	848	AACAACTGAGAGCACATGACGAAATGTGCGCTGACCACATGCTGGAGATCGAAAGT	4949	A_95_P117022	DV159810
5380	64	25	1072	CGGGTACCCTATATTCTAAGACTTTAGATGTTTCACCTGAGATTGTCATAATCAACTG	4953	A_95_P008191	TA12790_4097
5386	64	31	88	AGATTACTCTCAAGGTGACCAGACTATCAGAGAGATTACTTTCAGGGTGGCCCGACT	4965	A_95_P095648	BP533282
5387	64	32	582	GACAAAGATGTGGTCGGGTTTTTAATTCTACTTACTTACATTTTCATTTGCATGGATT	4967	A_95_P019121	DW002855
5388	64	33	749	CCCAATTGAACTGCATCCAGTATGGCTTTTGTAAATAGTTACTACTATATCAGCTAAC	4969	A_95_P148497	EB677835
5390	64	35	723	GGATTTGCAGGAAGAAAAAGGACCCTTTTTGCTTTAGTTTAACTATCATCAGTACTGC	4973	A_95_P224562	EB447840
5391	64	36	520	TGTTGCATTTAAGCAAGCTACACCGAAAGCTTCCCAAACATCTCTCAAATAGTAAACC	4975	A_95_P152902	EB683232
5394	64	39	233	AGGCAGTCAGTTGATTTCAAATTCAATTGCCTTCTTGTTTGATGGTCGTCGTCTTCGT	4981	A_95_P103677	EH623004
5396	64	41	821	TCAGTTGGCAATTAAGCTTTGTGGAAAAGATGGCGGAACTGCTTGCATGGCTGCATA	4985	A_95_P296443	EB452161
5398	64	43	297	GAAGAAAGTCGACCGAGCCAAACTCAGTTTACAAGTATCAACAAGTATTTTGTCGGT	4989	A_95_P031726	BP137283
5399	64	44	761	ACCACAATTGTGGGAACCTTGAATGTCTTTGTTTTTTCCTCCCTTTTGAATGAGTAATT	4991	A_95_P010841	EB431255
5402	64	47	426	ATTCCTCTACACCACTTTGAAGCTGAATTTGACAATTCTAAAATACTCGAGGATGGCT	4997	A_95_P149259	EB679035
5403	64	48	283	GAAAAAATAGGGTTCTAAGAGAGTGCTCTTCTTCTCCTCAATTGTCCATCTACAATTT	4999	A_95_P005726	BP529971
5407	64	52	336	CGAGTGAGGTCTGTTAAAAACTTTGTGAATTATCAGAATGGATCTTGTTTGTGAATA	5007	A_95_P207492	TA18752_4097
5408	64	53	680	CTTATAATGTATAGCTTATTGTTGCTGCGCAGTGTAGGAGTTTTCTTTAGAGTGACTT	5009	A_95_P265661	FG198611
5409	64	54	793	TTGGTTCTTGAGCTACTGTTGTCTCCTTGCTTAGGTATGTAAATCATAACCTTTCTTTT	5011	A_95_P199357	EB443300
5410	64	55	319	AAGATAAAGAAGACACAAATTTAATATGGTTCGGTCAAGGTGACCTACGTCCACCAA	5013	A_95_P032721	AF057375
5411	64	56	148	TCTGTTCCGTCAAAACTATCCGAATCTGATTCTCACCGGATGTGAGATAAGTAGGCA	5014	A_95_P133757	EB435442
5413	64	58	600	AATGTGTAGAAGTTCTCCGTTTCTCTGGATGTCTGTGAAAATTATAAGTCAAGATCCC	5018	A_95_P027446	TC70136
5417	64	62	747	TGTTGAGCGCATTAAGAAGTATTGTGACATTTGCGGAGGTCCAGCTACCTTTATACA	5026	A_95_P150092	EB680158
5419	64	64	744	AAAGAAGTGCCTTGTGGAAATTTTGCAAATAGAGGTTGCTGTGGATTCCTCTCGAGC	5030	A_95_P029311	TA19358_4097
5421	64	66	753	GACAGTGTTAAAACTGGTTTTGAGTTTCTGTGGAATTTTGTTCCAATCTGCTAGAAAG	5034	A_95_P005116	TA12237_4097
5423	64	68	181	AACAGACTAATGTAGTGGCATTGCTGTTGAATTATGTGTTCCAAAAGTTTCTAGCCGT	5038	A_95_P189832	TA14872_4097
5424	64	69	460	AGAACCCCATACAGCAGTTATGGGGTCGAGATGGTAAAAAATTATCCGCACCAAAT	5040	A_95_P209077	TA19110_4097
5428	64	73	1473	CTATCGAGTTTCAAACAGTTGGCGAGACGATTTTCGGTGATAAGAGAATTATTGTAT	5048	A_95_P185657	TA13961_4097
5431	64	76	0	CGGATTTACCCGGTTTACATTATTGGAGTCTTGAAAGGAAGCAGCTCAACACACCAG	5054	A_95_P308383	A_95_P308383
5434	64	79	502	TCGGGCTGGATTTCCGCATTTCTTATTCATACTTTCTGCTATTTGGTACTATTAAACCA	5060	A_95_P286053	FS436570
5435	64	80	827	AGGTATTTGCATCCTTTCAAGTTCTTGCCGATCGTAAAGGAACGAACACTCTCATATG	5062	A_95_P261891	DV160431
5437	64	82	845	CTTTTCTTGGGGCTGTGATCTTATGATTTAGCAAAGGTCTTGTACTCCCCCTACTGCT	5066	A_95_P205452	TA18291_4097
5440	64	85	641	TATTCAAATGATATTCTATAGTGGTTTTGGCTGTTTGGGGAGGTACACCCTTCTTTCA	5072	A_95_P149387	EB679215
5442	65	2	726	AAGGCGTCACGGTTGTCTTTGTTAGACAGGGGTTTCATTTATACTATTGCTCACATTC	5075	A_95_P119072	DV162148
5445	65	5	776	GGCCATTTTAACAACTAGTGTTACGTGAATAACAATTTTGATTTTCTTCTGGTTGGTG	5081	A_95_P195627	DW004694

5447	65	7	316	GGTTTAACTTCGCCCTTTTTCCTTCTCAATGATGGTACTTTGTACTTAAATTTCTGAAG	5085	A_95_P006271	TA14481_4097
5450	65	10	682	ATTATGTAAGGTTTGGACTTCAAATGTTCTCCCATGTCATATTTGGTGACAAGTTGGC	5091	A_95_P136207	EB439855
5459	65	19	449	CTTTTTCTGGCATGCTCACTTGGCAGCTACTGGAAGCTCTAGTTAATCTTATGCCATTT	5109	A_95_P075685	BP526792
5460	65	20	1164	GGTATGAAGGCTTTTATGGATTTTACAAGGGGATGGGCACGAAAATCGTACAGAGT	5111	A_95_P206037	TA18419_4097
5463	65	23	724	TTCGAGTGACTTAGCAGTCGCCCTTTGTTAGTGGAGATTTGACAAAATGCTTGGTTTT	5117	A_95_P261131	EB678007
5465	65	25	887	CCGGCTTGGGGAATGTTTGTTCGACAATTTCATCTTATAATCGACTTTGTTAAATTTTT	5121	A_95_P234504	EB677577
5466	65	26	239	AATCTCTGTTCCGCCATTGATTTTCCTCCATTGTCAATCTCTGTTCCGCAGTTGATTTTC	5123	A_95_P097988	BP534285
5467	65	27	875	TCAAGCAATCTATGGATGTTCTGATGATGACAAAGGACTGTGCCCCTGCTGGTACAT	5125	A_95_P267741	DW000842
5474	65	34	753	AAGTACATGGATAGAGCTGCAAACAGCCAAGTCCGAGAGGTTGCAATCATCATTGCT	5139	A_95_P287303	FG175007
5475	65	35	327	AGGCCGAGCTATACATTTCATGATTTCACCAATATATCCTCACCAATCTGTTGTATTG	5141	A_95_P026036	BP131251
5476	65	36	536	TGTTTGGCGTTTGTCATACCTTGAGATAATATACAGGGAATTATGTGTTTCCATATCC	5143	A_95_P020081	EB446960
5477	65	37	498	CCACAGGCAACTGAATTTTCTCAAAAATTTGCATGCTTTGTTTGTCTTTCTCACTATAG	5145	A_95_P135947	FS399667
5479	65	39	675	AATTGGGACCAGCATTGAGCAAGGTTGCTTGCTGTGGAATGAACTAGAATCCATCGT	5149	A_95_P185117	TA13845_4097
5480	65	40	880	GTGTTTGGTTTGAGTGTTATTGTACTGTAAACGTTTCGTTTTTTGAAGAAGAAATCTC	5151	A_95_P178207	TA12181_4097
5481	65	41	487	GTCTTTGTACACGATTAGCAATACCGCACTTAATATTACTAATGTTGGAGTAAACTAC	5153	A_95_P264816	FG638060
5485	65	45	702	TGAATTTCATATATTATCTGAAGCTCATCTCCTGAGTTTTCCGGCGATGGCGTCAGAT	5161	A_95_P144572	FG164439
5487	65	47	480	TAGTCAAGTTCACGGCATGATAAACACCTCAATGCTAGTCTTGAATATTGATTTTGGA	5165	A_95_P286683	FG642353
5492	65	52	771	CATGCTTGCCATATAGCTAGGATTTACGTGTAATAGGGTTTTGAATAAGAGTGTCTTT	5175	A_95_P010121	DW000310
5496	65	56	754	TCTCGCCATATTATTTCCCGTTCGTTTTCTCGAATTTGTACCAAAGACAGAAAAATTTT	5183	A_95_P213992	TA20165_4097
5497	65	57	631	TGTTAGGTAATTCATATCCTCTCTGCTGGTGGTCCACTATCTCAGAACCATATCCAAG	5185	A_95_P037128	BP128917
5507	65	67	794	AGCAAGCGAGAAGAATACAAAGAACTTGTGGAGAAAGATCCCAGGCTTGTAGAAAT	5205	A_95_P193357	EB678282
5511	65	71	1210	TTGTACTGTTGTACCATAAATAAGCAGTTTGGCGGCCACAATGCAAAATTTGATTTGC	5213	A_95_P189312	TA14762_4097
5514	65	74	754	CCTCACATAGTTAGCCTACTTTATTTGGACTTTATTGTTGGTCCTTATGGATTTTTGTA	5219	A_95_P148092	EB677277
5520	65	80	582	AGGAGGCATGTTCTTCTAATCTCAATCCTCCATTCCCTGGTATAAAATAAGCTTCAATT	5231	A_95_P032396	AB032548
5524	65	84	0	GAAAAGTAAATGGTATGCTCATGAATGATAAGCAGTATAATGTGGCATTTTCTCCGC	5239	A_95_P310268	A_95_P310268
5525	65	85	673	TCTAAACAATTAACCAAGTCCTTTCTCTCTTCCCCTATGTTGGCTGCTCGTTCTGGGTT	5240	A_95_P299288	FG178141
5526	66	1	592	TGCAGAAGAACAATATATACTGACCCCCTCATTACTTTGAATTGATGATGTAGTTCTC	5074	A_95_P233244	EH618209
5527	66	2	794	TCAGCACTGTTACATCTTCATGCCAGGGCAGTGTGTTTGGTGATTATGTGAAAGAAA	5076	A_95_P293548	FG138251
5534	66	9	1119	ACTACCACCCTTGATACTGAGTTGGCCCCATGATTTTTACACGACGGGTTACAGTATT	5090	A_95_P007886	TA12921_4097
5537	66	12	813	GGAATTTTTACATTCCTATGCCACATACCTTATTACCCTCAATGTTTAAGGTTTGACTT	5096	A_95_P015776	AB050837
5538	66	13	567	CCATGTTATGGTTATTGCTGGCCTTGTATCCTAATTGTGAGGCATTTAGGCTTTTTGA	5098	A_95_P213092	TA19975_4097
5539	66	14	969	AGTTCACTTACTGTGGATGATCTTTTGTGACCTTTGAACTTATAATGGATTAATGTTG	5100	A_95_P124517	TA16780_4097
5540	66	15	949	CCAAGTTGCTGTTATGGTACCTCTCTGTAGTATCTATTATGGGAGTGTGTGATGTGGC	5102	A_95_P190537	EB677519
5544	66	19	805	TGTTTTGCTTGTGCTTTTGTACTGGATATGAGTTGGAACGTCTGTTTGAAAGCACTGT	5110	A_95_P011776	EB683024

5547	66	22	112	GCGGCGCTGTCAGAATAGAATGTTGATAAATTTTTCACTAAGAAATGAGTAGCCTTT	5116	A_95_P142252	EB445773
5550	66	25	486	GCTTGAGATCCTACCGATCCTTCATAATCCCCATGAATATCCATGATTCACTATTTCAA	5122	A_95_P033829	AJ633040
5554	66	29	798	CAAGGCAATAGGCATGATGTTATAATGGCTGGAGTGCGTCCTCTTATCCATGACATT	5130	A_95_P225902	EB441267
5558	66	33	46	CTTGCTTTTACTTCCTGATACCTGAAATTGTAACTTGCAGCAATTGAAAACGAACCAA	5138	A_95_P213802	EH618467
5560	66	35	493	AATTTATATGGGGTGATGATGCAGAGGATTTCCGGCCAGAGAGATGGTTTGATGAA	5142	A_95_P046071	BP131301
5569	66	44	769	CCCATCCAAATGAAGTCAAGTTAAGGCCTTTGCGCAATGTTTCTGAAATTCTGATGAA	5160	A_95_P160097	EH618737
5572	66	47	708	CAAACACAAGAGTCTATTCTTGTTCTTGAAGAAGCTGCATCTGATTTTAAAGAACTGA	5166	A_95_P302623	FG197710
5574	66	49	676	CTTTTGCATCAGACTCAATGTTTATCGATATAAAAAGTACAGGTAAAGTCAAGTTGCT	5170	A_95_P129322	EB429062
5576	66	51	847	GAGGTCCCCTTGTTGTATAACAAACCTTTGGTTAAATTCAATGTGTTGTATTCTGTCT	5174	A_95_P229334	DV160558
5578	66	53	436	AACACACACACACACATACGAGAGACAGAAGCGGGCAGAACAAAAGCAAAATATAT	5178	A_95_P096028	FS405146
5580	66	55	607	ATTTTTGGATTGGACTGAGTGTTGGATCGAGGGTTATAAATAAACAAATGGTTGTAT	5182	A_95_P202987	DW004949
5581	66	56	530	CCCTTAATGCTCTCGTGTATTTATTTATTCATTCAAATTGTGTTGCAATGTCAGGACTT	5184	A_95_P006621	EB683364
5583	66	58	386	TTTGGTCCCTTGGTTTCAAACAGATGATCTTTGTGTTATTGGAATTCAGAAGAATCAA	5188	A_95_P276758	TC67705
5584	66	59	856	TGAGGGGATGCCTCATAACTCGAATACTGTAAATCATTTAATAGCATGCGTCTTGGT	5190	A_95_P217752	TA21008_4097
5585	66	60	800	GGCTCTGTAATACTACAGTTCGGAAAATATGCAATGATGTTTGTCTACGTTCAAGTTA	5192	A_95_P107927	TA12124_4097
5586	66	61	225	GAGCTACTTTCTTGAAGTTTCTTGCAGAAAATGAGTCAGCTTTTGATCTTCTATATTG	5194	A_95_P155657	EG650183
5590	66	65	947	TAGGGTTTATAGGAAATTGTTGCGAGAGAATCTGTTCACCAGTTTTTCTTCGGCTGA	5202	A_95_P182817	TA13309_4097
5595	66	70	480	AATGGCTATAGTGCAACAGTGTTAGTATTTGTCCTTATTCGATGTAAATAAGGATGG	5212	A_95_P125447	DW005251
5601	66	76	852	TTCAGATTACATTTCACCCACTATGGTGCTCATAGGATGGTATTTCTGCTGCTGGAGC	5224	A_95_P295843	FG142060
5602	66	77	823	AAGGATGAGTTTTTAGAATGGGCAAAATCAGAAGCGCAACTTCTTGCTCAAGCTGCT	5226	A_95_P147477	EB451919
5605	66	80	3135	ACCAGTGGAAACGAAACAGTTGAAGAGTTTGCCAATGCATTGAGGCAAGTGTCTAG	5232	A_95_P240424	DQ213015
5607	66	82	409	GCAGACTCGGAGTGCATTGTACCAATACATGATGCTAAAATCTGTCCATAGTGCATA	5236	A_95_P155807	EG650273
5610	66	85	156	ATACAATCTGTACTTTCTACTAGGCCATATGTGTACTCAAGTGGTCGCACCCGTACTC	5241	A_95_P049306	BP132130
5611	67	1	977	TCTTTCCCCCCTTGTGTAAACTGCCTTAGTTTGGAGCTTGATTTGACCACTCCTAGTGT	5242	A_95_P229104	TA18446_4097
5613	67	3	94	CTGCGAATGAATGGAGCTTTTCTTTTATGTATAGAGAGAGAGAGAGAGAGAGAGAG	5246	A_95_P113107	CV021009
5615	67	5	982	AATACTGCTGATTAAAAGTGCCCATGATGCTCATTTCTTACATTTAAGTTGTTACACCT	5250	A_95_P237119	DQ365933
5618	67	8	604	TGTCCTAGTATTCAGCCATTTGGGTACGTAATTCCCTTTTTGTGCACTAATTTTTAAGT	5256	A_95_P291288	DW003644
5621	67	11	528	TCTTGCGTCAAACTGCACGCGAGTGCACATGACGTTCTCTAGTTTAACCGAAGCAATT	5262	A_95_P046846	BP131504
5623	67	13	605	ATTCGGAGTATTCTTGATTGCATTTTTAGTGTAGTTGATCTTCGCTATGAGATGATAC	5265	A_95_P001551	FG640794
5630	67	20	778	TGCTGGATCTTGAGCTGTGAAATATCTCCAGCTTATTATGAAGGAAAATTATCAACTG	5279	A_95_P021776	EB439530
5635	67	25	0	GCTGAAGGCACCTAAATTTTGCATTTGAAATTATAATATTGTTGGATTTGTTTGCCCC	5289	A_95_P020171	A_95_P020171
5636	67	26	2825	GTATGATTCGGCCTCTTCCTATGTAATCTCCTGCCCTTTTTAATGCAGTTTGTTTTAGT	5291	A_95_P249812	AF321137
5643	67	33	1135	GAGACTGTAAACTGCCATTGCGAATTATAGTTGTGCTGTAGTTTGTTTCGTATTTCAT	5305	A_95_P014981	TA14610_4097
5644	67	34	427	TTCGTTCACATTATCAAACTTGCGACATACAAACTTAAATACAGTTCCTGTGAGCTTA	5307	A_95_P211667	FG626323

5645	67	35	276	AGGATCTTCAACAGAAGAGTCATCATTTTCATCTTCAAGCAGAACCCCAAAATTAGC	5309	A_95_P062990	BP135662
5647	67	37	919	GACTGTTCAATAGTATACATTCTATAGTTGTAGACCTATATTGTGAAGCGACGGTGG	5313	A_95_P021646	EB438528
5652	67	42	820	AGACGACAAGGACTGTGGAGGACTTTGTAAAGGTCATTGGCAAGCCATATCAAGAT	5323	A_95_P273086	EB681364
5653	67	43	783	TTAGGCATACAAACCCGATGACATCCAACATTGTGAGTTTCAGCTGACTCTTGTGAC	5325	A_95_P254039	EH619468
5654	67	44	321	GCGTATTTACTTTGCCTTGGATTATTGCGTCTTTTTGTTTCCCTTTTCAGAACTTTGCA	5327	A_95_P102152	TA12957_4097
5658	67	48	589	TAATGCTTGGGTTCTCAGTTCCTTTGCCGGTCTTATTGTTCAATGGTATTGAGCTCATT	5335	A_95_P100603	BP535448
5660	67	50	820	GCGTTGAGTCCTATATTTAATGTGACAGCACTTGAAGATAAATGTAATGTGAGGTTT	5339	A_95_P246612	EB424973
5671	67	61	748	ATTCTTGAGAGCTTACGACGTTTCATGCATTAAGCCTTGTCTCGAGGACAGTTCTTTT	5361	A_95_P190842	TA15101_4097
5674	67	64	838	GCCCTTTTTGCTTGTCATTTTTAGGCAAGTATAGTAGTTTTCAGTTCTTAATGCTGTCT	5367	A_95_P010731	TA12837_4097
5677	67	67	567	ACATGTATCTAAGCTCTTGAACATTTAGCTTGACTTAATGATAGATGTTGACGAGTTC	5373	A_95_P301703	FG638349
5680	67	70	821	CTATACAATGGCAGTTTTGGCAATCATATTGGTGGGGTTGCTTTATGGTTTCTTCATA	5379	A_95_P291843	EB425061
5682	67	72	614	TTTTCAGCAGAACATGCTTAAAGCCTTATGAAGATACTTTCTTTGGATGCCTGGTAAA	5383	A_95_P156837	FG640413
5690	67	80	348	ACTGTAAGACAAAGCCCAGCCTGACAAAGGTTCAGGTAAAGATACCGATAGTGATC	5399	A_95_P103732	CV016663
5694	67	84	891	TGAAGAAATTGGGGCTGATTTTTATGTAAGCAACTTGCACAAGTGGTTCTTTTGCCCT	5407	A_95_P230849	EB428657
5695	67	85	432	TTGATCTCAACATTGTGATACGGACTGTTGTCATACACGAAGAGAAGCTTCAGTAGG	5409	A_95_P154617	EG649672
5696	68	1	2197	TGAAATTATGGCTAGGGGTACTTTCGCCAAACATCCGCATTGTAAACAAGCTGTAAA	5243	A_95_P111588	AF194945
5698	68	3	469	GATCCTTGTCACCTGGTGTAGTCTTAGAGTTTGTAACTGAATGGCAAATTGGAGAAC	5247	A_95_P196697	EH623258
5700	68	5	789	GACATTGTGAACAGCTGTCCACGTCATGGTATTGCTAGAAAACTTGTAAAAGCTGCC	5251	A_95_P296188	EB450614
5701	68	6	735	AATGTATCCGCTGCCAATGAGTACTAAAAGACGCGGAGCAAGGATTGCTGGAAGAA	5253	A_95_P292678	EB428060
5709	68	14	532	GATCATCTATGTGTAGCACTTACTGAAAACACTATCGTCTATGTGTAGCGTTTGAAGA	5268	A_95_P111577	TA12889_4097
5713	68	18	471	TTAGTACGCGGGCTATGTTATATATGAATAGTGGACCATTAAGACCATTTTATACAG	5276	A_95_P271916	FG636965
5714	68	19	422	GCAGCAGATAAACTTGAGGAGCAAACAAATGAAAACTCAGAGAAGATGCCTACAGT	5278	A_95_P086050	BP529441
5716	68	21	544	CTGAAACGTCTATATAGCTTTTGCTGCAGGTTACTGGATCAATGCCAAATTTTGTGCA	5282	A_95_P266666	BP534517
5721	68	26	813	TTAAACCATGTATTATACCTCTGGAAGGTGGTATTGCATCTGGATTCAAGAAGCCAG	5292	A_95_P125622	EB424706
5724	68	29	394	TGGTCAGTTTTGTTACAAGGTCAAACATTTAAGCACGTACAAAGACACCTTTTACTGC	5298	A_95_P098843	BP534667
5727	68	32	345	TTGGTGGGGGTGAGGATTAGTTGAAATTCTTGTGATGGAAGAGAATTTTCTAATAG	5304	A_95_P099233	BP534847
5733	68	38	656	TCATCTTCCGTGAAGTTCATGTTGTACCTGATTGTGTCCTTCTGTCGACTGAAGATTC	5316	A_95_P126162	TA16431_4097
5735	68	40	789	ATGTGATACTTGGCTAGCTTATTGCTGGACCGCGACGACCCATTTGGAAATGTATTA	5320	A_95_P283578	FG148386
5737	68	42	744	CCACTCAAACCATTTTTCACCTTGTAATATGCAAGATGCTTACAGGGATTTGGATTTT	5324	A_95_P115367	DV157540
5741	68	46	392	GTTGATAATTTTACATAAAAGGGGGCAGGGGGTTTGGGAATCCATTGCAATGAGCC	5332	A_95_P079665	BP527821
5746	68	51	898	ACTGGATTACAAAGGGCAACCTGCATGTCTGGCACAGTCACCTCAACTTCACAAACA	5342	A_95_P191137	DV161215
5747	68	52	308	CTTGAATAAGTTGTGTAGATGGATAGCTTGGAGCTAAGTTGAGTTACCTCTTGTTTTA	5344	A_95_P031916	BP533836
5748	68	53	608	TGGTGTGGTTTACAAGTGTAATGCTAAACAAGTAGACATACCAAGATGATTGGATCA	5346	A_95_P032081	FG644694
5751	68	56	495	GTCAAAGTGTAAAATAGCTACAGATTATTGTTTTGCCTGGTCTTCACAAGCTGAAATT	5352	A_95_P002296	TA16918_4097

5754	68	59	874	GATACAGATATCCATCTGGGTCTCAAGCTCCATATAATGTCACGGTGAGTTTGTTAGT	5358	A_95_P296893	EB680305
5757	68	62	123	TCAGGTGTGCATGGATTATAATCTATTATATGGGTGATACACTAGACTAATGACTTCC	5364	A_95_P130607	EB430659
5761	68	66	663	GAGCTTTTGTGCTGGTTTAATTTTTGGGCCTTAATGTTAGTAGCTTTCAATTGTTACTG	5372	A_95_P116487	DV159239
5762	68	67	998	GGTGTAGGAGCTTCATTATCAAGTGTTAGGTAAGTATCTAGGTTTGGTATGTTTAAT	5374	A_95_P216092	TA20629_4097
5763	68	68	514	CGTTAATCCATGAACAGGATCTATACATCTCGATCGGAAAAGAATCAAGAGAAAAAG	5376	A_95_P201017	TA17335_4097
5764	68	69	397	AGTCTGCTTATATGGGACACACTACTAAGTGATCCTGAAGGACCTCAGGAAACGTTG	5378	A_95_P266466	BP533691
5765	68	70	109	TTTATGGCATGTAATGGGCAGCTATTTCATGAATGAAGAATTTTCAGCTATTTCTCTG	5380	A_95_P113227	CV021064
5768	68	73	889	ATTTGGTTATGGACCCTTTCGACCTTGGATGTCTATAGCTCACTGGTGGCTCTGTCATT	5386	A_95_P226864	DW001145
5771	68	76	553	TAGTGGGGTGTCAAAATAAAAGGTGGGGGCAACTTTAGAGGTTCTGTGTCATGACA	5392	A_95_P052986	BP133061
5772	68	77	804	CGCCTATTGTTTTCTCCAATCTCTCTCCATTCTTCTGCATGTTGATGCATAACCTGTAAT	5394	A_95_P203957	EB677471
5773	68	78	735	TAACGATAATTGCAAGCAGCGGATGAGCAAAGCTTAATAAGGAATTTTTGCTTGAAC	5396	A_95_P152977	EB683289
5774	68	79	823	GCAGTGATGCTGCTTGATATATTCCTGTTCCCTAAAAGACTCTCTATCTTGATTTTATT	5398	A_95_P287888	FG172969
5779	68	84	540	GTTCTTTTAGAATCTCTGTTTGAATTCTGACTTGGATGTATACAAGTAGAATGCACGG	5408	A_95_P278863	AM824642
5785	69	5	180	CTGGGAAGTATTAAAATCCAATGCAACTGTTTTTTCTTTCTTTGTCCAGTCGTATCTCA	5419	A_95_P163582	EH622612
5787	69	7	439	AACAATTGGCGAGAAGACTAAAATAGTTTGGGAAAACTGTATCCTTCTATAGTTTGCT	5423	A_95_P124447	DW004283
5788	69	8	679	AAGAGGGAGGCTTGGTTGACTTATGTCACTCTCATTCCTGTTGTCACTGGGGTTATC	5425	A_95_P151237	EB681458
5790	69	10	435	GAGTAAGGTCTGTATGCACTACTCTCTCTAGACTCCACCGGTGGAAATACACTGAAT	5429	A_95_P071440	BP525705
5794	69	14	779	GCTATTCGACAGCACGGATTCTTCTACGGGTGGACTGCATTACTTTGATCCCTGTTATT	5437	A_95_P285438	FG151649
5797	69	17	604	GCCAAGAGAGTTGCTAAATCCTGTGGAGTACCCACTCCCAGCTGTTAGAATCTTAAC	5443	A_95_P000551	FG640862
5801	69	21	774	AGCATTGGTAAAATGAGCAACACATTAGATGAGCTTGTTTTCACGAACAATGATCTTT	5451	A_95_P128772	EB428503
5804	69	24	393	TATCCGAGATTGATGCACCAATTTGGATGTACTATTCTAATTTGCATTGAAGCATCAG	5457	A_95_P072990	BP526097
5805	69	25	282	ATTAGGAACAAGGACACAAGTTACCCCTCTTTGTAATCCACTTGGATTATGCCCCTCG	5459	A_95_P126717	AJ719141
5814	69	34	697	ACGGATTGACTCCTAATATTGGATCTGCTCACCATTTACTGTTGTTTGCTAAACAGCAT	5476	A_95_P136337	AF026389
5819	69	39	896	ACCATGGAATTGATGTTGATGTATAATATGTCATGGGAATGCTCGTTAAATGTTGTTT	5486	A_95_P247632	EB680718
5820	69	40	808	CAGGCACATGAAAGCGGAGAAGTTCGTCTCACCTAAGTGTAAATTATCAGCTTTGCT	5488	A_95_P146737	EB450851
5821	69	41	67	GGCTGGCTCGAAGTATTGTTTGTTATGTTGCTTAAGATACTGAATTCGAACTTATTTTT	5490	A_95_P105467	CV017474
5827	69	47	655	CTGTTAACAACCATCAAGCGATGCTTAAGTTTTATGTCAAGATAAGTACTGTGATATT	5502	A_95_P020501	TA12838_4097
5832	69	52	475	TGAAACACTCAGGCAAGCAGGCAAGCAGAGATTGTTAAATGCAATAAAGCAAAGCC	5512	A_95_P059316	BP134707
5833	69	53	452	GGGGAACCTTCTATCTTAATGCCCATTGAAAAGATTGATGTGCTTAAAGTTTTCAAAG	5514	A_95_P020551	FS406426
5835	69	55	751	ATTCAGATGTGTTGTGCACCTCTGAACACATACTTCTAGTCTGTGATTCACCACTGTAT	5518	A_95_P253354	EH620928
5848	69	68	994	GAGCTCGTCGAAATACTCTTCTAGTATTATTTATGGCCAATGTCCATTGACATACATTT	5544	A_95_P011596	TC43080
5849	69	69	566	AATTCTGAAGTCCAGGAAGAAATGCCAGAAGCTGCTGAATCACCACGTACGGTTGAT	5545	A_95_P080020	FG142351
5850	69	70	434	GAACTCTCTGATTCGCGCAATTGATATATAGGCCTTTTGGATATTGTATTTTCTTTAGC	5547	A_95_P088398	TA12644_4097
5852	69	72	281	TGGACATTTTTCTGTTGGGTATGAAATCTGAAGTTCGTAATTCCAACAAGTGGTGT	5551	A_95_P142117	EB445679

5855	69	75	633	ACTGGTCCTGTTATGGTTGTTAAGAGGTTTAGACATATGAACAAAGTTGGCAAGGA	5557	A_95_P238759	AF246967
5862	69	82	97	GAATTGCCACTTTTCATTCCATACTCTGTATACCATATTCTCAAGATGCAAAAGAGAT	5570	A_95_P112647	CV020775
5864	69	84	154	TACGAAGTGTTGGTCTGAGATTCATTTCGTGTTGGGGGTATAAATTAGTTGAAGTAA	5574	A_95_P045436	BP131138
5865	69	85	263	TTTCTTAGGTGGAAACAAAGTGTGGGTCAGTAATGGTCATGTTGGTGGCTTCTTCTT	5576	A_95_P214467	TA20269_4097
5867	70	2	794	ATTATTTGGGACCGAGCCATTGTAGTTGTTGTATATGGCCTTGTATTTACACACAAAA	5414	A_95_P290463	DV999676
5873	70	8	91	TGTGCTCATTCCATTGGGGGAAGGATGACTAAGAAAGATATGTCATTTTTTGGTAAT	5426	A_95_P032091	DV159517
5875	70	10	81	CTCTCTGCATATATAGCGATGTGATCCTTATAGATTTTCCTCATACTCTAAAAAAACCCT	5430	A_95_P006751	TA17411_4097
5878	70	13	734	ACTCTTATCAAATGCGCTACAGCCTAATTGATACCTCATGAGGAATTTTCTTCTGGCG	5436	A_95_P229299	DV157486
5884	70	19	478	GCTTGATTGTGTCAAAAGTGTTTACTGCTTTCGTTTTGAATCTATTCGTCATACAGTTA	5448	A_95_P175396	EH666079
5889	70	24	636	CTGAGTTCTGCGTCGTGTTCACTAATGTTGTTGTACCATTCTTTGTGTTTATAATGTAA	5458	A_95_P301353	FG636212
5893	70	28	882	AATGATCTCATGACTGAGGTACATTTGCTCTTGTGAATCTCAGGAAGACCTGGGTCT	5466	A_95_P258531	FG159147
5895	70	30	742	GAAGCAATGTGCTGTAGTCACTGCCGAACTGAAGGACTAGAGTTAAAATCAGCCGC	5470	A_95_P258481	FG161897
5897	70	32	777	CTTGATGTTTACTTGTCCATTTCGGAGGCTGCAATTAGAAACATATTTCGATTCTGAT	5473	A_95_P027336	EB680804
5903	70	38	268	GGCACTATTAGTCTGAGACTGCAGCTATTGTCTAGGGCATTAGTTTATATTTTACTTT	5485	A_95_P097573	BP534111
5904	70	39	705	CACTGTTCAAAGATCTTGTTCAATTTGCAAAAGCCAAGTCTTCCGTCATCGCCCAAAC	5487	A_95_P088578	BP530137
5907	70	42	353	GTTGAATAGGTATTCCCCCCTTTTTTCTCTGAAGGGATATCAATAAGCATCAGTCTGG	5493	A_95_P096233	BP533534
5908	70	43	754	TCAAAGGAATTGTCTTTTTCGTTTTCTGGCAGGGTATTCTGCTTGAGATTCTTGTATC	5495	A_95_P136032	EB439598
5911	70	46	682	ACTGTAATTATCAACAGCTCCAGAAAGTCAGTCACCAACCGGCATTATCAATCGTGA	5501	A_95_P195782	TA16192_4097
5913	70	48	831	TTTTTATATTGCTCGAAAACAAAAACCCATGAGTAGATGTGGTTTGGGAAGGGGGG	5505	A_95_P185782	EB431659
5917	70	52	498	GGTTGGTAGTGGACTGAAGAAGTTGAGTCCTGATAAATGTTTGTGAAGAGTGAATG	5513	A_95_P073245	BP526170
5922	70	57	799	GCCAGATATGCCTCCATTTGTACATCCTCTATTTCTATATATCATCATATTGTGAACTT	5523	A_95_P016451	TC45900
5925	70	60	732	TCTAGTACAAGAATATACATGAGCATTATTGGAATTCGGGATTGGTGCCTTTTATTCG	5529	A_95_P059650	EB446106
5931	70	66	441	ATCTGTGCTCTTGTTTTGGAGTGCAATAGGTGACAAAGATGAGAAGGTTTTGGAATG	5541	A_95_P157472	FG180507
5932	70	67	614	ATGGAAGCTATCCATTCCAAGCATGTTGATGCAAACCTACTCGCTGAGTTCATCCCTT	5543	A_95_P089793	FG635833
5938	70	73	318	TATGGCGAAATTTTTTGTATGACTGCGGAGTAAGAGTGGAACTATGAGATGTAAAA	5554	A_95_P085360	BP529260
5942	70	77	788	TACAGACATCCTATTGCAGCCCATCGGGTTACGTATGAGCTACGAATATATCCTTGAG	5561	A_95_P292418	FG137012
5943	70	78	259	GTTACATGAGTGATTACTGACTTGTGATGGTAAATCGAGTTGGTTTTATTATGCGTCT	5563	A_95_P094293	BP532644
5944	70	79	728	CATGTGGTGTAAGAATTCCTGTTCAGGTAGTTGATTTCCTTTTTTCCTTTCTAACTTCG	5565	A_95_P025861	EB445534
5947	70	82	1549	GGTGGGCTTTTGCTAGTTTTTGACATCCAAAGTTTTTGTATTTGAAGAATGATATCGA	5571	A_95_P009001	TA13194_4097
5948	70	83	371	AGTGCTTAACGTCAGGTTCCCTCCACATACATATGAAAAGTAAGCCAGCCGTATTAG	5573	A_95_P044616	BP130928
5951	71	1	289	TAACCAGCACTGGATTCTCTGATTTCCAAGGTGAATTATGCAGATTAAGTATTGACAT	5578	A_95_P112122	CV020528
5956	71	6	626	TGCTGAAAAAGAATTGGCAAAATGTAAGGTGGCCTGTACTTGAAGGGCACATGGGA	5588	A_95_P114127	DV157707
5959	71	9	713	TAAGGACCCCTCATGGGCTTTTGTAATCATATGTAAGGATCCCTCGTGGGCTTTTGTA	5594	A_95_P116102	DV158670
5970	71	20	327	GCTCTTTTGATTGTGAATAAAATATGGTGTAAATATGTTAGTTGTCTTGTCCCGCATG	5615	A_95_P040361	BP129804

5974	71	24	252	GAACTAGTGTAAGCTGTGTTGTATTTGCTACGGAAAAATGCATCAGCATTTCCAATTT	5623	A_95_P094408	BP532702
5977	71	27	669	AGGCATTTATGCTTCTGCATTTGCCTTCTTGAATTTTGTTTTTTGGACCCTATGAATTA	5629	A_95_P181757	DV159293
5980	71	30	1901	TATTAATTTGTAAACTATACTCAAAATGCAATGGAACTGTGTACTCTTATTTGCGGCC	5635	A_95_P238269	AF316320
5987	71	37	204	TTGAACCTCAAGGTAAACCAATTACAGAGTGAAGGGATGATGCTTCTTTCTTTTGAGT	5649	A_95_P217527	TA20953_4097
5990	71	40	804	CCTCTACGCCTTATGGCCAATGTTGTTCATAACTAATAGTCACTGAGAGATTTATGTT	5655	A_95_P185502	DV999374
5991	71	41	849	AATGCAGACAACCTAGCTGCCAACTTCAGTAGGGAACTTGCTGATTACATAATCTAC	5657	A_95_P116247	DV158867
5992	71	42	541	GTGCTAGCTATATATTGGTGGATGATGAACTTGGTGTGATGTCTCATGTCATGCTTTT	5659	A_95_P099783	FS419329
5996	71	46	421	CTGACACACTTGTTAGAATTTAGCAACATGGTCATTTCCAGATAGGAAGTAATGTCTT	5667	A_95_P061395	BP135249
6006	71	56	337	GAGATGGGAAAGTTGGAAACTCATTATTGAGCAGATGCTCATACCTTTAGAAAGTG	5687	A_95_P093733	BP532391
6011	71	61	1194	GGCTTTCTGGTCTCGTGTTTCTTATTTTGACAGATTGATGATGTATTATGATTTTCCAG	5697	A_95_P255399	TA14923_4097
6012	71	62	186	GAATTGCACTATCCTAATCCTTGTCATGAAGGTTCTTGATGGATATACCTGTATCTATT	5699	A_95_P140247	EB444209
6021	71	71	395	ACTCACTGTTGTGTCATGTGGAAAGCTCAAATTTAAAACAAGATCTTGTGCAACATTT	5717	A_95_P000996	FS417684
6025	71	75	422	AAGGGATACAATTGCTGAAAAGCTTTACTCCTCAGTTCCATGTTCTTAAGATTTTGTT	5725	A_95_P030871	BP530551
6026	71	76	888	ATATGAGAATAGACAGGTTAGTGGTACTCTTATTGTTGGCACTCATCTTGTTATGACA	5727	A_95_P020031	TA16858_4097
6030	71	80	1685	TGATTGTATTTCTATGTCACTCTGAAGACTTTGTTGCTTCTTGTTGGTGCCTTGATTTC	5735	A_95_P190067	TA14927_4097
6033	71	83	195	CAAGTTTTCACCTTTGTGTGATTTTCCAGTTTCAGAAGAATGTACGTTTTACCTACATT	5741	A_95_P144262	EB447413
6038	72	3	176	GGGTCTCTAAGGTAATCCATATTTAGATGTATACCAAGTGAATTCCTTTGGTGTTGAC	5583	A_95_P154362	EG649550
6042	72	7	295	CACCTAATGTACTGCTTTTGAGGTATATTGAAACTCTGATAGCCATTTTCGCTTTTCTTT	5591	A_95_P181347	TA12956_4097
6045	72	10	510	AAGGACATTTTCAGTAATATGTAGACTTTGGACTTGATAAAAGCTCGCTTCCTTTTCA	5597	A_95_P213722	EH623958
6054	72	19	847	GTACATGAGCTTGATGCTTCAAACTGAGCAGATTCCCTGAATGAGTCATAGATCCCT	5614	A_95_P252204	FG174513
6059	72	24	365	CCGAACCCCCTTCACCGAAAATTACACTGTATATGTAAGGTAAAATCTATATTTTATCT	5624	A_95_P006341	TA17902_4097
6062	72	27	834	AACTCTCCAGGAAATGTACCATCCTTTGCAGGTCGCCAGATGGAGAGAAATTATACT	5630	A_95_P214752	TA20329_4097
6067	72	32	824	TACAGACTTTGAGACATAGTCTTCACCTCCTCAGCCAGTATCATCAGGAATGCAGCAT	5640	A_95_P300788	FG156326
6071	72	36	657	TTCTAAAGACATTATGAGGGCCATCTCTCTGTCAGGGAGGGGATAGAAATGTTATCT	5648	A_95_P067555	BP136903
6074	72	39	602	GATCACAATAATGTCACTTAGTCCAAGCCATAACGCAGTTGGATTTGGCCAATGGCAT	5654	A_95_P063900	BP135903
6076	72	41	910	ATTTGACTTATGGTGGTATGGAACTTCGAAAAGCGAGGAGTTAAATTGCCATATTTCT	5658	A_95_P011391	TC40549
6077	72	42	916	CCTTTTGAATAAAGATTTGGTCAAAAATTAGTCACACGACTCACTTTGTCTTTGCCTG	5660	A_95_P126227	EB425480
6078	72	43	200	TTGGAAAAGGTTCTCCCATCCTCCTTATTCCCTAAGCCCAAAACCAAATAAAGCAAAA	5662	A_95_P173172	EH665546
6080	72	45	918	TATGTCCAGTTACTTGAGTCAGTGTGCATTGAGAATTCAGTTGGTTAATTGGAAAGT	5666	A_95_P133702	TA15451_4097
6081	72	46	2164	CTAGGCACAGATGTTTCTGTAATTGTGAACTTTCTGGCAGATGGAAGCTTAAGTTTTG	5668	A_95_P217602	Z28374
6083	72	48	421	GCACGTGGATCTACAGTCTACTTCTCAACTGGTATTGACTGTTCATTAATTCGCACTTG	5672	A_95_P072010	BP525845
6086	72	51	931	TTTTGGCAGAGCTGAAACTGTAATTACTGACTGTTGCACTGCGTTGAAGTGAGGAAG	5678	A_95_P221287	TA21789_4097
6089	72	54	1915	CAAATCAGCTGATATTCGATCCTTCCCCTTGGACCAGTTGTAATTCGCCGAACCATAT	5684	A_95_P119927	AJ305044
6105	72	70	486	CAGGATTTATTTAATAAAAAGAACGTCGGCTTTGTGACATTGTTGGGGTTTTTTCGTA	5716	A_95_P177677	TA12045_4097

6106	72	71	683	GTTGTTGTTGTTGTTGTTATTGTTGTTGTTGTTTTTGCTGCTGCACTATCAATGTAACC	5718	A_95_P193932	TA15777_4097
6110	72	75	281	AACCTCCGTGGTAAAGATTTTAATCTAACACTGCATTGGCACGTTATGCCAAAGACCC	5726	A_95_P108837	TA17015_4097
6111	72	76	346	ACAATATAGAAGGCTGGAAGCAAGGGTATATGCATATATGTTAGGCGTCGTTTTAAT	5728	A_95_P094078	BP532552
6112	72	77	776	AGAATTTATTACTCCTTCTTCGCTCGACTTTCTGCATCGATGGTAACATGCCACCACCT	5730	A_95_P290393	FG147498
6114	72	79	1265	TTGGGTAACTAAGCCCAATTTTTCTGGGCATTATAGACCTAATAATTCATTCAACTGA	5734	A_95_P094333	TA15200_4097
6117	72	82	528	TAATTTCCGATTGCTGGGCAAGAACCAGCATGAACGGCCTAGTTGTTGACGAAATCT	5740	A_95_P100373	BP535341
6126	73	6	977	CTTAGTTACGAGGTGATTGTTTGTGGATTGAAATTTTGGTGAGCTAATACTTTGTGAG	5757	A_95_P293348	TC72930
6127	73	7	487	GCTAGTCCGCCTTCTTGTTACGGAAGACTATATATATGAGTGCTAAGTTTAATATTTT	5759	A_95_P139937	EB443875
6129	73	9	608	CTCTAACAAAATGCACCTAAGATGTGGCCTAGTGGTCAATGAAGTGGGAAGAGATG	5763	A_95_P069165	BP137310
6130	73	10	653	GTTTTGGATGTGTTGGATATTTTGGGAGTCTTAAGTTTCTAATGTGAATTAGGTCTGT	5765	A_95_P120682	EB437412
6133	73	13	708	GGATTTGGTTTTGTTGTGGACGTGGTTTGAACATTTCTGGTTAAGTGATTGTAATTTG	5771	A_95_P195867	TA16212_4097
6134	73	14	361	GTATTATCTGCCAGTCACTAGCTGCCCCTATCAAGTTGTGAACTGCTTGTATCGTATG	5773	A_95_P179157	FS416927
6135	73	15	0	TTATTGTGTTTGTCCCTCCTTGCCCGTTGTAAGTTGTTGAATTACTTCAGGCCTGTGTT	5775	A_95_P027551	A_95_P027551
6138	73	18	398	CATGCCTCAGGAATCTTGATAGTTTCATAATTTGCATTTTCTCACCTGTGCTTTACCTT	5781	A_95_P094873	FG621848
6141	73	21	511	GGAAAGAACAAGTGCAACCAGGAGCTTTTTCATTCGAGTCTTGCAATTTCTTGAGCC	5787	A_95_P026001	BP128487
6144	73	24	725	GTACTTATTTTGTTGTAACTCATGCTGAATTCCAATCTTAAGAAGGAAATGGCTTCTC	5793	A_95_P146032	EB449863
6153	73	33	504	GGTCCAAAACAGAAGCTAAGTCAACCCTTCCAATTTTTCTAATAATCTATTTTGAGGG	5811	A_95_P093388	BP532238
6155	73	35	701	TTCCACTTATTGCTCAAATCATACTCTCTCATCGTGAATAACAAGGTTGTCCTTTGTAA	5815	A_95_P204937	TA18172_4097
6157	73	37	831	CCAAAGTTTATGTTGATTGCATTCTACGTTGATGCTCTTAAAGAAAACAACATCATCC	5819	A_95_P192717	EB438701
6159	73	39	220	CTGGCGTAAATCAGCATATACTGATTTCTTTTCTCAATGTTCAATGTATTTCTGGATGC	5823	A_95_P062135	BP135437
6172	73	52	2309	GTAGTTTCTTCATTGTAAATTTGTAATGCTTTTCTCCAAGATGTGGGATGAGTTGTTT	5849	A_95_P179782	TA12583_4097
6173	73	53	747	GTGAGGAAAGCTTTAGCAACTCTGTACAGAATTCCTGTGAATTCGCAAATTCTGATT	5851	A_95_P152917	EB683245
6175	73	55	1101	GGGGAGCCGATGATATTTCCCAACACTTGTCTAACAATGTAAGAATCTTGAGCTAAA	5855	A_95_P226179	EB643439
6179	73	59	836	TGCATACATGTTAATCTTACGGTTCACGGTAGTCCTTACATGTCTTTAATACTCAATGG	5863	A_95_P269406	EB424686
6180	73	60	808	GCTATTTGCACTCAAAAAAGATTGTACATCGTGATGTGAAAGCTGAAAACATGTTGT	5865	A_95_P151087	TA15718_4097
6184	73	64	596	CAGTTTAGACGTCTTCATAGCAAGAAGCTCCAGCATACATTCCGGTTCTACTCTCACC	5872	A_95_P304618	FG198773
6187	73	67	786	GACGGAAGTAACTATGAAAATGGAGCAAGCAACAATTAGTAATCATTGTTAGGATG	5878	A_95_P139332	EB443070
6188	73	68	831	TATTTAACAGCAGAGGAACAGGCCAAACTAAGAGAGAACAACCCGGGGAACTTGCT	5880	A_95_P121027	EB680105
6198	73	78	1373	TTGGACTGTAAGTTTAGGGTATAAGTGGGTTCAGTATTTCTCCTTTTCTTGATGTATG	5899	A_95_P130217	TA12917_4097
6199	73	79	483	TCCAATGGCATCTTGGACGATCAAAATGAAATGTAACACTTCCTACTTGATGTGCAAT	5901	A_95_P105102	CV017298
6200	73	80	612	GTGGATGTATAATTTGCATAAGTTCTGTAAATTGTACGAGCATTTTGAACGCGATAG	5903	A_95_P140282	EB444245
6202	73	82	808	GTACGGAGGTGTAATAGTTATTGTTGGAAAACTCTTGTTATTGTGTTTGGTTTTGAGT	5907	A_95_P178197	DW003366
6203	73	83	629	ATTTTAGATTTAGGGTGTGTTTGGAAAGCACTGTGTAATTACTAGGCAGTGTAAAGA	5909	A_95_P308793	FG643622
6207	74	2	707	CTTAGCATTGCCAGCCCCTTCCATGTAAGACATTATAAAAATCAGCTTACTGAAAATA	5750	A_95_P208682	TA19021_4097

6208	74	3	162	AAGGAACTCTACAAGGAAGCTCAGGATCATCGAAGTCCACAGAATCTAACACAAAA	5752	A_95_P046746	BP131476
6211	74	6	617	TTTCTGATTTTGGATTGAGTGCTCTATCCCAGCGAGTCAGGGACGATGGCTTACTAC	5758	A_95_P129262	EB428964
6212	74	7	1024	CTCATGTTCGCCTCACATATTAGAGATCTTTTCTGTAGTGAAATGTCATCAGTTATAG	5760	A_95_P208357	TA18951_4097
6219	74	14	1738	ACACATCTAGCATACCTTTTTAAGTCGCTTTCAGCACTGTTGGTTCTCTCTTTAATCTC	5774	A_95_P007431	AY553214
6227	74	22	1070	TTTTGGTTGATCCAAGCACCGTCTTTATGGATAGTTGTGCATTTACCTTGCCTTAAAA	5790	A_95_P249887	AB010878
6228	74	23	582	GATGAAGGTTATAAGTTACAGACCAGTCAGTCGATCATGTTTCGAACGTATCAATAG	5792	A_95_P272266	EB448670
6233	74	28	785	GTGAATCAAGAATTCCATCTCCAGTAATATACTCCTGCTTCAGAAAAGGCAGTATTTT	5802	A_95_P250877	DV160326
6234	74	29	452	AATATTTGGATTGATCATGTGTCAATGTGGCGTTGTAGTGATGGGCTTATTGATGCT	5804	A_95_P283783	BP128327
6235	74	30	811	GGTACAATCAAAGGCTGCTGCAACTGCATAGATCATATTTCACCTAGTTGAGATCAG	5806	A_95_P229599	DV159974
6241	74	36	670	TAGCATTTTGTTTCCCTATCCTTGGCTCCTTCACCTCCAAATGAAAAAGAGAGAAAAA	5818	A_95_P255354	EH614582
6244	74	39	770	GGGTCATAAGACATCGACCAAGGAGTAGTTCAAAGTATGAAGATACTTAATGTATTG	5824	A_95_P222322	TA22008_4097
6249	74	44	561	TCAGCTGGGATGAGATTTCTTTCTTCAACCCTTACATCCACTATTTTCAGATGTTTTGG	5834	A_95_P135847	TA18995_4097
6251	74	46	555	GTTGGCCCCAAATGGATTTCTCGGTCATCAGTTTTTTGTTTTTGTCATGCTTAATTCTT	5838	A_95_P314173	FG165774
6253	74	48	522	GATATTGACCGGTTCCTACAATTTAATCAACTTCCAGATGGAGGAGACCAGTTGAAA	5842	A_95_P138522	FG148973
6255	74	50	68	CAGGCATTGCCCTCAGACTCTTTCTTGGGTCTCCTGTTTTACTTTTGGTATTTATTTTG	5846	A_95_P090563	BP531001
6265	74	60	1168	CTTTTATCTTCTGAATGGAGAATAAACTATGGCCAGTGTGCCTTCTTGCTTATATTGA	5866	A_95_P002591	AY619950
6267	74	62	851	GCCGAGAAAACAGATTCATCCTCTCATTCTTGAAGAAGAACCAGTTAAAATAACTTA	5869	A_95_P247792	EB449524
6272	74	67	1504	TGCTTCAGATCTTTTTGCAATTGTAGTTTCCTATGTTCGTGTAAAGCATTTCCATCTCC	5879	A_95_P211722	TA19676_4097
6273	74	68	419	GATTCTGTGGAGATTTGTTCCTGGAATTCCCACAAATCTTGATCCCACAGGTACCTGA	5881	A_95_P088203	BP529986
6274	74	69	229	GGATATATATCAAATGGTACACCGAAGTGATACTCAATCAGATCGCATTCAAACTTTC	5883	A_95_P131742	EB432138
6276	74	71	1048	TTGATACATAGAACGATAGTTGCTGGACTATTAAATTCCTGTCGAAGTCTGGTATTTG	5887	A_95_P016846	TA16826_4097
6277	74	72	435	AAGAGTGGGCAGTCCTCAACATAGGGAAAGCATACAATTTTTCTGATGTTCTTGAAA	5889	A_95_P089818	BP530665
6279	74	74	883	ATTAAATTGGCAATTCTGCACCCTTCCACATTTCTGTCTTTACGCTCAATGAATGCGAC	5892	A_95_P011626	TA14282_4097
6280	74	75	309	GGATATTGTAGAGGTATTGTCTTCAGATTTGAAAGTTGGTTTAGTTTCTGTTTCTCAT	5894	A_95_P089223	BP530412
6283	74	78	569	GTTTTGTGTTATGTTTCCGGTGGATTCCTTTTCCCCTGATTCTTTTAGCATTCTTGTTGG	5900	A_95_P018141	BP533405
6284	74	79	793	ACGGAATAGCTGTGATAACATTAGTGTGATTGTGGTTGATCTGAAGAGAAGTCATAC	5902	A_95_P148077	EB677259
6285	74	80	1178	GAAAATTCTGATCCACCGTGATGGTGACAATGGGAAACAGCTTATATATGAAAAACT	5904	A_95_P015456	TA18679_4097
6288	74	83	421	GACTGTGAGGGCTCTAGTTCAGTTTGTACTCGATGCATTATGTTCATATATTATGTAA	5910	A_95_P293648	FG636961
6289	74	84	87	CACTGTATTGTGCCCTCTCTGTTTTCATTTGCTTTATGTATTAATGATTGAAAGATCCA	5912	A_95_P003341	FG638896
6292	75	2	342	AGATTTGTTTTTTGCATTGACCCAACCCTTGATTCTGCAGCTGACCCGGTTTAAGTGT	5917	A_95_P158642	EH616541
6301	75	11	479	TCTGATGTCTGCCGCCTTTTTCACTAGCAACCAATCCTTTCTGCATGGAGATGTATGA	5935	A_95_P277763	AM818948
6303	75	13	757	TAGTGATAAGTGATTATCCTTCAACTATAGAGAGCTGGAATAATGATAGCGTGGAAG	5939	A_95_P243932	EB682084
6305	75	15	516	AATATTTGTTCAGTCGATCTAAGTTTGGCTCCAAAACTGTACCATCTCGAGGTGGCTC	5943	A_95_P117462	TA12494_4097
6330	75	40	276	CAAACCACCGCCGACCTCGAAAAAATCGAAAAAATCTTCGAAGACGAAGCAGTGTA	5992	A_95_P104392	DV999016

6332	75	42	859	CATGCATTGTCTTTTTCGATGAAGTAGACGCTATTGGAGGTGCAAGATTTGATGATG	5996	A_95_P225372	EB444342
6338	75	48	383	GAGCATTTAGAAACACATTGCTTTTTGACCCCGCTTACATTAATATGAACCATTTTCG	6008	A_95_P023431	TA14313_4097
6340	75	50	266	TGTTTCAATAGCGTTCCCGGATTTATGTGCTAGAGATGATGCCAAAGAGGTCGCGAA	6012	A_95_P064340	BP136022
6343	75	53	541	ATCTTTTGCCCTTTATTTTCTGGCGACCTAACCAGAAAGCTTTAAATTCCAGCGGCCC	6018	A_95_P162972	EH621959
6357	75	67	573	GTGGTTCATTTACCGCGGTAAAATATTGATTGAACACATAATTATGCGAAATGGATC	6046	A_95_P181042	TA12886_4097
6358	75	68	782	AGCTTGTGTGGTTCCTGCAGATTTGAAGGAAGAGTGATTATGAAATTGAAAATCTAG	6048	A_95_P230584	EB439439
6359	75	69	686	GACACGCTACTTTGTTATGACTAAGACAATGATAATCTTAACGTGTAACCTGTAACAT	6050	A_95_P200012	TA17118_4097
6367	75	77	155	TGATGAGTACTTGGATTCTTTGGACCCGTATTTGGCTGAGTACCCTGCCAGGTAATAT	6066	A_95_P058156	BP134405
6368	75	78	468	GCTGATGCATGTTGCAAACTCAAAAACTACCTAAATGTATCACATTAGCAGAATAAT	6068	A_95_P039601	BP129594
6376	76	1	165	ATACTTGGAGCGACTGTAATGATCTCAACTGACTTTGGCCATGGGTTTGTGGACATT	5916	A_95_P069715	BP137463
6377	76	2	856	TTTATTGTTGTGGTAGTTGGTGGAACTCACTTCTGTGTGTATGACATCAAGTTCACCG	5918	A_95_P003356	DW001848
6378	76	3	729	TTAGCCTACAGGGAGGGGAGGAGAAGTACAGGAAGGCATGGACACAAATTTGTGA	5920	A_95_P150037	EB680099
6380	76	5	847	GGATTATGTGTACATATCACGTCATCTGTACATGCCATGTACTTCCTCTTCTTATGTAC	5924	A_95_P288138	FG163834
6382	76	7	584	AGAAAGAGTAGAACAAAGGCTCCAGGTCAGTGCAGGTGGGGTTCTTCACTTTGAAA	5928	A_95_P316393	FG188416
6387	76	12	853	TGTTATGTGAAGGAATGATAAGTAGACGCTGAGAGGCAAATCAATGATAAGTAATT	5938	A_95_P245437	DV999956
6391	76	16	793	GAGCCCTATTTATCTGGGAAGCATTTTAGAAGGACTTCTCATTATAGCTGGGCTTTAT	5946	A_95_P158877	EH616771
6392	76	17	898	CTATATAGAGACATGTTTGGAGAATTGCTTTTTGTTACATCGACAATCGTACTGCTTG	5948	A_95_P258586	DV157767
6394	76	19	121	TGTGAGTTCGATTTTTACTGTCCCCATTCCCTGATCCTCCAATGTAATAGAGAAAAGG	5951	A_95_P098148	BP534341
6398	76	23	170	GCATAAGATGATGTATTCCATAATTGACAGTGTATTTGCTTAGGTGAGTGTTCGTGT	5959	A_95_P109627	CV019388
6401	76	26	177	GATTCTGCTTTGTTTCAAATTTTAGCATTGGAAAAGCGTGGCTTTTTGCTATCGCGCC	5965	A_95_P095008	BP532976
6402	76	27	446	ATCAAACTTCATTTGATAGGCATTCCAGTCAAACCAAGCTTGAATACAAAATTCGCTT	5967	A_95_P074345	BP526445
6409	76	34	834	ATAGTCAGGTCCTAGTTTCCGGATCAAATTTTGTTGAGTGTTATCATTGCGGTTTTGG	5981	A_95_P191647	TA15281_4097
6411	76	36	352	TTGTTAATCTTTTTGCAGGTTCTTTCCTCAAGTGAAGTTGGATGATTCGTTTGTTACTT	5985	A_95_P131972	EB432401
6412	76	37	600	TTACTTTCAGTTGCTCCAAAGGCTCACCAAGTTAGTTCTGATCCCAGAGAGTCCAGAT	5987	A_95_P164932	EH624415
6413	76	38	429	CCTAGATTCAAGAGCTTTTGTTTTCCTATGCTGTGTTAATTACATTTTGATCAGGAGAT	5989	A_95_P003491	EB102901
6417	76	42	643	TGATTCCCGTACTTCTGGAAGGTTTCTGATTTCAATCTGAGTTGGCTTTGTCTTTGCAT	5997	A_95_P162472	EH621421
6426	76	51	571	TGAGTGATAATGCAAATGATTCTCAGATAGGCAAAGCAGCTGATGCTTGAATACTTG	6015	A_95_P135627	DV999569
6430	76	55	746	TTCATGCTTTAGTGGATTTGGTCACTGATGAATAAAGATGAGGAAACTTTGGTCAAT	6023	A_95_P146402	EB450438
6432	76	57	474	CTTCCTTTATATTGCACAAATTAGGCCCAGGCCTAATCTTTTTATTCACTCGAATAACG	6027	A_95_P152882	EB683210
6435	76	60	484	GTACTTTCAAGTTCCTATTTTTTACATGCTTGCTAGAAGATGAGGCTTTTTCAATGCCT	6033	A_95_P090903	BP531135
6440	76	65	780	TTTTGTAACACTTCACCCTACACTGTTGTAGAGACTATGTCCTTGGCGAAGGCTCTTG	6043	A_95_P125787	EB424886
6442	76	67	713	TATTGTGGGGTATTGGAACAGCTCTTGGAGAGCTTCCTCCTTATTTCATCTCTAGAGC	6047	A_95_P145062	EB448605
6445	76	70	731	GCAGAAACTTCTTAGAACAGCTCAATTTGAGCGCTGGATAATATGTTATACCAGTAT	6053	A_95_P012916	DV157680
6454	76	79	496	GTATCAGGTCCCTGCCTTGATTCGAGTTTAATTTTTTGCTGCTCTATACTTATTTCGAA	6071	A_95_P288643	FG639219

6455	76	80	944	GAAAATGAAGAATGGTTATCGTATTCTGCTGAGCTCTGTGGTGGAACACACATTTCT	6073	A_95_P187072	TA14266_4097
6458	76	83	320	GGGTGTTCCTCTTGATTGGATTTTTCCATGTCTCGTGTCTTAAACAGTTGAGATTTTTA	6078	A_95_P194447	TA15898_4097
6459	76	84	826	TTGGAAGCTTTCTTCTTGACAACCTTTGCTTTCTCCAGTTTAGATGACTAGATATTCTT	6080	A_95_P301368	FG161210
6460	76	85	852	TTTCTGTCTCTGCTACCAGAAGATAAGATGCGCGAACTCATGCAGACTCCTGTTCTTG	6082	A_95_P301608	FG167602
6462	77	2	383	GATTATCCTGAACCTATTCTCTTTTCAACGCTGACTTGTCTTGCAAAGGATTTCTGTGT	6085	A_95_P024946	BP131725
6463	77	3	810	GGGTGAAGTTTACTGAGGTTTAACGTCTTGGCTGCTAGTACTTGTTGACCTGTTGTCA	6087	A_95_P221692	TA21874_4097
6467	77	7	422	GTTGTTGATCAGTGTTTTACTGCTATGAAATTGCTGGCTAATGCTCGACTAAGTTAAC	6094	A_95_P195837	TA16205_4097
6470	77	10	757	GCTTCTCAAGGAGGGGGTTGTTGTAGTTAAAAATGGACATTTACTATTCTAACTTATC	6100	A_95_P160362	EB449711
6483	77	23	958	CAGCAAGCGGATTGATGTATTTTGGAGAAGTAATCAGAGAAATCTTGTCAGTTTATG	6124	A_95_P016581	TA12014_4097
6484	77	24	169	GAAAATGTGACAACCTGAGCCTGAAAAGTTGGAGAATACAGCTCATTATCACTTTAA	6126	A_95_P133592	EB435224
6488	77	28	456	CCCTAATGTTTAGGATTTATGGTACACCTCTCATTTGTCTTTTTGTATCTTCTTAAGGC	6134	A_95_P220447	FS393498
6503	77	43	1205	ACTGGTTTTCCACCTGTATGGTGTGTGATAAATCTTTATTTCTCTGGGAGTTGTTTCA	6164	A_95_P009756	TA13127_4097
6508	77	48	1888	CAGTTTTGAAGGTTTTCCTGCCTTCTGTTAATGGTTGTACAAAATAATGATGTTAGAT	6174	A_95_P032826	AF149981
6513	77	53	828	TGTTAAACCAGGGCAAACTAGTGATCCTAGAAGTGGTTTTGCTACTGTTGAGAAGGC	6184	A_95_P030376	TA15846_4097
6514	77	54	719	CGGCTGTGTTTTTCACTCTATGTTTTCGAAATGTCTTTGCTTCAAATGTGTGAAAACTC	6186	A_95_P011661	TA11894_4097
6516	77	56	628	AATAATTCCAGTTGAAGAGATGCTATTCAGTTTTGGGTGTAGACATTTGTACAAGGA	6190	A_95_P121517	DW001600
6517	77	57	334	CTTGACGGATTGATTAAGTGAGAATTTTTCGTGATAGTATTGATACTGGTCAAGGTTT	6192	A_95_P129632	EB429597
6522	77	62	508	ACAGTTAAGAAGTATGCCGATAATCTTCTGCATGCAATGGAGGGAGTTAGTGCTCG	6201	A_95_P127722	EB427299
6526	77	66	1062	CAAGAAATACCAAGAGGAGTGATCATGTAAATGGATTGTGGCTCGTGATGGACCAA	6209	A_95_P204717	AB193040
6530	77	70	192	ATCCAATTAGGAATTTGTTTCCTTTGAATTCTATCAGGGTCCCATTAGCTTGTATCGC	6216	A_95_P080625	BP528049
6533	77	73	880	CAACAAGTGATGAGACACAGAAACAAGAAATTCTCAAGAAATTTATGGCAGAGCAT	6222	A_95_P025086	TA17479_4097
6534	77	74	783	GCCACTGGATTTCTGTCCCACCTGATCCAAATTCTTTCTTCGTCAATGTTGGTGACTCA	6224	A_95_P011252	AB125233
6537	77	77	587	CCTGAGTTGTTAGAGGATTCGCTTGAGAATTACCCCCGAAGAGTTTTCATTTCTGATG	6230	A_95_P136457	EB440221
6540	77	80	343	ATTCTTCATGTAGGTTTTCACGAGCTTACAAGTATGGCATTGTCTTCTGAGGGGATAT	6236	A_95_P096438	BP533623
6542	77	82	461	CTGAAAAACGTGCTGCAGCAGTGAAGGCTTCAGGAAGAAGAAGAATCCGTAGTATC	6240	A_95_P108612	CV018923
6553	78	8	841	ACTTGGAGAGGAACTTGTTGCCATCTTCACTGAGGGATTTCATACATGAACACACTT	6097	A_95_P292403	EB427333
6554	78	9	424	CAGCGCGATCATCAAAGATATATAGCTTAAAGAAACTCCGAAGTTTCCTCTAAGTTG	6099	A_95_P064715	BP136129
6559	78	14	1038	TGTGGTAATATGTTGATATTTTGCAATCAATCGATTTGATTTCTTTTCCTCGTGGAAG	6109	A_95_P192382	TA15439_4097
6564	78	19	631	AACAAGGATGCAGCATATGCCTGATAGTGTGACCATTGGTCAGCAATATGACAGAA	6118	A_95_P136742	FG160232
6565	78	20	422	ACATGGTCTACAATTGATCGAGCTGCTTTTATTTGTGCTTCCTTGAGAAAGGAAAACA	6119	A_95_P096488	BP533648
6566	78	21	849	GTGTTGGACCGCGAAACCAATAAATGGAAGTTATTTTCTTGTGCAATTAGAACCTAT	6121	A_95_P011096	EB680130
6571	78	26	394	CTCCCAAATCCACCAAAAGAAAAAATATTTCTGCTCAATTGAAAGGGTGTTCCCTCAA	6131	A_95_P204702	TA18120_4097
6574	78	29	552	ATCTGTCCTCTACTTTCCATCCAGAAAAGTGTAAAATAGCATTGAGCAATGCCTGTGA	6137	A_95_P103442	CV016502
6577	78	32	388	GCGTGGAAATGGATCTTGACAAAACTGATTTTGGCTGATCTATCCACATTAAGGAGA	6143	A_95_P063185	BP135708

6582	78	37	1008	ATAAAGCGTGTCGCTGAAGTGAAAGCCGCTTTAGGCTGCAGATCCTTTTACTTGAAG	6153	A_95_P202522	TA17654_4097
6586	78	41	866	CAGCTGCAAAATTTAAGCTTGTGATCCTTGGATATTTAAGTTCACCAGTGTATTTGTT	6161	A_95_P226244	DV158744
6588	78	43	461	CTGTTTGTGTTAGTGGTCAGTTTAATCTAGGGTATTTTAATTTCTGTTGTTAAGGTCT	6165	A_95_P000736	FG635626
6589	78	44	1215	TTGTGATTAACTATGACCTTCCTACTCAGCCAGAGAACTACCTGCATCGTATCGGTCG	6167	A_95_P152712	X79141
6592	78	47	798	GTTGCTCAACTACGAATGGTCTATGTACATATGATTTCTTGTATTATCCAACTGCAGT	6173	A_95_P137897	DW002580
6593	78	48	913	AAATTGACTTACCACTTGTTCCATGGTAATGTGTCTAATGCAATCACTTCATTTCTCCT	6175	A_95_P014616	TA15703_4097
6594	78	49	172	ATTAAAGGAAAAGACCAAGAAATCCATAGCCCTATCAACGCCCCCTTTCACGTTAGC	6177	A_95_P131547	EB431869
6595	78	50	314	ATGTAAACATCGAGGTACAGCTGATAACTTGCAGAATATTTATCTAAGCATAGATGA	6179	A_95_P019461	EB447384
6599	78	54	1083	CTAGTTGACTTGCCATGGAACCCCATGAAATTTTTGGTGATGCTATGAGTATATAAAA	6187	A_95_P214822	TA20347_4097
6602	78	57	627	AAAGGAAAACTTGCATTTTTGGGATCTTTACACAAATAGCCGGCGATATTCATTGTTT	6193	A_95_P287268	FG635982
6605	78	60	600	TCGGAGATGCAAATTCTACTGGTAGAGAGATGCAAGTTCTTCAGTCAATCTAGCCAA	6198	A_95_P061270	BP135218
6606	78	61	544	GCTTTTATGAACGAGAATGTGATGGAGTTCAGATTCAAGAGAGAAGATTACTTCACT	6200	A_95_P060680	BP135059
6611	78	66	969	ATTGATCATGTCTCTATGAGGAAATGCTATGATGGAATCATAGACGCTGTGGAAGG	6210	A_95_P010171	TC59215
6612	78	67	779	CCTTGTATAACTAATGGAAGTCCAGATATTGTCAAACCATCAGCAGGCTCAAGAAGC	6211	A_95_P126432	EB425758
6616	78	71	314	ACTCCAATCTTTCCTTTGAATATCTTGTCCTCAGGCATGTCTGAAGTTTATTTAAGCTT	6219	A_95_P109767	CV019440
6619	78	74	759	TTGGAGAACTGCAAGCAGTCTTTAGCTGTTATACAAAGAATCGTGGAATCAACCTCA	6225	A_95_P253564	DV159957
6622	78	77	194	GTACTTTGGTTCATACTTCAGCCTCTTGAAACTAATGAAGAGAAGTCCCTTTCTCCTC	6231	A_95_P119982	DV999616
6631	79	1	1375	GTAGGGGTTGATTGTATCCCAAATCTTAGTACTGTCTGGATGAAAATTTTATGAGGA	6248	A_95_P002691	TA13816_4097
6632	79	2	483	TCATCCTTGAAGTTTTCTCTGTGTCTGTAAAACACGCATTGTTCAAGAATCAATATCAT	6250	A_95_P136357	FG644307
6633	79	3	773	ACATCCACCACAGATCAAAGCTTCACAGAGCGATCAATAATTGATTTTCCCATATACC	6252	A_95_P197012	TA16469_4097
6641	79	11	641	CTGCTATTGCACATGTACAGTTCCTTGAAAATAAATAAAGCATTTGCTCTGGGTTTGT	6268	A_95_P188302	EB433758
6643	79	13	1724	CTCTGCCTGAACAAACTATGTTTGGAAGAGAATGTAAGCTTGACTTTCCTTTGAATTA	6272	A_95_P007441	AB075948
6644	79	14	800	AATGTGATCCACTATTTCAGACTGATGGGATCTTCACCCATCTAGCTACATGGTGCAC	6274	A_95_P269766	FG159209
6646	79	16	801	ACTTGTACGTACTGTGAAGAAGTTAACTTTGACAAATACAAGGTTTGCTTGGAGTGA	6278	A_95_P253684	DV162053
6649	79	19	1145	TATGCTGTGTTGAATGAGCAGAAAGAGGTGAGGAATCCTCTTTTTAACTCTTGACTC	6284	A_95_P209852	TA19277_4097
6650	79	20	605	CGGGACAATATTCGGGTTTTCACCGTATAGTTTGATGAACATTGTTGGAACGCTTTG	6286	A_95_P128912	AB488495
6651	79	21	538	GGGCAGCTGGTTTGAGATTTGTCCTTGTTGTATCATATAGTCTGTCATATACGAAAAT	6288	A_95_P116532	DV159290
6653	79	23	915	ATGTATACATGAAACATACTCCATGATGCTTGGGTCATAACACTTTGATGCTCATTCT	6292	A_95_P192287	TA15418_4097
6658	79	28	367	TCAATTTTTATTTGTTTCAGATTTGGAGCATCCAGAGGCCGATTCGAGAGGCAAAGA	6301	A_95_P094263	BP532630
6659	79	29	468	AAGGTGTTGGAACGGTGTTTTCTCTCTAATATTTTTCCTCTCACAACGTTCTATAGTAT	6303	A_95_P036368	BP128714
6660	79	30	379	ATTTAGCAAATTCAGTTCCAGCACCCAAGCTCGTGTCAGGTTCGATAAGCATTGGCA	6305	A_95_P067760	BP136958
6661	79	31	603	CTCTACTGCACTTGGCTGCATCAATTTGTATGTTGGGATTATATTATAGTTTTGATTCT	6307	A_95_P223832	EH615961
6662	79	32	497	TCTGTAGAGCTTATGACTTGTACTACCAGTTTGGGATTGTAAATTTGTATCGAGATTT	6309	A_95_P079450	BP527768
6663	79	33	284	TTTGCTTGGTAGATATCCAGAAGTAGGGCTAGCCAACGCTGTGCCTTGAGATGTTCT	6311	A_95_P125522	EB102909

6664	79	34	580	TTGGGAAATATCCTATTCCTTAAGCCTGACCAGGTGGTGAAAGCCATGAAAGGGCCT	6313	A_95_P126367	EB425709
6667	79	37	627	TTGTTCAACATAGAAGATTGTACCTTGTTTCTTCTGGAGGGTACAAAGTTTCCAGCTA	6319	A_95_P183737	TA13525_4097
6670	79	40	328	GACCTTTGAATAATTGCTTACTGTTTCCTTGGTTATCTGGAAATTGTTTGGGGAATAC	6324	A_95_P093623	BP532339
6673	79	43	608	CTTTTCTTACTTGTGGGGCAGGTGGTTGACTGTCGCATATGCGGAAATCCCAATTTCT	6330	A_95_P163987	EH623041
6676	79	46	108	GGTTCTTGGTTTGTTACCTATGTATTTTAATCGTAATATTGTTTGCCACTGTGAACTGT	6336	A_95_P152217	EB682535
6678	79	48	429	TGACACTTTCTTCCATTATGCGTGTATCCAGTTTTCCTTTCTAAAACTGAAGTTCAAGA	6340	A_95_P020691	TA12997_4097
6680	79	50	869	CGCGCTTGTATCAACTTGTATCTGTAGAAAACTTAATTAATCTGCAGCAAATTACGTG	6344	A_95_P229414	DV159857
6685	79	55	687	GGATCTTTGAATAGGGACAATGGTTTCCCTGCTCGATATTGTGCCAAGAATCGGATG	6354	A_95_P162292	EH621249
6686	79	56	1180	GATGTCCTCTTTGGCTGATGTTGTGGACTTTTCTCTTATTAATCAAAGCTTTTTCCTCT	6356	A_95_P217837	D86722
6689	79	59	876	CACAGAAGCTTACATCACAGAGACAGATGCAATTATCAAAGTTGTATAAACATTATG	6362	A_95_P116497	TA17798_4097
6690	79	60	844	TGATAGGTGGTTGACAAGGCCTTCACAAGGGTAGATTGTGCCTGGATAATTTTGTTC	6364	A_95_P017746	EB449268
6692	79	62	622	TTCATTATTGATGAATTGCACCTGATTGGTGGTCAAGGTGGCCCAATCCTGGAGGTG	6368	A_95_P037318	BP128972
6698	79	68	225	GTTTAGTTCTCATCGAAGGGTTTGATTGTTCAGACGATGAAAACTAGACATATCTTGT	6380	A_95_P034399	AJ718674
6700	79	70	347	CATATTAATATATGTTCTCTTCCATTTTATCGTCCTTGGCTTCCTACTGTGCCGAGTGT	6384	A_95_P081290	BP528217
6704	79	74	853	TAGACAGTACGCAAAGCTGTTACTCGCTATAGCCCATCTGGTGTGACTCATTTTTCTG	6392	A_95_P227429	FG161617
6705	79	75	842	TACAAACATTCTGTTCTCATCTGGCACAACAGGAGAGCCAAAGGCAATTCCATGGAG	6394	A_95_P205377	DV162298
6708	79	78	806	ATTGAGAAGACGCATTTACTTAGCCTGGGATAATGCTTGTATCACCCTTCCTATCTTG	6400	A_95_P159017	EH616951
6713	79	83	586	TTTTTCGAGAATTTTGGATGCCCTGATTATCAAATGCCTTTGTGAAACGCTTTCTTTCC	6410	A_95_P019586	DW003011
6714	79	84	182	GGTCGTCTTCTCAGTCTATTGACAGAATATTCATATCAAAGGTTCATTTCCTCTAATTT	6412	A_95_P034588	AJ719184
6715	79	85	873	TCTTCAGCACTGCCCTGAGGGTTTTGAATGTTCAAGTTGGAGAGACATCAAGACTAG	6414	A_95_P245547	DV159373
6716	80	1	1240	GCTGGTGTATCATTTATAGTTTTGGTGTTTTTCTAAGAATTGCCTGTTCAAAAGATCCT	6249	A_95_P033091	AF352797
6720	80	5	535	TTGTCCTTTGATTGTGCTTATTCTACACTCTGTTATGTGAGTAGTGATCATATTTCTGC	6257	A_95_P263751	FG637333
6726	80	11	469	GTACGAAGCTTAATTCTATCTCTCGGGTACTTGTTACCAAGAATTTCTCTTCACGTAAT	6269	A_95_P114212	CV021495
6727	80	12	463	AGGCCTTTCTAATGTTTTTGTGGAGCTTTTTCCATAAACATTGAGAGTGTATCTTGTGT	6271	A_95_P028031	EB431080
6729	80	14	576	CGCATATCTACAATTTCTTTTCAAATGTCATGCCATTCAAGTGTAGCATTCAGTTGTTT	6275	A_95_P055186	BP133634
6730	80	15	770	AGCTTTTGGAAAGAACATCCAAGAATACTTGACGAGGAGGAGCCATTGCGGACGAT	6277	A_95_P218642	TA21221_4097
6731	80	16	490	AATGGTGGTTGTTTTTCTTGTTTCAATTTGGCGATAATGTTGCTATGCCTGGTTCTATA	6279	A_95_P018986	FG142809
6737	80	22	740	GGGGTTATAGCAACAGATCAATTTTTTGTACTTCTTGCAATTAATCGAAAAGTTGTGC	6291	A_95_P002046	TA16284_4097
6738	80	23	577	AAGATTATGTGTGGTATTATGCCAGTGATGCCTACGTACGAGAGGTCTCATTGGAAG	6293	A_95_P043496	BP130631
6740	80	25	647	GGCTCCAAACAACATGACTTCATTATGTTTAGTGAAATGGCAGTTGGAAATGGTAAT	6297	A_95_P280378	FG184459
6742	80	27	1715	GCAGCTTTTTTCTCGTGTTATGTTTTCCAAGTTACTGAAAACTCTCATACAAGCAAAG	6300	A_95_P184492	TA13708_4097
6743	80	28	333	CTTTCAATTTTTGGTTTTCTTTCCTTCAGTTACGCGACGAGTTTGATATGGCATTAAAC	6302	A_95_P025726	TA16842_4097
6748	80	33	331	GCTACTCATTTGTCAAGGTTCATACAACTCCAAGTGATTTGGGCGCCCAATGTCTACT	6312	A_95_P080700	BP528071
6749	80	34	1033	CTGAATGTTTAGTACATTTCTGAGCTCCACTCATAATCCATGACTGTTCCTGCGAAAA	6314	A_95_P028411	TA16149_4097

6750	80	35	406	CTCGCCAACTAGCCCTTTTGCATTGCACTTCGTCGCAAGTTGATGTTCAAGATCAAGA	6316	A_95_P100828	BP535535
6754	80	39	1478	GAGTTTCAAACGGTTGGCGAGACGATTTTCGGTGATAAGAGAATTATTGTATAATTT	6323	A_95_P021536	TA13961_4097
6756	80	41	726	TCAACTTACTGCTGCAACATTACCATCTGTGTGAGAAGTATATACTGTAGATTTCGCG	6327	A_95_P103437	EB683342
6762	80	47	444	CCAGGCTATATGGGTTAACTCTCTGGGGATAAAACTGCTTGTAAGGATCTATAGTTG	6339	A_95_P045491	BP131156
6767	80	52	764	TTCTTCATCAGATCTGGTTCAGAATTTGACCTCACAGCTCGACGAGTAGCTGCTACAA	6349	A_95_P228809	EB449914
6768	80	53	301	CGAGTTTTCTTTTATCAAGCAAGGGCATTTTGTCTGTAAAACTTCTTTCTGGGAAGAA	6351	A_95_P040501	BP129847
6770	80	55	440	AAGTTGCTTCTAAAGCACCAGAGTTGCACGCGGAGATTCAAAACAAAGTGCCATGCA	6355	A_95_P104497	CV017044
6771	80	56	893	GAGTTCAACTTGTTACCTTACTTTTGCATTGCCAGTAACTTTTGAGTCTTTTGGATGTG	6357	A_95_P198642	TA16823_4097
6774	80	59	362	GCCTTTGAAACACTGAAAAAAGGGTCCTTCGCGTTTTCTTTTTCTTGTTTCTTAATTTC	6363	A_95_P089563	BP530554
6776	80	61	701	CTGGTGGTTGCATTTGTAGTTGAAATAATGAGGGAAGCAAAGAATAAAATTGATCCC	6367	A_95_P026021	EB681115
6779	80	64	727	GTAATTTCATTTGTTGCGGACGATTTTTCTCGAGCTAGCAGTACATGTGTTGGAAAAC	6373	A_95_P314793	FG199468
6780	80	65	500	CTATGGAACGTTTTTCTTGAGAAATTGAAACTTCAACTTTTAGGTGCCAACATGTCGA	6375	A_95_P255584	EH616011
6783	80	68	435	CAAAAGACATTCAGCTTGCCAGAAGAATTAGGGGTGAGAGAGCTTAAATTGGGATT	6381	A_95_P195022	FS436591
6784	80	69	723	TAGAATAGGTACTTGTTGCACATTGGTGTAGATGGGAGTGAAGAGGAAAGGCAAAA	6383	A_95_P163157	EH622136
6787	80	72	1004	CATGCTTAGTAGAATGAGACATCACCAAAGTGACGATGTATGAGATTATATTTTGCTT	6389	A_95_P212092	TA19755_4097
6788	80	73	57	TGGTTAAGAGTGTTTATTAGACCCCAGACGTGACCGCAGAATCACTGTCAATGAAAG	6391	A_95_P111797	CV020376
6792	80	77	580	TGTGCTTTTATTGAACTGGAAGTGGTAACAAAGTGTGTTATATAACATGTTGCTGGA	6399	A_95_P032101	EB683726
6796	80	81	1156	AAGTACTATTGAATAGCAATCTGTTGTTTTGGGACCTTGACCTCATGCTTTAGATCAA	6407	A_95_P008731	TA12866_4097
6800	80	85	503	ATGGGAAGGCAAGATTTTGTCCTAGGAAAGACATTTATGTTTAATGACTGCTCAAAC	6415	A_95_P002326	FG643973
6802	81	2	849	AAGGATCTCTCTTGAAATACATTTTAGAGTCACGGGATCCTATATTCCAATGACCTGT	6418	A_95_P216297	EB680805
6806	81	6	393	TACTCTGAGCAAGAGTTGTAGCCAGATATTGGAATCAATCATAAAGATAACACTTCT	6426	A_95_P088613	BP530146
6811	81	11	1156	TTGTAACAGATTACTAGTACATTGGGTACTGGATCGCATCATATTCAATCAAAGCTTC	6436	A_95_P201697	TA17479_4097
6813	81	13	690	GCCCTCTATTTGAGCATAACATTCTTATTTTCGTTAAGGGTGTGTTTTATATGGAGGA	6440	A_95_P003606	TA12312_4097
6818	81	18	673	TATGCTATATTTTCAAGCACATGCACTTCACGGAGTAGTGATGATCTAATTAAGTGCT	6450	A_95_P000661	TA12654_4097
6819	81	19	625	GAGGCAGTGAAAATTAAGAGATTTAAAAAGCATGTTCGAAGCTTTTCATCGGGTAAA	6452	A_95_P064880	BP136179
6820	81	20	710	GATTTTGATAATTTGAGGCATGAAGGGGAGGATGGTGAGTTGCAACCTAAGGTTGT	6454	A_95_P291333	EB678797
6821	81	21	1112	AAAGCTGCTCGAGAAAGATGTGTTTCTGTGAACTGGGGAGGGATGTCACAGGGTTT	6456	A_95_P180287	AF352797
6827	81	27	663	TTCATCCACCTTTCCCCTTCTTTGAGTAATAGCTGGTGCTCCTCTGTGAATAATTGCCT	6468	A_95_P287733	FG190143
6834	81	34	648	AGACTGGTCACCCTGGCACGTGATTGTCAAAAATGATCCCGTGTGCAACCTATGTAA	6481	A_95_P066105	TA17246_4097
6835	81	35	1199	CTGCTAGTTAGCTTAGGTCTGAACCGTAGAATTTCGTTTGTTTCGAATTTTGTATGTT	6483	A_95_P238914	AB032536
6837	81	37	679	TAAGCTTTTTGCTGTATGGAGGAAGGTTATTTTCTATGCTGAGACGCTTCCCCATTGA	6487	A_95_P145622	EB449379
6840	81	40	876	TAGTAGATGTCCTACGCCGACAGAGATTTCTGCGAGACCCTGAAGTTATGACATCTT	6493	A_95_P247897	DW000180
6842	81	42	758	TGAGCTGTCTCGGCTTAGCTATTAGCTGTCTAAAAGCTATGGTAAATAAAATCCCATG	6497	A_95_P139632	EB443435
6843	81	43	1855	CCAGATGCTCACTCTGTCAGTTTATCTTACTTTGTATTAAGTAGTATCTAAGCTAACTC	6499	A_95_P188412	TA14565_4097

6845	81	45	194	GTTTCAGTGTGAAAGTTTGAAGGAATTTTTCTCACCGAACAAAGAAATGGCTCCCATT	6502	A_95_P158832	EH616723
6846	81	46	1634	TGCCTGTACAGCACGTTTTTGCCTGTAAAATGCCGTTACCTGTTGATTTCCTCTCTAAT	6504	A_95_P206572	AJ133453
6852	81	52	54	ATACATAATCTGGACATGGTTACAAATTTGAGGAACATTTCAGCTCCCCCCACCCTCT	6516	A_95_P050396	BP132385
6853	81	53	877	GGTATATAGATTGTGGTTTGTGATTCTGCTGGTGTTGTGACAACATTTTATATGTGCT	6518	A_95_P296108	EB450034
6859	81	59	828	GGTCTCCTTCCAGTGTTGCATCTTTACCATATATATTATGGATTTTACTAACCTAATAG	6530	A_95_P010551	DV999830
6864	81	64	621	CTGAGTGTTGGATCGAAGGTGATAAATAAGCAAATGGTTGTATGCTTCTGCATTATT	6540	A_95_P198252	DW004949
6866	81	66	573	ACGTGTCCGATTGACAATTTTGGGGTTAATTTGAGGGATGGTCACTTAACTTTCATTT	6544	A_95_P282418	FG636054
6868	81	68	495	TCTGTGTAGGTAGAAAGGATGTGTTTCTTTGTGCAAAAACTTGGGAACTCTAAATTTT	6547	A_95_P119507	DV162724
6875	81	75	561	CAGGGTATATACTCTTCTGCATTCACCATTAGAAATAAAAGTGTGCAAATAATGCTTT	6561	A_95_P025841	DW002115
6877	81	77	706	CTGTTTTTACCAGTTTGTTCAGCGTCTATCTAAAGTTCTGTCTTTAAGTTAGCTTAACT	6565	A_95_P266706	EB439799
6879	81	79	733	CAGTAATGTGCTGATAGATGCTGTGTGTGTTATCCTTGATTACTTTTTTGTTTATGTTC	6569	A_95_P190132	EB677573
6880	81	80	830	TGACAGTAGAGGTTCTTGGGTCTTGTGGGTGAAGTTTGAAATTCTAAAGTCACTGGA	6571	A_95_P115382	DV157555
6882	81	82	842	AGTCTGTTCCTGGTTTTTTGTTCTTTCCCTTGTCTTCCTGTGATGAATGGCTATTTAGT	6575	A_95_P017871	TC53016
6883	81	83	165	AATATCTATTTGATGAATGTTAGCACGGGGGAAAACGTAATGTAACGTGTACTTAGG	6577	A_95_P103032	CV016307
6887	82	2	834	GAGGCAACTAGTCATTGTTTCTCTCGATTTACTGAGAGGTGTTTCTTCTTTAATTGTA	6419	A_95_P119047	DV157598
6889	82	4	816	TGTGACTGAAGCTCAGATGACCACCAGCACGCTTTGCTACATTGTCATTTATTGCTGA	6423	A_95_P283963	FG139568
6891	82	6	70	CTCTGTGCAGCTATTTTAGCCTGTATAGCTCTGACATGTATATAATATGTCACATAATT	6427	A_95_P131372	EB431558
6896	82	11	654	GTTAGATCGTAGATGTCAACAATTGATGAAGATATTAGCAATATTGGATCATGTGTG	6437	A_95_P244297	EB683360
6903	82	18	1048	GCTTTTGCGCTTATATAATCTCTGTCTATTTGTGCTGCTGTTTGTATCTTAAAGCTATG	6451	A_95_P008791	TA13304_4097
6904	82	19	580	AAGATACAAGTCAGGATTTAGATGCAACTGGGAAGGAAGAATTGGGTACTGAATCT	6453	A_95_P122142	DW002182
6912	82	27	758	TACTCCTAGTGCTTGTATCGTTAATCGGTTGAGCTTAAACATTGAGAGCTAAGTTATT	6469	A_95_P108167	EB440260
6916	82	31	1116	CTCAGCTGCTGTACATAAATACATTGACCAGATTACCAGACCAATGCAGTTTTTAGTG	6477	A_95_P024271	TA18940_4097
6922	82	37	223	CGTGACCATTGAAAAGATTTCACTCTACGCTAGCTATTTCATTTATAGAGTTATGGAT	6488	A_95_P140842	EB444664
6925	82	40	808	GAAGTGGACAATATAAGTCTATAAATGAGGCACTTAATGCTGTGCCTAAAAAGAATA	6494	A_95_P010086	EB426940
6930	82	45	836	CCAGGAATGCTTTCGTTGGTCACTCGTATTGTTCTGTTTCTGAGCAAATGGACCTTTA	6503	A_95_P288948	EB445476
6931	82	46	550	AGCGGAGTCGTGTATCTCCTTTTTATTGCAGTTCATGCGAAGATAAAGAATACATAA	6505	A_95_P039086	BP129448
6933	82	48	493	CACAGAGATCAAATTGTTCACTTCTCTTGACTAGAACATTTCCATGTATAGACTGCAT	6509	A_95_P257529	AM808565
6941	82	56	508	CTTCTTCCTATTGTTATGGTGATGATCTATGTATTATGAAAGTTTGAGGCTAAATGGC	6525	A_95_P088813	BP530227
6943	82	58	534	TTTCCTGTCACCATTGTTAGAACTTTAAAGATTGCCAGCTAACTGAGAAATTTTCCTA	6529	A_95_P286308	FS412600
6947	82	62	806	ACTGTCCATGTGTCAATCTAAAGGTTGATTCAGCAGCTTTAGGAGTTGATAGGCCAG	6537	A_95_P270161	FG134970
6948	82	63	855	GTGCAAACTGTCCCCGATTTGTTTGGGAACCAGCTTAAATGAAAGTGCGAAGTTGTT	6539	A_95_P178177	TA12171_4097
6951	82	66	420	TTACGTCTTGTTTCCTAGCAGTTCCATGTTTGAATGAGTGTGGAGTGCATAATTTCTG	6545	A_95_P209012	TA19096_4097
6952	82	67	1580	GTATCTATGCCCCTGTAAATTTTTAGTCTCTAGCTACTGCACTATTGATCCTATTAATG	6546	A_95_P210682	TA19448_4097
6953	82	68	747	ATGCTTGTCTTTGTCAAGGATATTTGAGCTCTATCAACTTTGATGCCAAAGTTTTGGTT	6548	A_95_P102672	TA12018_4097

6955	82	70	500	GGACAGAAGAAGGGAGGTCTTGCTTGAGTAATCTTTCCTTATTTGAATGTGTAAAAA	6552	A_95_P304698	FG638411
6957	82	72	439	CCCGTATAATGTAATGAATATGACCCTGTTTACTTAAGTTGATCCTGCTGGGTTGAAC	6556	A_95_P021851	TA12197_4097
6961	82	76	76	TGTCCGAAAGCTACAAACAATGTATTAGTTGTTTGATACAATCTTGGCATGGCTTTCT	6564	A_95_P098018	TA18268_4097
6965	82	80	571	ATGACAGTGTCAGATAAGGATGATTTTGGAGGACAGACATGTTTGCCTGTCTCAGAG	6572	A_95_P054591	BP133478
6966	82	81	659	GCGGCTTCTGTTCTCGGGGAGGTTGAAATGATATATGAATATTATTATTGAAGAGGA	6574	A_95_P195192	TA16062_4097
6976	83	6	851	TGTGGTGTCATTTTACTTGGGCTGCTGACAGAGATGAGGAAAAAACTGATGGGCTTC	6593	A_95_P229634	FG159651
6984	83	14	299	GCTACTATCGTGGAGCCCATGGCATAATAATTACTCTAGTGGTGTGAATCACTAGTG	6609	A_95_P155742	EG650239
6990	83	20	737	CACACAATAGCACTGTGCTGAAATTTACGAAATTCAAGGTGCTTTAATGTCCTGTTAT	6621	A_95_P135192	EB438480
6993	83	23	821	ATTCCCAATATTTGGTTACCCCTTGCTTGTCAACTCTGCCGTTTACCGATTTGCTTGGC	6627	A_95_P220877	DV162339
6996	83	26	840	GAGCGTCTCAAGAAGAAAGGCTATGAAGTGCTCTATATGGTTGATGCCATTGATGAA	6633	A_95_P130272	TA15509_4097
6997	83	27	986	TCGGATAGAATTTCGTTTAGGTTTGTTAGCGGTCTTTGTTGTATTCACATTGTTGTTTT	6635	A_95_P216722	TA20766_4097
6999	83	29	491	TTGTTTGTGTCGCTTGCTGCAGCACTGGTAGAATCCCATCCTATAAGCACAGAACTTG	6639	A_95_P094473	BP532734
7000	83	30	1107	AGAGAACTAAGATGCATGATTGTATCAAATATTTCAATATCGATGCTTTGGTGACGG	6641	A_95_P011691	TA13363_4097
7004	83	34	816	CTATTCTGCAAATAATCAGGCAAACTTCTGATGATGCTTTATGTTCTAAAACGTTGAA	6649	A_95_P014671	EB450443
7008	83	38	267	ATATAGGGACGCAGAACACATGTAATTCTCCAGAATTCTTATGCCATGCTGTTCTTTT	6657	A_95_P142702	EB446132
7009	83	39	311	GCTATGCTTCTTATAATGTAATCTGGTTGGTGTCAAGTTTGTTTGTGAAAGATGGTTG	6659	A_95_P003586	TA13678_4097
7021	83	51	522	TATGTGGAGTTGTTGATGATGGGAAAGGATGTGGAGAAATTCCAACCTGAAGACAT	6683	A_95_P281208	AM791968
7026	83	56	492	GCTCTAAATACAAATTGGTGTGCACTTGTAATTGTGAAGATTCAAATGGTTTCTGCCA	6693	A_95_P209677	TA19241_4097
7030	83	60	1099	TTCCCAAATCGAACTGTATGTTGTTGTATGTATCAACCAATATTAAAGAGCACCGGTT	6700	A_95_P154167	M94135
7032	83	62	775	GCAGCTATGGATGTTTCTTTGCTGCGCTAATTCTTGTTGCATTTTCATGTATCAAATAA	6704	A_95_P212862	DV158792
7034	83	64	488	TAAAATTGAATTCTGGAAACCTTGCAATACTCTGCACTATGTTGCTCTCTAGTCATTAC	6708	A_95_P186487	TA14138_4097
7036	83	66	655	CTGAGGTGACTGACCATTGGGAAGCTTATACTATTTTTAAAGACTTGAACTTGATACA	6712	A_95_P144507	EB447883
7041	83	71	198	GCATGTCAAGTGAGTGCAAAGAACCCCAGCAGTTTGCAGTTTACAAGTTTCCAGTTA	6721	A_95_P115162	DQ460120
7048	83	78	0	AGAGAGTGCTGGAGTTCATGTGGAGAAGGTATGCAGATGACAAAAGATAATCCCAG	6735	A_95_P309343	A_95_P309343
7051	83	81	244	GGAGTAGGGAACATGAGAGTAAAGTTAGGTGAGTTGAATACTGTATGTTTACAGAT	6741	A_95_P143677	EB446915
7052	83	82	453	CGTACTTAAGTGCCAGCTGTTTTGATCATGTTGTTTAGCTATAATGTGAAAGTGAATA	6743	A_95_P005786	TA13604_4097
7055	83	85	858	GCCGGTGTAAAATGCTAATGACTATATTAACAGAGACTGTAACATTTGTCAGTTCTTA	6749	A_95_P021616	EB446173
7056	84	1	730	TACTTCACATGGAGAAGTAGAGGCCTGGGAGCTTATCAGCACTAACATATTGCGCAA	6584	A_95_P265341	EB428206
7058	84	3	856	TGATACAGGTCCTTGCTCTATCTTATTATGTTATCTCCTACTTCCCCGGAGGTTCAGCT	6588	A_95_P226229	DV161010
7063	84	8	762	CATGCTTGGAGATATGCCCCAACGCTGTTCGTCGAAAAGAAATGAACCATAACATGG	6598	A_95_P146007	DW000151
7066	84	11	733	CGGCTACAATTGTCAACTAATCCATATTTGGAGAGAAATGTGGAATTTTTGATTGAAT	6604	A_95_P148073	TA14583_4097
7070	84	15	671	CTTTTGCACACAGTACCAATTTGTGCAAGATCTGTAGTTTACTGAATATGTGGTTTGT	6612	A_95_P001186	DW003166
7071	84	16	805	CTGAGAAGGAGACCTATTCTTTATTGAACGTCGGCCCTAGAAGCAACAAATTGTTTA	6614	A_95_P218197	TA21119_4097
7072	84	17	198	GGGTTGTTTGATTTTTGAGTTTGTTGGTCATCTATCAAACCCTTAAACCCAGTTTGTTT	6616	A_95_P141262	EB445034

7082	84	27	188	TGTTCTCTTGTATGTACACTCAAACGGATGCCCAGTAATTATCCTCAGTTACTTTCTGT	6636	A_95_P132307	EB432770
7085	84	30	284	ACCCTTTACTGGTGTCTCCGTTGAGATCAACGTGTCCTACTTGGATAGCTGCTTAATG	6642	A_95_P105672	CV017561
7086	84	31	830	ATGACAGTTATCACCATTGGTGCTGAAAGATTCCGCTGCCAGAGTCTGTCACATCAT	6644	A_95_P224822	FG139197
7089	84	34	863	GGTGGCTCGGAAGTTTTGTTTGTTATGTTGCTTAAGATACTGAATTCGAACTTATTTT	6650	A_95_P176802	AF154660
7093	84	38	753	CGATATTCGAACATCAGATTATTTTATCCTGTAGCAACTATTCCTCACTTTTTGGGTTG	6658	A_95_P140297	EB444258
7096	84	41	651	ATGGAGGCAACAAAAGCAGTCAAGCCATTACTCGGAGACTACTACCAATTTGACGG	6664	A_95_P148782	EB678289
7098	84	43	401	TTTCACAATTACGTAAGTTGTATGTGACCTTGAGCGTCACAATGGTTAATTTTAAGGG	6668	A_95_P308718	FG643422
7104	84	49	410	GCTTAAAATGAAAATCTTTTATGAGCCACTCAAAGCAAGAAAGCCTGAGCGGGCTGT	6680	A_95_P130922	EB431045
7108	84	53	779	TTGGTGCTTTGTTTGTAAAATTTGTTGTTTCACATTCGTGTGGCGTATATGAGTTTCAT	6688	A_95_P000221	EB438050
7109	84	54	399	TTGGGGAATTTTGTTGGACAACAGCTATGTACATAGAAGGAAAAGTGACATTGTAG	6690	A_95_P104792	TA12994_4097
7118	84	63	702	TCGGAGGCCTTTAGTTGTCAGTACATGGAGTAGGCTGCTTCCTGCTTATCAATTTACA	6707	A_95_P148157	EB677366
7128	84	73	849	GCACCATAGGTGGTAGTTTCTACTATATACATAACCTGCTCTTGGTTCCAGATGTACT	6726	A_95_P009456	DV162425
7129	84	74	768	TTTTCAAGTATGTTTGCCTTGCTAAAGGATCCGGCATTGGCAATCCATCTCCACCATT	6728	A_95_P245292	DW004658
7133	84	78	961	AACTTATCATGATGAGATGGTGCTTTTTGGACTCTTTTGTTGCACATTGTAGCATGAA	6736	A_95_P000426	TA12032_4097
7135	84	80	813	CTCTAAGGCATGATTTTCCTAGGCAACAACGCTAAACAATTGATATACACTTTATCGT	6740	A_95_P199252	TA16953_4097
7139	84	84	553	ACCAAAAACCCCCTCTTTATTGGGGTTGTGGGAACTACTTTCATACTTCAGATCATTAT	6748	A_95_P036908	BP128858
7140	84	85	817	GAGCTTTCTGACCTCAGAGCGATGGTTCTCACTGTTATTTTAATTTTTCTTATGTTTGA	6750	A_95_P218887	EB677936
7142	85	2	1080	GCTGAAGTTTCTGCACAGCTGATTTATGATCTTAGGGTGTCCAATTCGACGTATTCTT	6753	A_95_P216637	TA20749_4097
7144	85	4	1286	CCCATTGTAATAAAGACTTGAGATGCTTTGTTATCAAAGAAAGCACGAGCCTTGATA	6757	A_95_P187327	TA14320_4097
7146	85	6	686	ATGAGCTTTCGTTTGATAGGGAGTATCCTTGGATTGGTGTTGAGAAAACCGAGCCAT	6761	A_95_P138032	FG160063
7149	85	9	1174	TCTCCATCTGAAGTGGAGCACCTCTGTATGTGTATACTCGTTTTGCCTGGGAGATTTT	6767	A_95_P195242	TA16072_4097
7150	85	10	1352	ATTCTTCCATAGTTTTTGATGTAGAAGATTTTTGTTCAAGTTGCTTATATTGCCCGTCG	6769	A_95_P023866	TA13974_4097
7158	85	18	755	CCTGAATTCGGTATTGTGAACCTATGACGTGTTGAACTTTTTTGTTTTGTATTCCAAGT	6784	A_95_P000061	DW000215
7159	85	19	545	TCTGCCTATTCCCTGTTTTATCTGGAATTAGGAAGCCAAGTTTACTTAAATGTACTAT	6786	A_95_P133222	EB434534
7161	85	21	438	GAATCCACGAAAATGGCCCTATTTCCGTAGTGTGAAATACCTGACAATAGAAGGAG	6790	A_95_P137822	EB680983
7163	85	23	730	CTGCTGGGTGTTTAATGAGCTAAAAAACATCCTTTATTTTTGTTGGCTTATTAAGGTC	6794	A_95_P244422	EH615725
7164	85	24	159	TATAACTGGTTTTTCGTAAGACTCAAACCCTAATATGCCTCATATTTTTCTGTTTCCCC	6796	A_95_P139437	EB443182
7167	85	27	254	TGTATCCTTCTGAATATATGATCCCTCACTATAGCTGAATCAGTTAGCCGCTTATGGT	6802	A_95_P129947	EB429882
7173	85	33	978	ATAACCCATTTGAAATGTATATATCACTAGAAGCAGGTCCCAGGTGTAGCTTTCTTCA	6814	A_95_P206032	TA18418_4097
7177	85	37	329	CTTCTTTTCTCGCCCATGGCTAAATTTGGTGTTCTAAGCTTAAGTAAACGTATGGGGT	6822	A_95_P102792	CV016201
7179	85	39	1376	CCAAGTTTCTTGGGTAAAGTTTGAGGATAATGGAAAATCATGGATTGAGATGTTAAA	6826	A_95_P179592	TA12545_4097
7186	85	46	0	AGAATCTCTTCTGTGAATGCATGTCAGCTTTTATGCGAGCTACTGAGCGATGTTTCAC	6840	A_95_P309738	A_95_P309738
7188	85	48	845	ATTGAGACATGCAGTATGCAGTTACCTTGGATGTCTACCCCACGGTTTTCTTCAGCTT	6844	A_95_P310253	FG172986
7190	85	50	1235	TGGATAAACAAGATAAGCGTCGATGGGCTCTTCACAGATTTCACAGGCAGCTTCACC	6848	A_95_P011956	TA14869_4097

7193	85	53	456	TTGAGAAATTAGTTACTGGTTTTTCTATGTTGCGTCTCCTTGGAATTGCAGTTTTCTCG	6854	A_95_P028081	TA13900_4097
7199	85	59	570	ACTCAAAACAACTCGATTGGAGTGTTTTGTTTACCATGTACTGGAATTTGTACAGTTT	6865	A_95_P192322	EB678300
7202	85	62	520	CACAAATTTGCTTGTGCTCTTTTAGTTGTCAGTATAGGGAATAATGTTCTAGGCAAAG	6871	A_95_P026176	BP528510
7211	85	71	848	ATACAAAGAAGCACTCATCACCTTTTTGATCCTGATGAGTTGTTGACGGTTGCTTTTG	6889	A_95_P126322	EB425654
7214	85	74	719	TTGAAGGGCTGAAGCTGGATGACATAGAAACTGGCATATACAATGTACACTGTCTGC	6895	A_95_P144162	EB447314
7215	85	75	775	CTTGAGCTCTAGAGGGAGAGAGCTAAAGATGTCATCTTTTTCTCTGGGAGTATTAGG	6897	A_95_P302118	FG172161
7220	85	80	727	GTTGCTGCATAATAGTTATTACTGGAGTATTAGGTTGTATTTCCTCTTCCAAGTTCTCT	6906	A_95_P153442	EB683711
7221	85	81	2010	GGAGAGGCTTGTATTGTACAGAATTTTCTACAAGTAAACAAGATTCTAGTGCTTGTT	6908	A_95_P028036	EF520286
7222	85	82	411	TGTGACACCAGGTCTTGGCACACACACTAGTAGAATTTTGGATTTAATTATTTTCTTG	6910	A_95_P049796	BP132249
7225	85	85	712	CAGTTCTATTCCAGCCTTTATTTGGCTTACGCTCATTTCATTGTTGTCAAGGTATTTGC	6916	A_95_P216012	EB679884
7227	86	2	762	GTAGCACTTAATACTTGTGGACATGTCTTCTGCAAGAAGTTTTGCGTGGGTCTGTGA	6754	A_95_P252654	FG640566
7228	86	3	823	TCTAATTTATGCCCGTGTAGTCAAGGCCAACACTGGAATGAACCCTGAGCTATCTTGC	6756	A_95_P011761	EB441379
7238	86	13	141	TTTCACTGGTCTTAAGTCAGCTGCCTCATTCCCTGTTTCAAGGAAGCAACAACTTGCC	6775	A_95_P113007	CV020957
7253	86	28	776	GTAGCAAATTTTGATGACATTCTTCTCAACTCTGATGCATTTATGGTGGCAAGAGGTG	6805	A_95_P192257	Z29492
7255	86	30	900	GAGTTCGATGGAAAATTGTCTCTGATGGATAAAACACCAGAAATGCACTTGCAATGT	6809	A_95_P225552	DV161327
7257	86	32	890	TCCATATGGCCTGTCAAATTATATTATTGATACCGACTCTCTAAAATCCTGCTTTTCAG	6813	A_95_P011751	EB681792
7260	86	35	951	GCTATAATTTGTTATGGCCCCGTGCAACATGTATGACATTCCGCTTAAATATTTCTCTG	6819	A_95_P008271	TA12344_4097
7262	86	37	1261	GTGAATGAGTCTTTTTGACATGGAAGAAGTGGTTGATGTTAGTAAGAAATAGAAAG	6823	A_95_P026451	TA17910_4097
7263	86	38	771	TGAGAGGGAGCTTTGCTTAGGTAAGTTCCTTCAGTCAACTTCATTTAAAGTGAGCTTT	6825	A_95_P126542	EB425874
7265	86	40	771	TGTATGATAAATATGCTATTGAAGATAGGCTTCTTACTGTCCGCCATTAGCAACTGCT	6829	A_95_P205797	TA18367_4097
7266	86	41	533	GAAGAAACAAATCTTCTAGAGGGCCGGGATATTCACATTCATTTTCCCGCTGGAGCT	6831	A_95_P051821	BP132749
7267	86	42	1036	CCTACCTTTTGTATTTTCAGTATGTATACTCCACATGAAATGAGTGATTACTGATCTTC	6833	A_95_P027981	TA16733_4097
7270	86	45	665	GATTGCTTTGACAGGTTTTATTGGTGTTTCCAAGTACACGTCCAAGGAACATAATTTT	6839	A_95_P179742	TA12575_4097
7272	86	47	2491	ATTGTCGGCTTGCTTGTACTAGTCTTTTGTTAGTGTACTACCTTTCATGTTCTGCGGAA	6843	A_95_P013486	X83730
7275	86	50	210	ATAGCCCCAATTCTTGCTGAGATTGCTAAAAAGATGCCCCATGTTAATATTCCTCAAG	6849	A_95_P108277	CV018765
7276	86	51	491	CTTGTCTTGTCTAGTAGTGTTGAGTATTTTAGGCGGTTTAAGATTTTGTCAAGTCTTTT	6851	A_95_P129847	EB429796
7280	86	55	289	TATTCCGCACGCCTCAGCATTCTTAGCTTTTGGCGTATTTACTTTGCCTTGGATTATTG	6858	A_95_P112107	TA12957_4097
7294	86	69	780	CAAACGTTCTTTCCTCGCTGCATGTAACATCTTTACTTCTGAATCAATTTGATTGAAGA	6886	A_95_P182302	TA13183_4097
7296	86	71	406	AACTGTACATTATGCTCAAAGATATGTTCCAACACATACTCAACAGTACTCTCTATCTC	6890	A_95_P100723	BP535496
7297	86	72	388	GTACTTATGTACCACTGTGAATGATTAATGATTCTGATTCCGACACAATTTATCCCTGT	6892	A_95_P196682	TA16391_4097
7300	86	75	264	GTTTACTCCCTCTACGCCCCCAAGGTCAAGAGCGTCATGGAATTGAACTAGTAACTTA	6898	A_95_P112727	FS383836
7302	86	77	578	GCTCAACAATTTCTACTCTACAAGCTACTTGTACCTACTCAAATTTTAACCTGTGAAGT	6901	A_95_P276813	FG639951
7309	86	84	816	AAGGTACAAGATAACATTGACTATGACCGCATTACTAGTTCGTGTGATGGATACACT	6915	A_95_P139227	EB442966
7314	87	4	319	CAGATTGTTACCGTGATGTTACCTTTTGTGGATCTGTATTTTACGAAAATTATCTGGG	6924	A_95_P161532	EH620238

7315	87	5	525	CTACTGCAAATTTAACAGTGGATATGAATGTTGACCCTAAGACATTTCTCAGTCTTTT	6926	A_95_P124712	DW004497
7321	87	11	793	TTGTGTACGACATCTTCTGGGTCTTTTTAACCCAGTGATGGTTAGCGTTGCTAAATCTT	6937	A_95_P200417	TA17204_4097
7322	87	12	900	GATAGCCTGTTGACGTGGCATGCATTCCAGAAAATTAGGGACGTGTACTTTGGAAAA	6939	A_95_P185302	TA13882_4097
7328	87	18	433	TGGCGACGTGATTTTGAATTCTCTACGGTTCCCTTTCTTCAGATTTGCATATTTTGTGC	6951	A_95_P077250	BP527198
7330	87	20	793	CAGCTGCAGCAGTGAATGATGAAGTCACGAATTCTGTACGTATACATTTGAGAAAGA	6955	A_95_P236694	FG140148
7332	87	22	851	CATGATGAGTCTCTAAAATGGTTGACGGAGGTGTCATTTGCATTGATTGGCTTTGAC	6959	A_95_P262736	DV159797
7334	87	24	678	CAGATTGGGATGAGCAGAGGGCTGAGTGGTTGAAAAAGAATCTTAATTTTCCTAATT	6963	A_95_P070930	FG132816
7335	87	25	806	CAGTTCCCCTCCCTTAGGTTCACAGCCAACGAAAAGTTTTTGTTTGTAGGTAATTGAA	6965	A_95_P116982	DV159759
7337	87	27	739	GCAACCGTTAGTTTCTTTCTTAACATGTTTTGTGCTGGATAGTTCACTTTGTCTTTTGT	6969	A_95_P117977	DV160995
7338	87	28	458	GTGATGTGATGTGGGAGGAAGTTATCATCTAGTTGTTAGGAATGAAATGTTAATTAG	6971	A_95_P114097	CV021441
7340	87	30	701	AGGTCCTAATCATGGTGGAGTGTTTCTTCTAGAGTTGTAAAATACTGGTTTGCCTGTT	6975	A_95_P162897	EH621890
7341	87	31	1401	GGGGTTTGGAACTGATTATGTCTTTGCTATTGTGTATTCATTCAGATTTTGGTATGAAA	6977	A_95_P184622	TA13734_4097
7348	87	38	0	TCATCAACAACTGCAACTGAACTTTGCTCATATGCGCGAGAGTATGGCATCCAGAGA	6989	A_95_P285598	A_95_P285598
7357	87	47	1329	ATCTTAAAGAAGATGGGAAGGGATACACCTAGGCAAGGTGGTCCAGAAAAGACGGT	7007	A_95_P238044	AY553214
7359	87	49	407	AAGGAGCCATTTTGTCTTCACTCTGAGAATTTCGGGTGTGAATGAGAATACCGAGCA	7011	A_95_P006876	NP916877
7361	87	51	465	GTTTCTTCTCTCTTGAAGCTACTAGGTTCTCCTGATGATGCCAGCCTTAGATTTCTGAG	7015	A_95_P038066	BP129169
7365	87	55	970	TGAAGAATTCCCTATGACACAGGAAAATTGCTTTCAGCGGTTCAATCTACCCGAGCCT	7023	A_95_P214522	TA20280_4097
7368	87	58	835	ATGAGACATTCCGCAACTTCAAGATTCGAGTTGCCGATTACATACGCTATCGGAGGAT	7029	A_95_P128917	EB428663
7377	87	67	766	CTGTTCATTGTTGGGGTTTTGTTGAACCATGTCTACGGAGACTGTAACTTTTTATTTAT	3665	A_95_P000026	EB439159
7378	87	68	797	CTGATAACGTTGGACATCCCAAAGATGTTGAAGAGGCTGCTGGTGATAAAGTAGCT	7047	A_95_P230589	DV158076
7381	87	71	418	CTTGTAAAGGGACGAAACCTTTATAAGTTGAAGACTTTCAGACGGGTGAACCCGCAG	7053	A_95_P222532	TA22054_4097
7382	87	72	686	CCATAATTTGCTTAGCCATGTTTTAATGTGTACCTTCTAAATGAGGTCATGTCCCATTT	7055	A_95_P129382	EB429240
7385	87	75	392	CTCCAAGCATCTCAGGTCTCTCTTTTCTCTCTCGTATATCAATATACTTACTGGTACTTC	7061	A_95_P094543	FS379071
7387	87	77	763	TGAAGAGTGTGTTTTTCATCCAAGTGAATTTTACCCTGTCTGGACACTGGAACCTGCC	7065	A_95_P133037	EB434087
7390	87	80	1268	CAATACCAGCAAGCGGATTGATGTATTTTGGAGAAGAAATCAGAGAAATCTTGTTGT	7071	A_95_P009411	TA12015_4097
7394	87	84	885	ATTTCCACAAGGTCACTGCTCCATTTTTGACAGTGCACGGGACATCTGATGGTGTTAC	7079	A_95_P002376	TA14115_4097
7398	88	3	614	TACCAGTAGTATAGTCAAAACCGCAGGCAGCAATTTCTCGAAAAAATGGTTTTGCATT	6923	A_95_P141157	TA15893_4097
7405	88	10	552	TGAAACTTTGATTAATGTGAGCTATTATGTGAATGTTTTTATAGAGGCGGGTGGATGT	6936	A_95_P122817	FG134826
7413	88	18	612	TAGGGCTGTTTAACAGAGTTTGGGGATGAAACAACTCTGAAATCTAAAGCTTGCTTT	6952	A_95_P250422	EB683598
7414	88	19	368	ATGTAGTCTCCAGTTGTGTTTTAGTTCGATGAATGTACTCACCAAAAACTCTATTTGT	6954	A_95_P265971	BP532939
7416	88	21	557	GCGCCCTTCTCTATCATTTGTGAATTCGATAGAATATCAATCAGGTAGACAGACTTTG	6958	A_95_P025486	FG639535
7418	88	23	1389	TTTTAGCTTACCAAGACAGTTTGTTTCTTCTCCCTCGCTGTAGGGTGGTGGGAGAGAT	6962	A_95_P203627	TA17893_4097
7427	88	32	576	CCTTAATGTTCATTGAGCATCTCATCACCAACGCTCTGATGGATAAGATGAATGGCAA	6980	A_95_P068175	BP137068
7434	88	39	616	GCTTTTAACAATCCCGAGAGAGCTGTTGAATACTTGTACTCTGGTATTCCCGAGACAG	6992	A_95_P190177	FG160178

7438	88	43	816	GACCATTTAAGACAAGATGGTCTATTACATACAACATGTGGAACTCCTGCATATGTA	7000	A_95_P243107	DW000648
7440	88	45	958	TAGATGTATGATGTGACTCCTTCAGAAAATAATCTAAAGATGGTTTTGTACCTTTTGC	7004	A_95_P177282	TA11933_4097
7444	88	49	865	ATCATGATTCTGGGAAGTGAAGCTCTCTGAACAAAGGAAAAAAGATGCTGAGAATT	7012	A_95_P277193	FG146297
7446	88	51	54	CGTCTTCTTTCACCACAAGCGTCTTTGGAAAATAAAAGTCCTCATATTCCTTCACCACG	7016	A_95_P034618	FG642309
7448	88	53	0	TCTGGGCATGTCGAACGGAGCAACTCCTTTACAATAACTAGCAATTTGATATATATA	7020	A_95_P030116	A_95_P030116
7455	88	60	878	ATCATGCAGTGTTCCAAAGACAAATGGTAAAGAGGACTGGAGTTGTGCGCTTTGCC	7034	A_95_P292653	EB427898
7464	88	69	636	TTAGCCTATACTCTTGGTCCTTTAACCCAGCCCAGTCGCTGTTAAATGATGAGGTTTG	7050	A_95_P300378	FG636919
7466	88	71	522	AAGTTGCTGGTTTATTTGTTTATACCGGCTTGTTTCAACCTGTGTCGAAGCGAGGAAT	7054	A_95_P125342	DW005134
7469	88	74	589	CTCTCTCAGAAATGAACAAAAGCAGAGTTAGATTTGCTAGCTGATTTCATCACCTTT	7060	A_95_P304358	FG638642
7475	88	80	611	GTTTTATCAGTTGTGCTGGTGTTGCAATAGCAAACTTCTCTAGTGTTGAAGAAAGTTA	7072	A_95_P031066	TA18216_4097
7479	88	84	781	CGAATATACTGCAACGAATCCGATTATCGGTTTTCAATAATGAAATCCATTTTCTTCT	7080	A_95_P011861	EB677971
7481	89	1	188	TACTCTCCAACCACTACTCCAGCTAGCATGGAGAAGGATATCAAGAAACTTTTGGGG	7082	A_95_P034339	AJ718476
7482	89	2	368	CTTCCCTCCTTAGCTTGACCGGCAATAAATTGGATTTTGATTAATGTTATATGACAGT	7084	A_95_P301693	FG635768
7483	89	3	642	AAACTATCAGAACCTATAACAGGGCAGACTATAGCAAAATGGGCGTTGCTGGGCAT	7086	A_95_P062270	BP135474
7484	89	4	610	GCTGCTCCCCCGGATGGTTGTTTAATTTATTGAAATTTCATACATTCTTTTAAAATTGC	7088	A_95_P016811	TA14193_4097
7487	89	7	1309	TAGAACCAACAAAGACGATGAAATTCATGAGAATAATACTTCAGGAGCAAAGCTTC	7094	A_95_P176502	Z48603
7488	89	8	857	AGATTTACCAGATGCTGGAAAAGTATATATTTTTGCCTGATCTACTTCCTGCAACCTT	7096	A_95_P232804	EB677793
7490	89	10	308	GCATGATCATGTTTGTGCAACTCATAGGTTACCTGTATAGTCCTGTTGTATTATTTGA	7100	A_95_P107517	CV018414
7493	89	13	1160	GAGGACATCAGCTCTTTGTTTGACCTCTCAACCTTGTTATCTCAATGTCACCAATTTTA	7106	A_95_P139322	TA11997_4097
7496	89	16	851	CCCTACATTTACCACAGCAAGGCTAGCAATCCATTTGTAAACTTGAAGAAAGAGTAC	7112	A_95_P218542	TA21200_4097
7501	89	21	642	AACGAAATACTTGGTGGCGCCTATGGCGTCTTTCTTATATTCACTGTATTTTACGATT	7120	A_95_P048081	BP131816
7502	89	22	437	TACGGTGAAGGAATCTAACAATGTGCAAGATGCGGACAATCCCCTCTAAAAGTCCAC	7122	A_95_P113307	CV021104
7504	89	24	750	TTGGAGCTTAGTATTAGGATTGTGGTGCGTTAGAAGACTTGTGCCTTGTTATTATTCT	7126	A_95_P135407	TA14351_4097
7508	89	28	734	CTAGTTGTCTGGGTTTACATGTTAGTCCATAACAGTACAAGTTAACTACGATTTGAGT	7134	A_95_P149707	EB679630
7510	89	30	456	CAATGGTTGGCTTCTGATGCACCTCCTTATGAGTTATCAGTTTCACTTGATGGTTGTA	7138	A_95_P052251	FG639495
7513	89	33	568	GCTTGATCATACATGTTCCTCCACTTTGGATATTTAATTATCATATACTCCCTCCGTTC	7143	A_95_P006696	TA15575_4097
7514	89	34	738	ACATGTTTCACTTGCCGTGTATAGATACATGGCTGTTGAAACATGGCTCGTGCCCAAT	7145	A_95_P295023	EB443550
7520	89	40	846	CTTGGTACAAGCGGAACTAAGGTCCATAGCAATGTTCAATCTTCAAACTATTTTTCAA	7157	A_95_P008896	DV159843
7524	89	44	964	GCATCAAGAGAAAGATTATCCCACATATTTTCAGTATACGAACATCACATGAATGAT	7165	A_95_P010471	TA17261_4097
7526	89	46	525	AGAGTTGATTTTCTTTCTGGCCCAAGTCCTTGGCATATTAACATACCAGGGGTTTCTT	7169	A_95_P074775	BP526555
7527	89	47	795	TTAAGCGCGTGAAAGAGGCTTCCAGATTCGCGATTTGAACATATCCGGATACCACAA	7171	A_95_P163102	EH622089
7533	89	53	685	CTATTATCAATCAATGAAACCCCTTGTTTCGATTTTAAAACAACCCACATGACGACAC	7183	A_95_P019151	TA12698_4097
7538	89	58	791	ATCTTCCTCATGCACTATAGCCCCCTTCGTGGTATCAGGTATTTGCATCCTTTCAAGTT	7193	A_95_P117502	DV160431
7541	89	61	489	TTGAAAGCAGCTTTTTCAAGTGTCAGTAGCGGGACGTTCTGTCAATCGGGGAAGGT	7199	A_95_P275673	AM803681

7544	89	64	1155	TTTGACTGATGTTGGCCATATTCACTGGGTAAATGGCAGTTACTGCCTCACTTTTTCA	7205	A_95_P185202	TA13862_4097
7549	89	69	489	GATTTTATATCATGTCTACGTACGGAGTGATGTTGCAGCGGGATCAGATATTCCCGT	7215	A_95_P051196	BP132586
7550	89	70	724	CTAGTAGTGGCGTATGAGGATGTTTTAGTTCTCATTTTGGCTATCAGATCAATTCAAT	7217	A_95_P190007	TA14912_4097
7551	89	71	807	CCTATAGCTTTTTGTTAGGATAAAAACGTTGAAGACTTTTAAAGTGGTCAGGTATGT	7219	A_95_P009201	DV162419
7556	89	76	893	TTTATGTGGGTAATCTTGCTCCTCTGGTGACACAACTCGATCTCCATCGCCACTTTTAT	7229	A_95_P259026	DW001309
7563	89	83	1044	TAATTGAGATTAAGGTTCTCTCCCCGTAATGATTTGGTTAAAGTTGGTGATGTTTCTC	7242	A_95_P178522	TA12270_4097
7566	90	1	679	AACAGTCAAACTATGTGGGTAGTCCTGAACTTGATGCGAGCTCTCAAATCTATCTCTA	7083	A_95_P029386	TA13901_4097
7571	90	6	832	AAAGCAATTAACTGGGATCGCGCTGAGATGTAGAAGTCTTCCAGTCTGCAGCAGATT	7093	A_95_P243067	EB451275
7572	90	7	1015	TGTAATCAGTGTGAGAGAGATCACCAAGGACTTTGTTGGTGGGCAATGTTTAGAGT	7095	A_95_P014841	TA13035_4097
7575	90	10	646	AGTGTATAAACAAGTTTTTGCTCGAGGTCATTGAGTTGATCATCTGTCTGAATAAGT	7101	A_95_P024281	DW004487
7578	90	13	1161	CAAATGGGAGGACATCAGCTCTTTGTTTGATCTCTCAAACTTATTATCTTAAATCACC	7107	A_95_P005121	TA11995_4097
7579	90	14	132	TTGGCTATTTTAGTACTGTGTTGATATGATTGAGTCCTGTTTTCCAGGTTGAGATTGC	7109	A_95_P150750	EB680873
7581	90	16	850	GTAGGCTAGCTTGTTGTCTTTGGTTTAACCCAGCAGTTAAAGTGACCTCAAACGAAA	7113	A_95_P199317	TA16969_4097
7586	90	21	845	GGCTTCGCTCCCTTTGCTAAATAACTCATTTTCAATGCCAATAGTTGTTCATATGTCAT	7121	A_95_P116992	DV159764
7588	90	23	551	ATTACTCAGCCAAACAATTGAATTGCACTGCTTGCAAAAGCCCCTCTGGGATGTTATC	7125	A_95_P212437	TA19836_4097
7589	90	24	856	TTTTGATCCGCTGCCGTCATGTCAGTCAATGATATTGTAAGAGCAGACTGCACTTAAG	7127	A_95_P310943	FG162423
7590	90	25	918	GTGACTTATGCAACTTTGTAAGGTGTTTGCTGAAGTGATATATCACTCTGTATTTACA	7129	A_95_P181747	TA13053_4097
7593	90	28	925	TCTGATCGGGGGCTTTCGTTAGGACCAGCTTTAAATTACTACTGGGTTTTCTTTATCC	7135	A_95_P230704	DV157855
7601	90	36	847	GTGACTATCATGCTTCTCTTGCACCTAATGAAGGCTATCCTGGAACACCTCCAGTTGT	7150	A_95_P216857	EB441655
7606	90	41	777	TTCACTAAAGCCTGAATTTATTGATATCATCAAGTCCGCAACAGTGAAAACAACTGGT	7160	A_95_P148152	EB677365
7610	90	45	836	GAAAAGTTTTACTGTTCGGTCATGGTTGTTGCGCCAGTTATATGCCCATGTGATTATT	7168	A_95_P208772	EB449346
7613	90	48	678	TCACTCAGTTTCTTTGTTTAATGGAGGCACATTCTCCCTGAGCGAGACCATTCATTTGT	7174	A_95_P288803	FG199314
7614	90	49	153	TTAGGCGCAAGACAGATACTTTTCCATCTTATTTAGCTTCTTTTGAAAAGCTGCTTTG	7176	A_95_P132782	EB433496
7621	90	56	835	CTTGTATTATCCAACTGCAGTGAAATTGTATGAAGGTTGTTTCCATGGTGGTTTAAAG	7190	A_95_P177952	DW002580
7622	90	57	218	GGTAGCTTATGGAAGATGCACCACTGGAATGAGCAACGAAAAGTTAGGTCCATTTT	7192	A_95_P110847	TA12840_4097
7625	90	60	856	TGGATACATGCTTAGTCCGGATCTGCATAAGTTTTGTTTTACATTTATCTGTGTTTTGG	7198	A_95_P241180	DV159117
7627	90	62	773	GACTACTAGTTTTGTTGTTGTGTATCCTAGTAATTCAAGCAATGCTCTGTCTCTTGTAA	7202	A_95_P177532	TA12000_4097
7630	90	65	500	ACAAAAAGCACATATCTACCAAATACTTCCACCTTGTTTGCAAATTTGTTGAGGGGA	7208	A_95_P081860	BP528370
7639	90	74	557	CCAAGTCTGGAAGTGATGTACTTGCAATTTATGGATATAGTAGACAAATACATGTCG	7226	A_95_P024866	TA21691_4097
7641	90	76	1236	GCGTTCGGTGCTTTACCTTCATATGTGAAGCTACTCTTTATCGATTAATTATTTATCCA	7230	A_95_P193667	TA15720_4097
7647	90	82	770	ATCTCATCAGATGCCTCTAAATTTATAAGATGCAGGCTTGCAGAGCATAGCCTACAT	7241	A_95_P298333	FG168498
7649	90	84	0	TTCTTGAGATGGTCATCCGATAGGATGTGCCCATCATATGCAAAAAATATGGGACTT	7245	A_95_P297983	A_95_P297983
7650	90	85	164	GAATAAGAGACTTCTGAATATTCACACCAATTGACAGTTTGTTATGCATGCGTGATG	7247	A_95_P034424	AJ718733
7655	91	5	613	TTGCAAAAGTTTTTCATTGTCCTGAAACTTCTGATTCTATGAGAAGGCCTGAGTTATT	7256	A_95_P153107	EB683431

7656	91	6	537	TTTCCGTTTGAAATTAAGAGAGGGAATCCAACCCGGACTTTCTTCCGCTTTTTACTTG	7258	A_95_P053261	BP133131
7657	91	7	466	TAACTAGATTTGCAGGTGCACTTGGCTGCAAAAAAGGAAAGGCTTGTTAATAATAAG	7260	A_95_P006986	U95924
7659	91	9	585	GCAGCGCTTTTTCCCCTTTATTTGGGATCCCAAATACATCATATAAATACTCTTCTTCTC	7264	A_95_P026046	EB445471
7661	91	11	764	ATGACATCTGCTCTATCTAGCCAGCAACTTTCATCTTCATGTCCTGCAGTTGATGTGG	7268	A_95_P096473	FG153654
7664	91	14	350	GGTTTCCGATGTTAATAACCACTCTCTTTTTGCTTGCATATGCTATTAACGTATGTTCT	7274	A_95_P125897	EB425028
7666	91	16	374	AGTGGTGAAATCGCCTTGATTACATTTTCTGTGTTGGTCTTTCTTTTAGCTTTGTAGAT	7278	A_95_P133312	EB434716
7668	91	18	819	TACGGAATTCGTAGACTACATAGTGAGGTTGGTTTGTAATGAACAATGACTGGTGAT	7282	A_95_P269736	EB426391
7669	91	19	1279	GCATATCTTGGAGATTGATTGGATTTCTATTGTTCCAACTTGTGTATTTCCCAGTCATA	7284	A_95_P197192	TA16509_4097
7672	91	22	606	GCAAAACATCCTACATTTTCCTTCTTTGCTTGGGGGAAGCTTTAAAGAAATTAGGATT	7289	A_95_P212657	TA19882_4097
7677	91	27	1577	TGAGCATGTCTCATTTTTTGACTGCTGGTTCTGCAACTTTGATATGCATTTTGTAGTAT	7299	A_95_P108912	TA11833_4097
7680	91	30	723	TTTACTAAACTTTTGACAAGCCAGCACCATCGCACCTTGACTGGCAAGTTGGACATGT	7305	A_95_P298583	EH623389
7688	91	38	800	ATTAGCCCGAGAAATTATGCCATGTCACCTGGAAGTTATGTTGGATCTGCTTACCCAG	7321	A_95_P021371	DV161271
7691	91	41	776	ATCAGAAGGCAGGCACCTCTAGGATTTGGATAACTAGTGCGATCTGGAAAGAGCTA	7327	A_95_P295743	EB447894
7692	91	42	449	AGGTTAATGAGGTAATTTTTACCAGTAGATGATGAGAATGCTGTAAAAGGAAACAG	7329	A_95_P159687	FG144962
7697	91	47	758	TTGATGAATGCAGTTTCATTATCAGCATTCCTGTGCTGTCGTTTCCGCGAATTAAATG	7338	A_95_P012481	DV160348
7698	91	48	620	ATATGCACCTCATGTAGCATTTCTTACTGCCTTTGCATTGTACTTGTCCTCTGCCGGTT	7340	A_95_P063870	BP135895
7701	91	51	352	AAAGGGTTTCTTTGGGGGTAATTTAGAGGGGAATTTGCTTGGGGGTTTGAACAATT	7346	A_95_P095728	BP533307
7702	91	52	638	TTTTTTGATGATGAAAGGACAGTGTATCATTGCCCGTTCTGCAATTTATGCCGGCTGG	7348	A_95_P137177	EB440893
7707	91	57	724	CCTTAGCCCGTACATATAATAAAGGTGCAGGTTGTAACACCACCTGCCTACTCAAACT	7357	A_95_P025181	EB679218
7712	91	62	271	CATTTGTGCAAGGACATGAATTCCATGGTGAGCAAAAGTGAAACACTACCAACCTTT	7367	A_95_P143462	EB446757
7713	91	63	756	TGGCTGGAAGCAAGCTGCGCAAATTGGATATTAGCTGGTTTTGTAAACTTGTTATAG	7369	A_95_P128372	EB428069
7715	91	65	760	CATGGAGTGTTCTGACTTTTTGCATGAACTATCTGTTTTAAGGGCGTTGAGTGATTCT	7373	A_95_P009216	TA16854_4097
7717	91	67	426	TCTGCACTAATGCTTACATTTAAACTTGGAAGCGTGTTCATATGTCCTTTCATCCTAAA	7377	A_95_P001506	TA19130_4097
7722	91	72	549	CCCCAGATGGACTAATATTTGTTGAAGAACTTAGAGATGAAGAAGATAGAGAATTAG	7386	A_95_P059680	BP134799
7728	91	78	550	GTTCTTTTTCTGGTAGATGTGTTGTTTCTCATGAATATTGGCAGCTAAATATCGGATG	7398	A_95_P035213	BP128407
7732	91	82	794	CAATTTCTACTTTCATCTTTTGTTCAGGATTGTTGTGTATAGTGCAGTTGCTTTCTTTG	7406	A_95_P198647	DV999246
7733	91	83	629	AGTCAGTTGCCTGCAGAAGATTGCCTTTGTGAGATATGCACCAATAGAAAGGGATTT	7408	A_95_P138207	EB441955
7734	91	84	701	GCAGAAGGCCCTGCTAACTGCTTTATATGCTACGAGCCTCTTACCAGTTTGTAGTTTT	7410	A_95_P146082	EB449944
7736	92	1	353	CACAATAGTTCATTATACCTGAGTAAAGAGGTTTTGGCAGTTGTCCTTTTTTGTCTTTC	7249	A_95_P028671	BP531178
7738	92	3	428	GTTCTTAGTAGTTTAAACCAAACGACCCCTTGGATTTATATAGACATGGTCGCATTGA	7253	A_95_P211182	TA19555_4097
7739	92	4	890	TATTCTTTGCTTTCTGGGTGATTGTTCACCTTTACCCCTTCCTCAAAGGTCTCATGGGT	7255	A_95_P187142	DV161313
7746	92	11	479	GGTGGCTGGGTTGAGTATTAGTTGCAAGTTACACTATTGTAGTTCCTCTGTTCTCAAC	7269	A_95_P184327	BP530524
7748	92	13	1194	GAAGCCACTGTGTTGCAGTTGTTAATGGGATATAAAAATAAATCCTTGTATACGATTT	7273	A_95_P016196	TA13049_4097
7750	92	15	754	GACTAATTGTTCAGTGTTACCAAACTAGTGTTGGCAGCATATGTTTACCTTTAGCTTT	7277	A_95_P273681	EH618301

7752	92	17	233	TACCTAGGTCAGTTTCAGTTGTGTCTTTTTTGTACAAGGGATACTTATTTGCTTATCAG	7281	A_95_P098773	BP534635
7756	92	21	492	CCTGTAGACATGACAGATTCTTCAGTCTTTTGCTTTACTTCGCTAGAATTCATTGTTAA	7288	A_95_P122797	DW002756
7757	92	22	778	AAAGAGGATAGAGAAGGCAAAGGTTGCTGTTTTCGTTCAAGGCGTTGATACATCTG	7290	A_95_P139087	EB442787
7759	92	24	802	ACGAGTATAAAGACGGCTCGCTGCATATAAATATGGTAGTGTCTAGTGTTAATACGA	7294	A_95_P188167	EB679714
7764	92	29	317	ACTGATACAATTTCTGTGTATTTCAACCCTTTTAGTATTTTCAGTTCCCCCTTCCCTAG	7304	A_95_P133502	EB435068
7771	92	36	465	CTTTTCCTTATTGCTTGGCTTGCTTAAGAAGTAAACTCAAAAGAACCCCTTTGTATTTA	7318	A_95_P091513	BP531390
7777	92	42	0	ACAGGGAACTGTTTAGTGTATATAGCTCTTACTCAGCTGTTTGACATCTAACTTATCC	7330	A_95_P029646	A_95_P029646
7781	92	46	629	GCACAAATTCACATAAGCTCCCCTCTTTGAGAATTGAAAAACTTCAGTTTCTTGAACC	7337	A_95_P063780	BP135872
7783	92	48	559	GAGAAACCGCGGAGTTTACTGTAGTTTTTCTTCCCGAGCCAGTAGAGCTCGAATTTTT	7341	A_95_P219417	TA21391_4097
7785	92	50	834	TACAGGAAAGATCCAAGAAACTGGAGGATTCATTGACAGCTGCACAGAAGCTTACAT	7345	A_95_P229999	EB438987
7788	92	53	360	TTTAGATATTTGGAGCCTTTGTTCTGCATACAAAGAGCGGGCGGGAATGCTTCCGAA	7351	A_95_P119422	DV162630
7790	92	55	900	GTTCTCTATTGCACTCCCTAAATAGGGTTCTTTTCACCTTTCCCTCACGGTACTTGTAC	7354	A_95_P176613	TA11663_4097
7792	92	57	951	CGCATAGCTGCTGCTCATTGGCTTTTTTCCTTAACAAGGTTTGTGCATACACAGTTTAT	7358	A_95_P223407	TA22245_4097
7794	92	59	826	TGGTAGTTTTATCTTCCCTGGGGCTCAGCATATCACATCGTCACTTCTCTGAAGAAGT	7362	A_95_P247832	FG142227
7797	92	62	568	GGATCCATTTCCTGCTTTCGATGAACCAATGGCAAAGCTCAGAGTTTATAATAACATA	7368	A_95_P291313	FG639427
7798	92	63	482	GTTGTCGTTCTTAAGGTCTCGATATTGTAATTTCTCATTGCAGATTCAAGGAACAAAG	7370	A_95_P004161	TA12412_4097
7800	92	65	629	CTCCATTTATGTATGATTTCAGCTACTTTGTCATGGTACGGAGGTTTGAATTAGGTAA	7374	A_95_P108482	DV999474
7806	92	71	1590	TCTCATTTCTCTGTATTGCATATGGACATGTAAATCTTGGATATATGGTTTTGGCAGCT	7385	A_95_P188147	TA14505_4097
7807	92	72	332	ATAGATCCAAATGTGCTGCTATCACAAATGGAAGATAGCAACTTGGATGATTTTTTCT	7387	A_95_P314428	FG170087
7808	92	73	787	TAAAACCTTGCTCACATCTTTGTCAGGTCATGCGAGTTGGGTTTTGAGTGTGGATGT	7389	A_95_P293243	EB431978
7814	92	79	1309	ATGTACAACTGTGGGGAAGTAACAGTAATATGTACACCAATGGAGCTTTTCCATAAA	7401	A_95_P253784	AB031321
7816	92	81	614	TTTGCTGTAACACAGCCGCAAATTTGCAGATTCTTAGCTGCTATTGTTTTCTTTATAGT	7405	A_95_P271341	EB442156
7818	92	83	868	CTGTGGATATATCTCCTAACCCTGGACGTTCGGACCCCATGTATATAGTATATTCCAG	7409	A_95_P201472	DW000412
7820	92	85	395	AAATAATGTCTATCCATCCGCGAGGATCATCACATTTGTTGAATTGTCATTAGATGTC	7413	A_95_P106577	TA12334_4097
7824	93	4	0	GGGTCTTGTGGGTGAAGTTTGCAAAGAGAAAAAAGTCCTAAATAGTCACTGGATTAT	7420	A_95_P010816	A_95_P010816
7825	93	5	2054	TCCCAGTTTTGTAAAAGCCAAATAATGTTGAGAAGTTTGTACCTTTTGAGGGTCGTTG	7422	A_95_P014831	TA15521_4097
7829	93	9	848	AGAGTACATGCAGCTGTTCGCGATGGCTTACTAGATGTTTCAGCAGAGTTGCTTCTA	7430	A_95_P231689	FG163124
7830	93	10	254	GCTAGCAGTGTGGCCATTGTACTCTATTGTAACAATATGTTTTACAGATAAAACCATT	7432	A_95_P144942	EB448503
7833	93	13	797	AATCTTCTTTGAGGTTTCTGGTTTTTGTTGGCAACACTTGTGATAAAGAATCTATTGG	7438	A_95_P176712	TA11739_4097
7835	93	15	1045	CAAAAATGATGACGGGTACCCTGTATTCTAAGACTTTAGATGTTTCACTTGAGATTTT	7442	A_95_P180627	TA12791_4097
7840	93	20	787	GTGGAACATCAGGATTCTAATCACTTACTTGACAGGTGACATCATTCTCATGGTATTG	7452	A_95_P120337	DW005082
7841	93	21	638	GAATCTGCCCGTTTCCGATACTGAATCCATTCCACATGTTTCTGTGATTTAAGTTTACA	7454	A_95_P178227	EB439272
7842	93	22	722	TATAAAGGCAGCCAATACCACCAGCAAGGGGACTTTCAATGAACTTGATAGGTTATC	7456	A_95_P164717	EH624024
7844	93	24	859	GTGGGCTCTTCAAATTTCATTTTTGAATGCACTTTTGTTGTAAGCCATTCTTCTTGATG	7460	A_95_P265316	EB679991

7845	93	25	566	ACCTGACTGGAGAGGTTGTTTCCTCTTTCCAGTTCAGTGATACTTTAATGCATGGTAA	7462	A_95_P001141	TA15333_4097
7847	93	27	1516	AACAATGTAAGCAAACTCATAGCTCTGCGGTGCGCAAATCTGCTTGCTAGTTTATTTC	7466	A_95_P015926	AY429423
7848	93	28	773	GTGCTAGTCTTGGCAGTACATGTTCATCTTTTTAACAAGTTATTAAACTCGAGAATGT	7467	A_95_P144577	EB448030
7852	93	32	493	AAGCAGATTGTCATGAATGGAGCAATGGGGAAGAACTAGCAAGCATCCTACTTCAG	7475	A_95_P139477	EB443235
7853	93	33	953	CAGTTTTGGACTCGATGTTTCTATTTGCTTAGTGATGCCATTTTTATTATGCGCCTTTT	7477	A_95_P000466	TA12129_4097
7855	93	35	485	CTTGTATGCGTCATTAGCACTTAGTTTGTATGAGCTTTTAGCGTAAATGATCCTTGTT	7481	A_95_P153602	EB683840
7856	93	36	295	ATGGTTAAGCAAAGCACGGTTATGCTCTTGATCGCATGTGATCACGGAGCTCAAGG	7483	A_95_P040816	BP129931
7857	93	37	1114	GTATCAATAGAATTTCTGTATGAATCTTTGCTTTTACATCTGAAGGACGTCGTTCAGT	7485	A_95_P191592	AB281271
7858	93	38	365	AAGGAATTTAAAATGAGCCCTGATGTTTCCGTTCCTGATCATGTACACCTCTTTAAGA	7487	A_95_P114242	CV021514
7859	93	39	279	AGCTCAGTTGTTTTGGTAATGTTTGTGTCCATGTCGGTCGAGTAATTTTGGTATTATT	7489	A_95_P100933	BQ842950
7860	93	40	674	ACAAAGTTGCTCGAGAATGGCTTTTTGATGATTAACATGTTGAAATTTTCAGTGATTG	7491	A_95_P273151	EB681910
7861	93	41	451	CTGTCCTAGTGTGTTGGGCGTTCTTCTTCTTCTTTTCGCCTTTATGTGACATTGTATCT	7493	A_95_P290363	FG635220
7867	93	47	547	GATTCCTAAACGACTATTGATCTACTTCTATTTGGTTTACTGCGATGCAGAAGAACAA	7505	A_95_P028376	EH618209
7869	93	49	805	CACATCTCCAGCCTTAGCTAGTGTGTATAGTAATAGGTTTTTTCTTCTCGTTTCATTCT	7509	A_95_P014571	TC47385
7872	93	52	722	ATAGCTGATTTCTGTTATATCATCCAAAGCGTCGAATCATATTGCCTCTGTGTTATTTA	7515	A_95_P214063	TA20180_4097
7874	93	54	717	CGTGTCTTGAAATATAACCTAATGTCCAGTTACCCTTTTAGATGCAAAGTTAGAATTT	7519	A_95_P135427	EB438874
7881	93	61	765	TTTGCCTATCTCCAAGATATACAGAAAGTACTTCCAGCACTTACTAGGAGAAGTGGT	7533	A_95_P296203	EB450783
7884	93	64	690	TGTTATTTATCAGTGGATAGGTGTGATTTGTAATGTGTGGCCTACGCTGCATTGCCG	7539	A_95_P192252	FG150164
7885	93	65	705	CATGTTATATTGGGTGTAGATCCAAGAAGCTCCTTTTGCCTAGTTCTTATGAGTTAAT	7541	A_95_P162287	EH621216
7889	93	69	479	AGTTCTTGCACTTACATACTATCATGCTGCTGACGTTTCTTTCCTGATTTTGGTCTGTG	7548	A_95_P005911	FS407121
7894	93	74	655	AGAGAAAATAATTCATGGGAAGCCATCTGGTATTGACAACACAGTGAGCACGTATG	7558	A_95_P136597	FG134879
7895	93	75	5	TTTTGAGCTAAGTTTTTGTTGGAAATGGCGGAGTAGTGAAGCCCTAGCTTCCGATCT	7560	A_95_P046091	FG139803
7897	93	77	482	ATGTGAATGCTATTGTTGCTTGGCTTCAAAGAAGAAAGTTTACTTGAATGAGTGTCG	7564	A_95_P023336	TA13918_4097
7900	93	80	1168	GATATTCCAGTAGACAATAGACGGAGATCAGTTATTGCATTTTTGAGTGTTAATGTG	7570	A_95_P219542	TA21418_4097
7901	93	81	635	TTGCCATAAATGTGATCATATCCAGTTCGTCATGTTTGTCAGACAGAATGTGAAACAT	7572	A_95_P015391	EB439146
7908	94	3	880	GAAAGGACTTATGTTATGCTATTCTGTAATTTTGGTCACTTTCTACTCTGCTTCTGTTT	7419	A_95_P218502	TA21190_4097
7909	94	4	515	GTTGGTATGGTTTTGGTTTAGGAATCATTATGGATTTACTGCTATCTGAGAAAGTTTT	7421	A_95_P016886	EH619999
7920	94	15	352	GTTGTAGAAGCATCTTACTGATCCCTGAACAATTTTGTAGATTCAGGTCAAATATAGT	7443	A_95_P308683	FG643244
7921	94	16	832	GCTATACACATGATTTAGTATAGACACTTGTTCATGATGTGCTTGGTTTGAAGATTGA	7445	A_95_P309788	FG172993
7922	94	17	752	ATGACTCTTATAGGGAGAATGCTCGATATCTTGGCAGTGGAAGGGATCATGGGTAT	7447	A_95_P148062	EB677243
7924	94	19	704	TGTGCACCATCCTTTATTCATGTTACGGACATTTTCTTGGATTAATACATCACTTAGAA	7451	A_95_P256339	FG635761
7925	94	20	2800	ACGACCAAGAAGTTGCTGATTGCATGCAGCCTTCGTAATTTTACAGGGGTGAGATTG	7453	A_95_P034673	AY219234
7926	94	21	711	TTTGTGCTAATGTTGCAGTAGCTCTTCAAATTTGGTCTTATGAGGTATTATAGAACGG	7455	A_95_P119367	DV162534
7928	94	23	709	TGTCAACCTTTGTTCTTGTGTAAAAGTCTGTACATGGTTTTGATATCTCTTTCCTAAGC	7459	A_95_P149667	EB679586

7929	94	24	1062	TGTGCACTGGATATATCAAATACATCTGAAGTGAAACCCAACAATGGTAATCAAGCT	7461	A_95_P009101	AB119470
7930	94	25	221	CCAAGCCCAAGTCCTGAACTACCTTTTCAATTAATGTTCTAATGGTTAAAAGGAGTTA	7463	A_95_P004291	EH616725
7936	94	31	796	TATATGTTGCTTGCTGGAAATGCACCACCTGTTACGCCAAGTGCAACATCTGCTCTAT	7474	A_95_P292923	FG159197
7937	94	32	425	TGTGTAGCAAGAAATAATCTTTTGGCTCTTCAAGCATCTCCCCGGTCTTTCTGCTTGA	7476	A_95_P308958	FG644183
7938	94	33	569	AGGCAAAATTGGTTTTGGGTTGTGTTACTGTTGCACCCCGCAATATTACGTCAATATT	7478	A_95_P182652	TA13269_4097
7939	94	34	74	GAAAAGGGTGAAAAATCAGAAATTGGAGAAAAAGGTTCTAGGGTTCTTTTCAGTTT	7480	A_95_P097453	FG624638
7941	94	36	828	AAATGAAAGATTCGTGAGCTCACAGAACAATCTGCACCATCATGCTGCTTTTCCAGA	7484	A_95_P298348	FG159026
7942	94	37	384	AGACATCTGCACAAGAGTGACTTGTAATGTTCTTAGCATTCTATAGTAATTTAGCAG	7486	A_95_P076640	BP527040
7945	94	40	1313	TCTGCCCTTACAGTTTGTTGCTGATTAGGCATTTGAAATGTTGCCTTAATTTTTGGAG	7492	A_95_P191487	TA15247_4097
7946	94	41	350	ATTTAACCATATCAGGAGAAGATGGTCAAAACACAGGCAACTTTATCACGGACCGAA	7494	A_95_P105472	CV017477
7950	94	45	468	CTCATCTGAATTTGGTGGCTCCTTATGTAATGAACATCTTAGAGGATTCTATGATCTC	7502	A_95_P180137	TA12669_4097
7951	94	46	466	TGATATACTTACCACTGTTCATGTGGTGATTTGATAACGTGATTAGGTGCATAATCAC	7504	A_95_P024976	FS390471
7952	94	47	652	CTCTATTATCTCTTTCGCGTGTCCAATTTTGGTGCTTGGATATTTGTTCTTGTTAGCTA	7506	A_95_P141467	EB445181
7953	94	48	907	AAGGGTGTACCTGATAAGGGCATCTGTTTTGCTCCTTGTTTGGATTAATATTTAAAAC	7508	A_95_P004086	TA12324_4097
7954	94	49	432	GTTCTGAATATCTTTTGTAGTGTCCAATGCAGAATAACTCATAATTTTGCCTAGCGGC	7510	A_95_P276788	AM841116
7958	94	53	727	ACAAGGGGTGTGATGTAGGCAACCTACCCTTATGGTTGAAGTATTAGTGGTTGATTC	7518	A_95_P147667	EB452184
7961	94	56	138	CCTGTGTTGTACGTACGCCTTTGGAACATTTTGGCTTAATTTAATACAGTGGTATCTC	7524	A_95_P098513	BP534515
7964	94	59	866	GCTTTTGCGCTTGTATAATCTACTATGTCTATTTGTGCTGCTGTTTGTATCTTAAAGCT	7530	A_95_P182797	DW000146
7965	94	60	128	AGGTGTTTTTCCTTTGGTCAGTTTTGTTACAAGGTCAAACATTTAAGCACGTACAAGA	7532	A_95_P214367	TA20249_4097
7968	94	63	70	ACAGTGATCCTTATGTTGTTGTCACCATGGGTGAACAGCGAGTGAAGACTCAGTTGT	7538	A_95_P109022	CV019112
7970	94	65	265	GGTATGTACATCCAAAGCATTCCACTGACATGAAATAACAAAATCAGAAATAGATGG	7542	A_95_P158667	EH616555
7971	94	66	710	GATTACTTGTTTTCTCGGTCACGGACTTGCTGTTATTGGAGTGATTGAATTTGAATTT	7544	A_95_P115797	DV158153
7977	94	72	315	GCGTAGGGGTATTCATTGGTTGGTTTAATATAGTCGGTTTTAAGATGTTATACCAAT	7555	A_95_P030611	BP527351
7978	94	73	686	CTACTGATTAATGGCGATACTAGGCTTCACAAAGATGTTCACTTGTAATTGTGACTAG	7557	A_95_P135792	DV999689
7979	94	74	689	AAAGAGAATGACCAGCTTGTATATAGATTCTGTGCCGTATGAAATCTGCCCTTTCTAT	7559	A_95_P213332	TA20024_4097
7980	94	75	375	TCACCTTTGTAAACCACCAGCACACTAGCGTTGATGAATGATTGAAAGCTTTAGCTTT	7561	A_95_P142797	EB446224
7981	94	76	635	TTTTATGCTTTTGTAGAAGAGGGAGCCTTCCTCTATTGGAACGCATTATGGTACCCTG	7563	A_95_P028276	TA18172_4097
7982	94	77	845	AGCATCTGGAAAATGAAATTTGTGGTGATGGACATTGGAGATGCATATGACATACTT	7565	A_95_P015661	TA15151_4097
7987	94	82	622	ATACTGGTTGTTGCCAAATTTCCAAATATGCACAAGGTTCGTATTTTCGGGATAAATG	7575	A_95_P306178	FG634510
7992	95	2	350	TTGGTACTCGATTGCGTCGAGTTTTACATAAATAGGCAGTGTATTCAGTTGGCCTTCT	7584	A_95_P161752	EH620373
7994	95	4	818	GCGTCTAATCTAGGGGTCTGAACTATATAATTATGTTGTAATATCTTGGTGTTATTGA	7588	A_95_P272746	EB677863
7996	95	6	766	TATGAAAGTAAATGTTGAAGTGGAGAAGAGGCTTTGTTTGGCTAGTAATGCTCTCTG	7592	A_95_P221617	EH622008
7997	95	7	384	TATGTCGATCAGAATTGGCAATGAATTCAATTAGATGCACTATTGTCTTGTTAACGTC	7594	A_95_P163097	EH622087
7998	95	8	350	GTCAAAGGATAAATTCAATGCAGGTCTTCGATCAGCGCTCTTGTTGGGAGCTACAGG	7596	A_95_P277213	FG625263

7999	95	9	1501	CCCCGTCTGTAATTCTTGTAAAATTTGTGTATACTTTTACGATGTATAGCAGATTGGT	7598	A_95_P239399	AY220484
8002	95	12	1411	CCAGTATCAAACAATCAGATAGTGCCAGTGTATGGTATAAATGAATATAGATCTCTCT	7604	A_95_P018926	TA12620_4097
8004	95	14	260	ATGCTTGTTCTTATTGTTGTTTTTCTTGTGTGTATGTATCGTGGCGTAATACAGGTTGA	7607	A_95_P210197	TA19348_4097
8013	95	23	853	AACTCGATTATGTCCCTTCAACAATCATGGCTCTTGAAGAGGTTGTGAAAGCTGCACA	7625	A_95_P258096	EB431820
8016	95	26	812	TAGATCTGGATTCTTTGGTGCGAGAGAGTTTCAGATCTATTCTCTCAGCGAGCTAGT	7631	A_95_P229989	FG163770
8017	95	27	73	GAGTGATCTCTTTGTCCTGTTGGTTTGTTTGAGATTGAATTATAACATGTAGCTGGATT	7633	A_95_P138757	EB442482
8019	95	29	549	AGTCCCTAACTTTGTACAGAGCACACATTCCAATTTCTGAATTATACTGAAACATAAGT	7637	A_95_P154077	EB684241
8021	95	31	865	CAGTCATCAATTTTGGCAATATTATAGCTTCGGTATTCAGACTTCAGTCTCTGTGTGCC	7641	A_95_P186292	EB451332
8022	95	32	626	CACTCTTTCTCTATGATAAGAGTGAGCTTGTTGTAAGTGCATGTGATCTTATTTATGAT	7643	A_95_P026141	EH615198
8024	95	34	977	GTTGAGGACCAACGGTCATAGCCACATTTGACCTGTTGTCTTCTAGCCCCATTTTTGAA	7647	A_95_P031701	TC76477
8025	95	35	405	GGAGGAATGGTGCTAGCCGAGGAGGAGCTCCAAAACATTATATTTATCTTTGTTCTTT	7649	A_95_P092783	BP531969
8026	95	36	851	GTTTAGTATGATGTCTTAAGACTTTGTTAATCATTATCAGCTTTCCTTCACTGGTTCCA	7651	A_95_P178212	DV158570
8028	95	38	903	CTGATTGGGCCCTCTCTGGTTTCATTTGCTTTATGATTAATGACTGAAAGATCCAGTT	7655	A_95_P213947	AY029330
8032	95	42	573	TGATGGACATTTGTTCTGCTAATTACAAGTCGGACGTTGGAAGTGTAAGCGGTTTTGT	7663	A_95_P063390	BP135770
8033	95	43	776	CGAGTTGTAGTCTTCCTGTATTTAGCTACAAATTGTGAGTGTAGGACAATAAATGAAT	7665	A_95_P117837	DV160812
8034	95	44	846	TTGCTACAGGAGGATATGCTTGCCATGCAGAGGATCAACCAATGGAACTTGGATTTC	7667	A_95_P179717	M64261
8036	95	46	789	GGTCTACTGGAAATATAGACTGAGTTTCTTCAAATGCACAGTCAATAATCAATGGCTA	7671	A_95_P179807	EB677669
8042	95	52	824	AAGGGAATTAATTGGAACTTGGAACTGTTAGACCTTACTAGGTTGTTTTCTATTATCA	7683	A_95_P180252	TA12699_4097
8043	95	53	415	ATACGAAAGCTTGCAGACAACTGTACTGGTCTTCAAGGGTTCCTGGTCTTCAATGCT	7685	A_95_P002596	CV017816
8046	95	56	481	CAGCCGAAGTGTATACACTACTAGCTCAAATTGCTAGTATTCTCTTCTTCTCAAAAGAA	7691	A_95_P263046	AM833705
8049	95	59	316	ATGCTGCTATTGACTTGGGGAATGAATTGGTAAGTAGGAAGATTGACTTGGTGTAT	7697	A_95_P163947	FS406206
8056	95	66	479	GGTGCGACTGTTTTGCACTCGTATGTTATGTAAGCTTTTACTTGTAATAGTTTTACTCA	7710	A_95_P207107	TA18669_4097
8058	95	68	866	CCTTAGAGCTGAAAGCCATTTTTAACTTCTAATGTGGAATCATAATCGATTCCTTTTG	7713	A_95_P013966	TA14348_4097
8066	95	76	938	TGGATCGCGTATTTGAGTTAAGGTGACAATGAATTTGCTTAATATCAGGTTCTCTGAAA	7727	A_95_P206432	TA18515_4097
8069	95	79	1365	ATATATACCTATTGACAAGCTCATAAAGGTGGGCATTTGCTAATATATGGTGTTTCAG	7733	A_95_P207392	U81312
8071	95	81	547	GTGTGAAGATGTATGCATTGACTACTGAGATGCCAAGGCAAGGTAATAAACCTAGA	7737	A_95_P057896	BP134333
8072	95	82	886	GGTGATGGAGGAGGGTTTAATACTGTTGTAACGTCATTTAATGTATTTCTCTTTCTCAT	7739	A_95_P007731	EB428028
8074	95	84	206	CTACGCTTGGAAAAGAAATGTAATTTTTATCCTTTAATTCATGTTCGGCTGTTAGCCCA	7743	A_95_P118237	DV161249
8077	96	2	599	TTTGTTGCCTGTTTAAGTCGTTACAACTTCCAATTCTAAATCCATTATGGGAAGTTATC	7585	A_95_P177117	TA11882_4097
8081	96	6	709	GATATTGAGGATGGTGAAGACTTGATTGATAAGACAATTTCAACACGTTGGAAGAA	7593	A_95_P161722	EH620360
8084	96	9	782	CCCAAGACCTCTTTTTACCTGTTTCTAGTTCCTATTAATGTCCAAAAGGAACACCTAAG	7599	A_95_P211902	TA19716_4097
8085	96	10	465	GAGTGGGTAAATCAGCATATACTGATTTCTTTTCTCAATGTTCAATGTATTTCTGGAT	7601	A_95_P130562	EB430609
8088	96	13	428	AGACCATTTTTGCGTTTTTACTTTATTCCCGTCTGTCCCATATATTGGAGATTTTTGCGT	7606	A_95_P022016	TA14504_4097
8089	96	14	521	ACCTCGATCTCGATCTATTGATCAATTTTTCGCCGGAGAATTTGTCGACCACAGGTACT	7608	A_95_P088348	BP530022

8094	96	19	955	GGAGCAGGTGTAAGCAATGAACTATATACAGTATACATGCGTAATTTATTTGCAAAAT	7618	A_95_P207287	TA18707_4097
8095	96	20	503	GGAGATCAACATCTCAGTCAGATACCAGAGTGCAGTTTCATCAGGACCAAACTCATTT	7620	A_95_P020411	FG168633
8098	96	23	276	GTTACCTCTGCATTCTGGTATTATGGATTGGTGTTCTGATATTAAGATATCTATTGTTG	7626	A_95_P011721	TA14031_4097
8099	96	24	809	TCTTTCACAATGATTAGAGTTGTCAAAGAGTTGAATCATCACTCTGAGTGCTGCTTCTT	7628	A_95_P248457	EB684243
8101	96	26	316	TCAATTGCTCAAGGATGTCGCCTTGAGGAACACAATATATGCACGTGTTGATTCAGC	7632	A_95_P135782	EB439340
8106	96	31	414	GGAGCTTAAGTTTGGGTAGGTTTCTGAGATTCTCATACAGATTTCTTGTTAAAGTTTG	7642	A_95_P101168	BQ843215
8107	96	32	611	TGTGGATCATGATAAGGATGTGAAGAGGATGAAGACGAATTTCGAAGAGTTGTGTG	7644	A_95_P138367	FG142142
8109	96	34	696	GAACCATCTGAAGATTCTACCAATCATGAAGCAATTGAACAATCCGAGGAACCAGGC	7648	A_95_P126477	EB425789
8111	96	36	757	GTTCATGCATTTTGTAGACCAACATCTAATTACTCCCAGAGTTAAGTAGTTTTTGAGA	7652	A_95_P250592	EB439564
8115	96	40	435	CAAAAGATGCACGCGCTAGAATAACGAATAAGACGGGAACACGTGGATTTAACTTG	7660	A_95_P042756	BP130436
8116	96	41	498	TCTTCATACCCCATTTATGGGACTACATTGGGTTTGTCGTCGTTGTAGTGTACTGGAG	7662	A_95_P263056	AM807618
8120	96	45	1958	CCTCCGAATAGTTTGGGAGTGAGGCATGATTGTTGGTTGTATTCATTTGTTTAAAATA	7670	A_95_P190087	Y09876
8123	96	48	494	GAGGCGCAATTGTTGTAATACTCCGGAAACAAGAGCGTAATGTCATATGCCAGATGT	7676	A_95_P129412	EB429294
8124	96	49	871	CAACTGACCGTCATGGCGGAATTGTATAACATGTACATTTGTTTATAGTTGTACAGTT	7678	A_95_P027456	DV159197
8132	96	57	423	GAAGATATACTGTTTCTAGCATAGCTATTACCATTGGAGCTTGTAGGATGTGGATACT	7694	A_95_P184377	TA13682_4097
8133	96	58	253	AAACCACTAAGAAGATCGTGTTGAGGCTGCAATGCCAAGGGTGCAAACACATGTTT	7696	A_95_P104237	TA12974_4097
8146	96	71	816	TCATTGGATGATTTGCAGATCTAGAAATGAATTGTTGGTGGAGATTGCAAGCATATT	7719	A_95_P267286	DV159689
8151	96	76	956	GATGGGTGTCAAGTACAATTTCCCGAAGTTCAAAATAAAGTATCACTGATGTTGCAA	7728	A_95_P009426	TA12687_4097
8152	96	77	800	ACTAGAATTCATGGGCTGGCTTGCTGGTTTGATGTACTTTTATGAGCACTGTACGAG	7730	A_95_P308688	FG172795
8154	96	79	585	GACTGCTTTCCCCATGTACTTTAAGCTTCATCTGTTTCCTGTTTAAGTCTATAGGTTCTT	7734	A_95_P097848	BP534228
8162	97	2	846	GATGTTTGCATGGATGAACTGTGCCTTCCCTTTTTGTTATCCGGTTCAGGGTCTTACAT	7749	A_95_P223512	DV159253
8165	97	5	252	AAGATCAATATAATGGACAGAATTCAAGTGTCCCCCTATACTCCTCAGGAGATGGGC	7755	A_95_P155207	EG649952
8174	97	14	799	ATCGAGAAGAGAGGAGAGGCAAAGCTGATGTTTTTTCTGATGATGTTCTTTCTGTCAT	7772	A_95_P300493	FG174638
8178	97	18	808	TACCTACTCTTGTTGTCAACAATCGACAATATCGAGGAAAATTGGAGAAAGGGGCTG	7780	A_95_P150057	EB680108
8184	97	24	815	CTCTTGTACTTGTTGAATATCCAGTAGAATCTGTTACACTTAAATATTTTCGGTCAGAG	7792	A_95_P208677	EB439408
8190	97	30	432	GTCCCTATTGTGATAGTTGATGGTGAAACTATGCTGGACTCATCAGATATTATTGATA	7804	A_95_P093653	FG158784
8194	97	34	1439	GCCAATGTGGTGACTCTTATGTTCTAAACTTGTACAGATTCAAGCTGCTACTTAATGG	7812	A_95_P214817	TA20345_4097
8195	97	35	1438	ACATTGTTTACTCTGCTTGTGGAGTTTTTGTACGGTCTTTAATGTGGTTCTTAGGTTCT	7814	A_95_P103102	AF120093
8196	97	36	550	TGGTGACCCATGTATAGGAGTGACAAAAAGTTTAGCTGTAGAAGCTTCCTGTTCGTG	7816	A_95_P150737	EB680862
8200	97	40	1343	TACTGGAAGTGATGGTTTCTGTTTGGAAGGGCGGGCACATGAATATAGTTGGCTTTT	7824	A_95_P208387	TA18958_4097
8204	97	44	765	AATTGTTTCTGTAGAGTTGATGATGAGGTAGGAGGGTTTGGTTGTGAAACAGACGGT	7831	A_95_P210107	TA19329_4097
8205	97	45	944	CTATGTTCCTCCTATTTGTGGAATTCGGTGAATGATAATTAATCTTCAAGGAGATTAT	7833	A_95_P026531	TA16388_4097
8206	97	46	794	GTCGGATTATGGCGCCATAGCATCTTTGAATAGTAGCTTTCGCTCATTAATTAGGAG	7835	A_95_P188832	TA14656_4097
8208	97	48	499	AGAAAAGTGCTGTCGAATGATTGTTGGTCAACCTAGATTAGAAATATCTTTGATCAA	7839	A_95_P302923	FG644087

8209	97	49	468	CATCCTTTCACTTTGTGCTCCACCATAATGCTGTTAATCTCTAGTGATAATTTACCTTG	7841	A_95_P287933	FG157352
8210	97	50	110	AGTCAGTCCTAGCCCAAAAGGTGATTCATTATTTCATTATTAAACAGGTATCCCAGAG	7843	A_95_P139857	EB443783
8212	97	52	854	GATTCACGAGCTGTTCTTTCTCGGGGTGGTCAAGCTATTCAGATGACAATAGAACAT	7847	A_95_P120632	DW000595
8215	97	55	212	TTAGGGGACTGCTGTATATATGGAAATCACCAAGTTCTTAATCCTTGTGTGAGCAAA	7853	A_95_P092058	BP531621
8217	97	57	898	GATTTATGATCTTGTAACTCGGATCCTCTTCCACGAGGTATCCTGCTACATAATTGTG	7857	A_95_P010791	TA16202_4097
8221	97	61	214	AGACTTGTGTGATTTGTTTTGATGTTCGCTTGTTTTTATCCTGTCTGAACACTCGTTTC	7864	A_95_P004361	EH618582
8227	97	67	880	GAAGACTGTTCACCGTTATCACTTTTTACTTTCTTTTGGCACTTTGTCAAAACACTCAA	7876	A_95_P210982	TA19513_4097
8233	97	73	772	TACAAAGGACGGCACTATAGCACCATTAGGAGAAGCTGGTTCCGATAGTTGATTGTT	7888	A_95_P121577	DW001660
8234	97	74	849	TTATCGGGTATTCTCCTCTTCCAGCATTGCCTCGATTATGAATGTGGTAACTGGTATTT	7890	A_95_P248237	DV999351
8235	97	75	123	TTTTCGACATTGATGAAACTTTGCTCTCCAACTTGCCCTACTATGTGACCCATGGGCTT	7892	A_95_P114337	CV021551
8237	97	77	198	GTCGGAGTAAAGGATCGTCAACAAGGGCGTTCTAAATATGGGGTAAAAAAGCCAAA	7896	A_95_P007106	NP918018
8238	97	78	883	TCTGGTGTGGAGGTTATGCGCAATAAGATTGGCATGAAAAGCAATGTCATCCGTAA	7898	A_95_P246122	EB451637
8240	97	80	340	ATCTCGATCTTGAACAGTGGAAACTAACACCCTTTCAATTGTATATTAGCTTTTTCCTT	7902	A_95_P099993	BP535160
8241	97	81	574	CAGCACTGTAATGCAGTTCTCTCTTTCTTATGCTAATGATAAATGGAACTGGTTTTTCT	7904	A_95_P019166	EB437086
8242	97	82	888	AGCACTACTATTTCCAGAATGAGTTTTCCTTGCTATGTATTTTGCACATCCTATTGCTT	7906	A_95_P247122	EB425471
8251	98	6	448	GTGAATAATGACTCCTGGACTGTAGATGACAAGTTGAGAAATGTGCTGACAAATATC	7758	A_95_P263906	BP525578
8255	98	10	459	CTTGTCCTGAAATAATTGATTTGACAGACTCACCTATTTTGGTCTGAAGTGGAGTATT	7765	A_95_P277273	AM843516
8261	98	16	380	ATCAAGATTTGTTGCTGAAGTTTCAAGTTCCTTGTGCTGGTGGTGGTGATGGAGGAA	7777	A_95_P310298	FG183282
8263	98	18	750	TCTCAGGTCCGTTCTTCTTAACTTGCTCTTGATTAATGTAATTTTGATGTCTCAATCAC	7781	A_95_P135652	EB439185
8265	98	20	244	AACAAACTTTCTTGTGTTATTCTGACGTCGTTACCTGAATAAAGTGAAAGTAGTTTGT	7785	A_95_P009921	EB432848
8270	98	25	467	AGGTTTCAGTTTGTAATTTCGGTATTTCGTTCCCAAGGATGGTTGCTTTGTTTAGCCTG	7795	A_95_P080225	BP527954
8271	98	26	686	CAGATAGTGATATTGTGTCTGGTTTATGGCATAACTGATGTTGCAATTTGTTATTTGG	7797	A_95_P115377	EB425143
8275	98	30	842	GCTCAGTTTCCACTTCTGTTTTGGCTTGGAAAGATAAGTCTTAATTGGTTCTTTTGAAA	7805	A_95_P295793	EB450832
8277	98	32	695	ACCATTGACAAATTTGGCATTGGCTGTCAAGAGGGACTCAACCTTTGCAAGCAAGGT	7809	A_95_P139317	EB682717
8278	98	33	549	ATAATCTATTTCGAGGGGCGTATAACTTTGTGTTGTCGCCTTCAAATCTCACTGATCC	7811	A_95_P021306	BP134065
8284	98	39	413	ATTTGTAAAGCGCACATACGGATTTAGATACTGCTGTATATTACGTATAGCATACGCA	7823	A_95_P213357	TA20029_4097
8285	98	40	184	CAAATGGTGGCTTGTCTGAAGAACCACTAGTTAGCGTGACTCACATGCATAAGATAC	7825	A_95_P107317	EB677644
8286	98	41	565	ATCCAATGTAACACAGAGATGAATACAGGATGCTTTCCTGGAAAAGGGAGAAGATA	7827	A_95_P044421	BP130871
8292	98	47	675	CGACCATAGGCAGATGCTTCGTGTATTCAGTTTTCTGTTTTGATTTATTTCACAATCCA	7838	A_95_P125347	DW005140
8296	98	51	585	TGTCCATATCATTTCTTGATGTAAACGATCTTGATAGCTGAGTGTCCTAATGTGTCATT	7846	A_95_P134722	EB437405
8300	98	55	867	TACTTGCGTTGAATGCCAGACCAGTAGCTCAGGACATCTATTTCCTACTTCGTCCTAA	7854	A_95_P151497	EB681708
8304	98	59	821	ATTAAGCCAAGGCAGGCTTGTTCGACTTTAGCCTGTAGTTATGTTGGACAATGTCCCT	7861	A_95_P244607	EB678191
8305	98	60	246	GAGGGAGGTTTAGCACGTCATTTGCACAACTTTATATATATAGTTTTAACGCAAAGT	7863	A_95_P109202	CV019185
8306	98	61	800	TGTTTGCAAATGGGGAGGAAGTTTAGTGGAAAGTAAATAGTTCATGGTTATGCAGT	7865	A_95_P198542	EB424705

8308	98	63	425	TCATTTCTTGGGCCTTTCTCTGTGCTGATCTAAGTTTGTTCATAATTTTATCCATGGAT	7869	A_95_P264941	AM822487
8312	98	67	524	TTTGCGTACTATCTACCTCCCCAAACCCACTTGTGGGACAATACTGGGTTGTGTTAAT	7877	A_95_P068785	BP137216
8314	98	69	664	TTCAGTACCTTTCTAGAGATGTTTTGCCTTTCTAGAGATGTGTTGTGGCATATCTTCCA	7881	A_95_P178677	TA12309_4097
8316	98	71	1095	GATTCGTGAGACTGATTCTTCAAACTCAAGCAAGAAAGACAGAAGTTAAAGAGAAC	7885	A_95_P193297	TA15640_4097
8319	98	74	643	GAGGCAAATTTTTGCTTGGTGCTCTTTGCCATGATTTTCGATTTATTATTTCATGAGTT	7891	A_95_P016071	EB429539
8321	98	76	825	GATTGAGGATCCACTTTGGGTCATGAATGTGGTTTCCTCTTATGCTGCAAACACGCTT	7895	A_95_P013981	AB120529
8323	98	78	854	AATTGAACATATCGTGGCAAACTGCTGCCAGATCTTCAAAGGCTCAGTCAACTATGC	7899	A_95_P229819	DV159724
8329	98	84	805	GATTGGCATTGGGTCCTAGATTGAAGGATTTCTATGAATTGTATGTTAGATCATGAG	7911	A_95_P130302	EB681752
8330	98	85	335	CTGGAGTGTATATAATCTGTTGCGGCACTAAGTTGATTGTCCCTGGATATTTAGTTCT	7913	A_95_P160957	EH619640
8331	99	1	897	AAAGCTCCGGATCTGGCACAATGCAGGCCAACCACTATTTTTAACTCCCTTTCAGTGA	7914	A_95_P245447	EB427825
8337	99	7	179	ATATGGTTGTTGAATGAGCTGTTTCTTCAGTGAAAATTTGAAGTTCCTCTTGTACGGA	7925	A_95_P107769	CV018522
8340	99	10	773	AGATGCTGTGTATATGTTAATGAAGAGACTTGGATATGGAGATGTGGAAATTATTGC	7931	A_95_P027166	EB427252
8343	99	13	1799	CGGCTGCCCTGATCATGTACTATAAATCTACAAGTATAAATTGTTAGAATCAACATGC	7937	A_95_P023086	TA13666_4097
8345	99	15	905	CTTTTGAAGAGAACTTTTGGTGGAATTGTTGGTTTTAGTCTTCTTTTGCCTGCTTATAC	7941	A_95_P007876	D85912
8348	99	18	2610	CTCCAGTTTTAGTTTGTCGTCGAAGTTGTCTGTTTTTGAATAATACCCTTAGTTGGTG	7947	A_95_P238104	AF127239
8351	99	21	790	GCCTTAGCTTTGAGTGTACACTTGAATTACTTTCTACTACTTGCCTGCCCTTTCATTTG	7953	A_95_P012616	DV159852
8353	99	23	1187	CTCCTGAACAGACTGATGTACGTTTTTAAAGCTATGTCTGTATGTATGTATAAACTCT	7957	A_95_P207967	TA18862_4097
8354	99	24	661	ATCAGATGTTGGAAACACTTGGTTGTTCATTTTCTTGTCAAACTTAAAACTTCAAGCT	7959	A_95_P033684	EB677750
8355	99	25	799	TCTCCTTATGGGACGTTAACATCTATGTATCAAAGTCATCCTTGCAAAATCAATGTTG	7961	A_95_P296688	EB678890
8356	99	26	470	GAGAATCGGGATGATTACTATTCTCCAAGGAGATGCAGGTCAAAATCTCCATCTGTT	7963	A_95_P148212	EB677460
8357	99	27	258	TATTTGTTCCCGTTGTAAATATGATGTTGATGCTGCGTATGCCTTTGTTGCTTAGGTTC	7965	A_95_P142637	FG640214
8369	99	39	1270	TCCCAAATATATATTACTCCAATTGCTATCATCCCTTCGCTGTCGTTATGAAAGGATAT	7989	A_95_P013216	TA14129_4097
8370	99	40	729	GGACCTGTAGTTGCTCCGTAAATTATGACAATGTTATATAGTTTCTTCATACTTGCTTG	7991	A_95_P016231	EB683870
8372	99	42	638	GGACTTTGGCCTTAGTGCAAATACTTTTCTGCTTTCAATTTCTAAGATGTATTGGGTA	7995	A_95_P016391	EB679128
8373	99	43	859	GGGTCGTACAAAAAGCTGAAAACTTTGGAAGCAGGCAACAAAGACTATGAAAAGCG	7997	A_95_P298873	FG155294
8375	99	45	376	CGAGTCTCGTTCAGAAAAACTTGCAAGGAAGCTAAAGAAATGTTCAAAAACTTCATG	8001	A_95_P134027	FG640186
8377	99	47	555	GCGTGAAGCTGGAAAACAGACATCTCATGGTGAGGTGAAGTTGAATGAGGTTGATG	8005	A_95_P054771	BP133531
8378	99	48	703	GGAAAATCAAAGTCCTTTTGCTTCAAGAATGCCCCTGTGCTTAGTAAGGTTATCCTGT	8007	A_95_P136697	EB428526
8385	99	55	555	TATGGTGCAAGGAATTTGAAGAGAATGGCATACCAGGATAGGTTTGAGAACTGGGC	8021	A_95_P136447	FG143463
8396	99	66	353	CTATTTCTGAGGCTAGAGCAAAAGAGATCCGCAATCAACCAGGGGAAACACTAATA	8041	A_95_P112067	FG136272
8397	99	67	127	TTTGGCTCAGTGTAATGCTCCTAAAGCCAAAGAATCTAATCCAAGCTGTCAAGTACA	8043	A_95_P094283	BP534288
8398	99	68	856	CTGGAAATGGGTCTTCAGAATTTCGAGGAGTACCAAGTGTGTGCTGTTACTGTTGGT	8045	A_95_P296958	EB680579
8402	99	72	752	GAGTTTGGCAATCTTTTTGCCCATTTTAGCAGTATTCCTTCATCTGCTTGGCTACATCT	8053	A_95_P019626	EB447882
8403	99	73	509	CCAAAGAAGGAGTAGTTGTGGTATCTCATGGTGGTGCAAAGTGCATGGACCATTAA	8055	A_95_P151477	EB681680

8404	99	74	663	TTTCCCGCTAAGGGGCTACTTGTATGAGAAAAAGAAGAGTCCTTTCCGAAGGCTTTG	8057	A_95_P053391	BP133164
8409	99	79	803	ACAAAAAGCATTCACCTTCAGAGAGCGGGAACATAGAAAGATCGCAGAGACTCGTG	8067	A_95_P294308	FG162382
8411	99	81	1201	TGTGGTGAAGCCAGATGTTAAAAACTTTACAAGCCTTATGTCATATGCTTGTGACCG	8071	A_95_P210972	TA19510_4097
8412	99	82	400	ATTATTGCACAGTTGCTTGGATCCACTGTTGCTTGCTTCCTCCTTGAATTTGCCACTGG	8073	A_95_P004971	EH666154
8416	100	1	737	ATTCTTGTACCCAGTGTGCGTTTTCCTGTTTTATGATATTTGCAACCTGTTAATCTAGA	7915	A_95_P244782	EH614145
8417	100	2	729	AAATTTGAGAATGAGCGAGCTACGTTGAGCTCTCAGAGAGAACGCGCAGCTGATAT	7917	A_95_P137457	EB441186
8418	100	3	979	GTTTCTGAATCTTATGTGTACGCAAATACAACTTTTATGATGACTACCTGGATCTTGC	7919	A_95_P179917	TA12616_4097
8425	100	10	737	CGACTGAAATAGTCATGATTCATGAACATGGCATCTTTGTGCAATGTGATTGATTGA	7932	A_95_P195532	TA16138_4097
8429	100	14	334	TGTATCTTGTAGAGATGTTGCCTGATAAAATATATATACACTCGTGACTCGTCTATAG	7940	A_95_P198044	EH621781
8434	100	19	485	GGTTTCTCATATTTCTCTAGCTGTGCTAGTGAATCTTGAATCCGAGTTTTTACATGATT	7950	A_95_P300798	FG644329
8437	100	22	2238	CCTCTCGTTCATTCTTGGAAGACATGTATAGAGACATTCATCAATTTAGAGTTGGAAC	7956	A_95_P143072	X60057
8439	100	24	860	AGTTGAGGCATTTATCCCTAATACTGGCCGTGGTATCCAAGGTGCAACTTCACACTG	7960	A_95_P027556	TA20092_4097
8441	100	26	1561	GACATCAAAGGGTTGTATCTGAAGTACAATGTCAAAGTATGAAATCATTCACTTATG	7964	A_95_P189707	X79138
8448	100	33	804	CTGCTTGATAGAATTATTCCTCCTCGTTGCAGTTATTTTTAGTAGTTGGATGTGATTTT	7978	A_95_P272501	FG157506
8457	100	42	955	GGCGTTCTATCCGTTGGTGTGGTACGGTTTTAAGTTCAGTATGGTTTGGTTTTTTATT	7996	A_95_P009331	TA12523_4097
8458	100	43	687	CAGAGGATTTTGCGTTTTACCAAGAGGTTATTCCTGGTTACTTCTACCTACTCGGAAT	7998	A_95_P231914	FG197322
8459	100	44	863	ACTGGAAAGGCAATCATTCTTTGTTTAGTTCGTCAAGTCTGCTTTAGTGGATTTTGCT	8000	A_95_P203977	TA17968_4097
8460	100	45	379	CACTTGATATGGCCAGTGCTACATTGATTCAAATATTGAATGACGACTTATAACCTTA	8002	A_95_P002246	TA13486_4097
8464	100	49	144	GCACACACTCTCTTTATACCAACTTTACCTTTAAAATTGGGGAAATAAAAAAGACGG	8010	A_95_P126007	EB425207
8468	100	53	575	GTTCATGTTAAACCCCTGTAATCTTTAAAGGCATCAAGTCATCTTGAGATTAAGTTTT	8018	A_95_P202117	TA17566_4097
8470	100	55	753	CGACATTAGTGACTTATCTGGAGAGGGAAATATTGAGAGTATGCTGTCAGTTGAAAT	8022	A_95_P136737	EB440491
8474	100	59	1358	AGCTAATACATGGTCTAGTCGACAGAATCATGGAAGCAACTAGAACTTCTTTTGTAT	8030	A_95_P203477	TA17861_4097
8475	100	60	679	GGAAAAATCAGTTATCACAATGTCTCCCTTAATGCAGACTTACATGGTGCCCTAATTC	8032	A_95_P161007	EH619708
8476	100	61	421	TCACTGTTGGATAGCTGGTAGTGAGTTCGACTTGATGGCTACAAGTTGATTGTCTTA	8034	A_95_P045541	BP131172
8477	100	62	757	TCAAAGCTATTGACCTGTGGAGAGGAGTATGACCTTGAACAGAAATGGACTGAATC	8036	A_95_P311483	FG142405
8479	100	64	633	ACAAAAAATTCTGCAGCAGTACGATCAGGAATGCCTATTTCCCATAATGTGGGGGCA	8039	A_95_P304428	FG186266
8484	100	69	791	ATTTGCATTGGCTTCCAAAATACCTGCTGAGGCTACTCCTTCAGCCACTGATGACAAG	8048	A_95_P128992	EB428762
8490	100	75	868	GCTCCGGAATTTGGTTCTTCCCTCCTTGCACTTCTCTTTTTATGTTGCTTATGGATCTG	8060	A_95_P025766	EB429415
8497	100	82	609	GAAAACTCGCTTACTGATTTTGGCTTAGGCGCCAGAGGATAGAATTCTGTGTGCGAT	8074	A_95_P049481	BP132172
8501	101	1	794	GTCCTCGTTTGTTTGCACTTAATCGAGCTCTGAATTTTAATCATTCAGATCTCAGATAT	8081	A_95_P201742	TA17488_4097
8506	101	6	423	GTAGACAGTGATGAATGGATGTATAAGAGGGGATGAAATAAATTTGAGACTTCCAA	8091	A_95_P308258	FG641836
8509	101	9	475	GCGTTTGTACTCCTTTGGAATCATGGTTGGTTGTAATTTGAACGATAAACAGTTTAGC	8097	A_95_P001586	FG637765
8511	101	11	742	TTTCCGAGGAAATGATCCAGACTCATTTGCCCTGCACCTGCAGCTGACATTTAGATTA	8101	A_95_P159727	EH618178
8512	101	12	534	AGCTTGGTGGTCTTAAGAATGGTTCGGGTGGGGGATTCTCTTAAGAATAAAGAATTA	8103	A_95_P007221	NP918186

8516	101	16	107	TAAGAGCATGCACTATCCGTTTTTAATCTACGATGTTACGCTGGGAACTATTTTCACC	8111	A_95_P107352	CV018333
8519	101	19	792	GCATTTTGTTGTGCAATTACTGTGTCAAGTACATTGGTTAGTCCGTTCATTGATGTAA	8117	A_95_P180882	TA12847_4097
8520	101	20	839	GTCATAGCACAACTATTGGATGTTCTTGTTGGCTTGATTATCACTTGACTTTAATCATA	8119	A_95_P227744	EB449440
8524	101	24	469	GTCATACTTTGCAGATGCAAAATTCTACCTAGATTCTTGTGAACCAAATGTGGATAAA	8127	A_95_P041751	BP130174
8525	101	25	224	ATATAAATAACCAGGATCTGCTGAGTTTACATGGTTCAGATGCCTTCCAATCATCGCG	8129	A_95_P155117	EG649909
8526	101	26	476	ATTGTTCACTCTACATGCTTCTCAGATTCATATTGATTTACCTACCCTCTCAGATAAAG	8131	A_95_P127777	TA17748_4097
8527	101	27	907	ATGTCAAGTCATGAAGCTACCATATTAATATATGTTCTCTTCCATTTTATCGTCCTTGG	8133	A_95_P015206	EB441030
8528	101	28	415	TCGCAGACTATTTCTGCTTGGCTTTCCTCAATTAAGTCATCTCTCGTTAAACTATGAAC	8135	A_95_P086385	BP529523
8531	101	31	384	GGTTCTTGGACTTTATTTATGCTTGGGGAAGCATTCTTATCAGTTCAAGAAAAAGAG	8141	A_95_P024326	BP535420
8537	101	37	3053	TAGGGAAGAAATGTACTGTACTGTACTAGTATGTCTAAGCCGAAAGGTTGTAATGTT	8153	A_95_P007297	TA12768_4097
8538	101	38	872	AGTCTGTTCGCATGTTGTCGCAAATGGAGGTGAGTACTGTGCTCAAGTATGCAAGAT	8155	A_95_P231389	FG160044
8542	101	42	230	ATATTTCACTTGGCTTCATGGTTTTGATCTCCAAAACTGTAAAATAAAGCGGTCGACA	8163	A_95_P096248	BP533540
8543	101	43	758	ATTGCCCCTTCGAGGTTTTACTTAGTCGTTGGTTAGGTTTTGTAAGTAGATTCATTTTT	8165	A_95_P290258	DV162430
8548	101	48	536	CTCCTAATTAAGAAGTGCAATTTTGTGCTTTCCTTTTACTTGGTTCCTTTAGCTTTGGA	8175	A_95_P125302	DW005102
8552	101	52	889	TAATGGTAGCCAGGTTCCTGCTGGTCATGTATGAAGCTAAAGTATTGATTTTGTATTT	8183	A_95_P217172	DV159981
8554	101	54	704	ACGTGCTGAACTTTCTAATCTGATGTAGAGCATGGGTTGCAGGTGATCATATGGGAT	8187	A_95_P161382	EH620127
8555	101	55	547	GTCAAGTGTGTTGTAGAGTTCATACTGAAGTTGCTTGTTTGTACTCTTAAACGGTTAT	8189	A_95_P221922	FG635938
8560	101	60	323	CTGTAGCCTCTTAAGTCTCTGAACTCTATTTCAATCTGAATATTTTCCTTAGTATTGGG	8199	A_95_P002706	TA14555_4097
8565	101	65	474	CGCCCTTCTATCGAATTCATTTTTCCTTTATCTTTTTTAGTATGGAGGTGCTCATTTGA	8209	A_95_P097953	BP534267
8578	101	78	333	GCAATCTCAGGCCGAATCTTGTGGCTATTGATGAATTGTATTAGTTTAGTTGTTATAT	8235	A_95_P159217	FG635710
8581	101	81	648	TTAAGATGAACTTCCCTCAATGACAATGTTGGTTGATATTCACGGCCACTTTTCGACT	8241	A_95_P030621	FG645098
8582	101	82	852	CTTTTCTTTTACATGTGAAACAGGTTTCTTTGGGACTGTCTTCAATTCGAAAGGGGAC	8243	A_95_P020021	TA13824_4097
8583	101	83	1934	CGTATCTGCGCATTACTCATGTTATTTACATTTGCTTGTAATACCATGCTTAAGCGATA	8245	A_95_P020721	TA16563_4097
8586	102	1	507	TTTTGAACAGGAAGTTTTGACTGATGTCGAATCTGAGTAACAAATTCTCCTGAGTTGT	8082	A_95_P207282	TA18706_4097
8592	102	7	773	CCTGATCATCGATCTACTTTTGAACCATTACTTGAGTTGTTACTGCTTTGAACATTTTA	8094	A_95_P027731	EB428593
8607	102	22	776	GAAACTCGATGAGAGAGCTTACGCCTTTTTAGCTGTTTCAGGCTATGATGGGTTAGG	8124	A_95_P146627	EB450702
8612	102	27	752	TCCCTTTGTATAAGAATCAGTTAGCAGAATGCCCAAATAAAATATGAGGCTCCTGTA	8134	A_95_P164132	EH623282
8613	102	28	85	GCATTTATATGCTTTGTATAATGGCACTTTGGACCCTGTCTTAGCTGAAACTAATACA	8136	A_95_P019891	EB682845
8623	102	38	301	GCCTCTCTTCATAGATTACAGCTATTCAGTTTCTCTTGAAAAGAGATGTATTTGTTGC	8156	A_95_P111777	CV020369
8624	102	39	2093	ACTATTTAGATCTGCTAAGCTCATGTAGGTGGTTTTGTTAGTGTACTTTTTTGGTGTTT	8158	A_95_P008141	X97913
8625	102	40	461	AGAAGATTGTATTTATGCGGTTTCTAGGGGTACAAATTCGTTTACCTCTAAGTTATGG	8160	A_95_P021581	TA15613_4097
8634	102	49	770	GTATGATGAAATTGGTCCCTCTATTGTCCACAGGAAGTGTTTCTAAGCTTGGTGAGA	8178	A_95_P146617	EB450695
8635	102	50	879	TGTCTTTGATGAAATGATGGTTTAATCTGCCTGTCATTTGAACCATTGGCTTACCTAG	8180	A_95_P190967	AB024575
8641	102	56	770	TCTTATCGTCTTCCGTTGTATACCAGATTGGATTGTTATGTAAGAGAGAAGGTTTAAG	8192	A_95_P114847	TA12745_4097

8643	102	58	770	AAATCATCAACATTTGCCGAAGTATGGGAAAAGCTGTCATTGTTGCCACCAACATGC	8196	A_95_P014931	TA18563_4097
8644	102	59	466	GCAGTTGCTTGTATGTTTTATTGGAATGTAATTAACGTTTGAATCGCTTGCTGTATAC	8198	A_95_P002756	TA11916_4097
8645	102	60	795	GACTGATTCCAGTGACTATCTTGATGCTAGAACTTTCGAGGAGTTACTAGAGCATCT	8200	A_95_P152092	EB682389
8646	102	61	222	CTCTGCTAGTCGCTCTATTGAATTGAAATAGAAATACATATCATGTTTCCTTCTCTTCC	8202	A_95_P028291	TA16554_4097
8649	102	64	866	TTTCGAAGAAGCAGTTGAAATTAACAACTCTGTCCCTCAAGGTTTAAGTAGTTCCATC	8208	A_95_P227619	EB427789
8652	102	67	741	TTCCAAGACAAGAAAGTTACTTGCAAAGTAGGGCAACTGCTCTTCAAAATGTTGAAT	8214	A_95_P127182	EB426644
8655	102	70	796	CAACTGCAGTGAAATTGTATGAAGGTTGTTTCCATTGTTGGTTAAAGAATATCGATT	8220	A_95_P149702	EB425537
8661	102	76	815	GTAGCGTGTTGCCCCCTTCATTGTTTTCAATTGAAGGTTACTTTCTGAGTAGCCAAAA	8232	A_95_P119967	DV999585
8665	102	80	1046	TAAAGTGGAGTTCTGCAGGAAAAAGTGGAGCTGCAAAAGGATCCAAGTGCATTAAT	8240	A_95_P193987	AB193039
8666	102	81	807	TAAAAGCTGCTACATTGGGTCAACATTTATGCCAAAGCTCCAGGGGAAGTTTTTGGC	8242	A_95_P267736	DV161485
8669	102	84	390	TTTTCCATGATGTAGGAGTTTAAATCGTAAGTCAGCTATTGCAGAACTTATTTGTCAT	8248	A_95_P110242	EH617354
8672	103	2	684	GACCTTGCTTTCTCCATGATCTTGGTTTATACTACTTGTTACCTTAGTGTGTGTTTGTA	8253	A_95_P119227	DV162334
8674	103	4	659	GGGCATTGTCTTAGTAAGAATTATTGCTCAGAATTTTGCAGTACTAAAAGGTTTTTAC	8256	A_95_P178077	EB678598
8675	103	5	845	CTCACCTTTTATAATAACCTTGTGTGGGCACTTTCAAATCATTTTGCACAAGTATGTG	8258	A_95_P219147	DV999968
8677	103	7	521	AATTTCTTAGCTTTGGACAGACTTTGAAAAATGCCTTGTCGCCTTACCGACTTGGGGG	8262	A_95_P153172	EB683478
8684	103	14	723	CGGAAAAGGGAAGTGGAAAGGGATGTATAAGATGAATTTGAAGTGCTTATGTTTCT	8276	A_95_P139832	EB443754
8691	103	21	906	ATGTGGATTGCGATTTGTTTGGATGGACCGATTTGGATAGATGAAGCTACTGTGGTT	8290	A_95_P180482	TA12754_4097
8692	103	22	424	TGACAGATTTCTCAGAAGCATCAAACAAAGTCGAAAGCTTATCCTTTCTTTGAACATT	8292	A_95_P265881	AM830968
8693	103	23	713	GACTTGAAAGAACATGTGATCCAGCCCCGTGATCCCAGCGAAGATACCTTTGATGAA	8294	A_95_P159422	EH617609
8695	103	25	739	GCATCTGCCATTTGATTCTGGACTCTTTAACATTTCAGAAGACATGAAACTATCGTAA	8298	A_95_P162342	EH621277
8696	103	26	624	TTATTACCAGAAAATGATCGAAGCCGATCCAGGAAATGGTCTCCTTCTGGCCGATTA	8300	A_95_P217117	FG162154
8699	103	29	260	GTGAATGTTGTATCCACTCATGATGATGTTTTCTTCTGATATGATACTTATGTGAGCA	8306	A_95_P096093	BP533472
8700	103	30	166	GAAATTGTGACAAAACCTCTCTATGAACTATTCAAGTGCAAGTGCAGAATTTGAGAA	8308	A_95_P012711	EB433346
8701	103	31	337	TTTGTTTTGCTGTTGATGATCGCGGTCCCGAACTGTAAATTACTGCTGCTTTCGTTGG	8310	A_95_P162952	EH621942
8703	103	33	344	AGTGAATTTCGCCGGCGAAACTTCGATTTTTTCGAGATCGGAGGTCTTCAAATCTCAT	8314	A_95_P242382	DQ460091
8705	103	35	774	GTAGTATCGAGTCTGTCAGTCTAATTAAGATTTTCGAGTCTTTTGTTATAGTACTTCCT	8318	A_95_P119887	DV999500
8706	103	36	437	TAGCAGTAAATGACTTCATGTTGCTGACACTGGAAACTGGTAGTTCTATTATTGTTGT	8320	A_95_P281858	AM783785
8709	103	39	1102	GCTCTGTATAAGTGTTGAATTCCATCCACATTCTTGTAAAATTTACGCCTAAATGAAT	8326	A_95_P028111	TA15042_4097
8710	103	40	451	AGGGTTGCTTAGTTTTGGTAAGGTTGATGATGTAATTCACCGTTACATAGTCAAGGA	8328	A_95_P181562	TA13009_4097
8715	103	45	1276	GGAGGGGTTGAGCATTGTTTCTCGTTTATCGACACAGTTGATATATTTATAAAATTTG	8338	A_95_P013601	TA15948_4097
8716	103	46	867	AGTGATCACTGAGCCTTGTGTACCCTATGTACTATCTCGAGGTGACATGAGTAAAGC	8340	A_95_P269756	FG159963
8718	103	48	247	CTGCTCTGTTGAGGCACTGAGTGTGTTATGCTGTATTGTTTTTTATGAGATTTGATAT	8344	A_95_P001166	FG622072
8723	103	53	848	ATTGTGGGTGCATATATCTCATCTAAACATGGGAATCTTGGAGAGTCAGCAGCTTTG	8354	A_95_P225732	FG157369
8725	103	55	618	ATGATTATGGAGACCCGTGTAAATACATAGATGTAATGGTGAACTGTTGCTTGATAT	8358	A_95_P286903	FG643169

8727	103	57	628	AAACAGCACGCTGTAGTGGCCTTGCAATTTGAATCGTGGATGTATAATTTGCATAGTT	8362	A_95_P295093 EB446390
8728	103	58	519	GCGGCCGCTGTGGGATTTATTGAGCAACGACATGAAGTACCACAAAATTTTAGAAG	8364	A_95_P280023 AM799744
8730	103	60	804	TTTGGAAGTGAAAGCCTTTTAGCGATAATCTTGAACGATATCCAGAAGTATATTCAT	8368	A_95_P217377 TA20919_4097
8736	103	66	506	AATGCAATCACTGGAGCAGTTTGGGAAGCTACTTGAGAGCTAACAACATAGATTATC	8380	A_95_P071195 BP525643
8738	103	68	88	CTTCGGAAAGTTGAGATGTATTATGGTCACAACTAACATGTATCTATATACTTCTGTC	8384	A_95_P129517 EB429473
8744	103	74	539	GAGTTCTTTCAAGATGTGATAATAGTTGTTCGTTAATGTATTGGTTAAACGCTTGTCT	8396	A_95_P124132 DW003980
8751	103	81	503	GCAAATTTATCTGGATGGGATTTGCAAAATGTTGCTGACGGGCATGAATCAAAGTTT	8410	A_95_P049626 FS412189
8752	103	82	452	GCTGGTAACTCCAATAATAAATTATCTGGTCATCTACAAGAAAAAGAGAGGAAAAGA	8412	A_95_P209252 TA19149_4097
8754	103	84	783	CATGTTCTTGATGTTGTATTCTTGGGGTTTGTTATGCGAAATTGGCAGGTTAAACAAA	8416	A_95_P243437 EB680757
8755	103	85	546	CTGCCGTGTTTGGAATTTGGCACCTGTATGATGATTACTTTTAGTGATGAAAGAGATT	8418	A_95_P120047 DV999725
8758	104	3	679	CTCGAAAAAACTCTTATTCTCGAGCTTTGCTGATGAGTGTTATAGTGTCCCACATTGGA	8255	A_95_P221688 TA21872_4097
8759	104	4	807	GCTTTCTGCAGCTGGTCATCCAATTACAATAATACATGCAAATTTGCCTGTTAAAATCT	8257	A_95_P009531 EB429945
8763	104	8	873	CATGTCTAAATGGTATGTGCGAATCTAGATCATATGGAAAATATCCGTTGACATGGTT	8265	A_95_P011571 DV160063
8766	104	11	769	GCGAGGGGAGAGATCTTCTGACTGTCATTTTATCATATCTTGAACCTTTTGTATTTGTT	8271	A_95_P012036 TA12171_4097
8769	104	14	809	TACATTACCTGCATTTTTCAAACCTTTGCAAAAGCCAAGAAGCAAGCTATATAGACCTT	8277	A_95_P206842 EB452141
8770	104	15	431	GGTTTTATGGAGCTGTTGAGTTCCAGCTTTGCCTTTATTTGGTCCTCTAATTGTTGATT	8279	A_95_P267153 DV158783
8773	104	18	844	GCTAGGCAACGGTTTCTTTTATGTCATTTGAGTCGACTGCGTTTCGTCATTCACAATG	8285	A_95_P014156 DV160978
8777	104	22	292	GCTGCTGCCCTGTTCTCATATATGAGATCAGCAAACTTGTATGCTAAAATATTTATACT	8293	A_95_P096893 BP533806
8778	104	23	856	CAAACGTACTACTCTTAGCATACTGTCTCACAGCTGAGATTGGGCTGGATTTCTTCTA	8295	A_95_P295553 FG162573
8782	104	27	1572	CTAATATCCGAATTTTATTGGCCGATGCATTAATGTTTTAGGCTCTCCGGTAAATTTGT	8303	A_95_P183652 TA13506_4097
8793	104	38	1655	AACAAGAAAAGCAGGCTGTAATCTTCGCAAAGTTATTGAAAATTTTAGATCAAGCAG	8325	A_95_P186097 TA14053_4097
8794	104	39	824	AACTTTTTGCAAAGAAACTTTCAACTCTAGGGACTGGATCTGGTATTGATCAATCTCTT	8327	A_95_P014006 EB426220
8795	104	40	217	GGGAAAGTCAAGATAGTAATGTCGTATGTGTATTACATGTTCCACTTCAAACTATGAA	8329	A_95_P092628 BP531905
8797	104	42	821	CACTAGTGTGACAGCTTCCGCGATTAGCCTTTTGTGATGTCTGAGTCTATTTGTTGTGT	8333	A_95_P228144 FG161660
8799	104	44	312	CAGATCAACAGAGAGCATGCTCTATTGTCACATTTTCCAGAGAAGATTCGACATTATA	8337	A_95_P067705 BP136944
8801	104	46	414	GGTCGAAAGGGTGTTGCCATAAAATTAGTGAAAAGTGATGAAATTAAACATTCCGA	8341	A_95_P102722 CV016160
8804	104	49	1009	ATTGTCTTGTCTTGTGTAGTAGACAACATGAATTCTGATTGGCTATGACATTGAACGA	8347	A_95_P024901 TA15942_4097
8810	104	55	445	TCTCAGTAATACAATAGGAGATTACGAGACTGTAACAGCAAATGTGGAACATGTCAT	8359	A_95_P274518 AM835908
8812	104	57	123	GAGCAACTTAATTCAAGAACTCTAGCTTTAAGCATGGCGAAAGTTTTTGTATTTGTTG	8363	A_95_P132247 EB432689
8813	104	58	827	ACGGAAGTAGTAGAATTCTCCCTTGTACATATGAATTTGCAGTAACTGATGCAATTGA	8365	A_95_P205492 TA18302_4097
8818	104	63	1309	TCTAGCAAAGATTTTGGAACCCCTTGACCACTGAGCTATGCTGCTTTTGGGTTGTGTC	8375	A_95_P191772 TA15309_4097
8819	104	64	508	TGCTTTTGACATTTGATACATGACCAATATGGAGCTTCATTTGTTCAGAATGTTGGTA	8377	A_95_P021411 TA21905_4097
8820	104	65	759	GAAGACTACAAACACTGTGCTACAAACATTAAACGTGCTGTTAGATATGTGCATATTT	8379	A_95_P272426 EB679363
8823	104	68	590	CTGTTTCCTTTCCCATTTTGAACCAGGGATCTGCACGGAACATATGAACACCTCTCTT	8385	A_95_P237224 TC66546

8828	104	73	884	AAGAGAGAGCTTGCAAAAAATCCAGCTCTGGCTAATGAGAACTGGGACAGATTTCTT	8395	A_95_P268391	EB446004
8830	104	75	857	ATTCAATATAGTGTCTTGTTCTGCCCACCCACAGGAAGAGATCATGAGACTTGTATCA	8399	A_95_P301838	FG163572
8832	104	77	247	GGAATTAGGCTTACCGATTATCTGGTAAATTTGGGAAACTAGTTTTCCTTCTTTCTTTT	8403	A_95_P001816	AJ718017
8835	104	80	1424	CCTTGTTCTTAATGTTTAAGGTGAAAGCGTAACTCTGAATACTTCAATCTACATGTTTC	8409	A_95_P003256	TA12366_4097
8837	104	82	204	TATGAGGACCGTTGAAAGCACTATCCCCAGCTTGGGATTTCTATTGTTCTTCTTTCTCT	8413	A_95_P212402	TA19829_4097
8839	104	84	586	GGAATAAATGTCTGCCAATATGATGGTTTCAGTATTTTGCGGAATGTCCCACTTTTCTT	8417	A_95_P207232	FG642695
8841	105	1	375	CTCATGAGTTGTGACTCCAGATCCAAAAGGTATCAAATATTATGGGTTATGTTATTTC	8420	A_95_P025321	BP535221
8846	105	6	863	AAAGATAGTAAACTCTGAAGCTGCTGCATCTGCAACGTGATTGGTGTTGCTTGTGGT	8430	A_95_P296868	FG163431
8849	105	9	1446	GGACAATCATGAAAGTGTAATGAAAGGATCATCAAACAGGTGATCAATCAATTTGAT	8436	A_95_P009696	AF097180
8854	105	14	617	CCTGTGTTAGAACACTGGTTATTGTATTCCTTCATTTGTCATAGTGTTCTTGTGACATA	8446	A_95_P193682	TA15724_4097
8855	105	15	96	CTTTGTTCTCCATTAGGACCAGAAATAGTTACTGCTAATAATATTGGACTAAGACGTG	8448	A_95_P145692	EB449442
8857	105	17	695	TTGTACGATCAAGCAGAGAAATTGAGGTCAAAGGCCCCCCGGTTTGAAGCTCATTCA	8452	A_95_P151802	AB001422
8860	105	20	750	TCGGTTTTGATTGAGGAAGCGAAAGATTGTGTTTTTATGATGGCGTCGCATCAGATT	8458	A_95_P146307	FG169607
8863	105	23	1080	GTTACTGGGAGATGGGATAGAGGAAGTGATTGGAGTATTAAGAACTTCTATAGAGT	8464	A_95_P206562	TA18545_4097
8866	105	26	754	GGACAGTATAATAGAAGTCAGAAATCCTGATCTTACCAGTATTTTTTGATAACCATGT	8470	A_95_P015796	TA16305_4097
8873	105	33	816	ACTCTGAACAGGAGAAAGAAGGATGTTTGTAACCGCTTGACCAAATGGGGTGATCC	8484	A_95_P290093	DV161928
8874	105	34	1345	TGATCCTTTGTTGAGCAAACTATAGGCTAGGTTACATATTTAATAAATCGTGACGGTT	8486	A_95_P021781	TA15435_4097
8876	105	36	1196	AGTTTACTGTTTCTACAACACTTGTGACAGTGGATTTATAACAGGAATTTCAAGAGCT	8490	A_95_P249332	AM087458
8879	105	39	339	AAGTTAGAGGAGAAACATCAAGCTTTGGAGGCTGAGAAAATTCAATGCGAGGAAAG	8496	A_95_P094378	BP532685
8880	105	40	725	TTCTCTTGTAATATTACATTTTCAATGCTAAATTGTGTGAGAGTCTGCAGTTGGATTG	8498	A_95_P013351	TA12160_4097
8889	105	49	873	AAGTCTCCTCTGTATGAGATCACATTTCAGTGTTCTGTGATGTTGTAAGTCGTGCAAA	8515	A_95_P258066	EB427958
8891	105	51	359	AGGATGAGAAATGAGCTCTTTAGACATCAGGAGATTGGGGAATTGATTGAGGTGGT	8518	A_95_P207387	TA18729_4097
8899	105	59	759	ATAAAGCAAATCACAGACATTGTCAGATCTCCGGTTTGATGCGGAGCTGTGCTGAGA	8533	A_95_P225517	FG172171
8902	105	62	817	TGCGCATTGTATATATTGCAACGATAAACAAGCAAGGTCATGTGGTTCCTTTTCTTTTT	8539	A_95_P213042	TA19965_4097
8905	105	65	843	TGCCATTTTTCCTTAGGCTGGTAGCAACTTTACCTCTAGCATACTGTTACGTGAATCA	8545	A_95_P186512	DV158504
8910	105	70	1090	TTTTGGTGAATGCTTGTGTTGGTGTGTAATACTTTTAACCCCATGGAAATACTACGTTT	8555	A_95_P014961	TA13160_4097
8911	105	71	716	ACGTCCACAAGTTAGAAATAGAATGATCCTCAATGGTCCTTCCGTTTCCCTTTCTAGA	8557	A_95_P161062	EH619773
8913	105	73	323	TGGCCCCTCATTGAGACTCTCAGAATTGACATGTTATACAATTGAAACTATGTAAAAC	8561	A_95_P093153	BP532162
8914	105	74	837	TTCAGTCTTCTAGTATGTAGCCTAAGTTGACATTTAAGCATCATTAATAATGTGCCTGT	8563	A_95_P246572	EH615692
8917	105	77	734	CAGAGGATTTGCTTGTAGTAGTAGCTATTATATAATAACTTGTAATGTAGCTCGGCGA	8569	A_95_P286893	EB678541
8918	105	78	761	TTCTTCTGTTTGGTGAGATCATACCACAATCTGTTTGCTCAAGGTATGGACTGGCCATT	8571	A_95_P129287	EB428997
8922	105	82	480	GGCTGTGAAGATCGATGCAGTTGATCTTAGCTTGCTTTTCTCGCTGATGTTGACTGTTT	8579	A_95_P172366	EH665352
8924	105	84	437	GTTTTGACCAAATCTTAAACATGTCAAAGAAGTAATGAACCAAACTTTTATTCGCCGG	8583	A_95_P205087	TA18205_4097
8932	106	7	353	GTCAGAGCCCTTTGGTTTTATTTTTCGGTTTAGTCCGAGTGTCCGAGCAAGTTTTGAG	8433	A_95_P082840	BP528603

8936	106	11	95	AATACTGAAAATGGGAAACAGAGGAAATGCCTGAGTGCGGGTTCGGGGTAGAGAA	8441	A_95_P070110	BP192522
8938	106	13	155	GGCTGTGTTTGGGTTGTATTCCGTACATTATACTATCTTTTGCTTAGACTTTGGTTTAT	8445	A_95_P154272	EG036058
8940	106	15	860	TTTGTTTCAAGGTCTGTTACACCTAGGTCTTCGTCTCCTTCATCATGAAGGACTACACT	8449	A_95_P216047	EB681108
8945	106	20	720	GTCGTGGGGTTATAGCAACAGATCAATTTTTTGTACTTCTTGCAATTGTGTATGAGAA	8459	A_95_P023031	EB678111
8948	106	23	765	GTTGGATTGCTTTGACAGGTTTTATTGGTGTTTCCAAGTACACATGAAAGGAAACAT	8465	A_95_P097948	DV158066
8950	106	25	821	TAGACGGAATCGTTTATACCGGTTCAGCAGACGGAACCGTCAAAGTTTGGAAAAGG	8469	A_95_P121097	DW001094
8955	106	30	846	AAGTTTGTGTAGTGATAGCTGTTTCTCACTCTATCTGGGCATCTGGGCTGATAGCGTC	8479	A_95_P255869	FG167225
8956	106	31	766	GGAGTAATGACTGAGTGTGACACTGATACACCCATTGAGCATGTTCTCCCATTGGAA	8481	A_95_P127932	EB427514
8957	106	32	794	GGGCCTCTTCTTTTTGTGTTGGTAATGACTTCATTTAATGTTCTTTCTCCCAATGTTCA	8483	A_95_P185007	EB677651
8959	106	34	811	CTCGTAAGATCTAAAAGTTGTTACTGTTGGATCATGCTTGTACTGCTCTTTATGTTCTA	8487	A_95_P010371	AY074787
8974	106	49	503	GAGCCCAATAAAGGGCAGTGTAAATATATGTATCTATGTCCATGTCTTTATCTCTGGA	8516	A_95_P056976	BP134096
8976	106	51	956	GTAAGTAGTGTTAAAGTTTCCAATGTTTTGATGGTGTCAAGTACAATTTCCGGAAGTT	8519	A_95_P180222	TA12686_4097
8978	106	53	1455	GTGTTTGCTTGGGTTTAGCTTTTGCTTATCGTGAAAATTTCACATTAGATCCTTGACCT	8522	A_95_P033364	AJ438616
8979	106	54	1462	CCTGCCCCAGGGAGCAGTTAGTGGTAGTTGAAACTGCAAAAATTTAGTTTGTTTGTT	8524	A_95_P011736	TA15485_4097
8981	106	56	928	GTCCGGCCAATTTTCAGTTCATTGAGCTCATTGGTATAAACCGACACCCTTCAGAAGT	8528	A_95_P216527	TA20725_4097
8984	106	59	715	ATGTTTGTTGATGTGGGGAGTTAATGTATGGGAGGAAAAGCCCAAATTGAACAAAT	8534	A_95_P161252	EH620000
8987	106	62	823	TGTTTCTGGAGATACTGGATTCGGCTCATTTGCCCCTTCAGCTGGTACTGATATCTAC	8540	A_95_P180407	TA12735_4097
8992	106	67	667	CGGAATAATCAACTTGTTCGCAAATGAACTTTTCCTTTCAAAGTAACCGTGATCAGTT	8550	A_95_P124667	DW004448
9000	106	75	813	GCTGCGCCTCCTTTTAGTGATTGATACTGTGTATTAGTTATGTAGTATATAAATTGTG	8566	A_95_P128547	EB428246
9001	106	76	2524	CTCTGTTGAGTTGAACTTTCCACCTTATACGACTATAATATCTTGAGAGGACTTTCTA	8568	A_95_P201612	D86506
9002	106	77	536	TCAGGACAGAATATATACTAAGGCGGGCCCTGTCCTAATAGCAGTCAATCCCTTCAA	8570	A_95_P063800	BP135878
9005	106	80	735	AGAGCGAGAAGAGAAGAAGCAGCGCCTCTTATTGAATCTGCATTTCAATGGCGTTTA	8576	A_95_P128058	FG136848
9006	106	81	301	TCATGGTAGTTAGCTTTCTTCTAGCTTCTCCGTTTTGTGTATGTACTGTAAAAACTATC	8578	A_95_P088823	BP530235
9008	106	83	422	ACGCAGGTAGATGCCAGTTTCCTCAATTATGTGGTGGAATATCTTTGTAGTAAATATA	8582	A_95_P052616	BP132971
9009	106	84	605	TCTAGCCCTGAGCTTTCAACTGGCGGAGGAGGTGGAAATATGGGAAAGAATCTAAA	8584	A_95_P150072	FG143015
9011	107	1	350	AACTACTGATGCAGCTGCAATTGATGCTGGTAATGTGCAAACGTAGCAACAAATTCA	8587	A_95_P108782	CV019000
9013	107	3	460	CGGATTGACATCCTTGCTGTATAAGTTTTTTCTTCTTCTTGCTTAATCCAAATTAAGAG	8591	A_95_P133352	EB441754
9014	107	4	447	AAGGTCGTCTAACTCAGTGTACTTGTACTATGTTGTATTGGTATAAGAAATAGACTAC	8593	A_95_P024346	EB435685
9015	107	5	224	TTGTCATGTATTACTGTAATCCGAATTAGTGATTTATTGAGAGTGACGATCGAGAAA	8595	A_95_P122977	DW002871
9021	107	11	413	ATTGGATCTTGAATGGCAGTTACTATAACAGATTACTGTACTTTTGTATCGTCAACAG	8607	A_95_P121842	DW001947
9022	107	12	1003	GGTATTGTTAGTACAATAGTTGATATTTGATGATTTCCTGTCTCATATGTCATGCAGC	8609	A_95_P024801	TA13396_4097
9023	107	13	477	GAAGTTGATGCCCACCATGTCAACCAGTAGGTTGAGATATAATTGATTTTCTTTAAAT	8611	A_95_P123227	DW003095
9025	107	15	1174	ATGATGCCGATGATGATGCTGATGATGCTGATGACAAGTTGGAGTCCAAGGATGAT	8615	A_95_P240269	EU984501
9026	107	16	539	CATAACCATTCGTGTTGGTGTATTGATTCTATAATGCTCTTATGTTTTTGCTCCAGGAA	8617	A_95_P024706	TA16508_4097

9027	107	17	909	GAAGCACTGAAAATGGCAATCTTTTGCCAACTGATAGCAACATACCATTTTTTGGTAA	8619	A_95_P009086	TA13860_4097
9029	107	19	829	TGCCATCTCATGAGTTCCACTCAACTATTGTTGCATATTGTGTTCTATTGCACGTCGAC	8623	A_95_P236294	DV160047
9030	107	20	884	TTTGGCATGTTGTGCATGCGTTTGCTTTCCTTCCCAATCCGCCTTGCTCTTTGAAGTAA	8625	A_95_P190882	TA15109_4097
9032	107	22	844	ACAGTGTCCGCTGCTATTGCTTGATACGAGAATGCCTTATGGAAGCTTGTCAATTGGT	8629	A_95_P253799	DV999942
9037	107	27	646	AGCTAGCCCTGCGATCGTCGATCAGTTTTGTGGAAAACAAAAAGGAATATAAGGACT	8638	A_95_P295188	FG200595
9039	107	29	751	AGATGAGGAGTGATTTATGCTTGGTTAGATTGTTGTTTAGTTGGATTGTTGTTTAGTT	8642	A_95_P161417	EH620171
9045	107	35	678	TGGTTTATGGCTTTTTCTTGTACATCTTGATACAGTAATATCAGTGTTGCTGGTTTTCT	8654	A_95_P178492	TA12264_4097
9049	107	39	547	TATTTAAGTGGAGAAGAATAGAGGGTCAAATCCGACACTACTCGTGACTTTGCAGCA	8662	A_95_P070725	BP525523
9063	107	53	502	ACATGAATGTGTTGATGCTTGTGGAGTTGGCAGGAACTCTGTGGGATTTCTTCTGAT	8690	A_95_P082155	BP528444
9068	107	58	428	TAGGGAGTTCGAGGGAGCACTTTATTTCTTTTTATTATCAACCCCACTTCTTTGTTTTA	8700	A_95_P279278	AM788929
9072	107	62	442	CCTTGTTAGTAGGCCACTCTAGTGTGTCCTTTGTTTTGATTTGTTTTATGTATTAACTA	8708	A_95_P015331	TA13462_4097
9076	107	66	524	AACCAGCAAGGACTAGAAGAGCTGAAACCACCAATCGTGTTACAGGAGTTTGTTACT	8716	A_95_P039076	BP129446
9077	107	67	741	GAGGGTTGACTTTGTGCCTGTTTGGGAGAGATGGTGTGATACTCATGCCTCAAATAT	8718	A_95_P277588	FG173377
9083	107	73	203	TGCTAGAAACGCTGTTCCCTCTCGGAAGATGGGAATAACCAGCATATATGGGGCTAT	8730	A_95_P107597	CV018459
9088	107	78	610	GCTTGTTCTTTTCTGTGCTTGGTATTGAAGTTTAGTTGCAAGTAGTAGTACTTTTGTTT	8739	A_95_P143197	EB446542
9089	107	79	808	ATTCAGTTTAGATGATGGTGGGATTAGCAGTCTTGTTTGGGATATGCGCATTGTGGG	8741	A_95_P289668	FG156027
9090	107	80	280	GCTCTACTGCTCAACAATTGTCGGCTTTCCTATCTTAATCGTGGCTATGATTGTAACTG	8743	A_95_P085350	BP529258
9094	107	84	317	CCTGATATTTAGTGCTTAATGCATATGAATATTTTTCTTGGAAATAGCAAGGAGGCAG	8751	A_95_P130842	EB430948
9097	108	2	789	GGAACGTGGTTACTGGTTAGCTTTTATATTTTTGATGTTATTGTCTTCCTATGGAAGG	8590	A_95_P124757	DW004568
9103	108	8	343	ACAGCACCGTGACATATGCATCATGGTTATACAATTACTAGTGGGATGTAATATACTT	8602	A_95_P160227	EH618903
9109	108	14	711	ATAATAACAATAAATCTTCACCTCCATCAAAATCCTCAAATTCAAATGGTGGTTCGCC	8614	A_95_P127312	EB426829
9110	108	15	847	ATGACATGCTTCCTGAGGAGTACACATTCAAGGATATTATTGGCAGCATGGGACCTA	8616	A_95_P206502	EB425509
9117	108	22	194	TTCACTCAAATCTTCAATGGCTACTAGCCATGGGAATGTTGGGAGGTATAAGGGGGT	8630	A_95_P113582	CV021207
9119	108	24	728	TCCTCCTCTATCTCTGCACTGCCTTTGGTTCTCTCCAAATGTTTAAGATTTATGGCGCT	8633	A_95_P217542	D26509
9123	108	28	830	TGGTTGTATTCATATAGGCAATCCATAGCAGTGTATCCAAATATGAGATTTCATAGCA	8641	A_95_P261741	EB437528
9125	108	30	384	CATAGATACATGTGATGCAGGCAGGCTCTTATTGTTCTCTATTTAGTAAGTACTCTCC	8645	A_95_P133647	EB435274
9128	108	33	646	TTGAGTATCAACTTGGTCAGCCTTGTTCAAAACAACTCGTATCTTATCATCATGACCTT	8651	A_95_P315638	FG181325
9135	108	40	895	GGGATTATGAGTGCAATGGTCTACATAAGCACTCTAAGGCTGTTTCCAGTGGTAGTC	8665	A_95_P249077	EB680583
9138	108	43	797	AAGATTATCAAATGGGTTGCCCTTGGGACAGTTATTTTGGAGGTAAGGTTAAGCAG	8671	A_95_P212057	TA19748_4097
9143	108	48	562	CTGTCTCTACAATTAGCATCCACAGGGAAGATGTAAAGCTAATACTACTGCAGCAATT	8681	A_95_P037751	BP129085
9145	108	50	280	ATTGTATCATTACATTTCTGATTGCTACCAATTGGTGAAATGTGGGACTTTCCCCTCCT	8685	A_95_P090988	BP531163
9146	108	51	480	GAAGCTTTTTACCGGATCCAATTAGCATAGCAGAAGGTTTTGTTTTTTGTCACATGCA	8687	A_95_P276448	AM783542
9150	108	55	250	TTTAGAGATGTCACTAGTGTAACCCAAAAAGTTAGAGAACCTGCTTTTCTGGGTACT	8695	A_95_P108572	CV018903
9152	108	57	494	CTTGCACTTTGAACGTGAAGATATGTTGAGTTCCTTAGTTTTTGTCATCTCTTTTGATG	8699	A_95_P013161	EH621686

9156	108	61	1849	GTGGCTAGTTAGTATTAAGTGGATATTAAAGCGAAAGGAATGCTTTCCTAGTTGTAA	8707	A_95_P239639	AY578143
9157	108	62	272	GTGGTGAATATGGTGGCCTTTTGCATGCTATACCTACAATAACCAAGGCGAAGCCAA	8709	A_95_P107747	CV018516
9158	108	63	1564	ATGTGAACTTGTCAATTATCTCCTGAGGTGAAAGAGTCCTTCAGGGAATAGTTTAAA	8711	A_95_P234194	AF127243
9161	108	66	794	ATGTAGGCCACGTTTCTACATTGTTCTTCTTCCATTGGTCTCTTTTGTTTGTAAATTGC	8717	A_95_P185527	DV999353
9164	108	69	99	GGCGTCATGATACGTAGGCAATCCCCATCGGATTCGATCATAGCCATAAACAAATTG	8723	A_95_P055041	BP133595
9165	108	70	787	AGCCCCTATGACAAGTTCTTGAAAGCAGCAGATGCTGACTGACTTGATGCTTTTACTT	8725	A_95_P162942	EH621932
9166	108	71	115	AATACCACCACAAATTGGTGAAGTGAATGAGATTTTCAAAGGATCTAGCCGTGCTTG	8727	A_95_P036413	BP128725
9171	108	76	597	AGAATTTCTAACCTGGTTGGTTCCCCTGCTAGGACCTAAAGAAAGAGCCAACTCTTCT	8736	A_95_P018341	DV159141
9175	108	80	665	ACAGGCTGGATGGGTGGTTAGGTTCGCTTTGGAATTTATGAATGTAAAATATATTTG	8744	A_95_P024081	EH617846
9178	108	83	367	GTCGTTTGTGGAACAAATACTCGATTTTATGAGTAATACGAGCCTGAGATTTTGGTG	8750	A_95_P097383	FG639624
9180	108	85	423	TTGCTGCTGTAGCCAAGTAGGATAGTGCAAAATAATTCTTTTTTCGTTTCTATTTCTGC	8754	A_95_P143002	EB446397
9181	109	1	864	GGCTAAACTTTTTGTTATAGTGAGAGTCGTCATCTTCTATCACTGATTATATACTGGT	8755	A_95_P204382	DV158532
9182	109	2	831	AAGTCATCTCTGAGTCTCCCCATGAGTCTCAAGCAAACAATCGCAGTGCACTAGTCAT	8757	A_95_P293293	FG162163
9185	109	5	653	AAGCTGTCAGCATATTTGTTGTGTAACCATATTCTTGAGATCTTTTCAGCCATAATTAG	8763	A_95_P154862	FG644355
9186	109	6	202	GGCGCGGTCTAACAAAATATTGGATATCTTTCTTTGGTTACGTTTGATGTTAAACATT	8765	A_95_P113677	CV021254
9190	109	10	403	GTCAGTTTTGATGCAATCCTGGTTGGATAATGGTCTTATTCTATTTAATCTGTAGTCTT	8773	A_95_P110707	CV019867
9197	109	17	810	TTGGGCAACTAGCTAAGTTACATGGATGCTATGTTGTAGGAAGTGCCGGGTCGAAA	8787	A_95_P118562	DV161665
9198	109	18	634	ATTGGAAGTAGAACACCTGAGAAGCGTACTGCAGCTGGAGAACCTAAATTAAGCTT	8789	A_95_P062390	BP135507
9205	109	25	469	GCTGATTTGGGCTGTAACACGAACTTATCGATATATAGAATACAAGTTGGCTTCTCCT	8803	A_95_P002726	CV018667
9207	109	27	2345	CAGAAAATAGTCCTCTCGTATTATCTGCACAGACACACAACAGGCAAACTTCCATCTT	8807	A_95_P257816	AB289457
9211	109	31	613	TTAGATGCAACTGGGAAGGAAGAATTGGGTACTGAATCTTATCTGAATGAAGAGTTT	8815	A_95_P228444	DW004322
9212	109	32	640	AACTTTAGCAATTTCCTCCACTTACTAATGATCTTGGGCACAGAGCCCCGGATACAAA	8817	A_95_P304613	FG152078
9213	109	33	486	ACTCTATATCATGCCCTGGTCGTTCAATGTAGTTGCTGTTTCTTCCTTCAATACCAGAA	8819	A_95_P214452	TA20266_4097
9218	109	38	77	GCTCTAAGGGTTTGAACTAAGAAAACCTTTTGGTCGTCGTATTTGATGATGAATAAG	8828	A_95_P003976	FG199117
9219	109	39	863	TTCTTGAGATATATCAGCAAGTTGCTCCCGCTGCTTTGCCATTACTGAAGAACTCTGA	8830	A_95_P271306	FG133114
9220	109	40	786	ATGATGTGTAAACTGAATTCACGACCAGTAATGGCTTTTCGTCCCTCACTTTTTATGTT	8832	A_95_P248482	EB451478
9221	109	41	439	GTATATATTTCTTAGCCTGCTTAATATTTGTAATCTTAGGATGCGTTGTGCATCTGTAG	8834	A_95_P028196	TA19070_4097
9222	109	42	512	ATCCATATATACACGTGTAGACTTTTTTGGACTCGTGATTATTGAAACCAGACTTGCT	8836	A_95_P028296	TA17676_4097
9225	109	45	1539	GATAACCTTTAAATGTGGTCGGTCGGAAGCTATTGGTATTTGCATGCATTTCCATTCT	8841	A_95_P017736	TA14955_4097
9228	109	48	1083	GGTAGAGTTAGGTTTGTGCTGTTCTTTTAAGAATCCACATATGTAGTTTGTGTGTTAA	8847	A_95_P176392	X92443
9231	109	51	1131	TGTTTCTGTGAACTGGGGAGGGATGTCACAGGGTTTTATTGTCGAGCCACAGTATTT	8853	A_95_P258551	AF352797
9235	109	55	350	GGGCCTTGGCAATTGAATGACTTCTTTATTGAAGTTAAAGAAGTTGCATTTCCTACAT	8860	A_95_P027916	BP530550
9236	109	56	851	GCCAATTTTTGGTGCTCTCTGTGTATCTGAGTTTTCTACCCTTCTCTATCAACCTTAACT	8862	A_95_P224582	DV158521
9239	109	59	523	AGAGGCTCATGTACTTAGTGACACCCTCGTTTTGGAAAATTTCTGTATTTAGTTATGA	8868	A_95_P308333	FG642090

9241	109	61	756	GACAGCTTTGTCCAACAGTTCAATGATGCCTTTGTTTTAATATATACTACTATTTCCCG	8872	A_95_P017146	TA14623_4097
9244	109	64	554	TTCTTCTCTGCAACGTACTTGCTGCATGGCAGAATATATTGGTTAAGGGTTGATCTTT	8878	A_95_P248272	EB678649
9246	109	66	818	TTGTATTTTAGTTTGTGTTGTCTCCGCCTGCAGTTGTGTATGCCTCTTCCCTCTTATGG	8882	A_95_P144642	EB443735
9247	109	67	451	GACCGGACTGGAGGACTATTTCTCAAAGTAGAATATTCCCTTCTGAAAATTTGTGTAT	8884	A_95_P110517	CV019760
9251	109	71	291	CAGTGCTATAGCAAATCTACTCTGATGCAAATTAAGGACTAATGATGGTCCGTTTAAT	8892	A_95_P001626	EH623740
9252	109	72	560	TCGCGGGCTCCCTTATTTTGCAATTTTTATAGATTGTTTGAGCATTATGTGGCATTGC	8894	A_95_P210922	TA19498_4097
9262	109	82	562	AGTTGATTAACAAGTACAGGGAAAATCGTCCCGAGAGTGAGGATGAGGTGGTGATG	8914	A_95_P038006	BP129155
9265	109	85	792	TGATTACGTCTGTTATGTGTTGTTCTGATTCACCTGGTATTCTATCCTATATTACATGT	8920	A_95_P151122	TA15633_4097
9272	110	7	1007	CGCCTCCAAAAACTTGTAATCGACTATTGTAATTGTGATGTTTAATTTCATTCCCCCTT	8768	A_95_P012596	TA14366_4097
9274	110	9	1457	AGAAAAGACTACTGAAGTGCTTGGTGAGGGAGGATCACTTACGTACCTCACATTCA	8772	A_95_P259441	TA12251_4097
9279	110	14	1781	CCATGTTATGTATTGTGCTCATTTATTTGTTTTGTATGTCGACCCGCGAGCTAATTCTT	8782	A_95_P180572	AF220611
9282	110	17	829	ACGAGTGCATGACAGCTTTTGAAAGGTACTCAGTACTTACACGTCGTAATATCAAGA	8788	A_95_P020871	EB678158
9284	110	19	707	CTTAAGCATCCCCCAGGCGATGAGATCTATAGAAGTGGTACACTGTCAATGTTTGAG	8792	A_95_P127772	EB427345
9286	110	21	543	TTTGACCAGCCATATGATAATCTATGTAGTAGTTAGTCTCTTATCTATTGCCTCTTGAG	8796	A_95_P260276	FG643134
9288	110	23	797	ACATAAAATCGAAAGATGCAGATGGCCGACCTGATGAAGAAGTTGCAGATGAGTAT	8800	A_95_P159197	EH617159
9294	110	29	811	CTACAGCACCAAGTTGATGAGGGAAGATGGAGGCTACGAAGTCATTTTGAAGGCTA	8812	A_95_P269472	EB425343
9295	110	30	161	CTAGTGGTAGTAAGGATATTGATCAGAAGAGTCCCAGGATTAAGTCAAGAAAAGGG	8814	A_95_P133622	EB435254
9297	110	32	486	GTTGAACTTAGGTGTAGCTATTCGCTGGTAGCCTGTATTCCAGATTGTGTACCATGCT	8818	A_95_P060220	EB428797
9298	110	33	746	TGTGTCGAAACAGAAGGACATATAGCTTGTGGGTCCTCAAGTGGTGGTATAGCTTTG	8820	A_95_P311743	FG144289
9302	110	37	457	TGGCATGCTGAAGTCATATTGTATCACTATTTATGTGCTTATCGTTGATGCCAGACAA	8827	A_95_P114597	EB678991
9303	110	38	792	AAATTGAGATGCTTCTTAGAGAAAATACCATTCTCAAACGTGCTGTTTCCATCCAGCA	8829	A_95_P018356	DV159715
9304	110	39	632	ATGTCATGGAATACAAAGCCCATGATGCTTCCTTGCGTGACAACTCATCATACCGCA	8831	A_95_P271871	EB445862
9305	110	40	368	TAGCAGGGGCTACTCAAGGTTGTGTATTGCAGGGGTTCCTCTCTTTTTTGAACCTTTT	8833	A_95_P152512	EB443661
9310	110	45	486	GTTAGCTGACTGGGAAGTTGTTTCCTTGCGGGTTACTGAATTATCTATCTTCTTCCAG	8842	A_95_P106827	TA14707_4097
9311	110	46	793	GAGGAACTCTCGTGTCTTGTTTCTTTCATTTACTGTAAGACATTATGGTCACATTTAA	8844	A_95_P244592	DV160610
9322	110	57	729	TCTGAAACATCGTGTGGGACATAGAGGTACTTAAGGAATACATTTGCTTCTTGCAAT	8865	A_95_P232759	DV160268
9324	110	59	741	GTTGGTAAGAGCTGAAAACATGATGCGGGCCATTACATATGCTCGGAAATATCTTGC	8869	A_95_P136847	FG139248
9326	110	61	729	TAGATCCTCGTCATTTGGAAGCACTAGGAGTGATCCTGCTGATGCATGGAAGATTTG	8873	A_95_P316758	FG193831
9329	110	64	570	GCAGTGACTATGTACTAGTTAAGATAATAAGACCAAACTGGTGTGGTTTACAAGTGT	8879	A_95_P263651	FG644694
9331	110	66	875	GGCTGTCAGATTTTGTGCATGTGGATATGTCAATTTTGCACTCTCTATGAAGTTTCTA	8883	A_95_P200602	EB443292
9332	110	67	795	CAGAAAACAGCCCAAATACTGATGGCATACACATAAGCAAATCTAACACTATAAAAC	8885	A_95_P214532	TA20282_4097
9334	110	69	1879	GCATTTATAGCTCAAGGCTGGCTATCAACAATGGCTTAATTGAATTTAATACTACTTA	8889	A_95_P190307	TA14985_4097
9340	110	75	581	TGCTAGAATTTTGTTGGTTTGAGTCCATTTTGGAGCTCGCTTGTGAGATCTGCTCGAA	8901	A_95_P160942	EH619629
9342	110	77	845	ATGGTGCAATATCTCTGTTCATTTGTTGTTTAGAGAGGTTGTAGAGCTTCTGTAACTT	8905	A_95_P243177	EB426408

9344	110	79	819	AACCAGCTGAGATCTAGTCGAAACTTTTGTATCGACATCATTTTGCTGATCATCATTC	8909	A_95_P236134	DV160005
9353	111	3	1470	CCGTGAAATCACTTCCTTAATCTTGTACTTTGTTGTGAGTTTAATATGAAAGAGCCTT	8926	A_95_P193507	TA15688_4097
9354	111	4	89	ATTGTTCTCTGGGTGGACGTAGGATTATTTTGATCCGAACTACGTTAAATCTTGTGTT	8928	A_95_P064595	BP136093
9355	111	5	768	CCTAGAAACTGCTGTATTCATTCTCGTCCAGTTAGTTGATAAATAGCCTTTACCCTTTC	8930	A_95_P188557	DW003989
9356	111	6	450	ACTCTCATAAAAAGGGGTTCAAGTGCATATTCGATCGAGGAATTCTGCATCTGTATTT	8932	A_95_P132607	EB433168
9359	111	9	877	TTGAGAAAAGATCAAGAAATGCACCAGTAGGAGTTCCTCCCAGCAAGCTTTGAGTTC	8938	A_95_P191782	TA15311_4097
9371	111	21	774	GGAAGATTTAACCACGAGTTTTTCTCCTTCTTCTTCCTACTTTTCATTGTTGGTTATGA	8962	A_95_P217802	EB677687
9376	111	26	796	GTCGGGATAAGTTATACTGGTATAAGTTATGCTGGGATTAGTTATGCTAGGATTGTT	8972	A_95_P208567	EB451348
9379	111	29	792	ACTTTTGCTTTTGACAGAGGGTATTAGAGCCTTGTGAAACAGGAACTTTGAGATGCT	8978	A_95_P012186	EB439152
9380	111	30	673	GCATGTAGTTGGAGTTTGCAACTTGCAATTGCTTTCTCTTGTTTCTTATTACTTTGGAA	8980	A_95_P197947	EB438995
9381	111	31	345	CCATCTCCAAATCTTTTTGACAAGGTTTGTTTGATGTTGTTTCATGGTTTTTCTGTTTG	8982	A_95_P006491	FG625247
9385	111	35	1385	CTCCATCTCCCTTTAGTGTGTAACCTTTATGTAATGAACTACCAGTTCTAAATTATGTC	8990	A_95_P185997	AY660024
9387	111	37	840	TATAGCTCTGATGTATATGGGATGCTTATCATCGATCGGCAGCGCAGTCTTGCAAGG	8994	A_95_P297853	FG163881
9392	111	42	1937	GTTGAGCATTATATATGTTCTGGGGTTCTGCTAAGTCTACCTGTTATCATATTCTGGC	9003	A_95_P018476	TA16281_4097
9394	111	44	581	CCCTTTAGCTTGATGTATTTGTTGTCTGTTTAAGTCATTACAATGTCCAATTCTGAATC	9007	A_95_P285843	TC55285
9400	111	50	99	ACAGAGTTGGAATAAGGCTTTCCCCATTTGCAAGCTACATGGAATCAGGAGACTCAA	9019	A_95_P215517	DQ460062
9402	111	52	581	TTTGAACATGCAGGTCTATGTTTTCTGCTCCTTTTCTTTTCCCCCTTTCTTGGAAGGGA	9023	A_95_P001196	DV999385
9407	111	57	471	AGAGCAAAATTTGCATGTTGATTAGCATTCAAATGTGATTCCTGCACCAGTTCAATTG	9033	A_95_P252809	EH621250
9412	111	62	529	GTAGCTAACTCTATAGAGCTTATGACTTGTACTACCGGGATTTAGGAATATGTTCATT	9043	A_95_P300058	FG643213
9415	111	65	824	CAGATATTCGCTTGTTTGTCACCCTGATTAGGTTTGACGAGGTGTATGCTGTCCACTT	9049	A_95_P123342	EB450387
9416	111	66	582	CCTTTAGCTTTGATGTATTTGTTGCCTGTTTAAGTCGTTACAACTTCCAATTCTAAATC	9051	A_95_P028026	TA11882_4097
9419	111	69	593	GTGAGTTATGAGAGGAAAAATTGAGGTATTTATTGTCATGTTATCAGGCCTTTGCCA	9057	A_95_P005253	TA15502_4097
9420	111	70	796	CAGACTGATAAAAATACCCATTTCCTAATGGCTTTAGAATATTGTAGAAGATAGGGC	9059	A_95_P148657	EB678062
9423	111	73	202	GGCATTACCTGCAGATTCTGTTCCCCAGACATGGTTTTCAGGTTGAACTTTGTCGTTC	9065	A_95_P066715	BP136669
9426	111	76	695	TAAAAATGTCCTAGAGGCTGTCTATAAAGAGGGAGGACTCCGTGCACTTTATCGAG	9071	A_95_P298423	EH620917
9428	111	78	1053	CCTTCTAAAATCAACTATGAAAAGCGAATGATCAAGATGTTGGAGAAGTCAAAGTCG	9075	A_95_P210712	TA19454_4097
9437	112	2	405	CCCCGTATTCCTCTGCTGTAGTGGTAAACACATACTACATTAGCTTAATCTTTACTGTC	8925	A_95_P130917	EB431042
9439	112	4	752	TTGTGAATACAACTGTGAAATTGTTGTGTCTGGTCCTCAATAAAGGCGGCTCTGGCC	8929	A_95_P211797	TA19692_4097
9441	112	6	527	TGAGCTTCATAAGTTTATGTAATTGATTAGGGCCTCATGAATCTTGAACTGCCTATTG	8933	A_95_P216397	FG628560
9442	112	7	176	GAAGGCAGGTTTATTGACAGAGGTTCTGATTCTGTAGATTTCTTACTGATAGTACTTT	8935	A_95_P134857	EB437723
9443	112	8	279	TTGGGTACTTGGGGCTGAAAAATGTTAGGTTTCTAAGTTTTTGCTTGTTCAATGATGT	8937	A_95_P000091	AJ717873
9445	112	10	429	CTGGGAGGACATTTCACTTTCATTGATGAATACTCCACATTTCAGATTTGATACTATC	8941	A_95_P064445	BP136053
9446	112	11	258	CTGACATCAACTGAAAATTTGAATAATCGGTACTTTCCTAGGGATAAATCACTAGGTT	8943	A_95_P114647	CV021703
9447	112	12	828	AAGTACTTGAAGTTGTTGCAGGCACTAAAGGCATCACTGACATAGACCAACTGGGC	8945	A_95_P295933	EB448824

9459	112	24	900	CACAGTTTCGAGCTTCCTTGTATAGACTATTAATTTGTAGACAGTAAACCAAATGAAG	8969	A_95_P124727	TA21470_4097
9462	112	27	663	AATTCTACATTCAGGTTGTCACCTTTTTAGTGATGAAAAACGCGACTTCTGGTCGTGA	8975	A_95_P124137	DW003984
9464	112	29	1724	TGTAATCCTGTACATAGTTGGTCCTTCAATTTATATTGTACGCAAGAATCTTCCTGGAA	8979	A_95_P197307	TA16534_4097
9470	112	35	1457	GAGATACTATTCGTTTATCGCATGTATTAATAAATGTTTATCCGTCTCTGATGTTGGA	8991	A_95_P187577	TA14378_4097
9476	112	41	600	TTTTACAGCAACAAATTGAGGTTCTGCAAAACCAACTCAAGCTTTTAGAGAACCCAAA	9002	A_95_P273046	EB681049
9478	112	43	1314	CAAATTATTCTTGAGAGCTAGGAAAAGAATACTTTGGTTTATGTTGAGATCCCAGGGT	9006	A_95_P197722	TA16625_4097
9481	112	46	880	GCTTGAAACATTTCACTAGCCATACTGATGTTGTTCATGTTTTACGTTCTGTCTTTGAA	9012	A_95_P227609	EB427794
9482	112	47	653	TGATAATACAGTCGCATGCACCCATCCATTTCTCCATCTACTTCTGAAATCCTTTAATCT	9014	A_95_P270876	FG195996
9483	112	48	187	ACTCCATATCTTGGGATGGTTTACGTTAGATGTTGGATTTAGTCTTATTACGGTTATCT	9016	A_95_P129697	EB429659
9487	112	52	467	GGAGGAGCAGTTGATTTAGCAATTTTTAGTCTTCATCTATCTGGTGTTTCATCCATTTT	9024	A_95_P028106	BP528067
9490	112	55	735	CAGGCACGAGATTAACTCAACAGGCACGAGATCCTAGAGTTAATTATTTATTTGAATT	9030	A_95_P159542	EH617797
9497	112	62	191	GTTTGATAAGTCTCTTTATGTTTGCCTTCTTTTGCAGATTATTGATCTGTGGGAGAAA	9044	A_95_P133922	EB435631
9498	112	63	1519	GATGAGGATTTGTAGCTGTATTGCCTTTATGTTTGATGAGTAGCGAACTTATTCGTCT	9046	A_95_P207837	TA18831_4097
9501	112	66	216	AAAGGATGTTGTTGCTCCAACCATTGCACATAAGATTAATAACAACTCTCTCTCTCTCT	9052	A_95_P220637	TA21650_4097
9506	112	71	872	TTTTTGCTTCTTCTACCTATGGGGATATGGGGAATCACTATTCTCCCATGCCTGTCTGG	9062	A_95_P246232	EB451951
9511	112	76	1012	GGGAAAAACCCTGGTCCTTCAGAGGAAAAATTTTCCATGTTGCAAAGAACTAGGGG	9072	A_95_P171511	EH665158
9513	112	78	875	ATATTTTGATGGCATTTACGTTTTCTTCAGCAGAAATGCAAGCCAAGCTTGATAGAAA	9076	A_95_P227814	EB426348
9515	112	80	739	GCTGCAGTTTATGTTGTACTAAGTGATTCAGCTGTAAAGAGGAGTGAGAATGTATTTA	9080	A_95_P180092	TA12657_4097
9516	112	81	546	TGGGGATGATCCGATAGTTTTATTGATATGGTGTGCGATTTCTATTGATTGGTGATAA	9082	A_95_P211247	TA19569_4097
9518	112	83	434	ACTGACAAAAGGATCAAAGTTGAGGCTACTTCCACTGCATTTCAGGAGTGAATTAGA	9085	A_95_P071205	BP525645
9520	112	85	316	CACTGAAACTAGTCGACGGTGGGGAATCACAGAGAACTTTTATATATATCAAGGATG	9089	A_95_P150822	DW000398
9523	113	3	566	GTCAAATATTCAGTTCAAACTCTTACCTCAACTGGCAAGGAAATTACCTAACAGTTTAA	9094	A_95_P301238	FG636454
9529	113	9	1179	CATTTATATACATCATCTGACCCATAGGAGAACATACTTTGCCAGCAAGGCAGCCACC	9105	A_95_P159407	TA15129_4097
9531	113	11	846	ATCTGTAATCCAGTGAATTATTTGTTGTTGTTGTTGTTAAGTCTGTAATCCAGTTGGT	9109	A_95_P020376	DW003318
9533	113	13	530	CTGTCAATTTTGTCAGGGTACTTAATGTTTATGTTTTATCAAAGCATCAGAGGTGTTA	9113	A_95_P283683	TC59158
9536	113	16	1240	ATGCATTACCATCAGAACATTTTTTCTATAAATCTACCAGGCGCTCCCGTTTTCAAAAA	9119	A_95_P238329	AY029749
9538	113	18	600	AATAGCAAGAAACCGGTATAATACTTCGGTGGGGTCTAAGGCGAAGGTGGTCACAA	9123	A_95_P063880	BP135897
9541	113	21	542	GTAGCTGTTTTAGCCCTTTTTCCTCTTACTATCAGGACAATTATTAAGTTTTGGTTACT	9129	A_95_P223337	FS387202
9547	113	27	849	TTCTCTGGCAGGTTCTCTATTATCTCATAGTAGATGTCCTACGCCGACAGAGATTTCT	9141	A_95_P199557	DW000180
9549	113	29	922	CTTGGAACTAAAGAACATATCTTAAACTATCTTGCCTTCCCATTAGTTATATGTGTCTC	9145	A_95_P218387	TA21163_4097
9552	113	32	79	TAGTGATGAAGAGATGCTAGAATGGGGGCTATCCCCTGAGATGATAGCAGACCAAA	9151	A_95_P101443	CN498832
9553	113	33	557	ATAGCTGATTCACTCTCTCCATATAAGCTTATAGTAAAACTCCATATCAACTGTACTG	9153	A_95_P047556	BP131686
9554	113	34	764	CAGGAAGTTAGCAGTTGAGGATACAGCATTTTGAAATATGAATGTATCTCGTAAGAT	9155	A_95_P179392	AY074787
9555	113	35	805	GTGGAAGTTGTGGAACAAATGGCAATGCAGATGAGTTCTGGATTGGCTGTGATATTT	9157	A_95_P205277	DW004725

9557	113	37	513	ATGGTGAAGTATGTATGGGGTTTCGTTGTGCTTTGCTTGAAATGTAGTGAATATTTCT	9161	A_95_P001101	FS405424
9558	113	38	813	AAATTCAGAAAAGGATGTTTCAAAATCCGACAGATTTGCTCGTGCCGTGCCTCCAGG	9163	A_95_P213982	EB679271
9559	113	39	609	TTGTTACCGTGATGTTACCTTTGTGGATCTGTATTTACGAAGTTATCTGGAATTAAGT	9165	A_95_P000421	FG167411
9561	113	41	742	AGAAAACCGAGCTAATATAGTTGAGCTATCTTAGGCTAATTGGAGCTGTTATTTGTG	9169	A_95_P270186	FG640788
9562	113	42	444	GCCGGAAGACGTCTACTTTAAATAACTTCTGTCTTGAGACAGGTTTGCTTATATCTTA	9171	A_95_P131452	EB431745
9564	113	44	389	GGAAAAAGTGGAAAAAAGGAAACGTACTGAAGAAACTCCGCAAACTGGTGCAGCT	9175	A_95_P086708	FG644997
9567	113	47	677	ATCAGAGAAATACGGTCAGGATGCCACAAATGTGGTGATGAGGGTGGTTTGCTCTA	9181	A_95_P159157	EH617116
9568	113	48	793	GCTTCGAAGATTTTGCCAGTGATTGAATGAACATTCAGATGGTACTATTTTGTCTTGA	9183	A_95_P219382	DW001838
9569	113	49	841	GGAGGAATTCCTAAAATTAGGTAGGAATAAGGATTTCCTTCTTGATTCTGAACTCTAT	9185	A_95_P220387	TA21596_4097
9577	113	57	677	GATTCCAGTAAATTGTTGGAAGATTTGCAACAAAATCGCGATCAAAAGTGGTGGAAT	9201	A_95_P315628	FG184961
9579	113	59	721	TTTCTGCTCCGTTGTCGATAAAGGTCCCTAGTCAACTTCCCATTTAGATAATTTTTGAA	9205	A_95_P136297	EB439998
9584	113	64	908	TGATATATACGTCGTCGATATTTTGGCTCTTCATGCATCACGGTCGATGTATATCGTA	9215	A_95_P247162	EB447545
9585	113	65	1693	TTTTGCTTTTGGTTTATCCTTGTTATTTCGAGGAATCACAGAGTAACATGTTTGCCTTT	9217	A_95_P016036	AY639865
9588	113	68	758	TTGTAACTGTTTTCATATGTAGCATCTTTGCTGTTGCATTCTCAGATTCCGCGAAGAA	9223	A_95_P146558	TA12573_4097
9589	113	69	455	GTAAACAGAATAGGAACTAGAACTATTTGGCAGTTGTGATGGAATGGGAACAGTAT	9225	A_95_P025761	EB643491
9591	113	71	687	TAAATACACACAGCTTGCAAGTGCAGTATTTCATCAGACTTCATCACCATCTTCAAGT	9229	A_95_P256194	FG197449
9592	113	72	787	ATTTCTTCTTTGGTGGAATGCGTCCTGCAACGACTACTACCCATTTTAGCTTTCGCCCT	9231	A_95_P214832	EB441356
9593	113	73	771	TCTAAATTCATGGAACCTGTTCGTTATGCACTTTTTCACCAGAAGGAAGTCACTTGAC	9233	A_95_P236029	EB439796
9599	113	79	867	AGAATGAAGGCAGATAAACTGTTCAAGACCCCTATTTTGGGATCTCGTCTTCAGCGG	9245	A_95_P251157	EB438096
9600	113	80	737	CAGTCGGCAATCCCTCACCCAAGAATAATGGGAAATATTTCGTGATGTTGGAAGGAA	9247	A_95_P164697	EH623971
9603	113	83	446	ATATTACCATGCAGATATGAAAAGCGTACTTGAACAGCTTGCTCCACACCTTCTCACT	9253	A_95_P069695	BP137459
9604	113	84	287	AGATAAGAGCATCACAAGATCAGATTCATATTTTAAGGAGCTGTTCAATCAATGTGG	9255	A_95_P160297	EH618990
9607	114	2	222	TCGATCACTGTATGAGTTTTGCCGGAGGCTTGGTTCAATGAAAAATCGTTGTTTCAGT	9093	A_95_P091808	BP531503
9608	114	3	688	ATCATTACTGTCTTTTTTGTGGATGTCAGTATGAGTCAACCGAGGCGCTGCTATCTAA	9095	A_95_P149572	EB679470
9612	114	7	874	TTACTAATTAGTAATTACTGGCTGACCAGCTTCTCCTGCTGCACCTGGTTCTAGTTAG	9103	A_95_P245267	EB679204
9620	114	15	756	ATTTTCCTGGCGGAGGCACTCACTTTCACTATGGAGCTGATAGTACATTTGCTTCAAT	9118	A_95_P164437	EH623678
9624	114	19	535	GAACCTGGATTTTGCTTTTAAAATCTTGCTTGAGGCAGACATTGGAAATTATAATGA	9126	A_95_P226839	FG645200
9632	114	27	882	TTGTGGATAGTTGTCTCAGTTAAGTGTGACCGTTTATCATTGTGATGAGTCCGTCCTT	9142	A_95_P149997	EB680048
9633	114	28	1256	ACATCCTACCTTGCTGGGTTGATCCTGCTTTTGAATAGTTTGTGCTATGTATCTAGGAT	9144	A_95_P306818	TC51772
9635	114	30	829	ACTGTCAAGTGCAATCCCGAATATGAAGACTTAATTCTGAGCGCTGGAACTGATTCT	9148	A_95_P127832	EB427394
9640	114	35	839	ATTTGGGAGTCACCCATTCAGGAGAAGTGACTGTACTGGGACATACTCCACTAGTAT	9158	A_95_P311513	FG142986
9641	114	36	711	CATGTCGATGCAACTCTTGTTTTGAAGCCTTTATATTCTTTGATTTGGTTTCTTTCCGA	9160	A_95_P200897	TA17308_4097
9642	114	37	813	CCACATTTGTGAATAGTGCCAAACCCTTGACAGTTTAGTTTAGGGAAATTCATTTTTT	9162	A_95_P194687	DV159906
9644	114	39	221	AAGCCGTTGGCTATTTATAAAATAACCATTTAACCCCCCAACTTTGTTTTAACCCCAAA	9166	A_95_P104597	CV017089

9647	114	42	980	GCCTACTCAGGTTCTTTCTTATCTAGGACCAGTAATTTGTCAAATGTACAAAAAGAAT	9172	A_95_P183362 TA13441_4097
9648	114	43	1359	CGGGTTTGCAGTTAATTATCTTGTTTGATGCTTGTCTTGGTATGTCTTCTGTTAATTTG	9174	A_95_P199367 TA16979_4097
9650	114	45	826	AGATGATAAGAACAGAAAGTCAGCTGCCCGTCTAGAGAGCGAAACAGCTTATCAGT	9178	A_95_P307953 FG169124
9653	114	48	335	GTAGTGGTATTATCTTTGGACTTCCGCCTGTTTAACTTACTGTTTTAGACCTTTATTAT	9184	A_95_P242312 FS433138
9656	114	51	1885	CATGGTGCTGTATAAGAAGTAAGTACTATTTTGAACATGAGGGACACAATTACCTTT	9190	A_95_P012486 M61904
9658	114	53	396	GGAAGTTTCAAGACCACTTTACAGAATTCTTTTGCTCGAGGAACTACAACAAGCATG	9194	A_95_P038631 BP129321
9659	114	54	314	CACAAACAGAATTGCCAGTCTGTGTTGGCCTTGAGGTTTTGGTGGATAAAAGACCCA	9196	A_95_P126762 DV998762
9660	114	55	863	GGATGTCATGAGATTGTTTGAGATATTCCACGACCTCAGTGTCCAAGTGTACAACAA	9198	A_95_P268076 DV999490
9666	114	61	160	CTTAATGTAGTTCTCCTTTCTATCTGTATATGGTGTCGATAAAGTATGATTGAGTGGA	9210	A_95_P112752 CV020816
9668	114	63	678	TGCTGAGAAGTTGTCCTTAAAAATGGCAAGCAAATGCTATTCAGATTCTGGACATGA	9214	A_95_P294993 FG197328
9669	114	64	1086	AAGGGAAAGTTTATTTAAGGAGAGATCCATGTGATTAATTGACTAGACATTTGGTCC	9216	A_95_P008077 TA13785_4097
9672	114	67	864	GGTTATAGAACCCTTGTTGAAAACCAGCCCGTTTACATCCATCCTAGCAGTGCACTTT	9222	A_95_P231229 DV162553
9678	114	73	375	TTGTAAGAAGTATAGCAGACTCAGATCCTCTTTCTAGTGGAACGATCGGTTATTTTCT	9234	A_95_P133367 EB434818
9680	114	75	665	TTATGAGAGGGTACAGTTCTTTGATTGTTTAGTCATTATCAATGGAGCTTCCGGTTAT	9238	A_95_P266781 FG635845
9682	114	77	454	TGAAGATTGAAGAACATTGCATCAATGATTTGGTCAATGCAGACAATAGTTGAACGG	9242	A_95_P150202 EH624123
9688	114	83	1418	GCCCCCCTTAACTATACACAGTAAAGATTGAGTCTTTTTTCCAGTTCTTGTTTCCTTTC	9254	A_95_P220382 TA21595_4097
9692	115	2	713	AGTGAAATTGTTTTGTTTTGTTCCGTTCCGTTCCAGTTCATGGGTTCTCAAACTTGTCT	9261	A_95_P140362 EB444295
9702	115	12	3115	GAACAGTATGAAGGATTAGAATTTGAGGCATCACATCATGCAGCTTCATTTTCTGAA	9281	A_95_P024661 AB071435
9708	115	18	1380	GCCTTTAGGATTTTAGTTGAACTTCAATTGTTGCCGGAGCTTAAAACGCATATTATTT	9292	A_95_P021151 TA12420_4097
9711	115	21	688	TGTTATGCCCGGAACATTGGCGGCCACATATGAAAAACTTGGCGGTGAAGTAAAAT	9298	A_95_P293968 EB438959
9716	115	26	437	AAGTTCAAATTTGAAGGAGATAAAAATTGGGTCTGAGCCTGCTGCTTTGACTGCAGA	9308	A_95_P083575 BP528793
9717	115	27	1373	TATAGGCTGCTCTCAACCACTTTTTGTTATCTTCATGTATATAGCTCGTAGAGCATCG	9310	A_95_P201642 TA17468_4097
9718	115	28	1018	GTTGTATCACCATTATTTAAATTGGTGCATGCAATTATGTAAATTGCCTCCCTTTTCTC	9312	A_95_P020271 TA18887_4097
9722	115	32	268	AAATTTTAGTACTTGGATCCGCGTCTCGTCGTCTGCCCTTCTCTTTTCACTTGGACTAA	9320	A_95_P033814 TA17615_4097
9727	115	37	625	TAGCAGCGATTGTCACTCAATTATCCTGTAGTGTATTATCAGGCACAATATGTACTTT	9330	A_95_P216712 TA20764_4097
9729	115	39	246	CATACATCACACATGTTCACATTTTCATTGTTAGTAACAGTGATGCTTGATGTTGTGT	9334	A_95_P098553 BP534544
9730	115	40	615	GATCCAACTGCAGACCAGCAGTTGAAACAATATATTTCTTGTTTTGTTTCAAATATGC	9336	A_95_P283673 TC51838
9732	115	42	1439	CTTCTGTTTGATGATTGTTGACGGTGAACCACCAGTTATAATTATCACCTTGAAATTC	9340	A_95_P000326 AB032546
9736	115	46	1351	CTCCTTAGTGTACCCTAAAACCTGTTCCATTCTCAATGAAAAAGCATTAATTTTTCCAT	9348	A_95_P019141 TC54601
9738	115	48	493	AGGGCCTAGTGCTACTTTGTGTTGTATCATTTCAACTTTTACTCGTATCTTGATATATG	9352	A_95_P025356 EB682879
9744	115	54	748	CCATTGATCCTTTCGCAATGTATCGACCGACCTGTTTAATATGATAAAAGTCCAATTTT	9364	A_95_P129622 EB429592
9745	115	55	955	CTGGTGCTAGCATCAAGAGAAAGATTATCCCACATATTTTCAGTATACAAAATCACAT	9366	A_95_P200692 TA17261_4097
9747	115	57	32	CAGTTCAAAGCTAAGGACGTGAGACTGCGCCTCAATAATATATTATTGTAATAATGT	9370	A_95_P128187 EB427716
9750	115	60	213	CGGATCATGAATTTTCTAGTCTTACCAGACTTTTATCGTCTTTTTGAATCTTTTGGAGG	9376	A_95_P132152 EB432603

9753	115	63	1275	GACCCGAATATCTGAGCTGCAGATTGTTTTCCTTGTTATATTTGCAATTGGCTGGATA	9382	A_95_P016461	TA15106_4097
9759	115	69	273	AATTACTGAAATTGTTTTGGTAGCCGGTGTGACACCTTTCGTGGTTGCGGGAATCGA	9394	A_95_P150632	EB680765
9761	115	71	1118	TGGAATTGTAACTGCCATTGCTCTACATTGCCATGAACTTTAGTATTCAACCTTACTCC	9398	A_95_P195967	TA16235_4097
9764	115	74	870	GACTTTGTTAATCATTATCAGCTTTCCTTCACTGGTTCCGCTTTCTCTTGAAAGTTGTG	9404	A_95_P008756	DV158570
9766	115	76	788	ATGGATTTGTAATGGTTAAGCTTCATCTTTGTATACATTTGGCTCTAACATGCGGATG	9408	A_95_P019366	EB677167
9773	115	83	728	GGAGAGATAAGAGTGTTTTTCCCATTCATTAGAAATTTTAGCATGGGATGTAGCATT	9422	A_95_P014381	TA11720_4097
9776	116	1	748	GGGCTCTCTGACTTCAGCAATAAGCTGAAATAATCTTGTATTCTTCCAATTAACTTAC	9260	A_95_P267311	DV159761
9777	116	2	829	CTTATGCTACCAATCAACGAATGTATGTGTGCTGTAGCACCTGATATGCTCGCATCTA	9262	A_95_P227434	EB425341
9778	116	3	712	GGGTTGTGTTGGGTCATTTTCTGCGAATTATGATATTAACTGCTTAAACCCTGGTTTA	9264	A_95_P193087	EB678134
9779	116	4	854	GGTGCTTAATGCACCATTCAGTTTAATAGCTACTGTGTGTAACAAGAACTATGTTATA	9266	A_95_P213812	TA20128_4097
9782	116	7	784	GTGAACCTAAGGCTCCTCCTTGCCGGGATTTAGATGCTTGCTCTGCTGAATAGATTTT	9272	A_95_P187792	TA14426_4097
9783	116	8	794	TAGGCAAGCATCTTTCAGTCGTTTTAGAGGTGGTTTCTCTTCTATCATGTACAAAAAG	9274	A_95_P126342	EB425683
9785	116	10	551	CTTTATTTTCTGGCGACCTAACCAGAAAGCTTTAAATTCCAGCGGCCCCTGACTGCTT	9278	A_95_P257109	EH621959
9788	116	13	712	TCTCATGCTGCACGGACAACTCACATGCTAATAATATCAATCCGCCCATGTGTTGTCA	9284	A_95_P314983	FG199812
9792	116	17	337	AAGTTGGTGGTGAAGCAATACCAGGTCTGGCGCCTCATTACAAATTTTCTCTAATTCC	9291	A_95_P103777	FG143827
9796	116	21	574	TAGCCTGTTTCAAAAGATAATGAGGTTGGCTATGTTGGAGCTTGCTTTGACTGATAT	9299	A_95_P018491	EB678172
9801	116	26	453	GTAGTAGTTGTTGTTGTTGTCGTCGTCGTCGTTGTACAAAAGCCAATTGGTGAACAG	9309	A_95_P139922	EB443834
9803	116	28	157	AGATGTTCTTGCATCACATGACAAGCCATTCCTTTCATCATCGGCTTATGTGGTGGGG	9313	A_95_P102357	CV015990
9806	116	31	819	TATATAGTTTTCTTTGACCCCGCAGCTGAGCTCTCAAAAATCTGCAATATCTGCAGAT	9319	A_95_P014416	EB449539
9808	116	33	1202	GCTCGGTAGTTTGTGCCTGTTTATCTTCTTTCTTATTACTAAGATATATGACAAAGGAT	9323	A_95_P123292	TA13567_4097
9810	116	35	491	CTAGACTAGCCCAAAATTGCTTTTACAATGGGCAATGAATTTGATTACAGAGACTTG	9327	A_95_P019791	TA14991_4097
9814	116	39	1685	CATTTTTGGTTGTGGAAGTGAAGAGAGCAAGTGGTGATACATTGGAGTACAACCAG	9335	A_95_P134317	TA13774_4097
9815	116	40	631	GACATTACACCCAAGTTTGAGGAACGTGATTCATTTCGTTGTGATGTAGACTGCAAA	9337	A_95_P203427	TA17851_4097
9818	116	43	508	TTCCCCCCTCTAAAGCTAGAGTTTGAAAAGATAAAGGATGTATTTGAAGGTCATTGA	9343	A_95_P044046	BP130776
9819	116	44	827	GAATCTTTGTTTAGCTGCAGCAACCCTCTTCAAAACATAAGGTGCAGGTGGTTGGAT	9345	A_95_P266971	DV157633
9821	116	46	457	GACTTCACGGTGTAGCTTGGAAGCTGCAAATACTCTTTTACAGTAGTCAAATACTGT	9349	A_95_P133377	EB434825
9822	116	47	635	AAGCTGAAAAAATTGTCCAGATTAAACGAGCTGAGGGTGATGCTGAGGCTAAGTAC	9351	A_95_P135162	EB677602
9823	116	48	752	CTCTCTCTTTCCATGCATTCCCTTCCTGTCAATCTGTATAACTTTGACTCAGATCAGAG	9353	A_95_P246882	FG150796
9825	116	50	200	AGAATGACGAACAAACTGTAGGTGCGAGAATATTGCTTCTAAAACATAAAGTTTCCC	9357	A_95_P217512	TA20950_4097
9827	116	52	688	AAGTCAGAACAACAGTGGTTGTGATTGGCAATGTACTGTACCATTCTCTCCTCCCTAT	9361	A_95_P284268	FG151259
9829	116	54	672	TGTTGTTGGTGGAAGAGATGGTGTTCAACAGTTGGGCTTGGAATTGGGCTCTACAG	9365	A_95_P303428	FG151438
9832	116	57	609	AACCGCTCTTTCAAATTCCACAGCTGCACATTTCTGATCATTTTTACTTCTATGTTAAT	9371	A_95_P262576	EB445150
9833	116	58	487	TTTGAGTGTTATTGTACTGTAAACGTTTCGTTTTTTGAAGAAGAAATCTCCCATTCCG	9373	A_95_P159462	EH617704
9846	116	71	285	GGCGTGTACAATATTACTCAACTGAATATTTTAGTACAGGCGTACGTTCGTACATGCT	9399	A_95_P097758	TA20565_4097

9849	116	74	469	CAAAACTTACGAAAGCCTCTTGGTTCGATAAATAAGCTCCATGTGACAGGTTTTCTAT	9405	A_95_P187732	TA14411_4097
9850	116	75	665	ATCATCTTTTTGAGCTTTTGGGCCGAAGTGCACTACAATTCAATCTATCCGCAAGGAG	9407	A_95_P298978	FG645447
9851	116	76	809	AAGAGCTAGCCAGATCTATGGACAAGGACATTGAGATGAGCTATAAATAAGTATTTT	9409	A_95_P254944	EB449161
9853	116	78	816	AAATATCAAAAGCTTCCGAGCTATTAAAGAGGGAATCAACGTCACTACGAGCCGCAC	9413	A_95_P266456	DW003912
9856	116	81	862	GCACAATATCTTTAGCTGCTTCTAGTTTTGGGATTCACTATAATGGTGGAATTTCTTG	9419	A_95_P211612	DV159929
9858	116	83	575	CGATTGCTTCGAAATTATCTTTCTAATCTATGATGATGAACTGAGGATTTCTTGCTGA	9423	A_95_P184402	FG634402
9860	116	85	895	CTCTCGAGGATGGGAATAACAAGCATATTTGGGGCTATATATTTTTAGTTTGCCGAG	9427	A_95_P017901	TC44187
9866	117	6	631	TTTCAATGGCACTGCACTAGGCATTTTAACTTTTATATACATGGATGATGCTGCTTTCG	9438	A_95_P207202	EB679579
9868	117	8	558	GACGGGATAGATGGTAATTCTCAGTTAGTTGAATTCTTGAATAGGGAAATATTTTGC	9442	A_95_P297468	EB683673
9869	117	9	855	ACCAAAGGGCTTTTGTCCTTTGGTACTGACTATTTGTTGTTTATTGGCATCTGGTTTTT	9444	A_95_P271446	EB449461
9870	117	10	762	ATGTACTTATGCTGCTGTGCTAAACTGTGGTATCAGGAGATTTGGCTCTATGAGCACT	9446	A_95_P265241	FG151976
9874	117	14	719	CTGGATAGACTATGATGATGCTATATCAATCTCTGTCAACGAGGAAGTAACATTGAT	9454	A_95_P138997	EB442705
9878	117	18	694	AGAATGTTTGGAAGCTCAGGCGCAAGATTAATTGCTTATCCTCATCCTAGCCCTTACC	9462	A_95_P292723	EB428286
9879	117	19	704	GTTGAACACGTTTCAGAATTTGCATCTAATGTTTAGTTCAACTGTTTGGCATTTGCAT	9464	A_95_P177262	TA11928_4097
9885	117	25	1587	GTGCATTAGGGAAGCAGCTGTACTGTTTACTTATATGTTCATTCGTTTGCTGACAATT	9476	A_95_P179012	TA12404_4097
9890	117	30	810	AAGAGTTGATGGGCAGAAACGAACAAAACCTATTCAGAAGCTGCAGCAACACAACT	9485	A_95_P297033	EB680939
9897	117	37	605	CACATGCAACTTATGCTTCACTTGATGGAGTCCTTTATTGCCAGCACCATTTTTGCTCA	9499	A_95_P305863	FG201356
9898	117	38	1349	GATGATAAGAGTCAGACCTGTTTTGTGATTCTTTAAATGTTTCTTTGAATTGGAGAGC	9501	A_95_P012086	AJ438614
9899	117	39	611	CTTGATCTTGTTGACCTTGTAGCTTTATCCGGGAGCCACACAATTGGAAACTCGAGAT	9503	A_95_P139372	FG146483
9900	117	40	3868	GAATCTCTAAAAGTCTTGAAGATTTCTACAAATGAGAATCCCGCAGATATGCTGACC	9505	A_95_P007056	TC55284
9902	117	42	739	GTTGTTAGTGGCCTAAATGTTGTCCATTATTTCCTGTACATTATGGAAGAGTTGTCTTT	9509	A_95_P015666	TA16785_4097
9906	117	46	802	TGAAATGGAACATATTTCAATTGCTTCTCTTCCGGGGATGTACGAACGAACTGTGAC	9516	A_95_P019921	EB427335
9914	117	54	721	ATCTGATGTGGAAAAGGTGGACTCTCTGTAAACCCAAAGATGGGGTGATGCTTTGCT	9532	A_95_P201727	TA17485_4097
9915	117	55	407	GAAACTTTGTGTATCTAGGGCGAATTTCCCCCCTTTCAATTTTTGATTCTGTTATTTGTT	9534	A_95_P095838	BP533362
9916	117	56	461	ATGATACTTTGGGCCCCATCTTGTTTTCAATTAATAGAGGTCTGAATCAATGTTTCAG	9536	A_95_P121402	DW001464
9919	117	59	764	AGCTTCAGGAAGTATATGTCTTTGTGGTTACTGAACTGATGATGAAATGTTTTGTTTC	9542	A_95_P011811	EB681685
9920	117	60	1054	AAATGTTTGAATGCAACTGCGCGGGATTATATTTACATTTCGTGCTGAATTTCACGTG	9544	A_95_P024761	TA14159_4097
9921	117	61	340	GGGTTACAAATGTTGAAACAACTCATTACATACTTGGATCTGTTGCAGGACCACATC	9546	A_95_P070170	BP192543
9922	117	62	609	GAGGAAACTCGCATGGAGGAATGAACAATTCACTTCCTATATTCTATATTCTCAAACT	9548	A_95_P089513	EB677527
9925	117	65	753	GAATAGTGTTACTCATTTTCTAGAATTGGTTTCTTGGTACTGAATGAGCCACAATTTG	9554	A_95_P031501	TC46025
9926	117	66	824	CCTGAGGTACAATTTACTGTCCAATGTAACCTTGGATAACTGATCAATACATCCTTTA	9556	A_95_P296533	EB677605
9927	117	67	470	CTCAAGTGTACGATTTACCTGTGTTTTGAAACTTTCTGAATGTTTCGTGCCTAATAAAG	9558	A_95_P005466	TA12358_4097
9929	117	69	0	AATGCCAGTATTGGAGGGTGTATTAATCTACTGATCCTACAGAAGTGGAAAGATTCTT	9562	A_95_P031051	A_95_P031051
9930	117	70	893	GCGCATGCGTTTTTTCCCCCCTGCTTTAGATGTAGATATTATTTTGGCGTTTTTCTATTT	9564	A_95_P217457	TA20936_4097

9933	117	73	1020	GTACTTAACCAAGTAATTTAGAGGGGTCCTTCGGTAGAATGTAATAATGTGAATATG	9570	A_95_P028551	TA12679_4097
9937	117	77	637	AATCGGTGCACGTGGTTGTAATCTTCATTTTAACAATGAACTTTTCAGTTCAGCACCA	9578	A_95_P122422	DW002400
9939	117	79	549	TTAGGGCCATAATTGTATGGATATTGCATCTCTCCATCTCTTTCTCTTGGTGTCGCACA	9582	A_95_P236774	TA18727_4097
9954	118	9	876	AGAGACAGAACAAGGTTACTATGGTACAATGGTACAGATGTGGAAGTCTGCGCATG	9445	A_95_P219057	EB449531
9955	118	10	308	GTGAACAGTCCGAAACACGAAAATTCGGTGAATATGAGGGTAGAGATGAACTGTGT	9447	A_95_P026221	DW000146
9958	118	13	583	TGGTATCACGACTTAACCATTGTAACACTAGACTTCCGGTACTTAATGTTATTGAAAC	9453	A_95_P203097	TA17781_4097
9960	118	15	564	AATAGATGAAGAGCGTTATCATGATGCTTCAAGATTGTGCCAAAAGTACGGGAAGT	9457	A_95_P156767	FG160166
9962	118	17	579	TGCGTCTCCAACTTTATGATCTTCTTCAGCAGTGTATGTATGTGAAAGTGTCACTCTT	9461	A_95_P219117	FG645464
9966	118	21	399	TACTAACCTTTGTGCTATCCATGCTAAGAGAGTGACCATTATGCCGAAAGACATTCA	9469	A_95_P107002	FG641470
9967	118	22	660	CACGGTTTTTGGTGTTTGAAACACTTGAGGAATTAGTAATGTTTTTCTATTATGCACT	9471	A_95_P149922	EB679934
9974	118	29	861	AGGGTTGGTGCTTCGTGGATCTCATTCTGAATGTTTAGCTTTATATTTCATCTTACGT	9484	A_95_P199572	EB424673
9982	118	37	687	TATACGGAGACCCGTTTTTTCACAAGAAGAATGAATCCCAGTTCAAAAGAAGGGGG	9500	A_95_P162492	EH621448
9985	118	40	216	GGGATTAAACATCTGATTAGATGTGGCTAATTTTGCTCATGGAACCTTTTTCTGTACG	9506	A_95_P107547	EH621391
9986	118	41	876	CAAATTGGCAATTGTTCAAATTTGGAGTTATGTACTATGAGCTGGTCTCATTGATTCC	9508	A_95_P189592	TA14820_4097
9991	118	46	444	AACAGTAGTAATTTCTGTTGACCATCTTCTTAGTTGTAGATTCAGCTTTGTAAAAAGG	9517	A_95_P142987	EB446380
9992	118	47	750	CCATTGATAAAGTCACTGAAGCCCAGCCTCACAACGGATCATTATGTGTAATATATA	9519	A_95_P104267	DV159758
9999	118	54	248	CTAAGCTGAACCAATTAAATCTTAATTATGCAAACATGGATGGGTGTTAGCCTTTCAT	9533	A_95_P102617	CV016109
10000	118	55	617	AATTGGAATGATATAAAGAAGATTAGCATACGCCCCCAATGCAAGGATAACGAGCAT	9535	A_95_P233044	EB436935
10001	118	56	352	TTCAATTTCGTACTGGTTTCATCGCCCCTTCGTCGAGTGTATTGTGGAAGAGGAGTTT	9537	A_95_P076785	EB681161
10003	118	58	1016	GGCTTGTCATGGTTTGGATCTGGTTTGTAAATTATTATTGACAAATAGATCTTGCCAC	9541	A_95_P017906	TA12822_4097
10006	118	61	846	AACTTCTTACGTCCTGACATTTATTGGCTTTACGGAACACATTTTATACAATCCAACGA	9547	A_95_P231204	DV999740
10011	118	66	753	TTAATAAGTACTGGTTTCAGTCTCTCGTATGCCCAAAAAGGAGAGATGGCCGACAGG	9557	A_95_P292228	FG143890
10012	118	67	182	GTAAGCTGGCTGCGCATATAGACTTCATCAACGCAGAACTTGAGGTTGAATGAAAA	9559	A_95_P060855	BP135107
10013	118	68	96	GTTGGAGTAAAAGCAGCTGAATGGCACAAAGTGCAAATAAGAATTATTTTACTAGTT	9561	A_95_P132887	EB433697
10017	118	72	458	TCGAGTGCTGCTTTTAGTGAATGAGAAGCATCTTCTATTCATTTCTGGTGGCCAAAGA	9569	A_95_P271331	AM843409
10018	118	73	687	CTAAAGTTTGGTTGCTAATTTTGGATTTCCATCTCGTCTGTTGGCTGTTTCGTGTAAG	9571	A_95_P268806	DW003107
10020	118	75	760	ATCCGAGAGACATGAGATCAGTATAAACTTCATCGCATAGAGCCATTTGCGTGACAT	9575	A_95_P160162	EH618805
10022	118	77	648	GGAGTGGGTGTGGGGGTTTATGTTCTACAATTAAATATCATGTACTATTAGTAATGC	9579	A_95_P201027	TA17337_4097
10028	118	83	920	AATGTGAATCCAGAACCTCAGAATGTCCTTCCTGAGCCTAAGAGCTCTAGCACAACG	9591	A_95_P190922	TA15117_4097
10030	118	85	565	TTGCTGATTCGCGACTTTTGCCTTTGCATTATTCTTCTTATAATATAGCTAATGACCTG	9595	A_95_P222307	TA22005_4097
10033	119	3	845	GATTGGGAGAATGTTTTGAAGTTTGGATTTTGCACTGATGGTTAGAGTTTTGACAAT	9600	A_95_P012906	TA12892_4097
10035	119	5	820	ATGTTCAACTTTCTTTTTCCTAGTGAAAGTGTAAGACGATGGCCTATATTATTTCCCGT	9604	A_95_P185427	TA13910_4097
10041	119	11	1063	TGGTGCAAACCAGTATGATTTTCTGCTTTGACCTATCCAAAAGGTTAATTGATGGATT	9615	A_95_P014621	TA16696_4097
10050	119	20	829	CCGCTGCTGCGTGTTAGTGAAATTGAGAGAATCAATAGCTTCATCTGTTGATATTGC	9632	A_95_P289493	EB678011

10054	119	24	602	AATCCCAGGGTCTTAATACGTTGATTCAATTATTTATTACTAGCATGGAGGTTCATCA	9640	A_95_P201002	FG644605
10058	119	28	867	CCAGGATCTAGCCCTTGTATCATTACTATGTTGTGCATCATCTTAAATTACTCATTAAC	9648	A_95_P246352	EB678725
10059	119	29	831	GTCTAAATGTCTACAGTATTTTGCTACATGACACGTTAGTCATGTCCCGTGATGCAGT	9650	A_95_P015681	EB677928
10060	119	30	777	ATATGTGGGCAGAGGCATATAAGTGATGGCATCATAGTCTCTGTTACAAACTCAGTA	9652	A_95_P037936	TA12762_4097
10062	119	32	616	AACTGCTGATTCTGGTGTTGCTGCTGTTGTTGCCATTTGGTGGATTTCCAGCAATTAG	9656	A_95_P056396	BP133943
10067	119	37	731	CGTGAAGTTTTACTGCTGTAGGGTATTATTCCAGGCTCATTTTGTTATGACGTTTTAG	9665	A_95_P014756	TA11873_4097
10077	119	47	322	TCTGTAGCATCCAAACTTGTCCATGTATATCAGATTTTTAAGATGCTAAGCATCTTCTC	9685	A_95_P114052	CV021418
10078	119	48	448	ATGTGCCAAAAGAGGCTTCTGTCGAACGCACACTTTTTTCATCAATCTTCAGAAAATT	9687	A_95_P136857	EB440570
10080	119	50	338	TTGCCGATGAACGAAGACTAAAGACAAGACAGCTAATGGAAGAAGAGAGAATCCAT	9691	A_95_P054011	BP133331
10082	119	52	833	GTTAGCAAAACTTAGACTAAGGTTCTCTTACTTTTCTTTCAGCCTAGTATGTTAGTTGA	9695	A_95_P228119	DW004819
10084	119	54	510	TGCAATACTCTGCACTATGTTGCTCTCTAGTCACTACATCATTATGAAGCCCATTCGC	9698	A_95_P013141	TA14138_4097
10086	119	56	807	AATCTTTTTGGGATAGTCGAGGAGCGCCCTAGCTGGCCTGGACACTACTGTTATAAA	9702	A_95_P021636	EB426600
10087	119	57	839	AATGCAAGAAAAAGTCATAGCAATCAAAGTTCAGAAGACCCTCCATCATCCATTTTG	9704	A_95_P179902	TA12613_4097
10092	119	62	826	GTCGTATCTCGAAACACGTGATATTTAGTGCTTAATGCATATGAATGTTTTTCTCGGT	9713	A_95_P013721	TA15116_4097
10093	119	63	758	GGGAACCTACCTTCTTGTTCACAAGCTGCAAACGATGCTTCTTTTTATAATCATAAAA	9715	A_95_P164192	EH623339
10094	119	64	478	AGGCGTAATAGTAGTTGTTGTTGTTGGAAAACTCTTGTTATTGTGTTTGGTTTGAGTG	9717	A_95_P178192	TA12178_4097
10100	119	70	855	AGAGGGGGAGAAAAATCTTGGTCCCCATGATCGTCTAATTCATGTTTACCATTTCAC	9729	A_95_P229529	EB682588
10101	119	71	346	TTGTTGAGAAGGCTAAAGAAGAAGGCTATGATGTGAGCAAGCTAAACAAGACTCAA	9731	A_95_P156692	EH614617
10109	119	79	1690	TGGAATTTGGAACCTGAGAACAGAAAACCTCGACTCATGGTTTCTAGGCCAAGAAAC	9746	A_95_P186757	TA14194_4097
10110	119	80	790	GGCAGCTTCAGTGTTGACGTTGATGCTGCTCCCTCTATTTTACCTTATTGTCTATTTGT	9748	A_95_P209847	EB439165
10113	119	83	635	GGTAGTCGTGACCGCTGTTGATTCTTTTTACTACTATCATTATTGTTGTTGAACATTAC	9754	A_95_P207032	DV999819
10125	120	10	764	TCTTGGTTACCTTCAACCAATTAGCGGAAGGGGTTTTGTGGTTGTTACTAATCAGCTG	9614	A_95_P268476	DW001859
10132	120	17	705	AAGGCCAAGTCGGAACAGCTGAATATCAGAAGCTTCTTGCTTCAAGGTTGAAGAGC	9627	A_95_P033399	AJ632711
10137	120	22	498	TGAATTCAGACGAATTGAATTTCTGGGGTAGCCGTAAAAGTTTTGAAATGCTGAAGC	9637	A_95_P264801	BP528807
10142	120	27	287	AGCCACCCCCCTCATCCACTAACTCTAGTAAGTTATTGTTACTAGATTTTGTGGTTTT	9647	A_95_P134162	EB436085
10147	120	32	356	TCAGTGTATCTATTTAATCTGTTTTTGAGTGAGCCACTGATTCGTTTGACCTGTATCTT	9657	A_95_P097258	BP533958
10149	120	34	655	TTAATGATCTTCGAGTCGACAACTTCGCCGTAGTGAGCAAAAGCATCTCCTAAAGTTC	9661	A_95_P189682	TA14840_4097
10152	120	37	838	AACTCCATTTTGGTGGTTCCGTACTGTCACTTTGAAGTTTGGAAGCAGTCGCTTGGTC	9666	A_95_P200292	EB426680
10157	120	42	1517	CTTTTGATCAACCAGCTGATACTAATTCTTGATTGAACTGTCATCTTTTGAGCTCTATT	9676	A_95_P017566	TA15028_4097
10163	120	48	781	CGTGGAAGAAATTGGATTTAGCTGTTGGCTGATTATTTTCAGAAATTTGTAGTTGGA	9688	A_95_P013906	DV159892
10165	120	50	261	GAGGTCGACTAAGCTGTTGGTGTTGTTCCTCTTCTGTTTTATAGTAATTATCAGTTATT	9692	A_95_P102592	CV016096
10167	120	52	748	CCTCAGTAGTTTGATGTGAAGATACTATATATTTTTCAGCCTTTTGCGAAAAACCCAT	9696	A_95_P189322	FG171924
10168	120	53	488	ATGATTAAATTGGGCCGTGGTGATGAAAATGGTGGTGGTGTTACCTTTGAAGGTTTT	9697	A_95_P252949	FS409302
10170	120	55	881	CGGTTTGGATACCGAAGTTGTTTTCACGAAAAAGAGTTGATCGAACCGGTTCGGGTA	9701	A_95_P283383	AM851016

10171	120	56	226	ATCCAGCAATTCTCAGCAGAATGAGGAGAAGATGCTCAACACCTGTCTGATGCTAAA	9703	A_95_P164772	FG148948
10173	120	58	816	CAGGCCCATATGCTATTTAAGTTTGTAAATTTAGGAGATGTTCAAGTAAAGACCTGAT	9706	A_95_P194912	EH615319
10174	120	59	159	GGTGAAACGTGAGGAGAAGCTTTTGATCAAGCAGTTAGAGAGAAACAAACGAGAA	9708	A_95_P068655	BP137183
10176	120	61	187	TGTGAAAATCTTGAGGATGCGAGCACATGAGCTAATTCTGACCGATGCAAGAGATA	9712	A_95_P105642	DV999385
10178	120	63	514	GTGTCTTCTGTATGATGCCTACCTGTTTAACTTCAGTTAACATCGACTGGTTTAAAGT	9716	A_95_P188217	TA14521_4097
10183	120	68	730	TTGTTCTTAAGGTTGATGATTGGCTCTTCTGCCATGGTGGCCTTCTTCCTCATCATGTT	9726	A_95_P150452	EB433813
10184	120	69	628	CATCTCAAATTTGCCAAAGGCTAAAGATGAAGATACATCTAACCTTCCTTGTCAAGCA	9728	A_95_P189147	EB424654
10185	120	70	839	TCAGCTCAATTGTTTGGATATTGCTCTTGGAAGAGCTGATTAAAACTGATCCTGGGCT	9730	A_95_P236054	EB448164
10187	120	72	1202	TTATATGCATCTTTGTGTGGAGGACTGGATGTGGTGGTGGAAAGCATTCTATGCATC	9734	A_95_P215722	TA20550_4097
10188	120	73	488	GCCTATTTCCCAAATATAATTATAGCCCCTAGTCAATATACATATATTACTCCCTCCGT	9736	A_95_P204047	EH622076
10193	120	78	478	GATTGCTCACTGTTAAAGTTTAGACCAATGCAGCTCTACATCTGTAGATGAAAAAATT	9745	A_95_P146842	EB450993
10199	120	84	504	TGAAGTCTTACATATCTAATGAGCCACATTATGGTTGATGCTGGCCGTCTGCACTCTT	9757	A_95_P050446	BP132397
10205	121	5	810	TATAAAGATATCACACTCAAGGTGAATGGAAGTGCTTCGAAGCAGGAGGTATTCGG	9767	A_95_P195382	DV158230
10210	121	10	774	CATTATCAGCATTCCTGTGCTGTTGTTTCCAAGAATTAAATGCTAAATCTTCTTTGAG	9777	A_95_P012746	DV160348
10212	121	12	321	TATCGAGCCTAATAGTTTCTTTCTACCATTGTTTAATTGTAAGGATGTGCTGCTATTCA	9781	A_95_P004571	EH621092
10215	121	15	802	CCAGTTTTGTAACATAACTGTATTTCTTATAGAGACCCCTGGCTTTTCATGTCAAGAA	9787	A_95_P022686	TA17003_4097
10216	121	16	581	TTATTAACATTAATGTATGGACATGGGGCTTTATAAATGCGCGTCACTTCCATTTGCG	9789	A_95_P015811	DW002308
10220	121	20	130	CCGTATGTAAAATCTAGTGGGGTGTACTTGGGTTTAGTTTTTGCTTTTCATGAAAATT	9797	A_95_P141872	EB445487
10222	121	22	1334	GATGGAACTTGGAGCTTTGTGTTATTGTGCAAGCTTCTTACTCATTCAGTTATTTCAT	9801	A_95_P013021	AB017694
10223	121	23	640	TTACTGCTGGCATTGTCTTGTGCTGTGATCTAGATGTTCTTAATAATGTCATGGAATT	9803	A_95_P013556	EB431060
10225	121	25	710	AGTTACCATGGGGAGTACTGCTGTATTACTTATCGGATGGAGGACACTCTTGTTCAG	9806	A_95_P188572	DV999990
10226	121	26	506	TTTGTGTCCATTGCGTTCTTGCAGAGGTTTAAATATCCTTTCACTTCTAGTATAAACCA	9807	A_95_P180242	TA12694_4097
10228	121	28	1004	TTTACGTGTCCATTCAAGATGTCCAGTGTGCAATGTTAAACGTGAATGAATGCATAGT	9811	A_95_P013651	TA15113_4097
10231	121	31	246	CACGCGAAATGCACAAATGGCTGAAACAAAGCTAAAACAAAAACTCAAATGAAGAT	9816	A_95_P096883	TA18314_4097
10235	121	35	1362	GGAGGGATTTTTTCAGATTCATCACCAGAAATATAGTGCTGCAAACAAATCGTGCTG	9824	A_95_P195897	TA16218_4097
10249	121	49	1741	GTGACTTGACCTTAGTCCTTATGGAGCTTTCGTTTCAACCTTGTGCAAGCATATTGGA	9850	A_95_P193277	AJ344535
10252	121	52	1614	GCCTTCTTAGTCCCAGCTTCATCATGTGTTTGGACTAAATTAATTTTGTTTCATGTTCA	9856	A_95_P193897	TA15770_4097
10254	121	54	586	GGCCAAGTGTAGCACCTTGGGATATTTAGTAGCTTGAGTTTTTACTTTTTCACAGTGT	9860	A_95_P222362	TA22017_4097
10255	121	55	469	GTCTCTGATTCATAAGGTATTCTTATTGCGCGTGGAGCACTTTCCTTCTCCACTTCTTT	9862	A_95_P053336	BP133151
10269	121	69	619	TCGTTTCAGCAGTATCAAAATTAACCACTTCAGACTCTCCTTCAGCAATCAGCTTTGG	9890	A_95_P218317	FG641433
10272	121	72	189	AATATTCTTTAGTAAAAGGCGAAAGAATAGTTCGCTTTGTGCCCATCGCGTGGCTGC	9896	A_95_P142227	EB445749
10274	121	74	562	GTTGCAAGTTGGACTCTCCTCTTTTCAGAAGGGAAAGGAATTAAAATGTATCAATGA	9900	A_95_P270526	EB432745
10275	121	75	84	GAAATATAGCTCATTCACCAATCCCTTTTTCTCTTGGCTGTTTCTATACAGTTAACCTT	9902	A_95_P106362	CV017874
10276	121	76	680	GGGACAACTAATGTGTGATGGCTTTTGTGTAAACTATGTGCTATATACACTTTGCTAT	9904	A_95_P201982	EH624166

10280	121	80	659	AACGGGTGTTACTAATATGGAAAATAAGGCGTTTACGCTTTAGCAAGCAGTGTTATC	9912	A_95_P179602	TA12547_4097
10281	121	81	486	GTTCGCTGCAGTATCAGGTCCCTGCCTTGATTCGAGTTTAATTTTTTGCTGCTCTATAC	9914	A_95_P096318	FG639219
10282	121	82	837	CTGCAGACTTGCAAAAGATAATGCTTCCTTTTTTCACATCAGTATATATGAAGTTTCT	9916	A_95_P258668	TA13753_4097
10285	121	85	1032	AATGCTCTATACTTCATTTGTTTAAACAGCAGAGCCTGTTTTGCAGATGATGATGTTC	9921	A_95_P213967	TA20160_4097
10288	122	3	1149	AGGATCCTATACAAGAAGTTTAGGCAGTTTAGGGTCTCAGTGGTTTTCCCAATGGCT	9764	A_95_P213952	TA20157_4097
10289	122	4	858	TGTTGCAGGGGTTCATACAATCATGCTTGGTTCATATACTGACTATGATGAGTACTCT	9766	A_95_P118972	DV161905
10291	122	6	336	CTATGAAGACTTGCATATTTAATAAGGGATTATGAGGTCCATGATCCCCTATGTTTTT	9770	A_95_P005131	CV018107
10294	122	9	373	GCCTCGCCGCCTCCTTGAAAACTCATGTTGTATTGATTTTCTCTTCGTGCTACTTATTT	9776	A_95_P097693	BP534162
10298	122	13	726	GGTTTTGGATCGGGGTGAGAAGATTGAACTGCTAGTGGATAAAACTGAGAACCTTC	9784	A_95_P296238	FG634419
10299	122	14	524	GACACGAATTAGAAGAGAGTTGAGACAAGCTGCGAGACCAAGAATTATGTTGGGCA	9786	A_95_P053236	BP133122
10306	122	21	680	CGTCCTTGACATTTGTGTATGGACTGGGTATGAGAAATTCTATAGTATTTGTTTCGAT	9800	A_95_P008406	TA13639_4097
10316	122	31	786	CCTAAGTAAACTGATTATTCATTTACCATTCTCTGGAACAAATAGCAGTGGCTTTCAG	9817	A_95_P228864	EB451816
10322	122	37	651	AACCGCTAATGTATTCCCGTGTAATAATATTCCTGTTTTTGAACTGAGGTTCTGTTCAA	9828	A_95_P015526	TA12008_4097
10326	122	41	312	CAGAGTTCCCATGTACTTGTTGTCGACATAGGAGAAAACAACCTCTGCAAGTTTTTGT	9836	A_95_P213142	TA19985_4097
10327	122	42	279	TTGGGTACTTGGGGCTGAAAAATGTTAGGTTTCTAAGTTTTTGCTTGTTCAATGATGT	8937	A_95_P000091	AJ717873
10328	122	43	561	CAGGGCATTGATGCCTTTTGTTTGATCAGATTTTCTTATGCTTGCTAAAAGAATGATC	9839	A_95_P108412	FS436012
10330	122	45	893	GCATATTCCCGCAGTATGAACATTTCCTTAGTATAAAAGAATCCAGTGTGTTTGCTAT	9843	A_95_P181582	TA13014_4097
10334	122	49	513	TATGAAGATCTATCTATGAAGGCCAAATCAAGATTTAGTGTCTCTTTGCGAAGTCTTT	9851	A_95_P053651	BP133236
10335	122	50	486	GAGTGTTCTCCCTGAACAAAGGGAGATGGGATTGTGAAAGAAAAGGCATTGTGGTT	9853	A_95_P122242	DW002268
10336	122	51	713	ATTGAACTGCTAGTGGATAAAACTGAGAACCTTCAGTTCCAGGCTGACAGCTTTCAG	9855	A_95_P146777	EB450884
10337	122	52	823	TGAAGAAGAATGTGAGGCTGATGAACCAAAAGTTTGCTGAACCAAAATCTGGAGAA	9857	A_95_P157432	EH615494
10339	122	54	694	GTCCACTCTTGGGTTACCCACTGTAACTGAATTTGTGGAGGTAAATTTCTCTTTTATTT	9861	A_95_P217382	TA20920_4097
10343	122	58	826	AACTAACAACATTAGGTAGGGCATAGTCAGATTGCAGTTAACTCCATACTGTGATCTT	9869	A_95_P271731	EB445042
10346	122	61	489	TTCGTCACTGTGTACTGAAGTATCAGTCTCTTGGGAGATTATGTGCTTAAGGTTGCAA	9875	A_95_P083270	BP528720
10347	122	62	810	GGTAGAACTGAATACAAGCTAGCCGTCTTGCTATATGCCCTAATCAGTGTAATGTTAT	9877	A_95_P273041	EB680971
10349	122	64	100	AGTTGCTTTCACGGCTCGAACCTGTGACTTATAGGTTACACGAAAACAAGTTTACCGT	9881	A_95_P242162	AJ719139
10352	122	67	666	AAGAAATAGTTTTGGAAGGAGCGGAAGAGAAACGGGAGGCAATTAGGCAGCTTTG	9887	A_95_P260241	FG642865
10356	122	71	544	ATGCTCATGAAGATGTAATTGTTAAGCCTGCGTCATAGTGTACGAGCTTCTGCTTGCT	9895	A_95_P198897	FG628825
10360	122	75	614	TTCTTTATGGTTTCTCAAGTATTCTACTAATGTTGAATGACCAACTTTAAGGGGTTCGC	9903	A_95_P023767	TA14039_4097
10364	122	79	492	AGGTTCTTATTTGCTGTAGTGTTTAGCAAAGTGCAGTTTAAGGTTGTGTTGTATAAGT	9911	A_95_P089288	BP530435
10366	122	81	763	AAAGTTTGGGTGCAAAATCACTTCAGGTGGTCTTTCTGCAACAGAATGGGTTCAAAT	9915	A_95_P116177	TA13182_4097
10372	123	2	900	CACATTGCATGTACAATAAAAATGACATATATTGCATTGCCCTCTACTTTTTTCGGCTT	9925	A_95_P134207	TA13354_4097
10374	123	4	1484	GGAGTGGAACTGAATTTTGACTTGATGTGTTAGTCTCCTAGGGATTCTATTAAACATT	9929	A_95_P208077	AJ344538
10375	123	5	200	ATCAACTTGCCAATTCAACCATCCACCTAACAGGAAACTGGTAAGGAAAGCATATCC	9931	A_95_P133462	EB434968

10376	123	6	845	GCAATACAGTTTAGCAAATACTGATATTTCTTCCGTACTAGTGGGGAATGAAAGTCC	9933	A_95_P192647	EH616239
10382	123	12	687	CTCCATTTTGGTTATGGAGTGGGTTCAGTTACTGTCATATCAGAATACAAATTGAGTT	9945	A_95_P016216	EB684198
10388	123	18	207	CTCAAGTGGGACAAAGCCACGAGCTTAAGTTGGAATATAATCGTGTATCACACCTTG	9957	A_95_P106402	CV017888
10389	123	19	150	CTCTAGCCAGTACTATGTATTCTATTGACACAATCTCTTATCCACTGCAGAAAAGTTTT	9959	A_95_P129987	EB429951
10390	123	20	622	ATTTAGTCAAATATAAATATTTAGGTGTAAATGCCCGGTGCGGGTAAGCATTTACCA	9961	A_95_P250207	DW001637
10392	123	22	466	CAATGTAATGTCTCAATGGGAAGGATTTTGTGTGTCCCAGACTTGGTCGACGGATTT	9965	A_95_P002241	DW004871
10396	123	26	1038	ACAATATGCTTGTATTATCTACTACCTGGGGAAATTAGCTCCATACAGTACGTGATGA	9973	A_95_P010196	TA15624_4097
10397	123	27	868	AGGTCCTGAGAGCATGCATACTAGATAGTGTCGCCATCCACTATGGTAGAAAAGTTT	9975	A_95_P272556	EB450931
10398	123	28	363	GTCTTTCAGCCTTTTATTTGGCTCCTCTAAGTTTATTTCTAGTTGTTGAGGTACCTATC	9977	A_95_P138637	FG625004
10399	123	29	645	CTCATAGTACTTAGTTATGTAACTTTACGTGTCTTATAATGGGAAACTGCATTGCCAT	9979	A_95_P123217	DW003092
10401	123	31	478	TGCCTCATGTAATATAGCTGTATGCTCATATTCAAGGCCGAAGAACTTTCGTGTTAGA	9983	A_95_P134172	EB436143
10404	123	34	887	CGGAGTAGGTCCCTCCTCCATTGCATTGGATTATAAACTGTATAAGTTATTTACCTTT	9989	A_95_P019231	EB425276
10406	123	36	408	TCTGGGTGATTTAGCCAATCTTGTTGGGACTATTCCTCATTCAATTTTCAATTGTTCAA	9993	A_95_P306683	FG635964
10407	123	37	2107	AGAATAACAATCGCCTGCGGTTGACTGCTGGAATGTTGAGCTCAAATAGATGCTGCT	9995	A_95_P188252	TA14529_4097
10412	123	42	725	TATTTGTTGCAAGTGCTTTCTTATCTCTGCTTTTGCTATCTGCACACTATACAGCTCGA	10005	A_95_P133252	EB434566
10417	123	47	2617	CGTAGGAAGATCTTGGGATTGATTGTTCCAATATCAATCATTCATTGCAAAATACATC	10015	A_95_P212937	AB032538
10422	123	52	318	GATTTGCCCCCTAAACTCCAATAAAAGGGATGCCCTCTTCCATCTCTGAACTATACAT	10025	A_95_P098043	BP534308
10423	123	53	322	AGTCAATATCAGTCATTCTTGCTAGCTCATTAGCCTTTGCACCCCCTTCACTTGCTGAA	10027	A_95_P102682	TA12603_4097
10424	123	54	446	ACTTGTGAGCATACCTGAGTAAAGTAATTCACTTGGTATATTGTACCCCGGTTAATTA	10029	A_95_P141922	EB445531
10427	123	57	741	AAATACAACAGCAGATCCTGCAGCAGATACCTACTTTGCAAGCACCCTGCGATATAT	10035	A_95_P153507	EB683766
10428	123	58	836	ATGCTTCAAGTCCGTTTGCACGGATGAGTATTGAATATTGAGGAGGGCTTATATCAT	10037	A_95_P135487	EB438979
10432	123	62	313	CCAAATTCTTTTTACCCAAATCCTTTCAAGTCCTTCCGATCAATTGGCGAGAATTTTCA	10044	A_95_P092208	BP531695
10437	123	67	997	GAGGGTGGGACTGAAGATTTCAGCCCCCATAATGTAATTTATTGATTTGTCATTAAT	10054	A_95_P011061	TA17064_4097
10438	123	68	834	CAGGCTATAGCCAAGCTGGAAAAATCAGTTTGTTTTGAGAAATGCTTTTCTCAAAAG	10056	A_95_P190192	TA14957_4097
10448	123	78	1056	TGTGCCCCTCTAAGTGGATTTACCGATGCCAAAGATCATAATGGTGTGCAAGTTGGC	10075	A_95_P238739	AB032198
10451	123	81	866	CTGATCAATCACACTGATAGCTTCAATAGTTCACTGAAATTTATGGATATCACCTATG	10081	A_95_P017291	TA12621_4097
10454	123	84	431	TGTGAGACTCTCAAGTTGTGTTAGTGGTTTGTTTTAATTATGAAAGCCTCCTGCCGTT	10087	A_95_P179147	FS416927
10455	123	85	390	GTGAACTTGTTTGTGAGACTGGCAAGTTGTGTTAGTGGATGGTTTTAATTCTGATTT	10089	A_95_P024051	TA14666_4097
10456	124	1	603	GTTTCTAAGTTGGGATTTTTGAGAAGATGATCTTCAGAGGTGGGGGGTCTTGTGTTA	9924	A_95_P060425	BP134993
10459	124	4	1547	GTTGTGTTATGGCATGTTTTTGGAACTTTGATGCAACTATTGGAGCAATCTCTTTTAG	9930	A_95_P011816	TA13725_4097
10462	124	7	363	TGAAGCTCAGACTATATTTGATGCTTTGTCTAAAATCGTTGCCTGTGTGCTGGGACAA	9936	A_95_P156922	FG643894
10464	124	9	532	TTGGCAAGCTGTGCATATCTTCTACTTGTGGAACATCTCTATAATGTAAAGGAATAAC	9940	A_95_P131802	EB435034
10465	124	10	760	GGCAGAGATTGTAATCATCAATTCTATTATTGTGTCCTCGAGAGCTCTACTACATAGA	9942	A_95_P206892	DV160757
10467	124	12	818	ATGGCTCTGATGGACCAGATGGTCATTTCATTCGGGGTAATACAAAGTTTACCACGA	9946	A_95_P290733	DW001012

10470	124	15	1587	GACGTGTATGTCTACAAGAATGCTTAGAATACCTTGTATTATCCCTATATTGAGAACT	9952	A_95_P008651	TA12972_4097
10473	124	18	744	TAAGCATGGCTTTGCTTGAACTTTTTGCTCTTCCCACTTCGCTAGAATGCTAAATTGTC	9958	A_95_P160107	EH618757
10474	124	19	739	GGAAATAGAGCAAAGGTGAGTCCCTTTAGTTATAGTCATTCTTTTCTTCTTTAACCTT	9960	A_95_P141282	EB445053
10477	124	22	504	ATGCAATCCAAAGCCGTTCTCTTGCAAGTTTCTGTCGTGCTATCACATGTATAATAAA	9966	A_95_P163377	EH622289
10479	124	24	778	TAACCCATCGTGGTGTTGCAAATAGTGTTAGATTTCTCACCGGTCACTCAAGAAAAG	9970	A_95_P018166	DV161248
10480	124	25	711	CAGTCCTGCTTCTGTAAATTTTTTGTGCTTTCAAGCAATCCAGCTGTATAATACACAA	9972	A_95_P203067	EB440029
10481	124	26	603	TCTCCTCCTCCTCAATGGGCTTAAAACACTATTATTTATAATGGGCTTATTTCCCGTGG	9974	A_95_P060940	BP135132
10482	124	27	193	CATCGTGGTGGCATCTGTATTTTTCATTGTCTTTCATCATATTGTAAAATTGATTGTCC	9976	A_95_P106862	CV018094
10494	124	39	561	TGTCAAAGTGAGACACAAGATACCTGGTTTGCAGTTGACTCTCCTCGAATAACACAG	10000	A_95_P055346	BP133677
10501	124	46	373	TGCGTCTTTTTCAAATGAAATGTCTGCTGGCTGGAGTAATACCTCATTTGACTCTTTAT	10014	A_95_P149477	EB679332
10505	124	50	212	TGTTTGACCTAATACTAAAAGTAGCTGTGAATGGGAAACTAAAGGAGGATGAGATG	10022	A_95_P032556	AB210290
10510	124	55	760	AGTAGGGCTATGCATGATTTCATGCCTATTGGTGTTTCTTATTTTTACTGCTAGTTGG	10032	A_95_P125132	DW004936
10512	124	57	226	TGTAATAAATGAAGCCCGGATGGCACACGTCATGTACCAATTTGGAGATGGATTTG	10036	A_95_P156352	EH613727
10513	124	58	547	GTTTATTCGTTTTTGTGACTTTTACTCGTGGGCGGTGGTGACCGCGTACATGCTATTT	10038	A_95_P108947	BP530129
10515	124	60	865	CATTAGATACCATTCATTTTATGCTCTGCATAGATCTGGAGCTTACAAGCACCTAATG	10041	A_95_P287833	EB427882
10519	124	64	354	TAAAGAGGCGAAAGGAAGCTGAATGGTTTATTGAAGGGGATTTTGACGCATATGTA	10049	A_95_P161217	TA14884_4097
10521	124	66	140	GATCGATGGGTACCCGGTCGAATATGTTTGCAGCTTTATAAATATAGTATATTTCTGC	10053	A_95_P120927	DW000908
10527	124	72	888	CGGCATGTCCAGAAATGGAATTACTATAGTCTTATTTAACCTTGTAATTGTGGATTCC	10065	A_95_P217472	TA20940_4097
10533	124	78	914	GTGTTTACTATGTAATGTGGGAGGCTCAACGTGCCTTTTGATGAATTTAAGTCATTAT	10076	A_95_P000796	AB213651
10535	124	80	241	AATGTGCCAGAAAAATAACAGAACAACGTTGAGCTAAAAGATCTGGTGATTGTTAT	10080	A_95_P109037	CV019121
10536	124	81	417	GCGGATGCAGGTTGTAGTACTAGTTGAGGAAATGCTTTTAATTTTAATTCCAGACAG	10082	A_95_P097208	BP533931
10540	124	85	142	CCACATATCAGTTCATGTACTGTATCTCCCCAATGACTGTTTAATAAAAAGCTTAATGT	10090	A_95_P129532	EB429494
10541	125	1	807	TCGTTGGATTAATAGGAAAATGATGAGCTTGGTTCATGATCATTATCCTGGAATCAT	10091	A_95_P215972	EB427456
10547	125	7	856	CTTTTGTGCCATAAGGGAGAAGAATGAAGCAGCAATGACAAGAGAAGAATGAAGC	10103	A_95_P131787	EB432202
10552	125	12	480	CTGCAAAGAGCTCGTTGAGGAGATGGAGCTTGTTGATCTCTTATTACTCGATGATTG	10112	A_95_P222962	FG629636
10554	125	14	634	ATCCTTAAAATGGTGGAAATGCTCAGAATCTCTAACTGAAATCTCCCTCCGGACAAC	10116	A_95_P260451	BP128854
10555	125	15	157	AAGGGCAACTTCTATCCTTTGGCATTTCCAATTCCCTTTGAGACAGCACTTAATGAGC	10118	A_95_P157317	FG640154
10560	125	20	225	AGAGACCTTAGACGCTTGCAAATTACATTTTGTACAATGATGGTCTGTCTCCTGTTAA	10128	A_95_P143817	EB447009
10562	125	22	560	AATATTCATAGGACTCCGAGCACGAGACTTCTTGGCTAATATACCTTGAAGCATGGG	10132	A_95_P241390	BP129934
10563	125	23	588	TTGGCTTCAGGGATTGCTAAAAGAGCTTGGTATTGGATACAAAAGTATCACAATTTTT	10134	A_95_P046286	BP131356
10565	125	25	437	ATGGCTATCCAAGGCTTCCAAATTCTAGTCAATTTATGGCTCCTTCAATATTTACTATC	10138	A_95_P083400	BP528751
10567	125	27	1946	CCTTTCTGTACTTATCATTTTCAAGGACTTGGGACTGGTTATACCAAATATTTGGGGTT	10142	A_95_P154227	EF051140
10569	125	29	562	GGGTTAGCATCTTTGATGTCTTTGTAAAGATTAGTCTCTTGTCAAATTGTTCTTTGGTA	10146	A_95_P221622	TA21858_4097
10573	125	33	801	GAAGATGAATCCAACGGAAGAGCTAGTAAGCGGCAGGTGAAGCTAACTGATATTG	10154	A_95_P209007	EB426833

10574	125	34	147	GCAGATAAAGCATCACAGTAGGAGTGTCCTTTTTCTTTTTATAACCAGAACTATTCTA	10156	A_95_P152262	EB682586
10579	125	39	688	AACCTCTAACTTTTGTCTGTCGCCTGAAATTGTACAGAAACCTCTAATGGGAATGTCA	10165	A_95_P122417	DW002399
10582	125	42	485	TGGGTTGAGGGAGCCTGTGCAAATGTTTGTTCTTGGGAAGACAGAATTGAGAACCC	10171	A_95_P036228	BP128677
10583	125	43	867	CCCACCGACAAGGTGTGAATTTTCTGTCATTTTTCTGATCATGACTATTATTTTGTTGA	10173	A_95_P180307	TA12712_4097
10584	125	44	699	GCAACCTAACATGACCATCTCCCCTATATTTGCTTTTAATGACAGTCTTTACTATACTA	10175	A_95_P192767	TA15525_4097
10592	125	52	705	GGTTTGACTTATTGTCTCTATCTGGTTCATTTCTGCTGTCTGAAATTGGCGGTCAACG	10190	A_95_P137612	TA16714_4097
10593	125	53	414	CCCTATTCACTGCTTTCTCTGTATATTCTTTACGTTCATGTCAAAGCAAACATTTATGA	10192	A_95_P028681	EB431359
10594	125	54	306	GCTTAATTGTCCGTATACGTGTAACAAAGTGAATTTGTATCCGTAGACATGTTACTAT	10194	A_95_P033241	AJ344584
10596	125	56	300	GTCGCTCCATAGTCATTCTTTTGGTGTCATGAGTATTATTTTGCTATTAGTCTTATGTC	10198	A_95_P131347	EB431534
10599	125	59	836	TTCCTGTGAACTTGCAATTGCATGGATATAATTACAGGTAGTTTTGACGCCATTGTTG	10204	A_95_P248707	DV158976
10604	125	64	734	AATTTCTCTAAACTGGCTAAGGAGAGCCCACAAACACTCGTCCGTGCTATAAGGGTT	10214	A_95_P212942	TA19944_4097
10610	125	70	90	CATGCCCGATGCTTTCTGTTTATTCTTGAGTCTATTTGTATTATAGTACTTAGTTACAC	10226	A_95_P161987	EH620690
10612	125	72	474	GGATTATTGTAGACTGACCTAGAATGTTAAATGTGATGACTTTTGCCTTCATGTGTTT	10230	A_95_P278013	FG643399
10616	125	76	716	GAGGAATAACCTCTTTGTTGACAATGTTAATGTAGAAGAACAATGTCAAAATTTAGG	10238	A_95_P127472	EB427008
10619	125	79	432	CCTTTTCTGCGGTGTTCCATTTCTGTGAATTGGTTCTGTAGAAGCGATGGTTTCTTCTG	10243	A_95_P006531	FG198048
10620	125	80	196	AACTTGGCTTACACATTTGATTTTTCTGGTTGGGGGAATTTTCTTTATTGGGCTTAGA	10245	A_95_P093308	BP532214
10622	125	82	854	GAGGAGCAAAAGAAATTATTATATGAGAACTATGGAAAAGATGATCCTGCTTGTGTT	10249	A_95_P024846	EB426351
10623	125	83	316	CCTGACTCGTTTATACGTTTCGTCTGTGTAAATGTCTCTCAAGTATAAGTGTTTTTCAT	10251	A_95_P090478	BP530969
10628	126	3	1061	CTTGGTGATGCTCCAATGCACTTGGCTTGGCATCAATATAAATTGTTCCAGTTATCTC	10096	A_95_P211602	TA19651_4097
10630	126	5	837	TCATGTTGTGGATTTAGCAGATGGACATATAGCTGCCTTGCAGAAGCTATCCGATCC	10100	A_95_P222147	EB682214
10637	126	12	0	TCCAAAATCCACCAAAAGAAAAAATATTTCTGCTCAATTGAAAGGGTGTTCCCTCAAG	10113	A_95_P023676	A_95_P023676
10640	126	15	830	AGAAGAATACCTGAATGCAGAGGCTAAGTTAGTTACGGTGTTCAGTGTAGTGGACG	10119	A_95_P118607	DV161686
10644	126	19	466	TAGGCGATTCAATATTTCGCCAATTTTGTTGATACGACTTGTTGGAATTTGGCAACCT	10127	A_95_P262501	TC74788
10648	126	23	635	ATCGTAAATTCTGACGGGGAATCACGGTTGTATCAAATTTGCGAAGCATGCTTGGTT	10135	A_95_P295373	FG643778
10655	126	30	684	GTTTTAAAGAGAATGACCAGCTTGCATATAGATTCTATGCCGTATGAAATCTGCCGTT	10149	A_95_P071765	TA20024_4097
10656	126	31	864	TTGGATTTGCTTAGAATGTGCTAGTTGCTTTTCCAACAAAGATGGTTTCCGTTACTTC	10151	A_95_P015371	TA13072_4097
10657	126	32	432	AGTCTTCGGCTAATATTAAAGCCCCAACAGATCACATTCGAAGAGAACAATTTAAGT	10153	A_95_P074365	BP526450
10667	126	42	335	CAATTTCGCGTGGTTTTCTGATTTGAGTTTTTTCAGCTGAGAAAATTTGGGAAAAAAG	10172	A_95_P101098	TA12306_4097
10668	126	43	773	GATCAAATGAGCAAATGATAGGTGAAAGCAGTGAAGACACTATCTAGAGTTATGAT	10174	A_95_P251372	EB447310
10670	126	45	378	CTCAGATCCGCTTGTGATATGAAATTATTGTTGTTCTTTAGCTAACCTATGAAAGAAT	10178	A_95_P141212	EB445001
10671	126	46	884	GCATTCAAATCGATAATTTTGCAGAGGGAAATGCACTACCTACAAGCTAACTCTTTTT	10180	A_95_P119462	DV162682
10672	126	47	837	CCCGATGCTTTCTGTTGATTCTTGAGTGTATTTGTATTATAATACTTAATTACACGACC	10181	A_95_P197692	TA16619_4097
10675	126	50	840	GTTCTGCAATCTGAATAGTTTCCGCACCAAGTTTATATTAGGTTTCTCCATCTTTCTGG	10187	A_95_P227795	DV161398
10684	126	59	458	TTAAGAGACGTAAGCTACCCATAAAGGGGTTGAAGCAAAGAGTTGGTAAGGCGATT	10205	A_95_P158077	FG137231

10689	126	64	628	AATTTTGACACCCGACTGAGACCAGTGTTAAGGGCTCTGAAGTGTGATCACTGGTTT	10215	A_95_P135447	TA13035_4097
10692	126	67	366	GTCCGGGACTCTTGGGGTATAATATAGAACATTGTATGGGAGCTTAACTTTTGGTAC	10221	A_95_P092568	BP531865
10695	126	70	621	AGCAGTGTATATTTTCCAAGTTTCAGTGGGTTGGGTATAAATCAACCACAACACCCTT	10227	A_95_P021336	FG638986
10696	126	71	346	GGACAAGCTTACACGAACTTAGACAATTTCTTCAGGTACCTAGCATTTTTGCTCTCTC	10229	A_95_P096213	BP533523
10698	126	73	845	AGCAAGTGGAGCATAAATGGAACCGACATGGATTAGGTGGTGATAATCTTGAAGGG	10233	A_95_P285813	DV162116
10703	126	78	903	GGGACAAGCCTCAATCTTGATTCTGATGCAGTTGTTTCTTCTATAAGTTTTTCAATATC	10242	A_95_P007801	EB429936
10705	126	80	874	AAACTTAAGCTGGAGAAGTTTCTCATGAGCTGCTACAAACTTTTGTTCTTTGAGTCTA	10246	A_95_P291793	EB424895
10711	127	1	819	AATTTCCTTGGGGTGCTTTGGATGATGTTGTGATGGGTGGAGTGAGTCAAAGTACAT	10257	A_95_P227459	DW001357
10713	127	3	326	ATTTAATAATAGGGATGATATGCTATGTCGATCTTATTAAGTGTGGTGGATGGACGT	10261	A_95_P109007	CV019107
10716	127	6	872	TTCCACGGAGCTTCTCGTTGCTGTTATTAATCTTTTCGTAGCATAAAAGCTTAACCTGC	10267	A_95_P196987	TA16462_4097
10723	127	13	426	TGCCATGCTTGAGTGGGATGAAACATGGGATTGAGGATAAACTGACAGAAAAGGAT	10281	A_95_P085065	BP529185
10726	127	16	1029	ACATGTGGTTCGAACTCATGTATTGTTCTGCGGCTCTTTTCTATTCAAAGTTTTCAGCT	10287	A_95_P020486	TA16369_4097
10729	127	19	184	CTGGCAGTTTAACACAGACGCTATATTTGAGGATTGGAAGTTCTATAGATTAATCATT	10293	A_95_P094788	BP532869
10734	127	24	543	AGGGGGTAACTATGGATGTTGTATGGAAATAAGTATGTGATTATGCATGCATACGG	10302	A_95_P153142	EB683453
10736	127	26	832	TAAATCGTGGTCATCTCAGCATCACTAAATGCTTTAAGCAGAATGCCGAGTAACGCC	10306	A_95_P255609	FG147452
10741	127	31	627	TTGTTCTAGGAAACGTTGTGTTCCCTCAGACCTGATCAGACAGGAAAAATGAAACAA	10316	A_95_P157687	EH623052
10743	127	33	629	AATGGCATTCCTTGGAATTCGAAATGCAATTCCAGTATTCAGTATGGTTCCTGCTCTC	10320	A_95_P125512	EB102905
10746	127	36	375	GGGAACCTTGCAATACTCTGCACTATGTTGCTCTCTAGTCACTACATCATTATGAAGC	10326	A_95_P186492	TA14139_4097
10748	127	38	558	TAAAATTGAACTCTCCACCATTCTCCTTAACATGCATACTTCACAAGAACTACATCTTA	10330	A_95_P046676	BP131459
10751	127	41	685	TTATATTGGCGTGCTAGCTTTATATAAGTCATGGAACACACTGTCTCGCCTGGTTGAT	10336	A_95_P066215	BP136535
10754	127	44	702	TGGCCAGCTTTGCGAGATAATGAAATTTTCTTGAATTTGGCTTCGTTGATATTAGTAG	10342	A_95_P180467	EB679246
10762	127	52	473	AAGGAGTTGAAGTTGTGTATTTCTGTCCAAATGAAAAGCCCCTGGCAGACTTTTATG	10358	A_95_P073580	BP526245
10767	127	57	801	GCTGGAAGTGAAGTACGATTCCGATTTGATTAACATTCTACTTGTGAATATTTCCTTG	10368	A_95_P117602	DV160541
10771	127	61	666	CTTGTAATAAACTTTGCCATCAGTGTGCACTTAAAATAAATGAATAAGTGGGTGTTG	10376	A_95_P033414	AJ632718
10778	127	68	774	GGCAGAAAATTTGATCGGTTTCTCCATGAATCATACATTGAGGACAATAAAAATGGT	10390	A_95_P314238	FG168120
10782	127	72	842	AAGAGTATAAAAGGTCTTCGAGCAGTCTTTGGCGAAGTGTATCCTGATCCTGTCCGG	10398	A_95_P227354	EB682108
10783	127	73	433	AGTGTAGCAGTATCGCCTTCTCTACTATACGCTCCTCTATCTTCTCAGCATCAGAATG	10400	A_95_P276078	AM783100
10785	127	75	745	GACATGGGAAGACTTTTCGTTCCTCACCTCGCAATTTCCAGATTTCAACCTGAAGATC	10404	A_95_P156972	EH615037
10787	127	77	269	TTTTGGACTAGATGCCTGTTTGAATTGGTTATGTATGACGATGAAATGAAAAAGGCT	10408	A_95_P132207	EB432656
10791	127	81	872	CTGCTGTTATTATAGCTGGCAAGGAAGGAGTCAGTGTTCAGAGCAAGTGAAACTCTC	10416	A_95_P187367	EB679898
10792	127	82	209	GTGGCTTTATAATAAGCTGTTGAAAAAATCAGGCTGAGTTTGTTCTGTAGTAGCTTTC	10418	A_95_P099943	BP535137
10797	128	2	794	TGCGGAGGTGAATTTGAAATCAAAAGCAGTTTTAGAGTATTGATCGGGGCTATTTGA	10260	A_95_P142667	EB446089
10800	128	5	158	TTCCATGATCTCGCCGAGCTTTTTAGGATTGGCGGACAGTGTCCAGATACAAATTATC	10266	A_95_P001826	AJ718115
10801	128	6	487	GATTGAGTTATTGCACATTTTACTGGGTCGACCATTCAGAGTTTTCAGCCTTGATACT	10268	A_95_P170234	EH664856

10813	128	18	1437	TGGATTCTGTGATCGAATGCCACTAGACAGAATTTCTCAATATGAGAGAGCCATTCTA	10292	A_95_P025451	TA12737_4097
10822	128	27	729	ACGCATGTTATATTGGTGTAGATCCAAGAAGCTCTTTGCCTAGTCTATGAGTATTTTAT	10309	A_95_P162412	EH621341
10824	128	29	540	TATATCGTTTCAGATATAATTCTTAGGCTTGGATTGGACTGGGGCGGCAGGAATTTG	10313	A_95_P071835	BP525804
10825	128	30	812	TGTGTATGTATGGTGTACCCCTCCTAATCGTGAACGGCTTCCTTGTCTTGATCACTTA	10315	A_95_P150207	AY660024
10827	128	32	500	GCACCACTATACCATCATTGACTACAAAAATGTCTTTATTCAGCCGAACTCAAGCTAT	10319	A_95_P125402	DW005190
10830	128	35	869	GTACAAGTGATACGGATACATATGTACGTGATTATTGGCGAAACAGCACGCAAGTG	10325	A_95_P223027	DW000906
10831	128	36	806	GTTCGGTTTGAACCTGCGTTTAGAGGTCATATTGAGAATTTGCTGATTATAAACATCT	10327	A_95_P186112	TA14056_4097
10838	128	43	609	ACTTTTGCTATTAACCGAGACCAATTTAAGTTTGTTGAACCTCGATTGACTTATGGAA	10341	A_95_P214512	EB428418
10839	128	44	961	CAGTTGTATTTGTGAACTGGATTTATTAAAATGGTACACCGAAGTGATACTCAGCAAT	10343	A_95_P007646	AB119468
10840	128	45	269	TTGATGGATACAGCCCCATCTACAAAACAGATGACTGGTCTAAAAGTGGTGATGTAT	10345	A_95_P109327	CV019244
10841	128	46	204	ACACATCCACCGTGGCAAGATTTCCTGGTTTTCTCTCTGATTAAAACCTCCATATAAGT	10347	A_95_P104297	CV016932
10842	128	47	834	AAGAGAGTCAGTATGAGCTTCTTGTTGAGGCCGAGAAGATAAGTTTGGGAGCATCAT	10349	A_95_P231719	FG159329
10843	128	48	597	GTATCCGTGGCAGTCTCAAGAAGTAAAATAATAATAATAGTCTTTGTGGGTTGACAT	10351	A_95_P002086	FG644428
10853	128	58	397	ACAATTTCCTTCACACAATTTTTACTGCTGTCAGTTTTCTTGAGGTTAAATCTACCTGT	10371	A_95_P129962	EB429906
10856	128	61	144	CTCAAAACCGTGGATTCTTATACATAATAGGACGAATTGTACAAGACGAAGTGGGG	10377	A_95_P065645	BP136390
10857	128	62	477	ACACGTTTATCCAGTTTGATCCAGCTCCAAGAAGGGGACGAACGGATGTAAAACGAA	10379	A_95_P112177	CV020558
10858	128	63	384	GTTGTGGAGGTGTTGCTTCCCAATTTTTTGGTTATCTCCTCTCTGCATTTTACATCTGG	10381	A_95_P090383	BP530929
10864	128	69	778	TACTTGGGCATTGGCCTTGATGTTTTCATTGTAATGTTAATGTATTGCTAGTTTGCGCT	10393	A_95_P026651	DV999095
10873	128	78	451	AAGAAAAAAGACAGCAGCACCTTGCAAGAAGATTCTGGTGAATCAGAGGAGGCTAT	10411	A_95_P076235	FS377087
10874	128	79	549	ATCAAATGTCGTTGGGTTGTTTGGTAAAGTGATACTGACTACACTAATTTCACGTTTG	10413	A_95_P068365	BP137111
10880	128	85	492	CCATTTGTATCGTGCACAATATTTTCACGGTGTCTTCTGGTTCTCACTTGGCAGGACAA	10425	A_95_P047881	BP131767
10881	129	1	398	TACTCAAATCTCAGTTCCAAGTCCTAAAAGTGGTCCTGTACATTGAACATCTTCCTATG	10426	A_95_P109752	CV019435
10882	129	2	561	TCCAGAAGTTTTGAGGCCAGGTACATTATGATTTATTCACAGATCAATTTCCCTTATA	10428	A_95_P225087	DV161940
10884	129	4	467	CCACTTCCCATTCTTACCATGAATGTCTCTGTACAGAATTACCCAATTAATCTATACTTT	10432	A_95_P308343	FG642093
10887	129	7	282	TAAAGACGGTACCGGTTGCGTCGTTGTATCGGATCTCAAGCATATCCTTACTAGTATT	10438	A_95_P111892	EB683945
10889	129	9	1125	GAGGCCACTGCTCATAATTTTGTAAAATTTTATTTAGCCGTTTGAATAGAGAAGCATG	10442	A_95_P201507	TA17439_4097
10891	129	11	853	ATGAGGATATCTATTCCAGTGCAAATACGCTGCCATTGATCTTGCAACTGGAGTACCT	10446	A_95_P296988	EB680653
10900	129	20	474	ACATCATGAAACCTAGGTACAGACCACAATTGACAGTTGCTGTTCTCATTCCTTTCTT	10464	A_95_P191597	EB425970
10902	129	22	383	GAGTTTCAACTGCTGTTGGTATTAAATGGTTCACGAGAACAAACTTTATGCTGATATG	10468	A_95_P024961	TA18401_4097
10903	129	23	588	CAGAAAGGGAACAAGGTGCTTAAACGAGATGAATTGGATAATTTTGTAGCGGATAAT	10470	A_95_P089293	FG642298
10908	129	28	612	TTGATCATAGCACAAAAATGCCAGTTTGGATTTGTAACATGTATGAGTAATCTTCCCC	10480	A_95_P228539	DW000999
10912	129	32	1527	GTAACTCTATTTTGTGAATCTGAAGGAGTGACAGTTAATCGAGATTGAAAAAGTCCTT	10488	A_95_P197117	TA16493_4097
10913	129	33	1009	ATATGCTCAGCGACTTTGCCTTCAACATTTTATTTTAATTGAGATTAAGGTTCTCTCCC	10490	A_95_P008341	TA12270_4097
10915	129	35	344	TCCAATGCTGACTTATATGCTCAGTTGCAAGAAGAGTGGCGCAAAACTAAAAAGATG	10494	A_95_P217087	FG638032

10919	129	39	792	GGAGACAAAGTACTACCAAGTTGTAGTGTTAGTCGAGTTCATCAAAAAACAGTTATT	10502	A_95_P271141	EB439824
10922	129	42	239	GCACGAACTACTTTGGAATTGAGACATAGTTAATTGATTGATATTGGTGATTGGTGTT	10508	A_95_P077390	BP527234
10924	129	44	576	CGACGTTGTTAAAGTGATTCTTCTCCAACAGGTTCATTATGCTACTTCCTCCTTATTTT	10512	A_95_P091223	BP531260
10925	129	45	486	GTTTAAGGGCACATTTGCGTCCTACCATTGGCATTGGAATATGATCTCAGTTCTTGGA	10514	A_95_P249642	FS417360
10926	129	46	565	GCACTTCTGCCCTCCCAAAGGCTTAAGGCAAATTACAAAGGAAATCCGCCTAATATTT	10516	A_95_P197527	TA16582_4097
10929	129	49	761	TTAAACAGACATGGAATGGCAATGCTGATAGGCATATTCCTGGATGGGAGAATGGG	10522	A_95_P235364	EB426628
10931	129	51	626	GACAAATAGGACTCATTCCGACTATTATATTGATCATCAATAAGAGGGATTTCTCTGA	10526	A_95_P181057	TA12889_4097
10933	129	53	1328	GTGAATCTCCTAAGTGGAAATATTGAAGATACAGGATCCAAGTTTATAGCCATTTCTT	10530	A_95_P008936	Y14431
10936	129	56	96	GACTCGCAAAATTTTTGCGTGTAGGTTAAGCAACTCTCTTGAACATTCAGATCAAAAG	10535	A_95_P010886	EB450337
10937	129	57	398	TACCCCCTTTTGCATGTAGTACATTCAAACAATCCTTGTATATTAAAGAGTATGCAGTT	10537	A_95_P215837	TA20575_4097
10941	129	61	112	TAGGTTGCTTTTGTGGATCATGGCTGAATTGGCTTTACTCAGGACTCATCAGACTCAT	10545	A_95_P115227	DQ460200
10942	129	62	182	TGGGAAAATGTTCAAAGTTGTCCCTTCTCCCTAAACTTTGCCTTCCATTAAAAGTTGG	10547	A_95_P118282	DV161293
10945	129	65	823	AAGTACATTGCTTCAATTGCAAATATGCTGAACTTTCCGAACAATAACCTGAACAATG	10553	A_95_P150347	EB680433
10947	129	67	786	TGTTTGAATTAGTTTGGAAGGCGTAAGTGAACGCACATGGACAATGAACCCCAGGAT	10557	A_95_P235459	EB432254
10948	129	68	794	ATGATTCCTTCATGCTAACTGTTTTGCCTTTCCTCCATTGCTTAGAGATGTGTAAATTTT	10559	A_95_P163602	EH622640
10950	129	70	765	GCATTCAACCTCATTTGTGAGACACATAGGTATATTAGTTTGTGACTATAATATATGC	10563	A_95_P265886	FG643711
10951	129	71	780	GAAGGTTGAGCTTTTTAGTTGGCCGACCTTGGCAAATTCAATGAAACTGATCTGTTA	10565	A_95_P263606	FG641644
10952	129	72	693	CTCAACCATTAGCACTCAAAGAAGTGATGAAGGCTTCTTTTGAGGCCTATCTTATGGT	10567	A_95_P304903	FG199258
10958	129	78	302	TAAAGCCACGAATGCAGCTTATGGAATCGGACTTTTGAATCTGATACGTTTGGTAGG	10579	A_95_P077165	TA20316_4097
10959	129	79	339	TTGAGTCCGGTGATTATGCCAACAGAAGAGCCTGAAGCTATAAGCCTTTTGCTGCCT	10581	A_95_P133307	EB434714
10966	130	1	606	GGTGTTCTTCCCAACATTAACCCAATTTAGTTGCCTAAGAAGACTGGAGGTGATAAG	10427	A_95_P107687	EB447792
10968	130	3	2636	TCTCGACGTGTGTGATCCCCCATCACCACCCATTTCCTTGGAAAGTAGACTTAATTTT	10431	A_95_P016996	TA15059_4097
10975	130	10	762	TTGGAGGCTTAACAGTACAAGTGCAACTAATGGTTACGGATGGGACATGCAATTTCT	10445	A_95_P230229	DV999783
10979	130	14	300	GACTTTCACCATCTTTGAAGAAACTTCTTGCTCAACATAATGTCAGGTGGGGTTGTGC	10453	A_95_P110222	EB431631
10981	130	16	616	AGCTCACTTTTACGATTGCTTTCTGGATGTCCTCTACTCGGAATATGTCACAGTGACA	10457	A_95_P062920	BP135644
10983	130	18	710	ATCATCGATATGCTGTAGATCAGCTAACTTTTTCCGTTTTCTGAAAGATGAAATGTGG	10461	A_95_P159737	EH618182
10985	130	20	875	TCAAGTCAATTTCACGCTGTTGGAGCGTAGATGGAGAGTTAAGTTTTACAGTTTTGA	10465	A_95_P259226	DV157889
10986	130	21	116	TCTGGGGGACATTTGCTTTCATGGACAGTCTCTGAAGAGAGCTTGAAAACCGCAATT	10467	A_95_P069845	AM816107
10990	130	25	303	AATTCAGATTGCAGGAGCAAAGTGAAAGCTGCTGAGGGGGAGTTGCAACATCGTAA	10475	A_95_P040966	BP129969
10996	130	31	367	TATTACAGCTTCGTACTTGTAATATGCCTCTGGCTGCTACTTTCTTAACAAATTATTGT	10487	A_95_P096168	BP533503
10997	130	32	503	TTCATGGTGGTTGTGATGTTTTTGATGCCAAAATTAGTAGAGAATATGGATCCCGAA	10489	A_95_P104607	TA13106_4097
10999	130	34	560	TTAGTACTGCTGGTGCTTCTGAGGTCGTCTCATCAGCACTCAAGACTTGTATTAATAG	10493	A_95_P288763	FG641047
11000	130	35	883	CACTTCTGTGTGTATGACATCAAGTTCACCGCGAGAATCAGTTCAATCTTAAAGGATT	10495	A_95_P009691	TA12879_4097
11004	130	39	1583	ATTAAGCCTTGTTTGTCATTTCTTTGCTGTGGCAATCTATGGTGTTGGCCGCTTGCTG	10503	A_95_P191387	TA15224_4097

11006	130	41	474	ATGGTGTATTCACCAGAAAGAATAGTGATCTGTGTATGCAGAGTTTGAATGGGTTTT	10507	A_95_P021831 FG638812
11007	130	42	633	ATCCATGTATTATGAAAGTTTGACGCCTAAATGGCTGAAATCAGTTGAATCTCCTATG	10509	A_95_P019751 TC54833
11009	130	44	656	CCCTTCCCGAATCCCGCGCATAGCGAAAATTTAGTGTTAAGTGTACGAGCTGTCTTTT	10513	A_95_P122937 DW002850
11012	130	47	808	TTCTGCGATCTGCTGCTTAATTTGATGGCTCTTCTACTCTGCGCATGCATTACTATGAC	10519	A_95_P295768 FG164981
11025	130	60	456	CATCTTTCCTTTTGACATCTCTCAAGTTGCACCTAACAGTATTTCGTGTAATGTTATGT	10544	A_95_P223617 TA22291_4097
11027	130	62	1099	CTCTGCCAACACTATTATCATGTTGGTACGTTTGTTTTAGGTACAATATTTCTAAGAGT	10548	A_95_P199642 TA17038_4097
11029	130	64	542	GCGGGCGTGCCTGTTCGTCCAGTGTAAAATTAATTGAGAATTCTTCCAGTGTAAAGA	10552	A_95_P123152 DW003058
11034	130	69	242	AAAGGAGGATAAGGTAGTGGTGATAGAGGGTACTATTACCGAACGATGTTAGGGCT	10562	A_95_P110202 CV019619
11037	130	72	127	GAAGACTATCACTGATTTCTTTAGGTCCATCATCAACTTCATTAACGTGTTTTTTGCAA	10568	A_95_P108012 FG635120
11038	130	73	543	CCAGTAGTCCTCCATCTTCTCAGTTACTAAAACTTGACTTTGTCTGATGTATATACTAT	10570	A_95_P221452 EH622684
11039	130	74	871	AGTTTGATTTTTTGGAACGAACTCTCATCTCATCCCCCATTGTCTCTTACCTCGGGCCA	10572	A_95_P294163 EB439934
11043	130	78	812	TATACCTAGGATGATCACTGGATATGGAGCAATTCGCTCACATGCTGGTTCAGTAGCT	10580	A_95_P311633 TC41992
11049	130	84	549	GATTGTGTTTCCAACTTTATAATCTCTCTTCAGCCATGTTATGTATTTGGAAGTGTCGA	10592	A_95_P152787 EB683132
11052	131	2	810	GGTGTTGATAGCTATTTTCAATCTCTAGCTAAGATGACATATGAGAACAACATTTGGT	10597	A_95_P214842 EB449765
11063	131	13	630	TCAGAGGCTTTATATGTTGCAGAACAGAAAGCTAGAGAAGCGGTTGCAATGCGGTC	10619	A_95_P121477 DW001549
11065	131	15	325	AGTTCCATTTTCAGTCAGGGTATTTGATTGCGTAAATGTTACATTAAACACGTGTAGA	10623	A_95_P090183 BP530839
11068	131	18	602	CTTGACTTGTCAGGATTTGCCTGATACTCAAACAGGTTTCTTTAACTTAATCAACATGT	10629	A_95_P186997 DV999544
11069	131	19	543	TACATCTTTACTGGCAGATCTCAATAACTGGCACCTATTTTGCCATCTTTACAAGCTAA	10631	A_95_P252419 EH620138
11071	131	21	504	TAATTAAGCTCCTTTCTTTGATTCTGCTACAGGCCCCTAATAGATATTCCGCAATAGAG	10635	A_95_P068815 BP137222
11076	131	26	816	GCATTAGCTGGCACTGGTCTTCCCATTGATAGGTTTATGACTTCTGATTCATTGGGGT	10645	A_95_P205272 DV161936
11078	131	28	440	TTGTTTAGGTTGGTGGTATGAAAATAAGGTGGTTCCAAACAGTTGAGATTGCATCTC	10649	A_95_P094713 BP532842
11081	131	31	742	CTTAGAACTTCAGAACTTATCTTAAACAATCTTGCCTCCCCATTAGTTATATGTACCTT	10655	A_95_P208852 EB683961
11082	131	32	429	GTCGTTATTAGGATGTTAACTTTAGTAAGCTCTCTATAGAGTTGTGTATCACCGGTTTT	10657	A_95_P153942 EB684093
11086	131	36	818	TATTACACTAAGAATTTCATGAGCGTGAGCATTCCATGTGAGACTGTTGACACACGA	10665	A_95_P249137 FG160796
11092	131	42	516	CAAGGAACAAAGTTCATTTCTAGAAATTACGATGGTTATATTCTGGCTCGTTGTTGTT	10677	A_95_P241330 FG644689
11093	131	43	544	TAGTACGTTTGGGCTATTAGGATTTTGGGGATCTTTAATTCTGTGAGCATTTGGTTGT	10679	A_95_P026951 BP526356
11094	131	44	923	AAAGCTACTGGTAATGCGTCTCTGAGTTGCATTCGGTCCTACAAAGGAATAATGATC	10681	A_95_P229474 EB680954
11096	131	46	3005	GAGGCGTACTCTTGATTTCAGTGAATGTGGATCACCTGGAAAGGGAAAGGAAACTG	10685	A_95_P238434 AB056123
11102	131	52	532	CACTCTGGTCGTACGTGTGATGATTGTTTGATAATAGGTCAGTTGAGTTCATGTAGTC	10696	A_95_P213257 TA20009_4097
11105	131	55	557	GGTTTCTACCGGCGGCATGTACAATATCGCGTCTATATTAGAGCATATTTAAAAATTA	10701	A_95_P234979 FG633459
11107	131	57	234	AGGACCATTTCCTATCCCGGTTGCAGTTGATATTATGCTTCAGATTGCGAGAGGAAT	10705	A_95_P059525 BP134763
11116	131	66	264	ATCAGTGGAACTGCTTCTCAAGTCCAAACAGCACAACAATTGGTACAGAATTTCATG	10723	A_95_P092263 BP531724
11120	131	70	861	GGTTTATGTCCCTATATACCTATGTTCATGTGTTTATGCGAAATACTTTGTTGGTGTAA	10731	A_95_P266966 DV157625
11121	131	71	823	AATACGCAGACATGATGCAACTTTTCCTGCTCTTATGGCGAGGGAAATGGGGTTCAT	10733	A_95_P254714 EH616218

11122	131	72	134	GAAGTGTCCAGCTACACGTGCATGGCAGAATACCTTTTGCTCTAATTCGCAAGGAAA	10735	A_95_P041916	BP130219
11124	131	74	585	ACCCTTCAGTTGTAGTGCCGTTCAGTTTTGTTTCTCATCTGTAAAGAATATCGATTTAC	10739	A_95_P123747	DW003636
11125	131	75	700	CTTTTTGGATTCTTCTTGGCAAACGAGTCTAGCTTTTCCCCAACATTCTTGCTGAGGA	10741	A_95_P211452	TA19613_4097
11127	131	77	1440	GTGGGTGAGATGCAAGTTGTGGTAGAAATAGTGAGATGTGTTATGATTTATTAAAT	10745	A_95_P184062	AJ438615
11129	131	79	780	GTGTTTATGTGGTCTCACTTGTTGATGTGGTTCGTGATTCTTATAATGTATACAAGTA	10749	A_95_P017366	TA15605_4097
11130	131	80	1102	TGTACCTTTTCGAGGCATTTGTAAACTACTGAACGTCTGAGCTCTTGCCCATCTTGTG	10751	A_95_P176287	U44760
11132	131	82	789	GACGAGGAATGAATTAATGGTGCCTTAATTTTGTCTTGTATATGCATTGAATTATCG	10755	A_95_P131497	EB431800
11135	131	85	499	CTGTTACGTGAATCACTCCAATAATCATTTGTACTCAAATACTGAACCTCATTTTTCGT	10761	A_95_P008711	EB446681
11141	132	6	573	GTACCAAGCATTACATGTATGGATTTCTTTCTCCCAATTTTACCTACAACCTTACATTG	10606	A_95_P124877	DW004687
11143	132	8	854	AGTCTTTGATTCCAGTTATGATGGACCCGGTTTTGGGAAATGAGAGGAAATTGGTGA	10610	A_95_P034499	TA13733_4097
11145	132	10	606	CTGTGGATGATTTTAGCTTTAGGAAGTGTGTAGATCAGATACAACCCCTTCCAGCGA	10614	A_95_P203217	TA17806_4097
11147	132	12	387	ATAACCAGCTCTGTTTTGGTGCTGCTCAGGGCGCAGCCAATTTTTTCATGACATTCTT	10618	A_95_P060380	BP134981
11148	132	13	695	AGAGTGTGGTTCATGAAAACGCTTATCTCAGTGAATTTCATCATTGTTTCTCTATACC	10620	A_95_P137812	FG167434
11149	132	14	125	GTCGCTGACCAACTTTCGGGCTGTAATTTTCAAGTGTACATGTCGTTCCTTCTAAGCT	10622	A_95_P089748	BP530637
11153	132	18	443	CGAGCCTCGGAAAACAACTCAAGACCATATTGATTTACAATCATCAAAACCAATGTG	10630	A_95_P065155	BP136256
11156	132	21	740	CACCCCGATGTCGGGCTTGCGTATTTATTCTGCACTATTCATTTAAACTTATATCATAA	10636	A_95_P235579	EB678672
11160	132	25	1503	CTCACATTACTGCGATGGTACTTTCTTTGTTGTAATGTGTTAGCAATTTTGTTGCCTAA	10644	A_95_P199767	TA17063_4097
11165	132	30	760	CAAACCCAGGGGTAGAGGAAATAGTTTCTACGGTAATGAGAACATGGATGGTTTAA	10654	A_95_P138127	EB441864
11169	132	34	2485	TCGACTCGAAATCCCTCCTTTGCTGTCAGTTTATAATTTATATTTGGATCTTCTATAGC	10662	A_95_P204672	TA18114_4097
11171	132	36	1711	GTGATCAAGGACATGCTTTCTATGCGATTGTATCTGTGGTTTATATTTGTTTCGATAG	10666	A_95_P202862	TA17731_4097
11177	132	42	737	ACTTCAATGATTCATCCAAATGGGTTGGAGAATGTCACTTGGATTTGCAGCTGTTCCA	10678	A_95_P315613	FG198033
11179	132	44	780	GAATCATTATAGCATGCAAATGGGGTGGAGTGATATAGCATAGCATATCCGTGTCGT	10682	A_95_P027101	EB681640
11183	132	48	541	TCCTGGTTATGATCAGCAACAAGGTTATAGCTCTACTCCCGGTTACGGGAATGTACC	10690	A_95_P002211	FG149075
11190	132	55	741	CTATCTTAAGTGCATTTACGTCAATGTAAAATTGTGCGCCATTGATTAGGCAATTTTA	10702	A_95_P187207	DW001436
11194	132	59	389	TGTGGTTGTGTATTCCTTATCTGGGTTACTACTGATTAGTGCAAAATGTTCTAGGTTT	10710	A_95_P212767	TA19905_4097
11196	132	61	845	ACGCACAAAAGTGGCTGTACTTGGTTGGGCCTTTTGGTCATATTTATCGTTATTTCTA	10714	A_95_P193577	TA15702_4097
11197	132	62	514	TCTGCCTATTCCCTGTTTTATTTGGAATTAGGAAGCCAAGTTTACTTAAATGTAGTAC	10716	A_95_P121932	DW002007
11206	132	71	554	CATGTGGCCTGAAACACTTTCCATCTAGCATCTTTTGCCTCTATTGGGATTTGAACTCT	10734	A_95_P141792	EB445416
11207	132	72	514	TATCATGAAAGTTGGTTACTGACTCTGACTTGCTTCCAGTGATAATTAATTCGCCAGT	10736	A_95_P038806	BP129374
11212	132	77	975	CATCCGTCATTCCGACAATTGAAATATGGATTACACCATGGACTTTTGATCTTGGTAG	10746	A_95_P194787	TA15974_4097
11217	132	82	823	TTTATTCTACACTTCCCCAGCTATGCAGCAAAGATATTTGATCAGCCCATCCCTGGGG	10756	A_95_P311348	FG147526
11218	132	83	649	CAGGAAGACATTGCCTTCCCAAATGATCCACGAGTACCTATTAAGGTCGATGATGAT	10758	A_95_P221997	FG174018
11226	133	6	791	TCGATATGAGTATAGGTCTAGCAAGATATGCTATCCTTTTAGAAGCATTAACTTGACT	10773	A_95_P212722	EB684210
11228	133	8	453	TTCATGTAGAAAGAGACTAAACTATGCTGTCAGTCCGAATATTTTAAGTTTTGTGGTC	10777	A_95_P003666	FG637596

11229	133	9	436	GTGAGTTTTTAGGTTATTACTATTAATAAGAGATCTTGACTCTAGTGATTTGGCTCCG	10779	A_95_P182502	TA13230_4097
11230	133	10	801	GTTTAGTCTAGTGTGCTCTAATTTCATTCATTCTTTAACCCATCCTCCATTACATGACTG	10781	A_95_P287718	EB451943
11236	133	16	768	ACGTTTGGATTTAAATCTTGAAAGAGGACGCATTCGTGATGAGCTTGCCAATCAAAA	10793	A_95_P253134	EB426249
11237	133	17	833	GGGATTAAGAAAAGCATACCCCTAAAGGTTTGGGAGATATCAGTTTGATTTTGTAGT	10795	A_95_P232664	DW000015
11241	133	21	363	CGGTAGACATTGTCTGATGTTACTGTGTTGTACGTATTGCATATTAAACTATTTCTTCC	10803	A_95_P159712	EH618158
11242	133	22	744	TAGTGGATTGCATTTTGTTGCTTTTAACTTGGTGGATTGTGGCTTGTAATTTTAGCTG	10805	A_95_P027206	DV160701
11249	133	29	814	CTTTTTCATCCTTGTGTGTAAAATGCACTTGATGATTTAAGGGAATCCGTAAGTTACT	10819	A_95_P193727	EB425276
11251	133	31	1178	GTGTTAAATTAGTAACTTCTTTGTGTCCTTTTAATTCAGACATCTTTGGAAGGCACTCT	10823	A_95_P103337	TA17132_4097
11257	133	37	1041	CAAGGGTGTACCAGAGACGTCAAATGTAAAGAGAAATTACCAGTTTTGTTTCACAAA	10835	A_95_P240219	AY141105
11258	133	38	330	GTTACGCCTTTTTCCTTGGGTAGCATTATTTTTTGTAGGATAACATAGTGTGCTTTTTG	10837	A_95_P212827	TA19918_4097
11259	133	39	809	AATTATGTCATGCACTCGACTTTAGCCGCATATTACCACTTAATGAAGCCTTCTTTAG	10839	A_95_P119652	DV999112
11262	133	42	279	ACGAGAGTTACTCCTGGTATTTCCTACTTTTGAGTTGTACCATTACAATTATCATCCTA	10845	A_95_P002036	FG642822
11265	133	45	902	GTAAGTGCCGCTTTAGATTAATTGGAAGTTGAGTATAATAATCTGCTTCTCCTTTCAG	10851	A_95_P010626	TA12520_4097
11266	133	46	56	GGCAGAATTGCCATCTCATCTGTACAACATTATTTGTTGTAATTATCCTGTGTATACAT	10853	A_95_P089048	BP530322
11268	133	48	558	TTTGCATTATTGCAGCATAGACAACTGCAGTCACTTTAAATATTGATTGGCGTTCTGA	10857	A_95_P286058	FG634699
11271	133	51	866	ATTCTGATGAGCTGCAGATTAGTTGAAATTACCGGCTCTACTTCAACATGCACTTTCT	10862	A_95_P304833	FG155267
11272	133	52	427	GCACTATCAAATGTAATTGGAACATTGAGCATGAATGCAAAAAGAAAAGACCTGATT	10864	A_95_P089318	BP530453
11274	133	54	821	ATATCTTAAGGAGCTTCCACTGTCACTACATGACACTGGATTGATCACTGCGCTGCTA	10868	A_95_P246967	FG157245
11278	133	58	809	GATGAGCATCTTATTGGTGTAACGAATATTGACAGCCATATGTACATGGCAGTTGTT	10876	A_95_P225177	EB445311
11279	133	59	281	TTTGGGATCGATGTACAACAAGTTTGACGTTTCAGTATTGGAAGGAATGCTTTGTGTT	10878	A_95_P117542	DV160481
11280	133	60	0	CAATTTATGTAGCATTGTTCGACCGGGCCAAGGAGTTTTGAAGTTCCAAAGTTACGG	10880	A_95_P021066	A_95_P021066
11282	133	62	130	GCAGCAGGTTGTTTGAGTAATGGTTAGTGACATATCCTATGCATAAATAGTGTATTG	10884	A_95_P118362	DV161393
11285	133	65	1468	CATGGCTCAGTTTGATGTTACTTTGGTGAGCCAGCAGTCTTGTGCTTTGCAAGTTTGT	10890	A_95_P222847	TA22121_4097
11286	133	66	589	TTTTGGAAGTGGTGGTTGTTTGGTTTCAAGTAATTGAAGAACTTACTTCCTTGTTACT	10892	A_95_P005936	TA11726_4097
11287	133	67	244	TGCATGTTAAGGTAGGACCACGAGAATTAGAATTTGATTAGAAGTGTCTCTTATCATT	10894	A_95_P134127	EB435986
11288	133	68	203	GGAGATGTGAGTTCCAAATGCAAATTTTGAGTATACGACTGTGGTTTTCTAGTTTCTA	10896	A_95_P115212	DQ460183
11290	133	70	164	ACTTCGGTGATTCTTTCTATAATGGCCTTGGTGGAGTCTTGCCCGGTTTTAGGAGACT	10900	A_95_P161952	EH620608
11293	133	73	1715	ACACTTGTGACAGTGGATTTATAACAGGAATTTCAAGAGCTGTTGCTGCTTGTTGATT	10906	A_95_P008816	TA12710_4097
11294	133	74	874	GATATAGTTTGTATCTTCCCGTCAACGGCCAGAATACATTGCAATACCCTGAGTTCTT	10907	A_95_P219172	TA21341_4097
11295	133	75	78	CTTCGGGTCAGGTTGATGACTTACAATTTGTTATTGGTATAGTTATTGATATGTGAGT	10909	A_95_P257509	EH623795
11302	133	82	526	AGTTATCATACTTGTTATGTTAGTGCCAGAAATGCTATCCACACATGGTTCTACTGGA	10922	A_95_P106217	FG200594
11305	133	85	863	TCAAAAATCCACTTTACAGTGTAACTTTTACCTTGTTAATGCAGCTGATCCTTTCTTGT	10928	A_95_P184992	TA13817_4097
11307	134	2	490	TCATTGTCTCCTATTGGTAAATCACCTGCTTCAAGTATCGGATCGAAAGAGCAAAAG	10766	A_95_P122652	EH618914
11309	134	4	483	TGTTCCCTATCCATCCCATTCTTGCTTTGAACTTTGAGTTGTATATGAAATGTCTAACA	10770	A_95_P285673	FG643284

11312	134	7	419	CACAGTGCTGCCTCTGTTGAGTTTGTCATTGTCCTTGGTGATTTATCTGATGTTTGTG	10776	A_95_P056146	BP133884
11321	134	16	777	TGGCTGCTCTTGTGCACATGACAGATGAAGATCTTAAAGCTATGGGAATACCAATGG	10794	A_95_P205167	EB438545
11322	134	17	566	AACGAAAGATGAAAAAACCATGACTGGGGCAGTTAAGGCTTGAAGAAGAATGACC	10796	A_95_P020261	EH622432
11323	134	18	463	AAGGTCCTTGTACACAGAACAAGAATCATGTAATATCTATTCCGCGGATGATGTAAA	10798	A_95_P141237	EB445013
11324	134	19	357	GGCTGTGTCGGATTGGACTTTCCGCATTGTTATCGATATTTCCGCTATTTAGTATTGTT	10800	A_95_P004606	EH621994
11327	134	22	704	ATGGCAACTCATCAAACACATACAAGGCATGCACGTAAACGTCTAATTTCATTTCATT	10806	A_95_P299308	FG187855
11328	134	23	176	TTCATCCTAAGAGAAAGAGAAACAGCCACCCATCTCTAACCTCACTCAAAAATCAAA	10808	A_95_P168486	EH664439
11330	134	25	889	CCTTTGCTGTAATGAGATAGTAATTGTTTACCGTGGAAATATGGATGTTTCTTTAGCT	10812	A_95_P264681	EB678751
11336	134	31	367	CTTGGAAACGATACATCAGTGGGAGTCTTTCATCCAGTTGTTGGAATGTTTGGAGAG	10824	A_95_P092858	BP532022
11337	134	32	566	ATGATAGATTGCTATTGGAACCATGCTAAAGTGCACTGCGCTGAGTAGTTTCTTTTG	10826	A_95_P063050	BP135675
11340	134	35	0	CAGAAAGTTTAAAATATAATACAAGGCTCAGGCCTTCACCGTCAGCATCACCAATGA	10832	A_95_P302438	A_95_P302438
11347	134	42	413	TTCTGCCGTTGAGAATTATTGCTCTTAGATAGTGTGACTGTACTTTGCGTTCTTAATTA	10846	A_95_P121712	DW001818
11354	134	49	789	CTATTTCTTCGGTGGAGTGAGCACCACAAAAAACTAGCCAATTTTATAAGGTTATTTC	10859	A_95_P138142	EB441880
11358	134	53	415	GAACCAGCTCGATTAGCCACTAGTATACTTGAGAATTTCAGTTTACTCAAAAGACAAT	10867	A_95_P001256	FG638255
11363	134	58	551	GATGGAGATTAACAGACCCTGCATTATTTCTTGAATCATGTAATGACTTCCTACTGTT	10877	A_95_P197597	TA16598_4097
11373	134	68	476	TGTCCAACCTACGTGTCCTCCTGCTAATGAAAATCTGATGGAACTCTTGATAATGATT	10897	A_95_P137847	FG169100
11375	134	70	605	CAACTGTAAGTCGTACATGAACAGTTTGTGTACTAGTTACACATTTCCAGAAGATTAT	10901	A_95_P122622	DW002611
11380	134	75	782	GTGCTTTTGGTGCTAGTGGGAGTAGATAAGGCACTTGATTTCGGGCCTAATGTGAAA	10910	A_95_P208657	EH620836
11381	134	76	315	TGCCTTTTATTAACTCCCGGGTTCTGATATGATCAGTTTATGGGGCTGGTGGACAGAT	10912	A_95_P103077	CV016329
11382	134	77	392	TGAGTTGTTTATTTAGTAGCATTTGTAAGATTGTAGGATAGTCATGGGTGCCTTGTCT	10913	A_95_P062155	BP135442
11387	134	82	761	AGCCTTAAGCAGAGGTCTCGAGCTAATAATTGAAAATGGTTGGAATGATGCGTGGC	10923	A_95_P126577	EB425895
11397	135	7	755	GCCTCTTGTTCATTTTTTCGTACACCTGTATAGAGACTTAAATCAATTCAGAGTTCAG	10942	A_95_P192722	TA15516_4097
11398	135	8	739	GATATGTGGATACCTCTTGGTTCCATCAGTAGAAATAAAGGCAAAATACATACTTTTA	10944	A_95_P179137	TA12435_4097
11399	135	9	842	TGGGAGTATTATATGTCTCCACAGCTAAGCTTGCATTTTGTAGTGATAACCCTCTCTC	10946	A_95_P210867	EB425346
11400	135	10	555	TCCTCTTAGAAAAAGGCATTTGTATGCAATAGTAGAATGAATATGCAGTTTTGAGAC	10948	A_95_P205267	TA18242_4097
11402	135	12	765	GCAGACGACCTTATCTGCGTTTGAATTTTAAGCCATTTGGAAACAATTACTACTATGT	10952	A_95_P142727	EB446140
11413	135	23	1221	GCACTGAACGTCTGAGATCTGTTATTGTACTATTTAGGTCTTTCTTTATTGTAGGTGA	10972	A_95_P009721	TA12692_4097
11414	135	24	513	AGTGGTTAAGTACTGCTGGAAGTAACGTTCCCATCACTATGACCAACTTCTCTGGTAG	10974	A_95_P207567	BP530590
11416	135	26	1664	GGCTCCATGAGATGTGCCAATTTGACCAGAATGAATATTAAGCTATAACAACATTCA	10978	A_95_P011846	TA14346_4097
11417	135	27	671	TTGCACAATATGTTGTGCTTTGGTGAGGTTTATAGGTCTAAATGACAGGGCCTATTTA	10980	A_95_P163147	EH622114
11418	135	28	1622	CCCCATGTTATTTTTGTCTAAATAAAGGGCGAGTATATCAGTTATAGACAGCTATCCT	10982	A_95_P110607	Z48977
11420	135	30	465	ACCAATTGGCGAAAATTGACATGTACGTAGCAGCTGCTGGTATCAACCACAAAGAGT	10986	A_95_P053741	BP133263
11421	135	31	468	CTTATAGTGGCGAGTATAAGCTTCCTAACTTGTCCGATTTATGGAAGGGTAATGGGA	10988	A_95_P110992	TA13525_4097
11425	135	35	495	CATGGAGAATGAACAATACCAGTATGCCTTAGTGCTATACCTGCATTTTATGCCAATT	10996	A_95_P028661	DW003697

11426	135	36	899	CAGGTATTCTTTGTACAGTTGAACTGCTGCATTTTCAGTCCACTTACTTGTTCTTTGTT	10998	A_95_P200322	EB430285
11433	135	43	782	TTGAATTCCTTTCCACCAGAGGAATCTCAAGCATTTGTGTTCCTCAAGCCAGAAGAG	11012	A_95_P200627	EH622710
11435	135	45	647	TCATGTGACTTTCTCTCTTCTGACAGTTGTATTTGGAGGAGCAAAGATACGTCAGTG	11016	A_95_P135217	EB680885
11437	135	47	416	GCACGTATGTCACATGTATAAGTTTTCATGTCATGTCAGGTTGTCCAATATTTAGTAT	11020	A_95_P090368	BP530926
11440	135	50	747	GCAATTCATGCTTGCCATGTAGCTAGGATTTACATGTAATAGATTTTGAATAAGAGT	11026	A_95_P010281	TA14530_4097
11442	135	52	294	AGTCAGAGCGCTTAATACTTTATCTACAACCTTGAATGTAATACACTAGACTTTATAC	11030	A_95_P201237	TA17380_4097
11444	135	54	725	ATGTCAAGCGTGCTCCATACTCATGGGAAGATGCTTCCTATTTGACACGAAGGTCTC	11034	A_95_P262041	EH619270
11445	135	55	708	GTTTCCTTCTTTCTATTCGGTGTATGTTTTTCGATTCCTACCAAGTTATGAGACCTAAT	11036	A_95_P000226	EB438050
11449	135	59	1073	GCCTTTACTGCAAGTATTATAGTATTCCATTCCTATATGCTTACACTAGTCACAAGCA	11044	A_95_P211272	TA19574_4097
11453	135	63	259	GTTTATGTAAGTCAATTCGTTGTTATCGGGATGTAGGAACAGTTCTAATGAGCTTAA	11052	A_95_P091868	BP531535
11456	135	66	499	TCATGTATCAAAACTTTTTCATCTCATGTCCTTTTGATATGGTTTCTACCCGCGGCAGG	11058	A_95_P202657	TA17682_4097
11458	135	68	846	TAAGGTGCCGAAGGACAATTGATAATGGACAATCTATAATGTCTGAAGTTTTGGCAG	11062	A_95_P020251	EB425529
11460	135	70	916	CCAACATTTTATGCGTTTTAGGTGGTTCTGGACCTTCTTGGTAATCTTGATTTATGATA	11066	A_95_P215697	TA20545_4097
11461	135	71	636	GGACCCCTTGTAAACATTGGAGTTTAAAGTGGTTTCTTTTATGTTGAATGTTATGATC	11068	A_95_P021481	TA16412_4097
11463	135	73	875	ATTCTTAGCTATCAAGTCGGGGGAAAGGCAGAGCAGGATATAGAACTGCTTGTGAA	11072	A_95_P296628	EB680438
11464	135	74	614	TTCCGCTGTTTCTTTTGGGCTGTATATTTAAGTAAGTTGTTTCGGTCACTTGTAAATTC	11074	A_95_P310153	FG135369
11469	135	79	441	TCATTGGAAGAGCTGTGGTTGTTCATGCTGATCCTGATGATCTTGGAAAGGGTATCA	11083	A_95_P160342	EH619039
11472	135	82	464	TTGCAAATGAGATACCTGTGGGTATCATTAGTCCTTCTAGGTGATCTTGTTGAGCAG	11089	A_95_P077480	BP527257
11474	135	84	793	GATCCAATTCGTGATTGTGATAAGTGGAACCGCAAGTTCCTGTATCTGTAGCTTGTA	11093	A_95_P163517	EH622562
11479	136	4	613	CTCATATTGTGCTTGTCTGTCTGTACGGAACGATTTAATGAGCATCTAATTTCTCTGTT	10937	A_95_P019631	TA16064_4097
11480	136	5	799	TGTCCAACTGACTGCAATTTGTGTGACCTAAATGAGTTGTAACTGGACATTGCGGAC	10939	A_95_P016646	DW002460
11483	136	8	1880	GTTCGTTTGCTGAGATAGGAGATAATTACAAGCAAATGATGTGGATATATTCTGCAT	10945	A_95_P221482	TA21828_4097
11484	136	9	129	CTGGTTTGTTGGTGGTGGTGTTGCTGCTTCTTTTGTTTTCAAATTTTAATGTTTTTTGG	10947	A_95_P147262	FS437774
11492	136	17	695	CTGGTAATGGTTTCATTTCTTTGCTCTTCCCAATTGTAAAGAATGACTTGTAAAAGTG	10962	A_95_P194947	EB446333
11493	136	18	637	ATGGATTTGTATTGTCGACTTGTCGAACAATAGATTTTTGGCATGACACATGCTTAC	10964	A_95_P300603	FG644499
11494	136	19	842	TCTCTTTGGTGTCCGGTAGAAGAGTGGTGTTTATTGCTGTTTCTCTGGAAATGTCCTT	10966	A_95_P230764	EB677730
11497	136	22	531	CGTGTGAGCTCTGTAGAGGCAAGATATTATTTTTACCTTATAATGGGTGCTTGAGTA	10971	A_95_P122052	DW002106
11498	136	23	978	CCTGAACTTGATACGAGCTCTCATATCTATCTCAATAATATCTTAAATGCCTGTGGTTA	10973	A_95_P185392	TA13902_4097
11499	136	24	560	GTCAAAGCTAATCCTCAAGATGTTGAGAATGCTACGTGGATGTTGACTGTATTCAAC	10975	A_95_P051691	BP132720
11502	136	27	881	ATTCTCTACAATCGAGCGCTGCAGACTATATGGTGGTGCATATGACAGCGAATTGCA	10981	A_95_P294168	FG163876
11505	136	30	1714	GTTGGTGGTGTGATATGATATTGTAGTAAGTTAGAACCATTTGCTTTTTGGTGTATG	10987	A_95_P007486	D45204
11506	136	31	801	GATGGCATCATAGTCCTGTTACAAACTCAGTAATGCAATAACACTCTTGTTAAGAACA	10989	A_95_P010871	TA12762_4097
11512	136	37	716	CAGTTTCTACTACCTGGTCCATATGTTTTCTTCTTTGATCAGTAAATGGTAGTACATAG	11001	A_95_P231369	EB451089
11514	136	39	778	GTCCTGCAAGGTTTGTTTCTTGCTGTTGAGGTATGTAGCTCAGTTTAGACAATGTAAT	11005	A_95_P118022	DV161036

11517	136	42	1353	TTGCGGCTTTATAATCGTTTTTGGCATCCAGTTGATGATTCTACAACAGCCAAATCAT	11011	A_95_P238959	AB084124
11520	136	45	582	GTTTGGTGATACTTGAGACTTAGCCTTACATGGGAATTACTTGTTCTATGCTGTAATT	11017	A_95_P246437	EH617143
11522	136	47	863	GGTTGACGAATGCCTTGCTCCATCTTATGCATGAGAAAGTCTTTGTTCAGTATATGGA	11021	A_95_P217742	EB678124
11523	136	48	398	GTTGAATGTGAAACAGAATAAACCATGCTTTTCGTCCATGGACTAATAAATATGTTCT	11023	A_95_P000916	TA13631_4097
11524	136	49	684	CTCCATTAGTTCAGTAACTGAGCCTGGCTTGGTTGTGCGTGACTGACTTTTCTTCATT	11025	A_95_P267916	DV162718
11526	136	51	485	TTATAAAGCCCCAGTGGTTTGTCAACTGCAAAAGTATGGCCAAACAGTATCCAGAGC	11029	A_95_P058101	BP134388
11530	136	55	276	AATGATGTAAAAGAATCGTGGGAAGATGAAGAGGAGCCTGTTCCGGCACCTAAACC	11037	A_95_P164802	EB426099
11536	136	61	382	ATGGATTCTGGTCCAGTATCAACCTTCCAGGTTCACATAGCTTTGGTCTCAAATATTC	11049	A_95_P043896	BP130739
11540	136	65	174	TTCCATCTGTAGTTTTGATGTGACATTTTGGCCGTTTAGCCTTGAAAATGTTATACCT	11057	A_95_P104062	CV016826
11541	136	66	381	TTTCCTATTTTCGCCAAAAGAGCATAAATCTGAGTTGGGAGAGTTTGGGTGGGGTTG	11059	A_95_P001311	BP526377
11545	136	70	824	ATTGTGGTAACAAATGTTGTCCGGTCTGGGTGCTGCTGTTCTTGGTGATCGATTTCCT	11067	A_95_P157782	EH615815
11550	136	75	752	GATCTGTATTGTAATTGCCTTCTGGGCCATTTTAACAACTAGTGTTACGTGAATAACA	11076	A_95_P013506	DW004694
11551	136	76	522	ATGGGCTACTGGTTGGAGCAAATCTCATCTAAGAAATTCGCTTTCTAAAAAGAGAAT	11078	A_95_P107052	CV018189
11552	136	77	1242	AAAGAAGAGAATCACAAACTGCTGAACGGAAATTCTGGAGATCCTGCAGAATGGAG	11080	A_95_P194607	TA15932_4097
11555	136	80	829	TCTACGTTAAACAGGCTATTCAAGAATTCAAGCAGCAAAGAATGGCATCTTCTGCGC	11086	A_95_P025751	EB447103
11562	137	2	562	AGTGAAGTTTTGTTGCTTGACAACTTTGGCCTTTTTGGTGAATATATATGGCTTGATG	11099	A_95_P248392	EB682951
11565	137	5	286	TACATCAACTCTACGGCAGTGTACACAGAGGGGTGAAATATAGAATTTCTTTTACTT	11105	A_95_P027966	EB446714
11566	137	6	594	GTGGCATCCCTTACTTTCAATGTTTTGATGTCAGTTTTACATTTTAGCTTTTGAGTGTT	11107	A_95_P149627	TA12981_4097
11567	137	7	688	CTATTTTCATGCTTGCATCAATTGAAATTCTGGAAAATCTGAACACCAGGAATAATGG	11109	A_95_P140502	EB444403
11571	137	11	850	GAAAAAGAAACGAACATTTGTGCTCCGTAAGGATGGGTTACCGGATGCAGTTGTGT	11117	A_95_P198412	DW000157
11581	137	21	500	GTGACAAGAAGAATTTCTGGTACAGGAACAGGTATAGGTTTAGACAAATAGGTTTCT	11136	A_95_P073655	BP526268
11587	137	27	935	AAAGAGTATGGGCTAATCGATGGTGTCATCTTGAACCCCATGAAAGCCCTTCAACCA	11148	A_95_P016141	TA14085_4097
11591	137	31	615	CCAAGTTTAATTTGTTGCCGGGGTTTGACGTGTGTTGTAAACAAGTTAAAGGTTTTCC	11156	A_95_P119617	DV999065
11605	137	45	271	GTCTCAACATTAAACCACAAGACATCTCAAAGTAACATTGGAACCAACCCTGAAAAG	11184	A_95_P094833	FG639902
11613	137	53	403	ATATCAGCTAATTTGCCTTACAAAGTGGAGATTCGTGGTGGCAAATTTGGAAGGGC	11200	A_95_P113722	EB681361
11618	137	58	916	CGAAAGGAGACTCTCACGAGGTTCGACTCCATAAGTAGTACCAGTGGTTTTGATCAT	11210	A_95_P233024	EB677877
11623	137	63	384	AGCATGTTGTAGTTGGTATATACTCGTAATGCCTATATAATGTCCAGTAGATTGACTT	11219	A_95_P214962	TA20379_4097
11624	137	64	730	GAAAAGAAATCTGTTAACGTCGATGAGCAATGACAGAACGTCGTTAGAGGACTAAA	11221	A_95_P145907	EB449668
11626	137	66	730	CACAGCAGCAAGAATGAATCCATCTGCCAAAATGCAAAATATAAGCTATTATGTAGT	11225	A_95_P149372	EB679208
11635	137	75	1958	GATGTATCAGTGTTTCTCATTGTGACCCCATACTTGGAATTCCTCTTGATTATCATTAT	11242	A_95_P007341	AY578144
11641	137	81	627	AATGTCATGTCATTCTCGTTAAGTATTGTGTTAGCTACATTTTTATCTGTTGCCCTGTG	11254	A_95_P182992	TA13352_4097
11646	138	1	640	GTCCCGATGGTTTACGTACTGTTTTGTGAAATTACCTTCTTATCTATTTTGTAAGACAA	11098	A_95_P206607	DV157653
11654	138	9	473	TCTTGCTCCAGAGGTCTTGGAAGGACAGTAAGTACTGATTTTGAATTCCTACGCCAA	11114	A_95_P079070	BP527676
11658	138	13	1186	TTGAGACGTGGCCTGTGCATCTACTGGTGCTGTGCAGAAACTACACAAAGATATAGT	11122	A_95_P204012	TA17975_4097

11661	138	16	962	CAAATTTTGTCAATTGTTAAAGCACGAGGGAAGAGGTGTCCCTTCTTCGCTTAGTTTT	11127	A_95_P195207	X60059
11665	138	20	904	GCAGATTGTTTCATCTTTGCTAGTATGATTACGAGTGAAAGCTCTTAATGCAATCTTA	11135	A_95_P021531	TA16260_4097
11667	138	22	382	TGCGATGTCAGATTTTGAAATCCCATTATAAAGGGATTTGATGAATGCAAATCACCTT	11139	A_95_P182062	TA13124_4097
11668	138	23	407	GTATGATATAAATAGTGGTTCACCTATGCACAGTAGCCTGCATTTGGTGGATCTTGC	11141	A_95_P238569	AB053097
11681	138	36	418	ACACGCTCTGTATTTTCCTGCCATTGCTTTGCCTTCTGTTTGTTTTTATGTAAACAAGA	11167	A_95_P122862	DW002807
11686	138	41	382	CCTAAGCGATATCACTTGGGTACAATGTTTGTTCTTTAATTTATTGAACGGATGTGCA	11177	A_95_P026806	TA21992_4097
11688	138	43	278	CCGCCCCAAATAGTTTGGATAAAGAAAGCTTGTTGATATATTAGTAGTTATATCCTTC	11181	A_95_P114612	CV021687
11695	138	50	496	GGAGCCCTACTCTTTCATCATGCTTCCCTTTTTCATTGTTGGAAAATATAATGAAAGT	11195	A_95_P062730	BP135589
11696	138	51	743	TATTTGGGGCCTTTGATTTGATACGGCACCAAAGATACCAGCGATATGCAAGAAAAT	11197	A_95_P313563	FG158379
11705	138	60	798	GGATGTATGTTTTCTCTGGCTTTGTGTTAATTCTTACAAGAATAAAGATTTGGGTTCT	11214	A_95_P270111	EB677791
11709	138	64	392	TGAGTTCCTTAGCTTTATTTTGTAGGAACATATGGACTGAGCTTAATAGTATGTTGTC	11222	A_95_P039801	BP129657
11712	138	67	382	TCCATATCTAGTATAGTAGCAGCTTACACATCAGCTTCATTTCTTCTATGAATAGAAG	11228	A_95_P098893	BP534687
11716	138	71	104	ATATGTAACACAAACTTCGGAGACTCATGGCCTCCCTAAAATTGAAGAGGTCCTGCC	11235	A_95_P067590	BP136916
11719	138	74	178	TTTCTTGGATTGTACTGGAGTTACAGCTTTGGGACTTGTTGCAGCTCTTTGCCTTGTT	11241	A_95_P154377	EG649559
11724	138	79	353	AATCTGGGGTAAAGGTTACCATACCACGTTCCATAGCGCATCGGATCTAACCACTAT	11251	A_95_P113872	CV021352
11725	138	80	675	GTAATTTTAGTTTGTTGATAAAATCTGGTTCCTTTCTCTGTTCTGGCGGTTTTGTACCA	11253	A_95_P120137	DV999876
11729	138	84	1780	GCTACTGGTGACTAGAACATAATAAATGTATGTCAAGTTTTCTGGAGGTATACATGT	11261	A_95_P010596	TA14042_4097
11732	139	2	144	GTAAATGCTCGGTTAAGAAAACGAAGGCCCTAGTGATCTGGGTACAAAACAAAGCC	11266	A_95_P041946	BP130228
11738	139	8	855	TATTTGCATGACCAACAAGATTTGTCCTCCTGCATGGCTGAGTGAGCAGCTTGAAGT	11277	A_95_P311133	FG164937
11739	139	9	771	GACAAACAGCAGGTAGGTATAACTTCAGAAACAAAGTTTTCTTAGTCTTGCTGTTGTT	11279	A_95_P294128	EB439747
11744	139	14	921	GATGTGTCAAAGGCTTTTCTACTGTCGTTGTGAATCTATTGTCATGCAGTTAACTTAA	11289	A_95_P181947	AB079023
11753	139	23	60	GAATCCAAGAAGTCTTGGAAATCGTTATGTCTCCCATGCCACATTTTTGAAAGAAATA	11307	A_95_P004066	EB643438
11754	139	24	1087	GTGCACTTTTGTTCTCCAACTTGATGTTGTGAGTACCTGGCATTCTTCAGCAATCTGG	11309	A_95_P213957	TA20158_4097
11755	139	25	1402	ACTCGAGTATTAACATCTACCGAATTTGGGGAAATACAGAATTTTGTAGTCAGAATTT	11311	A_95_P007492	TA13337_4097
11759	139	29	691	TATTTCAAAATCTGGTGAGGGTGTAGAAAGTGTAGATCATGTTGCTCCATCTGAGAA	11319	A_95_P142612	DV159622
11766	139	36	426	TAAATTTTCCTTCGATTGTACTAAACATAATTGGCTTTCCCCGTCCAAAATCCACGTCA	11333	A_95_P082115	BP528435
11767	139	37	530	GGTTGAAGTTGGGAGCACGCCCATATAACAGAGGAATACATTCAGTCTTTTCATTTC	11335	A_95_P160317	EH619013
11771	139	41	672	AAGCTATGCAGGACGCTGCTGATGCTGCAAAAAGTGCAATGGTTAGTATAATTGGA	11343	A_95_P138912	EB442625
11776	139	46	963	CGTTATATGATGTATACGGATTATGATTTTGATCCATCGATCCATCATAATGGAACGT	11353	A_95_P202907	TA17741_4097
11777	139	47	105	GCCTGCTGTCAACCCCTTTTTGTTATATCTTCATGTATATAGCTCGATAATATTTGTGT	11355	A_95_P102177	CV015906
11781	139	51	442	TGGTTCAAAGCTGGATCTCAAATTTAAGCGAGGGTGGACTTGACTACTTGGGCAATC	11362	A_95_P104037	CV016814
11783	139	53	282	TTCATGCAAATTGTAGCTTCTCAGATGTTTAAGCCTATGATGGATATGATAGATGGG	11366	A_95_P111792	CV020374
11784	139	54	356	CCCCCTTTACCTTAATTACCCAAATACTTCAAAGCATTATGCACTACTTTTCTTAGGTT	11368	A_95_P028676	BP533879
11785	139	55	724	GGACAGTGGAAACATGTCGACATTGTTATTTTCATTCCTGAAATGAGAGTTCATTAA	11370	A_95_P215772	TA20561_4097

11787	139	57	2369	CACACAAGATGTTGTAAGTTGTTGTTGGACATCGCTAATGTCTATTTGCCTTCTAAAA	11374	A_95_P239319	AF435452
11792	139	62	739	TTGTCTTCTCGGATCCCTACAAAGTGTCACAATATAATCGCTGTACATCTCCTTATCTA	11384	A_95_P137702	EB428815
11794	139	64	740	GGCTGCAAATTTAGCCAGTGTTGGCTCCGCTGATTAATTATGGATTGGTTTTGTTGC	11388	A_95_P214672	EB678917
11795	139	65	1256	ATTGGCCCCGAATCACTTAAATGTACTTCCCTTGCAACTCAATAAAGTGATACTCATA	11390	A_95_P159537	TA17140_4097
11797	139	67	681	TGAAATCTGTTGGGAAGCTCTCTAACGATGAGTTGCACAAGTTTCTCCCAATGGAAC	11394	A_95_P063635	BP135833
11801	139	71	959	GCTAATGGGTATTGATCTCCTATTTCTGTAAATGTTACACTTTGTTGATGTAGTGTTCT	11399	A_95_P196102	TA16265_4097
11803	139	73	769	TCCCCTCAGGAATAATTGTGATTGATCTGCTTTCTCCTTGTACAGCAATAGTGCTGAT	11403	A_95_P273826	EH623341
11807	139	77	678	GTTTTGAAACCGGTGGGAAAACCTTTATCTATGGATGTGGCAACTTTTGGCAGAACT	11411	A_95_P120442	DW000357
11810	139	80	341	TTGGAGGGTCTGCTTTTCTACTTGCATTCTATTATTTGACAAAAGCGTATGACGTTTT	11417	A_95_P127007	EB426424
11819	140	4	747	GCATATCCATAATGCTTTGCTTACTCTGAAATCATTGTAGCACTATTTTCTTTCAAGCA	11270	A_95_P214527	DV158255
11824	140	9	287	GCATCGGCCCCCTGCCATTTTGTAATTTTTGTAACTTGGGATCTTTCTCACATTCCTTT	11280	A_95_P088488	BP530091
11826	140	11	660	GTTGTTTACCTGCTTCTTGTATTTCGTTATCATGTACCGGACATAGTCATTATAATGTG	11284	A_95_P125387	DW005177
11828	140	13	89	GGTGACTCTGATGGAAACTGGAGGAATTAGATAATTGAGAAGATGTGGATTTTAGT	11288	A_95_P106807	CV018069
11832	140	17	0	TCACGCCAGCGGAAATAGATGATTACCTACAGAGTGATAGATTTTCTTTTCGCTTCGC	11296	A_95_P297133	A_95_P297133
11840	140	25	428	GTGCATTAATTATAGTTACGCTTATGAGTCGCCGTTGCCCGTAGGCAGACATGTAGT	11312	A_95_P181212	TA12925_4097
11842	140	27	0	AGGTCTCTTTACAACGTTCTGAAAGCATATTCTGTCTTTGACCGAGATGTTGGATACG	11316	A_95_P297758	A_95_P297758
11845	140	30	728	CCTTTTGTCTCACTGACCAAGTGCATAAACATCAGGAGGCAGAAGAGTTAGTAACTT	11322	A_95_P263961	EB449438
11847	140	32	263	GGATTCGATCCCGGTTTGGTTGATGGAACATATTAGATTTGATTTTGTTTCAAGATGA	11326	A_95_P092863	BP532023
11848	140	33	442	TCCCGTCGTAAGGGCTTATGTGTGACACTATGGAGTGATAGGAAATAATAATTGTTA	11328	A_95_P196312	FG622275
11849	140	34	489	TTGAAGTTTTCTCTGTGGCTGTAAAACACGCGTTGTTCAAGAATCAATATCATCTTGA	11330	A_95_P020391	FG644307
11854	140	39	496	TTAAGAGAGGACAAGCAGTTTAGAAGGGACTACCCTGGTGCATCTACAATTTCAACA	11340	A_95_P239819	AJ496227
11855	140	40	395	CTGATGATTCTCAAAGTCACTCTGCCACAACTAACTTTGCAAGTATATTTGCTTTCTC	11342	A_95_P159937	EH618507
11869	140	54	236	GGGCTATTTGGGGAATTAGGCTTAGGATTATCTGGTAAATTTGGGAAACTAGTTTTC	11369	A_95_P002226	AJ718017
11870	140	55	238	TACTTGCTCCCAGGAATTGCAATAGCACATTGTTATATAAGGCTGCCAAGAGTTTTTT	11371	A_95_P099513	BP534956
11875	140	60	854	AGGTTTCTGTGGAAAAGTAAAAGACGACCTGCTAAAAAAGTTATGGTTGTAAGTGC	11381	A_95_P246952	EB426347
11882	140	67	234	GGGTCTAAATACGGCTCCTACAAGTTTGAATTCATTGTATCTGATATATTGTTTGAAC	11395	A_95_P027176	CV016731
11884	140	69	517	ATTCTCCCTATTACTGTCATGGTGGTGGATTATAACTGAAAGGTCACTTTTTTGGGTT	11397	A_95_P027666	TA17147_4097
11889	140	74	876	CCAGATTATTTGTGTTAGTCAGCTTCTTTCCTATGGATATGAAGATGAGTACGGTATG	11406	A_95_P203357	TA17837_4097
11891	140	76	755	CCCGTCACTAGAGTGAAAAGTATTGAGCTCGATGATGTACTTTCCACCAATGTGTAA	11410	A_95_P164757	EH624061
11892	140	77	791	AAACACTGCCCCTATTGTAACTAGGCAATGTTTAGTCTTGCATTCGTGAGCCAGTTGA	11412	A_95_P194167	EH622303
11893	140	78	572	TCCCTTGGGAACCAAATCTTCAGAAAGTTAGTCAGACTCCGAATGGACTGGATCCAA	11414	A_95_P082460	BP528518
11895	140	80	453	ACAGTTGAAGCAAAGTATGAATATCCAAACATGGCATTCAATTAGCTGTAATGGAAG	11418	A_95_P211982	TA19732_4097
11896	140	81	576	GATGACCCAGATAATGCTTATTTTGCTCTTATTTCACAGCATTGTATCCCTTTACACTC	11420	A_95_P139162	FG144494
11899	140	84	1209	TAGGCATATCAATGTATTGTGTGTGCCAAATTCAATAATATGTTGACGACCAAGTTC	11426	A_95_P031626	TA18069_4097

11902	141	2	837	TCTGGAGTTTACAAGCATGTAACAGGGCAAAGTATGGGAGGCCATGCTGTTAAGCTT	11431	A_95_P245427	EB438565
11904	141	4	514	GTGGATTAAGTGTTGATGAGGATGTTACATAGTAGCTAATGTTGTGGTGATTAATTA	11435	A_95_P124057	DW003905
11907	141	7	574	TATAGTCAATTTTTGGCCTAAATTTGGTGCGCCTGATTTGTTAAACACCAGGAAGCTT	11441	A_95_P143307	EB446652
11916	141	16	614	TACATCCTTATTGAGCCTTTGCTGCCTAATCCCAAATGATGGGCGTTCGTTCCACTGAT	11458	A_95_P297933	FG639155
11917	141	17	362	ATAATTAAGCCATTTTTCTCCTGCTGTAGTTCCAGTGTCCTAGGAGTGGTAACACTTT	11460	A_95_P051801	BP132744
11918	141	18	332	TCTTCCTCTAAACTTTGTCGCGGGTACCTTTGTGTACATATTTATGTTAAAGCTTTCCCT	11462	A_95_P140817	EB444644
11919	141	19	415	TGCTGCAGCTTCATTTGGTCAGGTGTATAAAGGGAGTATACTCAATGGTTCAAGTGT	11464	A_95_P088128	BP529967
11927	141	27	1421	GTCACCTAAGTTGTTACTTGCACATATATTTCCTGACCACATTTTGTTGTCAAGTTTTGT	11480	A_95_P027486	TA14793_4097
11929	141	29	791	TAAGGAGTGGTACACGAACCATAGGCGAATTTAGGATTTAAACTTAATGAGTTCAGC	11484	A_95_P021916	EB677429
11934	141	34	524	TCTCTCTACTTCCTAAATGGATGTTTGAGCTTTCATTGCCAGCATTGCTTATGATTTAA	11494	A_95_P019821	FG641597
11938	141	38	991	CTAGTGATGATAATGATCCACAAACCTTGTAAATAAACTCCCTTCTTTTTCTCCATTCCT	11502	A_95_P010391	TA13920_4097
11940	141	40	847	CCAACTAAGGTTGATAGAAGTGGTGCATATATTGTAAGACAAGCTGCAAAAAGCATT	11506	A_95_P188517	EB677645
11951	141	51	908	TGGCACCTTTTGATGTGCAGAAGTTTCAGCCCCCATATGTGCATTATGATGCTGCTTTT	11527	A_95_P227534	DV161802
11952	141	52	1590	CAGTGGTCACATTTTCTGAGATGCTAAAGAGCATCATTATAGATGTAAACGAATTCGT	11529	A_95_P018481	TA14633_4097
11953	141	53	596	AGGTACTTTGTTCTGAATGATGTCTTTCATTTGTATGAGAGGGGAGTGAGCTTCTCAA	11531	A_95_P164967	EH624431
11956	141	56	68	GCCCTCATGTATTGCCAATGTAATTTCTCCTCTAGCAAACCATTATGTATTACAAACTA	11537	A_95_P202232	TA17591_4097
11957	141	57	832	CCCAACTCTAAATGGATGGCTGCTTGGTTATCCTATAGTTTACCTATTTGGGATGTCT	11539	A_95_P146727	EB450849
11959	141	59	646	TGTGTAACATGGGGTCTAATCGTGATGGTGATGGTTTACACCGTGGGACATATATCA	11542	A_95_P316698	FG196196
11962	141	62	120	GAAATTAACGGTATTATAGTCAGCCGCCTCCTCCAACACCAGTAGTTACAAATCACAC	11548	A_95_P170064	EH664817
11965	141	65	106	TACATGTAGTGAGAAGGTAGACTTTTCCCATGTGATGCCACCTTCCATACATCATAAT	11554	A_95_P108867	CV019042
11967	141	67	786	GAATCGACAATGTAGTCTTACAACAGAAATTATGAATACCTAATTGGTTGCCTATTGT	11558	A_95_P009381	TA13492_4097
11969	141	69	193	TATACTTCCAGAGGAGCATTCAAAAGCAAATCCGAGACGTGAATCCCCTCATAAGGT	11562	A_95_P132647	EB433208
11971	141	71	0	GGCTGTATTTTAACCAAGCTTTCCCCCTTCACTCTTTCCATTGTCAAATAAAAATAAAA	11566	A_95_P285963	A_95_P285963
11974	141	74	778	CTCTGTATCATGGTTGATTTATTTTAGGGCTCTCAAGTCAGGGCCATATGCTATTTAA	11572	A_95_P014916	EH615319
11976	141	76	162	CAAATCGGGGATTATTATCGGGGGATACAAACAGAGTTGTTCTCATAAATACAAATC	11576	A_95_P092078	BP531630
11977	141	77	1392	GCATTTGGCTGTAGACATAGTGATGATTCTTATCAAATGCATCACATTCACACTCAAA	11578	A_95_P251732	AJ271749
11979	141	79	784	ATAATAGCAGATCAGTGCTGCAGTCGTGATCTCACAGGCTAAGAGAATCTCCTGAAG	11582	A_95_P312248	FG160767
11980	141	80	776	CGCGGTGTTTTCTGTATCTTGATGGCTTTGTAATTTTTATTTACCTGAATCCATCTGGA	11584	A_95_P296083	EB449797
11981	141	81	698	TGGATTCTGTTATATTTTCCAGCACAAACATTGTGCATGCGAATACAATGGATGGCTT	11586	A_95_P162437	EH623509
11988	142	3	661	ATCACGCTTTGGTAACCCTCCATGCGACAATTCACAAATATTGTGTGATCAGCTTGAA	11434	A_95_P315018	FG194337
11991	142	6	501	TTATACGTAGTTTCTTGATTGTCTGGTCATCCCCTGCTATGTATGTTCATGCCGTCATA	11440	A_95_P004691	TA15684_4097
11995	142	10	610	GATGCCAATTACTGTAGCTTTCAATCATTTTGGAAAGAGATGGTACAGAGAATGCCA	11448	A_95_P005991	BP128327
11998	142	13	1931	CCATGGGTTGTTCTGCGCTCTTTTGTATTTTCTGGGTTTTGGGGATAATTGGCTTTTCC	11454	A_95_P188742	TA14638_4097
11999	142	14	433	AAACTTAACTGAGTATGTATTTACCTGTCTCCATAATGAAATGTGTAGTTGAGCATCG	11455	A_95_P156202	EG650462

12000	142	15	703	TTTCTACAATCATTGGGTCTTGAGAGTATGCATTACATTTCAGCTGAAGAAGTTGATA	11457	A_95_P164797	EH624132
12001	142	16	443	TTTTTGATTCTCAGGACAGGTTGAAATTGGCTGATTTTGGATCTGCGGAGTGGTTTGT	11459	A_95_P217727	FS407656
12010	142	25	630	AAGATGTTTTTGGTGCAACAGATGCTTTTCAGTGTCAAATGGAATATGAGTGCTATG	11477	A_95_P210817	FG641774
12014	142	29	773	TGTGGTGTGTGCAGGTGTGAGAAAAATATGAATGAGTATATCTCTCTCTCGCCTCACT	11485	A_95_P216347	TA20685_4097
12017	142	32	805	ACCCACTTCTAAAGGACTGTGAACTCCTTATCATGGATGCTTTGCGGCCAGATAGAT	11491	A_95_P146992	EB451223
12019	142	34	808	GCGCCTATGGGTAAGTAAGGCAGCAAGAAGGTACTGTGATTTTATTTGCAAAATAA	11495	A_95_P263461	EB450466
12025	142	40	427	TAACAAGTCCATTGAGATTCGTAACTTCCTTGGCGAGAAGAGGGTTAGGAAAGTGG	11507	A_95_P102577	TA11943_4097
12035	142	50	362	TGCCATTTGTGAGCTCAATTATGGAGCTTGCCTAACTCTGTAATTTAAAAGATACTCT	11526	A_95_P151702	EB681945
12037	142	52	352	ACTTTAGCTACTTGTCTGTTGTTGCCTATTAGCTTCATCGTTGTGTTCCCCTCCAAATTT	11530	A_95_P024266	FG636220
12040	142	55	641	CTTAACAATGGATTTCACTTTTTGGTTTGTGTAATATACAGCTCCTGGATTTCATCTCA	11536	A_95_P177812	FG158081
12041	142	56	313	CTTCGTTTGATTGGGTTGCAACGTGATGATCTGCCTACAAAACCCGAGATGCTTACAA	11538	A_95_P058136	BP134401
12044	142	59	585	TGTGGATGCTTGGTTGGATTCGTTGCATTATGGTTGTGTTGTGAAGTATGAATTTAGT	11543	A_95_P065865	BP136446
12054	142	69	349	GCTGCTGTTCTGTATTGGAATTATTAGTTGAGCTCTACTGCTTGTTTGCTTAAGAGGT	11563	A_95_P163687	EH622784
12056	142	71	774	TCGAATTCTTGTACTTGGGCAGTCTGCTTCGCTTGCAAATCACAATTTTGCTGTCATCT	11567	A_95_P218662	TA21226_4097
12062	142	77	752	TAGTCGGAAGAAAATAACTGTAGTAGTCTACTGTTGTTTGTCTGCTTCTTGAGAGAC	11579	A_95_P142297	EB445810
12063	142	78	380	CCTTCATTTGATCGAAGCTTAAAACCCGAGGATCTGCCACAAAGGAAGGACAAAGAT	11581	A_95_P127217	EB426686
12068	142	83	553	AACTTCTGATTGAAAGAGAAGATCATGGAATTGCACTATACACTCTGTTGAAATAAT	11591	A_95_P031826	TA16803_4097
12070	142	85	816	ACCGACGCAGTGGACTTTATTATCTTCCTCCCTTATAAAGGCACCAACTCTCACAGATT	11595	A_95_P301478	FG171813
12072	143	2	606	TTCTTTTATTTGCTACGTTCCCTGAACAGTTAAAGAAGTGGACAAGAACAAGCCTGCT	11598	A_95_P216647	TA20751_4097
12073	143	3	627	TTCCTAAAGATGAATCCCCTTCGCATTGGGTTGAAGGGAAAGCCTTATCCCTCTGGA	11600	A_95_P161042	EH619747
12074	143	4	347	GACTGCTCTATGTGTAAATACATCAGTTTTTATCCCACCCTTTATAAGTTCATAGTGCA	11602	A_95_P030156	CV020316
12075	143	5	280	CTGCTTCAGCTAGGTAAGTTCCAAGATTCCTTGTATTGTGCTTTCATTTGAATGATTA	11604	A_95_P006796	EB431057
12076	143	6	785	ACCGAACTCGTAGTTATAAGGCTGCCTCCACCCTGAGTAGTACTATGGTCTATTATTG	11606	A_95_P296303	EB451287
12078	143	8	225	TATGAATTATGACAGTTGATGAGACCTCGATGCTTGCTATAACCTACTTTTGGTGTTT	11610	A_95_P202397	TA17625_4097
12079	143	9	545	TCCTACTGATCAGGACAGCATGTTATGTTTATTTCACATAGTTTACATTCCTCTTCAAG	11612	A_95_P307203	FG637773
12080	143	10	457	GAGGACAAATCAACTCCTTGTATATACTATATAGGATGTAACTTATATCCACTGACAG	11614	A_95_P027326	BP134187
12086	143	16	90	GTCTTCTTAAATATTGGAACTCCGAAGCAGTCCAGAAAATGTCCAAAATCAATACCG	11626	A_95_P144322	EB447310
12087	143	17	289	CCCTAGTTTCCAATCCATGTTGACACAACTGGAATTAAGTTTTATGCATTGAATTTGA	11628	A_95_P208517	TA18985_4097
12091	143	21	809	GCTCATTTACTCCAAGTATACCCTGCAATTGATATATGAGCATAGCTGTATCTTCGCT	11636	A_95_P296808	FG136523
12092	143	22	641	ACGACTTCACTTTTTGTTGGCACTTCGTAATTTTGAGATGTGATATTACCATGTGAACT	11638	A_95_P017926	TA17390_4097
12093	143	23	586	GGTGGTACTTGAGAGTTAGCCTTACATGGGAATTACTTGTTCTATGCTGTAATTATTA	11640	A_95_P027491	EH617143
12094	143	24	872	ATACAATCATGCTTGGTTCATATACTGACTATGATGAGTACTCTGATCAATATAGATG	11642	A_95_P208147	DV161905
12095	143	25	481	ATGTGTTTCAAGGGTTTTGGATATCTGAAATATTTAGTAAGTTGGATACTGGATTCCC	11644	A_95_P263311	AM828261
12098	143	28	523	AAGGCTTAATCTTCCCAACTACCCCTTCGTCAAAGGAGTCTTCCAAGGATGATTCTTC	11650	A_95_P158652	EH616548

12101	143	31	887	GATAGTCAATTATTGTTGCTCTTCCCTGTACTATTTATCTTGCAGGGATTTGAAGCATA	11656	A_95_P294663	EB442981
12111	143	41	760	CCTCTTGCAATGAATACATCATTCAATGTCTGGGCAAAGGCAATTCAATGAAATTACA	11676	A_95_P119822	DV999410
12113	143	43	747	TTTTCCGTCACGAATGGGAAGTATATTGTAAGCGGCTCAGAGGACCGATGTGTCTATA	11680	A_95_P144637	EB451710
12116	143	46	649	TGTATTGGAGGATAGGAATGATGCGGAAGATGATTTCTTTTACCCAGCATCTGGATG	11686	A_95_P053896	BP133305
12117	143	47	840	CAGAATCCCACTTCAATGCCTCTAATGTAATCCTTATTGGCAAAAGCTAGTTAATTACT	11688	A_95_P018646	DV160117
12126	143	56	1927	TGGTAAGGATGCTTGTGAATTATGTTACCATGAGACAAAGGAAATGGTGCCCTGAAA	11705	A_95_P239534	AY081175
12133	143	63	79	GTCCTCAGCTTTGATGAATTCAGAGTTATGATGACAAGTTAGAAGAGTTCAGAAAGA	11719	A_95_P003201	CV021135
12136	143	66	472	CTAGGACCTCATAGGATAAGATGTCATATTTTCCTCATCTTTTAGTCCATTTTCCCTGTT	11725	A_95_P049366	BP132145
12139	143	69	838	AATATGATGGTGGGTGCTTCTCACATCAACTGCTGTAGGAAGCTGCGTAAAGACTAC	11731	A_95_P266586	FG144602
12140	143	70	710	TCTCTAGATTGAAAGAGCTGCTCAGCCGCCTATTTTTACCCCTTTTCTCGTATCGAGCT	11733	A_95_P130722	EB450467
12141	143	71	377	TTGTCTAAAAGCATTAGCAAGCCTGCATTGCTGGCCGACGATCCAAACATGTACTTG	11735	A_95_P278793	AM838831
12142	143	72	1041	CACTGTTTTGGATGAATAATTCTGCTGGCTGCTTGTTAAGAGATTTTCTCATGTTTCAA	11737	A_95_P007026	TA20978_4097
12145	143	75	346	CAGACAATACAATGTTAGCACTATTATACAATGGGTTTCCGTAGTTTGAATGAAATG	11742	A_95_P002411	FS416760
12146	143	76	346	AACAACAACAGCAACAATCTGGTAGCTCTGGCTTTATGGAAGGATGTTTGGCTGCAC	11744	A_95_P000591	FG193869
12151	143	81	849	CTATGACCGACGAGCTTTAAGATGTGAATTTGTACGGTAAACATTGAAGTTCTCCTTC	11754	A_95_P013066	TA13881_4097
12154	143	84	950	TTTGCATTTTCTGTGTAATATTTGGTGGGCGTTTGGACATAACAATCGTAAAATTTCG	11760	A_95_P029681	TA16286_4097
12156	144	1	344	GGGTGTATGGGTGGTTGTCATTGAAGATAATGTGAACATGGACTATATTTATTATTT	11597	A_95_P133067	EB434138
12160	144	5	871	CTTGTATGCAGAAAGTATGAAATGCATTTCCTGCTGAGGCAGCAAAATGCTGCTTTTA	11605	A_95_P200542	TA17229_4097
12161	144	6	1049	CAGGATCCATTTGCTGCATCTTTGACTGTTCCACCTCCTTCATATGTACAAATGGCGGA	11607	A_95_P112872	TA13518_4097
12162	144	7	98	CCGGTTGGCATCAGATCAACACTTTAATCAGCTTATAATGCTATACTTGATCTGATAAT	11609	A_95_P163872	EH622917
12163	144	8	437	AATAAACATTCTCGCCCACATTATGGGATGAAGGAAGACAGATTAAAAGGGCAATG	11611	A_95_P283293	AM799615
12164	144	9	625	GGTCTGAGTGATTTGGAGCGAAGCAACTAGGAGTTGGACGAGCTTGTATATCTTGAT	11613	A_95_P135772	DW000043
12169	144	14	535	CTGTAAAAACTGCTCTATGTGATTAGTGATGACATTCATTATTCCAAACAAACCACAC	11623	A_95_P021091	BP534904
12171	144	16	854	GGCCTTGCCCCATGTAGTCTTTTGAGGCTTTTCATTTTATGCTAAAGCTTTCTATTTTTA	11627	A_95_P009676	EB449882
12172	144	17	17	ATATTTCGTCAATGCAGCTTGCAAGCTGCAGAGAGGAGAGTCATATGTAACTTTATAA	11629	A_95_P095798	AJ718758
12174	144	19	818	TCCCAGCAGCATGGCATATACTGGCCTTTATGATATGTTTAGATTCTTTTTTGTTCTTTT	11633	A_95_P187872	EB678181
12176	144	21	794	GATGTTGATTGAAAATTGTGACACTTAATCTTTGTAGCAGTGGCATGTCAGTTCCTTA	11637	A_95_P245807	EB451770
12178	144	23	822	ATCGACTGATGAAAGGAAGAGAATTGAAAGTGCCGAGTTGTTGTGATGTGGGCTGT	11641	A_95_P285228	FG148388
12180	144	25	1106	GGTCTAGATTAGCTCAAGGATGAAAATGTTGCTGTTATTGGATGTTGATATTGATGTT	11645	A_95_P214827	TA20348_4097
12181	144	26	685	CCCCTCAGTCCATCTGATCTACAATTGGATCATAATTCAACAAGTAAATATACCTATCT	11647	A_95_P017166	TA13094_4097
12182	144	27	692	GATCACCTATTTGAAGTCTTGCTTGACTGAAAGCGCTCTCTGATGCAACAGTTGAAG	11649	A_95_P289468	FG643691
12185	144	30	745	CTCTCATACATTGCTCTTGATTTCGAGCAAGAACTAGACACATCAAAGACTAGCTCTT	11655	A_95_P128138	EB427675
12187	144	32	502	CTTGTAGTGAAATTAGAGCTGGCCATCTTAGTGGTGACTGTCATTACAAACGGGAAC	11659	A_95_P071180	FG177765
12194	144	39	310	GGTTGTCTCTGCTGCATACAGTAGAAAGAGTGTGTATCTCAAAATAAACTGATAAAT	11673	A_95_P157492	EH615541

12197	144	42	901	TAAAGTCAGATGGCCTATTTTTGGCAGCTATTCTTGGTGGAGAAACATTGAAGGAGC	11679	A_95_P296943	EB680517
12198	144	43	491	TCATACTTCCTTTTTCCCCCTCCATTAGGTGTTCTACATCATACTATACAAGGCAAACT	11681	A_95_P255774	AM842133
12199	144	44	439	TGGCATATTTTGAAGTCATTTCTCACTTGGTCTGACCAAACAGACTCTACTGGGGAAT	11683	A_95_P033594	AJ632860
12200	144	45	400	CCCGGACTAAGCCCAGGCCCAACGGCTATTTAATATTGTTTTAATATTATTTTTAGCG	11685	A_95_P037493	BP129019
12202	144	47	441	TTCTGTCAACTTTTCCTACTTTACAGTCACATTAGGAGCAAATCCAAGTTTCTGCGTG	11689	A_95_P273136	AM818734
12203	144	48	734	GAACTTGAGCAAGTCATAATTGGTGACTTTCTTAAGCTTCTTCGGTAGAATTGATATG	11690	A_95_P272796	EB678279
12204	144	49	252	GGGCAGTGCTCTTAGTTCTGTAACTAATTTTGTTAAAAGTTGTGGCTTATGAGCAACC	11692	A_95_P213672	TA20098_4097
12206	144	51	0	CTGGGATTGCTTGTAGAGCATAGTGAAAATGCAACTTAGTTCAAATTGTAATCCTTA	11696	A_95_P309318	A_95_P309318
12209	144	54	496	GGGTTTCTTTCTGAATTGTGGTGGTTGTGCCTTGATTTTCAGATAATAAATTTGGTTT	11702	A_95_P002436	TA12805_4097
12213	144	58	556	GGTTGTGCTGTCATGAATATGGATTTCAGGTTTTCTGGTGTTATATCAGAGTATTGGT	11710	A_95_P153977	EB684143
12214	144	59	1045	TTTGCGCCATTCTAGGTAATGATGTAGTAATATACTCCATTCTTTGAGACGATTGTGG	11712	A_95_P008011	TA16773_4097
12218	144	63	432	CTCGATATCATGGAGAACGTGCCACCAATATGACAACATATCGAGATGCCCTTATAT	11720	A_95_P145202	TA14564_4097
12222	144	67	483	GATAGCTGATTCATACATGTAAAGACATGCCGCAGATTATTCTTTCAACAATGTGTAA	11728	A_95_P025561	TC59594
12224	144	69	870	GATGTTCCTGCTCCCACTAACACAGATTTGTACAGTCTCTCCCAACACTAAAATGCAT	11732	A_95_P233634	FG159928
12227	144	72	730	ACCATGGTTGATGGTACCTCTAACGATAGTGTTAATGGTGCTTAAAGCTGTTCTTTTC	11738	A_95_P232319	DV999927
12239	144	84	627	AAGTATATCCAGATATCTGTTGAATCCTGATGAGTACTCATATATCAAGTTCATGAGG	11761	A_95_P027441	TC67685
12241	145	1	812	AAAGAGAGGAGCCAGATATTGGTGATTCCTCTAATTTTAAATAGTGACTTGGCTCTG	11764	A_95_P215067	TA20404_4097
12242	145	2	1098	ATCTCCCCCTTCATTTTATTTGAACTTGTTTGATTCGGGCAGAGTTAGTGAAAAAGAG	11766	A_95_P027661	TA21617_4097
12246	145	6	547	TAATGAGGCCCTTCCATCTGATTGTAGACCAAACTTCTCTGCTGCATGGTTGACAAAG	11774	A_95_P262341	BP135370
12250	145	10	694	GATTATGATGGCGTATATGATGATATGAAAATGAAGGCTGTCCAACCTCGAGCTCAG	11782	A_95_P138047	EB441765
12251	145	11	687	GTTACACTGTAAGGCAAAGCCTTTCTATTTATCCTGCTGTGTTAAAATTCCACTAGTA	11784	A_95_P288528	DW003497
12252	145	12	512	GCAAGGATACCAATCGATTGGTATTGATTGATTTTGGTCTGAGCTTTACATCAACCCT	11786	A_95_P148307	EB677576
12259	145	19	715	GTGTTTGAATCGATTTGATTTGTGGAAGATTTGAATCTTTTGTGATTGTTCGGTGTTT	11800	A_95_P215602	EB438670
12261	145	21	809	TATGATGAATGACATTGAATTAGTGCTTAAGGCAATGGTTTCTGTGCATTGGTATTTC	11804	A_95_P205852	TA18379_4097
12262	145	22	907	ATACGATGAAGGAGATTGGAGCTACTTCCAAGTCATCTGCTGTGTTTATTCCCCATG	11806	A_95_P126487	EB450618
12272	145	32	0	CAGAGCGTTGTTGTGGATCTTAAAGTGATTCTCAAGCAAGAGAGAGTGAGATGGCT	11826	A_95_P258596	A_95_P258596
12275	145	35	823	ATGGCTTCAAGCAATTTGTAGTGGGTCAATTATGTATTTGAGTGTAGCATTATGTTTC	11832	A_95_P206047	TA18421_4097
12277	145	37	591	GATGCAAGTGGGATGTTCCTTTCGAGAGTATGCTTTCGTTTTGGATTCTATTGGATTA	11836	A_95_P161527	EH620236
12279	145	39	684	AAAGTTTCGCCCCCTGTTGTTGAGACTCACTGAGTACAATGGATGGTACTGACATTCT	11840	A_95_P134727	EB437409
12281	145	41	503	CCCGGTGTTTCGAACAACAGGAGAGATTTTGTACATGCTGTATCATTACCTAAAATCA	11844	A_95_P066600	BP136643
12286	145	46	155	CGATGACAATGATGATGACGATGACGATGACTGATGACGATGACGATGAAAGATAC	11854	A_95_P064610	EB445150
12289	145	49	270	AGAGCCCTCTTAATAGCCTGCTGCAATACCTTTAATTGGAAGAACAAGGAAGGATGC	11860	A_95_P002093	BP129711
12302	145	62	0	TCAAACAGATCTGCCTAGATCTCTCATTGATGACGTGAATATGCCAACACAGACACC	11886	A_95_P236104	A_95_P236104
12305	145	65	898	GTGGGTGAAGCGTGGTGAATCCACACATTCTGTTTGAAACATCAAATAATTTATTCA	11892	A_95_P194032	TA15805_4097

12306	145	66	819	TGTTTCGATGGATGTTTTCTGCAGACTTGCAAAAGATAATGCTTCCTTTTTTCACATCA	11894	A_95_P013901	TA13753_4097
12310	145	70	839	GGTTGAGTTTGTTTAAAGCTTGTTCAAGTTTAACAAATTTGAAAGTTGTTGGTCTGGC	11901	A_95_P023971	EB449629
12317	145	77	544	AAGGTTTGGCTCATACGTATGTTACTTTATCTGTGTATGACAGAGAACTTTTAGCCAT	11915	A_95_P121902	DW001989
12318	145	78	264	ATTTGAGATATTGTCCATTTGTCCTCTGGTTAAGGAATGCCCACATGAGTTCGTCAAA	11917	A_95_P092008	BP531602
12319	145	79	513	TTTTGGCCTATTTCTGACTTCCGTTACTTCTAAGCTTCAAGCATGAAGGAATTCAAAA	11919	A_95_P158332	EH616324
12320	145	80	862	CTCAATAAGGCCCTTGATACCTTCAACACTGCCGTTGTATCTCCTATATACTATGTTAT	11921	A_95_P208347	TA18949_4097
12333	146	8	416	GCACCTCTTGCATATGCTGAGTTTAGGTTAAGTAGTCTAGTTTAAAATGTTAACTTTC	11779	A_95_P211212	EH621285
12338	146	13	684	TCTGAAAATTCAGAGTCAGATTTGAGTTCGCAGCGTGTGACACTTGGATTGAATGCA	11789	A_95_P086500	FG152206
12339	146	14	752	GAGAGGGACTGGAATTTGGAGGCTAATGTTGAGAATGGCAAAATGCTGTATGCAG	11791	A_95_P244017	FG638547
12340	146	15	822	AACTTGTCATACTATTCTGGATCTCTTCTCGTGCACGCTGTCCTTTTCTTTTCCTAGTGT	11793	A_95_P126612	EB425931
12342	146	17	779	AGCAAACATCAAAAGGAAACGCCCTCCTCCAAGAAGAAGTAGGAAGTGTGGTCGAA	11797	A_95_P121247	DW001268
12343	146	18	112	CATGTACTCGAAAGAACCATATTTTGATGTATATGTGGAACAGTAGCAATTGGTTTA	11799	A_95_P257419	EH623419
12345	146	20	231	AACTCTGGTCACCGCTCACAGATAATCTTAATTTCCGGCCAATTATTGAGTTTTGGCG	11803	A_95_P158912	FG643060
12346	146	21	613	CCTTCTTTGTTTGTGTTGCTGCAATTACTATGTTGATAATTCTATGTTCGGAGCAGGG	11805	A_95_P129237	EB428951
12350	146	25	875	TAAATCTACAGATGACCCTCTCCTCCCTATCGCTTTATCACTATTATTGTGCTCCTGGG	11813	A_95_P288203	FG167361
12354	146	29	349	TCATCCATAGAAGGAGTTTAAACACAAGATTGGTTATGTCCTTTTCAGTTTAATCAGC	11821	A_95_P105277	CV017392
12357	146	32	768	GAAGCATGCTCTGACCCTCTTTACAGATTTTATTGCTGTTTTTGTGCGAATTTTAATCA	11827	A_95_P135927	AF390556
12358	146	33	378	CTGGAGAACTTTTTATGGATGTCACTTGATTCATAAGATGCTTGGTTTAATCAACTCT	11829	A_95_P023146	AM824341
12359	146	34	725	TGATCATGTATCATCCTTTGCTTTCTCATTTTGCCTTCTGATGGTAATAAGTGGATGGT	11831	A_95_P182182	TA13150_4097
12363	146	38	365	GATGGAATAGCAACTCCAAACCACTTCCTTAAGGCTAAATGTCTTTTGCTTTTGTACA	11839	A_95_P131342	AM806952
12364	146	39	698	GAATGCTTCTGTAGTACTGTGCGAACCAGACTTTAGAATTATAGAATTATGGCAATT	11841	A_95_P026546	EH618938
12367	146	42	835	GCTGGCATTGTAGAATGTGCCTTTGTGTCTTCTCAGGTGACTGAACTTCCATTTTTCG	11847	A_95_P230799	DV157984
12372	146	47	439	ATCAAATACAGCATTTAGTGTAGTGGGAGCCTGGGTTATTGAGAGTTTTGTACATCA	11857	A_95_P204352	TA18047_4097
12374	146	49	706	TGATCGTTTGTTTGAATACAATCAGACACTTCGAAACCAGTTGCAGTCAATAAGCCAT	11861	A_95_P144677	EB448177
12376	146	51	682	TGAAGGTCAACTTTACTACAGTTTGGCCAGGAATTTTGAGAAGTATTTGTGGTACTTT	11865	A_95_P232594	FG643793
12377	146	52	1445	AAGGGTATCTTTATCTCCTGGCAATTTGGTCATTGACGACGAAGATTTTTGAGTTGG	11867	A_95_P303508	TA15330_4097
12380	146	55	766	CCTCTGGTGGAGACTTAGTAGAAATGAGAACTTGAGAAGTAATGAATGTTGTAATA	11873	A_95_P117947	DV160934
12381	146	56	693	GTCATTTAGTTGATGTTAGAGTCTGTCATAGTCCAGTTAAGTTTGTCGAGTCTTTTGT	11875	A_95_P206782	TA18593_4097
12390	146	65	627	ATTTCCGGTGAGAATCTGCCCGTTTCCGATACTGAATCCATTCCACATGTTTCTGTGA	11893	A_95_P132745	EB439272
12392	146	67	520	TATCAATGAAATGGATGGGAAAGAGCTGCTCGCTCAGCCAATACATGTTGATTGGG	11897	A_95_P148178	EB683371
12393	146	68	758	TAAAAAAGAAAATTCTGCTGATGGTTGAAGTTGGTGGTCTGCATGAACTTGCTGGTA	11899	A_95_P153112	EB683435
12399	146	74	909	ATGTGTGAATGGAGAAAGCTACTGGTAATGCGTCTCTGAGTTGCATTCGGTCCTACA	11910	A_95_P008081	EB680954
12401	146	76	630	CTATCTTTAGTGCATTTACATCAATGTAAAATTGTGCGCCATGTATTGGGCAATTTTA	11914	A_95_P090943	TA14293_4097
12402	146	77	266	TCCTATTGTCTTGTTTGTGACAAGATGTACTGCACTTTGAGTGGTATTGTGTCTGCAG	11916	A_95_P112202	CV020573

12403	146	78	772	AACTATTTGCTGAGTTAGAGGGTAGATACCAGTTCTAGTTCTGGCACAGCAGTTCTC	11918	A_95_P241694	FG147471
12405	146	80	385	TTTTTCGTCGAGATTTGCGTCGATTTCGGTTTCAGCTAAGTCTTCAATGGATTTGGGC	11922	A_95_P089613	BP530570
12406	146	81	737	ATGAGCATACCATCTCCTAGTCATTTCTGCAATTTTCCTATTTTCTGCGTTTAGGGGG	11924	A_95_P028986	EB428319
12409	146	84	391	ATGAATCCAAAGATGGACTCTTGGATCTCCCAGATTTTCCTCATGGTTTCCCTAAGCC	11929	A_95_P050731	BP132468
12412	147	2	392	TTTTATGATGGCTGTGTCAATGTTGCTTCTTTGTTTTGTTACAGAACTTTAGGTTTCCT	11934	A_95_P105752	TA15420_4097
12417	147	7	689	ATATACATCATCTGACCCATAAGAGAACATACTTTGCCAGCAAAGGCAGCCACCGTT	11944	A_95_P159447	EH617653
12421	147	11	549	CTCGATGTATCTCAGGGTATATACTCTTCTGCATTCACCATTAGAAATAAAAGTGTGC	11952	A_95_P122057	DW002115
12423	147	13	812	AGTCAAAAGGAGAGCATGTAACCATCAGATCTTGGTGAACTCATTTACATTAACCGA	11956	A_95_P115462	DV157688
12425	147	15	365	ATGATACTACGACGACTGGTTAGGTCGTCTGTTTGTTAAAATGAGATTCATGGCTGA	11960	A_95_P129857	EB429800
12427	147	17	830	TGAAACTCTTGAGAAGTGGGTCACTGGTGCCTTTGCTGGTCATACAGCAGTTTGTTT	11964	A_95_P150382	EB680474
12429	147	19	520	CACTACAAAATATTTCCTGCCATCTTGATTAATCTTGTAATCGCTGTGATTTTAGTGTG	11968	A_95_P000231	CV020114
12430	147	20	1680	GCTAGATACTTCTCATTACCCCTACAAGAGAAGACTAGATGCTGTAAAAATATTCGTC	11970	A_95_P130902	DQ399915
12436	147	26	789	CTGAGAGGAACTCTCGTGTCTTGTTTCTTTCATTTACTGTAAGACATTATGGTCATATT	11982	A_95_P018521	DV160610
12437	147	27	198	TAGATGGTGTTGCATTGACACTCTGCCAGTCAGATCCTGTTCTAAATGATGGGTGTA	11984	A_95_P158897	EH616784
12440	147	30	519	GTTGCTGCAACAATGTTTCAAACATAACACTAAATCATGTGAGACCTTTGTATTTGCT	11990	A_95_P268646	DW002369
12442	147	32	702	CCCTTAGTAAGGGCTGTAAATGGATACCTCTTTTGAAGTGTTCCATATATATGTGAAT	11994	A_95_P013821	TA12500_4097
12443	147	33	817	CCGAGAACATCCAACAAGATATCAAGACACCAATATTTATTTCCATGTCAGCATTTGA	11996	A_95_P126157	EB424698
12445	147	35	874	AAGGCCTTGATGAAATGGCTGGCTGATTTCTTTCAACAATCAAGTTGAATTCTTGTTG	12000	A_95_P015451	EB425092
12448	147	38	844	TGATGTTTGATCAGCGACAGAAATCAATGGGTCTTCCAACAAGTGATGAGACACAG	12006	A_95_P231634	EB425013
12451	147	41	657	TCTCATGGAAGTTCAGATAATCAGAGACAATGCTAGTTCCATGTTCTCTCAATGTTTC	12011	A_95_P027826	DV159784
12459	147	49	313	GATAACAGAGGAGACCTAACTGGTACTAGCTCAACTGAATTCCCTCTTCCTTTATTTT	12027	A_95_P133782	EB435466
12462	147	52	678	TTAATATGTTTATCAGTGGCAGGGTTGCAGTTGTGGCATTTGAAAGACCTTTTTCGA	12033	A_95_P292073	FG643223
12464	147	54	756	TTATAGGCGTCTGATTCACACTTGCATCCCTTCATTTGGTAATCAAAATGTTATTTGTG	12037	A_95_P272801	EB678285
12465	147	55	247	AAATGGGTCGGAAATATCAACGAGCTGTAAAATTGCCAGCTTCACATTCAACGGAAT	12039	A_95_P103917	CV016751
12468	147	58	546	ATGAGGACGAACGGAGCTCTGAGGTACTGTTATGCTGCTTGTGAAGATTGAAATGT	12045	A_95_P160332	FG636077
12469	147	59	679	CTAGTGGCAATATCCTGTCATGTATGTTATTTAAATTTGTTGTGCTTGTGATCCAGTA	12047	A_95_P020816	DV999581
12470	147	60	649	ACTTACAGAAGGTAGTTGGAGTGAAGCATTTGATGGCCTTGGAATTTCTTTACTGTT	12049	A_95_P148327	FG152390
12472	147	62	295	TAGGGGTTCTATCTTAGTGCTGTGATGATCATCTGTAATGGAATTCTTGCTATTATTC	12053	A_95_P143137	EB446478
12478	147	68	798	GTTCTTCTGGTGAAAACAATGCTTACATGGTCGTTTATATTACTGCCATCGCATTCAA	12065	A_95_P268581	DW002225
12479	147	69	290	GACTGTATTTAGTACATTTTTGACTTTAGTTGTGTTCGGACCTTAATAGATGCTCATG	12067	A_95_P093853	BP532448
12482	147	72	514	GATCCACTTGGTTGGATATCTTCCCCTTTTGATTTAAATTGACTATTATCATTGGTTCC	12073	A_95_P022516	TC59898
12488	147	78	743	GGGCTTGGTTGATTGTCTGTATTTATCCGATTGTTTGACTCTTAAACACCATATTTATG	12085	A_95_P021561	EB682980
12492	147	82	577	TAAAGTAACAACCCAGGCACTCTCAGCTGCTGGTAGAAATTCAAGCATTGCGTGGAA	12093	A_95_P068320	BP137101
12495	147	85	980	GGCTCCTGTAAAGAAAATGAAGGGGTCAAATAATACATGATTGAATCTTGGCTTAAT	12098	A_95_P194872	TA15996_4097

12497	148	2	1000	CTCCAACATGCTATCAGTACTCCCTGAGACAGTTGGCTCCTTAGTAAGTCTAAAGAAA	11935	A_95_P202477	TA17645_4097
12498	148	3	741	GCGGAACACAAAGGCGTAAAGACTGTGTGGAAGATTACAGATTCATATAATTATTGT	11937	A_95_P025171	TA17191_4097
12499	148	4	806	TTGAGAGTTCTGATACCATTGACATGTCAAAGCAAGATCAGACAGAGGTATCCCGCC	11939	A_95_P309023	FG167278
12501	148	6	622	AATGCTCTTCTCCTCCTTATATGGATAATGGGCAATTAAGATTGGATTCTTAGAGCCC	11943	A_95_P091498	BP531384
12505	148	10	0	GAGTACATCTCATGGTGAAATGTGCTGCAACTTTCGATGTTGTAATATCAAGTTTAAG	11951	A_95_P024101	A_95_P024101
12508	148	13	421	GAAATTGCTAAGCGAGGATTAATCCAATTCCAGGTCATACCGTCTCTCTCTCTCTTTTT	11957	A_95_P060245	BP134948
12509	148	14	786	TCTATATGGACTCCCTCTTACCAGCAAACTTGTTGATACAAATTATATTCAAATCACCT	11959	A_95_P196957	EB429912
12510	148	15	418	ACCCTCTTGTTGGAATTTTGAACACTTCCTTTCAGCTCAAAGCACTTATTTCGTAGCTT	11961	A_95_P022691	TA13685_4097
12512	148	17	600	CAACACGCTGTATAAAGCATTCTGTTTTTATGTAGAGTTCAAGAAACGACGCACTTGT	11965	A_95_P216367	EH621105
12518	148	23	426	AGATTATGGACCCAAGCAAGCTCTGTTTATTTGGTTATTAAATGGCTTTAGGATATGT	11977	A_95_P132072	FG638602
12519	148	24	996	GAGTAGCCGGCGACGTTTTATTATGCGTATGAATTGTCACCGTGTTTATGTGAATAT	11979	A_95_P205757	TA18358_4097
12521	148	26	608	CAGTCTAGAGAGCTGATTGGTGTTATTTCTTATTTCCTTAAATCTAGATAACTGGTGA	11983	A_95_P204447	TA18068_4097
12525	148	30	1391	GTTGCTTATATTGCCCGTCGTAGATTCTTTTTGTTAAGTTTATTTTAGTCCTCTTGCTG	11991	A_95_P185712	TA13974_4097
12526	148	31	529	CAGGCTCCGTTTAGAAAAAACCCAATTGGATTGGTAAGATATCTATGATTGCTATTCA	11993	A_95_P020631	EB432836
12530	148	35	1679	TCTATGAAGTAGGACGAGTGTCCTACCTAATTCAATGCTAGGTAACCAAGTTAGTAT	12001	A_95_P176372	TA12737_4097
12534	148	39	337	TCTTGAAGTTCTTGCAAGTGAAGGTGCAAATTATCTCGAGAGATCAATGGAAAAAAG	12008	A_95_P087798	BP529881
12535	148	40	708	ATGCTCCACTTCTTGTTAAAAACAAGGCAGCTGAAGTGTTGTTTGGAAACATCAGAG	12010	A_95_P260511	EB425659
12540	148	45	841	GTCTATGATCGAGCTCTTCAGACCGTAATTTCATCATATGGATAGAATTTCACCAAAA	12020	A_95_P219297	DW003605
12543	148	48	348	CCTTCTACTTCTAATTCCAAGAAACAAGAAGAAGGAGGAGGAGGAGGAGAAG	12026	A_95_P158097	EH616183
12544	148	49	633	TAAGAAAAAATCGAGATTTGGGGTTGAGATTTTGGGAACCCTTGCCCAGATTTTAAAG	12028	A_95_P257539	FG643524
12547	148	52	278	GTCCGGAGAGTTGAGGACAATATCTATGCGACTATGCCATTAATTTAATCAAAACTA	12034	A_95_P214317	TA20239_4097
12549	148	54	369	TGGGCATTTTCTGAGCATGTTAGACTCTGTTCTTGAAAGAGACATGGTGCCTACAAT	12038	A_95_P110337	CV019692
12551	148	56	579	GATTAATGTGAGTGTAACTGCTGCTGCACCCCTACAGAATGAAGAAGAGTCAGAGG	12042	A_95_P307913	FG195867
12552	148	57	452	TCTGCGTTTGTATCCCACAAGAATAAGGGGAAAAAATTTCAAGATATCGTTCATGTTT	12044	A_95_P137007	FS416181
12555	148	60	646	GTTTCCCGATCAAGGACTGGACTTTAAGAGATTAATACATTTTGGAAAAATACGGTTT	12050	A_95_P016806	EB443154
12556	148	61	513	TTAGGGTTATTGGGTAACTAGGCTTATCTGGGAAATTTGGGAAACTAGTTTTCCTTCT	12052	A_95_P000101	FG167017
12561	148	66	343	TCGCGCAAAACGGTAATATATCGCTTGATGATGTGATTGAGATTGCTAAAGATGATG	12062	A_95_P102937	CV016268
12564	148	69	183	CTATTTGTGAGGTCTCGGAAAGAAATGGACTATATTGTGACTTTTGGGAGAAATTCA	12068	A_95_P091313	BP531296
12568	148	73	777	TCCTGGAGAAGATGATACAAAGTCTGCAAGAATAGGGAGAAGGGCTAGGATGCTTG	12076	A_95_P136057	EB439617
12570	148	75	935	GAACCTACGACGTGTCAAACTTTTTTGTTTGTATTCTAAGTGACTAATTCTGTTGATA	12080	A_95_P011546	TA12287_4097
12573	148	78	298	CCAAAATTTGGTTGTTATGGGCATGCTATATCAGTTTGGCACCATTTTTATGTTGGCG	12086	A_95_P155037	EG649867
12576	148	81	788	TTGAGAGGTAGTCCGATGTAGAACCTCATTGGCCTATATCAAGAAATGAAGGGCTTT	12092	A_95_P181352	DW005137
12582	149	2	756	TATATTATGTTTAAGAACATGTGCTAGGAAGCTGGCCTTGTGTTTTGGCTGCAACCG	12102	A_95_P195622	EB678692
12585	149	5	875	TATTGTACTGATCTATAACAGTCAGAAGATGCGTTCTTGGCGTGGATGGTTCAGCCA	12108	A_95_P229859	FG161194

12587	149	7	450	TATGCACTTGGGGTAGAACATTTACTTTTGTGGATATTATTAGCTTGTTGGACGAGTT	12111	A_95_P131647	TA18424_4097
12590	149	10	860	TTCAACAAATCATATTTGGAGTACATTGTAGATAGTGCAGGTAAGTATTATGGCACT	12117	A_95_P268541	EB436962
12592	149	12	893	CGTGGGATTCCTATGGAAGAACTATGGAAATGAAGAGTTTCTGTTGCTTTGATTTGT	12121	A_95_P009196	DV998963
12593	149	13	290	TACTGGTTGACAATGGGTCTAGTGCGAACATTTGTCCTCTCTCCACATTGAACAAGCT	12123	A_95_P038021	BP129160
12594	149	14	436	GAACTATGGAAGATCATACTGGTCCGACTGACTGCAACAATTAATGATTTTGATTGA	12125	A_95_P211312	TA19583_4097
12596	149	16	309	CTAAAGTGATTTCTAGAGCAGTTTTCCCAAGCCTGAAACTTAGCATTCAGCACATTTC	12129	A_95_P208482	TA18978_4097
12604	149	24	581	AGAACAGCAAATGCAGATAGGCATGCTGGGAATATTCTTGTGAGCAGGGAAGGAG	12145	A_95_P128752	FG155230
12610	149	30	878	CTTGACAGAGATCAAGGAAGGTAACTGGAAAAGTGGCTTAGTTGTTGAAGGGATTG	12157	A_95_P254064	EB424810
12613	149	33	734	TATTTACTCATGAAAGGACTCATACAGAGTAGATTAATAAATGGGTCGCCCCCGGCC	12163	A_95_P117882	DV160844
12616	149	36	591	CGTTTGGCTGTGTTTATATAGTGCTTGAATTCACAGCAAATTGAGCAGAGTAGTTTA	12169	A_95_P122032	DW002099
12625	149	45	1231	GATCCTTGTGGTTACTCCATGAATTCTATTGAAGGAGCTGCACTTTCTACTATTCATG	12187	A_95_P018976	TA14024_4097
12628	149	48	114	GTTAAAGTGGGCTTTAGTGACTGTTGTCCAATTTGGTATTGGTAAACGTTTTTATGTT	12192	A_95_P127277	EB426804
12632	149	52	600	GAATCTGTAGCTCAGGTTTGTTTCCCTTGCAACAAGAAATGAAGTTGGATTCAATTG	12199	A_95_P147797	EB643455
12633	149	53	472	CAAGGTCAGATTAGTTCTCTCGATGAATTGAATTATTACGATGTTGCATCTTATGCAC	12201	A_95_P162872	EH621868
12635	149	55	859	CCGTGCCTAGTAGATACATATCAGCAAGGGATGTTCTTTCTGCTGTTACTCAGGGATT	12205	A_95_P245922	FG158620
12638	149	58	647	CTTTTTCAGCTATACGATCTCAAGCAACAAAGGCTTTCATTGAGAGGCAAGAGGTGA	12211	A_95_P184487	TA13707_4097
12643	149	63	27	TTCTGGACTATGTGAAGTTCTTAAGGCTTCAACGTTAAGGGTACTGAGCATGACGTA	12220	A_95_P064985	BP136207
12644	149	64	753	CAATGTGGCTAAATTTGTGGGATGTTATCGCGCATTTTTTGTTAGTGTAGCATAAAAT	12222	A_95_P023016	TA13495_4097
12645	149	65	248	ATTTCTCTATAGTTGGCTACTTCAGAACCTATCAAAAGGAGAAAAGGCTATTTCAGA	12224	A_95_P155442	EG650068
12647	149	67	586	GTTGAGACAGAAGGATGTAAAAGAAAGGGAGGTCATAAATTGGCAGTTTTGGTTCC	12228	A_95_P216357	TA20688_4097
12649	149	69	556	ACAACTACTCGATTGGAGTGTTTTGTTTACCATGTAATGGATTTTGTGCAGTTTGATA	12232	A_95_P018321	EB427220
12652	149	72	653	CTAGCCCTGCCATCGTCGATCAGTTTTGTGAAAAGCAAATAGGAATATAAAGACTAA	12238	A_95_P020611	TA21272_4097
12653	149	73	313	TATGTAGTTTGTGATTCACGATGTTCCGGGTTTTGCTATTGCTTGTGTATGTTTGACC	12240	A_95_P107917	CV018599
12663	149	83	605	TTCTGCAGCTAATACTACCGGGTTCTGAATGGTATTTGCTGGTGTTTATGTGGATGCC	12259	A_95_P061770	BP135343
12677	150	12	1080	GCAGATGATATGCCTTTATTCCGTGTTTAGGTTAATTATCATCTTCTTTGCAGAATAG	12122	A_95_P019291	TA17097_4097
12680	150	15	825	ATTAATACCCCAGTCAGAATTTGGTCTAAGTAACTCTTTGCTTGTTACTTTCTTTACCC	12128	A_95_P023651	EB438728
12683	150	18	742	GGGGAGATTGTGGAAATTTTAAAGCCTGATCAACTCTCTGAAGCTAAACATCCCACG	12134	A_95_P286568	FG640162
12687	150	22	446	ACTTTTGTACCAGCAGCTTGTGTTTTCGGCTCATCATGGACTGATTGGCACCGTGTAT	12142	A_95_P153972	FS421124
12689	150	24	316	CCCATCGAGTCCCGTGGTTCTAGCACAGTCTCTTTTTGACTATGTAAGGCTTAAATCA	12146	A_95_P141562	EB445262
12690	150	25	386	TAATAATCTGCCCGTCTGTGGGATCCTTTCATTTTCCCATTAATTGTCACATTTCTAGT	12148	A_95_P186872	TA14221_4097
12696	150	31	750	GCGGGGTTCGTCCGTCGGTTTTGAAATACTTGAGTTTGGTATTTTCTGCATTTTAAAA	12160	A_95_P183227	TA13409_4097
12697	150	32	288	CTTGTAGGCACTCTTGTTTTGAAGTATTCAAGTTGTTGACATTTTGACTTTGGTCAAA	12162	A_95_P108742	CV018985
12700	150	35	807	AGGCCTGACGCCTTATACCATCTTGTACCTTTTTACTTTCTCTTCTCTGTCGTGTACATT	12168	A_95_P030426	EB681836
12701	150	36	466	CATTGATGTGCCGTCTCATATAGCTACTGTAAATTGATATGGCGGCCGTCAGGTGTA	12170	A_95_P092608	BP531883

12703	150	38	357	ATCGTTGTGTAGAATTGGATCTCAGATGAGGGAGAGTGATTTGGTTGATTGGTTTGT	12174	A_95_P127347	FG140084
12706	150	41	440	GTGAGACATATGGACATTGTACTCCTATGTTTTATCTTTGTTCAACTAGCTCAGCTTAT	12180	A_95_P123327	TA12982_4097
12707	150	42	543	AATGTTTGCAGATCGGATGTCCATTTCATAAATGTTTGCTGTCTGTTTATCTTGCTTTT	12182	A_95_P098533	BP534535
12713	150	48	780	GGCTCAACATTGCAAATTGTGTATTATCAACACTTTGTTTGTGTTGCTGCAATTACTA	12193	A_95_P215372	TA20470_4097
12714	150	49	436	CATTTTGGATTGAGGAACTTGAGAGGGCAAAGGGTTGATTGTTGAATGATCTTATTC	12195	A_95_P194387	FG636318
12715	150	50	784	AGGCAAAAGGATTCTCAATTGAAGGGCATCCAGTTATTCGGAGTCTAGTCGAGATA	12196	A_95_P264191	EB450911
12719	150	54	807	GTAACATCAGATTTCTCATCCTAAGCCTTGTTATTTCATTTGTCATTGTGGGTCTTCAT	12204	A_95_P184817	DV162582
12723	150	58	709	ATTCTGAACTCCTATTTAGAGGTAAAGGCATGCTTGTTCCAGGTGGGTGGTGCATTG	12212	A_95_P192477	FG144933
12726	150	61	377	ACTTTTGGGATGTCTCTATGGTGACTGAATGAGTTAGTATGGGGGACTTGCTCCTTT	12218	A_95_P111857	CV020401
12734	150	69	725	CTCTTCTGTCTCTGTGCTGTGCAAATGATTTGAGTTAATTGAACCATGAATCCGTTTG	12233	A_95_P213627	TA20089_4097
12736	150	71	865	TAGAACGACATGTGCTGGGCATTGGACTGATGGAGCGCTGCTATGTTTATTGATATC	12237	A_95_P232864	FG158951
12737	150	72	296	GACCCTTTCTTAGGCAGATACTATTGGGATATACTGACCAAAATGTATACTTGTATCC	12239	A_95_P111272	CV020131
12738	150	73	264	GCAGAACACCCTCTTGTGATTATCTAATGCAAAATCAACGTGTAGAAGGAATAAAAA	12241	A_95_P043716	BP130688
12739	150	74	452	CTCTGTTACCTGCAGTAGTTACATTTTTCGTTTACCTTACCATATTGCACTTTATGTGC	12243	A_95_P177072	TA11870_4097
12741	150	76	509	AACCGCAATGCATCAGATCATCAGGTTATATACCTAACCTTTATGTAACTCATTCTTTT	12247	A_95_P035278	BP128427
12742	150	77	726	CTTCTGCAGAAACTTTTAGAACAGCTCAATTTGAGCGCTGGATAATATGTTATACCAG	12249	A_95_P258381	DV157680
12744	150	79	1221	CTTCTGTTGCGTAGAGTTTTGCAAAAGAGAGTTAAAAATCATCCTGGATTTCAAAGT	12252	A_95_P028781	TA12612_4097
12747	150	82	909	TTCCATGCCAATTTTTGGGGACAGATTATTTATTTAGTTGTCACGAATTTGCTGTTGA	12258	A_95_P199647	EB424807
12750	150	85	931	GTTTATTAAGTCTTAATAGATACTTTGTTTCACCTACGGTTGCATCTTGCTGGAGATT	12264	A_95_P013056	EB680644
12751	151	1	833	AGTTCGTCCTTTAAGTGCTGAGGAAACTGTAAATGGAGCTGTTGAAGAAACTGCAC	12265	A_95_P200362	TA17192_4097
12752	151	2	787	ACAAGTATAAGGACTCAGCTGATGGACTCTTTGGTAGTCTTGCAAGTAGAAATACAA	12267	A_95_P267196	DV159037
12757	151	7	854	GGACATAATTCAACTAAAAGTTGCACGACTTTTGGAGAATACAAAAGCAAAACATCC	12277	A_95_P218227	EB425360
12760	151	10	492	CTTGCTGTTGGTGTTTCAAATTGCTATGTCACATTACGTGATTTAGAGGTCGAATAAT	12283	A_95_P260141	AM848538
12761	151	11	625	GGGGAATTTTGTTTGTAATGTATCTTCTTAAGCTTTCTACGGTGCATGGTCCAGTTAT	12285	A_95_P088658	BP530168
12764	151	14	414	CGTCCTGCAGAATATGCAAGACAATAAGCTTAATGTAGTGTAAGAATGTATTTGGAT	12291	A_95_P140662	EB444533
12765	151	15	854	AAATTGATTGGAGGGTCTAGTGAAGGTGGTTCAGCTGTATTCAGACTGGATTACAA	12293	A_95_P191142	DV161215
12767	151	17	430	ATCGCCCCTTCTTTCTTGGATTTTGGACAATTGACATTCTCTATAGCATTAATTAGTTC	12297	A_95_P000856	EH621051
12772	151	22	773	GCTTTCCATGATAACACTTTTGGCTTGAGTAAGCGCGTGTCTGTCACCAATATTTCAT	12307	A_95_P022221	EB680374
12775	151	25	366	TATTAAATAGATCATGAGTAGGTGAATGAGGGCTGGAAGGAACGATTGGAAGGAG	12313	A_95_P099143	BP534807
12776	151	26	907	CCTGTGATTTCCCATTTGCTTTAAAATAGGTATTTGCTCCACATTAAGGCGGAAACTC	12315	A_95_P176432	Y09505
12779	151	29	824	CGGGGAACAAGGTTTCAATTGTCGTGTGTCTCCTATTAATATAATTTGTATTGAATAC	12321	A_95_P030236	EB425650
12781	151	31	901	GTTCACCATGGTAGTTTACCGACCCTTTCCTAGTTTCTACTTTTGTGGATTATATTTAA	12325	A_95_P242187	EB679195
12782	151	32	838	TGTTTTATGAGCATGTAAATACAATAACCCTCGTTGGGCTATTGATGATGGAATGGC	12327	A_95_P304033	FG133447
12787	151	37	801	GGTCATATCCTTTGCCTAACAGGAAGAGGATAGTAATTCTTGTTTTTCTGGCATTAAT	12336	A_95_P219812	EB448302

12788	151	38	835	CCTATGCCACAAACTTTGTTCCCGGAAAGTGAATTTAACAAAACTTGATCTCTAATTT	12337	A_95_P260071	X52744
12790	151	40	241	TGTGGATTAGGATTACTTCGTCTTTTTTGAGTCCGGTAATGTAATTCTCCGTTACATA	12341	A_95_P003921	TA13010_4097
12793	151	43	764	TAATCCTGAAAATGACGGTTGTATCAATGCAGTTCTCCTCGTGTAGTACCTTTTAGTA	12347	A_95_P237179	EB677494
12794	151	44	820	TCTCATTTATACCCATGGTAAGGTCTGTAGGGAATGCTCGGGAAAAGGTTCTGACAA	12349	A_95_P117727	DV160677
12797	151	47	747	TCTAATCGCGCATCTTCTAGGGCAATTCCTGATCAACCATATGCTGATAATCACAGTG	12355	A_95_P150247	EB680334
12798	151	48	197	CCACTGTTTTGTTGTTTGGTGATGGTATTTCTAGACTTATTTTAGACTTTGGTAGCTGC	12357	A_95_P089773	BP530648
12799	151	49	563	ATGATTAAACACAAAGATGACGTGGGCTCATCCAGTGAATCTTGACAAGGGAGATG	12359	A_95_P159557	DV157557
12803	151	53	789	GTGGTCTTTCTGCAACAGAATGGGTTCAAATGTCTTAAAATATATGTAACTCAGGAC	12366	A_95_P159772	TA13182_4097
12822	151	72	903	CTGCTTGAAGTGTTTCTTTTTCATACAGTGTTCTTCTGTTTCTTGCAAATAAAAGCGTA	12404	A_95_P180652	EB678678
12830	151	80	703	TACAGAAGACCCTTGCTTGTTCATGCCGAAGTGCTACTAGATCATGATGGGAAACTG	12420	A_95_P138807	EB440641
12831	151	81	608	GACGAAAATTGTGTGGATATAACTGTGGGCTTGCTTTTATTTAAATGGAGTATGTTT	12422	A_95_P003891	EB444373
12835	151	85	1584	TAGAGACTAGTGTGGAAATGCGAGCCCGATACAAGCTTATGAAATAAAACAAGTGT	12430	A_95_P031116	TA13207_4097
12836	152	1	905	ACCAGCTTACGTGTACCTAAACTAGCTTTGGTGGCTATTATATTTTGTCATGCTGTTG	12266	A_95_P208912	EB678190
12843	152	8	2319	CTTTGGCTCTACAAACTAGTGTAATCGTCCGAGAAAGAGAATGAAATGTCCAAACGC	12280	A_95_P221527	AB454418
12844	152	9	769	GCACATGAAGTATCACCTGATGATGAAACTATTGCGGATGTTTTAAGGATTGGTTAT	12282	A_95_P139297	EB443026
12845	152	10	348	GTCGGATCTTGGTGGAAACACTTGAATCGTTCAGTCGTTGAAGTCCATTCGTGCTTC	12284	A_95_P067360	BP136851
12846	152	11	1180	ACGATATTGTAAACCCCCCTGCCTGATCTGATTAAAGTTTGTGGCTTTCTATGTGTTC	12286	A_95_P183367	TA13442_4097
12850	152	15	753	TTATAGGATGCTTATGCTTTTGCCGCTGGGGGCAGAGGGTTGGTGTATAGAGAAAT	12294	A_95_P291903	EB425366
12851	152	16	1259	CACACGACAGATCTATTTAGGCATTTTATTTTATACCAGTAGCTATGTCAAACCTAGA	12296	A_95_P190742	Y11209
12852	152	17	896	CTGCCATAACTTTTCACCGGAAAATATTGTGAAATCACAAACTACTAATATCGACTTC	12298	A_95_P011046	EB426682
12853	152	18	320	GTTCTCAATTGTATGTAGGTGAAAGCTAGTAGTTCTGATGAGATACAAAATCTGATC	12300	A_95_P139977	EB443917
12855	152	20	451	TGACAATCTTTTGCTGCAGTATTGCATGAAAATTGTCTGAGCTTAACTAAATAGCATT	12304	A_95_P273596	AM822174
12856	152	21	863	ATTACTTGGCTGTACAGAAGCTCCTCTACACACAAGGACTCAGCTCTTCACCAAGTTT	12306	A_95_P229114	DV161644
12860	152	25	785	AATTACACATTAGATAGCTTTGCCAGAATAGGACTAGAGTTTTCTCAGTCCACATGCT	12314	A_95_P285483	EB448976
12862	152	27	706	CATTATCGGGTTTAAGCCCTTTTATCTTGAGACTAGTTCAGCTCTTTACATTTTTGAAC	12318	A_95_P100913	DV160879
12866	152	31	795	TTTGGTTTATGTTCTGTTTTGGACCTGCTTTTAGTCGTTGTATTGAAGATTTTGTTGGC	12326	A_95_P272531	TA12360_4097
12867	152	32	255	ATCCAGGATTTGAACTTTATTGGTTCAAGTTCGGAATGCTACAAGTCTACTACAACTC	12328	A_95_P089343	BP530461
12869	152	34	548	TCATGCACTGATGTATTAGTTCTGTTGTTTCAGTGGAGTTCTAACTTTTGGGTTTGTG	12332	A_95_P147952	FG625361
12874	152	39	706	TGGCAGACTAGCCATGTTCTCTATGTACGGATACTTTGTCCAAGCCATTGTTACCGGA	12340	A_95_P002581	TA11665_4097
12877	152	42	699	CCAAATTCTGACACACTCTTTCGCTTCTCTATTTCTGATGATGAATTGTGATGATTTGC	12346	A_95_P206792	DV157565
12878	152	43	108	GTGTACTCGAATAAACTATTCTCTGGTTTCAGGTGCAATGAAAATTAGTAGGTCTAAT	12348	A_95_P116662	DV159431
12880	152	45	318	CATTGGTATCGTGGAGGATAGTCATCGTAAAAATTCTTAGGTATTTTCCTCTGTGGG	12352	A_95_P101393	CN498817
12882	152	47	114	AATGAAGGGACACTCTGACCTTCTCACTGTTTCTCGATTCACAACAAACAAACACCAC	12356	A_95_P104312	CV016936
12883	152	48	699	CTGGATTGGATCTCTCTAATGCCTCATCGATTTATCAGCATTTATGAGCAGGTTGCGC	12358	A_95_P159787	EH618241

12889	152	54	584	GTGGCTCTATTGTTGTCTGTTTAACTGCAGCACACATTTGTTTCAACTTCAGTTTCATT	12369	A_95_P122147	DW002185
12891	152	56	618	GCAGATGATAAGTATATACTTTATGTTTGTTTCCCGATCAAGGACTGGACTTTAAGA	12373	A_95_P188997	EB443154
12894	152	59	534	CTATGGACTTGTGGTATGGATTCTTTGGCATTTGTACATGGAGCATTTCATTGGGTTG	12379	A_95_P044566	BP130915
12896	152	61	783	TAATTGATACAAATAGCCCATCAACGACGACTCTATTAAGGGCTAAATTCTCTGAATT	12383	A_95_P256454	EB449193
12898	152	63	1333	AATGGACTTGGACAAGGATGATGGTGGAAGACCGAAGAAAAGTCATCCTAATGGA	12387	A_95_P198202	TA16727_4097
12899	152	64	653	ACTACTTCAATTAGGAAACCTATAGGTGCAAAGAAATCTGGGAAGCCAGGTGGTGG	12389	A_95_P138337	EB442079
12900	152	65	181	GCATATAAGCGAATGTGTCCCTGATTGAAGTCAAAGTATTTGACCATAGTTAAAACT	12391	A_95_P095723	BP533306
12902	152	67	663	CTTCACATTAGAAATGCCTTGTATATATGTGTATCAGCCTATCAGGTAGATGTGCTAG	12395	A_95_P260191	BP129638
12903	152	68	836	CAAGGTTTATGTGTTGTTTTTAGTTGTTAAGCTTTGTTAGTCTGCCGGATGATATTTT	12397	A_95_P227214	DV160739
12908	152	73	692	AGGTTGGTTTAGATGACGATGACAACGATGATGATAATTCATCTCACACACCTACAA	12407	A_95_P140002	EB443948
12910	152	75	736	AATGTGTAGGTGTTCTATCTCTTGTTTAAAATGCAAGTGAAATGCTACTAGTGTCCAG	12411	A_95_P018936	TA15542_4097
12913	152	78	388	CATCTTACTGTTTTCGTCTAAGGATGTCGTCAAGGTAGTCTTATCATTCAGCTTTCAG	12417	A_95_P205212	TA18231_4097
12917	152	82	336	TGTCGAACCCACAGAGACTTGTATCAACTATCCACTAAATTTACCAAGATTGTTATTC	12425	A_95_P099628	BP535004
12918	152	83	887	TGGTCATCTGATGGAAGTAAGGTAACAGCTGGGAGTTCTGATCGCATGGTTTATATC	12427	A_95_P206472	DV157626
12921	153	1	817	AGAACTTCCTTGGGGTGCTTTGGATGATGTTGTGATGGGTGGAGTGAGTCAAAGTA	12431	A_95_P205682	DW001357
12924	153	4	743	TAGTCAAGAGTGCAAATCTAAAGAGCCCTGAGGTTTCACTTTTTACAGCCTTTTTCAA	12437	A_95_P316243	FG187377
12926	153	6	420	GGATTCCGACAGAACTATCAGAGACCTTCGTCCAATTTCACCAAGATCAGGAACATT	12441	A_95_P086165	BP529467
12931	153	11	762	GACAACAAAGGATTTATGTGAGAGGTTCCTGTGTTATTTCATGTCACCTTCAAATTTA	12451	A_95_P183212	X95752
12933	153	13	698	TTTCGAGAGGTCGTTTGAGTTGAGCTTTCCTGACATCGAGCTCTGATTGAGGTGTTT	12455	A_95_P160532	EH619215
12934	153	14	930	GTGCATCTGCTTCCCTCTGCCTCTTTGTAACTTTAATTTGTTCAAATGAACTGTTATGT	12457	A_95_P013631	DV999488
12937	153	17	795	AAGACAACATTCTGCTGAGGTTTCAATTCTTCAACCCTTTGCTCATTCGTTTTTGTCTA	12463	A_95_P116187	DV158763
12942	153	22	501	AAGGAGGATCTCAACATTTCTGAAGGGATTTCAATCATTTCTAAGAGTATATATCCTC	12473	A_95_P219592	TA21428_4097
12947	153	27	484	ATGACCTATTGCAGTTGTCTTTGTTGTGTCTGCTGCTTTTTATGTGAAAACTTTTTCGG	12483	A_95_P164452	EH623701
12951	153	31	881	GACACATTCCTTTGATATACATGGTGGTGGAATGGACTTGACTTTTCCTCACCATGAA	12491	A_95_P118712	DV161777
12959	153	39	603	GGCTGCAAGGCCATGTACCATTAATTTAGACTTTCCTTCACGCAGTGTAAAAACAAG	12507	A_95_P222972	TA22146_4097
12961	153	41	374	TTAACTATGGAGACTTCAGAGCAGAGATTAAGTCTGTGTATGCCCAAGAATCCTTCA	12511	A_95_P080545	FG141460
12966	153	46	749	GTTGGGATTTTTTCCCGAGATATTCTTGAGTCTATTGTACTCTAATTCTTTTTCCACTG	12521	A_95_P029106	EB425632
12967	153	47	806	TATTGTAGATAGCATGGTGTTCAATGACTAGCTAGAAGAATGAAGAAAGCGATATT	12523	A_95_P214617	TA20300_4097
12969	153	49	167	TCTGAGTTTGGTGTCCTGTCTCGACTCTCATGTATGATTGATGATGGATATTCCGGTT	12527	A_95_P142382	EB445861
12972	153	52	2185	TCATTATGTTAGTGTGAAAATGTAGGGAGCTCTGCAGCCTAAAAGCTTAATAAGCCT	12533	A_95_P259856	TA12447_4097
12974	153	54	783	ACATATGATGATAATGCCATTACTAATGCTGTTGACATTTATAACACTGCCAGTGGCG	12537	A_95_P127287	EB426811
12978	153	58	806	TGGCTATCCCTTACAATTACAAACGCTATCATTAAAGATTTTCTGATCTTGAAGGGCC	12545	A_95_P258952	EB429556
12984	153	64	651	GTGGTGACAAAAGGTTGCTCTTTTGGCTACAGATAACGAAGAGTTAAAATCTCTGAT	12557	A_95_P153282	EB683555
12985	153	65	964	GTCCAAGGAAAACCTATTGCAGATTGTGTCAAAGCAGGGTGTTATGCATCGAATGTC	12559	A_95_P146147	AY695053

12987	153	67	695	CCATTTTCAAGAATCAAGACTCATTTTTGGACAAATAGAATACTCTCTCTCTCTCTC	12563	A_95_P016906 DW004524
12989	153	69	119	ACTATGAGCACAATCAATAACCTTTCGAGATGTCCTTCCTCCAGGTGCTTGTATGCAG	12567	A_95_P034354 AJ718525
12992	153	72	749	TCTTTCTGATATTGGAGTACGTCGTGATGTCACGAAGATCCCTGTTGAGAGACTTGT	12573	A_95_P012731 FG159939
12994	153	74	722	TCTTATGTGCACTTATTTCTTTGCCTGTTATGCTTGTGTACTGTAATTTAGATGCGTTG	12577	A_95_P296493 FG645393
12997	153	77	681	TTATCTACTTGTCCTCGTTTGTGATGAAGTTCAATTTTTGATGCCGTTGATGGTTTTTG	12583	A_95_P183402 DV158478
12998	153	78	851	CCAATCTTTTGCCCAACTTGTTGTGTGAATATCTTTACAGATTATCTGAAGACTTCACT	12585	A_95_P267396 DV159937
12999	153	79	520	TGGCAAAGCTCAGAGTTTATAATAACATACCTCTCAAGTACAACTCTGTGTTTTCACT	12587	A_95_P152862 EB683192
13002	153	82	1503	CCGGACACAAACAACTTCTTTTGTCATTGTGTTCATTTATCTAATGAGAAATGCCGTA	12593	A_95_P177242 TA11920_4097
13003	153	83	1624	TGTTTTTGTACTTTGCTGTGTGCATTGCATAATATGAGGGAAATAGGGAGGGTCCGA	12595	A_95_P217077 AB014484
13006	154	1	802	TTTAATCAGGAAGCATGCGGAAGTGGTTGCAGATGATGATGCTGTCCTTCGAGTCTT	12432	A_95_P228939 DV161110
13009	154	4	830	AAGACAGGAGCAAGCTGCGGAAAATGGAATTATTCCACACTTGATGCATTTTATCAT	12438	A_95_P297273 EB682598
13017	154	12	829	GGAAATACAGAATCAAATATTCTATACAACGGTCTGTTCTTGTCTTCTTAGTTTCATC	12454	A_95_P127317 EB426843
13019	154	14	826	TACCTCTGTTTGTTTGGGGGGTTTAGCTGACAATGACATGTTTGGACATAGTTTGTGT	12458	A_95_P021036 TA15464_4097
13026	154	21	41	GGTATCCGAACTGCTCATGTACTTTGCGTTACGCAACTTCTTAAAACATAGGCTGAG	12472	A_95_P153437 BP129154
13027	154	22	564	CCTGGCTGCAGGAATTTTGATTAGCCAATATTTAGTGGGGAATTGCTTATTAATTATT	12474	A_95_P035903 BP128595
13028	154	23	526	CTGGACCAGAAATGCAGCATCTTATATTCTAGCTTTATTTTCTGTATTTGTTGTTCTCT	12476	A_95_P124042 DW003889
13033	154	28	597	CAGTCTGTGTTACTCTTCCTAGCATTTTCTCTTTGATCAGCCTTTGAATTTGCAGCTGT	12486	A_95_P288283 FG641025
13034	154	29	424	GATGCTAAACATGTATCGAATACTATTATCCAAGTAATAAACCAGTTAACGTACCCCG	12488	A_95_P218032 TA21082_4097
13035	154	30	423	GTTAGAAGAGATGGAAAGGTTTGCTTTGGGTACAAATTGTATCTTGAATGAGATGC	12490	A_95_P210897 TA19493_4097
13044	154	39	838	GGGTAAAGAAGTTATGATGAAAGGGTTTATGGTAGGTTCATATTATAACCACTTTGA	12508	A_95_P135507 EB438993
13046	154	41	551	AGGAATTACAACCTGATGAGGAATTCTCTACATTTTTTGTGAAGCGGGCACTTCTGTT	12512	A_95_P031196 BP133364
13051	154	46	2742	TTCAATCCTTCTGGTTAGTGTGAGCATCCCAGGCAGTGAAAGTTGAAGGTTTCTGCTT	12522	A_95_P025971 AB117525
13055	154	50	1160	GGCTGCAGTTTGAGCAAATCCCCTGATTATCTCTATATGTGATTCCATTCTTTATGACT	12530	A_95_P010246 TA15744_4097
13062	154	57	1494	CCCTTAGATGTTGTAAGCTTATTGGAGTGGTTCCAATCATTCAGCTTTATAGCTCTCA	12544	A_95_P207082 TA18663_4097
13067	154	62	790	AGTTCAAAGAAGAAGTCATTCTCCAAGTGGGTTTTTCGGCTATCGTTTAACGACCGT	12554	A_95_P283463 EU123523
13068	154	63	202	GATGCTTCTCAGGATAATGAGAAACGGAATGGTGAAAATTCCAATATTTCTTCTTTA	12556	A_95_P079375 BP527745
13072	154	67	122	AGAACCTGGTCCTAGCACTATCAACAATGTGTGTGAGGCTGTGAAATGTGTTGTGGT	12564	A_95_P001846 AJ718660
13074	154	69	818	ATGTTTCAAATTCATCGACCTAGACACACCCCTTCTGTTGGCAGAGGATCCAGTTTTT	12568	A_95_P245007 DV159814
13075	154	70	1188	AATGTGACCATTGCTGCCAAGCTTGCAGGAATTTCTGGTGATCCGTTTACTGGAATTT	12570	A_95_P190172 TA14953_4097
13078	154	73	321	GTATATATTTCATACCTTTAGGGTCCCAGCATGTTCTTATTTGATGTTTAGTCTTTGGA	12576	A_95_P129567 EB429551
13082	154	77	402	TAGACAGCACTGAATCCATGGTATGGATCAAATCATCAAATACACTGTCTAGAATCT	12584	A_95_P111097 EH617567
13084	154	79	615	CAACTAATGCTCTTATCGGTGCAGTCAGTGCTATAATATTCTGTGGATACATTGTATA	12588	A_95_P108777 EB424839
13089	154	84	897	TGGAGTTGATCTACAAGCATGCAGTCCCAAAGCCTAAAAATGAGTGCAGCAAATCTA	12598	A_95_P009631 TA12329_4097
13090	154	85	383	ATATTATGGTGGATGTCTACTCTTCCTCCATGATCTTCATGTCAAATGCTTAATGACAT	12600	A_95_P161237 EH619980

13091	155	1	786	TTGGGTCGGTGGCTTCATGATCTTCTTATGCCTCAGCTTCATCACCTACCACTATATCA	12601	A_95_P219447	EB425891
13094	155	4	1666	GGGCCATTCAAGTATATCTTAGTGCTTTTGTATTTTTACTGTTTCTACAACACTTGTGA	12607	A_95_P132347	TA12710_4097
13095	155	5	398	TGAGCTTTGAGCAATTAACTATGGAGTATGCTCTTATCTGACTCTTGATTCTGTTACAT	12609	A_95_P287558	FG634597
13098	155	8	404	CCACGCATTCCCTTTGTCCATTGTCGAATTCTTTATGTATCTCGCCCATTACCTGTTAA	12615	A_95_P256804	EH621028
13099	155	9	478	GAAATGTCGGCTGTGTGACCTTACCTATGCGGCTCCAATTTATGTCGATATCGAATAC	12616	A_95_P085395	BP529269
13102	155	12	578	GCTGTTGTATCTCCTTTTCCACCTTCTGATAAAATTGGAATAAACTCTGTACAAAGGG	12622	A_95_P128072	FG160326
13105	155	15	1208	ATGTTGTTTCTCATGTAATCCTCCTTGAGCTTTTGATTTACCAGGAATACTTATTCTCG	12628	A_95_P020756	TA14528_4097
13106	155	16	132	ATTAAGTTGACGGGCCCTGCTCCCGCCATAGTTGATAATGACACAGATGTTATTACTC	12630	A_95_P110927	CV019970
13108	155	18	474	TGTACATATGTTTGTTGTCTGTCATCTTTGTAACCTGTATCTGACATGTGCAACAAAAT	12634	A_95_P004151	EB683227
13111	155	21	840	ATCACTAGATGTAGCTACTGTTTCACAGGGGCAGAACAGGTTTTTCAGTGTGCTGAT	12640	A_95_P137957	EB441679
13115	155	25	304	TAGTACTGCCTTGGCACTATACAGAGTGCTTATCTGCTGGAAGTTGAATATGGGACA	12648	A_95_P113067	FS429988
13116	155	26	1217	CCTAGAGCTTGTGTAATCCTTGTTGGCTTTTGGTTACATGGTGCTTGCGGTGGATTAG	12650	A_95_P004341	AY748245
13119	155	29	768	TTCATTCTGGGTCTAGTATAGTTGCTTGATGCTACTCCCTCAACTGTTGTTCGCTGCGT	12656	A_95_P258291	EB440265
13129	155	39	876	GTTGCAGATGGAGTACTGGTTTACATGATTGGAAATAGAAATAGTGATATGGTCATT	12676	A_95_P205512	DV999401
13132	155	42	2007	AGAAGTAATGGGTCGGGACAAAATGAACCTAGTTCACCCCCTCATGATGAAAATATC	12682	A_95_P240324	DQ156499
13143	155	53	731	TAATACCGCTACAAGGATGTGGTACAAGTGAAGCTTTTCAGCTACTGAATGATCGCT	12704	A_95_P227154	EB446517
13148	155	58	634	CTAACTGTTGAGTACATAGATCTGGATTTCGTTAATGGCGCATTGTATTGAATTTAAG	12714	A_95_P274198	FG636122
13154	155	64	1033	ACCATTGTGTATGTTAGTTTGATGTTGATTTCCGTAATGACTAATGAGTATGTTGTGT	12726	A_95_P212357	TA19817_4097
13156	155	66	759	GCGATTAACATGCACTATTTATTTGTCTGGTGTTCATTTATCACCTATCGATTACTGTC	12730	A_95_P029166	EB425809
13159	155	69	378	TTAGCTTGGCTAGTGACTTAAGTTGATAGTTTTCTGAATGTAGACTGAACTCCCTTTT	12736	A_95_P187647	TA14393_4097
13165	155	75	431	GTATCTTTTTGCTTTGACTCATTGAAAAGGGGAAGTGGTACCAATTGCAGTTCTTGCA	12748	A_95_P244042	FS407121
13169	155	79	203	ATTTCTGAAAGTGGGTTGTAGGAGTTATTGCACAGCGACCTGGAATCCAGTTAGGAA	12756	A_95_P158422	EH616387
13171	155	81	652	GTCTTCTTTAACACGTCTCTCAATTATTCTTTCAGCTGGCCGTTCTATTGGATTCAGTT	12760	A_95_P037358	BP128982
13173	155	83	691	GGAAATGAGAACAACTCTAGTGACGACTCCAATTCTGCAGCAGAAACCAATGAAGC	12764	A_95_P152482	EB682795
13174	155	84	394	CATGTGTCTCAGACTTGGTCTACGGATTTTTTCGAATATTTTCCAAAACATGTAATGC	12766	A_95_P094328	BP532669
13176	156	1	446	TTCTGCTCTCCGTCAACGTTGTCAGTGCTATACAGAGGATAAAGAAAGACTTAGTTTT	12602	A_95_P205228	TA18234_4097
13181	156	6	445	CAAAAATTGAAGGATGTGGGAAGATATTTCTGAAAATGACTTCTGGCAAGGTAGTC	12612	A_95_P081540	BP528281
13182	156	7	482	CAACTTTGGTGTTTGCCTTGTGTGCATGTTTCCTTTGACTCCTGGTTAATACTATCTTTT	12614	A_95_P121672	DW001786
13186	156	11	151	GAGCATACTGGTTTTGAACAATGCTTGACATTATTGCTTTCAAGTATATAAGTTTTGG	12621	A_95_P161697	EH620348
13188	156	13	905	GCTTCCCTTCCTGGGATTTAGGCTTGTTTTGATTGATTTCTAGTGAACTTTCAATTTTA	12625	A_95_P211747	TA19681_4097
13189	156	14	551	AGGGAACCCAGTCCACCAAGCAGAAGTAATGGATTTCAAAACTGTGTCATAGATGTG	12627	A_95_P066890	BP136717
13192	156	17	747	CACTCCAGTATAAAAATGGAGAAATTATAGGGCTTAATCATGTTAGTTTAGTGGTTG	12633	A_95_P131287	EB431445
13199	156	24	388	GATGGGGACTCAGAAAGCTTCTATTTCAGTTTGATATTATTTCCAATAAGTATATCAG	12647	A_95_P220432	TA21606_4097
13202	156	27	464	TGGAACAATTTTCCCAACGTGACATGTCCAGATCTTACTTCTATTTTAATCAAGCTGA	12653	A_95_P020706	FS389605

13212	156	37	175	CCGGTATTTTGTGATTCTGGATTGTATTGGTCATAACCTGCATCGTTAATTTTATGAT	12673	A_95_P140472	EB444360
13213	156	38	844	CTATTTTGTCTTTACATACAGGTAGCTCAGTTGATTCTCCCTTTTGGATCAATGTGTAA	12675	A_95_P229539	DV160249
13215	156	40	726	TTTATGCCCCATGAATTTGACATCCTCTCTATTTGAAGAAATCATATCAGCCAGGAGA	12679	A_95_P125637	EB424731
13217	156	42	0	CAACATTAGGTGCAAGAGTGATCTTATCTTGTGCTTCTTTCCCTGATGCTGGCTCATA	12683	A_95_P314978	A_95_P314978
13220	156	45	96	GTCAATGGATGATGGACTTAAGTGGAGATATGGATTCCATTGATGGATGAGATGGA	12689	A_95_P113512	CV021168
13223	156	48	820	TGCACCTTGAAGAGGACGATACAATTGCTACTGTCTTGATCTTGTAAAGTCGTCCCTA	12695	A_95_P228244	EB449537
13231	156	56	905	TGTCTCTTGCTCAAATGGGGATTCCAATGCACCTCATTTTTGCAAAGCACCGCTTCAT	12711	A_95_P116557	DV159314
13234	156	59	573	CCCCACCACACCTTCTGTTAAAGCTTGTTGATTGTTTCAGAGAGATTGCTATACATTTA	12717	A_95_P192482	EH615132
13238	156	63	582	CCAAGTGCATATCTGATGAAACAATGAAGACGTAAAACGCAGATGTCTTTCCTCATT	12725	A_95_P066770	BP136685
13242	156	67	424	CTATTGGCACCTATGAAAGTTCCCTTTGTAATGTTACTGTTTGTCTAAGTGGAATTTTT	12733	A_95_P133197	EB434494
13243	156	68	522	TTTTTTGTGTCCCTCCTCATCTCTACTTTTTAGAGCCAAAGTGCTTGTAATCAGGTTGG	12735	A_95_P300998	FG641516
13248	156	73	865	TATCATGGGAGGATTTACCAGTCTTTTCTTTTCGGGTTGAAATAAGAATATTGCGACT	12745	A_95_P232439	EB426018
13250	156	75	338	CACTAATTGCCAAAAGGAAGTTCTCTTTCTTGGGGAACTCGAAGAAGTGCTGGAAG	12749	A_95_P207597	TA18775_4097
13254	156	79	1656	CAAGGGCATTTTAAGTCTGTGAGATACCTGTCTATAATGCTGTACAGTCTATTTGCTA	12757	A_95_P265351	TC50731
13256	156	81	846	GGCTTCAAGTTTAGGTAGCTTGTAGTTTGTATTCCTGTTAATTTAATCATGCTTGCTCT	12761	A_95_P149887	EB679882
13257	156	82	690	AGCATCCGGGCCATCAAGACGGAAAATTGTTTTCCCATATACCTGAAGGAACCATAT	12763	A_95_P309053	FG184306
13261	157	1	739	ACAGCTACCTGTTCTCTATTTTACTGATGCAACTGTCTGTTGATTTACAGATGCAGTA	12770	A_95_P246632	EH622517
13267	157	7	451	AAGCCTCTTGGTTCGATAAATAAGCTCATATGTGACAGGTTTTCTTTGTTCAAATAGA	12782	A_95_P001026	TA14412_4097
13270	157	10	879	GTAGGATATTAGTAAGTTAATGAATGTGTGTAAAACGGTCAATATACTGCTACCAAG	12788	A_95_P181517	DV158914
13275	157	15	1784	TCTCTTCTGCATATTCATATCTGTAATAAAGTCAGGAGCTGTATGTCGAGTTTAAATG	12797	A_95_P016816	TC49390
13282	157	22	679	TAAGCTGTTCATTCCCAAGGAGACTTGCAGTATTGCTTTCTCCTTGTCTGGTGTGAGA	12811	A_95_P116687	FG140162
13284	157	24	683	TATTTTCTGCGAGAATGTTTGGAAGCTCAGGCGCAAGATCAATTGCTTATCCTCATCC	12815	A_95_P015721	EB428286
13285	157	25	198	GCATATCGTGTATATGTGAAGAAGTGCTACAAAGTTTATCTTATAGACGACTACATTA	12817	A_95_P132107	EB432551
13286	157	26	664	CATTGACCCTCCGGTTCTTCAACCTAAAAAGAAAGAACTTATATACTAGTTTTGCCTTT	12819	A_95_P148847	EB450360
13287	157	27	948	TAGGGAATTATTTGCCTACAAAAACAAAAAACAAAAGGCCCACCCGGGAACCAATC	12821	A_95_P011371	TA14146_4097
13290	157	30	605	ACAGCTTGTGACACCATGTCTTGACACACACATATAGACGTTTCTTTTGGATTGTTTA	12826	A_95_P287953	FG640153
13293	157	33	97	GCAGAACAATAATCCGCTGACAAAACTTCCAAACACGGACGTGTATGTGCTCTCCTA	12832	A_95_P107027	FG144865
13296	157	36	749	ACAGTAACTAATAGAGATACAAGTGAACATACAAGTCTCTCCTTTAGGGAGCTTTAT	12838	A_95_P162517	EH621473
13297	157	37	880	TAACTAGTCGGGCTGATGCTAGCCATATTAAATTCACTACATGATGAATCCAAATTTT	12840	A_95_P223697	TA22308_4097
13298	157	38	766	AAGTTCTGTGTTGATGTAATTTGCTTCTTGTTTTGCCACTACTTTGTTCAGTTGCTTGT	12841	A_95_P181492	TA12995_4097
13301	157	41	221	GTGTGAACTTTTCCATGTTAAGTTGAAATATGGGACATATGAGCTACTAAGATTCCTT	12847	A_95_P164962	EH624430
13304	157	44	486	ATCGAGAATGTCTCCTTGGATAGATGCTGGACCTCTCAATATTCGTTCAAATTGCCCC	12853	A_95_P090098	BP530799
13308	157	48	390	TGCTCTATCACTTATCTCTTTGGCAGAGGCTCCATTTCCACCTCTCCTGTTTCAATGTT	12861	A_95_P129067	EB428823
13313	157	53	769	AATTCCATATCGTTGGTGTCCTTGGCTGCAGCGGTCATGTCCTTGACATATTCGATTG	12871	A_95_P014221	TC44168

13314	157	54	1001	TGTTTACGAATAACGTTGCTGCTCCAGCTGATTTCTATTTATTCAAATGCAACTTGGTT	12873	A_95_P026741	TA14717_4097
13318	157	58	649	CACAGGTGCTTCTCTAGATATACTGAAGCAATAAATGTAACAAGTTTTCTGTACAGTG	12881	A_95_P203557	TA17878_4097
13330	157	70	815	GGGTTGCTTGTTTTTGATATTCTGATTGTGAGAGAAGGTTCAATATGCAAAAAGGTT	12905	A_95_P194657	TA15945_4097
13338	157	78	991	GCTAGGGGGTTGTCTTATTGGAAATGAACAACTTTTAATATTGATGTTTCAGAAGTTC	12921	A_95_P007631	TA12296_4097
13340	157	80	703	TCAGTTACAGAATCGGCTTGTATTTGCATCCCTCCGCGAAATATATATTGAAAGCATC	12925	A_95_P160472	EH619173
13342	157	82	397	CTGCAACCATAGTTGTGTTGTATTTGCTCATTAGGTGAAGTAATTCAACTAACTAGAT	12929	A_95_P130757	FS393322
13344	157	84	1028	ATGTTGTTGGTGCTGATGTTGTTGAGTTCAACCCACAGCGTGATACTGTTGATGGCAT	12933	A_95_P010186	TA14510_4097
13346	158	1	569	TTTTACATGAGTTGGAAAGGAATTCGAAATGGAGCACACATATGGCAGAGTGGTTTA	12771	A_95_P214097	TA20188_4097
13347	158	2	711	GGTACATCTATGACAGAGGATTGGTGAAAGAAACATCTTATAGTTGGATTGAGATAA	12773	A_95_P029141	EB439733
13356	158	11	361	TTTAGGCCTAATATTCGTGTATCAAATTGCCCGCAGTTGTTAACTCACAATTGTAGCTA	12791	A_95_P052206	BP132857
13366	158	21	757	GCTCAAGACAATTTGCCTTAGGTATGTATTATATCCTTTATATTTTGGGGAAGAAATG	12810	A_95_P200852	TA17299_4097
13368	158	23	116	GTAGAAGAGGAATCAGTGATCTGTAGGCATTTTTATTGATTTCTGTGCAGAAACGTCA	12814	A_95_P168431	EH664424
13371	158	26	765	ATTCGAGTAACAACTCGGACATGTTTGTTGGGGGTCAATCACTGCAAAACTTAGCTCA	12820	A_95_P147682	EB452193
13372	158	27	875	TTGAGAAATCCTCTGTAGCTGGTTGGTTGTTTCGCTTTGATCTATGGTAGTGCACTAT	12822	A_95_P185897	EB424739
13374	158	29	712	CACAGTTGTTTCAAAACTTCTTCCTGGTTTGGCTGAACTGATGAACTTCATTGAGGTG	12825	A_95_P017831	BP130210
13375	158	30	722	CCGCATTATTGTAATAGTCTCTTGTTATTCCGAACGGCCGAAATAAATGGAGATTGAT	12827	A_95_P148922	EB678509
13376	158	31	404	GACCAACTTGAAATGGACCAACAGGTTATTTGCTTAGAATGTGAACCTTTCTAGCTTA	12829	A_95_P097438	BP534048
13381	158	36	382	AGCGTCAGAGTTTGGACAAACTGTCTAGAAGCTTCCTTATTCTACGTCTAATCTTTCAA	12839	A_95_P293493	FG643621
13386	158	41	400	ACCAGATTGCTCTTGTCTGTGTTCAAACCAGTCAGGGATCTCGACAACATTATGATCC	12848	A_95_P094758	BP532862
13388	158	43	891	AACCCTAAGTCTCCTCTGTATGAGATCACATTTCAGTGTTCTGTGATGTTGTAAGTCG	12852	A_95_P235204	TA13446_4097
13396	158	51	1395	CTTGAAATGAGATCTATGCTTGGAGGTTGGTGTTATAGTTCATTACTAAAGTTCTACT	12868	A_95_P023796	TA15200_4097
13397	158	52	459	TTTTTGTAATGCAGGTCAAAAAAGCAAGAGGAATTCAGATAACAAGGGTCCAAACAA	12870	A_95_P278833	AM848505
13398	158	53	759	AAGATGGTGTAAAGGCTTCTCCTAGGGACTATAGCATTCCAGGATCAGGAGACAACA	12872	A_95_P127892	EB427451
13400	158	55	799	TAAAAGAACTACTACACAAATGGGCCATGGTCAACTCAGCTGCTGAGTCTGAAGGAG	12876	A_95_P309883	FG136392
13402	158	57	763	TTGTTGTGTACTGGGGTTTGGTAAGAGGCAGTTGGATGTGTTTTCTCTGGCTTTGTTT	12880	A_95_P222297	TA22003_4097
13405	158	60	274	AGGCTTCTTAAGCGCTAGTATTCAACCCCTCCTTTAAAGGTGAAAGGTGAGTTCTTAA	12886	A_95_P110247	CV019640
13410	158	65	663	TTTCTAAGAGTTTGTAGATAACAAATCTCCTGATGATTCCTTTCCTCCTGAATGGGTGT	12896	A_95_P311068	FG139766
13412	158	67	754	ACACCCAGAAATTTTTTCCAGCTTGTAGTGCTGCTTCTTACAACCCTGGCGCTCTTTCT	12900	A_95_P180052	EB679219
13421	158	76	803	GAGGCTATCAATCCGATTTCATAACTAGTTGGTACGTTCGAATAATAAAAAGAAGTT	12918	A_95_P270401	EB431749
13427	158	82	861	CTTCTCTTATGGACAAGAAGGGTCACGTATCTTCTTTTGAATTGAGCAATAAGAAGA	12930	A_95_P178682	TA12310_4097
13429	158	84	437	GGTTTGTTAAGAATGGTCTTTGGTCACTTCATGTGGATTTTCCCCTCTGTTCCAAGGT	12934	A_95_P127752	FG147794
13432	159	2	608	CTTATGTGAGGCCAACGTGCAATCAAGCTATTGAGTGATTTCTACACAGATCTGAACT	12939	A_95_P058476	BP134482
13433	159	3	484	TGTAAGGAACTAGCAATATAGCTAAATTTTGTTTATGACTGCCTTGTTTGGCTGTTCTT	12941	A_95_P022426	TA14801_4097
13435	159	5	193	GTGAAGGCCTCAAATGTGCTAGTATAAGTGATATCAGGAAACTGGATATTAAAATGT	12945	A_95_P141652	EB445325

13438	159	8	430	CAGCATGGTGCAAATCTAGTGCCTTCATTTCTAGTTCTATTAATCCCTCCACTTCGACG	12951	A_95_P094168	BP532590
13443	159	13	874	CTTAATAGAGCTAAAGGCAAGAAGACCTTGTACTCTTTTGCTTTAAACCACTTGTTGC	12960	A_95_P230179	DW000183
13448	159	18	814	TGCATCTGTTGTACTAGTCACTCGCTCACTATTTTTGAGATATTTGCATCTGATTCTAC	12970	A_95_P000461	DV161017
13452	159	22	769	TCCTGGATTTGTGGACTGTGTTTATCCTGATGCACCTAAATGAATTTACAGCTTAGAT	12978	A_95_P157222	EH615261
13453	159	23	701	GTTGGCATTAGTTATGCTGAGATTATATCTTATCCACTGTTTGGTTTGGTGTATTGAA	12980	A_95_P120482	DW000413
13456	159	26	798	ATAGGTAAGCTAGCCCCTGTATGTCATTATTCATTTTCTGAGCTCAGTCTACAACCAC	12986	A_95_P009791	EB428177
13458	159	28	476	ATCCTCATCTTCTTCTTCTTGGCTTCTTGTCAAGCAACTCCAATCTGAAGTACTTGACT	12990	A_95_P072960	BP526090
13459	159	29	433	TTAAGGCTATAGGGGAAAATGAAGAAGTGTATAGAACTTCGGCGGATGACATGAAG	12992	A_95_P110412	CV019718
13463	159	33	577	GCTACAAGTGTTCGTTGTTTGATCGGTACACCAGTTGTAGGAAGGAATTTAGTTTTA	13000	A_95_P121857	DW001953
13466	159	36	453	GTAGATGACTTTTTGCTGAGACAATATGCTCACATTCTCCCACATAGTTATTTTGTCA	13006	A_95_P058891	BP134589
13467	159	37	428	GAGAGCTTTCAAGATGTTATGTCCATATGATGGTAATGAAGAGTGAGAGATTGGAT	13008	A_95_P008956	EB682455
13470	159	40	796	GCAAAAAGTGGAGGATTTGTTATCAGATGACAGCATAAGAGCAAACTCACTTAAGT	13014	A_95_P115497	DV157724
13472	159	42	938	GTTTTGAAAAAGGAAAACCTTTTAGTTGAGTGGAGTCATCGTTGTAGTCATTCACTTT	13018	A_95_P191357	TA15218_4097
13474	159	44	519	ATGGCATTGATTACGTTCTTTCTGTCAAGACAGTTGTTTTTAGCTGTTGGCTTCGTAA	13022	A_95_P032116	TA12512_4097
13476	159	46	441	TGTCTTGCACAATTTCAATTTGGCTCGCCGCTTTTGCTCGACAACACTATTGTTCTCAG	13026	A_95_P066080	BP136501
13479	159	49	577	ACCTGAATCAAGCTACATCAATGTTCTGGTCCGCATTTTATGCAACCTGTGTTGGCTA	13032	A_95_P204662	FS409048
13480	159	50	1234	GTCTACTTACCTCAAGATGAGTTAGCACAGGCAGGTCTCTCCGACAATGACATTTTTG	13034	A_95_P186367	TA14111_4097
13481	159	51	203	TATCATCTGGATTGGCTGGATTTTTACTTTTCCAGGAGCCACTACCAATTCAGGGGTT	13036	A_95_P155882	EG650309
13482	159	52	119	GATCAGTGAATCAGCCATATACTCAATGAACAAGGTGAAAACTAAGAACACTTGGA	13038	A_95_P046291	BP131358
13493	159	63	539	CCTGACCTTAGTTATGTACAGAATGTTTGTCATTTTGCATGAATGCATGAAAATGATG	13060	A_95_P006461	BP135407
13494	159	64	550	GCACACACCATAGTTCTGTCACTTCTTTGTTCTTCACAGAATTCTATTGAGAATTGTTA	13062	A_95_P219312	EH615351
13497	159	67	843	CATGTAGCAAACTATGTATAGTATTCTTCTCTCTATGCATGTCTGTCGGGTTCCCGCG	13067	A_95_P263101	FG163595
13498	159	68	235	ATTATTCTGAAGGGCGGAAGTCCTAATAAAGGTACTCCTGGGGTTATGCATGGGAA	13069	A_95_P029221	TA19047_4097
13500	159	70	517	TTTGATCTGGACATGTTTTATGAAGTCCTCGCCAGCTGACAACTGTGTATCTGCTAG	13073	A_95_P025671	TA14517_4097
13504	159	74	779	AAATGTAACATATGGGTTTACTGCCCGTCAGAGACAGGATGCCACTCTCCGGACATT	13081	A_95_P289538	DV159765
13506	159	76	841	TCTTGTTTCAGTGTTAGTGCAACTACACCAGAAGACATGGTGATCTATGATGGTCTTT	13085	A_95_P013566	TA17008_4097
13508	159	78	198	CGCTGTTCAGTACCTCTCCCGATATGTCGAAATCAATATGAGTAGAGTTTCTGTAAAT	13088	A_95_P077590	EB425809
13509	159	79	358	CGTCAAAGCAAGAAAGACATTCACTGTTTGTCTTGAAACCTGTATGTAAGAAATCAC	13090	A_95_P085285	BP529241
13511	159	81	500	TCCTTATTGCTTGGGCTTGCTTAAGAGGGTATACTCAAAAGAACCCATTTGTATTTAG	13094	A_95_P161597	EH620274
13514	159	84	865	CTTTTTCCTCAAGGAAACTGTTCCATAATAATAAGGATGCCCTTTTGGATGTAAATTC	13100	A_95_P290408	DV999295
13518	160	3	817	GTTGCCTACTGTGTTTTGATGATTTATGTTTCGAGAATTTTGGAGTGTTTGTTCTTGC	12942	A_95_P198207	DV158366
13519	160	4	684	CTTTCATGTTGGTTTCTCTTGACATTGACCAGGATAGTCCAACTAAAAAGCTTAATGT	12944	A_95_P275483	TC63004
13530	160	15	204	TGTAGATCTTTTGAGTGCTTTATATCGGCATTATTGAGAATGGAAATTTTGCCCTGTC	12965	A_95_P100578	BP535437
13532	160	17	577	TAGGTATCAAGGAAAATCCATTCTGGCTTCAAAAGGGACGTTTCTTTTGATGAATAA	12969	A_95_P035398	BP128462

13533	160	18	707	TTATATTTTCCAGCACAAACATTGTGCATGCGAATACAATGGATGGCTTTATCATCTTT	12971	A_95_P014301	EH623509
13534	160	19	311	CCCAACATACACCTGTGTACAGTTGAATAATCCTGCTTCTGCTCAGTGTGCAGTTTATT	12973	A_95_P111057	CV020030
13536	160	21	233	GAAACTGGAGAAGCACTAGTATCCTCTGTCGACAAAATGATATTTGTTGGATCACCT	12977	A_95_P136727	EB440488
13539	160	24	451	GTGCTCTCTGTTATTCTGTGTTTGCTAAGTAGTTTATTGGTGTAACATAAGACTTGTG	12983	A_95_P060455	BP135001
13540	160	25	454	GCTGAAACAACATGTAGCTAAGGAACTTCACAGTTTGGAAATTGCACAAGGTTGATT	12985	A_95_P001251	EH620046
13542	160	27	481	AAGTATCTTGGAGACTTAGAAAGCTGGAACAAGGCTGAAGATTCTCTTGCGGAAGC	12989	A_95_P035558	FG142279
13544	160	29	780	TATTTGATGAATGTTAGCAAGGGGGAAATGTAATGTAACTTGTACTTTGGTTGTCAA	12993	A_95_P187477	TA14354_4097
13546	160	31	469	GAAGAATGTGGGTGGAAAGGTTCTTGGTTTCTTTTATTAAGTTCCTTATGCTGACAA	12997	A_95_P157412	EB439805
13549	160	34	901	TTTTGGAGCTCCTGATTATGCTGAAGCTATTAAAGGAATCAAGACAAGCAAAAGGCC	13003	A_95_P243857	EB429842
13550	160	35	795	AGATGAAATACTAGTGGAAAGGAAAGGGGGTCCATGGGAGTGACTTTACTACTGCT	13005	A_95_P311568	FG143668
13551	160	36	325	GAGTGCTTATCTGCTGGAAGTTGAATTTGGGACATTTTAACTTTCAATAATATCGCCA	13007	A_95_P109672	FS429988
13554	160	39	265	TATACGAGAGGTGCTCAAAGGATACATACCAGATACGCGGCCCATGTACTTATGAGA	13013	A_95_P110962	CV019986
13557	160	42	780	GTGACAATTCTGCTAAAGGTCCAGTTGCTAGCAAAATGAGGATTCACAGATCTTATC	13019	A_95_P148582	EB677946
13558	160	43	465	CCCCAACAAACAAATGTGGTATAATTCTCTACTGTCCCTGACTAGAAGGGGAGATAT	13021	A_95_P047681	BP131717
13561	160	46	553	CTATTAGAGTACTGCAGCAAAAGGGTTCATACCTGTTTTGGCTTTGTTGAAACCAGTA	13027	A_95_P041941	BP130226
13565	160	50	475	TGTTCCTTTTCATTGTCATATCTGTATGTATTCGCAGTTTGACCTTTGATTAGACTACC	13035	A_95_P103547	CV016564
13568	160	53	479	CTATTTGTTGCATAGTGGACCATGCCCCTATTCTCCATTCGTTTAAGGTATGAATACC	13041	A_95_P255849	AM817974
13569	160	54	813	AGAGCTGAGCTTGTATAGTGAAGTGAGGCATCAACCTAAAGCTGGATATTTGTCACA	13043	A_95_P307123	FG148524
13571	160	56	432	AGTGGATCTGAGACCTCAAAGCCTACAGTTCACTGCCCCATAAAAGTTTCACATGAA	13047	A_95_P093663	FG635489
13572	160	57	2258	CCAGAACCTTTGCGCTGGTACTTTTATTTATGGCTTTTGACAACTTTGGATTATTTCTTT	13049	A_95_P234239	AF190655
13573	160	58	344	CTGTCTTGTCCCTTTGCAAGTGAGTTGTTATGTGATTTGTAGTAAGATGAATATATTT	13051	A_95_P085420	BP529274
13574	160	59	950	CAAGTTGAGTTTTGTTGTGACGATCTCAAAATTTTGCATCTTGTTCTTTGCCTATGTTT	13053	A_95_P177172	TA11899_4097
13575	160	60	349	GGTCCCCTATTATCTTGCAGAGCTAACAGAAAAAGTTGCAGACAATGACAGGATAAA	13055	A_95_P070530	EB680539
13576	160	61	712	TAAGTTTTGCATATACATTATCCTCCCCAGACCCCACGTGGTGGAATTCACGGGTTTTT	13057	A_95_P164187	EH623329
13578	160	63	965	AACCTTGTCCTCAGCTTTGGTCTTGCTGTCCTCATTTGTGATCCTGTGATTTTCTTGCTT	13061	A_95_P192927	TA15561_4097
13583	160	68	251	GGAAGGCTTGATGTTATTTCCTTAGATTGTGATTAGGTACTGGACAATTTTAAGAACT	13070	A_95_P111147	EH619918
13586	160	71	673	GAAAGTGAGATGGATTTCTCTGCTTTATGATCTAGGTTTTGCAGAATGCTCTTGAATT	13076	A_95_P182482	DW003915
13587	160	72	563	CGCTAACGCCGGCCAATGCCACCTCTATTACCATTTTTTGTCGTGAAATCTTTGTTCTT	13078	A_95_P284548	FG637689
13590	160	75	799	GACTAGTTTATGGAACTATAAATTGATCGATAAATAATCCCCTCCTCCCCTTTTTCCCT	13084	A_95_P017161	TA21967_4097
13597	160	82	798	GATATTTTTCTATATGCAGTATTCTTTAATCTTACCATGAGTTGACGTTGATGCCTGGA	13097	A_95_P180082	DV157481
13598	160	83	402	GATGTGTGGAAAACAATGTATTGCAGGATAAGTGGTCATCGTGCTTATGATGTGAG	13099	A_95_P079520	BP527786
13599	160	84	800	ATTGAGTACACCAATTGCTTTGATGCCAATCTTGACACTTGTGCAGCTGCTCTTGCTG	13101	A_95_P291853	EB427579
13606	161	6	736	TAGAGGTTTTCCTTCTCTTAAACCAGACCTAGAATCACAGAAAGTTGAGTGCTAAAC	13113	A_95_P202967	TA17755_4097
13611	161	11	754	ACACTAGGGATCGAGGCTCTACATATGCGTAGCCTTTCTTTTCTTTTTGTTAATTTCTC	13123	A_95_P010236	EB439033

13612	161	12	1365	GGGAGATTGCTTGTGGCTTAAGGTGACGTTTGTTTGAGATTTTCTAAAATTAAATTTG	13125	A_95_P222132	TA21965_4097
13613	161	13	386	ATTGACCAGTGCTATATAGATCTGGAATTTTGAAGAAGAAATATGGAGGAGTTCGTT	13127	A_95_P092358	BP531762
13616	161	16	197	TTATTCCTTGGCGAATGATTGATCTTGGTGAGCATTATTTTCTAGTTTCTCTCAAGGCT	13133	A_95_P034164	AJ718241
13619	161	19	558	CAATATGTTACCTCACAGGTGATTACATGCTTTGACATTCTCGTATGTTGGGGGGTCT	13139	A_95_P080190	BP527945
13620	161	20	305	CAAATAGATATGGTGCCGTACTAGATAAGTTCTGTCCTTAGATATCCTTCTATCTCCC	13141	A_95_P108972	CV019089
13626	161	26	337	TTAAAACAAGTTTGGAATTGGCTCTACATCTTATTCTCATCCAGAAGCGTAAGAGTTT	13152	A_95_P133427	FG643621
13627	161	27	681	AGCATTATGTAATGTCACCATTTTGAAGCAATGCCATAAGGGGCGGATCCAAGATTT	13154	A_95_P192962	TA15568_4097
13629	161	29	383	TGCAATCTTCAATCAACTTTGGTTGTCGCATGGAAAATTTTGGACTATGCACATCTTA	13158	A_95_P006261	FS381087
13634	161	34	387	GTCAAATTCAATTGTTCTTGCTATTAGGTAGGTGGATTCACACCTATTATACTTTGCCT	13167	A_95_P281583	AM796827
13636	161	36	689	GATACTGCTGCCCATGACAAGTACGTGCGCTTTGTTAATGTTCCTTTTGTTGATATGT	13171	A_95_P017621	TA12435_4097
13637	161	37	543	TTGTTGTCATTTCTATTGTCCGGGTTATTTCAGGGCTGTAATTCGGATATTGTCTTGTG	13173	A_95_P148902	EB678440
13644	161	44	710	GAAGATGAGAAGAGTGTCCAAGCAGCTTGTAAGTATGATAGGCAAAAATAATTGAG	13187	A_95_P272781	EB679187
13645	161	45	688	ATTCGAAAATCAAGAAAATGGATCAGTATGTTACCGCCACTGCCCTGCTCCATCGAC	13189	A_95_P137997	EB441707
13650	161	50	421	AACTTTGCTCACTTTCCAAATATAAGTGACTTTGTATTTGTGGTGCCTTTCCCTATCAA	13199	A_95_P108397	CV018816
13653	161	53	638	TAGTTGGACATTTTCCTTTTTATATGTCCTTAGGGCCTCTCGAGGGTCGACGAATTCC	13205	A_95_P164217	EH623365
13658	161	58	518	TAGTAGAAGAGGGTGGCTATACAATTGATGCGGTCAGTGTGGAAATGTCGGGCGAT	13215	A_95_P074690	BP526533
13661	161	61	764	ATGTTCTGATGTTGTGAGAGATGAAAACTGTGTAGACAATGTAATCTTTGTGATTAT	13221	A_95_P029956	DV160716
13676	161	76	519	GCTGATGGCAGTGGTTATAACGTATCATTGAGTGTGGTCAACAATAATCTCAAACCA	13251	A_95_P103587	CV016589
13677	161	77	632	ACAGGTTGTGGGTAGTGTCGGGTATTGGAATTAAAGTAGAAATATTGATGTTTGTCA	13253	A_95_P151612	EB681852
13678	161	78	356	GGGTGCATGGTTCCATGTTCTCAAATTCTTGTTGAGTTGTTTCCCAGTTGCTTTAATTT	13255	A_95_P002741	TA16339_4097
13680	161	80	102	CATTCAATAAGATGAAGATGATGTATGTGGTGGAGGACGTATTGTCATCTAGGAATA	13258	A_95_P132892	EB433703
13681	161	81	837	AATTCACAAGGTGAAACACCACTGGATTGTGCTCCTGCCACATTGCAATTCAAGATG	13260	A_95_P226139	EB439999
13682	161	82	496	ACTGCATTCTTGAATTCAGAAAAGATAGGGTTAAACTGTTCTTGGTACTTTTGGTCTA	13262	A_95_P187558	TA14374_4097
13685	161	85	658	ACAGAGAGTCTTCCTACTTGCAGTGTTGTATCTGATACTGAATCGAGGAACTGAGTG	13268	A_95_P301228	FG182635
13686	162	1	0	AGATTCTGCAGATGATTTGTAGTGACTACTAGTACTTTTGTAACTAGGCTGTCTACTG	13105	A_95_P313883	A_95_P313883
13695	162	10	729	GTAGGTGAGTTAATGTCAAAGCTTTGGTAGGATATACTACTTCATTTTCTCTGTTAGC	13122	A_95_P198992	TA16897_4097
13696	162	11	734	GGTGAAGGCCCAAACAAGACTAAGATAACTGGCAACAAAAATACCTTGATGGTCTC	13124	A_95_P314988	FG199121
13698	162	13	229	GGCCTCTTCAAACTAAATGTAATGGTTGTTGACAGTATGAATAAAATTGCAGCTTCTT	13128	A_95_P211897	TA19715_4097
13700	162	15	1086	CCATGCATGATGAAGCTTGAATTCTGCTAGTTCATTTGGGTATTCACGTTATTATTTTG	13132	A_95_P023091	TA12370_4097
13706	162	21	540	GTGGAAGGTTTTTAAGATGTACCTACAGACAATATACCGCTGCCTGATACATGAATA	13144	A_95_P221312	TA21794_4097
13714	162	29	898	GGTTGAAGTTGTGATAGTTCTGTATACTCTTTCTGCATTGTATAATAAAGGATAACCA	13159	A_95_P210737	TA19459_4097
13715	162	30	428	TTGGCCGTTTACTTATCTCTAATTCCCATCATCGGTGGCTGTGGTCTTTCTGCTCTTAC	13161	A_95_P011071	DV158401
13716	162	31	503	TGATGATTTAGCGCGGGGAGATGAAGAAATAAAGGTACATGCAAAGGAGCCCTGTC	13163	A_95_P131302	FG143691
13718	162	33	449	TTAGCGAGGTTCCTGCTATGGTGAAGTGAAAGATCTTTCACTATAGTGGGAAGAAG	13166	A_95_P071050	BP525606

13719	162	34	362	CATGCATCGTTTTCTGATGATGACCTTTACTCTCCAGTTGCTCAGTAATTAACTATTTTT	13168	A_95_P097293	BP533969
13722	162	37	674	ATCTTGATACTTGGGGTGGACACCTTTGAGTTATGGATGTATTGGGTGCGGATGTTG	13174	A_95_P063830	BP135886
13729	162	44	303	GTAGTACCTTAATGCTGTTTGTATGCTGCATCAAAAGAAAGCAATCTGTTACAGAACT	13188	A_95_P164332	EH623500
13731	162	46	143	CATTGGGTGGCCTGCCTAATTGCATACCAACTATGTAAATTTTTGTAAAAAATGTAGC	13192	A_95_P002966	CV020097
13737	162	52	598	CTAATGTTGGCTTTCTGCTGGTTTGATATAAGTAATGTATTTGTTCTTGCTTTTCTGCG	13204	A_95_P026041	EH623514
13738	162	53	525	CCCCCTCACGTAAAATATACTGGATGTGATAGGATTTTAATTGTATCGTTGCAGCTAT	13206	A_95_P001901	BP129353
13739	162	54	573	GAGGTCCCAATATAGTTGTTTCCCAAGAAACAAGAAGAAATACAATTAGGGGAGTA	13208	A_95_P124207	DW004062
13741	162	56	4313	TAAACTATCTAATGGTCAACTGGTTGATTTGATTCCGTGGTGCCTGCCTAACACTGCT	13212	A_95_P251627	AY567977
13743	162	58	940	TTCCTGCACTAAATGATGTTACTGCAATGGAGTTGCCTGATATTGTTGCTGAGGCTG	13216	A_95_P242967	DV159439
13746	162	61	902	ACATACCGCTGTCTTGCCTTCACGCTTGTGAGAATCACTTTTTCATTCAGAAAGTTGTT	13222	A_95_P208727	TA19031_4097
13747	162	62	751	AAGATGAAGTCAACAACATTGAGCCTTTGGATCTCTGTGGAAACCATCCTGACTGCC	13224	A_95_P244077	FG139319
13752	162	67	645	TAAAATTGGGAAGCTTTGGAGGAGTTGTCGTTTGAGCAGTGGAATAAGCCACTCAG	13234	A_95_P000901	EB451750
13754	162	69	187	GATTGGTTACGAAGTTTGTCTCTGTAGTGTTTTCTCAGTTTTATCCAACACTGTTTACT	13238	A_95_P097593	BP534118
13755	162	70	813	TGTACCTGTTTTGCTTGATGAGCATATTGGAGAGGGAAAAGTCATTGAACGACTTTG	13240	A_95_P294028	EB440637
13761	162	76	417	AGCCAAACCTCGAGATTTATTCAGAAAAGAACCTTCAACGGTAATATCTTTCATTTTG	13252	A_95_P048966	BP132049
13766	162	81	642	TTATATTTTGGTTTCCCCCGAAAGCTTGTTGTTCACAAGGCAAAATGGCATCTCTTTTT	13261	A_95_P014606	BP130287
13767	162	82	777	GATCACCTTTTGGTCAAATTATTCTATCGACACGTTAGTGTAAGACAATCTATTTGACT	13263	A_95_P004201	X65700
13769	162	84	779	ATTGTTGATGACGCATCTGCTCTACTGGGATATTTTTAGGGCATTGGCCCCAAGATCC	13267	A_95_P255379	FG136640
13773	163	3	951	TAAGCATCATGAAACTGGAGAGTCTCTCCCAGAAGACATATACAAGAAGCTTCTTAC	13274	A_95_P014511	TA15524_4097
13774	163	4	549	GTCTTTCGTTGGATGTTAGGGTTAGTGATGTAAATCAAATGACTTGTTTCAGTCAAAC	13276	A_95_P003466	DW003379
13776	163	6	369	GCTAGGGGGTCTCTATAATTATCAGAAACTTTTCTTCTGGAACACTTTGAATCTTTCT	13280	A_95_P220452	TA21610_4097
13783	163	13	96	GTATCGAAAAGAGAGCATCATGTATAGTAGTGATTCTTATGCAGTTCTTGTTTGCTG	13294	A_95_P132302	EB432768
13784	163	14	809	TATCATATGATCATGGTAAATTTTATTGTTGCTTGCCTGGGCCAAGGGACAGAGAAG	13296	A_95_P197732	EB681120
13785	163	15	828	CTGCTGCGCTACTGTTGGTATGTCGATTACTTGTGTATGTGAATAATGCCATGCAACT	13298	A_95_P147227	EB451494
13787	163	17	877	GGGAACTATGTACATAAGGCATAGCTGCTATTCATTGGCTTTCTTCCTTTCTTTCTTTT	13302	A_95_P226064	DV158290
13790	163	20	570	CTTTCCTTATGGAAGAATCTTGGATATTGAGGTCGTAGATGGTGGACTGATATGCTC	13308	A_95_P047146	DV999838
13793	163	23	869	CAATACTTTGATTTGAATAATCTGTCGTCTCGTCTAATGCTGACAAGAAGATGTTGTG	13314	A_95_P272791	FG158149
13795	163	25	682	CTCTTGCAAAACCAGAACGTTGAACAAGTACTAGACGGTCTCTTATAGAAATGCAGC	13318	A_95_P306973	FG151496
13797	163	27	497	TGGTAGATTTGGCCTGGAGTTTATTTTTCTATTCATTGTTCCAAGAACACAATGCAGC	13322	A_95_P098583	BP534557
13799	163	29	500	CTTGCTCCATTTGTGTTGTAATTTTATTAATCACTATCGGTTATCTTGGCCCTAGTCGA	13326	A_95_P021186	FG644605
13812	163	42	872	GGGTCATTTGTGTATATACCCAAGAACACCAAGTGTCCTATGCAAATATCTACTTATT	13352	A_95_P236544	DW000893
13815	163	45	51	GGAGAAAACCAGTCATTTGTAAGGACACGAGAAATCATCTTAATATACTGGTTTACT	13358	A_95_P256319	EH618738
13816	163	46	952	CTTGTACAGTCTTGTAAATCAAATCAACCTTATTCGTCTTCCAATTTATTTCTGTGCTG	13360	A_95_P203012	TA17764_4097
13821	163	51	440	GTGGGGAAGCATATATTTATCTGGTTTAGGATAGTTTCCTTTGGCTTGACACTATAAG	13370	A_95_P114247	CV021515

13822	163	52	335	TTAGTCCTGGTCAAAGACTTTAGCTCGCATATAATTGGTGACTTGTACAAATAGATAT	13372	A_95_P141882	EB445504
13826	163	56	544	TTTCTGCCTTACTCTGGGTATTCAAACTTCCTATGGATATTTGATGATATTTCAAGTCA	13380	A_95_P183317	TA13431_4097
13831	163	61	1434	GCCTCCAAAAACTGATGCGACAGTAGAATGTTTACTTTTCTCTGTGCCTGTTATAGTA	13390	A_95_P192672	TA15504_4097
13832	163	62	776	GAGCTCCATCAGCTCATTATTTCCTTTCTTCTTTAGGCTATGAAAGCGTTCTATTTCTG	13391	A_95_P189477	TA14797_4097
13833	163	63	379	CTGTTCATAGTTTTAGCTGGGGTTGTTAAGTGTTAACTTGGGATACACTGTTTAATGA	13393	A_95_P004336	TA13705_4097
13834	163	64	589	CTCTTGGATCACTTTAAGCATTCTGGGCCGAATGGGCAGCATGTTTGTATGGTATTTG	13395	A_95_P128377	EB428075
13835	163	65	662	CAGCGATTGTCAGTCAATTGTCCTGTAGTATATTATCAGGCACAATATGTATTTTCGT	13397	A_95_P136162	EB439792
13836	163	66	326	AGCCTCTTACAGTAAGCTTAAACTATAGGGATGTCTCTATGGTGACTGAATGAATTTA	13399	A_95_P109837	CV019462
13840	163	70	542	TGCTTATGCTTGATTGAGTCAGCATAATAAATAAACAGCTGCCAAGTTGGTGTATTTT	13407	A_95_P222527	TA22053_4097
13841	163	71	826	AAAGTGCATGCCAACAACTTCCAAAATTTGCTACCCTTTGCAAATTCAGTATGAGAAA	13409	A_95_P011506	DW000343
13844	163	74	1402	GCTAAGGGAATGATAGTGGATCATGTGCTTGACATGTATATACATATTTCGTATTAG	13415	A_95_P025466	TA14191_4097
13846	163	76	222	CCATATTGTGCCACAGAATGATGGCCTTCATAAACCATTGTGGAAACGCTGGAGAAC	13419	A_95_P146337	EB450358
13849	163	79	808	AATTGGACTATTTAGTTGGGGCAGTTTCAAGTCCAAAGAGGCCATTTGCTGCTATTGT	13425	A_95_P008581	Z48977
13852	163	82	721	GGCTGGACCATAATGGGCTCTTATTTTTCTTTCCCACTTCAGAATTTTAAAGTTTTTGT	13431	A_95_P202057	EH615240
13854	163	84	505	GCCATCGAGTTCCTGATTTTTGATTTTTTCTCTTGGAGTGGATTTGAACTCAAGCTTGT	13435	A_95_P088863	BP530252
13856	164	1	1123	TTTTGTAATGAGACCCTGAGCTATAGCGAAGTAAATAATGGACTGAATCATTTTTTCC	13271	A_95_P204562	TA18092_4097
13857	164	2	832	TGATGATGTATCTGTGGATATAGCTGTACTCAACCCAGTGCAGAGACTTTGTCAGTGT	13273	A_95_P307393	FG141895
13858	164	3	656	GCCAATTACTTTATCCCAAATTTGATGGGACTACTATGTTTACAATTGACACATCATG	13275	A_95_P031036	TA14624_4097
13862	164	7	367	GGTGGAAATCCAGCACGTAGATGATTTCAGTTCTAGTTTTGTGTTATTTAATGAGGA	13283	A_95_P029711	BP533659
13864	164	9	911	TGTTAAGTATTTGGAAAGGATGTCTAGGCAAGTAGGATGCGCGCCAAACTATGAGA	13287	A_95_P268206	DW000064
13869	164	14	426	TTTTCATATGCTTTTCCTTAATGGGTCCGGTGCCTGTTGGTTACATCTCGAGGCTATTT	13297	A_95_P081210	BP528200
13870	164	15	812	AATCAAGCAGATAGGACTGCAGTAGTTCTGCCTCAAGGAACCTCTAGGTGTGTAGA	13299	A_95_P269936	EB428068
13871	164	16	890	GAGGAAGACGATGATTAGTTTACTACATAACAAGAATTTTGGATTCTTGTCGCTTAT	13301	A_95_P260046	EB677659
13873	164	18	808	GATCTGTGCTTTCACGATTTTGGTGTGTGCATGCTGTCTCCCATGGGACTAATATTTC	13305	A_95_P299693	FG139470
13875	164	20	867	GGACTTCAGCTCTCTAGAAGTACAATCATATACTTCAAGCACAATGATATGGAGTCCT	13309	A_95_P296433	EB452117
13876	164	21	492	AATGGAAGAACAAATAATTCACGGTGATGGGCTATTGGTGAATTTAGCAAACGAAG	13311	A_95_P040086	BP129731
13878	164	23	445	GCTTCTTGACGCTTTGCATTTTGCCTTTTTTCTATACAGTGACTACTTGGGGCCTGAAA	13315	A_95_P158957	EH616859
13883	164	28	2616	CAATTTTGTCTGTATTGTCATTATCCACGTCTAAGATAATGGACCTATGTTTTCAGCTT	13325	A_95_P250777	X77915
13885	164	30	820	TTGGACAAATGGATGATAGAGAACATAAGTCTGGAGAAGAAGTTTCTAAACATACT	13329	A_95_P127222	EB426697
13886	164	31	868	ATTTACTACAATGCCGTTAAGTCCTCCGTATTTGATTTTTGACGTGGATTACTCCTAAA	13331	A_95_P196852	EB680458
13889	164	34	848	CATCAATAATCGAGATCTTGGAACATTCAAGGTGGACATTAGCAATACCAAAAACCT	13337	A_95_P126097	EB425332
13891	164	36	768	CACACAGCTTATCATATTCAGACCAGACTTGATTATTGTGATTTGTGTAACATGAAAC	13341	A_95_P015576	EB438873
13895	164	40	1152	TGTTTACATTCTATGTTGACTTATTCTTCTGGATGAAAGTTGTATTTGAGGTGTGCTG	13349	A_95_P192367	TA15436_4097
13898	164	43	780	GGCTGAATTCATCTGATATTGACAAAGAAGCTGTTCTTTCAAGTTCTCTTAGCTAGAA	13355	A_95_P254779	EH616966

13899	164	44	843	TATCGTGACTGAGGGTCGAATATCTGCTTGGGGAGGGTACATCAAAGTATCGATTTG	13357	A_95_P296058	FG143518
13903	164	48	938	ACGTTGCAAAATTTTTTCCCTCTCCTTGAATACTCATCTGTATTTCAGATCTTATGCTG	13365	A_95_P196857	TA16434_4097
13904	164	49	657	CAGACAATTACTTTTGGATTCATCTTGATAAGAAGGTGCCTACTGGGGCTGGTCTTG	13367	A_95_P136612	FG134239
13909	164	54	696	CAATGAAGCTAGAATACAGCTTTACTGGCCAAGATACATGTCAGTTTTTCATTTAGTT	13377	A_95_P022371	TA13932_4097
13915	164	60	704	TAGCTGTTAGCAGGATTATTTGGTTATGTTTCTCATTGACTTCATTGATTACCAAGGT	13389	A_95_P213007	TA19958_4097
13917	164	62	508	ATTTTCCTCTCATTTTGAAGATATGGTTAGGCCGCTGCATTCTGGGCCAGCAAAGTAG	13392	A_95_P005806	BP528616
13923	164	68	558	TCTTTTCCCTAATCACTCCATACTTGATGAGAAAGAAGAGTGGGTAACTTTTCTCACC	13404	A_95_P158517	EB427996
13926	164	71	763	GAGAAAGAGATCGAGAAATGAGGACTTTTATACAAGAATTTGATGACTTTGCCACTG	13410	A_95_P159167	EH617126
13931	164	76	189	GTCCAATGTAGTCTATTAGTGAAACAGATGTCTGTACTGTACCTTAAAACAACACTTC	13420	A_95_P096083	BP533466
13934	164	79	730	CATGCCATATAGCACCAGCTTTCGAGATATTCTTAGATATCGTTCTCTATACTGATTG	13426	A_95_P117337	TA14846_4097
13935	164	80	559	AACTTATCAAACCAATGCATCTGTAATTGGAGCTGTTCCTGCAGCAAGCAGTGCTTCC	13428	A_95_P138782	FG141527
13938	164	83	346	CAACCTGTGTCGAAGCGAGGAATTTTGCTAAGTGTATTCAAGATTTAATATACCTGTA	13434	A_95_P058041	BP134370
13948	165	8	298	CGGCAGGAAACATCCACCACCTTCACATTAACATGTTTCATGAATTTTAAGGTGGAA	13453	A_95_P043051	BP130512
13951	165	11	515	GAAACTGGTTTAGCAGCATACACAATTGAGGCATTGGTTCTTAGGCTCCATAGTATT	13459	A_95_P041451	TA15600_4097
13952	165	12	830	ATTTATCATTATGATCAGTGCACAGTGGTGGTGGACTCACTTGCATCACAGTCAGCTG	13461	A_95_P291613	FG143021
13955	165	15	416	TTATGGATACACTTAGGGCATGGCGATAACGAACCTCTTCATCTTGAGCTAAAGCGT	13467	A_95_P108677	CV018951
13966	165	26	888	CCTATCAAATGATCTTTGGCAGGAGCTAATTGTGTGATACATAACAGTGTTGTTACTT	13489	A_95_P250407	Y11002
13968	165	28	575	GGCTCAACATTTGAGAGTTAGTGGCGTTTGGACATAACAAATGTGAAATTCTGGAAT	13492	A_95_P066335	BP136573
13969	165	29	0	CTGGGTGCTCTGTAATCCTAATAGCATGACTCATCTGTTTTTGTAATATCATGTATTTT	13494	A_95_P018961	A_95_P018961
13973	165	33	815	GTAACAGGCACATGGGAATATGCAAAGTATATCCATTTGCAATGGAATATAATTTGA	13502	A_95_P179597	EB450661
13974	165	34	813	GCCATATGTTCAAGTTCTCTCCTGATTTCCTAGCACACTCGAGCCTTTTCTTGATTTCTT	13504	A_95_P244722	TA12753_4097
13978	165	38	489	GTTGGGATATATAGTGCTATATATACCCAGCCTCATGGAATAAAACTTTCATAGTTTC	13512	A_95_P127907	FG625527
13982	165	42	240	AGTCAACTTTGCTTTCTGTACTTCTACATGTATAATGGGAGGGAAGTGGTTGTGCTTC	13520	A_95_P142847	EB446260
13984	165	44	271	ATTCGGGAAAGTATTTCAGGTGAAAAAGAAGGGCACATCAGAAATTTATGCAATGA	13524	A_95_P077635	BP527301
13985	165	45	785	GATGAATGAAATGATCATAAGAGGACACACACTCTCTCTCTCTCGTAAAGTAAAAGTT	13526	A_95_P269136	FG645381
13987	165	47	219	TTTGATATGCTGGTGCTGCTGCTGTCGCATTGCTTGGAACAGCTTACCTATACTCTTTT	13530	A_95_P112002	CV020471
13991	165	51	770	TCGATCATGAAGAAGTCTTGTAGGAAAGATGATGCATTATCACATGCCAATTCTGCTT	13537	A_95_P289253	DV158351
13992	165	52	262	CCATGATGCTTGGGTCAATAACACTTTGATGCTCATTCTTCATTCTTATATTCTAACCA	13539	A_95_P028531	CV017661
13998	165	58	744	GATTCTTAAGGGCTTGAACATTTCACTTGTAAATGTGTGTGTGTTTTACTTGCTAATC	13551	A_95_P268736	DW005219
13999	165	59	108	CTACCTGATTTAGATGTTGCAGAGCAAAGCTGTGCGATTGTGTTGTATGTTATTCTTC	13553	A_95_P241450	AJ718321
14000	165	60	672	GCGAAGTTTGTAGATTTGGTTTTACAACTGAATGGCTGCAATGTAGTGGGTGGCAAT	13555	A_95_P015181	EB679266
14002	165	62	650	CCATTTTGCTACTCTGATTGCTTCATAGGCGCTATTTGGTCCCTGTTAAACATTCTCTG	13558	A_95_P189162	TA14731_4097
14005	165	65	993	GACTTCTTAATAATGCTGGACAAGGCATGTAATGTGGTGAGAACTCCACAAATTCCA	13564	A_95_P210477	TA19406_4097
14011	165	71	746	TCTCTATCGTACAAGTGGTGACAATTCTGTGTTGTACGACCCATGATCTGGAGAGTTA	13575	A_95_P162457	TA16083_4097

14014	165	74	103	GGTCATGGAGGGGTGGTGACTATGATTTCTTGGGTCGTATTTAATGTCTTGAAATTTT	13581	A_95_P237409	X68590
14015	165	75	625	CGGTGTTTTGGGTAAGTGGCTTTATGTTCGTTAATATATGCTGATCTGCATGTTTTACA	13583	A_95_P177977	TA12115_4097
14019	165	79	370	ACATGTGTCGGTATGATAACATTGAATTTTGCAAGTGTAATGGTTAAGGTGTGGTTCT	13591	A_95_P213127	TA19982_4097
14026	166	1	787	ATGATATTCTTGTGGACGCACTTGTATCACCTTCCGGTGTGATTCCTATTAGTCCAGCT	13440	A_95_P136492	EB440257
14028	166	3	1307	GGTGTTAGATGGATCGTTGAATTTTACGTATAAAGTTTGCTGGAATAGCTTCTGCTTA	13444	A_95_P189137	TA14726_4097
14029	166	4	322	TGCTCCTTGTTGCTGTCACAATTGTATTCATGTTAAGTTCTTTATGAAGTTGGGTTGA	13446	A_95_P094738	BP532855
14031	166	6	306	TTGTATTTGCTTTCTTATTCTCAATAATGATTACAGTTCGATGGTGCATCTCCGGTTTCA	13450	A_95_P132962	EB433862
14034	166	9	813	CCATGTCTTAGTTAAAGTTATGCTTATGAAACTGATGAGCTACAGGTCAAGTTCATCA	13456	A_95_P216972	TA20823_4097
14035	166	10	440	TTTTGTCCGTTTACGAGTACGTCGCCGAATCAAGATAGTTCGACGTCGATTCCAATT	13458	A_95_P107682	CV018489
14041	166	16	874	GTGGACTCTAGCATCAACAAATCTGTTATAATAGAGAACCTTTTCTTCTGTATGAATC	13470	A_95_P009391	EB427816
14042	166	17	744	GTTGCGCTTGAATTAATACATTGAATTGAGTACTTTTTATTGAGATGCATCCCGTTTT	13472	A_95_P012931	DV159000
14043	166	18	1025	CAACTCGAAAGGGGTTACATTAGTCTGGGAAAAGATATTTTGTTTTGCTTATAATGG	13474	A_95_P011271	TA14015_4097
14046	166	21	803	TTGAAATTTGGTGATGGCATGGAACTGTTGTCTTTGACCAAGCTAGTCGTTGCTGGAA	13480	A_95_P015686	EB446842
14049	166	24	770	CGAGGACTAAGAAAAGGTTTCGTTTCCATTCTATTTGTATATTTGACATATGCTCCCTT	13486	A_95_P202012	TA17542_4097
14051	166	26	856	ATGCATGGGCCAGTGTTCCTACATATCCTAGTGGTGTTATTGGGTTTCTTCTGTGTTC	13490	A_95_P016286	TA20570_4097
14053	166	28	814	TTACTTTGTAGTAAGATTGATGGTGTAACATAGGTTGTAGGATAATCGAACTGGTCTA	13493	A_95_P013641	EB450467
14055	166	30	925	GATTGGCTTCAGAATGCATCGGTAAATACTTTACACGCACCACTAAAAATGGAAGTC	13497	A_95_P028981	EB680234
14058	166	33	521	CATTGGTTTGCTCCTCCCTATGTAATTTAGATTATTAACGATTTTAATGGAGGAACAC	13503	A_95_P091728	BP531478
14060	166	35	553	ATTTACCAAGAGCGTCACACAATGGTTTACCAAGGATGGAGTTCTTGTGGAGGGGCT	13507	A_95_P034364	FG636765
14063	166	38	291	GCCGGATTTTGGTTGCCGGATTTTTAGGGTAGAATTGACATCAATAGCTAGGTCTGG	13513	A_95_P062875	BP135632
14066	166	41	884	TCTCAGCAGAAAAGGCATTCATGAACAGCTTTCTGTCCCTGAAATAACAAATGCAGTT	13519	A_95_P298453	FG142676
14068	166	43	678	TTCTACCCTTTGTTGGATGTTCTACTGGGATGCTGAGATATTAAGACTTTGTTACCTTA	13523	A_95_P124102	EB443533
14077	166	52	681	GCAACAACAAGTTGGATTTATCTCGTCTTACTCGCTCTTCTTCTATTTGGATGGGCAAT	13540	A_95_P145377	EB425395
14079	166	54	1534	GCCTGATACCTGCAAGGGGGTCTTACCACTTTAATTTTATTTTATGTATTTGATCTATC	13544	A_95_P011241	U84972
14082	166	57	797	TTGCATCGGAACACCATTTGGTTCAGCATGGCTAAAAGAAACTTTCTTGAAAGGATA	13550	A_95_P207342	EH618818
14085	166	60	510	ATTAATTTGCGAGTCGTGATGAGTAATCAAATCCAAATATGCGCAGTGGTTCCAGAG	13556	A_95_P149027	EB678689
14086	166	61	513	TTTTGTTGTAGCGCTGGCCACTAGCTACCACAGCTTTGCTGTATAAAAGAGATGTCAA	13557	A_95_P304423	FG645419
14091	166	66	142	CTATAGGCTGTATCTTGAACGCTCAAACATTTTGATCCTTTATGGAATTTGTTTCTTTG	13567	A_95_P031926	EB435446
14092	166	67	769	GTACTGAAGATGGGTGTCAGCAAGGCTTTACTTTTGATCCATCGACTGGTGTTATGTA	13569	A_95_P205062	TA18200_4097
14095	166	70	673	ATTCTGGCTATTTTGTTCATTTCAAGATTCCTGTGCTCGGAAGACCTTTTTGATCAATA	13574	A_95_P314973	FG179245
14096	166	71	62	CCACGGTTGTGGATTATTGTTTCAGTTTGTAGCATTTTAAATTATTGATGTTGTAGGG	13576	A_95_P160817	EH619517
14098	166	73	208	TGGGTTCATCACTTACTCTGATCCCACTGTCGTTGACACTGTTATTGCTGAAACCCTTA	13580	A_95_P157042	EH615090
14099	166	74	164	GATTTCTTGGTGGAGCCACAGCTATCTGGGTTCTCTTTGAGGTAGTAGAATACCATTT	13582	A_95_P156277	EB680718
14102	166	77	848	ATAATGCCTTTGCGATTCTCATGTTGTGTTGAGTTTGTTCCACTTTAGGTGTGTATTTC	13588	A_95_P117817	DV160787

14105	166	80	481	TGAGTTTATCCCTTTTGGAATTGGATTGTTACTACAATGTTATTTCTATGTGGTGGTTC	13594	A_95_P020571	TA12507_4097
14107	166	82	410	AAATAATCTCTCTGGGATCAGACTGGCTCTCGGCTTGAGCATTGTACATAGGTTTGA	13598	A_95_P204552	EH621290
14108	166	83	467	ACTAATTGTGCACTACAAATTGATCTGATTGCTGCAACTTTTGAGGAACACCACTCCG	13600	A_95_P006381	BP532606
14109	166	84	836	TAGAAGGTATTAAGCAGTTTTATGTGAATGTAGATAAGGAAGAATGGAAGCTTGAG	13602	A_95_P182363	X79135
14111	167	1	473	TGGCTGTTAAATGTCTACAGCAAACACTACCACATAAACTGAAAAAGGTTGAGAAAG	13605	A_95_P134212	EB436283
14112	167	2	481	TTGCTGGCCCTGATATTATACGTCTCCCTAGATTATTCCGATTTCTCCAACGCCCATTA	13607	A_95_P034893	TA14479_4097
14118	167	8	811	ATCACTCATCCATTGGCAGGTTTCCTAATGCACCTGGTGCTATGATTTACCCCATTTAT	13619	A_95_P208472	TA18976_4097
14130	167	20	660	AGTGGTTGTGGTATGTCACTTGTCTTAGTTTAGCGTTGTTCCCAGTGTCTGCTTGATT	13642	A_95_P067315	BP136837
14133	167	23	364	TTTCAGAATGCCAAAGTTCATCTCCTAAAGGTCGAAGCAGTAGTGATAATGCACAAG	13648	A_95_P064065	BP135947
14135	167	25	2087	TTCTGGGGTTTGTATCCCGTGAGGGTATTCTGCTAGTATTGCTTGTTCATAAGATTGT	13651	A_95_P015376	TA15967_4097
14136	167	26	247	GCTCTGTAAATGATTTGCTTGTCAATCATTAAGTAGTTCAATGAGTTCCTCCTTTTCAA	13653	A_95_P110977	CV019992
14139	167	29	199	CATTGAGGATTCTACGACGCTCTTGAGATCATTGACACATTTGTTCATTTTTCATTTCT	13659	A_95_P111027	CV020010
14140	167	30	504	GAACTTGGAATAAACTTCGGTTGTAATGTTGTATGTCTTTAGCTTGGTGTTAATGTGG	13661	A_95_P299468	FG645576
14145	167	35	795	AGTTGCAATTGATGGAAGTGGACAATATAAGAGTATAAATGAGGCACTTAATGCTGT	13671	A_95_P196497	TA16352_4097
14154	167	44	821	TAATAAAAGCTGGTTTGAGTGTTCGTCTTCTATTCCCTGTATGCTGTAACTGTTATTAC	13689	A_95_P146382	EB450422
14157	167	47	830	TGTCTGTTAAGTTAGAGGAAATGGAAAGATTTGCTCTGGGTACAAATCTTATCCTGA	13695	A_95_P227639	EB427690
14159	167	49	872	GGTGGTTCTCCCAGTAGATCAACTCAAAGCCATTACTCCGTCAACTAGTAAGATCAAT	13699	A_95_P229644	EB450979
14163	167	53	764	ACACCATTAAACTCTGACACAGCTGTCTTCTATTGGCATATAATTACAAGTACGTTTT	13707	A_95_P188362	DV158374
14164	167	54	1611	CTGTGGTATGGAACTTGTAATAATACACTTGTTTCCATCTTAAGCAAAGATTCACTTA	13709	A_95_P010496	AJ319873
14165	167	55	771	TTCATGGTTCTGTTCCTGTGGGAAGGGTGCCAGCTTTGTATAACAAATCGTATTATTC	13711	A_95_P209817	TA19270_4097
14177	167	67	848	AAGCTTGTTTGGATGGTTTGATAGCCATGTTGTTGTATTCCAAATTGATATTCCACTA	13735	A_95_P233729	EB432598
14179	167	69	2242	CCCTGTCCTAAGTCTATGCATTTCCCTTTGATAGTGTAACTAAAGCTATGTCATTATTA	13739	A_95_P018241	AF435451
14180	167	70	243	GGGCTACCCATGGCATTGTAAGCAAAATTTAGAAGAATGTTAAACTAGGAAATTTCA	13741	A_95_P132367	EB432845
14183	167	73	803	AGTGATCTTATCCTTTTCCAGAGCTCGATGTGGATCTCGAGAGTCGAGAAAATGACG	13746	A_95_P292308	FG135867
14185	167	75	844	GTTTGCACAGTACTGATGTCAAGTAATGCCAAAGTTTATTGCGCTGTGTTGCAGTCTT	13750	A_95_P310073	FG134932
14189	167	79	756	GGACATGTGATTGAAATTTTCCAACTGGATTTTATGATTCGACATGGTAAACATCCTC	13758	A_95_P013851	DW000482
14191	167	81	838	TTTGTGCCTGAAAGCAATATCAAGCATAGTAATACCATTCCTTTGGTCCTCTTGTTGG	13762	A_95_P014656	DV160066
14193	167	83	749	GCCGTAGAAAATCCTATGCCCTAAGATCCGACTGTGTATAGACTTCTATAGTTACGAT	13766	A_95_P184222	TA13643_4097
14207	168	12	453	AAGACCACTTCTTATGAGGAGGAAGCACTTAGAACCATGAAAGCATTTTGGCTGCCT	13628	A_95_P039116	BP129459
14209	168	14	708	CTTCTTTATGTCAATTTCTTCTGCTTGCTCGATAGCTGCTTCCTTTCATGGATTGAGCA	13632	A_95_P135417	EB678847
14230	168	35	478	GGATCTGCTTTGTATGTAATGTCTAATTTGCACCTGCTATTTTGTGCTTCAGCTTTCAT	13672	A_95_P276598	AM801363
14232	168	37	735	TTAGCTAACAGTAGAAACTCTGCCACAAACAGTTGGGGCTTGTAGATCAAAGGCAG	13676	A_95_P160582	EH619262
14233	168	38	825	CTTCACTGCACAGCGCTATGTCTTTGACGAAATGATGGTTTCTTCTACCTGTCATTTGA	13678	A_95_P136167	EB439795
14238	168	43	839	CTTGTGCTCGATGTTCTAGCACTGGAGCTCTTGTTCTTATCGAGCCTGTTTCAAAATTT	13688	A_95_P012461	DW000246

14239	168	44	756	CAAGAGCTGAGGAGAAGAAGGCATTGGCTTACCAGAAAAAGAAGACTGTAAATATG	13690	A_95_P148337	EB677622
14240	168	45	806	TTAAAGTGAACTAGAACCTTGTCAGTCATGGTATTTTCCAACGAGAATGATACCAAA	13692	A_95_P117447	DV160357
14244	168	49	570	TGTTCAGCTACTGTAGTGGTAAACGCATACTGCATTACCCTTACTGTCTTCCATAAGG	13700	A_95_P153322	EB683615
14247	168	52	259	CTGGCCTGAAAAAGAGCGGACAGAAATGAGAATGTTATATTCTTCCTCCCTAGTATT	13706	A_95_P105707	EH616159
14248	168	53	549	CATGGTATAGTCGAGACCTTTCTTGTTTTCCATTTATATTAGTAGCATTTTATTCTGGG	13708	A_95_P214407	TA20257_4097
14249	168	54	321	GTTGGATAAACTTAGAGAGCTGTCTATTATTCACTGAAACCCGTGTTTGTTAGCTGGT	13710	A_95_P106162	CV017781
14254	168	59	762	AGCACAGTCAAGAATGTTACTTCTGTTATTATAATTAACTGTTGCCCTATATTTTGCCC	13720	A_95_P012791	TA12536_4097
14257	168	62	869	AACTGGTGAGAATAGCCTTGGTGCTGATAATGATCCTAAATACATAAACATTGGCAA	13726	A_95_P126422	EB425749
14258	168	63	788	ACGATCAATCTTCTTGAGTTCAAGAACTGCTGCTCATTTGCTGCTTACTTGTTTGTGTA	13728	A_95_P191327	TA15212_4097
14261	168	66	468	GATCTTGGTTTTTCGCTAATAAGCAGGACCTTGAAAGGAGCAATGACCCCCATGCAA	13734	A_95_P163267	EH622281
14263	168	68	463	AGCCATGTCAGCTCAAATCCAAAGTAGCAACTCCATAGTTAAATGCTAACAAATAAG	13738	A_95_P274703	AM791671
14265	168	70	718	AGAGTCCGCGACTTGGCTATGCCTGAGTTTTGTACTAGTATATATTGGTTTTTTCTTC	13742	A_95_P122477	DW002444
14268	168	73	862	AAGATGCATTTGATCTGAAAAAGACTGCTCAGAGGCACACGTTTGGCTGAAGCAGTT	13747	A_95_P227089	FG155288
14270	168	75	887	GCTGCAAATTTAAGCTTATGATCCTTGGATATTTAAGTTCACCAGTGTATTTGTTGTGT	13751	A_95_P195647	TA16163_4097
14271	168	76	755	TAGACTGAGATGTTAGTCTTCGGCAGATCTCTAAGCTAAGATTTTCACTTTTATGAGA	13753	A_95_P136272	EB439961
14273	168	78	524	CTCCAGTATACTGTTTGTATTCGCTTACTTATACAGTCAATTACCAAGTTGCCTTAGAA	13757	A_95_P151142	TA21558_4097
14276	168	81	878	GAGGAAAGAGAATGAGGAAAGAGGTTTTGGCAGTTGTCCTTTATTTTCTTTCTCAAA	13763	A_95_P206342	TA18493_4097
14277	168	82	767	TTTGTGAGGAGAGCCCTCTCGTATTTGATAAATGGCCAGCCAGAACTTGCATTGAGA	13765	A_95_P145752	EB449496
14278	168	83	0	ATGTAAAATGCTAGCTCGTGCTGCTCCTATGACATTTGAGCGCAGTCAGAGTGGTTC	13767	A_95_P313888	A_95_P313888
14280	168	85	137	GTGCTTGATTGTTAGATTTCAAGGATGGGTATGATGATACCTTTTTGAGTAATTAGCC	13771	A_95_P111517	CV020242
14282	169	2	754	CTAATATGATGAACTTTCTCCTAGGGTAGAAATCTTAGTCGGATGAATCTTTCTCCTA	13774	A_95_P119787	DV999343
14283	169	3	694	GTCGATGATGATTTGAAGCAGCTATTCAGAGGTATTGAATTACCACGTGACATGCTT	13776	A_95_P073715	FG174018
14284	169	4	438	TGCATGCCATCAAAAGTGCACCTTGAATAGAAATCACTTAATGTTTTTCGCCTCAAAA	13778	A_95_P091823	BP531510
14286	169	6	160	TTTAATCACGTTACACGATGATGATGATGAAAGTATGTTCAAACCTTTGCCAGTGGG	13782	A_95_P023446	EB445713
14287	169	7	815	GTGTTGTATGCATTAGTTAGAAGTGTGATTTTGTGTCAAACTTATCAGACAGCTTTGA	13784	A_95_P218762	DW000456
14289	169	9	470	GTGGAAGTGTTCTGCAGTTGCCTTTTCTGATCTTTCAGCTTCGCATTTATATTTATATT	13788	A_95_P198812	TA16860_4097
14291	169	11	545	AGCGCTCCTGTCTGGAATATGCTGTTCTAGATTTTGATTTACAAATTCAAGTATAGAG	13792	A_95_P203337	TA17833_4097
14297	169	17	479	TGTCAGAATTAGTATTGTAAATGCAACTGTAATAAACTCAATTCTTCTTAGCGGCCGC	13804	A_95_P266106	AM793907
14300	169	20	175	TTCTTGAACTCAGAATCGATTGTTTGAATGATGTCAATTGGACTGGGGCCTACGTATT	13810	A_95_P162737	EH621737
14301	169	21	424	AAGAGATCATAGGGATGGATCACGTCAAAATGGTGGTTATGAAGAGTTAGAAGATG	13812	A_95_P073895	BP526333
14302	169	22	640	CAAGACTTTGATATATCTAGCTGCTTCTGCTTTCTGCTGAAGTTATTGCTGATTGTTGC	13814	A_95_P163452	EH622499
14305	169	25	706	AATGATGGATGATATTCTGATGGAATTTTGAGCCGTTGGAGGTAGAATGTGTGCTAT	13820	A_95_P207402	TA18733_4097
14306	169	26	856	GTCAGTATTGAACCACAGAAACTTTCTGATCTGTTGAGATTCAATATTGGAGGATTA	13822	A_95_P228324	EB678983
14309	169	29	1384	CCCTTTTGTCCCAAACTAGTTGTGCTAACTTGAATTTGACAGTCAAAACTGTAAAATTT	13828	A_95_P198147	TA16716_4097

14314	169	34	301	TCGAAGCCAGCACTGCCTCGTGGAAAACCTCTGACCTTTAAATATACGCTATATGCAT	13838	A_95_P015626	EB444079
14316	169	36	860	GTATTCTGGTGGCCTGTACAAATCATAAGGGTTGCTCCTAAAAAATTTTCTTTCCTCTT	13842	A_95_P222577	DV999307
14317	169	37	783	TGTCATGAATTACTTGGTGGAGCCAAATGGGATGAAATGGACTTCCAACTTCTGAAA	13844	A_95_P022356	EB450549
14319	169	39	574	GCCCGTCGTCCGAATTCATGTAGATGGTATGTACATTAGCACATAAAAAATAGTACA	13848	A_95_P042796	BP130449
14320	169	40	480	GTTTAAGCTAGGGTACTTTAAGTTTCTGTTGTTAAGGTCTGGATATTGTAATTCCTCG	13849	A_95_P006061	FG635626
14323	169	43	704	TGAACCTTGAGATTGAGAAAACATCTTTATGATCTCGGCGTATGATTCAATTACCATG	13855	A_95_P118217	DV161237
14324	169	44	462	AATGACAGATTAGGTCTCAACGGATACTATGCTGGGAATGGAAATCTTACATTCCAG	13857	A_95_P281903	AM789234
14331	169	51	121	AATTTAAGGGTTGAGACATGTGTTTTAAATATGCATTGTGGTACGATGATTTGCTTTG	13871	A_95_P031086	TA19607_4097
14334	169	54	504	CAAGGGGGTTCAAAATCTACATAAGGTCATGAGTTCAATTCCCACTAGATACAAAAT	13877	A_95_P001486	BP129233
14335	169	55	683	ATTCTGGTGCTTTAGGTTCTAGATTCTGTTGTTCCACTTTTCATTCTAGATTTATGGCT	13879	A_95_P238879	AB032528
14336	169	56	874	CACCACCCGGGAAAGAAAAAGGAAGTCCTATGTATATCATCAAATTCCAAAACCACC	13881	A_95_P222872	EB439038
14339	169	59	880	CCCCTAGCTTTGAACGTTTTCATCTCTAAATGTTTTTCTCGCTTCCTCAATTGACAGAA	13887	A_95_P183602	TA13496_4097
14342	169	62	1962	CGAGCACTAGCACTTTCTTTTAAATGTAGCCTTTGCTGAGTAACTGGATAAATAAATT	13893	A_95_P186637	TA14169_4097
14343	169	63	834	TTGCGATCAGTTTACCGTCATGGTGGTACTAGAAGTGTGCTTCCTGAGTACCATTCAT	13895	A_95_P148967	TA17097_4097
14344	169	64	723	TCTGGACATGACTGTGGGCTTAACACTTTCTTTATAGTGATGACCCTTATAGTCATCTT	13897	A_95_P139282	EB680583
14352	169	72	278	GTGCTGCAAAACTGTTTTTGACTGAGTTATTTGGTTGCAACCTCTATTTTCAACAAGT	13912	A_95_P100688	BP535484
14353	169	73	437	ATTACCCTCTTCTCGAGTCCCTATATTGATCCATTGAAGCTTGAGAACGTTGTAAAGA	13914	A_95_P120037	EB427837
14354	169	74	762	GCAAGGCATCCAAAATGAAACCAAGAGTCTGAAAAAATCTCTCAAGGATGTGGTTA	13916	A_95_P240678	EB427259
14357	169	77	790	TCGCAAAGTGTGTTATGTGCGAGATAACGAGAGAAAATGTTTGTGATAAAAATTAA	13922	A_95_P117387	DV160311
14365	169	85	871	TCTTTTCATAGCAACTCTGATCCTCGTATATTAATTGATGGTGCCCAATATTTTGAACC	13938	A_95_P014481	TA16928_4097
14369	170	4	1585	AAAGACAACTTCTGTTTTCTGATTTGGAGAAATTAAATGGGTGGAGCTTTTGCATGG	13779	A_95_P202372	AJ344537
14370	170	5	211	CACAGATGTATATCTTCCACCAGTATAAATGAAGTTCTTTGCTACCTCAGCAAACTTC	13781	A_95_P133092	EB434217
14371	170	6	224	AGAAAGAGCTGGAGAAGTCAATGAAGAAGCCGGATAAGAAAGCTAATCGAGTCGC	13783	A_95_P126852	FG624146
14373	170	8	615	TAAATTAGGTGTTGATGGATGATATTAATGCTGGTATGAGCGCTGCGAGTTGCAGGT	13787	A_95_P046916	BP131521
14376	170	11	350	GGTTGCGGTATTGTGTTAGTTTGTAGATTTTGAAAACTATTGAAGTCTGTTTCCCTAA	13793	A_95_P001911	FG642183
14377	170	12	1515	ACACCTTTTAATGAGTGCTCGTGTAATTTTCTATGAGGTCACGACTCTATTTTGATTTC	13795	A_95_P176807	AJ007496
14378	170	13	783	TGATGACTTGCATCTTGCAACAATGAGCTTGGATCTAGCTGTTCTAGTATAGTAATAT	13797	A_95_P189507	DV999471
14381	170	16	721	GCTTGCTGTTTACTTGAGGAGAAGTTTGTAATCATCAACTGCTCTATCATTGTATTTCT	13803	A_95_P248702	EB440103
14382	170	17	795	CCAAATCTAGCAGTGGCTATTGTTGGATGTTTCTGATATTGAGCTATACTAAAGATTG	13805	A_95_P012911	DV159784
14386	170	21	755	AAGTGTAAACGAGGGAAAGGGATCAGGTTAACAGCAAGCTTCCGAAGATCAGAGT	13813	A_95_P258251	FG156089
14388	170	23	1295	GGTTTGAGAGCTTTTTGTTAGTCGATAAGATTGTGTTCCCATTATTTCTCTCTTGAAAA	13817	A_95_P007571	D26509
14398	170	33	827	TTTGAGACCCAAATGCTAGAATCTATCTACGCCTCACATGGTGGGAAAGCTTTATCAA	13837	A_95_P310588	FG158077
14400	170	35	156	TTTCTCCCCTACCCTATTTTGCGGAAGTAAGCAGTGGTTTTCGATAAATTATCGGGGT	13841	A_95_P065160	BP136258
14408	170	43	219	CAGCCCCTACTCCTGGCTTCATAAACTCTTTCCCAAATTTGTTTACACTTGAATTTTCA	13856	A_95_P069530	BP137409

14414	170	49	380	GTAGTATTCTGTAGTAGTCTGTGAGCTAGTGACACCAGACTCTGGGTAGCATTTTGG	13868	A_95_P144027	EB447213
14415	170	50	245	GTGTTGTGATGGAACTTTTATCATCAATCAAGGGTGTTCAGCGTGATATTGAATTTTA	13870	A_95_P131727	EB432113
14416	170	51	592	AAACTGGTGATTGTACTATGGTACTCTTTCTTATCCAGTTTAGGTCTCTCCTTTCGATT	13872	A_95_P091548	BP531408
14419	170	54	855	CAAAGTACATTATGATGGCAGACCTCTTTAGAGAGATCCTCAAAGTTTATGTGTTGTT	13878	A_95_P269926	EB428013
14424	170	59	785	AATGATGATGGAGATGACGTGATGTCTCCACCTTTTTCTCTCTTTTCTTGCCTCCGTG	13888	A_95_P195462	EH623218
14427	170	62	729	CGTGGTTCTTTATCTTTGAGAAAATATCTTTTTCTGTTTGAGTGCAGTTTCTTTGAGTG	13894	A_95_P126972	EB426380
14428	170	63	815	GATGGTCTGCTTTAGTAATCGTTATATAAATTTTTTCCTCTAGTGGAAGTGGGATTCT	13896	A_95_P012231	EB439212
14433	170	68	630	AAGAAAGTGCAGCAGCTCTGAAACCGAAGAAACGCCATTTCACGAACAAGAAGAAG	13905	A_95_P097898	TA13766_4097
14437	170	72	1465	GAGGTTGTTTCCGAAGACCCTCAGCTCATATTACAACGTTTGTAAGATCTATTTGTAT	13913	A_95_P190532	TA15036_4097
14443	170	78	316	CTCCTGATGATGTTTTGAAGCTGCTGGATCGCTTCTACAACTTGGAAATGGTGAAAC	13925	A_95_P051966	AM829948
14445	170	80	133	CGGTATGTACATGAAATGAAGCACTATTAGTCGTTGCTTAATCACTTCCCTTTTTTCA	13929	A_95_P088843	BP530241
14449	170	84	570	ACTTTCCTACTTTGTCAGATGGCTGGTTGAGTTGGTTATGTACGAGGATAGTTTCTGA	13937	A_95_P022466	TA13628_4097
14453	171	3	737	GAAACCAGTTTTTGTTCCAAAATCTGAGAGAGACACCATAGATGAGCGTGAGAAGC	13944	A_95_P204812	EB438536
14456	171	6	861	AGGTTGCATTAGTTATTCTTTAATGGTCTTCCTCTTCCCCAGCATGTAATATTTCACAT	13950	A_95_P227004	EB678186
14460	171	10	781	ATTGCTTATTAGTGGCTGAACCCATGAAAATTTTGCGTTTGGTTGATCACCAAGTCTT	13958	A_95_P177217	TA11914_4097
14463	171	13	1949	GACTGGCTTTTTATGTGAGGTACAGGATGTTTTTATGCGGTTATATCTTTGCTTAAGA	13963	A_95_P030886	TA15238_4097
14470	171	20	578	CCTTGGCTTGTGGACAGTATAACATGTGCCTTACCTAAATAGAGGCAGAATTTGTTTT	13976	A_95_P244347	FG640417
14474	171	24	25	ATACGAGCTCATTATCTAATGAGGAATCAGCAAACTTAGCAAGTGTTACTTCACTTTC	13983	A_95_P034044	BP129575
14475	171	25	302	GACGAAGAAGACTTGAGCAAGTCATGCATGCAAGGAGTTTAAAATTTTCTTTGTATA	13985	A_95_P090233	BP530869
14479	171	29	485	TGATGCAGCAGAAAAGAATCCTGTTGAGATGCCTAATAATGTCGTCCTACGAAGGCT	13993	A_95_P083280	FG164240
14480	171	30	203	GCCGAGACACAGGATTCATACAAAAGACATAGCTACATATCTTATGTTGTTGTTAATT	13995	A_95_P033294	AJ344603
14485	171	35	971	GCCCTACAAACATTTGTGTTCTAGGTTCTTGTGAACCTATAGCTTTTTGTTAGGATAA	14004	A_95_P183302	TA13426_4097
14489	171	39	557	CATCATGGGAGAAGCCATGAAAGGTTCTGGGTTACGCTTGAAAGATGAAGAATTGG	14012	A_95_P301718	FG640148
14492	171	42	737	AGAGTCTGATAACCTCGTGGACCAAGAAGAATTTCTGCTACAGGAACAGGTATAGG	14017	A_95_P148802	EB678313
14495	171	45	555	TTTTAGATCTTGTTCTCTCTTAAGAGGCATATTTGCTGGTGTAACCTCTAGATGGTGT	14023	A_95_P006126	BP528513
14498	171	48	761	CCTTTGTCTGCCATGACATTGGCTTATTGTATTCTGTAGCCATTGTTTACTCTGTACAA	14029	A_95_P264296	FG144751
14499	171	49	303	CGATATCCTTCCCTTCAAGAATTTCCCACCTATATAAATGTGAACTCATTAGTTTTGGT	14031	A_95_P093188	BP532173
14502	171	52	600	GGCGTTGCTTTCTTACTTGGTGGCTTCTTTATTCTACTCAAATATTTGGGATATTTACT	14037	A_95_P019876	TA12236_4097
14506	171	56	827	TTGATTCTACAACCAAAGCAATCCTTCAGGAAGCAGTCAAAGGAGAACTCTGGCGTT	14045	A_95_P259351	EB428843
14507	171	57	820	CCAAATATGGCCTCTGAAGACTTCATGACCAGGAACCCATTTCAGTTTCCATTTGGAG	14047	A_95_P297243	TA14721_4097
14509	171	59	572	TGACTAATGGTGCTGATGAAAGGTAGAATGGCCTGGAAGGAGCTATCATTGATATT	14051	A_95_P261961	FG641103
14510	171	60	486	TCCTGAATGGGATTTTAACATGCATGCTTTGTGGCTAAAAAGAATGGCCCTTCTCTGA	14053	A_95_P293158	FG638602
14511	171	61	728	ATGAGTGAAGCAAACAACAATGGCATGGACTATTCAACTCCCAAGTACCAGGCCTTT	14055	A_95_P221957	TA21929_4097
14512	171	62	748	AACTGATGATTTAGTGCCGCTACAGCAACTGTTGGTTGATCAGCCTAACATCCCCAA	14057	A_95_P161257	EH620008

14524	171	74	759	TGTGCTCTCAAGGATGCTCGGGGTTGGTGTATCATCCTCAAGGACAATATCTATTGA	14081	A_95_P193537	TA15694_4097
14530	171	80	447	TTAAGCTCCCGTCCCCCCTAAAAAATCAGAGTACACCACAAGGGATTATGGCAAAAG	14093	A_95_P163662	EH622753
14534	171	84	827	AATGTTCTGAACTGTGAACTGTAGATGGACATGTACCAAGTAATAACTGTTAAGTTT	14101	A_95_P289183	DV157974
14536	172	1	587	GGGTAAGGAACATCTTTCTAAGGGAGTTTTGATTTTGATGCGGACAGAAACCTAATC	13941	A_95_P047551	BP131685
14538	172	3	540	TATTTGAACCCTATATGACATGGGACCTTTTTACTCTTTTGGCTCAGTGCCTTACAGAG	13945	A_95_P073775	BP526298
14541	172	6	535	GTCAAACTCTGTTACTTTTCGGAGAATTAGGATTTGGTGCTTAGTATCTGTTATGAAA	13951	A_95_P027691	EB445484
14542	172	7	793	ACAGCTTCGCCTGATGTCATACCATGTACCTCGAAAGATATTGATATCAATTTTAGTT	13953	A_95_P198532	EB445932
14545	172	10	672	CTTTGCTGTATATTATTCACCTTTAGCATGTCAATATACACATAGTTGAAACACACGTC	13959	A_95_P304458	FG635717
14546	172	11	805	CTATAGTCCAGCTGCCCAGTTGGTGTCTGTTGGAATGATTATACATGGTCATACTCTT	13961	A_95_P120622	DW000590
14548	172	13	631	CGAATACTTGGATTATGAATCTCACAGAGGAATGAATATTTTGTAGCGAGGAAACCA	13964	A_95_P116292	DV158972
14549	172	14	846	TTTCTGGTCGTCGGTCTGGATTCTGATTTGGCGAATGACTGGATTCAAATCATCGTCG	13966	A_95_P012901	EB451168
14550	172	15	204	TAACCTTTTGTTTATATTTTTCGTGACTCTAGGTTGAGGAGAAGGGAGGTTCTGCTAA	13968	A_95_P049541	BP132189
14551	172	16	513	TTAGGGTTATTGGGTAACTAGGCTTATCTGGGAAATTTGGGAAACTAGTTTTCCTTCT	12052	A_95_P000101	FG167017
14552	172	17	475	AATCTACTCTTTTTGTAATCTAGATGTAGAATTTGTTTCCCGAAGCTGAAAGGCACAA	13971	A_95_P266481	BP533801
14554	172	19	860	AGAGTGAAACTGTTCATCCAAATTATCGATCTGATCATGAAGACGATTTGACTTTGAC	13975	A_95_P226939	FG145978
14555	172	20	1279	CGTGTGATATTGGAAAGCAGTTCAACAAATTGCTATCCGCATAATTCTTATCAGTAGT	13977	A_95_P030971	TA16020_4097
14559	172	24	788	ATTAGCTAGATTGAAGCTTAATTGGAAACTGTCCAGAAGCGTTTGGCTCGTTGTGTTT	13984	A_95_P288918	DV157727
14560	172	25	513	CAGCAGTTTTGGAATTTACAAAGATGTGGCTGTAGATGAAATCGGCTGTATTTGATT	13986	A_95_P265001	AM827696
14561	172	26	517	GGGGATATGTTGTGATTATCGTCGTGCTGGCTTGTATCACCATTATTTCTACATTTAT	13988	A_95_P001686	EH620909
14567	172	32	337	TACTTAAGGGAACCTGGAAAGAAGCAACAATGTTACATGGTTCTGATTCTTCTAATCT	13999	A_95_P069940	BP192480
14571	172	36	797	TCACATTTGTGGATTCTTGACTGGATTTCTCCTTGCTTTGTCTGCTTCACGCCCTCACA	14007	A_95_P308828	FG169612
14576	172	41	624	GCGGTGAATGTTTTAACGCATACTGCTGATGTAACTATTGATAAGTGGCAGCTTTCA	14016	A_95_P138842	EB442568
14578	172	43	1227	TAACTAGATCATCATGGATAACCAAGAACGGAGGACCAGATGTGGGGGAAATTCCT	14020	A_95_P203722	TA17915_4097
14584	172	49	741	TAATTGCTAATTGGATGATCAATATGTGCGGTGATTTGGAATGCGATGAGTTATTTA	14032	A_95_P115682	DV157996
14586	172	51	759	GCCGTTGTATCATAGGTTGTGCCGTCATGAATATGGATTTCAGGTTTTCTGGTGTTAT	14036	A_95_P181182	TA12919_4097
14587	172	52	809	ATTTGAGAAGTGTTGCGGAAGAATTTGCTCGCAAGACGAGAGTATGACTCTATGCTG	14038	A_95_P263721	FG164682
14588	172	53	427	ACACCACTTCTAAATTACATTGGTTAAAGACCTTTAATTCTGCTGTTGCTTACCCTTTC	14040	A_95_P110812	CV019923
14591	172	56	580	CTTGGAGGCTCAACAGGAATTAGGATCATCAAACTTGTAGAATTTGCTATATGTATA	14046	A_95_P122282	DW002302
14601	172	66	651	GCTTAATGCATCGGGCTGATCTTCTTGAGCCCCTTTCTTTAGTTCTCTTCATGAACAAG	14066	A_95_P105122	FG147325
14602	172	67	271	CAGTTCTATGTTGTGTTGCAGTATGACATTGAGTTGAATCTTAGTATGTTGTACACTT	14068	A_95_P005821	EH617454
14609	172	74	233	GATGCATTACTCACTGGTACCTTACAAATGATGGTATAGAGTTCCATCAAGGACTTAC	14082	A_95_P112717	CV020796
14610	172	75	1022	GATAGTAGTTCTGAAGATGATGGTGTAAAACGAGGTTCTGAAGGGAAGCACAAAAG	14084	A_95_P207922	EF051139
14613	172	78	628	GTGGATCTGTATTCGTGTTCACAGTTCCATTCTGACTTTATTTGGATAATAGATTGCAT	14090	A_95_P001341	EB678288
14614	172	79	261	GAAAGTTTGAACCCAGTCTTCTCGGTCCCTTGAGGTTGCTTGTCCTTTTTGTATTGTAG	14092	A_95_P154487	EG649607

14616	172	81	855	CATGTACTGGCTCTTATATGCTAGACATGTCCCTGTCATAATTTCAGCTTTGATCAGC	14096	A_95_P255134	FG155952
14621	173	1	446	TAAATTACTGAGGTTATTGGTTCCCCAGAGGACGTAAGATATACTAACCTACCACAT	14105	A_95_P284883	BP133207
14622	173	2	873	GTAGCCTTCCTGCATCTGATCTTTAGGAAAATCTCTTATCTATTAGTATTCTCGAAGTA	14107	A_95_P228349	EB447626
14623	173	3	1630	CATCTGTATGAATTGATCTCGTGTACTATGGCTTGCTACTAAACATGTGCAATTCTTC	14109	A_95_P119082	TA18893_4097
14624	173	4	362	GTGTCCATGAATGGTTCAGTGTATTGATGTGAGCGAGAAAGTTTCTTTTTTGGAGCG	14111	A_95_P264341	AM783661
14628	173	8	495	GCACCAGGCTGCCCTTTATAAATTTGAGCTATTATTCCCTCTTTGATATATTGCAAGA	14119	A_95_P114757	CV021742
14633	173	13	731	TGGATCGTATGTAGAGAAAACTTGCCTGCAGTTCTGCATTGAGTAATTCAGACTGAA	14128	A_95_P135402	EB438808
14637	173	17	0	CGATTTTGTAATCCCACTTACAAATGTTTTCCTTATGTTACACGGTCATTTTCACGTAG	14136	A_95_P018966	A_95_P018966
14639	173	19	445	TGTTCGAGTTCTCTCGTCGAGCTTATACCGTTGTATTTGTCTTCATGTATATTACAGAT	14140	A_95_P095768	BP533331
14641	173	21	784	TGTGAGCACCTTAAAGTTTTGATACGTTATTCGCATTGTATCTGAGCTATTCCTATTTC	14144	A_95_P009891	TA11947_4097
14647	173	27	204	GGTGAACTTTGTGCTCATAGTGAAATGAACAGTTTTTGGAAGATTGTTTATACATTG	14156	A_95_P140617	EB444512
14655	173	35	613	GGCTTCTCCAAGATCATCAAAGGTTATTGATGTATCATATTAGAAGTTTGGCTTTGAA	14172	A_95_P152887	EB683228
14662	173	42	403	TGGTGTTCACAGGTGGTATAAGAAGTGAATACAATATTGTACTTTGGTGTCTGTAGT	14186	A_95_P067970	DV160708
14665	173	45	2591	GATTCAGCCCTTTGTCGCTCCGATTCGTACGGAAAAACAAATAAATTTTACAAAAAG	14192	A_95_P021496	TC59934
14666	173	46	802	TTGCAAAACTGTGTCTTGTGTTACTTCCCGTTCTGCTTGCATCTCTGGTTGCCATTTCT	14194	A_95_P016716	EB428777
14671	173	51	968	TTCTAGTTGTGTCCCTCTTATCGTGGCAGCGTAACATAATACAAGCTTTCATGTATTG	14203	A_95_P199048	TA16908_4097
14674	173	54	16	GTGCCAATTAGTAACCAGTGTTTAGATCAACTATGGTGTTATTTTTGGGTCTTATGTT	14209	A_95_P242212	AJ719169
14678	173	58	869	GTACTCATGGAAATAAATCACTTAATGGCTGTGATGGAGTTTGCCAAATTAAATCCT	14217	A_95_P009276	EB451572
14682	173	62	383	CGGATTGCATTTGGAAAAATTATCTCAGGTTCGTTTCTCTTAACTTGTTCTTGATCAAT	14225	A_95_P093728	BP532387
14683	173	63	994	CCCACTGAATTTCCATTGACAAGAAAGCTTTTTGTTTACCAAACACAGGAAACTAGA	14227	A_95_P187397	TA14337_4097
14684	173	64	395	AATATATTGCTCGGAGGTAAAGTAATATCATGCGTGACAACTGCAGAGCTTGTTCCA	14229	A_95_P042386	BP130345
14686	173	66	805	CGGAAGTGTATTTGCATTGTTATTTATGCTGTGTATGCTGAAGAAGGTTTATCTGGA	14233	A_95_P184527	TA13715_4097
14687	173	67	673	CTGCAGCACTCGTGACCTTGCGTACATTGAGAAGTATGTGGAAAAAATTGCTATGTC	14235	A_95_P261216	FG182506
14688	173	68	826	GATTAGTAAGAGGTAGGGGTGATTTAGTATATTGATGGGTCAGTGACTGCAAAATC	14237	A_95_P284918	FG144419
14690	173	70	1557	TGTAGTGCATAAAAAGGCCAGCTACTGTGCATCTATGTTTCTATTTGAACACATATTG	14241	A_95_P188842	TA14659_4097
14691	173	71	818	CCATACTCAAACCAAGATTAAATTGATACAACTTCTAGCCTGTTTGGCCAAGCTTTTT	14243	A_95_P123542	TA13459_4097
14695	173	75	463	GCTGGCTCCTCAAATGTATGATTTTCCTGAGTTTCGAAATTTTCAGAATGTTTCGTGC	14251	A_95_P178842	TA12357_4097
14697	173	77	738	GGAATGTTTTAAACACATTTCTAACAATATCTTGCCACAACGCATTACTTCTTTTTCCG	14255	A_95_P210832	TA19480_4097
14701	173	81	412	AAGTGCAACACTAAAATTCTTGGCATAGTAAGCATGACGTAATGTAAGCCAAGGTTC	14263	A_95_P033689	AJ632906
14709	174	4	514	TTAGAGGCTCATGACTAGTGACACCAGATTCGGGCTTTATTAGTGTATCTTCGTACTA	14112	A_95_P224232	EB643437
14713	174	8	688	TGAAAGCCTTGTTGGACATTTTTAATTTTGCTTAAGTTTGCTGAAGTCAGTGCTGAAT	14120	A_95_P296518	EB677507
14716	174	11	599	TTATTTGGTGCCCAAGCTCGTGTTTTTGTAGCTTTGTTTAAATCATATAACGACGTCT	14125	A_95_P218637	TA21220_4097
14718	174	13	107	GAGGTTTTTGTAGCAGTTTTTATCCCTGTTAGAAGCTAAGGGGTACATTGTTCATTTA	14129	A_95_P032976	AF211717
14719	174	14	702	CACATGTGGAGTACTGAAAAATCTTTGATCTGGAACTCCATGAAATGAATATTGCTG	14131	A_95_P304678	FG190124

14720	174	15	513	AATGGAGATTTTATTATGATGTGACCGAACCCACAGGGTTGCCTACGTATCCCCTCTT	14133	A_95_P281098	AM835641
14722	174	17	682	CTAGTTATATAGCCTGTGTTTGTATGCTTTCATATCCAGAACATTGTCAGCGATTCATA	14137	A_95_P146292	EB450285
14723	174	18	273	GTTTTGTGAGGTTCCTCCCACAGACCTCAAGTATCCCTTTTAGTAATATTTTAAAATTT	14139	A_95_P105262	CV017381
14724	174	19	1321	GTTTGCTGTTTCTCTTATGTTCTCTGTTGTGAATAAAGATTCCGAATTCCTGTCCTAAA	14141	A_95_P005841	TA11844_4097
14726	174	21	456	TAATGTTGTTCCAATCCTGCATCCACAGAAATGAACCATTTCAGGTCTATTTGACCTG	14145	A_95_P264366	AM845282
14727	174	22	716	TCAAATTTCCTCCTCCAGCACTGCAAGTAATGCAACAACTGTTGGTTCATCGTTCACAT	14147	A_95_P127487	FG142863
14728	174	23	720	GAATGGTGAGTTTCATTTTTACTGTACAGCAGAGGGTGCCTGCCCTTATTAAGGGCT	14149	A_95_P159617	EH618005
14730	174	25	587	TGCTGTGATTGAAGAATTTGTGATTCAGATTATGATGAAATCCTGGATGTGCTATTTA	14153	A_95_P015916	EB683945
14731	174	26	823	AAGTGCTATTGGACGTGACTGGCTTAGACTTTACGCCACTACACTATCTACCCTTTGT	14155	A_95_P117347	DV160229
14732	174	27	794	TGAAAGCCTATGCACATGACATAGTATGGTGATGGTTGTTTCTCAATCTACGCGTACC	14157	A_95_P229159	FG167705
14734	174	29	760	ATCATAAGATGGTGCAAAAGTTGAATGACAAATCCTTATGGCGCCTAGCTGTGCGTG	14161	A_95_P248802	EB451550
14737	174	32	369	CTCTTGTCTTGAAATCTCTACGATAATGCATTGACAGTGTTACTGTTTATGTTTAGACA	14167	A_95_P209912	EH623749
14739	174	34	656	TATATCGAGTTCGTCCATTAAATGTGCCTGAGTCGTCTGTGAACGTACTCTATATGTG	14171	A_95_P266551	FG637949
14740	174	35	1116	GGAGGATATCAGCTGTGCTTGTCTCTCAACCTTTATGATCCATCCTGAGTTTTGGTAT	14173	A_95_P191607	TA15273_4097
14743	174	38	738	TAAAATATGAACATGGGAGGGATTTTAGCCTCTGTTAACTGGTGATTGCCCAGTTTG	14179	A_95_P211597	TA19650_4097
14744	174	39	279	GGCTGTTAATTGATGTTTGTTATTCATGGACACAGCGTGGTCTAATGTTTGGTTTTCAT	14181	A_95_P134772	EB437540
14746	174	41	580	ATACATTGTAGAGATGAATGTCTTACACGAGAAGATCAATGCAGCAGATTATTTTCCC	14185	A_95_P261296	FG639994
14748	174	43	468	GAGATGCAGATAAGTACTGTAAAATTTTGCTATCAAGGCTGTCTCATGGACATGGAT	14189	A_95_P125947	EB451857
14750	174	45	635	TTAGTGATCTCTCTCCCTCTTTTTCCAACTCTAAGTGATAGCAAATGTGGGATGTAGTA	14193	A_95_P305183	FG637455
14757	174	52	1473	TTCAGCGGGCGCTGAAAACATCGAAGAGTTGGGGAGAGTTTGTCATATTTGATTAAA	14206	A_95_P249647	U66402
14762	174	57	98	CCCCCAATTAAAATGAGCATAATGTGATGATTACTCCTTTTAACGCTCTAAAGTAAAA	14216	A_95_P132322	EB432787
14764	174	59	681	ATATGGAAGTAGAGGGTAGTTACATGTTGTGGGATAATTTCACTATAGAGCTATTTCC	14220	A_95_P145502	EB449259
14765	174	60	395	TCGTCTTACTATTGGGAAGTATAATTTCTTGGCAATAACGGGGCTGATGATATGCTTA	14222	A_95_P184017	TA13591_4097
14768	174	63	749	TTGATGTTTGAACAGCTTCTTGTTAAAATCTCGTGTACTTACCTTATATGCCACAGTGG	14228	A_95_P000721	EB678578
14780	174	75	957	GTGCAGTTCTTGTATATTCTGATTCTATGTACTCTTACACTTGTGTGGACAATGTGATA	14252	A_95_P193842	TA15758_4097
14781	174	76	705	CCTCTCGTTTTAGTGCTAACCATATATGAATCACCTAAATAGGCAGTGGATTTTGTACA	14254	A_95_P215127	TA20416_4097
14783	174	78	799	ATTCCTTGTTCTCTGTTTTTTCCTCAATCAATTACTGGTGAAATGAGTTGGGATTGTTG	14258	A_95_P133867	EB440118
14785	174	80	1325	TTTGGCCACAATGAACGAATTTGTGCTCGTCTTTGTATCTTTAAGATGCAATCAATAGA	14262	A_95_P079015	TA17519_4097
14792	175	2	352	AAACTTGAGGGGAAGTGGGGTTTATTTTGGGATGTTTTTGGTTGAATATTGGAATTG	14275	A_95_P003616	EB434108
14795	175	5	857	AATGTTTCCATGATCTGCCGAATACGGGCATGACATGGCATGGCGTTGCTGTTGTTTT	14281	A_95_P144192	EB447351
14797	175	7	414	TCAACAGCCTAATAATATGCTTTACTCTATGTCATATTTGCGCTTGGTTTAGTGACATC	14285	A_95_P001056	FS425927
14798	175	8	742	TAAAGTTTGAAGTTGACGTGAAGTTTTTGCTGCACACAAGTTGGGTTCTTGCTGCCCG	14287	A_95_P253424	EH623247
14801	175	11	452	GATTTGCAGATGCTCTGTCTCTTTCTAAAGTCATTGCTGAAGGTGTTGCTGTCGGATT	14293	A_95_P123447	DW003303
14802	175	12	773	CTGCTAAAAATGTAATCCATGTGATGTTGTCTACATAATCGATCCCGTGCGATTTCGT	14295	A_95_P244692	DV159065

14803	175	13	769	CCTTTCCGATTGTGATGCCTTTGTTTTTTATGCTCTGCCAGCTCCAATCTTCGTATCTA	14297	A_95_P014706	EB428320
14804	175	14	0	TGGAACGATACAGAGAAGATTATGGTTCTTGCGCAAGGATGGCACAAACAGTCAAG	14299	A_95_P280988	A_95_P280988
14805	175	15	430	GAGCAGGCCATGAAGAGAGATGTCAGGATGAAATACTTTCTGTAAACTACTTTTTTG	14301	A_95_P000096	EH619820
14807	175	17	258	AAGTACTTAGTTGCCAGCTGTGTTGGGTCCCCAACCGATAGCTCGGTCATAAAAAAG	14305	A_95_P129902	EB429847
14810	175	20	823	TCAGTAGACAAGGAGATCAGTTGGCCTGAGCTCAAGCCTTGTATATATAAACGGCG	14311	A_95_P190297	DV160394
14818	175	28	700	AGCTGAAGAATGTACAAATCCTCCTATTTCGTCTAATATTAATATGTGCCTTTGCGTT	14326	A_95_P029866	EB681703
14819	175	29	741	CTCAGTTTAGCTGTGGATTTGCTGAGGGAGGAAAATGTTATGCTGAGAAAGAGTGT	14328	A_95_P215057	TA20402_4097
14823	175	33	750	GGCTTTAAAATGAATAGGTTAAGTACCCAAACTTGATGATCATTTTAACCATGGTGG	14336	A_95_P130347	EB425306
14827	175	37	494	TGTCTGTATAACTCAATTAGCCAATTGATGACTCTGTAATCTGTATTGAGAGCCCTGT	14344	A_95_P308758	FG643555
14828	175	38	430	GAGCAGGCCATGAAGAGAGATGTCAGGATGAAATACTTTCTGTAAACTACTTTTTTG	14301	A_95_P000096	EH619820
14829	175	39	864	AGTTCCTGATAGTTTTGATGCTCTTATTCCTGTTGATGACAAGGATTCTCATGGGGAG	14347	A_95_P213822	EB678087
14830	175	40	848	TTCTACTCCTCCCTCAGGGTGTTTGTGCTATGATCAGCTTGTTTTGACGATCTTTGAG	14349	A_95_P253169	FG143546
14835	175	45	465	ATGAAGCCAAGTATCGTATTTCAATGTCTTCATTACATCGGATGTAATTCGCTTGGAT	14359	A_95_P215142	EH620700
14837	175	47	386	ATACTCTCTGTATCAGTATTCTTGCGTGATGGTGACGCTAATAATTTGGTTTTAATCCT	14363	A_95_P143177	EB446520
14840	175	50	81	ATGGTCTAGGTGTTGTTGAGAATGGACAGAATGTCCATTGATGAAGCAAGAAAAAA	14369	A_95_P012831	CV019646
14842	175	52	198	GATGATTTTGGTTGTCAATTAGGGTTTCAATTTCTTGTCGGTACTTGAATATTGTAAG	14373	A_95_P161847	EH620431
14843	175	53	1049	TTGTACCCTTTTATGTACTTGCTACTCTTGTACTTGGTTTATTTCAGTCAGCGCAAGCT	14375	A_95_P016471	AB044153
14847	175	57	1189	GGTAATAGGTTCGCTATTTGGTATGAATTGTTTGCATCTGTATTATTTGTTGCCTACA	14383	A_95_P194517	TA15913_4097
14852	175	62	211	TTCTCAGGACCTGTTGTCACTCTGAAAGTATTTGAAGACAATGTTTTGGTCCGTGAGT	14392	A_95_P157522	FG645304
14853	175	63	495	CTCAGATGATGGAACTTAGTCAAAGGTTGCAATCTCTTAATGAAATCCTCAGTTACAT	14394	A_95_P071790	BP525792
14856	175	66	417	CCAGCTCTTTCAAGTAGAAATTTTTGACATTGTCTTCCTTCTGGGCAAAATTTTCCAAG	14400	A_95_P143437	EB446733
14858	175	68	400	CTATCTTCCTGTCTCCCTCTGCTCATAACTTTGTCCAAGAATATGGATGCTATAATGAT	14404	A_95_P073095	BP526127
14859	175	69	333	TGAACCTCGTTACAGACTTATGGTTAGGAGGATAATGGAAGGAAATCGTCGAATGG	14406	A_95_P078715	BP527584
14863	175	73	796	ATGGTTGATGGAGGAGGTTAGATTCTGGGGAAAAATGGTTTTGGGTTCCTTTTTTCC	14414	A_95_P145567	EB449312
14864	175	74	255	CTTGTCCTTTTAGCTAGCAAGTCTCAAGGCCCATCGTTAATAGAAGCATCTAACATCC	14415	A_95_P138547	EB442291
14867	175	77	845	TTTCTAGCTGGTGTAGCCAAGTTTATTTATTAATACGCAATCTGGATAAGTTGTCTAG	14421	A_95_P188602	TA14607_4097
14868	175	78	2072	GATCAATAGGTGCGTGCTACCCAAACAAGATTAGTAGTTGAAATAGGTTTATTCTTG	14423	A_95_P196872	AJ002315
14869	175	79	580	TAGAACCGTTAGTGTTGTAATTTGACATGAATAAAACATTTATAGGGCACTCTCTAG	14425	A_95_P125452	DW005252
14871	175	81	914	TTCATTGGCACTGGTATTAGTCCTCTGGGTTGTGTGGTCTAGAGTTGTGATTTGAATG	14429	A_95_P119792	TA17553_4097
14875	175	85	1065	GAGTCTGTTGCTGGAAGAGATTTGAACTCTTCAATTTACTTGTCCCTATTTAATATCAT	14437	A_95_P203507	TA17867_4097
14877	176	2	704	TTTTGGTGCATCCTCCGGTAGTGTGTAATTCTTTTGACCTAATAAATGGCACTTGGTTT	14276	A_95_P001061	DW004427
14886	176	11	737	GTGACATATGAGATAGGTTGATTCGACCTGATAATGAAGTCAGCTTGGTCCAAAGA	14294	A_95_P204572	TA18094_4097
14887	176	12	784	TGCTATGGATATCGCAAGAGGCATGACTTATCTTCACAATGAGCCGAATATTATAAT	14296	A_95_P118632	DV162248
14889	176	14	741	CCCTTGATATCGATCCACTGTCAAAATCTACATGGTAGAAATAGTTTGTGAATAGGA	14300	A_95_P117487	DV160408

14891	176	16	788	CTTCTTCAGCCTTTTGCATGAGCTGATTTCCGACATATATTATCTTGTTCAAGTATCCT	14304	A_95_P218632	TA21219_4097
14894	176	19	660	ATAGTTTTGAGCGAAGATTGCGTCTTGGCGGTCCACTGCTGAAGGAAAATATAGCA	14310	A_95_P151212	EB681450
14900	176	25	1439	TTGCCCATTCTTTGTATGACAATGCCTTCTTGGATGAGACTAATGCATTGACATCTCTT	14322	A_95_P210637	TA19438_4097
14902	176	27	354	AAGCACTTTGTGTTGGTGCTGGTAGTGATTTACAATCATTTTGTGTTGGTGTTGGTAG	14325	A_95_P131657	EB432021
14905	176	30	161	GCACCGGGTTGTCCTTTTTTATCTGATTATGTAATTTAGATGTAGGATTGCTATGTAG	14331	A_95_P213617	TA20086_4097
14906	176	31	641	AACAAATAGTGCAGGCTATGGTTATCAGGCCACCAGTTGACAAACTTACAGTGGTGC	14333	A_95_P061110	BP135181
14918	176	43	792	GAGCGGACCTGCATCTGATTCTAAAGTCAAAGAAACAGTTCCAGCTAACTCTCATGG	14356	A_95_P138462	EB442219
14919	176	44	795	CCACAAGTCCAAACACCTTAATGATGATTGAGAATTTCCATGATAGATAAAAACTAT	14358	A_95_P128027	EB427581
14921	176	46	668	AACGTTTTGCTAAAATGATTATGAACATGCATGATACTGCAACAATTGCTCTCCTCAT	14362	A_95_P016626	TA13924_4097
14924	176	49	533	AGAAGAATGAGTCCGAAAGCAGTTCAATGTATCAAATCCTCTTTGATGTACGAAACT	14368	A_95_P260266	AM819928
14926	176	51	489	CAGAATATAGTGAAAGGATCATTCAGCAGATGATCCAATCTAATGTGAAAGTGGGAT	14372	A_95_P098478	BP534491
14930	176	55	420	AACAACAATAGAAAAACATAAAAGACATAACACAGCCGGCACCTGCCACACACGGA	14380	A_95_P097488	BP534071
14931	176	56	364	CCCTCATTCACAGTGGATAGCCTTGGATCTAAAACTATTTCTATAATGGATATGTTAT	14382	A_95_P024716	TA15752_4097
14934	176	59	658	TCTTGTGAAAAGCCACAACCACTGGTTGTTCTTTGATGATGAGAACGCTGAGATCATT	14387	A_95_P028151	EB451747
14938	176	63	862	CTTATCTGGAGCCTGCCCCATGTATTAATTTAACGATGAGAGTTGCAGTTTTCATTCC	14395	A_95_P195772	TA16190_4097
14940	176	65	711	CAAGGAAAGATATTCAGAGGTAAGTGCATATGATCCTCTGGGATTTATTCTCTGGAT	14399	A_95_P157332	EH615384
14942	176	67	915	CGGCTATTTTCCTCATTATGGCATGCCAGTTATGAATCTACCAATCTCATCATCTACCG	14403	A_95_P289988	DV161627
14947	176	72	662	ACGCTCATTTTATGTGTACCCTTACACAAGCTATTGGTGTAGCTGATGGCGTTGGTG	14413	A_95_P139552	FG156212
14949	176	74	935	GTAAAATCATGGATTATCATCAAGATTCATGATCCAAGTTATGTCTATCAGTGGCGTT	14416	A_95_P009376	TC71430
14955	176	80	550	GTAATTTTGTAAGGCGTATGTCATACCTTGAGATAATATACAGGGAATTATGTGTTTC	14428	A_95_P113312	CV021106
14956	176	81	535	ACTTCATTATGGGGTTCTGCATCACCTGTGTGGATCGAAGGGTTCATTACCAAGGAA	14430	A_95_P053771	BP133270
14957	176	82	783	ATCCTAGGACTGGGTCCCCTGCAGCTTCTAAATCAGATGATTCAAAGAGGAGAACAT	14432	A_95_P297178	EB681987
14958	176	83	461	TAATTTTTGACTCTGTAAAATTAGTGGTTTCCCAGTGTACCATATATTACACTCCCACA	14434	A_95_P124242	DW004097
14961	177	1	667	TGTTTTTCTAAAGGCTGCTGGATATCTCGATTGTGCGGTTCGAAACGTTCTTCCCCAG	14439	A_95_P137662	EB441388
14962	177	2	510	GTAGTGGTGATGGGATTGTAAAGGTATTTAGATGAACTCTTTATCCGTTTATAAGCT	14441	A_95_P029396	TA17997_4097
14963	177	3	427	CTTTAAGCGTTTGTGTTGATAAATTTGGATGCTCTAACTGGTTTGTAATGCAGTTCTC	14443	A_95_P094983	FG641634
14973	177	13	1515	TAAATGCATCTTAAGTGATAAGTTCTGACAGATCCCCAACTGCTATACCAGTGGCAA	14463	A_95_P009966	TA14306_4097
14976	177	16	976	GGTGTATTGTGGAATAGTGTTTCAGTGAAATAAAAATAAACAATATCACCTGGCTCG	14469	A_95_P010166	TA14977_4097
14979	177	19	1700	TAGAACTCATTTCATCTTACCTGTTGTCCTTGGGCATTATTGCCAATGATCCATAGTTG	14475	A_95_P257514	AB505625
14982	177	22	985	CTGCAATTCATCTCTGAAGGAAGGTTATACTGGTACTTGAATTCTTCTGTAACTATTTT	14480	A_95_P215782	TA20563_4097
14984	177	24	1800	AGAGAGCTCTTGATGCCTCGTGACAGGCCAAATATGAGAATAAAATTAGCTCTATTA	14484	A_95_P164587	AB505625
14988	177	28	627	AGAAGTCTGAGTATATATATGTATGCAGAACTTGAACTTTCAATGAAGGACTTGAGT	14492	A_95_P117622	DV160550
14989	177	29	777	GGGTGTAGCTGCAGTTTCAGTAATTTGGTTTCATTACAGTTTCATATTTGGAATCATT	14494	A_95_P253984	FG142249
14990	177	30	559	GATATTACGGATCTCCAAATATGTGCTTTTATTGAACTGGAAGTGGTAACAAAGTGT	14496	A_95_P153462	EB683726

14992	177	32	566	GTAATGGAGCGATGCACTTTCCATCGGGTTCCTTAATATCCTTGTAAGAAATAATACT	14499	A_95_P273726	EH619367
14994	177	34	550	TAGATCGCTGTATTATTGGTAAACCGGTTCCTCTCCGCTTCCACCTGTTTCCCAATAAA	14502	A_95_P142067	EB445622
14995	177	35	287	GTTTTCCATCACCACCAAATAGTGGTGCCACAATTGGCACCCTTGACTTTTTCTCCATT	14504	A_95_P125772	EB424846
14998	177	38	1429	ACCGGCACAACCATTTATATCTTCCACTCATTCTTATGATTTGTATCTTGTGTGTTGTA	14510	A_95_P031266	TA16601_4097
15000	177	40	879	GTTGTGTAGCCATTATTAACAAGTCACACTTGCAGCATTCTAATTGTATGAACTATAA	14514	A_95_P007736	DV999303
15003	177	43	2360	TGGAGAAACCAAGGACTATGTAATCTCCCCCGTCTTATTAAATGCATTTACTTTTGTT	14520	A_95_P010116	AB110952
15014	177	54	1077	TGCAGTTTGTCGATTAATATGAGTTATTCTCGGGGTAAAGGCTAACCTCAGCCGTGT	14542	A_95_P291108	TA15454_4097
15026	177	66	770	AAGAATGCTGTATTTGGTGATAGCAGTGCTTTGGCACCTGGAGGTGTTCGTATTGGT	14566	A_95_P146602	EB450673
15028	177	68	521	CCCCTTTGTCTAAATGGTTCCCTCTTGAACTTGTCTGTGTTACTTTTGACAAGATAAGT	14570	A_95_P050676	BP132455
15033	177	73	703	TTGTATAACTTAATGACCCAGACTCTCTGAGTAGCCTAGAGCTATATTGGCAATCTTT	14579	A_95_P124642	DW004426
15041	177	81	858	GAGATTCCGCTGCCCAGAAGTTCTGTTCAACATCATGATCGAATGAAGCTGCTGATT	14594	A_95_P259311	FG158261
15043	177	83	524	GCCCGACGTCTCCTCTATCTTATATTTCATTTTGTTATCTCATATATTCGAGACAAACA	14598	A_95_P153587	EB683821
15046	178	1	236	AGCCAGCTACTGTTTGCTAAAAGATGAGGTGACCAAAAGAGTGTTAAACCAACTTCA	14440	A_95_P210697	TA19451_4097
15051	178	6	681	ATATTGGAGGCATGTAAAACTTTGTAGCTTGAACCAGATGAGCTGCTTTCCAGTTTTT	14450	A_95_P115722	DV158039
15057	178	12	161	CGGTGTTTTTAGCAAGAATGAAGGGGCGCTTAATGTTTGCTTCGAAGGAGCTGATG	14462	A_95_P258921	X06134
15061	178	16	1022	TCCCATAAAATGTAAACTCGTAAGCTGTGATGAGTTAACAGGTTTGATTTGACATGT	14470	A_95_P013236	TA14283_4097
15062	178	17	845	TATCCTTGCTGCTACAGTTTGGTTGTGTACTTTCCCATCTGTAATCTCTCACTATTTTG	14472	A_95_P015496	DV158412
15064	178	19	228	TGCTTTTGTAATCAGTGTGAGACAGATCACCAAGGCCTTTTGTTGGTGGGCAATGTT	14476	A_95_P181665	TA13036_4097
15066	178	21	390	GCTCTGTCCATTAGCTTCACATATGTTTCTCTGTTTTTGCATTGGATTTTGAGATTTAC	14479	A_95_P089328	BP530456
15069	178	24	771	AGCTTCAATTTGACTACCAATATTTTTCCTGTTGGTCCTTTACTTGCAATGGGCAGTCT	14485	A_95_P304668	FG148050
15074	178	29	1029	CACCTCTACTGGAAAGGTAATTGGTCTTTCTTGAGAATCTTGACAGGTTGCACTGTG	14495	A_95_P196232	TA16295_4097
15076	178	31	399	AAGAGGCTACAAATCTTTGTTTAATTGTGTTGTTTGCATTTGGCATGTTTTGAAGACT	14498	A_95_P282128	AM784687
15078	178	33	512	TCAGTCCCGTCTTTGTACAGTTGTATTTCTATTAAAGGTCTGTAGACAGTTATGTATA	14501	A_95_P106632	CV017986
15080	178	35	679	AGCGAAGAAAATGGAAATATTGAAATAGCTTCTCCAAGCACTGGAAGTCAGGCCCC	14505	A_95_P218232	TA21126_4097
15087	178	42	478	GTTCATGAAGTAGACATGGATGCGTACAGAAAGCCAGCTAAGTACTTATTGTGAATT	14519	A_95_P279153	AM830119
15089	178	44	905	TATGGGCAATACCAGAGAAAGCTAGTCCATCTTTGTATGGACTCCCAACCTTTCTCTG	14523	A_95_P296638	EB678894
15094	178	49	664	AGATTGAAAAACTGTGTCCTGGACTTCGGTCTGACATTCAGGGAAACCAAGCACAG	14533	A_95_P066735	BP136675
15096	178	51	535	AGTAGTTGAAGTTGGAACCAAGAGAACAAAGAGGCATGGATTTTTCTCGGCTCGGA	14537	A_95_P307668	FG644332
15097	178	52	578	TCAGCTTTGTTTGTTAAGCATAGTGATCTTTTTATGTGCGCCTGGTGGTCAGTGCTAG	14539	A_95_P155862	TA14797_4097
15098	178	53	907	TCGATAAAATTGACCATCTCAATCTCATTAAACCAGAACCTTCTTCCAAAGTTGGAAT	14541	A_95_P239914	X67159
15099	178	54	2231	GATGCTTCAGTGAAGATATGGTTGTAACTTGTAACCAAACAAAAGAAATGAGACTTT	14543	A_95_P033389	AJ627182
15101	178	56	829	CAGTCAAAGATAGATGCAGGCTTTGCAGTATATCCATTTTTGCCATAATTTTGGGACA	14547	A_95_P229784	DV159792
15104	178	59	618	TATTCTAACAGAAGCCATTCCAAGGGGAAGGTAATACCTTTTATGCTGGTGTATTTGT	14553	A_95_P048316	BP131874
15107	178	62	443	GTTTGAGGAGCTTTCTGGGATCTCAGGACATGGAAGTCGATAGTAAAGACCATGAT	14559	A_95_P156592	TA15919_4097

15108	178	63	717	TACTATTGCCCTTTTGTTTTCCCTTTTTGAGCGTGTATTATTCATCGTAACGGGGAAAG	14561	A_95_P157742	EH615781
15111	178	66	240	AACGCATTCACAAGTGAAAAGGAACCATGCTGTTTGTTGTCAAATAAATCACTTAATT	14567	A_95_P214477	TA20271_4097
15113	178	68	827	CTCCTACTCAATCAGCTAGCCTTTGAGTAAAGATCAGCAAGTGAGGTTATTCTTGCCT	14571	A_95_P265171	EB425594
15115	178	70	589	CATGGTATTTCCTCATCCTGTTTGGATTAAGGGGATTGTTCAGTCTCATTCTTGGAGA	14575	A_95_P158132	TA14284_4097
15117	178	72	448	TTGGATCGCGCATTTGAGTTGAGCGAAAAAACAATTTGCTTAATATTTAGTTTGGGT	14578	A_95_P125282	DW005063
15120	178	75	708	AAAGAGTTTATCAGCATTAGAAAGCCTGCTGGTCTGCTTGAGGATGGCCTTATGTCC	14583	A_95_P298073	EH616346
15125	178	80	133	TACTTCGGTGTATGTTTTTCGATTCCTACCAAGTTATGAGACCTAATAATTATGACAC	14593	A_95_P107882	CV018573
15129	178	84	503	TACGCGTATTGCCATAGCGTATTTTGTGAATTTTGGAGATTGGCAACTTTATTATTTG	14601	A_95_P125222	DW005018
15131	179	1	415	TCATGTTCATGCATGGAGGGGTTTTATCTGAAGTTATGAAATAGACATTTGCAGCGG	14604	A_95_P270916	AM824464
15135	179	5	860	GTTTAACTCCATCGCCTTTGAGGATTCGACTTGTTAAGCGTCTTAGTGGGACATTACT	14612	A_95_P118332	DV161343
15140	179	10	432	CATGTTTGTATAACTACGAATACTCCGAATTTTTCATTATCTAGCTTGTAGTCTAGCTC	14620	A_95_P133237	EB434552
15144	179	14	827	CTCTAATCCGTGTTATTTGTAATCGTTGCTGGTTCTGTGATCAGTTTGTCACTAGAGG	14628	A_95_P217232	EB679623
15146	179	16	496	ATGAGTTATATGCTTGTGGTATTTTGCCCTCCAGACTTTATGTATTACGAGTTTTTGG	14632	A_95_P003476	FG641760
15150	179	20	414	GGACGGACTGAGGACTATTTCTCAAAGTAGAATATTCCCTTCTGAAAATTTGTGTATA	14640	A_95_P003241	AJ272037
15154	179	24	548	GATCACCTAGTACCAAGTCCATTTTCTTTTTAGAATAGCACAAGCTTTCGTGTGTATAT	14648	A_95_P268796	EB445968
15155	179	25	477	GCATGGTTCTTCTTCCTGTAAATTCTTGCACTGGAATGTCCATACTCTCAACTGAAAG	14650	A_95_P131717	FG640545
15157	179	27	531	ATTCTTTATCGGATCATAAAAACCCACTTTCCGAAGATCTTTTCCTTCTCTTCGGGATC	14653	A_95_P279403	AM803568
15158	179	28	630	AAGCATTTGATAAGGCATTGAAAGGGGGTAAAGGGTTTAGCTCTGGCTGACTCGTG	14655	A_95_P045896	BP131257
15162	179	32	771	TAGTGAGCTGTCAGAAATATGTGGTGAGGGGGCTAGAATGGTTCGTGAATTGTTCC	14663	A_95_P162957	EH621945
15164	179	34	422	GTCCCTTATGGGTGATTTTTTGTGTGTATAAGAAGAGCAAACGATTGTATAAAGCGA	14667	A_95_P155642	FG642661
15167	179	37	492	TGCTAAAGAGAAGAAAACCACTGAAGACGGTGGCAAGAAGCAGTCGTCTTCTCCTA	14673	A_95_P131762	EB432151
15170	179	40	405	AAGAGCTCTGGCGTCACATCCAATGAAAGCCAATAAGAAGGGTATTGGAGAGAACA	14679	A_95_P102637	CV016117
15171	179	41	184	CGCGAAGATGATTGAGCTTTTCTTCTGTGCCCTTCTGGCTCTTCTCCATCACTTTTGTT	14681	A_95_P114937	CV507090
15172	179	42	791	TGCCAAGGCTGATAAGGCTTAAGATATTGAGTTTGTTACTTTTTTCATTGTCGTATTCT	14683	A_95_P145627	DV162568
15173	179	43	711	GCAGAATTCACAAGTACATTTACCAAGTTGATATTTATGACTGGTCGAAGAAGTGTT	14685	A_95_P128567	EB428254
15175	179	45	368	CATATAGGACCATGGCATCATCTCAATTTTGGTAGGGAGGTACATTAGTTTCTCAATA	14689	A_95_P094183	BP532593
15178	179	48	879	ATGTATATGAGTACTGAAGCTTACATCTGATGATGGTGATCTAGCATATAGCTGGAT	14694	A_95_P146062	EB449921
15181	179	51	305	TTTCAGCAGATCCAGAAACCTTTGCCAAGAACCGTGAACTCAAGGTGATCCACTGCA	14700	A_95_P106872	CV018096
15193	179	63	486	GTGCTTAATATGATCAACTCTAGCTAGTAACATTGTATGTCCTTTCTTGCTCTTCTTTG	14724	A_95_P109992	TA12099_4097
15195	179	65	436	TTAGTGATGGGTTTGTGATTGAAAAGTATGGTTATTTGATGTTTGTGCTGCCTCTTTT	14728	A_95_P195377	TA16102_4097
15196	179	66	676	CATACCTCCTTGGTTCTTTGCTGGTCTTACCTTTCTGTCACCTTTATTAATCTGGGCAA	14730	A_95_P047916	BP131776
15200	179	70	3	AGCACTGGAAGAATGCGGTGATGATCTGGATTCTGCCATCAAAAGACTAAATGAGC	14738	A_95_P150337	EB678788
15201	179	71	125	TACATTGCTTTGTACTTTCAAGATAGTAGGACGCCGAGCCCATTTAGCTGGAGAGTTT	14740	A_95_P067480	FG155271
15206	179	76	880	CAAACAAGGCGAATGACTCCACCTCTATATTGGAGTATCTTGAGTTTGTGATAGTTTA	14750	A_95_P059096	TA16369_4097

15208	179	78	207	TACTGTTATGAAAAGCCGCTGATAGTTTGTCTACAGTTTTCTTTTGCTTGATGATCTGT	14753	A_95_P100208	BP535265
15215	179	85	361	CAGAGCCAAAATGGGTAAGATATCTTAAATTGAATCTTCTGAGCCATTATGTTCAGA	14766	A_95_P147937	FG182925
15216	180	1	129	CTGATATGTTTGATCCGCGCCTACAAGCAAAGATACTTAACGTGGTCGATGTGTCCTA	14605	A_95_P141967	EB679730
15218	180	3	141	CCAAGTGAGCGGAACTAAATTTTGACTTGAAACCTTAGTCACCTAGGGATTTGATTAA	14609	A_95_P129777	TA17494_4097
15226	180	11	626	ACCATTTATTTCCGGATTTATCCCTTGTTTGAGCATTATATGTAATGGGCCTTCCCGCT	14623	A_95_P060270	BP134955
15227	180	12	823	GTAGCAGTAAGTTTCCCTGTTAAGTAGCAGTGAATTAAGTTTCCCTTGTTCTATCATAT	14625	A_95_P177842	TA12087_4097
15232	180	17	848	GGGGTTTAAGTGTGGTCAAAGGAGCTGGAACACACTTCTCACACCTCATACTTTCCTT	14635	A_95_P240199	FG164541
15233	180	18	702	GGTAATAATGCCTTTAACATTTCTTAGCTTCCCTTTGTGAGACATCATATGGTTGTCTT	14637	A_95_P028431	EB439386
15234	180	19	244	TCACAGCAAGCATGGGAAGACTCATAAAACTTCAGATTTGGGCATCAGCTGGACAA	14639	A_95_P104412	CV016999
15241	180	26	714	TGACAAGTTGGCAATGTCAAATGATGCATACTCTAATAGTGTAGGATCAACAGCTTTA	14652	A_95_P015316	DV158577
15243	180	28	545	AGCTCCCTAAACCCTCCATTGTGATAAAACATTTCTTTGTAGTGTTACACTGTAACTTA	14656	A_95_P001581	TA20683_4097
15248	180	33	796	GTGTGTGTGTTTTGTGTCGATTAGCACAAAAATATGATGTTGCTTTCCAGGTTTTCTGT	14666	A_95_P296718	EB679073
15249	180	34	743	TGTAATAGAAATAGTGCAGTTCAATGCAAACATTCGAGTTTGGTTAATGAAATGGTCA	14668	A_95_P199852	DW003387
15251	180	36	402	GTGATAGCTTTAATTCCTCTTTAGTAGCAGTGGTTTGTGTAGAGCCTGATGTCTTTAA	14672	A_95_P064470	BP136063
15255	180	40	693	CTGATGTTATTGCCTTTGATAGTTCTCAAAGAGTATATGTGTATAACAAGCACAGCTG	14680	A_95_P026761	EB445608
15256	180	41	477	GCGTAACGATAAAGTTGCTGCTATGTGATTAGAAGGTTACGAGTTCGAACTGTAGAA	14682	A_95_P093408	BP532250
15257	180	42	99	GAAAGTTTCAACAATTTAGTCTTTACTTGGAATGTCAACCTCTAGATGATTTGTACAC	14684	A_95_P127997	EB427568
15260	180	45	625	AGGTTCAACAAGCACTAGCAGCGGCAACAATAGTGAAATCACAGCTTTATGGTAGTC	14690	A_95_P139602	EB443405
15266	180	51	300	GTGATCCTTATTTTTCTTGACATTGTTGAGAAGAGAAATAAGGTTCTGCAATGTTGTT	14701	A_95_P095043	BP532990
15267	180	52	708	TGACAGTGAGCTTGTTGAATCCTTTAGTAGTGGGGATGATGATGATGATCTCTTGTA	14703	A_95_P148957	EB678562
15269	180	54	825	AGCAACAACTGACACTTTGCACTGATAGCAGTTCTGTGTAGCATTCAGAGGGAGTCTA	14707	A_95_P304738	FG162079
15270	180	55	2215	GCTGCCATTAGGGGTTACCCTTTTCATTTCTGTTGTACTGTTCTTTTGTTTGTCAATTTG	14709	A_95_P015882	AF004232
15272	180	57	1150	TTGTCCGAGTGTAGAGATTAGAGAATGCAAGTTAGGTTTTGACATGCTATATTCTCAT	14713	A_95_P193592	AF289466
15273	180	58	356	GACGAGATAGCAAGGATGATTAACAGCTGACATGGTTAATGCCATATGCTTTCTTCT	14715	A_95_P131582	EB435034
15276	180	61	592	TTGTAGTGAAGAGGGGTTTGGAACTGATTATTATGTCTTTGCTATTGTGTATTCATTCA	14721	A_95_P124357	DW004209
15278	180	63	1140	AAAGAATTGGTGCTTATTGGTTTGAATCCTACGTCGGCTAGTTTGTTGGCGATAGCTT	14725	A_95_P033954	AY220479
15284	180	69	637	TGATTTGGGTGCCAATGTCTACTTTTGCTTCTGTTCTAGCCTTGTCTGAACTGTTTCGT	14737	A_95_P101083	TA12299_4097
15285	180	70	932	CAGCTCTCGTGTGATTGATTTGATCTGCCATATGGCTTCTGTTGCTTAAGGATTTGAT	14739	A_95_P003386	M14419
15287	180	72	878	TTTGTCTATGTTTATTGGACGCTGTTGAATTGTACTGTGTATTCAGACGGCTTTTATGT	14743	A_95_P283478	Y08161
15288	180	73	834	GTTCTGATATGATTCTGGTTATGTTTGACGATGAAGCTTTTATTAGAGTAACTTGGTG	14745	A_95_P185892	TA14012_4097
15292	180	77	482	GGAACAGCTTGAAGCATCGACACATCAGGGATTAGACCAACAACTTCCTTCTTTCAAT	14752	A_95_P132062	EB432485
15294	180	79	568	CTGGGTACCTGCATGTCAAACGTATTATTCGCTCATGTTACGGTATTTTATTATTGTAT	14756	A_95_P135017	TA18968_4097
15296	180	81	673	ATCGAACTGTTCCAAATGTTTCTGGGAATTCTTGCTCTGATTGTAACCATTTGTATCTA	14759	A_95_P130972	EB431106
15301	181	1	917	TATTACAGCTTGATCGGGATCTTTATGCTTGCTTAATTTGCGAATTTGACTATGGCCT	14768	A_95_P184967	TA13809_4097

15303	181	3	526	TGGACTGGATGTGCAAAACATTCCATTGGAGAAGACAATTCGTTGGCTTTTGAACTG	14772	A_95_P063745	BP135860
15306	181	6	346	AGTATGCAGACATCTTAAACCTTTGCTTGTTATCTCACTTTGGAAGGAATGTACATCA	14778	A_95_P098348	BP534430
15309	181	9	916	GTTACATCACTTTCTTAGAGTTCTTTGTGCTGGTTGTCTCATTTTATGTACTCACTGGC	14784	A_95_P200192	TA17157_4097
15311	181	11	786	ACGTGCGCTTTCCCAATTTTTACATCCTTCAAGAATGGCTTTGATCTCAAAATACTATG	14788	A_95_P146322	EB450324
15316	181	16	1174	GGTGTATAGGTGGAAAACATCTTGAAATGCTTAAGGGACTTATGTAAATGATGTTCT	14797	A_95_P202457	TA17640_4097
15324	181	24	580	ACAAGGTGAAAGTTTTAGGTCAACATTATATTTCAGGATCTCATTCTGAGAATGTGTT	14813	A_95_P271711	EB444918
15329	181	29	959	CTGACCAAGAATTTAGCTTTTATTTGCAACTGATCTTAGTCAGTTGTTTTGTGCACTCT	14822	A_95_P183037	TA13362_4097
15330	181	30	1156	AACCTGAAAGTATAGATTCTATCTGGAATCTGAGAGGAATCCTGAACACCTCATGGC	14824	A_95_P188202	TA14518_4097
15332	181	32	287	AATCACAAACACTTGGAGGAGAATAAGCGTACGTTAAAGGACACTGAGCTTGACGA	14828	A_95_P080930	BP528131
15339	181	39	738	ATTCAACCTGTCAACCAAGCCCTTGGTCGCTTTCCAGCTTTGGAAATACATTCCATGA	14842	A_95_P145162	EB448723
15343	181	43	456	AATCTGAGTCTTTGGTCAAAGCTAAAAAGAAATTCGGGTTACTGATAATCAGGAGAC	14850	A_95_P307228	FG637951
15345	181	45	637	AAGCCTTGCCTAATTTTGAATTACCTTCCCGTGTAACTGTTGCTAGACTCTGTTTAAAG	14854	A_95_P269101	DW004055
15352	181	52	1739	CTGTCTATAGTATTTCGAGTTGCAGGGTGAATGTCTATACTTTACGAGTCATTTTCTA	14868	A_95_P026511	TA14068_4097
15361	181	61	569	TGCAATTTATGAAACTTGGAAGGACATATAGGAGTAAATGTTACAGAGATGGTGGT	14885	A_95_P088238	BP529993
15368	181	68	529	CGATGAGAGGAAAGCTAGGTTGATCGAAAGACTCAATGCTTTGAATGCTGCTGGTG	14899	A_95_P032221	BP131873
15369	181	69	470	CCTTAAACTGAGCTTTTCCATGCAATCAGCATTAGGGTTTTAAACCCTAAACTGAACT	14901	A_95_P263026	AM845812
15371	181	71	1243	TTTCTACATGAGAAGGACATTCCTGGTCATTTTCTTGATGACGAGAGGTTCGCCAAG	14905	A_95_P013501	TA18942_4097
15372	181	72	335	ATTAAAGTGTTTAGCTGATTCATTTCCAGGTCAATAGTGTCACACCTCCTTTTTTCGCC	14907	A_95_P005851	BP532771
15374	181	74	412	ACTTGCTGAAGGTCTCTGTAGCAAAGATCCAACTTTACTTAGGCATTACCCCTACATT	14911	A_95_P105147	CV017317
15377	181	77	126	TATTCGTTTCAGGTATGTTCCATACTAAATCAGTGGTTGCTTGACGTTTATGAAATGA	14916	A_95_P042011	BP130244
15379	181	79	585	GAGCATTATGTCCTTTTGTGTAACTTTCCTTAATTTGGATATTTGAAAACTTGCTCGGC	14920	A_95_P300418	FG139817
15381	181	81	651	GTTTCTCGGATCTTTGACTTTGTCAGTTGAAGGGAGACAGTAGAACCTCTTTTGCCTT	14924	A_95_P004541	FG133250
15388	182	3	721	CCATTCATGTTGGGTTGCCAAGAAGACCGAGATCTTTCAATATGTGAATATATTTATT	14773	A_95_P183382	EH620397
15394	182	9	219	TCGTAAAATGAAAGAGCATTTTGGTGTTGATCCATCAGCCATCCAAAATAATAGTGC	14785	A_95_P140627	EB444515
15400	182	15	117	ACTCTGATTCTGGTCTTAAGAAGCTTGATGAGTACCTCCTGACCCGTAGTTACATCGT	14796	A_95_P114367	CV021562
15401	182	16	776	CTTAGCTGGTTCTGTGCTATGCCATCATTTCTCTTAAACTTTTGGTCACTTGCATCTCG	14798	A_95_P291783	FG640499
15402	182	17	359	GATAAGCGTTGGTTTCGAGTTGTAATACTGCTATCTGTTTCTGCTTACATATTTGTTAT	14800	A_95_P179212	CV020529
15404	182	19	812	TAGACCTTCACTGATGGCTGAAAGTTGGGAGTGTTTCGTCTTTAAGTTATTTGTGTAA	14804	A_95_P230079	EB431969
15405	182	20	837	GAACTCTTCCATTGTGATTGTTTTTTGTATGGTGGAGTTTAAGGGACTGAATTCTTTT	14806	A_95_P206437	EB430245
15406	182	21	782	GTGCACTGTTAGTAGCTCTGGGTCTAGCAGAAGATTGGAAAAATGCTGAGAAGTTG	14808	A_95_P265626	DV999652
15408	182	23	727	GGGATTGAACTGATTGTGTTTTAGACCAAATGGAGGAGGAAAGAGGAGATAGTCG	14812	A_95_P128477	EB428179
15410	182	25	512	ATTTGAGTTTCTTTCTGTTGACAATCATGGAATTTTGCTGTTCTATTGCAAGGATGGG	14816	A_95_P124942	DW004722
15420	182	35	286	GGTTCTCTGTGGAATGGTACTGAAGTTAAAATTAAATAAAAATGAAAAGCAGATCTC	14835	A_95_P001326	EH619214
15422	182	37	109	CAGTCAAATATTTTCCTAGTTTCCAAGCACATTTTCTATCAAATTCAGAACCCGTCTGT	14839	A_95_P212062	TA19749_4097

15424	182	39	228	ATACAGCAATGCTGATTTCATTGCCTATGATTTGGCAATGGTGTTACAAACAAAACA	14843	A_95_P008231	X68604
15425	182	40	356	GAGCACCAGTAGAGTTAAATGTTTGCTGCCTTTTTTAGTCACAGATTGCTCCTTTATA	14845	A_95_P055746	BP133784
15428	182	43	758	GCATGTTTGAGTTGTTGTAGTTACGACTTCTCTGTGAAACAGTTGTGTGAATAATTTT	14851	A_95_P190312	DV162434
15430	182	45	1667	TCAAACTGTTTTGTGGCCATGAAATGACCCCTTTTTTATGGCCATGGGTTGTGTGATG	14855	A_95_P014771	TA14394_4097
15432	182	47	1645	GTGTCATCATCAATGAATGCTAATCCATTTACTACTTTGATGAGTTTAACCTGCTGAC	14859	A_95_P201422	TA17420_4097
15433	182	48	326	ATTTGTAATTTTGGTGTTTCGATCCAAGGATTGTTTCTTTGCTTTGCCCGATTGACTTG	14861	A_95_P099338	BP534892
15437	182	52	573	GCCCAGAGTCTTGGTTTGCATTATATGGACTTAAATAATCCAGGTGCTGTGTCTTTGT	14869	A_95_P062610	BP135559
15439	182	54	1220	CCTCCCTTCTCGATTTCCTCTACTATGTCCTATTAGTTGAGAGTGAATTTGGATCAATA	14872	A_95_P194367	TA15876_4097
15441	182	56	788	ACAAAACTGGGCATCAGAGCTGTTAAGATTGCCAATGGAAGTCAAGGAGGACGATG	14876	A_95_P010711	EB438558
15446	182	61	829	CCTAAGATCTTCTCATTGATGACGTGAATATGCCAACACAGACACCATCAGTCATATT	14886	A_95_P189812	TA14868_4097
15447	182	62	0	GTTGGAGCCATTTGCTTACGGTTGCACTTTTCATAGTTATTATGTTATAAGAAGTGAG	14888	A_95_P253299	A_95_P253299
15448	182	63	755	TTGTGTGAGTATAGGTTCCTTATTTTTGATACTGTGATTGATATTGGAGTCTGACCCC	14890	A_95_P199007	TA16900_4097
15449	182	64	824	ATGAATTAGCATAGTCAGGTCCTAGTTTCCGGATCAAATTTTGTTGAGTGTTATCATT	14892	A_95_P229604	DV157649
15452	182	67	806	CTGGAATTAGGTTGTTTTTTAATTTGGTGACTCTGTAGTTTGCTTTTTAAGCCTAGGTT	14898	A_95_P016926	DV998783
15455	182	70	472	AGCGGCATTTGCACTCTAGTGCACTCTTTTGTTTTGAGTGTTTCAGAACTCCATTAAA	14904	A_95_P037338	FG626433
15458	182	73	552	GTGAAAACTGATAGGATTGTTTGGTACTACTAATTGGGGGGTTGTTTATCCTTGTTTT	14910	A_95_P028161	BP130458
15459	182	74	256	CCTTCACAGGAATGAAATTCAGTAACACTCGTTCCATAAAATAAAACAACATTGGAA	14912	A_95_P212147	TA19768_4097
15461	182	76	631	CACAAACAGATTTTTCTTTTCAAGGGTACCTTTCAGATTTCACTATGGCAGAGACATA	14915	A_95_P206707	EB444599
15462	182	77	478	TTGTTGAAGGCTATGATGTGATTAAGGAAGGCTGAGGCTGATTGCGATCTGGATCT	14917	A_95_P063540	TA11676_4097
15464	182	79	765	AGCATACACCGTCGTGTATTGACGAAAGAATAGATGCAATCTATATCTCTCTTAAGT	14921	A_95_P183502	TA13472_4097
15466	182	81	455	GACCTATTCAAGTTTACATGGCATGTGCAATGTTCTATTTTGTCGAAATCACAGACTC	14925	A_95_P084350	BP528995
15470	182	85	861	ATATTTTTCTAACTGGAAAAACTGAATGTTCCACTGCTACATCATTTGCCGCCATTGC	14932	A_95_P267361	DV159872
15475	183	5	555	CTTGGTGTTACCGGAAGTTGTTGATTAATGACCAGTTAAATCCAATTTTTTCTAGTGT	14941	A_95_P203372	TA17840_4097
15478	183	8	393	TCTCTGAACCTTTAGTAGGGGATATGGTCTCTGTATAACTGGTTTTGTCAAGAAATGT	14947	A_95_P033994	AJ718012
15479	183	9	510	GCTCTCCAGAATCTGAGGTATGTAATTGCTGTGTACTTTCAAAAGCAAAATGTATGT	14949	A_95_P129607	FS388031
15480	183	10	557	TATCATAAGAGAAGAAAGCTGGCAGGTTGGATCCTAGGGTAGATTCCTGCTGTTGA	14951	A_95_P047406	BP131649
15482	183	12	803	CATGGATGGAGCATTTCAACTTTTACATGCAAGATGTACTGCAATTTTATGGATGTGT	14955	A_95_P017286	EB678991
15484	183	14	3973	GTGTTGATGAAAGGTGATGGTAAGGGTGAAATGTTTTTGCAGAATTCAGAAGAACG	14959	A_95_P018821	TA13319_4097
15486	183	16	879	CTAGGTGTAGAATTGACTAGTTCTTTTGTCTGAATAGTGGTCTGATATACTTGCTAAT	14963	A_95_P023541	TA15369_4097
15487	183	17	535	TCAGTACTGGGACTTTTGGGATTCATTATCATGTCTATAAGAATTGCCACAATAATAC	14965	A_95_P018331	TA14339_4097
15490	183	20	957	TCTGACTTGCTTTTGCTAGCTATAGTTGTAAAAGCCCTCTTAAAAATATGGTCGTTTG	14970	A_95_P220967	TA21721_4097
15497	183	27	566	CCATGGTTGGATCTTGCAATTGCTAAGTACAAATCTTATTGGTCTAGATATGTAATGT	14983	A_95_P262826	FG635943
15499	183	29	767	TCATGTATGCCTCGGCTTATTATCCATATGGTACGTTAACCGGTGTTAAAGCCTCCATT	14987	A_95_P201077	TA17347_4097
15500	183	30	453	ATGCTGCTGGTGTTCTTTATACATCAACCAAGCATAGTGACCCTTCTGATGATGTGAT	14989	A_95_P137027	FG146239

15501	183	31	692	TTCTAGTTATACTGTATTGATTCTTCATTTAGTGCGCGGGAATTACAAATGCCTGTAG	14991	A_95_P253124	FG635430
15504	183	34	514	GAGTCTTCTTGTTGATTTGTACTCTTCCATTGACATGTCTTTGTTTGTAATGCAGTAAC	14996	A_95_P003406	TA12168_4097
15513	183	43	914	TGAAGCTGATGGAAGTGCTAAATTAGGCGCTGTGGAAAAGACGTTGGGAGCATCTT	15014	A_95_P189412	TA14783_4097
15516	183	46	360	GGTTGTTATCCATGGCAGCTCAGGATTTTTGCCTAAAGTACTTAATTTGAGCTTTTTA	15020	A_95_P163117	EH622105
15520	183	50	210	TTACTGCATAGCTATTAGTTATGATGAGCAACCCTTTGTGATTATTCTGGTTTGTCCTC	15028	A_95_P090953	BP531151
15521	183	51	744	GAAAAATAGCTCGACGCCAGGATGATAAAAAGCTTAACACCTCTCATTCTTATTACTT	15030	A_95_P030351	TC74407
15523	183	53	976	CCCTTAAACTGTAATCGTTACACATAATTTTCTAAGATCAGGAGGATAGGTTGAATTC	15034	A_95_P002421	AJ291738
15525	183	55	920	GTAATGAGTCCGGAATCGTTCGATTATGTGGAAGGATTTGTGTTTGTGAATAGTGAT	15038	A_95_P220272	TA21573_4097
15531	183	61	843	GCCTATGTTGCATTGATTTGAACAGGAGCTGAGACAGCAAGAGTACCTCATCAGTTG	15049	A_95_P259501	FG147028
15538	183	68	89	GGACACAGTCACACAGGTATAACTGATGTAAAATTTAAACTCCTGATAATAAAAGGA	15062	A_95_P131202	EB431330
15547	183	77	849	GCATGGATCTCATGCTTGAGATGTAGCCATATATATATATATATTAACCGCTTGAAGT	15080	A_95_P128492	EB428190
15548	183	78	708	TTTTCAGTCAATGTGCCTGGAACTAGTGCAAAGGATGTTATGGACATGGTCCTCGTA	15082	A_95_P221062	TA21742_4097
15549	183	79	252	GTGATAACAATATGTTGAAACTATTGAACGCATGTGAGGTTGTAAATGTACTGAGTG	15084	A_95_P091203	BP531251
15551	183	81	818	ATTACAATTATGAGCTTCTATGGGATCATGGGATGTGTGCCGATACTAGCAGAGGA	15088	A_95_P012151	DV161682
15552	183	82	914	TCTCAACAAAACTGCTGTTGAAATTGACCCTGTAACTGCTTCTGAAACTGAAAAGTTT	15090	A_95_P222378	AB091430
15553	183	83	488	ATCTGAATGAAACCTTCTTTGTTGGTAATGTTGATGAAGCATCTCAACGGTTAGTCCA	15092	A_95_P080660	BP528060
15557	184	2	633	CTTTTCTGAAGAAAGCATATGGAGATAGCATGCATAAGGTGCTGCGTGTTGGCCCTG	14936	A_95_P137162	EB440885
15558	184	3	692	TCACAAGTGTTGCTTCATTTTTCGTCAGTCGAGTAGACACACTTGTCGACAAGATGCT	14938	A_95_P186217	FG157511
15560	184	5	632	TTTTCAAGGGTGCTCCTGGATGCTGCACTATGATTGGGCCTATGAATACTGAAGTTA	14942	A_95_P159372	FG161814
15561	184	6	502	GATCTCTTGATGTTTGTATTAGTCTTAGCTTCTTTCGTTTCCTCTATAGATCCAGGAAA	14944	A_95_P153247	EB683528
15567	184	12	1165	GTTGATTCTTGAGGAAAGTGATAATGGGGATGCTGCGTCGTCAGTTGTTTACTCTTT	14956	A_95_P070630	AJ299256
15568	184	13	466	TTTTGGTTTACCATACCACGTCCCATAGCGCATCCGGATCTAAACCCATAATGAACCG	14958	A_95_P159237	EH617190
15572	184	17	0	TTGGGATATGACAGTTTGGCAGCTCTACTGCTCTGAGCTAAGCTGATCTTCTTGTTTG	14966	A_95_P310248	A_95_P310248
15573	184	18	611	TCCCTTTTTCTGCTGGGAGGTGTCAAAGAACATCTAATCTATAGTTTTGTAAAGGAAC	14967	A_95_P220882	EB677573
15574	184	19	443	ATCAGCTTTATATATTATATGTATGGTGTCCCCATACCATTGACATGGGGAAATGTTG	14969	A_95_P160797	TA12063_4097
15575	184	20	174	GGGGATGTTACTGGAAATGTAGAAGATAGTGATCATCAGCAAAGTGACTTGTAATTT	14971	A_95_P013006	EB444167
15576	184	21	1692	GACTATTTGGAACATTGACCCGCCCTAAATAGTTTGGATAAAGAAAGCTTGTTGATA	14972	A_95_P182677	TA13276_4097
15578	184	23	469	AATGTAGGGGTTTGGGGTAGGGAGAAGAATTCATGGTTTCATGTATAGCAAGAAAT	14976	A_95_P050796	BP132486
15579	184	24	746	TCTGCTCAAGATTCAGGAAGGGATCATAGTGCATTGACTTCAGGGTCCTTGGATCAA	14978	A_95_P187392	EB678951
15583	184	28	579	GTAAAATGTAAATGCTAAGAAACATGTAGGAGGTAAGGTATATGTCCCCCTCCTTGT	14986	A_95_P160612	EH619290
15585	184	30	768	GGCAAAGATGAAAAGAAACCAAATGAAGGATGGGTTTGTGATGGTGAAGTTTGTTC	14990	A_95_P229424	DV160405
15586	184	31	561	AGGCTTTGCAGTGTATTTTGGTCCAGAACTTTCTCAATTCTGGATATGTAGTCGAATT	14992	A_95_P017396	EB678867
15587	184	32	171	TTTACCATCATTCAGGGTGTTCTCCCATGAAGAGCTTTGAGGAATTCGGCAGAGAAA	14993	A_95_P104197	EH621670
15588	184	33	457	CCTGTACGTTAAGTTCAAGAAGAACCCCTGTTATTAGTCCACATAAATTTTGAAGGAA	14995	A_95_P027116	TA17677_4097

15594	184	39	630	GATTAGTTTTTGGTGTCACCTCAGACTCTGCTTTTTAGCTATAAATTTTGTTGACAGC	15007	A_95_P028391	EH622574
15595	184	40	770	ACTATGACTGGTCTGACCTTGCAGATAATGGGAAGTTAAAGGATTTAACAGTGGTAG	15009	A_95_P268276	DW000395
15597	184	42	1038	CGGTGGTTGATCTGAAACTTCCCATGATTTGAACCTAGTTTCTATATAGAAATATTTT	15013	A_95_P220357	TA21590_4097
15598	184	43	834	AGTCTACAGAAACTGGGGTGCAACGCCGAGCTTATAGTTGATGAATTTGGTGAGAA	15015	A_95_P151202	EB681442
15599	184	44	597	TGTACAACACCCTTTGAAGCATATTGTTGTTAATCCTTCTCCTTTGTTGTAACAATGGG	15017	A_95_P293393	FG640186
15601	184	46	516	CCGTCTGTAATTCTTGTAAAATCTGTGTATCCTCTTACATGTATAGCAGATTGGTGAA	15021	A_95_P121682	DW001791
15603	184	48	855	TCTCGTGATCCCTCCTCTCATTTCATGACTCGATATGAAAGCAATGATCTGGAGGTGT	15025	A_95_P230134	FG141642
15605	184	50	761	GATTCATTAGATTAGTGCAGCTGGTGTAATCTGAGTGTTATATCTGGAAATAGAGTA	15029	A_95_P253769	DV999561
15606	184	51	659	GATACTTGATGATTGTATTGACTACCAGCAGTTTTGGTGAGTTTGAAGTGATCAACTG	15031	A_95_P266956	DV157573
15610	184	55	709	AGTTTTTACCTGCTCCGGCATTTTGCACTAGAAAGGATGTGTTCAATTATAATGGTTT	15039	A_95_P195302	TA16086_4097
15611	184	56	1225	ATGAATGTAAGAGCAGATGCAGGATAAAGATGTGAGGAAGTATAAACAACCTTAAC	15041	A_95_P185732	TA13978_4097
15615	184	60	695	CTTTTGACGTGATACAAGCACACCATGCATATCCTCTCTTTTTGTCAGCATAGTTCTTT	15048	A_95_P096718	EB429106
15621	184	66	111	GGATCAAGAAGTTGAATCTCTTATTGTTCCGACGAAATGCTCTAAATTACGGAATCTT	15059	A_95_P133082	EB434152
15625	184	70	703	TTGAATAATGCACCTTGTGAAGAATTAAGTCCATCCATGTACACTTGATATTGGTGAA	15067	A_95_P304993	FG637399
15626	184	71	524	GCTAGGATAGAATAATATTGACGTATCTAGACCAAGGGATGTACCTTGTATGAAATG	15069	A_95_P066645	BP136653
15630	184	75	1415	CTGATGGACCTTGGCTCTAGTGCTATATTCTTTTACTTACAACTATGTGGGTATAAAT	15077	A_95_P208452	TA18972_4097
15631	184	76	610	GTTCTGCTAGTTGTCAGGGTTTATGTTAGTATGTGAATACAAATCAAGGGATGAATG	15079	A_95_P159592	EB678380
15632	184	77	765	CAGTTGACGACAGTTGATTTTCTTTCCTGCTAGATTAAAGTTTACCTTTACTCTTGTAC	15081	A_95_P120177	DV999934
15633	184	78	669	GTAGGGGTATGGTTTTTCATTTATCGTTAGATCAAGTGTTATCTGTTTCTTACTTACCG	15083	A_95_P026026	EH623982
15636	184	81	286	CTCTTGCTTGGACATATCGTAGACAAAATTTATTGCGTGAAATAGTGGGCTACCGTG	15089	A_95_P089928	BP530726
15637	184	82	398	ACCTCTTATTTCTGTTCGTCTTGAGAAGTTATGTGCCATGTTGTGTACATTTTGAGTG	15091	A_95_P057486	BP134225
15639	184	84	689	TCTGCCATACCTGAACTTTCAGTTTAGGGTTTGATGGAGCAAACATGTCTTCGAAGC	15095	A_95_P017271	EB683455
15640	184	85	414	TCCCCAGCCCACTTGAACAATTTGAAATAATCTCATTGATTCCTGACGAAAATAGGAA	15097	A_95_P057446	BP134217
15641	185	1	224	TTTTTCTTTTGAACAATAGTCCCAATAGAATAGTTGACCTGTTCAAGTTCTGTTGCCCT	15098	A_95_P099813	BP535076
15642	185	2	849	GAGTTCATTGGTTTTTATGAAATGCTGGTTGTTGAACCTCTTTTTGGCAATATAAGCA	15100	A_95_P223897	EB677784
15644	185	4	226	CTCTCTTGAGGCACTAAATGTTGATCTATTTATGATTATGTTCGTCGATTTTGCGAGA	15104	A_95_P004456	EH619941
15645	185	5	0	TGAACATCAGCTGGAAATCAGCACTGAACTTCTTCCTACCCATGGACACGATCTTCAA	15106	A_95_P316883	A_95_P316883
15646	185	6	381	GATATACACTTCGATTGTAGCATAACTAAGATGTTTCTACTCTTTCAAAGTTCTTCACG	15108	A_95_P094973	BP532960
15647	185	7	977	AGCTCCCAGCTTATGTAATACAATGCTTGCTGCATCATTATTCAATTACGTGTAGCTT	15110	A_95_P197912	TA16666_4097
15648	185	8	811	CTACAGTATCTTTTTGGTTATTCTCACTGAACAATTTAACGATTGGCATGTCAATCAGT	15112	A_95_P199947	EB444224
15652	185	12	544	CGCATATGGTCCATTGTACTCAGGTGTTTACTTGACCTACTTAATAGTCATTTGAAGT	15120	A_95_P134007	EB435774
15657	185	17	467	TGATTACAGATCTTACTGGTTTGCCAATGTCCAATGCATCTTTACTAGATGAAGGGAC	15130	A_95_P121002	DW000972
15661	185	21	473	AACTTTTCTGTTGCTCCAAAGCTCCCCTTCTCACCCCTTAAATATGAGTTCAGTTAAAA	15138	A_95_P158357	EH616350
15665	185	25	889	TTTTCCTGTTGCTTCTGATTATTCAGGTTTATGTCCAGTTACTTGAGTCAGTGTGCATT	15146	A_95_P229759	EB425050

15666	185	26	431	ATTATAACGACTGGTTAGGCCGTCTGTTTGTTGAAAATGAGAATCATGGCTGATTGT	15148	A_95_P090048	BP530780
15671	185	31	488	TGATGTTTCTATGCCATACAATACCTGTATCCAGTAGCTCATAGAACATGTGACAAAG	15157	A_95_P183572	TA13490_4097
15674	185	34	482	TGGTTCACGGCAACCACTAACTTTTGCGGAGACCTGTATTTTTATTAAAAAATCCGTT	15163	A_95_P253399	TC53947
15678	185	38	4589	AAATGCTGTTCCACCTCCTTTGGCATATGCACTGGGAAGGAAACTTAAGGAAGCTGT	15170	A_95_P032611	AY567977
15682	185	42	69	GTCTTTTAAGCTTGCAGCTTTGATTTTGTTTGGATGTGTATTTTCTTTTGTTGGGGAG	15178	A_95_P130222	EB430267
15683	185	43	311	GAAAGCAATTCAGCATAACAACAAGATATTGAAGGATCTCAAAGAAAGACTTTTGCT	15180	A_95_P107097	CV018206
15686	185	46	586	TCCATTACAAGTATGGATAGGAAACGAACAGGAGGCCCCCTTTATTTTCTTTCAGG	15186	A_95_P167106	EH664113
15690	185	50	669	GAGCAATAGCGACTTAGTAAGCAGAAGAGTTAACAACTGCAAGAGATTTCACATAA	15194	A_95_P116442	DV159154
15698	185	58	501	GTCCTGTTTCTAATTGTGTTGGATATCCTTGAGCCTTAAAAGATAAAAAATGCACACC	15210	A_95_P160887	EH619582
15703	185	63	0	ATACCATTCAAGGCGAATCGAAGCTTGCCAGCTACTTGACTCCTAGAATTGACGATC	15220	A_95_P315588	A_95_P315588
15704	185	64	701	CTTATTCATGGAGCTTCAGCAGCAGTTTCCAGTTGTGCTTGGAAATCACATTTTATTC	15222	A_95_P202752	TA17702_4097
15705	185	65	848	AGTAAACATGCATTCTGTGCTTTGTCAGACTGCCCATAATCACAGCTTGCTACAGCAG	15224	A_95_P268606	FG146677
15706	185	66	1679	GATCAATGAGTAATACCAACCAACTTTTGCTTCTATGTTCAAAACTTGTCTCTCTTTCA	15226	A_95_P206042	TA18420_4097
15713	185	73	433	AATTGCAGAGTCAAGCTGCTGAGCAGTTCAAGCTCCTAATTTGAGCAAGGTTATATC	15240	A_95_P103462	DV158664
15721	185	81	151	CTTTGTGGATCTGTATTTACGAAGTTATCTGGACCTTATCTGCACTTTAGATTTACACG	15255	A_95_P104052	CV016820
15725	185	85	183	TTACATGCTGGATCACTGTGATCGAAAATGTTGCCTCTTGCCATTTGATACAATCGGG	15263	A_95_P108377	CV018809
15727	186	2	319	TGAGTTGGCTCTCCAGTTCAGAATACAAAAGAAGTCCTTCATTTGTGGATGTTATGA	15101	A_95_P088158	BP529976
15730	186	5	792	TACTGCATCTGTAGAACATCTGCCATTGTTCTGCATCATCCACTGCAAGTGGTGCTTC	15107	A_95_P298278	FG169769
15734	186	9	832	GAATTGTTCGCGAAGGTTGCCAAAGGGAGGTTAAGGGAAGATATAGCACGTGGCTA	15115	A_95_P245227	EB680165
15737	186	12	826	AGCAGTGGCTATTGTTGGATGTTTCTGATATTGAGCTATACTAAAGATTGTTTTCCTC	15121	A_95_P187342	TA14325_4097
15741	186	16	775	GTACTGTTTTGGATTGAATATGACTATCTGTTGATGTTGCTGATGACCCTCTGCGAAG	15129	A_95_P243947	DW004424
15743	186	18	921	ACATGTGATTTCAAGTTATAATTCCGGATGTGACATTCCGTCCATCAGCTGACTTAAC	15133	A_95_P200977	TA17326_4097
15747	186	22	496	CCAAGCGTCCCTGCCGTAGCTCATAAGTGATTTTTTAATTTCATTCTGTTGTAATCCAG	15141	A_95_P095413	BP533184
15758	186	33	213	TGAGGAGCAACCCCATTGATCTTCGGCATCAGTTTGGTGGGCTTTAGTTTATAATATA	15162	A_95_P103937	CV016764
15763	186	38	814	GGCGCTGTTAGTGGAAGAGTAGTTTACAAGAATGTAATTCATGCTCTTGCCAGTATA	15171	A_95_P011456	DV160992
15764	186	39	317	AACAATTTCCAAAGTGTAGCTTTCTATCTGTTCTCTTCTAACAACCACTAATCCGGATG	15173	A_95_P108447	CV018833
15765	186	40	131	GGATTTAGCTACATTTTGGTGCAATTTGGAACTTGATCTCGAAACCCTTTCTCAGGTT	15175	A_95_P031161	EB445761
15766	186	41	538	CATGTCCAATGCTTGGAGAGCTATGTCAATGTTTGATATTTCCTGAAAACATGATTAG	15177	A_95_P138852	EB442579
15768	186	43	840	GGTGTTATCACATGCCTGATGTGGTTATGCATGACAGTATCTTGTAAAATGTAATTCT	15181	A_95_P254424	EB434745
15770	186	45	631	GAAGCGTAGTCCGTGAAATGATGTTCTGGCTCAATTTTTTGATAAAATATATTGTGTT	15185	A_95_P219792	DW005127
15777	186	52	822	TAGTTTGTGTTTAGTTCATTTGCTTTAACCCTTTTTAGGCGGTTCCTTTGCCTTCATGG	15199	A_95_P149177	EB678878
15781	186	56	623	ACTCCTGGTCATACGCGAGGGCATATCAGTTTTTACTTCCCGAGGTCAAAGACAATTT	15207	A_95_P159382	EB449939
15782	186	57	816	ATATGGTATGGATTACTGGGGTGCTGCCACCGCATCATCTATCTGCATACACGAAAT	15209	A_95_P292303	FG169614
15784	186	59	834	TAGGCTGGAATTCCATAATCGGGATATTCTTCTTCATTGGTGCTGCATTCTTCTCTGTT	15213	A_95_P291883	EB425309

15790	186	65	663	CGCCTGACTTGAATGAAGATGGAGATGATCATACTCCTCTTTAAGTACTATGATATG	15225	A_95_P211847	FG639450
15791	186	66	582	GAGGATGGGATTTGTATTGATTTAGGGTAGGGATTTAATAAGGTTTTAGGATCTGTA	15227	A_95_P059161	BP134667
15793	186	68	711	GCTTTTACGTGCTTGATGTAGTCATCAGATTTCATGGTCCTGCTCTTTTCTTTTTCAAC	15231	A_95_P216177	DV157720
15796	186	71	431	GCCCCGTCCACTGCCCACAAAATGGAATCTAAAGATTTAGAATGATATATGTTTATCC	15237	A_95_P100138	BP535234
15798	186	73	1330	CCACAGTGAACGAAATTTGTGCTCGTCTTTGTATCTTTAAGATGCAGTCAATAGATTA	15241	A_95_P201897	TA17519_4097
15804	186	79	186	CTGTAAGCTTCGTGGCATAGTTAGCTTAATTATCTTGTAAAATTTCCTACAGGTTAGA	15252	A_95_P029596	TA18101_4097
15806	186	81	827	CAAGTGTTTACACCAGTGTTATTGGGAGCCACATAACCACAATTTTATCACTACGCTT	15256	A_95_P310293	FG172952
15810	186	85	756	CGAGAGGCTCTTAATTCTGGACTCTTTTAACATTTTCAGAGACATGAAACTTATCCTT	15264	A_95_P156627	EH614400
15812	187	2	606	CTTAAACGAGATGAATTGGATAATTTTGTAGCGGATAATGTCACAGAGCTATTTATT	15267	A_95_P244477	FG642298
15817	187	7	651	GACAAGGAGAGTAATACAAGTGTATCATAGTTTACCTGTAAAGATTGAGGTTTCTTA	15277	A_95_P122077	DW002134
15819	187	9	683	TCCAGTGGATACTGAGAAAGTTGAGAAAGCAGCAACGGAGCTTGTTAAGCCTAATC	15281	A_95_P288813	FG641302
15822	187	12	685	TTGGAGAAGTATTTGAAGCAGTTAAGTCTGTTTTTGCCCCAACTGTTGAGAAGGTTG	15287	A_95_P157352	EB425244
15823	187	13	369	TCTTTCTGAATTGTGGAATGCTCCTGCTATTTTATCACCAAAGAGGATCGGTTTCAGC	15289	A_95_P096148	BP533497
15825	187	15	239	CATGTGTTATACAAGTGTAATCAATTAATATTATCTTGACCATGGACTTGCTGTCACA	15293	A_95_P129837	EB429793
15831	187	21	312	ATTGGTTCATTCTCACGGTCCACTAGCAATCTGGTCCCCCATATGCTTCGATTGTTTAC	15305	A_95_P040271	BP129783
15834	187	24	776	TGATTTGTTCAAGCCTGTAAACAGCAGACCCATGATCATATCCCATCCGAGTTTCAGC	15311	A_95_P261086	FG158633
15841	187	31	494	GGAAGTTGTTTTCTTGCGAGTTACTGAATTATCTATCTTCTTCCAGTAGAACTAGTCTT	15325	A_95_P021326	FG638771
15842	187	32	84	AACAAGAGAAAACCATCAAACTCTCTCCCTCTCCAAAAATGGACGATTGAACCCTAG	15327	A_95_P090663	BP531050
15844	187	34	714	GACATAGGGTACCAGAGAAATCTTTATTTGAATCAACTTCGTTTTTACTCTTGTTCGTT	15331	A_95_P001046	TA14635_4097
15850	187	40	212	CTTGTTGCTAATTACTTCTCTGGAGGATTAAGGGTGATTTAGCATAATTATAACAGTC	15343	A_95_P150477	EB680558
15851	187	41	786	AAGTGGATACATCAGTAGAGATCTCAAGCAAATCATCAACTTCCAATGAGGACTCAA	15345	A_95_P115932	DV157934
15853	187	43	1608	GATAATAGCTTCCTTCCTAAGGCTGATATTCCCTATGAGGCTGGCATGATGAAGGTG	15349	A_95_P193147	AY772945
15856	187	46	861	ATGTCGATCATAGATCCTACTGGTCGAGTGCTTTCTGCCTTTTCTACTTACCAACAAA	15355	A_95_P214037	TA20175_4097
15861	187	51	1010	CTGGTTCTGGTGCTTTGTTTCTAGTAAAGCATTTCAGTTGTATTTGTGAACTGGATTT	15365	A_95_P183472	AB071967
15863	187	53	435	AGACTCTCAAGTTGTGTTAGTGGTTTGTTTTAATTATGAAGCCTCCTGCCGTTGAGTC	15369	A_95_P179162	FS416927
15866	187	56	389	ATGAGAGAAGTGTTATGAGAAAATACATGTGTATCTATTGATCTGGTGTAAACACTT	15375	A_95_P213787	TA20123_4097
15869	187	59	2409	ATTTTCATGCTTGGTCCAGGGGTCTGAAAACAGGAATGTACTATCTAAGATCACGCG	15381	A_95_P034194	Y10862
15870	187	60	538	CACGCTATATGGAAGCTCATCTGTAATTTATCCATTTCCTTTGATGTGAAGTGATTTTA	15383	A_95_P148352	TA13703_4097
15875	187	65	889	CAAGATGAAAAAGAAGATGGAAGAGAGTGGGCAGTAACTTTTCATTCGAAAGCAAC	15393	A_95_P009191	TA16947_4097
15879	187	69	711	ATCTTGTGATTATATCCCATGGGCTAGCTAGTCGTGTCTTTCTGATGAAGTGGTTCAA	15401	A_95_P301483	FG200980
15883	187	73	62	CCTCCAAATAGCGACTGAATCTTGTTCAATACTTGAATGTATGATGTCAACATGTAAT	15409	A_95_P134242	EB436358
15885	187	75	1155	TTGCGCACGTCAGTGGAAAGATAACATTATGTGGTTTTATGATGAAGAGCTCAGAGT	15413	A_95_P203227	TA17810_4097
15886	187	76	799	TTTGATACGTTATTCGCATTGTACCTGAGCTATTCCTATTTCGGTTATGCATTAGCTTT	15415	A_95_P010411	TA11948_4097
15888	187	78	303	GTGATAAGCAAGCCATGTTGTAACTTAAGCATCCTATATAAGTAGTGATACTTAGGA	15419	A_95_P107647	CV018474

15898	188	3	233	TAGAGTTGAAAGAGTTTTTGTTAAGCCAACAAGAAGCATATGAGGTTAAATTAGGG	15270	A_95_P093458	BP532277
15900	188	5	893	CAAGTGTAATTTCCTTAGTGAGCAGCACATTCTTTTATTTGTCTGTGTTTGACATGTTC	15274	A_95_P230859	DV157578
15905	188	10	853	GATGATGATTTTACACTTGAAGCGGTTCGGTTATGGAAGCCACGGAAGTACTAAACC	15284	A_95_P206027	DW001171
15906	188	11	1641	TGTGCTGATGAGCCTGAATGTTTACAAGACAACTAGGTTAATTTACAGAAGTTTTCA	15286	A_95_P183967	TA13580_4097
15910	188	15	849	AACAGGCAATTGAGTGCATCACTGCAGCTGCATAAATCAACCAACCTCATTCTCCAAG	15294	A_95_P022481	EB426400
15913	188	18	3239	AACTTTTCCTGTTTGTTGCTACTGTCCAGTAGTTGCAATCATCCTGTTTGTTGTTTGGA	15300	A_95_P039516	AB041352
15915	188	20	1079	TACTCAGTATCTGAGTTTTTGGATGTCATCCACCTGTTTGAATGTTCAGAGATCGGGT	15304	A_95_P205787	TA18365_4097
15919	188	24	509	AAAGCTGACTAGCTGAGATTCAATCAGTTTCCCCTTATAAACGTGGAATGGTGCTCA	15312	A_95_P192582	TA15483_4097
15923	188	28	227	GGACAAAGGAAAGTGAGTGTGTGAAAATTAGTTAGTACTTATTTTGCTCACTATCTT	15320	A_95_P017456	EB434785
15931	188	36	863	ACAGTTGCATGTATCATCAGCAGTTTCTTACTGTATTGTTCAGTTGTGAAAGATAAAG	15336	A_95_P298068	FG141610
15937	188	42	486	GCGCGACTTGTAAAGTATGACGTGCAAGAGTCAAATGACAAATGTGTTTATTGCTAA	15348	A_95_P210862	TA19486_4097
15938	188	43	862	TGGGCAGTTAATGCTCTGCTACTATATTAGTTGTTGGAATTTCTGGCACTTTGATTAG	15350	A_95_P288953	DV999667
15939	188	44	760	CGGATAGGCCTTAGTTCTTTCTTGGCCAGTATATGGAAATCATGTGTTTTTGCTAATT	15352	A_95_P179952	TA12623_4097
15940	188	45	662	TGCTGAAGGAACAAGAGAGCTTCTGTAAATTCACCAAGGACATTGACGAAAATTGTT	15354	A_95_P293558	FG641828
15941	188	46	670	AGGACAGACACAGGAGTCCACTTCACTTTCTTCGCACCTTCTTCTGTGAATATTTGTTT	15356	A_95_P314993	FG179505
15946	188	51	369	ATTTGCTGCTAATGCACTTTCGTGCTTTGCGGGCCCAATTAACTTCCAAAAGAAAAGG	15366	A_95_P094153	BP532584
15948	188	53	915	CCCATCTGATGTTCAATTTCATGTGTCTGGACTAATGTAATCTTCTCAATAATGTGCTT	15370	A_95_P019456	TA14455_4097
15949	188	54	739	TTTGGGACCGAGGCGTAACAGTTGTTGTGGCCTATGAATCAGCAGGTTAATAAAATT	15372	A_95_P126382	DV999635
15953	188	58	700	CCTTTAGACGACGAATAAGAATTTTTATGTGGATTTGGTTTTGTTGTGTACGTGGTTT	15380	A_95_P011161	DV160976
15955	188	60	938	TGTCGATGTTGATATTGAGAAAGCAATGCAACGTGTCCTAAAGAGACATATATCTAC	15384	A_95_P289903	DV161328
15956	188	61	765	TAGCATGTGGGGATATAAACGCTTTTTCAGGAGAACATTATTAGAAACATCAGACTA	15386	A_95_P137307	EB441033
15959	188	64	858	TCTTCTGTGGGGTTTGATATATTCATTGCCAGAGTCGATTGTTGATGCTTGGCGCCTG	15392	A_95_P231334	EB438510
15960	188	65	835	GTGCTGATTGTTAAGAGTTTGTTGTGCCATTTCTCCATCATTGTACAGATATTTCATG	15394	A_95_P181962	TA13104_4097
15964	188	69	805	ATACCAAACCAAAACCCATCATGAGGACAATCAAAAAAGAGACGATGCTGAATCTCG	15402	A_95_P120512	DW000472
15974	188	79	775	TAGCACAAACGAACGAAGCCACAGCCAATTCATTACGTAACAACTTGGAACAAGTCC	15422	A_95_P289108	DV157571
15979	188	84	469	TTACAAGTATCACTGGGCTAAGGCGGTTTCTATTATGTTGAGCTGGTCAGATGATCT	15432	A_95_P278698	AM819186
15980	188	85	869	CGACAGAAATAAAGAGTTGAACTAGTCTGTATTATGGTTATTTAAGCACTGTAGCATT	15434	A_95_P291128	DW002773
15984	189	4	689	GGTTGGATTTTATGCCTATAGAAATGAGGCAGCCACCACCAGATATCCTGTACAGAA	15441	A_95_P244312	FG193046
15986	189	6	944	CTTCACAAACAAATGGCAATATGTGGTGATTTTGGCCGTGTGTTTGAAATTGGTCCC	15445	A_95_P007936	DV161215
15990	189	10	807	ATTCTGGCTATATTCTTTTCTGTGTCTTTCTATGATGAATGAAATGTTTCCCTTGCCCT	15453	A_95_P177087	TA11873_4097
15991	189	11	294	GCTTATAGTTTACCTAGAAACGACGATGACGATGATGATGATGAGTTACCTGGTGTA	15455	A_95_P155718	EG650227
15993	189	13	631	CATATTCCAGTGTTTCATCATTGTAACCCCATACTGGGAATTCCTCTTGATTATCATTA	15459	A_95_P118042	DV161054
16003	189	23	190	ATGTGATTGCAAGATCAGTGGCTATGCAGACGCTGCTCAGCACCTGAAATATTCACA	15478	A_95_P162862	EH617829
16004	189	24	771	ATGGGTGCAGCACATGCAGAAAATGAACATTTCATTTATGATATAACCTCGAAGGTG	15480	A_95_P150332	EB680417

16007	189	27	750	ATTGTTTTTCTGGTTGAGCATTAAGCCACTATAAAGAAACCTGACTATCTGCAGTTTT	15485	A_95_P187427	TA14344_4097
16008	189	28	377	CGATAGTTCGTGTGCTATGGATTCTTTGTATGATGTGGATCTCATCTCTGACACTGTA	15487	A_95_P082130	BP528439
16010	189	30	1462	GTATGCTCCCTTTACACTAAAGGGAACATATCTGAACTTCAATTTTCTGGTAATATAA	15491	A_95_P206957	TA18634_4097
16012	189	32	231	ACATCTGAGTAGTGTTTTTGCCCTAATGGCACTGAATTGAGATTCTGATATCCGTTTT	15495	A_95_P003306	TA13593_4097
16014	189	34	441	TCAACCAAGTGTCTCAGCTGCTGACATTGAAAAACATGAGAAATGGTTTTCGGAATT	15499	A_95_P067115	BP136776
16021	189	41	853	GAGTTGACCTTACTGAATCAGCAACCCAAAAGTTTGAACAGTTTGATACTTCAGTGG	15513	A_95_P215027	EB444165
16023	189	43	293	TAGCACTTGTCTCGCAAAGATTGATGCTTTGTTAACTGCTAATGACTGTATTATATTT	15517	A_95_P130742	AM840689
16025	189	45	666	ATTGTTGTGTTTGCGTTGAGGACGATTGCGGCTTATAAGTACCAATGGGTGGCAAAT	15521	A_95_P147627	EB452143
16026	189	46	695	CAGATTTTCAGACTAGTTTCATGTTCTCTTTTGCTGTAATTCCATTTTGGGGATATGTG	15523	A_95_P157032	EH615086
16032	189	52	374	ACCATTGACTGCTTGCTTTAGTTCCATGCTATCTCTCATCTATTAAATAAGTTTCTTGG	15535	A_95_P161482	EH620212
16034	189	54	474	TATTGTCAATGCAATTTGCAGCCTGAAATTATGATGATGCTGACCAATTAGGTACTG	15539	A_95_P089833	BP530677
16036	189	56	105	CGATATGACCTCTACCTTTGTTTTTTGCCAAAAAAGGATTGTAGTTTTCAACGAGATG	15543	A_95_P211927	TA19721_4097
16042	189	62	553	CCAACTTAGCTGCTTTCAATGTGGAGATACCATATCTTCACATCGTGTACATTGTTTAT	15555	A_95_P195457	TA16120_4097
16045	189	65	463	TTTTCTCCTTCCTCGTCTAGGCCATTATCCCAGCAGAATGTGTAATGGGTTTATGTTCA	15561	A_95_P038881	BP129391
16046	189	66	92	GACCATAGTTGCTAAAGTTTTTAATCAATTAATAATGGCACGTCGCGACTTCCTTTCC	15563	A_95_P133437	EB434931
16047	189	67	887	ACTAGCTAGCGAGCATACTCGTATGTACACTATATAATATAATCTTGTCTGCTAGTCA	15565	A_95_P198707	DW001909
16052	189	72	845	CCGATTTGTAAGAACGATGTCTTTATTGGACTGCGTTACCTAATATGATCTTTTACGT	15575	A_95_P014321	EB679064
16053	189	73	787	CAGTGACGACAATGGATTTTTGTAAAATGTTGCGTGTATTATTTGCTCTCAACTCTGA	15577	A_95_P184197	EB442957
16054	189	74	475	GATCTCATGATCAGTAGTACTTTAGACAATCTTTTTCCCACTTCAAAAGGCATAATAG	15579	A_95_P159887	EH618420
16057	189	77	372	GTCAGAGACTAGGAGTAGCATTTTCACTTGTTCCTCACATTCTGTAAAGCTTCTCTTAT	15585	A_95_P092948	BP532063
16058	189	78	466	TGCTTCTATTTTTCTGTTAGCTGACTGAGAAGTTGTTTTCTTGCGAGTTACTAAATCAT	15587	A_95_P026796	FG638771
16061	189	81	429	CTTTGGGTTTGTTGGGATTTTTTCCCGAGATATTCTTGAGTCTATTGTACTCTAAAATT	15593	A_95_P164172	TA12815_4097
16062	189	82	816	AGATTTTTCCCGAAACTCTTGAAGCAGTCAAGATGGGGGTGGTGGTTTTGGGTGTTG	15595	A_95_P160212	TA12680_4097
16063	189	83	718	CTGCCTTATTTTAGAAAGAAGTGATGGAAATGTGGACTCATTTCAGAAACTAGCTCTT	15597	A_95_P013921	TA14478_4097
16068	190	3	256	TGCTCGACCCATTGAATTGGAAGTGCAATAGAAACGGAGATGAGAATTGTTTTGTTT	15440	A_95_P006186	TA16599_4097
16071	190	6	909	ATTGTCTACAGTTCAAGGGCGATGTGCTTGATTGACTTTGGGTTGCCAGTTGGTGAT	15446	A_95_P230579	DV161310
16073	190	8	1311	GAACCAGGAACCTTGGCATTCTTTTGCGCTTTATTGAATTGGTATAATGGAGCCTACC	15450	A_95_P190907	TA15114_4097
16077	190	12	450	TGCTTACTGAAGCATGTACTCTTGTTATCTAGGCTTCTTGTGTGTCTTCTTCTTATTGG	15458	A_95_P061225	BP135207
16078	190	13	1515	GACACTATAAGCAGAATTTTACTGCTTGACAATTGCAAGTGTGCTTACATGTTTTCAC	15460	A_95_P012691	TC42677
16082	190	17	1679	AGCTGAACTTCATTGCTCCCGCTTGTCCTCATCATCATGTTCCTCTTCTTTTAAAGATG	15467	A_95_P239414	AY640382
16083	190	18	727	TTGGAGATCCTCAATTTCCTTCCTTGTTCCATAGACTAGCCACCACCACCAAAGATGG	15469	A_95_P241815	FG142490
16086	190	21	722	TGTGTATGTTATAGGTTTGTGGTGCATGTCAGCAGTGTGCTGTCTGTAGATTCTCCA	15475	A_95_P202952	TA17751_4097
16089	190	24	464	AAGAATTTTACAGATTTTGATATCTCCTTCAAATCTAAGCCTGGTGCCATGCCTGTCTT	15481	A_95_P055631	FG153655
16090	190	25	730	ATGGAAAATTTGAAGATTTTTCCCGAAGCTCTTGAAGCAGTCAAGATGGGGGTGGT	15483	A_95_P148607	TA12679_4097

16092	190	27	226	AAGAGTACTGAACTTCTGATCAGGAAACTCCCATTCCAGAGGGCTTGTTCCGTGAAA	15486	A_95_P032306	AB001555
16097	190	32	313	GGGGCTGGGGCTTAGTTCGAGTTCTTTATTTTGTTTTCATCTTTTTCTTGTTGTCACAA	15496	A_95_P076905	BP527114
16098	190	33	750	GATTATGTTCAATGTCTAAGAGATTCTGTAGGAGCTAGTGATGGCTAATGGTTTAAT	15498	A_95_P013671	DV158020
16099	190	34	386	GGGGTAAACTGATTGTTTTTCAGGTTGTTTGGTTGATCAATATTGTAATTGCCCTTGT	15500	A_95_P093743	FG153629
16100	190	35	914	GTCTCTTCTACCATCCAATCGTTAAAGAAAGCATCCCCTACAAGTCTTAAAATCTCATT	15502	A_95_P186497	DV162062
16102	190	37	260	AGTATGTTTTTATCTCGTTGAAGCAACCTCCTTTTTTCCCCCTTGACTAGTTGACTTGA	15506	A_95_P034169	AJ718252
16103	190	38	862	CCTCAGTGGTTCAAAGCCATACTTCTTTTTGAGTTCCCTTTGTACAGTCGCAATCTTCC	15508	A_95_P136372	EB440122
16120	190	55	295	AATCTCAACAGGCTCATCTCTCAGGTTATCTCATCGTTGACCGCATCTCTGCGATTTGA	15542	A_95_P234679	AJ718154
16122	190	57	189	TCATAAACGTGTTGATGTACCAGACTTACATAGTTATCAGTGGTAACTCTTCATAGTT	15546	A_95_P132182	EB432645
16126	190	61	595	ATGTAGCCTTATCTCAGCCGCTTTTTTAGAGCATATGATATACGTAATAAAACTCTCA	15554	A_95_P143117	EB446459
16142	190	77	750	TCATCCTGTGTAGGGATTGGTGGGGATCCTTTCAATGGTACAAACTTTGTTGATTGC	15586	A_95_P146507	EB450562
16146	190	81	214	GCTGAAGAAATGGGAAATCTAGAAGTCAAGCTCTTGTTATCTTTTGTGACTTTTTTCT	15594	A_95_P130262	EB430299
16153	191	3	1199	GGGGTCTTATTCATGGTTGATTTGCTTCTTAAGTTATCTTTGCTGGTGTATCATTTATA	15606	A_95_P012466	AF352797
16154	191	4	608	CTGCACTTGGCTGCATCAATTTGTATGTTGGGATTATATTATAGTTTTGATTCTCCAA	15608	A_95_P222552	EH615961
16155	191	5	0	AGCCAATCCAAAATCAGATAACTTTGGGATGGTATCCCTCCCCAAGCAGAATATTGA	15610	A_95_P269146	A_95_P269146
16157	191	7	738	GAAAATTCTGCTCCTGGTCACTTCTCGACAGTGATATAGTGTGGAGATGATCTGTGA	15614	A_95_P273958	FG145625
16160	191	10	1589	TCACATATCATGTGTGTGATAAATTCCCACCGATAGTAAGCTGAATGTTTTTAGGCTA	15619	A_95_P139842	AM851012
16162	191	12	919	CCTGTAGATTTATATATATGAGGCTATAATGCAAATGCAAGGGTTTGGATGTTTGGA	15623	A_95_P266746	DV162641
16169	191	19	631	TACATAATTGAAGGCGAGGAGATCAATGTGTTCACAAAGGACATTCTCAAGTTTATC	15636	A_95_P299643	FG639706
16170	191	20	657	TGTGCAGTGAGGCTAAGCACCAAGTGTTAAATCTTCTTTCTACATATTGGTATAATGA	15638	A_95_P198772	TA16852_4097
16171	191	21	471	CAAACTACTGTTTCAGAAATAGCTCCAGCAATAATTGGTTCATCAGCTAAGGATTTTG	15640	A_95_P264981	AM839155
16173	191	23	855	CTAAACATTGCAAGTGGGCTGTTGTAACCTTAGCCCAAAATGGGTGCATGGCAAAAC	15643	A_95_P245652	EB424878
16175	191	25	674	CTCTGATAGATGTCGTTGCTATGTGTTACAAGTAATTTACACTGACATGGATCAGTTA	15647	A_95_P208722	TA19030_4097
16176	191	26	526	TGCTAGTGCTCTCTTAAGAGCTGTATTTGATCTGTACTTAGCATGGAATTCAATTTTC	15649	A_95_P090153	BP530831
16177	191	27	532	TTCCTTTCAGGTCAAAGCACTTATTTCTTGGCTATACTTTTCTGGTGCGTTTAGTACAG	15651	A_95_P096968	EH620311
16178	191	28	841	GATAAAGTAGCTGATGGTCCTGAAGCTGCTAAAATGATTGAGGAGGAAAAGGATGT	15653	A_95_P203857	TA17943_4097
16180	191	30	326	GTAAAAGAGATGTTAATATCCGTCTGCTTGTAGAACACATTGTTGGAAAAGAATGTT	15657	A_95_P130132	EB430135
16182	191	32	852	TTTCGGGCTTAGTTGGGATGGTTTTCCTTGTTCTATCACGTTTATTTTGCATTTAAGAT	15661	A_95_P199212	EB425297
16183	191	33	848	ATTGTCTTTGGACGCTGGTTTGGTTCTCACGGACTGCATTGTCATGTTAGCTGATAAG	15663	A_95_P269491	FG134412
16184	191	34	915	GTATGGAAAACTTATGTTTTACAGTTTTGGACTCGATGTTTCTATTTGCTTAGTGATG	15665	A_95_P246637	EB678829
16190	191	40	330	GATTTCAAGGTCTGTGCTTTAATTTTGCTACCTATTTATGACTTTTGTGTGATCATAGG	15677	A_95_P163387	EH622428
16194	191	44	506	ATGGTGCGATAAATCTGGAGAATAGCAAAGCAACTAAAAGAATGTGGTCTGATAGT	15685	A_95_P198322	FG645435
16199	191	49	611	GTCTTTAGGGAAGAAATGTTGTACTGTACTAGTATGTCTGAGTCAAAAGGTTGTAAT	15695	A_95_P208298	TA18938_4097
16200	191	50	226	TTGCCTATGTTGGAATTCACCCATCATCCTCAAATTCGAGTGGAGGTATCAATGATGG	15696	A_95_P151687	DV162331

16201	191	51	737	AGGAAAACCTTGAGATCATATCAGCAACAGTTCATGACAGGGTCCGGACACGTGTA	15698	A_95_P152052	EB682346
16205	191	55	917	TACGCAGTCGACAAAAGAATACGACTTTTCCTCTCTGACGCAGGGAATGTTCTCAAA	15705	A_95_P245982	EB679909
16206	191	56	646	GATTGTTATGGGAACTTTGTATTACGGATGTCTACGATAATTTAATGAAAGGGAAGA	15707	A_95_P210802	TA19473_4097
16207	191	57	36	CTTTATGGGAATGCTCAGAAATTTCAAGCAATCGAGACAGATAATCGCAGGCAACG	15709	A_95_P223937	AJ718543
16208	191	58	577	AATATAGTATAGGAAAATATGTCCTTCTCCTGCCCCACCAATCGATACAAGATGCAG	15711	A_95_P107727	CV018510
16209	191	59	571	GCCCGTTGAGGGTTTTCTTTCTTTTGTTGTTTTAATATAAATTCTTGTCTTGACCCAGA	15713	A_95_P026056	TA18908_4097
16210	191	60	540	GCAATCCAGTTTTGTGTTTTTCTTAGCTGTGGCTTTTGAACCATCCAATTGCTTTCAAA	15715	A_95_P026446	TA13256_4097
16219	191	69	753	GTTACTGCTCTGTTTGGGATATGCTGTGCTATCGAAAGAGAGTATGAAGAAGCGCA	15732	A_95_P019061	TA12425_4097
16221	191	71	308	ACTGGAATTTGTGTGACTTTTCAGAACTTGTGAATTTGGTGGTACATGTACCTTATTT	15735	A_95_P119002	DV162081
16224	191	74	1405	AAGGATCATCAGTGGGGTTACAGGTGCTGCAAACAAACGATCAGAAACAGCTATTG	15741	A_95_P208352	TA18950_4097
16236	192	1	517	TTCGACTGTCGATTCGAGGTTCTGGGTTTATTAACTTTCGGTGTTTCGGTCCAAGGGA	15603	A_95_P048811	BP132007
16237	192	2	494	CCCGAGAGGGTACAAGGGAGTTTTTTCCAATTAAAGGACAATCGAAACAAGATTGG	15605	A_95_P143427	EB446728
16238	192	3	291	GATGTCTGGAGCAATTGTGTATTTTGTTGACAATGAGAAACCTTGTTGTACATATCA	15607	A_95_P132192	EB432650
16241	192	6	431	CTTTGGGGGAGGCATTAGTGTCTCATATCAAGGTATCAAAAGGTGTAGAATCTTCAT	15613	A_95_P111262	CV020127
16242	192	7	872	TGGAATCATCCTTGCTGGAGCTGGTCTAGGATATTGGTTGGTGCGGAAATTTGTTAT	15615	A_95_P011401	EB428037
16252	192	17	698	GGTTCATCACCATTTTGCACCGATCTTTCTCTATCTTCAGGTGGCAGTAGCTCAGAAC	15633	A_95_P040986	BP129974
16254	192	19	445	TCTCAAAGAGGGACTCACCAGATACAGGTCAAAAGAACTTAGAGAAGAGGATGAGA	15637	A_95_P032181	BP532124
16256	192	21	247	GTATTATCAAGAGAAGGAAGGGTTTATACATTCTCCTGGGGGAATGAAACTAAACTT	15641	A_95_P136992	TA18912_4097
16260	192	25	675	ATTGGTTGTGATAAGTCAACAAATACCGCGCGAGCTTCAATTGATGTTTTATACTTCT	15648	A_95_P135977	EB439547
16262	192	27	525	TTAAGGAAAAAAGAAGTACACCAGAAGGGAGGGACATCGATGAGATATTCAAGCTT	15652	A_95_P123497	DW003354
16263	192	28	748	TGCTGTTGGGCAGACAAATGTTATGCGAAAGAAAAAGCTTAGAGCTCACCATTTTGA	15654	A_95_P230534	DV158163
16264	192	29	876	TGCTGCTGCTGTTCTGTAATTCTGTTTGGGCAAGATGACTTATTTGTAGAGTACTATC	15656	A_95_P009141	EB424984
16268	192	33	375	GAAATAGATGCGATTAAGAGTGGTTTTGGACACTTGGAGCGCTTCAGAAGACATGA	15664	A_95_P077625	BP527298
16273	192	38	789	ATCATTGCAGCCGGAGAAGGTTGCTGGAGTTATTCAGACCAACATCCTTTGGAAGTA	15674	A_95_P164762	EH624074
16274	192	39	682	CATCTGAGCTTTTGTTGGTAGATTTCTGTTGTTACTGAAATTTTAGATGATACGTTGC	15676	A_95_P288133	FG640182
16277	192	42	356	GAACATTTGAAAATCGGAATACTCCATAATTTTCAAAATATCAGTTGAGCTCGGTCCC	15682	A_95_P023876	FG622950
16278	192	43	429	TCCGTTGATGATTATGCTATGTATACCTTAATCTACATATGCCAGAACTTGCTTGTGA	15684	A_95_P042201	BP130296
16279	192	44	525	CATTACTTTGAATATGAGGACCCAAATGGAACAGTAAAAGAAATTTGGCGACAGGT	15686	A_95_P052451	BP132927
16281	192	46	782	CTTTAGCGTTGTCTCCCTTGACGAAGAACAAATCGCTGCTAATCTTGTCAAGAATGGT	15690	A_95_P192157	EB678171
16282	192	47	364	CTTGGGAAAAAGCAACTCCCATTACTCCATTTACCAACATTGATCTTGGATTGAGGTC	15692	A_95_P102827	CV016224
16285	192	50	547	GTAAATACTAAGCTTTTCAGATCTATGGTACTTCGAGAGTTTTACGAATTGGTTGCTG	15697	A_95_P119187	DV162265
16288	192	53	307	ATCGGCCACTTATAGCCAAGTCAATGAATGTATCAGGTGTAATTTTGTAGATTTAACT	15702	A_95_P195667	TA16167_4097
16289	192	54	333	ATCAATCAGCCTGCCCAAGAATCTCATTTTCAGAGGCATACTGGTTATGAGTCCAATC	15704	A_95_P058831	BP134574
16293	192	58	554	CTAGCTTTATTTTCTGTATTTGTTGTTCTCTGTGTTTGATTGAAAGGAGTTGATTGCTG	15712	A_95_P027216	DW003889

16302	192	67	1211	GCTGGCTGCTGCTGTTTACAGTAGATCAGATACTAAAGTGTTTCTCATAACAAGCTTG	15729	A_95_P249857	AM087457
16304	192	69	305	GCTTTGGAAATCATTCTACACAAAGGGGAAGGTCGGTCATGGTTATAACATTGGAA	15733	A_95_P070090	BP192518
16312	192	77	766	CTGTTCATTGTTGGGGTTTTGTTGAACCATGTCTACGGAGACTGTAACTTTTTATTTAT	3665	A_95_P000026	EB439159
16316	192	81	314	GATATGGTATTTTAAAGTGGTTAGTCCGAGTACATACATGGTTATTATGCTCCCATGG	15755	A_95_P113667	CV021246
16318	192	83	367	GCTGATTGGGAATGAGTAACATTAGTGTCTGTTAGGCTACAAGTTCTGTAAGATTAT	15759	A_95_P202212	TA17587_4097
16320	192	85	504	AATGACTTTGATAATGGTACGTTGCCATTCTATTTGATGCCGTTGAGGAGTTCTAGG	15763	A_95_P151597	EB681832
16322	193	2	576	ATGATGTTCCTACTACTTATAAAGACGCTGTCCAAAGTTCAGAAGAAGATAAGTGGA	15766	A_95_P261861	BP133763
16331	193	11	2610	GGATTATCTAACCAAACAAATGAATGAATGAAATAAAGGACGGTGGCTTTTGTGAA	15783	A_95_P258326	AB263747
16342	193	22	861	AACTTAAATGGAAGAAAACCATGTAGCTGTTGAGATTTCTGATAACATGGAGCAGTT	15804	A_95_P201212	TA17375_4097
16343	193	23	581	GAAGCTGAACTATCTAAGCTGAAAACTGAGGAGAAGATACTTAAAGATACGGTTGA	15806	A_95_P119017	DV162099
16345	193	25	443	TGGGTTCATGTTTGTACTTGGTGGTGTTGGGATTGTGATGTTGGATTTGGCAACTGA	15810	A_95_P097578	DV159157
16348	193	28	279	TTGGGTACTTGGGGCTGAAAAATGTTAGGTTTCTAAGTTTTTGCTTGTTCAATGATGT	8937	A_95_P000091	AJ717873
16350	193	30	1054	CCAAACTGCCCCTACTTATTAAAGAGCGTGGCACAATCACTATAAATAAACATTATTT	15819	A_95_P022661	TA17435_4097
16355	193	35	694	TGTCAAGTTTCCTCAGTTCTTCACCGGCAAGAGGAGGCCATGGAGAGCTTTTCTTTTA	15829	A_95_P144912	EB448466
16357	193	37	814	CGGGTAGTCGATATGTGGTCACATGATGGGAGTTTTGAAGTTTTTATTGACAATCAA	15833	A_95_P133897	EB435594
16359	193	39	179	TATATCACGCCACTGTTGCAATTTGGGATTTTTGGTTGAGCTTGGATAATTGTTTGTC	15837	A_95_P100178	BP535252
16375	193	55	682	AAAGGGGAGGATAGGAGTATGTTTCTCCTTACACCAATGAATGTATCATTTTGACCC	15868	A_95_P243967	EB681148
16376	193	56	719	ATGCTTAATGGATGTACACTTTTTTGGTGGAAGAGAAAGTGAACATTAACTGACATC	15870	A_95_P250622	FG642423
16377	193	57	1761	CTCACTGATCAGAAAATGGTCCTCTTGTAGTATCTTTCTCCATCTGTTGTAGCACCTTT	15872	A_95_P239420	AY639145
16378	193	58	529	CAATTGGCTTGGTTGATTTCTTTAGCATGATAAGAAATGTAGGAGGATTTGGGTAAA	15874	A_95_P041376	BP130076
16384	193	64	553	CCTAGTACCAAGTCCATTTTCTTTTTAGAATAGCACAAGCTTTCGTGTGTATATATTCC	15886	A_95_P202872	EB445968
16390	193	70	752	AACTGGAAGAGATACATCACCAATGACAAATTTAAGGCTCAACGACAAGCTTCTCAC	15898	A_95_P146912	EB451085
16392	193	72	1512	TTTGTGGTTATGTTATCCTTTTCCAAGTAAAGCAGTCGTGGCACTGATTTCCTTCAGGT	15902	A_95_P017296	TA12455_4097
16393	193	73	416	GGGGAAAATTGATGCAGCTGTTATTTGGTTATATATTTATTCCCCCTCCCTCGTCTGC	15904	A_95_P071550	BP525731
16394	193	74	1038	ACTTTTGCTTTTGGCGTCTGTTGGTTGTCATAAACAGAGGAAGATAGATAGTTGGTTT	15906	A_95_P199072	TA16913_4097
16395	193	75	710	GTTGTAGAGCTTTAAGTTTTGAACTAAACCTTTTGGTCGGCGAATTTGATGATGAATA	15908	A_95_P019126	TA22209_4097
16396	193	76	778	TGATGCCGCAATATTGCAGTGTATCAATTAACGATAGAAGCTTTTAGAGGATTGTAT	15910	A_95_P141427	DW000158
16400	193	80	818	TATGGGTGACTTGTCTGGATTGGTGAACAAGATACAAGACGTGGTCCCAATGGATC	15918	A_95_P267731	DV161452
16401	193	81	839	ACTCCTGCTACGGTTGTGAGTGAATTTATACTTTTCTCGCAATTTATGGTCTCGTTGTA	15920	A_95_P226514	DV999521
16404	193	84	766	TGATGTTGAAGGAGCAAATTGAGGTGCTTCTTAGAGAAAATACCATTCTCAAACGTG	15926	A_95_P218537	TA21199_4097
16408	194	3	110	ATGCCCAAGTAAATTAAGTAGCCTACTCTGTGACGCCTTTTTCTCAGTTGTTTGACTT	15768	A_95_P040231	BP129772
16409	194	4	314	TCAGAAACGGGGGGAAGAATCAGTTACTTAGGTTTGAGTATTATTAAGGTGTTTTAT	15770	A_95_P158187	EH616256
16419	194	14	2030	CTATGGAGTTTCAGTTACCTACACTTTCCACTTATGGATTGAACTAAAGATTCCATTTT	15790	A_95_P188417	TA14566_4097
16426	194	21	687	TTGCACTGCAATGTGTTAGATACCTCTAGTAAGCTATCATCAATGCTGAATAACTACT	15803	A_95_P131097	EB431220

16430	194	25	369	GGTCAAAACAGATGTGTTATGTGGTGACTGCCATGGTGCTGGATTTCTTGGTGGATC	15811	A_95_P029006	CV019724
16431	194	26	481	TAACAGCACTTGCAGTAGCTATATGATCCAAATTCACTTGGATGTACTAGCTTTGCTG	15813	A_95_P026581	TC68927
16435	194	30	443	CTTGGTTTAGGTGTAACCTCTCAGTTGTCTTAATGTAATAATTGACAAGTTACAGCTG	15820	A_95_P098208	BP534364
16436	194	31	96	TTCCTCGGGAATCTGTCGTGTTAACCTAGTGTACTTGTTATACATTAGCCATTGACTC	15822	A_95_P164047	EH623173
16438	194	33	464	TAACTATAGCATCCAGAGGGGAACGTACTTGTTGATGGTCAAAGATCTACTGTCGTT	15826	A_95_P198277	TA16744_4097
16439	194	34	448	CATGTGTCTTTGTGGTTTTTGTAAGTTGAGATGCTTATAGTCTTAGGGCTTGTGTATA	15828	A_95_P125357	DW005153
16443	194	38	891	GGGTACTCTATATAGAGACATGTTTGGAGAATTGCTATTTGTTACATCGACAATCGTA	15836	A_95_P008121	DV157767
16444	194	39	87	GAGTAGCTCTTTTCTCTTAAATTGTTCATACTTTTGTCCAACTCCATGCAAAGTCTCCT	15838	A_95_P129577	EB429568
16445	194	40	782	ATGATGGCATGAGACGCCAATGCGTGACAGAGCATGAATTCATGAGTCGCTAGAAC	15840	A_95_P234259	FG155496
16451	194	46	893	CAGCAACCCTTTTGTTACACCTCAAAAAGGAGTACAACGGCATCTTCTGGCAAGAAG	15851	A_95_P185247	TA13871_4097
16452	194	47	1921	GTTTTTTGGTAAGGATGCTTGTGAATTATGTTACCATGAGACAAAGGAAATGGTGCC	15853	A_95_P034653	AY081175
16454	194	49	503	CCGTTGCAGATCCCTCGTCCAATGCAGCCCATTGCTTCTTCAGGCTTATTTAAATTTTG	15857	A_95_P006856	AY045572
16456	194	51	542	CTGGAGCAATTGTTAATTCAAAAGATGGTTCCCTCTCGGGTGATTTCTTTGTACATCT	15861	A_95_P123192	DW003074
16458	194	53	208	GCTATTATATCCTTTCCCATGGAAGACTTTCTTGCAGTTCAAATCCGAAGAAATTTTG	15865	A_95_P027961	TA20238_4097
16459	194	54	0	CAATACAACTTTGAGGGAGGAACTGGGTTTTATTCTAGTATTCAGGCGTTTTTGATAT	15867	A_95_P020076	A_95_P020076
16465	194	60	252	AGTTGAGGCTGCTAAGCAGATTTCTGCTGGTATTCAGAGCACCCACTCATTTAAACC	15879	A_95_P112477	CV020700
16466	194	61	1616	TTGCGAGATGTCACCTGCTAAATGAGACTGGTTGGATTGCTTGAATCCCCTAGTAGT	15881	A_95_P259606	TA13128_4097
16468	194	63	424	GTGTACCCATTCAAGGCATTCAACCAGACAATTGAGATATAGTCTATGGTTTCGCTTA	15885	A_95_P305418	FG636725
16470	194	65	458	GAAGGTTCGAGCTATCAGCACTCTTATGCAATGACATGATATCTTTAAAGGAATAAA	15889	A_95_P016721	BP534468
16472	194	67	815	ATGAGGTGACTGCTGCTATCTTCCAATAGAGTAGCCAGATCAGAGTGAGTAGTCTAA	15893	A_95_P311218	FG141044
16477	194	72	749	CTGTGTTTGCATATTTTTTGATCGCCTTCTCATATGCACAAGAGATAAAGCTATAACT	15903	A_95_P025196	TA17041_4097
16480	194	75	639	GTGTTGTCCCTCCGATTTTGGTTTTGAGGAATTACCCTTATTTATATTAAACCTTCCAA	15909	A_95_P221467	TA21825_4097
16484	194	79	347	TCATAACACCATTATGTTGAGATTCCTTGGACCGATACTTCGGAAGTGTCTTGTGAGC	15917	A_95_P112667	CV020782
16492	195	2	297	ATTCAAACGTCTTATCGTGACTTGAGGTGTTTCGCGCACCTACGAAAATGATGGTTTT	15932	A_95_P042471	BP130368
16494	195	4	721	ATTGAAGACCTGAAAAGAGTTCTTAGCCATCCTCAGGCTCTTGCACAGTGTGAGAAC	15936	A_95_P135172	EB438457
16498	195	8	0	ACAAATTTGGATTATGATATTTTCATGCGAAACGGGGTTGGAGTTCTTGTTGTTTTGT	15944	A_95_P296573	A_95_P296573
16503	195	13	481	GAGCTGTAGTCAAGCCTGGAATTTGTTCTGGTGTGTTTTAGAATTTACTCAAATTTCA	15954	A_95_P105507	FG644201
16504	195	14	917	TATTTGCCTTCAGATATACACCACAAGTGCTGGTTTTCATTGCCCTCTCCTGCTTGATC	15956	A_95_P202497	TA17649_4097
16505	195	15	602	GGACAGATGTGCGTTGTTACTTGTTTCATGTTGTATTTGTTATTTACGTCTAACAGAA	15958	A_95_P122517	DW002492
16507	195	17	311	TTTTGCAAAATGGCATGGGTTCCTTGTATGGCAATTCGAGACTGAGCGCGGATTTGT	15962	A_95_P105922	CV017693
16511	195	21	386	TTGAATGAGAAATTGCCTTCACTAATTACCCAGTCAATGCATGTAAGAGGCTTTTCAC	15970	A_95_P203202	EH615570
16514	195	24	515	TTCCCCCTTTTGTTTTTACATGTGAATTGGTTTGTTTACCTATTTTATGGTGTCATCGG	15976	A_95_P097268	BP533963
16521	195	31	383	ACATGTGGTTCCTTTCTTGTAGCAAATGATGCTGCAGAGAGGACTCAGTCTCATGTC	15990	A_95_P214947	FG142908
16523	195	33	327	ACGTTGCTATTTCTTTGGTGTTGGCTTTCTTGTATACAAGAAAAACGGTTAGAATCC	15994	A_95_P211557	TA19639_4097

16527	195	37	350	CTTCTTCAGCTCTGCAGCTCCTATAATCTTTCAAGTTGTTTGAGAACAATCTGTGTGAT	16002	A_95_P053061	BP133081
16529	195	39	916	TCCCGAGATATCGTCTGTTCTGTCGGCTGTTTTAGAAAGTAATGGGACTCAATTTGAT	16006	A_95_P258581	DV162128
16532	195	42	541	GCTGGACAACTTTGGCCTTTTAGGTGAATATATATGGCTTGATGATAATATGCTGAA	16012	A_95_P197262	TA16523_4097
16535	195	45	405	GCATGAAAAAGGCCAGCCACTGTGCATTCTCTTATGTTTCTATTGAAACAGATTCTCT	16018	A_95_P188847	TA14660_4097
16537	195	47	345	CAAATTTCCTAAGACAAATGAGAACTTCCGCCTCATGTTTTGACACAAGGGCCGATTT	16021	A_95_P104337	CV016949
16538	195	48	1889	GGCAGCTGTAATTCCCCATTAAGATATTTGTATAACATAAATCTGTCAAAGTAAGGT	16023	A_95_P007411	AB063573
16539	195	49	1102	AACAGTTTGCTGGGGACAAAGAGACCGCTGGTTAAGCTTTGATGGTGTAGAAGATT	16025	A_95_P214897	TA20362_4097
16541	195	51	676	AACCTTCCCCTCGAGATAACTTGAACCCTTAACTAGAATCTCAATGGTTTCGTAGATC	16029	A_95_P127157	EB426620
16542	195	52	491	CTGATGTGACTGATGTTCTAACAGTGACTTTGATCAACGAGTTCTGCGATATTCCTCT	16031	A_95_P202617	TA17674_4097
16544	195	54	508	TCAGCACTGTAGTACAGTTCTTTCTTTCTTTCTTTCTTATGCTATGATAAGTGGAACTG	16035	A_95_P021906	TA13884_4097
16546	195	56	3032	CCTGTACAGCTTCTTGCTAATACTAGTCCATGATAATATTCAGCTTTTTTGGTTCTTTT	16039	A_95_P032426	AB071436
16549	195	59	1144	GGCAGAGAACATGCAGCCTGTTCAAGTTGATTAATGTCCTTTTACAATAATATATACT	16045	A_95_P014021	TA17144_4097
16552	195	62	1541	TTGAGCTTACAATTGTTAAAGAGAAATACCATGGATTCATAATGGAGCTGTTCCTGC	16051	A_95_P191452	TA15240_4097
16554	195	64	475	GGCTGGTTTTGAGACTATCGATGCTTACTATTTCATACATTTCGGTTCCAATTTAGAT	16055	A_95_P125062	DW004896
16556	195	66	516	GTACTCGCCAGAAAGAATAGCTATCTGTGTATGCAGAGTTTGAATGGGTTTTCAAAA	16059	A_95_P181902	TA13088_4097
16559	195	69	507	CATGAAAGTGATACTCAGGGTGGGCATATTGATGGGGTTAATTTCTTCTCTAGTGAC	16065	A_95_P160417	EH619110
16563	195	73	384	GGTCTCTTCTTTCAACATGTAGATCGAGAGACCACTCAGTGAATTTCATTAATTATTC	16073	A_95_P032391	AB032547
16564	195	74	707	TTGGGGCCGTCCGATGATCTCACTGTCGTTCGTTGACTGTTGATATTGTTAATATTCC	16075	A_95_P135002	EB438075
16569	195	79	640	AGCAAGTCCTGATATGAAGCTAAGCAAAGGACGCGCATATCATGTTGTCATTGGTCC	16085	A_95_P272046	EB447061
16570	195	80	908	TGGAAGCCATGATCTCTCGTTGTCTGTTGAAACACTGACAGAGCTAAGCAAAGTGAC	16087	A_95_P185152	EB680105
16571	195	81	458	TAAACGTCAAACATCAAGAATACTTTGCTGATAGCCCATCTGCTGGGTTAGATCCTG	16089	A_95_P105137	FG638862
16579	196	4	764	TTCTTCTTTTTGCTTTGTGTGGTCTTTTGCGGCTGTTTTGGTTGCCTCAGGGCTTTTGG	15937	A_95_P215617	TA20527_4097
16584	196	9	761	ATTGTCTAAAATAGTGGGCTTACATGAGCTTAAGCAGCAACTCCGGAAATGGGCAA	15947	A_95_P139052	EB442754
16588	196	13	803	TGAGGAAGTGGGAATGCATATGTTTTGCGTCTCCTGAAGTATCCTTCAGCAAATTAG	15955	A_95_P010486	TA15278_4097
16589	196	14	226	CAAGGCTTGTAGGTCAGGAAGTCTTTGAAGACATTGCTTATTTTGGGCTTAATTTATA	15957	A_95_P137392	EB441134
16590	196	15	837	GTACTTCCTTTCAACTAGTGATGATAATGATCCACAAACCTTGTAAATAAACTCCCTT	15959	A_95_P224882	DV999092
16596	196	21	394	GGTATTCCTCTTCTTCCTTAGTGATCTGGAAAACTATCTGAGCCAACTTATTCTGGAG	15971	A_95_P045936	BP131266
16598	196	23	822	CCAAAATGTACCTCCAATACTCTACTGAATTATTTATTACAAGATTACCTGCCGGTTTT	15975	A_95_P188017	TA14477_4097
16600	196	25	273	AAGGGAATGCAGAAATTTAACAGTGTTGACAGTGTGTTCATCCAGTCTTGTTATTTA	15979	A_95_P163057	EH622071
16601	196	26	611	TCCTCTGTTCTATCACAGAGCAAGGTCAGGAAAGAGTTTGTATTGTCATATGAAATC	15981	A_95_P189517	CN949733
16609	196	34	125	GTATGATTTTGTCCTGGATCTAATCTCCACCTAGTTGATTTCTTTGACCCGATCAAAAA	15997	A_95_P254864	FS391062
16611	196	36	366	AGGGTTTGTGTGGGTAATGATTGTAGATCGTTTTATCACCTGTTGTGGATTAGAATTT	16001	A_95_P005826	TA16418_4097
16615	196	40	875	TCCACTTCAAGTGCAACAAGAAGCTACTACGTGAATATCCACATCTGTTCAATTACAC	16009	A_95_P228314	EB450387
16618	196	43	426	GGAATAACCCATGGAGGAATTCATCAGATTCTGACACATCCTCATCCTCATCTTCTCC	16015	A_95_P115142	EB449164

16620	196	45	850	AGCACAAGTATAATGCTTTAGAGTCCATCCGTTTCCAACCTGGTTTGATTTGTATCCA	16019	A_95_P187767	TA14419_4097
16621	196	46	733	CTGTCATCATCGTCAGTATATGGCAACAGTTATATCGAGCATAGTTATCGCTCCAAAC	16020	A_95_P013061	EB439836
16622	196	47	885	GATGTGCCTTACCATATATTCTTCTTTGCAACTGTCATTGGGATCATTCCAGCTGCTTA	16022	A_95_P265311	EB440010
16623	196	48	725	TTGTCTCGAGACTTTACCTTTTGGGCTTTACCTATCACTGTCAATACTTATATGCAGTT	16024	A_95_P286268	DW000312
16630	196	55	472	CCGAGGCTTTGTCACGAGATTCTTTCTCTTGTATTTCTTTGACCTTTATTTGATGTATA	16038	A_95_P031396	EB683293
16639	196	64	1659	GCTGTCATGAATATGGATTTCAGGTTTTCTGCTTTCAATTCTTTCATTAGAAGGATAA	16056	A_95_P026331	TA12920_4097
16642	196	67	264	GGCATCATTGGACTTGAAGTACCACCTTAATCTGTAACCACAATTTTTGGACTTTAAA	16062	A_95_P033314	AJ344613
16644	196	69	49	CTCTGCGTTCATGTGGCTAGTATTTTTTCAGTTTGGCTCATTCAAACTTTATTTTTGTG	16066	A_95_P131077	EB431207
16645	196	70	761	TTCATATGGAGGTTGTTGAGCCTCAGCCTAATCGGCCTAAACTCCAACTTACCCTTGT	16068	A_95_P132017	EB432449
16646	196	71	361	GTCAAGAGGAAAGAAATGCCAATGGGCAATCTGATGGATCTTCAATGGTTACTTGG	16070	A_95_P095788	BP533342
16647	196	72	430	TTCCATAGTTGGCAATGTAGCTGCTCAGGTGACTGTTCAGAAGTTTATTTGTTTAATT	16072	A_95_P287493	FG633763
16651	196	76	831	TAGACTACATAGTGAGGTTGGTTTGTAATGAACAATGACTGGTGATGCACAATGTTT	16080	A_95_P012666	TC44437
16652	196	77	933	AATCTTATGCGACTTTTTGTTACTAGAATTATGGGGATGTTTTGACTCGTATGTCAAC	16082	A_95_P191952	TA15349_4097
16655	196	80	480	TCTCTTTGTGGCAACTTGCTTTATGCTGGAATGGGTTCTAGTGCTGCAAGAGAAGCC	16088	A_95_P041171	BP130024
16657	196	82	391	CTAGGGGAAGGAAGATTAAGGTGGAAACTCTAAAACTTCTCATATTTGCTTGATTTG	16092	A_95_P026286	EB437588
16658	196	83	511	ACTGTCCCAATGTAGACTCTCCTGTCCAATGATGAATTGAAATCGAAGTTTCTGCTGT	16094	A_95_P211197	TA19558_4097
16663	197	3	835	TTCCAACTTTGCTCATGGTGTTATGTGAAGGAATGATAAGTAGACGCTGAGAGGCAA	16103	A_95_P186232	DV999956
16666	197	6	443	ATGGAAAGCAATTAACCTGTACTTTATCATCATCACCAAGTCCATCTACTTCAGCTTC	16109	A_95_P060570	BP135027
16667	197	7	606	TCAGAGGAAAATCGCATGGAGGAATGAACAATTCACTCCCTATATTCTATATTCTCA	16111	A_95_P201297	EB677527
16675	197	15	292	GTTGTTTTATCATCCCTGTGGTGAATGTACATTCGTGTATAGTGCAATTTTCACCTTCC	16127	A_95_P213562	TA20074_4097
16679	197	19	467	AACGTGGACATGCTTGATGGGGTAACAGTTGTTCGATCTGAAAAAGGGTTTAAGGT	16135	A_95_P004801	EH664411
16682	197	22	581	ATGGTGGAAATCAAGGTTATGGAGGTTCTTATCGACACGGTAGAGACTATCATCGC	16141	A_95_P140587	EB679251
16692	197	32	472	ATCTGTAGTCTTGATTAAGAAAGAACCAGGGGTTTTGAATCTTCAATGACTTGATGA	16161	A_95_P183137	TA13390_4097
16693	197	33	756	AGGTGGTATGCTAGTGTCTTGGACTTGGTTTTATTGTCTTAGAATGTTGTTTCTTGAA	16163	A_95_P246457	EB444815
16696	197	36	130	TGTTTGCTTGTTCGATTTCTACCACTATATAACCCCTCCCCAATTACCCTTTTGGACAG	16169	A_95_P241535	AJ718381
16698	197	38	902	GGCCATCTCCTTTAAACTCTCTTACTTGAATGTTGCATTTTTCCTAACTTGAGCAAAAA	16173	A_95_P214917	TA20366_4097
16700	197	40	862	AGCAGATGTGCATCGACTACATGAGCGCGAAGAAACACTTTTCTCAGTTTATACTGA	16177	A_95_P272611	FG157459
16701	197	41	404	TAACATCGAGTGGGCTCCTGATTGTTAAAACTCGAAATGTATTCCCTTATTCTCCAGG	16179	A_95_P076090	BP526891
16702	197	42	834	AGGACTCAACAGAGAGGATGACGAGTCTAGTAGTACCTGTCCCTACTATTTTAGAGC	16181	A_95_P246567	DV157934
16704	197	44	1726	GTGGTGTGGTATGATATTGTAGTAAGTTAGATCCATTTGCCTTTTGGTGTATGATTTT	16185	A_95_P034773	AY639866
16705	197	45	385	ACTTTCCCTTGTTGATCTTGTCGTCAAGAATCCCCCCTAGATTCAAGAAGAAAAACCA	16187	A_95_P162312	EH621258
16706	197	46	957	AATGTTGAATGCAACTGCGCGGGATTATATTTATATTTCATGCTGAATTTCACGTGCT	16189	A_95_P176467	Y16644
16709	197	49	824	GGACAGGCAGATAACAATCTGAAGCTTATGTTCTTACTTGTTGGATTTCTTGTGTTCC	16195	A_95_P294183	EB451619
16713	197	53	824	AATGAAAGCAGTCACCCTGAAATTGGCCAGACAGTTACGTTCTCCTGAGTTTCAGCT	16203	A_95_P264536	FG156146

16715	197	55	412	CTTACGAGTAAGCAGTAAGTTTTGACAATCCCACACCAAATTGTACCAATTTATGTAT	16206	A_95_P223007	TA22153_4097
16716	197	56	343	TTATACCAGTTTGACAAAGGGTGGCCCCTCTTTCCTAATTATTACAATGAAAAGTTTC	16208	A_95_P143222	EB446556
16717	197	57	953	GCTCAAGGATATTTGTAACCTAGCTGTTTCTGAATCTTATGTGTACGCAAATACAACT	16210	A_95_P179922	TA12617_4097
16719	197	59	652	ACTAAAGGAAATGAAGTCCAGCAAGAGGAATCAAGTGATCCAGTTATTGGGGGTGC	16214	A_95_P065540	FG194561
16723	197	63	369	AAACTATAATTGATGGGGTTGAAACAGTCGATGATGGCGGTGATTGAAGCAGCGGA	16222	A_95_P159007	FS423299
16726	197	66	964	TGTTGTAATATCATAATATGGGAATTGGATTATTATGGGAAAGTGGTTGGAGGGAA	16228	A_95_P222927	TA22137_4097
16731	197	71	816	GATTGGTGTCAGAAGTCTCATGACTACTGCAGTGACTATCATGCTTCTCTTGCGCCTA	16238	A_95_P120647	EB441655
16733	197	73	288	GGAGAAAAAGTTGTCAAATAAGTGTGTGTGTGTCCCATGGCTGTTAATGACAAA	16242	A_95_P091403	BP531339
16736	197	76	792	GCTGAAACTATCTTTGTCATCATCTGTTGTTCTTTTTGCATGTGCTTAATGCCATTAAT	16248	A_95_P268776	DW002989
16739	197	79	804	ACAATGGGTGGGATGGCTGTGAATGGACTCCACATCATGCTAGACACTTTCTTTACA	16254	A_95_P305603	FG134987
16740	197	80	661	CAATGCAAGCGGCTGTTGATAGATTAAGTCATTCAACAAACTTCCTTAACTTTTTGGC	16256	A_95_P160497	EH619192
16741	197	81	646	AGAAGCTTGTACTCTGACTGTAGCCTGTGACAGATGGTAAGAAATGAAGCCAAATT	16258	A_95_P132162	DV999374
16744	197	84	822	ATTAGTCGATCCATGGACCTCGCCAATTTTCTCTGTTCTTTTTTCTTTTCTGGGACGTG	16264	A_95_P031781	EB443556
16751	198	6	328	TCAGAATCCTCAAGCATTCCTTCAAGTTCAGCAACTCCATCCGAATCACCGGGAATGT	16110	A_95_P094703	BP532840
16752	198	7	266	TCACTTGATGCCCAGATGGGCTTTATTGACAGTTTGTTGGTTCAATGCATCCACTTTA	16112	A_95_P210907	TA19495_4097
16760	198	15	908	GGTGTATGGTGTCTTTAAAACAGCCTTGGATTTAATACCATGTATCAAGTCCTGATTT	16128	A_95_P181972	TA13106_4097
16768	198	23	411	AAGGGACGGACTGAGGACTATTTCTCAAAGTAGGATATTTCCTTCTGAAAATTTGTG	16144	A_95_P003621	AJ272037
16770	198	25	1376	AAATGCATCCTCCATCTCCCTTTAGTGTGTAACCTTTATGTAATGAACTACCAGTTCTA	16148	A_95_P017186	AY660024
16773	198	28	741	TGTGCATGTCTTGAAGAGAAGGAGATGGGAAAGAAATAAATGGAAGTTGTAGTTTC	16154	A_95_P024456	DV158596
16774	198	29	859	GGTATGCCCTGCTCTACATTATGGACGCGGCTTTATCGGTTTATTTAGAGCACATTTT	16156	A_95_P215727	TA20551_4097
16775	198	30	811	GGAATTTCTCACCTTTAAAAGCATCGTTTATTGATCTTCATGTGGGAAGCCACACTCA	16158	A_95_P292913	EB428959
16776	198	31	533	CTGAACATTCTGTCCATTTGCTTATGTTCCTTGAATTTGAGTATTGAGGTCTTTTGAGC	16160	A_95_P019026	TA13020_4097
16777	198	32	780	CTTGGACACCTAACTTCATCGTAAGGTAGTGGCTAAGATATCTATTGAATATTTGATG	16162	A_95_P015736	DV160851
16783	198	38	857	GCTCGCGGAACTAGACCTTGAAGCTTTGATAAATCGGAAAAGAAAACCATCTTATGT	16174	A_95_P225862	EB431697
16788	198	43	758	CACGCGCAATGCAATTACCAATTCTTGAAACAAGACAAACTGAATATTTTGATTTGG	16184	A_95_P151392	EB681596
16791	198	46	806	AAGATCCAAAGGTGGTCGTTTCAGTACTAATGAAATTAGCTGGCGGCTGTCCATCTC	16190	A_95_P131087	EB431214
16794	198	49	218	ACAAAATCGGGCATTGAGGCAATCCAACCAGTATCTTGGCTTGGCAAATGGATGGG	16196	A_95_P141037	EB444841
16799	198	54	754	CAAAATGGTTCAGACAACATTGTATGCTGTTGATTAATACTTTGGTTTAAGACCATCT	16205	A_95_P016661	TA13240_4097
16802	198	57	1522	ATTGAAGCAATTTCTAGCTGAAATGATGTAACTTTTGGCTTCTATATGCTGTTTTGCT	16211	A_95_P184947	TA13805_4097
16803	198	58	518	ATAATCAGTGTAGCTCCTGGATCAGTTTTATTTAGTCTCCTCCTATTTTTTCAGGAGTT	16213	A_95_P316413	FG188473
16805	198	60	898	ATGTGAGAGTTGTTCTGTGCTTAGCTGGAAGGATGATTACCCTATAATTTAGGTTCT	16217	A_95_P180472	TA12752_4097
16810	198	65	577	TTGCAGTCTGTCTCTTTTGTTATCACACTCTGGAAGGCAAATAGTTTAGATAATTAGT	16227	A_95_P048601	BP131958
16818	198	73	841	GTTTTTTGCTGGCTTAAGTCTCATGGCTGTAAGAACTACATGAAATAGCATTTTATTG	16243	A_95_P211112	TA19540_4097
16822	198	77	400	GCACGTGGTCAGATCGAACTAGCAAAAAATGTAAGACAGAGGCTGACATCTCCCAA	16251	A_95_P071500	BP525717

16828	198	83	477	AGGAAAGAAATCAAGTGCTTCTGGGTTTCTCAAATCTCCCTTTCAGTCCTACCAGTGG	16263	A_95_P100733	BP535500
16834	199	4	1047	GCAAACTCATGAATTTTTGCTTATATCCATCCCAAATGTTCATTGAGGGACCAGTTTTT	16274	A_95_P016986	TA12618_4097
16839	199	9	0	TTGAGGACTCAATCCCAGCCTATCATCCTGAGTGTCAAGAGCTATATCATGTCTAGAC	16284	A_95_P310403	A_95_P310403
16840	199	10	727	CTAACCTTAGCTTGGGGGATTAGGAGTTGTGTCCTATTTGCTATGTGCTTCTGTTGAG	16286	A_95_P284363	FG133725
16841	199	11	458	ATGTACAGATGAATTTGGCCATCGGAAAGAGCATAGGTGGAACCTTCCTATGGATG	16288	A_95_P045136	BP131060
16842	199	12	620	AACCAAAAAGGAGCGCAAGTGGAAGGATAAGTATCATCCAGGTTATTATATTGCAAA	16290	A_95_P125722	EB424789
16844	199	14	448	CGTCACGCATTCCGTACCAAGATTCATCATTGTCACGCGTTTCCTTCCTTTATTTTTCTT	16294	A_95_P274253	TC69625
16845	199	15	137	ATGGCTGTAGACATATCAAGAATAGTACTTGTGGTGAGTAAAGATTGTTGTTGCTGC	16296	A_95_P217167	TA20870_4097
16848	199	18	583	CCTATGTTTTGGAAGTGGTGGTTGTTTGGTTTCAAGTAATTGAAGAACTTACTTCCTT	16301	A_95_P154137	TA11726_4097
16853	199	23	342	CGTGTGACCGGATTTTGATAATAAAATGTGATAGTGTATTCTCAGATCTGGTCGAATT	16311	A_95_P091183	BP531246
16855	199	25	1275	TTTTCTATCTGATGTATGGCAGCGGATTGGTTTAATAACAAACAATATTGGCGTTGTG	16314	A_95_P002881	TA12047_4097
16856	199	26	640	GTAACTGTAGCGGGAAGTAGAATTGGAATAGTTTGTATACTAGTGTATCATTTTCACA	16316	A_95_P134337	EB435329
16861	199	31	811	CTTCCTGTGTCCGTTATGCTAGGTGTCTTGTTTTACTTATTAACTCGGCTATTGCTCGA	16326	A_95_P145547	EB449289
16862	199	32	203	GCTACACCTGCTAATTGGCTTGGAAGTTCAGAGGCATGAAATAATATAAATTTTAGAT	16328	A_95_P158847	EH616737
16864	199	34	639	AGGATTCTGAGCTCCCAGTAAACCTATGATTGATGACATGAAAGAGCAAATATTTCGT	16332	A_95_P223242	DW002575
16875	199	45	657	TTGTGACACCAGATCAGTTTGGGGTATGTAGTTTCTAGGTATTGTTGACTTCCGCATG	16354	A_95_P265266	BP530311
16880	199	50	1256	GCTGATTTCATTCGCCTTTGATTTGGCAGTGGTGTTACAAACAAAACAATGTTATTCTT	16364	A_95_P179632	X95933
16885	199	55	798	AGCGTGACTAATTAGCCACAGGATAGTCTGTTTCAGTTAGAAATGTATGTTCGCTAT	16374	A_95_P145212	Y16644
16887	199	57	1251	TAGTGGGGATTTAATTGTAATGTCAAGACTGATTAGCAAATTCCTACAAGTCCACTTA	16378	A_95_P010106	TA15152_4097
16888	199	58	755	CCACATGGTGATTCTGTTCTTTGATTTCTCGACTTCATTTATTCGCAAGGACATTTTATT	16380	A_95_P119297	DV162399
16890	199	60	704	TACCATGAGTGGCTAAAACCCATAGTTTTGGGGTTATGATTTAGCCATGAATATTGTT	16384	A_95_P130882	EB431005
16891	199	61	1315	CGCAAGAACAATAGTTGTGTATTTGTTGCAAATGCATTTCGGTTGGTGTTTTGTTTAA	16386	A_95_P007581	TA14073_4097
16893	199	63	365	AATTGAAATACCAGGACATCAATAATCCTGATGTTTGGATAGCTGGTCCCTCCTATAT	16390	A_95_P042861	BP130466
16895	199	65	503	AACCAACTATATCGGTTTGGACTGGTTTGGTTTTGTCGGATTTTTTGGATTTTCGGATT	16394	A_95_P036338	BP128705
16896	199	66	777	TACAAAATGGATGAACATGACCCCGATTCGGCCTACTTGCGATTGCAGTTCTCGAAGT	16396	A_95_P250082	DV162343
16897	199	67	796	GCTAAAAGACTCAGTCACCCGAGTCATCGTTACAAGAGCAGACGATGATATGAAGCA	16398	A_95_P196442	TA16340_4097
16898	199	68	458	CCCTAGATGTGCCTGTTACCTAAAGAAAAATATGTTATTAATGGCCTTTTGTTATGTG	16400	A_95_P087158	BP529725
16909	199	79	321	AAACAGGGGAAAGCGAAGATTGCTGCGGGTGCATTGTTGCCTCATCAGATAATCTTT	16422	A_95_P067045	BP136757
16913	199	83	736	GTATAGTATATAAGCTTGGGGTGAAAAATTCGTAGGCAACAGGCTCTAGGTCAGGC	16430	A_95_P303363	FG171806
16925	200	10	580	TAACTTTCCATTAGTTGCAAGTGGAAAGACCTCTAGTCTTCTTCAAACCATGTTATGAT	16287	A_95_P001176	EB432436
16926	200	11	1069	TGTGATTGTGACCTGAAGGGATCACGACTATAATCGTTTATAATAAACAAAGACTTT	16289	A_95_P007591	S44869
16927	200	12	622	CTGGAATTAAGTGAATTTAGATTTACAGTCTACAATTGCATACCTGTTAACTCTTGCG	16291	A_95_P006256	AF154644
16929	200	14	742	CAAGTTGTTGTGGATAAATGATTATACTGTGCTCTTCGTAAACATAGGATGCATTTGT	16295	A_95_P177897	TA12099_4097
16935	200	20	316	CCCGCAATAGAGTAAAACGTAGAACAAAAATGGTCTGGAAAGCATCGTCCAAACAGA	16306	A_95_P196542	TA16361_4097

16936	200	21	679	TGGATGATCACGTTCTTGATGTACTGGAGGGTAATGCCAGCACCTTTAGCAATATGA	16308	A_95_P237579	FG195217
16937	200	22	663	GAGATGAACATAGTTATGGCGGAACTTGCATCTTTTCATTTTATCAAGTTTCTGTACC	16310	A_95_P116132	DV158708
16940	200	25	695	CTTCATTTGAGAACAAATTCAAAGAAAGAACGGGCTGCCTGGATAGAAGCTCTGATA	16315	A_95_P287153	FG186420
16946	200	31	1261	TTCAGTGTATGCATGGTTGAATATCATCTGGAATGATCCTCGGATTGATGTATCTGG	16327	A_95_P017141	TA15454_4097
16954	200	39	795	TGGTTAAACCACAAAGCATCTGTCTCTCTTGCCTCCTGCACTCATGTGCATTACATCA	16343	A_95_P225012	EB450071
16956	200	41	865	TTAAGTAGGAGTCTTTCTCCCCTTTTGATATTTTCACTTCACTGGGTTTCCTGGTCAAA	16347	A_95_P189212	EB428320
16957	200	42	780	GGGTGGCCTCAGCTAAAGCAAATCTTGATTTTGGATCGAAACTGGCTATTATAATTT	16349	A_95_P021846	DV162505
16958	200	43	743	GAGTTTAAATCTCAGCATTGGCAGTAAATTTTGTTGATGTTATGCAAGCTAATCCGG	16351	A_95_P219857	TA21485_4097
16960	200	45	249	ATTCCTGTCTATGGTCTTCGGCATTACCCCTTAACAGAGCTATGTTAGCTGTTTCACTC	16355	A_95_P144927	EB448482
16961	200	46	805	TGCATTGCCTCTGCTTGAAACTCCAGAAAATGTTGATTATGATATCGCCAGAGACTTG	16357	A_95_P150807	EB680929
16962	200	47	535	AGTTTGGAACTCTTTGTGAAAAATGCTTATAATAACTGCCTCCTCTCATATTGCTTTAC	16359	A_95_P026146	TA13077_4097
16965	200	50	1063	TCATGTTTGTAAGAATGTGGCATTACCAGTTTTTACACAGGCGGTCTGCTGTTGCGA	16365	A_95_P109592	TA15601_4097
16967	200	52	1842	TATTAGAGTATGCGGTTCTGGACCTTGTGATATAGTTAGCTTGTGCTTTCTTCCAAAA	16369	A_95_P251422	AF116915
16968	200	53	456	TGTTTTGTGGTTTATTTCTATGTTTCGATGGGCTATCGCCCCTTCTTTCTTGGATTTTG	16371	A_95_P182782	TA13301_4097
16970	200	55	1217	ACTTCTAGATGATGTTGGGATACCCTAATAAAATGCTTCAATGTGCTGTGCTTTCTGG	16375	A_95_P020166	TA17814_4097
16973	200	58	1421	CACTTCCTCTTGTGACAAGAGAATCTTCCATGGTTGATAACTTGAAATTACTAATGAA	16381	A_95_P003991	Z48976
16975	200	60	620	TGTTGTGAAATCATTCGGACCAGAACTGGTCTATCAATTTTGATAAGCTGAATAAGA	16385	A_95_P214347	TA20245_4097
16980	200	65	511	AATTAAAAATAGAGCTAAGCTGAGGTTTGAAGCTGAGTCGAGGCGTCGGTTCGAAC	16395	A_95_P036433	BP128730
16983	200	68	568	AGGGTGATCTTATCGATGACTGTAATTGGGTGTTTGAATCTGTTAAGCAATTTGAGA	16401	A_95_P258866	FG640166
16986	200	71	255	GTATGCTTCAAGATTCAATTTTCCTGATTGTAAGAATATTTCCTCATCAAGTACGACT	16407	A_95_P141907	EB445519
16995	200	80	230	ACTTCTTGTTCGATGTAATATGTTTTGAAGTGTCGAACACTTAAGACGCAGGTTGTTG	16425	A_95_P121202	DW001222
16996	200	81	386	TGTGCTAGAGATAATAGCTTTTGCTGAAAATGTGTCTGCCAATCAGAATTTGCAATG	16427	A_95_P132612	EB433169
16997	200	82	803	GATTTTAATTTCCTGAAACAACCTACTATCAGAGAAAGTCAGCTGTGGCATTAATGT	16429	A_95_P295478	FG132886
17002	201	2	828	GATGTCTTTTCATTTGCTTTAATTTTACAAGAGATGATTGAAGGCTACCCACCTTTCCA	16438	A_95_P025906	DV161181
17003	201	3	659	TTGTCATATTTACCTCATGCTTCGGGAAGATTGTCGGCACCATTGTCGTCTCACTCCTT	16440	A_95_P208837	TA19057_4097
17006	201	6	987	TCTGTGTCCAACATAGTTCTCTTTCCTTTTGCAGAATCCTCCCTCTGTAGACTTGCAAG	16446	A_95_P008686	TA12105_4097
17013	201	13	182	CTATTTCGTGCTTGTTAAACTGTGTTCACTGCTTCTACGGTGGAATATAATCATTGCG	16459	A_95_P100363	BP535339
17014	201	14	874	CTGACCGTCGTGGTGGAATTGTATACCATGTACATTTGTTTATAGTTGTACAGTTTTT	16461	A_95_P227674	DV159197
17017	201	17	426	AGCTACAGGAGGTACCAAAGAAATTTTATGTTAGATTTTTCCCTCTGTAGAAAGCTCT	16467	A_95_P091048	BP531192
17022	201	22	501	ATGCCAGAACCAGAGCTTATCGATCATGCTGGTCTTGATTCTGCTGTCTATATACGGA	16477	A_95_P073360	BP526196
17024	201	24	794	ATGGCAAAAGGAGGAATGTTCAGGCAAGATTACAACCATGTCCACCACCCCTATACT	16481	A_95_P015931	DV158862
17028	201	28	90	CATCTATGTGGTCGATTCAAGTGAATGCAAGTACTAAAGATGATGAAGAAGATGAG	16489	A_95_P034034	AJ718058
17030	201	30	762	GGGAGTAAACTGATTGTGTTTTAGACCAAATGGAGGAGGAAAGAGGAGATAGTCG	16493	A_95_P016411	TC50620
17033	201	33	1567	GGGCTACTTGCTTAAGTTCTGGTTTATTTATGCCTACTCTTTAATGTTGTTATTTTGAG	16499	A_95_P160102	TA14230_4097

17034	201	34	731	TTAAGGAAGGTTTGGCACCAATAAATTTGGTAGTTGAGACTGAAATGCACCGCGCA	16501	A_95_P151667	EB682378
17035	201	35	374	CCTAAAGCTCTGGGAACAACTCAACATGTTCATCTAACTTGGCAAACTTTGGAGTGTT	16503	A_95_P041421	BP130090
17037	201	37	174	CCAACTATAGTTTAATCTTCTTTTTGCATATATGTATCTATAGCAGTTCCACCCTTGGC	16507	A_95_P164082	EH623212
17038	201	38	559	GCTTCTTCGTCATCATTGTCCTAAGATTATTCCTTAATCTTGATAAGTCTTAACTGGCA	16509	A_95_P017851	TA17289_4097
17042	201	42	856	GTATTCTCCTCTTCCAGCATTGCCTCGATTATGAATGTGGTAACTGGTATTTACATATC	16516	A_95_P186797	TA14204_4097
17045	201	45	841	AATGTTTTGTGTAGAACCAAGAATCAGCATAGAAGCTAATGATTTGACATGTGAAGA	16522	A_95_P216822	TA20787_4097
17052	201	52	783	CAAGCAAGGAAGGGCTTCCCAGAGCCTCTAGCTTATCAAGTATTGATTCTATAATGA	16536	A_95_P138487	EB442237
17053	201	53	853	TTGATGCCGCAAGGGGACTCGAGTATTTGCATGAGAAGGTCCAACCTTCAATAATAC	16538	A_95_P245052	DV161386
17071	201	71	1633	CTGTATGAATTGATCTCGGGTACTATGGCTTGCTAATAAACATGTACAATTCTTCTTC	16574	A_95_P208112	TA18893_4097
17076	201	76	1014	CGTGGAACAATGTTTCCCTTCTTGGTGAACTACTTGTATGTTACTTAAATCTCTTGTTA	16584	A_95_P195212	X60060
17079	201	79	1406	CCATTTCCGATGTAATGTTGATGATGGTAGTGAAGGTTATTCCAATTTGTATAATGGC	16590	A_95_P198937	AJ488194
17082	201	82	1087	CAACACAGTAACTTTATTGGTACTGAACATGGCATTAACTTTGCGATTAACGAACTAC	16596	A_95_P030501	TA17907_4097
17086	202	1	236	TCCACTGTGCTGTGATTTTGAAAAAAGCATAACCCTTCTATTGTCTTCTTTTTACCATG	16437	A_95_P197272	TA16525_4097
17087	202	2	1972	CAGAGATGCTGATGTCTCACATTTTATTGTGTTCTTCATGTCGGAGAAATGTAAAATA	16439	A_95_P012966	AF129003
17088	202	3	889	TCCTGTTCTTGATGGAAAGACTTCCAGTTCAAGTGTACAAAGAGTTCCTGTGAGGAG	16441	A_95_P184747	TA13764_4097
17090	202	5	440	TAGGCTATTATGAGTTCAAGACAGGCCGCTATGGTGAAATTGGTAGACACGCTGCTC	16445	A_95_P065230	BP136275
17097	202	12	41	GGTGCCCTTTCATGGCTGCCCAAAATCCAAAAATCTTTTCTCCAAAAAGAGCCTATCC	16458	A_95_P113287	CV021096
17099	202	14	266	ATTGTTTGAACTTTGGATCTTCTACCACGTGCCACGGTACCACTGATTAACGATAAAA	16462	A_95_P209477	TA19199_4097
17101	202	16	933	GGTATGAACCTCCATAGATTTGTTTCAAGATAATGAATGTGCTAACGTAGAGATCAA	16466	A_95_P015781	TA14437_4097
17103	202	18	155	GACATGATGTCATCTGATCCATTGGATGCTGGTACACAAGCTCATCACTCGTCCTTGA	16470	A_95_P234374	EH617354
17105	202	20	253	TGATACCTTTGTGTTTCCCTGACAGAAGTATAAGTCAACAGTACAGCTGGAAAGCAA	16474	A_95_P038801	BP129373
17110	202	25	770	AAATACAGGAGCTTTGGCTACTCCATTGGTGCAGCAGCTGATTTGATGAGATGATTG	16484	A_95_P228234	FG158536
17119	202	34	859	GAAAGCTGATACAGGAAGGAGATTTCTGATCCAAGCTTTTCTGATTCATTATCTTTAT	16502	A_95_P229239	DV162712
17121	202	36	457	CAGGGAACTGTAACGTTACAATGCTCCATATTTCATATTATATGGTCCTCCATATGAT	16506	A_95_P002481	FG637164
17124	202	39	435	GTATTAATGACTCTTCCGGTCCCTTTTCTCATCTGTGAAATTTATTATGTTATCCAACC	16511	A_95_P257054	EH621667
17127	202	42	469	TTCACCCAGAGTGCACTAAGGACAGAGATATATAAGTAATTTAATTAAGAGGGGGG	16517	A_95_P113682	CV021255
17129	202	44	711	TTTTCTTTCTCGAAATTCTCTGAGTCCTTAGCTGTGTTCCTAAACCCTTAGAGGCGGA	16521	A_95_P030646	EB447172
17131	202	46	1095	AATATTGGGGAGCCGATGATATTTCCCAACACTTGTCTAACAATGTAAGAATCTTGA	16525	A_95_P187502	EB643439
17139	202	54	802	TGTAGTGCATGGAGGTGAAAGTTATGGTGTGTTTTCAAGAATTGTGGTTGGTGGATT	16541	A_95_P289703	EB449854
17140	202	55	809	CGACTAATAGGATATAGTGGAAGATTGTCACGACTTGATTTTGCTTTTGTTCATTTGT	16543	A_95_P009586	EB679346
17146	202	61	671	TCAGAATGTTGGAGCCATCGGATGTTTATCAACAGAGTCAGATCTACTTCTACGCTCT	16555	A_95_P301758	FG643145
17148	202	63	563	TCGCACATCTTGGGATGGTTTGCGTTAGATGTTGGTTTTAGACTTATCATGTTTATTT	16559	A_95_P159962	EH618563
17152	202	67	477	GCGTTGAGTCATCAGATGGTTTAAATCTATGAATTTGATTCTAGTTTGGCATTTGTAC	16567	A_95_P261631	BP132909
17156	202	71	126	TAAGGTGCATGAGCACATTCAGGATTGTTTGATATCTGAGTAAAAGTTAACATTCTT	16575	A_95_P162227	EH621119

17163	202	78	1237	ATTTGGCTAGAATAGGTGTGAAGTACTATGGAACTATTCGGCAGGAGGAAGAACTT	16589	A_95_P014011	TA16664_4097
17170	202	85	170	TGGAGAAATCCACTACCCTTTACCATCATTCAGGGTTGTTGCTCCCATGAAGAGCTTT	16603	A_95_P104667	TA11636_4097
17173	203	3	820	AGGTTGTGACAGATGATCCTATCGATTTTATGGATCAGCCTCCAGCAGGTCTTGTTAT	16608	A_95_P229944	EB441417
17174	203	4	544	AATATAGTAGTACGGATGATGTGCTATGTTGATCTTATTAAGTGTGGTGGATGGAG	16610	A_95_P105357	CV017422
17185	203	15	809	AATTTGAAGATTTTTCCCGAAACTCTTGAAGCAGTCAAGATGGGGGTGGTGGTTTTG	16632	A_95_P010016	TA12680_4097
17188	203	18	757	ATTCCAGCCTGGTTTTCCTTCAGTTCTAAAGATGGTACCAATGTAGTCAGTGGGGATT	16638	A_95_P269891	TA21000_4097
17191	203	21	764	TACACTCTAAATGCTCGGATATCCTTGCTCTTACTTGATCAACTGAAGTGGAATGGCT	16644	A_95_P195347	EH617306
17192	203	22	488	AGCTTAGCAAGCAAAGTAGGATACGGCCTGATATTTTTGATTGATCATACAAGTCTG	16646	A_95_P276853	AM802729
17195	203	25	680	GATGAGCTCCCAAGATGGTTTTGCCATCATTACTTTTAAATTCTGGTACATTGATAGT	16652	A_95_P014311	DV160945
17201	203	31	1361	ATTGCCGCTTCATTGTATGATCCTCCACGTTCTCATTAATCTCCAGAAGTTTACAGTTG	16664	A_95_P016776	TA12497_4097
17202	203	32	843	GACCTAAGTGGACAGCAAGGCTTTTCTATGCAATAGTAGCTGTGCTTGTTGTTTTGCT	16666	A_95_P289113	DV157663
17203	203	33	1565	CGGTACTGTTTGTTACACTGAACTTCTACTAGGCGATTTGGGTATTGAATATGTAAAA	16668	A_95_P259721	DQ229077
17204	203	34	535	GGACTAGACTTGCTCAATTATTAATGTGTCAGTCCTTGTTCTACTTGTTTAACTCTTGA	16670	A_95_P206757	TA18588_4097
17208	203	38	680	GTGATCTGCAAGCAAGGTTAGACAATTTGAGGAAAATGTAAATTGCTTACAGATTGA	16678	A_95_P248172	FG190544
17209	203	39	810	AATGCATATGGTTTCTATACCATCATCGGAGACGAGTGATCTGGAACATGCTTGTCC	16680	A_95_P117492	DV160414
17210	203	40	726	GGTCCTCTTCTGGTTAACCTTACCATGTACAGATGACTCTTGCTCTCTTATCCAATAGC	16682	A_95_P216027	TA20615_4097
17211	203	41	866	CCAGGACAAAGATAAATTGATAACTAACTTGAAGACTATACAGGACTATCTCTGTTC	16684	A_95_P148577	EB677938
17215	203	45	743	GGTAGGGATTGGAGAGCAATACATTTGGTTGATTAAGTAGCTTGAGTTTGATTTTGA	16692	A_95_P164257	EH623394
17217	203	47	512	ACCTTTTGTCCTTTCTTGGTTGTGCTTTTGATAGAAGAAAACACCATGCAAATTGTTT	16696	A_95_P022651	DW001744
17218	203	48	336	GTTCTCTTATGTTTTCAAACTTGGCCCTGTAAAGTAGTGGTACAATATAGTAATTCAA	16698	A_95_P096993	BP533846
17225	203	55	80	CCACGACAGAAATAAACTGTAGTTTCGTTAATGTTCTTGTAGTGTAGTTTCTTCCCAA	16711	A_95_P147482	EB451925
17228	203	58	556	TAGTGGAGCTAGATTTTAGTATTTTCAGTTTCTCTGCAAGCCTATTTATAGGCAGTTC	16717	A_95_P124037	DW003888
17229	203	59	793	ATCCAATGCCTTAACTTATTGAAGTCCTAAGTGAGGACATTTGTGCTTGAAAGCAAT	16719	A_95_P011146	TA12856_4097
17233	203	63	571	GCTATCTTGAGTTTACTTTGTGAACTACTATTAAGTAGGGCATTGTACTGGAATTTTG	16727	A_95_P000801	EH619079
17234	203	64	937	CATCCAATTACAATAATATGAGCGAATGAATGTCGGATATATGCATCATTATGGACG	16729	A_95_P185337	TA13889_4097
17236	203	66	410	ATAATGTTGTTGCTGGTGCTGCTTGTGATGCTGATCTTGACAGTCTCGTAGCTGATG	16733	A_95_P051881	BP132772
17238	203	68	790	ACATATGTAGGCCACGTTTCTACCATTGTTCTTCTTCCATTGGTCTCTTTTGTTTGTAA	16737	A_95_P010311	DV999353
17239	203	69	709	GTTCAATTTTTGATGCCGTTGATGGTTTTTGTTTGATATGCATTTTGTGTTCGTTGTCT	16739	A_95_P014626	DV158478
17240	203	70	644	GGACTAGCGTTCTGATAATCTGATCTAGACGACTTGATCTTTGAGGAATTACTAATA	16741	A_95_P051321	BP132614
17243	203	73	828	GCACTTTCTTACCTTTCTGATGTACCACGACAAATTCAGCGTCATGAGCAGTGTTGTC	16746	A_95_P289928	FG141437
17247	203	77	267	TGGGGGTTAGATTTGTGGAGTTAGGTTTGTTCTTTTGTTGCCGTTTGTGGATTAGAAT	16753	A_95_P152122	EB682425
17248	203	78	272	CTGTCTTTTTAAATGTTTCGGGCGGTGTAAATATGGTCTGTCTATGGAATAAAGTTGT	16755	A_95_P089228	BP530413
17253	203	83	466	GAATAAAGAAATAAATTAGGGGTGCTCGGGTATTGGTTGGGGGAATCCGTCTCTAT	16765	A_95_P087793	BP529880
17255	203	85	388	CCGCAAGGTATAGTAGAATGAACTCGGTGGAAAAGGCTATAGAGAAAGTAGAACTC	16769	A_95_P096103	BP533476

17257	204	2	882	TAAAATCAACCAAGCTGTTTTTCCCGGACTTCAGGGGGGTCCCCATAATCACACAATT	16607	A_95_P278078	EB427822
17258	204	3	583	ATTCGGAAAATTCAGACAAATCCAAAATCTTTACCTTTCACATAACAGCCTCACTGGC	16609	A_95_P102127	EB425603
17259	204	4	392	GAAACACATTGCTTTTTTGACCCCGCTTACATTAATATGAACCATTTTCGTGTCAAATG	16611	A_95_P187297	TA14313_4097
17266	204	11	528	CTATGCTCCTTGAATCTTCTCTAGGGGATTGAAACTTTTGTCGTATATCCTTTTGTTCC	16625	A_95_P022541	TA18459_4097
17274	204	19	812	CCATACTCTTCGGAGCTAGTATATATTTTGGTTTCTACAATCTTTAAATCTGCTCCTCT	16641	A_95_P147157	EB451395
17278	204	23	282	TACTGGAGCAGCTTCGAGTCATCAGTATGCTCATGACGGAACTCTGAATCTTGTGCA	16649	A_95_P168131	EH664357
17279	204	24	693	TAGCTGAGACAGAATAGTGTCCGATTTTCATGTGTGAAATGCTTTCTTTATTTAGCTG	16651	A_95_P027231	EB438892
17283	204	28	803	AGGATAAAGAGAAAAAGAGAGATAAAGGTGGTCATCATGATTCTGGTGCTGATCAT	16659	A_95_P248017	EB426879
17286	204	31	767	TTTTCAATGCTTTGCCACGACTGGTGATGGCTCCATTGTAGTTGGATCACTTGATGGG	16665	A_95_P202382	FG144026
17294	204	39	801	GAACCAAGTCTTTTATCTTTGCCTTCTTCCGCAGATTATATCTTTATGCAAGAAACTTT	16681	A_95_P248677	EB451516
17295	204	40	454	GCGTATGCGTGGCATGATGTTTGTAGTCTGTGCATTATTACTTTTAACATAAATTTAA	16683	A_95_P022146	EB430490
17304	204	49	128	GATTTGCCTGATACTCAAACAGGTTTCTTTAACTTAATCAACACGTATTTTCCTAGTGG	16700	A_95_P103657	CV016628
17307	204	52	665	AATCTTTTTGTGGTGGGTCTCAATGGGGCTCTTGATATTGAGGACTGAGTGTCCAAG	16706	A_95_P210592	TA19429_4097
17312	204	57	0	GCATTCCAGTCAAACCAAGCTTGAATACAAAATTCGCTTGAAGGCTTCAATTGAGGT	16716	A_95_P264156	A_95_P264156
17321	204	66	615	TGTTTCTCCTTGCTTGGATTCAAGGGTGAATGAGATCAATATGGTTTTGTTAGGTTCT	16734	A_95_P300333	FG639683
17325	204	70	461	GCTGGAATGTAGACCAAATCCCGATATGTACTTTGAGTTATCTAAGAGTAAATAGTT	16742	A_95_P140092	EB444052
17333	204	78	702	TTGATCGGGAGTAATTTATCTTCGAGAAATGTTGAGCGCCTCTGCAATTTTAGCTATA	16756	A_95_P259896	TA14213_4097
17341	205	1	212	AATAATCTTTCCTGCCTTGGAGAAGAATACTAGAGGCCACTGGAATCAGGCAGTACA	16771	A_95_P068735	BP137202
17343	205	3	863	CAGATGTCATGGAAGAGAAATGTAATTCTGCTGCAATCTGCTTTGTTTCATTCCTGCC	16775	A_95_P008926	DV161279
17346	205	6	449	ATGGCCTATCCGATCACTTGCTTAACACATTGATTTTTCTGTTCTGGGGAATTTTCTTT	16781	A_95_P002001	BP135342
17347	205	7	877	TGAGACTTGTCGTGTTCAACAGTATCCCTTCACAAACAACCAAGCTATACCTCCAATG	16783	A_95_P116467	TA16664_4097
17349	205	9	675	GTAGAGCTTTTTTCCGCACCAGAAGTTTTGTTTGGATTAACTTTTGAATGACAAATCT	16787	A_95_P178657	TA12305_4097
17352	205	12	412	GTGACCATGACATGTTTTCCGGAACATTATGAACAAAGAAGCTTCTGTATTTATCAAT	16793	A_95_P121917	DW002000
17353	205	13	708	GGTAATTTAGACGAGCTGACTTGATAGCTCGAACGGCTTATGTATCTGTATTTTGGT	16795	A_95_P017601	TA12651_4097
17361	205	21	487	ACTGTCCAACTGCAAAAAGCAGAGATAGCTGGGACCGTACTTGTTTTGTTTTTAGTG	16811	A_95_P123712	DW003582
17364	205	24	562	GATTCAGAAGCTGGGTTTAGCTTCATTTGGTTATTTGTTGTTGTTTCATCAGGCAATA	16817	A_95_P160387	EH619086
17368	205	28	3831	GTCCTGAGCTTTGTCCTGAGCTTTATTGTAATAAGAACACAGTTCTCATGTTTTAATA	16824	A_95_P033181	AJ302018
17369	205	29	859	TTAATACAGAAGCTGGAATTCTTGAGGTTATGGGGGCTCCACTCTCTGGAACAGACT	16826	A_95_P273331	EB428953
17373	205	33	742	ATGAGTTGTTGCGTAGAGATTGTTTTGTTTTTCAGCATCATGTTATGTGGGCTAGGCA	16834	A_95_P302758	FG182677
17380	205	40	830	TTTGGCCAAATTCGGAGTCCAGTTCCCTCTCCTTTCCTCACTCTTAGATAAATCTAACT	16847	A_95_P130572	EB430626
17382	205	42	573	CAGATCTATAGCCTAAATTATGGAGCACGTAAACTAATGGTCCCTCCGCTAAATTAA	16851	A_95_P304578	FG636318
17390	205	50	756	CTTCATGTGCTTTAAATTACTATATCCAAAGGAGTACAAAGAACACCAGTTAGCCATT	16867	A_95_P021971	DV160358
17392	205	52	687	GTTTCAAGCTCGCAATGAGTTTGAAATCTCCTGACACTGGAGTTGCCGATCCTTTACT	16871	A_95_P162082	EH620847
17394	205	54	475	TGTTCACAGCATGTTTTTGCTGACATAACTAATTATAAACCCAAATTTTCCCTGCTCCA	16875	A_95_P027081	BP132176

17395	205	55	811	CCTACGGGCAAATTCAAGCTAAAGAAGTTTGAATAGATTCATTAGCAGAAAATGAAC	16877	A_95_P009946	EB679273
17397	205	57	608	CACACTTAGGTCTTGAAGATTTGAAGCTTTTGGTTGAGAATTGCTTACTCATTTATGC	16881	A_95_P027566	EB681194
17402	205	62	642	GGGCTGCATGTTCAACTTTAGGATGATGACATACTTGTACAGTTTCTTCAGGATAATA	16891	A_95_P067865	BP136984
17403	205	63	409	ATCGAACTTGATAGAGGCATTCAAAACTGTACCAATAAACTGATTACTTGGGTAAGA	16893	A_95_P197122	TA16494_4097
17404	205	64	783	TGATATCGATATCTCAGATCATTGGGGAGCAGACCATCTGTCTGAGATGAGCTGAGA	16895	A_95_P253379	FG161776
17408	205	68	876	GGTTTCTGTATTCAATTTTAAGGGCAGTTGCTTTTTCCTCTGAAGAATCTAGAACTACT	16903	A_95_P216967	EB678001
17410	205	70	181	ATGTAATTTTACTCGTTCAGACCATCCTTTAAGGTAAAGGAACATCAATAGTTGTGAT	16907	A_95_P149902	EB679891
17416	205	76	322	CAGGAGACAGGGAGATTAGAGAGATAGCATTCGATTTATATTGAAATGAATCTTCAT	16919	A_95_P102642	TA12506_4097
17418	205	78	594	TGGCAGTACTCTCGTACCTTTGTAGGCACTCTTGTTTTGAAGTATTCAAGTTATTAAC	16923	A_95_P205742	TA18355_4097
17419	205	79	957	AGGATCCTCGTGAGGTTGCTGCTGCTAAAGCAGATTTGAATTATATTGGCTTGGATG	16925	A_95_P184572	TA13724_4097
17420	205	80	418	TTGGTCGGTAGCATGTATCCTCTTGTTCAAGTTCCTGTATAGAAATCTGAGTTCAATG	16927	A_95_P026921	TA20171_4097
17422	205	82	832	TTGCTGATATCAAAACTCAAATGTGCTGCATAGTTATGGTGGCGATATTGTTCGTCTT	16931	A_95_P117377	DV160284
17428	206	3	975	TGAGGGGTGATGATGATAATGAAGGGGGCAAGGATCACAAGCTTTCTGGTAAAACC	16776	A_95_P238989	AF154643
17431	206	6	545	TTGGAGATGGCGGACCATTTGGCTGGTTGAATCATTTATGCTTTAGAATTTGGCTTTA	16782	A_95_P258056	TC58159
17438	206	13	62	CCCTTTGCACTCTTGGGGCGGACAGTTCCAATTCTGTAATGTCATATTTGCCTCAAAA	16796	A_95_P102212	CV015925
17440	206	15	772	CCCTCCCTCTGTTCGTAGATTATTTGTGTTGTTTTGTGTTTGTAATGGTCTCTCTATTG	16800	A_95_P221907	EB429111
17441	206	16	881	AATCTCCCTCTCCCAGAGCGCATTGTTCGTTATACATATGCATTGGTTGGGATCAAGC	16802	A_95_P207127	DW001038
17444	206	19	354	GTCTTCGAAGGTTTCACAGTTGGTTTTCATCCAAGGTCATGGGAAATTGTTTACAATG	16808	A_95_P080770	BP528090
17454	206	29	343	AGAAGCGTTGCTCTCTTGTGCTTCTTGAAAACATAGAAAAGGCTGATTTTCTTGTTCA	16827	A_95_P156002	EG650363
17455	206	30	656	GACTACCTTGTATCTATATATATCTGTTACTTACCAACGTTAGCTGTAGTTGCCACCAT	16829	A_95_P234919	FG638862
17457	206	32	221	CTTGGAGAAAAGCAGAGAAGAAGATTTTGAGGATGATGGTACTTCATCTACAAAGA	16833	A_95_P140042	EB443985
17458	206	33	551	GAGAGATGATTTAATTTGATGTCATCTAAATTGTAAGGAGTACGCTTATTCGGTCATC	16835	A_95_P120167	DV999916
17462	206	37	485	TCTTGACTATTCAGAGTTCTGCATATTCAGAGTACCTGCAGTAATCTCAATCGATTCCC	16842	A_95_P056596	BP134001
17464	206	39	934	GCCAGAAGTAAAACGTATACAGCGGCTCCTTTTTGCAACTTATGTTATTGTTTATTAC	16846	A_95_P217422	DW000754
17465	206	40	1313	GATGTATGGAAGAAGCATCCTGTTTGGAAGAAACTCTTCAAGAATGAATGATCAATC	16848	A_95_P223472	TA22258_4097
17466	206	41	249	CCTGAAACATACTCCATGATGCTTGGTCAATAACACTTTGATGCTCATTCTTCATTCTT	16850	A_95_P105892	CV017661
17469	206	44	690	TAGCAGGTTTCTTGTGCACCTTTAGCAAGTGGAATATGTTTAAATCATCTTGATTTTT	16856	A_95_P003691	EB679961
17471	206	46	267	GTATCCAAATAGAAGCGTTTCATGTCTTCAAGCTATTTGCCGCAAATCACAATAAGCC	16860	A_95_P030838	TA20626_4097
17473	206	48	493	CTGGTTACTGAGAGTAAGTATGATGATGGCCGTGATGCTAAAATCAAGAAGTCACA	16864	A_95_P153302	EB683590
17474	206	49	261	CTCGAACTGAGAAAAAAGTTAGTTAATAAGCTATTGTTTCTTGAGAGTGCTGCTTGT	16866	A_95_P028021	TA15160_4097
17476	206	51	858	AACGAGCCATTTATGCGGAGCAAGAAGCTAATGAAGCTTACAAACAGATTGATAAA	16870	A_95_P145427	EB449178
17479	206	54	807	TGATTTTGCTCAAAAATCTCTCCTCCTTTGTGTCGATTTAGCGACGAGATCCGGGATC	16876	A_95_P239464	FG152875
17480	206	55	346	AGAAGATCAGAAGGGTGGATCCAACTCTGGACATGGAAGCAGATGAAGGTGATGA	16878	A_95_P155842	EG650290
17483	206	58	792	ATCAATTTAGGGAAGTTGTTAGGCAAAGGAGGAGCAGGTGGCGGTCAGTTTTGAGA	16884	A_95_P145092	EB448633

17490	206	65	876	TGGAGAAGAAGGTTGAAGAAATTGATTCATCACTGGTAACTGCTATACCTGGAGTTG	16898	A_95_P124492	DW004310
17491	206	66	620	GTTCTTTTTATATTTTCCTACTGTATAACTTAATGACCCAGACTCTCACAGTAGCCTAG	16900	A_95_P223002	TA22152_4097
17493	206	68	770	CTTGATTACACAGCTACAAAGGGTGCAATAGTTGCATTTACTAGAGGACTTGCTCTTC	16904	A_95_P148402	EB677708
17495	206	70	831	GCAGTGAAACAAATGAAGTATTTGTGTACCATAAGGCGATCTCCAAACCTGTTACTT	16908	A_95_P269946	EB428076
17496	206	71	543	TAGCTGTCTTGAGTTACTACTTTCTTGAACAACTATTTTTAATCTAGGCATATTGCACC	16910	A_95_P002191	TA14971_4097
17497	206	72	974	GGCATTGCAACAAGTTCGTGTTAGTTGTAATGCTATTAGATCTGAGCATTTTTTCATT	16912	A_95_P018311	TA14739_4097
17498	206	73	0	ATAGTCGGTACGATTAACATGGGGCACATCACAGTTGTGAGAGGAAGGAACAATAT	16914	A_95_P263621	A_95_P263621
17501	206	76	290	TATAGTATAGCTGTCGCTGATATTTGATTCTGGAAGAGGAGAGCTAAAATCTTCAAC	16920	A_95_P090683	BP531059
17502	206	77	446	ATGTGTAACAGGAGATGTGATGAGCTAAATGTAGGGCTCAAAAAGTTTCTTTTGACC	16922	A_95_P067835	BP136976
17504	206	79	601	TTTCCTATTGTCTTGTTTGTGACAAGATGTAATGAATTTGAGTGGTATTGTGTTTGCA	16926	A_95_P000881	TA13413_4097
17506	206	81	233	GGTTGAGGGAAGTATTTGTGCTTTTATCCTTCATTTTTGTTTAGAGAAGCACCATGTA	16930	A_95_P142862	EB446271
17508	206	83	575	AGGATTGATTATACAGAGGTGGAAATATGGTGCTACTGAAATTATGTGGTATATCTT	16934	A_95_P244372	FG643880
17511	207	1	745	ACGGCATCCAAAAGGATGTGTCACGGATACTATCGTTCATGAATGCAGTGAAATCTG	16939	A_95_P146947	EB451123
17516	207	6	578	TAAGCCTGATTAGTCCAACAAGAGTTTGCTCTCAACTGCAGAGTTTGACAACTGATAT	16948	A_95_P117757	DV160704
17517	207	7	1382	TGTAAAATTTTTGGTGACCAGTTGTCAGAGCAGTTAGATCGTGATGGTGGACTCCCG	16950	A_95_P214862	TA20355_4097
17520	207	10	787	GTACAGTTGACTTTGTAACCGTTAATTTTGTTGTCGTACGCAGTGTAAAGCTTATATT	16956	A_95_P213902	DW003088
17521	207	11	657	TTTAATGTAGCTTAATTTCATAACAGGCTGGTGCATCGAATGATGAAGGGTCCCTCAT	16958	A_95_P049361	BP132144
17522	207	12	405	AGAAGACCGCTGCTTAAGAACTTTCTGATTAGTGCAATTGATATATAGGATTTATGG	16960	A_95_P002311	BP534280
17523	207	13	798	AGAAGTACTTGGAATGTCAGTGAGGAGCTGTTATTTAAAAGTTTCTTTAGCTTACCAT	16962	A_95_P272666	EB452029
17525	207	15	700	TCACAGTTGTACAGTGTAGTGCTTTTGTAATGGCTCGTTGGTCTTCATTAATTGTACA	16966	A_95_P272786	EB678213
17526	207	16	283	TAGACTTGAACTTTGGATGAATTGTACCCTATGTCACTTGTCCTGAATTCCCTTTTTCA	16968	A_95_P164072	FG199807
17530	207	20	871	AATGCCCTGCTACTATATTAGTTGTTGGAATTTCTGGCACTTTGATTAGTTTTTCCATC	16976	A_95_P031271	DV999667
17535	207	25	359	GTTAGTTTGAAGTTGTATAGTAATTTATTTAGTGTACCAGGTGCAATCAGCAGGACT	16986	A_95_P053091	BP133088
17536	207	26	282	TAACACTTGGTGGTTTTTTAATACGAGGATATCTTGTACACAAGTGTTGTAGGGAAA	16988	A_95_P033544	AJ632822
17540	207	30	808	TTCCTTGTCAAACAGATAACGGCCTTTTATATATTGCAGCTCTTATGTTCCTGGCCAAA	16995	A_95_P177147	TA11894_4097
17541	207	31	844	GCTCCAGTAAACTCCTAGATTGTTCTAAAGCATTGGATCTTCCATATTATGTATTTGTA	16997	A_95_P198777	EB426417
17543	207	33	92	GAGACATAAAGTGAATATGGATTGTATTCCTTACAGATTAACCAAGTCTACTGCAAT	17001	A_95_P139707	EB443582
17551	207	41	415	ATCGCAGGATTAGCTAGTGGGTTATTATCCTTCATTTATGAAATTCAGTGCTGCCTTTT	17016	A_95_P088633	BP530161
17552	207	42	1127	AGTGCTTCCTTTCAACTAGTGATGGTAATGATCCACAAATCTTGTAAATAAACTCCCT	17018	A_95_P016121	TA13921_4097
17558	207	48	378	ATTTGTTTATGCTTATCCTCTTCACGCAGCGTCTCATCTTGTTTTGAGGAGCAGAGGG	17030	A_95_P086225	BP529480
17564	207	54	0	AAATTTTTGCCTCACAAGGAAAATTGATTTGTGGTGTGATCCGTTCCAATCCTTGTCC	17041	A_95_P030176	A_95_P030176
17575	207	65	454	TGTGGCTAGTAATTCATTTGTGTGATCTGTAGAAAATCTGCAGACACCATTCATGTCA	17063	A_95_P256169	EH618184
17576	207	66	917	TTTTCTGGATTGCTCCTCTTGGTGCGATGAATTTTGCTGGCTATGAGCTAGCAAGGAA	17065	A_95_P209857	EB424838
17579	207	69	507	GCACCTGAAATATCAGAAAGAGTAGCTTGTACTGCTGTATCTTTTAGGAAGTTTGTA	17071	A_95_P002221	FG637017

17582	207	72	879	CTATGTTAAGACTTGCATATTCCCGCAGTATGAACATTTCCTTAGTATAAAAGAATCCA	17077	A_95_P010521	TA13014_4097
17583	207	73	248	ATTCTAGAGGCTCAGATTTGTGACACCGGGTCCTAGTGAGATTATATTGTGTATTTTG	17079	A_95_P027381	BP534488
17585	207	75	348	CTGCCTGGGATAGAAGCTCTGATATCAACAAGAAATCTTTTTCAGTTGAGACCTTTAA	17083	A_95_P079730	BP527835
17586	207	76	862	TAGATGGCTGAGTCACCTGAATGTTGGTGAGTTTATTTCTTTCTGCACATTGATAGAC	17085	A_95_P227809	EB678753
17587	207	77	761	TTTATTCTACAGTATCTGAGATGAGAGACTGGAGTGTAGCCAAAGCAGCTGGTCTGC	17087	A_95_P305358	FG167679
17590	207	80	369	TAGTTGGGGAGGAAATCGAAGTTGAAGCCAAAGTATTCACGTGTTGGGAAGACAAT	17093	A_95_P068830	BP137226
17591	207	81	811	CTAACTCTTGTACTTGTTGAATATCCAGTAGAATCTGTTACGCTTAAATATTTTCGGTC	17095	A_95_P093433	EB439408
17592	207	82	861	GCTGTGCCAATAAACTAAAATTTGAAATACCATCTTTCTTTTGGATGATGGCCTCCTTT	17097	A_95_P244912	DV159753
17595	207	85	441	CTTCCCGATATCTTCAATCCTAGCATTTCTAATCATAGTCCTACTTCCTTGATGAATACT	17103	A_95_P265741	AM796086
17596	208	1	157	GATGCAACCGTCTTAACCTCATTATGGACGTTTGAACCTGTGCTCTAAATCATCGAATT	16940	A_95_P154717	EG649728
17599	208	4	770	GGCCTGTGAGATGTTCTCTTGTTATATTGCATTTTCAATCAATGCTAAATTGTGTGAGA	16946	A_95_P108762	TA12161_4097
17601	208	6	734	GTGCATACATAGAGCTTTGTTAAACAGCGATGTCCGACATTTGACTCGTGGAGCTGAT	16949	A_95_P212912	TA19936_4097
17603	208	8	796	TTTCGTGTTCCAACTGTTGATGTTTCAGTGGTTGATCTTACAGCGAGGCTTGAGAAAG	16953	A_95_P214717	EB425616
17604	208	9	524	GTCCCAAGAGTGTTATGGGAAGAACAAGTTGGTTTTTGTATAGAATATACTGTATGCT	16955	A_95_P209237	TA19146_4097
17605	208	10	668	GAAAGGATGTTTCCTCTTTTAAACTTGTATTCTGCTTCGATCTGTTTTAGAACTTCTGA	16957	A_95_P212587	TA19868_4097
17609	208	14	729	CACCCATACAGTTGGCTTAGTAAGGTTTTTCTAGGATCCAAATGTAGTAATACACTTAT	16965	A_95_P231234	EB440239
17611	208	16	497	AAACACGGATGTTATTGTGTTGTCAAGGATCCAAGACAATCTGGATCTGAATTTTGAA	16969	A_95_P303788	FG638864
17612	208	17	586	CTATATGAATTCTCGGTTACCATGTCACTCTCACTCTGTTTAAGCTCATCAAATATCTT	16971	A_95_P233504	FG639166
17633	208	38	706	TGAGGTAGAACCTTTTGTGATGTTTGAAGAATCTAAATAAAACGTCAGTTGATTGTG	17011	A_95_P147722	EB452239
17634	208	39	805	GCACCACAGCTATTGCATGTCGATTTTAATTTCCTAAGAGTTTCTTGCTTGTTGAAACT	17013	A_95_P097088	TA11961_4097
17635	208	40	4821	GTCACTTCACTTTAAGTTTGATAACTTAGTTGTTACCATTTCGGCTGTACAATATTGGC	17015	A_95_P025026	EF520731
17639	208	44	468	TTACGAATAAATCTAAGGTTTTACTCTTGAGATGCATGATTGATGTGTATGCTGTTTG	17023	A_95_P180552	TA12775_4097
17640	208	45	343	AGGGTGAAAGCTACTGGATAACTTATGTATATATTTAGACGCTAAGATTTGAGCAAT	17025	A_95_P209672	TA19240_4097
17641	208	46	790	CTTTTTGTAATGACTGTGTAAGACGATGGTGGAATATATGTAATTGCTGTCTGTTTTA	17027	A_95_P014461	TA12122_4097
17642	208	47	913	TGCAGCAGCTTCTGCGTAGAACTGCTTACGTGTTTCATCTCTGTATCAATAGCTTGCA	17029	A_95_P227554	DW000208
17651	208	56	649	TGGACTTTACTTTCCTAGAGATGAATCCCTTCGCATGGTTGAATGGAAAGCTTATCCT	17046	A_95_P161032	EH619740
17653	208	58	711	ATCCATGAAGGAGATGAACTGCTTGAGATAAATGGGGAGAGGCTTGATGGAGTTGA	17050	A_95_P150732	EB680859
17658	208	63	385	AGTGATGATCCCCAGCTTATCATAACTTTGGAAGAAGGGCGTGATTATGTGTTGGTC	17060	A_95_P157622	EH615676
17660	208	65	804	GCAATGCCAATCATAATTGATAACTATGGGGGGTTTTTTGTACCAAAACCAAGCACCC	17064	A_95_P013781	TA13953_4097
17664	208	69	402	ACCGTCAATTCTACCCCGAGCTATTGGAGAAGGAGGTCACATATTACAAATCGACGTT	17072	A_95_P161377	TA17844_4097
17668	208	73	366	TTCAGTTCTGCAGATGTAGTCAAACAAAATTCACCTCAATCACCATTGAACCTGGTGT	17080	A_95_P104487	TA13616_4097
17673	208	78	1759	AAGGGCCAAATCTCTATGTTACCATAATACAATGTGGTGGTTTGGATTTTCTATTGGA	17090	A_95_P003851	TA11817_4097
17681	209	1	749	AGCAGTAGTCAATCAATATAGGATGGGTCACTGTCTCAGCAGCAGCGCTAGAAGCAA	17105	A_95_P308488	FG147652
17685	209	5	591	AAATGTCTGCCAATATGATGGTTTCAGTATTTTGCGGAATGTCCCACTTTTCTTTTCTC	17112	A_95_P245477	FG642695

17690	209	10	841	GGAGTGCTTTGAAACAGTTTTTATCTGTTTACTGTGTTGTGGATTCTTTATTGCGTGTT	17122	A_95_P184872	EB424704
17691	209	11	253	ATCTTCAATATGAGCTTCTACGAGGGAACTCTCTCTGAAAGTGGTGCTGGTGGATAT	17124	A_95_P102347	DW003761
17692	209	12	328	GGATAATGTTAACTTATTTGTTTGAGAAAAAACCTTGTAGGGAACCGGTTTCCCCTTG	17126	A_95_P089138	BP530364
17695	209	15	296	GCTGAGACGATATAGACCATATAAGTACTGTATTTTTGGAATTGCTAGCACTTGTACT	17132	A_95_P155167	EG649930
17699	209	19	358	GATCCTGTTATATGAATCCCCTAAAAAGTTAAAGGGAAAAGAAGGATAATGCTGCTT	17140	A_95_P118167	DV161188
17700	209	20	713	TCTAATGGATATGGACAGTGGTTGTTACCAGAAGATGCAGAGAGGATTACCAAGTC	17142	A_95_P218307	EB440007
17704	209	24	859	CAAGTCAATGTTTTGTGTACTCTTTGTTGCAGCTCGAAATTCACATTGCATGTACAATA	17150	A_95_P008006	TA13354_4097
17705	209	25	1105	GTAGTAATTGTTGTTTTTATCTTTGGACAATGTATTTCCGGTTTTAGTGGAGAAGGGT	17152	A_95_P206292	TA18482_4097
17708	209	28	632	TAAGGTGAGTGTTGCTGATTCTAGTGTTCGTCCCTTGGAGGTGTTTATGTACAGTATT	17158	A_95_P069950	D87821
17709	209	29	411	TATCTGAATCTGGCTACTATTGCTCCTTTGTTGATTATACTTGAGGTCGTTTGTGCGAA	17160	A_95_P286208	FG644682
17710	209	30	681	GATCAGCATGATTAAAAGGTGACTCGGAACCTCTTGAAGGCAAAGCTACAAATACCT	17162	A_95_P222282	EB438136
17711	209	31	1490	CCTATGTGTGGCTGTTAGTTACTATTTGCTAGATTCAAGTTAGGACTAGGTTACTTTAA	17164	A_95_P197267	TA16524_4097
17712	209	32	496	TTCATCTTCCAAAAATGTGCACAGAAGCAGGCTGATAAGGAATCTGAGGCCGTTTTCT	17166	A_95_P002576	FG147651
17717	209	37	883	GAACTATTTTGTAGGACTTGCGTCCAAATATAAAGACGTTATGCATTTCCATTGATAC	17176	A_95_P202172	TA17578_4097
17718	209	38	633	GGAAGAGGTTATCCAATCATTTTGCAAGTCTCTTTGTAGTTGAATTAATTTTTGGGGC	17178	A_95_P155192	TA18703_4097
17725	209	45	1338	GTCGCATTGACGATTCTAGTTGAGAATATTAGTAATGCAAAAGTTTTGTTGTTGTGGT	17191	A_95_P251832	AY395738
17727	209	47	746	GTTTTTGTATTTGTGAGTTTCTAATAAAGTTCTCAAATGCATGGTGTTTGGTATGGGG	17195	A_95_P246647	EB429369
17730	209	50	2512	CTTTTGAAAGAAGCTATTCAGGAACAAATGGACCGTTTTATACTTCAGGAACAAGCAT	17201	A_95_P017531	TC75692
17731	209	51	1131	CTAGCTAAGATGTCTGAAGACAGCCTATTGCCATAAACCAGTGAAGCATAATCTATTT	17203	A_95_P242737	AB433897
17734	209	54	726	TAAAAGAATGCAGGCTTGCAGAGCATAGCCCTACATGCAATCCATTTCACGGACCACA	17209	A_95_P161312	EH620054
17743	209	63	428	TGAAAAATGACGGTCTGATGCTCCAGCTGAATTAGTACGTTTAGGAGCCAAGTGTTG	17226	A_95_P093428	BP532257
17745	209	65	1099	GGCTAACCGTGTACCATTCCATAGCAAAATTAGTAGCTATTATCACTATATATTTGTG	17230	A_95_P019951	TA15403_4097
17749	209	69	271	CCCTGTTTTGAGAAAGTCTACAAAAGCAATTTTTCATGGCAAATCTAGAACTTGGTAG	17238	A_95_P222357	TA22016_4097
17754	209	74	173	TGAATCTCCTGGTGCCTGAAAATGGTTAGCAAATGTGAGATGCTGACTGCCAGTGTT	17248	A_95_P104652	CV017119
17758	209	78	0	CTGGGAGAACATTTACTAAAGAAGTTGTACAAGCTATGGCAACATTCAATGAGAAAA	17256	A_95_P258811	A_95_P258811
17760	209	80	1190	CATCTGGTTTCATAGGTTGTTTATCAACTATGCAGACTAACGAAGTTTTGCAGTTGAT	17259	A_95_P032201	TA14050_4097
17764	209	84	789	TTAGAGTTCATTTCTTTCCTACTTGGAAATTTGAGCATATGAACAGCCGCATTATGTCA	17267	A_95_P188752	TA14640_4097
17767	210	2	373	ACCAATGGCTTGCCTAATGTTGCTTTTCCAAGAATGCTACTATTATTTATGTTTGAACC	17107	A_95_P023741	TA13130_4097
17768	210	3	622	TGAGGACTTCATTGAACTTGTTGGCTCTAAATGGAAGTGCAGAATTATCTATTACTAC	17109	A_95_P015986	EB435292
17770	210	5	245	GTGGATGACTTTCTTCCTGATCTTTGTTATGTACAGAATGTTTCTCATTTTCATGAATG	17113	A_95_P121167	DW001168
17771	210	6	334	GGATTAGATCTAATCCTCGATACCTAAAATAATGATCCTTCCTTTATTAGCCTTTCTCCA	17115	A_95_P111707	CV020338
17776	210	11	450	ATAGAACAGCGGCTGTGAAGCGAACGATTCATTTTGTTTACTGCACTAACTTTTGCTC	17125	A_95_P193687	TA15725_4097
17783	210	18	373	GTAAATTGAAGACTTGCTGACAGATTGCAAAGCCACAGGAGCCCAGATCATGTATCT	17139	A_95_P087383	BP529780
17787	210	22	668	AAGGTCACCTCTTTTGCTTCATCTCGAGATAAATGGGTATAACTCATACCTTTTCTTCC	17147	A_95_P225222	EB445165

17792	210	27	849	ACACAGTAGACGAGGATCTGCTTGTGTAAAGATGGCACTCATGATGATTGCACGAG	17157	A_95_P224932	FG147089
17793	210	28	0	TTCAATGCAACATGGACATGTCATTTGCTGATCCATCACCTATCTTGTTCATCCCTAGC	17159	A_95_P259286	A_95_P259286
17794	210	29	220	GAAAGCATTCAGAAGGTAACCAAAAATTGTATTGGAGATGTGGAATTTTATGCAGG	17161	A_95_P031996	TC76975
17796	210	31	758	GAGGTTCTTGGCTTCTCAAAGAGCCTACTTATTTTGCTGTGGAAACTGTATTTAAATA	17165	A_95_P017521	TA12515_4097
17799	210	34	1855	TGCCTTCTTAACTCTGCGACCATGTTTGTCAATATTTAATCCTACCTCCTCATTAAAA	17171	A_95_P237584	Y13466
17800	210	35	436	TTCCCCCAATTAGACCAGCCAAACTAGGCAAAAAGGGAAGTGCCACTGATATGAAA	17173	A_95_P239559	AM847113
17801	210	36	487	TAAAACATATTCCCTCTGTTGTAAACTTGTCACCTTTCAGTTTGAGGTTCGATTTTTCC	17175	A_95_P021076	FG631866
17806	210	41	184	TTCTCAAGAAAGGAGTAAAATTTTGCTAGATATAGCTGATGCACTGGAAGCAAATGA	17184	A_95_P136762	EB440509
17808	210	43	476	TTGCTTCTTTCAAGAAAAGTTCTATAACTTTTTTCTCTTCCCCGACTGTTCTGAGGATC	17188	A_95_P100323	BP535324
17810	210	45	499	ATTGCTTGAGTTTCTTATCGTCGGTGCTCATTTGTACATCCGAACAAAGGCTAATATA	17192	A_95_P091113	EB678107
17811	210	46	902	GAGGCTGCAAATTCAGCATTATTAAAAAGCTATGGACTAGTCCATGAAGACTGTATA	17194	A_95_P229904	DV159496
17812	210	47	286	CCGCCAAAGCAACTTTGTAACTTATATCATTTCCATTTCACAAGGGTTCTATTCATTTG	17196	A_95_P216487	TA20716_4097
17817	210	52	647	GTTGAAAAAATGGAGTTCAACTGAAGTTTTGGGGAGTTTGGTTGACCAAGTCCTGCTA	17206	A_95_P308083	FG644587
17818	210	53	1404	CGTGGCCATTAGGCAGTGCCATTGAAGTTGCATCATCATTGACTTAACTGGGAAATG	17208	A_95_P206857	EF051589
17820	210	55	841	TTACGGAATTTAGGGCCTTAGCTAAGTGGTTCCAGTGGCTATTGCCAGTAAGTTACA	17212	A_95_P273201	EB682721
17827	210	62	727	CATTATCTATATGTATTACGGTTCAAGGACAAGGCGCTTGCTTTACGGAGATGAAAA	17225	A_95_P292698	EB428134
17829	210	64	262	ATTTACTGCCACCCCTCCTATGAACCGAGAGGGGAACCATAACTATTCTTTGTCGGAT	17229	A_95_P034224	BP129934
17837	210	72	298	GTTCCTATCCGTCTAGGGTTTACTCGTGCCCTTTTTCCTTCTCAATGATGGTATTTTGT	17245	A_95_P188033	FS437228
17838	210	73	458	GAAGTACAATCACAGCACTTCTCCATTGTAACATTCTTAAAACATGCGGATGAAAA	17247	A_95_P022431	BP132516
17839	210	74	413	CAGAAAGATGCCTGCGAGAACTTCAAAACTGAAGATAGTAGGCAAAATTTTGCATC	17249	A_95_P220362	TA21591_4097
17842	210	77	1439	TACTGGATCAGCACCAGTTGTAAAGATAGCCTGTTTGGTCCAATTCGGCACGCGTTT	17255	A_95_P176417	X98161
17846	210	81	177	GACATACTCTGTGACTAAGAGGTAGGTTGATCACTCATTTGCACTTCGAGCAATATA	17262	A_95_P141902	EB445518
17853	211	3	536	TTCTCTGTACGCCCACATTTGTCAGATGCACCATTTATATTGCTGTTCATACTAATATT	17275	A_95_P266581	BP534234
17856	211	6	657	ATTATTCAACAAAATGCCAAGCTCAACCGAGAACTGGAGCTTCTGAGGCATGGACGT	17281	A_95_P305543	FG199826
17860	211	10	550	GCTAAACGTGTTACAGAATCCTCTTCTGTTTCTGTGCTATGCAAATGATTTGAGTTAA	17289	A_95_P121742	DW001833
17862	211	12	371	GGGGTGAAATGCATCTCTCTTGCGTGCTCTGTTTTCTTTGAAAGGAGGAAAATCCAG	17293	A_95_P092453	BP531808
17864	211	14	838	CTAAAGAAGGCTCCTGCTGGATTTGGCAAATCATGAGTTTACTGAAATCTACCAAAA	17297	A_95_P269006	EB678914
17868	211	18	746	TAATTGCGACTAGCTGATTTTTACTAAAGAATGCCATGACTTAATAGCTTTTGGTGTT	17305	A_95_P017001	EB437994
17872	211	22	422	TTTCGCTGATGAAATTGGTATTCCTTTTATGGAAACAAGTGCAAAAAGTGCGACCAA	17313	A_95_P156867	FG171924
17876	211	26	556	ATTGCGAGATGACACTTGAACGGATTATTGTGAAATGTGGCTATGTTGTAATAGATA	17321	A_95_P219607	FG640950
17877	211	27	350	AGGTGCTTGAACGGCTATGTGTTCTCGGTAATGATGTATTTTTAAACAGTTTAAATCA	17323	A_95_P107152	CV018234
17879	211	29	771	GAAAAGAGCTTAGTTCTTCCAGTAGTATCGCTGGACACACATCTTTTGCTCTGCTGTG	17327	A_95_P309558	FG142534
17887	211	37	767	GGAGAAACTTCATGTTCATGTAATTTTACTTTGTTTGCCAGTTTACCTGAGCCTTTCTC	17342	A_95_P258071	EB677495
17890	211	40	394	AAGCAGAGATGTTTGATGACCGTCCTAGAAAACCTGGTCGTAAGATAGTATGCCGA	17348	A_95_P023286	FG642251

17892	211	42	1393	GTTTGCTAATTGATACTGTCAAGCAAAATTTAATTCTACAATTGGTGGGTGCGGCAG	17352	A_95_P008416	AB032545
17893	211	43	902	GGCTTTAGAAAGATTTTACAGTGGGATACTGATATCGAAATTGACATGCTTCTTGGA	17354	A_95_P221857	TA21908_4097
17894	211	44	299	CTAGAGCATACATTTAGTGCAAAAAGGACTTGTTCAACTTATGCATACATAATCTGCA	17356	A_95_P194757	EH617633
17900	211	50	841	ATGGGGTGTGATGTTGCAGCTTGGTGCTGTAGCTTTTGAGGCTACAAGATTGGTTAT	17368	A_95_P217772	EB427867
17903	211	53	210	AACCAAGATGTACAAACTTCCACACAAGGAGTGACAGCTTTTAATCTTTTCCCTCGTA	17373	A_95_P033744	AJ632934
17904	211	54	686	GTTTAGAGGGAGCAGATTTGGTTGCAGATTGTAGTCTCATACAAAATCAGAACACCC	17375	A_95_P266641	EB683902
17905	211	55	774	CCGGAGACAATATAAGATCCTTTCAATTGTATGTTTAGGTCATAATGTGCTGTTTTTC	17377	A_95_P218842	TA21264_4097
17907	211	57	712	CAAACTTCAAGGACAGCTCAGTTGGATACAAATTTTACAGACAGAATCTTCTTCTCGA	17381	A_95_P221247	EH622995
17908	211	58	1096	CTGATTATTTAATATGCTGCAACCATCTATACTTGAGATGTGCAAATAGAGCTATGTT	17383	A_95_P014386	TA16663_4097
17909	211	59	587	TCTTGCAGCCAAAAACCATTCCATCCCCATTCGTGGGTATATATCATGTGTTGTTGGC	17385	A_95_P120857	DW000825
17914	211	64	360	ATTTCGGGGTTTTAGTCCAAGGATTGTTGCTCCGTTTAGCTCAAATTTTCAGCTTTGTT	17395	A_95_P097523	BP531659
17919	211	69	587	TTTCCATCCTGTATAATTTGTTGAAGTGATATCATAAACAGCTGGTACAGGTGGTCAT	17405	A_95_P082995	BP528647
17922	211	72	319	TAACTTTGAAAGACAACGTTACCTGTACGAATTTGGAAGTTGGTTGACAAACAACCC	17411	A_95_P102852	CV016231
17923	211	73	274	CCTAGTGTTAGTCTCTCTCAAGCTTCGCTCATTGACATTTTCTTGTATAAGAGGTGCA	17413	A_95_P127567	FG135867
17924	211	74	111	AGCTGTATTGAACCGGTCTGAGAGAGAACTGAAATGGCATGTTGATGAGATCCCAC	17415	A_95_P156727	EH614748
17925	211	75	384	CCATTAGAGTACCTTAGAACTTCGAGTTATGGCATAAGTGAAGCACTCTTAAGTTCAT	17417	A_95_P130107	EB430105
17928	211	78	2334	CAGTGAGTAGGTGTTTGCAGAAAGCATTAGAAGTATAGAAATCATCAATGAGATAG	17422	A_95_P306688	AB263747
17930	211	80	494	GAGAAACGTGGGGGAGGGGGCTTTGTTTCTTTTTGTTGTTTTTGAAATATTATTAATT	17426	A_95_P061695	BP135325
17937	212	2	771	TTTCATTATCAGCATTCCTGTGCTGTTGTTTCCGCGAATTAAATGCTAAATCTTCTTTG	17274	A_95_P234394	DV160348
17940	212	5	309	AAGGAGTACCGCACAAAAGGTGGCAGACTGAGCTCACCAACATTTGCAACAGGATA	17280	A_95_P103142	CV016362
17942	212	7	0	CCGTTCAAGGCAAATCGAAGCTTTCCATCTACTTCGGTCCTAGAGTTGACAATCTTGA	17284	A_95_P239669	A_95_P239669
17945	212	10	280	GTTCAAGATTTTTGATGTACCGTCTATCTGAAGTTGATTGTCACGTTCTAATGGTTTT	17290	A_95_P004531	TA17295_4097
17947	212	12	1214	GCGTCTCTTGTAGTAAAAAATATCTTTGGGTTATTTGTTCCAAGGCCTAAACTAGTAA	17294	A_95_P028286	TA20135_4097
17952	212	17	401	AAGATCTTGTGTGAAACTTTTATTCCCTTGGGGATTTGTATTCTGCTTCAGCTGAATT	17304	A_95_P031006	FG626648
17953	212	18	426	GGAGTCCCCTTCTATTCTCCCCTATGTCAATTACCTTATGTACTTCTTTTGTTAGACTCC	17306	A_95_P098943	BP534702
17955	212	20	394	GATATGGCCAGTGCTACATTGATTCAAATACTGAATTAGACGTCACTTATAACCTAAT	17310	A_95_P022461	TA13487_4097
17956	212	21	839	ACAGGATGCTAGGGTTATTCATTTGCACAGGAAACATGAATGACACCTTATATAAAA	17312	A_95_P229574	DV160201
17961	212	26	831	TCTCGAACAGTCGAGAAAAGATCAAGAAATGCACCAGTAGGAGTTCCTTCCAGCAA	17322	A_95_P191777	EB450564
17963	212	28	149	GTAGGCTGTGACTATATTGTGCTACTCATGTTACTAACCCAACCACCCCCCAAGAAAA	17326	A_95_P067680	BP136939
17964	212	29	723	AGTGAGACTGTCTTTTCTTCTTCCCTCACTATTATCAGGTGGAGCCTTTTATTGAATAT	17328	A_95_P015821	EB439146
17966	212	31	587	GCTCTCTTCCCAGTTGTAATTTGTTGGTATGATCCAATTGTTTTTAGGCCCTTTAAGTT	17332	A_95_P042746	BP130434
17972	212	37	1134	ATTTAGTATGCCTGATTGGTCAACGATGTGTATATAAGTCTTGCCAGCTTTATCTACG	17343	A_95_P191882	TA15331_4097
17977	212	42	448	GGGATCACAGTGGGTTTGTTGTTGTCATTGTACTATTTGACGATTCACTCCACTTTTT	17353	A_95_P131217	EB431362
17978	212	43	505	GTGGTTTGGAGTTTCTTTCTTGGCCGTCTAAATTATGGGCTTAAGGTTTTCTTTATTCC	17355	A_95_P198512	FG642795

17979	212	44	123	GGGAATACATTCCGCTTCGATTTGCAGAACACATTACAGAAGCTATCCGAACAATAT	17357	A_95_P042911	BP130478
17981	212	46	781	TCAGATACAATTACTTTTGGCTATCCATCATCATTGGGCTCAATCTAATGTTTTCTAGC	17361	A_95_P127352	EB426901
17983	212	48	464	GCAAAATAACGAGTTAAGGAAGTTTTCGGACTTTCCTCAGTTCTTCCCTCCCTCTCTCT	17365	A_95_P071240	BP525655
17984	212	49	654	TTGGTGATCGGGTGTCAAGTTTGTTTGTGAAAGATGGTTGTAATGTTACTATAATAA	17367	A_95_P016221	EB431066
17988	212	53	1071	ATCTCTGCAACTCTCCTGTATTTGGATGCTTCTTTTTCCTGATTGGAATGACCAATTGA	17374	A_95_P251767	AB119476
17991	212	56	772	CTTCAGCGTCCTCAAGTCTTTTTATCAGCTTGAAAGAAAAGGCAAAATTAATGAGGTA	17380	A_95_P179207	TA12449_4097
17998	212	63	753	ATACCAGAGACATACTGAGTTATGCAAATGAAAAGATTCTGGTGAAGCCTTAGCACA	17394	A_95_P189227	TA14745_4097
18002	212	67	632	AAGAGATGCAGCGTGTGTGCGCTTGGATTTGTATTTAATTTCTTGAACTTTGATTATT	17402	A_95_P134787	EB437562
18003	212	68	807	ACCCAGTTTCTTCAAATGCACAGTCAATAATCAATGGCTACAGATTAAAGCTGTTGTA	17404	A_95_P010021	EB677669
18004	212	69	455	AAGGTGAATGAACCTTCCTCCCTACTGATAAATTTCGTCATGGAAAACGAGTACTAGA	17406	A_95_P261581	BP132748
18006	212	71	656	CCCTAGTTTTTTGGTTTTTACTTACTCCACCAGCAGAACAAGATATGGTTAAGTTTTAT	17410	A_95_P030346	TA11873_4097
18007	212	72	906	CGAAATATGTGTTCGAATATGGTGATAGTCTTTAGAGCCTCACATTGTTTAAGTTGAG	17412	A_95_P258201	TA11901_4097
18010	212	75	681	GTGTATGTATGTTAGCTGAGACAGAATAGTGTCCTATTTTCATGTGTGAAATGCTTTC	17418	A_95_P030056	EB438892
18015	212	80	415	ATATACTTGAGTTTCTGGGCAGAGGTGCACTACAACTCAATCTATCCTCAAGGAGACT	17427	A_95_P091448	BP531357
18022	213	2	710	TTCCTTGCCCAGCCTGCAGAGAAATATCCGTCAATATTCGCTAAGGATTCTATATTTG	17439	A_95_P160422	EH619111
18023	213	3	91	CCAACAATTAGTCCCGATTTTGAGGAGTTTATTTTCCCCAAAATTCTTGTTAAAGTTTC	17441	A_95_P130142	EB430151
18024	213	4	377	TGCGCTCCCATAGATGTAAAAAGTGTATCATTTGGGGATCATACTATATTTGTGAGTG	17443	A_95_P003676	EB433911
18029	213	9	904	AGATGCCAATTGATAGAGCTTGAGCCTGCTAGTTTTTCTGCTTGTAACCTAAACTGGA	17453	A_95_P244957	EB679726
18031	213	11	826	CTCGTGGCGTCACATGTGTCTTGAGTCACTAAATCTATTTGATCTTATTTTTCCCATTCA	17457	A_95_P218467	TA21181_4097
18037	213	17	742	ATGTTTCGTAGCCCATGAAAGTGACTTTGGTGGAGCGGCTGATTATCACACATTGCT	17469	A_95_P160182	EH618839
18043	213	23	676	AAGCTGACAATCAGCGTCATGCTGGGGATAATTCTGATTCGAGCTCGCTTATTCATG	17481	A_95_P001051	FG148930
18044	213	24	1097	CCTAACTAAGATTGTTCCTTGAAAGAGATCCGTATCTTGTACGCCTTTTGGATTTTATT	17483	A_95_P191207	TA15179_4097
18048	213	28	672	TCTTTCATCTTTTTTAGCTGAGGTTTATCGGAATCGTCTCTGTGCCTCCAGGTGGGGTA	17491	A_95_P256464	FG140967
18051	213	31	406	CAGTAGAAATTGTTGTGTACTCGTTTCTTTGTTGAATGCAATAAGAGTCCTCAATTTT	17497	A_95_P154872	EG649794
18055	213	35	480	GATTTGCACAAACTTCGAGAGGATTTGCTGCAACTGCTGTCTAAAGTGTCTACCTTAG	17504	A_95_P170741	EH664973
18056	213	36	618	CAGGGATGATGAGCAGAAAGTGGCCTAAGATTATTGCCACTAAGTAAGAATTAGTTT	17506	A_95_P153292	EB683563
18057	213	37	1556	GGTTGGAGTACCTACTATCAATTTTGTCGGTGTGTCTTTGTTTTGTATTGTAAGTCTAA	17508	A_95_P179672	X79141
18058	213	38	49	CGAAGTCACTAGAGGAATATTCTGATACTTGACAGGCTACCAAAAATCGTAAAAATG	17510	A_95_P104407	CV016994
18061	213	41	706	AAAGGTCCAATTTCAGGTTCATTCTTCGTCCTTTTTCTCCTATCATTAGATGATTCTATG	17516	A_95_P136452	EB440211
18067	213	47	1110	TGCTGTAAATTGATGGATATGTGGATTTTAGTAGCAATATAGCAAGTCTGGTGCTTT	17528	A_95_P024766	TA17938_4097
18069	213	49	816	GGGTATGCATCTCATGTAAGTTCATCAGTGTAAAGGTCTATGTTCTCCCCTTGATTTTT	17532	A_95_P116237	DV158848
18070	213	50	491	TTGCGCTCCGGAGATGGGTCATTTCATGCATATCTAGAGCATTGTTCCACTGTATGCA	17534	A_95_P091298	FG159805
18076	213	56	856	GCTCAAACCTTCGTTCACATACAATTACTAATGTCCAATCAAATGATGATAAGGTATCT	17545	A_95_P208197	EB424930
18080	213	60	150	TGTATTTGATGGGGCCCAAATGCTGAAATGACCTCTGTTGCTATGAAAGTTCAAACAT	17553	A_95_P241210	AJ718197

18081	213	61	533	CACATGTACTTTACGCAATCATTGCCCTTACTTTATGTATAGATACTCCTATGAAATCT	17555	A_95_P270741	AM832190
18083	213	63	369	ACCTGTTTACTGGATACTGCATACTTGTTATACACAAAAGAAAATGATGAACGGAGA	17559	A_95_P129672	EB429639
18090	213	70	984	CCGTTTGGATCATCTATTTGGAAAAAAGAAAAGCACAAGGATTAAAAGCTCCTTTAG	17573	A_95_P176942	TA11832_4097
18092	213	72	390	CGTGCTAGGCGGGGGCATTCAGCAGATAGAGATTTTATTCAACAGGTTCAACTGAA	17576	A_95_P308533	FG642724
18093	213	73	758	TGCCCCGATGCTCCTAGGAGGCCTGCAAATCGATTTAAAAATATTGACAAGGATTA	17578	A_95_P185912	EB434114
18094	213	74	642	ACCAGATTCATGATAATGATATCGTGTTTTTTGGTTATGGGTTCTCTGATTCTCATGAT	17580	A_95_P025417	FG637548
18095	213	75	1398	AGAGCTCAAGGAAATCCGTGGGATGGTTTCTTTTCTCATAATTGCTGGTTTGGAGAA	17582	A_95_P257836	EF110692
18104	213	84	627	AAACCCATGGTATTAGGAATCCATTACTCTTCCCTCCTGGTCTATGACAGTTTCCAATT	17600	A_95_P081785	BP528350
18105	213	85	511	TGTGCCGAGAGTGTTGCCAAAAAACGAGGATCCTAAATTGGTTAGTAGGAATAAGA	17602	A_95_P151762	EB682700
18108	214	3	790	CTCCTTTCCCATGGCACTTGGTGGTTTCTACTTATGGGACATACACTTATCAGCTAAT	17442	A_95_P195642	EH621524
18111	214	6	294	TGAATGTACAGTGGTGTTTTATGAATTGAATGTCTAAATGGGGATGCATTCCCTAAG	17448	A_95_P191792	TA15313_4097
18116	214	11	126	GTGGATTGCTACTATTTGCAAGAGCACTTTGCGGGCATGTTAGGCAAAGTCATGTTT	17458	A_95_P033894	AJ717866
18118	214	13	277	TTCTTCAATGAAACAGTTCACATTTTCCGGCCTCTCTTCTCTCTTCTAACTACGACTGA	17462	A_95_P066300	BP136564
18119	214	14	163	CCTCCAGCCTAGCCCAAATAAGAGTATTGTTTTTGTTGTAATGTTTATGAATGTCTAAT	17464	A_95_P139112	EB442808
18121	214	16	762	CCTGGAATTGATTTTGACGTTTCAATTTCTTTTTACCAAACTTCACGCGATCATCGTCT	17468	A_95_P024096	TC69715
18122	214	17	892	GATGGCCTTGTAAAGCTGTCGTGCGTTACCTGATAATATAATGAGATTTTGTTTGTGT	17470	A_95_P000146	X52743
18129	214	24	821	CAGATACGTAGTTATCCCGCTCTGGGTTCCTGATATTTACTTAATTGTCGAGGTCCTT	17484	A_95_P272326	EB449303
18135	214	30	854	TCTCACCATGCTTCTGAAGAAAGGAGAAAGAGGAGGACTTACCTCCCTTTGACATAG	17496	A_95_P292788	FG155230
18139	214	34	346	GTGATCTACTTGTGCTTTTTATCCATTCCAGCCGTGGAGGGTAGGGCTTCTATCCTTTT	17503	A_95_P092598	BP531878
18141	214	36	394	CATAATTAGCTATCGTTGAATCCCGGTGGACTGCTGAAGCTGGCTAACTACTGGGAA	17507	A_95_P075525	BP526751
18143	214	38	283	ATCCTTCTCATAATAAAGTTTACTTCAAGACTCCTGTAGGAATTGGAAAGTCTTTTCCT	17511	A_95_P161322	EH620068
18144	214	39	1516	ATGGAAGAATCAATTATGATGAGTTTGGTGCCATGATGAGGAAAGGTAATCTGGAT	17513	A_95_P063925	FJ026805
18147	214	42	800	GACTGTATACGTCTTTACTCTTTCTGATGCATATCGCGACGCAGGATAAAGAGGTGT	17519	A_95_P298553	FG160018
18154	214	49	818	TATGAATTCCAAGAATCCTGATATGGTCGTCTTCCACCTTGTAACTGACGAGGTGAA	17533	A_95_P151207	EB681448
18158	214	53	438	CCTAGGGTTTTGTATTTTTATAGCATCTAATATCCAATGTGATGAAAGGCACTGCCTT	17540	A_95_P252714	TC63485
18160	214	55	285	GGATCACGTCAGATAACGGAAAAAATAATTGGATCGAGATTCATAACTATACATCAT	17544	A_95_P012336	BP530730
18161	214	56	206	CGATAAATCTGCTTAAGACACTACTCCTCAGATCCTAATATGCTTATTGTCTTAAGTTG	17546	A_95_P118342	DV161351
18165	214	60	814	AATACACTGCGTCATATTTGAGTGTCCTCGTGTAATTTTGGTGCATGAAATCAGCGA	17554	A_95_P262496	FG139580
18166	214	61	805	TTTTACTGAGAAGAATGCTAACTTGCAGGGTGTGGAATTGAAGACTCAGGATGTTG	17556	A_95_P199602	EB425577
18173	214	68	694	AAGAAATGTACCGACTCTTGTGACGCCTTGTGTTTGTTGCAATAACAGAAAAATTGT	17570	A_95_P025406	DW004280
18178	214	73	162	CTCCCCTGAGCATCTGTATACAATTCTTAGTTTAGATGTCTAAATATATAGACATGGC	17579	A_95_P120637	DW000599
18179	214	74	893	GCGGAATTGATGTTAACTGTGCTGAAAGTGTATGCTTTTTATTGTGATGTTGTGTATT	17581	A_95_P014796	TA14870_4097
18182	214	77	1514	GAATATTGCATGTGTGAGTTTGACTTGAAACTTCTATTCCTTTTGCTGCATAGATGCA	17587	A_95_P006496	TA13272_4097
18183	214	78	797	GCAAACCAAACAGATGTTTGTACAGTAAGAGGAAGCAAATCGTGTTTTTGGTATTTT	17589	A_95_P009256	DV159699

18188	214	83	481	TTCCCAACGTGACATGTCCAGATCTTACTTCTATTTTAATCAAGCTGAAATGGTTTCAT	17599	A_95_P185122	TA13846_4097
18190	214	85	781	ATTTGCCGAAGTATGGGGAAAGCTGTCATTGTTGCCACCAACATGCTGGAAAGCATG	17603	A_95_P206647	TA18563_4097
18195	215	5	472	AGCTACATGATATGAAGTTCCAGTCCAACTAAACAAAGGTTGAGGTGGGTTTTTGAA	17612	A_95_P130942	FG623870
18198	215	8	515	CTGTTAATTGTTATGTATTTTAATAGGGTTTGAGTTTGATGAATACCCTGGTCGTGCT	17617	A_95_P074725	BP526541
18199	215	9	1333	ACTCGGGTGGTGAAGAGGTTATATATATAAAGCAGGGCTTCTGCTGCTGAAGGAAT	17619	A_95_P202167	TA17577_4097
18211	215	21	0	CTCTTTGATATGGATCCAAGTGTAATAACAGGTGCAATCGATCAAGATCCCATAGCA	17643	A_95_P302318	A_95_P302318
18214	215	24	862	GGAAGGAGGAAGACCACTCGATATAACTGTCACGAAACTGGATGTAAATAGTATTA	17649	A_95_P010011	EB427799
18218	215	28	759	ACTGCCTCCTCCCTCATATCATACCCTAAACCCTAATGATCTAGAGATTACTGTGTTAT	17657	A_95_P302403	FG177828
18219	215	29	803	AGCATCCCGTGCCAGGAGACAAAGTATGATTACGTGAACGGATGCAATTCAGATGC	17659	A_95_P126842	EB426202
18220	215	30	352	GGCTGCTCCCTGTATCTGTCGTTAAATCTGATATATGGAATTTTGAACTTTTTCTAGCC	17661	A_95_P029491	TA17540_4097
18222	215	32	645	TGTTCTATAGGTGTTTCCTTAAAAGAGGGCGATCTAGGGACCGATGATGTATGTTCC	17665	A_95_P155957	DW003703
18223	215	33	711	CTTCTTGTTGCTCAATTGGAACTTTTGTTTTCTTAAAGTTTCTAATTCTTCGACAGGCC	17667	A_95_P315028	FG199077
18224	215	34	1269	GAGTGAAGTTTACAGTTATGTTGTCTCCAAGCAAGACTAAGTATGTGTTGTATGCATT	17669	A_95_P178817	TA12351_4097
18227	215	37	580	TGATCACATGCTAAAATGATCATTATTGGTGATTCAGAATATACCTTGGCAGTTCTGT	17675	A_95_P156572	EH614292
18231	215	41	354	CTCTATGGATTTGGTGGTTAGGTTGTATCAGTAAGTGATTTTAGGTAAGTGTAATGG	17683	A_95_P104892	CV017209
18232	215	42	626	TGTGGCTTTTGATGATAAACTCCTCCTTGTCAAGTATAGGAATTGTGAATGTTGATTG	17685	A_95_P017791	EB426919
18233	215	43	313	AGAAAGTGAAGAATACTGCACTGTACATGTTGAGCCGCACCAACTAGATTGTCAGGT	17687	A_95_P090243	BP530876
18234	215	44	669	GGAATGCTTTCCCATAGGTGAACATGTATTACTTGACCTTTATCTGCAAGCTACTAAG	17689	A_95_P068390	BP137117
18235	215	45	463	GGTAGATGAGTTACTCTTTATATGCTGTGGTATTTTGCCCTCCAGACTTTATGTATTAC	17691	A_95_P019946	TA13616_4097
18238	215	48	682	CAGACTACATTTCCATATCCACTTTGAAGAAACCTGTACCATGACATAATCAAGGATT	17697	A_95_P194112	TA15823_4097
18241	215	51	246	CTTTTCTAAAAGCCTCAGGAGATGGGCAAGCAAATGGTCCAGATGATGAAAACGTTA	17703	A_95_P070115	BP192523
18245	215	55	1061	TAAATCATATGGTATGACCCCACTCCATCTTGCTACTAAGGGAGGTCACGTGCGAGTT	17711	A_95_P148312	TA15076_4097
18250	215	60	510	TCAAAAATCATACAGAATCCCTCTACTCTGGAGCTGCAAAAGGCAGCAAATCAAGGA	17721	A_95_P082600	BP528551
18251	215	61	265	ATAAGACTACTCCTCCAACCTTTGAATTGCCAACTATGGCTCAATATAACATCAGCAG	17723	A_95_P085700	BP529351
18255	215	65	806	TACTTGGCTTATTGAAGATGGTTCCTGCTGCAATGATAATCAAGCACATCATATCTTT	17731	A_95_P147067	EB451309
18256	215	66	134	TACATAGAACATGAACACAATCAGAAATACAATAATCTTTGTGGCCTTGGGTTTCGA	17733	A_95_P145647	EB449412
18258	215	68	776	TCCTACTTTTTCAGCTGATTTACATTCAAATTCTCATAGGAAAGTTTGGAGATGAGAG	17737	A_95_P297738	FG172791
18260	215	70	787	ATTCCATTACTGAAGCAAATCTTGGATTCTTTGAGACTGGAATACTAGCTGGTCCATT	17741	A_95_P161022	TA12711_4097
18262	215	72	1541	GGAGTTTCTGAGCTGTTGTTTATTGTTCATGTATGATTTTGAAATCCTTCGGATATGA	17745	A_95_P002976	AB264104
18268	215	78	184	ATACTACAGCCCATACCCCTAATTTCTGGTTACATTTTGGAATATCGTATGGGTGTGA	17757	A_95_P107477	CV018396
18271	215	81	617	TGGATAAACTTCCGTCTAAAGTCCCAGTTGACACTTGAAACTAAAGTTACTACTATCT	17763	A_95_P018361	TA12423_4097
18273	215	83	1584	CTTGTTTGGCGAGAAAAACAAAAGGTGATTCGTACTGAGAAGTTTTGTAGCATATCT	17767	A_95_P251723	X65974
18277	216	2	267	CCACTGTTACGGCACTGACAGAGCCTATTGATATATATAGTGAATGGATTGACGAGT	17607	A_95_P089768	TA14411_4097
18283	216	8	1097	ATATCGTAAACCGGTTGTATCATGGAATTAATGTTTATATTTGATTCCCGTACTTCTG	17618	A_95_P015861	TA14048_4097

18289	216	14	865	TAATGCATCTGTATAATATGTATTTCAGTGGCCAGAACTGCATCTTTGTAATTGTCTGT	17630	A_95_P182647	DV157864
18292	216	17	911	TTTGCACCACGCTCCCTGCAGCTGGTCATCCAATTACAATAATATGAGCGAATGAATG	17636	A_95_P011641	TA13889_4097
18295	216	20	407	TTGTATTGTATGTGTGTGCTCGTTTGTGAGACTCTCAAGTTGTGTTAGTGGTTTGTTTT	17642	A_95_P023611	FS416927
18296	216	21	287	CTTGTTGATCTTGGATCGAACAAACTGGAGGAGCAACATGCTCACAAACTCTCCTACA	17644	A_95_P102522	CV016057
18297	216	22	458	GGATTCAACTCTTGGTTGTTGTACAACATGGATGTCACAATTGTATTCATGTTAAGTT	17646	A_95_P001336	FG641133
18298	216	23	345	TGGGGTAGTCTTGTAGAAATTTTATCCGAATATGCGATTCAGCTTAAAAGACAGCTTA	17648	A_95_P110792	CV019908
18302	216	27	985	ACCATTCAACTTATCCTGATGTAGTGGCTTTTGGACTCTTTTGTTGAACATTGTTGCAT	17656	A_95_P000431	X97967
18303	216	28	461	TTTCTCAATCTGATATATTTCTGTAACGTGATTTGGGGTGTAATGTAACAGAAACGTG	17658	A_95_P000156	TA11669_4097
18304	216	29	843	CTCGATTTGAACTACGGCTTTACCAGATAAAACTAGGAACGATGGATCAGGATGAAG	17660	A_95_P269541	EB427988
18309	216	34	698	CGGATGATTGTGAATTTGCGACATTGCACATTTTTTCAGCAAGTATGTAAATCATATT	17670	A_95_P019961	DW001751
18311	216	36	586	ACGACTGGAAACCACCACTTCTATATTACCTGCTCCTTATTTCCTCAAATTGTGTGATT	17674	A_95_P005811	TA12644_4097
18313	216	38	744	GGATCCAAATCCAAATTCAGAATCACTACATTCTAAGATTATGGAGTCAACTTGGGTT	17678	A_95_P162037	EH620779
18314	216	39	848	TTGCTGAAATCCTGGTGGTTTACCTGGTGTATGAAGCACTGAACAGATGAAAGAGAG	17680	A_95_P288078	FG139528
18318	216	43	680	GGAAGGTTTAGTCATCAATCACTTAATTAAGTGATGCATCTATGCTCCACATTGCTTA	17688	A_95_P151642	EB681893
18319	216	44	955	GCATATCTCCAAATTCCATTCAGACACTGTTGCTCGAAGCTATGTATTGACAGCCCTT	17690	A_95_P204337	TA18044_4097
18320	216	45	667	CGGAACCTACATTGGTTGAGTCGTAAAAAGATGATGACTATTATGACTTTAGTATCTG	17692	A_95_P188902	TA14675_4097
18329	216	54	457	AAACGCTAGAATAAAATAGCTTTAGTCAAGGTTTGAAGTTCCATTCGATGTTTTCGGC	17710	A_95_P209662	TA19238_4097
18331	216	56	1826	GCAAGGTTATCATCCTTGAGTCTTAACAGGGGAAATATTGGCTAGATTTTTTGGATTT	17714	A_95_P004586	TA12215_4097
18336	216	61	791	TTTTCTGGAATATCTCAACAGTTGCTAGCCGTCCCGAAGCATGTCTTATGGGTATGAT	17724	A_95_P298623	FG148948
18339	216	64	660	GACAAAGCAACATATTTCTGTTAGTACTTCTCTTTCTGCGAGTTTTTATCGCAACCTTTT	17730	A_95_P028766	DW005049
18342	216	67	906	GCATGTACAATAAAAATGACATATATTGCATTGCCCTCTACTTTTTTCGGCTTGTGACA	17736	A_95_P183002	TA13354_4097
18346	216	71	93	TATCTAGATGAATTATCCCTATAGAGGAATCATCGTGGCGCATGAGGAGGAGGA	17744	A_95_P141122	EB444915
18351	216	76	791	GCAGGCTGAAAAGTCTCTCAATAGAATTTCCCTTTTCCTCTTATGCTGTTTTTCTTCCTT	17754	A_95_P265876	EH616818
18355	216	80	870	CCTATCCCCTCTGATGATGCTGGGAAGGAGGAAGTAATTGCAGCTTTGGTTACAAAT	17762	A_95_P227144	DW000809
18357	216	82	767	GTTGGGTGTTGCCAATATCTCCATAGAATTATTTATTGAAAAGCCTTGTTTGATTTGG	17766	A_95_P162207	EH621097
18358	216	83	867	TCTGGAAATTTGTTTGAAGCAATAGGAGACGCTGTTCGTTTGGTACTAAAGGAAAA	17768	A_95_P219092	EB447431
18359	216	84	681	TGTTCGAGCTTACATCCAATCCAGGTTCCAGATTCTGATATTGGATCACACTTTGGCAT	17770	A_95_P144937	FG157727
18361	217	1	871	ACACTCAGAGCGTCTGATGTAATGGCTGTGCTATCTTAGTTGGATATCGAGTTAATTA	17773	A_95_P016176	DV158991
18362	217	2	451	GAAGTTGGAGATGGTGAGGCTGGTGATGATAATCACATTGATACTCATCCTGCTGTT	17775	A_95_P071590	EB424987
18363	217	3	868	TTCATTGCAGATCGTTACTCATCATACCATTCGGTGTCTGAGTATCATGTATATGAATT	17777	A_95_P217002	EB682225
18372	217	12	1396	CTTAATTTCAAAGTGACCTCCGAAATTTATTTCTGATGTCCCCGTATACAAACAAGTTC	17795	A_95_P007521	AF321140
18374	217	14	845	AGCTGTCTAAGCTCGTTCTCTATTTCGTCCATACTTATATGCTCAATGATGGCAATCAT	17799	A_95_P229569	DV159750
18376	217	16	815	ACTTGAATCTTTTACCATCACTGATGAAGAGTGACTGCATAGTAACTTGATTGTGGCG	17803	A_95_P268026	DV999271
18377	217	17	500	GGATATGATAGATGGGAAATAATGTAGAATAAGTTATGGACTCAACGCCTCGGAGT	17805	A_95_P123597	DW003466

18378	217	18	815	GAGACAAGAGGATTATGAGAGAGAGTTTAATTTTAGATTCGAGGAGAATGCAGGG	17807	A_95_P149077	EB678729
18379	217	19	892	CAAAACAATCATGTCGGAGAGTTAGGTAATGCATACAAGATATTGCTGGCCTTTTCA	17809	A_95_P282893	EB680466
18382	217	22	807	ACAGATTATCCAGAGAGCCGCCAAGTTGTCCGATTCCACTCCCGATTACATGACATTT	17815	A_95_P230714	FG157344
18383	217	23	582	TGGCTTTATTTTGGGACTGAGGCGTAGTAGTTGTTGTATATGGCCTTGTATTTACACA	17817	A_95_P140137	EB444089
18386	217	26	821	GGCACATGGGGATATGCAAAGTATATCCATTTGCAATGGAATATAATTTGATGCTAT	17823	A_95_P250077	EB450661
18395	217	35	630	CTAGGAAGAGGTTATCCAATCATTTTGTAAGCCTCTTTGTAGTTGAATTATTTTTTGG	17839	A_95_P207267	TA18703_4097
18400	217	40	68	TATCCTATGCGCCGACGTATTTTCCTAGTTTGGATGCTTGCAACAAACTTTTCTCATGC	17849	A_95_P032141	CV021711
18405	217	45	442	CACCTAGTATTTTTTGCCTCTCTTGGATTTGGAGTTGCAGGGCTTTATTCTATCAATAT	17859	A_95_P141042	EB444843
18407	217	47	899	TACTTCTAATGCTTCTGGTTCATTATTGGCAAGCTCTACCTCTGTCCTGGACCGGTACT	17863	A_95_P217522	DV162291
18410	217	50	1342	AGACTTTGTATCAGAGATAGCTTGTTCCGACTGGCTCAAAGTGCTACACAGAGGCAA	17869	A_95_P199442	TA16995_4097
18417	217	57	836	AATCAGAAATTAGCTCATCCAGTGATGATAGGCGGAGGAAGAGGAAGAGATCTAAA	17882	A_95_P027476	EF051139
18420	217	60	2363	CGGACACACACAAGATGTTGTAAGTTGTTGTTGGACATCGCTAATGTCTATTTGCCTT	17888	A_95_P210327	AF435452
18423	217	63	829	AACCTGCACACAAGAGACAGCGCCAAATTTCCAATGTTGAAGGTCAGTACTCTTTGT	17894	A_95_P121927	DW002005
18425	217	65	678	ATTGTTCTCAATCATGTGTATAACAAGCGGAAGCTACAGTTGTTTCGGACAGTGGAA	17898	A_95_P291173	TA20561_4097
18431	217	71	522	CCCCACCGCCAAAGAAATGAAAAATGAAATCTGGTGGAAGGATTTGAATGAAGCAA	17910	A_95_P124537	DW004346
18433	217	73	495	AAGCTTCAGATGAAGGTCTAGAAGGAGTGAGTGGTGAAGAGGAATCAACAGATGA	17913	A_95_P052061	BP132816
18434	217	74	685	GACAAACTAACTGTATGCTCTTGATGAGTTGATTGAATGATAAATGATGAGAAGGG	17915	A_95_P014136	TA18995_4097
18435	217	75	589	GGAGGAGCTTGAAGCTAAGGCACTCAAATGTTTTACTTTTTTGGTTATATATGACAA	17917	A_95_P268631	EH615283
18436	217	76	176	ATGACTTCTGCTGCTATGAAAGTTCAAACGCCGCTTGTTTGTGTGAAATTGCCTTTAT	17919	A_95_P034134	AJ718198
18438	217	78	703	TTTGATTAACTCGTTTTAGGAGTTGGAAGTATGTTGTATCACTAATAGATGAGTTGCA	17923	A_95_P146267	EB450252
18443	217	83	1069	AGTAGTCAAGCTTACACATAGTAATGTGCCGGAGGAAGACAGATATGGAAATGCAA	17933	A_95_P034549	TA15200_4097
18449	218	4	706	CTTGTTGATGTCATGTTGTGAATTATGAAGATGGTCATGTATAATTGCCTCCAAATGA	17780	A_95_P116512	DV159279
18451	218	6	208	AGCGGAGGAGGCAGAGGTGCTGGAATGAACATTCAAGACATATTTAGCCAGTTTTT	17784	A_95_P176222	T18328
18457	218	12	264	CTTTTGGCTTCTATTTGCTGTTCTGCTGTAATTATCCATTTGTTATTGGTACCGCTGTT	17796	A_95_P009706	TA13806_4097
18464	218	19	1289	GAGCTCAAAGACTCTCTTCTGTTTGTATAGCTTTAAATGTGTTTTCGTACACTTTTTGG	17810	A_95_P192732	TA15518_4097
18465	218	20	405	AGACGAACAAGGCAGTTCAGATTGTCTCTCCGTTGCCTAAGGATTGCAAGAAACAGA	17812	A_95_P083420	BP528755
18466	218	21	494	TCACAAGTTATTATGACTCTGATGTGACGGTGAATCTTACTTTTCCAAATGAATTTGC	17814	A_95_P281278	AM821017
18472	218	27	738	GTGTTCAGCTTCTTGATTTCGGGTTTGATGTTGTTCTATCACTTTACCGGGTCGGGTT	17826	A_95_P128397	EB428100
18477	218	32	115	GAAGAAGATCTAGAGTAAGTAATACAAGAAGAGGAAACCGCCATTTGGGTTATGAT	17834	A_95_P030601	BP532130
18478	218	33	1035	GTGTTGGTGACTTTGCTCGTATTTATAGTCTTATTTGCATGTTGCGTAATCATCTTTGT	17836	A_95_P008136	AB119480
18481	218	36	509	CTAGGTTGAACTTTATCTTACTGTTCTCCTACAAGAAAATCATGAAATCCGTCTCCTTT	17842	A_95_P061355	EH623004
18482	218	37	273	GATGGTGTTTGCATTCCAACAGATCCACTTCCTTTACCTTCAGATATGCATGTATCTTC	17844	A_95_P095143	BP533037
18501	218	56	1174	ATAAAATGGGAGTCATTCTTCCTTTTATTGTGAAATAGTAGTAGTACTTTTGGTTCCC	17881	A_95_P007656	TC40222
18502	218	57	719	TCGTCAGTTGTCAGCAAATGGCGTGTGATTCTGAGAATTGATAAAAGTGTTAATCGA	17883	A_95_P310573	FG136991

18503	218	58	523	CACTTGGTAATGCAAATCAAGGTTGGGTTGCTCCAACAGTGAATATGGGATCAACTG	17885	A_95_P083950	BP528896
18506	218	61	754	GCTGTGATGAGAAGTACACAGCGCGATATCTTGTTCATTGAATTTAATAGTAAGAAT	17891	A_95_P252674	EH623728
18507	218	62	601	AGACTCGTGACACCAGATTGTTGGGTTTATGTAGTTTATTGTTATTTTGACTTTCCGC	17893	A_95_P157367	EH615412
18509	218	64	500	CGTTATACATTGTCTGGGTGTTTAAACGAACGCTTTCTAATATGGTTAATTTCAGTTG	17897	A_95_P293783	EB437715
18515	218	70	539	AGGCTGATCAATATTTGAGATTAGAGCGTTGTATGGTTATGTACAGAAGTTGGTATA	17909	A_95_P124802	DW004605
18516	218	71	1707	TACATGGGTCGTATCAAAAAATTGCAGGAGTACCTGACAAGGTGCGCACAATTGTG	17911	A_95_P170556	TA15521_4097
18522	218	77	713	GTAGTAATGCTTAATGGATGTACACTTTTTTGGTGGAAGAGAAAGTGAACATTAACT	17922	A_95_P155577	FG642423
18523	218	78	873	AGTATGCTTCTTTGCGTGCAGAGCCAGATTTCAGTGTGTTAGGAAAAAGGCTGGGA	17924	A_95_P119032	DV162127
18526	218	81	623	ACTTTCACCTCTATCCTGGATATGGCTGGAGTTCTCTTGCCATTCTTGAAGTGGGTCA	17930	A_95_P121312	FG161763
18532	219	2	0	TTATGTGAGCATGGGGATGTTTCAGTGAGCATTTCTGGAAGTTTGGCGGACATTGG	17940	A_95_P248222	A_95_P248222
18536	219	6	760	CTTTGAAGCGGCATACACTTGTCTTACGGAAAAGAGATATAATGCGGAGAAAAGCA	17948	A_95_P208652	TA19015_4097
18539	219	9	414	TGTAACAGGGCTGAATTTCAGACTCCTGTCCAAATTTTGAACTTAAATGATTTATAGA	17954	A_95_P099663	AM828280
18540	219	10	637	GAAAGTGTATTTGGGAGATGAGTCTAAGCCTAATGCCCCTGCTGGAAAGAGCAATG	17956	A_95_P138817	FG145780
18543	219	13	811	ATTTTTCTCTTCATGTGTTTGTCTGGGATAACAGCCTCGTTATGCGGTGGGGAAGCAT	17962	A_95_P136962	EB440696
18545	219	15	753	ATCAATCCCCTGAACTCGATCAGAAATTCCCGTTGTCAGTGGACCCTTCTTTTGAAGG	17966	A_95_P000116	FG157904
18548	219	18	745	CTTGTAAAGAATGATGATGATGCTCTGACTTCTAACTGGAAACGACTCCTGTAAATA	17972	A_95_P206587	TA18550_4097
18550	219	20	1227	CAGTCATTGTATTGTTGAATGACAGGGATAAGAAATATTCCTCAATTGTACGAACTA	17976	A_95_P010081	TA14849_4097
18552	219	22	0	TGTATGTTTGGACTGAAGAAATGTCCAATACTTTGAATTTCATTCACCTTATCCATCTG	17980	A_95_P304773	A_95_P304773
18553	219	23	1758	TACAGAAGAGCTGTTGGCAGCTCCCTTAACTCAGAAACTATTCAGTAATTCCTTTTCT	17982	A_95_P221947	X92967
18554	219	24	2455	TCTGTTAATTAGCCCAAAATTCCTGTTACCATGGGCAATGAATTTGATTACAGAAACT	17984	A_95_P190327	Y11996
18555	219	25	1735	CATTGTAAGCAAATGGTAAAGTCCTTCCTTATGTAGGATTTTGGTTCTTTTCCAGGAA	17986	A_95_P182027	TA13117_4097
18558	219	28	684	TAATCTACTATTGGAAGCTGCAGCTGCAGTTTTGTCTCGTAGTTCCTCTAGTATCATT	17992	A_95_P232364	DW002772
18559	219	29	728	CGTCCACTTGTAGGCTTATGTGTTTCTTGTTTACACCATATATATAGGGTATTTTCCCC	17994	A_95_P161307	EH620045
18560	219	30	1352	GACCCAGTCTTTGCAACTCTGGATATGTTTCTTGTTTTTGTTGTGTTATGAATGTGTA	17996	A_95_P009326	AJ133422
18561	219	31	827	ATTTGGTGATGAAATCAAATTTCATGCTTTTAATGATGCAGATCTCCTCTAGTTCCTCT	17998	A_95_P187057	DV159114
18563	219	33	364	ACGCACCTCATTGGTGTTAGTGAACTTGTTTTATTGATTGAGATTTCTCATCATCACTA	18002	A_95_P130372	FS429628
18567	219	37	801	TCTCAGGGCAAGAATCGTGAAAAAACAGAATGCACTTTGTAGCTGGATTTCAAGGTC	18010	A_95_P272596	EB451374
18568	219	38	102	GGTTTTTACTGAGTGTACATGCTCAAAGATGGGTTCTATGCATTGCCCCCTCTTTTGT	18012	A_95_P120792	DW000751
18570	219	40	3102	GGGCAGTTGTCTACACAAGAATGTGTTCTTTGGTTTCAATTGTATCAAGAGAAATCA	18016	A_95_P025156	AB032541
18572	219	42	918	AGACACTCCTTACCAAAAACATATCTGACTTATTATAGGTGGCAGTTAACCTTGTCCT	18020	A_95_P015726	TA15561_4097
18580	219	50	792	GCACTCTGGATAGTGGAAAAACATCTTCATTTGCAATGAGTCAAATATTAGAAAAGG	18036	A_95_P216017	TA20613_4097
18581	219	51	839	TGAGAACAATCTTCTAGAGGCCGGGATATTCACATTCATTTCCCGCTGAGCTGTACTA	18038	A_95_P284758	FG159803
18583	219	53	860	CTGCTTGCTTGTTTGTGTGATGAGCTTGCTTCATATTACAATATTTATAGTTGAGTTG	18042	A_95_P014681	EB679140
18585	219	55	1138	CATCCATCCTCTTGCATAGTCTGTGGAATGGCTTTGTATTCTTAGATTTAATGAAATG	18046	A_95_P008506	TA14305_4097

18587	219	57	685	ATTGATCTGCCAGCAAGCTGATGAAGTTAGTAAACTTGGGGGTCCTCCAAAGTAATC	18050	A_95_P164527	EH623769
18589	219	59	166	CTCGTTTGCTAGCAGAGGATGGTATGTAATGAAGTATTTCTTTGATAACAGTAGTCA	18054	A_95_P141642	EB445312
18594	219	64	661	GGGGGTACTTTGTGGAAAGTGTAAATATGTGAAATGTAAAATCTACAACCTCTTGGA	18063	A_95_P214612	TA20299_4097
18597	219	67	327	GAGATGCAGCAACCACACTTTCATCAAGTTCTACACAATCAACAAAAGAATGCGATT	18069	A_95_P086090	BP529450
18598	219	68	684	GCTGAACCACAGGCTGCAGAAGAGACTCAAGATTAGTCATAATTATGAAAATAGTG	18071	A_95_P126982	EB426388
18600	219	70	86	TTCCACTACTTGTGGAAATGGATCATTGTATCAATCGGAATTGCTATCCATTGTTAGT	18074	A_95_P030111	CV016797
18611	219	81	1714	GTGTCTCTCTAGCAATGCCAACTTCTCAGAAGTAATAAAAAATGTATTGATGAACTTC	18096	A_95_P014366	TA15877_4097
18615	219	85	389	GGCGACTAGCAGTTTCATTCTTACTGGATGTGTTACTTCTTTGATTTCTTTGTTAGAAA	18103	A_95_P219892	FG641158
18618	220	3	671	TGCACCTGGATTTTGGGTTGGAGTTCAGTTTGATGAACCAGCAGGAAAACATAAAG	17943	A_95_P253524	FG641440
18627	220	12	687	AGGGCTGTTATAAACTCTCCATTTGATCTGCTTTGCTTCTCTGCTTCTCTGCTTCTTTG	17961	A_95_P135692	FG643304
18628	220	13	1151	CAATGGTTATGGTAGTGTATAAACAAAACTTGGCACTGTTTGCAAATTGCAAATAAA	17963	A_95_P200302	TA17179_4097
18630	220	15	641	CAGGAGACTGAGTACATGAGAGAATACTATCAGTATGTTATCTATTTTCTCATTAACC	17967	A_95_P137532	EB441250
18631	220	16	420	AGTAATAGCTTGAAGGCCTCAAGGTTTCCCTTTTGTGCTGTTGTTATGGCTGCGACAA	17969	A_95_P014426	AY740530
18632	220	17	809	GGTTTTCTTATTAATGACATCTCATTGTCAACAATACTTGTGGGTCAGCTACCACATT	17971	A_95_P003841	DV162691
18636	220	21	717	GAAGGTTAAGGTAAGACATTTGGTTGATGATAATAAGAAAAGGTCACGTTCCTTTGC	17979	A_95_P149897	EB679885
18637	220	22	867	TCTTGACTTTTGAGACTTGTCGTGTTCAACAGTATCCCTTCACAAACAACCAAGCTAT	17981	A_95_P229314	DV162045
18638	220	23	423	TATTTGTGTCGGATTTTGGACCTCAACCAGAGAAAGAGAAAGAGAAAAAGAGTGGG	17983	A_95_P122922	DV999293
18641	220	26	1300	ATCCATTTGTGCTCAAAACCAAGGGACCAGATGTCAAGCAATGTGGACTTAACTGCT	17989	A_95_P197492	TA16572_4097
18646	220	31	151	CACTTGGCTTGTAAGCTTTGAATTCCAAGTTTTGAACCCTAAATTGGCAATTGCTTAT	17999	A_95_P006626	CV016052
18648	220	33	480	GAGAGATCGGCCTGGCATATAAATGAGGAAAATCTCTCTCTTTCTCTCTCTCTCTCTC	18003	A_95_P095238	BP533092
18649	220	34	911	CGTGTAGGCATTTGAAACAACAGTTCTACTGTACTGATATGTCATTTGTAGTTATGAG	18005	A_95_P003961	EB425137
18651	220	36	126	TCCTCTGTAAGTTTCTTTATTAAATGTTTTGGTCATACACCCAGAGCAATGTATTTGTG	18009	A_95_P066045	AM819908
18652	220	37	924	AAAGAAACTGTCGAAAGTTTGAAGGAAAAAAGGTTTTTTGGAGGCTCATCGGCTAT	18011	A_95_P240394	AY911855
18654	220	39	265	TCTCCACTGTAACTGTCTACACCACAGGCCCATGATTTGTTTCTAAATATAAAGTAAA	18015	A_95_P033774	AJ632967
18658	220	43	418	ATTAATCAAATGCTTAAAACTGGAATCGCGGAAAGAGCTCATGTTGGTGATTCTCTT	18023	A_95_P076970	BP527130
18659	220	44	662	GTGTTGTCGAGATTTTATGCCGTGGACAAAGCAACACTGTGGAGATTGTATTTCTAC	18025	A_95_P287863	FG198220
18660	220	45	675	GCCTTGTCTGAACTGTTTCGTACAACAATTTTGATGTGAGACCAAGTGTTATTACTGT	18027	A_95_P004076	TA12299_4097
18661	220	46	769	GGGGGTTGTTGTAGTTAAAAATGGACATTTATTATTCTAACTTATCATGTGTTCCTAC	18029	A_95_P238694	EB449711
18662	220	47	592	GTATTTGCTTTGGTCTTTACATCTTCTAGGTGTAATTTGGTAAATGGATCTCGACCAG	18031	A_95_P209447	BP130751
18666	220	51	1391	GAACATAGACTGCAAGTTGGCATTATTGTTCTGTGGACCAAGTCCCCCTTCCCCAAAA	18039	A_95_P024876	TA16043_4097
18669	220	54	627	CTTTGGGCTTAGTGCTCATTCGTGCTTGACCTATCTTATGTATGCAATTTAAAACGTTT	18045	A_95_P001661	EH617929
18676	220	61	166	CCATCGAGGTCCAATCCCTTCTATTTTATCTTGAATCCTTTGATTTTATCATTGAGATT	18058	A_95_P134372	EB436614
18677	220	62	372	AATTTTTACGGTGTGGCTAATTTAATTCTAAAAATTAGCTGGGGGTGGCGGGCAGAA	18060	A_95_P104982	CV017249
18683	220	68	765	GTTTATAAGGGTTTACTGTAAGGATTTATCTGTTGGGGTTGGGCCCAATAAGTCGTC	18072	A_95_P028361	EB426542

18686	220	71	815	CCTTTGATGTTTTGGATGCTCCAAGTTATTTGGTGTTCCATGTAATACATGTATGTTAC	18077	A_95_P283613	FG638542
18689	220	74	403	ATCTTCTGGAGTAGAAAATATTTACAAGAAGCTTTACGCATCGATTCCTGGAAATGT	18083	A_95_P065415	BP136325
18690	220	75	847	CATCACTTGGCGAAATTCAGTTGATAACAACGAGTATTTGAGAATAAAGGCCGTGAA	18085	A_95_P148597	EB677958
18691	220	76	1019	ATGAAGTTCAGCTGCTTGTAAAGATACTCTTTTATGTTCTAATGCCTAATGGACTGAA	18087	A_95_P023751	TA16718_4097
18692	220	77	1823	GCTCCCTTAACTCAGGAACTATTGCAGTTTAAGCCAATTAGAGTTGAGATAATAACA	18089	A_95_P217622	X92966
18693	220	78	196	ATCAAGGACTCGGTCGCGTTCTTTCTTCCATGTGAGAACTGTGGTTACTCTAGCTTAC	18091	A_95_P040286	BP129787
18695	220	80	105	TACCACAATATCTGTCGGTCTTATAATTTGTGTTGGCAGGAAGGGATTTGTTTAAATT	18095	A_95_P023186	EB445368
18696	220	81	540	TTCATGCTCGTTTTCATGCCCGTGTGGGATATCTTAGCATTGAAGAAGAGATCAGAG	18097	A_95_P108267	CV018754
18702	221	2	715	TCCAGCACAAACATTGTGCATGCGAATACAATGGATGGCTTTATCATCTTTCAGTGTT	18107	A_95_P181882	EH623509
18704	221	4	0	TGATCACATTTCATGTGTGGTATCATTGTGGTACGTGGTTGTACTCGGATTACGACTC	18111	A_95_P292023	A_95_P292023
18706	221	6	832	AGATACATTTGTGTTCTGTGCAGCTGTCTGTTTCAATAGCTGGCTTCTTTTCTATTTCT	18115	A_95_P266946	DV157514
18707	221	7	882	TGCAAACTATGTGAATGGAGTTGTTGGTAAAGGGTGGAGCTGTGTATAACAAGCAT	18117	A_95_P230484	DV158244
18712	221	12	839	TGATAAAAGAAGAAGCATCCCTCGGAACTGGCGATCCTGAATTTCCAAAAGCTATTT	18127	A_95_P292748	EB428339
18714	221	14	1507	ATTTGCTCATGGAAATCCTTGCTTGGTAATGATTCTCTACTGAGTTACCTTTCTATTCT	18131	A_95_P027281	TA14519_4097
18716	221	16	856	GAGATTGAAGTAAACTACAGTTTCAGATTTTCTTGGTCATTTGACATGCCATTCCGAA	18135	A_95_P183252	EB678237
18717	221	17	196	ACAGAATCGAATTGCTCTTGTCTCAAGTTGAGGGAAAAGACATCACTGAGCTGATTG	18137	A_95_P104622	FG645200
18722	221	22	597	CCGCTATATATGGAAAATCCAAAGTGGGAGCAACACATGCTATGCCAACCAACTGG	18147	A_95_P171786	EH665222
18725	221	25	724	AGAGTATAGGCGTTTCTTGAGTTCTCGACTTGAGCTTATTTTCCTTCTATTTCCCCCCT	18153	A_95_P120387	DW000280
18730	221	30	127	GTACGAGTGTTGGGAACTGCATGTTACAATAAATGTATGATGGTAGTGTTTGAAATA	18163	A_95_P154867	EG649789
18732	221	32	372	GAACTAAGGGATTCCACCCTTAATATCAAATAGCAATGGAAGTATTATGTCTGGATA	18167	A_95_P110477	CV019747
18734	221	34	230	ACCTCATGCTGGCTGTCTATTACCCGAACTCAGTGATAAAGAAACATCGTTGATCCA	18171	A_95_P111172	CV020081
18735	221	35	0	CAAGTAGAACATTGTTGTTGGTCAGGCCATGTATAAGCATTGAAGCTTGGGAAAGTC	18173	A_95_P247642	A_95_P247642
18737	221	37	1509	GAGCTCATTCTATGCCTTAAAAACTACTACTAGATAACTGCGTAGTAAATAATGCTTG	18177	A_95_P255199	DQ350357
18738	221	38	798	TATGAGCCAGAGGGCAAATGGATTTAGCAATGAATACATAGTGGTTACAATCTTGGT	18179	A_95_P229694	DV159967
18739	221	39	257	CGGTCTATCCGCCCTTAAGTGGTATTACCAGCCATTCTGGAGAAGCTGCAAAAATAA	18181	A_95_P034688	AY237826
18741	221	41	1235	CGGAAATGTAACTGTTCTGGTTATGCCATTTCATTGTATCATATTGCCTCAACTATTAC	18185	A_95_P209922	TA19291_4097
18742	221	42	699	AATAGGTCTGATTCAGGAAAAAGCACTTCCTTCCTCCCCTAGTCCATTGTACAGTCCT	18187	A_95_P137627	EB441351
18746	221	46	568	AAAGTTAGGCATTACAGAGTAAACATAGATGGCAATGTTTGCACTGTCATGGTGACA	18195	A_95_P132567	EB433069
18749	221	49	1124	CATCTCAGAGGTTTTGTGTAATACAATATATTGTGCAACTTATCTTGCATAGGGAACA	18201	A_95_P007846	TA12488_4097
18750	221	50	139	TAAGGTGAAGCATTCACGGCACCTTGTGAACGTCTCTCTGCTTGTTGACTATGCTTTG	18203	A_95_P104822	CV017186
18752	221	52	479	CATGCCCCTAGTAATTTAAGTATTTAACCCCAAGGAAGCAATATTCGTATACTTGTAC	18207	A_95_P273371	EB684268
18756	221	56	1398	CTATTTTTTATAAGAGGAGCGACACCAAATATAATAGAGAGGGGCGGGGGGAGAG	18215	A_95_P122572	DW002555
18758	221	58	864	TCATATAGTTTCTGCTGATGTACGAGGAACTCATCGTCAGTTGATTGTGGAACTGTGT	18219	A_95_P310953	FG144423
18760	221	60	502	TTGTTCCGCACTGGGTGGTTATATTTTTTCTCATTCCCGTTATTGCATTATGACGTGAA	18223	A_95_P266221	FS391824

18763	221	63	456	TGTCCTACAGAAACTGGGGGATCTTATAGCAGCATATTCAAATAATCTGCTCAAGAG	18229	A_95_P072340	BP525938
18764	221	64	390	CTGCTTCTCAGAATTCTTCTCCATTTGCAGCATCAAGCAGTCAAGAATTTGGTGGTGG	18231	A_95_P148907	EB678463
18767	221	67	1183	ACAATACCAGCAATCAAATCCAGTAGACTTCTTGGCGAGCGACCAGTTCAATCTTTCA	18237	A_95_P018251	TA17597_4097
18769	221	69	743	CTTGAAGATAGGAAAGCAGTGGATAAGAGAGTGAGAGTGAAATGAGCTTGATCTG	18241	A_95_P298303	FG146934
18771	221	71	23	GGAACCGTAAATTTCCATTTTGGTTGGACTATCTACTATCAATTTTATCGGTTTGGCTT	18245	A_95_P110127	CV019594
18775	221	75	780	GAAGCCGGATATTGTTGTTCCAGGGAATTTGGGCTTGTTGAGTGAAGCATATGATCG	18253	A_95_P194402	TA15886_4097
18777	221	77	783	TCAATCATTGTTGCATCTGCTTCCTGTGTCAAGCCAGAAGGGAGAAACTAATGCTGA	18257	A_95_P305108	FG136365
18782	221	82	754	TTTGCCTGTTGCTGCACTTATAGATGAAAAGATCCTTTGCATGCATGGTGGTCCTTCT	18267	A_95_P118372	DV161400
18786	222	1	242	CAGGCATATTTTGTTTTAATCAAGAAGTGAAAAGGTTGTGGCTGGATAGGCCAGCTG	18106	A_95_P062200	BP135456
18787	222	2	600	TGTGAGTAACTTTATTTGTTGTGTGATTTTTCATTCTTGTTTTTGTCATCAGGGGTCCT	18108	A_95_P123337	DW003204
18789	222	4	1950	ATGAAGACTGCAGACACTGAAGTAAAGAGCGAAACTCTTGCAAATGCTGTGCACCG	18112	A_95_P233144	U01961
18791	222	6	830	AAGTAAATAGTTCATGGTTATGCAGTGTAGTTCCGATTACTTTAGGGGCTACCTCGG	18116	A_95_P013376	EB424705
18795	222	10	113	AATCTCAGAGGGGTGGTCGGATTACTTGCATGGCCAGTTACAAAGATGCAAGCTTAT	18124	A_95_P108507	CV018866
18799	222	14	2458	TAACATGTGTTGATGATTCCAGCTCACTTGTTATAATTATCAATTCCGCTCTCCCTCTA	18132	A_95_P027611	TA12261_4097
18802	222	17	0	GTATCATTGTTACCGTGGTTGTACTTTGATGTACGACTCTTTGAGCTGTTTCTTGACTG	18138	A_95_P242107	A_95_P242107
18805	222	20	438	TTTCTCACTGTGGCCTATGTATTGTTGGTGATATGCAAAATATGTAAAAGGGCACATT	18144	A_95_P025211	TA17662_4097
18807	222	22	1394	CAGGATACCTGCAATAGTTTCATGCTGAGTTGTATATATGATCTCTTCATTTTCCAAG	18148	A_95_P031151	AF211537
18808	222	23	779	CTAGAACTTCTGCAGAAGACATGGAAGAAATGTGGAATCATCCCAGTGTGAGCAAG	18150	A_95_P233374	DV161185
18810	222	25	293	TGATGGAAACTAACTTGATGATGACCAAGATGGCTGATGGCTTTGTGCTAACCTGAT	18154	A_95_P110482	CV019749
18815	222	30	409	CACTTGAGGACATTGAAAAAAGGGCTTTTTTCTTGTTTTTGTGTAATTTACTGAGCAT	18164	A_95_P178667	FG196229
18817	222	32	449	GTTCAATAGTAAAAGACAAAGTCACTAATGCCCTTATAAGCATGGAAGACTTAAAAC	18168	A_95_P072245	BP525911
18821	222	36	384	GTAAAAAGGGTAGGTGTTGATATATTGGAATGAATGGTTGTGAATGCACTATGTTTC	18176	A_95_P120787	TA17047_4097
18829	222	44	701	CACTGACATGCATTGCATTTTTGCTGTAAGGACAAAACGATGTATCTATTTAGGTTTT	18192	A_95_P301278	FG640610
18830	222	45	615	CCTCACCGTTTAAGAAGTAACCATAGAAACGAAGGAACCCACTATTTATTTTTTGATT	18194	A_95_P192922	EB433140
18831	222	46	111	CCTCCTTGGTGTCGATCTGTCAGAAGTGACCCTTAAAGAATATCTAAAGTGAACTTAT	18196	A_95_P094133	BP532579
18833	222	48	1150	GAGGTTTCGTGTAATACAGTATATTGTGCAACTTATCTTGCATAGGGAACAAGATAA	18200	A_95_P179362	TA12489_4097
18835	222	50	443	TGATCCAACTTAGATAGTTTGTGATGTTAGAGCAAAGCTGAGGATCATTATTTTTGCC	18204	A_95_P192037	TA15366_4097
18837	222	52	576	TGCTGGCCTACTTGAGAAGTTGAGTGTTGAAGATAAGAAGTCAGAAGAGAAGAGCG	18208	A_95_P125267	DW005060
18838	222	53	2087	CTGCACTAACTAGTTTGTAAATCTGAAACCAGAGTGACAAAGGTATTTGAGATTTAA	18210	A_95_P222167	TA21975_4097
18839	222	54	679	TCTTGGGACCAATTTTACCATATATGATAGTCAACCCCCACACAATGGGGCAAAGCC	18212	A_95_P138622	EB442362
18842	222	57	1699	TCACATTCAGAGGACCGGAGAAAGAGAGCCATGGTTTTATTTGAAAATGCTGCTTTC	18218	A_95_P188657	TA14619_4097
18845	222	60	21	CTTTCGGAAGGGTGGTTTACCGCCTATTGTCATATGGATCACTGTATTAAACATGACG	18224	A_95_P190512	EH663872
18846	222	61	291	GTTTGACCCTTGGTCGGAATCATTTGCTTACAGTTTAAGAGAGATTCTTCATTTTCTA	18226	A_95_P089688	BP530605
18847	222	62	629	TACAGGAAATATGGGCACCCTGGAACTGAAAGATGTGGTGATATATGAGCTATGCT	18228	A_95_P270676	FG634009

18849	222	64	680	CTCCTAGAGTTCAAAGGTTTTGAAGAGTTGCTGTTATTTGGCATATCAGGATATTATA	18232	A_95_P184662	TA13744_4097
18851	222	66	1027	CAAGATGCGAGAGCATCCGACAAGCTTATAATACTCTATATATATAGATTCTACAAA	18236	A_95_P111287	TA13160_4097
18853	222	68	945	GACGCGGCTTGTCATTGATGCTTGTTGTGTAAAAATCTTGATATGATATTCCATTTGT	18240	A_95_P019256	TA16669_4097
18857	222	72	1270	CTGCCAAATTTGTCTCCTCAAGAGCTTTCGATTAGTTATTAAAACTTCAAATCTGTATG	18248	A_95_P197002	TA16466_4097
18858	222	73	879	CTGGAGCGTAGACTCGTTTCGTGCTTCCGAAATATGTGTTCGAATATGGTGATAGTC	18250	A_95_P115822	TA11901_4097
18865	222	80	870	CTACTGGGATGTCTTGCTGGAGTGGAAATGGTACTTAAGGATGTTGGTTATCCAGTG	18264	A_95_P246187	DV159853
18867	222	82	811	TAGGTGACAGAAGTTCTCCTGAAAGTTGCAATACTCCTTATAATAAGATTGCAGTTTG	18268	A_95_P000871	EB678587
18875	223	5	371	TCATTCGTGGTTTTGCCTCCACCAGCTGCTTCAGTGTATAAATGTGAGCCTACATCTG	18283	A_95_P137487	FG159598
18879	223	9	704	TCTCGTAGTTCCTCTAGTATCATTAGCTGATGCTACAAAGTCCCAACAAAATAATATC	18291	A_95_P023726	TA18847_4097
18880	223	10	702	ATCCGAGTTTCTTGCATTTCTGAATCTATAAAATCGAAATGGTCTGCTGCTCAGCGAG	18293	A_95_P306233	FG150142
18881	223	11	22	TGGGGAAGCATATATTTATCTGGTTTTGGATTGTTTCCTTTGGCTTGACACTATTTGT	18295	A_95_P014371	CV021131
18883	223	13	158	CTCACTTTGCGAGTATTTTTATACAACGCTTATTGAATAGATATCTGGGTCTTTGGTTT	18299	A_95_P147492	EB451952
18886	223	16	780	TTGATGTTGGAGGAGAGGTGTATGATCCCGAAACAAATGCATGGGTTGAATGCCAA	18305	A_95_P292548	FG167375
18887	223	17	455	GATTCTTGATCTCAGACCATACACCTATCTTGGGGTAGGGGTAGAGAGGTTGTTTCT	18307	A_95_P277403	AM809125
18894	223	24	408	CTTCCCGTCTTTGTAGAATGTTCTTCAAATATTGATGACGATTATTTTAAGTACATGCC	18320	A_95_P094218	BP532608
18898	223	28	261	ATACTATCACTAGGCTGCACCCATGTAATGATGATTCAAGATTTTGAATGCATTTCTA	18328	A_95_P177962	TA12112_4097
18900	223	30	960	CCAAATTCAAGCAACTATTATTGCAAAAACTGAGTTGTCCAAAGTTGGATTCCCCTGA	18332	A_95_P187442	TA14347_4097
18901	223	31	1042	AACTCTGCCAGCTATTAGAACAACATCCAAAGTTGATGCAGATGCTTCAGGAGAGGT	18334	A_95_P208817	TA19053_4097
18905	223	35	222	TACACTCCTTGAGTTATATGACTTTCCTCCCTATAGGGGATTTGTGGATGCCCATGCT	18342	A_95_P101238	CB337254
18906	223	36	861	GCTTTCTTTTTTCCATTGTGGTTGCATGTAATTTGCACTTGTTTAAAGATGCCAGTTTC	18344	A_95_P242972	DV158734
18909	223	39	409	TCTGAGGTGTTAGTCGAGGTCAAGTTTGTTGGTTCAAGTCCTTGTAGCGATTTGTTG	18349	A_95_P097703	BP534166
18910	223	40	715	CAAGATGTCAATACATAATCCGTGAATACTCAATTTGATATTGCTGTTACCGGGCACT	18351	A_95_P204237	TA18023_4097
18911	223	41	1732	CAAGAATTTGCTCTGTTGCAGCAACTTCCCTAATTGAATGGTAGTACTTATGTGAAAA	18353	A_95_P240074	Z93768
18912	223	42	0	AGGACGGATTGACAGATCAGCATGCAGAGCAGATGGAGATTGTTTTGTGTGCATGA	18355	A_95_P295923	A_95_P295923
18915	223	45	910	TCATGAATGACAAAACCTTAAAGGCCTTGCATTCATCTTTTTGTATGTTCAATGGTTG	18361	A_95_P205067	TA18201_4097
18918	223	48	822	ATACATATATGGGATCTTAGAATGCTGAGTTTCAGTCCTTGAGCTCCCTGGACATGCT	18367	A_95_P292428	FG159966
18919	223	49	801	AGAGGTGGAAGCTGTCCAATTTATTATTACTGCCTTATTCCAAAATGGATAACCAAAT	18369	A_95_P135727	EB439252
18920	223	50	1165	GTGCTTTTATCTTCTGAATGGAGAATAAACTATCGCCAGTGTGCCTTCTTGCTTTTATT	18371	A_95_P006281	AY619950
18921	223	51	577	TGTGCATTTAGTCTTGTTACCGTTGAGGTTTTATCGAGTGTATCTTTGTTGATCAAGT	18373	A_95_P029441	TA14154_4097
18924	223	54	673	TGCTATGAACAGATTTGTGAATGAACAAATGAAATACGGCATACGAGGAAATATGA	18379	A_95_P227079	DW003523
18925	223	55	460	CCCAACCATCTGTTCTCACATTTTTTATTTTCCCTTGGAGGGTTTGAGCTATGTAATTT	18381	A_95_P023356	EB445361
18933	223	63	323	TATGTGGGTGTGACGATTCTGCGTGACAATTATTTGTATGTTGAAGCCGAGGAATAT	18396	A_95_P100228	BP535273
18935	223	65	903	TTATTCAGAACCAACATCGATGAGATGTAAAGCCAGAAGTAGAACGTAAACAGCGG	18400	A_95_P148632	DW000754
18936	223	66	1105	ACAGTTATGTTGGTTGAGATTCGATTCAAATTAATGGTCGTTACCTATTGGTATTTTG	18402	A_95_P214462	TA20268_4097

18937	223	67	110	AGCCCTGCGAATCATGTTGAATATATGTATTTTGCTTTTCCCCCTTTATTTCCTGAATG	18404	A_95_P030981	TA18011_4097
18948	223	78	822	AGCTCTGGTGGTCTGCATGATTGAATATTCTAGTTAAATGTGTAGCATGTGGCTTGGT	18426	A_95_P020436	EB432890
18951	223	81	254	AACTGTCTGCAAGTTCGTGTTATATTTATGAAATCCCAGATTTAAAGACTTTTTCCGC	18432	A_95_P027271	TA14452_4097
18954	223	84	777	AGGATGGACTGTCCCAAGCTTTGTAAAATTTTTGACTCCTGCATCTGGTCTTCAAGGA	18438	A_95_P152012	EB682276
18957	224	2	780	TTGATCTTCCATCCCTTGTGTTCAGCTCCAAGTTGAAATCTAACACCTGCGGGCATCTT	18278	A_95_P212297	TA19803_4097
18960	224	5	643	ATCGCGAGTCTAAAATAGATTCCATGTCTCAACATCTGGTTTTTGTCATTTTTCTCCAA	18284	A_95_P136767	EB440510
18964	224	9	1006	ACATGGAGCAGATCATTAGGGACTCTGTTGAGAGTTTGAAGATCAAGGGCTTTATTT	18292	A_95_P011421	TA14585_4097
18968	224	13	808	ACAGCTCTGCAGTATTATTCCTATCAGTGTGGACCCTATGTTGTCTGCATTTTCTTGG	18300	A_95_P310338	FG135966
18970	224	15	1846	CACATTTGTTAGTGATAAGTTGGTTGTAGCTGAAAGTTGCAATCATTCGGTTTATCTG	18304	A_95_P184752	TA13765_4097
18975	224	20	629	ACTCTGGTCCCATGTTGTTAGTTTGCCTACTGAATATCCAAATGTATTCTATTAGTGAA	18314	A_95_P203392	TA17844_4097
18982	224	27	682	AATCCTTTTCCTATGCATCGGGAGATATCGTTCCCATGTTTGCTGGTGAAATGCTCGA	18327	A_95_P306613	FG636844
18983	224	28	838	CTTGTCCAGGGTTCAGTTTGCTATGGTTTGATTAAGATGATATGAGATTTGATCTCTA	18329	A_95_P000241	TA11743_4097
18988	224	33	508	TGAATCCATTTTTGGAGCTCGTTTGTGAGATCTTCTCGGAGCTGGGTATTGAGGTTTC	18339	A_95_P262751	BP136794
18991	224	36	782	AGAGCCACTAGCAAAATCTGGCGCCAATGTTATTTTACTTTCAATTACTCTAATATTGT	18345	A_95_P001576	EB678787
18995	224	40	643	CATATATATTTTCTGATTCTTAGCTCGGTGGTACTATCTTCCTGGTGTGTATTGGTTAT	18352	A_95_P047726	BP131730
18997	224	42	892	GAATGTTATGATGGGTATGTCCTTGCTTGTTGACTAAAGAGAGATGGATTCTCAAATA	18356	A_95_P180302	TA12711_4097
18998	224	43	394	GAAACACTGCGCCTACACTCGTTTCATGTCTTTTATAAAATTCTCTGGCATGATTTCAC	18358	A_95_P090433	BP530952
18999	224	44	340	ATGGGAATGTTATGTTTTTAAGTTACAGAAGGAACTGCTTCTGCATTTACCTCATTGG	18360	A_95_P093903	BP532467
19000	224	45	91	AGCGATTAAAGATGGTAATTACCCCCTCCCCCAAAAAAGATTTTTTAAGTTGAGGAAA	18362	A_95_P033694	AJ632907
19001	224	46	799	CGATCTTTGAGATCATTTCATGTATTCAGTTAGAGTTCGTGACTCAGTATCACCAGTCT	18364	A_95_P284298	EB683736
19007	224	52	323	TGCCTTCGGGTACAATTTTGAGAATTCGCGTGACACTTTTGGTACACGACTTTAACAT	18376	A_95_P095588	BP533248
19009	224	54	194	GAGGTGAAAGAAATGCTGTAATCTAATTGTATCAAGTACGCAAGGGCTGTTTCTCTTA	18380	A_95_P093948	BP532496
19011	224	56	809	AGTCATGGTTACTTCTGCTGATTCACAAGTTCGAATACTTTCTGGATCCAACATCATCT	18383	A_95_P152282	EB682625
19012	224	57	914	TATACTACCTGTGGCAGCTGGTAGAAATTCTTCCTTCAGCACTTGTGCTATACATCCT	18385	A_95_P014406	TC42345
19013	224	58	518	GTGGGTCAAGAGATATGCAGTTATGAAGCATGAAAAATACAATTCATTCATAGTGCA	18387	A_95_P060000	BP134886
19015	224	60	590	TCATGTTCAAGGAAGAAACATGACATCTGGTGCAATTCTTCGTGGTTCCATGCACCTC	18391	A_95_P006881	FG162981
19017	224	62	748	TGTGCACTCTTGGATATGGTTTGTAATCAATTTGTGCCTCTGGATAGTTTCTTGTTTTT	18395	A_95_P003396	TA12760_4097
19028	224	73	1361	GGATGAATGGTTTGAGTTTTGCAATTCATTTTATGCTGCTGTACTGTAAAAAACTGCA	18417	A_95_P202187	TA17581_4097
19036	224	81	544	GTGGGAGGAACTGGGTTTTATTCTGGTATTGAGGCGTTTTTGATATTTTATAAAAGCA	18433	A_95_P088943	BP530279
19037	224	82	559	GCACTTTGTATTTACACTTCTTGCATCTGTTATTAGCTCACATTCTAAGGTTGTGATAT	18435	A_95_P161352	EH620095
19041	225	1	433	GGGCAAAAAGTAAAGTCTAAGCGCATATGGCACGAAAAGGAAATCCTATTTCGGTAA	18442	A_95_P075615	BP526774
19043	225	3	456	TTGGTGTGGAAATCAGCATGTCAACTAATGCATCTTCCTTTATAGTATTTCGAATGTTT	18446	A_95_P022751	TA14181_4097
19044	225	4	380	TTCTTAAATACTTTAGACGGAGCATCCTCCGGTGAAGTGGTAACGTGGAGAGCTGAA	18448	A_95_P081555	BP528287
19049	225	9	1350	ATATTGTTCCAAGTTTCTTGGGTAAAGTTTGAGGATAATGGAAAATCATGGATTGCG	18458	A_95_P008381	TA12544_4097

19051	225	11	548	CTATCTTGGGTTGACACTGACTGGTTTGTGTATCTACTTTATTAAGATGTTCTTTTCCA	18462	A_95_P024721	TA16574_4097
19054	225	14	787	AAAGACAATGGATTGAAGCATGTCACTTTTTCAACTGCTGATGGAGCCCTAGAAGCA	18468	A_95_P013281	TA18410_4097
19056	225	16	629	GCTGGAATACGAGTGCTATTCAGATTGCCGCTATGTGCTTGTACTTCACCTGTGTTTA	18472	A_95_P122807	EB678148
19057	225	17	546	GAAAATATGCAAGCCTTTGAAAGCTCTTGGAATACATACAGTGAGTCTGCATCCTGG	18474	A_95_P092798	BP531978
19059	225	19	1030	CGGCGAACTTGTATATTTTACTTTGAATTCATCTTGAGAATGTTGGTTGCCCAAATTA	18478	A_95_P013736	TA12594_4097
19062	225	22	1474	TACTCCTCTTTTGGTCAATCTGAATACATGTGTATGTGTCTAATCCCAAATGATGCCT	18484	A_95_P218237	TA21127_4097
19065	225	25	618	AATAGGAATAGGACACCGAGCCCTTATGGACCTCTGTATGATGGCTTCAAAGTTGGC	18490	A_95_P138927	EB442637
19066	225	26	955	AATGACTGCAAGAATAGTATCTTGGACAGGTTATTCCAAATTAAATAATTGGCTGAT	18492	A_95_P024506	TA11806_4097
19067	225	27	1913	GGCCACTATATTTCATGTGCTAGGTTACTTTTTGTGTGATTTTAACCTTCTGTACACAT	18494	A_95_P195042	TA16032_4097
19069	225	29	1038	ATTAGTAAGAGGCTTCAAGTATGAGCGTTGTAGATGACATGATGTCTTGGTGTACGA	18498	A_95_P215822	TA20572_4097
19071	225	31	776	CCTGGTGTATGTTACCCTTCATGAAAATCATATGAGTGAATAATGGGATTTCTTTTCT	18502	A_95_P176652	TA11689_4097
19075	225	35	890	CTGAAGGAGCTCATCTCCATATTGTTCATCTGTCTGATGCTAGAACTTCACTAAACCT	18510	A_95_P245877	EB440641
19078	225	38	515	CAGTCTCCTAATGGGTACATATCAAAGATCATAAAGAGTTTTCCGTTCTTATGAGTAA	18515	A_95_P037213	BP128946
19082	225	42	768	GCAGGACTTCTATTTACCAGGCGAGGCCACTCTTTTTTAGTAATTATAAAATAAAGA	18523	A_95_P195922	EB448388
19086	225	46	0	TGTCCCATTTGAACGATGTTCCTGTGTAAAGTTGCAGATAGTTATTTATTGCCGAAGC	18531	A_95_P029061	A_95_P029061
19091	225	51	199	AGGGTGAAGTGTGAGGATAAAGCGAGCGGGGCCTAATTAGGTTATCTGTTACATTT	18541	A_95_P211357	AJ718047
19093	225	53	765	TACCTACCTGCTGTGTTAATAGTACTATCTTCCCATTCTCATTGACTGAACTATTAGCT	18545	A_95_P195132	EH622432
19095	225	55	590	CTCTGCTATTTGGCTTTCATTTTTTCATGGATTCAGAAGCTGGATTTAGCTTCATTTTG	18549	A_95_P045566	BP131181
19096	225	56	527	CAAGCAGTTGTAACATAATCTTTTTATCATTCTGCAGCTGCCATAATTTAATGCCCCTA	18551	A_95_P123637	DW003499
19101	225	61	866	TCAAGCATTTAAGCAAAGTGTCGCAGTTGGAGCTGTAATTGTTACTAGATGGATGGC	18561	A_95_P293218	FG134918
19102	225	62	1089	TTAAGCGCCAAGAGCCTTGCCGGAACTACAGTTTGGTATCAGTTTGAAAATATTTGG	18563	A_95_P216147	TA20642_4097
19103	225	63	827	AGAATTGCTCCAGGTTTGGCATCTCAGTTCGATTCACCATACACAGTACCAGTCATTG	18565	A_95_P008911	TA14564_4097
19104	225	64	673	GCCTGTTCAAAAGATTCCTGGATTTTTTGTATTTGTAACATCGTGATTACCAGTGTTA	18567	A_95_P017656	TA12707_4097
19105	225	65	3458	TTCTTTTCTGTACTAGCTTGCTTACAAAGTCGGAACCCACATTGGTTGAGTCGTAAAA	18569	A_95_P188907	Y10804
19112	225	72	107	ACTTGTTGGAGTTAAATTCGTGGGTTATGGTTGTTTGCCCTTGTACTGGGATGGCTCT	18583	A_95_P139222	EB442961
19117	225	77	565	CAGTATTAGTGACTTCCGCTCCTGCTCCCTTGTAATCTAAGAAGTAAGAACCATTCGA	18593	A_95_P103122	FG162563
19118	225	78	293	TAAACAGTCGTCCAAATTTCAAAGTACCCAATTGATGGCTTAATGCCATTGTTAAACT	18595	A_95_P154522	EG649624
19119	225	79	1018	GCATTGAGTCTCGTCATAAGATGTGTTTTCCTTTTGTAATGGAATAAAAAACTCTTTG	18597	A_95_P210852	TA19484_4097
19120	225	80	0	TATGTTTGGGCCGATGGGCTATAAATGAATTTTGCTCTATAAAATGGGACTCTTTATT	18599	A_95_P299333	A_95_P299333
19121	225	81	326	AAAGTGCCTTTTCTTACATCCCGAGTGTTCTCTGAATATTTTGATGGCTTTGTAATTTG	18601	A_95_P305878	ES658986
19124	225	84	0	GATTAACTCTCTTTAATCATATTACATAGCACGCTGCGCTTGTTGTTTGAGCGGCCGC	18607	A_95_P263806	A_95_P263806
19125	225	85	449	AGCCTTGTGGCTAGTAATTCATTTGTGTGATCTGTAGAAAATCTGCAGACACCATTCA	18609	A_95_P216057	EH618184
19131	226	6	698	GGTCTCCTGATGATGAATTTCGCCACTGGTTGCATATTTGAGTATGATGCTAAGCAC	18453	A_95_P241315	FG198197
19135	226	10	847	CTTGTGATGTACCATAATCTCAACTAGGCTGATCTTCATTTGTCAATCCATACAGATTA	18461	A_95_P210767	EB678281

19136	226	11	726	CTTTGTTGATGCTGGTTATTTTATCCGTGCGAAGAATCAAAAGCAAGCAAGAGGCTT	18463	A_95_P292398	EB427326
19138	226	13	933	AGAGTATGACATGAAAATTTCAGCTTATGACACTTCCAGTTCCCGTGCAGTGATCATA	18467	A_95_P309503	TC47602
19141	226	16	238	GTCTCTACCTGTTTGTAATATTATTCTAGACAATTGTGGAAGTCATCAAACCTAGTCTT	18473	A_95_P095608	BP533257
19143	226	18	255	TGGGTTTTGCCTACCCACCCAATTATGGAGAACAGTGTGATGCATTGTATTATCCTTC	18477	A_95_P176217	T18327
19146	226	21	822	TATTCCGTGCACAAGAAGCCTGAGCATGAATGGTGTCAGCACTAACCAATTGTATAA	18483	A_95_P242777	EB428460
19147	226	22	630	CTGGTGTAAGGCTATATGCCCAATTCTACAAAAAGACTACTTTTAGATTTTGTATCTC	18485	A_95_P159572	EH617840
19150	226	25	607	TCCCGTCTTTTCTGGGCCTTTTTGTATTGAATTATTGTTTGGGGCTTTTTTACTTGTGG	18491	A_95_P019496	TA17318_4097
19156	226	31	789	ATTTTCGCGCGGTGTAGTCTAGAGAAGAGAATGATGCAACACTTTTGAATAAACCTT	18503	A_95_P012276	EB438347
19167	226	42	1128	GGAGAATTGCGGGCTGGTAGGGAAAAATGACTTTTCTAACAGAAATTAATTCATTAG	18524	A_95_P156112	TA15739_4097
19170	226	45	813	GACGATCATTCAGGAACTGCAATGTTTGCTCAATTTGCTGAACTTAACGGGCGATGA	18530	A_95_P127027	EB426443
19171	226	46	812	AAAGTTGCTTCTCTCAATTCTGCCATCCTGAGTGCTGATACCCTTTCCCTCGAAGTACA	18532	A_95_P227159	FG156975
19178	226	53	792	GAACTTATGATTCAAGCAGGCATCATTACCTCCTTCTCTTCATTGCCCTAGCTCAGTTT	18546	A_95_P144752	EB450832
19182	226	57	481	TTGTTGGACTTGCAGTAGCTATATGATCCAAATTCACTTGGATGTACTAGCTTTGCTG	18554	A_95_P181152	TA12913_4097
19183	226	58	658	AGTATGAAGGAAACCTCGATGTCAATGGGGAGGATTACTCTGTTGAACCTGCTGAAA	18556	A_95_P120727	DW000694
19185	226	60	1050	GATTTGAGAGCTCTTGCCAAATATACTCAGGGATTCAGTGGAGCTGATATCACTGAG	18560	A_95_P070885	TA14230_4097
19189	226	64	1783	GCTTGTTTACTTTAGTTTGGTCCCTATGACAAGTGTAGATTTTTACGACATTTGGAGT	18568	A_95_P176307	U73937
19190	226	65	672	GTAAAATACTCCTTTTACAAGTTTAAGGTACTTCGCGATGAATGTGAATTGTGCTTGC	18570	A_95_P287448	FG639700
19194	226	69	569	ATGGCGGATTCGGTCTCCCTCTCAATTTTCTGATGTATTTATTTTTCCTAACACCAATA	18578	A_95_P122642	DW002623
19198	226	73	338	GATGATGGCCGATATTACGTACAAAAGAATTGTAAATACTCTGCACGCTAGTCTTTTA	18586	A_95_P159657	AM830473
19202	226	77	474	ATTCTGCAGCTTATGTGGGTGCAATCCAGTAATCCTGCAAAGGATGTTGGTGTTGGA	18594	A_95_P096593	BP533689
19204	226	79	0	TTGTACCCGTTGATGAACATGTGAGGAATAGCAGCAAGAGTAGGATATGAAAGAAG	18598	A_95_P224177	A_95_P224177
19205	226	80	434	AATGATGTGTTTGAAGAGAAGGTTAGAACATGCTGCGAAATTTCTATCGATAGAGTT	18600	A_95_P304158	FG638884
19206	226	81	446	ACTTGAAGAGATGTATCAGAGTTTGCTCTCTCGCTTGATCTTTGTTCTTGTTTTCTTTA	18602	A_95_P037806	BP129099
19209	226	84	1553	ACAGATTTCTTTCGAACAAATGTGAATTGAAGGGGAGGGGACTTCTTGATTGTTTTA	18608	A_95_P019316	TA13825_4097
19210	226	85	398	TGATCTAGAAAAATCAGCACAGGATAGTGAGCAGAAAGGGGATTCAGTGGATGAG	18610	A_95_P139462	EB450728
19215	227	5	2129	TTTCATTTGATGAGAATGTCTCTCAGTTTTTTGCACATTCACTGGTGTATGTTACCCTT	18619	A_95_P013111	TA11688_4097
19224	227	14	499	ACATGATGTATGTTTTCTCTCTCTTGGGAATTGGTTCTCTAAAGAAGCGTCTGCAGTA	18637	A_95_P252859	EH619757
19226	227	16	137	CCTCACAGGCAATAATGTCAGGAACATTGATTTTTGCTTCTTATTCAATCTGTTTTTCC	18641	A_95_P132987	EB433910
19227	227	17	522	AAGTAGGGCTGCATATTCTTTGGGATACCTGTGTACCGCTACATTTTTGAGTGAAAC	18642	A_95_P091338	BP531303
19230	227	20	712	TAAGTAATGTTGAATTCCAGGACAATTGGTGCAGAGTTTGGGTGGATCTTGGTACAG	18648	A_95_P252704	FG185867
19232	227	22	881	GTTATTAGAAACTTTTGCTTTTGACAGAGGGTATTAGAGCCTTGTGAAACAGGAACT	18652	A_95_P185672	TA13964_4097
19234	227	24	350	TGACATATGGTTGTCTATCCTATCTGCCAAGTTCCATTTAAGGGGAGTGGTGCATTG	18656	A_95_P089733	BP530626
19235	227	25	555	TTCGCAGAAGAGAGAGATACAATTATAGAGAAGGAGCCATACTCCAGTGGCAGCAT	18658	A_95_P138432	EB442203
19237	227	27	445	CGATGTACAAACTTAAAAACAGTTCCTGTGAGCTTAGTTTGAGCAGAAGTGAGTATG	18662	A_95_P025651	TA17917_4097

19238	227	28	746	TAAATTCCAGAGGATTCCTGTCGGCAAGATCGGTTACTGGTTTCCTCGCTGATGTTTA	18663	A_95_P310398	FG136120
19244	227	34	259	TAGTACATCTTTCAAGTTAAAGCTCTACTTTCAAGACTCAGCCATCATTGCTGATTTTG	18675	A_95_P132932	EB433790
19247	227	37	835	GAAGTACCTTCTGGTTCCACTCTATGTGTATTCATGGATATCCATCTTCAATATCTTGG	18681	A_95_P292938	EB429014
19248	227	38	563	TGAGCTGGAGTTGATTGACATATTTTTATTGGTGCTTCTTTACTCATTTCCAGGAGTTT	18683	A_95_P209962	TA19299_4097
19251	227	41	837	GGGGTCTATTTGTTGGGTGTATTATTGTTGTGATAACGTCATTGGATAATTTAGCACT	18688	A_95_P229724	DV159219
19252	227	42	776	GTTGTGTTTAGTGAAAGTGTGAAATCACAATGTAGTTGGTTGGTCTGAAATAGGTTG	18690	A_95_P119542	DV998886
19255	227	45	897	GAAGAACCAGTTGGGAATATATTCTAGCACTTTTTTGCATTGGATTACAGTTTATGG	18696	A_95_P291713	EB424685
19257	227	47	682	AGGAAGCTGGCCTTTTTGTTTTGAGGTTATAAATCTTTTGACTAGAATATGTGGGTTG	18700	A_95_P289053	FG641473
19267	227	57	1488	GGTCGGTGATCTGATTGTAATAACATACTTCCTTCTGAATGTTAATTGATTTTGTCTG	18720	A_95_P182442	L29275
19272	227	62	909	AGGCTCAACAAACAGGGATTTTGTACCTTTACCACCTACCTCCCTCCAGTAAAGCATG	18730	A_95_P197742	EF051138
19277	227	67	451	TAGTAAACAGATGCAACAAGTGTTATAGTTAACTTCAAAGCTAGTAGACCAGATTTG	18740	A_95_P134877	EB437765
19280	227	70	410	CTGCTTGCTTCTCTGGAAAGGAAAGATTCATATGATCATTTGTTATTCAAGAGTCAC	18746	A_95_P031536	BP135385
19285	227	75	183	TTGATGTTTAAAGAAGTGTAACGATCCGACCGGTCGCTTTGAGCTTTTGCATTTTGCC	18755	A_95_P158867	EH616756
19290	227	80	310	GGAAGATGGTGGATGATATGGTTGGTGGTAAAGCTGCAAATTTGAATAACGTATCA	18764	A_95_P071398	BP525693
19291	227	81	845	GCACAAACACCAGTATGATTGGGATGCTGCAACATCTGCTAATTCTGCGCAATATGG	18766	A_95_P249002	FG141593
19296	228	1	578	CTGGCTTGCTGCAAACACTTCCTATTCCTGCACTTTATTGGACAGATATTAACATAAAT	18612	A_95_P306303	FG642762
19299	228	4	844	TCAGCCGTTCAAAGTGACAGAGAACAACATGGAATTTCCTTATGACCGCTAGATGTA	18618	A_95_P232579	EB438485
19300	228	5	842	TTTGCCAGCGGGAGTTGAATATATTAGATTCTCTTCCCAAACCAGAGCATTTCAGGG	18620	A_95_P145247	EB448849
19304	228	9	272	CGTTTGTGATGATCGCCATTCAGAATTGATTCCGTGTCTCGACAGACATCTCATATTT	18628	A_95_P170396	EH664893
19307	228	12	325	TTCCCCCTCTGAGACTGTGTTACCGGAAGTTGTTGATTAATGACCACGTTAAATCCA	18634	A_95_P080405	BP527996
19314	228	19	635	TATGACACCCATTGCTCTTAGGAAAGTTGATGAATAGGCTGAGAACAACCAGCCCGC	18647	A_95_P164052	EH623175
19315	228	20	822	TAATGGCACTTCCAGCTGGAAACAGAGATGATCTACCACTGAACCAATACGAGTACA	18649	A_95_P017411	EB440363
19320	228	25	328	CTTGCTGCAAGGGTTTTAAATGCTTTTATTTTGTGAAAGAGTGATATCGTGCATCCTT	18659	A_95_P241609	BP534117
19323	228	28	1824	CGCGAGCTAATTCTTTTGTATCCTTTTTGAATAATGTTGCCTTTTGTGAGGTTCTTGTT	18664	A_95_P009861	AF220611
19325	228	30	888	TTAGGCCGACAATATCACCTTTCTAGTTACATCAGTCCGACAATCTTTTGGATTTACA	18668	A_95_P009716	EB426099
19326	228	31	817	CATAGCTATCTTATTTTGACAAATCAGACCACCTATGAGCTCGTTAGACGACGGCGC	18670	A_95_P216742	TA20771_4097
19327	228	32	503	AAGCTCAAACTCAGGGGAAGTATGGTTGGTGATATTTACGTGAGGTTCCTTAGTGGT	18672	A_95_P266676	BP534541
19337	228	42	501	TCGTTGTCTTCCAACCATTTCCATTGGTTTTCATGAACCAGCTTGGTAGTTTCGACTTC	18691	A_95_P185802	FG623230
19338	228	43	118	TTGTACCATCTGGATGTATTGGACCTGGGAATGAATGTAATGCTTTATTACACCAACA	18693	A_95_P110652	CV019834
19345	228	50	599	TTTGTCGATTCCGATGTCTTCGTGAAGATGAATGTTGGGATTGTACTTGACGAGGGC	18707	A_95_P001856	FG144547
19346	228	51	1100	TTCCCATGCACGGCATGTTAGCAGATATGGAACTGTTGTGTTGAATTGGCATGTTATT	18709	A_95_P135027	TA18105_4097
19349	228	54	596	AAGATCTAAGTCAGGATTTAGATGCAACTGGGAAGGAAGAATTGGGTACTGAATCT	18715	A_95_P203122	DW004322
19351	228	56	692	TGTTTGTGTTGGCAAATATTATGACCTCTGCTGAAGAGTACACGTTTCTATTTTGTGT	18719	A_95_P295393	EB445884
19355	228	60	677	AGAAAGATGGAACACGTGATAATGACTGGAAATGTCCTAAATGTGGAAATGTCAAC	18727	A_95_P155847	FG143076

19356	228	61	139	GCTGCTTTCCACATTGCAAGGAACTAGAATTTTACTTCCCCCAAAAATAAAACTGTAT	18729	A_95_P033979	AJ717979
19357	228	62	362	AAGTAAACTGTGAGCATATTACCGCTTGTCTTTTTCATCAAAATTCTCGCTTATCCCTA	18731	A_95_P147402	EB451797
19359	228	64	413	GATAACTCAGTGTATCGCCTCTACTTTTGGCTTGACTCCATCTGAGGATGAGGGTGAT	18735	A_95_P161592	FG160077
19363	228	68	720	AACTTCAGTACTCGTGGGCGTGGATGAAAAACTTAATATTCAGGTTGGATTTTCATCT	18743	A_95_P290288	DV162520
19367	228	72	378	CTGTATGGTGCATATGAGAATGCTTGGTTCTTCCCCTATTTTAAAGATGTATGATTTC	18751	A_95_P003766	EB436307
19371	228	76	156	TTTGGAAGATTGGGAGGCCTACTAATTTATGATAAATACACATGAGTTTCCGGGGAC	18757	A_95_P070280	BP192578
19372	228	77	824	AAATTTGCTGCAGAAACTTGAAGGACATACTGATACCGTGATTTCGGTAACTTGCCAT	18759	A_95_P224487	EB451710
19375	228	80	93	TAAGGCTAACCATATAGGTCTATGATTACTGCACAGACACTAGCTCGGTTCCCTGTTG	18765	A_95_P102302	CV015968
19379	228	84	592	AGAAGCAGGCAGCATTATACATTGGAGAAAGGCTTATGAAATCTGTGTGAAGAAAG	18773	A_95_P060690	BP135063
19383	229	3	760	GTATGTGATGATAGGTTCTCCACTAGTACATGTCTCATATCCTCGGAGAGCATAAAC	18780	A_95_P099458	BP534936
19386	229	6	454	GGGCCTTTTTGTATTGGATTATTGTTTGGGGCTTTTTACTTGTGATCGTGGAAATTTAT	18786	A_95_P141762	EB445401
19389	229	9	177	ATCATACTCCAAGTGGTCCTGACACATTTGAAAATGGCGAAGGTTTTACCCCCCACTA	18791	A_95_P147902	EB643486
19392	229	12	485	AGTCTGTCTATAGTATTTCGAGTTGCCGGGTGAATGTCTATACTTTATGAGTCATTTT	18797	A_95_P186172	TA14069_4097
19395	229	15	734	GAGATTTCTAAGTGTTCTAGTTTTGATTATGATGCAATGTTGGGAAATGAGCCCTTTC	18803	A_95_P208902	DV159975
19396	229	16	354	GGCTATTGACATGATGAGAAGGAAGTATGAGCACGTTCCGCAGTTGAAATACATGC	18805	A_95_P157832	FG142745
19409	229	29	612	AAGCTAACTTGAGCTTCAGTTGCTTTCCAGCTACTACTAATATATCAATTAGTAGTAG	18831	A_95_P187482	EB445354
19410	229	30	340	TCGAGATGTCGCTCCCCGGATAGGTTATCACAAGCCTGCTTTGATTGAATCATCTTTCT	18833	A_95_P021171	DV157598
19414	229	34	1386	GACCATGGGCAGATGCTTCCTGTATTCAGTTTTCCGTTTTGATATCTTTTCACAATCCA	18841	A_95_P034763	AY619953
19417	229	37	602	CCGGTTCTTCAGCTAGTATGTTAGTTTTTGCAATTAATCTTGAGTAAACAATCTGTAC	18847	A_95_P005981	EH617048
19421	229	41	697	AGCAATACTACACAGCTTGGTGTGAGTTTTGCTGGTGGATATTTGGGCTGGTATTCT	18855	A_95_P159487	EH617741
19422	229	42	816	GTATCCACGAATGGAGGCAATATTCATTGTTTCAAGCTATAACCCCTTGTGGCTTATTT	18857	A_95_P298513	EH622237
19430	229	50	661	GGCCTAATGCCGCTTTTGATGTATTTCGGTCAAAATTCTATGTGGAAAATGAGAGTGT	18873	A_95_P258416	TA12009_4097
19431	229	51	1138	CATTTCTGATGTATACTTCGAATTATTAGGCAGAAGGGACTATGTCTTCCTCAAGTTAT	18875	A_95_P018801	TA15093_4097
19433	229	53	249	GCATCCTTTGGAAATGCTTTACTGCTTCACTCATTTAATGACATATTATGTTGGGTAC	18879	A_95_P184602	TA13730_4097
19435	229	55	495	ATTAATAATTCTGACTTGATATATCAAGCAGCCTCAGGGGATTCGGATGTGGGGATT	18883	A_95_P075345	FS411604
19436	229	56	179	CGTGCTGCAGCTCAAGAATGGTTTTGTTTAAAGTATTATCTTGTGTAACTTGTTCTGT	18885	A_95_P210762	TA19465_4097
19443	229	63	1687	ACTTGCATTCTAGAAGGAAGCTCGATTCATGACCGTCTGAAAACTGCTTTCTGATTGG	18898	A_95_P214482	TA20272_4097
19450	229	70	0	AAACCACATTCGTCGCGTGAAGCTGATTTGATGATAGCTGGTGACTGAAGCTGCATG	18912	A_95_P309963	A_95_P309963
19452	229	72	782	CATTCCTGGTGGTTGGGAGTTGGTCTTATGATGAGTAATTCAAGTTTCAGGTGAGAA	18916	A_95_P161992	EH620691
19453	229	73	264	CCATGGAGTAGTTATCTTTAGGGTTTGATGGATTTTGTGTATTGATACTTGTTTGTGG	18918	A_95_P209522	TA19208_4097
19456	229	76	815	CAACAGATGAGGCGTCAAAACATTGACTCAATGAGCGGCCAATTCAATTAATTATTT	18924	A_95_P205237	EB424983
19460	229	80	521	CATGTCACTTTTGTCTGTTCTCCTCAATCTTATTTAATAGTAGGGCCTTCGTGTGTCTGT	18932	A_95_P031686	DW003455
19463	229	83	799	CTGGCTCTCCGAACTTCATATGCTTACTTTAGTTTAACATGGTATTATCGGATATTTGA	18937	A_95_P184347	TA13675_4097
19474	230	9	261	TTACATGTCTGAATGTTTAGTACATTTCTGAGCTCCACTCATAATCCATGACTGTTCTT	18792	A_95_P097278	BP533966

19475	230	10	217	GCAGTCATCAGGGTGACAGTACACATTAATATGCAAGTGAGTATTTCCTACAATTAT	18794	A_95_P009511	EB448560
19477	230	12	749	TGATATCAGTTCTAGGTCCAATGTCCTTTGCTGGCCATTCCCTCACAGACTATTGGTT	18798	A_95_P311603	FG143367
19479	230	14	221	AAGTTGCGCAGCCAGGAGGATGAATGACCATATTTGGCTTTCAAATGATATCTACTA	18802	A_95_P112962	CV020938
19480	230	15	861	AGTTATACAATATTGTGATGACCTCGACGAGATCCCTCCTAGCTTTGCCGATATTCCA	18804	A_95_P115482	DV157713
19481	230	16	641	AAGATGTTGATGCTTTTTGTGAACTGTGTGGTATGTCTAATGACATCCTGGTTTGTTG	18806	A_95_P019146	EB432106
19482	230	17	818	AAGGATTTCTCGTTTGTAAACAGCTAAGCTAATATGGTCTCGAGTCAGTTTGGTTAA	18808	A_95_P009826	TC41163
19483	230	18	970	TGGGTAGTCCTGAACTTGATACGAGCTCTCATATCTATCTCAATAATATCTTAAATGC	18810	A_95_P014611	TA13902_4097
19488	230	23	885	CCCTACTTTTCTGTTACATTTTTCTAATGTACCGGCTGAGTTTGGTCATTTTTGAGAAT	18820	A_95_P249752	AJ309009
19489	230	24	296	TTATTTAATTGTACCCCCGGACTGGTTTTTGCCCTATTTAAGTAGGCTAAGAATTTTCT	18822	A_95_P052511	BP132942
19491	230	26	489	AGAATCTCAGACTGCATTACATACTTTTTTGTTGTCCGAGTTTTATGTCAATGTACAA	18826	A_95_P029696	EB445136
19494	230	29	539	TAAGATTGAGTAGCAGCTTTTTATCTGCTTTGTTCTTGATTTCCTTAAGTTCCTGCTCT	18832	A_95_P312693	FG151860
19497	230	32	1374	CAGTGATATTTCCGTAATTACGCCATTTCATTCTGTCATTTGCTTATGTCATACTTCAA	18838	A_95_P011991	TA14296_4097
19501	230	36	778	GTGCAGCTTATCAATGATCTAGGCGAGTTGAAGGATTGCAGAAACTCCTGTAAATGA	18846	A_95_P163557	DV999212
19502	230	37	279	CAACTGCTGATGAACATGGTCACTATCTGACCCAAAAATATATGTGTTTAAAAGCTTA	18848	A_95_P105087	CV017290
19504	230	39	565	CTGTTTTAGTGTGGTTGGTGTTATTGTCCTTTATATTTGGTTAAGATACTGTGGATCT	18852	A_95_P108017	FG622663
19506	230	41	769	TTATTTTTCGCACTGCTAGGCTATCTGGTGCTCATAACCTGTATGATCGAGAGTGCGC	18856	A_95_P312993	FG160784
19507	230	42	268	AGGGGCAGAAATTTCTTTATGTATTTGATTTTGCATTGTTCCCTGTTGATGGACTTCC	18858	A_95_P156217	EG650470
19509	230	44	661	TCAGCATTGCTGTGATGATTTTGTGCATAGTCTTTTACAATGTGGCACATAGACTTCC	18862	A_95_P135622	EB439134
19512	230	47	875	CGAATGGTAGTCTAGAAGAGCATATCATTTCTTTCCATTCTTTGTCATGAATATTCGG	18868	A_95_P212337	TA19811_4097
19514	230	49	682	CTGGTGACTTGAAAATGTCCTTTAACAGCAATATTCACTTTGGATTAGAGATGGTCTA	18872	A_95_P023491	DW003798
19515	230	50	738	GGATGAATCAGCGTGGTTTCTGGATATTGGAGGTCATTGTTGTTCATGTCACCAGCA	18874	A_95_P246532	EH621518
19516	230	51	306	ATTGTGCTCCTGAGTGGTTTATTTTCAGTTTAGCAGTAGACCCTCTTTCATTGTATTTG	18876	A_95_P135577	FG629295
19521	230	56	864	ATTACACATTATCGAAGGAGCTGATCATGAATTCACTTCGCATCAAGATGAGTTGGC	18886	A_95_P117152	DV159941
19525	230	60	835	TATGTTACTGCAGCAGCGAAGCCTTTGATGTGTAATACTCGTTCCGGTTAGAATGCC	18894	A_95_P183082	TA13375_4097
19526	230	61	289	CGTGAAATTATGACACCAGTTTTGGGTGGAGTTTTACTTCGGATTCATATTTGTAATA	18896	A_95_P093758	BP532399
19528	230	63	708	GCATCATTTCAATAGGAGTCACTGCTTTTCGTGCATTGTACTGGCTGAAGAAATGTA	18899	A_95_P251507	FG644568
19530	230	65	612	TAAAAGCAGCGGAGCCAACACTCATCAGAAAGGAGATAAGCAATATATCACTTGAA	18903	A_95_P269811	EB433245
19543	230	78	194	GGGTCGACATATCTCTATCTATCTTTGGTCTTTACTGTACATAAGTAAGTCTTACGTAT	18929	A_95_P211502	TA19625_4097
19548	230	83	683	GTGTGATGATTCTTTTGCTTTAACAGGCTTATTTATTTGTATGGAGTCATCATCCCATG	18938	A_95_P291603	FG165897
19550	230	85	1023	GATTGGAGCAGCAGAACTCAAATGCATATTGCGAGGCAGTGATTAGATAATAAAA	18942	A_95_P192312	TA15425_4097
19551	231	1	756	GCATTCATTGACGCGGACAAAGTGAATTATCAAAAGTATCACGAGAGATTGCTGCA	18943	A_95_P226154	FG194205
19552	231	2	897	GTGAATGTTGAATGAGATTGAATATAACATGGTTTTGCTGTCCCAGTGCATGCAAAT	18945	A_95_P238629	AB023479
19555	231	5	313	GTTAGCCTTTCTTGAAACTCGAATTTAACCTGTAGATAGTATTGAGCTGGATTAATTC	18951	A_95_P048931	BP132041
19557	231	7	1080	CGCATATCCCTAGAATGAGCTTGTAAATTATGGTTGTGCCAAACTTATGATTAACAAT	18955	A_95_P022871	TA12945_4097

19566	231	16	925	GGAATAAATCTGAACCCCTATAACCTGTGTATCATCATTGTTGTATCATCAGTACATT	18973	A_95_P193837	TA15757_4097
19568	231	18	701	TATCCAACCATCAGCCTATCTTCTCATCTCCGCTGCACTATGTTGATAAGGAAATGCA	18977	A_95_P287018	FG639578
19569	231	19	92	GCAGATTTTATTCGCTAAGAACTAGGAATTCGGAATTGCTGAGCTCGCCTAATATTGT	18979	A_95_P132847	EB433632
19571	231	21	624	CAAAAACCGTACTTTGAGACCAAAAGACTCAGATGGTCGTCCAGATGAAGAAGTTG	18983	A_95_P041661	BP130150
19576	231	26	847	TATGATATATAACCGGTGGAATGGGATTCTTGAGGCGGAGTATGGGTTCATGCACCT	18993	A_95_P295413	EB446027
19582	231	32	860	GCTACAAGAAAAGCAATTTTAACGGTTCATTAGAAGAGCTTTATTAGCTTCTCGTTCC	19005	A_95_P187347	TA14326_4097
19583	231	33	729	CTTGAGATGGCTCCCTGATCCTTTTCTTCTTTGTCATTTTTTCCACGTTTGTAACATTGG	19007	A_95_P216312	DV158438
19586	231	36	802	TGTATGGTCGCCTCCACCTTTACATTTGCTTATATGCAGAGATCAGGGTACAGAGTGA	19013	A_95_P267996	FG153457
19589	231	39	250	GCAATTTTCTGGGGATTCTAATGTATTCTGAATAGTACTTTGGTACTATTGTTGAGCC	19018	A_95_P007351	BP533064
19590	231	40	559	TCAGCCTAGCTTTAGCTTCTGTTGCAACAGTATTTTACTGTATGAAATTTGATACCCTT	19020	A_95_P017921	TA17887_4097
19591	231	41	204	GTGGTTGTGATGATGAGTGGAAGGAAGAATGGAAGGGTTATTTTATTACTAGTATCT	19022	A_95_P104962	TA17047_4097
19592	231	42	888	TTGGGGCTTTGACCAGTTTGAGACAGCTTTATGTTGCACATAACAAGTTAACATGTCT	19024	A_95_P137257	EB440979
19594	231	44	511	GGGGCTGTAATAATCTCTATAATAAACAGATTTGGAGCTTATTAGTAAAAGCTGGGG	19028	A_95_P121407	DW001469
19598	231	48	400	CATATTGTACATTGGTGTCTTAAGGAAGAAGTCCTTGAGTTATGTGATCTCCTCAGG	19036	A_95_P026696	BP135949
19600	231	50	1109	GGAAGCAGGTTGTAGTATTAGTTGTTGAGGAAATACTTTTAATTTTATTCCAGACAGT	19040	A_95_P182122	TA13138_4097
19603	231	53	822	ATTCTTTTTAGCTGTATGATGAGGCAGATTCAGGATTTAGACGGGATATATCAACAG	19046	A_95_P291818	EB424969
19604	231	54	649	TTGTTTTTACACTCTTTTATCAGGAGAAAGGAAAGTAGAAATTATGGATTGCCCCAA	19048	A_95_P134652	EB437237
19605	231	55	369	GTCTCGGGCCAGGTCCATTGTATAAATAGAGACAATTAGCTCTATTCAGTAGTAGTTT	19050	A_95_P068595	BP137169
19606	231	56	680	CTGGAATCAAAATAATTCCTGTGCGGCTCTCTTTTTAACAGTCTTAAAGTTAAAGCTG	19052	A_95_P196422	TA16335_4097
19607	231	57	261	GACTCACATGATGCCTCCTTGGTTTTCCTATGTTGATGCAAAAACAGGAACGCCCGTT	19054	A_95_P241955	EG036055
19608	231	58	415	TCTGTCCGATATTTCTTTGCTCGTAATGAACTAACTGTTTGCAGAATCAAATGATAGT	19056	A_95_P088898	BP530264
19611	231	61	818	TTTCATGCTTTTTGACATGGATGGTCATCAAGTTCTTCAAAATACAGTTGTTCAAGTT	19062	A_95_P199832	TA17076_4097
19613	231	63	86	AAACGAAAGCTATCTCCGAAAGAAGAGCCTGAGCCAAAAAGGTTGCAGCGGATTGC	19066	A_95_P034144	AJ718211
19616	231	66	826	GGGGCAGCAGTTATCAGAATCACCAAGCAAATACTTAGAATGTTATTTATTTAATGT	19072	A_95_P139532	EB443303
19619	231	69	0	CAGTTTGAAACATTTGGTAATGGGGAGTCTGATAAGCCAAAACACACAGAAGAAAA	19078	A_95_P293468	A_95_P293468
19623	231	73	402	GTGCTGAAAGTCTTCATGATGAGTTTGAAATTCTGTATCTAATGGCGTGGCATAATT	19086	A_95_P133887	EB435581
19626	231	76	769	GGTACCTGTTAATTCTGCCAATAATAAGGATCATTATGTCCTCTCGTGAGTACTATAT	19092	A_95_P011896	TA12183_4097
19627	231	77	876	GCTTCAGATATTAAGATAGCATTGGATGGAGGATTCAGAAAGATCTGTAAATATGTT	19094	A_95_P022761	TA18270_4097
19631	231	81	659	GGAGAACCTTATCAGAAAAATTTATGCTATGCGCTTCTTGGAGGAGTGAGATGCATA	19102	A_95_P297728	FG634385
19632	231	82	618	TTGTTTGTGCTCATGGAGCTTTTAGGGTTCCGGAGGATTTGTTCCTTGATGATCAAGA	19104	A_95_P122707	DW004634
19634	231	84	1877	GGTACCCAAAGTGGAGACGAATTGTTGAATAATTAAAAGTGTTTATTTCTTTCTCCCT	19108	A_95_P183207	TA13405_4097
19635	231	85	664	CATTGCTAAGGCCATTGGAAATTATCTGTGGGGTCTGAGTAATCGTATGCAGGAAAA	19110	A_95_P056231	BP133902
19640	232	5	737	CCAAATGGCTGTATGATGGTTGTCACAACGACTTGAGACCTCTATGTTCTGTTTTTCT	18952	A_95_P281463	FG642462
19644	232	9	716	GAGGCTTCAGGCAGTATTGAAATGCATCAGTTGATAATCTTGCCTTCCTATGAGCATT	18960	A_95_P203672	EB680704

19647	232	12	273	TTGGGAAGCCATCGACGTTTCTGATGGACTTTCTATTGCAGAAGTATAACATCACTAC	18966	A_95_P081035	BP528156
19651	232	16	606	GCACACTGGGCGTGATTGTGACAAGTTTCAAAAGGTAGAAAAAAGACAGAGAAAGA	18974	A_95_P188912	EH614541
19652	232	17	621	GTGGCTCTTAGTTGGACTATGTTCTCTTTTGTTTATAGTACAAACACGGATAGCAACT	18976	A_95_P307728	FG639284
19654	232	19	2861	GCGGGTTAAACCAAACCCATTATTTTTTGCTCGAACTATGTATACGTATGCAAAAAGA	18980	A_95_P212947	TA19945_4097
19666	232	31	828	ATAGTGTTAGGAGCTGCTATGACGAGGGAAGCGGACTGCTGAACTGACTATGAATA	19004	A_95_P292273	FG146921
19667	232	32	118	TCCAATGTCAGCTCTAATGTTAATATAATGACTGACCCTTCCCTCCCTTCCAAATCTAT	19006	A_95_P316313	FG188087
19670	232	35	517	GCTCTTGGTGTAAATTGTCTGCAAATTGTCCATGGATTTGTGGAAAACTATACATCTT	19012	A_95_P029446	BP529479
19674	232	39	692	CACTCCCGATATGGATGTATGATGTGGAGTATTAAATTTTAGTGGTTTAGATACGAT	19019	A_95_P213112	EB435618
19675	232	40	422	TGACCCCCTTCAGTGAATTCTGGATCGTAATTGAGTGTTCTTAATTACTCCTAGTATAT	19021	A_95_P095968	FS412034
19679	232	44	253	TGTGTTAGAACCATTGAACTTTCAATCTATTGGATCGACCCCCTTGATCTTCTGTTATG	19029	A_95_P133742	EB435391
19680	232	45	285	GTTTGGGATGCCAAACTCAATTTGTATCTTTTTGCACATCAATGATCAATGGTGATTG	19031	A_95_P136862	EB440572
19682	232	47	1285	CAGCAAGGCTGATTTCATTGCCTATGATTTGGCAATTGTGTTACAAACAAAACAATGT	19035	A_95_P179627	TA12552_4097
19683	232	48	845	ACCTGGACTTCAAATTAAACATGCCAACCCCTCTTAATCTCTCTTCTTCGGGTGTGTTA	19037	A_95_P126517	EB425828
19685	232	50	505	GTGCATGTTAAACATCTGAGAAAACCAAATGTAGGTGTTTGTAAGAGAAATCGAAG	19041	A_95_P022496	FG640166
19690	232	55	362	CTTTCCTGCTTGGAATAATTTGGTAGAACCATTTGTCTTAACAGCTTCACTCTGGGAT	19051	A_95_P030811	BP136525
19692	232	57	512	TTTCCTGTTGAATTTGAGACATACAATGTTTTCATCGAGAGAAGGGAGAAGAGAGA	19055	A_95_P161192	EH619949
19697	232	62	888	GTTTTTATAATTGGGGCCACAAACAGGCCTGATATAATTGACCCTGCACTTCTGCGAC	19065	A_95_P258806	TA14230_4097
19699	232	64	454	GGTGCAAACTTTTGTGCTGAATTGCTGCTTTCTTAGATATGATGTAGAGATTAGGAA	19069	A_95_P212922	TA19939_4097
19701	232	66	845	CGGGTGTAGAACTCTCCTTGTTTTTTCAGGTGTAGTTAATGAATCAGCTTTTCAAGAT	19073	A_95_P010651	EB682950
19723	233	3	300	GACTATGTGGTACTTTGTGCATTTAGCTTCGGTACATCCCTCTCCAATAAAAGTAGTC	19116	A_95_P125257	DW005053
19726	233	6	509	TTTCACTTGTGATGAAAGAAGGTGTAGCAATTGTGGGATTTTCACGGGGCGTTCTGG	19122	A_95_P212747	EH616394
19729	233	9	0	AAGCTTTAAAAATGCAGCGTTGTGCCTGTTTGTTTCAGTGAACAGCAGATTTGATAC	19128	A_95_P024131	A_95_P024131
19730	233	10	428	GAGAGAAGTTATGTGAAGCAATTGACAAAAATCCCTTGAGCTGTCTGGTCATAGGG	19130	A_95_P113232	TA12319_4097
19731	233	11	177	GTATGATAGTTCGCTTTCTCTAATAGAACTATGTAGTTAGCTGTGATGTAACTGAACC	19132	A_95_P098248	BP534387
19734	233	14	428	TCTTATGGAAGTTTCACTACTTATGAGAGGATTCCTATCAAGCATGCAAGTGTAGGG	19138	A_95_P077825	BP527352
19735	233	15	423	TTATACAAGAGCGGCTGTGAACGAACAATTCATTTAGTATACTGCAATAACTTTTGCT	19140	A_95_P023496	TA15726_4097
19737	233	17	855	ACACTGGCGATTTGATTCGTTATCAAGAATTGTGCCGTGTCCATCAAGCTGCATTGAA	19144	A_95_P190762	TA15084_4097
19741	233	21	476	GCAGTTCTCTATGAACATAGTTTGAGCTGAGAAAAGTTGAGATGGGCCTTATGTTTC	19152	A_95_P232044	FG641634
19742	233	22	608	TTCGGCAGATCTCTAAGCTAAGATTTTCTTCACTTTTATGAGAATTTTGTACTGGGTTA	19153	A_95_P011491	BP530118
19743	233	23	380	ACAAGTGCATCTTTGAAGTTCACAGTCTTGAACCCCAAGGGGCGAATTTGGACTATG	19155	A_95_P147702	EB426400
19744	233	24	550	ATTCAGGGATAATTATTCGTTTCGATATGGTTGCTCTTAAATGTCCCATTATTAGAGG	19157	A_95_P178747	TA12334_4097
19745	233	25	244	CTTCTGTTTATGTGCTTGATTCATTAAACGCATTTGGTCCAGCAGTTCTTTAATCTTTT	19159	A_95_P031311	EB444332
19748	233	28	274	CAAGCTGATAAACACACCTTTCTAAATGTAGAATGCTGCATTAGATTGTTAAGGTGT	19165	A_95_P001771	AJ632774
19749	233	29	816	TTCTAACTTACTGCTTTTGTTAGCTCGCTACCAGATTGTACTTGTGATTACTTGTTGTG	19167	A_95_P273131	EB681678

19751	233	31	714	GAAGGCTTAGATTTAGTGGCTGTTATAAGCCTCTTGCTTTTCTATCTTTATTTGGATCT	19171	A_95_P000676	EH615247
19755	233	35	226	GGGTTGTATGTTGTACCAAACAAACTTTCTTGTGTTATTCTGACGTTGTTACCTGAAT	19179	A_95_P132372	EB432848
19764	233	44	1502	GTATGCTCAGTATTTTTCCCTCCCAGAACTATGAAAGAAAATAGATTGAATTTTTGCC	19197	A_95_P186397	TA14118_4097
19765	233	45	490	TTTCCAGCAATCTCAAACTATTGTTCAACCTGGGTCACTGGACAGTGAAGCTGGTATC	19199	A_95_P091533	BP531401
19766	233	46	372	AAGGGCCAGTCTACTTGGTCTTACTTATGCAACTCAATATCTGAGCGTTCTCCTCATA	19201	A_95_P026926	TA17881_4097
19768	233	48	799	AAAGAGAGGGGATATCAATATCACACCCTGCCCGGTTTATCCTTATTGGTTCGGGTA	19205	A_95_P184917	AF014053
19769	233	49	434	GCTTAGTTTAATCCCTTTATCTTGGGCTTAGCCATTCTTTTTGTTTTATGTGTCGTAAG	19207	A_95_P278348	AM832067
19771	233	51	685	TATCCAGGGTAAAGTGGAGTTCCTTTCTTTGTAGCCATTTTCTTGAAAATCCACTATA	19211	A_95_P316678	FG197371
19772	233	52	617	TTGCTGACATCTAAATCTTTGCCAGCATCTATTGTGCTTCCTTGTGGATCTTGCTCACT	19213	A_95_P116857	DV999689
19779	233	59	0	GCATGGAAGGATTTCTTGTTTTGGATTATATCATCTTTACCCAAAATTTCGGAAATGG	19227	A_95_P259631	A_95_P259631
19781	233	61	505	ATTGGTCATCTGCTGGAGGAGAACCGCTGGATAAATGAATCCATTACCGCCCTCATA	19231	A_95_P120582	FS392203
19783	233	63	429	ACAACTCTACATTGATGGGGAGTACTTTGGTGGCTGTGACATCACTGTAGAAGCATT	19235	A_95_P103402	CV016485
19784	233	64	560	ACGGGTGCATTTCATGTAGCATGGCTTGCGATGTGTTTTAAATAACCTTGAAATAATT	19237	A_95_P065360	BP136309
19788	233	68	766	CAAGCTGCGCAAATTGGATATTAGCTGGTTTTGTAAACTTGTTATAGTGTGTAAAAC	19245	A_95_P269941	EB428069
19791	233	71	592	CATGCTTGTTGACCAGCTTAAATGAAATCATGGTGAGAAGATAGGAATAAAATGGG	19251	A_95_P132487	EB432978
19798	233	78	425	AGATGTTGAAGCTCAAATCCGTTGTTGCTTTGTTATTTGTTTGTTGCCGCTCTGTATC	19265	A_95_P094173	FG635922
19800	233	80	1012	AGTGTTTCACCCTCTCTCCCCCCTTGTATTAAATGTAATAATCTGTTTATCTTAATGCT	19269	A_95_P191547	TA15261_4097
19806	234	1	433	TTTTGTCTGTCTTTAGCTCTTTTCTTTTGGGTCACTGAATGGTCCCGTTGCTGCTTTTA	19113	A_95_P092113	BP531648
19809	234	4	1222	GCTACCTAGCTTGTACTTTGAGTATATTCCATGCGGCTTGTTATAGTTTTTAATAAGA	19119	A_95_P008001	TA12648_4097
19810	234	5	785	TAGGGCTTTTTGTAATGACTGTGTAAGACGATGGTGGAATATATGTAATTGCTGTCT	19121	A_95_P146017	TA12122_4097
19812	234	7	1282	CTGGCTGTTTTTGATTGCCAAAATACACTCAGAACTTGTTGAGTAGAGCAATTTGTAT	19125	A_95_P237854	AJ006228
19813	234	8	2339	GCATCGTCTAAAACAACGATTTTTATCAGCTGTAGCAAAGAAAGAAACTTCATAGAA	19127	A_95_P029026	TA12266_4097
19814	234	9	1450	GTTTAACCTCTCAGTTTCACCCCAAGTGTTTTACTTTTTGAGATTCAAACAACATCTTA	19129	A_95_P214932	TA20369_4097
19816	234	11	240	GCACCTGGGACTGTAATGATTGCCAAGACATGCAAATCCATGTAATTGTAATTCTTTT	19133	A_95_P092333	AM802310
19824	234	19	1441	ATTATGGAAAGAAAAGGCCTGGCCCCGATTCCAGACACTGGTCTTGATTCAGAGTTT	19149	A_95_P194002	TA15796_4097
19829	234	24	273	GCTTACTGTAAAGTGAACCTTTGTGGGTTGATTTAAAGACTAGTACCTTTTAAAACAG	19158	A_95_P067655	BP136933
19833	234	28	507	GGCTTATTAAGCAGTATTTTGTTGGGTTGGTCTTACTTAATAGCCAACATTTTGGCAT	19166	A_95_P220917	DW004366
19837	234	32	551	GGTTGTAATCAACCATGGGCATGTAACCGTAAATTCCGTTGATACAATTTATTATCTG	19174	A_95_P006266	FG633965
19838	234	33	106	AGGCTTGTTGGTTGAACGATTTTGTTATCTATTCATTTGCCTTACTTGTATTTGTCCGC	19176	A_95_P121327	DW001339
19839	234	34	723	TTGTACATCTTTATACAGTAATACTGCTTATTTAAGCCAGAAGGGGTTATTTGCGTTG	19178	A_95_P013421	EB429134
19844	234	39	584	TATGCGTTTTAGTCTAGGTATGCCTTCTTGTTTCAACACTTAGATTCTATCCATATTCA	19188	A_95_P005351	TA12063_4097
19846	234	41	740	TAGCTGCCCGTCGATTCGCAGTTCCGTTTTTCTCCATCCCTATCTTCCTATTAGTATATT	19192	A_95_P115817	DV158194
19854	234	49	964	TGTGGACCTCTATTTGTTTGGATGGACCGATTTGGATAGATGAAGCTAGTTTGGTTG	19208	A_95_P005061	L16767
19857	234	52	780	AGATAGCAATCAAGGTATCCAAGAGGGTTAGCACTTCCACTGGTAAGAGACGAGTA	19214	A_95_P204567	DV159964

19866	234	61	805	TGTTGTTTCCAATTTTGGTTTACATTTGAAAGGGTGTTTTTGGTACATTTGTCCTCGGA	19232	A_95_P258648	DV159788
19867	234	62	737	CAGGTAAAGATACAGCAAGTATCCCAATTTACAAGACAGAGGCTGATATAACTATTTA	19234	A_95_P242622	DW000916
19870	234	65	403	ACTACTATTGTAATTGCAGTACAGGCTTTTTACGAATAGATAATGCACTTCCTTGTGGA	19240	A_95_P130077	EB430050
19876	234	71	875	GCCAACATCTTGAAATAAGAATGGCATCTGAAAAACATTTCTGCTGTTGAAAAACACT	19252	A_95_P289788	DV160971
19881	234	76	404	GAGCAGTGAATATAGTCTTATTTCCAGGTGCTGATCCGGAATAAATAACATGAAGTTT	19262	A_95_P163252	EH622262
19884	234	79	689	AATCTGGTCTTGGGCTGAACTTTGCTGAGCTCCAGATTAGTCGTGGAAACTCTTGTTG	19268	A_95_P073500	EH620962
19885	234	80	428	GCATGTTAAATAAATGTTGTGGTTGTGTTTGAAATAGCTTTCACTGACTAGCATTTGG	19270	A_95_P154837	TA15535_4097
19892	235	2	873	TGTTTCACAGTTGTTAAGGATGTACCCTTTTGCCTTCGAGTTCTCTTCGGCTTTCCTGG	19282	A_95_P223052	TA22165_4097
19893	235	3	818	TGGTCCGAGCTGTGTAGCAATCACAATAATGTGGAATGTGGTGGAGTTTCTTTGAAC	19284	A_95_P270291	EB430842
19896	235	6	795	ATTCAAAGATGGAATCTTGGATCTCCCTGATTTTCCTCGTGGTTTCCCTAAGCCAGCT	19290	A_95_P126582	EB425904
19897	235	7	635	CTTCGCTTGGTCTTTTGAGGTGAAGATACTTATGAAAGGATGTTTCCTCTTTTAAACTT	19292	A_95_P087548	TA19868_4097
19900	235	10	418	TTGTACCTGACATCCCTTCGCTCCAAAGATGGCTTGAAATTGTTTATCAAAGCGCAGG	19296	A_95_P002101	BP528296
19904	235	14	455	CACCCAAAGTAGGGTCTTTGTGATTTGCATTATTTGCATTCAATTTTGGAGTATAGCAT	19304	A_95_P001446	FG642881
19907	235	17	845	GATGCTTAAGAAGGATTAATCTAAAGCTCAGATCACCGCCTAAAGGTGGATTGCCGC	19310	A_95_P116022	DV158516
19908	235	18	746	AAGAGGAAGATTTAGAAGAACTAAGGGCACGTCTCGCTAAAGTTAGATCCTAAGTGA	19312	A_95_P206997	TA18644_4097
19910	235	20	359	TAATTGTGCACCACCACCTAATGCACTTTTACTTATGCGATGTCGTTCTGCTCCACCAA	19316	A_95_P135897	EB439593
19911	235	21	531	ACCTTTTTGGTGTGTCCCTTCTCATTTGCTGGTCATGATGAGAATGGTCCTAGCTTGTA	19318	A_95_P107822	CV018545
19914	235	24	776	ATGATGAAATTGTACTTGCAGAGCCTTCAGAGGCCTTTTTTGCCCGTGTACAGAACCA	19324	A_95_P291583	FG172556
19919	235	29	251	TTCCTTAAAATTTATCTAAAGATCGAGTTGCAAATAAATGATGTTTCCCTGGTTCCGG	19334	A_95_P110317	CV019680
19921	235	31	581	CGTCATATGCTTGTGGAAAATGCTCTTTGCTTCCTCTCCTTCCAGATATTCCTCTACGAT	19338	A_95_P040711	BP129900
19922	235	32	716	GATTCTTTGCTTAGAAGATGTAAAATGATAGTTCCTGTGGGCTTTCTGCATGTTTTCTT	19340	A_95_P159647	EH618039
19923	235	33	615	AGCAAATGAGCTCTTCCTTGTTGCGAGATATTATATGCTTTAATAATTGCAGCTTCTAA	19342	A_95_P018271	TA14646_4097
19925	235	35	406	GCTGCAGCAAAGCAATACATTGAGAAACATTACAGAGAGCAGATGAAAAATTTGCA	19346	A_95_P085370	X71057
19926	235	36	818	GAGAAAATGGTTTCAAAGTTGTTACCCTTCTCCGTTTGAGCCCTTTGCTTCCTTTTTCT	19348	A_95_P203652	TA17898_4097
19930	235	40	392	ACTGGTCCACCACCAACAAACTCTTGTTATTAATTAATTGCTAGTAGCCATGTTTGTTG	19354	A_95_P090273	BP530884
19931	235	41	823	GAGGCGTCAAAACATTGACTCAATGAGCGGCCAATTCAATTAAGTATTTAACATAAAT	19356	A_95_P205827	EB424983
19932	235	42	1238	CTTTATTTCTCTGGGAGTTGTTTCATGACATGTATTTTACTGAGGTTGTCTCCCTGCTC	19358	A_95_P182077	TA13127_4097
19934	235	44	394	TTCGTCTAAGACAAACTGAACTGATAGACTTACCTTTTTTGATTTTCCTGTACTGTAAC	19362	A_95_P024536	FG644144
19937	235	47	1227	GCCATTGTCGCACAGATGATTTCTTCCTAGTATATACTAGTGAAATTTTATTGATGTTC	19368	A_95_P200167	TA17151_4097
19940	235	50	748	TAACCATGATCTTGAAAGGGTTGGCATGGGGATTCAGCAGAACTAGGATCCTCAGTT	19374	A_95_P213197	FG161520
19946	235	56	127	TTGTTATGGGCCGCCCATCTTCTCTGCGCCGGGACATAATTTAGACATATAACAAAGC	19386	A_95_P155387	EG650038
19947	235	57	458	CTAAGAGTAGAGTATTGCGTCCCCTTTGTATTATGACCATCATCTGATGAATGGCACC	19388	A_95_P039066	BP129444
19949	235	59	785	ATACATCGATAACACAGCATTCTCCCCTCTCTAGTCTCTGAACATCATAGATGCGCTAT	19392	A_95_P285073	FG165655
19950	235	60	107	CAATGTGCAGAAGGAACCTGTAGTTGCTCCCCCAATTATGACAATGTTATATAGTTTC	19394	A_95_P242407	DQ460102

19956	235	66	431	CTTCTATCAATAAACCAAAAAAGAAGTTTGAACTTGGTTGAAACCTGATTGAACTGCT	19406	A_95_P182092	TA13130_4097
19962	235	72	447	ACAACCCCAGATTTAAACTTATAATAACATAGCCTCATGCCGGATCCCTAGTAGGAAC	19418	A_95_P132722	EB433357
19965	235	75	476	TACCATTGACATGGGAAATGTTGTTATGATCAAATAGCTTAGCTATAGCTTTGTGTAC	19424	A_95_P003741	TA12063_4097
19967	235	77	215	ATGCTGTAACGGCGTGCGTGCCTATGCAATGTCCTGTCCATGCATAATGAAGTTTGA	19428	A_95_P178902	TA12371_4097
19969	235	79	0	ACTGTAATGCAGATCCTTCATGTTAGAATCAATGATGATCGTGTTTGTTAGCGGCCG	19431	A_95_P231114	A_95_P231114
19970	235	80	518	AGTAGAGCGACGATCTTGTCTTGTTAACAAGGGACAACCATGGTCAACAATTTCACT	19433	A_95_P010061	EB432801
19978	236	3	401	GGGTTGTGCTGTAATTGGTATTGGTTCTAGCTTCTACCAGTTTATGTTTAATCTTAAA	19285	A_95_P002891	EH623972
19981	236	6	987	TGAGGAGGAAGACGTTGATGAGGCACATTGATCAATTTTAGAGTTGGTTATTCTAAA	19291	A_95_P067100	TA14838_4097
19990	236	15	692	GTAATTCCATTGAGGAATCTGCTTTTTCATGGCATTCAAAGATCGTTGCTGACATGGA	19307	A_95_P282833	FG196092
19995	236	20	475	TCTCGAAATTGATTGTCACTATGTGCGTGAGAGTCTTAATTCTGGGCTGATATCTCTG	19317	A_95_P276128	AM783324
20000	236	25	967	GCAGCTTTCATATGCATACTTATTGCAGAAATATGGAGTATCATTATTAACAGATGGT	19327	A_95_P013741	TA16406_4097
20001	236	26	456	GTGATTGAAGATGATTGCAGTGTTGTAGGTATTGTGACATTTGCTAACATGTTAGAA	19329	A_95_P275908	TC66158
20008	236	33	562	GCAAGATGGAATTCTGAATGTTCCATGGTTTTGTTGTATCATATTTGACATCTTGGCT	19343	A_95_P125437	DW005234
20009	236	34	935	GCTCTGCCATTTTTGTTGTTGGATTGCAATGACATGAACTCTTGAACTTGTTCTGTGT	19345	A_95_P177922	TA12104_4097
20011	236	36	735	CATTAACATGTGCTTGATTTTCTCCATGACTATGTTTGTTTGGCTTGAATCCTGATCAA	19349	A_95_P136557	EB440325
20015	236	40	592	ATTTTGCCGTACCCTGGGTGGTTGGATTTTATTGTATACTCTGAAAACTGTATTTTTCT	19355	A_95_P222502	TA22047_4097
20022	236	47	93	TAAAGGAAAGTTCTAAACCTGAGAGAGCAAGTACTTTCGCTAAACGTGCTGCTCAGG	19369	A_95_P033884	AJ717826
20027	236	52	621	GTTTTGAAACTTCAATTACTTTGGGGTTTTCTGTTGTTTTCTGATAACGCTGTTGAACA	19379	A_95_P286198	FG639851
20028	236	53	293	GTTCCTATCCTATTACGGTTTAACTTCGCCCTTTCTCCTTCTCAATGATGGTACTTAGT	19381	A_95_P112347	CV020632
20029	236	54	650	GTGGTTTAAGAAACCAATTGTTCAGCAATTTCTTTTGAATGAGATTCCATCAAGGGCT	19383	A_95_P299748	FG635361
20033	236	58	909	AGATATTTAATGAAACTAAACTCTGCCAAGAAGCTTCTTGCGAACCAATCTCTTCTACT	19391	A_95_P223622	EB425095
20034	236	59	501	AAGCAAGTTGTCACTTACTAGTTCCTCCAACTTGAGTTCAGGTTGATCCTACTGGGAT	19393	A_95_P036658	BP128789
20040	236	65	888	TAGTAGTGAGTTATTGTTTCTTAGTCTAGTCGGAGCTTAGCTGTGTCCTCCTGATCTAT	19405	A_95_P119127	DV162197
20041	236	66	541	CGACTTGATTTTGCGAGATGTTGCAAAGTAAGAAGAAGAAGAAGAAGGGACAAATG	19407	A_95_P202642	BP131040
20042	236	67	602	GAAAGGTTGAATTGTGACCCTCTGTGAAACACTTAATTTGCCTTATGTGTGTAAGATT	19409	A_95_P032856	EH619487
20044	236	69	786	TTTTTGCTCGCGCCCTTGGAGATGGCAAAAGTTGTACCTGCCCGTTTTTTGCGAATTAT	19413	A_95_P202287	DW004236
20051	236	76	695	TCTTGAAACAGAAACAAGAACACCAAACAACACAGAGTAGTTGTTGCTCATGAAAAC	19427	A_95_P136567	EB440332
20059	236	84	615	GTGCTATTTATTGTGACTATGCTTTGAGATCTTTGATATTGGTAGCTTGTGAGTTGAA	19442	A_95_P266866	FG636593
20061	237	1	541	AGGAAGTAAGAAATGCTTAGACACTTGTTTGGGTGTTGAGAGAACCAGGCCTGATAT	19445	A_95_P042616	BP130405
20066	237	6	835	TGGTGGAGTTATTTTGCCCTCCTTAATGGTTACGATTTGCGTGTCTATAATTAAGTGCT	19455	A_95_P244122	FG143242
20067	237	7	1247	AGAGTAGTGTAAAGTGTATATTTGCGTTTGGTGTAATGCATGAATTTGACTGTGTTCT	19457	A_95_P202337	TA17612_4097
20068	237	8	345	AAACTTATGGGTACTGCTGGTGGTCTCTCGTCATTGGCAAAAATGCCTGCTTGTAATG	19459	A_95_P135222	FG145825
20070	237	10	0	CCTGATAAAACAAAGGCATCGCGCGACAAGTATGCCAAAATATCAGAGCAGGAGAC	19463	A_95_P315973	A_95_P315973
20073	237	13	133	CTATCTGTGCTCAATATACTCCTGAACAGACTGATGTACGATTTTAAAGCTATGTATGT	19469	A_95_P161737	EH620364

20074	237	14	215	ACAGGCTAGAGATTACGCAGGGAACGTCTCGAGTCCCTGTTTTTACTAATCAAACCAT	19471	A_95_P166707	EH664006
20075	237	15	610	GATTGCAAGCAACTTTACTGGGAGGGGACTCAATACCACAATGCAGTGCAAAAGTTT	19473	A_95_P299058	FG638357
20086	237	26	372	GTGGAGACTAAACTCATGTTATTGGAAGCTGTCATTTAACTGAAAACTGCTTTTGTTT	19492	A_95_P089253	BP530421
20089	237	29	516	GTACGGTTTTGAAAGATTCGGTTTGATAATCCTTGGTGATTTTGAAAATGTTATACCC	19498	A_95_P193517	TA15690_4097
20102	237	42	599	GAAGAGGGGTTTGGAACTGATTATTATGTCTTTGCTATTGTGTATTCATTCAGATTTT	19523	A_95_P012776	DW004209
20103	237	43	2330	GAGTAGGAAGGATGACTGATCACATTGTTTCAACAATTAAGTGATTGAAGAAAGAA	19525	A_95_P002851	TA12429_4097
20104	237	44	350	GGAAAAAGTAACTCAATTGGTTAAGTGGGTTCATATGGCATTCTAAGCCATGAAGTT	19527	A_95_P202812	TA17716_4097
20108	237	48	791	TAAATCTTCTACCTCATTCAGTGATTCTGATGCACACACGGGGTCAGATCTGTCCTCT	19534	A_95_P152292	EB682633
20110	237	50	545	CAAGTCATTTGGTTTCATCTTTGGTGTCATTGAAGACTCCTAGAAATCAATTTCCCAAT	19538	A_95_P148797	TA13527_4097
20112	237	52	858	TGAGTCGTCAACTGGTTTATCACGGATGTTGCTGAGTTCACCAACATGTCCAGTTCTT	19542	A_95_P149317	EB679157
20113	237	53	478	ATCAGTTCTCACAGCTATTTCTAGACAAGTTCATCCCTGTCACCCTGAGAGAGGAGTA	19544	A_95_P048061	BP131811
20116	237	56	761	TATTTCAAGGAAGTTTGGCACCATAAATTTGGTAGTGAGACTGAAATGCACCGCGCA	19550	A_95_P290678	TC41333
20117	237	57	492	AAGAAAGATGTTATTCTATTTTCAGTAGAGTGACGATCTTGTCAACAAGGCACAACCA	19552	A_95_P153922	EB684086
20120	237	60	143	TACCACTAGACGAGCTTGTTAAGCTCTTTAATGCTCGTCCTCGCAAAAGTTCCAAAGG	19558	A_95_P167251	EH664152
20121	237	61	747	GCATGATTGCTTTGTCAATGGATGTGATGCATCACTATTCCTAGACCAGACACCAAGT	19560	A_95_P215292	EB428682
20123	237	63	1050	CAGAATTTTACTGCTTGACAATTGCAAGTGTGCTTACATGTTTTCGCAATTTGTTGGTT	19564	A_95_P176862	TA11807_4097
20126	237	66	435	GTGAGTTTTGTATTAGATTTATGCTTCCATGAAATGAATGCAATATTCTAGCTGGTGT	19570	A_95_P137157	EB440883
20127	237	67	853	AAATGCTTTTCACATCTCGTGCTCACATCATCTTCTCAGTTCATCTTGCAATGAGTCAG	19572	A_95_P313473	FG157322
20128	237	68	836	TCAATGGTTCAAAGCCATACTTCTTTTTGAGTTTCCTTTGTACAGTCGCAATCTTCCCCA	19574	A_95_P268191	TA18465_4097
20132	237	72	504	CAGAGTGTTGGGAAGAAAGCTTGTCTTATAGGTCAAGCATTGGAAATTAATTATTTT	19582	A_95_P019401	DV160201
20134	237	74	1174	CATTGTGTATCTGCTTCAGGGAAAAAGAACGAACTAGATCAATAATTTCTGGCCAAAA	19585	A_95_P231584	AB036735
20136	237	76	583	GGTTTACTGACAAGCAAAGGAGCTTGTTCTAATCAGGCATTACTTCCCATGGGCTCTA	19589	A_95_P050941	FG168352
20140	237	80	266	CGTGACACCGGGTCCTAGTGAGATTATATTGTGTATTTTGTTAAATTCTTCAGTACTTT	19597	A_95_P029001	BP534488
20145	237	85	611	CAATTCGAGGTTTGTGTAAAGCCAAACCTTGCTAATGTAAAATAAAAAGAAACGCAG	19607	A_95_P143162	EB446508
20146	238	1	1178	TCTCTGATAAGATCATGTTCTCATTTGGTCACAGATACTGCATGGTTTTCTAATGTAGT	19446	A_95_P103942	TA15170_4097
20150	238	5	396	TGTGCTTTGTCTACTGAGGTCTCAAAGATGTTCTATGCTATTTCTGTTTGCTGTTTCTCT	19454	A_95_P006961	TA11842_4097
20152	238	7	484	AAGGTCCAGCAATGTGGGAAAATTTAAAAAGTTCACTTCAATCCAGCTAAGATGATT	19458	A_95_P044841	BP130986
20157	238	12	858	GGGGTGAAGTTTGTTTTGTATTTGCTGAACTTCAGCATTCTAGGAGTTGAAATTTTTG	19468	A_95_P126042	EB425236
20158	238	13	454	TATTGACGCCTGCAATTTGTCCTCTTGAAGATGCTGGAAGGAACCTAATTATGGTGA	19470	A_95_P058346	BP134454
20161	238	16	719	AGAAAACATCTTTATGATCTCGGCGTATGATTCAATTACCATGTATTTAGCTATTGAG	19476	A_95_P010056	DV161237
20163	238	18	784	CAATGCTATGAAGTATGGATGGACTGTTTGCTTAGTGAAATGTGATTTCGTTTCTAAG	19479	A_95_P135392	EB438786
20164	238	19	796	CTTGAGGGCTCAACATTACAAATTGTGTATTATCAACACTTTGTTTGTGTTGCTGCAAT	19480	A_95_P223817	EB683080
20166	238	21	870	TACCTCTGTACTGCAGTGATGAGAAGTATATTGTTTCAAAGAAATTTTTCAGTAGCAG	19484	A_95_P009166	TA14865_4097
20168	238	23	387	CGACGTCCTGATAATCGAGCAGAGTCACCTTTCACTTTAGTCTATTCAGATGTTTGGA	19488	A_95_P151162	EB681401

20179	238	34	474	GCATGTTGCAAACTCAAAAACTACCTAAATGTATCACATTAGCAGAATAATAGCTGCT	19508	A_95_P026566	BP129594
20189	238	44	610	GCCTGGTTTTGCTCTCTTTTAGAACACCACAATTACTATCTTTCATTACAAAAGGTTCTT	19528	A_95_P225152	EB445473
20195	238	50	581	ATACGTACCTGTCCTCCCTTGGATTTTTGTTTGCGCTCATCATTTTTAATAATTTAGCT	19539	A_95_P191377	TA15222_4097
20196	238	51	1451	GCCTAATGATAGAATAATTTAAGTGTACCCTTTGAAGCCGTGTTTCTTCTCTGTATCAA	19541	A_95_P182202	TA13158_4097
20200	238	55	753	TTCACGGTGACTTGGGACACATAAATCTCCAGGTGGCGACTCTGATCTTTATAATAAT	19549	A_95_P300643	FG173876
20201	238	56	686	GCTTGGATACTTGTTGTGGTAATTCTGTCCGACAGTAACCGATCTTGTAGTTTACTGG	19551	A_95_P164652	EH623917
20204	238	59	113	ATGCTCACTTCAAGGTGGATCGAGAACTTCAGGCATCTGTTGCTGTGTATGCATTGAA	19557	A_95_P034319	AJ718441
20211	238	66	704	AGGGAGCTAGTACTAGTAATGCTACTAAGCCTTCTGATACTAACAGCATTACATCTAA	19571	A_95_P129052	EB682225
20216	238	71	917	CTCAATTAATGCACAGTTGAGAGTAAAGAATGTTGGGATGCGCTTAAGCCTTTGTCAT	19581	A_95_P245802	DV157766
20219	238	74	0	CTTTTACCATCAAAATGTAAACAGAACAGAAGAAAAATGACATCTCTCAACCTGGAGT	19586	A_95_P029651	A_95_P029651
20220	238	75	193	GTCATTGGGCTAAACTTAATATGAAGAAATCTACTGGCAGTACTTTGGGACATATTT	19588	A_95_P048841	BP132016
20223	238	78	1615	GCATGGCTATAAACAAGGCGCTGCGAGAGATGAACAATTGTCAATTCTTTTATATAAT	19594	A_95_P208622	TA19009_4097
20225	238	80	712	TTAGCACCCCCTCTATGTCGTCTCATGTGACCACCTAAAGCTTGTCCTGAGTTAAATT	19598	A_95_P316793	FG194848
20227	238	82	667	CTTGTCTCTGATGTTTTGAGACCTTAGTCTGTTGTAACATGGAAGGAAATGAAAATAA	19602	A_95_P018176	TA17448_4097
20229	238	84	880	CTTCTGTATTACTGCATTTCCTCATTGAAAATAGACTCGGGAATTCGGAATAGTTGTA	19606	A_95_P013461	TA12161_4097
20232	239	2	855	GGTAAAGTCACTTTTTGTTGGCTTGAGGATGAGGAAAGGACAGAATGCATATGATTT	19611	A_95_P297428	EB683457
20238	239	8	615	GGGCTAATGCTACCTTTTTCTGTAAAATTAACATCAAATCCAGTGTGTCGATGCATTC	19623	A_95_P253714	FG642800
20242	239	12	644	CAATGGTCCTAATCCCATGAAAGACACTAGTATCATGTTTTCCATAAAAATTGTTCTCA	19631	A_95_P283873	FG639842
20246	239	16	901	ATCATCATTCAACCAACTGAATCTTGGTTTGGTATTAGTGACCAAGCGCTTATTCACT	19639	A_95_P212627	TA19876_4097
20247	239	17	2483	GTCTACCTTCACTCATGTACATGATAAGCATTTGTACAGAACAGTTATGGTTCTGTTTA	19641	A_95_P007301	AY046898
20248	239	18	1328	GTTGGTGTGTCGTGTATGAATTAATCGCTTGGTACCTAAAATAGATGAATGTGACTT	19643	A_95_P182982	TA13349_4097
20249	239	19	1116	TTCTGGTATTGCTGCACCTATGTTAGATGGGTTGTTGACATCCATTTGTGTTAGGTGG	19645	A_95_P134227	TA15207_4097
20256	239	26	774	GAACTTCTGGACAAAGATGCCTACATTGGAGAGTACGGCACCAATTTGACAAAGTG	19658	A_95_P298173	FG137301
20259	239	29	785	AATACGCTGCTGATGCTGTCTGCACAGTGCTTCGGGTAGACCAGATTATAATGTCAAA	19664	A_95_P149437	TA15640_4097
20263	239	33	433	TGTGTGGTTCAAGGCTGGATACCAAATCTTTAGCAGAGGCGTTGGACTTTGACTAACT	19671	A_95_P176527	TA11626_4097
20267	239	37	357	TTTCCATTGCAGTTTGAATCCCTGAACCAGATATTTTCATGGGGTTATCTGTCCTTCCC	19677	A_95_P103537	CV016555
20270	239	40	357	GCAAAGTGGCAATGTTTTCAGCATATATGTTTCTCTCAATTTCACCAACTCTATATATG	19683	A_95_P074995	BP526612
20271	239	41	1109	TTTCGAGGCATTTGTAAACTACTGAACGTCTGAGCTCTTGCCCATCTTGTGCTGAAAA	19685	A_95_P237344	U44760
20276	239	46	763	TTCAGACTGCGCTGTAGTGACTGAGCTAGGATTTCCTCGAATTTTTATGCATCTTGCCT	19695	A_95_P135147	EB438412
20279	239	49	409	GAGCAAGCTTCTGCCTAATTTGCCTCTATTACTATTGTGACTGATTATAATGGAAGATA	19701	A_95_P003481	TA15496_4097
20283	239	53	669	TTCTCTTTTGATTTGTATTTGGCTTTGTTTATATGTGTGAAGGCGTCCCCGGCCGTAAT	19709	A_95_P202687	TA17688_4097
20286	239	56	483	AAACAGAGGTGCCGAAGAAAGCAAACTGACACTGAAGCCCAAAAAGGTTGGAGCTA	19715	A_95_P159417	EH617603
20291	239	61	489	ACCAGTTACGCCAAGACTCCCCTTTAAAATAGCAAAGAATAAGACCAAAGAAAATGT	19725	A_95_P143647	EB446890
20303	239	73	594	GGGAACTGCTTTTGTTAGTGTGTTATTAATTTGTTAAGAGGCTTTGCAGAACTGCTTTT	19749	A_95_P003711	EB439100

20304	239	74	1204	CTGATAAACAAAGCCCATTGTGCTTTGTAAACGCTTATTTGGATTTTGATTGTTACTC	19751	A_95_P208427	TA18967_4097
20306	239	76	563	TAGGCCTACTATGATACTGATATTGTTCAGGACTTCAGGTGTTATTACCGTTACGCTA	19755	A_95_P203587	TA17884_4097
20308	239	78	791	GCTGCAGATGTCTCTTTGTGATTCGATATGGTTGTGATGACACCGAGGAAACAGTTC	19759	A_95_P140412	EB444327
20312	239	82	496	AACTAAATAGCGACGATCAGTAGTTTATAACACAATTACACTTCCCTCTCTTCTGCTAT	19765	A_95_P264411	AM782197
20315	239	85	614	AAGTTTAATCACCCTTCCAGAAGAAAATACCAGCAGGGGACAAAGGAGAAGGGAAA	19771	A_95_P147732	EB452258
20317	240	2	467	CTACTCTTGTTCCGATTTATGATCTTGTAACTCGGATCCTCTTCCACGAGGTATCCTGC	19612	A_95_P164617	TA17325_4097
20322	240	7	205	TAATTCAAGTTTGATTGTGCATTAAGAAACTATCAAATCCTGGTCCAGTGGATTTCTT	19622	A_95_P023486	CV016449
20326	240	11	760	AAACCCTAACCGGGAAACATCACCCTTGAAGTTGAAGCTCTGACACTATTGACATGT	19630	A_95_P157738	EH615777
20328	240	13	618	TGGGTGACCGTATAATGGCTGAAAAGGTTTCATATATTTTCCGGAAGCCTGAAGTTT	19634	A_95_P151757	EB682012
20333	240	18	826	ACGCTGTTGCAGGATCAGGAACTGAGTTTTTATTTCTCTTATCTAATTCGTTCCACTAC	19644	A_95_P117277	DV160122
20338	240	23	333	ATTTGCCTTTCAGTGATGTGGCTCTGTAATTGCAGGAATATGAGTTGTGGTTTATTAT	19653	A_95_P101243	CB337256
20347	240	32	1209	AGATACTGCATGGTTTTCTAATGTAGTTCGTTTAATTCTCTATTTAATCCTCAGGGTTC	19670	A_95_P191167	TA15170_4097
20349	240	34	244	CAAATTCGTGACACCGGGTCCTAGTGAGATTATATTGTGTATTTTGTTAAATTCTTCA	19673	A_95_P089308	BP530445
20355	240	40	199	AGCCTCGATTCCTGATACATTGAGAGGTATCTGGGCGCATCTAAAGGTTCGTATACC	19684	A_95_P088198	BP529984
20357	240	42	698	TGCTGATGGAAGTGTTCTGTGGCCAATAAGCTATGAAGAGGTAGAATTTGATGAAA	19688	A_95_P196632	TA16381_4097
20359	240	44	646	GTCGCTGTGCCTCATTTATCTCCAAATTTATTCATTCATACATTCAAAGGTGATTTTCT	19692	A_95_P207472	EB683911
20361	240	46	762	ATGCGATTTGCATTTGGCTTTAGGTACGTAACGTCGTGACGATCGATATGGGTTTGT	19696	A_95_P286868	FG166173
20366	240	51	434	ATTCTCTTCTCTTGGGTCTGAAAATGTCAACTATGATACTTGGACTTTGCTGAATGAT	19706	A_95_P220757	TA21677_4097
20373	240	58	740	CAGATTTGGGGTCAGTTCTGTTTCGTTCTGTTGCCGATAATTCTTATTTTTTGCTACTG	19720	A_95_P254014	EH616635
20374	240	59	625	AGAAGTGGCGTTTTCAGTGGCGTTGCACCTCTGCAGTTTAGTTTCTCCTCTATTTTCCT	19722	A_95_P302413	FG637459
20377	240	62	412	AGGGGGATGTCCTTATATGTAGTCTTTCCACGTCAAGTTTGAAATTGGTTGATGAGA	19728	A_95_P084890	BP529140
20378	240	63	240	TCCAGTAGGCAGCTTTAATTGGTTTGCAACTCATGGAACTTCTATGAGTCGAACTAAC	19730	A_95_P155307	FG140044
20383	240	68	490	AAGGGTGGTTGGAACTCTTGGCTACATTGATCCTGAATATTATAGAAGCGGACGGCT	19740	A_95_P145957	FG144874
20384	240	69	532	TGCATCTTCCCTCGTAGAGTGGCGTCTTTTATAAGAAAAGACTTTCTCAGTGGAACTA	19742	A_95_P148817	EB678356
20386	240	71	859	CTGAGAACTAAAGGTTTATGTTGGATATCAATGTTAAACGCATGGATGTTACTGCTT	19746	A_95_P268136	DV999599
20389	240	74	484	TGAGCAGAATTGCTGCTCTGTGCCATATTTTTCTGTTACCACTATACAAATGTATACTA	19752	A_95_P154062	EB684227
20391	240	76	222	GTAGTGTTAATGCCCTAATGGCACTGAATTGAGATTCTGATATCCGGATTAAAAGTT	19756	A_95_P104142	CV016866
20396	240	81	888	CTAGACTAGATACCATCTCATATCATGTATTAAAATTCATCATCATCTCAACGTGAAC	19764	A_95_P022391	EB678149
20411	241	11	878	CTTACAGTGGACATTATCGGCCGACGGATGATAGCCTTGACAGTTTTTTATCAATTCT	19793	A_95_P206897	EB426751
20414	241	14	979	TGAAGATGGTACACCTGCTACTGAGGCACAAATGGGAAAAGATGTTGTGTCGTTCTT	19799	A_95_P011036	TA16055_4097
20417	241	17	367	GCCAAAGGAAGAAAGTGATGATGATATGGGATTCAGTTTGTTCGATTAGAAGCTGT	19805	A_95_P103138	TA13775_4097
20418	241	18	1940	TACTTGCATGGCCAGTTACAAAGTGAAGCTTATTACACCAGAGGGAACAGTTGAGTT	19807	A_95_P103342	AF223573
20421	241	21	481	CCTGTTGAGGTTGAATTGCAGGAAACAGAAAGCGAAGAAGAACTTCTTGATGATGA	19813	A_95_P003561	FG164295
20422	241	22	1772	TTGTCTACAGACACAGATATGATGCGAAATAAATTCCTTGTGCCTTCAATTTATCTGT	19815	A_95_P014391	Z29492

20427	241	27	759	GATTACAGAAAGAGTGACTAACACTTATTTTGCCAGAATAAACTTCCGCAAGCCAGG	19825	A_95_P141512	EB445207
20431	241	31	304	GAAATATCCCCTTTGGCACCTTCTTGTTGTAAAGATGAGGAACCAGAAACCTTTATTA	19833	A_95_P081095	FG132709
20433	241	33	410	ACAAAATTGTTGTGTCAATTCCTAGATTTGTAGTCCCTTTGTAATCCAATTTCCCGAGT	19837	A_95_P309028	FG644418
20439	241	39	605	TATCGGCTCTTATAGTTTGTTTCCACCAATCCATACCATGGTAAAATCGGGTTCCTTTG	19849	A_95_P021016	TA18651_4097
20440	241	40	98	GTAACCTGAAAAGTGACAAATAGCCAGTTTGTACCTTCATAATAACCAGTGACAAAT	19851	A_95_P220652	TA21653_4097
20444	241	44	415	TTCTTTTGTTGTAGTAAACACAGTAAAGCTAAAAGGAGCAAATGATTGGCTGGTTCT	19859	A_95_P017951	FG636272
20445	241	45	590	CACTCTAGTTTCTAGGGTTGTGGTTGACATGATTATTAATGTTTACTAACTACATCTTC	19861	A_95_P019931	TA22171_4097
20450	241	50	515	ATCCTAATATTTCGTTGTGTAGCTGCCACAAATGAAATGTAAATCCGTTGGTTCTTTT	19870	A_95_P307063	FG637219
20454	241	54	364	TTGTGCAGTAATACAACTACCTTCACAGACGCTGCTTCTCTCTGTGTCTGATAAAGCC	19878	A_95_P242132	AJ719117
20462	241	62	608	CCTGGCTTTGCTCTCTTTTAGTTTTAGAACACCACAATTCATACAAAAGGTTCTTTTT	19894	A_95_P209932	DW001479
20463	241	63	401	GAATCTGCTCGTTTCTGTAATCGAGATTTATTTTCTTCATTGTAGACTAGAAGGAGCT	19896	A_95_P143892	EB447083
20467	241	67	2243	CGTTCATTCTTGGAAGACATGTATAGAGACATTCATCAATTTAGAGTTGGAACTTTTG	19904	A_95_P008446	X60057
20469	241	69	782	TCTTGCTGATTTTAATTCCTCAGTAGTGACATGACGCGGCTTGTCATTGATGCTTGTT	19908	A_95_P232774	EB449667
20473	241	73	208	TCCTATTACTTTGTATTCCGCCTCGCACCATGTCTTTTCAAGAATACTTGGCACTACGA	19916	A_95_P108902	CV019054
20476	241	76	371	TCTTGGCTGTTAGAAGGGTAGGGGGAAAAGCTTCTTTTTCTCTGTATTTTCAGTTTTA	19922	A_95_P067450	BP136869
20477	241	77	446	CTCTATCAGGCACTGCTAAGTGCTTGCATAGTCTGTGTTTTTTATGTAAGCTTAATTA	19924	A_95_P134702	EB437373
20478	241	78	117	TTACAGGAGGCTGATGAAGGTAGGAGTTTGTTGAAGGAAGAATGTGGTAAACACG	19926	A_95_P031496	CV507122
20479	241	79	684	TATCAAAGAAGTTGCTGATGCTGCTTCTTGATTCAGGGGCTCTTCGAGTGTCTATCAC	19928	A_95_P231539	FG643775
20487	242	2	820	ACGATAGAGATGATCTGACGAGCACTGAGATGACTACGAGACAACGTTGGTGAGAT	19776	A_95_P303138	FG159394
20490	242	5	457	GCTACAGAACTTTTTTCTCTTACAAAGATTTCTATTAGTACCACTGTACGAAGTCCCG	19782	A_95_P062095	BP135425
20491	242	6	352	CATTACTTCTGAGACTTGACTTGTTCTTCAGTTTTTTAGATACAGGGAGTAGTATACT	19784	A_95_P028731	BP532761
20493	242	8	315	GATGGTAGAACAAGGGAACGTTTTTGAGTTTGTCGATTGTAATTGCTACTTGGTCTA	19788	A_95_P142257	EB445774
20496	242	11	851	GAAGGTTCGAGCAATTGTGTTTGATGAAATAATACATAAACCAGGACGTCATTTCTA	19794	A_95_P197832	EB432554
20498	242	13	529	CTTCGTTGACCTTGACCCCATAGTGTGATTGCGTGTTTTAGTATCTACGGGGAAAATT	19798	A_95_P055556	BP133729
20501	242	16	589	TCTTGAAATAATTCCCCTGTTCAACCTATGATGGGGGGCTAATATCACCAGTCTTGTG	19804	A_95_P192822	TA15539_4097
20502	242	17	916	CTCAGCGGTGGATTCAAGCTCTTCACTTGATAAACTAGTGATCTGAAATTTTTCCTGA	19806	A_95_P011521	TA17424_4097
20503	242	18	607	GAATAAAAATGTGTTCCGGATTGCGGGTGCATTCATGTGACGTAATCCAAAGACATG	19808	A_95_P069130	BP137303
20504	242	19	546	TTTTGTATGGCACTCTGGTGGCATACTTCAACATGAAACTATTCCCCAATTTGAATCG	19810	A_95_P059820	BP134838
20507	242	22	1444	TTGTTGACGATTGCCAATGTTCCCCCTGCTGATTATGAATTATCTTCATTAGTCTTCAT	19816	A_95_P120322	AJ438264
20509	242	24	533	AATCAAGCATTGAAAAGGCCATTTAGGGATATTAACTTTGCATTTGTGTTGCCGATTC	19820	A_95_P130102	EB430102
20510	242	25	808	TATCAGTTTGGTTTGTTGGTGGCCTGACCGTCTTCCATCTGTATCTTATTGGCACAAA	19822	A_95_P223852	DV159414
20511	242	26	752	GCAAGTGAATGCATATGGACAATGAACCCTTTCTATGGCTGTATGCACAGCAGTTGT	19824	A_95_P145722	TA14842_4097
20514	242	29	1354	CCAAACTGTTCCACTTGTGATCATATGTGCGATCATATGAAAATGACAAATATTACTG	19830	A_95_P012141	Z84821
20517	242	32	811	TTGATCACACAATCAATGTATGATAAACAATTAGACAGTGGACGTGGTACACTTTTG	19836	A_95_P153157	EB683472

20521	242	36	723	AGCGAGTTCTTTTCATGAGATTTGTATATTGTTGGTTCCCTGTTTACTCTTGAGTTGTG	19844	A_95_P183012	EH619479
20522	242	37	885	CAATGTAAATGCTCTCCGTTTGTAAGTTTCCCTCTGTTTTTTATGAGTTTAACTATGCT	19846	A_95_P020296	TA16759_4097
20528	242	43	264	GTTTCATGAAGACCTTAATGTACCTGTGATACAATGATACCTGTAATCCTAAGCTTCT	19858	A_95_P142107	EB445660
20533	242	48	1526	GGTCTATGTTGCCATTCCCTGGCTGCAAAACTGTTTATCAAAGGTTCGCTATGGCATG	19868	A_95_P007976	TA14794_4097
20536	242	51	688	GCCAGCGCACTTTGGTGTGAAGATAGCTTCGAAATCTCTGTTAGGAGTTATTCGTTT	19873	A_95_P125687	EB424762
20538	242	53	253	GCAGACAAGTTTTCGATTGCTTTCATATACGTGTGGTTAGCACATCTCAACTATTATT	19877	A_95_P155502	EG650107
20540	242	55	768	CCAGTATTGTTTGCATTTTGGTGCTTGCTATGCGTCTTCAGCAAGGCGATGTATCTTT	19881	A_95_P128557	TA13632_4097
20543	242	58	263	CACAGCCTTGAGACAGGAAGTTGATGATCTTCTGGAAGTAATTGATGAGATATAATT	19887	A_95_P033924	AJ717916
20544	242	59	601	CGCGCACACATGAATCTACAATTGACAAAAGATTTCAAGAGCAGATGGCTACGATG	19889	A_95_P232724	BP128844
20546	242	61	562	TTGTTGTGAAGTGTTAATTGGATAAACTTCCATCTAAAGTCCCAGTTGACACTTTGAA	19893	A_95_P017706	TA12424_4097
20547	242	62	529	CTATGCAGTTAAAGGACAAGTGTGTACGAGATATAGCGTTGAGATGTAGATGGATG	19895	A_95_P144202	EB447365
20548	242	63	1163	CTTGGGATTGAGCCCCTAGATTCAAAGCAAAACTGAATAAGTAACACATTGCTATTT	19897	A_95_P195282	TA16082_4097
20550	242	65	142	CATCGGCACAGATTGCATACTTGAATGCTCTTCGTTTTGGGCTCAAGCGCATTATATT	19901	A_95_P111167	CV020080
20551	242	66	375	TGTGGTTGCCTATGCAAAGATATGTCCGGTTAACATGCTTTAACACAATTCTTTCAAT	19903	A_95_P094848	BP532899
20555	242	70	117	GGTTCTTTTTTGCATCGGTGGTGTAGAGGGTTTACAAACTTGTTTAGTTGCCTTGCTA	19911	A_95_P119292	EB438473
20557	242	72	871	GTAGCTTTGGGTTTGGTGGTCGTCTTAGCAGTACATATTCAATCTTATTAAGAAGTTA	19915	A_95_P183347	TA13438_4097
20560	242	75	836	AACTGAGTTGGCATGTGACCTTTAGGCGGTTGCATATGGCCCTTAATACCTAGTGAA	19921	A_95_P268111	DV999555
20561	242	76	234	AGGAACGTGACAAGATAGCGGTTGGTGATGTTCTCTGTGAGATAGAAACTGACAAA	19923	A_95_P208637	EH665894
20565	242	80	497	GCGGATAATGTCAGAGCTATTTATTGGCTTCAAATTCACATATTGGAACTATAGACCT	19931	A_95_P022386	TA17015_4097
20568	242	83	83	GCGTGTTAAATAAACGTTGTGGTTGTGTTTGAAATAGATTTCTCTGACCAACATTTGC	19937	A_95_P211777	TA19687_4097
20569	242	84	399	CAGAATTACTCTCCTTGTAATTCTTTTGGTCTTCATGTTTGTATAACTACGAATACTCC	19939	A_95_P022861	EB434552
20575	243	5	191	GCACAGGTTTTGAATTATATTAACGGTAACAAGCTTAATATTGACTCAGACCTATTGC	19950	A_95_P052291	BP132884
20576	243	6	687	GATCAAAAAATGGAAAGAATGCCCTAAGTGCAATCCCATTGTGGAGAAGGTTGATG	19952	A_95_P255359	EH614541
20579	243	9	658	GTCATGGTACGGAGGTTTGAATTTGGTAACTGCCTAATAAAAAATTGCTATGTCTTTG	19958	A_95_P000846	DV999474
20583	243	13	795	TGAGCCACTACTAATTTTGGGGACATCCTGTGTTTGCAAAAGAACTGAAGGCAGTCC	19966	A_95_P250327	DW005132
20585	243	15	553	ACTTTTGGCCAAAAGGAACCAATTTGTTGTGTGCCTCCTGGTGTTGGAGGCAAAATC	19970	A_95_P005956	BP134460
20587	243	17	674	GTATTGTGTATATTTTGCGTTTTCCTGTGCTACTGGAAATCGTACATAACACAATATA	19974	A_95_P135327	EB438720
20590	243	20	603	CACTTATGACATTCCCTGTGTTCTGAGTCTTTTATTGCCAAGAAGAAGGTTCCTAGCC	19979	A_95_P220192	TA21557_4097
20593	243	23	362	CTACAAGGATAGCACTTTGATATATGACAAATTCTTCGTGATAAACTCACTTAGTGGA	19985	A_95_P110873	CV019944
20594	243	24	466	ATCCGACTAGCCAAGAAGAATGGTGAAAGACTTGGATTACTTGCTTGATATCAACTT	19987	A_95_P114172	EB432747
20599	243	29	895	ACCTGAAATCTGGTAGAGACATGGTGGAGAACACACATATCGGTGATTGGTACTCTC	19997	A_95_P010941	TA15436_4097
20602	243	32	918	TGGATTCACAACATTGGTTATTTATAAGACGTCATCTTGAAAAGATGTTGCTGTTACG	20003	A_95_P011591	TA14999_4097
20605	243	35	564	GCTATGAACTAAGTTGTTGTAAACAGTAAACTTGCTAATGTTGGCTTTCTGCTGGTTT	20009	A_95_P246422	EH623514
20606	243	36	552	GCACATTGCGCCGTATAGCTTATACATGATGTTTTCCTATCTTTTCTGCAACATTAATT	20011	A_95_P142437	EB445895

20608	243	38	789	GTGCATTCTCTATTACGGCTGTGTTTTTCCCTCTATGTTTTCGAAATGTCTTTGCTTCCA	20015	A_95_P258276	EH618193
20609	243	39	743	ATTGGTGGTGTTTACTACTACCAGTGCATGTTGGAATTGGAATAAGATTAGATTTACT	20017	A_95_P180872	TA12845_4097
20616	243	46	765	CTTTAGAGAGGTATGAAGTCAGAGAGAAGAAGACTTCCAAAAAGAGACCAAGAGGC	20031	A_95_P126312	EB424807
20619	243	49	547	TGCCGAATCCTTTCAGTTTTGGTTGAGTCACGCAAATTAAATTTGCTTGTTTATGTGCT	20037	A_95_P121382	DW001420
20622	243	52	573	CATATTCCTGAGATCCTTTTTAGTGTTGTATTCTTGTAGGATTTCTGGGATTCTATGAG	20043	A_95_P153357	EB683643
20627	243	57	874	ACTTGTGATGGTACAACTATTTGGGAAGCACCAACAAACTTTGAACACTTACACTATC	20053	A_95_P244292	EB425283
20629	243	59	424	GAGAGAAGATTTAGGTGGTGTCATTGGCTTTTTCCCTAGGAGAAGTTTGGAACCTAG	20056	A_95_P027996	TC61180
20636	243	66	869	TGTGTGAACTTTATGATCATGATGACTCTTATCTCTGTCCCTAGTTCTTATCATACTCAT	20068	A_95_P183672	EB425023
20640	243	70	909	AACTTGTTAATAGCCTCCAATCTTAGACGATGTTAGTGTTTCTGCAATTGTTGTAAACA	20076	A_95_P292613	EB427773
20641	243	71	154	GTAAATCTTCTTTGTTATTGGTATTCTCAGTTTAAGTGGGGAAGATTTGGTGATAGGC	20078	A_95_P024881	FG626149
20642	243	72	747	AATTGAGGTTTTTCAGGACATATATGAGTTGAGCACATAGACAAGAGTGAAGCTCCT	20080	A_95_P014146	DV158160
20643	243	73	129	CAACTGTACGTCAAAAAATGCAAGCTGAAATGCAAGCTGAGATGAGTCGAAAGTTGT	20082	A_95_P090033	BP530774
20644	243	74	508	CTACTTTGACTTATTACCTTGTTTTGTTTTACCTTGAAACAAAAAGGGATTTGCTGCCA	20084	A_95_P240895	FG642146
20649	243	79	713	TTCTCAGACAGCCACCCTCTCATCCACTAATTCTAGTAAGTTATTGTTACTAGATTTCGT	20094	A_95_P295628	EB447232
20650	243	80	175	GGTTCACGGCTCAAGGTTCAATCCTTGTTTTCAACTTGAAATTCAAGAAAGTATTGAT	20096	A_95_P092348	BP531758
20651	243	81	271	TTGGAAAGAGTGGGAAAGTCATAAATTCGATTAGAGCCGAGATCCAAGGCGAAGGT	20098	A_95_P056111	BP133874
20655	243	85	453	GTACTACTCATTTAGGGGATTAACCTTTGTATAAATGAGACTCTCTCTTAGTTTGCTCC	20106	A_95_P012706	CV020046
20656	244	1	958	GGTTTACTGCTTTCGTTTTGAATCTATTGTCATACAGTTAACTACCCTGTGTTTGGATA	19943	A_95_P251907	AB079021
20661	244	6	590	TCAAACAGCTATGTAAGTTGTGCTTCTCACTCTCGGATATCTTAGTTTTGGGTTTTGCT	19953	A_95_P205032	TA18194_4097
20662	244	7	530	GAGGTACAGTTCCTACTATTGAGAACTTTCAAATGCTTGTAGTCGCTGAAATTTGTGA	19955	A_95_P254804	EB444586
20663	244	8	116	ATTGTCTACCAGAAGTTTGCTAGGAGTTCCTTCTGTGGGTCTCCAAAATCTGTTCTGCA	19957	A_95_P148612	FG645419
20668	244	13	782	CGTTTCACCGACGGATGCAAGAAGATGCGATAATAATCCCAGTGACAACCATTGAGA	19967	A_95_P271041	EB449152
20671	244	16	538	CACGAATGGAAGGATGCTGATATCTGTTGTTTTCAATCCAATGAAATATGCAGACGAA	19973	A_95_P264556	FG638865
20675	244	20	353	GGCTGTGATGTATGTATTTGTTGAAAAGTGAAGACATTGCAGCTATTTATGTACCTAA	19980	A_95_P108037	CV018643
20682	244	27	100	CCAATAAGGGAACAATGTTCGTCTAACTTGAAGTCTAGCCTATGCAAGGCTTTTTGAT	19994	A_95_P100798	BP535522
20683	244	28	127	TACAAGGGTTGCCCTTCCATAAAGCAAGTAAAACAACCGCTTTAGGCCCCATATTTGT	19996	A_95_P131282	EB431443
20690	244	35	515	TCATTGATTTGTACCAATCTGTAACGAAGTGCAACTTTCAGAGATTACGGTTTTGTTTT	20010	A_95_P096178	BP533507
20695	244	40	230	GTGGTATCTCTCTTATTACGGCTACAATCAGAGAAAGTCTGTAAAGTGATAATATTCC	20020	A_95_P107912	CV018587
20700	244	45	320	GCAGTATAAGAAGTACTATTTTGAACATGAGGGACACAAGACCTTTATTTTTATCTGG	20030	A_95_P097313	BP533981
20703	244	48	611	ATTCTCATGATTCTCCAAATCAGGGTGAAAGGTCAATATGTACATGTACCAAGTATTT	20036	A_95_P300243	FG635635
20705	244	50	494	CGCCTTCTTGTTACGGAAGACTATATATATGAGTGCTAAGTTTAATATTTTACAGTCTC	20040	A_95_P021721	EB443875
20707	244	52	563	AAGGATTGGTGCTGCTACTACTCTTGAAGTCAGAGCTACAGGGGATTCCTTATGCATT	20044	A_95_P069500	BP137402
20709	244	54	262	ATGAAGGCTCTTCCATGTATCTCCGGGGAAAGAGAGAGTAAAGAAGGAAGTGATCA	20048	A_95_P145022	EB448561
20711	244	56	869	CGTGGCATGATGTTTGTAGTCTGTGCATTATTACTTTAACATAAATTTGACCATCCTAG	20052	A_95_P267056	DV158046

20714	244	59	576	GTGGAAAAGAAGGTGCAAGAACAATTTGCTACTTTCATGACCAGAATGCACATGTAC	20057	A_95_P098543	BP534540
20715	244	60	831	TCATTTAACTCTTTTTCTTCTAGTTGGACTATAGGTACCGAGGATCAGTCAGTTTCCAG	20059	A_95_P226949	EB449952
20719	244	64	899	TGCATCTACCCTAAATGTTTTGACTAGGCGCTGCTGCAGGATGGCTGAGTGATATATT	20066	A_95_P222702	TA22091_4097
20720	244	65	384	GTATTTTCATAACCATGGGCAAAACTAGGGGTTTTGAGACCGCAATGGCTTCCTTCTC	20067	A_95_P158377	EH616362
20722	244	67	858	TGCTATTCATAATACGTTAACTAGCAAATTCTCATGGTGGAAGCTTAAATGTGCATTG	20071	A_95_P022366	TA11832_4097
20726	244	71	2390	CTTCCCTGTTGTACACTGTCCTGGGGCATTTGGTATCATCTTAGAATCAGCAGAAAGA	20079	A_95_P063445	AM851007
20728	244	73	581	AGATTCTTAAAGTCCAACCAGAGAATTGTTTGATCGACCAATAAGGAACAGATTATTT	20083	A_95_P196702	AF211537
20730	244	75	442	GGCAGTTGTTCAGTTTGACAGTTATATTTGTATATGACGAGAGACATCTTAAACCTTC	20087	A_95_P306398	FG635140
20737	244	82	770	TAAGAGACATGTATGACCAGAACATCTGGAAAGAGTTGGAAAGGAAGCCGATGCCC	20101	A_95_P297973	EH615487
20742	245	2	428	ACTTATAACTTACGTCACAGGTTCGAGCCTTGCGTCATGCGAACTAAGCCTGGTATTT	20110	A_95_P036803	BP128827
20747	245	7	774	TTACTAGAAGGCGAAGAAGTTGAAATCCTTATAGGCTGTAATAAATGTTACCATATG	20120	A_95_P177932	TA12106_4097
20749	245	9	883	AGCTGATGGAACAACTTGAAAATTCTTCTGTTTCCTCTATAAGTGGGCAAGATGGCAT	20124	A_95_P202577	EB427823
20750	245	10	638	ATTTTCTGGAATACTGGGTTGGCTTTGTTTTGGCATCAATTCATGCCCCCACTACAGT	20126	A_95_P300228	FG643798
20751	245	11	839	AAGGTACAAGAGGAAATCACCCGTGAATTTGCTGCAATCATGGCAACTGGAACATTG	20128	A_95_P246067	EB428701
20752	245	12	697	CGGGTTTTGGGATAGTCTAGTTGATGTTACGGAAGTGCATAACATTATCACCTTTTGT	20130	A_95_P205962	TA18404_4097
20760	245	20	379	TCAAGATGGCAAATGATTGCATTGGTCCAGACGTTGAGAAGATGGTTCATGAAATAC	20146	A_95_P048036	BP131804
20761	245	21	1550	GCTTAACTTACATGGTGAGATTGTTGAGGATTTCCTGAGACTGAGGGATGTCTATAA	20147	A_95_P022311	TA15002_4097
20762	245	22	443	AGCCAGAGGGATAGCTGCATAAGCTGAATTATATGCCATTTAATCCATTCAAGTACA	20149	A_95_P021361	EH615846
20769	245	29	828	AATGCATACAGCAGTTTCTCACTTGCCTTACTTCATTGCCAAGGCTAATCACATCTATG	20163	A_95_P127427	EB426979
20770	245	30	448	AAGTTCCTCTAATTCCAGTTCTCTTTCCAATTCACTATGATCCTGCTGAGCTTGAATCC	20165	A_95_P026631	BP533680
20771	245	31	628	ATGGTAACTAAGAATTCAACAGTTCGCTGTTGCTAGCTGTGGAAATATTGGTGTGGC	20167	A_95_P058191	BP134415
20775	245	35	599	TTGTGTCAATTGCTGCTCCCCCGGATGGTTGTTTAATTTATTGAAATTTCATACATTCT	20175	A_95_P186752	TA14193_4097
20776	245	36	876	CATAATCCTGGAGAAATATGAGTGCATTTGCCATGATAACTGTAGAAATTGATCCTA	20177	A_95_P270416	EB677719
20781	245	41	584	TTTGCTTTGTAATCTGAGCTCGAGATCTTGTGAATTGGAAATTGCAGTTGTTTGAGGT	20187	A_95_P202997	FG645282
20782	245	42	402	CTCGTCCTTTCATTACCATATGCCCCTATTCTGAAATTTGCTGACATGTAATTGGATAA	20189	A_95_P120777	TA14883_4097
20783	245	43	701	CTGGCGGCTTCTGTTCTTTGGGAAGTTGAAATGCTATATGAATATTATTTTTGAAGAA	20191	A_95_P195187	EB425378
20786	245	46	486	GCATCTCAATTCCTGGAACTTTCCGTGTTGCAACTGAGAAAACTGTTTTTGCCACACC	20197	A_95_P066485	FG199650
20791	245	51	735	CAAGAATTTGCTTATTGTCATTTACCTTTCCTCTTAAGGAATGAGGAAACCACATTTTG	20207	A_95_P216652	EB435837
20792	245	52	1091	CGTTGTTTCCTTGATTATTTGTTCTTCAAAACTGTGATATGGTCATTCTGTCTAGTGCA	20209	A_95_P183532	TA13481_4097
20793	245	53	1394	GGTGCTGCATTAGTCCCTTTTGCTTTCATTTTTTGAAAATCAGTTCAAGTGGAAGAAT	20211	A_95_P019516	TA13916_4097
20812	245	72	792	TTGGGAGGCTAAGGAATACGGATTGGTTGATGCTGTTATCGATGATGGCAAACCAG	20249	A_95_P216977	TA20825_4097
20813	245	73	786	TCATTCTGCATTTTCTGAAGCCTGAAGAACAGTTGACATTTTCGCAAGCTATGTGGAT	20251	A_95_P289578	DV160054
20817	245	77	702	TTTTCGTCAAGGGAAGTACATTGGAGGAGCTGAGTTATCAAGCAAATGAACGAAGT	20259	A_95_P220177	EH616351
20820	245	80	695	GCCTTCGGGTGCTGAGACGGACAGTACTTATGATTCACGTAAACTCAATAGTTTTAT	20265	A_95_P269121	FG640413

20823	245	83	997	TAGTGTGTGAAACTTGAGTTTTACATTTGGAATGGGGACTGAAGTTGACGCATTCTG	20271	A_95_P191417	TA15233_4097
20825	245	85	1207	ATTTGACTGAGGAAGACAAAGCTAATTTGATTAAGAAGCTTGAGCAGCAACAGCTA	20275	A_95_P012006	TA17212_4097
20826	246	1	416	CCTTTCAGTATGATATTTGGTTCCTTTTAGATGAATTGATGAAACTTGGTAATAGCAC	20109	A_95_P154332	DV157719
20827	246	2	243	TGTTATATGAACTGAAGTCATGCATGTTCTTGCTTTAAAATCTGTAGGTCTTGGCCTTT	20111	A_95_P104107	CV016852
20830	246	5	531	AGCTCCTTGACGGACATTCCTCTCGTTTCTGTCATGAGATCTCTTATCATCACCTGTGT	20117	A_95_P076910	BP527115
20831	246	6	1451	TACGTGTTGCTTGGTGATACCATTATTGATGTCTCCACCATTTATTGTTGACTTCCGAG	20119	A_95_P188772	TA14644_4097
20832	246	7	981	GTCTGTTATTAGACGATGATGTTGTCACTCTCTTCCAGCTAAATAAGATAAAGACTTC	20121	A_95_P258396	D85912
20833	246	8	561	ATGCCTTTAAGTTTTAAATTTGGAGGTTTGGTGCGGTTAATATGAGCCAAAAGCTTG	20123	A_95_P307883	FG639914
20839	246	14	131	CAAGTAGTCCTTTCAAATGCTTCTGTTCTAGGGTTTTGAACCTCTTTTTTGTCGTTAAA	20135	A_95_P003661	TA13102_4097
20842	246	17	578	GCGGTGGTGACCGCGTACATGCTATTTATTTGATTTTTACTATGGTTATGGTCCATTG	20141	A_95_P005561	BP530129
20846	246	21	651	TGGGGATTTTGTAGTTGAGTCGCGGTTGTTCCTATTCGGTTATTTATGAGATTTTTAC	20148	A_95_P157627	EH615679
20849	246	24	677	CATCTAACCAATCGTTGACTCTCTTCACCTTGTACATCATTCCTGCTATTTGGCTATCT	20154	A_95_P316858	FG196716
20850	246	25	856	TATTCAAAGACCTTGTAACTCTAGAATCTGGCATTTTCTTGTCCATAAACTTCTGTTGA	20156	A_95_P009961	TC41290
20852	246	27	409	TTTTTATAGTGTTTTCATGGAGTTTGGGGTGGTTGTTGGCTGATTTTAGGTGAGGTCT	20160	A_95_P077965	BP527393
20860	246	35	637	CCTCAAGGATGGGACAAGACTTATTGTTTGAGATACCTTGAAGAATTTAATGAAATT	20176	A_95_P001041	DV162559
20862	246	37	811	CTGTGAAGCAAAAGGTCTTGTGATTACCTTTGTTGGCATGTTTATTTTCTCTTGGACA	20180	A_95_P013391	TA15497_4097
20865	246	40	1018	GCTCTCCTTGGCCAGTTTAACTGGTTGATTTTAACGGAGTCATATAGATATGTTTCTT	20186	A_95_P208667	TA19018_4097
20872	246	47	469	CAGCTTTGTTCTAGTTGTCGTTCTTAAGGTCTTGATATTGTAATTTCTCATTGCAGATT	20200	A_95_P101103	TA12412_4097
20873	246	48	843	CCTTTGTTTGCAAACTGAACAATATGAAATCACAAACCGTGGAAAATTTAGTTGTAGT	20202	A_95_P031896	Y09506
20874	246	49	863	GTGGACATTGCCAGGAAGCGTCTCCTTAAGTAAACTTAAGTTGTTGTAAGTGTACAA	20204	A_95_P208757	EB438033
20875	246	50	252	GTTACTTGGTTTTTTAATTCATGAGCGCAAGTCTATACAAGCCCTTTTATAAAAGGGT	20206	A_95_P214142	EH624317
20877	246	52	736	AAGCTCCCACATTGCTGGTAAATAGTGGGGAGGAGAAGGATAAGAAATTTGGTGCT	20210	A_95_P156967	EH615034
20879	246	54	280	TTAAAATTTGCGATATCTGGGCAAGACAAGCCCTCTAATAACTCATCAATTGCGACAC	20214	A_95_P098828	DV157864
20882	246	57	509	TGGCTGATTGTCGTTTCTGATGGACTTTTTCATTGCCTCTTAGCTGTTTCACTTGTTTCT	20220	A_95_P124837	DW004632
20883	246	58	633	GTAATGTGTTTCGTTGTACCATCTGGATGTATTGGACCTGGGAATGAATGTAATGCTT	20222	A_95_P021516	DV160348
20884	246	59	420	GTTCCCCACCCCCCAATGACAAAGAACAAATAGTTAAAATTAAAGCTATTTCTTCTAC	20224	A_95_P050491	BP132409
20886	246	61	865	AAGGATGACTATGCAGTTGTCTTGTTGGTGTCTGCTGCTTTTATGTGAACTTTTCGGT	20228	A_95_P252374	FG168352
20888	246	63	51	TGTTGAATGCATCATCACCAACAGTGCCTTTGAGCCGTCTTCCATGATGGTAAAGTGT	20232	A_95_P033839	AJ717803
20890	246	65	544	ATCTTGACATTCATTATCAAGGGACAACAGCTTGAAAGGACTCTTCAGCACCAATTG	20236	A_95_P034070	AJ718098
20893	246	68	539	AGATCAACGACAGCTTTGGTTCCTCCTCCAAAGACCAGGTTACTCCTAAAGAGGATA	20242	A_95_P049836	BP132258
20898	246	73	840	CTTACGTAGATCAGCAGGGCATGTTCATTCAAAGTTCTCGTCCTACTCTTTGTTTTATG	20252	A_95_P245152	EB679261
20900	246	75	746	GTTACATCTTTAGTGCTTGTTTGTGCTTGTGATGGACATTTTATTTTGGGTTATCTTTC	20256	A_95_P161132	EH616479
20904	246	79	219	GGTAGCTGAAAAGGATGTTGGCCAAAAAAGGACATTTGCCTAATAGTTATGAATTAA	20264	A_95_P017436	TC72449
20906	246	81	334	CACGTTAATTATGTTACTCCAACTACGTGCCTGTAATATTTTGCCCAAGCAATGGCAT	20268	A_95_P115282	DR752037

20907	246	82	63	ATGACGCGAGCTTCTTTTGTTGCTGACTTGAATTGCATTCTGAATTGAATTCCCTTTTT	20270	A_95_P002061	BP192620
20915	247	5	726	GATTTCGTAGATCCAGCTTGTGCAGCTACTGCTTTGAGTGCATTGCAAGGTTACAAAA	20285	A_95_P307513	DV162343
20916	247	6	573	TTTCGACTGCTTCGAAATTATCTTTCTAATCTATGATGATGAACTGAGGATTGCTTGCT	20287	A_95_P184407	FG634402
20919	247	9	690	TTCCAAGTATTCATTGGTTACATGTCTGACTGATGTACTGTGTTTTATATACAAGAGGA	20293	A_95_P013381	EB440030
20923	247	13	279	CGGCCTGTGATTGTATAGCACAGAGATTGTACATAATATGGTGTGAATAATAGAAGT	20301	A_95_P141812	EB445446
20928	247	18	742	GCAGAGTTCCATTTCGTGTCAGTTACTTTCCTGAGATCTGCCATTTTGTTTATTCATTT	20311	A_95_P183842	EB426399
20935	247	25	1116	GTGATTTACTGAGTCGTGAAGGTATAGGAGTTTTTGACACAGCATTACCCTAGAAAAT	20325	A_95_P200372	TA17194_4097
20936	247	26	1056	GGCTCTTGCCCTTCGGAAATTCCGAATTGAAGGGTTGAATGCATTAAAATTTTGACTG	20327	A_95_P192147	EF051141
20939	247	29	864	GGCCTTAAGTTCTTTTCTTTATTGGGGTAGTCTTGTAGAAATTTTATCCGAATATGCGA	20333	A_95_P193272	DV158451
20940	247	30	663	TGACGAGGAGGATGAAGAATAAGCATTTGCACTAGAACGGAAAGAAAGCTGTTGGT	20335	A_95_P100893	TA12891_4097
20941	247	31	327	CAAGAAACAACTGTAATGCAGATCCTTCATGTCAGAATCAATGATGATCGTGTCTGTT	20337	A_95_P025676	FS411044
20942	247	32	47	ATTTCACAGATTTTTGTATGAGAACGTTGCTGAGTTTTCTGCAACATAATGTAATCTG	20339	A_95_P031676	EB437988
20947	247	37	2038	CTTCGGGTAATTAGAAAGCTGTTTACCATTTAATAAAATGGATTTTTGGAAAGCGGC	20347	A_95_P214632	X81855
20949	247	39	700	TAGGGAATTGAAGTTGCAGAATTTACCAAACTGAACCTGTAGTTTTCTACTTCTGTTG	20350	A_95_P177692	EB428593
20964	247	54	713	TAAACACGTCCCTTGTGCGGGCGACGTTGTGGTTGGCTTGTGGACTTCTATTTATTTTT	20379	A_95_P119447	DV162665
20966	247	56	403	ATCATGATGGACTCTTCTTCTTTGATACTTACCTACCTTCGGACTATCCGCATGAGCCA	20383	A_95_P084620	BP529066
20969	247	59	781	GATCTTCCAGATACTCAGGCAGCTCGAATCAAAATTGTTATTCCTTGGATCATCCATTT	20389	A_95_P247597	DV161190
20972	247	62	787	TACGCTGATGTCTTGTCAAACTGCCAGTAAGTTATTGTCTACCCACTGAGAGCACACT	20395	A_95_P242757	TC50758
20973	247	63	1130	TTCACGCTGGCATGTATCAAGATGAATAGGACTGATCTGGCTAAGAAGGCAGTGGAT	20397	A_95_P018721	TA16633_4097
20976	247	66	517	ATTGCTACATCATATAATGTGCATAGCGCCTGTTACTTTTAAACATGTGTTTCCTGGTA	20403	A_95_P024061	TA16142_4097
20979	247	69	784	TTGTTATTCCTGTGCCATACAAGGACGCTAATACTCTAGGGATCTTTGATGCCTGTGCT	20409	A_95_P118147	DV161163
20980	247	70	727	ACAAGAGGCAAAACGCTTGGCAACAATTTCAATCAACTAAAGGTCAGACTAAGAAG	20411	A_95_P216122	TA20636_4097
20982	247	72	561	CTCTCAATATATATCCCTACCCCGACCATGTATTTTCACTTTTTACTTAATACGTGATA	20415	A_95_P203502	EH615689
20983	247	73	491	TTGAAATTCTGCGAGACTGGGAAGATAAATTTATTGAGAAGTATGCCAGGGTGGGG	20417	A_95_P123592	DW003463
20984	247	74	45	CTGAACGGTCATATCTATTTGTGAAAGAGAGTGGCTTTTCAGAAAAGTCATCTCTAAAA	20419	A_95_P134037	EB435823
20988	247	78	866	GGGCTATAGTTTCTCTTGTTCTAGGTTTCTAGTGAAAACAGTAAAAGAAGTATTCTCT	20427	A_95_P177647	X97967
20993	247	83	1251	GACTCTAGGCTCTAGCTTTTTGCTATCCTTGCAGAGATTGTATTATTTACTTGTTGATA	20437	A_95_P179522	TA12526_4097
20995	247	85	729	TAGTCCTTCGGAAGGGTTTGTTGACCCGTTGAAACAGTTTGAAATCTCATATTCACGT	20441	A_95_P148107	EB677303
21009	248	14	147	ATAGGCTTGAATGCCGATGGAAATTTCCAAGTAAAGAGTGGATGGCATAGTGGGTGT	20304	A_95_P146682	EB450776
21013	248	18	637	TGTGTAGAGCTGGCGCTGGAGCAAAAAGAATTACCTTTGTATTTAACACAATTTTAGA	20312	A_95_P157847	EH615885
21016	248	21	571	TTTCCTCACAGGTAACAAGGATAAGTGATATAATCTGGTAACAATGCTTTTTAGTTGG	20318	A_95_P133817	FG641828
21018	248	23	1432	TCCAATTGTTTGCGAATGAACATAGCTCGTGAAAAGTTCAAGAGTTTTATAACAGAA	20322	A_95_P022506	TA15718_4097
21021	248	26	595	GGATCAGTTCAGTTTGAAATTTCAGGTTCCTCCTGATTTTCCTTTTTGCTGTCTTCTTAA	20328	A_95_P111182	FG640251
21023	248	28	492	AGTAGAAAAAGACTATCTGAGCTCAGGTAGGAGAGCATGCGTAAAACTCCTTCCCTA	20332	A_95_P266321	BP533240

21025	248	30	182	AAACCATATATAACTCCATCGACAAGGTTCAGATAGACAGGGTGCGTGCCTCCTCAA	20336	A_95_P088868	BP530255
21026	248	31	0	CTCTGCATGTGTAACTCGGTGTGATCGATATTGTGATGAGGTACTAAATGTTTTAAA	20338	A_95_P017741	A_95_P017741
21034	248	39	491	CGAAGTAAGAAGTCAAGGTAACAAGCTTGTGGACAACAGTCAGTAAAGATCTGGTG	20351	A_95_P011576	TA16364_4097
21038	248	43	1447	CCTAGTTTGTACGGGACACCAGTTTGCTATTTGCTATCAATCTATCATTTTCTTGCTCC	20359	A_95_P018236	TA14362_4097
21040	248	45	795	TGTATGAGAACTCGTTCTTGCAACCCTTGGGTTCTGTTGATAGATTTGCGAGCTCAGA	20362	A_95_P307238	FG137860
21041	248	46	595	CGTATTGTTGCAGCATTCATGTGTGTACTTTGGCTTGAATGGACAAAAAACTCAATTT	20364	A_95_P206407	TA18509_4097
21045	248	50	296	GAGAATAGCACTTTTGTATTGTGTCTCTCTCGTCTCTTGCCTTTACATTCAACAGCAG	20372	A_95_P046686	BP131462
21047	248	52	687	TGGCATTTTGAACCATGTTTGTCTTTCTCCAGAAATTTGTGGTACTGTTTAGCATATCC	20376	A_95_P115917	DV158976
21048	248	53	354	TTTTAAAAGGCTGGATGATTCTGGAAAAGTCCAGAGGGCTTCGTAAGGAATGCCCTA	20378	A_95_P103602	CV016597
21049	248	54	829	CCATAGTTTATGAAGCATTCATGTGAATATTTGCCTGTCTATGTAACCCAGACCTTTTT	20380	A_95_P211317	DV158454
21053	248	58	223	GGGGTTATGTAGACTGATAATCTCACCCTTTCTTATTCCTGAATTGCATTTGACTTGTT	20388	A_95_P002446	CV016592
21055	248	60	734	GGCAGTGGATTCCGAGGGCAAGCATTTTCAGATGGTGGGTTGATTATGAAAAAGAT	20392	A_95_P306328	FG167098
21056	248	61	985	GAATAAAGTTAATGTGTGAATTGTGTGATTGTGATCTATGGGATCGCGACTATAATC	20394	A_95_P179847	M15173
21063	248	68	1030	TCATAGAATGGCCATGGCTTTCTCTCTTGCTGCTTGTGCTGATGTTCCAGTCACCATTA	20408	A_95_P196522	TA16357_4097
21065	248	70	896	CTATAGTTTTCCTCTAGTATATTATTCGAAGCCGTCATCTTCTTGTTGCCATTTTGCAA	20412	A_95_P289123	DV157776
21066	248	71	709	GTTGTATGTGGCCTTGTCAGCTTTCAGTTTTGGACGTATAGTTGTCTTTAGCAACCTTT	20414	A_95_P195559	EB438896
21069	248	74	1027	TGGATGCTCCAGTGAAACTCTCTTATTTTCGTGGAAATGAATTCTTGTTTTTACGGAG	20420	A_95_P007671	AB119466
21078	248	83	886	CTAACTTTGCAATAAACAAGATAGTAAAATGTGCATTTAACGAGTTGATCGATCCAT	20438	A_95_P289738	DV160762
21081	249	1	421	GAGATATTAAGACTTTGTTACCTCTGTTGGATGTCACTGCTGGTAATGCTGTCTGTTA	20443	A_95_P023066	DW002423
21082	249	2	299	GTGATGACATTCAAAGGGGATAACTGGAGCCAAGTTGTGATATGGCTTATTTTTACG	20445	A_95_P100713	BP535494
21084	249	4	510	CCACCAGAGTCTAGGGGAATGTCCAAGCTAAAATGGATCGAGGAAAGGAAGAATA	20449	A_95_P156292	EH613641
21086	249	6	469	AACCCAAATGACACAGAGGAGTCAATATGGTGCTTCCTCTGTGAAGCTCAACTGTAT	20453	A_95_P071285	BP525667
21088	249	8	594	CAATCCCTTAATAGTTGGGTCAATGCCAAATATGCATCATTCTATCTCTATTTCCTTCT	20457	A_95_P058921	BP134599
21089	249	9	344	GCTGGGTGTACCATTTAGGTGTGTATATGATCATGGTTCAAAAATTTGTTTCAAGGTT	20459	A_95_P027766	EB443765
21091	249	11	836	TAAGTGGAACCTCTGCTGTATTGCTGTATTCTGCAATAATATTGTGGATTGTGGCATA	20463	A_95_P228989	DV161013
21092	249	12	863	TGTGCAAGCTGTCCCCGATTTGTTTGGGAATCAGCTTAAATGAAAGTGCGATATTGT	20465	A_95_P008146	DW000274
21093	249	13	723	CGTACTGGTGGTTGAAGAACAATAGTCGAATATGCCCCATCCAAATGAAGTCAAGTT	20467	A_95_P179612	TA12549_4097
21095	249	15	435	TAGGTTCATGTGGTTGGAAGATAATGAAATCGGGGAAGTTCCGTTCGTTTGGAACTT	20471	A_95_P135962	DV159900
21096	249	16	802	GAATGACATATACTGTGTTTTCTTGGGAAGTTTGAACAACTTATGTGCCTTAAACAAG	20473	A_95_P026201	EB441754
21098	249	18	595	GTCGATTTACCTGTTTCTTCCCTTGCACTATCAAACATTAGGCATTTAACCATTTGCTT	20477	A_95_P090618	BP531027
21100	249	20	785	TTTCAAAGATGCCTTTGCAAGAGCCCCAAGCCCCTGAACAACTAAAGTGCTTCCTTTC	20481	A_95_P194632	EH622289
21102	249	22	265	CTGTTGCTTATAGGGGTGTTGGTGGAGCTCCTTTGTGTAATATATATGTCATCTTTCG	20485	A_95_P129872	EB429804
21104	249	24	519	GTTAGACTAGTTTTGTTTTTAATTTCTCTGTAAAGCTGCTGCATTTATAGCAGTTGGCA	20489	A_95_P121447	DW001515
21105	249	25	610	CTCCCAATCAACAAAGTGTAGAATAGCATTAAATGTTGTCCTCTCCAGAAAAAAGAG	20491	A_95_P194017	EB677535

21112	249	32	0	TCAATGGCAACAACATGAACATCATAATTCTCAGCCATGTAAAAATCACCTCCCCCTA	20505	A_95_P316738	A_95_P316738
21115	249	35	451	TGTAATACATATACTGTGTACATGGCTTCTTGGGTTGAAAGATATTGACTTGTGTTGT	20511	A_95_P021911	FG644966
21119	249	39	851	CGAAAATCTTCCGTTCTTCGTCGATGTCTTTTGAAATTTAACTCTAGCCTATGAAACAT	20519	A_95_P222582	TA22064_4097
21121	249	41	482	GCTGATTTTTCGCGTCTCACAACAATGTTGTAATTGATTACTTGATAAGACAATGCAG	20523	A_95_P220572	TA21636_4097
21123	249	43	283	TTTGTAGCTGATGACATTTCAGACCCATATGAGTCTCGTACAATGCTTCTTTTCTTCCG	20527	A_95_P108442	CV018832
21127	249	47	687	GTCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAAAGTTTTGGTGCCGGAGGAA	20535	A_95_P238509	AB055500
21130	249	50	761	CTTGGGGTCTGCGCTTGGTGTACTGATGAATGGTACCATCTTAAGTCAAATTATCAT	20541	A_95_P015296	EH622808
21148	249	68	799	GGGTTTGTGATGGTGAAGTTTGTTCCAAAAGTTAATTTGGTTATTATGGGTTCTTAG	20576	A_95_P016576	DV160405
21149	249	69	259	TTGTTCTGACATCCATGATGTGGGGAACTGTGAACTATGTAACTAGGGTGCAATGGA	20578	A_95_P133302	EB434706
21152	249	72	779	ATATAGAGAACATGGGGTCATGAAAGTGTACCAGTGAGAGCGTTGGCTCCTTTGTA	20584	A_95_P150887	EB681018
21155	249	75	883	TCCTTATGCTGTACATCAGATGAAGGCGTAAGTCAAGATGGCGATGCTGGAGATGA	20590	A_95_P204767	TA18135_4097
21157	249	77	993	TGGGCTTGTTATGGTTTGGATGTAAATTATTTTTTGAGAAATAGATCTTGCCAGCCAG	20594	A_95_P180772	TA12823_4097
21158	249	78	1038	GCTACATTTTGCGCCATTCTAGGTAATGTAGTAATATACTCCATTCTTTGAGACGATT	20596	A_95_P130137	TA16773_4097
21161	249	81	106	ATTGGCTCAATCTTAGAATAGTGGTTGGTTTACGTGATCACAAATACCCTCATTCTCT	20602	A_95_P092133	BP531658
21164	249	84	178	CAATTGTGGTCACAGTACCTATTGTAAACTGTATAACCTATTTATAGACTACTTGCCTT	20608	A_95_P090668	BP531051
21171	250	6	194	AGTGATGTGGTTGCTGGTATGACTGGTACAAAGTAAGGATAAGATACTTGTGAGGT	20454	A_95_P109052	TA13487_4097
21173	250	8	679	GGTACACAAAATATGATCATCAGATTTTGGATGCAAGTCTAGGTTGAGTTGAATGCA	20458	A_95_P123617	DW003483
21174	250	9	478	TGTTTAGGGTTATGGTGAATGTGGTTTGTGATGGTGTTTAGTTGTTTTTTGCTTGAAA	20460	A_95_P268851	DW003245
21180	250	15	402	GACTATTTATCCCAGATCATTCCTAGTGTAATCTCGTCGTCGTCATATGCAGCAATAA	20472	A_95_P055091	BP133606
21181	250	16	651	CAAGTGCAACTTGGTAGATTACTGTATGTCCTAGTAATCCACTGTATCATTGTATGTC	20474	A_95_P121432	DW001499
21182	250	17	479	GTCTCCTTTGCCTACAAATTATTCTTGAAATTGATTAGTATTTTGTTTTCCGGGGGAG	20476	A_95_P162322	EH621265
21183	250	18	1365	CCACCAGCTGCACCGAAGATTTTGCACAGCATGTTGATAAAATCATACTGTTCCAATT	20478	A_95_P238689	AY061648
21185	250	20	469	CAAGGGTGATACTATGGATGATATATACAGTTTACCTGTGTGATATGCCATAGAATA	20482	A_95_P019906	EB683600
21187	250	22	2971	ACATGTCAAAGTACTTCGTTTCTTAACCTCTCACTGTTCATGTTTAGTCATTGTTTGCT	20486	A_95_P222742	AJ133502
21194	250	29	662	GGTATTACCAGTTCTAGGGAGTTGTATTATGATTTGATATTATCAATGGCTATTTGCC	20500	A_95_P100683	TA20739_4097
21198	250	33	370	GTAATACTTATTCTTGTAAGCATTGATTGTTTCGAGAGGAATGGTCATTGCTCAGGA	20508	A_95_P233289	TA18497_4097
21199	250	34	688	TAAAATGAGTGAGGTTTTGGAGATGGTGAATCGGCTCGTGGAGGCAACTGAAGCA	20510	A_95_P144732	EB448246
21201	250	36	1122	GCAACATCTTTGAAATTGACAGCATTTGGCATGTTGTGCATGCGTTTACTTTCCTTTC	20514	A_95_P018226	TA15108_4097
21203	250	38	502	TAGCTCAACAAAAACATGAAGTTCTGAGGTACCGCCACCACACTCCAAATAAGTTTA	20518	A_95_P262166	BP134733
21205	250	40	328	GATTTGCACGACCATTTGTTGATAACTATGAGTTTTTGGTTAAGAAGGCCTGAACCC	20522	A_95_P110542	CV019776
21209	250	44	450	TTATACAAAGCACCAGATAGCTTCTGAGCTACTAAATGGTGGGCTAAAGTTGGTCGC	20530	A_95_P160217	TA13884_4097
21210	250	45	690	AATTTTCTCATACAAGCGTGGATTTACTTATCGGAGTTTGAGCATGACAGAGCCCCA	20532	A_95_P151472	EB681675
21212	250	47	377	CATTGAAGTACAAGCATTTTGTATTGAGTTCTCAAGGATTAGAGAGGCCGCGGGGCT	20536	A_95_P100658	BP535472
21214	250	49	991	GCATGCTTGGCACCTGTGCTTCTAGTAATTTTTCCTTTTCTTCTGTAAACTGCTTTACT	20540	A_95_P012561	TA15251_4097

21216	250	51	243	GCAGTTGGAACATGTATTGGAGAAAAAACTTAGAGGTGTTGATTACTAGGACATGAA	20544	A_95_P102432	FG644264
21217	250	52	630	CAAATCCTCTTCATTCAGGCCTTTCCTTTTAAAGAGGTCAATCAACATATCCACTGTAT	20545	A_95_P305768	FG195555
21220	250	55	995	TTCTTGGCTGGAAGACGTCTACTTTAAATAACTTCTGTCTTGATACAGGGGCTTTGCT	20551	A_95_P182372	TA13199_4097
21221	250	56	575	AATCATGAGCTTGAGGGCTCATCTATGTAATGTTTCCAGATAACTTATGTCCGAAATT	20553	A_95_P113367	TA13071_4097
21223	250	58	1040	TACGAGAACGACTTCGAAGTAGTTCACTGGCTAGCTAAGAGGCATGGAATAGTCCTG	20557	A_95_P215957	TA20600_4097
21224	250	59	698	AGACTGATCCTCGACTTCCCAGGACATACCGCAATAAGGTTGCTACTGCAAATTTTGT	20559	A_95_P152302	EB682646
21226	250	61	656	ACCTTGATCGGGGCGGATCCAAGATTTAAACTTTATGGGTTTGCAGTGTCACAAAAC	20563	A_95_P123082	DW002998
21227	250	62	827	ATTTTTGTCTTGATGGGTAAGTAGCTCCTGAATGTTTATATTCATTTTTGAGCTGCTCC	20565	A_95_P245627	EB439032
21232	250	67	398	GAAATTGCAAGCAAAAAGGCAAAGGTAAAGAAAGCGAGTCTTGGGCGATGTAGCT	20575	A_95_P098298	BP534407
21237	250	72	680	CTATTCTGGACTCACTCAGTTTTGCTCGATTTAGTGCTGTAATTGCTGAATTTTGTTCA	20585	A_95_P284123	FG635995
21242	250	77	518	GCAGACAAGTTTTCGATTGCTTTCATATACGTGTGGTTAGTAGAGCACATCTCAACTA	20595	A_95_P201907	EH623306
21243	250	78	2124	GCTGAAGTACAATCAACACTTCTCCATTGTAACATTCTTAAAACATGCGGATGAAAAA	20597	A_95_P236429	AY123847
21247	250	82	1061	GAGAGACTTCTTCTTTGTGACTGAAAATGTTGTCACTCTTGTACCTTCATTTGTAATTG	20605	A_95_P212867	TA19927_4097
21249	250	84	401	TGAAGTGAGCGCTTAAAAACTTGCACATTTCAGGTTTCTATCTCCCATATATTTTCGCA	20609	A_95_P027651	TA21922_4097
21250	250	85	1513	GCATTTCCAGCGTGGAAGATTTTTACACGATGATTCCAGCTTTGTTGTATCATTTTAG	20611	A_95_P008636	TA14928_4097
21256	251	6	598	GCAAAAAGAAGTAGCAGCAAGTTAATGGAGCAGCTTTGTACAACGGGTTGTCCATCT	20622	A_95_P285513	FG643114
21258	251	8	566	TCTGCTTCAGATAGCATTGGATGGAGGATTCAAAAGACCTGTAAATATGTTCCATTTG	20626	A_95_P210017	TA19311_4097
21259	251	9	819	CTCTGCATAAGTGAACTCTGATATGCTGTTCGAGATCGGTTGATCTGGTGATTGCTCC	20628	A_95_P146487	EB450550
21262	251	12	298	TTGGTGTTGGGGTTTCTGTTCTACAGTTGAATATCATGGACTATTAGCAATGCAATAT	20634	A_95_P214397	TA20255_4097
21266	251	16	417	TTCCACTGCAGCTGTTCTTGATTAGTAGTGTAACAATATCACAGCAATCATACAAAAG	20641	A_95_P040641	BP129883
21267	251	17	417	ATGACCTCAGGCTATCAACAGATGAGAATCTTATCAAGCGGATCAAGGATGGATTAG	20643	A_95_P103877	CV016728
21269	251	19	220	CTACACAAAATGAAATAAGAATCTCTTCGCTCTCTCTCTCTCTCTCAATGTTCGGACCG	20647	A_95_P072875	BP526072
21270	251	20	493	AGGAAACCTAGTGCCCCTGTATTCATATTCTTATTATCCCCTTTATTGTGAGTTGTTAT	20649	A_95_P097303	FS408454
21274	251	24	985	CCATATCCGACGCTTTGCTTTTATCATAATTGCTTACATCTTGATAGATTGTTCTAGTA	20657	A_95_P204417	TA18061_4097
21275	251	25	597	TTTCCGGTACGGTCTGTTGTGTTTAGCTTCGTCGGCCTGATTTTCTTTGTAAACCCACA	20659	A_95_P064905	BP136186
21276	251	26	320	GGACCTGATAATCGGAAAACTAGTTTATGACTTGTTTTTGTAGGACCAATGAATGTTT	20661	A_95_P001306	FG137063
21277	251	27	141	AGTGGCACATCATCATCCGCTTGTGGAAGTTCAGCAAGGTTAGAACTGCAAAATGGG	20663	A_95_P156077	EG650397
21278	251	28	1567	TCAGACATCTCTTTTTCCCCCTCCCCCTTGTGTGATACTCCTTATGTGTAATATAAATTC	20665	A_95_P210807	DQ129870
21284	251	34	608	TTGTCGATATTATGGAGTGATTATCAGAACTTCTTCGTTCGGAAATTATTGAACGTTCA	20677	A_95_P208702	EB447309
21286	251	36	548	AGCTCTTGAAACATTAAAACGTGTAGTCGTTGCTGGAAACCGAACTAGGGATGCCTT	20681	A_95_P033834	AJ704986
21289	251	39	782	CATTTCCAATTTTTGAAAAGATTGGATTTTTCTTGGAGGGGTCTGCCTATAGATAGGC	20687	A_95_P209427	TA19188_4097
21294	251	44	821	TGTACAATTTGGATGGAACTCATGTTGCCGAGCGGATTAATTCGCCAAATAAGTAGTA	20697	A_95_P126917	EB426304
21302	251	52	694	TCTATTCGTGCCTCACGACATGCCCTTTTTGGCCTTAGTTGAGCATGTATTCCTCATTT	20713	A_95_P261306	DW003630
21303	251	53	588	TGAGGAAGTGAGGGAAGGATAAGTGCTTATCCTTCAGTTTTGTAATAAAGTTTACTG	20715	A_95_P208107	EB443661

21305	251	55	753	ATCAATCCCCTGAACTCGATCAGAAATTCCCGTTGTCAGTGGACCCTTCTTTTGAAGG	17966	A_95_P000116	FG157904
21310	251	60	643	ATCGGATGACACTTGAGAGTGAGCATGTCTCTGCTCATTTACATGAATGGGTTGATC	20727	A_95_P042926	BP130481
21312	251	62	888	ATTGGGCAAAGGTAGAACATATTGTTTGAATTGTAGCGAACCACACTGGATTTTGAG	20731	A_95_P118612	DV161692
21315	251	65	351	AACAACTGGGATGATATGGACGAAAATCTGGCACCACAACATTTTACTGTGAGCTCG	20737	A_95_P053246	BP133124
21319	251	69	776	CGGTGGCATTATGTTTCCCCATTAACATTATGTTGGTAGTTGAATGTTTCTGTTGAGT	20745	A_95_P246767	DV999273
21320	251	70	637	TGTCAAAGGATCGCTTTCTCGAGTGTATGAGTATCACTCAGAAGGACCACAGTTGAT	20747	A_95_P055486	BP133714
21322	251	72	337	CATTTAGTTCTTTATGATAAACTTATTTACTCTGGCAATAAAGGCTGTCTTTCCCAGCA	20751	A_95_P076915	BP527116
21323	251	73	1010	CTGCTGCAGAATGATTGCCATTGTGCCTAATTTCATTAATCTTTAATGTGTAATGTGT	20753	A_95_P250742	AF154645
21328	251	78	72	GTCAATTGTGCAGTTTGGTCCTACGCTGGGTAGATCATATATATTATTCATTTTTATC	20763	A_95_P257174	EH622168
21329	251	79	216	AAGAAAGACCTGATGGGTTTCTAGGTGAGGCTGGACTGGATGAAGGTTATGATGAT	20765	A_95_P143722	EB446938
21334	251	84	434	ATAGTGAGTACCAAATGTGAGCTGTTCGATTCTGGAGTTGGAAGCCTCAATGCACCA	20775	A_95_P085000	BP529167
21338	252	3	602	ATGCCACTCTATCGTGCTGTATATGATATACCAAGTTCTTTGATGCTGGTTCTTTTTAT	20617	A_95_P056281	BP133914
21353	252	18	808	TGTGTTCATGACGAATACCTTATTCCAGCCGTGCCATACTCTTTCTCCATAAGGTTTTT	20646	A_95_P234134	DV999274
21354	252	19	774	TAGGAGCAATATATGCAGGTCACATTCAGAGAAGAAAAATAGGGACCAAATGATGT	20648	A_95_P022671	EB683173
21359	252	24	559	GTTTCTGTTCATGTTGCATATGGAGCAGGACTAACCATACAATTTGTGCACAATGTG	20658	A_95_P316058	EB427619
21360	252	25	387	TTCCGAAAACCATTTCCAGACATAAACACTTGGAATGTCAATTTCTCAATATATCTCT	20660	A_95_P013001	TA14187_4097
21366	252	31	657	CACCGCTGGTGTCGAACAATGTTCAGTGTTTTCATCTAATGGTTAGTTCACGTTACTG	20672	A_95_P014401	DV161017
21367	252	32	868	GATGATCACATTCGGCATCATGCCCAAGCCCTTAATCTTTGATTTGGTTAAGCTTCTG	20674	A_95_P185832	DV157903
21369	252	34	717	CAGCAAGTGGGAAATGACTTGTGTTTCTTTGGAGTATTGACTTTTTCCTTTTGGAATG	20678	A_95_P201067	DW004423
21371	252	36	518	TTTGCATTGGCTTTACTTCAGCCTTTTACTCTTTTTGGGGAACATTTAATTCATACTGG	20682	A_95_P159582	EB439146
21379	252	44	837	TTCCTATTGTGCAGATGATGGAGCATATCCGCCAACAGATGATATCATGGTCTGACG	20698	A_95_P118212	DV161232
21382	252	47	116	CTGGTGGCCTATACCTGTATTCTTCTCGAGCCTTGAAATGATCAGATTTCATTTCAATT	20704	A_95_P132087	EB432513
21383	252	48	620	TGGGCGGTGGTGACCGCGTACATGCTATTTATTTGATTTTTACTATGGTTATTGTTTA	20706	A_95_P181302	EB683516
21384	252	49	412	TACCAAGATAAGTGCTGCGACGTGTTATTCCATTGTAATATTTAAAGGTGCACATATT	20708	A_95_P090043	BP530777
21385	252	50	642	GCTGAACTTTCAAACATTCGGCTGATTTTGCATGTAATCAATTCGATGTTGATGAGTA	20710	A_95_P149652	EB679561
21387	252	52	785	GGGGGCTGATGCTTGATCCTTTTGTATGTTGTTTTACTTTAATTTTGGTGTTACTGCT	20714	A_95_P269461	EB424813
21388	252	53	1110	ATTCCTCAAATTCTTGAACAGCAACAGGAATATTGATGCTAAAATTTGCCCGCTTTTC	20716	A_95_P207002	TA18646_4097
21396	252	61	92	AACAATACTTGTGGGTCAGCTACCACATTGCTGGATGTGCTCATTTGTAATGTGAAA	20730	A_95_P108577	CV018906
21399	252	64	691	AGTGCTATACTTTCAGAATACGAGTTCTATATCCTGTAAAGATGACATTCTGGGTTTG	20736	A_95_P162887	EH621882
21401	252	66	854	GATCCACGATTTATGAATGGACATCATATTGATGGGTTAGTTCCTAACCAGTGGCAA	20740	A_95_P296733	EB679155
21402	252	67	768	GCATGGGATGTAGCATTACTAATAAGAGTTCTTGAATACAATGGAATAAGGGAGTTT	20742	A_95_P176682	TA11720_4097
21404	252	69	524	ACCAACCAATTAGGTCTTCTGAGGGATCAGGGGGTGCTTAATTCTGACCACATGAAT	20746	A_95_P214362	TA20248_4097
21405	252	70	415	GGGTCGGGTCGGTTGTCATCTTTGTTTTGGGTGTTGTAGCAGAGATTATTTTGAATG	20748	A_95_P274348	AM790664
21406	252	71	680	ACAGGGTCAATTAATAGGATTTGAGGAACCGAGGTAGCATTAGGCCCATTTGTTTAT	20750	A_95_P234364	EB679945

21407	252	72	321	CTTGATTGATACATAGATTGAAATCTCTATTTGTGGTATAGGGGTGGGGGCACTTTCT	20752	A_95_P088333	BP530019
21413	252	78	912	GGTGCTTCGAGTGAAAACGAATATTCTATCCGGAAATAAATACTGTATGTTTCTTGTC	20764	A_95_P010771	X51426
21417	252	82	600	CCAATTACTACTGCTCAGGTGAGGAGCTAAGGAAACTATTGGTGCATCTGCTTACAT	20772	A_95_P183467	U64923
21420	252	85	606	GATTCCTGATGTCGAAGACTGGAGATGATAGAGTAGATCCTACTTGTGGTGGATGA	20778	A_95_P061050	BP135164
21428	253	8	239	ACAATTGCTCAGTCTATTTGATCGAATTGATAGATACGAAACCCTCCCCATTCTTTGG	20792	A_95_P223087	TA22174_4097
21431	253	11	840	CACGCTTGTTTCAGGATCCTGAAACTGGATATGGACTGATAAATTATCAAGGCTTTTT	20798	A_95_P242752	EB449817
21432	253	12	81	CAACCCACCTTATGATGAGACATTTAATTGAACCTACTACTGTTTATCTTATCATGGAT	20800	A_95_P112857	CV020883
21436	253	16	154	GTTAGGTGGTATCTTTCTTATTACGGCTATAGTCAAGAAAAGTCTGTAAAGTGATTGT	20808	A_95_P213132	TA19983_4097
21438	253	18	806	GTAAAAATGGGTTCCTGACAGTTAGGTTGAAGAATTATTCAACAGACCGGAACAACC	20812	A_95_P128157	EB427700
21440	253	20	879	AGATGCCAAGACGTTGCATATCCCTGTGCTGGAGTTCTTGTAATAATTGTTTGGTTGG	20816	A_95_P022731	EB428177
21441	253	21	161	CAACCTCAAGCTTCCTTATGTAGGATTGAGCATTGTATCATTCAATTAATTGTCAACC	20818	A_95_P116767	DV159584
21444	253	24	339	AACATTTCCATGCAGGGAGGCCAGGAGGTGCCAAAGTTTGAACAAAATGATGATTT	20824	A_95_P134002	EB435763
21446	253	26	318	AAACTGAGTGCAAAGCTTATATTTGGTGCTGACAGCCCTGCCAATTCAAGAGAACAG	20828	A_95_P114522	FG157348
21449	253	29	361	TCCTTTCAAAGGCGGATCTAGAATTTTAGTTCTATGGGTTCAACATTTAAAGTTATGG	20834	A_95_P221117	EH623811
21454	253	34	672	CGTGCGTGAATAAAATGTCATCCATTTCTAACAAGGTTCATGTGTTGATTACACTTGT	20844	A_95_P134882	EB437768
21457	253	37	555	CTTTGGTGACCTGAAAGATGACCTGATAGTGCAAAATGTCAAATGTATACAAAGTAA	20850	A_95_P215342	DW003929
21465	253	45	802	CCAGGTAGATGAAAGTAAGTAGATGATGAGGGAAAGGAGTTCAACATTTTGTTATT	20864	A_95_P220037	EB679789
21471	253	51	1010	CCGCACCAGTAAGATTAACCTTCAACTGGTAATGCAAACTCATGAATTTTTGCTTAAA	20875	A_95_P248427	AB286177
21478	253	58	0	GTGCATTTCCATTATCAGCATTCCTGTGCTGTTGTTTTCAGATTAAATGCTAAATCTTC	20889	A_95_P251919	A_95_P251919
21480	253	60	457	GTAATATTGGTAATTCTACCCCTCCAATTTTGGATGCCGGAGAAAAGACAGGAAGCA	20893	A_95_P282458	AM827545
21483	253	63	1167	GGGTTGCTCCTATGCCCCCTATTACCTAATCTTTATAGTCTGATACTAATAAAACAATA	20898	A_95_P016676	X81853
21490	253	70	987	CTCCCAATATATATTGTCCTTTTTGCACTGAGAACTGTCCAAAATCATTAATGTATCGA	20912	A_95_P196002	TA16244_4097
21495	253	75	805	CCAGCCAAACTAGCTGCATCTTAGCCTCATCTAGTTCATCTTTGAAGAGTATGGTTCC	20922	A_95_P235994	DV157850
21497	253	77	707	TGTCATCCTCAATATCATCATCTTTATCAAATCGATGAGCCTGGAATTGATTTTGACGT	20926	A_95_P269046	FG187755
21500	253	80	126	CCATTTGAATACACGTCGTGATCTATTGTAATCGAAAAGCTTTGGCTGAATGATTTGG	20932	A_95_P033864	AJ717852
21503	253	83	861	CCAGAGGATAAAAAGATCTATGCCGCTGGAGGACGAACAAAAGTACCCATATACGT	20937	A_95_P222317	EB681947
21505	253	85	648	TCTGCAAGATGGTTAAACAAGTATCTAAGGGTATGTGCTAATGTTCAATCAAATGGC	20941	A_95_P121457	DW001525
21509	254	4	225	ATGATATGAGATTGATGTACAGGTGGAACATTACTGATCGTACTAGGAAAATTCACT	20785	A_95_P132337	EB432811
21514	254	9	799	GCTTTGGCATTGTAAATTTCGCTTCATGATCTCTTGTATGTTTTCATCCAATGTTTCAG	20795	A_95_P016081	TA17875_4097
21515	254	10	839	TCATGTGAAGGTACTATTAAATAACTATAATCGTGTCATGGAGCAGCTCGACCTCCAT	20797	A_95_P248787	EB426734
21517	254	12	647	GAAGATGGGGTTGTTAAAATCTTGAATTTAGAGGAAGGTGGGGCTTTTAATGTTAG	20801	A_95_P115792	DV999531
21518	254	13	670	GGAGAAGTCAAGTGATGAGGAGTTAAGTGAAGCGGAATATGATTCAGCTGACGAT	20803	A_95_P248437	EB439929
21521	254	16	467	TGTTTAGTGTATATAGCTCTTACTCGGCTGTTTAGCGGCCGCTCTTTGTTAGTACAAC	20809	A_95_P260686	AM807444
21522	254	17	716	AGAACGGAAGACTATGCCATGTTCTCCATGTTTGGATTCTTCGATTCAGGCTATCGTC	20811	A_95_P105297	TA11627_4097

21525	254	20	219	GATGAACCATGGTGTATCCTCTCATTTGACACAGATCATAAAGAAATATCGAACTTTT	20817	A_95_P096973	BP533841
21527	254	22	480	ATGGGTTTAAGTATTTTACTGAGCTCCTACATTGTTAGATTCAGATACAGTACCCTTG	20821	A_95_P122672	DW002651
21541	254	36	997	GTGTAGATGACTGATGATATAATAGAGAGCATGTATCCAAAGCTGCAAAACAATATG	20849	A_95_P020211	TA15644_4097
21546	254	41	658	TTGTCTCGGTACTTCAATCTTGTTAATCTATTTACGGTAAAGGGCCAAATATACCCTTG	20857	A_95_P180757	TA12820_4097
21547	254	42	431	ATAAATGGGACGGGGTTTTGTAACCCTATGACCCATGTAATTTAATGAATATGACCTT	20859	A_95_P022926	EH623004
21556	254	51	508	TGCGGAAGAACTTATTAAAAAAGTGTGTTTGGCCTTGTAACAATTTTGCCCCATAACA	20876	A_95_P159277	EH617309
21558	254	53	814	GGAGTGTCACCTGATGCGCATTTGTTTTTAACAATTTTAAGAATTTTGCTTTGCTTTGC	20880	A_95_P115777	TA12687_4097
21563	254	58	108	ATATTCGATCGCATAGAGTGTACGAATGGGTTGATTAACAATTCACAGATGAAAAAA	20890	A_95_P131387	EB431578
21564	254	59	1187	CCCGCCCAAATTGACTCAAATCTTTGCAATATTCTCAACTATGTTTTGGAATAAATGTC	20892	A_95_P020046	TA17922_4097
21571	254	66	576	AGACGAGTTAGAGAGGTCTTTAGGCATTTTGATCGCCACGCTTTGGATTTATTAGACA	20905	A_95_P086520	FG153827
21576	254	71	514	GAAAACCTCTGTCAGACTGTCACCTTATGTTTTGACCACTTATACGGTGGCTAATTCTC	20915	A_95_P205467	TA18295_4097
21577	254	72	750	TCTAGCATGTCCAGCGATGAAAAATCAAGAAGGGGCAAAATATCTGCCCGTGCTCTA	20917	A_95_P199427	TA16991_4097
21579	254	74	147	GCAACCGCTTACTTTGTAGCTTGAGTTGCTTTGTACTCTTCAACATTATTACCTCAATT	20921	A_95_P141087	EB444876
21587	254	82	715	ATGCAACAACTGATCCTCTAAGCTTGCATGGAAGCTGCCCTGTTATTGAAGGTGAGA	20936	A_95_P128262	AB471927
21588	254	83	451	AATTTGATGTAATTGCTTCACTGAAGAGTTTTATGTATTTTCTACTTGAATCAGCGGC	20938	A_95_P257524	TC68991
21594	255	4	889	AACTTCCCTATATATCTTTGGGCTAGCAAAGAGGTTGAGAAGGAGGTTCCTGCCGAT	20949	A_95_P184007	TA13589_4097
21597	255	7	762	TCAGTTCTACCCAGTAGAGGTATCAGGTGCACTATTATTGGTTAGCCGATTTGCCTCA	20955	A_95_P141612	EB445287
21598	255	8	864	CAGTTGTACTTCTCCCTCTATATACTAGGAAGTAACCACATGGATTGCTCATCAATGG	20957	A_95_P206177	TA18452_4097
21601	255	11	852	TGAAGCACGGATCAAAGAGAATCTTGATGTACTGAACTGGTCTATACCTGATGATTT	20963	A_95_P226634	DW000438
21606	255	16	193	ATACAGTAACTGCTTTTGTGGTTTTACTTGCTGCAATATCAATGAATCATCTTTTCTGG	20973	A_95_P143937	EB447132
21612	255	22	286	AGGGGCAGCTGTGAGCACGTGATTTTTGCCCTATATATGAATAATTCCAAAAACTCA	20985	A_95_P109472	CV019327
21614	255	24	780	ATTGGGTCTGACCTTGTAGTGGCTGATTATTGGGGATTCCTAATTGCTGTTATTAAGA	20989	A_95_P125117	DW004932
21615	255	25	486	AGCTAAGAAACGTTGAAGGATTTGATTTGCCCCAAAAAATTTGGGTGCTGCTTGACA	20991	A_95_P250532	EB438743
21616	255	26	694	TTGCACAGTTAAAGGATTTTCTGTGGATGTACTCAATTATTTAATCATTGCTAGCATG	20993	A_95_P179267	TA12464_4097
21617	255	27	769	CCTGACCACTCCTAAACTGTTTAACTAGCTTTGGAGGTCCTTTACCTCTTTAAAGTTTT	20995	A_95_P116212	TA13007_4097
21619	255	29	762	CCAAATAATAATAAGGGTAACAAGTTTGGAGCGATGGGAGTAGGATTGGGTTTGGG	20999	A_95_P292568	EB427708
21622	255	32	241	GCTAGCCTGCTACTATTAAAGCATGTTTGATCTATTGACTCTCTTATGGTGTTTTTATG	21005	A_95_P143112	EB446457
21632	255	42	452	GGTGTAGCAATGAGGTCCTTGAATGTGGAGAAAAGATGGATATTTCCTCTAATTATA	21025	A_95_P069495	BP137401
21633	255	43	162	CGTCCTTCCTCTCTCCTTCCTGTATTACTTCTCCATATATTTAGGGGATGTTAGGTCTG	21027	A_95_P175112	TA15543_4097
21639	255	49	532	GTAGGTCAATAGGGAAGTACATTAGTAAGTTTGTATTTGGTTGAAGCTTATGTCGAT	21038	A_95_P297673	FG639066
21640	255	50	1109	ATGTGTCCGTTTATGGGTCATCGAAAGTTGTGGGAACACAAGCTCCAGTTCAATTGG	21040	A_95_P015166	TA14363_4097
21641	255	51	341	AACTCAGTCTTTTCTTTTAGAACTCAGGTTTTAGTGTGACAATGTGATGTTTGGCAGG	21042	A_95_P055866	BP133813
21656	255	66	1760	CTGGCTTGCTTATGGTTATGTTTATTAGTTAATGTGGTTCATTTGTTTTCGTAGTGCAC	21071	A_95_P182082	TA13128_4097
21660	255	70	229	AGTGCAGATCTTTGATGAAGTAAGAATGGAAATTTTTGGAAGTGTCTTGGAAATGCA	21078	A_95_P030416	EB446468

21664	255	74	739	AGGAGGCATGGTTCTTACAGCAGGACTTCTATTTACCAGTCAAAGGAAAAGCCATAG	21086	A_95_P195927	TA16224_4097
21665	255	75	790	AGTGTTTTTTCTGCTGTTCGTCCTTTCGATAAAATGATGGGTACCATGGAGGTCATAA	21088	A_95_P254854	EH616823
21666	255	76	810	CTTTGCCTAACTGGAAGAGGATTGTAATGTCTTGTTTTTCTGGCATTAATAATTTTTCC	21090	A_95_P206097	EB448302
21667	255	77	267	GTTATAGCTGGTTATGGACCTGTTCACACGAGTGGACGATGGTTCAATGACATGGTT	21092	A_95_P113057	CV020985
21669	255	79	1092	CAGTACGGCATTGTGAAGTTACAATACTGGAAATACATTAATATTTGATGGGAAATA	21096	A_95_P190557	TA15041_4097
21671	255	81	382	GGGGGTAGTGATTGTAGATTTGTTCTTTAGTTTCTGATGTGGATTAGGGTTGGTTAG	21100	A_95_P201792	TA17498_4097
21678	256	3	107	GCTTGAAGTATGGATCAACAAGAAGATAAAAGAGGATGGAGGAGTCATTTGGGAG	20948	A_95_P091273	BP531284
21681	256	6	733	CTTCTAATTGATGAATTGTGGCTGGATGTTTAGATTTGAAATTGGTAAGCGCTTGTAT	20954	A_95_P221727	TA21881_4097
21685	256	10	868	ATTACCAAGAATTGTGCCATGTCCATCAAGCTGCATTGAATGCTCAACCAGCATTAGT	20962	A_95_P249047	DV161159
21689	256	14	317	TGGAGTTGCAGCGTTACATTTGAGCTCAATTGAGAGCAGTTTAATAGTAATCCTTGTT	20970	A_95_P089638	BP530582
21690	256	15	315	AGGGGTGTTCATCGATTGGTCTAGTACAGTTTTGAAAGATTTTGGTTGTGTATTTTCA	20972	A_95_P098838	BP534665
21697	256	22	915	TATTACTGTCTCTGCATGGTTTTGACATTTTAAAGGAACAGACGTACTAGTTCTAGCT	20986	A_95_P015466	TA14626_4097
21700	256	25	242	TGAAGGGCGGAAGTCCTAATAAAGGTACTCCTGGGGTTATGCATGGGAAGCATAAG	20992	A_95_P208792	TA19047_4097
21701	256	26	458	TGTGAAATTGACCTAATTGCTCGTGAACTCCCAGCAATAGTAAAGTGACCTTTTAACA	20994	A_95_P285968	FG644264
21703	256	28	153	TAAGTTTTGGTTGAAGTACCCGTTATGGTTTACTGTGGTTCCTGCTACTGTCCTCGTTT	20998	A_95_P154602	EG649665
21711	256	36	447	TGCTGAATTTCTTAGCTATGGACCTCAAAAGGAAGAGAGTGTCACTGGAAAACCTTT	21014	A_95_P264196	BP526620
21712	256	37	440	TCCTAATATGATATTTGTATGACAGGAAGCTGATTTGGGCTGTCACACGAACTTATCA	21016	A_95_P113657	CV021242
21718	256	43	853	TGGAAATATGTGCTAGATTTGCTGATGTATCATCGCTGATAATGGGGAGTAGCTGAC	21028	A_95_P237074	FG157342
21719	256	44	875	CCTCTAGCATACTGTTACGTGAATCACTCCAATAATCATTTGTACTGAAATACTGAAC	21030	A_95_P230144	DV158504
21722	256	47	738	AGAAAAGGCTTATATACTTGATGAGAGCATTGGCAACTTGAGCTTCCAGATAACTCG	21035	A_95_P236069	EB450465
21723	256	48	313	TTATGTTCCCATGGGTTGACAAGGCAGTTGATTCTGTGTTGGAAGAAACAAACATCC	21037	A_95_P070030	FG643216
21724	256	49	330	ACCCTATAGGCATGGTCTCTAAGTGATGTGGAATCAGAAACATTGAACCAATCCAAT	21039	A_95_P041601	BP130133
21731	256	56	873	CTGTTATCCTGCATCATAGGGTTCTAAGATTAGATTTTCACCAAATCTTTATGTTGTCG	21052	A_95_P024316	EB679979
21734	256	59	703	TCCTTAAAAATTGTTTGCTTCACCAGTTTCAGTTAGATTCTGTGTTCTCTCAAGGATGA	21058	A_95_P015031	TA12059_4097
21738	256	63	683	TCGGAAAGGGGAGGAGAAAACACTTTTGTTGTGATCACAAATGATTATTAGATATCA	21066	A_95_P116127	TA13214_4097
21739	256	64	285	CGTCAATCGTTGCATTTGTTTAATGATTATTGATTGTTGTCAAGTGAACTTAGCAAGC	21068	A_95_P070370	BP192615
21741	256	66	595	ATTCACCTACAAGCCACACCAGTAGTGTTTTGGGAGGAAATGATTCTGGGACTAATT	21072	A_95_P129162	FG164011
21745	256	70	833	TTTCATTGTCGTATTCTGATCGGATTTGAGACCGTCTTTATACTGAGTTTTGTTTGGAT	21079	A_95_P244618	DV162568
21748	256	73	442	ATTACATGTCTTGCTGGTCAGATATCCAGTGCCCATTTGTTTTTCAGAGGTCCTAATG	21085	A_95_P004911	EH665273
21751	256	76	267	GACGGTTTCTGTTGATGGATATCATGCATTTTAGCTATTCTGAGAAAACTGATGTAAA	21091	A_95_P135557	EB439050
21756	256	81	781	AACATGTGTTGATGATTCCAGCTCACTTGTTATAATTATCAATTCCTCTCTCTCTCCCTC	21101	A_95_P013596	TA12260_4097
21759	256	84	792	GCATAATCTTGGGGAAGTTGATTCTGCGATACCTGAACTTTCAGTTTAGGGTTTGAT	21107	A_95_P116012	DV158506
21761	257	1	518	GGTTTTCTTCACCATCGATTCTATTTTCCGTTCGCGGTTCGTCACATTTTTTGAGTTCA	21110	A_95_P240623	AM786200
21764	257	4	793	CCCACATCCTAGACAGTGTTATATGATAGCCAAATACACCTTACAAGTCATATAATAA	21116	A_95_P125017	DW004809

21766	257	6	666	TAATGCTGGTCAAGCCGCCTTTGATCAAGCTCTAGCATTAAGCAAAGTGTTGCAGTT	21120	A_95_P063410	BP135774
21767	257	7	464	AGTTATAGAAACCGAAAGAGAGAGTCCTTCAGATTACAGCGTGAACGCAGAAAGGC	21122	A_95_P103432	TA13935_4097
21769	257	9	817	AATGTTTCTGATGGCCTTTAATGTAAATTTCTTGCCCTCATGCCATACCCTCTGTAGTT	21126	A_95_P003446	TA14616_4097
21770	257	10	901	TTCCGCGAGACAGTAGCCATGCATCCCTTTACGGCTATATCTCCTTATGTTATGATGC	21128	A_95_P118717	DV161781
21772	257	12	821	CATTGAGATATCTGAGGAATGTCGCCACTTAATGTCAGGGATTTTTGTCGCAAATCCT	21132	A_95_P149397	EB679234
21775	257	15	422	GTATGAAAGGAAGCTGATTTGGGCTGTAACACGAACTTATCAATATATATCTCCTCTT	1861	A_95_P000051	FG625247
21785	257	25	638	TCGGCGTGCGTAACAATATGTATAGCCTTTTTGATGACTTGTTAATGGTCATTACTTT	21156	A_95_P215747	EB678865
21789	257	29	599	GAACCTTTGGAAGGTCCTATAATGTGTGTCTTATCTGAAGCTGCGAATCCTGTTCTCT	21164	A_95_P038016	BP129158
21790	257	30	466	CTGTAGAACCATAAAGATAATTAGCATGAACCGCATCCAGTATAAATTCTGGATTCTG	21166	A_95_P030736	EB437660
21792	257	32	334	TATCTGCCTTTACAATCACTGCTTCCAAGGATGGAAGACTTGAAGATCTCATCAGCGT	21169	A_95_P084955	BP529156
21800	257	40	195	GGCGTCCATGTCTATACTGGCTAAATGATTTTACCTTCACTTAATATGTAAAGTAGTA	21185	A_95_P108082	CV018662
21803	257	43	1104	GAACAATTTACAAGATTGTAGTGCATGTATTCCAAATTCAACAAAGCACTTTTCCCCC	21191	A_95_P011701	TA13554_4097
21804	257	44	832	TATAATCACTGGTAGTGACCCTAAGAACACACCTTGGTCATATCATAACGGGGTTCTT	21193	A_95_P164947	DV161952
21811	257	51	1037	GTTATCAGATGTAGCTTCCGAAGAAACTTCTTGCTAGAAAATGAATGATTGGTTTGAT	21207	A_95_P191552	TA15262_4097
21813	257	53	358	TCTGGGCTTCCTCTTTTCATGGACCGCCTTTAATGAAGTACTGGGTTACGATTGTTAA	21211	A_95_P112212	CV020575
21815	257	55	504	CCTAGCACAGATTTTCAGTAAAATAGAGGTTGCGTATCAGGAGGCTGTCTGGAAGA	21215	A_95_P065855	BP136441
21816	257	56	856	TCTCCTGGTTGTCATCACTTGTTGAAGATAAGTTCTTGGTTAAATCTTGTGTTACCGA	21217	A_95_P189262	AJ966358
21818	257	58	111	GAATTACACTAGGCTTGTATTGTTGTTGTTGTTGTACTAATTGCCAACAAAACTG	21221	A_95_P043466	BP130622
21819	257	59	979	CTCAGATGTCTAAATGGCTCCAGTCTGAAATATTGATTTATTAATAATGTGCAGCAAT	21223	A_95_P189887	TA14884_4097
21820	257	60	894	GCCACATAATGCACCAATAAGCTCATTCTCTTATGCTCTGGCCAGTATGCTCTCTTATG	21224	A_95_P244177	EB439523
21826	257	66	569	TAGGGCCCGTTGAGGGTTTTCTTTCCTTTGTTGTTTTAATATAAATTCTTGTCTTGACC	21236	A_95_P130632	TA18908_4097
21831	257	71	1235	ATGCTATAGGTGGTTCAGGTGCTTTCTTGTGTATAAATAGCAAAATTGCATTCACGAA	21245	A_95_P022041	TA18579_4097
21833	257	73	557	ATCGGAATCCGGCGGAGGTAAAAAAGGAGAGTATCTTAAAATGGCTGGAGATTTCT	21249	A_95_P023986	FG150164
21834	257	74	396	TTTCCCCTTGTTATATCTTGTATGTTTCAGTCGGTGTAAATAGGGACCTTTGATGTATA	21251	A_95_P307018	FG637133
21838	257	78	731	AGTATTCAAAGAGTTCGTCTCATTTAGTGGACGCGGGTCACATTGAGGATGAGAAGT	21259	A_95_P138822	EB442559
21841	257	81	708	AGGGACAGTAGTGGTGAGGATAATCATGATAATGGTATATCATTAGCTGGTCGTCTC	21265	A_95_P146227	EB450216
21844	257	84	762	GTTGCTATAGTTTGCAATAATGAGGAGCATCTTGTTGGTCGAATGCTGATACAATTGT	21271	A_95_P191217	TA15182_4097
21847	258	2	1609	AGTAGCCTTGCACTGCACATCGTTCCTGTGTACAGCATCCGTTTCTTTTATTCATGTGT	21113	A_95_P200497	TA17220_4097
21855	258	10	774	ATCCAACAACTGGGAAATCAAAAGGGTATGCTTTGTTTCTGTATAAAACGGTTGAGG	21129	A_95_P294438	EB441195
21857	258	12	868	CCCCACCGGCTGGATCATCTGCTGGAAAATTGAAGGTTTCCTTTGGTTTGTTTGTTGT	21133	A_95_P193887	EB425031
21861	258	16	710	GCTGCCTAGTTGCTAGATCAATTCATGTCAGTTTCTAGAACCTTTACTGTAGTTAATAT	21139	A_95_P142032	EB445607
21865	258	20	318	AGGCTATATATATGAGGTAAGTCTTATGTGCTAGAAAAAATGGGGATGAGATCTTCA	21147	A_95_P024587	TA19326_4097
21866	258	21	179	CTGACAAGGCTTAAGACAATTTGCTTCTTGCATTTTATCTTGTTATTCTGTCCTGTTCA	21149	A_95_P142902	EB446296
21868	258	23	401	CGTATTTCAATGTCTTCATTACATTGGTTGTAAGTCGCTTGGATTCTAATGTTCACTTC	21153	A_95_P201582	TA17456_4097

21869	258	24	885	GAGTTTTTGTGTTGACCTTGAATATCCTACTTATAGTGACTTGTTAATGTCTGAGCTC	21155	A_95_P186107	TA14055_4097
21879	258	34	1198	GACAGTTAGAACATGAATGCAGAGATAGTTGTTTTGGCAACAAAGTTTGTTGTACTA	21174	A_95_P206512	TA18534_4097
21881	258	36	776	TTTATTTGGCTATTCCGGCTTGTTTCAAGTTTAGGGACGTGCTTTATATCATATATCCA	21178	A_95_P138272	FG169948
21882	258	37	746	TGATCTTACTGATTATCTCATGAAGATTCTCACTGAGAGAGGTTATATGTTTACCACA	21180	A_95_P138662	FG147028
21884	258	39	701	CTCAGAGTATATGTGTAGAACAAGCACAGCTGCAAATTGTTATTACTAATTTTATGGT	21184	A_95_P202697	DW000495
21887	258	42	330	ATGCCGCACGTGGTACCTTCATACAAGTTTTAGTCTTTTTTGTATCTTAAATGGTTTCT	21190	A_95_P089143	BP530366
21891	258	46	660	CAAATCTATTGATTTTGATTGCTGTTGTTCACAGATCATCCCTTATAATATTGTTGCCG	21198	A_95_P164272	EH623414
21893	258	48	518	TATATAAGAGGAGGAGTGGACCCGAATCAGCCCATCGGGGTTATTTCTCTGAATCA	21202	A_95_P307458	FG638464
21894	258	49	1730	ATGGATGGAAGCTGAACTATACATTGCAATTGGGACTTATACCCTCCCTGTGTTTGCC	21204	A_95_P008786	TA11833_4097
21895	258	50	849	AACTGCTGATGACGCAAGAGAATATGGACATACTCATCTGTCTGAGATCATCAATTT	21206	A_95_P120292	DW000074
21899	258	54	552	AGAGGCAGATCCAGAATGTACACTTTGATGAGTTCAATCTTTAAATTTTTTGCGTTGA	21214	A_95_P286283	FG641422
21903	258	58	1278	CGTTAAGCAAAGGTTGATTTCACTACCTATGGTTTGCAATGGTGTTTTTAACAATGTT	21222	A_95_P008886	TA12158_4097
21907	258	62	7	CCAAACAAATGTAGTGGTTTCGGTCAATTTGTTGTAACCTTTCTGATAGTATGTTATA	21229	A_95_P288873	BP534554
21910	258	65	463	ATTTCCTTCTTAGCTTCTGATGTTGATGGGAATGTGCCCTTCTTCTGGGGTACTGATT	21235	A_95_P147047	TA13199_4097
21912	258	67	754	TAAACAAGTACTTCGTTCCGTCCATATTAACCAAATTCCATTGGCTTAGGTATCTTCTT	21239	A_95_P015566	TA18776_4097
21913	258	68	430	GAGCAGGCCATGAAGAGAGATGTCAGGATGAAATACTTTCTGTAAACTACTTTTTTG	14301	A_95_P000096	EH619820
21915	258	70	526	GTCTGTAGTAACCTTGCTTGGTTCAAATTCAAAGTGTAATCGGTTTCAAGGCAAAATT	21244	A_95_P127977	EB427561
21916	258	71	663	GCATTGAATATGTCTGATGCTGTGATCTGGTGCTGATATGTCTGTAACCCTGATTTGG	21246	A_95_P164992	EH624455
21917	258	72	844	GATGGGAGAGTCTTCTCCTGATGAGATGAGTTTGTACTCCAAGTATGAAAAGGAGG	21248	A_95_P128927	EB428697
21918	258	73	737	GAAAATGAATGTATGATACATTGATACTTCCATTGTCTTGCTAGACATTGTCATTGCA	21250	A_95_P283758	FG636470
21920	258	75	196	GCCGTTCAAGTGTATGGTATAATTTATTGGCTCTTTTGGTTTGGCATTTGTGGTTAAT	21254	A_95_P111277	CV020132
21922	258	77	876	AATCTATAATAGCTGACGGTGTAAGCATCATGTATCCTATCTTGTGAGTTGTGACAGT	21258	A_95_P232644	DW000398
21938	259	8	790	CTCTAGACGTTTAAATCGGATGTCAGTGAGATTTACTGCATGTTTGATCTGAGATATT	21289	A_95_P017156	EB437962
21942	259	12	443	GCTGATTTGGGCCGTAACACGAACTTATCAGTATATATCTCCTCTATATAATTATGTGT	21297	A_95_P114077	CV021432
21947	259	17	493	CAAATGTATATAGGATGTAATTGAACTGTTTATATGTTTTCTTCGGCCTTTTGGCGAG	21307	A_95_P028266	BP134638
21950	259	20	480	TATGGTTCAAGCAGGTACAATGTATTTAATTTGCCTGGACAGATGGAACAATATTTG	21313	A_95_P207607	TA18777_4097
21954	259	24	753	ATCAATCCCCTGAACTCGATCAGAAATTCCCGTTGTCAGTGGACCCTTCTTTTGAAGG	17966	A_95_P000116	FG157904
21955	259	25	493	CTTCATGGTGAAATGTGCTGCAACTTTCGATGTTGTAATATCAAGTATAGTTGAATGT	21322	A_95_P140697	FG633777
21957	259	27	566	TGAGGGCACATTTTGAACGTGTGGTTAATCAAAAGATGCTGAAACACTATACATGTT	21326	A_95_P040041	BP129717
21959	259	29	518	GTTCACTTTTCTAGTCAGCGTAAGCAGTAGGATTCTCTCGACGTTTATCTGTTAACGTT	21330	A_95_P089173	BP530375
21960	259	30	1172	CACCAATTCCCATCCCATATGTTGTAAGGCATTTTAATTACCTTTTCTTCATCATTTGA	21332	A_95_P000631	AY695055
21961	259	31	826	AGTAAAGGAGACCATCCATTCAGTAGTCCATGGACTACTCGCAACTCTATCCCCTAG	21334	A_95_P246197	EB452191
21963	259	33	535	GCTAAGTGATAACAGGATGTATAGATTTCGACACCTGCTGGGTTTGGTACTCTTCCCT	21338	A_95_P035703	BP128542
21964	259	34	505	TCTCGCTTTCTGTGGGTAGTTAATTTTTATGACAAGCCGTTGTTTTCTTTCATTGTTGA	21340	A_95_P021046	TA14086_4097

21965	259	35	767	TAGCAGTATTAGTGCTTCTGCTTAAATGTGAGACAGCAGCATATGTTGGAATATTAT	21342	A_95_P225172	EB447150
21968	259	38	433	GACCTCAACAATGTCAGGGATGTATCCTATCGAGAGGTATTGGGACACTTCAAATCC	21348	A_95_P087983	BP529932
21977	259	47	573	TGACTTGAAGCCTGAGAACATTCTTCTCAACTCCTCAGAATATGTAAAGGTTCCTGAC	21365	A_95_P137427	FG152454
21978	259	48	714	TGGTCTTGGTGGGTCCATCTTTGCACTTTTGGTACCTCTACTTGAGTAGATTGGTCAC	21367	A_95_P146522	EB450582
21981	259	51	850	AAATTCATGTAATATTTTGCACTTTGGCTGACATATGCCCAGCGACTTTGCCTTCAAA	21373	A_95_P258776	TA12268_4097
21983	259	53	253	TGCACTGCCAGTGTAACCCTTGCACTTGTATCTAAGTGCACAAATTAAATCTTAATAA	21377	A_95_P114217	CV021496
21984	259	54	218	AACAGGTTCCACGCTTCAGGATGAGGTGAACTTTGTAAATTGTTGTAGTATTATATG	21379	A_95_P068825	BP137224
21989	259	59	303	AGCTGATGATCTCCGGATAAACCTTTGGAACGGGACAAATAAGCTAACCGAAGGTTT	21389	A_95_P040266	BP129782
21991	259	61	728	GAAGTCCATTTGTATCCAGTTTTCTACATCAGACCCAATGTGCTCCGACCCTTCTCTGA	21393	A_95_P296398	EB451916
21994	259	64	885	GAAGTTGGTGCAGCCGGAGGCTGTTGACCGTTCAAGTAAGTTTTTCAAATTTCAAGT	21399	A_95_P116597	DV159351
21995	259	65	504	CACATTAGAGTGTAATTACAACGGAGAGTCAAGATAGCTCTATTCATTTTAAGGAAG	21401	A_95_P084165	BP528947
21996	259	66	1356	GATTGGTGGGGCGATGTAAAAGTAATCAACTGGTTGTTGTAAAGTGTAATGTAATTT	21403	A_95_P210397	TA19388_4097
21997	259	67	213	CGATTTTAAGAGTATTTACCTGGGCTCCAGAGAATAAAGGTTAGGCCAATTGATTTT	21405	A_95_P098283	BP534400
21999	259	69	531	CTGCGCTAACAGAGCGCATAGTTATTGTTGGTGTTAGAGATGATTCAAACTTATTGT	21409	A_95_P231999	BP128651
22000	259	70	559	AAAGAGGGCGATTGAGCTCTGCTGATTTTGTTATACTTATCTAGGTATATTGATTGTT	21411	A_95_P153537	EB683786
22007	259	77	1345	GTTTTAAGTTTTTATTTGTTTCCTGTTAAAAAGTGTTGTGATGGAAAGGGATGTGTCC	21425	A_95_P202342	TA17613_4097
22008	259	78	856	TTTTGCTCCATTTGGTTCTGGTTATGGAATGGGTCTTAATTTTGAACCAGGGTTAAGC	21427	A_95_P243607	DV161884
22010	259	80	352	GAAGAAACAGGTCTGGGAGAATATTATTGGTTTGTTCGCGGAACAAATTTAATGGA	21431	A_95_P081930	BP528387
22011	259	81	1845	AGGGGAGGGGTAATGAATAGGAGCTTAATCTGTTCATGGATGTATTTGTTTTCTTTC	21433	A_95_P005151	X61146
22012	259	82	640	CATTCGACTTTCTAGTTTTAATTCTATGAAAAGACCAGACTTCTTACGACTGTTTGGA	21435	A_95_P042466	BP130367
22018	260	3	141	AAGTGAAGCTTATTACACCAGAGGGCAGCTGTTGAGTTTGATTGTCCAGGCATGCAT	21280	A_95_P103717	CV016659
22021	260	6	712	GGGTGAGTTTTGAGTGTTCGAATGTGTACCTTTTCTTCTTTGCATCATCCATAAGTCT	21286	A_95_P149492	EB679361
22024	260	9	431	TGTTGCTTACTATATTCTTGCCACTTCAAGTAATGGATATGATCCTAAGTACTTAGGTT	21292	A_95_P107572	DV999315
22025	260	10	899	TGATCCTAATGGCATGGGGGATTTACTTGGAGTACTTCAACTGTTTTCCTTGGTTACC	21294	A_95_P205322	EB679843
22026	260	11	780	GATTGCAATTGGACAGGCACCTGAGCAAGAACTTGAATCTTTCAACAACTGTTCCAA	21296	A_95_P225272	EB444939
22029	260	14	668	TCCCCGTATACAAACAAGTCTTTTGTCTTCTTTGTCATGTGTCATTTATCTATGAGAAT	21302	A_95_P159117	EH617071
22033	260	18	1060	GTTGAGCTGCCTACGTTCTTTGCAAAATAATGAACTGCATACCAATTTTTCTAGTAAA	21310	A_95_P016516	TA15214_4097
22034	260	19	738	GGCATTTTCGCTGCCTTGTCTTTATTTTCCTGTGCTTCTGATTATTCAGTTTATGTCCA	21312	A_95_P159327	EH617408
22042	260	27	832	CATCTTGTTTATAATCTGTATCACATAAATTAAACCCCCCAGTTTCATGCTGCTCGTTA	21327	A_95_P135602	EB439109
22043	260	28	393	AGACAAAGTTGTGGCTTCCGGTGCAAAAAGAAAGCGCAGGGAAAACAGAAATGCT	21329	A_95_P071720	BP525776
22044	260	29	784	GCATATCTGCTTGTACAGTTGCTGCAATACTATTTTGTTTCTGAATTTGGACAAAGTG	21331	A_95_P011686	EB426714
22045	260	30	0	GCGATAACAATTTTCATTTGCCTTGTATGGATGTGCAGTGTGTCAACTGGTTTTTCAC	21333	A_95_P011766	A_95_P011766
22048	260	33	123	CAGGCATCTGTGTGTTCTTGTTTATCTATGGATCATCCTTTTGGCATTTTAATAAAGTC	21339	A_95_P140892	EB444693
22054	260	39	198	GGTCTGTTCCTACTTTGATTACTATTACTTGCCATACTTTAGCCGATTAAATGAATGCA	21350	A_95_P141942	EB445545

22055	260	40	81	AGCGGTTTTTCGGTATGTTAATTATAATGTGGCTTTTTGGTCATTTTCGTCTGACATG	21352	A_95_P286313	CV018987
22057	260	42	685	TTTGGGATCAAAGGGGGTTCTGATTACATTGGTAGGGGTCCTCATGTTGATGAATAA	21356	A_95_P157882	EH615909
22058	260	43	1153	CAGGGCAGGACAGCTAGGATTTGCCTTACTGCTGGGCAAAATAATTTTTGTAATTAG	21358	A_95_P021896	TA16466_4097
22062	260	47	388	TAGCAGAAGCTCGTGGCAAGAAGGCAAGTCAACAGACGAGATGATCAATGGAAGT	21366	A_95_P142007	EB445591
22063	260	48	479	AAGCTGCCCTCTATAGCTGTATCATAGTGTTTTAGAGATCACTAATAGGTTAATGACA	21368	A_95_P198807	BP530158
22065	260	50	407	ACAATACTATCCAAGTGTGGCAGATGGCTGAGAGCATCTACCATGATGACGATGAC	21372	A_95_P034234	EB684021
22066	260	51	288	TTACAGTGATGCAAGATGATGTTTCCGACAATCCTCTCATCCAAGTTTGTGAATCGTT	21374	A_95_P078500	BP527531
22070	260	55	716	AAATAGCAGAGATGAATCAGGTATTGGTGGCTATGCACAAAGGTAATCTGTCCAAG	21382	A_95_P146302	EB439249
22076	260	61	1243	ATTCTTAGAACACTGTACACGTTCAAGAATGGAACATGGAGCTTACTCTAAAATCAC	21394	A_95_P192217	EB643449
22077	260	62	618	AAATTCAGAGTCGGAATGAACTGCACCGTGAAAGTCGACGTGAAAATCGAGATTAT	21396	A_95_P153622	DW002335
22087	260	72	793	GTGTGGTACCTGCAGATTTGATGGAAGAGTGATTATGAAATTGAAAATCTAGAGTG	21416	A_95_P196287	TA16307_4097
22089	260	74	499	CCATGGAGCTCACGCTGGATAACATAAACAAGGGAATTCTAGGACCTGATTTTATGG	21420	A_95_P160927	EH619619
22090	260	75	382	TGGACCTTGATTTATACCTGTTGGATGGAATTGTGATAATGTTTATTTTTAGAACCTG	21422	A_95_P006616	FS422353
22094	260	79	964	TGATAAGCCCGTACAAGAACATGCTCCTACCAAGAGCCTATCTATCGATCAATCATTC	21430	A_95_P141632	TA17597_4097
22101	261	1	774	GTATAGGCTATCTGGTGATTACAATCCATTGCATTCAGATCCAACGGTTGCAGGAAT	21443	A_95_P292853	EB428754
22109	261	9	449	TGTGCTAACAGTTGTTCACTGCAAATTTCATGTCTTTTACACCGAATGTTTCTCTTTGT	21458	A_95_P037028	BP128892
22113	261	13	207	TTCTGGTTGTGAATTTCAACTGTGGGCCACGGACTGTGGCAGACTGGTAATGAATAT	21466	A_95_P003856	EB443145
22114	261	14	681	ACATAGCTGGTCTGTGGGGTTATGGTTGGTCGATTCGATTAATTGATCAGCAACTTT	21467	A_95_P262641	FG636378
22124	261	24	340	TGCTTTAAGTTTTGCATCATCTCGCTTTGGTTTTGAACTGTGAAGGATTTCAGCCACA	21487	A_95_P181002	TA12875_4097
22126	261	26	781	TTTCTCTTTCTGCTGAGGCGCAGCTTCAGGGGTCTCTTGTTAAACTTTCAGCTTTCTTA	21491	A_95_P135087	EB438311
22127	261	27	634	CAATTTTCTGATATTGGTGTCTTTTGTTATCTGACGTTGTGTCCTCTTTTGTTTGACTG	21493	A_95_P025756	EH618496
22131	261	31	957	CAAGAAGAACTCTGAAAATAGTCGCAGTGTATGTAGCTCTGTATGTATATGATAAAG	21501	A_95_P025836	TC52442
22132	261	32	763	TCCGTTGCCTCCTTGCTGACCTTGGATGATGCAATTCATAATTCAAGCTTGTTGTCTGT	21503	A_95_P137942	EB441669
22136	261	36	218	AAGGACCAAAATGATGTGCATGAACTGTGGGAAGCTTGTCGGGTATGTGTATGATG	21511	A_95_P194977	TA16019_4097
22137	261	37	220	TTGGTACCGGATTCAAGGGATTAGTGCACCCTTCAAAACAACATAACAACATTCCTTT	21513	A_95_P131122	EB431250
22138	261	38	969	CCAAAGAACAGAATAACTGTGGTGACTATACCCTTTCTCTTCTTGTATGGTTTTAACT	21515	A_95_P195227	TA16069_4097
22140	261	40	150	GCTTGAGCCCCGTAGGGTCATGGGGCTTTGTTATAATGGAGATATAGAAGTTTAAAT	21519	A_95_P093048	BP532122
22143	261	43	1076	CAGCATGCTGCAACTTCATGTATTATCATTTTGTTCCCAAAAGTTCGTTTGAGAAGTA	21525	A_95_P220632	TA21649_4097
22144	261	44	438	GAAATGCATTTCTTTTTGCATCTTGAACTTTTGCAAAGGTGTCCTTTTTATGGCCTCTT	21527	A_95_P028726	EB435748
22145	261	45	857	AGCCATTTGGAACCAATTACTACTATGTTAAGACTTGTATATTCCCGCAGTATGAACA	21529	A_95_P225022	EB426727
22147	261	47	537	CACGACTCACATCCAAGTTTTGGTGTTGTATGGCCACTAATCTTGGCAAATATATTGC	21533	A_95_P129732	EB429696
22149	261	49	799	GCGTCTTCAGCAAGGCGATGTATCTTTATAGATTCTACTTTTATAGAAGTTTATGGCA	21537	A_95_P009451	TA13632_4097
22151	261	51	753	GCTACGAAAGGTGTCTACTTATTTTGCTGTGGAAACTATAGTTGAATAAACTAGTTTG	21541	A_95_P179462	EB439805
22153	261	53	642	CTCACATGTTCATTGGCTATGTAACTTGAAGAGAAACATTATTTTTAGGGGTGCCAAT	21544	A_95_P266026	FG636756

22154	261	54	866	TGCTATGTTTGGTATGTACGAAGCACTAAAGCAGTACTTTGCAGGAGGCACAGACAC	21546	A_95_P245097	DW000396
22157	261	57	2289	TGTGGTTGAGTTTTATGTGTTGTGTTTTTGGACGTTAAGTTTTACTGCTGTAGGGTATT	21552	A_95_P258556	TA11872_4097
22158	261	58	827	ATCAAGGTCCAGATCACCAGCACCATCTCGCCCAAAACATTTGAGTAAAAGTCCAAAA	21554	A_95_P148342	EB677623
22163	261	63	845	TCCAATTTGCCTGGCTTGTTTGGTTCTGCGTTCAAAGTTGGTATTGATTCACAATTATC	21564	A_95_P000581	TA12317_4097
22167	261	67	80	TAGATTAATACACGATCTGTACAAGAGACAGTTGCTTCTTAACCGTAAAATACTTGCA	21572	A_95_P079330	AM793637
22170	261	70	881	CTTGTTTGAGAGTTACAAAGTGGTCACTGGGCGTATATTCTCAAAATACTATCTTTCT	21578	A_95_P214337	EB680047
22171	261	71	769	CAAGTTAGAGATTCTCATGCTGACCTATTGAGGCTGTCTTCCGTCTTTTATTCTCTTTTA	21580	A_95_P140762	EB444603
22173	261	73	589	CTTGCGAGTATGCAAACTTCTTGGTGGTGGTTACTGTGTTCAATGTTTTCTAATAACTT	21584	A_95_P188952	TA14687_4097
22174	261	74	773	ATTTCACCTCCTTGAACATTAGCCAAGTGCTTCTACATGTTGAGACTTGTGGCATTTTT	21586	A_95_P263321	EB678453
22181	261	81	670	TCTTTCCAATGAGTGGGTTGACTCCTATGTCCTCCTCTGAATTCAAGCCTTTTTCCTTTT	21600	A_95_P164397	EH623635
22183	261	83	271	TTTCAAACCCAGAAACTGAGATGATTATGCCAACGTTAACGACGTCGTTTCAGACCC	21604	A_95_P004286	EB450495
22186	262	1	477	AAATTGTTGGCGGCTTTATTTCCCTTTTCTTTTATGACATGAACTGAACACCTGGTTGC	21444	A_95_P185372	FG632147
22190	262	5	825	ATGTATTAAGTTCAACATTTCCCCATCTAAGTTCCTCAATTGCCAAAGTCCAGTCACCT	21452	A_95_P218462	TA21179_4097
22193	262	8	1139	CTTTGCTTTTACATCTGAAGGACGTCGTTCAGTGATATATTAGTTATAACTTATGAGCT	21457	A_95_P011441	AB281271
22196	262	11	885	GGGACTAGATATTGAAACAATCCAACAACACTATACTGTCTAAAGAAGCTGCAAATCA	21463	A_95_P292633	EB427846
22197	262	12	1543	GGAACCTTATAAGCCTTTTGTAGGGTTGGCCAAGAAAGTTATGTTATTTGTATTCTTG	21465	A_95_P237544	D79979
22200	262	15	792	TTCAGATGAGAGAGACTCAGCTGGCTTTGATCCAAGATTTCTTGCTGGTGATCAGTCT	21470	A_95_P270201	FG139295
22202	262	17	845	CATGGGAGCATTTTTGTGGCCCCATCATTTATATATGAAAGTAATACTTTTGTGATGC	21474	A_95_P149747	EB679700
22203	262	18	874	GTTGAGAAGCAAGTTGCACTGAGCCATAGTTCTGTAGTGTTAAGATAATTTCTTCACC	21476	A_95_P221067	TA21743_4097
22204	262	19	573	CACCTCACATATTCCAAAGTACATGGATGACACCTCTAAACATTGTATCTTCCAATTTA	21478	A_95_P046586	BP131437
22205	262	20	1348	GCAGTTTTCTCAAACTGAGTGTCTTTGTGACTTCTTGTTGTTGTAACACGTCCGTTTTT	21480	A_95_P198592	TA16812_4097
22206	262	21	861	GTATATGAAGTCTGTTCTTTTTCTGCTCTCTTGTTCCGATTTATGATCTTGTAACTCGGA	21482	A_95_P253619	EB424993
22208	262	23	1801	TGGGTTTCGACCCATTAGAAGTTGTCTTGTATTTTTCTCTAAACCTATGGACTATCTTC	21486	A_95_P028071	TA14479_4097
22210	262	25	370	AGGCGGAGAAAAGAAGAAATGAAACCTGTATCCTCAGTTGATGATTGAAGAACCCAA	21490	A_95_P000826	FG643022
22212	262	27	436	TCGCTCTCAAGTTTAGTCTACAGTGTTCTATCTGTTCCATGTATAATGCTCTTAACTCAA	21494	A_95_P195352	TA16097_4097
22215	262	30	438	GGTTTCGTTCTTCTTCTGTGTTCCCGTTGGGAGTTCAATTGATTTGCGATCGAGTTGT	21500	A_95_P093213	BP532181
22217	262	32	562	CGTTAATCCACTCCCATTAGTTGCAACACTTGAAAAGCGAGAGGATTTGACATGCTGT	21504	A_95_P143667	EB446903
22223	262	38	713	AATGAGCAGGTGCACCAGATATTTTCCCAGAATGCTTTTGATTCTGTGATGCATTTTG	21516	A_95_P135052	EB438192
22224	262	39	774	TAATGTTACTTGCCTAGATATTCGATAAATTTTCCCTCTGAAGGTATTTGGCGTTGTG	21518	A_95_P010266	EB677709
22229	262	44	503	GTTTAGAAGTTTGGCCTCCTATTTCTTGAAGTCTGGTAATATGGTCCTTTTTTCTCTCT	21528	A_95_P030371	EB444420
22234	262	49	265	GTAATGGGTCTAAGCAGGTGACATTTAGTAATTCTGTATTAATTCTTACTTCTGTACC	21538	A_95_P106407	CV017890
22238	262	53	75	CTCGAGATGACATGCAGAATAAAGTCTTTCTTCAATTTCAGCTGCTCATTTTAGTTCAA	21545	A_95_P089178	BP530384
22239	262	54	681	GAGGAAAGATGGATTTTCTCATGTATATGTACTCTCATATGGAATGAAAAGTTCCAT	21547	A_95_P129172	EB425604
22243	262	58	886	GCTTAACGAGTAGGCATTGGCTGGTTGGAATTATTTTTCAGCAGAATGCCTTTGCGGA	21555	A_95_P295418	EB446037

22252	262	67	394	ATTCTGATCCAGAGTATGTTCCTATCCACTGAGTAAGTAAATAACTATCAAGAACGA	21573	A_95_P233009	BP529129
22254	262	69	422	TGACATGTTGAGTAATTTTCTTTCTCTTGCAAAGTTATTGGCTGAGAAAATGGCCGTG	21577	A_95_P234204	TA18423_4097
22257	262	72	810	GGCTCTATTGACTATATAGAGTTCATCACTGCCACCATGCATAAACACACTGAATTCT	21583	A_95_P029941	AJ549110
22258	262	73	767	AATTGGTGAATTATTTAGTGGTAGTGGACTTGCTATGCCTGTTGAAATTGTTCCTTTT	21585	A_95_P192587	EH624379
22260	262	75	498	TGCCGAGGTATTTACCTGGAGTTTATTTTCCGTTTGTTCAATCAACTACTGAAGAAAA	21589	A_95_P202717	TA17694_4097
22261	262	76	816	GTAACTATTGAAGCATAACCCTTGCAGTCCTATAATGACATTTTTTGTTTGGGATACA	21591	A_95_P010066	EB438084
22262	262	77	785	ACTGTGCTAGCCAAAGGCCTTTTGGCCAGTAGGGACCTTAATCATTTATAGTACTTTT	21593	A_95_P185877	TA14009_4097
22263	262	78	724	AAGCCAATAAAGCGGCATTGGGAAGATTTTAACTTGAGGCAGCAGGCTAATAAAGT	21595	A_95_P138442	EB442211
22266	262	81	325	ATATTGACTGTCTTGAAGGATCATAAAGTATTAATAAATGGAGCCTGGTGTTTCAAG	21601	A_95_P216577	TA20737_4097
22276	263	6	159	GCACTTGCTTGTAAGCTTTGAATTCCAAGTTTTGAACCCTAAATTGGCAATTGCTTAT	21620	A_95_P110077	CV019573
22277	263	7	781	CAAAGTAATAAGGCACAGAGTTCTTGTTTGGTTTTGTCATCAGAAGAGAGCTTTTAG	21622	A_95_P250988	DW000060
22280	263	10	836	ATGTACGCTTGTAATAAGTCCATGTTCAGTTACTGTTGACTCTTAACAATTCATGTTG	21628	A_95_P291448	EB678771
22282	263	12	735	AACAGAATAAGCAGAGACTGGAACTTGCTCGTCAGGTCATATTGGCTGAAGAAAAT	21632	A_95_P119007	DV162089
22287	263	17	618	TTGTAATTCTACTGAGGTCCTTGAAAGCAATAAACTCCTGTTGTCTCAGTACTTCAAT	21642	A_95_P022276	TA12820_4097
22290	263	20	1722	GAAGACCAAGATGTGTTGAATAAGTTTTGAGGAATGGAGGTGGTGTGCTATTGATA	21648	A_95_P176642	TA11687_4097
22292	263	22	310	GGGAGCCATTTGGCCATAATGATTTTAAGGCATTTATATTGCTAATATCTTGGAAATA	21652	A_95_P162977	EB433468
22293	263	23	747	TTTGTCTAGCGTGAAAACAAACAAGTCACCAGGATACTATGACGGCAGATACTGGA	21654	A_95_P002651	EV849919
22298	263	28	931	TGTGGAAGAGCGATTTATGGACTCAGACAAAGTTGCCCCTCCTATTCGAATAATAGT	21664	A_95_P205477	TA18297_4097
22299	263	29	531	AAAGCTGTTGCTGGATTGAATCGAACTTGATTTTTGTATGTCATCAAGAAACTCCATA	21666	A_95_P202882	TA17736_4097
22301	263	31	709	CACCATGGAAAAAGAAATTCCATGAATTAATTGTTGAATGAGGAGTTCATGACTAGC	21670	A_95_P227414	EB427201
22309	263	39	837	ATTATCACTAGACGGTGCTCTGCTAGATTGCTGTTGCCCACATGGTTTGTATCAATGC	21685	A_95_P226704	FG158801
22317	263	47	582	TTGGGTGTTCTTGAAGGGATGTTTGTATTTTGGATTTTCAATTATGTGACTTTGACCT	21701	A_95_P131957	EB432385
22321	263	51	620	AGCTCAGTTGTTTTGGTGATGTTTGTAATCCATGATGGTTGAGTAATTTTGGTTGTAT	21708	A_95_P003986	TA12776_4097
22326	263	56	565	CCCGGATCTTGAGAAAATTGAACTTGTTGATTTGTGTGCAAATAATTGAGTCTGGAT	21718	A_95_P010431	DW003182
22334	263	64	808	CTGCTTGCACCCAATTCATGTTGTTTTTCATTTAACTTCATTCTGTGGAGACCCTAAAC	21734	A_95_P125082	DW004904
22336	263	66	478	CCCCCAGATCAAAACTGAGAGAGCCTTAGTGGAGAAATGGCGGATAATGAAAAATG	21738	A_95_P087783	BP529878
22339	263	69	235	GAAAAGAATCAATGGTAGTAGGTTACTATAGCCTATAGGTGTATTTAGTTGGGAATT	21744	A_95_P155492	EG650101
22340	263	70	536	GTTGCAGGGCATCAACATAAGAAGTGCTGAGATGCAGGACACAGCTAAATCCTTTTC	21746	A_95_P282508	FG638289
22346	263	76	930	AGCGCATTTCTGTACTTTTCAATTGTTCTATGATGGGAATAAAGATGTGATTCCTGGT	21757	A_95_P184707	TA13755_4097
22359	264	4	1213	ATTTGTGGTTGAATTATGTTATCCTTTTCCAAGTAAAGCAGTTGTGGCAGTGATGTGA	21617	A_95_P014271	TA12453_4097
22364	264	9	2185	TCTTGTGCAGCTAGCAGTGTGGCCATTGTACTCTATTGTAACAATATGTTTTACGCGG	21627	A_95_P239109	AJ305044
22369	264	14	271	AGGTCCTTGTGTTGTTTGTTCTGGAGATGTACCTAATATTAGTATGTTACTATAGAAG	21637	A_95_P132042	EB432475
22371	264	16	405	TTTTGGATGAAATGGTTTTTCCGTTAACCATCTAATTTGTCTAAAGGGAGTCTTGGAG	21641	A_95_P154412	EG649582
22374	264	19	581	CTCCTTGTGTTTTGACTGCAAGCCAATTTTGTGTTTTTCTTAGTTATGGTTTTTGAACC	21647	A_95_P130502	EH622594

22378	264	23	759	GTTGGACACCATTAAACTCTGACAGCTGTCTTCTATTGGCATATAATTACAAGTATGT	21655	A_95_P011526	DV158374
22381	264	26	819	CTGTTGGGAGATATACTGCTTGACCGCTCAAATTCTGCAGTAATGACGCGTTACGTT	21661	A_95_P230294	EB678800
22384	264	29	730	ACAAGCCATCGGATGGATATCATCTGTATGATTGACTGGTCTTGTGTCTTATAATTTT	21667	A_95_P136147	EB439775
22385	264	30	806	GAGCTATTGTAAATTCTGATAAAGCAGGTTGTCAGTGGCTTCGTTCCTTTGTCCGTGC	21669	A_95_P255149	EH618915
22389	264	34	481	CCTCCGGGTGTTTCAGTAAACCAATCTAACGGGTATAGATCGCCTTACGATGGATAT	21677	A_95_P109657	DV157864
22390	264	35	618	GGAGCAAAGATGGCGCAGACAAAAAATCGGAGAATGGGATCAATTTTGTTAAATTC	21679	A_95_P102097	CN949777
22395	264	40	136	GAAAATGACGACTCCTTCAGAAAAACAAACTTATTCAAGTTCTTTTTCCCAAAGAAGT	21688	A_95_P034249	AM807789
22401	264	46	0	TCTTGTTCATCAATCGGAAATCAAGACAAAGCGGGCACTACGGTAAGACGTGAAAA	21700	A_95_P027106	A_95_P027106
22402	264	47	800	TTAGGCTTCTGGCGGAGGTTAACCGGTTAACGGAGAGACTGGTAATAGTGGAAATT	21702	A_95_P291948	EB425643
22403	264	48	445	ACAATGGGAGAGGGAAAGTATCCATATGGAAGTAGCATAGCTGTAAGTGCGGTAA	21704	A_95_P265801	AM819791
22411	264	56	847	TCTTGTAACTTTTATAAGGTGGCATCACCACTCAAGAGAGTATTATCTGGACCTTCGC	21719	A_95_P178697	EB424771
22422	264	67	266	ATATCTCATGCATTGTTGTCCGATTTAAGGGGTAAATCCATGAGATTTATCCCAGTGT	21741	A_95_P094928	BP532935
22424	264	69	824	AAGATCATCTTTGCATGCTTCAGTTGTCTTTTCTTATGGATGATCTTTGTACCCTCTTG	21745	A_95_P294968	EB677552
22427	264	72	335	CTGCTGGAGCTTGCATAAGAACATTTATATGCTAATAATATAGCCGATGGACCTTGA	21751	A_95_P110102	FS422353
22429	264	74	320	CTGTTGCAGCTTGTAATTGTAGTGTGAGTTCATATGTAATAGTTTTGCTTTTTTGGGT	21754	A_95_P129802	EB429755
22435	264	80	705	TTTGGTTTGTGTAATATACAGCTCCTGGATTTCACTTCCTCATACATGTTTAGCTTCTG	21766	A_95_P016111	TA12078_4097
22437	264	82	816	AATCGGTATCCATATGAGGACTTGTCTCAAGTTCTGGCCCAACTAGTCTCCAGTTATG	21770	A_95_P224947	EB446595
22440	264	85	847	GGCATGAGTTAGCATAGCGATAAGCTGTATTTCCTTGTATTATGCTATTAGCTTGATT	21776	A_95_P201997	EB677546
22442	265	2	911	GGTTTTTACATTATTGCCATAGTCCAAGTGTACCATTACTTGTGAGATGTATATTTGT	21779	A_95_P272581	EB451306
22443	265	3	157	ATACTATAAGATTTTAGTTTGGAGATCGGTTTCCCTCTTGATCTTACTCAGGACTCAT	21781	A_95_P241855	DQ460163
22447	265	7	1025	CCCAGATATCCAGGAAGAGCTGATCTATAAATGTCAATGATAATTATGGATTCTTTG	21789	A_95_P025426	TA20044_4097
22448	265	8	546	ACTTGTTTAACTGTGTTTAAGTTGTTGGACTTGTTGGACTGTGTTAAGTGTTTAACTG	21791	A_95_P003471	DW003643
22450	265	10	479	CGGCCTGCTATCAGATTTTGTAAACTTTCCTGTTGAATTTGAGACATACAATGTTTTC	21795	A_95_P021406	EH618371
22459	265	19	247	TGGTGGTTTTGGAAATTCCGAGAGTTCAGATCGCTCAACTGGTTTTGGAGGATTTGG	21813	A_95_P136037	TA20284_4097
22463	265	23	739	TTATCACCTATATCCCTCTTGATGTTCTCAAATTCATCAGCCGTTACACGTTGAGTGGT	21821	A_95_P127512	EB427027
22469	265	29	239	CTAGCATTTAAAGCAATAGTGGTAGCTCCTTGTATGTTGATAAAGACTGCATATTCA	21833	A_95_P160337	EH619036
22470	265	30	879	AACTCTTCCGACTCACCCTGAGAGTGTCCCAATTAATGCACTTATTGCAGTAAAAGGC	21835	A_95_P230399	DW000005
22472	265	32	696	TTGGTTTTGTATACATCCTTTGATTGTCCTCTTTTAATAATATGGGTTAGAGGCGGCA	21839	A_95_P017941	DW004740
22474	265	34	804	ATTAATCTCGACCTCAATCTTCCTCCGCCAGAAAACATGTAAAACTCTCTGTTTTACAT	21843	A_95_P011681	EB424796
22475	265	35	595	AACTGGTAAGAAATGCAAAATATCAGCTTTTAACCGGTTGACGGAGTGTTCCTTCAG	21845	A_95_P068430	BP137128
22477	265	37	316	ATCTTAGGGATTGGGCCTGTCCTTGTACAGAATATGGTTTAGTAACCGAGTTTTTAGT	21849	A_95_P156877	EH614951
22484	265	44	349	ATTCATCCGCAAGCCACTATGGTTCCGGGGGATTGATACTAATGAGATTAAATTCTTT	21863	A_95_P105682	CV017564
22485	265	45	876	AGTCAAGTTTGTCGTATCGGTACCTCCCACAAGAAGTGATGTCCTTCATCCTTGTGAT	21865	A_95_P245782	DV161522
22486	265	46	219	TATTGTGACCAGCTCGAGAATTTCTCATGGATTGCTAACATCCTTCAGACTTTTCTGC	21867	A_95_P099493	BP534950

22489	265	49	779	GGGACTTCCTGTAGATAAATATGTGAGCTCCCTGGCCTTTGTGTATTTGTAAATATTA	21872	A_95_P146582	EB450652
22505	265	65	271	CACCCCATAGTTAGGTATTTGCACAATTTTCCCTTTCCTTTAAATACTGATGTATTGAA	21903	A_95_P150252	EB680344
22507	265	67	765	GGAGCGTGGGTTTCAAGTTGTAATACTGCTATCTGTTTCTGCTTAAATATTTGTTATC	21907	A_95_P003276	TA12450_4097
22512	265	72	825	CGGATAGTATAAATAATAAATGTGGTGAGGAAAAACAAGCAAAGGGCGGTCACATA	21917	A_95_P226369	EB681955
22515	265	75	844	GGTGCTCTTTTCTTTTTGTGTGCTTAGTTTTCAAGCCATGTTACATTGTTTGTAACATC	21923	A_95_P220727	EB447664
22516	265	76	690	AGATTGCAAAGGCACAATTAGAAGAACAGAAAAAGGATGCTCTTGAAGCAATGGAA	21925	A_95_P147117	EB427847
22518	265	78	561	GAACCTCTCCTGTATTCTGCAATAATATTGTGGATTGTGGCATAAGCCTATTAAGAAT	21929	A_95_P020881	BP128373
22522	265	82	518	GTCCTGAACTTAGCGTAAGGACATGTTTTTCCAAATGATTGTAATGTGTATATCTTCT	21936	A_95_P121462	DW001529
22523	265	83	653	CAAAGATAACAATGTAGATGATACAGGGGAGAGAGTCTCATGTTCAGTCTGCTTAC	21937	A_95_P151272	EB681482
22524	265	84	500	CGACGTCTGATGAGTATGACTGAACATACTGAACTGTGTGATAGACTATTGTTGACA	21939	A_95_P154672	EG649697
22528	266	3	823	CTCCTAGCCCACCTACTTTTGAATATAAATAAGAGCTGAAATTTTTTGCAGGTTGGTT	21782	A_95_P192022	DV157650
22530	266	5	864	CCATGACTATGTCCGAATTTTCATCACTCTATTATTCCAACATTTGTTCAAAAGTGAG	21786	A_95_P217682	DV162696
22538	266	13	803	TCGTGGTTTTCTAGCTGGTGTAGCCAAGTTTATTTATTAATACGCAATCTGGATAAGT	21802	A_95_P011006	DV157631
22541	266	16	450	GGCAACTTGAGGCCCTTAACGCAGATTAGATTACTGAAATATAAAGAGACACATGTT	21808	A_95_P280423	AM838397
22542	266	17	570	ATAATGTTTTGGAGCTTGCAACACAAAGGTGGAACGCCAGAGACCATCCTTGAAAG	21810	A_95_P042521	BP130380
22548	266	23	1021	CACCGTAATCAACTATGTTTAAGGACTTTTCTGAGACATTCTCGTGTGTTACAATACA	21822	A_95_P009866	TA13119_4097
22550	266	25	772	GTTATTGGTGCATTGAAGATGAGGACCTATTTGAGTGGTATGCCTGAATGTAAGCTT	21826	A_95_P247342	EB440965
22551	266	26	906	CTTTTTGTGTTTCCTGGATTTGACTCATCAAAATCCTTTTGTGGTTAGTGCCATATAGA	21828	A_95_P028886	TA15660_4097
22553	266	28	828	GCAAACATTTGTATTGCAACTCCATATTACCAAGACTAGTATGGATCAGTGCTCCTCA	21832	A_95_P147357	EB451738
22554	266	29	534	CAGACGTAGCACCGGCTGACTCAAGTGGTTCAAAGAAAGAAAAGGTTAAAGAGTTC	21834	A_95_P222157	FG134412
22561	266	36	440	GGACTTTCGTGCCATTATTTTTCAATTTAATCGCCTCCGTTAGACGATCGCAGCAACA	21848	A_95_P087518	EB430886
22563	266	38	818	TGTTTTGCACATTTAAGTATTTCAGATACGTCGTTGTCTCCTAACAGTTTTCAGAAGA	21852	A_95_P013861	EB451303
22566	266	41	722	TTTCAGGAGGCAAGACAATGTGCACCTAGTATAGTATTCATTGATGAGATTGATGCT	21858	A_95_P138277	EB442022
22571	266	46	897	CCTTCAATAATACACAGGGATATAAGATCAAGCAATGTACTCCTATTCGAAGACTAC	21868	A_95_P139157	TA15002_4097
22572	266	47	300	AGATTTGCTCGCGACGTGCAAAGTTTTCCAGGAATTAGTTGTGCTTGAGCATGCTGC	21869	A_95_P169031	EH664574
22573	266	48	239	AATTGTCGGGGCCAAGATGATCTTTCAGTTATACTGCCATCAGCACATATAGGACCG	21871	A_95_P204292	AJ719171
22579	266	54	676	AAATATCAGCAGAATGGAAAATATAAGGAGGTCAAAGAAGTGGCTACTGTTTGCGT	21883	A_95_P136507	EB440264
22582	266	57	767	GAGCTAGAGGAAGATGATCTTACTTAAATTGATCTTCTCTGAAACTGGTTGTAAATT	21889	A_95_P248612	EB445511
22584	266	59	810	CAAAGCATGTAAGAAGTGCTGGCCTTTGGTTTGAAGTACTGTAACAAAATCTTCCCT	21892	A_95_P115417	DV157619
22585	266	60	302	ACAGAAGTATTAGTCGATTTGACGCCTATTAGCACTTCCTTTAGGATTTTGCTGTTTTT	21894	A_95_P029741	BP530883
22587	266	62	175	GGCTCCTGGCTATGTAGGTTAGATTCTACTGTACATTTATCGTCATAAAAATGAACTT	21898	A_95_P111507	CV020237
22589	266	64	562	TCTTCTTGTCTGTGTGTCTTCTGAAGGATTTTGCTTCAAGGCGAAAATCATTTGTGGT	21902	A_95_P199717	EB433985
22590	266	65	688	TTCCTCGTGAGCTTTTGTCATTGACCTATTGGTTGATTATTATAATGGAATGGCTTATA	21904	A_95_P130287	DV158468
22596	266	71	327	GAATCTGCTAGGACTCTGGTTGTTTGCAAACCCTTCGAAGAAGCCTATGAACAAGCC	21916	A_95_P242427	FG627369

22600	266	75	466	ATTTTGAGAACGATGAGGTCTTAGGTTCAAATCCCCGCGGAGAACAGAAAATACGA	21924	A_95_P076445	BP526985
22601	266	76	95	ATTCTTCCCGAATGCGTAGTTAGCTACAAATATGGACGTCATATGTCAGGTCAAGCA	21926	A_95_P033974	AJ717975
22609	266	84	872	TTGTATTGTTTACAGAAGTTGGGAGCTTCAGCTCGACTTTGCTGATAAAGTTGGTCA	21940	A_95_P202447	EB678643
22611	267	1	649	AATCTGTTGGTTCAATTTCTTCTTGCTTAGTGACTTTCTGACTTGATAACAGGGTGAA	21943	A_95_P063200	BP135712
22615	267	5	535	AGCTGATGACGGAACTACTGCAACTTCTTATACACCTTCTCTGCCATATAGTTATGGC	21951	A_95_P150292	EB680374
22616	267	6	273	GCCTTAGGTGAAAACTGAAGAAATATCTGAAAATCTGAACTTAGATCTCACTGTCTT	21953	A_95_P100398	BP535348
22620	267	10	679	TCCTCAGTGGATTGGCTGTTCTCTTGTACCGCTAGTATAAATGAATAAAAATTAATGT	21960	A_95_P016296	EB439650
22622	267	12	839	AGCACCATTTGAAGCCCTTAGAGTAGGCAAAGATCCTTGTTTCCAGCAGCTGTATCAT	21964	A_95_P196537	TA16360_4097
22631	267	21	354	CAATATGGAGTACGACGTTGATGCGGATTAACTCCTATGGCAGAACATAAACCGAGT	21981	A_95_P155692	EG650203
22633	267	23	791	AAAGAATTGCTGGTGCAAAACTAGACCTGGAACTGCTTCTCCTAATCCAAGAACTGA	21985	A_95_P284773	EH618908
22635	267	25	195	AGCTTCCTCTTAAAAGAACACTGATAAGCAAAACAGCATAAATCGAAGGAGACATTC	21989	A_95_P130257	EB430295
22636	267	26	642	GTGACTTGTTGCAGGCTCGTGGTTAATTATTGCGCAATGGATGCAGTGTGACAATTT	21991	A_95_P018101	DV157502
22641	267	31	796	GCATTGCAATGAGGTTCCCGCTGTCATTCTTAATATAAATTAATGAGTATTTGCTGTT	22001	A_95_P263156	EB679730
22644	267	34	509	TACGAAAAAGCGACTTTGAGATTACCCTTTTTTGAGTTAGGAATGTCTGATGGCCCG	22007	A_95_P160772	EH619483
22645	267	35	864	TTTAGAGATAGATTTGAGAACCTGCTAGGGGACACCATTGTGGAAATTCAAGTTGG	22009	A_95_P247742	EB441079
22647	267	37	876	AGTCAATCCTGCAGTTTGGGAGATTAGTGGACACATGGTCTTGAAGAGGAAGGAGG	22013	A_95_P247617	DV998879
22655	267	45	1042	TTCATGTTATTATATGGGAGCTAATATTTGTAGTTAAAATGATTGTGGTGGGAGGCCT	22029	A_95_P196867	TA16436_4097
22657	267	47	494	CTACTCTTTGGGAAAGTGGATTATTCTGATAGTGTTATTGTTTCAATATGGTCCTTGCT	22033	A_95_P228194	FG635177
22664	267	54	797	AGTTCATCATCAAAAGTGTTGATTTTGGCAAGGAAAGTGAAACCTTGCTGTATTATTT	22047	A_95_P201467	TA17431_4097
22669	267	59	424	GTTCATATTGTTGATGTTCCAGGGGCATTCTCGTTTGCGTCCGAAACTAGATGGGTTT	22057	A_95_P219992	TA21513_4097
22670	267	60	772	GTATTAGCAGGTATAATCTAGGAGCCGACTGCATAAATTATCCTTCACATATGTTTAA	22059	A_95_P149732	EB679681
22673	267	63	755	AAGTTCTTGACTGGAGCGTCCACCGTTGGCAGCATTGCAATTCCGATTATCTTAAAG	22065	A_95_P269746	EB439815
22679	267	69	745	AACCGTCTTTACTGTGAGATTAGAGGATGGAACTTGAGAGGGACAATCATGTGATCT	22077	A_95_P297648	FG198080
22688	267	78	681	CAAACTTCACCGATTATAGCTGCCAGTTTAAATTCGGGATTCTACCTCCTCAGCCAGA	22095	A_95_P190117	DW000151
22692	267	82	362	CCGATCAGATCAAAGTTGACGCTCTCAAACGCGCTGAACAGATCAAGTTTCAAATCC	22103	A_95_P160482	FG161364
22694	267	84	340	CGTGTTTCTGGCTCTCTATCTCTATCAAAACCAACTTTCTAAATTCTTCTGGCCGGAAG	22107	A_95_P103907	CV016747
22696	268	1	811	ATGTTTAATTCACTACAATCTGTGCAGTTTCAGTCTTGACTTTGTTCCAGTTTTGACTA	21944	A_95_P123802	EB679147
22700	268	5	762	GGATGCCGGCTAAGTTTAGTTGGTTGTACAATGTTCTGTCTATATGTTTTCTTTTCATA	21952	A_95_P201407	EH621143
22701	268	6	473	AGATGTTAAATGGTGCCATAAATCAGCGGAATTTGTTGCATGAACAACAGTTATGGT	21954	A_95_P274033	AM836818
22704	268	9	766	CTGTTCATTGTTGGGGTTTTGTTGAACCATGTCTACGGAGACTGTAACTTTTTATTTAT	3665	A_95_P000026	EB439159
22710	268	15	546	ATGCTAGCAAATGTTACTGTTGGTGTTTAATGAAGCAAACGGTTAAGACCTGTACAT	21970	A_95_P139627	EB443430
22714	268	19	618	AATAGCGTGTCAAGGTATTGTCTTCTGATCCCATTTTTCATCCATCTTAGCAGTTCCAT	21978	A_95_P028241	BP129197
22716	268	21	802	CAGGTACTTCCACTTAGTCTTATCATCCTTGAGGCGAGACACTTTTATAGAGACTTCG	21982	A_95_P115432	DV157637
22720	268	25	547	GCTATGGAAGAATAGCTGTATTGCAATGATGAGTTCCATTGTCATTTCTTTGAAGCA	21990	A_95_P051876	BP132770

22721	268	26	1340	ATTGAATTAAGAGTATACGAAAACCGAATATGGTGGCTATTCATTGACCCACGCAAA	21992	A_95_P195932	TA16225_4097
22724	268	29	779	GTACCGAAACCAAGCACCCTCGATGAATGTTTTATTTTATGTGACACTTTTCTTTTAAT	21998	A_95_P011101	EB677998
22727	268	32	858	AATTGTTTCCCAATATGTTTCAATGGAGATAATGAAACCTCCCCAAACAGATGATCCA	22004	A_95_P194887	TA15999_4097
22730	268	35	501	TTTGATATGATCAGTTTTTGGGCTGGTGGAGAGATTGTCCCCTTTGATTTCTAAAAAA	22010	A_95_P285998	TC56231
22732	268	37	92	GAATAATTTTTCATAAGTTATAACCCTCACAATTGCTTCCCTCTCCCGTTCTCCAGATA	22014	A_95_P113507	CV021167
22735	268	40	1257	ATGACAAACTATGCATGATTGATGTTTCTTGAACTTCTGAAAGAAGGGAATTTCTTGA	22020	A_95_P239219	AJ608156
22737	268	42	1828	CAGGATTTTGTCTGTTTCAATTTCACAGATTTTTGTATGAGAGCGTTGCTGAGTTTTCT	22024	A_95_P183997	TA13587_4097
22739	268	44	222	GCAAAAAATATCCCCAAGAGCTAGTTTCTCTATATTTCAACTCTGTCAAGTGATCATGT	22028	A_95_P132457	EB432942
22742	268	47	803	ACTCAACTCTAACTGAATGCTTTTCAAGCTTTTCCAGTGGTGTACACTTCCTGCTGGC	22034	A_95_P021676	TA15423_4097
22743	268	48	505	TTTTTGTGGACGTTGGTGTGTCAATTTTAGAGGTGCTATTTAGCTCTCTCTTTTTAGTT	22036	A_95_P122047	DW002104
22745	268	50	1193	CTGGGTATGCAGGAAAAGGGTTCTGTTGCTTTTGCTGTTGATTACGAATTTGCAGCA	22040	A_95_P209172	TA19132_4097
22747	268	52	1063	ATTGAAAAAAGGGTGTAAGTACATTTGATCAAGCTTGAAAATCAAGAAATGGCCTT	22044	A_95_P209147	TA19125_4097
22749	268	54	918	GAAAACGGAATAGCTACCCCCGATCGATGTGAATATCAAGAAAGGCTGATTTACTAC	22048	A_95_P034768	AY627865
22750	268	55	327	ATCACTGGTTTTGTTATTGCATAGTGTGTTTGCTTAAGGCGAAAAGAAATAGATCAAT	22050	A_95_P100973	TA12722_4097
22753	268	58	404	GCCATTTAACATCAACATTTGGTTTCAATAGTTTGCTCCAAGTTATGGTCGAACTAGA	22056	A_95_P185818	TA13997_4097
22754	268	59	400	ATTAGCTGAATCTAGTATTGTGGAGAATGATCCTGACAGTGATGTGCACTTGGCACC	22058	A_95_P079455	BP527769
22758	268	63	416	TTTCCTGTTGATGTTGGATAATCCTCTCTTATGAGAAAGAGGAAAAGCTGTACTTTTA	22066	A_95_P089078	BP530340
22762	268	67	571	AGAGTGTTCTTATACGCTTCTGATTCAACGGAGATGCTGCTGTAAGTTGCCTTTTTCA	22074	A_95_P192982	TA15573_4097
22764	268	69	156	CAATGTGAGATATTCTAACAAAGTCTTTCCCACTTACCGTGGATGATATTAGTACATC	22078	A_95_P131737	EB432136
22765	268	70	355	GTGCTAGAGTCATTCCGCTTATTTATACTGAGCCTCCTGAATTCTTCAATCAAAAACTT	22080	A_95_P110817	FG148134
22769	268	74	116	GCAGTAATTTAAGGGTTGAGACATGTGTTTTAAATATGCATTGTGGTACGATGATTT	22088	A_95_P211422	TA19607_4097
22776	268	81	875	AGAGGACTTGTCTAAAGTATGTTCTTTGACATTGCCATTAGCTGCTACTATTGAACTT	22102	A_95_P234254	EB449886
22777	268	82	487	TGCAGAGGAGATTGGTCTTTGGATACCTGTTGCAATAATTAATAAGGAACATGATGA	22104	A_95_P145582	EB449334
22782	269	2	212	ACCGAAGATTATCAGCATGAGGATGAGAACACATTAGCTAAGGTGATAGCCGGTTTT	22112	A_95_P159902	EH618448
22790	269	10	849	AAATGTAATGTTATCTGGTGCTGATTGTTATATTTTGGTTTCCCCCGAAAGCTTGTTG	22128	A_95_P216237	DV158578
22791	269	11	861	TGTTGAAATCAACTTGTACATTCGCTCCTGGCTTCTAACTAGCATGTGTAAACAATCA	22130	A_95_P020661	TC52386
22793	269	13	785	GCGTTGAATTGTACTGTGACTTTGTTGTTCATATTAGTATTGAAATGTTGCGGATCAT	22134	A_95_P204157	EB426734
22796	269	16	1561	GGTTAATGCCCTTCCTGTAACAATATGCTTTTGTTATGCTCAATAACATCATGTTTGTT	22140	A_95_P193882	TA15767_4097
22797	269	17	515	GGGTAAACCACCTGTTGATGAATACGGACGCCCTTTATACGGAGATGTATTTGGTGT	22142	A_95_P148042	EB677223
22798	269	18	769	CTACCTCCCTCTCACCTCAATGTAATTTGTAATACAGTATATAGTCTCTGTTTCATAGT	22144	A_95_P195117	TA16047_4097
22801	269	21	100	TGGCAGCGTAAGCTGATATCTTTTGGATTATTGGTGAATAATTGCTTGCTTCCTTGCG	22150	A_95_P006741	DW002879
22802	269	22	208	GACATTTGAGTAGTGTTTTTGTCCTAATGGCACTGAATTGAGATTCTGATATCCGTAT	22152	A_95_P028281	TA13592_4097
22803	269	23	682	TCAAACTCCACTTTTCATTATAAATGCAGCCTATGATCATTGGCAGGTAAGGAACATT	22154	A_95_P287143	FG644072
22807	269	27	667	GATGGGACTAAGAAATAGTACTGTAATGGAAAATACTTATCACCAGGTGCATGTACT	22161	A_95_P015441	TA15029_4097

22809	269	29	829	CTCTCCTGATTTCCTAGCACACTCGAGCCTTTTCTTGATTTCTTAACAGTTAAATGAAT	22165	A_95_P180477	TA12753_4097
22812	269	32	872	CCAATATTTTTTAGTCAGTGTTATTAGGCAATGATGTGGATTACCCGAGGAAGTTTTT	22171	A_95_P234324	EB678760
22814	269	34	705	TTAAAAGGCAAGATCTCCGACTACTATGGAAGTGTATGAAGGAGTGATTAGAGGGG	22174	A_95_P144722	EB448234
22815	269	35	1074	CCTGGCACATATGAATATAAGAATGGTCTGCGTGTGAAAAAATATCGAGGTATGGG	22176	A_95_P148617	AY433959
22817	269	37	0	AGTCTCTTTTGTGGATGTGCAAAGATCACGTAAACTTCCCTGGTGCTCGTAGCAAAA	22180	A_95_P296633	A_95_P296633
22822	269	42	455	TACTCCATAAAATGAGATTGCAGGGTGAGAAATTTTCATGTTTTGAAGTGGTTGTCA	22190	A_95_P082720	BP528575
22824	269	44	461	CTGTAGATTTCTCTGGGTATTCCGGATTGTTTGAATGCTCATGATTAGTGACACCTCG	22193	A_95_P281853	AM809865
22826	269	46	117	TTGATGAGGGTGAACATCCATTATTTGTAACTTGGAAGAAAGCAGTGAATGGTGGG	22196	A_95_P078320	FG622424
22827	269	47	689	ATCCGTCTCTCTCCATCTGTAAGAGGTTTGAAAAAATAGTGACTGGAGTTGCTCTCTC	22198	A_95_P255429	FG643894
22829	269	49	701	CAGGTTTTCCTCATCTCACCTCTCCTATGTTTTAGTCTTTTTCAAAGCAAAGCAGTACC	22202	A_95_P246302	EB677787
22835	269	55	91	TAATCAATCTCGTAATGTCCTCTAGCAAGAAGCTTATGTGTTCGGAAGGAGGACTCA	22214	A_95_P061485	TA21256_4097
22836	269	56	1567	TAGGAATTTAAGGGTTTTGTATGGTTTTGCCTCTTGGAAAGCTATGACTGGCTTGACT	22216	A_95_P187927	TA14458_4097
22837	269	57	1582	TTGGGTCTTGCCACTTGTGGATTGCTGTAATATGTTCAACTTGTTTTACGTTGCAATG	22218	A_95_P201277	TA17389_4097
22840	269	60	287	GAACAACATTCAGCTGAGGCAACCAAGTACTTTTTGTCAAAGTTCAGTGACCTTCAAT	22223	A_95_P102442	CV016020
22841	269	61	743	TTTCAACTGCTGCTGATTGCTTTGGTGTTGCTTAGAATTTGTCTTTGCTGCGTTTCTGG	22225	A_95_P180077	TA12653_4097
22844	269	64	774	ATACATCAGTAGAGATCTCAAGCAAATCATCAATTTCCAACGAGGACTCAATAGAGG	22231	A_95_P021541	TA13329_4097
22847	269	67	518	ATGTCGTCTTCAGAAGTTAAACTCATGAATGAAAGCAACGAAAAGGATCGAGTTTAT	22237	A_95_P223202	TA22199_4097
22850	269	70	755	GAGGCTGGACATACTATGAAGCACTAAAGAAATGTGGATGGAAAGGTGAAGTGGA	22243	A_95_P197862	EB425092
22851	269	71	770	ATAAGCAGCTTAAGACTGTGACTGACTACTGAAGATGTGTTTTGTCATACAAACCAG	22245	A_95_P164197	EH623345
22853	269	73	494	GTTATGTGAATACAGTCCATATATGCAGCACGATGGGTCCATCATTCCCCGTGTCATA	22249	A_95_P083485	BP528771
22862	269	82	797	TGCTTAGATCCCTGTAGCATGGTGTGACAGAACTCAGTAATGTACGCTTGTAATAAG	22267	A_95_P124397	EB678771
22864	269	84	806	GGTACCTCACACTTAGTTCTAACCATTTGATTTGTTATTGCATCCTTCCAATACCTTTG	22271	A_95_P032641	AF019202
22867	270	2	784	GCTCTTTGGCTTCAGTATTTTCTTCTGCATTGGAATTAATACACGTTTGAAAATTCATC	22113	A_95_P215802	TA20568_4097
22871	270	6	841	GGAACCTCTGCTGTATTGCTGTATTCTGCAATAATATTGTGGATTGTGGCATAAGCCT	22121	A_95_P187627	TA14388_4097
22874	270	9	615	TGTGGGGTGTTTTCTTTCTCAGTTGTAAAATTGTTTGCATGTTTCCTATTCTGTTATGG	22127	A_95_P197327	TA16538_4097
22878	270	13	428	GTCATTTGCTCTTCAGAACTCGATGCTAAATTGACAGCAGAAGTCCATTCTGATCCTG	22135	A_95_P039506	BP129563
22894	270	29	812	TGCTTGGATATTTGTTCTTTTTGGCCAAGATTATACTTCTATGGTATTGGCTGGTCAT	22166	A_95_P189172	TA14734_4097
22895	270	30	674	TGAGACTTCATCAGAATATGTCAATGCTATGGCTGCAGAATCCTGAACTGAGATTTG	22168	A_95_P157762	EH615794
22898	270	33	551	CTGCATCACCTGTGTGGATCGAAGGGTTCATTACCAAGGAAGAAGCAGAATCTTCAC	22173	A_95_P021441	BP133270
22900	270	35	745	AAGAGGTTGAGTTTCGTATCATGACTAGGCTGTCATCTAGTGGTATTATCAAGATTT	22177	A_95_P148997	EB678640
22902	270	37	153	TAGAGATCATGTGCAGCTTAGTGATTTGTTGGATGAACGCCTTCCATGTCCCCTCGAA	22181	A_95_P035988	BP128614
22903	270	38	0	AATGATGCCAAGCTGCAAAGAAAGGAGTGAGAGCAGTCAATGGTTTGGTTGATGTT	22183	A_95_P309388	A_95_P309388
22904	270	39	817	GCTGTACTGGCTGTGATCTTACATTCACATTATTCTAGACATTAATAAAGTCTCTCAT	22185	A_95_P009251	TA17404_4097
22905	270	40	1114	CAGGAAAATCCTATTAGTGTTGAGTGGAGTCATCGTTGTAGTCAATTCACTTTTGTAA	22187	A_95_P191362	TA15219_4097

22914	270	49	388	GACCAAGTGATGGAGCAATATGTAGCATCTTCATCAGTTGTGAGCTTCTACGTACCA	22203	A_95_P104687	CV017132
22915	270	50	489	CCAAAGTTGTTTGCTTAGTTCTACTTCAAACTGTTGATAGCTACTTAGTTTGGAACTCT	22205	A_95_P109572	TA13077_4097
22919	270	54	67	GGACATAAATATTGCTGTTAGGAATTCACTTTTTGCAGTTGGAGATATAGAACATGG	22213	A_95_P147612	EB452125
22921	270	56	444	TAGACCACAGGAGTATCCCATTGTTTACTCTTTTATTTCTAATTTTGGTCTTGGAAAG	22217	A_95_P216927	TA20811_4097
22925	270	60	428	GCCACACTTCCAATGTATACTTTTGGTAAAAAGGTTTGTGGTTATTTATGATATCCAC	22224	A_95_P030721	TA19787_4097
22929	270	64	473	TTCTCTTCGATCTTCTCTTTGATTGCTTTTTATGAAGTCGCACTGGGAGCTAGTGTTTG	22232	A_95_P087948	BP529925
22935	270	70	862	GTGTTCTCATTCGTGCTTGGTAATGCAATTGAACTGTGAAGCTTTAAACATGCAATTC	22244	A_95_P218987	TA21298_4097
22941	270	76	938	GTAGTCGGGCAAGACATTTGTTAATATTGTTTAATGGGGCAAAAGAAGTCATCGTCT	22256	A_95_P014886	TC49215
22944	270	79	754	CTTACTGCCGGCCAACGTTTGGATTTAAATCTTGAAAGAGGACGCATTCGTGATGAG	22262	A_95_P126882	EB426249
22948	270	83	1536	GTCTTCTAAACTGTAGTATGCTGTTGTTGAAGTCAAAATATGTTCGTTTGACTGGTTA	22270	A_95_P177052	AJ421412
22949	270	84	2545	CTGTACACTATCTTGCCAAATTTTCTCATTGACAAAGAATTTAGTGGTCTCAATTAGA	22272	A_95_P215017	X95576
22954	271	4	466	TCTAAATTGGAGTCCATTTTATATTTTGCCTGGAAGCTGAATTTGCAGGTGTCACTGG	22281	A_95_P073115	BP526132
22955	271	5	810	TATGCAATCGTACAAGAATATCGATGTCAACGCCCCGTTTTCAGTTGCATTTGAAGCT	22283	A_95_P222062	EB427385
22957	271	7	1212	GTTCCATTGGGGATGTGATAAATTTTATGTCAAAATTGTGAGGCAATATTTATTCTGC	22287	A_95_P189962	TA14901_4097
22958	271	8	835	AGCATTCTGAACTGTCTGAAAGTGTCACCATTGTGGTGTGAGTGAAATGTACGCAGC	22289	A_95_P294548	FG136761
22959	271	9	4550	GTTGGTTTCTTGAAAATTTGACTGCTAACAAATTAAACTGCCGTTACAGACACTTAGT	22291	A_95_P007271	AY169238
22962	271	12	461	GTACAATCTCAGCATTTCTCCATTGTAACATTCTTAAAACCTGCGGATGAAAAAAGTT	22297	A_95_P050916	BP132516
22964	271	14	238	TTCTTCATCTGGTGAAGGGGGGCTTTGACTATGATTTGGTTATCATTGGAGCTGGTG	22301	A_95_P104047	CV016817
22966	271	16	422	GTATGAAAGGAAGCTGATTTGGGCTGTAACACGAACTTATCAATATATATCTCCTCTT	1861	A_95_P000051	FG625247
22968	271	18	782	AGTTAGCAATAGGGTATGCCCTCTGGTCCTTTTTTCTTTCTCCTTTTTTCTTGCACCAC	22308	A_95_P187052	EB425115
22969	271	19	641	CAACGAATGCATAGTGTTAGTGAAAATACTCTATCTTCTCATGGTTATGCAACGAGT	22310	A_95_P306953	FG636850
22971	271	21	1788	GAAACTCCCAGGTTCCCTGTTGTAGTTTCTTAAACCAATGTTCACTGTTAGTGGTTTTT	22314	A_95_P195947	TA16229_4097
22973	271	23	748	AACACCACTGTATTATCTTTGTTGAGGTATAGGCTTAGAATGCCCCGTGTGCTTCGAG	22318	A_95_P135687	EB439224
22976	271	26	713	GAAGAAGGCCTTGCCACAGATACCCACACTTCAAAGCATGGCATAGATAATGATGCT	22324	A_95_P137262	EB427218
22977	271	27	99	AATGCAGACACAGAAACTGGTATCCAGGAAGTATCTGGAAAGCCGTTACTCAGGAC	22326	A_95_P242582	DQ460191
22980	271	30	717	TATGCAACACGCATGCTATCTGTTATTTTGACAGCATGATTGGTGTATTATTTCTGGT	22332	A_95_P013871	DW001454
22981	271	31	1363	GATTCTGCCAATTACAACTGCAGTTGTTTAGAACAGTGCCATTTATTCCTGTTTGGTT	22334	A_95_P212207	TA19784_4097
22985	271	35	699	AGTGACTATTGAGGTTGATGACGAGCATGTAGGTTTGGTCATGGAAGCACTTTCTCA	22342	A_95_P119157	DV162231
22992	271	42	417	GTTACCTGTTCACTACTATAGGATAGAGTCCAACGGGTACTTGTGCTGTACTGTGTG	22356	A_95_P173872	EH665711
22994	271	44	169	TCAAAGAGTCGCATTGTTTGGGAATGCAGTGCAAATTGGGTGGTAAATTTCATCCAA	22360	A_95_P028776	TA16088_4097
22995	271	45	1444	GAGCCAAGTTGTGAAATGGCTGTACTTTACTACTTTAGATACTTAGATCTTTTATGCA	22362	A_95_P009741	TA15085_4097
22996	271	46	0	TGCCCGTTTGTAGATGAGTTAAGACTATGTGAATGCAGCCCGATACAAGCTTATGAA	22364	A_95_P259146	A_95_P259146
22999	271	49	253	GCTTACAAATGCAAGGATTGAAGGCCAACTCTGAAGTGAAAGTCTTATAATTTCTGT	22370	A_95_P015011	CV018922
23002	271	52	220	CACCATGTTGAAGCTTTCTTTTTGGTTATTCTCACTGGACAATTTAAAGATTTGCATGT	22375	A_95_P026936	EB446137

23003	271	53	95	GTTAGAGGATATTCCCTACTACGCAAGCCTTGTAAAGTTATTGTAAATATTCTTACAG	22377	A_95_P141317	EB445072
23010	271	60	323	GGATGAAGACTTCCAGTTCTTACAACCCATTGATCTTATCACGAAGGATGTATATGA	22391	A_95_P042541	BP130384
23014	271	64	739	TCCCAAAAGATTCTGCTTTGGGAAGATTAAGGGGAAGTGGATATGTGGCTGGAGAA	22399	A_95_P217967	TA21064_4097
23017	271	67	862	GTTTCAGAACCTCTATTTTTGTGCGAAGTGATTATCTAGCATTTCCATTTTGCCTGAGC	22405	A_95_P008101	DW005137
23019	271	69	893	AGCCATGGTAACAAAAGGCATTATTGAGCCTATATCTGATACGATCATCAACCTTGTA	22409	A_95_P244167	DV161257
23020	271	70	630	GAAAGGAACGTCCATCTATGTCTCCCTATTCTGATTATTGCGCATTTGCATATAGAAA	22411	A_95_P303418	FG635358
23021	271	71	1626	CTTACTGGTCACTTGTGTATAAGGGTTCCTTGTGTGTATATATAATGATATATGCTGC	22413	A_95_P015386	TA14704_4097
23022	271	72	656	CCAAGTATGCTCGGGAAGATGATGACCTCGAAACCCTGGAAAGAGATGTTAGTGAA	22415	A_95_P037088	BP128908
23024	271	74	86	TACAGATTATCAAAAGGCGGCTATGACTGCCAGTCAAGCAGTCTGGAGATTCGGTTG	22419	A_95_P104642	CV017108
23027	271	77	744	AGGGTGTCGTTTAAGCTACTCTTCCTTATATGCTATACACCTGATTCTATGTACAAACA	22425	A_95_P136282	EB439968
23028	271	78	812	AGCCAGTAGCCATACTGCATCTCTCTCTCAATCTCTTTCAAATTGGGTCTGCACTCTAG	22427	A_95_P291838	FG165288
23029	271	79	616	GTTCTATGAATTTATGCACTTACTGTTTGCTTTGAGATATCACATCTGCCTGATTTGTC	22429	A_95_P005271	DW003255
23031	271	81	923	GTTGCCCTGTAAAATTTACCTAAGGCTGGAACATTGTCAAAACTCCATATTATTATTC	22433	A_95_P007961	D87821
23032	271	82	0	TTTCCCAACGTGACATGTCAGATCTTACTCATATCTTAATCAAGTTGAAATGGTTTCAT	22435	A_95_P233879	A_95_P233879
23033	271	83	744	GTGTGAAAGAACATTGTCGAAAAACTAATGATCGACAGAGTATATATATTATTCCCG	22437	A_95_P208417	TA18965_4097
23035	271	85	711	ATGATTCCTACATCTTCATCGGCAATATGCAAAGAGGAGTTGATGTCATCTCAGTAG	22441	A_95_P265296	FG187123
23036	272	1	594	CGACTCCAAATGCTTGACTAGTAATTTGATGTTTATAGACGTTTTTATCCATGTGGTT	22276	A_95_P185697	TA13969_4097
23037	272	2	791	ATATTGCAGCTCTTATGTTCCTTGTCAAACAGATAACGGCCTTTTATATATTGCAGCTC	22278	A_95_P258156	TA11894_4097
23043	272	8	467	GGGGCATTATAGAGAAAAGAAGGTTGCTGAACTTGCAAGAGTAATAGTAGAAGGAT	22290	A_95_P275843	AM792691
23045	272	10	421	TTAGCTAACCTATGAAAGAATGGTTATGAATCCCACATATTAGTACTAAGCTGTGTGT	22294	A_95_P024376	TC64810
23046	272	11	1001	GTGTCTTCCCTGTACCAGTAGGATTAGTAGTTAGCCTTGTATTCTATTATTGGTAAATT	22296	A_95_P010621	TA13551_4097
23047	272	12	316	AGGCAGTTAAAGCACATTCTTTACTGTGAATACCACTGCTGGTAAAACAATGTAACTA	22298	A_95_P132622	EB433174
23049	272	14	841	CTAGTGTCCATGAATACTAGCTTAACTGTAATGACTTGAATCCTTTAGTCGTCTTGTTT	22302	A_95_P014846	EB448428
23050	272	15	291	TTACGCGGTCAACGAACTCATACTAATGCTAGGACTTGTCGCAAGCTAATTCGGAAA	22304	A_95_P007226	TC76984
23052	272	17	187	TCCTCCTTGTTATGTCTTGTCAAGATTAGATTCATGTACACATAATGGACACTGATCAT	22307	A_95_P131037	FG626184
23055	272	20	372	AGAAATGTATGGGGCTTTCTGGTGTTCTCACTGCCAGGAACAAAAAGAGATGTTTG	22313	A_95_P031191	BP527417
23059	272	24	180	ATGTTACAGTTCACACTTATTTCAATGAGCAGGTGGTACTGATAATCTCTGCGCAGGT	22321	A_95_P089363	BP530472
23060	272	25	719	CCCTCATCACGAATCATAATAGTTATGGTGCTGCTGTTTCTCTTTTTTGGATTATCTTC	22323	A_95_P019721	EB430118
23061	272	26	104	ATCTAGTTAAGCCAAGGCAACTTGGAGATCCATCTTATTTGTCGTGGAACCGAAACC	22325	A_95_P162827	EH621828
23065	272	30	2441	CTTTTAAACCTCCTGTACATGTCCAAATTTGCTGTGTTTTTAAAGGTGTTGTTTCGAGT	22333	A_95_P183422	TA13453_4097
23067	272	32	420	TTGTTCGTACATGCATGGTGTAAGTACTCAAAAACATAATACATCTGGTTGATCATGT	22337	A_95_P090313	BP530902
23068	272	33	742	TATCAGAAGCTCAACAAGAGGGAAGTACTATATCAGGGACAATGTTCCACAGGGGA	22339	A_95_P137982	FG144580
23070	272	35	653	AGAGTACTCACCGGTAGACTATCAAATAGTTGTATTTCATAAGATACTCTATATCGAG	22343	A_95_P288148	FG640697
23071	272	36	568	TGCATGGTCTATATGATTTCCTATGGCTGCTTTTGTGATTCCTGATGAAATTGTCAAG	22345	A_95_P012166	DW001649

23072	272	37	897	CTATGTCCGTAAATGTTTGATATTACAGCTTGATCGGGATCTTTATGCTTGCTTAATTT	22347	A_95_P009651	TA13809_4097
23075	272	40	825	TCTGTCAACTCTCTGAACTTCCATCCTGTTCATGGAACATTTGCAACTGCGGGATCTG	22353	A_95_P003516	EB424826
23076	272	41	772	CTTTTGGGCTGTCTCTGGTCGATTACATGAGATGCTTAAATGGGATCCACATTACATA	22355	A_95_P128962	EB428739
23085	272	50	432	GCTATTTCTGTTTGCTGTTTCTCTTATGTTCTCTGTTGTGAATAAAGATTCCGAATTCT	22373	A_95_P176987	TA11842_4097
23087	272	52	985	CAGCTTCCAGATTTTGGATACTTTGTCTCTGATCTATCTATATACAACGATCTACTGTT	22376	A_95_P177362	TA11956_4097
23088	272	53	2849	GCTTTGAGTGATGATTTTTCAAATGAGATATAAATCCACTGTAGCAGTTTATGCTTCT	22378	A_95_P239574	AB196792
23094	272	59	848	CTGCATTCTCATCATGTCTACTTATTATTATCTCGTGTGCACTTGGCCGCGTATCATAT	22390	A_95_P310123	FG168503
23095	272	60	317	TAGGACAATTTCCAGTTGTAATGATGTGATTGTATTGAAATCTTGAGGCAGGCGCCC	22392	A_95_P142487	EB445941
23099	272	64	36	GGGAATGTGTATTGTGTTAGGAATTCTAGTTGCTAGGGTTGAAGTTTTTGTTGTATA	22400	A_95_P120502	EH616876
23102	272	67	435	GTCAAATTAGGGGTGTTCGATAAATTGGGGAAAATTTATCCTTGATTGATAGTTAGT	22406	A_95_P105307	FG164975
23103	272	68	188	GCCCTACTATTGACAAAAATATCATGCTAGTGTGATGACAATCTGGAATAAAAATGG	22408	A_95_P079250	BP527717
23106	272	71	775	ACTGATGTCAGCTTTCTTTGTACATCATCTCTCTCTTCTCGCAGTTCACGAGACGCTCT	22414	A_95_P271321	FG171937
23109	272	74	185	GCTAGCTAATTCTGCACTTTTAGCTTACTTGAGGGAAACTTCGATATAATGTAGATTC	22420	A_95_P110752	CV019883
23111	272	76	279	CGAATGTTGAGGAGTTAGGGTTGCTATTACCGTTGTTGTATTATGGATTTTGAAATT	22424	A_95_P015196	TA14982_4097
23112	272	77	537	GGTGTTTTGAGCTAAAAAGTAAATTACTTTGTACCATGTGTGGGAAAGAGTATCCCT	22426	A_95_P017122	EB428883
23113	272	78	1210	GTGCGTTGTATACGGAAGACTTGCTCTTTGATACTAATGATGAATAACAGTTTCTTAT	22428	A_95_P011171	AB024511
23116	272	81	484	GAAACATTTGGTGATATTGCCATGTGCTGCATGGTTACTTTCCTTAGTTTAATATTTG	22434	A_95_P030366	FG139988
23118	272	83	781	CGTTCTATGGATTAATGTCCAAGAACTGATTAGCACCTGTTTTGTTCGTTAACTGTAT	22438	A_95_P117422	DV160333
23119	272	84	796	GAATACAAAGGGCTAACTCTAAAGGAGGCAACAGATTATGTTATAAAAGAATCTAC	22440	A_95_P116472	DV159213
23125	273	5	580	CACTAGTGAAATCAGAAGAATTGTTATAGGTCGTGAGCTCTTTAAACATCAATAACT	22451	A_95_P270836	EB436402
23133	273	13	593	ATTTTTCACCATTGTTTCCTCTCCAAGTAAATATTTTAACCCCCAAAGCTTCAGATTGT	22467	A_95_P121677	DW001787
23134	273	14	686	CCTCTTTTTTGCCCATGGATTGGCTTAAATTTAAGTGATAAGTGAAGTTTTGGGTTTC	22469	A_95_P148732	EB678193
23139	273	19	690	CTCTGCTTTATGATCTAGGTTTTGCAGATTGCTCTTGAATTAAATTGAATGAGTAGTT	22479	A_95_P182477	DW003915
23141	273	21	967	ATGCAAAAGACTTGTCTAATTTTTCGGTTTTCGGAATAGATGGTTGGTTGAGTTGGTT	22483	A_95_P184157	TA13627_4097
23150	273	30	518	GTGGTAGATATGATTACTTTCTGGATTCAAACAGTTCTCTTTGTGTTTAGGTTTTGCA	22500	A_95_P110002	FG158081
23151	273	31	863	TAATGTTGCCTTTTGTGAGGTTCTTGTTTAATACTTGCAAGTGGCAGCTTAGCTTTTG	22502	A_95_P015961	EB445720
23156	273	36	426	GTGAAGAAACATTGGCTCATCCTACTCTCCTTGTTTGAAAGTATTTTATGAGGTTTAA	22512	A_95_P096743	FG643824
23160	273	40	826	GAGATCTTACAGCTGGTGACCCACTCTAACTTAATTCTGAGTCTTCTGTTCCATTTTTC	22520	A_95_P219517	TA21413_4097
23163	273	43	1808	GTTGAGTGTCCAGTTTTTGTGTGAGAGAAACAATTACTATGAACTATGTAGACTTCT	22526	A_95_P239889	X63106
23169	273	49	653	GTGAGATCAATCGGGATATGGTGATTGATGCCACTTACAAGGGCAACAAATCCAGA	22538	A_95_P034274	FG147699
23171	273	51	770	TCAGTGTCTCTTTCCTGCAATTGATCTTTCGCTGATTGAAAGTGACGAGGATACCCTC	22542	A_95_P272981	EB680661
23173	273	53	791	ATGCAAGTAACTTTCTGTACGAAGGGAATTGGTTTTCATATCTTATTTTGTTATCCCG	22546	A_95_P178577	TA12284_4097
23182	273	62	874	CTGATAAGGAGGTCAAATGATTTATTTAAATTGCATTGTGTGGCTTGTCTTTACTTGT	22564	A_95_P228199	EB678646
23186	273	66	419	GATCAGCATTGTGTGGAACTTGTATGAATTTTACCCTTGCAGTAACAGTTTTGTAACA	22572	A_95_P140232	EB444179

23191	273	71	1061	CTTCCTGAGACTTTTAGCATTGAAGATGTAAAGTTCAGATGAAGCATCAACACCTATT	22581	A_95_P194742	TA15965_4097
23195	273	75	701	GGACAATGGTTTCCCTGCTCGATATTGTGCCAAGAATCGGATGTTGATTAAAACAAC	22588	A_95_P256889	EH621249
23204	273	84	629	TTGTTTTGCTTATTAGCTGAGCCGAAGTCCCAATCTTTCTTGGCTTTGAACAAGCAAA	22606	A_95_P128522	EB428230
23209	274	4	445	GCCTCTTCTGTGTATTCAGATGGATTTAATGTATTACTTGAACAAGTCCAATTTTTCCC	22450	A_95_P009316	DW002313
23214	274	9	880	AGGGCTTCGACTTTCTTCCCCCATTTACCCTTTTGTATCTTTAGCAATGTTTTCTCTGCA	22460	A_95_P015336	DV157622
23216	274	11	331	CACGCTGTTGATCCTGTCTACAGTGTTTCCCAAATTTGTTGTCTTGTTAGTTATTGTAA	22464	A_95_P100638	BP535465
23219	274	14	309	AATATTTTAGTACAGGCGTACGTTCGTACATGCTCATTTTATGTACTCCCTCCGTTTCA	22470	A_95_P215787	TA20565_4097
23220	274	15	543	TTTTCTTAGTGTCGTAGATTCTCCTTTGTACACATAAGTTCACGTGTCTGTGAGTTACG	22472	A_95_P057961	BP134349
23221	274	16	739	ATCTATTTGATGAATGTTAGCAAGGGGGAAAATGTAATGTAACTTGTACTTTGGTTG	22474	A_95_P013041	EB444220
23226	274	21	987	CTGTATCCTCTTAATTCAATTGTTTGTTTCCTTACAGATGCATCAACATCTATCAGCAT	22484	A_95_P199817	TA17073_4097
23231	274	26	857	CTGCATTTGCTTTCTTTTCCTGTCGATGTTACAGAGATGTAATTCTATGAGATCATGAT	22493	A_95_P029871	TC42205
23236	274	31	797	TATCATTATATATGCCCGGACCCACCGTATTTTTTCTTGTTTTTCCATACTTGCATGGC	22503	A_95_P158527	EH616464
23242	274	37	1265	GAACCAAAACAATTTTCCACCTTGTGAAATCTCAGCTTCAATAAAAGTTTCCTTCTTGT	22515	A_95_P177167	M14417
23245	274	40	360	AATATCCAACGTGCTGCTGTCTATCAGTACTCTGGCTAAACGGACCCTAATTCCTGAT	22521	A_95_P107487	CV018400
23249	274	44	645	AAATTCAAGGGTGTTATAATGGGAAGAGCTTGACCGTGAATCAGCCCACACACGTGT	22529	A_95_P138322	EB442052
23252	274	47	579	GACCAAGGGTTCCAAGATTTTTCTCGGTTTTTGTTTTTATATGCAATCCCGGAATTGT	22535	A_95_P160032	EH618660
23253	274	48	693	CACACATTTTTCACCCCAACAGCAAAGTCTTTTGAGTTTATATATATACATGCTGCTCT	22537	A_95_P152822	EB683157
23254	274	49	542	ATGCATATTTGTATTAGACTATGTTGGTGTGGAAATCAGCATGTCAACTAATGCATCT	22539	A_95_P130007	FG637879
23255	274	50	433	TGCTAACAATAAAGCATCCCATAGGGTGTTGGAGAAGGCTGGATTTGTTAAGGAGG	22541	A_95_P096583	FG147325
23258	274	53	4120	GTATTTAGCTTAGGGAGTCCTAATCCTCATGTTGTATAGAGCTATATGTGTATATTGT	22547	A_95_P200612	U52078
23262	274	57	824	TACAAACCATCTTGGTTTAGCAAGCGGTTCGCAAAACCAAGTATCCCAAATACAGCA	22555	A_95_P285793	DV999492
23267	274	62	462	TTTTGATTACTGATTCCATTCTGTCCTGGCACCTTGGCAGAAGGATAAATGATACAAA	22565	A_95_P060665	FS382718
23271	274	66	420	TTGACAGGTTGCACTGTGTTTTGGCAGAAGTGATGAGTTTGTCGAGTTCAAGACTTC	22573	A_95_P096188	BP533513
23280	274	75	765	CCGTGTTATATGGTTGTCAGTTTGAACCCATATGTTAATTTGCTTGATTGTTGAATGA	22589	A_95_P272716	EB679392
23282	274	77	627	TTAGCAAACTCTAAAAATGGGGAGAATTGAAGGTGGAGGAGATCAAAGATGTATTG	22593	A_95_P308008	FG643465
23284	274	79	204	CAAGAACACAAATTTCATTGAATCTTCACCTGCTTTTATCAGCGCCATTTCTTCTCATT	22597	A_95_P093873	BP532456
23286	274	81	470	CCACTTTCTGCTCTGTAGGAGTCTCGGTTTCTGATTTTACTTCTTCTGTTGCCTTTTCAA	22601	A_95_P253044	BP528671
23287	274	82	727	ATGACGACAAGACTAGTACCTTCACTTGTGCCTCTGCTGATTACTTGATCATCTTCTG	22603	A_95_P022586	FG160313
23289	274	84	487	ATACAGATAACAACAAAGAGGAAGGTCTTCGGGATGGCCCAACAATCAGTATCTACT	22607	A_95_P070800	BP525540
23292	275	2	1433	AATTTTATGCCTCAGAAGGAGATTATGTGCCATAGATAAAGTTGAACAGGGGGGTG	22612	A_95_P263366	AM851011
23296	275	6	863	GCCTTTACACTGGATGTTTGTATTGTAATATTTCTAGATGTGCAGAAGAAAGAACCTT	22620	A_95_P209717	TA19250_4097
23299	275	9	777	ATCATCATCAAATGACAAAATCAGTCAGATGGGGTGAGAGTGGTGGGGAATGAGTC	22626	A_95_P312853	FG152714
23309	275	19	954	GCACACCTGATCTATGCCCAAGTCATCCATATTTTCTGAACTTAAATCATAGATCAAT	22646	A_95_P009666	TA14046_4097
23310	275	20	633	GGTTGATTATCTAATTCTACTATGGCTAATTTGCTATGAAAAGTCAAACCTCTTGTAG	22648	A_95_P214087	TA20186_4097

23311	275	21	790	ATTTCTTTGCCAACCCAATTTGGGTGTAATTTCAGTCAAGTGCAAGGGGTGGTTTAA	22650	A_95_P204637	EH615699
23312	275	22	654	ACTTTCCTCCCGATTCACTGTTGAACTACGTACCTTCTATATAGTTGCTTTTCTGAGTG	22652	A_95_P028371	TA18058_4097
23315	275	25	502	AACTCGTATGGGGCTACAGCTACACCATAGTTTTGTTACCCCAAATGCGAGGAAGTA	22658	A_95_P219682	TA21446_4097
23317	275	27	512	GTGCCTGACCATCGGATATGCAGTGGAGTATCCTACATTTCTTTTTACATTTTTCAG	22662	A_95_P308193	FG641465
23318	275	28	390	TGAGAACAATAAGTCACCAGTGCTACTACGCATGGTAGATACTGGACCATGTGGAA	22664	A_95_P104762	TA11718_4097
23320	275	30	909	TTGCATGGGTTAGTGGAACTTGTGCTAGACTCTTCAAGTCGGAAGTACAGTTTGGAC	22668	A_95_P011901	TA13067_4097
23321	275	31	1221	AATAATGAGCTTAGTTTTAGACTGCTTGTATTGCGCAGGGCTGGTACTGCTTGCTACT	22670	A_95_P013291	TA13313_4097
23324	275	34	746	GTTTGGTCATGTGGTGTTACATTATATGTGATGGTTTGTGGGGTGCATACCCGTTTG	22676	A_95_P157807	EH615838
23325	275	35	1139	GAAAGTACCTGTAGTCAGCACTGAGTCAATTTACAGAAGAATAAACTGTCAGTAGAA	22678	A_95_P206242	TA18469_4097
23327	275	37	109	GCTTTTCAGGAACTTGTGTATAATTGATGTGAAGCTGTTTGTTTAGTCAAGATTTGCT	22682	A_95_P065760	BP136418
23328	275	38	609	AGATACTCCCAGTGGAAGTCCGTTGCTGAGACTGGATTTTGTATCACTTACCCTTTTA	22684	A_95_P033494	AJ632788
23332	275	42	732	TAGGAATGCAATTTCTGGCAGTTTTCTTTAATAAAGTTAAAAGGTGGGGAATCACCA	22692	A_95_P115727	DV158045
23333	275	43	819	GTGTCAGACGGAGGTTGTCAAGTCTGTATATCCCAAAGAATTTAAAGAAGCGTATTT	22694	A_95_P230100	TA15601_4097
23342	275	52	611	ATCGTTCTGCCTTCTTCAGTTTTAATATCGGATTTGGAATTCAACTATGGAGTTTGATC	22712	A_95_P279833	FG643534
23343	275	53	181	ATATACAAATTTACAAGAGGCAAAGTAATATCGGCGAGATATCGTTTCGGTCGTCAT	22714	A_95_P213097	FS409145
23346	275	56	520	GATCTCTCCCTTCTATCCTTGTTATTAATTAGTATTTCGTAGATGGACATGCATTAGGT	22720	A_95_P278878	AM840564
23355	275	65	752	CAAGATTCAGGAAGGGATCATAGTGCATTGACTTCAGGGTCCTTGGATCAATCTCAA	22738	A_95_P229264	EB678951
23356	275	66	1819	GACCTGATTTTACGGTGCTTCCAATTGTTGAGGAATCAAGAAGGCTCACCAACATAA	22740	A_95_P191027	TA15141_4097
23364	275	74	55	GGTTGGATTGTTGTTTAGTTGGATGTTAACTTTGAATGTTGCATTTTGATGTTTGGTT	22755	A_95_P132552	EB433046
23365	275	75	702	TGTTTCTCCCTGAATTGGTAACAGAATTCGTTTGAGCTCTAACATTTCCATGGTATGC	22757	A_95_P195197	TA16063_4097
23366	275	76	175	GGCCACTATATTTCATGTGCTATGTTGCTTTTTGTGTTTTTAACCTTCTGTACACAGAT	22759	A_95_P141022	EB444818
23368	275	78	725	AACTCCAATAAAGGCCATAGTCTTGACCAGGGAACACAAGGCTATATATCCACAAGA	22763	A_95_P291643	DW005133
23369	275	79	613	ATGCTGCTGCTGTGTACTTCTCATCTTCCTTAAAACATTGTGTCATTGGGTATTTTAAT	22765	A_95_P022601	FG634827
23371	275	81	529	TCAGCAGGACCTTTAGCACCTCCTATGAATATTTCAGCACTGCAAATTATGCCGCATG	22769	A_95_P063660	BP135840
23376	276	1	761	TTTAGCCTTCAACCAGATATCTAACAACTGTGGTATGCTCCACTACACATCTGGTGGC	22611	A_95_P034439	DV161194
23379	276	4	745	GTGTTTGAATTGGCCATTGTGATTACACATTTTTCTCAGGGTATATACCTGAAATAAG	22617	A_95_P223437	TA22251_4097
23381	276	6	811	AGGAGTTCTGATGTAGCAACGAGGAAAAAGTATGCTAATCTGGTTGATTCAGTCAA	22621	A_95_P145992	EB449806
23386	276	11	957	GTTGAAAGCTATATGCAGATTGTTTTTGCAGTATCTGCTGTCTGTCTCTGTATCCCTG	22631	A_95_P008291	DV161541
23387	276	12	541	GTGGACAATACCTCTGATGTATCCCAAATAATAAGTTGATAAAACTCCTGTGATTGC	22633	A_95_P006191	TA17267_4097
23388	276	13	547	TGGAAAAATGGAGTAATCACTCTCAACACTTTGTAGAAGGAAATTGGCTTGCAACTT	22635	A_95_P124362	DW004210
23394	276	19	850	AAGTTATAGTGATCTTGTCGACAGTGTCGCTCTAACCAGAGAGTGATGCAATGTGAC	22647	A_95_P227279	FG148938
23395	276	20	420	TCACAAAGTTTATCGACATCTACAGGGGGTGCAATTCCATCCTGAAAGCATCATCAC	22649	A_95_P071220	BP525648
23398	276	23	329	AACCAGAGGATTTATCGTTGCGAAGATGTTGGTGATTTTAGATGTATTTATGGTCCA	22655	A_95_P062675	BP135575
23401	276	26	519	CAGGCTATTAGCTATTTTGAGTTTGTGAACAAACAGTTTTTGATTTGGGTATTGTACT	22661	A_95_P019871	EB683230

23403	276	28	639	AATTGGTGGTAATGCAGCAGATCTCAAAGTGAAGAGGATCACACCAGCATTTGCAA	22665	A_95_P053316	BP133146
23404	276	29	768	GGGTGTTCTGATACTATAGTCCTATAGTTGATGTGATTGTAACGTAAATTTTGTGTCT	22667	A_95_P268831	DW003203
23410	276	35	435	TATTTTGTATGACATGGGGACATGCTATCTTTTTAAGTGTGGGGTGGGGGATACTCT	22679	A_95_P274613	AM780197
23415	276	40	1115	CACGAGAACTGAGGAAATCTATGTAGTAGGCCAATTTTGTACTCATTTTTTGTCGTTA	22689	A_95_P010746	TA14579_4097
23420	276	45	1303	TAGTTGTAATAATCATCCTTTAACCCAATCCTGAGTTCAATGATTGACATTTTTCGCCG	22699	A_95_P194162	TA15834_4097
23421	276	46	650	ATATGACATCCAACAGAATGCTGGCATCCGTTTAGTCGCAGAAAAGTTGATCCTGCA	22701	A_95_P054281	BP133394
23424	276	49	650	CAGGGGAGATGCTACTACTATCTAGTTTTGTTTCTTCGACTACTATCAATATAGAGAG	22707	A_95_P184047	TA13599_4097
23428	276	53	314	GTTTTCAGATTCAGATAGATGCACATAAAATGTCTGAGCGTTCCTCTTTGATATGGTT	22715	A_95_P162352	EH621296
23430	276	55	798	ACTGCAGTGAAATTGTATGAAGGTTGTTTCCATGGTGGTTTAAAGAATATTGATTCC	22719	A_95_P010961	EB425537
23431	276	56	849	CTTCCCGTTCATAGACCAAGGGAAACTCTTTTTAGTAAGTGTTAGTGTTCCAATAACC	22721	A_95_P246942	DV161533
23433	276	58	255	CCAATAAAGTTCTTGCTTTAGGCTCCAAAAATTCAGGGCCCCTAAAATCATTTCTATA	22725	A_95_P033474	AJ632773
23435	276	60	294	TAGGTGGTGTCACAGTTTATCGTAATCTAGTTAAGTTTGTTGAGTCTTTTGTTATCGT	22729	A_95_P142052	EB445613
23436	276	61	441	AAGGCACCTATGGTACTGTTTATCGCGGTACCTATGACAATCAAGATGTTGCAGTGA	22731	A_95_P201262	FG162155
23437	276	62	666	TGATCATTGGTGTCAGTTTCTACAGGCACGGCATAACAAGGCTATTTCACGGGATAC	22733	A_95_P136132	EB643439
23440	276	65	551	GGGAGATATTGTGATTCATTCATTCATTCATTGTAGGCAGGAATGAAAAGGTCATAA	22739	A_95_P037921	BP129130
23449	276	74	79	TCGACTTGTTTATCGAACAAGGGAATTGTTTTGTGATATATACTCTGGAAATTGTCCA	22756	A_95_P002701	TA18356_4097
23450	276	75	448	AATACTGTGTTACTTTAAACTAGAATTCAGGTTCTTTGCTTGGCCTATTTGCTGCCAA	22758	A_95_P093878	BP532458
23452	276	77	742	CTGCTTTCATGAAGAGGGTAAAAAGGATTTATTCAAGCTGAAGTAATATTGCTGGCT	22762	A_95_P026111	EB439094
23453	276	78	872	GATTCGTTCTCTAGTGGAGTACTTCTTATGCACGTGAACCCTCGTCTCTCCGTCAAAA	22764	A_95_P208617	DV157933
23456	276	81	612	GTGGGTGTAACAACTTGTCAACTTTTTCTCTGTGTTGCCTATTATATATCGAGTTCGTC	22770	A_95_P141802	FG637949
23458	276	83	715	ATCCTACAAGGACAGTACCCTTATCATGCAGCTCCTAAGGGATAATCTCACTTTGTTC	22774	A_95_P045591	BP131186
23463	277	3	634	GATAACGAGAGTAGAGAAAGTGGTGGTGCAGAGCTCTGTGAAGCCAATAATAGAG	22783	A_95_P136157	EB439786
23465	277	5	1007	CCAGACAACATTTTTACTTGGTTTGCGTGCTTTTCTTTTGTAACATTATTGAGCGTTTG	22787	A_95_P025741	TA17830_4097
23469	277	9	713	TTATGAAGCGGATGGCTTAGTTTATGACCTGGTGTTGTTGCTGCTGTAAAGAGGCTG	22795	A_95_P027706	EB681224
23473	277	13	709	TACACCACCAGGAAACTCCACTAATTTTCAGTTAATGCGGCACAAAGACACAAGTGT	22803	A_95_P303353	FG197665
23475	277	15	775	TTGCTGGGATGATAGTTTGAGTGGGGCTATGATGGAGGCAACAAACATATTGCCAG	22807	A_95_P162002	EH620733
23476	277	16	526	CATGACAATTATTCTGTGGCCCCTTCAGCGACTGTTGTTGTCAAAGGCCTTTCACAGA	22809	A_95_P064415	BP136045
23477	277	17	529	CGAAGAGTAATTGATCAAATTCGCGGCCGGTCCTATGAGGAAACGCTTATGATACTA	22811	A_95_P248432	AM794263
23478	277	18	368	TCCTTCAGGGCTTGTATAGTTCAAAATATTTGTATCCCATTTTGTAGGTTGATGCTGA	22813	A_95_P089448	BP530510
23482	277	22	736	GACTTCCTCCATGATTATGGAGTAGTTTCCCTTAGAGTTTGACGTATATAGTATTTTG	22821	A_95_P149222	EB678920
23483	277	23	700	TACTTAGTTCTTCCGGTTAGCTTTTTATTCAGTGTGGAGAGGGGGGATTTGATAAGC	22823	A_95_P207712	EB677626
23486	277	26	1308	TGTACCATCTCAGAAGGATCATTATATGAAATGTCTTGTCTGCTTCTGCAAATTGGTG	22829	A_95_P208597	TA19002_4097
23489	277	29	805	ATGTCAGCAAGTACAACCACACTACGTTACCCAGGATACATGAATAACGACTTGGTT	22835	A_95_P286913	AJ278739
23491	277	31	251	GATGGTTGTATTGGCTACAAGCAGTTTTGGTTGAGTTTGAAGTGATCAACTGCTTTT	22839	A_95_P130112	EB430110

23492	277	32	381	CGTGGAGGTGAATCTATTTATGGTGAAAGTTTTGCTGATGAAATTTCAGATAAGCAC	22841	A_95_P108067	CV018655
23498	277	38	242	AGTTTTGTGTATAATTGTGCTGTCATGGGTTGCTGAGATACGGAGTTTGCCGTCCAT	22853	A_95_P155062	EG649879
23506	277	46	281	AAGAAAATGAGAAGTTATTTGATCGTTTGACAGAGAAAGCCTCTCTAGCTGGATCAC	22868	A_95_P077145	BP527174
23507	277	47	538	TCAGGTCAAAGCACTTATTTCTTGGCTATACTTTTCTGGTGCGTTTAGTACAGAGTTA	22869	A_95_P004516	EH620311
23508	277	48	693	GTACATATAGTTTAAGGAAGCATATTAGGTGTTGTCTTGAACGTCTTCCTGAAATCTG	22871	A_95_P235829	FG643574
23515	277	55	100	ATCCTGCTTGGAAGACTGCAACTTCTCGAGATGTTGATGTGATAGGCTAGAACCATT	22885	A_95_P032996	AF211772
23523	277	63	554	CGCCATTTCGTTATATTTAGTGAAACTGTTAATAGGGATTCGATCGGACTAATTTGAA	22901	A_95_P225782	FG631576
23526	277	66	1936	CACTGGAATCCCTATTTTCTATTCCAATTTCCAATTTTAGTAACTCTGAACATCATGCA	22906	A_95_P013911	TA13844_4097
23527	277	67	855	TTGTTGAGAACCGAGCATTGACAAGCAAAAGGTCCAAAGACAATTTCAGTTAAACAT	22908	A_95_P180502	TA12761_4097
23528	277	68	606	TATGAATCATAGAGGTTGAAGTGTCTCTCTCCCTCCTCATTTTCCCCTTTCATGAATCC	22910	A_95_P194707	EH618843
23529	277	69	631	GACTGCGTACATGCTATTGATTTGATTTTTACTCCGGTTATTGTTTATTGTTACTACCA	22912	A_95_P089913	EB683516
23535	277	75	630	TATAAGAGTTGTTCTTATGCAGGAGGATAATTTATAGCCTTCATCAGTAAAGGTTTG	22924	A_95_P290938	FG635699
23541	277	81	162	GTACGTTGATGCTGCAGCATTAGAAGATAAAATTATTGGAGAGAAGAAAACTGTTG	22936	A_95_P140237	EB444185
23542	277	82	300	GCATTTCAGAACCTGAAATGAATTTTGCTCTTTGATCTGAAATGGACAATCTCCACAT	22938	A_95_P097138	BP533891
23543	277	83	928	CTTGTAATGCTGAATTCTTTTGAGTATACTATTGAATGAGTTTCCCTCGTTCACCAGG	22940	A_95_P191297	TA15204_4097
23545	277	85	566	GCAGGAGTATGTAAGTTTTTGAAGATTTCCAGACCCTTTTTTGAAGAATTGTGAATTG	22944	A_95_P011671	EB683603
23547	278	2	774	GAAGCATGATTGGGTCAGATTCTTCAACAACTGATTATCCAGGAAAAATTCCAAGTG	22782	A_95_P262901	EB425832
23555	278	10	599	CCATGTTGAAAAGCTCCTACTTTGGCCCCCTTTGATTTAGAGTTAATCTTTTATTCTTA	22798	A_95_P097903	BP534255
23556	278	11	777	TGATAGATTGGAATATAGAGCCAGCCTGGAAACATGTTTGCACTCTATCTGGATATC	22800	A_95_P148217	EB677461
23557	278	12	585	CACATACAGTACCAATCTATGAAGGTTACGCCCTTCCTCATGCAATTCTTCGATTGGA	22802	A_95_P187363	FG134864
23559	278	14	427	ACTGAATTCTATAAGATGATAGACAAGATATTGTTGAAAAGTGGGGTGGGGATTGA	22806	A_95_P092903	BP532039
23560	278	15	197	TGCTTTCTTTTATTAATGGATCTTCGGAGTATTCAGCCATATGCCCCGCATCGGGTCC	22808	A_95_P137437	EB441175
23562	278	17	485	AACTACTTGACTAGTGTTTATGAAGAAGGAGATGCTAGATCAGCACTAATCGCTATG	22812	A_95_P240594	DQ218337
23563	278	18	854	GATTGCCTCCACTTATAGCGATGTCCTTTCTGCAAACATCTTGGATGTTGAACAGTGC	22814	A_95_P292583	EB427721
23564	278	19	420	GTCTTTCTTGTGCTGAAGTTGCTGAATAGCCGTAGCAGAACTGATGTTACCTTTTTGT	22816	A_95_P152932	EB683258
23569	278	24	486	TGATTCAAGTGAGCAAGTAGCTGTTGCCAAGATTTGGTAGAATTTCAGAATGAGATA	22826	A_95_P307643	FG639010
23570	278	25	1120	TTCTGGGACGAGTTGGAAGAGGAATTCCTAATTCTTACACGGATGAGACTGATCACA	22828	A_95_P176317	U92011
23572	278	27	349	AAGCGCTTTTATCATCAGTTGATGTCAAACAGAGTGTTTTAAGCATCGACGAGTTTAT	22832	A_95_P101373	CN498813
23574	278	29	611	TTTGAGTCTTATACCTTGGTAGTATTATGTTATTGTCGATCCAGGGGAATCTTTTTGTT	22836	A_95_P143132	EB446477
23577	278	32	738	AACTACTTCACATTTTCAGATTGCTAGGTACTCCTAATGAAGAACTCTGGCCCGGGGT	22842	A_95_P146707	EB450817
23581	278	36	750	CTAGAATAATTATGTCCTATGCTCATTAATCAGATCTATGTTCGAGAGAATAACTTGG	22850	A_95_P214297	DW003320
23588	278	43	534	TATTCTGCCAGTTATGGCTTGTTCATAAGATTGTCTATATTGGGAATGTTGTCTCTTCA	22863	A_95_P006326	TA15957_4097
23590	278	45	423	TTTTGTTACAGGGGTTCCAAAGCTGAACAGGTCTGAACTTGAAACAGCATGTGAGGA	22867	A_95_P139197	FG166170
23592	278	47	815	CTTTTTCCGACTGACATCCAAGTTCCGTTGGTTATTGTACTTCTTCTGGTTGTTATATT	22870	A_95_P147632	EB452145

23593	278	48	759	TTATAGGGAGAATGCTCGATATCTTGGCAGTGGAAGGGATCATGGGTATGAACCTA	22872	A_95_P267451	EB677243
23594	278	49	767	ACATCTGAAAATCGCTTATATGTCACCAAATGGCAAAGGTAGTACAGCACATGATGT	22874	A_95_P028536	EB448450
23595	278	50	644	CCAGAAGATCGATGATATGGTTGAAGAAACAAGGGAAACTCATAGTGATCAAATAG	22876	A_95_P272061	EB447231
23607	278	62	1337	AGGCAAGGAGACTTGTTCTCTTGTCTCTGTTTGTGAATAATAAAGTCCGAATTATGGT	22900	A_95_P012331	TA11989_4097
23611	278	66	712	CAGCACTGGAACTGTATAATTACCCCGTTTTTCATAATTTCAGAGTTATGTTCTTTACA	22907	A_95_P236949	FG135742
23614	278	69	862	ATCGAAAGCTAGTTCTTTGGTAGTCATTTGGCAAAACTTCTAATGGTTGCATCTTGCA	22913	A_95_P295053	EB444005
23615	278	70	474	ACGGCCCTTGTCAATTGTTGTTGTAATAATTGGCTATTAGCGATTGAACATTTTGCTT	22915	A_95_P306368	FG635097
23616	278	71	964	AGCAGCCCTGTGTATTCAGATGGATTTAATGTATTACTTGAACTAGTCCAATTTTTCC	22917	A_95_P181672	TA13038_4097
23617	278	72	2803	TGGGGACATGACCGAATCAATTTGATGTATGATTCGGCCTCTTCCCTATGTAATCTCC	22919	A_95_P179312	TA12478_4097
23618	278	73	526	AGAGGGGTTTGGAGACGTGAAAGACGAAAAGGGGCAAGAAAATCTGTCTTTTGTAT	22921	A_95_P041746	BP130173
23620	278	75	668	TTGCTGCTGCTGCACTTTCAATTGCAATTATCTGAACCAGTGACATTGCTTACACCAA	22925	A_95_P246337	TC72511
23622	278	77	949	GTAGAGCCAAACCTTGCCGTTTGGCAGCAAACGATCTTTGATTTGGTCCTTGTTGTTT	22929	A_95_P015646	TA18745_4097
23623	278	78	650	ACTGGAGACAGACTGAATATATGGATGGTGAAGATGGAGAACTATCCTGGTTCAAT	22931	A_95_P214207	EB449640
23625	278	80	1503	TTTCAGTAGTACTGGTGGATCAAATGGCCATGAGTTTGCTACTCCAGTTCCAACATTG	22935	A_95_P217657	TA20981_4097
23627	278	82	492	GCTAGTATTACACATTTGTTAGTGATAAGCTGGTTGTAGCTGAAACCTGTTTATCTGT	22939	A_95_P024336	DW003577
23628	278	83	792	CCTTGTCTGCTTGTTTGTGTATGACATATTTTGGGTTTTCTATTCCGAGAGATTCTTTG	22941	A_95_P184277	DV161576
23629	278	84	777	AATCACTTGACAAGGTTTGTCGGCCTATAATGATGAAACCTAAGCCAGCTAAGCCGG	22943	A_95_P226534	FG132790
23630	278	85	410	CCCACTGCTTGGAAACCTACCTCCATGGTGTGTATTGACTAAGAAGAGCTATATAAG	22945	A_95_P078765	BP527598
23637	279	7	923	TATTCTGAAGATGTTTCTGTAGCCCCTGCTTGTGCTATTCAAACTTTTCTAGTATTATG	22958	A_95_P206552	TA18543_4097
23645	279	15	565	CCACAGCACTCATGCATCAGAAGTCTACACGCTTATTAAACGTCTTTATTACTGCATA	22973	A_95_P024746	BP130288
23646	279	16	760	CTATGGCAGGGAAAGAAACCTATATCTAGTGGCATTTGTTTTTGTTTAGACTTTTTGA	22975	A_95_P006321	TA15419_4097
23647	279	17	427	CTGTAAGGTTTTCTAATATGATATTCGTATGAAAGGAAGCTGATTTGGGCTGTAACA	22977	A_95_P003141	CV020904
23652	279	22	98	AAGAATGTAGGGAAAAATACAGATGCTGTGTATGAAGTGAAGGTGAACGCGCCGT	22987	A_95_P105387	CV017445
23658	279	28	883	GGGAAATTTAGTTCTAGTGCTGATGCTGGAATTATGGTCTGATGAAATTTTCGATTCT	22998	A_95_P176437	Y09506
23661	279	31	572	CAAAGCCGCGAAGATCGTTAAACTTTGAACGGCGAACGAGATATACTCCATAATGGT	23004	A_95_P114782	CV021755
23662	279	32	1351	AGCAACTGATATCTAGTCTCCAACTGTGTTGTGCTTGTGCTTTTTCTGGCATTCTGAG	23006	A_95_P183352	TA13439_4097
23663	279	33	552	GTTGACAAGCGTCAGTGGATGACAATATCTAATTGTGGCTTTCTTGGTGTTTGTATTA	23008	A_95_P150877	EB681015
23667	279	37	428	GGAATCAAACACTCAGATCTACTTGGCAAGTTGGCAATGAATTCCTCCCTTCCAACTT	23016	A_95_P282503	AM806329
23668	279	38	782	GTGATTCTCACACTGCGAAGTAATGTAATTTGGCATGAAAGTTGCATGCTTTTTTAGT	23018	A_95_P296508	EB677472
23672	279	42	235	AATATTAGAGAGATGCTTACTGGCGCTGCATTGATGGACGAAGCAAACAGGACAAC	23026	A_95_P207862	FG158493
23674	279	44	1100	CATATGTGTTGTTCTATCGAAGAGTTAAAGTTCAACAAAATGGAGTTGTGGGAGGG	23030	A_95_P214217	TA20214_4097
23679	279	49	723	GTCGGGTCTTTACTGTAATTGGTCGTTTTTAAAACTACCAGTGCAAGTTAGAATTGG	23040	A_95_P026081	FG168780
23680	279	50	476	GCACTGATAAGCAATAAGTACATGACATGTATCTTTCACATAAGGCTTATCAACCAA	23042	A_95_P252914	FG633958
23681	279	51	401	TCAAGAGGAAAGATTCACGAACCTCAAATTAATGTGGAAGAAGAATTGAAACCGTT	23044	A_95_P096278	BP533555

23683	279	53	1244	TGCAGGATGAATGTCACTGTGTACCTTTGGATGTTTCATGTCTATTCTTCTTTCCTTTT	23048	A_95_P000401	AY220080
23686	279	56	853	CTAGCTTTTATTGTATCAGATAATGAAGGCAAAGGTGTCGTGCCTTAGCTTTGAGTG	23054	A_95_P193207	TA15621_4097
23691	279	61	766	AGTGTCTCAATTAGTTCATCAAACCCCAGACTGTTTGTGTCTGGGTCCTGTGACTCAA	23063	A_95_P121222	AF249743
23693	279	63	751	GGATTTTACTGGGTAGTTGTTGTTGTTATTCTTATACTGTCGTTATGTATCCCTTT	23066	A_95_P006226	AB257509
23694	279	64	1220	GCTGCAAGTTAGGGATTTTATCAGAGGAATTTAACGTTCCTTTTGATCACACATGAA	23068	A_95_P033061	AF289466
23695	279	65	736	ATGGGTCTCCAAGGCTTATGAACGCACTGTTCAACTTATAGAGGAGCACAAGGAAC	23070	A_95_P216462	EB447668
23701	279	71	307	TTGATGCAAGACTTGTGTCTGTAGAGTGAAAAATAACGGGTTTGCAGTTAATTATCTT	23081	A_95_P199362	TA16978_4097
23703	279	73	421	AGTGGAGTATGAGAACTTGTAATAGTAAACCTTCTAGCAGCTTTTTATCCTGACCTTT	23085	A_95_P132762	EB433475
23707	279	77	439	TTCCAAGATAAGCACAAGTTTTCCCGTTGAAGCGCAATTACTCGGTCTCATTTTGCTG	23093	A_95_P025046	BP533776
23709	279	79	389	CTCTGCTTGTATTCTGGGGAGCCCTGAAAATTTTCCCCATTCCTTGGGCTGTAAAAGT	23097	A_95_P094433	BP532711
23711	279	81	396	TGGCTTGCCTAATTCCGTGCTGCGAAAGAATGCTACTATTATTTATGTTTGAACCTTT	23101	A_95_P000786	EH620721
23716	280	1	748	CTATTGCCAAACAGTTTTGGAACAATCTGTAATCCAGTTTGTGTTGAGAGCTATTAGT	22947	A_95_P213412	TA20040_4097
23718	280	3	694	CAGTAGCATTTACATATCTTACTATCAGTACGGCATTGTGAAGTTACTATACTGGAAT	22951	A_95_P015226	TA15040_4097
23723	280	8	746	GCTTGACATGTACCTTCTGCTGTTTTGACTACTGACTTGTGGCATTATATAAAAAATT	22961	A_95_P117172	DV159969
23724	280	9	0	CCACGTTAAATCCAATTTTTTCTAGTGTTGTAATGTCTTAATACAAGGTTGGCTTTTG	22962	A_95_P025591	A_95_P025591
23725	280	10	1716	GCGCTGCTACTATGTCCTTTGTGCTTTTAGCTGTTTGTGTTATTTTGCTTGAAATTTAA	22964	A_95_P011796	TA14578_4097
23727	280	12	1719	CACTCGATTGTGTTGGCTTAATTATCTGTTGTGTACGATTCCTATGAATCATGGAATT	22968	A_95_P032911	AF198498
23729	280	14	664	TGGCTTCTAGCACTTGGAATGAGGTCTCTGCATCAAAAACTTTGATCACACCTATCCA	22972	A_95_P119232	DV162340
23731	280	16	491	ACTGTATCTGTTATAAATTCAGAGGGGGACACTTGTAGTGACTGTGAATATGCATAC	22976	A_95_P130117	EB430114
23734	280	19	363	TAATGTTGGTGCTTCCTTCCAACTATCATCTGGCAATTACTGCCTGCAAGCAGTTAAC	22982	A_95_P066055	BP136496
23735	280	20	326	CTCTATCGCGCTGAGTATAATATAGAGCTCCTTGATGCTGGTTCATTTTATTAAATGA	22984	A_95_P095258	BP533102
23736	280	21	849	CTCTATCGGGCACTGGTTATAAGTGCTTGAATAGTATGTGTTTTTCATGTAAGCTTAA	22986	A_95_P208737	DV999621
23738	280	23	746	CTGACTGAGAATTGTTGGATATGGACTTCATACAGTCTGAGAGAGCGAATACGACG	22990	A_95_P285803	FG166736
23739	280	24	860	GCGTCTTTTGGTATGGTCTCATGCTTGAAATGTGGCATCTATATTAATTCTTGAATTT	22991	A_95_P267921	DV998765
23741	280	26	372	GATGCGATCAGTAGAGGGATCTTTATCTTTAGTAAAAGATGTTACTGCTCTTTTGAA	22995	A_95_P005716	GH986496
23742	280	27	179	ACGACACCACCTGCAAATGGTAAAACTTTCTCTACCACCATGCAACTTATCTTGGCTA	22997	A_95_P062790	BP135606
23747	280	32	741	CTTTCTGAGACATCGTATGGTTGTCATTTTATTAGTCTCTGCAAAAAACTCGTGCCGC	23007	A_95_P007001	TA14674_4097
23748	280	33	283	ATGCCAATGACAGAAGTTGAATATGGATTTGTGATAATGCTAGTACCTTGTCATTAG	23009	A_95_P105227	BP534328
23749	280	34	227	GCACGACCTCTGAAGATGGAAAGCATCAATCTATATACCTTACAAGTTATAAGACAA	23011	A_95_P106227	CV017813
23750	280	35	658	CATGTTCTTGGATTATAGAAGTAACAATAGCTGGATGGGCAAGAAAGTAAAGAACA	23013	A_95_P233074	FG640747
23751	280	36	205	CTGGTCATTGCTGTGTGTGTTTGCTTATTTTATCAAAGCACTGTATTTGCTTTCTGTGG	23015	A_95_P006501	CV016456
23752	280	37	712	ATGGATATTAAAAGGCTTCAGTTGCTCTGCCCTTCCTATTCAATTTTACTGTTCTGTTT	23017	A_95_P189222	DV158664
23753	280	38	116	CCTTGTCACAGGTTGCATAAGTAAAGAATGAAATGGCTGATCTAGATTCTTTACTCCT	23019	A_95_P107472	CV018391
23756	280	41	968	CAAGTACTATGCTATCCTATGTGTCATTTGGATTTGCGCTTTGTCTTTATGTAACTGTT	23025	A_95_P223302	TA22220_4097

23757	280	42	519	TTCTCTGAATATTCCAGCTGACAACATGCTTTAAACCTCTTTAGTTCATAGTTGCTTTG	23027	A_95_P209842	TA19275_4097
23759	280	44	1483	GGGATTTGATGAATGCAAATCACCTTCCGTCAAATTATTAAGTTAGCCTGAATGTTAT	23031	A_95_P008546	TA13125_4097
23762	280	47	681	TTTGATTTCCTTGCTTGTATCACTTCCGGACAGAAGTTTTAATTGAAATCCTCTTAAAG	23037	A_95_P117637	DV160554
23763	280	48	843	TTAAATCCAGGCCAATGGTCTACACTACAACATTTGAGACTCGAAAATAATCGGCTC	23039	A_95_P126492	EB425810
23764	280	49	778	GCCCCCAAGAGAAAGGTGAAAATAAGCAAGTTATGAAGAAAGTAGCCTCTAACGGT	23041	A_95_P129047	EB428811
23765	280	50	814	ATTTCTTAAGAATCTGTCTTCTCTGCCTTTGTTGAGTGAAGGTTGGTTCAAATTGCCT	23043	A_95_P129042	EB428808
23766	280	51	850	CAGATAACAAGGGTGGATAGTGCTTGATCTATTCTTGACTTGTCTACTATTCATCTTA	23045	A_95_P197557	DW004644
23768	280	53	104	AAACTCCGACTGTTTCAATCAGCCTAACTTGAACAAATTTGTGGGATTGGGACGACC	23049	A_95_P192537	TA15473_4097
23769	280	54	796	TTTATGGATCCTGTATGATGAATGACATTGAATTAGTGCTTAAGGCAATGGTTTCTGT	23051	A_95_P228469	EB679710
23770	280	55	276	ATTCTTCCTATGTTCACTCCAACGAATCCCATCAGATCAGAGGCTTGCGATTTGAACA	23053	A_95_P110852	CV019939
23774	280	59	351	ATCCAACGGAAGTGTCAAATAAATGGTTGGACTTGTATATGTTACGGATTTACCATC	23060	A_95_P109032	CV019119
23780	280	65	436	GGTGATAATTGTGGGGAGAACTTATTTTTCTTCTCGTTTTAAAAGGCCAATGCTAATT	23071	A_95_P026491	TA12980_4097
23785	280	70	487	ATGCCTAAACAGAGTAACAACAACAACAACAACAACCCAGTATATAATCCCACTAGT	23080	A_95_P123197	DW003075
23786	280	71	310	TAAGCATCCCTTAATCCCCTAGGCGTGTAGTGGGTGCCAACTGGTTATATTCGAATG	23082	A_95_P160872	EH619574
23788	280	73	1415	GGTAGGAGGGGAATTGTGTTGGTGTTTACCTGTTAACAAAATGAAACATGTTTTATT	23086	A_95_P204412	TA18060_4097
23789	280	74	171	CAATGTGTAATCTCTGCCATGTACTATAGTCAACTTGTTTGTAAGAATAAGGACTACG	23088	A_95_P114222	CV021500
23790	280	75	115	GTTGGTTATAAGATTTGTTATCCCAATGGGTTGGTCTGTAAGCATTTGTTTGTTTTTG	23090	A_95_P144072	EB447233
23791	280	76	743	GAAAAAATGTTCAACATTTGGCATGCAGCACAAACGTTCTACGTCCTTTCCACCTGG	23092	A_95_P245617	EB451352
23794	280	79	659	TATCATTACTGTTGGATATTTTCTGAGACTACTTGTGGGTTCAGATCCTAACAAGTTC	23098	A_95_P284413	FG643166
23798	280	83	821	TGTAGGAAGAGCTGCAAAGCTTGTTAACTTATTATACTTCTTCCTCTAAATCTGTTCA	23106	A_95_P216037	EB447902
23799	280	84	482	ATGTTTTCTTTGTGTAGTAATTGGTGCACTGCTGGTAACATATTAAGCTAAGCCCGGT	23108	A_95_P259446	EB437617
23800	280	85	300	GGCACTAAAATCCTTGGATTTCAGACGAAACATGTCGTTCATGTCTCACTAGCGCAC	23110	A_95_P095498	BP533214
23805	281	5	1047	CTGCTCTTTTCTTGATGCTGAATTAAATGTTAGAAGGTGGACGCACAAACAACATTAT	23119	A_95_P008036	TA16363_4097
23812	281	12	510	GTCTTTTAGTTTTTACCTGTTTTTCAGTGATAATAAGTTTAGCGAGACCTCGAAGCTA	23132	A_95_P125322	DW005120
23814	281	14	856	CAGAATGAAGAGAGAGCTGATGGGTTCAATGGATATTGTTTGTCACTGCACTTCTCA	23136	A_95_P227929	FG144415
23819	281	19	592	ACCGAGGTCACTGCTTAAGAAGACAAAAACAACTTTTGTTCTCATCATGTTGTATCTG	23146	A_95_P276523	FG185842
23821	281	21	444	TAAGTGCAGGGTGGGTAAGGTTGATGTGTGTAATCTTACAGTATAGTTTCAGCTAAG	23150	A_95_P252589	EH622151
23822	281	22	410	GGGGTTTTCTAAATTAGGTTTTCGAAAGAAGGATGAGAATTCCTCTGTGGATAGTTT	23152	A_95_P097818	FG643580
23823	281	23	270	CCTTTAAGACTCGTAACGTACGTATTTTCAGCAATGGGAACAACTTGAACATACTGCA	23154	A_95_P093968	BP532507
23824	281	24	1172	GGAGGACTGCTTTATCCAAATGGATGGGAATATTCTTTTAGCTGAATAAGCTATGTA	23156	A_95_P309148	AJ299250
23826	281	26	246	TTCTTCGGAGTTGTCGGGTCTAGAAGTTTTGTGTATATATGTAGATATGATATGGGT	23160	A_95_P156907	EH614997
23829	281	29	727	CTTGTGCAAGATTATGTACTCTTATCAAATACACTACAGCCTAATTGATACCTCATGA	23165	A_95_P013841	TA15344_4097
23833	281	33	1077	GGCACATAGCTAGCTGTACTTATCAGGTCTTTTGTTTGCTTATATAATAGCTTTGTTA	23173	A_95_P214067	TA20181_4097
23835	281	35	821	ATTGGGTTCTGAAGAAGAAAGAACAGATGAGGAAAAAAGGGAACGCAGTTCCTCC	23177	A_95_P255014	EB678811

23837	281	37	430	TACAAAAGCTGGCCTTTCCACACTGCACTTACTCTGTCTTGGATATAAAATCTGGGTGT	23180	A_95_P065250	BP136280
23842	281	42	700	TTGCCTATTTAGTACTTGTTTTATGTTTTGCTACTTTTATGTACTGCCGGGGGTAGAAA	23189	A_95_P239469	EH619964
23848	281	48	808	CCAGACGAAGAATGAAGTGGATGCCACTGCATATACTTACTATATACATGTTATAATT	23200	A_95_P207642	EB680934
23849	281	49	981	TACCAACTCGGAGGTTTATTTACTGTCATTCGTTATAGAGAATGATGTTAATGGTTGT	23202	A_95_P187077	TA14267_4097
23850	281	50	378	AATTACCTAACTTCAAAGGACTCTGAATTAGGTTCGACCACTGGAAGAGTCAAACCTT	23204	A_95_P062210	BP135458
23851	281	51	853	TTATTCTTTATGATGTTCACGGAAGTAGCTCGCTCAATTCTGAAGGACTGGCGTTGTT	23206	A_95_P311363	FG155210
23858	281	58	580	TTGTCCACATTGTCATGCTAGTCCTATAAGCCAATCATGAATCCTTCTAATAAATCTTA	23220	A_95_P133947	EB435655
23862	281	62	882	AGTTTAGTGAGGTTTTTGTTCATCAGCTCATTCATACAATTGAATTTGTACTTGGAGCA	23228	A_95_P230909	EB682574
23868	281	68	1083	GTGGGAGAATGTATCTGATCGGGGCATATTTTCTATAGAAGGACCTTCGCTTTTCATT	23240	A_95_P007811	TA12835_4097
23873	281	73	728	GGTAAGACAGAACTGGATTTGATAGCAGAAGTGATTTATATGAATGTCACTTTTTACT	23249	A_95_P014866	TA12646_4097
23876	281	76	284	CCTTGCCCGCAAAAGGGCTAAATGGAATTCTTTAACTCCTCTTGAAGGTTAAATATAC	23255	A_95_P079005	BP527662
23877	281	77	679	AAACTCTCACATAGTTTGTTTACAAGTGCTTATATTCAGCCCAATCTCAGTTATTTAGC	23257	A_95_P017041	TA16614_4097
23886	282	1	229	GGGATTTTGGTTGATTCAAGCACCGTCTTTATGGATAGTTGTGCATTTACCTTCCTTG	23112	A_95_P103182	CV016385
23887	282	2	172	TATGGCTGACTCGTCGGGTAAATCACACGAAACAGTAAAAAATTGTAAAACGGAGG	23114	A_95_P132277	EB432721
23898	282	13	971	CTATATCAAGTTGAAGTGGGAAAGAGCATGCTACTTTTGCGTGAAATATGAAAAAGA	23135	A_95_P011356	TA18829_4097
23903	282	18	298	GCTAGTGTTCTCTACACATCTGTTGACCCTCTTCTCAGTCATTTCTGTCTCTACATTTCA	23145	A_95_P074055	BP526374
23904	282	19	308	GTTTCTGCTTGAGGCCCTTTGAGAGGGTTATCTGAGGGAGGGTACTTTTAATAACATT	23147	A_95_P107257	CV018282
23913	282	28	1075	GAGAACTGTAATGACACTTAAGGTTTTTGGCTAAGCTTTCTTTTGATTTCTTTTGGAT	23164	A_95_P014181	TA18990_4097
23915	282	30	851	ACCTTTTGGCCTGTGCAGATTAATGTATCTGTTTCCTCCCATCGTTGTCCTGAAAATTT	23168	A_95_P011946	DV157804
23919	282	34	823	CATGTTGAGGGAGTGTAATATTCTGTTCCGGATATAAAAGAACATAGTGACTTAAGT	23176	A_95_P204712	TA18122_4097
23922	282	37	740	ATTGATTTAGCCAAGAAAGCTGTCTCTCATATACTATTTAGTCAATGTAGCTGTCTCT	23181	A_95_P226669	EB678380
23923	282	38	442	CTCGTGAACTTACTCCATAAATAAAGCGATTTCTGTTTTCGTAGCAAAGTGGTTATGT	23182	A_95_P021316	TA13919_4097
23926	282	41	218	AATTCAGATAATGCGTGATGCTGATACAGATCCACATGCTGCAACCAGACCTGTCGA	23188	A_95_P153167	EB683477
23927	282	42	799	TTCCTGGTCAGGGTACAACAATCAACGTCAGTGATAACTCTGCAAATGTGAAGAGAG	23190	A_95_P117427	L29271
23932	282	47	794	GATCCTAAATGTTGTAATGCATACTTCATACCTTCACGGGTTTAAAGTATCTGATGGT	23199	A_95_P014036	DV160403
23934	282	49	733	TGTGCTCTGTCACCTCAACTGATTTGTATCACCATTGAATACTTAGCTTCATTTGCCTT	23203	A_95_P272416	EB449916
23935	282	50	739	GTTATCCGCTACTATATTCAATGCACATGTTACTGCCATTATTTGAATCTTAGCTTGTC	23205	A_95_P207077	EB679684
23937	282	52	498	TAGCTTCCTTTGATTTGTACGGCTTTTGTTGTGTAATGGACAGCTAATCATCTATGAA	23209	A_95_P129912	EB429850
23938	282	53	606	CCTTCTCAATTCCTGCAGTCCTGATATCCAGATGGTATATCTCTGGATACTGCATATG	23211	A_95_P030071	FG170078
23942	282	57	864	CTACAATAGAATGCTATATATCCTATTTGCTATGTAAAATGGTGGGAGGTGGAAAAT	23219	A_95_P120462	DW000389
23943	282	58	659	GGATCTGATGTACTTCAACAAAGGCAGGGTAACCGGAAAAACATAAAAGCTACTGA	23221	A_95_P123737	DW003603
23948	282	63	757	AAAGCTTCAGAGGAAGTAGATGCTGTCGATGGTGACACAGCGTCAATATACAATCTT	23231	A_95_P271856	FG134195
23949	282	64	210	CCCTGTGTTTGGATATCCTCCCAGAATTTCATTTATTTTTCGTCTTTTAAATATTGGAG	23233	A_95_P008296	BP531102
23951	282	66	805	ACTACTACGGATGATCCTGTTATCCGGCGTTGGCTAATGAAGATAAAGCTACTGTTTT	23237	A_95_P197727	TA16626_4097

23952	282	67	472	TAGTGGACTTCATATCTTCTTGATCTTTTATTTGGTTTCTTAGTTTTTGGCCTAGGCTG	23239	A_95_P091588	BP531424
23953	282	68	611	TATTTCACTATGGGTCAATCTCTTTGATTGCGGAACCGTGTAGGTCAGCTCATCTTGC	23241	A_95_P127102	FG201107
23956	282	71	753	AATTTCATGTGTGCGTAATCAATTGCTTTCGCGAGCTGCTGCTGCTCTGCAATACAAC	23246	A_95_P135922	EB439469
23959	282	74	298	ATCCAAATTGTGGATCCCAGTTCGGTTCCCTCCAACATTCCTTACGGTTATAAACGGT	23252	A_95_P106792	CV018062
23961	282	76	493	AGGTGTCTTCTGTATGATGCCTACTTGTTTAACTTAGGTACATCGACTGGTTTAAAGT	23256	A_95_P188222	TA14522_4097
23967	282	82	1734	GCAAAACTAATCATTTAGATTTTGCTGCAAAATTTCTTCGTGTGCTCGTATTGCTGGA	23267	A_95_P206082	TA18429_4097
23968	282	83	519	CTGCTTGGAGCGAAGGTGTCCCTGGTCTAGAAATATAATATGTAAATCGATAAATTT	23269	A_95_P293668	EB436838
23969	282	84	666	ACTGATGTTTTAGCAAGTCGCTTATTTCTCTGTTCTGTTGGGGCTCTGACCTTGTAATT	23271	A_95_P302913	FG635924
23970	282	85	606	TCTCTAGATTTAAAGCAAATAATTTGAAGCGTAGTCCGTGAAATGATGTTCTGGCTCA	23273	A_95_P249722	DW005127
23971	283	1	781	TCACAAGCGGATTCAAATGTGTTTGATGAAGATGGTGTATTGGATATCTCATAAGCA	23274	A_95_P292513	EB427587
23973	283	3	441	GATCTTCATTTTGCGCTTCATCCTGTACTGATTTATGTCAAGCTTGAATAAAATGTGG	23278	A_95_P276353	AM779996
23978	283	8	616	ATGGTAAACGTCAGTTTAAGGGGCTAATCGATGTTTACTCTAAGACATTGTCAAGTG	23288	A_95_P145112	FG144055
23982	283	12	1538	GTCGTCTGTCTTTCATGCATTTCATGTGTTGTCTTCTTGATTGTGGTCATAGCTTTGAG	23296	A_95_P192032	TA15365_4097
23990	283	20	0	TACCATTGACCAAATCAAAGAAGCAGCAGCAGGAGTTAAGGTGTAAAAGGTTCACA	23312	A_95_P008986	A_95_P008986
23992	283	22	472	CCTGCCTGCTTCACATCCCATGAAATGTTAAGAGGTCAATTTTTGTATTTATAGCATA	23316	A_95_P212742	TA19900_4097
23993	283	23	1095	TGTAAAACATGAAACTCCAACTGTGTCATTATTTGTTGCTATAGGATTGCTCATCCAG	23318	A_95_P212217	TA19786_4097
23994	283	24	649	TATTGGTGTTGGTGGCATTGATTACAGTAATCACATAGCTTCTTTTTCCTCTCGTGGC	23320	A_95_P054236	BP133383
23995	283	25	465	ACCTGCAATGCATCTATAGTGTCACTTTCCTATTAAGTTCGAACCATTCTGCATATCAT	23322	A_95_P279463	AM835066
23996	283	26	628	CGAGTAGACAAATGTATCCAACTAGTCTTGTTTTGCAGATGTGATAATATCCCAATTC	23324	A_95_P025946	BP133301
23997	283	27	377	ATGTTAGCTTCTGAATTTAACCGCTGTTGGTGGATCTAAAGACTAGTACCTTTAATCT	23326	A_95_P114087	DW003761
24000	283	30	900	CACTGAGCTATCTCTTGGAGATTAATGCTGTAGTAGTTTGAATCACAGTCTAGTTGTA	23332	A_95_P008236	EB677852
24001	283	31	808	GATGTCCCTCTTGTTGTAATGCTCCTTAGATGTATTAGTGGATTCACATTTCTTTGTAA	23334	A_95_P241555	EB678009
24002	283	32	750	AAATTCCACTCAGATCTCACATTTCACCTGTGAAAATCCGGCCCTTGCCAGAAGCTAT	23336	A_95_P293943	EB438793
24013	283	43	1264	CGGTGAAACGCATCTCCAATCTAAAGGCGATTAAAACTCTCTGTTGAGTTAAACAGA	23358	A_95_P023386	TA15188_4097
24015	283	45	952	TCACAGAGCACTTTGAGGTCCTGGTTGTAGTAAATTTATAGCTTTCTTTGTTTCATAA	23362	A_95_P184597	TA13729_4097
24016	283	46	516	TTCAGTTTGCACACCCATGTGTATTCCCTTTTCATATATTATCAACTCTGCTCAATTGA	23364	A_95_P190517	TA15033_4097
24019	283	49	836	GGCAATATCGTTGGGGATTGTAATATCTTTATTGGTCATTCTTTTGAGATTTAACGTG	23370	A_95_P147417	DV999323
24021	283	51	872	AGAAAGGGCAGGTTTCACTGGATCTAATTTTGATTGGTTGCTCCTCCATCAGGCAAA	23374	A_95_P245762	DV999286
24023	283	53	579	GAAAGTGATGATTCATTGGCAAGTACGGAGGATTCTTCTTCGGATTCTGATTCTGAT	23378	A_95_P137302	EB441025
24031	283	61	867	GACTGTTTTATATAGCTTTTTCCTAATGGGGACTTTAGGTTTGATCTCTCTGCTCTCTC	23394	A_95_P248092	DW001749
24032	283	62	375	ACTGAAAATGGTAGTACCAAGGATGACCTCAGGCTTCCAACAGATGAGAATCTTCTC	23396	A_95_P115718	EH664552
24034	283	64	352	TCTTAAGAAGAAAAGTTACCTTGCTGCTGTTTCTCAAGACGAGGAGTCACAGCTACG	23400	A_95_P195412	EB434170
24036	283	66	788	CGCAAGATCTCTCATGTACTTCAAACAGATTGTGCTGTTTCAGTTGCGGCTTCTTGTA	23404	A_95_P240149	AJ966361
24044	283	74	291	AAGTAGGGGCAGAGTTTGGAGATTTCTCTTTATCTTGCATATTTAAATCCACCTTAAC	23419	A_95_P105202	CV017354

24047	283	77	145	ACAAACTCGGTGGTCTTTTGAGGCAGAGCATTTCTGAGAAATGCACGTAAGTGGCA	23425	A_95_P104257	CV016912
24054	283	84	774	GAGTTCAAGTATATCATTGTAGAATACATATGTACTAACTGTAGTACCCACTTTTCGG	23439	A_95_P203617	TA17891_4097
24055	283	85	0	AACTATCTGACTGACCAATATGCATATTTGCAAGACTGATCGACCTTCTTTCTTTCTTT	23441	A_95_P264136	A_95_P264136
24059	284	4	823	GGAAGTGCATTTGCATATTAGCTTGCATCATGCTTTCTTCTTTTGTAAACTAATTCTGC	23281	A_95_P010456	TA13522_4097
24064	284	9	247	TTTTGTCCCATTGAACGTGTTCTGTGTAAAGTTGCAGATAGTTATTTATTGCCGAAGC	23291	A_95_P060170	BP134928
24066	284	11	429	TAATATGTCAAGGAGAAAAAGACGCTCTAGCCTGTTTGATATTGTTGCTGATGAGTC	23295	A_95_P156212	FG156321
24071	284	16	611	CCGTTCATAGTGGAGTGACATTTTTTGATGTCCATGTAAGCATAGTAGAATATGATTG	23305	A_95_P264291	FG640840
24072	284	17	842	GGGTGTTTTACATATACACTTCTACTCTATGAATGTAGTAATTTGTGTGCCTTTTCTGT	23307	A_95_P014236	TA12103_4097
24074	284	19	774	TGCCGAAGACCGACGAAATTCAGTTTAAGGAGGAGTGATTCTTAGTGTTAGATTGCA	23311	A_95_P163712	EH622807
24075	284	20	97	ATGGCAGTGTCAAAGAACTCATTGCCTGAGATCAATTACTTATCTGAGCCTCATTGGT	23313	A_95_P136902	EB440602
24089	284	34	826	TAAGGTGATGGAGTAGGGCTATGTTAGGATGAATTAAAGAGGCTGCATGGCCAGTT	23341	A_95_P253319	EB424967
24091	284	36	170	ATGTCTTCTTCTGAGGTTTGCCGACGACACATATCTGGAAAGTTACATAAGCACCATT	23345	A_95_P004191	X72212
24102	284	47	670	TAACTGAAACTCGTAGCCCAGCCACATCAGTTGAGTATAACGACAGGGTGACTAGTA	23367	A_95_P222042	EB433061
24104	284	49	435	ACATGATGAGTGGAGAAATAACGTTTCGTTAACGGAGTTCTAACGCACGTGTAAAG	23371	A_95_P104057	CV016825
24106	284	51	239	GACGAATCAGATTTGAAATTGGACTTATCCTCCTTGTATTCGAATGCCAAATCCCAGG	23375	A_95_P053251	AM840678
24111	284	56	773	TAGTCTGCATCCATCTTACAGATCCTTTCTCAACAAACATGGTGGGAAATCTCAGGTT	23385	A_95_P127267	EB426796
24115	284	60	829	TATTTCTGATGTACTCATGGATGGGGTGATTTCGAAACCGCTGGGCTATGATCTATTG	23393	A_95_P289043	FG162032
24116	284	61	2894	GTACTTCAGTAACCACTGTCAAAGCTAATCTTTAGCAATGAATTGCACGCCATCTTTTT	23395	A_95_P217392	AF194945
24118	284	63	204	CTTATGCTAAAGCTTCCGATCTTCCTCCCATCAGTTGTAATTGTTGACTAATTGAAATA	23399	A_95_P110612	CV019809
24121	284	66	785	GCGGTTGCAGGTTTGTGAAGTAATAATCATTCTTTCGTTTTCCCTTATCATTATGGTTT	23405	A_95_P285258	EB679218
24126	284	71	1217	CTGTTGAATTTTCATCTTTGATGGCTTTAAGATAGCGTGATCGATTTTGCATTGTCAAT	23414	A_95_P018461	TA11803_4097
24128	284	73	1046	CACTACCCAAGAAGTTGTTGATGCAATTATAGCTGCTCTAGACTAATCAGCACTATAC	23418	A_95_P150597	Y14432
24129	284	74	447	AGGAATGTTCCACTGTACAAGCACATTGCTGACCTGGCTGGTAAACAAGAAGTTGGT	23420	A_95_P162817	EH666157
24130	284	75	831	GCAGTTTCATCCTAGAGACTCTAAGCCCGTGATGAATCTATGGATGTTTATAGAACA	23422	A_95_P287138	FG148784
24139	284	84	790	GTATCGGAAATTTGCTTGTTTATACGATCTATGATTTTCTGGTAGCTCGAATTCTTTTG	23440	A_95_P194272	EH621684
24143	285	3	497	TGTGTTCATCAATGGCCACTCAAACACAGTAGTGCAGATCATTGGATTGAGTGTGAA	23447	A_95_P073265	BP526174
24144	285	4	354	TGACATTAACTCCAACTTTAACCAGGAGGACCTGTACAAGCTGATACCCATGGTTTCT	23449	A_95_P156107	EG650414
24145	285	5	891	ACTGCTTTGAATTTCAGCAGTTTGTCTACATGTTGCAGTGTACATGTTACAGTGGAAG	23451	A_95_P011321	DV999505
24147	285	7	369	TTAACCTCTGTATGGTCTTTTGAAATTTTTAGTGCATCCTAATCTTATCCAGAAACGGA	23455	A_95_P059840	BP535201
24149	285	9	752	GAAGGGATTGTTCTTCCATCTCCTTTGTAATTCACTAGTGCTTCCTTTATTGACTTGAT	23459	A_95_P117777	DV160733
24153	285	13	578	GGTGTGAAAAGTTTACGCGTCCTTTCTTCTCTCACCATAGTGACTCTTTAAGTTCTGTA	23466	A_95_P263346	FG635797
24154	285	14	72	CATGTCTGGATCTTGTGATCCCTGACTGAACGAAACACAGAACATAAACAAAACAAA	23468	A_95_P103147	CV016363
24155	285	15	835	GTGCCCTCCACATTGTATTTTGGCAAGTAACACATCCACGATCGACCTCAATGTTATT	23470	A_95_P232389	EB428507
24158	285	18	498	TGGACGGAATTCCCGCCAACAAAGAACAAGCGAACTTATTATCATCCAAAGGCATCC	23476	A_95_P275398	AM818672

24159	285	19	651	TTATCCTAAAGTAGGTGATCACAGTATTTCCACCCTCCAGGCGTATTTAGCTTCACATT	23478	A_95_P060445	BP134999
24163	285	23	26	GGAAGGGTGGTTTACGCCTATTGTCATATGGATCACTGTATTAAACATGACGGTTGG	23486	A_95_P015831	EH663872
24165	285	25	581	TATTTTTCTCAATGCCGCGATCAAAACATAGCCAAGAAAGGAAAGCAATCATCACAG	23490	A_95_P053886	BP133302
24166	285	26	466	TGAGAACAAGGGGTTTGATATCCCAATAGTTACTTCAGTTTTAGGAGATAACATTCTC	23492	A_95_P132777	EB433494
24167	285	27	866	ACCTGCTAAAAAAGTTATGGTTGTAAGTGCCGCTTTAGATTAATTGGAACTTGGAAG	23494	A_95_P179487	TA12519_4097
24170	285	30	759	ACTTGAAGATTAAGGTTTTAGGCTGCAGTTGTCAGCTGTTATTTTTGTCCACATCTTTT	23500	A_95_P192127	TA15386_4097
24172	285	32	466	TCTCAGATTTTGTACGTGGAAGACTCGACTTAAGCAAGAGTTACATGAATTGGAAAT	23504	A_95_P079240	BP527715
24175	285	35	491	TTTGTACACTCTCGGCTTGAAGCGAAATGAAATATTAATCAGGCTTTGTTCCTGTTGA	23509	A_95_P140157	FG623196
24181	285	41	605	TTGTAATCTGAAAGTTGCTCAGTAGTGAAGTTGAAATCCTACAAGGGTAGGTCGTGG	23521	A_95_P153152	EB683464
24184	285	44	407	CCAGATGTGGTTCTTCAGCAGGCGGCATTGATCAGTGATAGAAGTACACTCTTTTCAT	23527	A_95_P110832	CV019930
24185	285	45	367	GAGTAGATGGTGCTTGTTCCTCAGAGAGGTGCTTTGGGAAGAAAAAGTAAAAGCGA	23529	A_95_P212632	TA19877_4097
24186	285	46	549	ATGGAGCTTAGTTCGTTCCAAGTTTCAAGTTTATTCTTATTTTATGTTGAGCACCCTGT	23531	A_95_P200742	TA17272_4097
24190	285	50	381	AGTACCTTTGACAAATAAACGGATAACGACTCTGTGTTGCTCTCGATAATGCTCGTGC	23539	A_95_P102487	FG644307
24198	285	58	492	GGGATCTCTGGAGACCTTTCTACTTCATTGTCTTCCCTTGGAGACCTTTCTACTTCATT	23555	A_95_P073060	BP526114
24199	285	59	1085	AAGACATCTTGGTAATTTTGAAGGCCTGTACTGCTCATTTACTGTCTTGGTATTTTCGC	23557	A_95_P189192	TA14738_4097
24206	285	66	1025	ATGTGCCACTTGTTTTGCAATCGACTTGTGCAAGAGAAGGCCTACCATGATTCTGATT	23571	A_95_P007771	TA13610_4097
24207	285	67	860	AGCTTCATGAACTATCCTTAGCGAGCTCTGCCATATGAATAAAAAGGAAAGGTAATA	23573	A_95_P137652	EB441385
24210	285	70	624	CTGGTATATACTTGTCTAGGTCGTCAAAGTATACTGGGAATTATGTCCTGCACTCAAC	23579	A_95_P306763	FG636154
24217	285	77	789	ATGGCTGCACTGTAATTTGGCTAGCTGGAAATTATGGTTTTGCCCTTCATTTTTCTCTA	23592	A_95_P180942	EB438484
24224	285	84	382	TTTCAAGGGTTTACATGATCTGCATGCTGCGAGGTTTCGTATCCCAACTGTTCCACAA	23606	A_95_P156932	EB680094
24225	285	85	641	GCTAGTAATTTGTCTATCCAGGTCTTCACGTTTTATATCAACAGTAGTTTGGTGTTTTA	23608	A_95_P211307	TA19581_4097
24230	286	5	447	TATTGATGAAAATTTTAGTTGGTGGTTGTACTGCAACGCTTTGGACAGTGCTTTATCC	23452	A_95_P025731	TA19830_4097
24234	286	9	672	GCAAAGAGTGGTTGCAGATCAGCCAATTGAACTAGCCCCTATGTTTTCTGAGTTCCTA	23460	A_95_P041811	BP130189
24235	286	10	694	CTAGAGATCGGTTATCTACTTAAGATTGCTCATTTGAAGCATCAACGTCTGTTATCTCA	23461	A_95_P262696	FG195144
24237	286	12	1553	TAACTTCCATGGTGAGATTGTTGAGGATTTCCTGAGACTGAGGGTTGTCTATAATTTT	23465	A_95_P190377	TA15002_4097
24240	286	15	381	ATGGCGTTCGCAGACCCGATTTCTCCTTCTATCTCCACTTATTATTCCGCATTTTTGGCA	23471	A_95_P090698	BP531062
24242	286	17	757	TATTGAAACAGTGGAAGCTGTATAAGAGGAAAACAAGATGAAGCATTTGACTGAAC	23475	A_95_P202852	TA17729_4097
24243	286	18	881	AAATTTCCTTGGACAGTCACTGTGGTATGATGCTATTCTACTTTTGCTGGAGCCAAAT	23477	A_95_P253429	FG158652
24247	286	22	674	CAGATGTCATGTATATAGATACTTGTATGGCCTTACCGGCCTGTGTTTTGAGTGTACA	23485	A_95_P152737	EB683091
24249	286	24	762	ATATATATCAAAAGCTTTCGATCTTGGTCGTGTTTTCATCCACTTCTGGTCTGTTAACT	23489	A_95_P127537	EB427062
24250	286	25	459	TCTACATGCATTGTACACAGCTTCCATTCTACATATATCCAAAGCAATATAAGTCCTTC	23491	A_95_P122367	DW002356
24256	286	31	1003	TTGTAACTGCCACTGCTCTACATTGCCATGAACTTTAGTATTTCAACCTTACATGTAAG	23503	A_95_P012196	TA16236_4097
24257	286	32	1682	ATTTACTCTGTTATTTATCACATTCAGAGGACCGGAGAAAGAGAGCCATGGTTTTATT	23505	A_95_P014731	TA14619_4097
24261	286	36	824	AAATCAGGAAACTGCAGGAGAACAGCAAGATAAGGTGTTTGTGCCGTTTAGTCAGG	23512	A_95_P216802	TA20783_4097

24271	286	46	827	AATTCGTCGAAGGCAATGCTAAACCAGTGAACATAGAAGTGGCTTAATTTTACAAAC	23532	A_95_P222372	EB677671
24273	286	48	435	GATCGAGGTCCATTGCTACACCTTGTTCTTATTTAATTTTTAGTGATTCTTCTTGGTGT	23536	A_95_P142717	FG643597
24274	286	49	803	CATTCCAAAGACCTCTCTTTTGGATAGAGCATTCCGCGATTTTTAACATGTTGATTATT	23538	A_95_P226359	DV999856
24278	286	53	685	ATGTTATTCATAGCAATGGGTACAGGGAAAATGCATTGTCGCTCTGAAGCAAGGTCA	23546	A_95_P025381	DV158470
24291	286	66	201	TCACTCAAGTGAATTGGTTTCGAGAGCATTCCGCCAGTTTTTGGCGGCTTTCACTTTC	23572	A_95_P139537	EB443313
24293	286	68	312	GAACGGAATGAAGAATGAGCAAGCAATATCGGAAGTTTTGTGCTGGTCAAGAGATC	23576	A_95_P167941	EH664311
24297	286	72	959	ATTTTTCGGAAATCAGTGTAGGGAAACGTTTCCCTACTAAAGTGGGAGGTCAGTGTT	23584	A_95_P007871	TA13446_4097
24300	286	75	847	TTGCTTGCTTATGATGCTTTTCTATCCAAGATACCTATTCCTAGTGGCAATGTGTATGC	23589	A_95_P229899	DV159511
24301	286	76	564	TGCTTTTGGGTCAATACTCCACAGGCAAAACCACATTCACTTAAACATTTACTCAAAA	23591	A_95_P056376	BP133939
24304	286	79	502	GCGCCAGCTGCTCAAGGATCTTAAACTACTTAATCCCACTGTTTTTAATCTTTCTTACT	23597	A_95_P068070	BP137042
24305	286	80	841	ACATACATGTTCTCAGCTGGTGATGATAAGCAAGTTAAGTGCTGGGACCTGGAACAA	23599	A_95_P205952	TA18402_4097
24312	287	2	766	TCTGGTTATGCTATACAACTTTGAGAGGAACTGGGTTTTATTTTAGTATTCAGGCGTT	23612	A_95_P149167	EB678864
24315	287	5	758	ATTATAGGTGGTATTGTAAGCAACACATTGAGACCGCCTGTGCCAAGCTTCTGTGAC	23617	A_95_P287873	EB450940
24320	287	10	374	CCAAGCGTGTGTCGTATATGTAGCATTTGATAGTTTTGATACGTCAAAATTGTTCTTG	23627	A_95_P308748	FG643512
24321	287	11	2055	CATATCCCATTAAATGCTGTTAGCCTACCCTCTGAAATTGATATGCTAGCAAAATATTT	23629	A_95_P200957	TA17322_4097
24328	287	18	855	GTGGTAGAAAATGAGAAAGAGATATGGACTGAGCATAGTTATCACAAGCATGGCTG	23643	A_95_P284718	FG169521
24330	287	20	1209	CGTATGTATTTCTATTTCTGCATGGAACTCTGCGTAATCCAATTCGTGCAGTGAATTCT	23647	A_95_P184042	TA13598_4097
24331	287	21	872	AAGTGAATCAGTTAGATTCTAATCTTTCATATGCAACTGTGTCTTGTCTCGTCTCCTCT	23649	A_95_P204687	DV160259
24332	287	22	872	TGTCACTTCAACATTTCATATATTCAACTCTAGTAGTGACTTTCGTGTTTGTGATCATG	23651	A_95_P242767	FG160334
24333	287	23	579	CTTTGCTGAATTTGCATGTGGTGTTAGTTTCGTCTGTTAAGATGTACAATTATCTGAA	23653	A_95_P019466	DW003772
24335	287	25	598	CTTTCAGCTTGGACTGCCCTTTCTGGTTTTATAATGTGTCCCTAAATAATATAATCTAT	23657	A_95_P198757	TA16849_4097
24336	287	26	1013	CGAAGAAGCCCTGGTCGGTTAAAGAAGAGAACTACCATGAAGAAGATAGTGAAGA	23659	A_95_P135582	AB017694
24338	287	28	868	AATTATTGCTGCTTTATGGCGAAATCTGGAGCGTTTTGGCGTGCTCTGAGCAACGAT	23663	A_95_P185847	TA14003_4097
24340	287	30	894	TAAGAATGGTAACTAATGACGTTGGTATCCCGTGGTGGGGTAGCTACTCCTTATCAT	23667	A_95_P269486	EB424905
24343	287	33	1259	TAAAACCTGGGTTTAGGTTGCTTATGTGCATATCTATCTTCCCCCTCCCTTTCTGCCTCT	23673	A_95_P188377	TA14557_4097
24344	287	34	1227	GTTCCAAGAAACGCGGTGTAGTCTGGTCTTTATGACATAATTTATTTTTATTTTTTGG	23675	A_95_P027021	TA17581_4097
24345	287	35	791	ATCTAGTGATTTCCTTTCCCCTTCTACTACCCTGCCATAAAGCAGCTGTATTTTTTAAT	23677	A_95_P011881	EB426498
24347	287	37	319	TCTTTGCTTATCTTCAATCGCATTTTGTACTAGACACGTTCAAAGTTGGAATGACGAA	23681	A_95_P095628	BP533269
24349	287	39	526	CAAGGAGGGAACATCTGATTAGATGTTGTCTAATTTTGTTCTTGGAGTTTCTATGTAC	23685	A_95_P223022	TA22158_4097
24351	287	41	757	CCTGAAACTCTTCATGTTTCCAACAAGAGGGCAGCTGTGAGCACCTATTTTTTATTAT	23689	A_95_P302533	FG139104
24354	287	44	826	AGTCGGCTTACTTAGCGGATGTTCAAGAAAAAGAAAAAGCTATCCATCTATAGCTGG	23695	A_95_P270881	EB437031
24356	287	46	661	TGTCTAACCTTGGGTTTTTACCAAGAAAAAGACTGCCTTTCTTGTTCATATTCTCTAGC	23699	A_95_P300773	FG637873
24366	287	56	503	TTGTTCAATCCAGCAAGGTTAGCCTTTTTAACATTTTCGAATGTCAAAGGCATTTGAT	23718	A_95_P054721	BP133516
24368	287	58	637	TTTGGTAGAATTGGAGATGTTTTGTGTTCAAAGTTGGAATTTTGAGGGATTTGATTG	23722	A_95_P221277	EB678015

24371	287	61	774	GGTTATATCTTTAGTGCTTGTTTGTGCTTGTGATGGACATTCTTTTGGGTTATCTTTTG	23728	A_95_P183177	TA13399_4097
24376	287	66	792	TTGAGCGGCTTGCTAGGGAAGAGGGTATTGCTGACGGAAAGGGATATTATACAGAT	23738	A_95_P272106	EB447660
24379	287	69	782	TAAAAAAGCATGAAGTGTTGCGGCCAGGTATTTATCTTCCACAACCTGCTGCATTAC	23743	A_95_P120557	DW000523
24384	287	74	482	ATACCTAAGAGCAAGTGGGATGAGGACAGCCAGAGTTCAACTTCATAAAGATTTGT	23752	A_95_P044491	BP130895
24387	287	77	582	TGGTGCAGATGCTGGTTACCTGCATTACTTTTGTGAAAACTGACATTATATGGTTATT	23758	A_95_P307888	FG639922
24389	287	79	467	TCTAATTGGTTTGGTGCATGTTCATTTTCAACAATGAAGAGGCAGATAATGGCACAT	23762	A_95_P113747	CV021296
24393	287	83	646	GCCGTTAATTTCTATATGGCACCTGAAATCACTGCCCAATCCTTTTGGAGAATAGTGG	23770	A_95_P300598	FG638437
24394	287	84	217	GCTCTTGTCAATTTCTCAGAGGACCCATCACTGGGTGATAGAATATCATATGTGTTGA	23772	A_95_P157963	EH616022
24397	288	2	446	ACTTATTTAGGTGAATTCTTTACGTAGGTATTACAGAGGAGCTGGGCAGGGATTGTG	23613	A_95_P038586	BP129310
24400	288	5	0	ATGGGGTAATTTTCTGCTACTCTTATGTCCAATAATGTAGACAAAATGGTACAGCGG	23618	A_95_P265491	A_95_P265491
24402	288	7	681	GGATGTGGGTTACCATATCCCAAAAAGAAAGAGAAAAAAGTCTCCTACATGTAATTT	23622	A_95_P267701	DV161349
24403	288	8	773	CTTTCTTGTCATGAGGAGTTCATGTAGATGGAATTGCGGAAAAGAAAATGACCATTT	23624	A_95_P026216	TA22102_4097
24404	288	9	552	TTACTCTGCTTTAATGGGAAATTGTTTGATGTGCAGCATAGAAGAAGTCTTGTTAAC	23626	A_95_P048686	BP131980
24406	288	11	1408	CAATCCCGGCTAATTCTGTATACCTGTGATTACTGTAATAATGTACCACTTCTATTTTT	23630	A_95_P178877	X75088
24410	288	15	686	TTCCCTCTTCTCTAACATGCAGTCTGTAAGGAGGCCGAGGTCCAAGTTTAGTTTATGG	23638	A_95_P304168	FG635257
24416	288	21	520	GGGTGTATACATTATATGTTGTAACCGATACAAAAGGAATATAACATTTGGGGTTTG	23650	A_95_P151222	EB681453
24418	288	23	197	CGCGAATCCAGCTCAAATAGAGTTCTATAGATTTGGATATAAATTTGTCTTAAGGCA	23654	A_95_P093793	BP532412
24422	288	27	400	GGGGACAAAGTTGACTAGTGCTGACTATGGAGGCAGCTGATGTTTTATGAATGCAC	23662	A_95_P032506	AB120521
24424	288	29	787	GCTAATGGAGATGGGAAGCTTGGCACTCAAGGGCTTATTACTGTTATAGAGAGGAT	23666	A_95_P126257	EB425523
24427	288	32	987	ATGTGCAATGCTCTCAACAATTTTGTACGTTTATGGGTATGATGATACCAAATTTTAC	23672	A_95_P017766	TA16133_4097
24428	288	33	285	CGAGTTCAATTAATCCCATTACAGATCGCGTGTAACTATGTATACATATAGGTCAAAA	23674	A_95_P148872	EB678400
24431	288	36	322	GGAGTGAGCCATTTTGAAGCTGGTGATTCTAGAACCAAAGAATATGTTAGTTTGCTA	23680	A_95_P102947	TA12168_4097
24434	288	39	787	CATCAGATGAATTCAATCCATTTTTGTGGTCATGTTCTTTTGTTGCAATCTACCAGTAT	23686	A_95_P012476	TA13493_4097
24436	288	41	644	ATAATTCACTCTTTGCTTTTGGCGCGGCAAGAATTGACATAATCAACCTGAGATGCG	23690	A_95_P183397	TA13448_4097
24437	288	42	782	TGATGATGAGTACATAGGTGGTCCCAGACAACAAATCCGACAGCCACTGATCAACA	23692	A_95_P244537	DV999592
24438	288	43	746	TATGAACCTACTATGGAACTTGAGAATTTGTGTGTGTGTGTTGGTGTATTACGTACTT	23694	A_95_P003786	TA11883_4097
24439	288	44	514	TGTGTAGCCTAGTATTTCAGCTGAAAGATGAAAGTTAATGGTGAAAGAGCTGAATG	23696	A_95_P262936	EB446476
24440	288	45	489	CTGGTCTTACCCAACCATTGTATTTCTGTTTGTAAAGTTTACAGAAAGCAGGACAGAA	23698	A_95_P115127	DQ437541
24448	288	53	430	AGGTGGTTCCAAACAGTTGAGATTGCATCTCAACGCCTAGAACTTTGCATGCCAAAA	23713	A_95_P094608	BP532793
24454	288	59	141	GCCCTCCACACGCGTGCTTCTTAGTTCTACTTCTTATTTTCATCAAGTAAATTGTATTC	23725	A_95_P100943	BQ842958
24457	288	62	281	GCACTACTTTTCTGGTTACCTATGTTTATATCAGCCTGTTTTTAAGACAACAATTCCTT	23731	A_95_P309118	FG644729
24458	288	63	664	GGACGATGAACTCCCAAGATGGTTTTGCCATCATTACTTTTAAATTCTGTACCATTGA	23733	A_95_P182842	TA13316_4097
24465	288	70	577	ATTTGATGCAACATTCCTTAAAGAGATGCCTCTATGGGTCTCTTTCCCCACTTTACCTG	23746	A_95_P068585	BP137164
24468	288	73	958	GAAGTCAGGGTTAAAGTGAGGGATGTATAATGTTCTTTGAAACTAATGTATTAGCTA	23751	A_95_P222522	TA22052_4097

24469	288	74	289	GCTGGTACTGTAATTTGATTTTGGGAACTTAATCTTGGTTGTTTTGAAATTATGGTCG	23753	A_95_P025201	TA13570_4097
24470	288	75	313	TTGGAAGGCTTTATGCCTGATCAAGGATATTTGATGTAGGATCTTCATTTTTACTAGT	23755	A_95_P100448	TA12797_4097
24472	288	77	424	CCTAAGCTTCCAGGCATTAATGACATTTTCTGGGATCACATTCTTTCTACAAGCCCTCT	23759	A_95_P085860	BP529398
24474	288	79	787	ATGCACTTAACCTGAAAGTGAAGTCAGTGAGGTACACTCGTGGTAGTTTCATCTTCC	23763	A_95_P013931	FG142227
24479	288	84	511	CAAAATGCAGCCTTCTCGAACACGATCTATATAAAATTTCACAGTAGTTCTGGCTAAG	23773	A_95_P184342	TA13673_4097
24481	289	1	756	CTTTATAAAGCTGGAGAAAATAGATGGGGAACTGATGAGAAGACTTTTATACGCAT	23776	A_95_P128782	EB428512
24482	289	2	824	CAAACGACAGATGATGATGCTATGTTCTGTATATTTGGCACTTCTATTATGGTTTAAT	23778	A_95_P216532	TA20726_4097
24483	289	3	60	GAAAATTTCTTGCATTTTCTGTCCTAACAATCTTGGTTTGTTCTCTCCTTGTTAATGGC	23780	A_95_P128042	FG624980
24484	289	4	926	TTATCTTCATTCATGTACGGACATTTGATCATTGAATGGCCTGAAGTTCCGTGTTCAA	23782	A_95_P220617	TA21646_4097
24486	289	6	421	GGAGCTGTTGTATCTCATTTGTTTACGAGAGTTTGTTCTGTAGTTTCTTTCAAATTTCA	23786	A_95_P202392	AM817228
24494	289	14	802	ATCATCCTGCATACCGTTACTTCCAGTACATGCTAGTGGATCTGCATCAGTACTTGCG	23802	A_95_P253644	DV161442
24498	289	18	0	ACGGAAAGCCATTAGCGCACAGCAATCTTCGTTGAAACAAAACAAACCCTAGCAGC	23810	A_95_P266186	A_95_P266186
24500	289	20	542	TAGATATGTCCCCTTCACATTTGGCAAACAGCGTTACAGCGGGAAGAAAGAAACAG	23814	A_95_P149647	EB439032
24502	289	22	633	CCACTTTGTTGGATGGTGAATGCAATGCCCATCTGTTCTCACATTTTTTGTTTTCACAA	23818	A_95_P058551	BP134501
24503	289	23	496	GTGGAAGAGAAAGTGAACATTAACTGACATCCTTGTATGTGTTTATCGAGCAATACA	23820	A_95_P121887	DW001969
24507	289	27	1852	GACTGTTGAATACACTGTAATAGTGGATGACGTTCTTAGCAATCCCTAAATAACACTT	23828	A_95_P023706	AF426837
24509	289	29	105	CCGTCCTTCATTGTAATTGTAATCTGAAGGAAAAGGATGGTCTTCTTAGAAATTCATT	23832	A_95_P090128	BP530816
24511	289	31	545	ATACAAAAACCCTGTCTCTCAGTACCTACACCATTGACTGTCGGAAGATAGGTTCTCA	23836	A_95_P081880	BP528375
24516	289	36	195	TTATGGTGCTGGATTTTGGAGAAGTCCCTCTCAACGGAGTGACAACATGGAAACAAT	23846	A_95_P133712	EB435348
24520	289	40	364	CAAGGCACCAAGATGATCGATTTTGTTGTAATGTTTGGTTGATGTGCTTATCCTCGAT	23854	A_95_P122287	DW002306
24522	289	42	713	AAGAGTATAAAATTCCTCAGGGTGGCCTATTCAATTTTGTCATATGCCCACATTACCT	23858	A_95_P269956	EB428227
24525	289	45	623	AGCTCTTCCTTGTTGCGAGATATTATATGCTTTAATAATTGCAGCTTCTAGTCCCAAA	23864	A_95_P188782	TA14646_4097
24528	289	48	267	GCTTAAGTTGCAGCCTACATTTTGCAGTGAGCCTTAGTTCAATTTACAGGAGATTTAG	23870	A_95_P107587	CV018454
24531	289	51	500	CCATCAGTATTCGGCAGCTAAAACATTTGCTCATGTGTTTGGGTTTATGGATATTTGT	23876	A_95_P186692	TA14180_4097
24534	289	54	499	CGACGTGGTCACAACCCACCTTTGATGAGACATTTAATTGAACCTAATACTGTTTATC	23882	A_95_P286548	FG635493
24535	289	55	835	ATGCTTTGTGCTTTTGGGATGAATTACACTTGCATCACAAGAGGCAGATGGTCATAA	23884	A_95_P292503	FG139517
24538	289	58	136	AGAAGCAAGACCATCATTTACACAGATAACAAACAGATTGCGCGCCATGTCACAAGC	23890	A_95_P034209	AJ718283
24539	289	59	636	TATTGCACTAACTTCTAACTTGCCAGTTGCTTTGAGGTGCGTAATTAAAGTCTCAGCA	23892	A_95_P116892	DV159674
24543	289	63	789	GAAAGGTTTCCTGTACTTGCCAAGGTTATCTGGTTTATCTTTACTTTGTTAATTCCCAT	23900	A_95_P269291	EB450319
24544	289	64	819	ACTTCTGATGGGCAACATGCAGTTAGTGAGTGCTTTCTAGATGACATTGGGCAAGAC	23902	A_95_P293838	EB438212
24550	289	70	560	ACTGAAAAAGTTTGTCACTCTATCCCAGTCATTTGTAATTGTAATCCGAAGGTCGAAG	23914	A_95_P151037	EB681257
24551	289	71	1753	TACTTCTCATTACCCCTACAAGAGAAGACTAGGTACTGTAAAAATTACTCGTCTAAAG	23916	A_95_P182942	TA13341_4097
24557	289	77	524	ACGTACGATGAGAGGAAAGCTAGGTTGATCGAAAGACTCAATGCTTTGAATGCTGC	23928	A_95_P048311	BP131873
24560	289	80	864	GACTCGTCAATATAAGGTACCTGTCATAATTGCTGACTTTTCAGCTTTTACTTCTTAAT	23934	A_95_P208187	TA18913_4097

24566	290	1	602	TGCCAAACATCTCCCGACGATCAACTTTGATCATTTGTTTGCGTATTTATATGATCATT	23777	A_95_P129107	FG136481
24568	290	3	199	TTTGGGCCTATTTGCTTCTTGGATTACTGGGACTAGGGAGATTTTGACAGTCATGAAT	23781	A_95_P036663	BP128790
24578	290	13	622	TACTGATGAGTGTTTGTCCTTTCCTTTTTCTTTATTTGGGGGTTGGGGTTGGGTGAGG	23801	A_95_P195127	TA16049_4097
24579	290	14	466	GTTACATAACCAGCATCTTTGCTTGGGTTCATATTATACACTGGATCTGGGATCTGGT	23803	A_95_P238824	AY081941
24581	290	16	458	ATTCTTTCATTCTAGGAAGCTGGAGTAGTATAATACTACTGCACTAAGCTGCAGTGTA	23807	A_95_P262941	BP530854
24582	290	17	450	CAGCTCAAAGCACTTATTTCGTAGCTTTACTTTTCTGGTGCATTTACAACAGAGGTAA	23809	A_95_P004686	TA13685_4097
24589	290	24	441	AGGGGTATTTATGTAATTCATGTGTTGGTTCCACGTTTCAGCTCTTTTCATTCTATTGC	23823	A_95_P125462	EB041772
24590	290	25	537	CTCAGACTTGTTTTGTTAGTTTGGAGAGACTTCGCTTCATGCTTTCTACATTATTTTAC	23825	A_95_P153472	EB683730
24591	290	26	359	CTCCAAAGGCTATTCAAGCAATTGTGTTGTTAGATCCACCAGTCTACATTATCCACAC	23827	A_95_P053526	BP133201
24598	290	33	607	GATATTGGGAAGAGGATTTGTCCGTTATTTGACAGCAAGTGTGATGAATTTTCAGTG	23841	A_95_P243872	FG642795
24601	290	36	776	TATAAGTGTCTATATATCTGACCGGTTAAGGGGGAGGTTTTGATATTTCCTGCCAAT	23847	A_95_P272226	EB450882
24603	290	38	876	GCTGCTGCTGTCGAAGCTTTTGTGTGACATAGTATTTTTCCTTCTGGTGTGCACTTTA	23851	A_95_P267726	EB450082
24606	290	41	871	GATGTGTTGGAGTGAGACTCTGAAGATCTGAAGAACGAAATTTTAGAAATTGTTTTC	23857	A_95_P234189	DV998837
24609	290	44	382	AGTTGGGTTGGATTTCCGTCTTTATCTATACTTTCCGCTATTGGATATTATGAAAGAG	23863	A_95_P098598	BP534564
24617	290	52	798	TTTGCATCATATTCTTGTTCGAAGATACGCACTCGAGCTCAAACACTCAACCCAGCTC	23879	A_95_P311113	FG168999
24618	290	53	690	CCTTTAGCAGCTTGGTTGGATAGTTGTTACCCTGTATTATATTGTATTGGTACTCTAA	23881	A_95_P161702	EH620352
24620	290	55	1640	ACCATTGTGTCATAAATGAAGTTATCTCCACTATATATGCACGGGTCATTCGTTGCTG	23885	A_95_P199512	TA17010_4097
24624	290	59	906	ATCGTGCTACGGTGATGTGAAATGATACTGTATGAATTCCAAGGAGTGCTATATCTA	23893	A_95_P204527	TA18085_4097
24626	290	61	825	TATTGAAGATCCTGATGGTTACAAGTTTGAACTTTTAGAGAGGGGTCCAACACCCGA	23897	A_95_P137977	EB441692
24628	290	63	403	GGATTTCCTGCTAAAATATTCTTCAACTGGTGAAGAATGTGCACTTCCAACTGATTTT	23901	A_95_P054781	BP133533
24629	290	64	771	TGATTTTGAAATGGACGGCGTTGAGCTGACCCCTGAAGAACAAGCAGCATTAGCTG	23903	A_95_P218147	TA21108_4097
24632	290	67	683	GAAAAACACAGGGGAGCTATTACTGTCATTCGGTACTCTCCAGATGTTTCCATGTTTG	23909	A_95_P151842	DV162033
24635	290	70	1987	GTAACTCCAACTCTTGGTTCTCAGATAGTCCTGTAGTATATTTTTAGTTTTCAGAGTA	23915	A_95_P026826	TA13109_4097
24636	290	71	451	CTACTCCCTTGGTATTGTCTCATTGGGTACATGTATATTATTTGTGATGAATGAGACG	23917	A_95_P212247	TA19792_4097
24638	290	73	782	ATCAACAGAGAAAGTGCATGCTAACAATGTAGCTCATAGAACACCATGTAAAATTGT	23921	A_95_P149737	EB679689
24640	290	75	312	CTGTGGTCTTGCTTGTGTTTTAATGGTTTTGAGGACTCTCGGTAAGGATTATGATATG	23925	A_95_P151562	AM818734
24642	290	77	877	AGCGGCTTATATTAATTGTCTCCTGCTCCAGTATAGTAAATTATGGGAAGCCCGAGTT	23929	A_95_P218457	DW001338
24643	290	78	1403	CCAACTGCATGGTAAATTCTAGTACGGGACCAATCCCACCATTTAACCTTCCTAATAG	23931	A_95_P013081	TA13401_4097
24645	290	80	394	AACAGCGTGTAACATGCGATATCCAACTTTTTATTCATCAGAAATGTTCCTTACCCTAT	23935	A_95_P133357	EB434809
24649	290	84	490	TACATGAGTTGCATCTCTTGTTTGCGATCCGCAGCGCAATAGAGTCTCCTTCAGAGTT	23943	A_95_P055476	BP133712
24652	291	2	526	ATGGGAGGAGCATTGTAGTATTGTTGAGTTGAGTATCACACAAGATGTAAAATCCTA	23948	A_95_P140532	EB444428
24655	291	5	317	TTTATTCCTATGGAAATTGTCTGTAAACCTAAACAACTCTTACCGCATATGTAGCTGCT	23954	A_95_P028701	EB451322
24659	291	9	344	GGCAGGGCATTGGTGGGAGCCATGTAATAAGTGAATAATTGTTTTCTATCCTAAATA	23962	A_95_P178987	TA12399_4097
24661	291	11	218	GGCAATTGAGAATAGTCCTTCTTTACAGTGTATGCCTGAGCTATTGGAAATGTCCTTT	23965	A_95_P131847	EB432273

24662	291	12	557	TAGAGTCTATTTGGGTTATCATACGGTCGCACAGGTATTTGCTGGAGCTACTTTAGG	23967	A_95_P156872	EH616675
24665	291	15	780	TGTAGATTTTCATATTTGTTCATCACTACAAAGGTCTGATTCTTCCTTGCTCTATTTGC	23973	A_95_P150552	EB680665
24666	291	16	834	AACTGAAGCAGCTTTGCTAGTAGTACTGGAGAAGTTCTTTGAGGTGGTTTTGAGCCT	23975	A_95_P148837	EB678368
24667	291	17	979	CTGCTGTTCTCCCAATATATATTGTCCTTTTTGCACTGAGAACTGTCCAAAATCATTAA	23977	A_95_P018401	TA16244_4097
24668	291	18	612	CGGTGCATGTGGAGAAAATCCAAGAAGTTGGCTATAAGATATTTATTTCAAGTGCAA	23979	A_95_P307983	FG640354
24669	291	19	892	GCTTGCAAAAAATCCAGCTCTGGCCAATGAGAACTGGGACAGATTTCTTCCGCAGTT	23981	A_95_P012526	TA20719_4097
24672	291	22	765	GGATAGCAAGCTGTGACAATCTAAAGACTTGAACTAGGACCATTTAACATATTCTTTT	23987	A_95_P010101	DV159747
24674	291	24	349	GTACCTTGTTTCTTCTGGAGGGTACAAAGTTTCCAGCTATACATTATGCATCTTCTAAT	23991	A_95_P159367	EH617504
24675	291	25	349	GCTGATTTCCCAAGTGCATAGATTATGGATGTGATTTTCAAATCTCACTAGCAAACTG	23993	A_95_P133047	EB434099
24676	291	26	826	GAAGAGCTGCAAAGCTTGTTAACTTATTATACTTCTTCCTCTAAATCTGTTCAGAAAC	23995	A_95_P272146	EB447902
24681	291	31	480	TGGGAGGCAATATTTCAAATTTCATTTGGCAAAATATATTTGAGAGTCGAGGTTTCC	24004	A_95_P266191	BP532909
24682	291	32	645	GGATCTTTGATAAATTACAAATGTGGATCAGTTGAGACTAATGTTTGAGTCTGGTAT	24006	A_95_P029211	TA13069_4097
24689	291	39	627	TCCTCTGACGGATGCGAGTATAGTCTTGATGTAGGTGAGGATGACTCATAATCCTTT	24020	A_95_P051941	BP132789
24690	291	40	896	AATGGGAAATTTACTCGTGACCAGTCACTTGTATATACTGCTGTCCTCGACGCTCACG	24022	A_95_P012011	EB440534
24692	291	42	305	AAGCTGTATAGAGACAATCTGCATTTCAGAACCTGAAATGAATTTTGCTCTTTGATCT	24026	A_95_P025951	BP131112
24693	291	43	263	CTCACATTGTTTAAGTTGAGTTTTGTTGTGACGATCTCAAAATTTTGCTTGTTCTTTGC	24028	A_95_P133537	EB435095
24698	291	48	690	TTCCAGTACTACTTAATGACGCCGGGAAAACTGGCTCACTCAAAGCAGCTTCTGCTA	24038	A_95_P300293	FG190228
24699	291	49	706	ACTGACCAAAAAAGTCAAGTGATGTAGTTGTTTCCTTCCCATTTTCTTCCTGTTTTTCT	24040	A_95_P022381	TA13660_4097
24700	291	50	319	TTTGAGCCTAATTGGGAATTGAATGATAGAGATTTTTAGGGTATGGAAGAGGACTG	24042	A_95_P143302	EB446644
24703	291	53	434	TTGTGTAGGCAACTGTGTCACCTAGTTTGTGTCTCGTTCAAGTGTTACTATTTGAGTT	24048	A_95_P226425	EB437833
24705	291	55	823	CGCCCGATGTCTGAACTCTTGAATCTATGTGTTATTGTTCTTTAATGCATCTGTATAAT	24052	A_95_P008116	DV157864
24707	291	57	1398	CTGTGATGTCAAAATTGTATTATTTGTTTTGGCTGGTAATCTCATTGGAAGCTGTGAC	24056	A_95_P221592	TA21851_4097
24708	291	58	904	TAGCATCCACCAATGCTATAATTTCTGCTGCCTGTGCTTTGGAGACCTTGAAGCTTGT	24058	A_95_P220082	EB427964
24709	291	59	131	TTCACACCTTGAACGTAATGTACATCTCGAATGAGCACGCCCATGTTTCTACTGTTAG	24060	A_95_P241885	AJ718708
24713	291	63	825	CGATCAAGCTTATATACTGAAGTTTGACAAGGATACAAACATATATAAACAGCCAAG	24068	A_95_P290178	DV162082
24722	291	72	790	GTAAAGAAGTTAGGCCAGCAAGAGATGAAGAACTTCCATCTGCTTTCGTGGAAGAG	24086	A_95_P255884	EH616991
24723	291	73	397	ATATGGCTTTAGTTATCGTCGTCAATCTTCAGAGTTATTGCTCTATTGAGGGCTGGGC	24088	A_95_P095848	BP533364
24725	291	75	535	CTACCTATCCTTTGCAGACATATCTGATTTGGAGAAGCAACTTTCAGATCAATCAAAT	24092	A_95_P072370	BP525944
24730	291	80	863	GTTTGTGTTATCAGGTCCTTGGCACTAGATTCTTATCCATTGTCATGGCTAAATATTTA	24102	A_95_P013131	EB451357
24737	292	2	312	GATGAGGCTCTTAACCAAGGATACTAGAGTTTTCATTCTAAGCTTTTTCTCTTATACTT	23949	A_95_P102182	CV015908
24740	292	5	606	CGAGTCTGTTTTTCGCTTTAAGGCGTGTTTGATTTAATTTTGTTGAAATTCTATGGGG	23955	A_95_P177572	EB432034
24743	292	8	324	GGAACTCTTGTGCTTGGAAAGCTGTCCACATTTGTAAAAATTGATGACTCTTCTGGTT	23961	A_95_P122092	DW002140
24750	292	15	827	CAGGATATGATCTGGAGTTCTTTGAAACAGTTTTTATCTGTTTACTGTGTTGTGGATT	23974	A_95_P008641	TA13791_4097
24756	292	21	667	ATACCATTTTGCTACTCTAATTGCTTCATAGGCGCTATTAGGTCCCTGATAAACATTCG	23986	A_95_P117782	DV158020

24760	292	25	413	ATTGAGGGGTATGTGGAGAAATATGGAAAATCTTGAGATGAATTTTGCTCTACGTG	23994	A_95_P114982	CV507107
24761	292	26	489	CCTGATCTATGCCCAAGTCATCCATATTTTCTGAACTTAGATCATAGATCAATAATGA	23996	A_95_P129692	EB429656
24767	292	32	579	TAAATCTTTCGGACCTTTATTTGTAGAATTCCTAGAAAGTTTGTGGATTTTGTGGCAC	24007	A_95_P307508	FG645125
24769	292	34	804	TAATATACTTCGGCGCTTAGCATCCTATGGCTGTAAAATCACTGTTGTTCCTTCAACA	24011	A_95_P152477	AJ319873
24770	292	35	905	CTATCAAACCAAAAGAAAAAGCTGTGTTTTGCCTTGTCTTACAACTTGTTTGGATGA	24013	A_95_P024371	TA18559_4097
24772	292	37	489	GCTTCTTCACTTAAAAGGGAACTTCACAGTTAAGGTCTATCTCATCTCCCTTTCTTAT	24017	A_95_P208662	BP530687
24773	292	38	733	CCATGGCTATCACCTATGCCAAGAAATGAGCAATTTTAATTCCAGGACACAGCTATG	24019	A_95_P234714	FG644997
24779	292	44	106	CTTTTTACTCATGAAGAGCCTATTGTGTTTGTCAGTCTGTATCCTATAATTCATGTGTA	24031	A_95_P130172	EB430216
24784	292	49	139	ATTGACACCGTAACTTCGGAAGAAGGTGTGCCTTTAGTAGGTGAACCATTTACTTGG	24041	A_95_P143732	EB446943
24786	292	51	164	TATAATGGGAGGTGTATTGGGTAAGAATGAATCTCCCTGGCTTCTGTCCCGGAGACA	24045	A_95_P148137	FG194427
24792	292	57	627	GTGTTAGGGTTTATGTTAGTCTGTGTATACAAATGAAATGATGAATGAAAGGCCCAT	24057	A_95_P241195	FG146706
24795	292	60	674	CAGAATTGACTCTCAGAGTTCACCCTATAATTTCGCTGATATTTTATATGTTTGACTTG	24063	A_95_P053831	BP133290
24797	292	62	305	CCAAAGGGCGAATAATTCTACATATCCTTTTGCTTTCTTTGTGTGTTCTCTTCTGACTG	24067	A_95_P091393	BP531337
24798	292	63	933	GTTTTGCTTGTATACTATTTCCCTCTCTCTGAAAGACTGGCTAGTAGTACTGAAGCTG	24069	A_95_P008991	TA12943_4097
24799	292	64	615	GGTGGGGGTTTGTTTGACGTTGTAAAATTTGATAAAGAAATGAGGGTATTATTGTCA	24071	A_95_P032071	TC74049
24814	292	79	725	GTCTCTGTCCATCCATGCTAACTTCTGGCAATCACTTGTATCACTTGTGGCTAAGTTTT	24101	A_95_P000526	EH623004
24816	292	81	421	CCTTTTCGGTTCTGATGAATGCATTTGTTACGCGATGTATTAGATACTAATTAACACA	24105	A_95_P276703	FG635575
24817	292	82	36	AAAGGAAATGAAACTAGCCAAGGACGAGCTCGAAGACATTTGAATTGTGTTGGCTT	24107	A_95_P132432	EB432894
24826	293	6	259	CATGGATCTTCTCGATCCTGTATGTGTAGTTCATATTTGGAGTACAATCCTATTATAG	24124	A_95_P029661	TA19597_4097
24827	293	7	763	TGAAGGACGTGATCTTGCTCAGGAAGGTAATGAAATTATTCGCGAGGCTTGCAAAT	24126	A_95_P246927	EB432816
24829	293	9	853	TTACCATCTTGCGCAGCAAAGACTTGCTTGGGTGTCTGTGTTTATGATTTCATTGCTC	24130	A_95_P269696	FG148776
24830	293	10	516	GTATAACAGTCGTAGAGTGGTTAGTAACATGAGCATCTCTGCTCCTGGTATTTTAAC	24132	A_95_P108137	CV018687
24835	293	15	805	ACCACAGTCTGAGACATACGCTTACTGGTGAAAACTGATGTTGTTGACGTGGATCTC	24142	A_95_P012021	EB424612
24837	293	17	259	CTCGTCAGCAAAGCAATTTATGGGTCATACTTTGGTCCATTAATAAACAATATGTTTG	24146	A_95_P110997	CV019999
24839	293	19	615	CAATAGCATTAAGCATTGCCCTCTGCAGGAAGACTAATGATGCTTTGAATTTTGTTTA	24150	A_95_P012471	EB431036
24842	293	22	167	CGTAGGTTCGAATCCTACTTGGGGAGATTTGATTGATTCTGAATTAAAGAATTCAGA	24155	A_95_P029086	TC72383
24843	293	23	1081	ACCTCCTTCATATGTACAAATGGCGGATTTGGAGAAGAAACAGCAATTGCTTGTACA	24157	A_95_P183707	TA13518_4097
24848	293	28	862	AATGAAAGCTGTGGCTGACTAATTAGACGTGAGTAGGTCAGTATCTCACCTAGCTAG	24166	A_95_P305328	FG144744
24853	293	33	767	GGTTGCTGTAGTAAACTAGCTGCCAAATTTGTCTCATTAAGAGCTTTCGATTAGTTAT	24176	A_95_P247157	TA16465_4097
24854	293	34	810	CACAGATGCCAAAGCAAATAGAGGATGCCAAAAATTGCGATCCTGACATGTCCTTTT	24178	A_95_P180132	TA12668_4097
24857	293	37	665	TTCAGTAATTGTTTGTGAGAACTTTATTTTGTCAAATTAATAGGAGGCACGGTTCATC	24184	A_95_P124587	DW004385
24864	293	44	744	ACAGGCTAGCTTCCTTGTTCTTGCTAGACAATTCTTTGTTGGAATGGTGGTGTTAGAT	24198	A_95_P264126	EH616914
24866	293	46	391	CGTCTAATTGACTCTGCAATGAGAAAAACTCTAGGTTTTGGTTAATTTAGGTGTAATG	24202	A_95_P092648	BP531912
24868	293	48	883	TGGTTTTTTGATGGCTATATGCCGAGGTTTCTGGTTGTTGGTGTAGTTTGAGTGTAG	24206	A_95_P268411	DW001352

24869	293	49	874	TACGCGGAAGCTTTGCAGAATTATTATGAAGCTATGCGACTAGAAATTGATCCCTAT	24208	A_95_P246537	DV999238
24871	293	51	666	CTCTTGTGTCTTTCTGAAAATGGGGAGGTTTTATTTTACTGCTCCGCCAATGAGTAAA	24212	A_95_P195617	TA16156_4097
24877	293	57	627	GTGAAGGAATGAAGTAATAGAATTCCAGAAAGCTCCAGTTTTGTTTATGAGCTTTAC	24223	A_95_P150932	EB681080
24878	293	58	480	CGAACAAGAGCTGGGATCAATCCTTTCCCTTTTGATTTTCGGTTTGGTCAAAATTCTG	24225	A_95_P091593	BP531425
24879	293	59	506	AAGAGAACTTCTTGAAGAACCAGAGGCTTCTAACACGGATGTATACGAGTCAAATCC	24227	A_95_P110897	TA13017_4097
24880	293	60	376	GCTTTAGTCGGTAAACTACTGAACTTGTTTCAACTTTGTGAATTTTGAGCAGCTTTTCT	24229	A_95_P163207	EH622180
24882	293	62	424	AGCACTTGTAGTCTGTAGTTGCTCAATGAATGTACTGTTCTATCAAGAACCATAACTA	24233	A_95_P117927	DV160902
24883	293	63	442	TCTGGAGCTACTAAACTTTGTATTTCGACTCGATTTTATGGTAGAAATGGATTAAAGT	24235	A_95_P125397	DW005183
24884	293	64	327	GGAGCAAATTTTGGGACAACTTCTAAACAGCCAGATTCTGAGGTTATTATATAAGAA	24237	A_95_P181592	TA13016_4097
24885	293	65	641	GGCATGTTGCTCTTCATCTTGATGGTCATTAGATTTTTAAGCCCCTATATTATTGTTCC	24239	A_95_P270611	FG642619
24886	293	66	154	TAAACTCTAAGCAGATTGCGCCAAAATGGCTGCTGAAATTTTAAAGGGAATGGGGG	24240	A_95_P315378	FG182040
24887	293	67	595	AGTTAGCGGGCACAAATGGTGCTACAGTCAAGGGATTTGAACTCATAGACGAGATC	24242	A_95_P292328	EB428944
24889	293	69	768	TATGGGCCCTACTGGGACTGTTGTGAAATTTCCTGAAGATATGGGTTTACCTCATTTT	24246	A_95_P118827	DV161900
24894	293	74	823	GTCCTACGCCACAAACTTTGTTCCCGGAAAATGAATACTATCACAAAACAATCTTAAA	24256	A_95_P003166	TA11664_4097
24895	293	75	706	TTGTGGCTACATTAATCACTGTCTACGCCAACTGGACGTTTGCTAGGATCCATGGGA	24258	A_95_P292264	FG194373
24897	293	77	874	TTAAACACAATCCCTGTCTCTGTCCTTAATGAATTCAATTACTGCACTTGTGCACAACT	24262	A_95_P269711	EB426072
24900	293	80	1148	GTTTCGTGAACTCAATGATCGGGGTTGGAACAGTAACAATCATAGTGTTTGTGGTCG	24268	A_95_P223452	TA22254_4097
24904	293	84	397	GTTGTGGAAACCATTTGAAGACCCATCATTCGTCTGGATTAGTTATATAATGACATTA	24274	A_95_P099648	FG636194
24905	293	85	852	AGTCTTTCCGTGTCTTTGTAGATCTAATCTGTCTGTATATAATGCCCTTAGCAGAAGG	24276	A_95_P009661	EB679350
24908	294	3	775	AGTACAATCATAACAAAAGATCATCATCTACTCCTAAGTCATTCCCTCCTCCTATTTCT	24119	A_95_P138237	EB441981
24917	294	12	859	GCTCAGCACACATTGAAACAATTTATTTTTGCTTCCAGTGTACATCTGTATTCTGTAAC	24137	A_95_P285668	EB432066
24921	294	16	495	GACACTATAAAATTCCAATATGAAAAAGGTGCTTTTGCATGGGAATTGCTGTCGGTA	24145	A_95_P104937	CV017229
24923	294	18	1990	CTCTTATGTGAAAGAAAACATCTCTGTGCAAGTCACAAGCTAAACAAGTTAGAAATT	24149	A_95_P195577	TA16147_4097
24924	294	19	908	GCTGTTGCTGCAGACTCGTAGAGAGAATGAGTTATGAGGAATAAGTAGGAGTTAAC	24151	A_95_P235169	EB424981
24925	294	20	604	AGAGAAGCCATCTTGGACATTGTGAGACAAATTTGCTATACCATTGTTACACTGAAA	24153	A_95_P133072	EB434140
24927	294	22	534	GCTCAATCGAACGTCTGAGATAGTTGAAGTTGGAAGAGAAGCGACAAGACAGAAAC	24156	A_95_P058521	BP134493
24928	294	23	430	AACTCAAATTTGATGACCACATTGTTTATGAGCAAGACTACCTCGTCCGCGTTCTTCA	24158	A_95_P103057	CV016321
24929	294	24	388	GCAACGTTCTTGCAGTACACTATATACCTGTCAATTTGGATATGAAATTTTGTTCGTA	24160	A_95_P308788	FG643619
24933	294	28	751	GTGAGTTATCCGTGCAGCACGTGAGTGTCCGTGCGATCAGATATAATATAGAACATG	24167	A_95_P314678	FG175728
24935	294	30	504	GACCTCATGAATGTAGTGAACTGCAAGTAAAGCTGATACTTGACAGCAAATATAATT	24171	A_95_P015421	EB444300
24937	294	32	970	ATAATATGATCAGAGGGGGGCGCCATTATAGAGGGTTTTCCCACAATTTTAGCCTGT	24175	A_95_P100558	BP535429
24942	294	37	104	GGTCACTGTAATAGGTTTATGTATGGTCAGTATTATTTTTTGACGTGTTTGGCAAGTT	24185	A_95_P135807	EB439364
24943	294	38	369	AAACGTGGAAAATATCTTCAAAAGAAACTGGGCAGTGGTAAGGAACCAAAATCGAT	24187	A_95_P079940	BP527888
24949	294	44	796	TTCTGAGCTATGTAAAATGAGGAAAATCTTAGCTGCTATGATGAACTTGTATCTTGAC	24199	A_95_P118052	DV161057

24950	294	45	731	GAGGGTTTCTTCTGTGTGATATGCTGAGTACATTTCTGATGATATGTTCCACATATTAT	24201	A_95_P234114	FG645193
24951	294	46	1102	CCAAATCGAACTGTATGTTGTTGTATGTATCAACCAATATCAAAGAGCACCAGTTCTT	24203	A_95_P178252	M94135
24953	294	48	798	AGTTCTGCCATGGCACAGAGAGCACATGACCTGTCAACATTAAAGGGTTACAGTGGT	24207	A_95_P009876	EB681289
24958	294	53	469	TCGCCGGTATGACTCTTTCTGCTGGAGATTAGAGTCTTTCTGCTGTGGAACAGAATGT	24217	A_95_P080445	BP528005
24963	294	58	291	ACTAGCTACTTATGTTCATGTTTTAGTATTAGGCCTCTTGCCCAAATAAGCAGTCTTGT	24226	A_95_P113972	CV021387
24966	294	61	879	CCGAATTGCTTAATGCGTTGCTCTTGCTGTGAATCATGTTGAATACAATCAAATCTCT	24232	A_95_P210567	TA19424_4097
24971	294	66	864	CATTTGTTACTCTGGTCGAAGGTGTTCCATACAGTGATGACCTGCGAAAAAGTCTTGT	24241	A_95_P205297	TA18249_4097
24972	294	67	538	ATTGGGACAGAGAATGATAATACGGAGCTTCATTTTGTCTTTTCTCATTCTCAGATAT	24243	A_95_P308948	FG644146
24976	294	71	526	TTCATGTACTTTAAATGAATGAAAACCAAAGAAGTGCCATCCTCCGTTTTCATGTCTGT	24251	A_95_P026941	TA12013_4097
24978	294	73	749	GACCACTGACAGCTTTGTCCAACAGTTCAATGATGCCTTTGTTTTAATATATACTACTA	24255	A_95_P188677	TA14623_4097
24984	294	79	848	CTCTGAGGAGATGGAGTTTATCTGTTATCTATGCTTCTTTGTATATGTACGCTAGATAT	24267	A_95_P298578	FG168370
24985	294	80	829	GAACCATAATCGGATTTTTGGTAGCTTACCAGAAGGATTGAAAGATTTACAGTTACA	24269	A_95_P013371	EB425603
24987	294	82	3141	CAGATAAATCAGCTTCTTGCTAACCTTGTAGTATGTGCAGTTTACATCATACAACATTA	24272	A_95_P222832	AF203476
24990	294	85	528	CTGGAAGAACGTAAACTTCTATGGTAGATTGTATAGACATTCGTCGTTTTATCCTGTT	24277	A_95_P123672	DW003534
24992	295	2	824	ACAACTACTGCGCTGATAAAAAGAGGTTTCCTCAAGGCTATTCTCATGAATGCAAGA	24280	A_95_P017356	EB446133
24995	295	5	960	TATGTTTGCTTTAAGTTTTGCATCATCTCCCTTTGGTTTTGAATGTGAAGGATTTCAGC	24285	A_95_P011906	TA12876_4097
24996	295	6	807	AGGGATACACTCATTCTATCTGCAGTCATTGTTGCTTGCACTTTGTTTCTTATTATCTAT	24287	A_95_P142372	EB445856
24999	295	9	440	CTGCCCAACGTATAAAAAATACGCCGATTTGCTGCAACATATGCATTTCACTATGTTCA	24293	A_95_P153037	EB683356
25000	295	10	428	TGAGCATCTTCCACCCCCTTCTTACTTTGTACTGATAGTTAATGAGGAAATGAATCCC	24295	A_95_P104307	CV016934
25001	295	11	458	TGAACAGGAGATAAGAATCTCGTGGAAGATGAGACATCAACTTCTTTCTTTTGATAC	24297	A_95_P099718	BP535040
25007	295	17	833	GATTGGGAAAGGCGATCCAGAATCATAGGAGGCGTTGCTAGGGGAATTCTTTATCTT	24309	A_95_P116567	DV159321
25008	295	18	1063	CAAGAGTGGGTACGCTGCACTCATAATTATATTAAGGGAATGTTTATTTAAGGAGAG	24311	A_95_P184852	TA13786_4097
25015	295	25	345	AGTCTAGTAGTTACCCAAACCTGCTCCGTATATTTTGCATATTGTCAAAGTGAGATCC	24325	A_95_P140447	EB444350
25016	295	26	688	AATGAAGATAATAATGATGAAGGCATGTATTGAAGGTTGCTTGTTGGGTGGTTTTCG	24327	A_95_P149582	EB679481
25017	295	27	760	ATCATCTCTCTCTCTCTCTCTCTCTCTTCATCACAGATAAATAAGTGCAACGCATTGTAA	24329	A_95_P160192	EH618859
25020	295	30	277	GTGGTAAACAAGAAATTGCAATTTGCATTCAGTCCAGCAATAAAGTTCCATTTCTAGC	24335	A_95_P133142	EB434371
25022	295	32	1514	AGATTGTCTCTTGTTGTTCTGGTTGTTTGGGCAGTTCTAGGTTTAATGCCTCGCTCTCG	24339	A_95_P015091	TA14104_4097
25027	295	37	571	ATGTAAATCCTGCAGAATCATGTAATTTGGCGGGGAGTAATGTAAGGCCGTTTAGAA	24348	A_95_P114567	TA13622_4097
25028	295	38	795	TGAACTCATCAGGAGGATGAACTAAACAGTAGCCAGCAGTTTTGTTTTCTTTACAAGT	24349	A_95_P119337	TA12229_4097
25029	295	39	804	CGGCTTCTGAAAGTGCAAAGGAAATTGGCATTTTTGAATAAACGCACAAAAGTGGCT	24351	A_95_P254579	EH621504
25031	295	41	388	AAAGGGTCAGGTGTTTGATATATTGGAATGAATGGTTGTGAATGCACTATGTTTCTCT	24354	A_95_P026351	TA17047_4097
25032	295	42	279	CACTCTTGGCAAACACCTCATTTGTATTTGAACTGCACAGTTAATTACCATACAAAAT	24356	A_95_P155147	EG649922
25033	295	43	635	GTTCTGTAACTGTAGCGGGAAGTAGAATTGGAATAGTTTGTATACTAGTGTATCATTT	24358	A_95_P198297	EB435329
25036	295	46	436	TGATTCAGATCTTGAGGGATCAGTCAAAGATGACTCAGAAGCTGCTAACAATCCACCT	24364	A_95_P120732	DW000697

25039	295	49	892	ACAATGGGTAATATTTTCTGCTTGGATGTTTTATTATGCAATCATGCTGTACTTTGGT	24370	A_95_P258771	EB447549
25042	295	52	671	ATTTCTGTTGATCATGTTGCTCATCTTAAACCATCTGATGGAGGTTCTGCTGCTACTC	24376	A_95_P207377	FG172968
25043	295	53	605	AGAGAAGAATTATGTACAGTTCGAGGAGGTCTCTCTTATCCTTATTTCCTTTTGGTGG	24378	A_95_P042406	BP130350
25045	295	55	521	GGCCGTAGTTATATATGTGAGGTGCATGTCCTATAATCGTTTGAACTGTTTTTTCTGT	24382	A_95_P019451	DW002669
25048	295	58	733	GTCCTCTATGTTGCTTCTATGTTAACTTCTGTGATTATTATTGATAAAGTCGGATCGTT	24387	A_95_P187417	DV158956
25052	295	62	596	GAACATAGACAGATTGTCTAATCCTCTAATTTACTAGGTAATTATCTCAAGCCCCTTG	24395	A_95_P303503	FG635016
25055	295	65	692	GCAGCACGAGTCGCTGCATATAGGTTTGGAATGTCTCTTCGCTTGATGTCTAATATAT	24401	A_95_P151752	EB682010
25057	295	67	629	TAAAAGATTTGACAGTCTTCTCCATATCTCCCCTCCGTGTTCTTCATTACTTCATCTGA	24405	A_95_P060410	BP134989
25059	295	69	524	TAGGGTTTGGTTCTGTTTGTTTGGTCTTAATCTAGGGTTCTGCCGATGTAAAAATAGT	24409	A_95_P000911	EB447085
25068	295	78	1893	GTATGTCGCAACCAAATTTGTTGTACTGCAATTCTAGAACCAAGACTAGCAAAGCGT	24426	A_95_P206542	X99405
25069	295	79	1746	TAGTATGTGGAGGTGTTACAGCTAACTGTCTCTGGTTTTCTAAACCGAAAGAGGAAA	24428	A_95_P124257	EU418730
25076	296	1	768	CCAGTACAAGATTTTATTCAGGGAACTTTCTCAACAAAAGAAAACTCATTGAGTTCCA	24279	A_95_P131757	TA13620_4097
25081	296	6	406	TTCCCTAAGTATTTTGACTTCTGTCTAACATTTGTTTGAAGTGAGATGTTCTTTCCAGG	24288	A_95_P150677	EB680812
25082	296	7	602	AAGTAATTGTTATTCCTGTGCCATACAAGGATGCAAATACTCAAGGGATCTTTGATG	24290	A_95_P056386	BP133941
25085	296	10	521	CAACCCTTGGAAACAAAAAGCTTTTACATTTGATCGTTCTATATATCCACATCTCTGTG	24296	A_95_P021556	EH622255
25086	296	11	772	TGGTCTTATTTACAGTAATGTGTTCATGAACCATGCACATGCCCCTCTATCCACCGATT	24298	A_95_P108127	TA13827_4097
25088	296	13	401	TTACGCAGAGCATGTTATGAGATGATTTTTGCGGATTAAAAGTCACAGATAGTTCAG	24302	A_95_P097378	BP534013
25092	296	17	853	TTGAATGCCATGTTAAACTTTGCTCATTGGTTTAATTAAGCTCTTTGCAGTTCTAACTC	24310	A_95_P197052	U91727
25094	296	19	459	GATTTCAATTGATCTCTTTTGAAGGGAATGGGGGTCCCTTGAAGAAGATGAAGATCT	24314	A_95_P266001	AM808208
25101	296	26	204	CGTTTGGCATTACAAATTCTTCTCTAGTTTGTTGGCATAACCCTGTTCATTCAATTATT	24328	A_95_P130637	EB430685
25105	296	30	496	ACACCGTACTTTGTGAATCCAAACAGTTGAGGGGCACTAAATGAGATTAATGATCTC	24336	A_95_P226749	FG641328
25107	296	32	985	GGCTAGAAAGCAATGGTGTTGACAACTAATTATATGGTGTTAGTAAAAAGAGTAGC	24340	A_95_P026481	TA16566_4097
25111	296	36	662	AGAAACTGAGCTTCTTACTTTGAAGTTACAGCTGAAAGCACATTTGGTTAAAAGAAC	24347	A_95_P222692	TA22089_4097
25113	296	38	494	AAGTGAAAAGCCAAAAAGAATGTGGAAATAAAACGCTTTCTGGTTGGGAAGTGTCT	24350	A_95_P005651	EB449928
25114	296	39	778	ATAGTGATGATGAGTACATAGGTGGTCCCAGACAACAAATCCGTCAGCCACTGATCA	24352	A_95_P016521	DV999592
25120	296	45	953	GGGATTAAGATTGACATACTGCTCTGAGCATATTGTCCTTCCTTTGTTTTTCAAAGAT	24363	A_95_P018116	TA13265_4097
25121	296	46	726	GGGTTGGTGTGTATAGAATATAGCTGTTGCTTTTTACTTTTCCTATTTTAGAGAACAC	24365	A_95_P146157	EB450063
25123	296	48	828	ATGTAGCGCTGAAATCATGTGAAGTGGGGAGGGAGAAACACTGTGCTTGTTGATGC	24369	A_95_P288493	FG158472
25124	296	49	988	ATGGTAATAGGACTTTCATTTCTCAACCTCAGAAGGCAAACACTGATGCCAATCAAAT	24371	A_95_P212897	TA19933_4097
25126	296	51	777	TTTTGCCAATGGCTGATGATTTCAAGAGTGCTCAAACGCATTCTCCTGCTGAAACAAT	24375	A_95_P182757	TA13294_4097
25134	296	59	453	ATGGCTGCATAGGTTGTCGTTCTCTCTATGCAAAGAGATGAGAGGTCCGATTTATAT	24390	A_95_P083840	BP528868
25140	296	65	297	GTATTATCCGAAATTCGGACTGATTTTTTGGGAAGTTATGCAATAAATTTACTCGGAC	24402	A_95_P033534	AJ632813
25142	296	67	335	CATTTTGGTGATACTGTCGCATCTACGTTCAAGATGTTGAATAAATGTGTTTGCTTGT	24406	A_95_P133232	EB434548
25146	296	71	309	TACCATTTACATCTTCGATTGACATTGCAGACTGCATGTTGAATGCTTCCATATTAAA	24413	A_95_P094753	BP532859

25151	296	76	329	TAGGAGCATTCTTCATCTTGTGCCAAACATAGAGATATTTTGCACACAATTTTACAAG	24423	A_95_P044576	BP130919
25156	296	81	830	TTATTGTGTCTAATCATGGGGCTCGACAACTTGATTATGCTCCCGCAACAGTTATGGC	24433	A_95_P147597	EB452103
25159	296	84	798	TTCAAGTCTGTCACTGTCCATTCTAGTCCTCCATGAACTGCTGATAAAGTCCTGATCCG	24439	A_95_P293033	FG147247
25160	296	85	747	GAGCAGGAAAAGAGTACTGTGTTTCCATTTTATTGTATTTATGCATCAACTGTGGCG	24441	A_95_P303148	FG645303
25163	297	3	130	GCAATACAGGTAGAATAGCTACGTCTAAATCATAAGGTGTTGTACTACCGTTAGGCT	24445	A_95_P112407	CV020660
25164	297	4	452	TTTGTAGCTGTGTTGCCTTTATGATTTGATGAGTGGTGAACTTATTTGTCTCATGTTTC	24447	A_95_P001541	EB643434
25166	297	6	754	TGAGTTGGTCCCTTCAAATTGGCAGCTATTACCTAATTGATAAAATTCAAAAGCCTTG	24451	A_95_P014046	TA12310_4097
25168	297	8	384	ACATTAGGAACAGCTGCTTCATTCATTGTTCCTTCTGCCTGAAAGAACATGGTGAGG	24455	A_95_P064075	BP135950
25169	297	9	895	CCTGTGCGTTGATTACTGTTGGTGATGAGAGCGATTTACAATTTATTGTAACTTTGTA	24457	A_95_P178822	TA12353_4097
25173	297	13	749	CCACTTTGCAGGAGAACCTAAAATCATTGAGAGCTGTTTGTGGACTTGATATGGATG	24464	A_95_P127912	EB427475
25174	297	14	867	CTTGTAAGCATGAATTTGGTTGATGCTTGATCTCAGTACTTCTGAAATTTGCTTTATTG	24466	A_95_P048526	TA15300_4097
25177	297	17	1144	ACTGGGTCCTTGATTCCCCCATTACAGAAGTACCGTCTGGTAGTACGGATAAATTCAT	24472	A_95_P203897	TA17952_4097
25178	297	18	734	AATTTGGGGCGAGAATATGTATCAGCTCTATAGAGGCGGCTACCATTCGCCCTCTTTT	24474	A_95_P146437	EB450494
25181	297	21	1326	TTGGTTCCTATACCAGAGTTTTAAAACCTAAAATGCTGTTATTGCTTGAATGTTGATG	24480	A_95_P193742	TA15736_4097
25183	297	23	702	TGTTTTGGTGCTGTAACATATCAAAGGCGTCTGGGCGTATCCTACATGAATTAAATG	24484	A_95_P235559	EB441645
25185	297	25	808	TGAGCTAGATTAGGATGTGAGATGACAATTAGAAATGTTCTGATTATCTGCCTGCAT	24488	A_95_P133672	EB435295
25194	297	34	581	CCAAGAGAATAATAGTCTCTCTACCTCCACAAGGTCAGGGTAAGGTATGCGTACACA	24506	A_95_P022956	TA21681_4097
25195	297	35	168	GACATGATTGCAGTCATTCATCGGGGAAAAGTTGTTGAAAAAGGCACACATCACGA	24508	A_95_P078345	BP527493
25201	297	41	147	GTGAATGCTTGTGTTGTGTGTAATACTTCAACCCCATGGAAATGCTACGTTTATTAGC	24520	A_95_P129497	EB429431
25202	297	42	657	TTATCCATTCTGGCCTTTGTAACACTCACTCGACTTGAAACCTTAACTGGCCAAAGAA	24522	A_95_P260906	FG635915
25206	297	46	1121	ATAGGATTGAGTCGTCGTCTACAGCATCTTTTTGGCCATTTTTCTTCTTTTACCATAGT	24530	A_95_P135242	TA15341_4097
25208	297	48	562	TTAAATTGAAACCTTGCGCGGCGAGGTATGTTCTTCACAAAATTGTTCTCAGATCTAT	24534	A_95_P285203	FG639462
25210	297	50	609	CTATCTGAGAAAGTTTTGGATTTTGATAAACGTTCATGTAGCTGTTTCACATGGTAAT	24538	A_95_P020851	TA12379_4097
25213	297	53	140	TTTTGATTTTTGATGTAATAACATGGACCGCAGACTGGAACCTCGACGGAACGACAC	24544	A_95_P130407	EB430452
25219	297	59	876	GATTTCAAGAACCCAATTAACCCCATCGATGCCGATGCCAGCCATAACAAAACTCTTG	24556	A_95_P258796	TA12763_4097
25222	297	62	386	GATGTTAAAGTTGATATCGACTTGGGCAGAGAAAGTCGCCATAATAAAATTTCCAGA	24562	A_95_P068280	BP137093
25224	297	64	271	TAGGACTCTTTATGGATTTGGTGGTTAAGTTTTTGGATCTGGGTTTTGGGTATTTTGT	24566	A_95_P025316	TA14098_4097
25225	297	65	407	GAGGTTGTGAATGTTAATTGTCTAGTGATTTAGGAGGATCTATTCTTCATATGGTGT	24568	A_95_P090413	BP530942
25226	297	66	698	AGGCAGGTTTTCCTCATCTCATCTCTCCTATGTTTTAGTCTTTTTCAAAGCAAAACAGT	24570	A_95_P013366	EB677787
25233	297	73	442	AGAGCTGGTTGTATGAACTTATACTGAAGTTTGGAATGCAAAGAAATTGGCGTTCCA	24584	A_95_P134812	EB437619
25234	297	74	264	CTGTATTCATTAGTCAATGGAGTATTTGAACCTTGGGATTTACCTGGCTTTGAAATAC	24586	A_95_P104342	CV016956
25235	297	75	432	TATGGGTAGAGGAGGAGAAGAAATGATTAGGCCTCCTGCAAAGTATATGAGAACTG	24588	A_95_P139057	FG161784
25238	297	78	1295	GACGAAGACTATGTAGAACCATATATTCTAATTTATGGTAGGTGACAGTCGAATTTG	24593	A_95_P183197	TA13403_4097
25242	297	82	145	CCACTTGTGAGGATATTTGGAAGTTGATGAGATCTTTCGAAGACATGTTATGAAGTA	24601	A_95_P158437	EH616390

25243	297	83	0	GCAAAAGTATTCTTATGGTTACTCTCTCCACATAGCAATAGATTTTGTCCATCTTCTCT	24603	A_95_P017311	A_95_P017311
25244	297	84	255	GTTCTACTGTACTGATATGTCATTTGTTGTTATGAGATGGTTGGAGTTTATGCCTTAT	24605	A_95_P133187	EB434452
25246	298	1	417	CAGAGGAATGTAATGCTTTTGAAATTTTATGATTGAGCCTAGCATATCTGCCGTTTAG	24443	A_95_P204097	EH618725
25249	298	4	409	CTGCTGTTAGAAAAGGGAACAAGAAGCAAGTAAAGGATGAGTTGGATCGGATTAA	24448	A_95_P125957	TA17381_4097
25251	298	6	573	TCCCTCCGATTGTGAGAAAGTTTGTTTTACAGTTGCAGTTGTATTTGTTACTCATTTGT	24452	A_95_P287333	FG642723
25252	298	7	861	CAAACTCTGTGATATGGGATCTGCTTTTTCATTTACTTCTGTTTATCTCGACAAACATG	24454	A_95_P226969	EB443281
25253	298	8	342	CCAATCATTTGAAAATTGGTCAAGGTGTTAGGCCCCTTTTATAATTAGGTCAACAAAA	24456	A_95_P175177	EH666023
25254	298	9	527	CTATTGAGCACATGGATGGACTGTTTGTGATCTTTGCTGGGAGGAAGTTCACTCAGT	24458	A_95_P040731	BP129906
25256	298	11	1189	AGCTGTTGCACAGACTGTAACTTCACTTTATGATCTTTACTGTGGTGGAGTGTTGTGG	24461	A_95_P028126	TA19612_4097
25258	298	13	579	CCGGTAGCCATGGTATGGACATCATGTTGCCAGTCAAAAATATGTCGTCTACTAACG	24465	A_95_P148812	EB678352
25260	298	15	817	ATATGCTGTGACTCCATTATTGGAAGATGCTCTAATGGACAGAGATCTCGTGCACAG	24469	A_95_P015561	EB425326
25262	298	17	838	ACGTTGTGGATCTGTATTTACAAAGTTCTCTGGAATGAAGTGAATGAAGATTTACCG	24473	A_95_P002476	EB450385
25263	298	18	384	GTCTGATTATGGTTAGTCTTACCTGAACTGGAAATGTTTTTGGTATTTTGTTACCAAC	24475	A_95_P025206	FG644421
25266	298	21	836	ACAGTTGCTATTGATGACATTGATATATCTGCTGGCAATCAAAGTTCAGCTGCCCGG	24481	A_95_P015946	TA17991_4097
25269	298	24	389	ATCGACTTTGTACGCTCCTGTGAAGATCTTCTAACTGAATTTAATTGTACTGCTAACTT	24487	A_95_P212087	TA19754_4097
25275	298	30	778	TCAAGGAACTAGGAATACAAGATTATCTGTTAGATGCACACCCCATCCTGTGAATAT	24499	A_95_P126912	EB426301
25279	298	34	373	GAGAAGCTAATAATTACAAGGGAGTTGGATTGGCCAGAGCAGGTGCTGGTGGTATA	24507	A_95_P108872	DV162343
25280	298	35	1466	CAGTTTGTTATGCTGCTGATGTTATGAATTTCATCTGTATGAGTTTTCTTCCTTGGATC	24509	A_95_P194442	TA15896_4097
25286	298	41	589	GGTTTCCCAGATGATTAATGGAAACTGATTGTTCTATGTATTTGACATGAACTGAAG	24521	A_95_P001461	FG636182
25288	298	43	458	GTACTAGAACTATTATTGGATGGTGTGTATGAGACTTCAAAGCAGATATGTTAGTGC	24525	A_95_P065355	BP136308
25289	298	44	484	GAAAGAAAAAATCTCTATTTGATAAGGCTTCTTCCTATACCTATGAATTCCATTGGAC	24527	A_95_P277173	AM808541
25290	298	45	98	GCAATATTGCTTACAAGAGAAAATAGAAAAGGATGACTCTGCAACTGTCACATCTTG	24529	A_95_P004146	EB682832
25292	298	47	1110	CGGCATGTTAGCAGATATGGAACTGTTGTGTTGAATTGGCATGTTATTTGCTATCTA	24533	A_95_P022236	TA18105_4097
25294	298	49	761	CAAGTCATGTGGTTATGACATCTTCCTTAAAAAGCATTTTTGCAACTTCATAGGGACT	24537	A_95_P286368	EH623686
25298	298	53	575	GCCACTGGATGGAAAAATTAGATTAGTGACATCACAATCAAAGATGTGTAACCATTT	24545	A_95_P020796	BP133356
25301	298	56	180	CTAAAAAAGGGATCTGAAAGTACAAGAACCAAATACCAATTTGACCAAAACCATCAC	24551	A_95_P155897	EG650320
25305	298	60	241	AAACAGATCGTGGACGAGCCAAAAACAGGGTCAAATCATTTCCGATTTCAAGCGAT	24559	A_95_P080590	BP528041
25310	298	65	755	TGGTTTTGTTAATGCAGATTGAGGAAATACCATATCAATGATCTGGTTCGACAGTTG	24569	A_95_P234269	DW000116
25314	298	69	490	ATATCAGCTTCTGGAGTTTGCAATGCTGCTGCCATGTTAGATTGCTCCAAAATCCATT	24577	A_95_P122892	DW005219
25315	298	70	782	GCCTTCTCTCACTACAAGATCATCTACTAATTTGCACCCTTAAAGATGTACTAAGAAA	24579	A_95_P207067	EB451448
25316	298	71	417	GAGTTAGGAGCACGTAAGCGTGAATTGGGTGAGGTAAAGTAGTTAAAGAGCAGTA	24581	A_95_P069220	BP137324
25322	298	77	647	GACATGATCAACTCTCTATTTGCTATGGAGATTAACTAGTTTGGTTGAATACCCTAGA	24592	A_95_P233824	FG637726
25327	298	82	202	GGAGACGAGCTGTATCATTGGAGTAGCTGATTGGTGTTTCATTTTTTGAAGAGGAAA	24602	A_95_P034948	BJ999183
25332	299	2	535	TGGGGCACTGAAGGCTCTGGTTATTCATACAATCACTTGAATCGTGAAAAAGAAAAT	24610	A_95_P134852	EB437708

25333	299	3	551	AGACGGTACTAAATGCAGCTAAGAATTACAAAGGATCCTGTGAAAATGACTTGACCT	24612	A_95_P085565	FG637100
25335	299	5	626	CAGAGTTTGCAGCAGAAAACTTGAATAAGAACATTATGGACGAGCTAGTAACGAGGA	24616	A_95_P139002	EB442706
25343	299	13	476	TACTCACATTTTGCAACATCAAAGTAAATTTCGGGTATCTCATGAAAGTCGGGACAAA	24631	A_95_P096998	FS413263
25344	299	14	550	CTCCCTTACTCTGGGTATTCAAACTTCCTATGGATATTTGATGATATTTCAAGTCAGTA	24633	A_95_P100958	TA13431_4097
25346	299	16	56	TTTCCTAATGTACTCCACCTCTGATGTTCTTGAAGGTAAAAAATAGCCTTTTCTACTGT	24637	A_95_P256284	EH622397
25352	299	22	948	GTCCAGAGTTGCTAGATTTGGACCGTCTGCTGTATGTATCTAGTCTTATAAGGGTGA	24649	A_95_P224397	EB449435
25354	299	24	776	CTTGTGCTGAGAGAAAATTGACAGAGGATGAAAGTACAGCTTTGGCAAAGAGGGAT	24653	A_95_P201417	EU294213
25355	299	25	539	TCTATTATTGGTGGTCTTGAATTTCTGGTTTTGAAGCAAAGCTTAAACTGACCATGCC	24655	A_95_P024076	FS438234
25359	299	29	859	TTATCAGTCGAATGCAAGTTCCACACAATGTCAAAAGCATCTCACGGACCCTTTCCAC	24663	A_95_P204257	EB425796
25360	299	30	410	AAGCTACCAGATGAGTAATTACTACTTCTGCTTGATACGAAATGACGATATCATCCCC	24665	A_95_P031321	TC75821
25366	299	36	243	TTCTCTGAGCTTTGGACTAATGGAAAAAATAACAGATGGATGATCTAACAAGTAGCC	24677	A_95_P129782	EB429741
25369	299	39	1544	CGTGAAAATATGAATGGTTAATGCTTCATGTATGTGTTTTAGTGTACTGTCGGTGGTT	24683	A_95_P115242	DQ813657
25375	299	45	982	GTTACGTCTAGGTAGATGATGCATTGTAAAGTGGTGGTTATTGAAAGTTGATAGTGT	24695	A_95_P016561	TA15470_4097
25377	299	47	714	GCTTGCAATTCTGAACACTCCACTGACTGTTTCTTCACCTATTCCTGGACTTTTTCAGCA	24699	A_95_P200087	DW000878
25378	299	48	647	TGGTGTATTCATGTCGATGGTTTAGTAGCTATTAGTGTCGGATTGGCGCACAGTTGA	24701	A_95_P056981	BP134099
25381	299	51	535	CCTGTTTCCCGTCTCCTTTAAACGTTGTCTTTCAGTTTCTCATAAAACATGTGAAAAAG	24707	A_95_P018446	EH617796
25382	299	52	693	TGCTAGTGCTGGAATTTTTAGCGAGCCACCTCAAAATGCTGGACAAGATTGCCATTCT	24709	A_95_P305363	FG193269
25383	299	53	521	GTGAACTCCAAGTTGTAGATTTGGTGAAAGGAAAAAGTGAACTATCTTCATTCCGTA	24711	A_95_P088523	BP530106
25384	299	54	1202	GAATAACTTGGGAATAAATGAGGCTGCAAGGCCATGTACCATTGATTTAGGCTTTCCA	24713	A_95_P186882	TA14223_4097
25387	299	57	749	GGCCTAATAGTGTATTAGAAGTTCTACTAATTAATTTTCCCAGGGGTGTACTTTATGG	24719	A_95_P116428	DV159134
25388	299	58	749	TAACCTAAACTGAGGTTCCAAGTCTGCAATCAGATTAGTCAGTTTCTCGCAATCCGCT	24721	A_95_P229409	DV160447
25395	299	65	519	CCATTACTATATTGTGCTGTTGCACCGACTATTTTGGCAGGTCAAATTGATCCCGTTCT	24735	A_95_P156342	EH622808
25401	299	71	767	CAGTGTGTGAGTTGTACTAGTTTTTGCCAACACAACATTAACCGTAATAAAACATAGT	24747	A_95_P000476	EB439640
25403	299	73	629	TACCTGTACGTGGAGTCTATGTACTATTCTAAGTTTTCACATTCACAGAAATTGTTGGA	24751	A_95_P273706	FG636077
25405	299	75	310	TGAACGCTTTGATTATCATCACTGGTTTTGTTATTGCATAGTGTGTTTGCTTAAGGTGA	24755	A_95_P026576	TA12722_4097
25408	299	78	489	ATTGAACTAAAACTAGTTACTGCTTGTGTCGTTACTGTTTCCTTTTGCATCTTTCCTTGA	24761	A_95_P209262	TA19151_4097
25409	299	79	861	AGAAATTCTGGCTTCTTGTACTTCTAAGGAGCTTGGAGTGAGTCAACCATGTCTAGCT	24763	A_95_P230404	EB678974
25411	299	81	415	GAAGATACCTCTACTGTAAAAGATTTGCCTGCCTATAATCTATTGAGGAGATAATGTA	24767	A_95_P076245	BP526933
25412	299	82	230	GTTTTGCATCTTGATTGAATGTAAGTTTTTGATCCAACTGCAGATCAGCAGTTCAAACA	24769	A_95_P177157	TA11896_4097
25414	299	84	513	AGAAATGGTGACAGCAACTCCATGCAGCCACATGTTCCATGAAGATTGTATTGTTCCA	24773	A_95_P124462	EB451554
25422	300	7	498	GTAGTAATCAGAGTAGTCTCTTGATATTTTCGTCAAGTTTCATAAAAAGAGTGCCAAG	24621	A_95_P297763	FG642661
25428	300	13	915	GTAGATGCTGGGCACTTTGTTAATTTCAAGTAAACAGTTTATCTCTGTGTGAAATGTG	24632	A_95_P200607	TA17242_4097
25431	300	16	777	TCTTATCTATCTGATGGCCAAATGATAAGATTCAAGCTGTAATCGAGGCGGTGTCTGT	24638	A_95_P253884	FG146936
25438	300	23	531	ATTTGTTAGGGACCACAATCATCCCTTGGTTATATCACCTTCCAAGAGACGTCCAACTT	24652	A_95_P045641	FS403398

25440	300	25	271	AGCATTTCCATCCATCGAACAAAATAGGAGGAGGTGGTTTTGGATTTGTTTTATAAG	24656	A_95_P162537	EH621481
25441	300	26	1524	CAAAAAACAAAATATTTCATTGAGAACATCTGGTTGGTTATGTCAGCCTCAATTTGCG	24658	A_95_P183932	TA13572_4097
25443	300	28	512	GCATATGAGAGTTCTGATGATGATGACTGATTTTGCTAGGATTTATTTGTCTATGATG	24662	A_95_P309273	FG645425
25446	300	31	800	TTCCCGGAGAGTTTAACGTGGTTGGATTTGAACCATAATCGGATTTTTGGTAGATTA	24668	A_95_P126117	EB425603
25449	300	34	778	GGTGTGAAACTGGATTGACAAATCTTGATGAGATGACACTTCTATTGTTCACTATCA	24674	A_95_P162822	EH621820
25450	300	35	942	TATGGAACTATGTCCGTAAAATGGATGATGCACTTCGTCAGTACTCTGCCCTTGACCA	24676	A_95_P118272	DV161275
25454	300	39	467	GCTATGGCTTCTAGAGTTGCAGCCTTTTGGAAAGATACTATTCCCTCCGTTTCAATTT	24684	A_95_P295618	FG635525
25457	300	42	712	AAAGCTTTGTATACCCTGAATCTTCTGTTCTATCGAAATCTTAAGCTTCAACAGGTTC	24690	A_95_P298263	FG638800
25458	300	43	730	ATCCCTTTTTGGAAATCAAGTTCTGCAGAAACTTCTTAGAATAGCTCGATTTGAGCG	24692	A_95_P184737	TA13762_4097
25460	300	45	411	CATAAGAAAAGCGAAGCCTCTAACAAGTTGATGTATATTCGTTGTTTGCACGAGAAA	24696	A_95_P119407	DV162609
25461	300	46	366	AGCAAAAACTTGGAGCAGGCCATCAGTTACTACGAGAAGGGAGCTGATCTTTAACA	24698	A_95_P106677	CV018003
25466	300	51	371	AGGTTTAACCCGATTGATTTGCAATTTTTAGCTTTGAAGCAATAAAGGTCCGATTTTC	24708	A_95_P108112	CV018674
25468	300	53	707	TTGTGGACAGGATGATTTATTGAAGATCATGGACTATTCCTCACTCCCCCATTTTTGC	24712	A_95_P294018	DV161190
25472	300	57	1443	GGTGATTCACAAATCTCAAGTATAGGTGTAGTTCAGACATTTCTTTGATCTTTGAGTA	24720	A_95_P023271	TA17973_4097
25475	300	60	779	CAAAACGAAAGCTGGTCAAGACTTAAGCACATGCTCCTCCTTACAGTAGTTGTGATG	24726	A_95_P163742	EH622823
25483	300	68	300	ATGTTTGTGGCTGATGGTGGTGAATGTCTTGCAGCTCAGAGTTATGCCAAAAACATG	24742	A_95_P027606	EB424783
25485	300	70	779	TGTGAATTTGGATATGTTTGGCAATCATCCTGCATACCGTTACTTCCAGTACATGCTA	24746	A_95_P138552	DV161442
25486	300	71	958	ACCTGATGTATGCCCAAGTCATCCATATTTTCTGAACTTAAATCATAGATCAATGACA	24748	A_95_P186062	TA14046_4097
25487	300	72	799	ATTCTCCTAGATTTCGCTGTCTAGGATTTTGTTAATCTGATTAGGCTGACATTGGCTA	24750	A_95_P265641	EB448253
25488	300	73	447	TGTAATTTCATATACAAGTTCCTCCCTCGTAACAGGGCACATCTTTGCATATACTATTT	24752	A_95_P163982	TA13652_4097
25495	300	80	615	TTTCTCTTCATGGTCGCTAATTTGATTCACACTCGCCATTTATAGTGGCAGCTTTGGAG	24766	A_95_P047846	BP131760
25497	300	82	887	AGCGTACTTGTGCCGTAAAGATTATGCTGATGGAGGGTTCAAGATGTTCTCTCTTGC	24770	A_95_P247507	DV998989
25500	300	85	827	GTATGTACCTAAGCATTATCACTTGGGTATAATGTATTATTTGTTGCCTTATCAGACG	24776	A_95_P221447	TA21821_4097
25502	301	2	445	AAAGCCAACTGATGTGTACGATAGGCTTCGAGCACCATTGGGTAATCTATTCTTTGG	24779	A_95_P117092	TA14500_4097
25505	301	5	0	TGGGTATCAGACTGGTCTACCTACATATGGCACAGCAAGCGAGCATCTTTTGTACTT	24785	A_95_P283738	A_95_P283738
25508	301	8	1212	ACGAAAGCATATACAGAATTTGAATGTGGATACAGTTGGTGTTGGCGTAATGGGCT	24791	A_95_P014356	TA18071_4097
25509	301	9	942	CCCTCTGCCTCTTGGAACTTTAATTTGTTCAAATGAACTGTTATGTATTCTTAGTTCAA	24793	A_95_P214582	TA20292_4097
25513	301	13	362	AAATTTCTGGACAATGGCGAATATGTACAATTACTATTACCTGGAATGGGGCGTGTG	24801	A_95_P114237	CV021512
25514	301	14	830	CAATTTCTATTTATGAGTCCCAGTTTTGTTTTGGGAAGCACTTGTAGGTTGTATAATC	24803	A_95_P120302	DW000090
25515	301	15	718	TTGAAGATGAAATCCTGTCGATAGCTGATCTCCGTTTTCTTGATCTATAATTGGAAA	24805	A_95_P190927	TA15118_4097
25517	301	17	188	CTTGGACAATGCAATTCCAGAAAGCTAGGTGTTCAGTGTGTTTCAATTTTGTTTATCT	24809	A_95_P132922	EB433719
25519	301	19	449	AGCTGCGTGTATAAACAGAGGAAACTTGTGATTTTTTCTGTCTCTGACTTTTAGATCT	24813	A_95_P197932	TA16670_4097
25520	301	20	122	CGTATTGATGGATGCAATGTTGTAACTTATAGTGCCCTTAATGCTCTCGTGTATTTAT	24815	A_95_P103012	CV016296
25522	301	22	453	TGAATATGACCCTGTTTACTTAAGTTGATCCTGCTGGGTTGAACTTTATTCTTACTGTT	24819	A_95_P178262	TA12197_4097

25523	301	23	474	ACTTACCAAAGAGAAACTTGGAGTAAACTGTTGCAATGTTTAAACCATGAGGGATTC	24821	A_95_P073130	BP526138
25525	301	25	2212	GATGGTTGTAAGTGCTGAAGACAGTATTAAGCTTATGGAAATTATGCTTTAAACTCA	24825	A_95_P009111	AY248907
25526	301	26	395	CAGAAGACCAATATCGGGTTCACAGCTAGAGTAGATGCAAAAATTAGGCAGTTGAG	24827	A_95_P083680	BP528826
25527	301	27	514	ACATTTTCCCAAAGCCTTCAAAAATGTGAACAAAGCTACTACTACAATGTCAGTAGG	24829	A_95_P191147	EB439763
25529	301	29	824	ACACAAAGTTAGAGGAAAAGCACAAAGCTCTGGAGGCAGAGAAACAAGAATATGC	24833	A_95_P011601	TA16021_4097
25534	301	34	2592	GTAGCCAAAGCTGTGTGATATATTTTAGCATCCTATATGCTATGGCTTAAGAATAAA	24842	A_95_P007316	AY248904
25536	301	36	760	CAAGCTAACTTGAGCTTTAATGGCCATCAGTTGCTGCTGCTACTACTGCATGTTTGTG	24846	A_95_P147452	EB424659
25539	301	39	886	ATATATGGCAGAGCCTCATTAGTTTGATTGATGTGAGGGACTGCTGCAGTACTCGAA	24852	A_95_P025446	EB450890
25540	301	40	341	CGTAATTTTCAACATGTTTTTAACGATGATAGTCGTGTAAGTTTGGTGCAGTTCAAGG	24854	A_95_P002896	FG198048
25553	301	53	985	GTTGTCCCGAAATTGGTGTGGCTTTTATCTGGGAAAAGTCTATTTTCCTTGGTTCATA	24879	A_95_P200277	TA17174_4097
25557	301	57	828	CATTTGGGTCTCTTTCTCATGTTATGGATGCATCTATGGAAGATCTTGCTCGTTGCCC	24887	A_95_P150017	EB680066
25558	301	58	522	TTGGTCTTTTCATGGAATGTGTTGCTATTTGTGACTTTTAGAAGGGTCTTTGCTGATC	24889	A_95_P231594	FS408551
25560	301	60	1196	CTTTGTGTCCTTTTAATTCAGACATCTTTGGAAGGCACTCTGTAAATTTCATGTTCAAA	24893	A_95_P010701	TA17132_4097
25570	301	70	641	CATCAGATTTGAAGAATAAAGTTGCGATTGAGAATTTATACCTAAGCGATATCACTT	24912	A_95_P249957	EX465326
25571	301	71	644	TATGTCAAAGTTTCATGTGATGATGAAGAAGAACGAGCGAGCCGTAGGATGTACAG	24914	A_95_P116392	DV159096
25573	301	73	788	AGAGGGATAGTTCCCATGATGCACATCAGCAGAGTCTAGACCGAATTTGTATTATAA	24917	A_95_P303963	FG136199
25574	301	74	350	CTCTTGTATATGATGGTGATTAAGAGTATTGATTAGTGAATCTTCAAATGTATTCCCC	24919	A_95_P301508	FG638239
25576	301	76	675	ATTCCATCAACCATTCAGGAAGAATTGGAGACTAACCCATTCATGCGGGCTGATCTT	24923	A_95_P189827	DW005092
25577	301	77	593	GGTATTGATGGAGCAAGTGAATTTGGTTCTTGATACACTTTTGGGTCAAATAATTTAT	24925	A_95_P178367	TA12230_4097
25578	301	78	697	GGGTGGGGTTTTCTGTTGTTTGTAATACACTAAAGTCAATTCCTTTTGAGCAATTTGA	24927	A_95_P152912	EB683240
25582	301	82	767	CAAGATATACTGAAAGGTGGTACATGGAATGCATGTTGCTGCATCTTGAATTCTTCTT	24935	A_95_P163442	EH622490
25584	301	84	405	GTCTGTTATTCATGAAATAACATCAGCGCTCGGGATATACTGTTTCAGGATTACAAG	24939	A_95_P087588	BP529831
25585	301	85	529	TCTTTTGCATCCAAGCCAATTTTGTAGTTTGATCACGCCCAACTATGCCTTATAAAAA	24941	A_95_P153882	EB684060
25587	302	2	1040	TCAGTGTCCTCTGTGAATTGACCTTGGGTATTATGTTTGCTGTCTGTTATTTAAGACA	24780	A_95_P018546	TA12116_4097
25588	302	3	842	CCAACTTTCAAGGACAACGGGTTTTTGTAAAATGCCACTGTATCATTTTTTCTTAACTT	24782	A_95_P010921	DV158142
25592	302	7	597	TGGTGTTTGAGGTTCTGTCATTCCCTGTTGCAAAAACATTTAATATGTGATCAGTATT	24790	A_95_P177622	TA12024_4097
25593	302	8	566	TGTTCTGCAATTTTGCGTCGTGACTGGTCTATTATTGTATGTAAGCAGTTCCTTCTTTT	24792	A_95_P124282	DW004137
25595	302	10	137	TTTGAAATCGTGATTGAGATACTGTCGGAGTCTGAGGTTGTTTCGTTGAGGTTTCCG	24796	A_95_P095113	BP533028
25597	302	12	696	AGAACAATAGTTGAACATTCCCATCTGAAGGAAGAAAATTTAAGGTCTTTGCGTGAT	24800	A_95_P118002	DV159892
25600	302	15	444	GAAGACGCTTACCCCGTTGGGGATGATGCGTAGTCTTGGTTTGTATTTTCTTTTGCTT	24806	A_95_P281193	AM837768
25605	302	20	686	TGTATTACTGGGCTTTCCATCAAGGAACTGAAATTTAATGTTCACATTTTACAGAGAC	24816	A_95_P191152	EB439763
25607	302	22	425	CCTTCTAATGTCAAGGAAGAAAGGAAGGAGACAGAAAGACACAGCAGAGCTGGTG	24820	A_95_P122022	DW002091
25612	302	27	508	TTCTGTCGAGTCTCGGATTTCAACAGCTGGTTTCCTTTTCAAGCTCGTTGCCAAGTTTT	24830	A_95_P056541	BP133984
25614	302	29	216	TATGCAGCTGAACTAAGCATTAGTTCCTTTCAATTGATGTATTGCTTATGTATTCGCTC	24834	A_95_P107612	CV018462

25615	302	30	274	ATCCCAATATACATTTTCTTAGATTAGAGAATGGTCATACCCCTCCTCCCCTTCCGTTT	24836	A_95_P131447	EB431733
25616	302	31	816	CACAAATCGTAGGCTTCCTCTGTTATCTTTCTAATCTATATCTGTGTCCATCAGTTCTCT	24837	A_95_P145352	EB449040
25617	302	32	677	GAACTTTAAAAATCCAGGATTGTAGGTTGTAACTGAAGCAGAGTTTTACCGGATTTGT	24839	A_95_P214422	TA20260_4097
25620	302	35	471	AATATATTGGTCCGGACAGTCTCAAGGTTACTCTGGCAACCATAATTGGAGCCATAG	24845	A_95_P086490	BP529548
25623	302	38	635	GTGATGGAATATGTTAGGGGTTGAGTTTGTACTTGTTATTACTTGATTGAGAAACAT	24851	A_95_P263291	FG644493
25624	302	39	612	AATGGCCATTTTGAGCTGAATGTTTTCAAGCCTATGATTGCTAATGCCCTTCTACATT	24853	A_95_P128387	TA18092_4097
25626	302	41	431	TCCTAATCAAACGGTGTTGGCTAAAATGGAGAAGATCCTTGGTGTTAAACTTAGAGG	24857	A_95_P092958	FG642155
25629	302	44	500	CTAGGTGTTAGTACTGGTGATAATCTTGATAGCGGAAACCAGAGGTCTTTTGGAAAC	24862	A_95_P105517	CV017494
25634	302	49	1229	GGGTAAAATTTTAGTAACTGCTCTTTGTACTATTGAGAGCTTGTATGCCTTACATTGT	24872	A_95_P201712	TA17482_4097
25638	302	53	809	GATGGAGATACTGACCTCTATGTTTCTAACATCCATACTGTTCCTCACACAGCACCAG	24880	A_95_P286878	FG136839
25641	302	56	301	GTGACACATCTCAAAAGAATTCCTTAAATGCTTTTTACTAGTAAAGCTACTTTGCCCTT	24886	A_95_P244452	TA12980_4097
25644	302	59	740	CTGAGACCTGTAAGAGAACTGACAATCTTATATTTTGTTGGTATTTGAACTACTCTTG	24892	A_95_P220012	TA21517_4097
25647	302	62	221	GTTTGCGCTTAATTGCTTTGACTACTTGCTTTGACTACTATCATAAAGTCACTTTTCGT	24897	A_95_P137637	EB441370
25650	302	65	1181	CACTAAATAGTTCCTGGATGATTATCGCACTATGAATGTTACATTGTAGTTCTGATTGT	24903	A_95_P201242	TA17381_4097
25651	302	66	1234	CCAAAGTTAACTGTTGGAAGATGATATTGTAGCTCTGAAGTGTATAATCTGATCTTCT	24905	A_95_P197577	TA16594_4097
25653	302	68	798	CTCTATTCAGTCACCAATTTTAGGGAATGCATCTAATTGATCAGATGCAAGAAATTTG	24909	A_95_P125792	EB424890
25655	302	70	846	ATGGTGAGAGGATTGGCAGGATGTTTGGTCCACTATCTCGACTGAAAGATGTGATTG	24913	A_95_P227199	EB424654
25665	302	80	2011	GAACTTTGATCTTTGTAGCAAATGATGCATGGGAGATATCCATATACTCTTTCCACAA	24932	A_95_P245277	AM746200
25668	302	83	998	TCTTGCTAAATCGAAATGTTGAGGGTTTGACTCATTTGATGAATTCTCAAAGAGGCG	24938	A_95_P226604	TC46839
25670	302	85	580	AATGAGGGGAAGACTATGGATCTTCCACCAATGAGCTGTAGTTGTTGAATTTATTTAT	24942	A_95_P196332	EB428726
25671	303	1	866	CATTGTGTCCTGTTCAATTTTTGAGTATTCAGCTACACAACAATCTGGTAGTAAAGTA	24943	A_95_P177892	TA12097_4097
25674	303	4	181	CTCTGATGCGGGAGAATCACACTGGGTTTATGGAATTAGTTTTAGCTATGAAAAAAT	24949	A_95_P138097	EB441814
25677	303	7	292	TGTATGGCCAACGTCTTACCTTCGTCATAAAAGTTTATCTGTTGAATCCTAAATTTGA	24954	A_95_P218097	TA21097_4097
25682	303	12	1073	TCTTGAAGGTTGGTGAAGCTGAGAAGAATTTGGGCCGGACAGCGGATGTAAATCTTT	24964	A_95_P017846	TA17945_4097
25686	303	16	589	GGTCTGCTTTATGCCTCAAAAGTTTAGGTTTAAAAACACTTGTGCATGTTGGTAAATC	24972	A_95_P122657	DW002636
25691	303	21	162	CTACTAAACTAAGGTTTTATCTCTCAGAGCCTCCTTGAATGTGAAATATTCTGAGATTT	24982	A_95_P080265	BP527962
25693	303	23	805	TTTCCCCTTCTACTACCCTGCCATAAAGCAGCTGTATTTTTTAATAAGAAAAGTTGCA	24986	A_95_P126662	TA16490_4097
25695	303	25	426	CAAGCGATTTCCTGCTCTTAAGGTACATGCTACCGTTACTCGAACAGAGGAACCAAA	24990	A_95_P128407	DW000208
25696	303	26	865	TTTGATCGAGTGACAGTAGTCTGAGATATGCTGATCTGATCTCTACACTCCCTCTGGG	24992	A_95_P235934	FG159665
25698	303	28	520	CAAGAGACTTGTTAGGTTGAAACCACCAACAGAGTTCTGATGAAGATTCCCCCCATCT	24996	A_95_P098388	BP534452
25699	303	29	844	GTACATTTTCAACATATTCCTTTTTTCTAGGAGCCAGGTAGTTCACCTGTAGTTTCTGC	24998	A_95_P294473	EB682884
25700	303	30	752	GTCATCTACGCTCCTAGTTATGTCTTTAAGAACGTAGGGTTATCTGTGTTTTATTACTA	25000	A_95_P217942	TA21058_4097
25702	303	32	226	CCATGTGCTTCGTAATGCTGGTCCTCCTAATTTTGAAGGAGATATTATTCTGATTCAT	25004	A_95_P261331	BP131668
25703	303	33	814	TGCTACACTATTGTGAAGAAAAAACTTAGTGATATGCTGGCCCTACTATATCCTATTG	25006	A_95_P195392	DV157600

25706	303	36	333	GACTATTTTCAGATTTCTACTGTTGTGAAGCTCTCATTTTGCTTGGATAGCACTGACTT	25012	A_95_P017591	EB425819
25707	303	37	781	AAGTTTCTGATGAGATCTGAGCATATTTCCAGAGTCGTCTCGGGAGTCAGCTTGTGC	25014	A_95_P310258	FG145186
25710	303	40	485	CGCCGACTTTGCAAATTCAAAAGATAGGGAGAACAATATTCGTCCTGACAAATGTCT	25020	A_95_P098053	BP534310
25712	303	42	454	TGAGTTTTCTTTTTCCTTTGCTGTACCTCATATATTCTGGAGACTCGGGCAGTTTTGTA	25024	A_95_P202317	FG642455
25713	303	43	554	GCTGGTAGTCATAGGAAACTGAAGGAATGCAATATATAATGAAATAAGCCTGGGAA	25026	A_95_P033769	AJ632965
25714	303	44	229	CTTTACTGGTTCTAAGTTTGGTTGACAGTTCCGTTATGGTTTACTGTGGTACCTGCTA	25028	A_95_P108272	CV018762
25716	303	46	687	ATTTTTTGTTCTCTGGAAATTTTAGCTGTTGAGGGAATGCATTTGTCGAATATGGCTA	25032	A_95_P117697	DV160624
25717	303	47	651	ACTCAGACTTGAGAAACTGAGCTTCTTATTTTGAAGTTACAGCTGAAAGCACATTTAG	25034	A_95_P265536	EB444722
25728	303	58	555	TTGGCGTACAATTCCATTTTTAGTTCACAATCCTGAACTTTCCCTTGTTCAAGCTCGTT	25054	A_95_P152497	EB682827
25736	303	66	794	TTGCCAAGAGCTGCTCGAAAGGATGTCAATGGGTGTGGAAGAGGAAACAAATTTGT	25069	A_95_P216537	EB450834
25737	303	67	2271	GATATGTAGATAGTTGAGACAACACCTTTTGTACAGCAGTTCGTTACACTAATACATT	25071	A_95_P031011	TA15408_4097
25740	303	70	244	CCTGAACATCGAGTTGTATTTGGAAGCAGGTTGCTTAGATAATTTATCTAAGACTATT	25077	A_95_P105867	CV017649
25741	303	71	859	CACTACTTTGGTCAGCTGCTTGTACAATTTCAATATTCAATACATTTCCAGTGACAAG	25079	A_95_P181497	TA12996_4097
25743	303	73	2652	GCTGGCAAAAGATATTTAACCTGCTCAATTGGAGCTTCTATAGTTTTGTTTGCATTTA	25083	A_95_P103692	TA12219_4097
25745	303	75	891	AATTTAATCTTAGACTTGACATACCCTTGGAATTACACACCCCAGTTTCTCCCGGATG	25087	A_95_P196087	TA16262_4097
25746	303	76	635	TCCTTAGTTTTGTTGTGGCAAATGCTAAAATTATGAGAGGGTACAGTTCTTTGACTGT	25089	A_95_P099558	FG635845
25747	303	77	804	CCGAAGAGGAATAAGGGAAGAAGGCAACGGCAACTAATTTTGAATTTTGAAGTGTA	25091	A_95_P213977	TA20162_4097
25748	303	78	336	TTTTGCAAAATGGATGGGTTCCTTGACTTGGAATACGAGACTGAGCACGGATTTGTC	25092	A_95_P176667	TA11709_4097
25752	303	82	758	GGACAACATTCTTCCTATATCCATTTGGCATTGTCATCGTCCTTTCACCCATCTTTATC	25100	A_95_P254569	EB438616
25753	303	83	354	GAAGAGGGGAACAAAATCTATTATTTCCTTTTTAGACAAACAATTGTTTCCTATGGTG	25102	A_95_P210027	TA19313_4097
25757	304	2	213	GGGAGGTTAGATGTCCTGTGAATGAACCTTTTTCCTTTTTGTAAAATTTTCAAGTCCA	24946	A_95_P140112	EB444070
25760	304	5	371	GTCTGTACCTGAAAATGCCAAAGATGCTGCTGTCAATCTCAAGAAATATGCTAAGTT	24951	A_95_P093938	BP532490
25761	304	6	573	ATCATAAAGCAATGTGCAAGATTCTTCCAGGAACATGTAACGCAGCTGGATAGAGA	24953	A_95_P160917	EH619615
25762	304	7	810	AGTGAGGCAACTACAAGAATATCCTATTATTCTCGCGAAGCGGATAGGTACCACAAA	24955	A_95_P290633	DW000676
25764	304	9	475	CACAACCGAAAGCAGAACCCTTAAGGTTTGGTTTTGCATGTCATGTTTCCTTTGTCAT	24959	A_95_P261301	BP131514
25765	304	10	861	CCCGTCTATTATTAGTCTAAGCGGTATTCAACTTAGATGTTACTCAGTTTTCACCATTT	24961	A_95_P254104	EB451857
25769	304	14	799	TCTTCTACGTGAAAAGTGTTGCAAGCAAATTGTGTTACAGTTGCTCTATGTGATTAAG	24969	A_95_P204622	TA18104_4097
25772	304	17	582	GCATTTGATCTCCTTCACAAATTTTAGTAGAACACTGACATTGATGCCATGAAAAGC	24975	A_95_P140647	EB444524
25773	304	18	394	TTGGGGTTCCCAGAAAACGTGTTATGTTGTAATGCATATAATCCTTCTCTAGGTTATA	24977	A_95_P072965	BP526091
25776	304	21	1027	CAACAACCTACGCACTATCTGTAGGCCAAAATCATTATGCAGAAATTGTAGCTTAATA	24983	A_95_P026316	TA16490_4097
25777	304	22	892	TTCTATGGGCCGAATCTTCGTGCCTCTTCTAGATCATCTGATGCTTCTTCATCATCAGC	24985	A_95_P273811	EB439979
25778	304	23	343	TGTAGTCTTTAATTATATGAGAAGGGGGTTATGTTTTAAGTCGAATGTCGTGTGCTCC	24987	A_95_P209692	TA19244_4097
25782	304	27	802	CAGTCCTCTATGGTTAAATCATGTTTACCATGAATTATAATTGGCCTGCAAGCATATA	24995	A_95_P023996	EB677551
25788	304	33	871	GTGTAGGTTATTAATGTTGGATGCTCGCTCAAAATAAGTTTTGCAACTTTTGGTTTTG	25007	A_95_P008556	EB425062

25789	304	34	751	CCTTATAGAGACCAGAGAGGCGTGAAAGGTTGCTTCTTATGTACATATTGAATTAAA	25009	A_95_P290468	DV999697
25790	304	35	699	ATTTTGGTATACTTGTCGCGCGATGCCTTTGTTTTATCAGGCCTCCCCAATTACAACGT	25011	A_95_P216772	EB428944
25794	304	39	407	TTCATGGATCATCTTCTGCTTTAGAGAAAAGCTTCTTGACGCTTGCATTTTGCCTTTTT	25019	A_95_P158872	EH616761
25795	304	40	558	TTCTCCAGAAGTTATGAGGCCAGGTACATTATGGTTTATTCACAGATCAATTTTCCTT	25021	A_95_P142402	DV161940
25796	304	41	792	TTTGTGCATTTTATCACCTTTGCAGCAGGTTCGTGCTGTGGTGTCAGGTCAAGTTGTT	25023	A_95_P121077	DW001083
25801	304	46	333	TCCGAAATAACATTCTTACTTGGCTCTCCTCCTCTTTCTGTACAACTAATTAGTTTAGT	25033	A_95_P085610	BP529328
25805	304	50	504	CATTCATGTACGAGCAGATGGAGGGGCCATTGGCAGAGAAACTCTTTTATTTGGTCA	25040	A_95_P095653	FG644694
25810	304	55	771	CTTCAGCTGGCGCTGAAAGCCTGAAAACATCAAAGAGTTGGGGAGAGTTTGTCATAT	25050	A_95_P218802	TA21256_4097
25811	304	56	450	CCTATGAGCATATGTATAGACTCACTCCTCTGAAAATTTAATCAATTTCCATGGATGA	25052	A_95_P001746	AF213464
25814	304	59	1172	CTCACTATTAGTCGGTTGATGTTTTCTTAAAATAAAAGAATCACTGGTTCCAGAATGT	25057	A_95_P178312	AB178953
25815	304	60	1171	ATTGCCTACTCCATCATTGTATTCACATGGATATGTGCTTAGTGACTTTGTATCAAGTC	25059	A_95_P025066	TA13222_4097
25816	304	61	417	AAGGTTTGAGAGAGAGGAAAAGCTAGGTTCTTTCTTTGAGATTCATTTTCGGATTTT	25061	A_95_P076325	BP526956
25821	304	66	797	TTCAGTTGAAGGCAACAAGGAGAGGCACCCTACATGTTCAACTTATATCCGTCAGAA	25070	A_95_P292158	EB426685
25826	304	71	509	GAAGCCCCTCTCCTCCGGTCTTTAATATATTTTGGAATAGCTATTTCCTATTTTAGCAA	25080	A_95_P144117	EB447270
25829	304	74	703	TCCTGAATCTTGGTTCTAAATGCATGTGATTTATTTTCCTTAATTACATTTGCTGCTGC	25086	A_95_P182382	TA13201_4097
25835	304	80	193	CGAGTCAAAATAACTCATATGAAACGGAGGGGGTATTTGTTTTTTGGCTCTTATTTCG	25097	A_95_P147807	EB643460
25837	304	82	868	TGGTTTCAATTTGAACTCTGAAGGGGGTGTTCTAAAGGTGAGCCCTGATGGTCTTCT	25101	A_95_P009981	TA16594_4097
25842	305	2	542	AGACTTTGTAATGTGATATGAATTTTGTGTTTGCTTTGTTACTGCCTTCTTATGGCACG	25110	A_95_P122042	FG638726
25843	305	3	812	ATCAGTTCAAAAATTGATTACTGGGCTTCCAGAATGAGCATTGCTTTACGTTTCAGTA	25112	A_95_P242877	DV999293
25845	305	5	286	GAACTGGTGTTTCAACTTTTTCATTCTTGCCGGTCAGATGATCATAAAATTAGTGCTTT	25116	A_95_P093508	BP532292
25848	305	8	705	AAAGGAAATACTCCCTTAGTTCTTTCAATCTGCTGGGACATACTGCACCAGTTCAGGC	25122	A_95_P135412	EB438829
25853	305	13	493	CCTGGGACATGATGTATGTTTTCTCTCTCTTGGGAATTGGTTCTCTAAAGAAGCGTCT	25131	A_95_P200667	EH619757
25856	305	16	331	CTGGAAAAGTTTAAGCTGGAAATGTTGATCAGTCTGATGGAAACTTTCTTGATGATG	25137	A_95_P103177	EB442583
25859	305	19	909	CAGTAGAGGAAACTTTCTTGTAGTTTAGTAGCACTTATGTTGAATGAATGTAAAGGG	25143	A_95_P203697	EB424837
25864	305	24	546	TAGGGAGAAAATGGATGTCATTGATCTGGAAGATGATACTATTGACGCTGAGATATT	25153	A_95_P101754	CN824837
25867	305	27	512	AATGCATTTAGCGGCTTTGGATAATCTATAAGGTCATTCGAGGAAGGTTTTTGATAC	25159	A_95_P209207	TA19139_4097
25868	305	28	532	ATGAAGATGGTGATGGCGCGATGGTGATATAACTGGAGCTAGTCGTCTTGTTCTTGT	25161	A_95_P161897	EH620471
25870	305	30	627	TTACCTGGTGTTTCTGTGTTGACTATGCATGAAAAAATTGGATCTGTGAAGAGCTTA	25164	A_95_P227084	FG635938
25871	305	31	870	TTGTTGCTTTGTTATCTCCTTACTCTGGTCAGTTGAAGTGCAGTGGACAAGGAAAGA	25166	A_95_P249862	EB679189
25872	305	32	1969	GGTGTGAAAGCTCCATTTTGCATGAAAGTTCGTCACGGTGGTGCTTGATTATAGTCT	25168	A_95_P147982	TA17155_4097
25875	305	35	348	GCTCTCCCGTGAAATCGAATGACAGAATCAAAGAAGACAAACGATGAGAAGAAGGC	25173	A_95_P109162	CV019173
25879	305	39	725	ACCATATGAAATCAGTTATTCTTCGAGAAAGCAGCTGGAGAGAAGCCACATTTCAAG	25181	A_95_P243057	EB445482
25881	305	41	856	AGAATTCTTACAAGCGCTGCGAACTTCCTGTGATAGTGTTGGTTCGCTTCTTGTCTTT	25185	A_95_P196847	TA16432_4097
25884	305	44	825	TTTACCTGTGTATGAAGAGACTTACAAGAGTTTGAGATCCAGAGGGGTACGTTTTCC	25190	A_95_P004101	DV159600

25890	305	50	657	GTCTATGCTGTTAGAAAGATTATTGCTGATGAAAATAAACCTAGCTGCATGGTGGCA	25201	A_95_P286483	FG638231
25893	305	53	574	AAAGTTTAAAATACAGCTTAAGGATGCTTTCCACACAATTGAAGTGCAAGGACTGCT	25207	A_95_P141052	EH617724
25902	305	62	504	AGAGAGCAAGATGTGCTCTTGAAGATAGTCTAAAGCGTGTTGAAGATATAGTACCA	25225	A_95_P083905	BP528884
25904	305	64	781	GGAGACACTTCAATGTAATTTTACTTTGTTTGCCAGTTTACCTAAGCCTTTCTCTAGTT	25229	A_95_P178692	TA12316_4097
25909	305	69	510	GGGGGTCTGCTCTTCTTTATTTTTCCTTCAAATAATGAGTAGCCTGACTAAGGTTTTA	25239	A_95_P220547	TA21630_4097
25913	305	73	544	TCAACGAGTCAATAGACTAATAGCCTGTTTGGCCAAGCTTCTAAAATCAGTTATTTTT	25247	A_95_P069765	BP137478
25915	305	75	851	ATCTAACTACGTTCATGTCACTACTTGCCCACCAAGCTGATAGAGCACTATCAGCATG	25251	A_95_P243902	FG164291
25918	305	78	463	GCTCCTGCTACTGTCACTGCTTTGAATCTCCTTAAATCAAGAGGATGATATCCCATAT	25257	A_95_P102797	CV016202
25920	305	80	274	CTGATGATAAAATGTTCAGATTTGTTTTACTTCTCCAGCACACTATGCCCACATCCGTA	25261	A_95_P097475	BP534063
25924	305	84	910	GGCGCGACCTAACAAAATATTGGATATCTTTCTTTGGTTACGTTTGATGTTAAACATT	25269	A_95_P177177	EB447510
25926	306	1	617	GCATAAAAGTGGGTGGATTTTCAATACCCCTGTAGATGCTAAAGCCATGGGTCTTCA	25109	A_95_P031636	AJ504731
25927	306	2	857	TAAATTGCCAGGCAATGCAAAGTACTCTGCTAATTCTGGAGTCCAGCCTTCTCCTATT	25111	A_95_P150542	EB680640
25931	306	6	421	AGTTGCTCTTGTTAAATGACCTGACTCTCGCTGAGCTGAAAGCTTTCATTCCAGAGCT	25119	A_95_P087603	BP529834
25932	306	7	2052	TTAGCTCATTTTCAAAAACGTCTAAAGGAGCACAATGTTCTTGTATCTTCTGGCCACT	25121	A_95_P238524	AB003038
25933	306	8	182	GTCTAAGAATTCCATTCCTTAAAGGCACACCCGTTAACAAAATTCTACTAACTCTATT	25123	A_95_P142112	EB445677
25934	306	9	597	TATCATGGGATTCTTTTTGCATCAGTATGCTAGTTTTGTCCTTGCAGTACTTTAAGATG	25124	A_95_P148247	TA12311_4097
25946	306	21	891	TACCTTCTAAAACGTTTTCCAGTTCCTTATGCTGCGTACTTCGTTGCCGTGGCAACTGT	25148	A_95_P289433	DV159365
25949	306	24	1518	GCAGAATTTTACTGCTTGACAATTGCAAGTGTGCTTACATGTTATTCGCAATTTGTTA	25154	A_95_P001731	TA11808_4097
25950	306	25	259	CTGCTACCTTCGATTTAGTTTTGAGAGTTTTGCCTTATAAGGTGAATTTCAACCCATG	25156	A_95_P161652	EH620329
25954	306	29	268	TTAGGACAATTCGATCCTCAATTTACGGCATGTTTTAGTTGACAATATGATTCTTGTA	25163	A_95_P002126	TA15252_4097
25959	306	34	901	TCTCTTGTGTATATCAGTAAATGATGATGCTTTTGTGATATGAACTGGGTAAAAGGT	25172	A_95_P195707	TA16175_4097
25960	306	35	594	TTGTCCCTCTCCCACAACAATATGGCTTCAGTCATCGGATCATAACCCTTTGGCTTTGT	25174	A_95_P287713	FG202802
25961	306	36	740	CATTAGTGTAAGAAGCTTCCTGAAAGGCCAATTTTCGTCATCAACATCAGTTTATTTG	25176	A_95_P222782	TA22108_4097
25963	306	38	960	CCTTTTTCAGGCTTGTAGATTACTGTCTTGATTCATATAAGAGAAGAGCTTGTGCAAA	25180	A_95_P223807	L29271
25964	306	39	809	GTAGGCCTTGCCCCATGTAGTCTTTTTAAGGTTTTTCATTATATGCTAAAGCTTTCTAT	25182	A_95_P198652	TA16825_4097
25968	306	43	818	TCATCTTCTATGATTTCTTCAGTAATGAAATGCTTTGGCAGGTGAAATGCTTTAGCAT	25189	A_95_P012631	EB438528
25974	306	49	411	TGCATTTTTAGCAGTAGTAGTGCTCCCAAATCTAAACTTTGGCTTCTTCTCTGCGGGC	25200	A_95_P052821	BP133022
25975	306	50	460	TGTGTTTAGTTCATTAGGTGTTGCTACCACATTTTTACTACCCTAGACTATAGTATCTT	25202	A_95_P261826	FG634286
25987	306	62	798	ACATCTTGATGTGGTATAGAGTTTCTCATTCTTGGAGGACTTGGCTGCTGCAGTGAG	25226	A_95_P261951	FG141797
25990	306	65	423	TGCTGGAGCAATGCTTAATTATTCAACTGAATGTATGGGCATTACAGACTACATCAA	25232	A_95_P192417	TA15447_4097
25991	306	66	850	ACTAATAGCAGCAATCCAAATAGGTTTCGGACATTATGTTTGGTGGCGCTGAAATGT	25234	A_95_P025291	DV157679
25994	306	69	844	TTTATGCATGATCTGCGACTGATTCACACTGATCTGAGCAGAAATATTCTCTTGTTCG	25240	A_95_P306503	FG155320
25997	306	72	838	AACTGCTAAAAGCTTATATCTTCCCCACTTGTGGGAATAAACTGGGTATGTTGTTTAT	25246	A_95_P011936	TA12054_4097
25998	306	73	356	TCCTACGAAGCAGAAACAGATACTTGGAGAGCACCTTTATCCTCTAGTTAGTCAACA	25248	A_95_P072690	BP526027

26000	306	75	487	TTGTTTGGGTTGGTGGTATGAAAATAAAGTGGTTTCAAACAGTTGAGGTTGCATCCC	25252	A_95_P288443	FS396507
26007	306	82	491	TCAGATCTTCTCCAGTCCTTTGTTTTGCAATATGAATCTATGATGATGTGCACTTCTCA	25266	A_95_P026051	TA14595_4097
26010	306	85	1561	GTTCTCATTAATTGACGTCCGTAATTTCTGCTGAATCATATATTAATGGGGGTTTCAG	25272	A_95_P015246	AF026389
26011	307	1	795	TTATTTGGTGGTAAAGTCATTGTCAAGGCAAACCACCACCACTAGCCACCACCACTA	25273	A_95_P233174	FG158371
26013	307	3	159	GTGCTGGTGGATATCTGGAATTAGAGTTTTCGAACATTTTCATCTTCCCTTTGCACGG	25277	A_95_P050861	BP132500
26015	307	5	1464	GAAGTGATGTCTGTTGGTATATTTCTTCTACATCACCTGTACATGTGCAATTATTTTG	25281	A_95_P198037	TA16693_4097
26019	307	9	156	TTTTCCGCGTGCTTTATTACGTTAAATAAATAAACAAGTTGGTGAAGCTTTCATCCCC	25289	A_95_P131182	EB431311
26031	307	21	750	CCCTGCTGTATAACTCTATATTGTGTCCTTTATGTATCAGTGAGAAACTATCAATAGT	25312	A_95_P279548	FG638649
26035	307	25	778	TAGAAGATAGTGGCATAGGTCTTGCAGCTGCTAAAGCAGCTGGAATGAAGTGCATT	25320	A_95_P188072	DV999306
26036	307	26	919	CAGTGTGTTTTGGAGATGTCTGTAACTAATTTTTGTTGTGTTCAGAACTTACTCAACA	25322	A_95_P192132	TA15387_4097
26039	307	29	764	AGACACCAAACATGAGTGAGATACGTTGGGCCCCTGATCCCAGCAATTCTAAGATAT	25328	A_95_P285603	EB429718
26041	307	31	385	CCGAAAACCGTTGATTGTGTTTTCATAGGATATGCGACAAATAGTAAAGCATATCGA	25331	A_95_P085135	BP529204
26045	307	35	897	CAAATAAAATGCAGTTATTCAGCTATCTAAGGACTGTAACCTCCTTTCTCTTACTTTCT	25339	A_95_P269641	EB426179
26055	307	45	1075	GAGGAACAAAAGAGAACGTTGTTTCCTTGATTATTTGTTCTTCAAAACTGTGATATG	25358	A_95_P011476	TA13481_4097
26056	307	46	375	GAAAAGCAGTCACCATCCCCGCCAGCTGTTAAGAAGAAATCTGGAGTAATTGAGAA	25360	A_95_P065670	BP136395
26057	307	47	407	GATGAAGATAGAGAATGCAACTCTAAAAGAGAGCTTAGAAAGTATGGATCATCTAA	25362	A_95_P085055	BP529182
26059	307	49	884	ATGCATTGCTGGAGAATGCTACTAGTGAGCAAGGAGCAAGAATGTCTGCCATGGAT	25366	A_95_P230659	EB450571
26066	307	56	810	GTTCAGGCTGTAATTTTGCTAGTTTTTGCGTTCTGATACTTTATATTTGTCCCTTCTAG	25380	A_95_P145742	EB677695
26069	307	59	501	AGTTTTGTCGAATTTCAGTCAGTAGGTAAAACGGTGGCTGATTTCCCGTAGAGGTCC	25385	A_95_P102677	CV016136
26073	307	63	247	GTAACTCAGTCATGCAAAGTCATGAACAAGTAGTGCCTTTGGTCTATTATTTTGTATA	25393	A_95_P164067	EH623194
26074	307	64	332	ATGGAGGTTGAGGTTGTTGTACAGTGAACAATGAACTGAAAATATTGCAGATACTG	25395	A_95_P154462	EG649597
26077	307	67	642	TCCTTTACTGTGTACTTCATATTGTGTAGTGAGGGATGATTGAAATGCGATCTCTTTA	25400	A_95_P218647	TA21222_4097
26085	307	75	885	CACCCCCCACTTTGTTAATCCGAGAAGCAGATACAAACATAACTCAGTTAGGCATTG	25416	A_95_P246097	EB680029
26088	307	78	331	CTACTGTAGTGATCCAGCCATCAACTATTGTAAATTTCCCAAGCTTTATAGCATCTTA	25422	A_95_P142837	EB446239
26090	307	80	1335	GATCTGCTTTTCCTGTGGCTGAGTGTTGAATGCCACACATCATTTCTGTGATTTCTCA	25426	A_95_P009901	TC59718
26096	308	1	362	GGCTATTGAGTACACATACAAATACAATGATACAAATACTCTTCTTTGCTATTGAGTC	25274	A_95_P095368	BP533159
26104	308	9	673	GATGTTTCCTCTTTTAAACTTGTCTTCTGCTTCGATCTGTTTTAGAACTTCTGAGATTA	25290	A_95_P232874	TA19868_4097
26105	308	10	437	AGTTTACATTTCGGAAGCAGTGAATTTATTAAAGGGAGAAGGGATTTTTTGTGTCAT	25291	A_95_P154782	FG635590
26107	308	12	807	CAGTTATTAGGCACTGCATACCACTATTATTTTGTCACCTTCATTCTATTGTTACAGTT	25295	A_95_P232159	DV159817
26114	308	19	803	GCTTATGTTATTGCCATGGTTGTAATGGGAAATTTTGTGATGTAATCAGTATTCCCAA	25309	A_95_P198697	TA16834_4097
26118	308	23	727	TCTCCTTGTGATAAATAAAACCGATTTGGCAGCAGCTGTGGGAGCAGATCTGTCTGT	25317	A_95_P226679	EB425900
26119	308	24	655	TGTATACGTCTTTTACTCTTTCTTGATGCATATCGCGGACGGCAGATACAGAAGGGT	25319	A_95_P163642	EH622724
26120	308	25	683	CTAAACACTTGTAGGTGCTATACTTGTTCAACATTGCACTCACTGGGAGGACATTTCA	25321	A_95_P261381	FG640951
26128	308	33	872	CGCAATGAAAGAACTAGATGCATCTTCTGAAAGTAATGGATTTCTAGCTACTCGTCT	25336	A_95_P254274	EB428671

26138	308	43	477	TGCGCGCAAAATGTGGTTCATTTAGAATGATGAAAATAAAATTTGTGGTACTGCAAG	25355	A_95_P142002	TA13269_4097
26140	308	45	53	CGCAAATAGTGGCATACGCCAATTTTTGGAGGGTTACAATGCAAGTTATAATTTTCTT	25359	A_95_P006611	CV021053
26141	308	46	386	GCATGTAAATAACACTTTTGGTTTATGACATTTCTTGTGGGTCATTAAGCTACGCTAG	25361	A_95_P049556	BP132193
26144	308	49	861	TGAGAATGAGCCCTTGAGAGATGAGAGACTATGTGTATGATACGTCTCCCTCGATCA	25367	A_95_P293278	FG167224
26145	308	50	410	GTAGCACGTAACTTGCCTTATCTTCCTTATTATTAATCTCACTTAACGGGCGATTATTT	25369	A_95_P238604	AB035705
26149	308	54	748	AATCTTCGTCAAACCCTAACCGGGAAACATCACCTGAGTGAAGCTCTGACCTATTGA	25377	A_95_P164112	EH623254
26153	308	58	488	TATCTGTTGGTCACTGGATGTATTCTGTATCTCATGTATTTATGGTTATCAGACGAGTT	25384	A_95_P113012	CV020964
26154	308	59	754	TAGGAAGAATATACCTGGGAATGCACAGCTTGATTGACATCATTGGGGGTCTAGCTT	25386	A_95_P137232	EB440958
26157	308	62	525	GCAGAGATGAGTTGCTTGTAAAAATTTTGGGTTTAATAGTTATGCACTAATCAGCGT	25392	A_95_P269036	AM787843
26162	308	67	498	GGTTTGTAACATGAGCATCTCTGCTTCTGGTGTTTTAACCTATGTTATTTCCTTTTTCC	25401	A_95_P112147	EH620447
26164	308	69	1322	AAGTTTGCCACTTTGTAATTCTACTGAGGTCCTTGAAAGCAATAAACTCCTGTTGTCT	25405	A_95_P180752	TA12819_4097
26172	308	77	456	GAAGCTCTAATGCACGCTCGCACCATGGGTTACAAAGTTGTATTTACTGATCATTCTC	25421	A_95_P074085	BP526381
26173	308	78	475	AAGCAAACTGGGTCCTTTGGTGAAGCTTTGGCTAAACACAAGGAACAATCATTTGGG	25423	A_95_P054241	BP133384
26175	308	80	1491	GGTTACAGGTTCTCAATGGGATCATTTGATAAAAATACAAATGTGGATCAGTTTGAG	25427	A_95_P012211	TA13070_4097
26183	309	3	825	GTTCAAGGATCAACAGGTATTACTATCTCCAATTGCCACTTTACTGACCACGATAAAG	25442	A_95_P009321	EB427133
26189	309	9	703	AGTTCAGTTCAGCGTCACAAACTTTTTTGTTTTCATGCCGGAGAGTTCTTAACAATATT	25453	A_95_P088403	EB435217
26194	309	14	387	TCTGTCTGTCCCTAGGACCACGCATTCCCTTTGTCCATTGTCGAATTCTTTATGTATCT	25463	A_95_P162172	EH621028
26198	309	18	427	TATCATTGCCTCTCATTGTTGATGTATCCCTATTTTGTGGGATGTGGACTATTACTATT	25471	A_95_P156987	FG639155
26199	309	19	282	CCATTCTTGTGTATACGTAGAGTGGACCAACTGACTCTTTTTGTTGTCTGTATGTAAG	25473	A_95_P095268	BP533104
26201	309	21	1747	TTACTTGTCTTGTCAGAGGATTTGCTTGTTCGATTCATAAAGGTTATTAAGTTTTGCA	25477	A_95_P185447	AY619948
26203	309	23	782	ATTACATAGCAGCTCTTGAGATGCAAGTTCGAGCCATGAGTGCTCTAGCTAACCTCCT	25481	A_95_P153262	EB683540
26206	309	26	716	CTGGAACTGTATAATTACCCCGTTTTTCATAATTTCAGGAGTTATGTTCTTTACCCTCT	25487	A_95_P013516	TA17108_4097
26212	309	32	833	TATTGGCTTTTGGATCAGTTTGGGACAGAACTCTGTCGATCAGATGCCGCTGGAAAA	25499	A_95_P310213	FG153523
26217	309	37	739	GCAAAGTCATGTGGATGGATGCTTTGACTTTGTAAATATTAAACTCTGAAACTTGTCC	25508	A_95_P216807	EB435414
26220	309	40	535	GGTCCTTAACTGTTTGTATCTGATTTGCAATGAAATTTCCTATTGTGATTAACTTACGC	25514	A_95_P222717	TA22094_4097
26222	309	42	891	CCAGGAGCAAAACAACAATGATTCGCCAAAAGTTAGCTTCTTTTTTCATTTGTTGAAT	25518	A_95_P244917	EB680018
26226	309	46	959	TATTTGTGACAAGTACTATGCTATCCTATGTGTCATTTGGATTTGCGCTTTGTCTTTAT	25526	A_95_P021661	TA22220_4097
26231	309	51	853	CAGCATGTCACAGTCTGTATGTATATGCTTTCGCAAGTGTAATTATCAAATTTGCTAT	25536	A_95_P272881	FG164564
26232	309	52	765	GCTTCAAAGAGCTGAATCAATGTCGTCCAATTAATAGCAAAGTTTCTCAGGAAATGTT	25538	A_95_P118263	DV161263
26233	309	53	828	GTTCAGACAACACTGTATGCTGTTGATTAATTGGTTTAAGACCATCTCGTTTTATACAA	25540	A_95_P182527	TA13237_4097
26234	309	54	863	ATTCAAAGATCTTCCCCTTCTTTCAGGACTTCGTCAAGCTATTTGCGCCATGGGCATGT	25542	A_95_P228594	DW000726
26236	309	56	1117	GGAGGATTGTATCTTGGTAGAGATTCATGTCTAGTTTTTAGGGCACATTTTTAATTTT	25546	A_95_P018811	TA15665_4097
26238	309	58	492	TTTGACTGTACGAACCTAATTATTTCACTCTGCCGCTTGTTGTCAAAGCAGGTACTCGA	25550	A_95_P074870	BP526582
26241	309	61	750	ATCCATTTGTGACCAACCAGAAGATTGCCGAGTTCCTCTTTGCAGGCAATTCAAAGC	25556	A_95_P223057	TA22166_4097

26244	309	64	735	TTTGATGAATCCTCTCAGTACTTGAACTTGAATTTCCCTCCAGCCAGCAGTGGCGTAG	25562	A_95_P223172	TA22193_4097
26248	309	68	815	CGTGCTCTGCAAATCCTACCATGGAAATAGAAGAAACATTTCTGTTAATTTTTCTTCTT	25570	A_95_P243652	EB425489
26252	309	72	1727	GCATCTGAGGGGAGGGATTTTACACATATTTATGTATGACAAGAGCTTGATTTGTTA	25578	A_95_P007406	AY366400
26255	309	75	404	GAGAATGAAGGTTATGAGGTCATTGTAATTGGGTTCTTTGAATTAACGAAATGGATC	25584	A_95_P207047	FG623545
26261	309	81	950	TAAGACTGATCTTGTAGTCGGGCAAGACATTTGTTAATATTGTTTAATGGGGCAAAA	25596	A_95_P197077	TA16483_4097
26265	309	85	911	AAGTATTTTGATATCCGAGGGATTCCAAGCCTAGTGGTTTTGGGCCCTGACGGAAAA	25603	A_95_P118737	DV161797
26267	310	2	1105	GTCATGTAACTCGTTATATGGTGTGATCTGTCACATGCTACACTTTCTGCAATGAATG	25441	A_95_P186727	TA14188_4097
26268	310	3	391	GAAAGAGAACTTCTTGAGCTACAGTATGTACAAAAATAAGACATGTCAAAACCATGT	25443	A_95_P150102	EB680162
26270	310	5	658	ATTGCTCCCTTTGTATGAGAATCAGTTAGCAGAATGTCCAAATAAAATATGAGGCTTC	25446	A_95_P153712	EB683919
26272	310	7	787	TACGTATACGCTACCCTTCCTAGACCCCACTTATGTTAATGTTGTTGGTCAATTTTACT	25450	A_95_P150977	EB681159
26273	310	8	532	GTCCGCAAGACTGTTGTTTTCTGGTTGGTTGACATATACATCATGCTGGGCAAAGCAT	25452	A_95_P033759	AJ632963
26274	310	9	253	ACAACCCTGTGATTCTGTTTGAGCATGTTTTGCTCTACAACCTCAAGGAGAGAATTTC	25454	A_95_P066465	BP136610
26276	310	11	285	GAGGAGCAATATGCTCACAACTCTCCTAATTCCTTACATTTTCTTGAGTCTCCCTTCGT	25458	A_95_P105032	EB428527
26277	310	12	475	TTCCGGTTCCGATGCTGTTGTTCGGTTTCTGTTTTCTTAGCTCAATGGTTATTTCTATT	25460	A_95_P203482	TA17862_4097
26279	310	14	645	CCGGATGCAATTTTTCTCAAAGTAAACTATGAAGAACTCAAAGCCATGTGTCATGCTC	25464	A_95_P265346	FG640689
26281	310	16	630	TTTGGCGCTGTAGCTTAGTTTTAGTTCAGTTGATAAAATTGTCAGTGTCTTCATACAT	25468	A_95_P049171	DW000180
26284	310	19	363	TGATGATGTTCTTGCTGTTTTGTTGATCTGCTGTTTGGGGAAGACCTTGTCTTATGTTT	25474	A_95_P094493	BP532739
26289	310	24	769	GTCTTAGTGATTGGTGTTATGGGCGTGGCTGCAAATATTCCTTTAGGCATATGGAGA	25484	A_95_P194677	EB425191
26292	310	27	931	CATTGGTTGTTGTAGGTGTTTTCAGATTGTGAATGAATGAAGTCTCATTGTTTTTCTG	25490	A_95_P198317	TA16752_4097
26294	310	29	783	CTATCCGGACATTATTTACTCGTGCAAGAACATGCGCTCCATGCATTCTATTCTTCGAT	25494	A_95_P151832	EB682078
26297	310	32	966	GCAAATAAAAGCGTACTTATACACTTGAATCTTCCAAAGGAAATCCTTGTTGAGGATC	25500	A_95_P009611	TA12795_4097
26300	310	35	876	CCGGGAGCAAACCATTCTGTTTTACCTTTCCCTATTCTGATATGTAACATTATGTGCAG	25505	A_95_P130602	TA12081_4097
26302	310	37	687	ATTAATGGCAGATTTTGGTGAGAGCGCAATAGGAGAGTGGCGCCTATTGATTCTGG	25509	A_95_P303278	FG149635
26304	310	39	1787	GAGGTGACTGCAGTTCTGGATATAACATTCATCTCTTTGATCTTAGCTTGAATGTATT	25513	A_95_P007721	L38260
26305	310	40	758	TCTTGACTATGAACAAGAACTTGAAACAGCAAAGACCAGCTCATCCGTGGAGAAGAG	25515	A_95_P011676	DW001087
26307	310	42	737	AGCTTATGATTGTGCACTTAAACTGATTGAGTGGATGGAAGTACTGATGATGGACTT	25519	A_95_P208322	TA18943_4097
26310	310	45	795	CCAGAAGTGTATTTGCCTTGTTATTTATGCTGTGTATGCAGAAGAAGGTTTATTTGGA	25525	A_95_P011921	DW000377
26314	310	49	1135	TGCTCAAGAAACAATCGAAGATATAAATGTGAATTCTGCCCAAACGATTTTACCGTTT	25533	A_95_P025011	TA21394_4097
26316	310	51	1245	CTTTTTGTGCCAACTAATATATTGAATGGTTTGGGGTATTTTTGCCTCAAAGTTGCTAT	25537	A_95_P256344	TC43686
26317	310	52	104	GGATTATGTTTCGAGATATAACAACATTACTACTTGATACTAACGGCGTTTACTGACA	25539	A_95_P112132	CV020533
26319	310	54	1056	GTTCGCAAGCCCATTTCAGACCTAAAGTAAATTGGAGTTTATAGTCAGTTAGCTTTAT	25543	A_95_P230559	AF053766
26320	310	55	394	TGGCATCATTTTGGGGTCACCTGTACGTATAGTCTCTTCTTGCTGGTTAGAATTATCTC	25545	A_95_P076765	BP527078
26323	310	58	1248	GGAATCGTAATGTGTACAAGGATGTTGCCTTTCTTGTTGTCTATCATGTAATTTTTTGC	25551	A_95_P182152	TA13144_4097
26329	310	64	815	CATGTTGTTCTGCTTTTGAAATAAACTAGTCTACGCGCACGTTTATTGAGAAATTTCA	25563	A_95_P243887	EB680330

26330	310	65	277	CCTTCAACCTAATATAACTGATTCTTGGTGTTTGTCCGCAAAAATGCCAAGTGATGCG	25565	A_95_P205252	TA18239_4097
26331	310	66	714	AATGGTCATATCTTTAACGTTGGTAATCCGAACAATGAAGTTACAGTCAGGCAGCTG	25567	A_95_P148112	TA17675_4097
26333	310	68	963	GAATGCAACTGCGCGGGATTATATTTATATTTCATGCTGAATTTCACGTGCTTCAAAA	25571	A_95_P226684	Y16644
26334	310	69	1206	TGGTTGAGAGAAATTGGCAAGGGGGATGAATAAAAGTCTGCAGGATGAATGTCACT	25573	A_95_P111912	AY220080
26335	310	70	568	AGTGGTCGTAGTTGGAGATAAATCATCCTAATCTGTTGATTTTGTTCTCCAAATCCTA	25575	A_95_P227054	FG640545
26337	310	72	841	TGTGTACACATTACCTGCTCTATGTTACTAGTATTCGATTTACGCGCTCAACTGAAAA	25579	A_95_P271086	TA19840_4097
26344	310	79	800	CTGCCTTTATGATGCACTAGTAAGACCTTATATTTCTTGAGATTGTTAAATTCTGCTGT	25593	A_95_P002566	TA11864_4097
26345	310	80	501	TCGGGGAACTTTGTCCTAATTCTATCTACCAAAGCTTAGGCAAATAGAAAGAAATGT	25595	A_95_P298558	FG636346
26346	310	81	450	CAGGTGCTGTTGCATTATAGGTTGGCAAAAGACGAGCTTGTTTATTATCAAATTTACC	25597	A_95_P001386	EB447417
26347	310	82	874	AGAATTTGAGACCGGAGATACCTCGTTGTTGCCCAAGTTCTTTGGCAAATGTGATGA	25599	A_95_P294613	EB441748
26350	310	85	765	CATGCCCCAATAGGAATTGTAAGGTAAGGTCTAGCTCAGTATATATTTGCTATTAGA	25604	A_95_P116517	DV159282
26353	311	3	754	TTTAAGGCTTAAGTGTGGAGAATTTCTACTGCTTCTGATTGGACATGTAAACGGGAG	25609	A_95_P126327	EB425660
26356	311	6	753	ATCAATCCCCTGAACTCGATCAGAAATTCCCGTTGTCAGTGGACCCTTCTTTTGAAGG	17966	A_95_P000116	FG157904
26358	311	8	127	CAGAAAAGCAAATAGTAATATATACCTGATGGCATTCTGATGCTGGGGGACACGGA	25618	A_95_P111047	CV020023
26360	311	10	515	CGTCAATCTCTTTCTCAATTGTACACTCAAGCAATCATATCTCAAGTATCAATTTTGCG	25622	A_95_P029421	DW003670
26362	311	12	739	TGCTGCAGCTTAATGTTTATTCGGATAGGCCTTAGTTCTTTCTTGGCCAGTATATGGA	25626	A_95_P248387	EF051129
26369	311	19	702	CTGTATACAAATAGTTCAGACTGGCCCTAACATGAAGAATCTTGATAAAGATTTAAC	25640	A_95_P197412	TA16555_4097
26373	311	23	538	TGTTTGTTTGTATATACTCTCCCATCTGTGATCTCACTATTTTGACTTCTAAGGTGAAT	25648	A_95_P299423	FG638572
26375	311	25	767	AAGCAGCAACTAAGGTCCATCTCTTCATTCTCTTTACCTCTTCAATTTGGTGATATAAA	25652	A_95_P197712	TA16623_4097
26376	311	26	891	GAGAATCTGTATGTTGTGGATGAGAAAGATACAGCTTTAGATACTGTTATGGAAAAT	25654	A_95_P227614	EB427793
26377	311	27	427	GAATCTAGTTTTGGGTGTAATTGGTGTTGCAGCAAATGCAACACTATGAAGGATTTT	25656	A_95_P214227	TA20217_4097
26379	311	29	283	TTCTTCAGATGAAGGATCAATCTGTCCGAAAATTGTCATCGTCCCTCCTGATGCTGAG	25660	A_95_P086545	FG640368
26381	311	31	319	TGGATTAACTCTCTTTAATCATATTACATAGCACGCTGCGCTTGTTGTTTGCCCAAAA	25664	A_95_P033819	AJ633029
26382	311	32	882	TGCTCTACTTAATGGTTTGCAGAATTCGCGTGTTTATACTTTAATGTGCATGTTGGTA	25666	A_95_P185592	TA13948_4097
26383	311	33	767	AGAGGAGAGAGGAGAGGGAGAAGGAGAGAGAACAATCCGTAATCAAACTTTTATT	25668	A_95_P213737	TA20112_4097
26395	311	45	1339	GGCTTTGGTTTGATCTTGTAGATATTTTGAGTGCTTTGTATCGGCATTATTCAGAATG	25692	A_95_P238789	AB022273
26398	311	48	547	AACCACTCAACATTATGTGTTTTCTGGCCATAATTTGGAGTTTGGATCAATCGCCTTCT	25697	A_95_P183222	FG137478
26399	311	49	131	ATGCTGCTTTTGCGCTTGGTAAGATATGTCAATTTCATCAGGAAAGTATCGACTCAG	25699	A_95_P154847	EG649783
26410	311	60	255	CTCCTCCTGAGGAACCATTAACTGATAAGGAAATTGAGGAGCTCATTGCTGAGCTTT	25720	A_95_P078645	FG641707
26411	311	61	261	AACGATGTGAAAGTAATCCAGTTCTCATCAATGCAAGATGCCTTTGATGGCTTCACG	25722	A_95_P052466	BP132930
26413	311	63	330	GTGTATTTGCTGGTGGCCAAGGTGAAGGAGATGATGCAGCAATTGGGAATCAAAAT	25726	A_95_P101988	U74325
26415	311	65	171	CCTTTTTCCTCTTAATTTAAGTCAAATAACAAACCTCTTGAGTGTACTTTGAAGCCGCC	25730	A_95_P159227	EH617185
26418	311	68	445	TTTCGTGGTTCTAGCACGGTCGCTCAATTGTCATATTTGGCTTATTTATCTGATTTTAA	25736	A_95_P090743	BP531076
26419	311	69	113	CGAAGGCGCCTTATGTAATTATATATAGCATAATCCAAAGGCTAACAACAGAAAGAT	25738	A_95_P140577	EB444465

26422	311	72	473	ATAATGTGGTGTAATGTGCTGCTGCTTTCCTTAGCCGAGAGTCTTTCGAAAACACCCT	25744	A_95_P072790	BP526052
26425	311	75	726	TGTTGCTTTTGAATGCGGTGCTCACTTTTGCGACTGCTTTCTCCTCTACTCGGAATATG	25750	A_95_P257059	FG636654
26427	311	77	513	TTAGGGTTATTGGGTAACTAGGCTTATCTGGGAAATTTGGGAAACTAGTTTTCCTTCT	12052	A_95_P000101	FG167017
26431	311	81	125	TGCTTGGTTAGATCTCAATAACCATTGGGCTAGCCCTTTTAGTCCTCAGCTGCCATTT	25761	A_95_P114152	CV021471
26434	311	84	860	TGTTGTTTGCTTGACAATTTAGCTATTCGTGACTCAGCTAATGCATCATCTTCTTGGTC	25767	A_95_P118687	DV161763
26436	312	1	321	AGCTTTCAGATTTACAGTCTCTCATGGAGTTTATTTACCGAGGTGTTACTTTGGTATAT	25606	A_95_P089538	BP530542
26439	312	4	766	GTTGAAACTTATCGACTGGAATGGAGAGCATTACTTCCTCACACTTGCAAATCTGTG	25612	A_95_P283988	DW003539
26447	312	12	784	CTTGTCGGAAGACATTGGTTTGTAACTTAAAATGAAAGGAACTGGATTGAGACAATA	25627	A_95_P183497	EB429193
26455	312	20	819	TTGGGGAAGTATGTGGAGAGGCTTCTTAGTAGTGGCTTTGTTAATGCCATCAAATCTT	25643	A_95_P117667	EB430351
26458	312	23	371	CGTTGTTTCAGTTTGTGTGTACAGGAACCACCAATAGACGGTGAAATTTAATAGATTT	25649	A_95_P003926	FS413762
26459	312	24	527	TGTACTCAGTGACACCGGGTTTAAGAGTGTTTATATATGTATTTGTGAATTTTCTTCC	25651	A_95_P019176	EB433277
26461	312	26	651	TGATTGAGAACAAAAACCGGAGGATTTGTTGCCTGTTGTGGTACCTTTCGGCTAACA	25655	A_95_P170094	EH664824
26462	312	27	172	GGAGAAGAGAAAGTTGGAAACTCATTATTGAGCGCATGCTCATACCTTTAGAAAGT	25657	A_95_P098023	BP534296
26464	312	29	847	AGGGGGGAAGAACTCAGTTGCAATATGGATTGTGGCCTCACATAGTGTCTTTTCCTG	25661	A_95_P031491	TA16203_4097
26465	312	30	296	TTTGTTGCCATCGCAAGTATGTCTTCCATAGACATGGCATTTTGTAATTCTTTATTTCCA	25663	A_95_P034883	BJ999149
26466	312	31	869	CACTTTGGCTGACATATGCCCAGCGACTTTGCCTTCAATATTTTATTTTAATTGACAAA	25665	A_95_P178512	TA12268_4097
26467	312	32	636	TGTCGCCTTCACATCTCCCTGATCGAGGTTTATGGATTATTTTATATAGTTGTGTTTGA	25667	A_95_P233714	FG641857
26468	312	33	340	TGATGAGGATTTGTAGCTGTAATTGCCTTTATGATTTGATGAGTGGTGAACTTATTCG	25669	A_95_P209067	TA19108_4097
26470	312	35	633	GCTTATAGAACTTGGCATTTCCACACAAGTAGCTGCAATGTGTACAATTTTACACATTA	25673	A_95_P149012	EB678671
26472	312	37	384	GGTGAATTCCAAAGGGAAAAGCTGTGATTGAGAATTAAGTGGCCTTCGGAGCGAGA	25677	A_95_P161572	EH620253
26473	312	38	203	GAATCCCTACATTGCTCTACTTTGTTTTATTTATTGCAAATGTGCTAGACAAAAGACCT	25679	A_95_P031506	BP531462
26475	312	40	798	GGAACTTGAGTTGAGACATTAGAGATTGCTGGTATATATTTTTAAGAGCTTGCTCGTT	25683	A_95_P246732	EB643454
26476	312	41	274	GGATAAGATGCTAGAGAGACTTAAGAATGCATAGAGTGATGTTCCCAATACATTATT	25685	A_95_P101853	CN824887
26480	312	45	815	TAATGCTTTTTGCTATCAAAGCCGTTGCAGAAGGAGTCCCTGAGCTAACAAGGGAAG	25693	A_95_P119162	DV162239
26481	312	46	814	CCACAGTAGGCAGATAGATGACTTGATTCACTTTTCTACAATAGGCTGATTGATGACT	25695	A_95_P226564	EB450058
26485	312	50	787	TGCTTCATCGCCAAATGTTCTTCAATGGCTTGTCCCATGTTGATGTCGTGACCCCTTTT	25702	A_95_P207647	EB679774
26489	312	54	678	CTTTGGCACAGTAGATCGTTATCCTTGTACTCCTATTTAAGTTGTATTCCAGCTCGCAC	25709	A_95_P005386	EB438907
26493	312	58	1391	CCTTTTAGGAAGAAATTGGCAGATGCATTTTTCATGCATTTACATTGCATGATCACACT	25717	A_95_P009296	AB066279
26495	312	60	1363	CAATTCTTGGTGAATCTGTCTCGGTTGAGGATGAAGTAGTGGTAATCAACAGCATTGT	25721	A_95_P194557	TA15921_4097
26500	312	65	1189	AGTTCCCTGAGTTGCTGCCAATCAAAGAATCATTGGTCAAATATGTATTTGAACCAAA	25731	A_95_P012121	TA16920_4097
26502	312	67	720	CATTTGATACTCGATCTGAATTCTGGAGCTTTGATGTTAAATTCTGATATACACCTGA	25735	A_95_P022251	TA13250_4097
26507	312	72	626	ATGCATGCATGGTTTGCTGCATTCGCTGATACTCGCTATGCAGTGGTTGTTCCTATAAT	25745	A_95_P019136	TA14564_4097
26508	312	73	1029	ACACCACCCAGTATAAGAGAAACATGAGTCAAAACCTTAGTGTTGTACTAAGGTTGTT	25747	A_95_P193127	TA15604_4097
26511	312	76	898	GTTTTATCTGCTACATCTAACTAGGGAAGTACTACGACTACTACTACGTGGTGTTCTAT	25753	A_95_P225577	EB443157

26513	312	78	543	ATTTTTGGTGTTACTGTGTATCCGAACGTGGATTATGCCTTTCGTAGTCGCTCTCTGG	25756	A_95_P162522	EH621474
26514	312	79	63	CTGACTTGGATTATTGATAGCTAAGCTTTACTTAAGGTCTTCTTGTAAACTTTTGCTGT	25758	A_95_P145067	EB448606
26515	312	80	563	TTAGTTGCTGAACGTTGTGATCTCTGGCCTCTGCCATATAAAATTTTACTATGCAACG	25760	A_95_P189132	EH622674
26518	312	83	1010	TGATTGTGATCTATGGGATCGCGACTATAATCGTTTATAATAAACAAAGACTTTGTCC	25766	A_95_P007676	M15173
26520	312	85	782	GGGAAAATTCTCCCTGGTAATTATTGTAGTAGGTGTTTGATTTATCTACTACACATGA	25770	A_95_P015411	EB450584
26523	313	3	612	AGGATCCTCTTCTTCAACAGCCAAGGCTCGTTCTCAAAATCAAACTGTCGTCGTTCAA	25774	A_95_P131632	EB679714
26526	313	6	552	CACTTTGTAGTTTGTTATTGAATGGTTATAAATGAAAAAGGGCTATGACTACCCGCA	25780	A_95_P021081	TA18792_4097
26529	313	9	837	TCATTACAATTCATTGTGGATGGAGAGTCAGATTATCCCTGATCTTCCATGTGTAGCA	25786	A_95_P285223	FG142087
26537	313	17	507	CATCATCTAGTGTATGTAAAATGTAATGAATCTTGTCTTGTGTTGGATTGGAACACAT	25802	A_95_P095488	FG636446
26541	313	21	1553	GGGAATACTGCTAGGGTTTTCTCGGGATGTTTTATCTAGAGTATGAGATTATTTTTG	25810	A_95_P008431	AF190657
26543	313	23	813	ACTGATGAGTGTCGATGGCCTAACGCGCGAAAATGTTGCTAGTCATTTGCAAAAATA	25814	A_95_P151987	EB682256
26544	313	24	654	GATTGCCGTTATGTGTACTTCACCTGTGTTGAGTAATACAGATTGCTCCTGTTCTTCG	25816	A_95_P198968	TA16892_4097
26547	313	27	594	AGTATTGCTGACACTAAATGGGCAGCTTGCTGTTGAAAAAGGCCATGCTGCAGATA	25822	A_95_P032291	EB449088
26548	313	28	103	TCCACAATCAGATGGCTTGTGCTCGATCTTCCATCATTGGTTGGGAATGGCATAAAT	25824	A_95_P171676	EH665193
26554	313	34	886	TATTTTCAAGTTGCATGTTGATGGAAAGCTGGTGATGTGAGACTTTCTTATGTTTCAA	25836	A_95_P011611	TA13458_4097
26556	313	36	561	GCTATGTTGCAACTTCTAGTCAATGACTTTGATTTGCTTAGTATATCAACTTTCATCTC	25840	A_95_P005236	EB442583
26559	313	39	182	GTTGTGTATTAAGAAACACCATTCCATCTCATGCAATTTCTGATATGTTTTGAGGATC	25846	A_95_P099033	BP534736
26561	313	41	521	GTTCGAAACGCGAATCATAGTATTCATTCTTATGGGAATGGGAATGAAAAACAAGA	25850	A_95_P270566	AM798360
26566	313	46	579	GAGAACATATACCCAGTTCTTACTGAGTTCAGGAAGAATCAGCAATGAGTTGAGAG	25860	A_95_P284403	BP131165
26567	313	47	109	GTTGCCTTCTGTTGTTTGGATGTTGTTTGTGTAATTTATGTAACAAGTTGTTGTAGGA	25862	A_95_P092168	BP531674
26568	313	48	223	GTTCGGTCGTGGCCTGTTATTGTTCTACTCTTAGGTATGTACACATCTAGCTGAAAAG	25864	A_95_P095483	BP533211
26575	313	55	810	TTATGAAGGTCATTGAGAGGCCATTGTCAGAAAATGAGCGCTTCATGCTGGCAAAA	25878	A_95_P261816	EB448369
26579	313	59	877	CATTGTTAAATGAGGAGCCTAAATTCTCTGTGGTTGAGATAGGTGTTTAGTTTTTGTC	25886	A_95_P005081	TA12257_4097
26581	313	61	1498	CTGGATGGCGTTCTTTTTGAACGTTTTAATTTATGTAGCATGATCTGTGTATGACAAT	25890	A_95_P217557	X83880
26583	313	63	768	AGGATGCTAAGCAATCACGATATTTCTTGAAGATGGTCATCCGATAGGATGTGCCAA	25894	A_95_P157537	EH615587
26585	313	65	428	TTCTTGTTTGGAGATTGAAGCAAAGACAAAAATTGGCTAATGGCGCAGAATGCCTG	25898	A_95_P005876	EB678658
26594	313	74	856	GGTAAATAGGGTTGACGCAACATTGCCAATATGGAGTTGTTCAATGGTTTTAAGCTT	25916	A_95_P245612	DW000372
26596	313	76	199	GGTGGTTTTGGAAAAGCAATGTACTCTGCTATCGCTCTATTGAATTGAAATAGAAAT	25920	A_95_P091768	TA16554_4097
26612	314	7	143	TCGTATTCTTCGAGATGTAAATTTTAAGATTCGGGGAACGGATCCTAGTATGGATAT	25783	A_95_P108222	CV018725
26613	314	8	663	CCATGTCCAAAAGCCTTCCAAATAAAGACCTCCTGATCAACCTTCAAGAATGCCAAG	25785	A_95_P132467	EB432949
26622	314	17	155	TCATCTTTTGCAGCGTTGTTGTGGAATTATGATGAAGTGCTGGACGTGATACATCGT	25803	A_95_P032196	BP533238
26628	314	23	196	ACTAGTCTTTGATTTTCATTGACCTGCTTTGACAGGCCAGAATAAATTTTCTTCATCCA	25815	A_95_P105067	CV017283
26631	314	26	449	TTGGGGTTAGGGTTTCGTTCAATAGTATTAGTCGGTTAATTTTTGTTGGTTGATTTCA	25821	A_95_P208442	TA18970_4097
26633	314	28	443	GTTGAGTGAAAATTTTATAGCGCACTCTTTGCACATCTTTAACTTGGTCCAATAATGT	25825	A_95_P111527	EH617796

26640	314	35	903	CAAGATGATCGGCTCTTTTCTATGAATCCTCCTTATGTAATGAGATTCTCTCTATAT	25839	A_95_P007706	TA13105_4097
26641	314	36	850	TCTTGTTGTCATAAGAATCATATGCTACTGGGGTAACAAAGGCACGCTATTCACTTGT	25841	A_95_P018876	DV158102
26642	314	37	444	CACATCCATCAATAAAGGTCCGATTTCTCCGTATTTATCCCTTTGTTACGAGTTCCTTT	25843	A_95_P093328	FG640666
26644	314	39	209	TGCAAATGTGGCATCTAGACTGCAAGTGTCACCCATTGCACTATGTTCTAAGTGAAC	25847	A_95_P103512	CV016540
26647	314	42	483	CTATCATCATCTGGCCTACTATTTCAAGCATCCTCCTATTTGGCAATTTGAGAAAACAT	25853	A_95_P049906	BP132274
26650	314	45	717	GCACTCGTAGTTACCCGTACTGTTTTGTTCGTATGCGTTTTGTGACAGAGCAAACACT	25859	A_95_P251467	FG635853
26653	314	48	570	GGTTCCAGGATTAAGTGGAATTTCACCAAGTTCTTGGTTGAATAAGACGGAAAATAA	25865	A_95_P106233	CV017817
26656	314	51	766	AATAGCGTCTAAGAGATGCATATAGCCTGTATTTAAGATCAGCTGCTTGTGTAGCAA	25871	A_95_P194327	EB450105
26658	314	53	721	GTACTACTGGATTTCTTTCATTTTTGGAGGATGCACCCTTCTCAGAGGGCTTTGCACT	25875	A_95_P136542	EB440321
26660	314	55	839	TCTGCAGTAACTTTAGGGTAAATTAATGTAATATTTTGCCCTTTGGCTGACATATGCA	25879	A_95_P148442	EB425860
26664	314	59	855	TTACAGTTTTGAGTGCATTGGAAACGTCTCGGTTATGAGGGCTGCTTTAGAGTGCTG	25887	A_95_P245992	EB678659
26677	314	72	782	TAAAGAGTTCCCCTTTCCGAACCAGGAGAACCTCTGTGAAATCAGTTTCAAGTAGTTC	25913	A_95_P138407	EB442174
26678	314	73	434	CTGTCTTAGCAGCCTCTTCTGTGTATTCAGATTGATTTAATGTATTACTTGAACAAGTC	25915	A_95_P122302	DW002313
26680	314	75	764	GAAGCTCATAGCAGAGGAAGCAAAAGATCACACCACCCTGTTAGCATTCTTTGATGC	25919	A_95_P218672	TA21228_4097
26681	314	76	287	TGGCACTGTATTTTGATATTGGGATCTTTATCTTGGTGGTTTTGAAGTTTGGGAGATT	25921	A_95_P109217	CV019192
26683	314	78	828	AGATGCGTTGGATATCGTAAGGGATCCAGAAGAAAGAGAGTGTTTCATTTGTTTAA	25925	A_95_P218107	TA21099_4097
26686	314	81	718	ATCAATCTACTTCGGCGTACATTTAAACGAACTCTTGTGCTGGGAAAGTTGTTCACAT	25931	A_95_P223072	TA22170_4097
26690	314	85	161	ATAATTGATCCACAGAAGGATAAGAAGTCGAGGGAGTTGTTTCCATACGTCAGTTGC	25939	A_95_P040061	BP129722
26691	315	1	1582	GTCGAAGAAAATGCAACATATTGCTGTTACAAGAACCACTGAAAGGGAGTTGATTG	25940	A_95_P188807	TA14651_4097
26692	315	2	596	ACAAACTATGTTTACCGTGTTTCTTTGCCGGCACCTGATTTTACCAGAGAAGTATCCT	25942	A_95_P046581	BP131435
26695	315	5	1829	AACTCCGTCTGAGACTCTAATAACATAGTGTTGTCATTGTGGATATGTTTGTATTACA	25947	A_95_P015846	TA12251_4097
26696	315	6	788	TTGCTCACACTTTATCTGGCCATCGTGATGGAGTAATGTCAGTCGAATGGTCTGCTTC	25949	A_95_P310908	FG172547
26700	315	10	442	TTCTGGCTTGGTTTGTTGCATCTGTTTTTTGGTGGTTTTGGAAAAGCAGTGTGGGGG	25957	A_95_P101503	CN498848
26706	315	16	1072	TCAACATGCTCTCAAATCATCTTAAACCGTCATGAGACTTATTTTTCCCGTCTCAATTC	25969	A_95_P202757	TA17703_4097
26709	315	19	638	ATAGGTACCCAAGAGCTAGGTTAAGATGAGTTTTCTTTTACATGTGTTTATGTGGTG	25975	A_95_P119412	DV162620
26711	315	21	830	TCAACATTGCTACTCAGACAGTTGCAGGCTATGTCTTCATGGTTGTTGCTGCTAGCAT	25978	A_95_P146967	EB451156
26713	315	23	1016	GTTCATAGATAGAGGATACACCTACTTTCCATTTTGTCAAGTCGATGTTGAATTCAAT	25982	A_95_P029401	TC48071
26718	315	28	738	AACTCTGGTATTTGATTTGCTTAGAATGTGGTAGTTGCTTTTCCAACAAAGATGGTTT	25992	A_95_P013971	TA13071_4097
26719	315	29	421	ATGAAAATAAGGTGGTTCCAAACAGTTGAGATTGCATCTCAACGCCTAGAACTTTGC	25994	A_95_P023661	BP532793
26721	315	31	812	CAGAGGTTCATATATGTCAAAGCAATGGTTAAAGCAGCCTGCATTCATTCAATCTTTT	25998	A_95_P259341	EB682828
26724	315	34	438	GCCACTAGAATTAAGCCTTGACTTGGTCTTTTGGATTTAGGTCCAAGGTATGATTTCT	26003	A_95_P044756	BP130966
26725	315	35	880	GGTGATTGATGCAATTAGAGCTGGAAGCTACTGCTAAATATTGTAACTAATGAACAT	26004	A_95_P204897	TA18164_4097
26727	315	37	333	ACATAGTAATGTGAAATTGTGAATCAAGAATTCCATCTCCAGTAATATACTCCTGCTC	26008	A_95_P132857	EB433648
26728	315	38	740	AAGAATTATGTCGGATTCTCTGTGTTTTCACTTTTCATGGCTGTGAGGCCTTTTCTGTT	26010	A_95_P184418	TA13692_4097

26729	315	39	701	AAAGTAATTCCCTAATCTAGCAGCCGACTCCTCTCCCATTTGTTGCTGAGAAATCTCG	26012	A_95_P301948	FG152175
26732	315	42	901	ACACTACTATATACGATGGGATAAATATATGCATTGAAGGCGGAAATTGCACTGCAA	26018	A_95_P292643	EB427886
26735	315	45	373	CCTATCCAATCATTCTACTATAAGTCCCTTCTTCATAGCTACCCAACTATGTAATTTAT	26024	A_95_P142427	EB445890
26736	315	46	574	ACATGGTTACTAGCTCCTTGAATTTATGCTATTTAAGTTCTCTTGTACTTTGTGGACTG	26026	A_95_P045731	BP131218
26739	315	49	778	GAAATAGAAAGACAGAGGATGAAATGCTTTCCTTAATCAGGTGGAAAATTCGACAG	26032	A_95_P117597	DV162682
26743	315	53	642	AAGAAGCAGTTGGTGCCATTGCTTTTAATTCCCAAGAAGGAGGACCTGGACTTTGTT	26040	A_95_P182072	EB430441
26744	315	54	479	ACACATTAGGTTCAACACGGATTCATATGTATACCGATTCATGAAAATGATATACAG	26042	A_95_P299483	FG643481
26746	315	56	849	TGCCCGCATGTCCAGGCTTCAGTCCCTTTCAAATGAGTACTTTTTATGTTCATTTACTA	26046	A_95_P226689	EB425964
26748	315	58	822	GCTGTCGTCTTTGGAAGTTCATTAGATCTAAAAAGAGTTTGAAGTTCATTAGATCGTT	26050	A_95_P229019	DV157735
26749	315	59	228	CTATTGAAGTTCTCTTTCCATCTGCTGTTGATTGTTTGTTGTGAATGAACTTCTTTTGC	26052	A_95_P027376	BP531067
26751	315	61	186	GGTTGGACATTTTTGGGGTTGGAAACTGAAATTCGAAAAAAGAACGAAAAGGATTC	26056	A_95_P096338	BP533583
26753	315	63	904	GATGGTAATCAAGATATGATGCAGATTGATGAAATTGATTCTAGAAATGGGGCTTA	26060	A_95_P198367	EB679747
26756	315	66	625	ATTTATTAGATAAAAGGTCGACGCGGGCTCTGCCCGTTGCTGCGATGATTCATGATA	26066	A_95_P029466	TA19036_4097
26758	315	68	725	TGGGTATGGTGGTGCTAGTGATCTTCCACATGCTGATGGTTTTGGAAGTTATGGTAC	26070	A_95_P136217	EB439884
26760	315	70	541	AACTCTAGATTACATACTATTCTCCTCCTTCAGGGGAATATCCAACCCAATTCAAGCC	26074	A_95_P028591	BP128599
26761	315	71	846	GCTGGTGATGTGCTTTGCTTCCCACCCATAACTTAGTTTTTTGTTTGTTTGTTTATATG	26076	A_95_P292578	EB427718
26763	315	73	818	CAAGAAAAACCTATAAGTTTCAGCACTTGGTTTTTCTTTGGTTTTCCTTTGGCTTTGGT	26080	A_95_P017226	EB438454
26764	315	74	2211	GGCAGTTCAATGAAGGGTATAATTTATTGGCTCTTTTGGTTTGGCATTTGTGGTTAAT	26082	A_95_P021031	TA11868_4097
26765	315	75	732	TTTGGCTTAGGCTCATTTCATTGATGTCGAGGTATTTGCTCTTATCATTTTTAGATTTG	26084	A_95_P149892	EB679884
26768	315	78	775	AGTAAGGGAGACACTTCAATGTAATTTTACTTTGTTTGCCAGTTTACCTAAGCCTTTC	26090	A_95_P012446	TA12316_4097
26771	315	81	687	TTGCCACAACAGGTCCATTTTCCTACTATTCTATCTCTCTTATCTTACCGTGAATGGAG	26096	A_95_P303383	FG194074
26773	315	83	791	CCGTCTGGAAAAGATGGCATATGTTCATTTATTCTCAAACTAATGAGGTCTTTTAGTA	26100	A_95_P009361	TA12569_4097
26774	315	84	674	AAAGTAAGTCAATGTTCAAGTAAATATTTGAGAAGTCGCCTGGAACTGTTTGAGAAG	26102	A_95_P116732	DV159518
26776	316	1	857	TCTTTAATGTACTAATGTACCACCTAGGAGCCCCTGGCTTCCCCCTCCTTGTATTTGTT	25941	A_95_P261941	EB424703
26783	316	8	543	GTATATATGTCCCAAGTTGTGGGAAAAGATATACTGCGTTGGATGCATTGCGGTTGG	25954	A_95_P042116	FG140087
26790	316	15	832	ATGTTTTGAGTCAATTGTGATAGAGAGATCTTGGATTGGCAATGAAGTTGGTGCTGC	25968	A_95_P219162	TA21339_4097
26797	316	22	829	TTATCAGTGATGGTAAAACAGCTTGTGCAGTGAGTATTTATGGTTCTCCGCGGCGTT	25981	A_95_P145267	EB448874
26800	316	25	486	GATGTGTCCAGTTAAATGATCCCACAACAAGCTTCCTTTTGCCAGGGGTTTTGGTGTT	25987	A_95_P050136	FG158367
26802	316	27	121	TTTCTTGTTATGGTCGAAGAGAATGGATGACCTCAAATGCAGTTGGTCGGTTAGTCT	25991	A_95_P112637	CV020769
26804	316	29	498	CAGTGTAAAGCATGCGTGGTGAAACTACTGTAACCAACAATTGGACGTTGGGAATG	25995	A_95_P023411	BP131493
26805	316	30	606	AGGGAGGAGGAACATAGAGTCTTTTCAAGTTGTACATTAGACACAGAAAGTGATAA	25997	A_95_P145077	EB448622
26807	316	32	823	GGATCGATGGGTTCCTGGCTTTATTTTTGGGCTCTTATTCATCAGATTTTGTACTAGG	26001	A_95_P254284	EH615257
26812	316	37	339	GTTAAAGGTGGTTTTGACTTCTGGGTCCTTGAAGTTATGGAATTTCTCTGAATTGGTA	26009	A_95_P095073	BP533000
26815	316	40	759	GCGTTTATGATAATGTTTCACCAGAGAAGGCTCAAGCTATTATGTTGCTTGCTGGAA	26015	A_95_P129282	FG159197

26818	316	43	871	AGACTATGTACTCTTGTTGTTTGTTTAGTCTGTAAATAGTTGGAATTTCACTACGACCT	26021	A_95_P061230	DV157623
26820	316	45	524	TTCCTATGGAGTAGGTCCATTTGGGTTTTGATAAATTTGGTGTATTGATGATTGTTTG	26025	A_95_P134332	EB436564
26822	316	47	243	ATCACGTTCATAGGGTAAAATACGTTTAGGGCAAAATTCCACAATTGCAGAATATGA	26029	A_95_P213032	TA19963_4097
26823	316	48	1123	TATTGGCAGTGTAAGAATGCCCCTTTTATGATGCAAGGAGAGGCTATATGCCTTTGC	26031	A_95_P013706	TA15324_4097
26826	316	51	1065	CTGCTATCTGTCTAGACGGATGTGAGTTTGATGTAATTAATCAATAAATCTCCAGTTT	26037	A_95_P034663	AY183722
26827	316	52	434	ACGTGGAAATTTATAAGCTGTGAGTAGGTGGTCAACAACAACAGGAAATGAAATAC	26039	A_95_P092408	BP531790
26832	316	57	624	ATTAAGGAGTGATGAAACCAGAAAAGAGATGCACCTTTTGAACTCATTGTATGCAAA	26049	A_95_P131437	EB431715
26834	316	59	812	CTATTACTTGTTACCCGGTTTGCCCATCATAATGAAGAAGAAGATGGTTATGATACTT	26053	A_95_P125632	EB424725
26845	316	70	657	CAAAAAATGTTCTAGTTGGTAAAGGACAAGCAACAGCCATGGCAGCTCTCAAGGAG	26075	A_95_P249067	EB435358
26848	316	73	128	GTACTCTTGTGAAGGTGTTAGTGCTATCTTTTCTAGCCACTTCAATTTAAAATATCACT	26081	A_95_P121052	DW001061
26850	316	75	167	GGTTCTTGGACTTGGTAACATACCTCGGTTACTTTGATTTGAAAGAATGAATCAAATG	26085	A_95_P131812	EB432223
26852	316	77	819	TGTCGTTCAATGGGTTGTAATTGAATGTTATTTCCTTCTTGCTACGTTCATATACTTCA	26089	A_95_P206987	EB451518
26855	316	80	798	ACAAGTGAAGAGTTCTCTGTTGCTAAGAATCAATCGTGGATGTTAGGCTCTGCTGTT	26095	A_95_P292183	EB426797
26858	316	83	654	TGAGTGAGCTTTAGAGGGAGGCTATTGTCTCTTTGTAACCATTTTGTGCATTAGTTAT	26101	A_95_P001496	TA19041_4097
26872	317	12	650	AGTTCCAAACCGAGGCTCTTCAGCATTTTGAAAGACATTGATATTCTTTTGAGAACCA	26128	A_95_P116937	DV159434
26874	317	14	428	TCCCAAGGGAGCGAAAACGAGGAATGAATTCAGAATTAGGGGTGGAGTTCATAAGT	26132	A_95_P087893	BP529908
26880	317	20	791	CATTTTTCCTGGCGACAGTCGTGAGTCATCCCTAATATATTGATGTTTGAACAGTTTCT	26144	A_95_P013606	TA12934_4097
26883	317	23	294	AGCACCTCCGGCTACTCAAATTTTATTCTATTTAGTAGAATGGCAAATGTCTTATTGTT	26150	A_95_P003731	FG638754
26884	317	24	1560	GTTGCAAGGATATGAGAATACCAAATGGGTATCATAGACTAATTGGGGTTGACTATA	26152	A_95_P025801	TA14079_4097
26888	317	28	777	ACTTGTCAAGTTGTAAATGCAAGCTGATGACTTTCTAACTCTAACTGCGCCCCCTGAA	26160	A_95_P117382	DV160289
26890	317	30	823	GCCTATACCTGTATTCTTCTTTGAGCCTTGAAATGATCAAATTTCATTTCAATTCAGCT	26164	A_95_P207777	EB450642
26903	317	43	507	AAGCCAAGAGTTGTGGAACATGATTGTGATTTCTAGTGTAATTATTCTCATCGTTGGT	26189	A_95_P221497	TA21831_4097
26905	317	45	393	TATGTACCACTGTGAATGATTAATGATTCTGATTCCGACACAATTTATCCCTGTTTGTT	26193	A_95_P030356	TA16391_4097
26908	317	48	494	TTGGTGACCTTAATGATTTACTGGAGCAAAATGAAACCAGATATATGACTTGAAAGC	26199	A_95_P021891	DW001874
26914	317	54	538	AAGAAATACTCATCGATTTAGGCTCCTTGTACCACTTCTGATAAAAGCTAAAAGAGC	26211	A_95_P144967	EB448515
26915	317	55	2420	CTGTCTTTTAGTCTTGTCAGAGTTTGGTAAGTCATTTTCAATGTAATGTCCTGTTCTGT	26213	A_95_P032536	AB186042
26917	317	57	1177	CCAGTATTGTTCTTTTTAGGAACATGGATTCTTGAGCTCTTTAATGAAATTTGGGCAA	26217	A_95_P189837	TA14873_4097
26918	317	58	759	TAAGGTCCAGCCTGTGTTCTGTTGTTCCTGGATGAAGTACTATTTGCTACATGTCCTG	26219	A_95_P148952	EB678548
26921	317	61	754	ACATCCATTTAGGCTTCATGATGCTCTAACCAATCGTTCCAAAGATCATTCCCACCTTT	26225	A_95_P215442	EH619741
26925	317	65	181	AGAACTCAAAAATACCACCATAAAAATGGTTGAACAAAGCAGGGTTCTTAACACCCC	26233	A_95_P136377	DV999293
26926	317	66	809	TAACATCTGTTAATAGTTGTCTCTGTTGGGATGAACTCAACTCATGGATGCTGGGGA	26235	A_95_P126992	EB426415
26931	317	71	741	GCTGCATGTTTATGTTGTACTAAGTGATTCAGCTGTAAAGAGGTGTGAGAATGTATT	26245	A_95_P010966	DV162548
26935	317	75	793	TGAGATTGAATCTCTTTCGATGGTACTGACTTCTCTGACACTAACCCGTGCTCGCTTTG	26253	A_95_P270016	FG138724
26938	317	78	785	ATGCTGTGTGCCTTTTCCGTCAACAGCTTATTTAGTGTTTACTCTGTATACGTATATCT	26259	A_95_P177912	EB437975

26939	317	79	552	ACTGTGTTGTGCTTGTGCTTTTTCTGGCATTCTGAGGTAATCCAAACATTGTAATTTTT	26261	A_95_P019076	DW004716
26946	318	1	767	AGCTGTTGGAATCAACTGTACTCCTCCTAGATTTATTCTGGATCTTATTCGATCCATCA	26107	A_95_P140372	FG138658
26951	318	6	1080	TTCATAGTGAACCGACGTTTGATCAAACTCTTGCTTGAGCATGATTCGAATAAACGA	26117	A_95_P023831	TA14141_4097
26953	318	8	1506	CTCTTAAACCCTAAAACTCATATCTTGTAAGCATACTTTTGCCAAGAGATGATCTGGA	26121	A_95_P021476	TA17215_4097
26954	318	9	665	GCACTTAGAAATCCTTGATCTCAATATCTTGGACTAGTCCTTATGTTGTTGCCTTCAAC	26123	A_95_P253369	FG642430
26955	318	10	361	AATATATGCAGTTTCCATCACAATCCGTATTGTGTTTGGTTTCATGTTTATTGCCCTGA	26125	A_95_P025691	DV161823
26956	318	11	472	CGCTGGTAATTCTTGTAGAAGGTGTTTGATTTATCTACCTACACATGAGGTTATTGAT	26127	A_95_P191512	TA15254_4097
26957	318	12	584	TTGAGGTTAGCATTCTTTCAGTCAGTGGCAATAAGCTAGTTGGTCTTAGTAGAATAGA	26129	A_95_P159132	EH617084
26958	318	13	1008	CTAGTGCCTTGGAGTGTGTGTATGAGAAGTGTCTGTGAGAACTTGAACATCTCTTTC	26131	A_95_P009491	TA15475_4097
26961	318	16	805	GTGAAGATCATAAATATTTGACGTTGAGTTCCTGCTGCTCCTGGAGTACTTTTTGCAG	26137	A_95_P233319	EB679770
26963	318	18	693	ATGAGCTTGAGGAGGAAGATGATATGGAAGATTTTGATGGTCTTGGAATTAGAGAC	26141	A_95_P137062	EB440802
26966	318	21	695	CTGTTGGAACACCTGGACACGGCTCTAGATTGTATGATAATACTGCTATGGAGAATT	26147	A_95_P136972	EB440704
26968	318	23	549	AGGAAAGGAAGCTCCGTTACTGTACTCTACTCCGATGTTAACCTCTCTAACGGCGAA	26151	A_95_P027946	TA15227_4097
26969	318	24	168	CTCCTCTTGAGATGTAGTGTAGTATCTTATCTTCCTTATTGCATGACATACTTTAAGGA	26153	A_95_P001411	EH619794
26970	318	25	311	TTTCCTTTAGGATTTGATGGAACTTTAGATTCTTAGAGCTTAAGTTAACGTTCCCTCAC	26155	A_95_P048426	BP131909
26976	318	31	393	TCAAGGAACATTATGCAACCATCATCAGCTATCTACAACCCTTAAAGCAATGGAAGT	26167	A_95_P097588	BP534116
26977	318	32	241	GCCCCGTCATGAAAGATTTTATCGATATATGAGAGTATTGTTGCTTCCTTTCTATCAA	26169	A_95_P003816	EB440105
26978	318	33	761	ATACTCCTATTACGGTCCCCTTAACCTTATGACTTGGAGTGTAGGATACCACAACGAG	26171	A_95_P293824	EB451261
26980	318	35	442	GAAGGAGATCTCAGTCTTTGGAGTGTATATTAGGAGTTCCTTTTGATTTAAACTTTG	26175	A_95_P101923	CN824929
26983	318	38	352	CCGCATATTTTTCCAAGGGGATAGAATTGTGTTGGATGGTGGAATGTAAGAGATTTA	26181	A_95_P033191	AJ310476
26991	318	46	326	AAAGCTAAAGAGAGATTTCAAAGACGGCGACAAATAGAAGCAATTAATGGTGCATG	26196	A_95_P080860	DW004768
26992	318	47	936	GAGTTATGAGGAATAAGTAGGAGTTAACCGTGAGATAATTGTAGGAGGGTTTAATT	26198	A_95_P012031	TA14873_4097
26993	318	48	251	ATGTAGACGAGCAACCTCCATTATTATCGTAAGAATAAACAGGTTCCTATTTTTTCAC	26200	A_95_P139232	EB442971
26994	318	49	116	AGCTTATGAATGACACCAAGCGTGCTAAGAGAAGGCTGTAAGTTCTGCTTTTTCCTG	26202	A_95_P034289	AJ718369
26996	318	51	921	TCACTACTTTTTGGCTTATATAAATGAAGGGACACTCTGCCTTCTCATGTTTCTCGTCC	26206	A_95_P185227	TA13867_4097
26998	318	53	319	ATAGGGAAGAAAGAACTCTTAAGGATCTGCACTGAAAGAGAATTCTTGCTAATGAA	26210	A_95_P081535	BP528280
27003	318	58	841	GATAGGCACACAATCATCATGCTCAAATGGACTGCGTTTTCTGTAGAATGATGATTG	26220	A_95_P224337	EB439249
27008	318	63	128	TGATGGTCACTTTGTCTTTGATGTCCTGTTCCCACAAAACTATCCTGATGTGCCACCG	26230	A_95_P225942	EB424860
27011	318	66	516	TGAGTAGTAGGTCGTGATTTTTTCACCTTTTGTGCCAGGTGTTTTCAATGTAAAAATA	26236	A_95_P265541	AM790765
27014	318	69	310	GGGTGGCGGGAGATGAAGATGAGGAAGATATTGACGATATTGAACACGAATTCAA	26242	A_95_P129187	EB428913
27017	318	72	1226	ATATGATGTTACTGTTGGACTGTAAGCATTGGGCTTTAAAGACTTTAAGCATTGGGC	26248	A_95_P208407	TA18962_4097
27021	318	76	489	GATCGTCGAAGGAACTAAAGGTAGGGTGGTACGATCTAGTGATAATGAAAGGACTT	26256	A_95_P267236	AM793576
27023	318	78	685	TTACCGAGGCAGAGAGCGTTTGTTTATATGTAGAATGATGACACAATTGATCTATTT	26260	A_95_P254484	FG190707
27025	318	80	459	ACATTGCAAAAAAGGGTGATGATGCTAGGCTGCATCGATGTGGCAGAGTATAGAGT	26264	A_95_P076360	BP526964

27026	318	81	726	GTGTTTTTTACCCTCATATGTACTTTCAGATAATCTTCCCTGTTTTGCATGGAATTTGA	26266	A_95_P278268	FG635823
27027	318	82	149	AATTTGAGATATATCTCACGATTGGAAGGTTCTGGGAAGGATTGGCTGGATGGATG	26268	A_95_P157452	EH615510
27028	318	83	815	AGTCATTCCTCGAGGGGGATGATGCTATGGAGCGTACTCTTCATATTCCTCAAGATT	26270	A_95_P243052	FG139530
27029	318	84	1467	TAATTTTGGTAGTGGCAAAAATTCAGTGTAGCCTTGAGTGGAAAGTTCTGAGAGCG	26272	A_95_P247657	EU375458
27031	319	1	1470	GATCAACCACTGTGAACTTAATCTTCCAGGCTTCTCTGTGTGTATATTGTTTTCTTTCT	26275	A_95_P152062	TA15973_4097
27032	319	2	519	TTTTGGTCATTCAACTTCCTATTGAATTGTTGAAGAGGAGCACTTAAAGGATGTGCTT	26277	A_95_P155932	EG650331
27035	319	5	421	CGACTTTTGGGAGCTAATACAATTTGTACGCTGAAGTTTTGCTGGTAACTCCAATAAT	26283	A_95_P286073	FS408169
27036	319	6	866	AGCTGTTTGAGTCGATCAGATGCACTGTACTGCTGTGCTGACTGATGAGAAAAATCT	26285	A_95_P235104	FG142893
27042	319	12	106	GAAGTATCAGAGAGGTAGAAGACACGACTCTGATAATGATGATAGTAATGATCTTG	26297	A_95_P119242	DV162344
27044	319	14	737	ACACATTGAAAGCAAGAATTTGGATGTTGCTGTGAAGCAACTTGACAGGAATGGTT	26301	A_95_P316743	FG194017
27048	319	18	301	AAAGTTGGGCTTTCTTAATTGGGCTTTAAATTTGTAGTGCTTTCTTTTCCTCTGGGTCC	26309	A_95_P213882	TA20142_4097
27049	319	19	603	TAGCCTTGTCGATATTATGGAGTGATTATCAGAACTTCTTTGTTCGGAAATTATTGAA	26311	A_95_P242942	EB447309
27050	319	20	1701	CTGTATCTGCACATTTATTGATTGTATTGCAAAGAGCTTGAAATCAACTACAGTTCTC	26313	A_95_P259986	AB286961
27051	319	21	603	TCATCAGACATCTCGCTTTGAAACAGCCATTCAAGCTGTTCGACATGTGGTTGCCACA	26315	A_95_P127327	FG174896
27052	319	22	488	TCCTGTTTGATGAAGGATTAATTGCCTTAAGCTGGTGCAATGGGATAACTACCTGCA	26317	A_95_P275918	AM788420
27060	319	30	867	TTGTCGGATTACTTTAACAATCTCTTTGGAGGCACCAAGGTTTTTATTGAAGCTGATG	26333	A_95_P248877	EB679127
27064	319	34	461	TTTTCAACATCTCCTGCCCCTTGACGATTCTGTCCAGATAAAGTAACAGCTGAATAAC	26340	A_95_P278488	AM802537
27065	319	35	388	CCACAGATGAGAGTGGGTTAGATGTTAGTTACTAGATTTCTAATTCCACTGTATATTG	26342	A_95_P211132	TA19545_4097
27068	319	38	199	GGAGAGGGATTAAGTCGCATTTCTGTTTCTTCAAGGTGTTTGTAAAAGTAAGATGTT	26348	A_95_P093603	BP532331
27069	319	39	596	TATATTTGTAATGAATTCATATCGTCGATCCAGGAATGTAATATCACCGAGCAAGCT	26350	A_95_P300453	FG638254
27075	319	45	700	TACAGAAAAGAAAAGAGGAGACTTTGCTGAAATAGGAGGGGCACACAGTTCATGG	26362	A_95_P135797	EB439356
27077	319	47	418	ACTTCATTAAATTGATTATGAAGAAGCACGGAAAGGACATCAGCGAAGGACAACGA	26366	A_95_P072845	BP526066
27082	319	52	674	GTTGACCTCGTCCTTGTATCCATGTTGTGTAAAATGTATATTGTAAGACCTAACATAA	26375	A_95_P295583	EB446978
27083	319	53	1558	TATTATATGTGAACTTGTCAATTATCTCCTGAGGTGAAAGAGTCCTTCAGGGAATAG	26377	A_95_P007981	AF127243
27085	319	55	854	TGATGGCTATCTGGATCATACTGTAAAAGCTTAAACTCATATGATATCTTCCCTGTGC	26381	A_95_P289148	DV157860
27090	319	60	789	TTCAAGATGCTTGTATGAGCCTTGGGTATGGCAGCCATATTCCACTAGCATATGAGA	26391	A_95_P281573	FG159896
27093	319	63	490	ACAAGAAGATCAGGGATCGAGCAGCAACATTTTAATCACATGATGAATTACGTAGA	26397	A_95_P054261	BP133390
27097	319	67	1474	TTAATGCTCTTCTCCTTCTCTCATGTAATAGAAATAGATGTGTGGACAAAAATCGGAG	26405	A_95_P218912	TA21283_4097
27098	319	68	490	TCTTTCAGCCTCAAGCATTGGAACTATGTGCAAGGAAAGTTGCTTCTGCATCCGGAG	26407	A_95_P006926	NP917038
27103	319	73	837	AATGTTGTTCCCATCCCAGGAGCCAAAAATGCAGATCAAGCTAAAGAATTTGCTGGT	26417	A_95_P290578	DW000445
27112	319	82	651	ACACCTTGGAACTTGGAATAGTATGAAAAATATCCGTGCCATGCTAGGCACATAATT	26435	A_95_P252414	FG645435
27113	319	83	749	GGCTGGTATATGTTTCTTTCAGGTGTGCATGGATTATAATCTATTAAATGGGTTAATA	26437	A_95_P016931	TA16516_4097
27115	319	85	284	TCTCTATGCCTGTTTTCCTCATCTCAAAAAGTGAACCGTTTAATTAGGTGCCAAACAT	26441	A_95_P109862	FS416927
27120	320	5	243	CCCTGATTTGGTAAAGGGAATTTTGGTACCTCTCAATAAATTTGATCCCCAAATTTAT	26284	A_95_P142807	EB446228

27127	320	12	223	TCACTGGAGACAGACATACTGTGTCAATCTTTTTGCTATTATGGATGAATCTCAATTG	26298	A_95_P089383	BP530479
27135	320	20	813	TGATCTTGGATGGATTTTTGCTTCCTCAGATTCTGTTCATTGTGTTCTGTAACACTACT	26314	A_95_P254154	EB426002
27136	320	21	451	GCCATAGACAATAATCTTGTTACATCAGGTCATCCAGGGAAAAAGCTAATTTAGTTTG	26316	A_95_P022716	EH623214
27138	320	23	652	CCCAATTTGGGGTGTAGGATTGATGATGATAATGTCATTGATGTTTAAATTCTACCCT	26320	A_95_P285698	EH622264
27141	320	26	399	TCACAGATCTGGTTGACTACTTTCCTCTGACTGCTTAGGTTGAGTCACACATTTTCTGC	26326	A_95_P106058	CV017736
27152	320	37	1153	CCATCTGCCATGCTTTTATTTGATGCAGTTGCATTGTACCTTAAATTCACTTGGTTCCT	26347	A_95_P027941	TA16625_4097
27154	320	39	148	GGTCCTGAGTAATCTAAATTTTTGTTTCATTTTTTCCCCTCAACACAGATAGGCAATTT	26351	A_95_P094243	BP532623
27155	320	40	501	AACAAATGTGCATACTTTCTGACAAGCAAATGTCGCAGACATGGGCGAAGATCTGCT	26353	A_95_P055016	BP133585
27156	320	41	798	CGGCACTTAACTGTTGTAATCTTCCGATTTTTACGTTTGATTCCGGCTCTGTAGTTGGT	26355	A_95_P152642	EB682971
27165	320	50	176	CTTTTGGGCAGCTCGTCCTTAAATTCATGTACATATTGGATACTATACTTAACTGTTAT	26372	A_95_P103837	CV016717
27167	320	52	331	GAATCTTTCTCTGTAGTTAAGGCTAGTGACCGCGTTTGTCTGCCATTTCTACCGTGAC	26376	A_95_P104452	TA15278_4097
27170	320	55	921	TTCGGGACATGGGAGTTCGACCCTGTGGATTTGGAAAATCCATTTCCTAACAATGAA	26382	A_95_P248027	EB679219
27174	320	59	619	GGATGGATAGGTGAAGACAGTGGCATGTTGCTAAATACTGTTAAAATCACATTTTGT	26390	A_95_P261876	BP133832
27180	320	65	464	TGACTGGAGCCCAAATTTTCCATTAGGATCATGAGTCGGATCCTAACTTGAGGAATA	26402	A_95_P052976	FG163875
27184	320	69	724	GCTTGTTACCAACTGGCAACTGGTATGGAAAGTGTTTAGAGAAATACATAGGAAATT	26410	A_95_P299103	FG645413
27188	320	73	346	CTTGGTCACGCATACTGTTTTTGAAATGAATCGAAAAAGAAAGTAGTTGTCCTCTCAT	26418	A_95_P308473	FG642531
27189	320	74	1123	CTGTGCTATAGTTGCAGCAACTGTTAACAAGGAGATTATTTTTTATATCCTGTAATAG	26420	A_95_P196402	TA16330_4097
27190	320	75	801	ACGCAACTATTATGAAGGTCATTGAGAGGCCATTGTCAGAAAATGAGCGCTTCATGC	26422	A_95_P144847	EB448369
27195	320	80	391	GTCCAGCAGTAAAATACATGTAACTCTATTAGATGATCCATGATCGTAGTATGGTATT	26432	A_95_P077090	BP527163
27203	321	3	529	GCATTATGAATCACCTTAAAGGGAGCCGTGATTTTCCTCGTTTACGAATAGGGCATT	26447	A_95_P157407	EH615476
27208	321	8	845	CCTAGTGCTATTGTTGATGAGATGAGGAAGTCATTGATCGACAGTTACGTTTGAGTT	26457	A_95_P224967	EB426172
27210	321	10	744	AGATGTTTGTTATCACTATGGGTTATAGTTTCTCTGTCCAGTTTCTAGTGAACACGTA	26461	A_95_P161247	EH619997
27211	321	11	293	ATGAACTGTTTAGGCAAAGGAGAATCTTAGCAACAGGGTAACATTGGAAGCATGAA	26463	A_95_P075630	FS424594
27215	321	15	480	GATGGTAATATTATGTTCCTTTTATGTTAGTTTGCTTTGAGGGATGTCATCTTGAGGA	26471	A_95_P061055	BP135165
27218	321	18	852	AAGTATGCCGGTGTCTTGTATGGTCTAGGTGTTGTTGAGAATGGACAGAATGTCCAT	26476	A_95_P235064	DV999544
27225	321	25	217	TAATAGAGAAGGGAGGGTGGCCTAATGCGGACACATCATAGCCTTTAATTACAGCTT	26490	A_95_P133597	EB435245
27227	321	27	514	TGGATGGTCACTCAAATCCCAAAGTTCAGATCATCGGGTTCAAGATGACGCCAATAT	26494	A_95_P071875	BP525812
27229	321	29	520	CGTGCACTTGTGACTCCAGTTCTGGGATGGTATTTAGATATCGCGATTTTTATGGAG	26498	A_95_P253444	EH622203
27238	321	38	876	AGTTGAAATTAGGTCATAGGGATCGTCGTATGGGGACTTGAACTATGTAAAATGAA	26516	A_95_P198597	TA16813_4097
27239	321	39	649	GCAGAGGTTGTTACATATATTCAAGAACAGCTGATTTGAGTTATTACTGTGTATCAGT	26518	A_95_P122737	DW002697
27240	321	40	846	GATCCCATAATGCATTTGCTTTCTGGGACTGGTAGAGTCGATATAGTGTCTGCATGC	26520	A_95_P270086	FG134963
27241	321	41	467	GTGCCCTGACTTCTATTTAGATTGTGTATTCTGCTATAGGTATATTCGACATGGTTTC	26522	A_95_P122607	FG638986
27242	321	42	777	TTAATAGCCCAATGGTTAATCCAGTTTCAGAAATATGCCAAGCTTGTTCTGATTAAGT	26524	A_95_P162577	EH621517
27244	321	44	372	AAAGGCGAATCTGAGCCTACCCCATTACTTTGATTTTGTTTTGGTTTTCCCTATGCTCC	26528	A_95_P076620	BP527032

27249	321	49	80	TTATACTAATGTAAAGAACTACGTTTGGGCTTGATCCCCATAGGAGCTTAGCCCGGG	26538	A_95_P034344	AJ718492
27252	321	52	832	TTGCTAGATGAATCGTGGGTGCTGACCTCCATTTCCTGTTCAATTCTTTCCATTCTTTC	26544	A_95_P119417	DV162624
27257	321	57	739	ACTTCTGATTCTTTGTTCTCCATCCAACCCAACAGGGTCTGTTTACCCTCGGAAATTGC	26553	A_95_P151137	EB427488
27265	321	65	834	TCTATACATGGCAATGACCGAATTTGAAAAGCTTTCTGAAGTACCTGATTGGTCATTT	26569	A_95_P236214	DV159985
27268	321	68	755	GCTGAAATTGTTGTGGATTATCCCGATAAGAAGGTAACTATTGTGCATCGGGGATCA	26575	A_95_P127947	EB427526
27273	321	73	777	TAAACATAGGATGCATTTGTACCATTTAAATGGATGCTTGGATTTGGGTAGTGAAAG	26585	A_95_P014376	EB442889
27275	321	75	146	TTGAATAACACCTCTTGCATATGCCTAGTTTAGGCTAAGTAGTCCAGTTGTTTTTAAA	26589	A_95_P099528	BP534960
27276	321	76	851	GTCAAAGTTGCTGAAGCCTGATCCGGAACTGGCTGATACAATTTATAAAAAGTGCTC	26591	A_95_P294658	EB441989
27277	321	77	275	TATTATGTAGCTTTTGCTGCTGTTGCTGTGGGACTCCTTGTTTATTCTGGAGGTGATA	26593	A_95_P266121	TA21591_4097
27283	321	83	310	CTGGTTCATCTTGTAAGTCACTCGAAGCATGAATGCAAAGATGAGAAAGATTTGAAG	26605	A_95_P094933	BP532936
27285	321	85	797	AGTTGGAGAAGGCTGGATTTCGTGGTATCTTGATAAATGCAGTTGTAGCTGCAGCTA	26608	A_95_P252499	DV158177
27288	322	3	1021	GGAAGGCGAAACGAAATTCTGTTTCAGTAATTTCCACCTTTCTTTTCTTTTTTCTTTCT	26448	A_95_P240144	AJ966359
27289	322	4	411	TTGGGTTCACCAGTTTCAATGTGTGGTACTCGTTCGACATATTGTAATAATGTCAAAT	26450	A_95_P130312	EB430338
27291	322	6	865	CTCGAATAGAAGACTGTTACATTGTCTCTGGAGATGATTGTATTGCTGTTAAGAGTG	26454	A_95_P152312	EB682654
27292	322	7	806	GAATTGTTTAGTTTTGAATTGTCTAAGGAAGCAGTTCCTAAGTCCTCTTCTTCTGATA	26456	A_95_P273051	DV999793
27294	322	9	423	GAGAGAAGCTACTGTGATGTCGATATTCCCTCTTAATCAGCTCGGATTGATGAAGAA	26460	A_95_P263898	BP525566
27298	322	13	814	GCTACTGGTGCTGCTATGTGCTGTTTGTAGAAGTAGGAGTGAGTATTTATTTTAATA	26468	A_95_P149782	EB679746
27299	322	14	503	AAGCATTCTTCGGATATTCTGGAGTTTGCTCAACTTAATGATAGAAGGATTCAAGTTT	26470	A_95_P022091	TA12410_4097
27309	322	24	807	ACGATGATTTCTGTTGTAATTTATACATTGTCTCAATGTGATTTTCTCGTTCCCAGGTT	26489	A_95_P214737	EB677283
27313	322	28	664	GTTGGAGGCATGTTGAAAATGTTCATAAGTGTTAAGTTCTAATTTAGCGACGTCCTAT	26497	A_95_P271971	EB446553
27319	322	34	511	ATTCATATTGGCTTCTTTAACGTGTACATAGTCTTATGAATATTGGACGTGCACTATTG	26509	A_95_P205602	TA18325_4097
27320	322	35	558	ATACTAAGCCCTGGGGAACTTCACTAAAAATCTCACGATGAACGTAGACGCCTCAGG	26511	A_95_P006306	TA15420_4097
27321	322	36	232	AGAATTAGGGTTTGGATGTGATCTGCTGTTGTTTTTGGGTTTGTGTAAATGCTCGTG	26513	A_95_P161877	EH620463
27322	322	37	156	ACGCCCGATGATTCAAAGTACAGAATGTTGATATGTACCATTTGTCCTCTTGTTAATA	26515	A_95_P109282	EH618781
27323	322	38	2807	AGTTTGATGAATGGTGATGGTAAGGGTGAAATGTTTTTGCAGAATTCAGAAGAACAT	26517	A_95_P227669	X83729
27325	322	40	518	CAAAACCATTTTCCAGTTAAATGCTATTTGGACAACTTCTCGTCTCGCTTGCAACTGG	26521	A_95_P223492	FG635017
27336	322	51	784	TTGAAGATATTGTTCGTGCAGCAAAGAGGGCAAGTTACAGAGCAGCAAAATCAGTT	26543	A_95_P117512	DV160439
27337	322	52	890	TGATAGAAGTTGTTAAAGGTTCAACAAAGGAGAAGGTCGTACGGGTCGTCATCTTG	26545	A_95_P292673	EB428039
27344	322	59	293	TGGACTTTCAACAGATCCAGAAACCTTTGCCAAGAACCGTGAACTCGAGGTGATCCA	26558	A_95_P105167	CV017332
27345	322	60	365	TTAGGAGTGTCCTCACGCTTAAAAATTGTTTTCTTGTTTCTCAATAGAAGGTTTCCTTT	26560	A_95_P307253	FG638033
27347	322	62	632	TTTTGTGCTGATTTCATTTTCAGCAAGGTTGTGGTACCCCTGCTGTGCTCCAACATAGT	26564	A_95_P284258	FG642918
27349	322	64	728	CATGTTCATTATCTATTGGTCTAGGACAATCTGTACTTCACATGATACACAGTTTAACT	26568	A_95_P017136	EB683285
27350	322	65	686	GGTTCATTTGCTCGTGTAATTGCTGAAATTTCTTATCGATATAAACTCCAATTTGCAG	26570	A_95_P149092	EB678740
27353	322	68	1077	GTTGATGCACAATTACTTGTCTCAGTTTGCTGTTGTATTAATGTCAAAGCTGTTTATG	26576	A_95_P194767	TA15970_4097

27354	322	69	806	CTTACATTGCTCTTGACTATGACAGACTTGAACAGCAAGACAGCTCATCGTGGAGAA	26578	A_95_P309458	FG133347
27359	322	74	435	ATTGCTGATACTGTGTATTAAAAATGATTCTCCCTTGGTTATCCAGGGGTGCTGTTAA	26588	A_95_P212667	TA19884_4097
27364	322	79	475	CATAGATTAGCTGGTATCTGTTATGTCTTCCTTATCAGTAGTTCTTGTATGTACTAGAA	26598	A_95_P094853	BP532903
27366	322	81	1113	GTGGTCTGATTATGTAATTTAGACCTAGGTTTGCTATGTACTGTGTACTTAGAGATCA	26602	A_95_P212132	TA19764_4097
27370	322	85	673	GAGCCAACTCCATTGTTACGTTGCTGTCAGCACTTATATGATTCTTTGTGGTTTCATTT	26609	A_95_P003441	FG643518
27371	323	1	1414	AATTGACGTTGTTGAGGCACTCTTGTCGTGTTCTTTCTTTCTTGTTAAACCAAGGCGG	26610	A_95_P239759	AJ006974
27372	323	2	930	GTCGATGTATATTGTAATACAATATAGATGAATGCATGTGCAGACTAGTGAGCTTGG	26612	A_95_P008261	TA12823_4097
27373	323	3	1087	CAAAAGATTTCCACTGTTCTCTCTCGAGTATTTATTAGTTACTACAACTTGATCTTTGC	26614	A_95_P196947	TA16454_4097
27374	323	4	730	ACCCCCGAATTACGCGACAAGTTGCACAAAACAAGGCTGCATATTGGGCAATTAGTG	26616	A_95_P121112	DW001113
27378	323	8	441	TCTGCAGTCCACGGAGGAAATGATGATATGATGGATGATCTTGATGAGATGATTTTT	26623	A_95_P093848	BP532446
27381	323	11	563	GTTTGGATGGACTCCAACACATGTAGACTTTCATGTATCTTGACCGGCATGAAATATA	26629	A_95_P221757	TA21887_4097
27382	323	12	742	TGATGCATGATGATATCAAAGGAGGAACGTGTATACCTGTAAATATTCTCTTTTTTGG	26631	A_95_P215077	EB426699
27383	323	13	696	ACATTAGAGACGACGAAGCAGAGCATTGTAAGACAATGAAAGCCTGTCAAACGCAT	26633	A_95_P126337	EB425680
27387	323	17	2117	GTTGTGTATTCATGAAATATTTCATTATGTTAGCGTGAAAATGTAGGGAGCTCTGCA	26641	A_95_P252079	DQ923119
27388	323	18	392	CTTTCCAGCACAATTTTCCAACCTGACGGGACAGTGATATGATGTGAAATAAATTCCC	26643	A_95_P155097	EG649896
27392	323	22	828	ATCGGGGGCAAGTATGGAGGAGATTACTGCTGCTGTTAAAGATGCTGTCACGAAAG	26651	A_95_P268096	DV999530
27395	323	25	516	ATTACCAGATTCCTTTGTACTTGCTGATTTTCACATAGTGAAAGAGTTGGTCATGGTT	26657	A_95_P123222	DW003094
27396	323	26	795	AAGGAATTGATCGTGACTTTGAACCTGTTCTTTCCATGACCCCTCTTAATTGAGATGA	26659	A_95_P268181	DV999785
27401	323	31	478	CAGAACATTGTCAAGAGAAAAAATGAAAGCGACAAGTGGTATTCTTACCCAATGTTG	26669	A_95_P274843	TC64030
27403	323	33	705	AGACTTCTCTACTAAAAGCTGTTTGCCTTTGAAGGCTTAAATTTTGTATGGATACTTG	26673	A_95_P015021	EB677251
27405	323	35	1176	GACTGCTTTATCCAAATGGATGGGAAGATTCTTTTAGCTGAATAAGCTATGTACTTCA	26677	A_95_P250542	AJ299250
27410	323	40	578	GTTTACAGTTGATGCTATAGTGTAATTTACCAACTACTTTTCAAGAGTTTCCTGGGAC	26687	A_95_P152867	EB683193
27413	323	43	553	GGTCCCTGTTCAGTCGTCCGTCCAAGATTTGGGTCCTAGATTTTTTCAGGGTTCAATT	26693	A_95_P091738	BP531480
27419	323	49	815	ATTGGACTCACACGGATTGTGCAATTCGTGATAACAGTTGGACAGTGCTTCTCCTGT	26705	A_95_P294648	FG160522
27421	323	51	1099	GAGGGATGGCTATCCTCTCGATTCTATAACGTTTCGATTTATAATAACTACTAGTACT	26709	A_95_P029216	TA16407_4097
27422	323	52	791	ATGATGAAACATTCAGACACATGGCTAGCATCTACAGTCATTCCCACCATAACATGTC	26711	A_95_P137407	EB441150
27423	323	53	820	TTCCAAGGCTACAGTGAGGGATGGCACTATATTAGCACAAAGTGCTGTAGGAGTTG	26713	A_95_P233679	DV159023
27424	323	54	782	TTTGAGAGGATATGGTAGCTTTCTCTTGTGTATATATGATGGTGGGTGAAGAAGAAA	26715	A_95_P159262	EH617285
27427	323	57	361	AGTCAGATGATGACATGGGCTTCAGTCTCTTCGATTAGAAGAATCCTAAGAATTCAG	26721	A_95_P204212	TA18018_4097
27429	323	59	923	TCGCTATAGCATTGAAGCAAGTGGCTACTCCTGAATACAAGACATATATGCAACAAG	26725	A_95_P020546	DV161209
27430	323	60	569	AACTCAAGGGAAAGGTTGAATTGTGGCCCTCTGTAAAATACTTAATTTTCCTTATGTT	26727	A_95_P178072	TA12136_4097
27436	323	66	800	AGCCAACTGCATCAAGGGGATATTGCCCATGTTAGGAACTGTTTTGGATCAGTAAAG	26739	A_95_P027546	EB679862
27437	323	67	541	AGTTGTACAGGTCACCCGAAATACATGTTAGTAGTTGGAAATTCTCAACGATGAGAA	26741	A_95_P261971	AM780931
27441	323	71	1387	TGTTTGCATTTGGCTGTAGACATAGTGATGATTCTTATCAAATGCATCACATTCACAC	26749	A_95_P033151	AJ271749

27444	323	74	807	CTTGTCTGAATAATAGTCACTCGTGTTAGTCTGAGTTTTGAATTGCCAAATGCAAATA	26754	A_95_P010201	EB425536
27448	323	78	1731	GTTCAGTTCCGTATATTCGCTTGCTTGTTAACTTGTAATTCGGCATGCCTGCCATTTTT	26761	A_95_P249782	AM851010
27452	323	82	463	AGCTATTGGAGAGAATAAAGCCACAAATTCCTCATCACTCATCTATGTAATTGTCTGT	26769	A_95_P103622	CV016607
27453	323	83	850	ATTATGCAAGCCAAGGATTACAAATTTCTCTCTTAGGCATCTCTCGTATGGCACACAT	26771	A_95_P205857	EB425159
27454	323	84	448	AGAGTGTTAAGGATGGGTGTTAGCAGCTAGGTTTTTTCCTAATATATCTTGCTTTCAG	26773	A_95_P062140	BP135438
27456	324	1	798	GGCTTGTTTTGCTAAGATAATTGAATAGCATGCAGTAACTGTTGGTGTTTTGTCTAAT	26611	A_95_P288558	DW000475
27458	324	3	497	AGGTGCTCTTTTTCAGGGTCTCTGGGATACTTGATGTCTGATAAATTGGAGATTCCTC	26615	A_95_P072295	BP525927
27465	324	10	519	CAAGGAAGCAGAGAGTAAACGAAATGAATTACTCAAATTCCTGAACGCAAGTTATG	26628	A_95_P071705	BP525771
27467	324	12	922	GAAGGGGAGAACAAGGATTTTTCTGATAACGGATTTGAAATGGAATTTTTGTTGTCT	26632	A_95_P194867	TA15995_4097
27472	324	17	480	CATGTTTCAGAAAGCCGAAAGATAAGACATGTAAATCTGACAATCTAAAGCTTCTCC	26642	A_95_P094478	BP532735
27473	324	18	1008	AAGAGCTCTTGAGCAATGCACCTAAGATAACTAGGATTTGCTGTTTCGAATGAATAT	26644	A_95_P121527	TA17173_4097
27476	324	21	275	CTAAACTAATGATTGAGTTTCCATCTATGTTTGGGTTTTCTGTGAGCCACACAACCCG	26650	A_95_P159182	AF205130
27481	324	26	405	CTTTGGTGCCTGAGATTGCTCATATGTACAAAACTGATAAAAGCAAGTACGAAGCCA	26660	A_95_P108693	CV020487
27482	324	27	805	CCAAGGTTATTCCTGGAGAATATGGTTTCATTGCTCAACTGAATGAGGGAAGGCACC	26662	A_95_P010601	TA12117_4097
27490	324	35	542	GTTGAATGTGAAACAGAATAAATAATGCTTTTCGTCCGGGGACTAATAAATATGTTG	26678	A_95_P025471	FG633777
27491	324	36	688	GAAGCGAAGAAACTACACATCAATTGAAAAGAACCAAGATGGTCTGCCTACTGATAT	26680	A_95_P055226	EB425809
27492	324	37	494	TTACATGCTCTACTTTCTCTCACACAGCTTGCTTCAGCAATTTCTGGCTTTGCCAGCAA	26682	A_95_P276623	AM789086
27494	324	39	738	TTTACGAGAATGAAGCTACTCAGGCAAAACTCTGGGATATACTTGCTGTCTATGCCT	26686	A_95_P003531	FG635366
27497	324	42	113	TCATTCCGGATGCAGCTCCTGGCTTCGTGATATGCTGCAAATATTTTGTCATATAACA	26692	A_95_P044901	BP130999
27502	324	47	115	GGTAGCCAATTCTTTGATTGGAAGCTGATGGTTGTATATTGAACTTTTTCAGAGTAAG	26702	A_95_P125852	EB424946
27508	324	53	400	ACTGGATTGGGCTTGTCTTTGGATAATGGACGTTTGGGTTCATGTGGTGACTCAGCA	26714	A_95_P125627	FG645115
27509	324	54	1456	GTTGGCAATTGAGCGAGCAGTTTATGTAATTAGGTAAACTAACCTCTCAAAACTTCA	26716	A_95_P014751	TA12350_4097
27510	324	55	172	GAAGAGTTATAGTAGCTACTTAGCTAATGAAGAGTTGAGATTGGAGTTGGAAATAG	26718	A_95_P099218	BP534843
27512	324	57	452	TAAAATAGGTCATCAGTGCCTACCTCTGCATGTTCTTATTCAAGAATCATGTTCTTGG	26722	A_95_P249477	TA21871_4097
27513	324	58	483	ACGGTGCGAATCTTAATAGCAGCCTGATGAGAGAGGTATGCCAACAATTCAAGATTA	26724	A_95_P280868	AM801892
27514	324	59	911	TAAGCTAATAGAGAAAAGTGATGGACCTGAGAAGTTCCAGCTTGCTCGTGGACTGG	26726	A_95_P225362	DV159609
27521	324	66	67	TTCATTTCCCAGTGTCAAACCATTACAAAGGGGGCAACAGTATTACTTTCAGAGTCTT	26740	A_95_P096343	TA19280_4097
27524	324	69	535	CTATGGTACTTGTTGTAGCTGGATTCATGAATGTGGTTTTCGTGGTTAACTTGGGTGT	26746	A_95_P223427	EB683624
27529	324	74	746	AAGGCAGAGACAGTGTTAAAACTGTTTTGAGTTTCTGTGGATTTGTCATCTTCTAGA	26755	A_95_P159242	EH617251
27530	324	75	1434	GCGTCAAAAGTAGTGAGGTATCTGAATGCTTGTATCCATTATGTAAAACCATATAAG	26757	A_95_P191192	AY748246
27535	324	80	872	GAACTATTACCATGACATGCATGTCATTCAGGATTTGCTTGTTCCTCTTTACAAGGTT	26766	A_95_P245727	DV162156
27542	325	2	828	CCTAGAGACGAACATTTGAGCATATGAGTTGTATACTTTTTGAAGGGTTTGAATAAT	26779	A_95_P267161	DV158881
27544	325	4	863	CACTGTGTATTATCAAGCGATGCTTAAGTTGTATGTCAAGATAAGTACTGTGATATTG	26783	A_95_P008551	EB448266
27545	325	5	837	ATGAACCATAGTTTCCATGCGACGTTGAATACTCAGCATGATGCCTATTCTAACACAC	26785	A_95_P118872	DV161947

27549	325	9	576	TGCTGTTCGAGTACTGGAGTATTTAGAGTATAGGAAATTTGAGGCTGATGATAATAC	26793	A_95_P276399	TC61186
27551	325	11	918	TTTGACTTTGAGAATGTATCAGTGAAGGCGGCATGGGAAGGAGAAAAGATTCGTGA	26797	A_95_P212462	TA19842_4097
27554	325	14	848	CTGGATGGGCAGCATTTTAATTTTGTGTATTAAATATGGCTGACATGTATGATCGCTG	26803	A_95_P245957	EB424987
27555	325	15	435	TTCCAAGATGAAAACCTGCTGCATAATTTGTGATTTGTAAATCGGATCTGGGATGTTC	26805	A_95_P205802	TA18368_4097
27563	325	23	1389	TCCTTTGAAGCAAGGGCTTGTTATGGACTTTTTGACAGTATGGATATTTAAAGGGCTT	26821	A_95_P188862	TA14663_4097
27571	325	31	1567	GTACCATTATGTTATTGAAGACTGAATTTGGGTGGCAATTATGATGTCCTTGTTTTGT	26837	A_95_P013916	TA12331_4097
27573	325	33	860	TCATCAGATCGCGTAAAGTATCAACTTTCTCGTCCCTGCTGTGCGCTCGTAAATGAAT	26841	A_95_P261856	FG158306
27574	325	34	722	TGTTGTTGGTGTAACGACGACATAGTAACATATGAGTTAAAGAAGTTGTTCGTCGAA	26843	A_95_P117142	TA14508_4097
27581	325	41	950	AGATAAGGAATTTACCTCGTCCAACAGATATTCCAGACTCCGGTTTGCTTTGCGATTT	26856	A_95_P215352	Z93769
27587	325	47	443	TATTTAGTGAGTTCATCTTTCTGGTCTTGACAAGGTAGACTCTGAGCTTTTTGACTTCC	26868	A_95_P200637	FG642292
27588	325	48	901	GTTTAAAGATGCCAGTTTCTTCAACCAAAACTTGAAGGTTGATCTCTTTCAAGGGATT	26870	A_95_P008186	TA13265_4097
27590	325	50	598	GGCATAGAAATAGTTTGCCTTGGTCATTCGAGTTTTAAGCAGTTATTTTATAAGATCT	26874	A_95_P124027	DV999471
27591	325	51	877	CTTGGAATTGTTATAGATGTCAAAATTTGAATTCCTTGGGGATCTCATTAGCATTATC	26876	A_95_P013331	DV157743
27592	325	52	122	GTTAGTATCTCAGTGTTCTAGCCTGTGTATATTGTAGCTTTGGGATGATACTTTGAGA	26878	A_95_P140327	EB444281
27593	325	53	2607	GCTTCTCCTTCTTTATCCGGTGTTTACACTAAACCAATAAATACATGACATGTCTTTTC	26880	A_95_P199692	AJ966362
27598	325	58	945	GTGCCAAGTAATGGAAGACTTCACCTGAACATTCTTCCAAATTGTAAGTAAAATGAA	26890	A_95_P019396	TA18614_4097
27599	325	59	788	GAAAAAACAAAATCGCTTACTAGCAACTGAGCTCGACGAGAAAGTATAGTGAGTCA	26892	A_95_P226029	EB450197
27600	325	60	887	TATTTCTGATGGACATCCTAGGTGAATTGTTGAAAGCTTGTTTGCTTGCCTGTTGTAA	26894	A_95_P205862	EB425041
27601	325	61	1404	AATTTTCAACTTCACATGTGTGAGATGCGAGACCATGAGCAGCCACAGATGCACAAT	26896	A_95_P162012	TA13109_4097
27602	325	62	281	CCAGAAGTTCTTTTACCGAATCAAATTGTACTCCAGCTTTATTGTAATTGGTAGAAGG	26898	A_95_P134287	EB436480
27603	325	63	132	TTTGGGATTGTATCCTTATAGTGCACTTTGAATTGAATGGAATATGGTTTTGGACCTC	26900	A_95_P095068	BP532999
27604	325	64	1134	GAGGATTCGGTGTTTGTTTGTCCTCTCAACCTTCGTTATCTAAATTTCACCAAATTTTT	26902	A_95_P016881	TA11996_4097
27608	325	68	746	ACATGGTACAAACCGCTACAGCACATTAAAATAGCTTCTGTATGCACGTTGGATTGG	26910	A_95_P136392	EB440149
27610	325	70	744	AATCCTTGGGACAAAAAAGCCAAGTCTCTCCCAGATTTGGGTGATGAAGATTACAAA	26914	A_95_P125707	EB424778
27613	325	73	731	TGATGAAAGAAATAGGGCAGTGAGATCGTCAATCAATCCAGATTCTGATTCAGACTG	26920	A_95_P250652	EB677239
27617	325	77	784	TCTTTTGGTTCGGGTACTAATTTCTGCCTTGGTCACGGAGAACAGCACAATGAACTTC	26927	A_95_P128332	EB427969
27619	325	79	554	ACCTGCGCTTATGGAGGCTGAGAATTGTTCTATTCAATAGTTGTTATGACTGTTATTA	26931	A_95_P053396	BP133165
27620	325	80	827	CTGAAGGCTTAAAACTTTGTTTTGAGGGTAAATTGACAATCTTCCTGAGTTTGAGTGT	26933	A_95_P179192	EB678033
27624	325	84	1850	CTGATTGTTGAATACACTGTAATAGTGGATGACGTTCTTAGCAATCCCTAAATAACAC	26940	A_95_P208967	AF426837
27629	326	4	703	GTTGTTATCCTTTTCCAGTTCCATCTATTTTGCGAAGGCTTAAAATCTCTGATGTCCTT	26784	A_95_P020306	EB682996
27631	326	6	1199	CTGAGCTAATGAGAGCCTAAGATATGTAACTGTTCTACGCAAGGATTATTTAGAGTA	26788	A_95_P029471	AF205130
27633	326	8	731	TATCCACTCCCAGTTTCAGATTTATGTTAAACGGCAAATGAAGGGTACTATGATTCTT	26792	A_95_P115527	DV157790
27634	326	9	747	TTGGCCACAAGCTCGTCAGCCTTTTAGCTCCGAAACCATTGAGTACATAAAATCACTT	26794	A_95_P130892	EB431016
27635	326	10	443	TTGGATAATCAGATCCGGCTTGTTCTTGAAAGTGGCTCTGCATTTGGGTGAGAATAT	26796	A_95_P179837	TA12595_4097

27638	326	13	938	CGTTTGTACTAAATCATATCAACTTATCATGGTCTGTACACTGTTGTATTCTGTGCACA	26802	A_95_P268186	DV999821
27639	326	14	671	TTGCCTCAGAAACGGCAGATGCCGGTTTTGGATGATTCGTATTTCAGGAGGAATTAT	26804	A_95_P121317	DW001325
27653	326	28	796	CCATGAAGGAATTTATTTTTTCTGGAAGACTGGATAATTTATGCAGTTCATTCTGCTC	26832	A_95_P186467	EB679484
27658	326	33	460	CCTTCAACTTTGCAACATCAGTGAGTACGTAAATTCATGTTTTTTCAAGGGTAGTTTT	26842	A_95_P068160	BP137065
27659	326	34	1629	TTTGCTGTAGGGATGGTTTTCCTATTAGTCCTTCGACAAGTTTTGTATCACACACGGT	26844	A_95_P022201	TA16637_4097
27663	326	38	704	CGCAGACCCGATTTCTCCTTCTATCTCCACTTATTATTCCGCATTTTAGACATATTTCTG	26851	A_95_P271841	EB679603
27665	326	40	2456	GGAGAGCGAAACATGCTGATTGTCATTCTGAAGCTTAAAAAGTTAATTCCTCTGCAA	26855	A_95_P203127	AF435450
27668	326	43	726	TGAGAACAAGACAATGACCCTCACAGCACATGAAGGATTAATTGCTTCCTTGGCTGT	26861	A_95_P195402	TA16107_4097
27669	326	44	799	ATTGTGGATGGTGATAAACCAACAGCGGAGGAGTTTCTGCAAAATCTGGCAGCAGT	26863	A_95_P189877	EB426728
27670	326	45	143	CTGACTCAGATGGTAGTGGAACCGAGAGTGGAGAAGAATTTACTGATGATGATTAT	26865	A_95_P118742	DV161799
27671	326	46	262	GGACCTGTTATGGTTGTCAAAAGGTTTAGGCAAATGAATAATGTAGGCAAGGAAGA	26867	A_95_P033036	EB425857
27676	326	51	504	CCAAGAAGAATTTCTGCTACAGGAACAGGTATAGGTTTAGACAAATAGGTTTCTCTT	26877	A_95_P021271	BP526268
27677	326	52	760	GCTTGTTTGTGCTTGTGATGGACATTTATTTTGGGTTATCTTTCGATTTAGTGATTCCA	26879	A_95_P019211	TA13400_4097
27678	326	53	794	CTTTAGTAGTTCTTGTAATGGAACATCAAGAATTCGGGCATTTCTGTACATGTATCAA	26881	A_95_P136487	EB440252
27679	326	54	330	GAGATTCCATCCCTTCGGATCGTTGCAGAAGCTGAAATTGATGATGATGAGTGGGTC	26883	A_95_P197102	EH616530
27683	326	58	694	AAGAATGCCTGCTCGTAATGAAATACTTGTCATGGTGTCTCTACCGAGTCCTTTGGCT	26891	A_95_P241480	FG636894
27686	326	61	1404	CAATTGTTGCCGGAGCTTAAAACGCATATTATTTTGGTAAAACAGAAGTTTTGACAA	26897	A_95_P179067	TA12420_4097
27687	326	62	109	CTACGCAGAGAACATGAAAACAGAGGAAAAAGCCCCTCAAATGGGATTGTTTATCA	26899	A_95_P088588	BP530140
27692	326	67	709	CAACGCACCTGTTCAAAGAAAAGACATAAGGGAGACCCGCTCTCATTTTACAACTTT	26909	A_95_P213602	TA20083_4097
27694	326	69	511	GTATGTCAGAAGTAAAGGCTATCGACTGCCTGGCTGGTTGTCAGGTTCTTTCTCATAT	26913	A_95_P274758	AM843365
27696	326	71	473	AGTGTTCGGTTGACTGCATCACAGGCAATGTGAATTTATTTTCTAACTTTTGGCATAT	26917	A_95_P072470	BP525968
27697	326	72	153	CGGTCAAATTTGTTTGTTCCTGCTATTAGGTATGTAGCTATGACTTTGTATGTTTCTGT	26919	A_95_P128682	EB428430
27698	326	73	639	GATTTGGCTAATAAAAGCTTGAGAAACTTCGTCTTTGTGACATTGTGGGTGTCATTTT	26921	A_95_P010326	DW004446
27701	326	76	290	ATTGTTTTACAACTCTGTATAATGGCCGAGCTAATTATTCAACTGAAGAAACTTTGGC	26926	A_95_P133087	EB434177
27705	326	80	393	ATTTCTCTTCACTGTCCGCTGATGGTTGCCATCCCTAACCAGACTCACATTAGCTAGTT	26934	A_95_P081780	BP528348
27709	326	84	242	GATGAAGTAAGAATGGAAATTTTTGGAAGTGTCTTGGAAATGCAACATTGAAGATC	26941	A_95_P143127	EB446468
27713	327	3	731	TTGAACCTCTGTAATTCCTATCACCATGAGTTGCTGCAGTAAATAAACATTTTGGAAC	26948	A_95_P003416	TA12319_4097
27715	327	5	809	CATTATGGTTTTGATTCGGAGGATGAAGAGGGTTTTGATGTGAATGCGATGAATGG	26952	A_95_P229935	EB428047
27716	327	6	1125	TAATGTTTATATTTGATTCCCGTACTTCTGGGAAGGGTTTCTGATTTCAATCTGAGTT	26954	A_95_P186072	TA14048_4097
27719	327	9	546	TTGTGCCGTTCATCTGTTGTAGACCTTGACCGAGCAACTTTAAATTCATTTCCTCTCTT	26960	A_95_P212282	TA19800_4097
27722	327	12	906	GATCGTCCTTGAGCTTTATGACTTCATATGCTGTACTCTTAACTGAAGCGAATTATTG	26966	A_95_P264306	DV162499
27726	327	16	306	TTACATTTCAACCCACTATGGTGCTCATAGAAATGGAAATTTTCTTGCTGCTGGAGCT	26974	A_95_P158032	EH616096
27734	327	24	113	AGCATTTTTCCTGTTTACAAATGAGCGTCGCGCTGCTCTACTTGTTGAGACCAAGAAT	26990	A_95_P070685	BP192699
27738	327	28	710	CTCTTAACTCTTGTTACACAGTTAACCCCCTTTTGCTGTTTTCTCATCTATAGTTAGAA	26998	A_95_P265561	FG642716

27743	327	33	120	AGTTGACATGGATAAGGAATTCGCCACACATTGAAAGATTGGTGGATGAGCTTGTTA	27008	A_95_P154692	EG649709
27746	327	36	811	TTACCCAGGTTCTCTGACTCACTATACCAAGAATGGGGTTTCTTGAAACGGTTGAGTT	27014	A_95_P201062	TA17344_4097
27747	327	37	445	TAATGTACAAGCAAGTGAGACTAGTCTCGGTTGCTGATTGATTCAGTAAGACTGTTT	27016	A_95_P030711	CV021010
27748	327	38	147	CACTCGAAGCTGTATCCTCGGATGTATGTTTGCAGCTTCTGTATTTTATTATTTATTCC	27018	A_95_P100313	BP535318
27749	327	39	760	ATTATATTATGAGCAAGTGCCCTGCTTCTCCATTTTCAACCCTAACCAAACTTTCATCT	27020	A_95_P163137	EH622111
27751	327	41	617	ATTATGAAGACATGGGTATACCTAGGGAAATTGCAAAACTCGGGGTTAGACAAGGT	27024	A_95_P022816	FG161776
27760	327	50	637	TCTCAAAATCCTATGACCAATTCGGCCAATGCTGCAAGTAGTGGTCAGAATGCTCATG	27042	A_95_P128162	FG163422
27768	327	58	615	GATTTTCCACATGTACTGAAGGTTTAGCTGTGTTAGTTTGGTCTGGTGAAGTCAAATC	27058	A_95_P043976	BP130759
27769	327	59	464	ACTGTCCCTTTGGCTTATGCAAAAATGGTGAAAAAGCTCAACTTTTGTGGTTGAAAC	27059	A_95_P157787	EH615819
27770	327	60	737	CAGGAAAGAAAGATGAGCTTGTCCCAAGTGAAATTGTGAGTCGATTCGCTGAAGCT	27061	A_95_P247212	EB429241
27772	327	62	695	GTGATCTAGTTTCTTGTGCCATTTGCACGAGAAGATTAGAATGTCTGAACATTGTGTC	27065	A_95_P305648	FG635815
27776	327	66	556	CTTGCATGTACAACCTTGATTGGGACCAGCCTTTTGAGGCAAGTCTTGGAAGTGAAA	27073	A_95_P208892	TA19070_4097
27777	327	67	246	TGATTGCATTGACGTTTATGCATTTTATTTGAGACGGATCGTTATACAGATTTTTCTG	27075	A_95_P151727	EB681975
27778	327	68	864	GTCAACAAGTTTGTTGACGTTTTCTGACATTTTGTTCTCCTAATATAATCAGATTGGTG	27077	A_95_P224067	EB451766
27779	327	69	371	AATTAATTTCCGCGATTAATCACTGTCACAAAATGGGGGTGGCCCACCGGCGATATT	27079	A_95_P294033	FS407656
27781	327	71	804	TCAGATCTGCAGATGGCACCCCTACTAGCTTCTTTGAGTATCAATTGAAAGGGTTCTG	27083	A_95_P024211	TA17379_4097
27783	327	73	452	CAAGAACCACTGAAAGGGAGTTGATTGAGGCTTGGGATGTGAAACTGTTAGTCAAT	27087	A_95_P007776	EB429702
27787	327	77	507	TAGGAAATTGTTGCGAGAAAATCTGTTCACCAGTTTTTCTTCGGGCTGAGACTTCAAT	27095	A_95_P164097	EH623231
27791	327	81	673	GATCTTCATAGGTAGATTGGCGGATACTTTAGCTGCTTTCTTGTTTCCTTGATTTATAA	27103	A_95_P017876	TA15235_4097
27792	327	82	726	CGCATGCTATCTGTTATTTTGACAGCATGATTGGTGTATTATTTCTGGTTTTACTTGCA	27105	A_95_P197477	DW001454
27795	327	85	889	AGGTTTCAGTGAAGATGAGGATCACCTTGCTATGATGATGGAGCTTCTAGGAAAGAT	27110	A_95_P289938	DV161437
27803	328	8	745	GTTCCTCAGAGAAATTGCATCTCATGTATCATATTTTGCGAGTAATGGTTGTTGTACG	26959	A_95_P027361	TC51269
27804	328	9	357	ATGGGCTGAATGAATTTGTTCTAACCTGTGTTGCTTTAACCCCAGGTCTGAATTGTTA	26961	A_95_P102632	CV016115
27805	328	10	914	GAAAAGTACAGCTATCCAGCTTCCTTTGCTGTCTGTGAAGGGCATAGCTTTTGTTTGA	26963	A_95_P193472	TA15679_4097
27813	328	18	803	TGCACTTTTGATACATGTTTTTCAGAATTTGATGCGGTTTAGGAGTTGTTGGTTCTGA	26979	A_95_P313158	FG155183
27814	328	19	661	GTGTGAAATTGGTTCCAGGCACTGTTAAGAAGGCGAAGACAGCCATGAATTTGTTCA	26981	A_95_P291683	FG639253
27816	328	21	1063	CATACCTGGTGCAGTTCTCAAAGGAGCTAAAGGTCTGGCAATATTAACGGTTGCAAA	26985	A_95_P200207	TA17160_4097
27821	328	26	619	CGTTTATTTCATTGGGAGGCTGTCCTTTCTTCTAAAACAAAAAAGCCCTCGACCACCA	26995	A_95_P099003	BP534727
27824	328	29	224	TTATATTGTAGTTTCAGTCGTTCAGACTGTAGCAGCACGAAAGTGACTCTAAATTACT	27001	A_95_P001216	AJ632923
27826	328	31	592	GTTTGTGCAGTGAAACTAAGACGGGATTGTATTGTTGTAGTCCTTGAACACAAGATA	27005	A_95_P127702	FG167680
27827	328	32	1928	GTACAACATTTTGGGGTTTGCCATCAAGAGACCTATTTGGTTATGTTATTCTTCGTTTT	27007	A_95_P208847	AJ577853
27834	328	39	1144	GGCATTGGTTACGTGCTTTGTTTTAAGACAGTTGTTTTTAGCTGTTGGTTTTATCTGA	27021	A_95_P026996	TA12511_4097
27836	328	41	1654	TAAGTTTTGCTCGCGACCATTGAAAAGCTTATACTATGATTTAGACCAATTTGTGTTT	27025	A_95_P014906	TA14747_4097
27837	328	42	543	ATTCTGCTCTCTTGGATAGAAGAATACTTTGCCCTGTCTTGTTCAAGAATTTATGAGA	27027	A_95_P218092	EH617170

27845	328	50	702	GTTTGTGCTAGGTCTAGATGCTTTTAAATGAGCAACGATATCAATATGAAAGATGAT	27043	A_95_P134642	EB437215
27847	328	52	653	CCGAGCACGATGAATAGTAGTTCGCATTTTCAGAATTATAAAAGGCTACTAATGTTG	27047	A_95_P195477	TA16125_4097
27849	328	54	826	TGAAGCTAACAAATCTAGGGAATTATTACATATACAGGGATTAAGGGCAAAAGTCCT	27051	A_95_P224752	EB440533
27850	328	55	569	TCGATTGGCATTCAACGGGAATCTCAAATTTCCTAGCAAGAATTTCTTCCTCCTCTGG	27053	A_95_P145002	EB448549
27856	328	61	261	GCTGCTTTCGTTCTTGCATCTTCAATTGACAATAAAGATAGCTGTGTGTTTTGGTCTT	27064	A_95_P093568	BP532320
27859	328	64	701	TCCTCTAGATCATCTCAGCTCCAACCGGCCTCCTCCTAGTTGAAATTTTTAATCTTTTTT	27070	A_95_P136522	EB440300
27861	328	66	573	TCTGCCTTAGCTCTGGGTATATTGAACTTCCTATGGATATTTGATGGTATTTCAAATC	27074	A_95_P000886	TA13432_4097
27865	328	70	761	CTACGACGTTTCATGCATAAGGCATTGTCTCGAGAGCATTATCTATAGGTACTAATG	27082	A_95_P259881	FG642013
27871	328	76	332	ACAGCTTTTGCTTTCTTGTGTTAGAATGTGCTCAAGTGAGATTTTGCTACTTGGAAGA	27094	A_95_P133582	EB435213
27873	328	78	935	CAGATAATGAACAAGTGCAGTAACTTGTCACAGTAACAAAGCGTGTTGCGCATTTGG	27098	A_95_P015571	TA15278_4097
27874	328	79	1101	CTCTTGATGCACAACCAATGTTATGTAGCAATTGAGAGTTAATGACGTTGAGCTTTA	27100	A_95_P218042	TA21085_4097
27875	328	80	726	TACTCTGTAGAGGATTCGATTTTTCCGGGGGCTATATAGTGGAAACTTTATGTTGTTG	27102	A_95_P219307	TA21368_4097
27879	328	84	150	AGGCTCTCCTGTTTGAACTATCTCGCGCAAAAGTTTTATAAAGTTTTCGAATCTATTTT	27109	A_95_P141367	EB445112
27880	328	85	269	ATTATACTGGTTTGCTACTGCCTGTGATCGGATAATGGGATATGGATACACCGTCTG	27111	A_95_P166312	EH663885
27882	329	2	776	TGCTATCTCTTGTATACTGCAAGTGAAATGCTTCTACTAATATCCAGTATTGTTTCATC	27114	A_95_P246902	EB437920
27887	329	7	1258	GTTTTTGGGACCGGTGATTACTGGCATGCTCCTACTATAACTGCAAACATGGCATTTG	27124	A_95_P013856	TA16537_4097
27888	329	8	659	TTTTGAGGTATGCATCAATTTGCTAGAGTTTGAGCATGACAAATACCCCAGGACAAT	27126	A_95_P125047	DW004864
27890	329	10	453	TCGAGAAATTAAATTTGAAGGCAAAGTGTGTCGGCAGTGGGCGAGGGAAATTGGTT	27129	A_95_P105897	CV017662
27894	329	14	402	CTAGTTTATTAGGTACTTGTGTCTGTTGAAAACAGGGGGAAATTATGGTGTTTAATC	27137	A_95_P107392	CV018347
27895	329	15	337	TTATGTACCATTCTGCTATTGCATCTCGGTCCGACGTACGATGTTTCAGATCGGAGAC	27139	A_95_P103297	CV016450
27896	329	16	755	CTTTTTGGGGCAGCATGGAACTTGATGAATTAGATGAAGCTGATATTGAAGATATAA	27141	A_95_P236299	EB448110
27899	329	19	406	TGAGATTGAAGGGGAAATCGATCTTATGAAGTAATAAGCCATATATGCAGTTCCTTT	27147	A_95_P209367	TA19174_4097
27900	329	20	1228	TTGATGATGTATTATGATTTTCCAAGAAATGCAAACTCTACCCTTTTTCACCTTCCCCA	27149	A_95_P190047	TA14923_4097
27901	329	21	629	TATTAGGAGCATGACTGGAGCTTTAATAGGCCAGAGACAGAAAGTGGATTTGTTAG	27151	A_95_P161667	EH620334
27902	329	22	714	TCACAGTGGATATTTATTACCCCTCATGACATCAGTATGGTGAAGCAGGACGAGAGG	27153	A_95_P269901	FG642339
27903	329	23	279	AGGATATTGGAGTCCAGAACTCAAACTCTGCTGTGGGCTGCTAAATTCAAGAAAGA	27155	A_95_P070105	BP192521
27906	329	26	704	GCAACCTATGGGATCTAGGTGCTTTCTTGTTGCTGCCTATGTGTAACTTTATCTTATG	27161	A_95_P123442	DW003300
27907	329	27	822	AAAGGGATTGAATCCTGGAAAGCATATTCAGAATATCAAGCGTCTGGAGCTTGCAT	27163	A_95_P126817	DV999762
27909	329	29	564	AATTGTGGAGATTGGTTACCTCAATGGACTTTTCGTGCTGGCTCGTTCAATTGGGCTT	27167	A_95_P148972	EB678581
27915	329	35	844	TGGCAATTGCTGGTGGATTCTTGATGTTATTGTAAGGAAAATGATCTTATGGGGGAA	27179	A_95_P003451	EB450812
27918	329	38	700	CAAAAGAAACATTTCACCACAAGAAGCTGAAAAATATGCTCCTGCTCATTTTATTGAC	27185	A_95_P292708	EB428200
27922	329	42	582	GCTGAGAAATGATTGTAAAAGAGAGAGGTTGTCTTGTTGATTTCTCTTCCATCGATT	27192	A_95_P017511	DV999315
27924	329	44	402	AGTTTTGTGCCATTATAAATCCTCCTCAGTCAGCCATTCTAGCTGTTGGGTCTGCTGA	27196	A_95_P186877	TA14222_4097
27942	329	62	643	AGGCGAGGTTCTTGAATAACGTAATACTGGTTGGTCAACATGGCATTTTATTCCCCT	27232	A_95_P288618	FG638803

27946	329	66	497	CTGGTAGAGTAGATCATTTGACACGGGTGTTTGTTGCACTCTGTACAATATAGATCTT	27240	A_95_P214687	TA20316_4097
27948	329	68	132	GATGATGTCGACTAAGCTGTTGGTGTTGTTCCTCTTCTGTTTTTTGTTTTATCAGTTATT	27244	A_95_P112292	CV020612
27950	329	70	472	GTTGCCTATTTGATGTTGCTCTCAAATTGCCTTCCTACATGAAAGCATAAACGGCTATT	27248	A_95_P162237	EH621129
27956	329	76	566	AATTGAGCATGTTTACTAGAAGTCTATTAATGAAAAGCTATGTCAGGAAAGCTGCTCT	27259	A_95_P139722	EB443604
27961	329	81	724	ACTTTGTACAATGGGTGTATCTGTATGTCAGTGAGTTGGAAGGAATTAAATGGCTTTT	27269	A_95_P119442	DV162658
27964	329	84	683	CAATGATTCATCCTTTATTAGAGTACTTGGATCCTTGGGTTGCCGTATACTTCATTTTT	27275	A_95_P001641	FG184528
27974	330	9	728	CAGAGAGGGAGTACTTGTATTTGAGGATGAAAATGAGGCTGCAAGATACTGTGACTT	27128	A_95_P146317	EB450322
27975	330	10	167	TGGCACAGTTTGGTCATGTACTGACTGTTGAAACTGCTCTCTTGAACCAAATGATTGT	27130	A_95_P122472	TA18158_4097
27977	330	12	702	AGAGTGCACAAGCAACACACGCGCATCACATATATCAGTTCGATTTATTGATTAAAA	27134	A_95_P303498	FG198624
27978	330	13	1014	CCAACCTTCATAAATGGAAGAGGAGGTCCATTTGTTGGCTATAGTTTATATTTTTACCT	27136	A_95_P008961	AF068724
27979	330	14	310	GGCACAGAGATGGATACTTCTAGGAAAAACAAGAAGATATCTGCGAACAAATTGGA	27138	A_95_P081650	BP528314
27982	330	17	752	CTTCGCTTCAGAGATACACTGCAGCTTGACAGGTGGCAGTTATCTGTTTGAATATATG	27144	A_95_P146832	EB450977
27983	330	18	1740	ACTCTATCCTTGATTTGGTTCAGTTTGGAGGAAATTCTTTAGACGTAAGAACTTTGCC	27146	A_95_P023621	TA12387_4097
27985	330	20	697	TAAGTGACAACAAGTTTTTACCTGCTCCGGCATTTTGCACTAGAAAGGATGTTTTCAA	27150	A_95_P016841	TA16086_4097
27989	330	24	759	TTGCTAGATGGTCGCTGCATGGCATGTTAGACTTTTGAGGTTGAGCCTAGCAATAGT	27158	A_95_P013156	EB678699
27992	330	27	225	CTGTTATTAGAGTGTGATGTTCTGAGTTTTCTGATACAATTACATGCTAGCTGCTATGT	27164	A_95_P147057	EB451298
27994	330	29	398	TCGATGCTATCTGAAGGCATGTATGGTGACTATACCACATCCTCAAGGACTTCAAAGT	27168	A_95_P279238	AM816248
27995	330	30	902	GATGATTATGGACCTTTGTCAAGGCTAATTTTGTGATAGGTTTCTCTTTTAGTTGGAT	27170	A_95_P024436	TA15458_4097
28004	330	39	661	CATATCCATTTCAGGTTGTACGATCTCGATTGCAGCAACGACCAAGTACAACTGGAGT	27188	A_95_P135477	EB438958
28007	330	42	562	GTATTTGAAGTAATCTTCATGGCAATCCTTATCTTCGTCACACTGACATTCCTCCATGG	27193	A_95_P223532	TA22271_4097
28009	330	44	198	TTGTCGTATTGGTTGATATTGGCCTTTGTATCATATATGGGACAGTAATTTATTCGAGT	27197	A_95_P112497	CV020707
28010	330	45	322	TGGGTACAGAAAGAAGTTCTATGTACTGCAGTACACCCCTAGTGTGCTTGTAACATCT	27199	A_95_P092023	BP531608
28012	330	47	735	GCCAACACAACATTAACCGTAATAAAACATAGTCCGTTAGCATTGCTGGTTTCTTAAA	27203	A_95_P004446	TA12140_4097
28013	330	48	673	ATCCAGTGTGTCGATGCATTCCAGACCTATATCTTGTATTCGTTTATATCTGCAAGATG	27205	A_95_P216062	TA20623_4097
28015	330	50	843	ATTGAGGCTCTGTGTGCCAAGACATACGAGGACACAACTCATAAACTCCAGGATATT	27209	A_95_P128662	EB428409
28017	330	52	274	CTTGTGACACCGGATTTTGGGATGATTATGGGTTGCAATGTATTGGAAATTTTTAAA	27213	A_95_P132492	EB432990
28019	330	54	485	TTGTTCTCTTGGGTCTCGTCTAGTTGAAGAAGAAGAAGCAAGCAGCCATAGATATCCT	27217	A_95_P276198	AM785983
28020	330	55	931	TTTACACTACGTCATCTGAGCAGCTTGTATTCTGCACCATGCAACGATGAACCTCATT	27219	A_95_P013801	EB425369
28023	330	58	337	AAGAATTTCGAGCGCATTCTGGTTGTCATTTCACACTCCCAGGATTTTCTCAATGGTGT	27225	A_95_P070070	BP192513
28029	330	64	858	GGGCAGCATGATCTTTGCAAGATATATCCGAATGTGTATGTTATTCAGTCGACTTTCC	27237	A_95_P139142	TA18679_4097
28031	330	66	1233	GCTCGGCTGATAAAGATTGCAAGGATGACTAAAGAACTGTTAGTACATGTTTTAAAA	27241	A_95_P212077	TA19752_4097
28035	330	70	671	CTCTTTATTTGGATCAGCTGGATTATGTAGGATAGAATTGTAAATTTACAGCACAGG	27249	A_95_P283888	FG637420
28041	330	76	316	ATGGTGTCATTTGTAAATATACCATCTTTGTGATGATCCGCGATCATGTTACAGCATT	27260	A_95_P140107	FG625819
28043	330	78	698	GCCCACAATGACTTACTTTCTGGAAATCTGATGCTTAATGAGGATAAAGGAAAGCTGT	27264	A_95_P123057	FG169254

28048	330	83	865	GACTAGTTGAACCTTAGAAATTCATTTCTTCTTTTTCGTGCCAATCCGGTAGTTTGTTT	27274	A_95_P018831	EB679147
28054	331	4	425	AATAGTTTTGATGGGCACCTTTGTTCGGAAGTCACCCAGGAGATAGGATTTTTGCCT	27285	A_95_P130957	EB431094
28057	331	7	1461	GAGTCAAGTGTTTGCCTACCTTCTTGCCATTTTTGCTTATTTTACAGCTATTAGATTGT	27291	A_95_P016921	TA12917_4097
28060	331	10	853	GTTGACTAGCATAAGTTTATGTAGCCTTCCTGCATTTGATCTTTAGGAAAATCTCTTAT	27297	A_95_P181102	EB447626
28062	331	12	339	CTGGTATATCTTACCCGACTTTTATGTCTTTTTGAATCTTTTGGAGAGGTTTAATTGTG	27301	A_95_P205147	TA18218_4097
28063	331	13	831	TTATGAATCATTTGTCCTTTGCTTTATCACTATTTGTACAGGGATTTGTTTGGGGAGG	27303	A_95_P204972	TA18180_4097
28064	331	14	625	GTTTCCATGAGTTACTCCCCTTTGAAATTTACTTTTGGTTGAAATATTTGCAAAGCACC	27305	A_95_P039186	BP129482
28069	331	19	641	AAGAATAATTTAGAATGAAGAGTGAGGGTATTGGTTTTGACGGATAACGTGGCCTG	27315	A_95_P004501	EH620311
28070	331	20	449	CATTAGTCCGTTTGCTTCTTTAAGATGATATTGATCATCTGTTGCATACTCACGCTTCT	27317	A_95_P026746	TA16770_4097
28071	331	21	596	ACGCATGCTTACAGAAATCAAGTTTTAATTCGTGCTACTGTTGTGTTAGGGTGCAATG	27319	A_95_P185492	TA13925_4097
28074	331	24	527	AAGTTCTGGTTGCGGATTTGCAATTTTTGAGGGATCAAGTGACAATTACTCAGGTCA	27325	A_95_P156712	DV158890
28083	331	33	868	TTGTTGTAGGAAAGCCCTCAACCTTCATGATGGACTACTTGGCTAATGAGTTTAACAT	27342	A_95_P245692	DV999727
28086	331	36	407	TGACAGAATGGAGTTTAAGGGGACAGATGATTCAAATGCATAGAGACAACCTTTAT	27348	A_95_P088443	BP530065
28089	331	39	580	GGGATATAGATACAGAATTGTGTACAACTATCCAAGTTCTGCTAGCATAAAATTGAG	27354	A_95_P046486	BP131409
28091	331	41	164	CGTGTATGCTCAAATGATTGATGATGCAGACGGTATAGAAAAAATAGAGAATCTTCA	27358	A_95_P070075	BP192515
28099	331	49	1211	GTTTTCAGGATCTTCACTTGTCTTAACAGCACATTTTGAAGGCTAATATCTCTTCAGTT	27373	A_95_P019041	TA14074_4097
28104	331	54	748	TGGAATTGATTACTTGTCGGTTGCTGCATTTGATGATTTGATACCTTTCCATCTTGTCT	27383	A_95_P295663	FG194438
28114	331	64	788	TATCTGCTAGCATGTCGACTTCACATAACAATCTTGTTCTTCGAGCCATGATGACGGG	27401	A_95_P298193	FG138924
28120	331	70	818	ATTCTGGGCAGTCAACAGTGTACAGTTTGCATGCATCAGCTACACTTCTTTTCCTGCA	27413	A_95_P242852	FG146943
28122	331	72	717	CCCGATAATTATGTTTGTTTCGTAGCCTTTCTTAGGTAAGTAGGATTTGCTTTTATCCT	27417	A_95_P025036	TA15399_4097
28125	331	75	654	GAGGATTTGGAATCCAGGAAATCTAGGAAGAGGAAGAAATTGAGGTCTAGACGTA	27423	A_95_P120407	FG141664
28128	331	78	666	AACTGTTTTGGTAACGCTTAAGGCTCGTTCCTCCCCCTGTTCCATCCTAACTTTATTAT	27429	A_95_P089113	BP530351
28129	331	79	788	AGTATTCGGTCTTTTAGGTGATGTTAGAGTTTGTAATAGTCTAGTTATGTTTGCCTAG	27431	A_95_P202412	EB679032
28130	331	80	768	TTCCTGAGCAAGCTGAATTTCTGAACAAGATGATCATCAGCTGATGTTGGTTTATATT	27433	A_95_P231509	EB426608
28131	331	81	873	TGGTCATCCTGCAGGACTTCAAGTGGTATGATTTCATTTTCAAAATGCATAAGCTGTA	27435	A_95_P227689	EB681843
28132	331	82	321	CCCTGCAATTTAAAGTTTTATGAAGGAGTTTGAACACTGGGAGTCGATCTCATTTTCT	27437	A_95_P026901	TA18797_4097
28138	332	3	800	ATCCAGAGCCTGCAGCTGGGGATGCTATTTTTGTACGTATATTTCAGCGATATTTGGC	27284	A_95_P267526	FG145967
28139	332	4	781	CGAGATAACCGAGCTAAAAGCTGGCACTCATGTCTTTGCAGTTTATGGTGACAATTT	27286	A_95_P245222	DW000634
28141	332	6	845	CAGACATTGTGCTGATATCAATGATTCAGATCTCCAAAGCTTGGGTGGTGAGCTTAA	27290	A_95_P241085	FG163772
28142	332	7	472	TGGAATCATATAACTTTCTATATCATGTTTTTGCTACACTAGGATACCTGAGCTTTCCC	27292	A_95_P208487	TA18979_4097
28155	332	20	134	TGATATTTAATTCTTTCCCTTGTACAGAGGTTTAGATCAATGCCTGTACTTTGCCTTGG	27318	A_95_P141017	EB444816
28157	332	22	790	TTCTATAAGAATTTTGAGCCTCGTGACTGTGCACGTGATACTAGCGCCTTATCAAGAG	27322	A_95_P296278	EB451118
28163	332	28	809	ATCCTAAATCATTTGATCCAGAACAAGAACGAGTACTGCAATGGGAGGTGACCACCA	27333	A_95_P157192	EH615220
28164	332	29	750	GCAATCATCTTTACTTATTGGAAATATTTATAGTGTGACAGATACTTGGCCAAGTGCT	27335	A_95_P179977	TA12628_4097

28170	332	35	651	AAGAGTTGATTAGCTAAACCGATGGCTGTTCATTGGATGAGCAGTGATCAACTATTT	27347	A_95_P219497	TA21409_4097
28171	332	36	386	CTTAGCAATCCTTTTCCTGAAAAAGATCAAAATTTTGTTCACATATGGCATGGCTGTG	27349	A_95_P093638	BP532343
28177	332	42	670	ATTTGACGACATAGATAATGAGACTCCCACGGGTCAGGGTATACAACCTGAGTTGTT	27361	A_95_P020836	TA21361_4097
28180	332	45	610	GGACGACGACACTTTTATGTCTACAGCACCTTGAATTCTGTGTTAACAATATGTGTGA	27367	A_95_P139452	EB443209
28183	332	48	655	GGGATGGTCTGGGGTCAAGAAACCATCAACTGACAATTTGTTTGAACAAAAAAGAA	27372	A_95_P253164	EH614269
28184	332	49	408	TAATCTTTCTTTTGCATCCAAGCCAATAATGTAGTAAGATCACGCCCAAATATGCCTT	27374	A_95_P006706	CV019425
28189	332	54	415	GGGGGTTAGGGTTTATAGTGTATAGTAGTAAGTGATTGTAAATTTCATGTTTGTGCT	27384	A_95_P110157	CV019607
28190	332	55	513	AGCAGTACCAGATTTGACAGTTGTATCTTAATTGGGCTTTTGCCATGTTTTGTAACAA	27386	A_95_P121522	DW001601
28191	332	56	794	TAGTGTCCTAGTATATGGATCTCTTGATTGTAATGCTGTACCTGGGTCTGCCTACTCT	27388	A_95_P204912	TA18167_4097
28193	332	58	462	GAGGTGAATAATTTCCTCATATTTGACTTAAGGTGTTTCTCTGCAATATATTTGTCCTC	27391	A_95_P029901	BP129902
28198	332	63	983	GAGTGGACCATGGAGTACTTTTGGTTCCCTTTATACCTATTTCATTTGCCTTTTCATTC	27400	A_95_P028001	TA17514_4097
28200	332	65	432	AACGAGGCCTAGTGCTGTTAAAGTTTGCAGTTATATTTGCCTGAATTTTGTTCGTTAC	27404	A_95_P212192	TA19780_4097
28201	332	66	551	GTTCAGTATCTCCTTATAATATCAAACTATATGGAGTGGTTTATGCCCATTTGCTTCTC	27406	A_95_P182607	TA13260_4097
28204	332	69	678	TGATGCTGCTCACAATAATAGCAGCAAAAAGCAAATCAAGTGGAAAGTCTCGACAG	27412	A_95_P285478	TA15934_4097
28205	332	70	594	GTGTCTTTCAGCTTGGACTGCCCTTTCTGGTTTTATAATGTGTCCATAAATAATATAAT	27414	A_95_P257851	TA16849_4097
28207	332	72	847	TTCAAGTTATCATATCAAGCTTGATATAGAGAGTTTACTTGCGAGCTTAACCTGATAG	27418	A_95_P116747	DV159539
28210	332	75	598	AGGCAAAACTGGTTTTGGGTTGTTTTGCGCCCGTTTTAAGGACTGGGTGTAAAGATT	27424	A_95_P247552	DW004850
28216	332	81	765	TCCATTAACATCTGTGAAGACTAGGTTTTCTGACAATGGGAAGGTTGCAATGCTTTA	27436	A_95_P126197	EB425445
28217	332	82	160	CTCAGTCTTACGAGGAGAAAAACACGTGATTCGAGAAAATTTTTGAAAAAATCTACG	27438	A_95_P155142	DV999238
28225	333	5	748	GGATACTTTCAGGGTGTTGTAGTTAAATATTATGTTAACAAGAGAGTATAGCTTGCT	27453	A_95_P151402	EB681601
28228	333	8	773	GTAGGGAACTTGAGAGAAAAGTTAGGTGAGTTGAATATTACTGTGTGTTTACAGATT	27459	A_95_P149272	EB679093
28229	333	9	924	ATATGAATATCCAAGCATCTGGTCAGGCAGTTAATGAAGAATACCATTCAAGTGAGC	27461	A_95_P005041	DV159546
28230	333	10	483	GTAGGAAAAAGGTTACCTTACTAAGGGCCTTTTCAAGCTGAATGTAATAGTTGTTGA	27463	A_95_P209047	TA19104_4097
28232	333	12	1346	CATGCAAGCAAACCTGCCAAATGCTACTTTAAGTTTATTTCTAACCTCTTTCTTGTGAA	27467	A_95_P208072	EU375458
28233	333	13	451	GCGATGGTTTTTCATTTCTACTAATTAAGTCATTCATCATTTCTTTGCCACTGTAGTCG	27469	A_95_P021631	EB426729
28236	333	16	531	TTGTGTCTTTTTGCTGAATGTTAGGGTTAGTGATGTAAATCAAGTGACTTGTTTCGAT	27475	A_95_P195847	FG637321
28248	333	28	604	ATGCACTTAGGGCAGAACATTTGCTTTTACGGATATTATTAGCTTGTTGGACGAGTTA	27499	A_95_P308243	FG641761
28251	333	31	441	GCTTCAGTAGACTTTATCTGATGAAGGCTCTTCACGAGAACTGAGGAAATCTATGGA	27505	A_95_P155877	EG650306
28254	333	34	487	TCCGTCACTTTCATGTGTGCTTTTGTGGTGAGATGATTTTGATAGTTTGTTTTCTTGAC	27511	A_95_P125087	FG138878
28255	333	35	900	GTACTCACTTTAGAGCTTACTCTTGTTTTGCTCACTTTGGTACTTCTCTTCCTGTACTCG	27513	A_95_P215637	TA20532_4097
28256	333	36	2275	GGGCATATCCCCTACACAACGTCCTATAATTAAATTCTTTGAAGTTTTTTGGTCTTTGT	27515	A_95_P007311	AB063576
28258	333	38	409	CCTGCACGCTCATGCAGGATTTAATAAAGGTTGAAGTATCTAATGTTTAAGTGTGGC	27519	A_95_P110207	CV019622
28263	333	43	754	CAAAAAGGCAAAGGTTGTTTTTCGACAGATTCATGGAGCTGAGATCTGTTAAACCAG	27529	A_95_P119252	DV162351
28265	333	45	646	TCGTGTTAAACTTTTCACTAAATGTCTCTGTAACCTAAGTTCTGCCAGTATATTGGTTG	27533	A_95_P021001	TA14213_4097

28270	333	50	898	TGTATATTTGTGGCAGCCCTAACAACAACAGTAGTATTTGCAGCAGCCATTACCGTG	27543	A_95_P267691	DV161322
28271	333	51	599	ACCTGTTCATTTCCTTATCACGGTAACAACTCTTTTATGAATAGCTAATTTTTACCAGC	27545	A_95_P200632	TA17248_4097
28279	333	59	398	TGTACAGAATTGTGCATGAACGTGAATTGGTTTTCAAATGGAGTGCTGAATTTCTCCT	27560	A_95_P009356	TA15160_4097
28280	333	60	966	ATTTGCCTAATAAATGCCTTTGTGGCTCTCCGTTGCCGGCATGTAAATAATTCCGGTG	27561	A_95_P193632	TA15713_4097
28286	333	66	208	GACCCCATTAGTGGGATTTTACTGGATTGTTGTTGTTGTTTACACCACTTTGGTTATA	27573	A_95_P241774	AJ718624
28288	333	68	827	ATTTGGAAATGCAGCACTTTGCTTGCTGATCGAGCTTCTTGTCGATGCATGTCATCGT	27577	A_95_P231799	EB677988
28289	333	69	771	CTAGATATGTTTGTGTTGAAGGTCTGATATTCGACTGGTACTGTCCAATGATGGAGCT	27579	A_95_P145372	EB449085
28292	333	72	632	TAGGACTCATTCCGACTATTATATTGATCATCAATAAGAGGGATTTCTCTGAACTCTC	27585	A_95_P016251	TA12889_4097
28304	333	84	942	TGTAGGAAAGCATCTTCCTGTGATATATTCTAACTTGTAAAACTTAGCTGGAGTGTGG	27608	A_95_P207897	TA18846_4097
28305	333	85	862	GTAAGATTCGCTAATTTAATGTTTTATAGAGGTCATACAGTGGCATCTGCCGTTCTAA	27610	A_95_P148777	EB678277
28313	334	8	173	CCTCGCAGCTGCTTCCTTTCTTCTATAAATAGAGGAGTTTTCAGTTCATTATGTACATA	27460	A_95_P124012	AM789368
28314	334	9	1663	TATAGACAGCTATCCTTTTGATGTCTTTCAACAAACTCTATCCTTGATTTGGTTCAGTT	27462	A_95_P008426	Z48977
28319	334	14	358	ATGTTGTAGAATCCGACCCAGCTTTGGGGCATAAGCTATTTAACTCAGGTTGGAGTG	27472	A_95_P097603	BP534120
28320	334	15	876	GGTTCTCTCCTTATTTGTTCTTATTAGCTGTGATGATGTGATATGCATCTCGTTCATAA	27474	A_95_P014836	TA16067_4097
28321	334	16	797	TCGTGACTTTTTGTAATTCACCTTCTAACTGTAACTTCATTCTTAAGTGGAACCTCTCCT	27476	A_95_P187632	TA14389_4097
28322	334	17	470	TAGCGTCTACCGATTTCGCCATATCCCCCTTTCTTTTTGAGATTAGGATCTCGTTGTGA	27478	A_95_P225762	AM812458
28326	334	21	599	GCATATAAGCTGAAATGATCTTGGAAGTGGGAATGGGATATGGTAAATGGGCATGT	27486	A_95_P195002	TA16024_4097
28330	334	25	864	CTTTGCCTGTATGCTGCTTTATTTCTGCCATTCAGAGAGACCATTTATAGAGATAACA	27494	A_95_P213052	DV159396
28332	334	27	275	GCTAGTTACTGTCTGATGAAGGCGTGATTTTGTAGGTTGAGGTTGAAAGTGCTTTAG	27498	A_95_P054876	BP133552
28334	334	29	862	GTATTTAGACCAGACAATTCTCAAATGGGGGAACTAGTATCACCTCAAAATTTGTAC	27502	A_95_P029201	TA21982_4097
28339	334	34	552	AGAGTTTGGTGATGTAAAGAAGAACTTTTGGTGTAATGTTTTACAGTTCTGCATCTGT	27512	A_95_P001871	FG190411
28340	334	35	753	GAAATGTAAAGCAGTGACCAGAAAAGTCAAGTGATGTAGTTGTTTCTTTTTCTTTTG	27514	A_95_P009831	EB431310
28344	334	39	700	GCAACAATCACCTATACACATTCAAGTACTATCTACGTTTATCTTCTCAGGTTTCTTGT	27522	A_95_P131522	EB431843
28350	334	45	817	CCTCCAATATCTCAAGGACATTACAACAACATTTCCGAGCTTTGTCTTTCATTCAAGA	27534	A_95_P120027	TA13706_4097
28351	334	46	383	TTGTCCGCTTTGACTTTATAGTGAGCCCTTATATGGTGTTAAAAGAATTTAGATGGTA	27536	A_95_P108737	EH619918
28352	334	47	380	AGTCTGAACTCTGTTGTTGCTTTGCTCCGTTGTTGCTCGTCTCTACTATTGTTGTTCTC	27538	A_95_P089728	FS406815
28354	334	49	82	GCCTGTTGTATTTTTACCCAAAACTTTGATCTTGTTAGAATTAGGTCCCTTTTACTTCA	27542	A_95_P106557	CV017950
28355	334	50	627	GTAAACACTGGGTACCAGTTAGTTTTTTCCTTTTATTTAATCTGCTGCAGCTTATCTGT	27544	A_95_P027986	BP134686
28365	334	60	1047	CCTCTGTGAATTGACCTGGGTATTATGTTTGCTGTCTGTTATTTAAGACAATATATTTG	27562	A_95_P105997	TA12116_4097
28370	334	65	580	CTTCAGAGGCAAGCTCAAATGTGGTGAAATGGAAAGAAAAACTTATAGGAAACTTT	27572	A_95_P261801	BP133500
28371	334	66	829	ATGTCTTAGCAAGTCGTAGCTAGTTGTCTAGCTTTATGGTAAATTCTTGAGTCTTAGC	27574	A_95_P126137	EB425387
28373	334	68	525	GGTTTTCTCGACCTAGTTTATGTATGCATTGTTATGAATAAACTGGCTTCCATACAGC	27578	A_95_P273356	EB684135
28377	334	72	495	TGACGTATTTTGCTGGTGTATTTCAATGTATGTTGCTCATTTGCTGCTACAATTAGTGT	27586	A_95_P090858	BP531122
28381	334	76	567	TACGTGTGATGTGGTTTGTAAAGCACCTTTCAGCCGTAAATTTTTTCTGTTAATTTCAT	27593	A_95_P196787	TA16416_4097

28382	334	77	418	CCACTAAGCAAGTTAGCCATTCTATTTTCTCTTGTAAGGAATGTTTTGAATGGAAGCT	27595	A_95_P142207	EB445745
28385	334	80	360	TTTCCCGGGCTACATTGAACTGCATTTTTGTATTTGGTCTGCACTTCCTTGCTGGTTAA	27601	A_95_P299348	FG634412
28395	335	5	399	GTCCAAGGTTGAGGTGGAAACATGTTAATACATGTGTACACCCAAATATTTCGAAAT	27620	A_95_P139667	EB443517
28402	335	12	898	CTTCTGACAATGGCATACAAAGTGATCCAAACGAAAAGCTGAATAATCTCATCATTA	27633	A_95_P009171	TA15054_4097
28403	335	13	435	CAGTCACTTGTTCTGGGAACATAAACATGGATTCTGGTTGGGAAATTGACTGCTATA	27635	A_95_P240885	AJ717982
28409	335	19	791	GACATATAATGAACACACTACACTGCATACAGAGCTCCTGAAATGTGGATTTGTATC	27647	A_95_P310108	FG135039
28413	335	23	219	GACTACTGATGTATCTTGTCTGATGAAGCAGGTCCAGAGTTCTTGTGGAGAGAATGG	27655	A_95_P068305	BP137098
28418	335	28	245	GTTGGCCAACTCTTGTTATATCACTTCTTAAATACTGTATTATAGCATGCACCATTTGT	27665	A_95_P214282	TA20229_4097
28419	335	29	441	TGGCGAACTCCTTCCCGCTCGTTTTGTTACTGTCACTGTTTTCGTGATGAAATTTTCAT	27667	A_95_P030441	EH617488
28422	335	32	601	TTCCGGAAAACATTCTGGTATACGCCAAGCTATGTTACTCTTTCCAAAAAAGTTATTA	27673	A_95_P000666	EH619838
28423	335	33	839	TGAGTTTTCAAAGCTGCTGGACTATGCTGATATGATTAAGAGTATAAATCCTGAGAT	27675	A_95_P147727	EB452255
28426	335	36	416	ATGACTGTTGCTTTTGTCTCGTGGACACAGAACTTATCTCAAACTTTTCACCCAATTCC	27681	A_95_P098343	BP534427
28428	335	38	109	GGCTGAAGCGATGGTGAATCCACACATTCTGTTTGAAACATCAAATAATATATTCAA	27685	A_95_P019811	CV015942
28430	335	40	672	ATTGATATTCTGTATGTTATGTTTTGGCCACTGGAATGCTTTCAATTCGAACTAAGTG	27689	A_95_P018416	FG637372
28433	335	43	769	TCTGTTAGCTCAAGGTGGATTGGTGGAAGTTGAGAAGAAGAACAAGAAAAAGGCT	27695	A_95_P136077	EB439653
28442	335	52	876	TTTAGATGCAAAGAGTAGCTAAGATGTCAGCTCAGCTGATATTCAGTCACTGCGTCA	27713	A_95_P290088	FG160077
28443	335	53	768	TTGGTCCTACCATTACAAAGAAACTTCTTTGTGGCCGTTTTGAGCTTGACAAAAAGAC	27715	A_95_P297893	EH614413
28447	335	57	236	TAGCAGAAAATGTACCTCAATCAGGGCATCTCTATCACCCTCAATATTGGGTCTCGTA	27723	A_95_P156147	EG650439
28451	335	61	609	CCAACAATGCTTTGATTTGATTTCTCTTTTGGGCACTGCCCAATGATGTTTTAAAAGA	27729	A_95_P206722	EB447449
28455	335	65	556	CAAAGATCAGAGAAAAATATCCCGACAGAATGATGCTTACTTCTCTGTTTTTCCCGTC	27737	A_95_P220157	TA21550_4097
28460	335	70	800	TTGTTCGGTTTGAACCTGCGTTTAGAGGTCAATATTGAGGATTTGCTGATTATAAACA	27747	A_95_P247402	DV162530
28463	335	73	385	AGCAATAATAAAGGGAACACCAGAATTTACGAGGTTCGGCTAATTCTGGCTACTCCT	27753	A_95_P085785	BP529377
28467	335	77	304	AGATTGATACAAGAATGCTTTTTTGGGGGGTGGGGGTTAAAATCCTCCATTTTGGTG	27760	A_95_P095138	BP533036
28471	335	81	1102	CGGTATCTTATCCTACATCAACAAAGAAAAGAAATCACATTGCAACATTTAGGACTTC	27768	A_95_P200657	TA17254_4097
28474	335	84	516	CGGCGAAGATGGAGATGGAGATTTTGGTCTACCTAGATTTTGGTAGAGAAATCGAA	27774	A_95_P081360	BP528233
28477	336	2	743	ACTGCCAGTAAAGTGTTAATCACAGGTTGATTTTGGGTTGATTTCACATTACATTTTG	27615	A_95_P216472	EB440076
28480	336	5	242	ACAAAGCATGGATGCTGGTAGTTGACGAATGTTGCTGAGTCGTCACATTGTGAATGC	27621	A_95_P081250	BP528208
28487	336	12	492	CAGATCAAAAGTTTTATCCATGTCAGCACGGATGAGGTTAATGGGGAGACTGATGA	27634	A_95_P020096	BP128355
28490	336	15	415	AGAGCGAGCGTTCCAAAGCTAAATTTGGATGATGTCTTTGAGCAGAAGAATCAAATT	27640	A_95_P079030	EB677602
28495	336	20	764	TCATGTCGACTCCAATGTAATGATGATACACCTTTGCAGTGGAAAACATTTCCTTAAT	27650	A_95_P116382	DV159091
28496	336	21	399	ACAAAGATGGTGATGGCAAAGTTGGGGCTGAGGATCTTAAGAGTTATCTGAATTGG	27652	A_95_P025151	FS409302
28497	336	22	184	TATATAGTTCCAGTTTGCAGGGAGCTTGGAATTGGGATTGTTCCATATGGCCCTGTT	27654	A_95_P095478	BP533209
28500	336	25	801	GCTGATTGATGACGAAGTGGAAAAAGTAAGGGCTTTTCCTGTTGAACATACTGCACC	27660	A_95_P151722	EB681973
28501	336	26	1345	GGAGGACTTCCGTAGTTTCTTGGTGTTTGAAATTTTCTAAAGCTCTATATTTTTCATGT	27662	A_95_P007851	AY064253

28502	336	27	863	GGAGGATTCATGTGTTGCAGACATGAAAACGTAACTAAATTGGTCCTTATTACCTAA	27664	A_95_P219077	EB426145
28505	336	30	400	GCGGCTTTGTTCGAGTCGGTTTAAATTGTTGTAATCACTAATGTTTTGTTAATTGAAA	27670	A_95_P140737	EB444590
28514	336	39	885	ACACCCAGGGGATGCTGTTCATTAGGATCCTTATAAATACTTATTTTATGGGCGCGTC	27688	A_95_P258678	DV159903
28516	336	41	300	GATCAGTGTATGGCTTCACAGGATTATCGAATGGAGTAAAGGATTTACATCTTTTCC	27692	A_95_P026461	CV017453
28517	336	42	517	CCTGCGCTAACAGAGCGCATAGTTATTGTTGGTGTTAGAGATGATTCAAACTTAATT	27694	A_95_P029666	TA18039_4097
28518	336	43	321	GACAGCATAATTAGTTATTAGGCTGAAGCTGATCTTAGCATTCTTACATGTTATGTTG	27696	A_95_P155722	EG650229
28522	336	47	536	ATTTATCTGTCTGTCTTGGTTTATGGATACTTTGCATGAACCTATTGACGAGAACCTT	27704	A_95_P193652	TA15717_4097
28527	336	52	350	CAACTATTTGTTGGGGATGTTGTGGTTCTCAAGGACCCTGTAAAGTCAGATGATTAT	27714	A_95_P132497	EB432993
28529	336	54	537	CAAGGGAATGAAAGTCATTCTTGGTGTGGATGATATGGACATCTTTAAAGGTATTAG	27718	A_95_P058121	BP134392
28530	336	55	242	GGTCATGTTTTAGTACGTCCATAGAGAAAGCATACGGATATTTGTAGAGAAATGTTA	27720	A_95_P130497	EB430531
28531	336	56	693	GATGACTTCAATTTGTGCTAATTGTTTACTGCCTCTGTTTTGTTAAAGTGAGTTGCTTC	27722	A_95_P139382	EB443128
28535	336	60	558	TTTAATTGGCTTGAGCTGAATATCAGGTCCTCCTTGATTTGTCAGGACCTGAACTCGG	27728	A_95_P042871	FG642918
28538	336	63	1237	ATACTTCTTTTTCCGCTTTCTCTTGGGAGGCATGTATATTATATCTACTAGCTTATGGA	27734	A_95_P177507	X79675
28541	336	66	750	GGGATGTGGGGGAATATTGATTTGTTTCTAATTCCCTTGGATCTGTTGAAAATTGTTC	27740	A_95_P196072	AB041515
28544	336	69	157	TCACTGTGAAATAACTCTGACCGCTATCCGCGTTTTTAAACACCACTGTGTGATTTAA	27746	A_95_P093783	BP532408
28547	336	72	212	ATACCATTTGCTTCCCCTTTGAGCCATACTTGTTTCTTTCCTACCCTCTCTTGGAAAAA	27752	A_95_P224187	EB643483
28553	336	78	1579	CTCGTGCAATCTATGATTTAAGTGTAAATTACACTCCGTTTGTAATTGCAGTGCAATC	27763	A_95_P212412	Z93769
28558	336	83	1067	TGGCAAGAATGGACCAACACCTTAACTTCGTTAGAAAGCGGATTCACATCCATCCTT	27773	A_95_P194407	TA15887_4097
28560	336	85	233	GATACGGAACCTCTCTGCTCGTCTACTCTGTTTGCTTCATATAAGGAATTAAAAGTCG	27777	A_95_P106962	CV018146
28562	337	2	206	AGATATGCTGATATCTTGTCTAAACCTGCCAATACGGTTATATGTCTACCCCGCTGAG	27780	A_95_P114302	CV021534
28565	337	5	896	ATAGAACTTTTTGTCATTTTTAGGTTAAGTTATGTTCTGTATGAGCACGCGAGACGGC	27786	A_95_P268151	DV999636
28566	337	6	665	TAGCAACGACAACAATGTGGATGATACAGGGGAGAGAGTCTCATGTTCAGTCTGCT	27788	A_95_P297084	FG197657
28568	337	8	568	AACTGCCTCCTCTCATATTGCTATACCTTTTCAATACTGGTGGATTATTTACTGTTACT	27792	A_95_P181862	TA13077_4097
28569	337	9	289	ATCTTCCTTACTCATGCAGAGCTGGTTCTTGCTCTTCTTGTGCTGGAAAAGTTACAGC	27794	A_95_P106267	EB442583
28570	337	10	813	GGGGTGGATTTTAAGCATTTCTTTCGTCAGATGTTTCTCTTAAGTCATTGTTAATGTTT	27796	A_95_P228109	DW001771
28571	337	11	365	TGCCAATGTTGTCACTGATAGGGTCACTGGGCGCACAAAGGGTTATGGGTTAGTTA	27798	A_95_P114028	CV021408
28573	337	13	632	TTGTTATAACAATCTCGAGGGAGAACACTCCTCTTTCTTCTCTAAACGGGGGGAATG	27802	A_95_P224842	FG634181
28578	337	18	782	TCCATGAGCTAAGTACCAATGAGAATCAGTTCCACTCTTGTGTCTTTCATCCTAGCTA	27812	A_95_P135442	EB438897
28580	337	20	898	TTACTTCTGAGGAAATGAAATGCAGTGACATGTGAACTTTGTTTGATTACTTTCTTGC	27816	A_95_P291823	EB424975
28585	337	25	751	CGATCAATTTGTCATAACTTTCTGTCCAGATCAATGGGGCACAGACCATTCGTCTGCT	27826	A_95_P146452	FG157506
28586	337	26	154	AATCAAGTGATGTTGCCGAAAGATCAGTCAGCAATGCTGTCAGAAAGGACCTGGAA	27828	A_95_P216872	AM789132
28589	337	29	222	TTCAATCCTGCGCTGAGTTTATGATTGAAAGAGATTGCTAATGGCTCCTGGAGCGGT	27834	A_95_P147872	EB643479
28592	337	32	524	CTCTCTATATCTTGCTGTCAAAGTTGTGTGGAATTGAGAATCAAGTTAATCCTAGTAT	27840	A_95_P009766	FG625013
28594	337	34	1116	GGCACCTATTAGGGATGGTTGTAAAGGGAATCTAAATTGCTTTGTATATATTGCAGA	27844	A_95_P012411	TA14462_4097

28597	337	37	441	GGGTTTTGAAACTTGAAATAAAGAAGTTATCGTCTTAGCTGGATCACCTTGATATTG	27850	A_95_P136917	EB440622
28598	337	38	537	TTAAGTTACATCTTTACTGGCAGATCTCAATAACTGGCACCTATTTTGCCATCTTTACA	27852	A_95_P190707	EH620138
28599	337	39	188	GCCAAGTGGCAAGCATTGTATCTAGCAATTGGTTTATAATGATGTTCCATGTAAATTA	27854	A_95_P078450	BP527516
28600	337	40	809	ATCCTTCATGGATGGAGAAGATACAGCGAACAATGAAGAGCATTTTCCGCTCTGTGA	27856	A_95_P118207	DV161225
28606	337	46	968	TGTGGATGATCTTTTGTGACCTTTGAACTTATAATGGATTAATGCCTGGCGTTATGTG	27868	A_95_P014701	EU880279
28613	337	53	621	GACCAGTACACGTACTCACACTTGTTTTGCCCTATCTTATTTATTTTGCTTCATGTTAT	27882	A_95_P124767	DW004572
28622	337	62	299	GATTACGTCGCCAAGGTGGATGATCTGGCAGAGGCTTCAAAGTCTATTACAACATTG	27900	A_95_P213772	TA20120_4097
28623	337	63	445	ACGAAATTTTTTGTTACCTTCTGGAGAAGAGGTGAAAAAGACTTGGCAAACAATGCT	27902	A_95_P194822	TA15982_4097
28624	337	64	740	GCAGATAAGGAAGAGGCAGATAAGCTAGTGGTGTTATTCTAGTTCCCTGGTTGTGTT	27904	A_95_P016156	TA15241_4097
28628	337	68	504	CCCCTGGTCAGTTTCATCCTGGTAGCTGTAGTTGTAACTCTAATTTGTTTATATATGTG	27912	A_95_P295643	FG635590
28630	337	70	839	AGAGCCTGCAGCAGATAAAGAGCTACAAGCATCACCAAAGATGCAAGCTTCATTGC	27916	A_95_P201837	TA17507_4097
28633	337	73	641	ACTCTCAACTTACCTGCATTTATGCAAGTTATTGAGTGTCACCGCGATGAGATCCGAG	27922	A_95_P302198	FG198195
28634	337	74	844	GGAGTTGGTGAGAACTACAAGAAACTCTGCACTTGTGATGGTACAACTATTTGGGA	27924	A_95_P194027	EB425283
28638	337	78	191	GACCTATCCTCAGCAGGCTGGTACTATTCGTAAGAATGGTCATATCGTCATCTAAAA	27932	A_95_P157982	TA12614_4097
28641	337	81	569	GTACTTTATCAGTGATGGCAGAGATTCAGATGTTGTAAAACTAAGTAAAACGAGTTC	27938	A_95_P124377	DW004216
28642	337	82	863	TTAGCTCATAGTTTCCCCGGTCAAGTTACATGAACAATATCTCTTTTCCTTTTCCCCTT	27940	A_95_P253754	EB440118
28645	337	85	123	CTGACAAGGTAATGCTTGAGATTTTTGTGCTCCAGGACTTTTTAAAGCTAATTGTTAA	27946	A_95_P004296	EH616876
28646	338	1	810	CCGTACCCATGATGGTAGAGAGTTCCATGCGTGATGTAAGAACAGAGCAGCATTGA	27779	A_95_P283713	FG142649
28648	338	3	390	CTACATAGAGAAGCGTTGTAGCTATTTGATGACATCAGTTATTAAATACCAATTGACT	27783	A_95_P003581	FG642300
28652	338	7	1013	AATGTACACCTTTCTTGACTTCAATAATAATGTTGGTAATAGCTTGGAAGTGTTCAAC	27791	A_95_P007741	TA12401_4097
28654	338	9	1062	TGCCCTTCGGAAATTCCGAATTGAAGGGTTGAATGCATTAAAATTTTGACTGCTAAA	27795	A_95_P237134	EF051141
28656	338	11	345	AACCTTGTTTTCTTTTGAATTGTTGAGGGATCATCAATACGGCATTTCTTTCTACTTGT	27799	A_95_P094811	BP532881
28657	338	12	263	TCTTCTAGAGTCAAACTCAACATTCACTGGGCTGCCTAAACTCCACAATTTTGCAATT	27801	A_95_P120712	EB425509
28658	338	13	657	TTGTAGAACCGTCAAACTTGACTTCCCTTGTTTAATTGACTTTCTTAGCTATTGTTTGG	27803	A_95_P189422	TA14786_4097
28662	338	17	637	CAGACGTTTACCTTATTGTTCGATTGGCTTTTGTAGATCCATGATTTTGTACTTCGTAT	27811	A_95_P268431	DW001404
28668	338	23	304	ATTTCCGCAAACTGTAACGTTCACTGCTTACTCTTGGATTATTTACTACGTTTTAGACT	27823	A_95_P113797	CV021321
28670	338	25	82	GCTTTGCAACTTGATCATTGGAATTGCAGGCTAAAACTTGCCATTTGTATAGTTTCAA	27827	A_95_P094233	BP532613
28674	338	29	597	ATGCTTCTGTATCAGCTCACAGCTTATGAAACAGTTCTTAATCTGAGTTTTCGGGTAA	27835	A_95_P307273	FG638065
28676	338	31	670	ACACAGTGTTCACAAGCAACATCCCTGGTAATCTGATGGGTGGAGATAAAAGGGAT	27839	A_95_P304043	FG187103
28678	338	33	545	CTGAAATCCCGAAATCCATATCTTCCTATACTGTTGAGATTGTTTGTGTTTCTTTCTTG	27843	A_95_P203232	FG144747
28680	338	35	886	GTGGTGATCCGGGCAATCCCATTCAAGTCTAAGTGAAGTCTCTTTTAACCACAGATTT	27847	A_95_P258766	DV999402
28684	338	39	571	AGAGAAACTTTGCAAGGAGAAAAACTAACAAGCTCCAATTGCACGGTCGCAGTGGT	27855	A_95_P181223	EB447549
28686	338	41	857	TCCTGTGTTGTACGCTTTTGGAACATCTTGGCTAATTTAATACCAGTAGTATCTTTCTT	27859	A_95_P015006	EB426212
28687	338	42	432	GAGCAATGTTATGGATGCATTTGTTGGCAGACAATTTACTAGACGCAAGAATTAATA	27861	A_95_P072670	BP526023

28693	338	48	653	ACTCCACAGGCTGAGTAGATTGACCATCTCTTTGCAATCAAACTTAAAATTATTGCTT	27873	A_95_P000701	EH617531
28698	338	53	420	GCTCGTGCACTTGTGACATCAGGTTTTTGGAAAATTCTAAGAGATATTTATGGTTTTT	27883	A_95_P220597	FG638076
28701	338	56	351	AGTGGAGCCCCATTAACTGTTGTACTAAGAATATTCATAATGGATGAGTTGTCTCTTC	27889	A_95_P193027	TA15583_4097
28702	338	57	536	GATTTCTCATGGATTAACTCTCTTTAATCATATTACATAGCACGCTGCGCTTGTTGTTT	27891	A_95_P020996	DW004723
28703	338	58	623	TGTATCAATGTTTGCTCTCTCAAAGACTAGCTCGAAAACCATTAGTAAATTGGCACAC	27893	A_95_P236384	FG195872
28704	338	59	173	AGTCAACCATGATACTTGGGGCCGTCTTGTTTTCACTTCATGGAAGTCTGAATCAGAG	27895	A_95_P110092	CV019577
28707	338	62	879	TGGTTACATTTTACCTTCTAACAAGGAAAAGCAATAGCAGATTTTAGTACGTCTCGGC	27901	A_95_P220797	TA21686_4097
28711	338	66	1756	CCATCACCATGTAACCACTTTCTACATTGTAAAAAAGATTCTGTGTTTTTCCAGCGTTT	27909	A_95_P020281	TA13986_4097
28714	338	69	680	CAGCTGCCTCATTTGGGCAGAATAAAAGCAGCCAAAGTTTTGGTAGGGGTCTTCTCT	27915	A_95_P121422	DW001485
28715	338	70	944	CTTGCAAATAAAAGCGTACTTCACATTTGAATTTTCCAAAGGAAAACCCTGATCATGA	27917	A_95_P007786	EB678678
28716	338	71	238	TCAATTTGGACCATAAGGTTCAGCTCAGACGCACGCTATCTAGCAACTACTCATCCAA	27919	A_95_P069010	BP137271
28722	338	77	492	TTATCACAGTTCAAGTATGAGCTGCTCTTCATCTACTCACTTCTAGCATGTGGTTAATC	27931	A_95_P112557	FG638231
28725	338	80	289	GTTACATTCACGTGTGTTGGGCAGCAGCCTTTCTAGTGATGAACAAGATGTGGCTTC	27937	A_95_P134927	EB437840
28726	338	81	867	CGGCATACTCAAGTGATCTTCTTAAGCATTCTAAACAGTTATTTACTTTTGCCGACAA	27939	A_95_P245857	DW000957
28728	338	83	900	TTTTGTCCTAGCCAGACATCTTGTAACGGTATCCCTCCTCCCTTGACAGATCATAAGGT	27943	A_95_P178407	TA12240_4097
28730	338	85	829	GAGGTTGCTGCTGTATCGTCAGTGCCCCAAGTGTTTAAAAAATTATAGAACCTTGAA	27947	A_95_P232004	EB426155
28732	339	2	73	AATGCTTAATGAAAGAAAGCCCTTTCATCCTAATCTCATCTACTGAAAAGGGGGCCG	27950	A_95_P044606	BP130926
28733	339	3	785	ACCCCGTTCTCACAAAGTTAGTGCCAGTAGGAAATTCCTTAAATTTTTTGCTGGTTAA	27952	A_95_P213282	EB681275
28736	339	6	798	CGACGTCACAACTCGTGAACATTCTGATGTCATTTTACAATATCAAGCAAATTGCATA	27958	A_95_P152662	EB428087
28738	339	8	819	ACAATGTGGTTCCTCTCTCTTCACGATCTTTTGGAGTTACTGGTAGTCCTTCAAGGTTT	27962	A_95_P217312	EB680073
28739	339	9	750	CTGGGTTGTTTGTTGTTGTTGTTGTTGTTATATTGTGGGGGGTATAAAAGCTCAAAAT	27963	A_95_P029706	DV157797
28748	339	18	761	CCATTTGAAAATTCATCAAACAAATCCTAAAGTTCCCAAACCGAGCCATATTATGAGT	27981	A_95_P216877	EB440248
28750	339	20	1093	GGAACTACTGTGTTATCTTTGAGGAATGTTGGGCTTTTTTCGTTTGAATTATCATGAA	27985	A_95_P000396	M14419
28755	339	25	893	TGGCTTTCCAGCAATTTCTAGGTTGTTAAAGAATAAGGTGGTCTATTTGAACTGATGA	27995	A_95_P179002	TA12402_4097
28758	339	28	849	GCCCCATTCCTATATCCAGAACTTGAATGGGATTTCAGATTACCATTAGTAAAAAGTA	28001	A_95_P206847	EB427446
28759	339	29	366	TGGCGTTTTGCTTTGTATGCGCTATAGATGCTATTGAAATTTTTGGTTAGTTGTGATC	28003	A_95_P003941	EB445445
28760	339	30	260	TGCTTTTGGCTAGGAGATGTATTTGTTATCTAAGAATAAAAGCTGATAGCTTCTCTCT	28005	A_95_P029791	BP530498
28761	339	31	793	TCTTGCTTCAAACAGGTGATTGGTTTTGTTGGTATGCGGTGATGAACATGCAGCCTT	28007	A_95_P137097	EB440831
28765	339	35	476	TGATTCATATTCTTGGCAGCTGCGGATGTTTTGGTTCCTGCTCTCTTCTTGGACTCTTG	28015	A_95_P274828	AM790347
28772	339	42	295	CTTGTGATTGGGTCTGATGCGCCTGTATATAGTTGTGTTATGCTATGTTTCCTCTTTG	28029	A_95_P131057	EB431202
28773	339	43	872	TTGAGTAAAGACCTCAGATCTCCCTCGGCAGTGTACACATAGGTTCGTATGATGATTT	28031	A_95_P216702	TA20762_4097
28774	339	44	607	CAATGTGATAGAATGTCACTATTACGCTTGCGGCAACACAGAGATACCTGGGTCCTA	28033	A_95_P055481	BP133713
28777	339	47	473	CCAATGCATTTTGCAAATTCACGCTTTCCAGTCTCTTCAGGCTCAATTGGTGTAGCAG	28039	A_95_P062770	BP135600
28780	339	50	286	CTATGTAAGCGGTTTGATTTATTTTTCATCTTAGTACTCGCCTGAAGAGATTCCAGGC	28045	A_95_P110907	CV019958

28785	339	55	345	ACAAGGCATTACCATTTATCCTGCCTGTGCTGGTGACTTGCAATCTTCAATCAACTTT	28054	A_95_P105532	FS381087
28789	339	59	717	AATTCGGATCCGGAACCATGTATGATTTGATATATGCAAGCGCTGTGTTTCTTCATAT	28060	A_95_P216962	FG136929
28791	339	61	416	TTGATGATGACGGTGATGGTAGTGTTAACTTTGAGGAGTTCACGAAGATGATGTCTA	28064	A_95_P196757	FG631576
28792	339	62	114	AATAACTTGGGCAAGTTTGGTTATTGGCAGATTTGATGCTGGAGTCGAGCCAGCCCA	28066	A_95_P089908	BP530719
28794	339	64	767	TCTGTCTGATGTAACTGATGTCGCAATGAAAGTTGAATCGAAAGATCTGAAGGAATT	28070	A_95_P148377	EB677668
28795	339	65	1259	TCTCGTTTCGGATGTTGTTCAGATTGATGTACATATGAATGAAGCATACCCAGTTGTT	28072	A_95_P026131	TA17129_4097
28797	339	67	1061	GTGCGTGTTGGGAACAAGAGTGATGTTGTAAACAGTAAATGTTGTGCTTATAATGA	28076	A_95_P210407	TA19390_4097
28801	339	71	1250	TGTACTTCAAAAACTTTTTTGAAGTAGGTTTTATGGAGTTTTACACCAATTCCGGCTT	28084	A_95_P007546	TA13068_4097
28802	339	72	168	AAGGGAAAGCCTGACTGAAGCAGTAAATGCAAGTCATCAACCTTCTTGGCATGCAA	28086	A_95_P096483	BP533642
28804	339	74	722	GCTGATAATTATGAGCAAGTGTTTTCTCACATGAAGCCAAATAGCATACTTGGGCTT	28090	A_95_P186643	FG160658
28805	339	75	556	CTTAGACCATCATCAAGCGAGAAGCTTGTCGACAACTCGGTGTCAGTAGTTTGGAAG	28092	A_95_P059081	BP134645
28806	339	76	776	CGAAGAGATCAAGAACAAACAAAGGGTCATTTCCACCTCCTATTTCTTGCATAGGGA	28094	A_95_P268081	DV999498
28808	339	78	1367	ATTTAATACTTCCGCCATTGTTACTCACCTCGCTTATTCTTATCCAAGCTGATGAACCA	28098	A_95_P122017	Y10472
28813	339	83	196	GCGGTGGTTATGGGAACCAGGGAACGTAGTTTAATCAAAAGTGTACTTCAAGGAAG	28108	A_95_P154797	EG649763
28820	340	5	681	AATTTTACGTCTACTGGATCTGTCCCTTCGTAGGGGCAATAATGGCTGCATGGACTTT	27957	A_95_P126547	EB451173
28821	340	6	573	AAAGACCTCTTTTGTTGGAAGGTTTCTGATTAATTTTGCGTGTTTGAGTTAAGGCTTT	27959	A_95_P018971	EB679098
28824	340	9	736	CGCTTTCAGGTTTAACCCGCTTCCTTAGTAGCCAGATGCATTTAGGATTCTGTCACTA	27964	A_95_P284178	FG170078
28825	340	10	739	TCTAGGTATCACGTTGAGCAGATGCTGATATTGTTCATATAAAAGTTCTTCGCAACAA	27966	A_95_P160757	EH619435
28826	340	11	894	ACAGAATTGACCTTTTGTAAGGGCTTCGGAGTTATGGACTGCTTTTCTTTTCCCTTTTT	27968	A_95_P010831	TA13869_4097
28828	340	13	270	AGTAACTGAGCTCCATTCCATATCCTTGATTTTTATTACATTGGCCATTTACAACTGTT	27972	A_95_P110382	CV019710
28831	340	16	500	AATTCCAGCTCTAATTTTGGAAATGTGTCGATGTTATCGAAAATGCCTTCATTTTCGA	27978	A_95_P052121	BP132837
28833	340	18	702	AACTGAATGGCTGCAATGTAGTTGGGCGGCAATCTGCAATGAGTATCCAAGATTTCA	27982	A_95_P015616	TA12798_4097
28834	340	19	141	TTTTCGTGGAGAACGATGGTTGAGATACCAATTTTTAGGTTGTTTTGGGATTGGGGT	27984	A_95_P155217	EG649955
28836	340	21	91	CTGCTTCTTTCCTTGGTGGTACCATGAGAATGACAGTATCAATTTGTGTCATACTCCTT	27988	A_95_P028171	EH664090
28841	340	26	949	GTGCGTGGAAGGTGTTTGAACTATTTTGACTCTTCAATGTAACGGATTTATACTTATT	27998	A_95_P009801	TA14092_4097
28845	340	30	433	TTTTGGGTGTTTGGGTCAGTTGATAAAGCGGAAGGGTAATCTTTCACGAATTGTTCA	28006	A_95_P097608	BP534121
28847	340	32	712	CCTTGAGATAGCTTCTGTTTCACTGTACATTCTGATTCGGCTGTTACTATTTAATATTC	28010	A_95_P116397	DV159102
28848	340	33	631	GCCCCTATTAGGAACTCAAACAAAGATACTGATGTTGAGGAACATTATGAGTGTGCT	28012	A_95_P062340	BP135490
28849	340	34	702	AGAGTTAACTCTTGACCTTGTTATTGTGTATGAGGAAAGCTTTTAGAGGCAAATTGTT	28014	A_95_P125382	DW005168
28851	340	36	423	TTGATCCTTACACTGGTGTTCCTTCACTTTATCAAACAGATCCATCTGGAACATTCTCA	28018	A_95_P277519	DV158532
28852	340	37	331	CTCATCCCTTTATGATTTTAAGTAGTTGTTCTTTACGGGATCTGGAAGTTTATTGGGC	28020	A_95_P105587	CV017531
28858	340	43	730	GTCTAGACTAGTGAAGTTTGAGCTTTGGCATGAAATTTGGAAATACTGAATATCATG	28032	A_95_P117997	DV161018
28860	340	45	104	TCGTCCCCTATCATGTTTGCTTTTCACACAAATTAAGCAAACTGGAACATTTTGTCCTT	28036	A_95_P118242	DV161252
28861	340	46	1130	CAGATTCACTATTCGTCAAGCTTTTGAGCTGGAAACATCAGATTTGTCCATTATTTAA	28038	A_95_P031236	TC66585

28862	340	47	810	GGAGTTCCTTTTTGCTAACAGGCAATTGGCCTTTCCTCTTTTTAGTTATACTATATTGA	28040	A_95_P202917	TA17743_4097
28864	340	49	774	ATAGATGAGGACCTCGTGGCATTGCTTGGAAAGTATTCCCCTATTCCTGTAACATAT	28044	A_95_P217067	EB450156
28865	340	50	451	GCAAAGAATAAGAACTTTCTACGCTTTGCTTTTGGGTCTTTGCAGATATTATCACATG	28046	A_95_P003996	FG644065
28867	340	52	388	TGATTTGCCTGGTCAGAAGAGAGATCCTCCTGAGGAAAGAGACCCATTAAGGATTTT	28050	A_95_P074245	BP526415
28870	340	55	609	CTTTTGACTCACTTTGCTCTCATTTGGTAACTCTTAGCTTGTCTCTAAGAGAAACAAAA	28055	A_95_P026646	TA12843_4097
28871	340	56	811	GTTGGGAACTTGCTCATTGTACATGTTTTCCGAGCTGGTTCTGTACACAACTACATAC	28057	A_95_P251487	EB451542
28885	340	70	773	GCTCAACTGATTTGATGATGGATTGCTTAGAGATTTGGACAAGTAAATGTACTCATT	28083	A_95_P195327	EB447714
28886	340	71	122	CTCTCCGTGCCATACAGGGTTTACTATACCATGTACAATAAAATGATCTTATGAATAC	28085	A_95_P162657	EH621661
28887	340	72	784	GTCTGTATCTGTGTGTCATTGTATGCTATGTTTCTGGAATAACAGTTATGAATAAGCC	28087	A_95_P000311	EB678624
28892	340	77	591	CCCTTTTGAAAGAAGCTATTCAGGAACAAATGGACCGTTTTATACTTCAGGAACAGC	28097	A_95_P262191	BP134817
28893	340	78	1559	TTGTATCGGTACTGTTTGTTACACTGAACTTCTACTAGGCGATTTGGGTATTGAATAT	28099	A_95_P115092	DQ229077
28894	340	79	822	TGACTCATGATGCACCTCAACTTTACTGGCTTTGTCTCACATTTTCTAGCATTCGATGT	28101	A_95_P292473	FG172609
28900	340	85	0	CACTAACAGCCACAATATAGAGTTTTATATCTTGCTATCTCTCAGATGGGCAGACATG	28113	A_95_P262186	A_95_P262186
28901	341	1	444	TTTATTCGTACATGGAGTGGGGGGAAATGGAATTTTATTTTTATTTCCCCGGCCGTAA	28114	A_95_P131912	EB432335
28903	341	3	700	GCTTCTATGGGTTAACAGCTGCATGAGTTTTATGAGATACCTCTGTTTTAAATCTTAT	28118	A_95_P150957	EB681112
28904	341	4	220	ATTTCAGTTGAGTTTGAGTCCTTTTAAAGCCCGTTCGTAGGTCGCTAGCTCTGTTCGA	28120	A_95_P189277	AM833831
28909	341	9	1489	TCATTAGAGACTCGAAGTGGCTGTGAAAATATAGTATGTTAATAGACCATTTTCCTC	28130	A_95_P007921	X75088
28910	341	10	1226	CCACAGGTAAAATTTAACACTGTGTAAGCACAGGTGATCATATGAATGTTTTGATTC	28132	A_95_P181257	TA12938_4097
28922	341	22	323	AGGCTGCATTTTTAGTTGTATGTTCCTACATATTTTAGCTTTTGGGACCTATATTCCTT	28156	A_95_P028101	CV015911
28926	341	26	636	ATCAAATGCCAGGATCTTCTGGCAACTGATCTTGATAACCAGTCGGATTCAATCTCAT	28164	A_95_P288503	FG641869
28927	341	27	774	AAATTAGGACATGTTTACCTTTGTCTCAGTGCTTGCCTATTTTCCAATTCTCATGATTC	28166	A_95_P238364	EB450213
28935	341	35	836	ATTCCTAGAAAGTCTCCTGGTGCTACATGCATTCACAATGCAATAACCCCACCAAATA	28180	A_95_P151152	EB681378
28951	341	51	513	ATCATGACGCCATTTTGGAGTGGTCTTCTTCTCATATGCCTCAATAGTTGTGGTATTA	28212	A_95_P235664	BP136509
28953	341	53	854	GGATTCTGATATGGTCAAATGTACCAAGTATTTGGGTTTTTACCTTGCATATGTATGA	28216	A_95_P010206	DV159955
28956	341	56	732	TGGCGATAGTGACTTGCTGCCTTTCTTAAACGATCTCATTTTCTTTGGTATTTTTGCTA	28222	A_95_P273116	EB681626
28958	341	58	875	TCTATGATTAACCAACAATACATGGAATAAATCTGACCCCCCTATAACCTGTGTATCA	28226	A_95_P009096	EB424911
28960	341	60	743	GACGCTTAACTGAGTTGTGGAATTCGTTATGAGTGTTATTGGCATTTTTGTACTAAGT	28230	A_95_P208692	TA19023_4097
28964	341	64	396	TTGAGTACTTTATGATGTTGAACCAGCTCGATTAGCCACTAATATACTTGAGAATTTC	28238	A_95_P006546	FG638255
28966	341	66	575	TTGTATCGGCAGATGTTACTGCAAACCCATACGTTTTTTAGGTAACATATTTGTGGTC	28242	A_95_P305268	TC56113
28968	341	68	443	TTAGACCACCAACCTCGAGTATGTACATATAAACAGATAACTCTTTGCCACTATCTAT	28246	A_95_P003881	FG641821
28973	341	73	897	AATGTGGACGTATGATGAACAGTGCATGTATAGCTTGTCATGCTGGAAACTGGCTGT	28256	A_95_P230669	EB439066
28975	341	75	4047	GTAATTTGTATCAGTTTCTTAAAATACCTTCTTCTCTTGCCCGTTTCGGGTGTTAAGAT	28260	A_95_P182852	TA13319_4097
28977	341	77	459	GATGTATGGTTATTGTTCCACTTTTCGGATCTTTACCCTAATAGCCGGCGATGTTCGT	28264	A_95_P133207	EB434512
28981	341	81	763	GTCTCTTAATCTTTGCATTTGCAGGGAGATACTCTATGAAAGTAGCTGGGGTTTGTT	28272	A_95_P289748	DV160786

28983	341	83	79	GTCTTTTTGTACAGTAACGCACTAGCAACAGTATCATTGCAAAAGTTAGAACTTTTCTT	28276	A_95_P164362	EH623576
28984	341	84	147	GGATCTTTCATAACGTTGTGTTCTCTGCTGATTACTTTAAAGTTTATTGTAGAGCGTCA	28278	A_95_P097308	BP533978
28988	342	3	804	CAATGTATTTTGTTGTGCGATTACTGTCTCAAGTACTTTGGTTAGTCTGTTCATTGATG	28119	A_95_P009671	EB679132
28991	342	6	780	TTTCATAAGCACGAGCAAGTAAAGGGGAGTTGACTTTCGTCACACCTATGTGGACTT	28125	A_95_P273491	FG140044
28995	342	10	640	GGATCAAATCTTGTTCTTTTGGTTCTAAATGTGCTTTACTGTGACCAGGTTTTAAGAGA	28133	A_95_P008061	DW003467
28998	342	13	1169	GTAGTTTTAATTTTCTGGCCAGTTGTTATTTCAGCAGGTTTCAGTACTGAAACCATTG	28139	A_95_P186017	TA14037_4097
29000	342	15	310	AGAAGATACTGTCAGATTAAGGGAGTTGACCCAGGCAAACAACTTGGACTGTGCTAA	28143	A_95_P002681	CV018508
29001	342	16	779	GGATTTAGGGTGTGATTTGAGAATCGAACTTAACTGCTTTTGGTTAATGCACAGTCT	28145	A_95_P177612	TA12021_4097
29002	342	17	851	AAATAAGGCTGTGAAGCCCATTCGTCCTATCATTGCTGGTTCTACCCTCATCAGTTTTT	28147	A_95_P296923	EB680455
29008	342	23	813	CAGGACACTTCAAGCTCAAGTTCTGACATCTCTTAGGACAAACCATTTAGTTTTCATGT	28159	A_95_P125902	EB680522
29011	342	26	756	ACATCGGGTGGAGAAACTATAGTTGCTGATTGCCATTTTATTTGCATCGGAACACCAT	28165	A_95_P022881	EH618818
29015	342	30	773	GCTTTGACAGGTTTTATTGGTGTTTCCAAGTACACATGAAAGGAAACATAATTTTGCT	28172	A_95_P012191	DV158066
29023	342	38	452	AAATAACACCAACTGTCAACTTGATCTCTCTCCTGGATCTCAAGCATGTGGCTTCAGG	28187	A_95_P081835	FG146160
29024	342	39	885	GAGCCTTTCTTATAACTGTGATGACTGACTTACTGCTTCAAGGATAAAGGAATACAAT	28189	A_95_P015041	TA12503_4097
29026	342	41	816	AAGTACTACTGTGCAAAAGGATCCACTGCAATCAGATGATGACACCATTGTACAGAT	28193	A_95_P290583	FG155272
29027	342	42	471	TTCTTAACTTGAATTTTGTGGTGCGCGAGATGTCATAGTTGCCAAAGAGGGGTCTCAT	28195	A_95_P275658	AM782821
29029	342	44	896	AAATCTATGGCACTCTCGCGTTTGCTGAGATGATCAAAAACTGCATGTCACAGGAGCT	28199	A_95_P251974	DV999997
29033	342	48	140	TTTTGTCCATTTGACGTTCTCCATATATCTTACACGAATGTTATGGAAGCTCCCTGTCT	28207	A_95_P144187	EB447346
29041	342	56	595	GTTTCTATACCTCTCACCTCACCTTTATATATTACTGAGCCGCCAAAAGAGGCATTGAA	28223	A_95_P205347	TA18264_4097
29042	342	57	580	GTGATAATTGGGGACGTTGCGTCGTCAGTTGTTTACTCTTTAATTCTACTCTATTTTTA	28225	A_95_P002606	TA12227_4097
29043	342	58	285	CTATATCGAGGTTCCGGTTCGCAATTTGGTATTTCAGTCCAATGATTGTTGCTTGTTTA	28227	A_95_P047806	BP131749
29045	342	60	689	TCTTGTACATCTTGATACAGTAATATCAGTGTTGCTGGTTTTCTCAGAAATTCAAGAA	28231	A_95_P164822	EH624164
29050	342	65	758	TGTGTTGTGCACCTCTGAACACATACTTCTAGTCTGTGATTCACCACTGTATGCCTTTG	28241	A_95_P215277	TA20449_4097
29052	342	67	796	GGGCATCCCTCTGTAGCATCTTTTCTTAAGTTATTATTTAAAAGGATTTGATCCATTCT	28245	A_95_P190367	EB438557
29056	342	71	346	TTCCTTACAATCTCTCATACAATAGCTTGGCCGCTTTACTGGATCTGCCAAGGACTGTA	28253	A_95_P102907	CV016252
29060	342	75	593	TTATCAAGACTAGGTTGCAGGTTCATGGGTTGCCAAAGATAGGAACTGCTAACGTTA	28261	A_95_P138837	EB442564
29061	342	76	599	TCTGGAAATGATAACATGGGCACAACTTGGAATTCACAAAAAACCGGTTGGTTTGCT	28263	A_95_P135892	FS406206
29063	342	78	748	ATACAAAGGATTTTTGGAAGGTGAAGCACATGGTATACTTTTGCATTCATATGTTTGC	28267	A_95_P152857	EB683191
29065	342	80	833	ACTGCTGTTGGCGAAGGATATTTTTGACAGATGCTCACATGGCGAAATTGTGCTAAT	28271	A_95_P199662	EB677741
29066	342	81	424	TAGCCTTTTGCCTAGTTTTGACATCTCCATTCTCCTTGGTTTCATGTAGAATTATATGGA	28273	A_95_P140052	EB444011
29067	342	82	1487	ATATTTCTCCTGGTTGCTTCTCCATGACCTGCCAAATGTCAAACGATTGTAACTGACAT	28275	A_95_P197647	TA16610_4097
29070	342	85	575	CTGCCATTTATTGCGTGCTTTTGTAGATTCTCTGCAACATAATTTCATATTGAAGTTCA	28281	A_95_P140147	EB444096
29071	343	1	949	TATAGTTGGCTCTAACTTAGGGTCCTTATATGTTGGTTCTGTTTAAATTAACGGTAGTT	28282	A_95_P216232	TA20660_4097
29074	343	4	546	CTTCTCACCGTTCTCTGCTATGTTGTACTAAAACATTCCGATTATATTGCATTCTTGAAA	28288	A_95_P092088	TA17414_4097

29075	343	5	618	GTTCAGCGCATTTTTGGTCTATGGCGTTTGTTCTACATAGATTTGAGTAAAGAAATGT	28290	A_95_P153052	EB683366
29076	343	6	93	CAGACTAATGTAGTGGCCAATTGCTGTTGAATTATGTGTTCCAAAAGTTCTACCGTTC	28292	A_95_P103112	CV016350
29079	343	9	826	TTTGCCAGAATTTTCCCCTTTCCCCGGTTAATAAGTTTGGCACCTCGGTCTTTGAAAA	28298	A_95_P243892	BP530068
29080	343	10	254	CCTGTGATCGTATTTTCTTGATTTAGTCATTTGAAACTAAGCAAATCATGACAGAGTT	28300	A_95_P206682	TA18571_4097
29083	343	13	636	CTGTGGTCAGGGAAGGCTGAGCATTAAGGAGATTAGAGAATTGAAAGAATCTTCAG	28306	A_95_P045551	BP131175
29091	343	21	517	GTGCTAGTATCAGTGCTTCAAAGTGTATAGAAGTTAAAAGAAGCAATACAGAGGAA	28322	A_95_P068740	BP137203
29094	343	24	208	GAGCAAGAGCAACTAATTGTGTGTGCCATATCATGCGCAGTGGAAATCATTGTAATC	28328	A_95_P143917	EB447105
29095	343	25	787	TCGCTGCTTTTCCACCCTGAGGTTATCTTTCAGTTAATTTTTTAGAGCTCCTTGAATCC	28329	A_95_P126527	EB425845
29097	343	27	676	TTAAAATCAGTTACCAAGTTGCCAATTCTGATTAAGGGCGTTCTCACTGGTGAAGAT	28333	A_95_P144957	FG140029
29100	343	30	327	GGGCGTCTGGGTATTCCCTCCCTGATATAAACTTGACAGCCATGTATTAGTAAAATTT	28339	A_95_P097563	BP534107
29101	343	31	149	ACATTAGAGCAAGGCGTCCAATGGCACAAAGTATTGGTCAGATTGCAAAGTTTAAG	28341	A_95_P158082	FG643824
29103	343	33	736	AGTGGTAGCTTGATTGAAGTCGACAAATCCTGCAGTCTCGTAATGATCCAGTGGTAT	28345	A_95_P270796	EB435854
29106	343	36	781	TATGATAAGAGCAATGCTGCCAAGAGTAGCTTCTAATGTGATTGCAGTCCTGCTTGA	28351	A_95_P146327	EB450327
29108	343	38	3179	CACCAACCTGGTAGTTCTTTATCTGTTGATTTCTGATTCTGGGAATATATATAGATGG	28355	A_95_P221292	AB015221
29110	343	40	386	ACTGTTATTGTTTGTTTTTGACATTTGAATGAGATAGACTGGAATGGCAGTTTTCCCC	28359	A_95_P127712	FS377589
29111	343	41	289	GTTGCCAAAGCGCAGTAACTCTAAGGTATCTTTGTGTATGCTCTAGATTCTGCTGCTG	28361	A_95_P156852	FG638507
29112	343	42	681	TCTGAATACATCCCTTTCCGAACCGATTGAATGCAACTGTAACTTGCATGATTTTATCT	28363	A_95_P316068	FG198287
29115	343	45	1558	GAAGCTGTTGGGCATACTTGCTTAAGTTTTGGTTTATTATATGCCTACTCTTTAATGTT	28369	A_95_P155777	TA14230_4097
29116	343	46	728	GCCCCTGTATCTCTTCTAAATTGTTGTAACAACTGGACTTGCTGTACAGATTAAGCTT	28371	A_95_P289303	DV158550
29121	343	51	123	AATAGAGTTGCTTTATTAATTTACGAGGTAGGGTCATGCCTAACCCCCCACCATGAG	28380	A_95_P129352	EB429137
29122	343	52	394	TGCCATGTTATGATAATCCAGCTTACAGTAATACTTTTGATGTCTTCATTAGAGGAGA	28381	A_95_P102847	CV016230
29126	343	56	668	GGAACTTTTTGAACAATTGTATGCATTAAAAGCGGTGATTATCTCTGGTATCAGCTTT	28389	A_95_P296553	EB677682
29132	343	62	610	CCAACTGTGGTTTGCTTGGACCACTGGATATAAACAGTAATGAAGATTGTTAAATCA	28401	A_95_P236259	FG642265
29135	343	65	442	GCAGCTTCATTGTCAGTATGCGTGTTGATTTGAGAAAGAGGTGAATTTGTATCAGTA	28407	A_95_P193137	BP533083
29139	343	69	585	CTGGAAAGCGTTACTGCATCAATAGTGCTGCCCTGAAATTGAAGCCAAAGTAAAAAT	28414	A_95_P112397	FG645193
29141	343	71	1311	AACTCAAACACCGTGATTTCATTGAGCCTTTTTTGGTAGTTTTTGACCTTCGCGGTAT	28418	A_95_P012546	TA15998_4097
29142	343	72	648	GAAAACTGGAGGTGAAAAGGCTGGCAAAAGAACATAAATCTCCTTCCAAAAGCAAC	28420	A_95_P109337	EH615247
29144	343	74	535	CAGTGTGGTCTATGATGCTGTGAACTTCCTATTTTCAAGATCATATTTGTTTTGGGTT	28424	A_95_P019286	TA16261_4097
29146	343	76	861	CAGCTACCACTGCTTAAAATGCGTGGTCGAGCTTTAGACTGATCAAACTTGTTTGCTG	28428	A_95_P243257	EB677187
29150	343	80	837	GTGGTCAATGGCTCTTGATTGTTAATTTGGAATGAATAGTTTATCTGAAAAGTCCTG	28435	A_95_P207482	TA18750_4097
29158	344	3	170	TTTTTAATAAACCCAGTTGGAATTCCTTGATCATCAAATCACCTCAGCTGAGTCTGCTT	28287	A_95_P104562	CV017070
29162	344	7	480	GGAGCTTGAAGCTAAGGCACTCAATATCTTGCATTTTGGTTATATGTATATGCGTAC	28295	A_95_P122327	DW002324
29167	344	12	927	ATTCTTTATCTCGTACACAATCCGCACATTTGGTGCTCTAACCTTTGCCACCATAATGA	28305	A_95_P023781	EB427932
29176	344	21	495	CTCTCCATATCACCTTTCCTTTGTCTATAAATTTAGAGGTTTGGCCTCATTTTTAAGAG	28323	A_95_P059131	BP134657

29177	344	22	869	TTTTGAATTTGAGCTGCAGCGAGTACTTCTCAGGACCATATGGAGAGGATGTTGTCT	28325	A_95_P245082	EB680256
29183	344	28	234	GGGCCTTGAGCTCTACTACAACTAATTCAATAGGTAACTTTTGGAATTTGAGGGTTTT	28336	A_95_P004241	EH614565
29188	344	33	670	GGTGGATCTTTGGTCCATTTTTGGTGATGTTCATCTTGTTTGGAATTGTATAATCACA	28346	A_95_P212347	TA19813_4097
29189	344	34	656	AAGCATATTCTTCTGGGGATGATTGGAATGACAGCACGCGATCAAAGGAAGAAGTT	28348	A_95_P303158	FG200231
29190	344	35	435	AAGTCCATTTCAGCTTGGTTGATGGTCCACTGCATACTCTCTAATTTCTTTACAATGTC	28350	A_95_P037453	BP129010
29196	344	41	1061	TCTTGAGAATGTTGGTTGCCCAAATTATGAGGGTTTTCTTTACGTCATCCTCATTCTGT	28362	A_95_P179832	TA12594_4097
29197	344	42	339	CCTCAAAAGGGGTGGGTGCAAAAATGTGAATACGAGGGTATACCTAAGTATTGCAA	28364	A_95_P076595	BP527025
29199	344	44	324	GGACCAGCATTGAGCAAGGTTGCTTGCCGTGGAATGAACTAGAATCCATCGTTCAAA	28368	A_95_P099158	BP534815
29200	344	45	587	TAGCAGTAGCATTGTAGAGTGTTTTACGTCCTCTTTTGCAGATATTGTACTATCATAC	28370	A_95_P296653	EB678635
29201	344	46	499	GGTGAAATGTGCTGCAACTTTCGATGTTGTAATATCAAGTATAGTTGAATGTGAAAC	28372	A_95_P184167	FG633777
29204	344	49	1470	GACCTTCAAAATTACATGTGCGTTTTATGCACCAGCTAAATTTTATGACAATGCAAGG	28377	A_95_P200222	TA17163_4097
29210	344	55	534	GTGCCAGACACGTTCATGTAGACTAGTATAGTAGAAAAGCTGGATCGAAAATATTTA	28388	A_95_P213827	TA20131_4097
29212	344	57	407	AAGATTTTCACATGTTTCAATTTTGCATGGGCAAGCTTCTCTCATCCTGTTCCCCCTTT	28392	A_95_P202832	TA17724_4097
29213	344	58	674	ACGGAGAGCTTACTAGGTGTGGCGTGTTTTGTAAATGACATGTAATCAATCTACTTC	28394	A_95_P268666	DW002417
29214	344	59	610	TTGCTGTAATCAGATCTTGTTATGACATTGTTTCTCTTTTCAATCCATGTTGCGTCATG	28396	A_95_P295068	DW003989
29217	344	62	723	TAATCGGAAGACTAGGACTGCCCTCTCTATCGTACAAGTGGTGACAATTCTGAGTTG	28402	A_95_P195287	TA16083_4097
29223	344	68	456	ATATGAGCTGGACTGTTTGGGATAGGTGGGTCATCAAGGACAATCCTACATTGAGA	28413	A_95_P090973	TA16928_4097
29226	344	71	548	CATGGCGGTTGGCAAACAAATGATTGATATATTGTCTCACTGATTACATTTTTCGAAG	28419	A_95_P233674	BP525990
29228	344	73	596	GTTTTGTAGATAGCAAGTCATGTAGCTGCAATAAACCGTAGTACAACTTGCTCGTTTT	28423	A_95_P124407	DW004247
29230	344	75	251	ACGTTAATGTATGGTGTCTTGGACTTGGGGCATTATAAATGCACGTCACTTCCTTTTG	28427	A_95_P027541	EB429909
29231	344	76	807	ATCATAGTCCTGTTACAAACTCAGTAATGCAATAACACTCTTGTTAAGAACTGAGCAT	28429	A_95_P180507	TA12762_4097
29238	344	83	20	GTGCAAGGTGCTCTCAGAGCAAGTTCTATAGAAACTACAGAAGAAAACCTTTTGCAG	28442	A_95_P186507	DV162646
29240	344	85	417	AGACCCCATTTATGCAATTGTACTGGGGTTTTGTTGTTGTTGTTGTTGTTATTGTGAT	28446	A_95_P223672	TA22303_4097
29243	345	3	456	TCATCGGTGGTTGTGGTCTTTCTGCTCTTACAGAGTTGAACTTCAACTGGATTGGTTT	28451	A_95_P115947	DV158401
29244	345	4	842	ATTGGCTTTGAGATCCTCGTGTCATCTCATGTGGTGATGCTGTGAGTTTCTACGAATA	28453	A_95_P267831	FG174143
29246	345	6	499	GCCGTTTTCAATTTTTGGTTGCTCCGAAGTCTGAACTCCCTTTCCATGTCTTAAGTTTT	28457	A_95_P181602	FG166414
29251	345	11	725	TGGATGGGCAGGGCTTTCTATATTATTCATCTTCGGTGTGCTTTCTTACTATACTGGC	28467	A_95_P297888	EH614391
29257	345	17	1502	GCACAACCATTTATATCTCCCACTCATTCTTATGATTTGTATCTTGTGTGTTGTATTCA	28479	A_95_P004626	D61377
29259	345	19	881	AACCTGCTCTTGGTTGCAGATGTACTTTCTCTAAAGGCATGTTGCTATAAGCGTTACA	28483	A_95_P008256	DV162425
29263	345	23	186	GCAATTTATTCTGCTATCCAAACACTATACCATTTGCTTCCCCTTTGAGCCATACTTGT	28491	A_95_P147887	EB643483
29265	345	25	419	TCAAGAAAAATCCAGAGCCTACTGCCGAAGAGGTTACTGAAGTGCACAGTCGGTTTA	28495	A_95_P113897	CV021361
29267	345	27	592	TTGGGGGTGCATTGGTTTAACTGTGTTTTGAAGCAGATGACGGTTAAATTGTTTTAA	28499	A_95_P122372	DW002359
29268	345	28	903	AATCGCTGAGAGAATCGATCGCAAAGACTACGAAAAAGCCGTTAACGACTGCTGGT	28501	A_95_P204522	TA18084_4097
29270	345	30	750	GTGATACCTTTTGTTTTCAGTGTGTGAGTTGTACTAGTTTTTGCCAACACAACATTAA	28505	A_95_P120242	EB439640

29271	345	31	128	GACCATTTTTTACTGGTAAAGAACCCCACGCATAAATATGTATACTCAAGTACTTTAC	28507	A_95_P113477	CV021159
29274	345	34	999	CAATAGCAGTGAAATGCGACATTTTCTCTTTATTCCATACCTGCCAATTGATTCATTCT	28513	A_95_P017016	TA16447_4097
29275	345	35	869	AGTGGTGGGGGAATTAAACTTTTGTGGATGATTGTAATTAATTGACTAACCCTTCTTC	28515	A_95_P291788	EB424882
29280	345	40	468	GCCGATTTTGAGATATTTTCGTTCAGAAACAACAGGTTATTTTTGGAGCTGCATTTTG	28524	A_95_P050516	BP132414
29281	345	41	819	ACCTGACATGGAGATCTATTCAATGTATGGAGTCGGCATTCAAACTGAAAGAGCATA	28526	A_95_P229179	EB682424
29282	345	42	1533	ACAGGATGTAATTTTATTGGCACTAACATCTTAATTATCTTCGGCCAGCAGTTTAATG	28527	A_95_P190572	TA15044_4097
29284	345	44	66	CAAATAGCGACTGAATCTTGTTCAATACCTGAATGTATGATGTCAACATGTAATGTAG	28531	A_95_P030821	EB436358
29288	345	48	1531	GATCCGTGTGTATTTAATGCTTTCATATTCCAACTGCTGGTGAAATGAAAATGCTGAA	28539	A_95_P199237	TA16950_4097
29295	345	55	353	TGAGGACCATTTAGTTGGAGTTGTTGGTTATGCTGATATCTTGGCTGCTGTTACTAAA	28553	A_95_P092763	BP531958
29302	345	62	570	CATGGGGTGCAAACGGTCATGTGTAAAATACAGATGTATTACGATTTAGTAGTGTAT	28567	A_95_P124542	DW004348
29309	345	69	2693	CTCTTGTATTGGTAAATGGTGTATCAGCAATGAATTTGCATTTGTTTATTACCCCCCA	28581	A_95_P240134	Y10861
29319	345	79	1415	GAGGGGGTGGAGATGGTGTTTTGTCATGATTATACAGTTTATACTTTTATTAAATGA	28599	A_95_P210382	TA19385_4097
29321	345	81	813	ACTGCATCTTGCATAACAACTCCATTGACACCATAAACTCGATGCAGTGATGGGACA	28603	A_95_P242662	FG159787
29323	345	83	790	ATACAAACCCGATGACATCCAACATTGTGAGTTTCAGCTGACTCTTGTGACGAAACG	28607	A_95_P186447	TA14130_4097
29324	345	84	626	GGTTGAAGAAGTTCAAGTATTTCGTTGTAATATTCATGGTACATTAACGGGGTCTGT	28609	A_95_P057721	BP134287
29325	345	85	872	TAACTAATGCCCTTGCTTAGCTGCTTAGCATATGCGCGGATGCTGGTTGTATTCCATT	28611	A_95_P011436	DV999648
29327	346	2	783	TTGACAGCAAGTTTTTTCCTGCTCCGGCATTTTGCACTAGAAAGGATGTTTTCAAATT	28450	A_95_P224592	EB447783
29328	346	3	573	TTGTCCTGTGGTTTGTGGAGGATTTGGTGGTACCTACTTCTAAGTTTTTAAATTAAAC	28452	A_95_P302873	FG640200
29330	346	5	655	GCTACTTTCTTGTTCGATGCATATTGTTGTAGTAGTTGGAGTTGGTAATCCCTACATA	28456	A_95_P023466	EB432693
29332	346	7	483	GTGTTGTTTTGGCAATATGGCTCCTTGCTTTGTGATCAATCATTGGTCTTAGTAATTTT	28460	A_95_P206687	EH620540
29335	346	10	234	ATCTTCCAAAAGAGTTGTCTCTTCTCCCACCGTCATCTCAAAATGGGTAAGGATTGTA	28466	A_95_P070430	BP192634
29336	346	11	364	CATTGGACTGTTATCGCCTGCATGTCATTGATCTTGATCCATCATCAGTGACTTCTGG	28468	A_95_P209567	FG641440
29337	346	12	637	TATCCGACGTCAAGCTGCAGAGCTTCGCTATATATTGCAAGCACCTAAGCTGAAGAT	28470	A_95_P224542	EB447892
29342	346	17	794	TCATTCTATATATGCACCGGTTCAGCAGCACACTGCTACAAACTCTTCGAAGGACAAG	28480	A_95_P139177	EB442895
29347	346	22	955	AAGCTTGCTTTTGGAACTCGGTTCCTACGGTTCACATATAAAGTGTTGTGAAGATCGG	28490	A_95_P187717	TA14407_4097
29348	346	23	1072	CAAGTGATGTTGTTCATCAGATACCTTCCTGATAAATGAAAAGGCAACAAGTCTTCTG	28492	A_95_P147737	EB643430
29351	346	26	979	TTGAATTGTGGGTGCTTCGTGTTTGGAAATGTCTTATTTCTAGGGGCACCTGTCTAGG	28498	A_95_P027746	TA14463_4097
29352	346	27	768	TGTTAAACAGCTTCCCGAGTATCATCCTTGTGCAGAAGAAGATGAGAGTGGGTCAAT	28500	A_95_P291678	DW005246
29355	346	30	839	CAAAGTACCAGTGCCATGTGTTTGATGTTGTGTATTCTTTCTTACTGTTAGAATACAT	28506	A_95_P295998	EB449343
29356	346	31	725	TATGAATGACATGTTTCTCAAGCTCTTAGGCTAAAAGAATGGAAAAGCCAATGTTCA	28508	A_95_P180947	EB438484
29358	346	33	215	TCTCAAACAGTCGAGGGTTGTCTTCGAGGTTTTCCGGACGGTCGATTTCGAATATATG	28512	A_95_P102417	CV016012
29360	346	35	687	GACATCCTAATGTAGCCCTGCATTGGAGTCAAAAGATGTTTGATCAAAATTCCATGA	28516	A_95_P219762	TA21463_4097
29363	346	38	1749	TTGAAGGGGGGAACATCCTAATGGATGAGTATGAGCACGTTATACATCTCATATTAG	28521	A_95_P014231	TA12737_4097
29365	346	40	591	AGCATCCAGCTATTTCAGAATGCTGTGTGTTAGGATTACCTGACAAAGACCATGGTG	28525	A_95_P056446	BP133955

29368	346	43	612	CATGTATCATGTGGTACTTGAATTGGTTAAGTATGATATACTCAACGTGCTTAGATGC	28530	A_95_P244027	FG644792
29373	346	48	799	ATAGAGAGATCGAGCCATTCTCTGCAGCAAGGTGTCGCGTTTATATCGATTGCGTGA	28540	A_95_P311788	FG158664
29375	346	50	799	CGAGAGTTACTGTTATTTGGCATATTATGTTTCCGTTTTGGCTATGCGATCAACTCAA	28544	A_95_P189347	TA14770_4097
29377	346	52	892	GGAAGGGAGTTCTCTTCTATATTAGTAGAGGTACCCGTAATCCTGTATTGCGATTTCC	28548	A_95_P218767	TA21249_4097
29380	346	55	1561	GTGAACTTGTTGGCTTCTTATGGATAGATATTAAGGCCCAAGTCTTTCTGTTAAATTT	28554	A_95_P014331	TA13580_4097
29381	346	56	782	GTAGTAGGTTATGCTTATTTCCTTGTTACTTCTAGAGACCCGTCATACCAAGATGTGT	28556	A_95_P116547	DV159298
29382	346	57	862	TTTTGTATCCAAGAGGATAGTTTTGAGAGCTTTAATAATGCAGACTGCCTTTGAAGTG	28558	A_95_P152942	EB683269
29384	346	59	551	AGAAGAGAGGACCAAACATTGGCTGTCTAATGTTACTTTCCTGTGTTTATTATTAGCT	28562	A_95_P124217	DW004071
29388	346	63	488	CATATGGCAATGTAAGATTAGGAGCTGTAGGAATTGGGAATAAGAGCTGAATTATT	28570	A_95_P152937	EB446750
29389	346	64	396	TCATGGAAAGTCGGAAATTATTCAGCTGAAACTTGGAACTGATATCTAAATTGTAGA	28572	A_95_P088413	BP530049
29398	346	73	326	GGAGATCAGACTTTCTTTGAGTAATTGCATCCTTCATAGTATATATCACATTGCTATA	28590	A_95_P095743	BP533315
29401	346	76	340	GGTTAGCTCGAACCCTTTCCGTATTATGATTTCAATTATGAATGAAAATTGTTGGATT	28596	A_95_P308413	FG642283
29402	346	77	766	CTGTTCATTGTTGGGGTTTTGTTGAACCATGTCTACGGAGACTGTAACTTTTTATTTAT	3665	A_95_P000026	EB439159
29403	346	78	597	AGATACTAAGTCAGGATTTAGATGCAACTGGGAAGGAAGAATTGGGTACTGAATCT	28598	A_95_P019551	TC55128
29417	347	7	909	TGTGATGCTGGCGATTCAGTCATTATGTTTGCACCATACTATTTCAATGCATACATGT	28625	A_95_P250967	DV999231
29420	347	10	871	TTCTTCGGATATATGATCTAAACCGACTCGATGCACCTCCAAGGGAAATTGACAGCT	28631	A_95_P245252	DV162345
29423	347	13	967	TGAGTTTGATACACAAAAAACTGCAAGATTACTGGTTGCTATTGTTGGCAAGTCCTTG	28637	A_95_P192057	TA15371_4097
29427	347	17	695	ATAGATACAGATGTAGGTTTCGTTGTAGAGAACTTCTACCCAGAGAACCCTAAATGG	28645	A_95_P293973	EB438961
29432	347	22	585	TAACAGCTTTGACTTTTCAGTCATTGAGGTTAGTCCCATATGAGTAACTCCTTTATGT	28655	A_95_P133912	EB435628
29438	347	28	415	CTAATAAATAGTTTCCGCTATATGTTTAGCTGGATAGGAGACGGGAGTACCCTGCAG	28667	A_95_P081645	BP528313
29444	347	34	715	TCTAAGAGAGAAGAAGCGCTGAAGCTTCTTGGAGCTGACAATTTTATGGTCTCATCG	28679	A_95_P263066	FG642025
29447	347	37	700	AGCTTTTACATTCTCTGGCAAAATGAGTGGATTTTGAGAGGTTTCCTAAGAACAAATA	28685	A_95_P298018	FG639910
29448	347	38	514	CCGCTACATCAAGGTACTCTTCTCGATTTTGACCATGTAACTTGATTTGGATAATTCAT	28687	A_95_P309088	FG644660
29452	347	42	398	TTGAAAAAGTGTGGAGTATTAAATTAGGGGGCTGTTGAGTTGCGTAAATAAAGCTT	28695	A_95_P118182	DV161197
29453	347	43	443	GAGGACGAATAAGTATTCATGCTTCGGAAGAGATATTTGAGCCTTGGAAAAGACCA	28697	A_95_P110697	TA13256_4097
29455	347	45	343	ATGCTTCAATGGCCATGTCCTCTCAAGTTACATGTACTTCATGGCGCCTCTTTGCTTGA	28701	A_95_P095868	EB682879
29457	347	47	380	GCAACATACTTCAGCAATTGCAGAACATGAACATCGTTGACTTTGATCCTAAGGGTG	28705	A_95_P103827	TA12309_4097
29460	347	50	702	AAGAAATGGTTACCATACCACTAATCGGTTCTAGCTATGATAGTTATGCTGGAACAT	28711	A_95_P202467	TA17643_4097
29464	347	54	214	GCACATCGTCCTTGTGCATTATAGAGAAGTAAAAGAGGTTATACAGTCTTATGATTG	28718	A_95_P003576	EB430167
29466	347	56	1005	GATGCTCCGGTGAAACTTTTTTATTTTCGTGGAAATGAATTTTTGTTTTTACGGAGCC	28722	A_95_P249697	Y11212
29467	347	57	650	TAACAATCATGTTTTAGTTGCAAATGTTGGCGATTCAAAGGCTTTTCTTTGCTCTCAG	28724	A_95_P302698	FG192418
29468	347	58	484	CCTGACTGATTACGAGTAGCGTGTATTTAAGTCTATGCAACTAAGTAATTTCTTTGCT	28726	A_95_P009526	DW003068
29474	347	64	1033	CCAGATATTAATACATATGACCTTGAAACTTACTGGTCTTAAAGGCCTTGCTTTACTA	28738	A_95_P010686	TA14508_4097
29476	347	66	512	GCATTTTGTTATGAGCTTTAGCTAGGGGAGTTTATCTACCTTTGAGAGGAATAATATA	28742	A_95_P001701	DW004070

29482	347	72	125	CAATGTAATCTTCCGATCAAATTTATGCTGCCAATAGCTGTTGCATTCATTTTCTTGTT	28754	A_95_P092538	BP531847
29483	347	73	910	ATTATTCGCATGGATCTTCTATCTGGCTTCACTTGTTCCAATGTGTAGTGTGTTATCTC	28756	A_95_P185082	TA13838_4097
29487	347	77	763	AAGTGGTTCTCTTACTGCTGTACAATTGACAGTGGATCTGAAGCCTAATCTACCAGCG	28764	A_95_P116572	DV159325
29490	347	80	1092	TCGGGAATCTCCGGATCTATGCTTATTTTCAACTCCCCGAAGCATTTCGTCGATTACT	28769	A_95_P033784	TA11649_4097
29491	347	81	803	TTGCTGTTTCTTCGGTGGAGTGAGCACCATAAAAAACTAGCCAATTTTATAAGGTTAT	28771	A_95_P196197	EB682700
29504	348	9	989	GCGATGGAAACATGTGGCTATGTTTTGGAATTTTGACATCTGATAACAAAAGTAATT	28630	A_95_P012976	TA15910_4097
29508	348	13	782	GTAGTTTGTAGGAGCAAGAGATTACCTTAGTCCTCCTGTTAATAGAGTGGCTGTAAG	28638	A_95_P151567	EB681758
29509	348	14	1141	ACCTAAACGGTGAAAGGCATATATTAGAAGAATCAAATGTTTTCCGATGCTAGAAAT	28640	A_95_P017221	TA13249_4097
29513	348	18	106	AACCAAGGCGGTTCCCGTTCTCAGGTCTAGAGGGATATTAAACATATATATCTGAGC	28648	A_95_P151297	EB681522
29514	348	19	760	CCCTTTCATTTGCTTTTATAAGTATTCCCCATTGTAATCAAAGTTCCAGAGCTAAACTA	28650	A_95_P016941	EB683010
29519	348	24	541	GTTGTAGGTGTCACAGAAGTGTAAATTAATCTGAAATGTTGTTGTATTCCAGTTCTCC	28660	A_95_P028931	BP129677
29521	348	26	579	ATGCTTGAAGTGCTCTTCAAACAGTATCCAGGTTTTAGGGAAGTTCGAATGATTGAA	28664	A_95_P024141	FG644997
29527	348	32	155	TTGATCGGTTTGTGACCAATTGGAAGAAGATGGTGAGCAAAACTAAGAGGCAGGCA	28676	A_95_P241795	AJ718638
29528	348	33	523	TCTTGGGCATGTAGTTTGAAGTGTTCTGGAAACACTATTTCTGCATCGAAGTATTTTG	28678	A_95_P093398	BP532242
29529	348	34	500	TTGAACAACTTTACATGTACGGAGCTGCAAGAGTTGAGAAACTACCTTCTCACAAAT	28680	A_95_P274043	AM803406
29531	348	36	483	AGGAAGGCTACATTACTCAGGATAAGAGCTAAACTAAACTGGTCATGTGACTTTTTC	28684	A_95_P015936	DW002874
29532	348	37	497	AGATTTGTAGCATATTCTGCACTTGAATAACGGATTGGTTTGTTTCTTCTTGTTTCGCT	28686	A_95_P091193	BP531249
29533	348	38	809	AAGATACCGGTGATTGGCGAAATCTTCTCCTCACTCTGGCTATTGTGATGAACTGTTG	28688	A_95_P310958	FG139193
29539	348	44	854	TGCATCACTATGTCAGACGAGCAGTTTCAGCTGCATTTGGTATCCGGAGGATGAAAT	28700	A_95_P313198	FG155310
29545	348	50	384	CCCTGCATTTAGTCTTGGCTTGCTAGTTAAAGACTTCCTTTTGATCATGTAATTAAATT	28712	A_95_P204617	EB433325
29546	348	51	901	CTTGTGTACCATTTCTTTTCCGTAAAAGACATACTGCTTAGTTTTTATGGTCCTACATT	28713	A_95_P185252	TA13872_4097
29551	348	56	840	AGATACATCTCTCCCTATCATTGTATAGGTTGCCTTCTTATACTTGTATGTCTCTCAGC	28723	A_95_P145702	EB439273
29555	348	60	625	AACTCGCCATTATTGCTCCGATCAAGTACTGAAGTCTAAATATACGTTGTTTGGAAGT	28731	A_95_P090218	BP530864
29557	348	62	773	TTCAAGATACACATATCCTCTAGGCAAAGGCGATTGAATGAAATTACAAAAATGTTT	28735	A_95_P186267	TA14088_4097
29562	348	67	473	GTGTATCAGGTTTTGTTTCCGCTTCAAATGTGAAACTACTGTGTAGTTATATCTTCTTT	28745	A_95_P030556	DW004407
29564	348	69	537	CGTATTGCTGCAGCACTGATAGAGCGTTACTTCCCTGGCTCTAAGGTTTTGATATCAT	28749	A_95_P135152	FG140309
29569	348	74	236	AGTGCAGTTCTTGCACTCTCCTTTGATACTTTAGACCCTTCATTTGCTTAGTAAATCTT	28759	A_95_P129437	EB429327
29571	348	76	853	TGGAAGCGCTTCCAAGCAGGATGTATTTGCTCAGATCGATGATGCATTAACACAGCT	28763	A_95_P195387	TA16104_4097
29573	348	78	810	ATTGGGATGCTCTATTACTTCTCGGCCTTGGGATATCTTCACTTGGACTGGGTTTCAA	28766	A_95_P267671	DW003261
29575	348	80	498	TAAGCTTCTTAACAACTTTAGTAATTCTGAACGATCAACATGCATATTTGTGAGCGGC	28770	A_95_P282148	AM818174
29578	348	83	296	TGTGAAAGCTAAGTTGATTTCGAAGAATGCTGAGAAGAAGATTAAGGAAGCTAGGT	28776	A_95_P114572	CV021675
29580	348	85	761	ATGCTTGGAGCTAAGAATACGGATTGTTGATGCTGTATCGATGATGGCAACCAGGAT	28780	A_95_P292063	FG159174
29586	349	6	392	TGAAACCACAGAACCAACAAGGAGTTTCTTGAGGAAATTTCGGCTACCTGGAATGGT	28791	A_95_P078340	FS423755
29588	349	8	814	ACTATGACATTTCCTTGGAGGTTCTCATTAAACCTTCTGGGCAAGCTGATTCATGTGT	28795	A_95_P030526	DW000811

29589	349	9	0	CTTGATTGGCAATTTTGATTGCCTGAATTGACAACTTTGTTCGTTTTAAATGAATGCG	28797	A_95_P252269	A_95_P252269
29590	349	10	270	CTGCCAGTGATGTATTTATATTTGCATGTATTATCCGAAATTCGGACTGATTATTTGG	28799	A_95_P028451	AJ632813
29591	349	11	680	CTTCTAAGATCTGCAAATATAGGTCGGTGATCTGATTGTAATAACATACTTCCTTCTG	28801	A_95_P216162	TA20645_4097
29592	349	12	603	CCACTGTAACTCTTGCATCACGTTATCAGCTTGTATTTTAGTAGTATTTCAGATTTCAG	28803	A_95_P208977	TA19089_4097
29595	349	15	789	CATGGATTCGCTTGCCCTCTTCCGTACATTTTTGTTCCAAAGCATATTGGCTAACTTTT	28809	A_95_P016186	EB684163
29600	349	20	766	GTTGTAAAACCATTACAATCGTTGTGTGGAGGACTTTGTTTCCAGTTTAACTTGGTTA	28819	A_95_P271121	EB439696
29601	349	21	191	GAAAAAGTGAAGCTCGCTCAATGAGAACAGCACGGATTCATCCATCACTTACCTCTC	28821	A_95_P210967	TA19508_4097
29604	349	24	1050	ATGGAGAACATTGTTCATCAGAATGCATTATTTGTGGCAAATGGAGAACATTGTTCA	28827	A_95_P013231	TA14467_4097
29606	349	26	348	GAAGAGTGCAAGTGCATTGCGTGGAAAAATTAAACAGCTGGAGTCAGAACTGCAG	28831	A_95_P104712	CV017142
29610	349	30	648	TGCCCTATATGTGATAGCATATCCAGTGTGTCATATTTGTCAAGACAGAATAACACTA	28839	A_95_P019416	TA13279_4097
29613	349	33	681	GGGGTATTGGATGAAGAAAAAATTCTGCCACTTGGAAAAGATATAACAGCTGTTGG	28845	A_95_P116647	DV159410
29618	349	38	526	ACCTTGTTGCCCCGCATGATTGTTGTTACGACAACACATTGGCTAAAGAAAGAATCT	28855	A_95_P021731	FG632147
29619	349	39	441	TGATTTGTGCATTACTGGTGTAAGGCTATATGCCCAATTCTACAAAAAGACTACTTTT	28857	A_95_P177662	BP534995
29620	349	40	124	ATTGTATACCTCCTGTTGTAGAGCCACGCTTTATCTGATCAAGTAGCATGAGTGAAA	28859	A_95_P103807	CV016701
29623	349	43	607	GTTTCAGAAGCTGTAGAATATGACGTAGGAATTTCTTTGATTTTATTCAGCTCTAATG	28865	A_95_P285883	FG643102
29626	349	46	722	AAACGACACCTTTGGAAGCCATTTCTGTAGATAAGGAAAGTCTGAGTGAACTGACTG	28871	A_95_P300918	FG196753
29630	349	50	641	TAATGTTTTGTTGTCACACCACTGGTGTCGAACAATGTTCAGTGTTTTCTTCTAATGG	28879	A_95_P108922	DV161017
29633	349	53	814	TGGTTCTTCTGTGTGTGTCTTTGAGATAGGGGTAAGGTCTGGGTTTGTTGTTGTTGA	28885	A_95_P218362	DV158095
29637	349	57	203	GTTCTATATTGTAATATTTGGATATGGCACCCCGGAGAGGGAATTGCAATACCCAGT	28893	A_95_P131382	EB431569
29638	349	58	915	GTGTTAGCCTATTTCTTTTTTCTTTGGGCTGATTAAACAAGAAAACACCAACGTTTCA	28895	A_95_P209667	TA19239_4097
29640	349	60	795	CAGTGAACGGTCTGAACCATTTTGTTTATGAGATTCGTGCATGTATCATTTCATCTTA	28899	A_95_P010891	TA12346_4097
29644	349	64	628	TGAGGCTATTACTGACATGACAAAGATCTTGGAATTGGAACCCTCAAATGACCAAGC	28906	A_95_P268661	FG644203
29648	349	68	401	GAGTTAGTATTTATGCCCCTGTATATATATAGGTACTGCGTCATTGATATTAATGAAG	28913	A_95_P090833	BP531110
29651	349	71	775	CCTTTGTCTGCTTGTTTGTGTATGACATATTTTGGGTTTCTATTTCCGAGAGAATTCC	28919	A_95_P156567	EH614287
29652	349	72	759	ACTCCATTAACATAGAGAATAGTTGATAGCGGAGCACAGTTGTGGGATGGCGCTGA	28921	A_95_P267411	DV160064
29653	349	73	753	CTTGCTATAAAATTTTCTTATCCTGGATATGGTGTTAGGTGTTGAATTGGATCCACAA	28923	A_95_P013417	TA12814_4097
29658	349	78	928	ATATCTTATGAATAGCAGACGTTTCTGTGGGAGCTGCATTTTGCACAAGCGGCTACA	28933	A_95_P212902	TA19934_4097
29659	349	79	787	ACCTGTACGAATTTGGAAGTTGGTTTAAAGTTTTGATACCTTGTTTCTCAGTGATACC	28935	A_95_P242697	TA11945_4097
29663	349	83	563	TTGGCTTTGATCCATTTTGAGTATTGAACCTTTTTTGCTATTAGCTTGAAGAAGCTTTC	28943	A_95_P031949	TA21989_4097
29665	349	85	563	CAGCAATCGAGGTCTATTTCTCCCTTTCTTCTGCAATTTTATGCCTAATATCATACGAT	28947	A_95_P304503	FG635940
29670	350	5	715	ACGACGTGAAATATTGGGCTCACGTCTTTGTTGCCTCATTCGTTTTTCGTACATGACA	28790	A_95_P301338	FG199627
29674	350	9	446	TCAGAGGATTGTTAGTGTTTCAGTTTGGTTGTTGTGTATACTTTTTATCTTGTACCTGC	28798	A_95_P280458	FG643681
29676	350	11	492	ACCTATCCAGAGGAAAGTCGGTTGTGGCATTAATGTGAATATTTATGGAAGTGTTAT	28802	A_95_P143032	EB446415
29677	350	12	770	GATGAGGATGATGGCAACAGTGAGGAAGTCATCAATGCCATTATGCATGATGTTGA	28804	A_95_P145332	EB448999

29679	350	14	110	CTCCAATCATGCTACTCAGACTATATGCTTAACACATGCAAGTCGAACCTTGGTTTTC	28808	A_95_P143992	EB447190
29681	350	16	540	TTCCTCTATTTTTGGGTAGTCCAGATGATATAGAAGAATTACAGAGTTATGGGGATG	28812	A_95_P149562	EB679464
29685	350	20	165	ACTGTGAATTCAGTGGGCTCGGATTTAATTTTGTTCTTCCTATGCATTTCTGTTTCTCT	28820	A_95_P130307	EB430336
29686	350	21	738	AACAAGATCCATCATTCCCTTTGCTTTCTAGAATGATGGCAGAACCTCAGACTCCCTT	28822	A_95_P300348	FG133179
29687	350	22	545	AGTCTGCACTCATGATATTTTCGTTCTATTAAGCTTGCAAGACAGTTTGTAGGGAGTT	28824	A_95_P106907	CV018115
29688	350	23	783	GAAATAGTCTAATCTGGTACATGTAACAACCAGATTTACAGTTCTGGTAGCCATAGTT	28826	A_95_P213582	EB683159
29689	350	24	861	CACTCACTTTCACTATGGACCGATAAGTACATGCCTCGATTGCAATATGCTGACTTTC	28828	A_95_P298758	FG143943
29691	350	26	348	ATTTGTGAAGTTCTCAAGAAAGACCTGGCTCAAGACACAGTCAATGGTTGGGGAGA	28832	A_95_P033939	AJ717935
29694	350	29	685	GGTGGATGCTGCGGCTAGTGTCAGATAGGTCTAAGTTGTAATGATACTGATAAACTT	28838	A_95_P284073	FG642702
29696	350	31	830	GGGTGTATCCTAGTGAGCTATGTTCGGAGAGCATTGTTCAACACATGGAGATTAGAC	28842	A_95_P293093	FG152454
29697	350	32	1322	GAGTGAAAGTGCTCTTTCGTGGACAACCTTTTTATTTCTGGTTAAAAGTTATCGTTCT	28844	A_95_P015816	TA15336_4097
29698	350	33	440	GCACTTTATTCGTACATGGAGTGGGGGGAAATGGAATTTTATTTTTTATTTCACAAAT	28846	A_95_P205102	TA18208_4097
29702	350	37	105	GGTTGCCATTGTGAATCTAGTTTTGTCATCTCAATATAAATGTAGATGTTGCTTGTAG	28854	A_95_P141217	EB445002
29704	350	39	1280	TCGTCTGATGATGTTTCTCCACAGCATGCTGGTGAAGAAAAGATTCAGACTCAGGTC	28858	A_95_P020811	TC50293
29708	350	43	876	GTTATATTTCAAGACTCCTCCACCCTTTTCCCCCTTTTCTGATGCTGTTGTCTCATGTAA	28866	A_95_P176972	CK720598
29710	350	45	853	CTCAGTTCCTTGGTGGAAGGCTTTATGATTGCGTTTTCAAATTTAATGAAGCTTTAAG	28870	A_95_P022111	TA17098_4097
29715	350	50	144	TACAAAGAACTCGAGAATGGATGTCTTTGGGAGGTTCAAGGGCAAGTAGGGTTGTT	28880	A_95_P107412	CV018357
29717	350	52	368	ACTCGATGCTTTTATAGCTGCCCGCCTAAATTCACACCCTGGAAATTTCAAAGTCATC	28884	A_95_P078805	BP527608
29720	350	55	702	TCAAGCTGCATCAAATATCACAGCGTAGTTCTTCTCCAACTTCTTGTGGAGTCTGTCT	28890	A_95_P126892	EB425446
29722	350	57	876	CCGAAGACTAAAGTTGTGCTATTTTAATTATGTTGGCATGAATTCAGCATTGATGTAT	28894	A_95_P198397	EB426241
29724	350	59	843	AGCCTGCAATTGTGTATGCCTCTTCCCTCTTATGGAGATATGATTCGCTAATGTGTTTT	28898	A_95_P010416	EB443735
29725	350	60	1011	GCATATCCCTCCTACATGAGTTAAGCATGCTTGTTTGATTATGAGTAATTGCCAAAAT	28900	A_95_P216152	TA20643_4097
29726	350	61	0	TTTAGGGAGTTTTTTACCAGCTTTTGGCGTTCTTCTCTGCCGGAACTTCAGTTTTTCCG	28902	A_95_P236779	A_95_P236779
29727	350	62	795	GCGGCGAATGGATTGCGTGTGTGACTTTTATTAAACAATATATATGCAGGTAAATTA	28904	A_95_P234649	DV160879
29728	350	63	338	GTCTTTGTCTGGCGGTCTTCCTGAAGGAAAAGAAGGAAAAATGTGAAGGAACTAAA	28905	A_95_P226639	AM826041
29730	350	65	1010	AACTGGATATGGTCACTACATCCTTCTATAGTTCCATTGGCATCAAGTTTGGTGTCAC	28909	A_95_P011466	TA15775_4097
29731	350	66	421	TTTGCCCAGTTGCATTATGAAGCATGGGTGAGATTTGTTGTTCTGAGCATAGTTACAG	28911	A_95_P052561	FG143081
29736	350	71	758	GAATCTGATAGAGCAGCAGAGGATGCGTGATTTGGTATTTGTCCATTGTAATTTGCA	28920	A_95_P147457	EB451895
29738	350	73	1743	TGTGCAACTTAAGTTGGGTTAAGTTTCAGCTCATCTATTGACGTTGTCTTCTCATTCTT	28924	A_95_P188622	TA14611_4097
29742	350	77	808	TTATGCTGCACCTTTCTGTCTAACTAAATCTTGTCTCGATCAGTCTTCTTGCTCCATTAC	28932	A_95_P029156	EB426381
29746	350	81	623	ATTTATGAACAGTATGTGGCATTGCATGTTAATTATGGAAAGAAAAGGCCTGGCCCC	28940	A_95_P241415	EB684021
29749	350	84	490	CTGATGTTATAGTCTAGAATATCCCCATTGTGTTCTTAGAATGATCATTGGAAGTTGT	28946	A_95_P203677	TA17904_4097
29756	351	6	2714	CCTGTTCATGGCCTCGCCAGTTTCCTTTTTGAAGAATAAATTTCAAATAACAAGAACT	28959	A_95_P010241	TA15676_4097
29757	351	7	1040	TGTAGCTCAGCGGATTGGCGTATACACAGCCAAGGACTATGCTGATATTCTGGAATT	28961	A_95_P012081	TA16904_4097

29759	351	9	896	CAAAATTTGCTACTCTTTGCAAATTCGGTATGAAACTGGTCTTTCAGAATCTACTCTC	28965	A_95_P190352	TA14997_4097
29761	351	11	285	TCACGAACTTGTGCGCCACGATGTTAAACAAGTTGTTTGTGCTGTATGCGACACTGA	28969	A_95_P148142	EB432321
29765	351	15	532	CTTCATTTTTCTTGTAATAGGACATTGGCTTTAGCATGGAGTTTACGAATCTTTCCGG	28977	A_95_P068250	BP137086
29766	351	16	126	GATTTTGGAAGAACCACTGCATGTGTTCCAAGGACATAGTGGGGAGACATTGGATG	28979	A_95_P274248	TA21917_4097
29768	351	18	395	TTTCATGGGTCTGAAATTTTGCTGCTCTACTGCTGATTCACTGCGTTGCTAGCTCCGAT	28983	A_95_P096518	BP533665
29771	351	21	255	TCCCCTGCTCATCTTGACTGCTGGTACCTAACTTTATCTTATGAAAACCTAAAAGAAG	28989	A_95_P095228	BP533086
29777	351	27	776	TTGCTTTCCATGAATTTGCTAAGGGACAGGCACGGTTAGCAAATGGCATAGCAGATG	29001	A_95_P228134	EB451350
29780	351	30	833	AGGTACAAGTGAAAAAGTTATTGCTGTAATAAAAGGGTGGGGAAGACACGCTTCGG	29007	A_95_P010301	DV999902
29781	351	31	945	GTTAGGTGGGAATCTTTTCCCTTCACCCATTCATTTATCTCATATAGTTGCCTTTTGCTT	29009	A_95_P009896	TA15282_4097
29785	351	35	321	CAAAACTTGATGTATATAGAAATAGGAGGCTGAAAGTGCCAGATTGGTGGAGATAG	29015	A_95_P032241	AM844046
29787	351	37	279	TTGGGTACTTGGGGCTGAAAAATGTTAGGTTTCTAAGTTTTTGCTTGTTCAATGATGT	8937	A_95_P000091	AJ717873
29790	351	40	811	CAGTTTCAACTTATAAGGCTTATCCTTCTTGTTGAAGTTGTGAACATAGTGTACATTA	29024	A_95_P134942	EB437933
29793	351	43	1024	GTTCAGCTGCTTGTAAAGATACTCTTTTATGTTCTAATGCCTAATGGACTGAAAGTTA	29030	A_95_P198157	TA16718_4097
29794	351	44	742	GTTGTCTGTGGGCGATGACCTGTTTTGTATTTGTATATTTGAGCTGTCTATAAGATAA	29032	A_95_P246182	EB681232
29803	351	53	720	GTGAGACAATTATGAGCAATATGAATTGTAGCCTACAATCTATTAGCTGGTTGAGAA	29050	A_95_P180802	DV157753
29807	351	57	769	TAGCTATGATGCCAAAAATGATATTCTTTTTCTCCGTCCATTGATCCCAATAGCCTTTC	29057	A_95_P016021	DV159904
29808	351	58	385	ATCTTCAGTCAGATTTGGATGTATCTAAAGTCGACCGGTTTTAATGAGGTCACCGACT	29059	A_95_P214562	DW003267
29810	351	60	599	GCCGTTTCATCGCAGTATGCAAGAGTGAAGAGGGAGATTTCACCAATTAATTTGTCG	29063	A_95_P305303	FG201973
29813	351	63	863	ATGCGACTCGTCTACTGGCTCTGATGCTTCGAAATCTTGGCTTGAGAGCTATACCAAT	29068	A_95_P226414	DV161544
29814	351	64	926	TGATCCTTTTGAATAGTGCTGGCAATGTTATTCCTGGCTATTCTGGTTCACGCCATTCT	29070	A_95_P116607	DV159363
29815	351	65	358	TGGTCATCTCCTGTTTCGTGATGCTTTATTCAGGTTATGAATAGAATAAAATGTGGAG	29072	A_95_P127087	EB447417
29819	351	69	854	CCACATAATTCATCATTCTCATCTGGCTGGATTTGTGTTTTGCAAATTTTAAAGAAGC	29080	A_95_P292638	EB427870
29822	351	72	1096	CAATATACTTGGCAAATTGTTAAGAAATTTTGTTCACTGTCCAGAGATCTACTTGGCC	29086	A_95_P176457	Y14432
29825	351	75	731	TGTTGTAGCCCTGATGAAGTAATATTTGGCCCTGATTTCCAACAATCTTTGTACTGTC	29092	A_95_P205152	TA18219_4097
29826	351	76	513	CGTCGTGCTAGTGGACTTTTCTTGTTTTGTTAACTCTTTGTTTCACAGTTAACCCCTTT	29094	A_95_P203082	TA17778_4097
29827	351	77	576	TATGGCGAGAGGTGGTCCTGCTAAGGATGACCTCGAATCGAAGAACAGTTGTAATC	29096	A_95_P054066	FG144419
29830	351	80	867	GTGGACACTGATCTCTCTAAACCATTTCAAAGAAATGTTCCAAAAGAAAAACTTTTCA	29102	A_95_P217887	EB425233
29834	351	84	825	GTATTCATCATCATCATCCTCATGTTGGTCATCCCAAAATTTGGATTTAATACCTTACT	29110	A_95_P294958	EB443115
29839	352	4	513	CACATATGGCTGGAGCGAACAAGTTTCGCAATGCTCAATTTTCATGGGTCACTGAGA	28956	A_95_P261896	BP133968
29842	352	7	119	TTCAGGGGGAGCTATATACATGGCAGTACTAAGTTGCAGTAAGTGCGTTGCACTTCA	28962	A_95_P034918	BJ999167
29843	352	8	455	GTATGCTATAGGTTTGCTGGTGTTATGTCGAAAGTTTTCTGTGATATTTTCTGAAATC	28964	A_95_P192907	TA15556_4097
29845	352	10	723	GCCTTTTTCTGAAGGCAGATCCCACAGAAACTAGAATCACAGATGTTTTATTCATAAA	28968	A_95_P135857	EB439411
29846	352	11	115	CCGCAGTTGTTAACTCACAATTGTAGCTAGCTTCATGATCCTTGCTACTTGTATTTATT	28970	A_95_P030636	EB432279
29847	352	12	290	GGAAGGTTGAAGAAATGTGTATGAAGTATAGGAAGGTGATTATTCTGGTTGTAAAT	28972	A_95_P161742	EH620369

29852	352	17	249	CTGTTAGCTTGTTGAACTTTAACCGCTGTTGGTGAATCTAAAGACTAGTACCTTTAAT	28982	A_95_P064655	BP136109
29854	352	19	308	AAGACTTCAAGCTTATTGGGGATGCCGCTACTGCTTAACACGTGCTAAATGAATGCC	28986	A_95_P108467	FG637164
29858	352	23	195	TTAACTTGAGCTACTTATGTATGGAGTTACTTTCTGTGCTACAATTTGTGCCTTTTCCC	28994	A_95_P139362	EB443105
29864	352	29	877	CAAGACTTTGATAAGCTCATTAATGATGGTCTCCAGGACCAATTGCTCTTGCTCTATT	29006	A_95_P115972	DV158471
29870	352	35	756	GGCACATTGTGCCATATAGCTTATACATGATGTTTTCCTATGTTTTCTGCAACATTAAT	29016	A_95_P129867	EB429803
29872	352	37	321	ACGGCTGTGAAGCTAGCTTGTGAACCTACTTTATCTGGTGTTTATTAGTATTGAATTG	29019	A_95_P133847	EB435545
29873	352	38	268	CCTTGTGAATCCTCCAACTTGTGCTCTTTGATCTTTACATATTCTCTGCATATATATGT	29021	A_95_P011981	TA14209_4097
29877	352	42	595	GCATTTGCATTACCATTTATCAGTCATTTGGGGTCAAAAGATTGCCTCTTAGACCCCT	29029	A_95_P123912	DW003780
29880	352	45	585	TGGTGACTACAGGGCGCGAGATAGATTCAATTCAAGGCAAGGACATTATCAAAGTA	29035	A_95_P097788	BP534194
29882	352	47	909	GGGCCCTCTCTGGTTTCATTTGCTTTATGATTAATGACTGAAAGATCCAGTTGGAAAA	29039	A_95_P230929	AY029330
29885	352	50	800	TGCTAGAGAATGAAAGATTGGCGGGGTCTAAATGAAGGATTTTGTAGTTTTTGTCGC	29045	A_95_P006841	NP916736
29886	352	51	848	GATTACTGATTGTAATATTTTGTGTTTGCATAAAGTGCTCATAGCGGCACTTCATTCT	29047	A_95_P201952	TA17530_4097
29887	352	52	695	GGGCTTTCCATCAAGGAACTGAAATTTAATGTTCACATTTTACAGAGACTGATTATTG	29049	A_95_P015956	EB439763
29891	352	56	820	ACATCAAGAACGTGATCATCCACGGACTCCATATTCATGACATTGTCGAAGGAAGTG	29056	A_95_P217717	EB428683
29892	352	57	688	AGATGTTATTCTAATTTCAGTAGAGCGACGATCTTGTCTTGTTAACAAGGGACAACC	29058	A_95_P182242	TA13166_4097
29899	352	64	775	ACAAACTAGTAGATTACATGACTGCAGACATGAAGCTGTCTATGATATGCGCAACAG	29071	A_95_P015191	DV157952
29900	352	65	220	TGTTGACGGTAGTTCGGGTGTGTATGGATTTAACTCTTTTTCTGGCTTTCCTACCCTT	29073	A_95_P110932	TA13705_4097
29901	352	66	856	TTTCTCCCTTTTTTCCTCTCTGAGAACGCGGAAGGAGGAGGAGAATCAGATGATTCT	29075	A_95_P194937	TA16011_4097
29909	352	74	849	TGGCCAATATGATGGGAGGATTTACCAGTCCTTTTGTTGGGTTGAAATAAGGTTATT	29091	A_95_P180717	TA12812_4097
29912	352	77	1117	TGTATGAGAACGTTGCTGAGTTTTCTGCAACATAATGTAATCTGCGATCCTTTTCCCC	29097	A_95_P015396	TA13588_4097
29915	352	80	798	ACAGACTTAGCTTCTCTGATGTGATGTTGGAATTGATATGGGACCCGAGTTGCTATG	29103	A_95_P230654	FG155645
29918	352	83	2690	GGGTGGGTTTGGGAGATATAAAGCTGCAAAGAGAACGTAAATTCAATAGTAAGGTA	29109	A_95_P007346	AF053104
29920	352	85	693	GCAGCGAAAGTCCTGCTACTCTATGGGGGGCTCTCATATAGACATCACTAATCTCATT	29113	A_95_P297558	FG187304
29923	353	3	869	AGGAGGGCGCAACAGTGTATATAAAGCTCAGCTTTCTGATGGAAAATCAGTGGCAG	29118	A_95_P118397	DV161441
29927	353	7	370	ATTGTTTGGCTTGCAGAATTGGTTCACATCTGCTGATCGGCTGTAGATTCGATCGTCT	29126	A_95_P104537	CV017059
29928	353	8	845	TAAATTACGGACTCCGGTATTGGATTTGCTTAGAATGTGCTAGTTGCTTTTCCAACAA	29128	A_95_P123787	TA13072_4097
29929	353	9	483	CAATTCATTCTTTTGACTCATTGTGAGGTTCTTGAAATATGTAGGGTAAAGTTGAAAG	29130	A_95_P276473	AM799834
29930	353	10	348	TCTCCGATAAGATGAGGGCTACTGGAGGTGGTGAAAAGAAGAAATGAAACCTGTAT	29132	A_95_P104522	CV017053
29931	353	11	930	GTTATGTTGTTTGGAATATGAATATGAACACACACATATACCCGGAGTATGTTGTGA	29134	A_95_P267246	DV159437
29935	353	15	500	GAGTAGCTTATAACTTCGTTGGATGTCAAATGAAGTAGTAAGAAACATATTGTCGAG	29142	A_95_P000321	FS412805
29936	353	16	236	CTGGAATGGCATTGTTGAATCCAATTTTTCGGTTATTTCAATAGGCTTAAGAAGGAA	29144	A_95_P103097	CV016343
29938	353	18	416	ACAGGTGGAGCAGCAAGTAACCAAGCTGGAGTACTAATAAGTAGGATCTCGCATTC	29147	A_95_P276608	AM784309
29943	353	23	859	TTTCTCAGAATTGTAGACCATACACACACCGGGATATGAAGAAATTTTCTTCGACGTT	29157	A_95_P192062	TA15372_4097
29946	353	26	719	GCATTGGTAGCAACCACAAATTGAAATCTACAAAATTTGGCGCAAGCAACAATTTGT	29163	A_95_P182917	TA13336_4097

29947	353	27	746	TGAGATCTTGGAGAGAGTCAGAAGCTTCAATAACATTCATAGTTGGAAGGAAATATT	29165	A_95_P215087	EB678557
29951	353	31	814	TCTTGAAAGATAAGCTTGAATCAAAGGTCTCGTGATTACAGACTGGGAGCCGCTTGA	29173	A_95_P191032	EH615740
29953	353	33	762	CTGTCTCTACCTCAACATTTGAGTTTGAAACTGTCATTGGAAATGTGTTTCAATTCTTT	29177	A_95_P105527	DW000646
29957	353	37	1410	TCTGATGTTTCTGTGTGTGCGGAATGTGCTATTCAATGCCATCTAGCACGGAATGACT	29184	A_95_P215562	TA20513_4097
29959	353	39	492	GCTATTCTAATACAATGATTGCTCTTGGATAATGTTGTCTCTTTTGAAGAAGGTGAGG	29188	A_95_P153397	EB683684
29960	353	40	867	TTGATAACAACGAGTATTTGAGAATAAAGGCCGTGAACTTCGGGACCATCACCGTTA	29190	A_95_P260751	EB677958
29961	353	41	868	GAAGAGGTAGATGCACTCTTGGACAAGTGCCTTTCTTCAAGCATTACATACGACAAT	29192	A_95_P008211	DV999212
29962	353	42	1313	GGCCAGAATTGCCATAACTTGGTCAAGAAAATTTTCTTGAAAGCTCTTTGTTATTATG	29194	A_95_P191162	TA15169_4097
29971	353	51	763	CCCAACTAAGATTGACCTATAAATCAGTAATTGATGCATACAGCTGTGTATTGTTACT	29211	A_95_P123932	DW003796
29977	353	57	429	AGGTCATTTTCTTTTGACGAATTTGTTGTTGGACAAGATGAAGGAGACAGCACGTAA	29223	A_95_P126702	FS435586
29981	353	61	694	GCAATCACGTGGGAAACATAGGAGCTCTGTATAAACATGTATAGGTTAAAAATTACA	29231	A_95_P235134	DW001858
29986	353	66	561	AAAGTGATAGTATTTGATGATTTTCCAGCTGACAAAGCTAGAGCAGTGATGTTATTG	29241	A_95_P150912	EB681065
29987	353	67	261	AGATCACAACCAAGCCACTGTTGACTATAGAAGATAGTGCGTGACACATGCAGAGG	29243	A_95_P005016	AF127243
29994	353	74	162	ATGCAAATGGTGGGTGCAGATTGGTTGAAGTCTGACAAACGAGAAGATGATCTAGG	29257	A_95_P116622	DV160201
29995	353	75	702	TTCCTGGTCAATGCAAAGGATGTTATTAGACCAAACTTGTCAGTCCGTGAAGGCATA	29259	A_95_P132252	EB432691
29998	353	78	751	ATGACACATATCTACCTTTCCTTTTGGAAGCATGCAATGACGAAAGTCCGATGTCCGC	29265	A_95_P310849	FG163453
30001	353	81	625	GGGAAATGTTACCTACCAATGGAAAAATCGTTCTTATGGACCATACAAATGTTCTAG	29271	A_95_P291518	FG640068
30006	354	1	770	GGATGATTGTGAACTCCTTGTTAGCTCTTTTTATTATCCCTTCTCCAACTATGCTCCAT	29115	A_95_P156587	EH614311
30007	354	2	836	GTGAAATCATACTTTGATTACCTGATGGTAGTTTGTGTATGGCCATGATTCATTACTC	29117	A_95_P216272	EB451507
30015	354	10	743	ATGGAGGTTACCAAATACCATACGGCTTCTTGTTCAATATTGTTACCTGTGCCAATTA	29133	A_95_P196592	EB451156
30017	354	12	767	AATTCTCGATATCTTGGCAGTGGAAGGGATCATGGGTATGAACCTAGAGTCCAATAC	29137	A_95_P117327	DV160221
30019	354	14	192	ACTTGAAGATTACATAAACTCTGTACGTCGGCCTTCTTAGAGTATCGGTCCATATGAT	29141	A_95_P103427	CV016498
30020	354	15	386	TTCAAGTTCTTGATTTCTGGTTCAGATTTGGTCGGTGTACTCATTCAATTCCAATTCAT	29143	A_95_P085325	BP529250
30023	354	18	632	GGTAATCACAGTGCATTTGAACAAATATGATGTTAAAGAGTAATACTTACCCTTTCTG	29148	A_95_P020201	DW005223
30024	354	19	340	GAAAAATGCTCTGGATCAAGTTCCATTTTGTGGGTGTGCTATTGGAGCTGTTGACGG	29150	A_95_P128152	FG167375
30025	354	20	722	AACTACTTGAATATGTTAGGGAGGAGCATCCAGAGTGGGAGATCAAAAATGGCTTT	29152	A_95_P285208	FG640001
30028	354	23	835	GCATCATGACTCTCTACACCATCCGAATATATTGTTGTACTAAAATTTAAAGTGATGG	29158	A_95_P156482	EH614055
30030	354	25	607	CAAAGCCAGATATTCAAACTGTGCATAAACTCAGATTACATCACGGATGGAACCGGG	29162	A_95_P047861	BP131763
30032	354	27	50	TTAATTTTTTAAGGGGGAAAGTCTACTAAGGTAGCTTGCTATCTGGGCTTTCGCGCG	29166	A_95_P112592	CV020749
30034	354	29	608	GGAGAGGTGTTTCCTCTTTGCAGTTCAGCGATACTTTAATGCATGTTAACTTTTGAAT	29170	A_95_P001136	FG137226
30041	354	36	164	GCAGAGATTGGGAAAATGTTTTGAAGTTTGGATTTTGCACTGATGGTAAGAGTTTTG	29183	A_95_P133322	EB434721
30045	354	40	668	CAGACTATGATCCTTAATAGCCCCCGTTTACTTATGAGATGCTTCCGAGGTTTTATTG	29191	A_95_P051736	BP132731
30051	354	46	737	GGTTATCGTCTGACTAAGCAAGGCAAGAGTGTTTACAACATGGGATGGAAGCAAGT	29202	A_95_P219367	EB425508
30053	354	48	617	TAGCTAAAGTACACTGAATTTGTAAATATGCTGACCCCCAGCCTTTAAAATCAGATTA	29206	A_95_P028356	TA13727_4097

30056	354	51	209	TAACTATTAACTTTTGCTATGTCGCAAGCAAATCTTGCCATAGGATGAGCATTTCCCT	29212	A_95_P100808	BP535527
30058	354	53	475	AATTATTGTCGTTTGAGGAAGTGGGAGTCAGAGTTTAAGCATTCCAGTGCCGATTTG	29216	A_95_P046131	BP131320
30059	354	54	878	CGAAGTAATTGGTTAACAAGTCTGTTGAACAAGTTAGGTTGACTTGGAAAACATCAG	29218	A_95_P204282	TA18032_4097
30060	354	55	821	ATTGTCTTGGTGAAATCTGAAGTTGCAGAACTCTTGTTCCCTCATGTGATGGTCAATT	29220	A_95_P126727	EB426077
30061	354	56	709	CTATAGGACAATCATAATCCTCTAGGGGACAGTTGCTTGGAGTTGATCATAGGTTGG	29222	A_95_P289333	DV158709
30062	354	57	257	ATAAGCTTAGGTCTTTGGAGTCGCTGCCTCTTAGCATTAAAAAGAATCCAAGCTTGG	29224	A_95_P104882	CV017206
30064	354	59	464	CAAGAAGATGATGTCTAAGGCTTAATGTCATTAACGGTAGGCGTTTAATTGAATTGA	29228	A_95_P022656	EB432036
30066	354	61	909	TGAACCAGACGATGTGTTATTTAAGTGGTGGAAGCGAGTCCAGCAAGATATATTGC	29232	A_95_P024166	TA12892_4097
30073	354	68	1951	CTGTACTTATCATTTTCAAGGACTTGGGACTGGTTATACCAAATATTTGGGGTTGAAA	29246	A_95_P297848	EF051140
30076	354	71	767	TTTTCCTTTGACATCTGATGCACTAAAGAAGGTCTTCACCGGTGAGGCTTCACGAGA	29252	A_95_P227339	EB678381
30077	354	72	418	GTTAGGTACCACACAATATATTTAGTTCAAAACTAAGAATATGCAGACACTCCACCTC	29254	A_95_P024621	EH615205
30079	354	74	430	TAAGCGTTTGTATTGATAAATTTGGATGCTCTAACTCGTTTGTAATGCAGTTCCCTAT	29258	A_95_P027501	FG641634
30080	354	75	686	GTAATTAGTCTTGAATTTGTATGCTCAATTTTACCCTTCTCGGGTTGTGATAAAATGG	29260	A_95_P116652	DV159412
30081	354	76	128	GAGCTTTTTGTTAATTGATCAGGTCTTCTCAAGAAGATCTGAGAAGGGGTTTCGTTTT	29262	A_95_P152132	EB682439
30083	354	78	856	TTAAGTTTCCTATTTCCAACAGCAATGCACAATCTTGGTTGCTGACAACATACCTGGA	29266	A_95_P245817	DW000156
30084	354	79	853	GGATTTTGCACCGATGGTTAGAGTTTAGACAATTTGTTTTTGAATCAGACGATGTGTT	29268	A_95_P010581	TA12891_4097
30086	354	81	513	TTAGGGTTATTGGGTAACTAGGCTTATCTGGGAAATTTGGGAAACTAGTTTTCCTTCT	12052	A_95_P000101	FG167017
30094	355	4	1384	CGCGTAGGAATGTTCATTGGTTGGTTTAATACATTCGGTTTTAAGATGTTACACCAAA	29286	A_95_P239069	AB077051
30099	355	9	427	TGCTTCTTTTGGCTCTTGAAATCAGGCTGATGGATTGGATGATTTAGGCACATGTATT	29296	A_95_P091693	BP531460
30106	355	16	270	AAGAAAGTACACAGCATGTGGTTTCAACAGAGAGGGTGTGGCCATAGCGGTGCAAA	29310	A_95_P038596	BP129312
30109	355	19	707	AAAGGGCAAGAGCTTCCGGAGGACGTTTTGCAAAAAAGTCAGATACTGATACTTCA	29316	A_95_P145527	EB449275
30114	355	24	845	GCCACTTGACAGTTTAAGTACCTTTGTTTTAGTGTTTGTACTTTTAATCGAAGAAACT	29325	A_95_P016356	TA15811_4097
30115	355	25	306	GTAAGTCAATCCTTTTGACTATTACAAATGTATTAAGCCATAAGGCAGTAATTGTTCC	29327	A_95_P133097	EB434257
30117	355	27	811	GCTCATGAATTCCTGGAGGATTCATTGTATGGCTATTGACATCAGTTTCTAATTCAAT	29331	A_95_P234934	EB424629
30118	355	28	787	AAATGTAGTGGTAAGCTGCTTGAAATTTTTGTCAAGGTAGGAAGGCCGAAGGTAGC	29333	A_95_P208362	TA18952_4097
30120	355	30	652	ATATAGGTAGCACCTTAGGTTGAGCGTGCAGTCATAGTCTGATGAAGCTATGTTTCT	29337	A_95_P283313	FG637159
30121	355	31	1328	TATGGTCGCGAGGCCCTTGATGTTATGCTTTCTTTCGACAAAACTTACTCATAGGTCG	29339	A_95_P239224	AJ608157
30122	355	32	431	GGACAAATAGGGGAAAGTTGGCCATAGACAATAATCTTGGTTACATCAGGGTCATC	29341	A_95_P109622	EH623214
30124	355	34	808	AGATGTAGTAATCAGAGTTCTAAGGAGGAAAGGCTCCGCTCTTGTTGTCATGTCTTC	29345	A_95_P196992	TA16463_4097
30125	355	35	402	CTTCAAGTTCTCAATCAGCATCAATAGAGAATTTGGATGAGTTAGTGATGCGTTTGA	29347	A_95_P095253	BP533101
30127	355	37	785	ACTATCTCTTGCTTCAGGTTCAGGTTCAGGTTCAAATTTGACAGGAGTAGATGCTGA	29351	A_95_P190912	EH620499
30132	355	42	865	GATGTATATCTGTATCTAAACCCCCTGTAGATTTTTGCATTGTAGTGTTATCAGCTCAT	29361	A_95_P270351	EB431314
30135	355	45	746	AGAACGACGATGGCATTGATGATGAAGGTACAGATGATTCCTAGTTAGTAAGCTTCT	29367	A_95_P151072	EB451434
30136	355	46	333	CTCTTTCCAAATGTAGAAACAAAAGAACCATGACGAGGCCTTCTCTCATCTTCAGTTG	29369	A_95_P043026	BP130505

30137	355	47	1520	GTAAGTAAACTCATAGCTCTGCGGTGCGCAAATCTGCTTGCTAGTTTATTTCTGAAAA	29371	A_95_P228424	AY429423
30140	355	50	972	ACATTCGCGAGCTCGGTTTGAGCTTATTATAATGTTACTTGCCTACGTAGTTTTCCCT	29377	A_95_P008516	TA13284_4097
30141	355	51	905	CCATATGTCACAGGGTTGTGGTTCAGTGCTCATTAAATTGATAACTGAGTGTATCATA	29379	A_95_P197882	TA16660_4097
30143	355	53	405	GATATGTGGGGTTCTTGCCCCAATTGCTTTAAAAATCAGTGATAAATGCCTTCTCTTT	29383	A_95_P089693	BP530609
30155	355	65	293	TTGTAAAAGCAGATGTAGGGAATTGATCTTTAGCAAATACCCGATCTTCAACCTGTG	29407	A_95_P026126	TA13159_4097
30157	355	67	742	TTTCTTCTTTACCAATGCAAAAGATTGCTGAAAGAGCAGAAATACAACTATCCTCATG	29411	A_95_P316838	FG196017
30159	355	69	335	ATTGGGATATGATACCCTTTGGAATCTCACTCATGGTGGCTGTTGACATTAACTAGTA	29415	A_95_P111902	CV020422
30161	355	71	662	ATAGTGGTGCTTATGATGTCTTTTGGACTGTTTTTTGTTGTGTGTAAGACCTTTTGAT	29419	A_95_P246317	EB430087
30162	355	72	727	TGCAGAAACTTCTTAGAACAGCTCGATTTGAGCGTTGAGCAATATGATGATAGATTA	29421	A_95_P228219	DW000115
30167	355	77	546	AGTCACAAGCCCAGAGAGAAGGTTCTGTCTCATTTTCCTAATATAGCTGCTGAGTGT	29431	A_95_P152517	TA16178_4097
30169	355	79	1198	CGAATAATTTTGCTGGCTGCTTGCTAAGCATTTTCCAGATTTGCTGGCAATTTGTATT	29435	A_95_P182592	TA13254_4097
30172	355	82	813	AGAGGAGAAATAGCAGCCAAATTGATGCCTTACACTAAACATCACCTTGTATTGTTA	29441	A_95_P152577	EB682912
30174	355	84	377	ATGTCTGGTCCTTGTTGTGACTGATGGAATTATCCTGCTTCTAAGCCCTATATTTGAT	29445	A_95_P186652	BP534468
30180	356	5	220	TGTTGTATGTGGATTGATCATTCCTAGTCCAACTTGTCACTAAAGAAACTATCCTTCA	29289	A_95_P098033	BP534304
30181	356	6	882	GTTTTACAGGAGGTATTGCAGTATTCTTGGAGTTAGTCCTGGTGACAATCTGGATTG	29291	A_95_P305858	S44869
30183	356	8	232	TGCATAATACACTTTTCAAGTATTTCCACATCTGGTTTCTTGCCGGAGCCTGTCTTTTT	29295	A_95_P131807	EB432218
30195	356	20	316	ATACAGACCCATACTAAACACAGATGATTGGTCTCCAAGCGGTGATGTCCTATGTAG	29318	A_95_P111352	CV020163
30196	356	21	1192	TGCGTTTAGAATGTTACAATGTACGTGTAATGTTAAGTGGAGTTGCTGCATAGCAGT	29320	A_95_P206137	TA18442_4097
30197	356	22	824	AATTTGATATCGCCTGGGTCAGCCATTTCTGTATCTGGAACCTCATCTCCGTTTCTTGA	29322	A_95_P193542	TA15695_4097
30199	356	24	646	TGTTCGGTATAATTTCCAGTTTGGCAACGGGCGAAATGTCTGTAAATTAATTTATAAG	29326	A_95_P000646	TA12585_4097
30202	356	27	1006	GTGTGTCCTTTGTTTTGATTTGCTTTATGTATTAACTACTGAATGATCCAGTTAGGGA	29332	A_95_P016981	U64923
30204	356	29	305	AAATGTTTTATGGTTGCAGCAAGGGAGCTTGTATTTCCTGGGGGGTGGATACACCAC	29336	A_95_P108487	CV018856
30205	356	30	216	AATTCCGTCGTTCAAATGCTTAGAGCCAAAAGGTGATGAACCCGGTTTGCTGACAGA	29338	A_95_P034903	BJ999158
30210	356	35	1672	GAAGGAACTTATGACTATACCTTATATTATGGCTCTATATAACGCCTGGCTGTTTTTT	29348	A_95_P239944	Z29492
30214	356	39	804	GTTCATATCCTCACTGTACCTCTTGTTAATTGTGCGAATGGATAATTCTTTGTTCGTGT	29356	A_95_P149057	EB678711
30216	356	41	848	ATATGGGTGATGTTCTTATCGAGGGTAAAGCTACTGGTTACTGTGAAAGTGGGTGCT	29360	A_95_P244397	EB447451
30217	356	42	856	GCTTCCACCTCATCCCATTGTGTTTCATATTGAAGTATGGTTTGAATAATTTGCTTAGA	29362	A_95_P201722	TA17484_4097
30220	356	45	806	GTGCAGATATTGTGTCAGAGAATGTTTGGATGAAGAAGTTTGTGCATATATTCAGTC	29368	A_95_P223217	TA22202_4097
30222	356	47	727	TAAATCTGGATCAGTAGTGAAGCCTGCCAAACGTGAAGAAAAACCTGTGGGAGAGC	29372	A_95_P013926	EB428701
30228	356	53	817	TTTAGTCAGTGGTGCTTCTTCCTCTTTAGACTAATAGTACTGCTGGTTTGTGACTCTAT	29384	A_95_P230614	EB425998
30231	356	56	637	GGAGATCAGACTTTCTTTGAGTAATTGCATGCTTCATACATCACTTTGCTATACGTAA	29390	A_95_P231864	DW002537
30232	356	57	159	CCGTGATGTGAAGCCCCATAATGTAATGATTGATCATGAGCAGCGTAAACTTCGGTT	29392	A_95_P128227	DV999924
30235	356	60	143	AAGGACCTCTGTTTTCCTCCATTAAAATGCATCAAATTACAGCCTCAAACCACCAACT	29398	A_95_P123607	FG622782
30236	356	61	0	TGTGTCCTATGGTGGGGAAAATGGATTCATTCAGCCTATGACTTATCTCTGCTGAGA	29400	A_95_P226989	A_95_P226989

30240	356	65	711	GTTTTCTTGATAAAAAGGAAGCCCGCTACAACCCAAAGATGTCACCCTATATACCAAT	29408	A_95_P120567	DV161110
30244	356	69	685	GGAAGAGAGAATAGTAGAGTACCTTCTGTATCTTAGAATCAGTTAACTCATGATTTCT	29416	A_95_P014736	EB435352
30254	356	79	867	AGAATGGGACCAGTGTGATGCTCTGGAAGACTTTCTAGCTATGGTCTCCTTACTGAT	29436	A_95_P297898	FG148963
30255	356	80	657	TGAAAAACACTTCATGATGTCCGCAATTCCACAAATCAGGAGAAGGTTCCCCACTCTT	29438	A_95_P065580	BP136369
30256	356	81	642	GTTATGGATTCTGTTATATTTTCCAGCACAAACATTGTGCATGCGAATACAATTAATG	29440	A_95_P018671	TA13080_4097
30258	356	83	836	CACCAAAAATCACATGCTGTATGAACGAAATCAGGAAACAAACAGATTGGAATACTT	29444	A_95_P118307	DV161323
30260	356	85	1051	TGGACATGTTTGGATATTTAACGCATGTAGGCATGCCACATTAATAAGATTGAGACG	29448	A_95_P204822	TA18149_4097
30265	357	5	809	TCATGGCTACTCAGTTTCAAGATGGAGAGCGTTTTAATCTCAAGTGTATAAAACATAT	29457	A_95_P269786	EB426716
30267	357	7	349	AAGAAGCAAGTTTGTTGCCTACATGAAGAAATATATCAATAGCCTTACACCCAAAGT	29461	A_95_P110392	CV019713
30268	357	8	419	CAAAAGATAAAAACGGCATGGTGCGTTACCATTGTAACTGTGAAACTCTGATCTTTC	29463	A_95_P100573	BP535433
30271	357	11	390	CGTTTGACATTTAAAGTTTCAGGACATTAATTGATGGAAGAGCTTAGAGGGACGAAA	29469	A_95_P123117	DW003019
30274	357	14	698	TATTGATGTTTTGGACAAGCAATTGCTTGAGGGTATGGGTGTGCTCCTGACAGAGGA	29474	A_95_P136692	EB440460
30290	357	30	323	GGACATGTACAACCTCATTCCACCAGTGTTGATTATGAATGTCAAATTATCATACACT	29505	A_95_P143822	EB447010
30294	357	34	1128	CCAGTAAGTTTTGTCGCTATATTCATTTGGTACAACACCTTTTGTGATACATTTTTGGG	29513	A_95_P008826	TC44547
30295	357	35	830	GCATATGATCTGGAGTGCTTTGAAACAGTTTTTATCTGTTTACTGTGTTGTGGATTCT	29515	A_95_P160202	EB424704
30298	357	38	464	CTGCCTGTACTTAACTTATATGAACCAATGCATATCATGCAACGTAAAAACATTCTTC	29521	A_95_P021816	TA17940_4097
30299	357	39	833	TGCTAATCAATTGCGATACCCAAACAATCACACACATTACTTCTCCTTTATTCTGCTCT	29523	A_95_P289808	DV161043
30302	357	42	1203	GATGGCCTAAAGCTCAAATTACTGTGAATAGTCGTGTTCATTTTCGCTTTGGAATTTT	29528	A_95_P011041	TA15689_4097
30305	357	45	1035	AACGATGAAAATGACATCACTGTGCATCCTACAACCAAATTTAATTGGTGTTTGGATT	29534	A_95_P011186	TA15797_4097
30307	357	47	1319	GCGAGGAGGCTTGTTCCCTCTTGTCTCTGTTTGTGAATAATAAAGTTTAATTATTGTTT	29538	A_95_P014336	TA11987_4097
30309	357	49	2097	AGTAAATAGTTACTACTAACCAATGCAACTTATGAGATGGATAACTAGTTGTGTCAT	29542	A_95_P014056	TA12496_4097
30315	357	55	573	ATTTCATTTTCGTGGATGCTGACAAGGACAATTACATCAACTACCACAAGAGGATAAT	29552	A_95_P005049	Z56282
30325	357	65	307	TTTTGTGGGATTACTGTTAAATGATGTGTGCAAAGAAGTGGGGGGAGCTTCTCCCGT	29572	A_95_P095033	BP532985
30328	357	68	173	CAATGATGGCTACTGGGACTATAACTTCTTATTTGGAGGTGCAGGTGGAGGAGAAC	29578	A_95_P241325	AJ718261
30330	357	70	621	TTCTTGCTATTGGAGGAATAGTTTGGCTTCTCGAAGATGGGAAATGGTTGTGAAATC	29582	A_95_P004921	EH665313
30333	357	73	440	TGACTTCCTGATCTTGTAGAAGCTGGTATTATCATTTGTTTATACTCCTGCATATTCTA	29588	A_95_P025706	TA14429_4097
30337	357	77	388	CAAGCAAAACTGCAGACAACAAGCCAACTTGGGATTTGAATGCTGCATTTCTTTGGG	29596	A_95_P081905	BP528381
30338	357	78	821	GTTAAGAATCGCGCTACAAGTTCTCCTAGTGAGGGCAGTTAACACTATCATAATTGC	29598	A_95_P147427	EB451837
30341	357	81	443	TATTATCCTTGCTTAACCCAAGGTTGATATCACAAGCTTGGGAGATTGCTGGCACAC	29604	A_95_P070665	EB425904
30345	357	85	837	TGCATCCATTTGTTTCTCTTTTCAGAACTGTCTACGACTATATGTTGTTGCTGAATAGA	29612	A_95_P218267	DV999170
30349	358	4	448	TTTGTCCCCCTGAGCGGACATGATAGATAGTTAGAATACCATGTACTTTATTTTGTTT	29456	A_95_P218272	TA21134_4097
30351	358	6	837	TGTTGGTGTTTTGTCTAATACTCAGGGTCGATGTGGTTAAGGTTAGAGAGCCATGCG	29460	A_95_P211322	TA19585_4097
30352	358	7	1600	TTTGTCGCCCTCTCAATGGAACTTTGCAGTTTCTGGTCTTCCCTGTTTCCTTGTGACTA	29462	A_95_P014556	TA15184_4097
30357	358	12	93	TTCTAGGATAGTAAACCTTTTGGACTTTGGTCGCTGTATTCTGTATCTGGATTCTCTG	29471	A_95_P112372	CV020645

30359	358	14	549	CTAGATGAGCTGTCTAAGGTGGTTCATTTACCGTGGTAAAATATTGAATGAACCCAT	29475	A_95_P181037	EH623214
30362	358	17	399	ACACTATGGTTGAGTCATGTGGAAAGCTCAAATTTAAAACAAGATCTTGTGCAACAT	29480	A_95_P198922	TA16883_4097
30364	358	19	623	GGTGCTTGACCGGTTATAGTGTTCTCGTGTTTTAGATGTATTTTTAACCATTAAATCA	29484	A_95_P104557	TA11779_4097
30368	358	23	1288	TGACTAATGGTTGTGATCATCTGTCACTGCTATACTATAGTTTCATCGTGTCAACGTA	29492	A_95_P200052	TA17126_4097
30371	358	26	489	GTTTGTCATCCGTTTTCTGAATGTTAATAGACTATTTCGATCATAGATATTGCCCTTTC	29498	A_95_P190677	TA15066_4097
30372	358	27	698	CCGGGAGGAATGACCTTTTGCATTTCTTCTTGTGAATCACAGATCTTTAACTATCTAT	29500	A_95_P122352	DW002352
30374	358	29	193	ATAAATTGTACCTGAAGAAGCAGTTATACGCCCTACACATGGGTGAAAGTACGATTT	29504	A_95_P242577	DQ460190
30376	358	31	514	TGACATCAGAACTTTGTTTAAACGCATCTTCAGAATGTCCAGGAGGCGAGTGAGGA	29508	A_95_P041331	BP130064
30377	358	32	691	TGGATTCTGCAATGTGAAAATTAGGGCAGATAGAAGCGAACACTTCCAACATCTTAT	29510	A_95_P050781	DV162700
30379	358	34	638	TTCAATCTCATTTCCGCTCCTTCTACTTGAGCCAATTGGCCAGAAATGAAAAAGAAAA	29514	A_95_P253304	FG168935
30380	358	35	483	GACTATTCTGTAATGAGGATGAGGTCGTGATATTTCTTTATATTCGATTTTCGAGTCT	29516	A_95_P219677	TA21445_4097
30381	358	36	552	TGTTTTGCTATAAATTGGATCCATTTCCTGCTTTCGATGAACCAATGGCAAAGCTCAG	29518	A_95_P123822	FG639427
30383	358	38	293	CTTTATTAAACTCGTTTTATAACACTACGTGGAGTTGCTTGGACTTCTTTCTCCCTTAA	29522	A_95_P180997	TA12872_4097
30391	358	46	691	AAATGCATATTGGACCATGGCGAAAGCAAAAATACATGCAAGCTAAGTGGCTAAAA	29537	A_95_P280288	FG195840
30402	358	57	986	GGCATAGTTATTGCTTCAGCATATACATGTCTTAGAAACTACACATCACATTTGATCA	29557	A_95_P190702	TA15072_4097
30403	358	58	842	CTAAAAGATCGATCATGGTCGTGAATATATGTTGGACCAATATAATGTGTCTTGAAC	29559	A_95_P195857	EB440123
30404	358	59	803	ATAACTGATGGCATCATAGTCCTGTTACAAACTCAGTAATGCAATAACACTCTTGTTG	29561	A_95_P011606	EB437936
30407	358	62	389	GCCAACCAAGGAACTCATAAGTCATAACAAACAACTGCAGAACAAGTTGTATTTTCT	29567	A_95_P124892	DW004693
30409	358	64	763	GGGAAAGAGAACTCCTTATTTCCCCAATAAATGTACATTGTTAGGTGAATTTCATAG	29571	A_95_P242892	DV999620
30412	358	67	110	CCCAATTGCAGTTGTTATTTTCACAGTGATAGTATTGGTAACTACTGTTTCCATGTCA	29577	A_95_P001276	EH623494
30413	358	68	818	CCTTGTAAGCAGTTGCAGTTGAAAGAGGTGTATCATTCTGGTAAACTAATTTTGAGT	29579	A_95_P244217	EB678794
30414	358	69	856	GACTGTTAACTAGCATTTCTGTGGAACATGAACTTAAAGATGATGTGATTATGAGTC	29581	A_95_P013316	EB677804
30415	358	70	787	GGCTTGCATCTTGCAACAATGAGCTTGGATCTAGCTGTTCTAGTATAGTAATATTATT	29583	A_95_P244687	DV999471
30416	358	71	1105	CAGTCAGCGCAAGCTGCAAAATCGAATTGTTGTGATATCCAACATTAATAAATAAAA	29585	A_95_P188977	AB044154
30422	358	77	510	AGGTTCCGTTTCGCAATTTTGGTACTTCAGTCCAAGGATTGTTGCTTTGTATAGCCCG	29597	A_95_P122082	DW002135
30424	358	79	375	GTTGAGTGTCATTGCTTATTGCATCAAATTAGGATAGAGGCCTCGGCAGGATGATGA	29601	A_95_P266426	BP533599
30426	358	81	1655	GAATGGACTCAAGATTAGTTGCATGTGCTGAAGATCATTTTCTCTTCTTTTTCCTTTTC	29605	A_95_P007826	TA11819_4097
30427	358	82	407	TTACACGATGATGATGATGAAAGTATGTTCAAACCTTTGCCAGTGGGCTATGTAAGG	29607	A_95_P093138	BP532157
30428	358	83	316	TCGATTTGAAAACCAAATCAGTTGAGAAAGAAAAGCCAAAGCAGAAGATGGACCAG	29609	A_95_P004621	FG642543
30429	358	84	552	CTAATTTTAGATATCCTTTGGCTCGGCTCCTCTACCACTTCAACTGGGAGCTTCCATAT	29611	A_95_P211327	TA19586_4097
30434	359	4	762	CAGATTGTGTTTCTAAAATGGAACGGAATGGAATGGAGGAGTTTGGATTCGTTTCGT	29620	A_95_P290523	EB678291
30435	359	5	902	TCTTTTTTGTTTTATTATACTTCTCGATTCTTGTTGATTGCAGCGGCCCCCGGCCGTAA	29622	A_95_P009091	TC40703
30438	359	8	342	TTGGTAAAAGGTTGTTCTGTTTTTGATGAAGCAAAGCCAGACCATTTCACAGTAAGC	29628	A_95_P094468	BP532732
30442	359	12	339	GAGAGAGAGTGTGTGCTTGATTTGTTAGTGATTTAGAAACTTTATTTATGATCGGTTT	29635	A_95_P005766	TA12138_4097

30445	359	15	759	TAGAAATGGTTCAGGACGATATTCTTCAGCAAGAAGGTCAGAGGCGATCACCTGTTA	29641	A_95_P149407	EB679258
30453	359	23	835	CTGGAGTTGGTTGATTATATCATCTCTTTTGCTGGGTTTAGCATCTGGCGTTTGAATG	29657	A_95_P194382	TA15879_4097
30455	359	25	145	GCTGCCTTTCTGAGTCGTTCTGCAGCTACTAGTATCTCTCCTTGTATTTTCTATTCTGT	29661	A_95_P001876	AJ719160
30461	359	31	489	TTTCCTACCAATAACTACCGTGTCACAAATGGTGCCGATTTTCTTGAATTTATAACCTA	29672	A_95_P095223	BP533084
30465	359	35	505	TCAGCTTCCCTGTGTGTAAATGATGATGAATACATCATGTTGAACACTGGATACATA	29679	A_95_P037208	BP128945
30472	359	42	812	ATATACCAGTACTAGTTCCCTGTTGTGAATCATTGTTCTTGTCCCCTCCCTTTGTCCTC	29693	A_95_P230554	DV158143
30474	359	44	734	ATGTGTTTGGAGCCAGTTCGTTGTGAACAGCTTACATATCTGGTGTTCCTGTGTTTTA	29697	A_95_P203092	TA17780_4097
30475	359	45	387	GGCTAACAGAAGCAAGGTTAATGTTTAGTTTGCAGTGAATAGATGTCTATGTAAATC	29699	A_95_P158952	EH616837
30478	359	48	320	GGAATTTGAGAACATAAATAGAGGAGAAGCTTTCCATCTTTCCTTTTGCTGTTGTTTC	29705	A_95_P067105	BP136774
30479	359	49	369	TCCCCCGTTTCAATTTATGTTAAACCTATTTCCTTTTTAGTCCGTGCCAAAAATAATGA	29707	A_95_P160542	EH619217
30480	359	50	873	TTTGGTTACATGGCTTGCATATGCTACGCCTTCTTTCTCATGCTCGGAACTGTTGGTTT	29709	A_95_P268781	EB438068
30484	359	54	805	CAGGGTTTGTTGGCTACGATGGAGCTTAAAGCAGCATGATTTGATTTCGAGTTGTAT	29717	A_95_P225597	FG144747
30485	359	55	948	GGAATAATCTGTTTCTTGTTCCTTGCCTCCAATCTTCTGATATATCAGGCCAATTTTTC	29719	A_95_P208232	TA18923_4097
30488	359	58	274	TTGCAGTCTAGCTGGTTTGGTTTACAAGTGTGATTGTATCTGGTTTGAGCATCCTTGT	29724	A_95_P095003	BP532974
30490	359	60	752	TATCTGCCTAATACTGACAACTGATGATGGGCGTATTTGTGTATGTTTTGATATTATC	29728	A_95_P123027	DW002919
30492	359	62	1551	CCTGCTGATGCCAAACCAGCCACCACAATGGGCGGTTTCCATTGAACAATATTAATA	29732	A_95_P010036	X82276
30495	359	65	98	TGTATATTAACAGATTGTGATTCTACTGAGGTCCTTTAAAGCTATAAACTCCTGGTTG	29738	A_95_P112907	CV020921
30500	359	70	350	GTTTTGCTCGCTTTTGGTGTACTCGTTTAAGTTTATCAATGCCCCAAACAAAAAGTTG	29748	A_95_P025161	FS415057
30503	359	73	804	CTCTTTGGTTCAATAAAACAGCAGTGACTTGTAAACATGCAATTTTTATTCTCTGTCCA	29754	A_95_P008316	EB449250
30504	359	74	845	CAACAAAGAGCTGAGCCAAATGAGGAGCCTCTGCGGCAATATATACTCTTTGATGTC	29756	A_95_P121332	DW001341
30505	359	75	338	GCTTTTTCTCGATGAAGTGCTTTAGCATTGCTTTATGCGTTTTGCTGAATTTACTGTTT	29758	A_95_P128767	EB428497
30506	359	76	753	TAAATTGTGTGAGAGTCTGCAGTTGGATTGCCCCAGATGGCCTAAAACTTTTCTTTGT	29760	A_95_P178137	TA12160_4097
30513	359	83	506	AGATCGGCTCCACTTTTTTGGTGCTAGTTATATGGTATGGGATATTTAGTGAACTGTG	29774	A_95_P122107	DW002148
30514	359	84	792	TAGGTATCTGTTTTTGGTGTAATTAGTATGATTACCTGTTGGTGATAGGGGTTCTTTT	29776	A_95_P033404	EB678137
30515	359	85	667	GCAATTCAATTACTTCAGTAATTGTAAGCAACTGCAAGTACCAAAGTTTCTCTGATTT	29778	A_95_P214487	TA20273_4097
30516	360	1	829	TCCAAAAAAGGAGTTGGTCCACGAAGCCTTTCAGGGGTTAAACTTGAATTTACCTCC	29615	A_95_P227194	EB680094
30519	360	4	416	AAGGACCAAGTTGAGAAAGACAGGTATCTATTTAAACGCAGAGATGAGCCTGGTAA	29621	A_95_P071520	BP525721
30523	360	8	495	GCTGTAAAACCTTGGTTATGGAACAATGGAAATAAGGATGTTTTGTGTAGGTTGTGT	29629	A_95_P293248	EB432042
30524	360	9	539	GGTGTATTTTGGTGATGAACAATAGAAGTTTTCTTGCGACCTTTTGAACTTTTAACAG	29631	A_95_P125262	DW005056
30526	360	11	1014	CCCTATTTATGTAATCCGTACAGCGAAATTAGTGCTGAATCATTGATTGTTGTATGAA	29634	A_95_P015061	TA17772_4097
30531	360	16	295	TTAGAAGAAGAGGGAGAGAGGAGGATGACGACTTTCGGACAATAGCAGAGGGTTA	29644	A_95_P058366	BP134458
30532	360	17	757	ATTTGGACTCGATGCTTTGATTCCGAGCACATCAAAAATAGACGACAATCAAAGGGG	29646	A_95_P263411	FG147854
30535	360	20	838	AGGATTACATTTACATTTCCTGTAATAAACTCATCCGCCAATATCGCTCTTGTTGTAGC	29652	A_95_P206387	TA18505_4097
30537	360	22	350	CAGTTGTTGCGTATGCTCGTCATTATGGATAGCGTCCTTTGTCGCAAAAGGGCTGAT	29656	A_95_P112822	EB680056

30538	360	23	333	AAGATTCAGGTATGTATATGGCTTATCGGAGGGAGAGTCATCACGAGTTTAGCAAG	29658	A_95_P103867 CV016724
30540	360	25	488	AGTGGTGTAGCTCAACAATGTTTCTTTTGCTTATTGAACAATGTATGTCTATGGCAGA	29662	A_95_P001891 TA15786_4097
30541	360	26	919	GCCACAATAAATCTACGCCAACTCCTTTCCACTTCAATAATTTTTAAGTCCATCCAATT	29664	A_95_P178242 TA12192_4097
30542	360	27	765	TGCAGACAGTCATACCAACTGGTAGCTGCAGTTCGTGTATTTAGTTCCCTATCCATCA	29666	A_95_P193662 EB433922
30546	360	31	364	TTTTAGATGGATATGCGCATTCTTTCTTCTGGGTTTGGCTTGTGGTCTCGCTGGCCTTT	29673	A_95_P102882 CV016246
30549	360	34	259	AAGATGCACGGTGTGGATGCATCAAGCTGTCAAGGTTGTCGATATTGTTGCACACTT	29678	A_95_P107527 CV018424
30552	360	37	691	CGCCTTGGAATAGGGGAAACTTGTAATATGTCTTATGAGATTTATTTTGGTGTTTCTA	29684	A_95_P195832 DV998762
30555	360	40	473	AGGGATCCTGTATAGAGCATTTATCGTTAGAGAGCATAATACTATTCTTTACCCTAGG	29690	A_95_P047491 BP131668
30556	360	41	626	AAAGAGGGTAGTCCTCAACATAGGGAAAGCATACACTTTTTCTGATGTCCTTGAAAT	29692	A_95_P265361 EB431914
30559	360	44	862	GCAGCTTACTTCTGGAGTAGATAGTTCAGCCAGTTGCTTGGAGCAGCAAATAACATG	29698	A_95_P258436 EB449748
30560	360	45	920	CACATTCGCGAGCTCGGTTTGAGCTTATTATAATGTTACTTGCCTAGATATTCGATAA	29700	A_95_P182712 L16787
30563	360	48	648	AAGGGATTTTGTTTGCTCAAGTTGCTGCGAGAATTTTTCTTGGTCACCTATAGTGACA	29706	A_95_P117457 DV160365
30566	360	51	763	TATGTTTGGCAACATTCTATGATGATCTGTGGTATCGATGGTGGGCGTGATTTCGAG	29712	A_95_P292888 FG170823
30567	360	52	801	CAATGTGCTCAGGAGCGTGCTATCAATTACCTCTTGACTCATGTTGATAAAAGTTCTC	29714	A_95_P163287 EH622295
30573	360	58	143	GATACGCTGGTTAAACTTACCAAAGTGCCAGGTACGACGTAATTTTTCCCTTGGATA	29725	A_95_P155172 EG649931
30576	360	61	532	CGTGTTTCCTCAAATTTGTCATTTCTGTTCTATTCGTTCAAATGATTAAGAATGCCTTG	29731	A_95_P046016 BP131286
30578	360	63	714	TTGGGAAAAGAATAAAACGTGTCTCGGTCTTTCGCTGCTGATGACTCCTCAGAGTAG	29735	A_95_P304868 FG151110
30583	360	68	463	TTTGTAGATTTAAGCTCCTGTATGGGGCTATCATGTACTAAAGCTGATAAACATATGC	29745	A_95_P188007 TA14475_4097
30584	360	69	838	TTTGTGGGTTTGGAGATGTTTGATGTCCATTTTCGAGACGTAGGAAAGCTCAGCTAA	29747	A_95_P287533 FG134245
30587	360	72	142	AGAGGCTCTAGCTGTGTAATGACAATTGAATGTGTGAATGAACTTCTTTCACATTGA	29753	A_95_P211932 TA19722_4097
30588	360	73	651	CTGGCTAACAGGTTATGCGCGTATATAAGGAAACACTTTGCCCATGTAAGCCTTTTG	29755	A_95_P122312 DW002316
30589	360	74	307	AACGTGGGATTGATCTTCACTAGAGGAGACCTGAAAAAGAAAGTCAGCGATGAAGT	29757	A_95_P147767 EB643445
30590	360	75	344	CAATTCCATTAAGGCTAGTCTTATCACTGTGGCTGAACATTATGTAATGAAAATCAAC	29759	A_95_P134712 EB437390
30591	360	76	715	ACTGGTATTTTCTTCTAACATTTGATTTTAAACCTACCACAATTGTGGGGACCTTGATT	29761	A_95_P238369 AB050843
30594	360	79	728	CTGGCGATTGTTTTTAATGTAATTTCACCCTCTCTCTCCCCTTGTATTGAATGTAATAA	29767	A_95_P191542 TA15260_4097
30597	360	82	719	GGTTTGTCAGGTAAGACAGAACTGGATTTGGTAGCAGAAGTGATTTATATGAATGT	29773	A_95_P023836 TA12646_4097
30598	360	83	647	GTTGATCCAGAAAAGTTAGTGAGTGACGTGTACAAGAGAACCGGGAAGCAAGCTAT	29775	A_95_P016686 DW000017
30604	361	4	306	GTCTTCCCCTAAAATTTACTAGGCTTTTGGATGTATGAATTGGTTCTAACCTTTTGGTC	29786	A_95_P094193 BP532595
30614	361	14	621	AGTTCTGACTGTTTCTGGTCCTGTGATTTCCCATTTGCTTTAAAATAGGTATTTCGTCC	29806	A_95_P202387 TA17622_4097
30615	361	15	908	CTCATGGATTGTTAGATACTTGGATTTTCTTTCTGAACTTCGAAAAGCATTTTCCTTTC	29808	A_95_P225487 L29276
30616	361	16	665	GTACAAAGTGTCTTGATAACCTTCAATGCTGCAGTCAAAAACAGCAGCCATATCACC	29810	A_95_P316643 FG194661
30617	361	17	1274	TTCCTTCAATGTAATCTTCTAATCTTGTAATTGTGGCTAATGGATGGTGGATGATGTA	29812	A_95_P309153 TC64979
30626	361	26	504	TGAAGATGATCCAGATCTGATGCAATTTAGACTCTGATTAAAAATGGAGTAGGTTTG	29830	A_95_P124957 DW004733
30630	361	30	1109	GAGTTTTGGCATGGATTGCTTTCGTTTCCTCTTTTGCTTGATGTTGTATAGCTAATAA	29838	A_95_P184207 TA13640_4097

30631	361	31	572	TTTGGCAAAAGTAACAACTTTTGGCTTCTGTATTTCGAGCTCTCTTAAGATGTAATCTT	29840	A_95_P018466	EH620543
30636	361	36	777	TTCTGTTGGAACTCAAATGTCCATATCTGTAGAATGTACTCGAGAACTAGTTGTGCTG	29850	A_95_P226319	EB438727
30638	361	38	631	GACGCCTATGGCGTCTTTCATTCATGCTATTTGACATTCATTTGTGTGATTTAAGTTTA	29854	A_95_P117807	DV160765
30640	361	40	859	GCCTGCTTGTTTTACTCGTTCATATACAGTCAAATCTCTAATATCTGTATAACAGTCTT	29858	A_95_P182957	TA13344_4097
30641	361	41	468	TAAATAAATGCGCTCCACTGTCAGCTTGGAACTGTACCCTTCTCTGGGTTTCTTACATT	29860	A_95_P072505	BP525980
30642	361	42	680	TTTCCAATTTTCTTTTGGTGACAGGTTATAGTATTGCTGCATACTGCTGATCTGCAAAT	29862	A_95_P000836	EH622594
30644	361	44	810	GAAAGCGCACAATGGTTGGTTGAGTTCCCAAGTCTACAATTCACATTGAGTGCAAAT	29866	A_95_P126607	EB425927
30645	361	45	577	GAGTATAGGATTGGAGGGGCATATTAGTCACTTTAATACAAGTTGTAATAGTCTTGT	29868	A_95_P022131	EB434942
30649	361	49	710	GTGTATTGGGTATATTCAGGATTATATTCAATGCTTGGGGGTGTAATGGATAATTAT	29876	A_95_P151787	EB682037
30653	361	53	540	AGGCATCTGAACGTTTTGAGCTTTGTACTAGCGGCTATTCTGCTAAAATATATTTAGT	29883	A_95_P210132	BP534671
30654	361	54	315	TGACACCAGTTCTGGGTAGCTCTTGTTTATGGATTTGTATCGGCATTAATTTAAATTG	29885	A_95_P099743	BP535049
30656	361	56	815	CATCATTCCCATTTCCCTCAATGGGAATTCTCTGTTTTGATATATATATATGGCACTGT	29889	A_95_P270511	EB677666
30658	361	58	205	AGTAGGAGCATAGGATGCTAGCTTTATACAATTGATTTGCTCAAATTACTATACAGTT	29893	A_95_P090223	BP530865
30661	361	61	845	TACTATAAAAGAGTTGTAAGACCTGCTCTCGCCTTGTGCTTACACAATTGAAATGTAC	29899	A_95_P017246	EB679251
30671	361	71	209	TTCGTTCTGGTTTAAAAATGCAAGTAACTTTCTGTACGAAGGGAATTGGCGAACAAG	29919	A_95_P107627	CV018466
30673	361	73	305	TCTGGTTGATGATTCCTGCAGCTATTTTTTGGTGTTTATGGACAGAGAGAGATAGAA	29923	A_95_P054231	BP133382
30676	361	76	849	ATGATTAAGTAGCAAAGGAGGAGGCCACAATTGTCATCTGGCTTTGGTCAATGCTGC	29929	A_95_P011011	TA14032_4097
30680	361	80	737	GGCAAGTTGATAGATGGACTCGGTTATGCTTTTGAGTTTTATGAAATTTAATGAGCT	29937	A_95_P222442	TA22033_4097
30682	361	82	716	GGTTGAAAACGCGATTAGCCGTGGTTTTGTGGTTTTGATTGTATTAAATGTGTCAATT	29940	A_95_P217642	EB433063
30690	362	5	582	CGTGGCCGCTGTTGATTCTTTCTTACTACTACTACTATTTGTTATTGATTATTACTGGA	29789	A_95_P187572	TA14377_4097
30692	362	7	708	GGAAGAACTATTTGAGGAGATCTGCATCTCTTTCAGACAGTAGACGCGAAATATCAG	29793	A_95_P300113	FG154262
30695	362	10	1581	GCTTGGTTAGTTAATGGTCATACTTTTGCGTATTTTGGCTTGTTTATCAAGCACAATTA	29799	A_95_P010286	TA11799_4097
30704	362	19	1944	CTCGGTGTACCTGTTACTTTCCTTATCACGGTAACAACTCTTTTATGTATAGCTAATTT	29817	A_95_P011291	AF124369
30705	362	20	479	TTGGGTTGCAAAAGCCTGTTGATCTATGCTTTCATTGGTTTAAATAAAACCTCCTGAA	29819	A_95_P058291	BP134441
30707	362	22	845	GTGATGTGATTCCCAAAATTGGTCTCTAAATTCCGGCTGATGAGTTTATTTTTATTTGT	29823	A_95_P198882	DV160910
30710	362	25	356	GTGTTATTATCGGATATGGTGGACCATTGCCATTTTGTAGTGTTAACAACTGTAATGT	29829	A_95_P032111	BP527510
30711	362	26	827	GCTTGGCCTTCTTGTATATGATTGATTACATGTTTCTCCTGTATACTAGTTTGTTTGTA	29831	A_95_P237494	U65390
30713	362	28	792	TGCAAATTCCAATCTTGAATGCACGTGTGCATCTGAAGAAGATTTTTCAACTACTCCT	29835	A_95_P145917	EB679074
30718	362	33	793	CTCGAAATTGCCATCTACATATTCTTGACTTAAATTCATACCTGTATTTGTCATCTCCC	29845	A_95_P019216	EB679955
30719	362	34	683	CCGTTTGGATTAGCTGATTTGAAGTAGCTGATAAGCATTAGGTGCTGAAATTGATTT	29847	A_95_P115967	DV158464
30722	362	37	750	AAAGAAGATGAAGAAACAGCAGCAGCTCAATTTGAGGCACCCGGTAATGACAGTGA	29853	A_95_P137467	EB441197
30724	362	39	2104	CAGGTGGAAATGTTGATCAGTCTGCATGGAACACTTTCTTGATGATGACCAAATGGC	29857	A_95_P113182	AF223573
30728	362	43	403	AAGGATGTATTCCCCATCATCCTGTCTTTCTTGGCCGTCAATTTTTCAAGAGCCACAG	29865	A_95_P083690	BP528829
30733	362	48	204	CAGCGACATTTGAGTAGTGTTTTTGTCCTAATGGCACTGAAATGAGATTCTGATATCC	29875	A_95_P091068	TA13592_4097

30736	362	51	890	TTGTTTAGTCTGTAAATAGTTGGAATTTCACTACGACCTCTTACCCCCAACTTATCATT	29880	A_95_P015361	DV157623
30739	362	54	728	GGTGTTCCATTGCTCATTTGCTAAGAATGGATGCATAAAGGATTGAAATTTATGTGA	29886	A_95_P002021	FG641754
30748	362	63	1145	ATTTAGTTTTCACTGGATGTATTGGCATCTCATTGCACTATCACACTTGCTCTCTATTT	29904	A_95_P178897	TA12370_4097
30749	362	64	418	TTATACAAGTAAAAGTACCAGCAAGCTTTCTTGTTGTTGCTCAAGTGCGATTAAGTTG	29906	A_95_P193817	TA15752_4097
30751	362	66	2335	CAGTACCCTGCAGTTTCTTTTCCTTGTTCATTTTTCGTTTCTATTTGAAGAGTAAACAA	29910	A_95_P007326	D83583
30754	362	69	845	TTTGATGATAGCTGTCAGCCATCATCTTATCAGTACTGGTTTTGCCCTTGTCTGCATGT	29916	A_95_P311318	FG163165
30755	362	70	437	TCAAAAGGGGCACAACTTATTGTTTGTAAAGTTGTAATGGGGCGGATACCCAGTACA	29918	A_95_P283078	AM820007
30756	362	71	693	TAATGGTCAAGCTCACCCAAATTTTCCCTTGGAAATGCCTGGAAGTGATGAAGTGGC	29920	A_95_P176202	X65700
30767	362	82	683	GACGTGAACAATCCCAAAATGAGTTGTAGTTTCACAATTGCTGGTAACTTGTTAGTTT	29941	A_95_P117192	DV160010
30775	363	5	1750	TAAGGAAGGATTTGCCAAGATTATGTGGCAGCTTTATGAATCTTTTGTGTTCCTCTCA	29956	A_95_P011926	TA12833_4097
30780	363	10	445	TTGTCTCAAGCGAGAGTGAGGAGTTATCTGCAAAGGCACAAGTATCTGAAATATTAC	29966	A_95_P276223	AM786095
30782	363	12	630	ATAGCTGTGAATCCTTCTCAAAAGATTCAGCCCGTACACCATTAACAGTTCCACTGCT	29970	A_95_P316258	FG194446
30783	363	13	201	GGAACATTGACCCGCCCTAAATAGTTTGGATAAAGAAAGCTTGTTGATATATTACTA	29972	A_95_P106737	CV018042
30787	363	17	473	AGAAAGAACAGATCTGCCTAGCAAGTGTTCATCTTTGATTCGTAGTAAGACCCAACA	29980	A_95_P013201	DV161939
30789	363	19	814	GTTGATCATCTGTGTATTTACTGTAAACTGCAATTCCTATTACCTGGAAATGTTATGCT	29984	A_95_P012131	TA14842_4097
30790	363	20	586	GGCCCTGTGCTTTCCATGTTTAATCTCTAGTTATATACTGGCTTTGAATGTGAATCTGT	29986	A_95_P161422	FG644316
30791	363	21	754	GAAGCAACCTAAGGCCTCAACCAAACATGTAGACTGGTTCTAAATCATGAAAATCCT	29988	A_95_P116957	DW000135
30792	363	22	758	TACCAGTGTGTGGACATTGTGGATCATGAGTCATTACTCATTAATGAATAAGATTCTG	29990	A_95_P124937	DW004720
30793	363	23	765	ACAGTATTTGGGATGGCTTACATGTTCGTTCACGATGGTTTGGTTCACAAGAGATTC	29992	A_95_P259461	EB450833
30795	363	25	843	ACCCGCTTCATGTGGATACACGTGAAGCATGAATTTCATACAAAAGAGTAGAATGTT	29996	A_95_P236114	DV999986
30796	363	26	701	TTTGCTGATGGAAGTGTTCTGTCACCTATGGGCTATAAAGAAGTAGAATTTGACAAG	29998	A_95_P244487	EH621158
30797	363	27	578	CTCAAGAACCTGTTTATGTTAATGCTAAGCAGTATCGAAGGATCCTGCAGCGACGAC	30000	A_95_P144302	FG136430
30803	363	33	783	TACTCAAGGACATATTATCCCTAAGGCATGCAGTAACTTCTAGAACTTTGGTAATCTC	30012	A_95_P146272	EB450258
30805	363	35	1681	TAAGCCATATATGGTTGAAATCCAGGAGTGACTGATGAGCAAGGTCTCAACTGAATT	30016	A_95_P029111	TA14918_4097
30806	363	36	575	ACCATTATGAGTTCAGTATCTCCTTATATTATCAAAATATGTGGAGTGGTTTCTGCCC	30018	A_95_P182612	TA13261_4097
30812	363	42	868	ATGTGGTTAAAAGAATTTGGGATTACATTAAGCAAAATAACTTGCAGGATCCGTCTG	30030	A_95_P296563	EB677800
30815	363	45	709	TTGACACTGTTCTCAATTACCATCCCGATAAAAGCTGTCAAGATGGGAGCTGGTCTTG	30036	A_95_P135302	EB438689
30816	363	46	779	TGAAGCACTCTGAGGCTGTAAATTAAGAAGGCCTGACGCCTTATACCATCTTGTACCT	30038	A_95_P143007	EB681836
30819	363	49	612	GTATATTGGAAACACCTTCTTGGGCAGCATATAATATAGTTCTATTGTAGAGCCAATA	30044	A_95_P192027	TA15364_4097
30820	363	50	429	CATTTTGGTTGTCAACTTCAGTACCACATCCTATTAATGGATATATTTGACCAGCGGC	30046	A_95_P275288	AM827414
30821	363	51	406	GTTGTACTTCTTGGAACCAGTGACCCTTTTCAGCAACAAATGACTTTGATTAATGATT	30048	A_95_P189637	FG645407
30828	363	58	766	CGATGACATAGAGGATGAATTGGGCATTGGACCACTTAATCATGTCATTTAGGGAGG	30061	A_95_P292108	EB448422
30830	363	60	644	GCGTGCCTTCGTTCATCTTGACTATGAATACAGCCATAAACCTGAACATGCTCAGGCA	30065	A_95_P146207	EB450974
30834	363	64	1806	GAAGCCCTATGAACCTGCATTTTGAATTATTGTGTCAAATAAACGTCTGTTTGTTGTG	30073	A_95_P014226	TA11926_4097

30838	363	68	941	CTTCTTGCTCAAGTTCCCTGAGGAATTATTGTTTTGTATTCAGGATACAGATTTTGCTA	30081	A_95_P206422	TA18512_4097
30839	363	69	425	TAAAATCTGGTTCATGTACTATTTTGTAACATTATCTGCCGTCCATCCTTTCACTTTGT	30083	A_95_P090058	FG157352
30843	363	73	1264	GACCTTGCATTTGCCTCTACATCCCAAAATAATGGTCTACAACATGTCAACTATTATTA	30091	A_95_P186537	TA14149_4097
30851	363	81	378	ATTTTCCAGAGTTTTGCATCTTCCATAGTGCCTCCCCACCTGCATCAACTGCATATGTT	30107	A_95_P264241	BP526819
30855	363	85	1138	TGACAGCAATGTCTCTTTGTATGGCTACTTTTAAGTGTGGAATGATGCGAATTACGTT	30114	A_95_P022306	TA12470_4097
30864	364	9	874	GCTCTTGTAATGTGATCTTGGTCTTTTAAGTTGGACCTTCTTGTGGAATTCTGTTAATA	29965	A_95_P159882	TA13590_4097
30865	364	10	883	TTGTTAGTCTGCCGGATGATATTTTGGTGCAAATATATGTGGTGGGCTTAATTTACAG	29967	A_95_P009176	TA13857_4097
30866	364	11	1075	TTGGATGATGATAGGATTGGATATGCTAATCAAGTTGAAAATATTCCACTTGATTGG	29969	A_95_P219877	TA21489_4097
30872	364	17	734	CTCTATGCACCATAAACTTGAATCTTGGATCATGTGGATTTTGGGTATGTTTTAATGA	29981	A_95_P119342	DV162464
30875	364	20	598	GTTGCAGCTGGTGCTACTGATTTTTCAGGATTACAAATTATTGATGTAAGTAAAGGG	29987	A_95_P127342	AB300776
30876	364	21	909	GCGTGAATAAAATGTCATCCATTTCTAACAGGGTTCATGTTTTGATTACACTTGTCTA	29989	A_95_P023881	TA16184_4097
30877	364	22	0	GGAAAACAAATATTTCTTACATCTGCTCTAGTATTACGAGCACTGAGCTCATATTGTG	29991	A_95_P249132	A_95_P249132
30881	364	26	835	GAATGAGTAAGCAAGGGTACCATATGTACATTGAATCTGTAACTTTCACTCCTACATC	29999	A_95_P135037	EB438153
30885	364	30	592	TCAAAGCTTAATGTAAATTTTGTATGTCGATCCAATACTGGCTACTGGTTCTGAGTAC	30007	A_95_P261466	BP132437
30889	364	34	1033	GGACCAGCTAGTTTCCTTTGGGTCTTTTGTGATACTTATGAATTGTTTCATTATTTACC	30015	A_95_P211657	TA19663_4097
30894	364	39	610	TTTTGTCACACGGTTGGAGGCCAGTTGAAGCTACTTCGCCGATTTCTTTGTTGAAAGT	30025	A_95_P191052	DW004979
30907	364	52	527	ACAGATTCCAGAACCAACTCCTTGTTTATCTCCCTTCTAGTGCATTTACTAAGTATTAA	30051	A_95_P222457	TA22038_4097
30912	364	57	573	CCTGAGTGATGTATAAATATATACTCCAACGTTATAAAGATAATAGGGCATGGGCGT	30060	A_95_P026411	EB433675
30914	364	59	227	CATTAATACCAAAACAAGTTGGCAACATGTACCACCGCCGTCTCTCTATGCTGCTTTT	30064	A_95_P160452	TA14823_4097
30917	364	62	0	TGAGGCATTCTATGAAATCTTTCTTAGCTGCCTCCTGCTCTTCTCCTTTTGTTGTCCAT	30070	A_95_P257791	A_95_P257791
30919	364	64	1794	GATTCTGATTCAGGAAGTTCTTCAGGGAGTGACTCTGATGCTGATGATGCACACTCT	30074	A_95_P225017	AJ504731
30920	364	65	431	GAGCTGAGACAGATTGTAAGTTAATAGTAGTATAGTTTACAACTGGCTTCGTTTAGT	30076	A_95_P030011	CV017299
30924	364	69	849	ATTAGCAGTTTTAAAGTCCAATGGACTCGCTGATTGTTCTTGTCCTTGTCCCGCCTTCC	30084	A_95_P148787	EB678294
30930	364	75	419	GTTGTAATAAATACTCACGATCCTCAAAAAGAAAAACCCATTGGTGGACAAGAATTC	30096	A_95_P197247	TA16520_4097
30932	364	77	1125	GTGCTGTTTGCAACTATGCAGATCTACATTTTTTGTGAGTGCAAGAACTACTTAATTA	30100	A_95_P027696	TA14498_4097
30935	364	80	600	CATGTGGTACTTGAATTGTTTACAGTATGATATACTCAACGCGCTTAGATGCTTGAAA	30106	A_95_P023306	TA13683_4097
30937	364	82	346	ATGTAGCAGAAACTGTGCATTGCTCTCCAGAGACTGAAAATTATGCAAGTTAGTTTC	30110	A_95_P033714	AJ632913
30939	364	84	119	CTATTAGTAACGGAAGTCCAGACATGAAGAGTCCACCTTCTGCTGATAATGGTTCAG	30113	A_95_P034778	FG164541
30941	365	1	389	GCCATTCCTTAAATGAAACATGCTTTGATAGTGGCTGAGATTGATCATCAATGCATAA	30116	A_95_P098753	BP534630
30945	365	5	738	ACTGTAATTGTATTCGAATTGGGTCTTTTTGCATTTCTGCCCTACAGCTCTTTGGCTTC	30124	A_95_P289353	DV158949
30950	365	10	530	AGTTCTGCATTTAATGTGGTTCCGCTGTTGCTAACTATTTATGACTGATAAAGAAAGA	30133	A_95_P264276	BP526949
30951	365	11	2237	CCTACCTCTCGTGTGCCATCCATCTTTTCTCCTTTAATGAATGAGGCTTTCATTATGCT	30135	A_95_P179397	TA12496_4097
30952	365	12	1218	GTTGGAAGTGAAGTGATCAAACACAAAGCAGATTCAGGAAGATGTGTATTTTTCCCA	30137	A_95_P030716	TA14129_4097
30954	365	14	466	TTCCTTCTAATGGCTGTACTTGGTGTACTAGCTTTCTTTGCAGAGATAACTTTAGCAC	30141	A_95_P064485	BP136068

30955	365	15	254	CCTTTGTTGTAACAATGGCCTTCGCCCAAAATGGGATTAGATTTAATATCATTGTTTA	30143	A_95_P032156	EB433693
30956	365	16	132	GGATGAGTCTACTTTGGAAATCAATGGGAAGCAGATTAAAGTCAGTAGCAAAAGGG	30145	A_95_P095303	EH665096
30958	365	18	454	CTTAATTTGGAACATATGTTGACAGTATGGGCTACGGCTATTTTGAGCAATCGTATC	30149	A_95_P100343	BP535332
30959	365	19	960	GTACATATACTGATATCCCCCTCCATCTCAACCTTGTAAACATCTTTAATGTATGTGAA	30151	A_95_P190817	TA15096_4097
30960	365	20	554	CCAGAAGGTGTTACTAATAAGATCTATGAGAACACTACGACAATAAAGGAGTATTTG	30153	A_95_P137207	EB440925
30963	365	23	394	GTCCAAGGCTTGGGAATCGTGAAGAAAGAACACATCAAAAATTCACGGGTTTCCTG	30159	A_95_P110762	CV019886
30964	365	24	465	GTACACTGTCCAGGTACGCAGTTTGTCTTACACTATATGATGTGTCAACTGAATGCAC	30161	A_95_P050561	BP132423
30967	365	27	1058	TCAGTGATTTATCCTCCAGTTTGTTTATAAGCTCTTTGTCCCCTATATATGGGATATGT	30167	A_95_P217362	TA20916_4097
30969	365	29	714	AACAGAAGTGTGCCCTTACTGTAAGGCGAAACTGTGGAGCATGCTGCAAGCAAAAA	30171	A_95_P279973	EB439536
30971	365	31	416	TTTTGAAACTTAATTCACAATTGCTAGTATCACCTCGGCTGGTGGGAAATCTAAAATC	30175	A_95_P120042	AM789623
30978	365	38	98	CATTGGGCATTATACCACACATGGTCTACAAAAACACTTAGTTAGTAAAATAAGTGA	30189	A_95_P144952	EB448512
30979	365	39	0	TATGCTGACATGCCGCACATGGTCCCTTCATACAAGTTTTAGTCTTTTATGTAAAAGA	30191	A_95_P287828	A_95_P287828
30983	365	43	736	CAAAAACAGTCCAAATGGACTTGTGGGATTAGAGAGAAGATTTCTCAAGTTCAACG	30198	A_95_P136912	EB440605
30987	365	47	256	AATGTCGGGTTCGAGTTTTAAGCAACTGTTGTTACTCTGTTAATAATGGAATAAAGT	30206	A_95_P125177	DW004969
30988	365	48	537	GATTTTTTAACCTTTCGTTAGTAGCTTAGCAAAGTTGTTACCGTCCTAGGTTTCAGCTT	30208	A_95_P220562	BP525818
30990	365	50	776	TATTGTCAAGGATGAAGATGCTGAGGTCTCAAAGGAAGATCCTGTCAAGGAGAAAG	30212	A_95_P149392	EB679217
30994	365	54	1304	ATCTTAAGGGTGTTGTTCAGTGGTACCATTCAACAATAGCAATGCCATTTTTGTTTGT	30219	A_95_P209057	AF191497
31003	365	63	784	ATCATGAAGCTCAGTTCAGTTTGCTTCTGGAACGTGAATCCTGCGTTCTGGCATCATT	30237	A_95_P309938	FG135371
31009	365	69	838	AGCTTCTTAGTACTGGCTTTGTCAATGCCATCAAATCTTCATGAAAAAAGGTTGTTTC	30248	A_95_P130327	EB430351
31016	365	76	526	TCCTCATGCTGCTCTCGCATCCACGTCATTCAACCGGTGCCATTATATATATTAAGGA	30262	A_95_P047541	BP131683
31017	365	77	758	AACAATGCTCAGAAGGATCATAATTCGTTGGGCAATTCGATCGTGTCGTGGAGTGTA	30264	A_95_P302943	FG147521
31019	365	79	566	GAGGGTTGGATATATCCAATTTTGTTGTAGGACAAGGAAACCTGTTCAGTATGTAAT	30268	A_95_P102037	CN949756
31021	365	81	1006	AAACCTCAAAGTTTTACAGAGTTCGCTTAGGTGATGGATCTGTTGAAACACTTTTAAA	30272	A_95_P221827	TA21901_4097
31027	366	2	348	GACAGCAGCTTATGAAGGGTCAAGTTGTATTCTTAAGCCCGTAGTATCCTCTATGTA	30119	A_95_P103347	CV016468
31029	366	4	2807	AGAAGTTGCTGATTGCATGCAGCCTTCGTAATTTTACAGGGGTGAGATTGGTAGAAA	30123	A_95_P239164	AY219234
31030	366	5	912	GAAAGCATCAAAGAAACTGTCGAAAGCTTGAAGGAGAAAAAATTCTATTCAGATGC	30125	A_95_P248947	AY911854
31033	366	8	610	AACCGGTTCCTAGCTCCATTTGAGTTCAAATTTGGCTAATCATTAACCAGTATCTTTCC	30130	A_95_P017526	BP530512
31034	366	9	713	GAGGCTGATTTTGTTTTCACTTCCATTTAGCTTGCTCATTACCTCTTGTGTGTTAATTA	30132	A_95_P289368	DV159060
31036	366	11	784	CGAATTTACATCTTACCGGTGAGTGATTCCACTTGTCATTCTTCACCTATGAATCCATG	30136	A_95_P025981	EB681743
31039	366	14	589	CGGCTGAACTTATATGTGAGCTGGAACTTTTACATAGTCCAAGTAACTTGATATATAG	30142	A_95_P286883	FG635003
31042	366	17	414	AGCTCGTACTGATGTTTCATAGATGTGGATTAGCAAGAAGAAACTTTGTCAAATTTG	30148	A_95_P144467	EB447819
31045	366	20	816	AGAATACATTTTTATGTGTGTAATCCCAAATGACGCCTCTTCAGATGTTGGCATTATC	30154	A_95_P206132	EB438385
31046	366	21	674	AGTGCGTGTTGCAGATGCTGAGCATTAAGCTCATTGTTCGAATACTTGCACAACAAA	30156	A_95_P234764	FG642251
31057	366	32	896	TGCTTCAGATGAGGAGATCCAACATCTGAGAAGATACGGTCGAGCAGTTGGTGTCTT	30178	A_95_P232629	EB426431

31058	366	33	768	GTTGATGAAGTTGCAACTTGAGAGTAGAAAAATGTAGTTCAGAATTAGTTTTTCTCCT	30180	A_95_P201482	EB681917
31059	366	34	129	AATATTACATTACATAGCATTGATGTTTTGCGTATCCTGGCCCGGGTTATTTCGACTTC	30182	A_95_P210602	EH617005
31062	366	37	749	GATTATTTAGGTGTAGTGACTTGCTATGCCTGTTGAATTGTTCCTTTTGTTGGGAATTA	30188	A_95_P164887	EH624292
31063	366	38	197	GGGCACTTTAAGGCCTCCTTAGAAGTTGATCTAAGTTCTGAAAAATCCATAAAAATGT	30190	A_95_P144717	EB448230
31064	366	39	1036	CTCCTATTGCACCTTTACCTTATTGGTTAACCCTGTTATGAACTTCTAAGCAATTCTATA	30192	A_95_P009576	TA14308_4097
31065	366	40	287	AGTTCTGGTCTGATTCCGGCAGTGAACAGTCCGAAAACACGAAAATTCGGTGAATAT	30193	A_95_P102707	DW000146
31066	366	41	356	GGCTGTAAGCTGTAAGGAATGACAAAGCCTCCACAATCCCAAATACACCAAAGGTCT	30195	A_95_P111977	CV020459
31069	366	44	776	GGATCTGAGGAAAGATTAATTTCTTGTTTCTCGTTCCTGAGTTTCTTCTTTCATTTAGC	30201	A_95_P240294	DV158685
31072	366	47	406	TTTTCCTGTACCTGTTTAGACCCTCAGATCAACCTGTTGTTATCCTTGGCCGCACTTTCT	30207	A_95_P088298	BP530008
31079	366	54	808	GAGCTGGGGCATTTTAAATCATTTGGTTTTGGCAATTGCTGGTGGATTCTTGGTGTTA	30220	A_95_P182402	TA13208_4097
31080	366	55	787	GTCTTCTGCATCTGTGCTCGGAAGTGTATTTGCATTGTTATTTATGCTGTGTATGCTGA	30222	A_95_P010716	TA13715_4097
31082	366	57	561	TCTATGGAATGTATGATTGGTCCTGAAGGAGATCTTACAGAGACCACCGAAGAACAG	30226	A_95_P059206	BP134682
31083	366	58	369	GTTTTTCAGGAGATATATGAGTTGAGCACATAGACAAGAGTGAATTAAGCTCGCCCA	30228	A_95_P148942	EB678528
31088	366	63	573	CTGTTGCTTAAAACAGAATAGATGATACCCTATACCTTTTATACCTCTCTCTCTCTCTAT	30238	A_95_P316498	FG188840
31089	366	64	739	TTGTCGTGGGCTTAAGAAAGCTGCTGAATTTTGATATTACAATTAGAGTCAGAAAGAT	30240	A_95_P298198	EH617940
31090	366	65	1357	CTAGATTTCTTGCTAGAGTAAACGGTTCAAATGCAATCTGACTAAGATTGAGGCGGC	30242	A_95_P232119	AJ414052
31092	366	67	1102	GAGCAGCACATTCTTTCATTTGTCTGTGTTTGACATGTTCAGTGTTGACCTCAATGCGT	30246	A_95_P016801	TA16297_4097
31093	366	68	661	AATAGGGAATTTGGGATGTGAGCACGGCTATCATTTGGAGTGCATAAAGCAGTGGT	30247	A_95_P132747	EB433422
31094	366	69	725	TGGGGGTGCAATATTGTCACTGTGAGAGTTGATAAGCACTGATATCCTTTTTATGTAA	30249	A_95_P163612	EH622658
31095	366	70	590	ACTGTAAACTGAAGCTTATTGTGACTGTCCCTGAATTGCTTGATTAGTTAGTTAATAG	30251	A_95_P124122	DW003976
31096	366	71	609	TAATGGCTTTCTGGTGTTACTGTCATTACCAGCTATGAAGGTCGTTTAATCATTTTGTT	30253	A_95_P022721	DW002470
31100	366	75	620	CTCTTAGCGAGGATGGTACTGCAGATGCGTGGTTCCATTAATCAAGGACATAAATGG	30261	A_95_P002818	DV157885
31103	366	78	699	GTTTGTTTCAAGTTCGTTGCTTCTGTTTGTTGTCGTTCGGGGCTTTAAATCCAGCGATT	30267	A_95_P309253	FG645389
31108	366	83	790	AAATGTGGTATGCAATCAAATTCTTTTATCTGAGAAGTACTACTGTGCAAAAGGATCC	30276	A_95_P120507	DW000465
31111	367	1	680	GTCTTTCTCATTCGAGTTTTTGTAGTTGCGGATTTAATTGTTCAGTTATGCTGTAGCAT	30281	A_95_P193802	DV158519
31114	367	4	659	TATGAGTTATGCTATATTTTCAAGCACAAGCACTTCACGGAGTAGTGATGATTGCTCA	30287	A_95_P235094	FG200594
31118	367	8	1038	CATTGGAAGTCTTGTGGAGGAGTTGCAGAGACAAAAGATGAAGAATATTCAGTTGG	30295	A_95_P216752	TA20773_4097
31119	367	9	180	CACCTAGGGATTTGATTAAACATTTATTTGTTTGGGCTTCACATGAAACTTCCTTTGAT	30297	A_95_P028251	TA17494_4097
31120	367	10	378	GTACATTGAGACCCAACATCACTTGTTTTTATTGTTGTTAGTAGTGTGAATTTCGTGTT	30299	A_95_P219507	AM808565
31121	367	11	839	GCATCTCAGCATTATGTGGTCACCTTGTGTAATTTCAGGATATATCACAGAGACGTGC	30301	A_95_P291283	FG157644
31123	367	13	505	CTTATCATATGTGTTTATGTGGGGACCTTTTTGTAGGCTCTTTTCAATCTTGTTACTCTA	30305	A_95_P186452	TA14131_4097
31132	367	22	390	TTGGGATCCTTGGTAGTAGTGCACTTAAAATGGGAATTTGTGGATGCAACAGTATTA	30323	A_95_P067340	BP136843
31136	367	26	768	ATTGGCTATTTTTTGTGCCAACTTCAAATGTTTTACTAGTTCACCACTGCTGTACCTTCT	30331	A_95_P196567	TA16367_4097
31138	367	28	549	ATGCAAGGTGCCTGAATTAGGAGTTCTTGATTATCAATGGGATGAAAAGGACTTAAT	30335	A_95_P068955	BP137257

31144	367	34	716	ATTAGATCAGGGACACGGGCATCACTTATAAGATTCCTTCAACTCTTGGTGGCTCAT	30347	A_95_P285248	EB427414
31147	367	37	604	GTATTTCGAGATCTTCTGGATTTTGGGCTTAAAATATACCGTTCCGTTTGGAAATTTT	30353	A_95_P202597	TA17670_4097
31148	367	38	800	TATGACTTGATTTCAGATGTAGATAAGGGTGTAAAACCGTTTTGTTTGCTAACTTTCG	30355	A_95_P030891	EB431338
31151	367	41	1056	ACAGGCGAGCTTAAATTTTTGACTGTTTAAGCAATATGAGAAACTCCACCGGTTATC	30361	A_95_P019726	TA16869_4097
31156	367	46	0	GCTGGAGGTTGAATTTGGGACATTTTAACTTTCAATAATGTGGCCAATAGACTTTCA	30371	A_95_P234044	A_95_P234044
31157	367	47	285	ATCTTACAAAGCCATTTGTTTCCATGTACTTTGGCGCGGGCTATTTGGCTTGGTTGTC	30373	A_95_P077020	BP527144
31158	367	48	829	TTAGTACTTTTTTGTTGTGGTTCGGATGGTACGGGTTTACCCGGGATCTTTATAGATT	30375	A_95_P309468	FG167388
31161	367	51	656	CTAGAAGGTCAAATAGCTATAGTTCTTCGCTATGTCTCTCTCTCTATATATGTAGTACT	30381	A_95_P293488	FG640583
31162	367	52	323	GTCGTAGAAGATCTCAAGTCACGGAGCACACTTAACTTGCCCCAGACAACTAAAATT	30383	A_95_P058471	BP134481
31167	367	57	583	CGATAGAATATCAATCAGGTAGACAGACTTTGGCCCAAATTGGTAAGAAAGAGAAC	30393	A_95_P240229	FG639535
31168	367	58	820	CAATTTCCATAGTTGCAATCATTCTTTTTGCTCAAAATGCATAGAGAGGCACGTCGAA	30395	A_95_P152232	EB682544
31176	367	66	311	CCTCTACTGATGGCATTTTACTTCTATGATCAGAAATGAACAATTACAACCCTCAAAC	30410	A_95_P019206	TA16840_4097
31178	367	68	346	TTTTTTAGCCCTTGTACGTGGGATATTCTGTCTGGCAATCACTTAATCTATAATATTGT	30413	A_95_P202087	TA17560_4097
31181	367	71	517	GTTGTTGACAGTTGTGGTTCCGAGCTTTCTATTTCTATCGAGGTCGTCTTTGGTTCAT	30419	A_95_P260806	AM809585
31182	367	72	921	CTTCCTCACCAGATATAATGGGAGAACCACTTGGAACTGAATCTAAAAGCACCACAA	30421	A_95_P031786	DV162276
31184	367	74	400	TTCTGCTGTAATGTAACTCGCTGTATACTGTAATCTATCACAATCTTGGAAGTTTGAAT	30425	A_95_P097583	BP534113
31185	367	75	497	GTTCAAGTATGAGCTGCTCTTCATCTACTCACTTCTAGCATGTGGTAAATCTGCTCTAT	30427	A_95_P020971	FG638231
31187	367	77	292	CTTGATCAAAGAAGATCTTTAGATGAAAGCACCAGATCTAGGAAGTGATGCATCGTC	30431	A_95_P029831	CV016585
31189	367	79	545	CTTTAGCTCCATCCTTCACAGTGAAAAAGCAGCCATTGGATGTGAATATAAGCTGATT	30435	A_95_P048191	BP131844
31192	367	82	1060	TTTTTCGTTCTTGAAAAAGGGTGGTAGTTCTTAGGGGCTAGTAGTAGTCAATTTGGAT	30441	A_95_P203932	TA17959_4097
31194	367	84	338	GATGATGGAGAGCTCTTTGATGGTGGATATGATATGAGTACTGGTGGTATTTGTGG	30445	A_95_P081385	FG638686
31198	368	3	803	TTTTGGGGTTGCTGGAAATTCTGCCACAGTTTTGTATCTAACCTTCAAAATATACAGA	30286	A_95_P218007	EB434642
31202	368	7	602	TCGGAGGGATTTCTTGTAAGCTTTGAATTTTCAGCTTTACTCATTTACCTCTTGTCTAT	30294	A_95_P251999	U66266
31205	368	10	813	ATTGAAAACAGAGTGGTTTTGTCTCCACATGCAGAGATGTTGCTAGAGTGACGGCA	30300	A_95_P295528	FG159719
31206	368	11	498	ATGCCGTATGCAGCTTCCCCTTATATTTCTATGAAGAAGCTGTTCCACACTTCGAACC	30302	A_95_P278998	AM839551
31207	368	12	697	TTAAAGAGAGGTGGCAATGGAAGATTCTTGAAAACTGCTGCCTATGGTCACTTTGGA	30304	A_95_P297348	EB683060
31208	368	13	900	CTGGATTTAGGCATTTCGATGACTCTTTGTATCACTGCTGAATTGGTTTGATATAAAA	30306	A_95_P032501	AB119475
31209	368	14	825	AACTATTTCAACCAATTGGAGAATACCAAGAAGCTTCTGCTGGTAGATGGTGGCCCA	30308	A_95_P126347	EB425699
31211	368	16	1569	ATAACTCCAAGTTTTGGATGCTGTTTGAATTTTTATTGAGAGTTAACTCTTGGCCTTG	30312	A_95_P179677	TA12562_4097
31215	368	20	95	CTTTATTCATTTGTGATCAACAACATTCTTCATTGATGCCAAGCGATCACAGGTTCAAT	30320	A_95_P031486	CV018605
31217	368	22	1638	ACTATAGCTGGTATAGATCCAGCCATGCTTTTCTTATTGGTTTATGAGTCTAGTAGTA	30324	A_95_P159307	TA12251_4097
31218	368	23	499	CACCCATATATGAACTATTTTGAACTTGCTCCTTGTGTTTTGACTCCAGCCCATTTTTG	30326	A_95_P164057	EH623176
31221	368	26	1450	TTCAACTGTGGATGTAACCTCAACTACCATACCCATAGGAGGAGATTGAACTTTAGT	30332	A_95_P196213	EF051136
31222	368	27	621	GGTCTTGCTGTTCCCCTTTTGGTGATCATGTCTATTATTTAATCAGATTGTTACATGAA	30334	A_95_P123422	DW003266

31223	368	28	739	GAGATGCTATTAGCATCTTCGCTTCTCATGATATTTGGATCGACCACGTGTCGATGTC	30336	A_95_P189562	EB427133
31226	368	31	70	TTTCGTATGTTGATTCTCAATTATGTAGCTGAATTGTGGCCCGAGTCTCAGCCTGCCC	30342	A_95_P104987	CV017252
31227	368	32	1325	TCGCGAAGAGGAAACTAGCAGCAAAATGTTGGATGGCAAAACTGATTTGAGTTCAC	30344	A_95_P228884	DQ672264
31228	368	33	554	TTTCCGATTTTTTCTCTTGGAATGGATTTGAACTCAAGCTTGTATTTGCCGGCTACATT	30346	A_95_P153727	EB683929
31233	368	38	757	AGATACATTTGCAGATGTGAAAATGACTTTCTTTGTGGGCAATGTGATCGTGGTTTG	30356	A_95_P203362	DW001694
31237	368	42	813	CAGTTCTTTGGAACTGTTTAGATGCAACCAACAAGAGCTCTAGCAAATTTCGTTTATT	30364	A_95_P252614	DV161053
31238	368	43	821	AAATTCTTTGGACAAAGGGTGAACCAGAAAGGGTGTGTCCACATATTCGTCTTGAAT	30366	A_95_P030361	EB438473
31240	368	45	798	TGAATCTTGGTGATATGCTTGAGCGCTGGAGCAACGGTATATTCAGGTCAACATTGC	30370	A_95_P250612	EB450250
31241	368	46	91	ACTCAAAAACTCCGACTGTTTCAATCAGCCTAACTTGAACAAATTTGTGGGATTGGG	30372	A_95_P192542	TA15474_4097
31242	368	47	545	GCCTCTCTTGATACCATTTATGCTACGTTGTTAGAAACTTTGTTTGATTTTGTTGGCTT	30374	A_95_P299948	FG626154
31248	368	53	806	TTCACAGTTTTAGAGTGCATAAGATGCGCCCTCGCAGGGATGTATGCAGACATTCCA	30386	A_95_P243317	EB447909
31250	368	55	1127	TGGGACCCTTACAAGCATCATTTCCATCTGAGAGTTTCTTCACTTGTACATTCAAATG	30390	A_95_P028046	TA13851_4097
31255	368	60	820	GGTGCTGCTACTAACCTTAGGAACAAACTTTTCAAGAATTTCAAGGTCCTTAGCCCAC	30399	A_95_P211227	EB424750
31256	368	61	611	TCTTTGCTAAAGTATGAATGGGTTGAAGCCGGTAATGTACAGGCCACTCTGAGGTGA	30401	A_95_P063875	BP135896
31258	368	63	828	AGTTGTATACCAGTGGTATTTCGTTCTTCCATTTTTCCTTTTTGGGTGTAGAGAGAGG	30405	A_95_P219157	EB446619
31263	368	68	637	CTTCACATCATGGGCACAAATTATAGCTTGAAACTAAAGAGAACTAACTATGTATCTG	30414	A_95_P138007	DW004524
31266	368	71	788	GTGTCTCCTGAAGTATCCTTTAGCAAATCAGACAAAAAATTAACTTTGAGAGTTCCTG	30420	A_95_P249087	DV159725
31272	368	77	734	CTGATTTTTCTTTTGAAACTGTCCTGATAAGAGGAAGCAAAGTTTCATTTATAGAGCA	30432	A_95_P012076	TA18471_4097
31274	368	79	831	ATCAATTGACTCGAACATGCTGTATAGTAGTCGAGTTTCGCGGATCTGACGAAGCAG	30436	A_95_P312713	FG158027
31277	368	82	532	TGTGTTCCTATGCTAGTGTAATGCATACTTGTGTCATTTAATTTGCCCCACTTAATTTC	30442	A_95_P123877	DW003760
31284	369	4	575	AGCTTCTTAGGTGGATTTATCAACTCAATCTGATGACACAAGCTTGCAAGAAAGAAT	30455	A_95_P069915	FG626716
31285	369	5	852	AAGTGCTTCTTTTCTCCCTAGTGGCATTTTACTGCTTCTTTAGTGAGATTTTAACTTGT	30457	A_95_P116357	DV159070
31289	369	9	904	TAAATCAGCTCTGTCCCAGTGATCTGAATGAGATCTCCAGCAACAGCTCAGTGCATTT	30465	A_95_P242467	TC43443
31293	369	13	640	ATCGGTCAAGATCTGAAATATGTGAAACCTCCTTTCTTTCTTTTCATGAAAAGGAACA	30473	A_95_P207682	TA18793_4097
31296	369	16	142	CACTATTTGGAAGTGGTTTAACTATGACTGTAAAGTTCCTGCTTGGCCAAGTGTTGTT	30479	A_95_P102307	CV015972
31306	369	26	1261	GTGATTAATTAGTTTCCCCTTGTAATGACCAACAAATGGCCATAGTATAGTTTTGGAT	30499	A_95_P249062	EU342421
31312	369	32	526	GTGAATCCAAACAGTTGAGGGGCACTAAATGAGATTAATGATCTCAAAGTATTGGCC	30511	A_95_P202972	TA17756_4097
31318	369	38	161	CTTTGTAATATATAATCCTCATGTGAGAGGATATGACATGTTGTAGCTTTCTTGGTGG	30523	A_95_P090438	BP530955
31320	369	40	839	CAAAGAGCTTTTCAAATTGTTGAAATCAACTTGTACATTCGTCCTGGTTCTAACTAGC	30527	A_95_P203777	EB439646
31325	369	45	546	CTATTTTCAGAGGATGGTATGTCTTTTCTAGCTAGTTGCCAAAACCTTGTCCCTCGAC	30537	A_95_P066320	EB681611
31328	369	48	730	GAAAAGGAAACGGGAGTTAAAATCATACTTCCATTATCGCGGAAAGAGGATTGTCT	30543	A_95_P287618	EB428479
31332	369	52	894	TGGCAATCATCTCCCAAGACTCTTTTTCAAGGGCTTTCATGTATTAGAATCATCTGAA	30551	A_95_P009311	TA14277_4097
31333	369	53	483	GGACTTGAACAACACTCCGCATTTTCGTACCTAACTGTCTACTCTTTTCTCTGTCCTTT	30553	A_95_P020841	TA17037_4097
31347	369	67	345	AGGTTCCAAATTCACTGTAATGTAAGTTCACCAGAAAAGTAGGTCTTCACGTATATCA	30581	A_95_P083735	BP528841

31348	369	68	586	GAAGGTGTATGGCTGTCTATCAGACTTACATCAATGCCATGATTGCGGATCCTTTCAT	30583	A_95_P062050	BP135415
31353	369	73	1447	CCCTTCTTTGTAGGACAATTTCCAGTTGTAATGATGTGATTGTATCGAAATTGTTATCC	30593	A_95_P027416	AJ438265
31354	369	74	470	TCATATTGGTGGATGCAATGTTGTAACTTATAGTGCCCGTTAATGCTCTAGTGTATTTA	30595	A_95_P063625	BP135831
31359	369	79	451	GATTTTGCCGGAAAGCACTATCATGACCTTAAGGAGAGACCATTCTTTAACGGCCTAT	30605	A_95_P125727	FG635539
31363	369	83	1049	CATTACTTGCTTGTGTTGATGACTTAGCTCGTATGTATAGTCTCATTTGCATGTTGTGT	30613	A_95_P180952	TA12863_4097
31365	369	85	2135	GGATAACTAGTTGTGTCATTCACTCGATGTGTGAATTCGTTTTTCTTTACTGGCATAAT	30617	A_95_P028141	TA12496_4097
31374	370	9	877	TGCCACTGTTAAGAAGGTATCTCTTGAGCTAGGAGGTAATGCACCTTGCATCATCTTT	30466	A_95_P231589	EB680600
31375	370	10	456	AATTTGCATTGCAAGCCTGATATCTCCTTACAGAACAAGATCGAGATGCTTGTCGTGT	30468	A_95_P075030	BP526621
31379	370	14	538	TATGCAAAACTGCAGGTTGTATGCTTCCAATCAAGTGATGATCGTAATTTGACTGCCT	30476	A_95_P284203	FG637809
31382	370	17	731	GATGGCAAAGACCGGTGTTATTTGTAGATGCATTTTTGTTTATCACATTCTGGCGCTC	30482	A_95_P269821	FG174896
31383	370	18	965	TTGAATGGATTGTGCTGATATTGATTCAGCTGAAATCAGACTGGTGTTTCCTTTCCAC	30484	A_95_P022791	TA17553_4097
31384	370	19	750	GGGTTGGCTTGTTTTATAGATCCCATAATTTACTGTTTCTGGAATTTGGATGATCTTA	30486	A_95_P206547	FG158098
31388	370	23	89	GTGTATAACAATGTCACTGATAATGTATTATGGTCCTCTTTTTCTCTTTTTTCCGAGGC	30494	A_95_P130807	EB430908
31389	370	24	188	TCGAAACCAAATTCTTGGCCGCTCTTCTCCTATCTAAAATTTACTCTTTGCCTATTAGCT	30496	A_95_P161492	EH620222
31398	370	33	672	TTGCAAGAATCTAATGGTTTTGAAACTGTATGATGGGTTCAATTTATGCGTCTTGACC	30514	A_95_P015701	TA14679_4097
31400	370	35	223	CGATTAATCAACAGCTCCGAGAGCTTGAGAGAGGGAGTTTGATTATTTCTTTGTGGCA	30518	A_95_P241575	FG167825
31401	370	36	167	GAAGGTTTTACGTTGTTTTGGTCAATTTTACGGGGAAGAAGGAAAATTGCAAAGTTC	30520	A_95_P095453	BP533199
31402	370	37	728	TTGAAAGAACATAAAGCTGTTGGATACTCTTTCGATAGGCCCCTTCATCCTTCTGAATA	30522	A_95_P206942	TA18631_4097
31403	370	38	419	TGGATGGTCTGAGTCAAGAACCATCAACTGACAATTTTGTTTTGATTGGTAAGGGTA	30524	A_95_P099488	BP534949
31405	370	40	711	ACCGGGCTGACTTTTGTATTTATTCCTGTTTCTCTAGTGTGCATTATCAAAAGTTTAGA	30528	A_95_P148757	EB678241
31407	370	42	729	TATGTTCCTTCACCTTCTTGTGTTGTTGGTGACCCTGTGTATGGATCTAAGAATGATG	30532	A_95_P126622	TA15758_4097
31408	370	43	813	TTTCTGGGGTTCACAATTTGTCCCAGATTATTACGTGTAATTTAGTCGGGATAAGATG	30534	A_95_P013956	TA14708_4097
31411	370	46	316	TCACTTGCTGTTTGTATAACTGGTATACTCTTCTGACAATTGTATTAAGCTTTTCAGCT	30540	A_95_P091538	BP531404
31414	370	49	431	GTTCAATCGAATGATATTGCATGTTGCTGGAATCCATTCTGTAGATTCAGTTAAAACA	30546	A_95_P284743	DW003998
31416	370	51	1019	TTGGTGTTGTTTCGGAACCAACCTTTAATGTTGGTGAATTTTCTACTTTTCTTTGGGTG	30550	A_95_P011131	TA15696_4097
31419	370	54	722	TTCATGGTTTGAAGTGAAGAATCTTCGCCAGTACTCTCTTTATGGCCTATATTCCAAT	30556	A_95_P192107	EB451025
31427	370	62	527	ATAATCTGGAGCTTGCTGTTAATCTTGCCAAACAGAGGAAACCTTCCTGGAGCTCGA	30572	A_95_P045211	BP131076
31428	370	63	958	GGCATTACCTTGTGCCGCCGCATCACCTGATCATTCCAATATTCTTTTGTTTCTTTTTAT	30574	A_95_P010531	Z82982
31436	370	71	722	TTTTACTAAACTTTTGACAAGCCAGCACCATCGCACCTTGACTGGCAAGTTGGGACAT	30590	A_95_P215452	TA20489_4097
31437	370	72	433	TGGATATTTCCCTTTAACTATTCATGTCAACTAAACGGGGGGATTGAAGGGAATTTTG	30592	A_95_P030161	TC74155
31438	370	73	367	TGGTTGGTGTGCTGGCACTTGGGCTTGTTCATCTGCCTAAACTTTTGGAACAATTGGA	30594	A_95_P111127	CV020067
31439	370	74	779	TGTTATGCAGGTTGAATACATACGACAAGTGTCTCATAACATACTTCACATGCCTAAA	30596	A_95_P214857	TA20354_4097
31441	370	76	690	GTTTATTCTGTAACCAAATCTGGTAATTTTACAGTCAGACAGACTTGGGACGCTTTTG	30600	A_95_P156832	EH614825
31443	370	78	422	CAGCAGCAACTACTCCTAGATCACCTTTCTATGTACCTTATTATGGGGCTTTTCTGGTG	30604	A_95_P089888	BP530698

31447	370	82	571	TATGAAGGGTGTGCCCTTTTGTATTATTGGAAGGGGCATGGATTTTGCTCACGGTTA	30612	A_95_P132442	EB432923
31450	370	85	748	GAGTCCTAAAAAATTGCTTGTTTCAACAGTTTCAGTTAGATTCTGTGTTCTCTCAAGGA	30618	A_95_P177742	TA12061_4097
31465	371	15	902	CTGCAATTCTTATCTTATACGGTCTACCTAGGTTGTTGACTGGGTCAATTCTTGCGCAT	30647	A_95_P020826	EB682391
31467	371	17	875	ATCTACTGGCATGAGCTGGTATAATACCCCGTGATACGGGAAGTGGCTGACCATAAA	30651	A_95_P022121	DV999868
31469	371	19	754	TTAGAGCTTAAAGGTAATAAATTTGTTTTGGAGAGTTTCTGGAGTTCAAAGGGGACA	30655	A_95_P161367	EH620115
31470	371	20	643	TCTTTGGTAAGGGACACCATAGCTGCCTGTAGTATGGTTCAGATTTTCAAATGGATTT	30657	A_95_P015276	EB426417
31474	371	24	339	CTCACAAATGGCGTACCTTCTCTCTCGATAACACTAAAAAATTGGCCCAGAGTACAGG	30664	A_95_P113732	CV021284
31475	371	25	705	ATTATATCGAAGTCCAGGACCTGGTGAACCACCATTTGTGAAGGTTGGTGACAAAGT	30666	A_95_P150277	EB680370
31476	371	26	72	GGTGTGCACAATCGATTACATACATGTATTTTACTGTTCTGTTGGAATTAATCTTGCTT	30668	A_95_P146027	EB449862
31479	371	29	722	AATGCAAACTCATGAATTTTTGCTTATATCCATCTCAAATGTCGATTGAGGGACTGGT	30674	A_95_P179932	TA12619_4097
31480	371	30	1130	ATATGTCTCTGACACTGATTAAATATCTGTAGTCTGGTTGCTGCAAGCCCTCAACGAC	30676	A_95_P243327	TC50283
31483	371	33	484	CTTCTTGAAGATAGTCCTTTTCCTGGTTGGTTTCTCTATATAATTTGCAACCTCTGGTC	30682	A_95_P208252	TA18927_4097
31485	371	35	837	GCTGTATATCTAGTCAAGTATGTGGGACAAATTGGGTTAAATGTATTCATGCAGGAA	30686	A_95_P184147	EB679701
31486	371	36	427	AGTGAACACAGTAAAGCTAAAAGGAGCAAATGATTGGCTGGTTCTTTATACTCATCT	30688	A_95_P306788	FG636272
31487	371	37	594	TTTGCTACCTAACTCGATGAAAGTAGATACCAGGCAAAGTATGTTTTAATCACAGGAT	30690	A_95_P143627	EB446869
31492	371	42	838	TACGTGGGGTTTTTTGGTACTAAAGTGTTAAAAGGAGCACAGAATTCTTAGAATTTT	30700	A_95_P232649	DW004645
31494	371	44	668	GATGATATGTTGAAGATGGAGAAGATCACTATTTATGTTGAACACCCCCGCCCTATT	30704	A_95_P137052	EB440796
31495	371	45	407	TGGAGCTGATTTATGTGGAGGATCTTTTTGCTGTAGATGGATAACAATTTCTTGAGAA	30706	A_95_P096378	BP533598
31499	371	49	845	CTTTTCGTGTGTGCAGAAAGAAGATGAGCTTGTCCAAGTGAATTGTGAGTCGATCGC	30714	A_95_P259511	TC41276
31509	371	59	781	GGAGATTTGAAGCATTCCTTCACTGTGAAGATTTGAAGAACTCAAGATAACTTCATTT	30733	A_95_P291753	EB424775
31516	371	66	1213	CTAAGTTTTAATGTTTGATTTGGAGGTAGATGCTATACTTCAAGTAATTGGAGTCGG	30746	A_95_P205818	AY319648
31522	371	72	529	CTGCTAGAGATTGTTCAGTAATTTGAGTGCATTTTTGTCTTTGTATCCCCAAATGCAAA	30757	A_95_P248552	DW002693
31528	371	78	458	CACGAAACTAGTCGTGTAGGTGTGTACCATATACTCTATGTGCTATTTTAATTGAAAG	30769	A_95_P127602	EB427139
31529	371	79	674	CTGCCCAAGCATTTTGTATACGTAACTTTGTAGTTTACTTTTGCCCTTTGTTTGTAGTT	30771	A_95_P226254	EB439183
31536	372	1	757	GTTGTCTTTTTTAGTTTTCTTTGTCTTGAATAATGGGACATTAAGCCAGCTACAGTTCA	30620	A_95_P127132	EB426581
31537	372	2	683	TTGGCGTTTATTACGTGGCACCGAGACAATGACCAACTTTGAGCCTCTGCATAAGTTA	30622	A_95_P139327	FG145736
31538	372	3	366	AAGAAGAAAGAGGAATCTGATGATGACATGGGTTTCAGTCTCTTCGATTAGAGGAAT	30624	A_95_P107222	CV018266
31540	372	5	412	AAAGAATTCAGAGCCCGGAGTTGTCTCATTTTCCAGCTGTTCCCTTGAGCGTATTTTA	30628	A_95_P005926	FG639375
31550	372	15	864	TACTTCTTTGACTGTTGTTGGCGAGGCTGTTACGGATGACATTGGAACAATTCGGAT	30648	A_95_P292298	EB428006
31562	372	27	742	ATTATAATAGGTAATAATAATTTCTCTCTCTTTCTATCTTCTCCCCCGGCCGTAATGGC	30671	A_95_P119992	DV999623
31565	372	30	829	TGTCCATATCTGTAGAATGTACTCGAGAACTAGTTGTGCTCAAGCTAACTCTTCGACA	30677	A_95_P011856	TA16924_4097
31569	372	34	170	ACTGCAAACTTATATAGCAGCTTCTATCATTTGTGTGCTTTCTATGGATTGATTGCACA	30685	A_95_P106212	CV017805
31570	372	35	825	AAGGAAATGGTGGCATGGTTAGAGATGCAGTAGACCATATTGGACTACGCACAATG	30687	A_95_P128347	EB428011
31573	372	38	379	TTCAACTGTTGCCGGAGCTTAAAACGCATATTATTTTGGTAAAACAGAAGTTTTGACA	30693	A_95_P179077	TA12422_4097

31576	372	41	494	AAGGAGCTCTTCTCCAGAAGCTGGTGACCTGAAACGCTATGCTATACATTATGATAG	30699	A_95_P026811	FG138693
31579	372	44	744	TTCTTTTCCCTGGAGTGACTGACCAGTGGTTTGCATGGCTATTTTCGCATCTAGTCTG	30705	A_95_P294743	FG148973
31581	372	46	425	TGCGAGAGTCAATATGCATTTACTGGAATCATCTTTCATCTTTGGTACATTTAAGGTG	30709	A_95_P046671	BP131458
31585	372	50	754	GTAGTTGCATATTTGAATAGAAGTGATGTAGCGGATAATAAGCAGGCTATAGCCAA	30717	A_95_P015531	EB677896
31588	372	53	164	GATGATGATGATGACAAAGATGATGATGATGATACTGAAGAACTCGGAGATGGTAG	30723	A_95_P139622	TA12746_4097
31596	372	61	332	TAGTCTACTGGAAGAAGGATCCACTGTAGGCAAGAGAAATATCTTGAAACAGAAAC	30738	A_95_P093493	BP532289
31600	372	65	434	AAGGAAAAACATGTCTGCTGCTGCTGCTATATTGTGCGGGAAGAGATCGAACTATTT	30745	A_95_P125817	FG150715
31609	372	74	246	GTTCCATCTTAGATGGTAATAAATTTGAGTATAGCACCATTGAACGGTGTTTTCAGCT	30762	A_95_P159112	EH617069
31620	372	85	1656	CTCTGGCAGGTGGCTTCGATACATAGTTACAGGTTCTTTCCTCAAGGCTAGGTTTTAA	30784	A_95_P024956	AM851010
31621	373	1	901	ATGTAATGTATTTAGAATTGGAAAGTGAACGTTCTTTTTAAGCCATTGGAGCCTCTTG	30785	A_95_P248782	TA14366_4097
31626	373	6	283	ATGATGGCTTGCTTTGACACAGAATTCTAGGGTTATAGCTTGAGGAAAGGATTATAA	30793	A_95_P059041	BP134633
31632	373	12	480	AGAATGGTTTGATACAAAAAGTCAAGAGAGAAAATTTGGACCTTTGAATGGCAGGT	30805	A_95_P232164	BP128741
31633	373	13	77	AATGGGGATATATTCAAAGCCGAGGTGCCCAGTGTTCGGTCAGGACACCTATTATAA	30807	A_95_P049736	BP132236
31643	373	23	461	GTCGGTATAGCTAAGGTACTTTAATTTCTGTAGCTAAGGTCTGGATATTGTAATACCT	30826	A_95_P109487	CV019336
31645	373	25	816	TCTTCATTGAAGACTGATGTGGGTGATGCCAGTGAATGCTCCTCATCTGGTGCTTTAG	30830	A_95_P138287	EB442026
31646	373	26	840	TTTTCCGTTTGCTGCCAGATCTTCCCAAGCCAATTTGGCGCTATCCGATTTCATTTCTT	30832	A_95_P246642	EB682809
31647	373	27	652	ACATATGAGGGACAGTTCGAGATCCTGTCTCTTTCTGGTTACTTTCTTCTCTCGGAAT	30834	A_95_P286708	FG186048
31656	373	36	655	TCCCCAAACTTGAAGTATATTGTACATTTGAAAGCTGCATGGAGTTGTGGCTTTTTGA	30850	A_95_P307753	FG641732
31660	373	40	582	GAGTTATGTTTCAAATTGGAATCAGAAATGAAAAAGTGGGCTCTACCCACGCCCCAC	30858	A_95_P085025	TA19965_4097
31661	373	41	1604	GATGTATTTGTAGTTCACTGTTCCTATAAATGGATTCGTTTTGAGTCGAGGGTCCCCC	30860	A_95_P237524	D31964
31662	373	42	498	GAATTGTCTACCTGTAGGCTCGTGAAGAACTATTCGGTCGATCAACTTATTCTCTATG	30862	A_95_P301853	FG637079
31665	373	45	344	TTTGTTGGGTATCTGCAAGGATTTCTTGCACAAATAGGTCACTTTGTGCAAATTCTGG	30867	A_95_P160672	EH619345
31669	373	49	413	TGCCATAAACCTTACCAGCTTCTCAATCACTAGATTGTATATGACTTTTGCAATCAAC	30875	A_95_P158817	EH616714
31670	373	50	55	CTAGGTGATTTCTTCCTGTCTATCCAAGCCTTGGTAGATAGAGTTACCTGGTACCTGT	30877	A_95_P092658	BP531915
31671	373	51	622	CTGTAGCTTTCTCTTGGTTCTAAACATATTCAAGGATTGTGGTTTTTTGCTGGTTCTTA	30879	A_95_P288233	FG641165
31673	373	53	366	GTTAGGAGTCGTGTGATGCTAGACCTCATGTGAAGGATTGGTGTGCTGAATATTTTG	30883	A_95_P051156	BP132576
31674	373	54	405	AGAGATAATGGCCTCTTGCATCTTATTTTCTCACTTCCCGTTGCCATAGAAAAGATCA	30885	A_95_P130532	EB430579
31677	373	57	327	GCTGTTGAAGTTGTACCGACATAATTTTGAGAAGTGAGCCTTTTTCCTTTTTCTTGTAT	30891	A_95_P034184	AJ718259
31678	373	58	470	AAGGAGCTTAGCTAGCGCCAGAAAATGTTTTTACTAGTAGCATATTTGTACCTGTTAT	30893	A_95_P099843	BP535089
31681	373	61	867	GGATTGGACTTCTTTGGAGTCTACTTACAGAGGCCGAGAAACAGGTTTATCAAGAAA	30899	A_95_P235679	EB678129
31682	373	62	1364	GCTTGTGAGGATGGTTTAATGCTTCAGCTGTATTTATCAGTTGTTTTAGGATATCTCT	30901	A_95_P179377	TA12492_4097
31684	373	64	394	TTCTCAAAATCCTATCTAGAAATGGGCCAAAAGTCTGACATGAGTGTTGGATGAATC	30905	A_95_P100403	BP535349
31687	373	67	561	AAGTATACGGCAAATTGCGTCCAACTTTATTATTGCAGCTGTTCAGGTGATAAGACA	30911	A_95_P159212	EH617174
31690	373	70	1407	GACTCATTAATTTGCAGGGAATAAGAGTTTAATCCTGTAATGCTTCTTGCTGTTCAAT	30917	A_95_P014071	X96727

31692	373	72	2584	TTGCACCTATGAACACCTCACACGCTGCTGTTTTCCTCATATATTGTACGTTGCTTGCT	30921	A_95_P027236	AB124647
31695	373	75	279	CTTTGTAATCGACTATTGTACAATATCTTTGAACCAGAGATAAAGAAGCGACGGTTT	30927	A_95_P029241	FG623741
31697	373	77	789	CTGAATTATTTCCTGTCTGTTCTTCCTTATGTATAGATTTCTGGTGTTTCATGGTGGTA	30931	A_95_P270971	EB438297
31699	373	79	1096	ACAGTACCAACCCAAAGCTTATGACTGAATCTCGAATCATGCGTATAGCTAGGGGAT	30935	A_95_P220692	TA21661_4097
31700	373	80	446	ATCTGTGAACTTGTATGTGAGACTGGGCAGTAGTGTAAGTGGATGGTTTTAATTCTG	30937	A_95_P232589	CV019600
31701	373	81	851	GCTGAACCTGTACAAGCTAGCACGTCGTTTAATCCTGAAGAAGCTGATGATAATAGA	30939	A_95_P241360	DV158562
31702	373	82	1148	CGGTGAAAGGCATATATTAGAAGAATCAAATGTTTTCCGATGCTAGAAATTGGAGTT	30941	A_95_P182572	TA13249_4097
31705	373	85	1734	CACACAACAGTGGAAAAGTTTCAATGTATGTAAACGCAAACAGTGTTAACGTTGGTT	30947	A_95_P181362	TA12960_4097
31708	374	3	884	CTTCCTCAGTTTCTGCAAGTGGGTTATCGTCTAATACCCTATTTTATATTTAATGCTGA	30788	A_95_P233709	DV162246
31709	374	4	333	AAGGGTGGAATTGGACGTTATTGGGAATAATTCGTCAAAGGATTCTTTTTAAAACCA	30790	A_95_P075010	FG635003
31713	374	8	793	CGTTGTACACAAATCCAATTGTTGACCTTGGGATCCAGCTTAGTTTCCGCTGTCTTTTT	30798	A_95_P234939	EB439485
31716	374	11	516	GATTAGTACGGTCTGTGTGATCCATTTTCTTAAAGCTGGTATACAGATGCTTTTCACT	30804	A_95_P021666	EH621297
31722	374	17	458	GTTTGCACCCTTTAGCTTGATGTATTTGTAGTCTGTACAAGTCATTACAATGTCCAATT	30816	A_95_P006451	CV020183
31723	374	18	782	CTTTGGTTAACTCAAGGTTCCAGCGGCACTGGTGAAGATTGATTGGAATATTTGATT	30818	A_95_P116267	DV158893
31725	374	20	642	AGATTGAACTTTGTAATTGTAACTTCATCTTTTGAGTGATACTGCTGCCTATGACAGT	30821	A_95_P018516	TA12434_4097
31728	374	23	617	CTATTGAAGTCTTGCTTCTTGTTCGGAAGAATTAAGAATAAGCATTGTGTAATCGGAT	30827	A_95_P300533	FG635390
31731	374	26	429	TTTGATTCTCAACCCAACTCTCCTCTTTCAGAGAGATGTATTGTTGACTTCAACTATTC	30833	A_95_P114312	CV021536
31739	374	34	506	TTATTAACGGTAGGGGTTGATCTGGACGAAAAGTATAACGGGGGACAAATGTAAAT	30847	A_95_P080430	BP528001
31740	374	35	729	AAAGATAAACAACCGAAAGCAGAACGACCTGCTGGTGGAAGGCGTGAAAGTAAAG	30849	A_95_P127727	EB427300
31743	374	38	241	TGAGATGAGGAAAATTATGCTGGCGATCGCCGATAGACTTGGATCATCGCCGATTCA	30855	A_95_P066990	BP136744
31744	374	39	655	TGACTTCCAATGCAGTCTCGTTCGTTACAATCCCACTTGTTCCTTAATGTGAAGAACTT	30857	A_95_P288038	FG186133
31749	374	44	676	TGGAGAAATTGGAAGCATCTGGGCTTCCTAATCTATTTTGGTGAAAGGGATATGAAA	30866	A_95_P158162	EH616240
31751	374	46	608	TTATTTTCTGTTGGTGAAATGGAATGCATGGGGTGCTGTGTAAATGCTCCAATGATG	30870	A_95_P110187	DV162733
31754	374	49	241	GATTTCTGGTTTAACACTTGACACTAGTGAAAAGCAGCTGGCACTTCTCTACCTTGCG	30876	A_95_P147857	EB643473
31755	374	50	839	TTGCTCCATGGCGTGTAAGCTGATTCTTTTGGATTATTGGTGAATAATGCTGCCTTGT	30878	A_95_P021811	DV159434
31757	374	52	399	AGTTGGAACTTGTTAGATCTTGTTAGGTGTTCCTCTATTATCAATCAATGAAACCTCTT	30882	A_95_P000671	FG627136
31759	374	54	36	CAACCCAGCAAATTGAAGAAGAACTGTTAACGTGGACGAGGAGTTGCATTTTCCCGT	30886	A_95_P074960	FG136839
31760	374	55	743	GCATCGGAAGAATGGTCAATTTGCATCTTTGAAAGCAAGTTCTGGATCTTCTAGCTG	30888	A_95_P137787	FG136761
31764	374	59	497	GTATAGTCTAGAATATCCCCATTGTGTTCTTAGAATGATCATTGGAAGTTGTTGTATG	30896	A_95_P019981	TA17904_4097
31766	374	61	830	TGTAAGATGTGTTCACATACAGAACCATGCCCTGATCTTTGTTGTCATACATGTGAAA	30900	A_95_P146937	EB451107
31771	374	66	438	ACTCTGTACAGAATTCCTGTGAATTCGCAAATTCTGATTGCTAATCCTTTTTGTACGTT	30910	A_95_P095323	BP533128
31774	374	69	759	GCTCTTATTCTGGACTCTTTAACATTTCAGGAGACATGAAACTATCTTATTTTCTTGGG	30916	A_95_P028246	EB449088
31775	374	70	392	GTTCAGCTTTGGGCATTGCATGTATCAACAAGCTAAACATGCTAATGGATTTAGTTAT	30918	A_95_P130612	EB430661
31777	374	72	597	CTTTATTGTTGTTGTTAGGGATAATTCGCACCTTTGTGGTTTGAACTTTATTGTTGGT	30922	A_95_P213857	TA20137_4097

31781	374	76	827	GTTTTGACGAAGTTATTGCTGAGGATCGAACTGAACAGTTCATTAATGTTCTCCAAAA	30930	A_95_P016056	DV160265
31782	374	77	32	CTTGCACCATAACCACGCTGGCACAAATTTCCTATGAAAAAATATGTATTTAACTTTC	30932	A_95_P003426	DW000536
31784	374	79	443	GTGCTGTTGCTGCTTTACCGCTTAAGGTTTGCTTTTAATTAATTGCGCCTTTTGAGTTT	30936	A_95_P005836	BP535069
31786	374	81	1064	TGTTGCTGCCAAATCCGGAGTGAAGCTAGAAATTCCAGATGGTGCTGTGATTGCAAA	30940	A_95_P250107	AB055502
31791	375	1	324	TGAAGTTGAAGGGGAGAAAGAGATTTGCTATCGCGCAAGAATTCTCTGATAGCCTTG	30949	A_95_P103377	CV016479
31799	375	9	814	AGATGTATTCTGCTGGTGCTGTGATGATCAAAGCTGTGAACTGTTGTGAGGCTGGTT	30965	A_95_P246667	FG153643
31800	375	10	1213	CTGCAGAGATGGCCTATTACAAGGCAATGGGAATTGATCCCCCTAATTCTACAACTA	30967	A_95_P015406	TA16293_4097
31802	375	12	301	GGTCTTGGCAGCCTTCTATTCATTTTCGGCAGCTCTCTTGGAACTTATATTCTAGCTAG	30971	A_95_P105117	CV017301
31804	375	14	586	TGAAGGCAGGCGAGTCAGTTATGGAACCCCAGAAAATGCAACAACAGCGAGAAAA	30975	A_95_P138942	EB442648
31805	375	15	451	CAAAGTGAATGCCTCAAGCTTTCCTCTTATTTCTCTTCTTGATACTGTACCTGTATATAA	30977	A_95_P202742	TA17700_4097
31809	375	19	844	CTAAACGTTCCATTCTATGTGGTGAGACATGAATTTGCTTTTGATATGTTTTGCATTAG	30985	A_95_P247132	EB438736
31813	375	23	513	AAATTCTTGCTCGAACAGGTAATCTTCTTTACTCTAGTATTTATTCTAACTCCCGTCCAT	30993	A_95_P022341	EB443868
31818	375	28	458	TAAGGAGAAGGAAATAGAGCCAATAAACTCCTGCATCCTCAACAACTGACCGTCCTG	31002	A_95_P050371	BP132380
31822	375	32	891	CCTTTGAGGGCTTCAGTTCTATTTAGAACGTATTTCAAGGCTGAAACTGTTGTATGGA	31010	A_95_P186542	DV158658
31823	375	33	288	GCTCATTGATATCACGAGTAGATTAACCAATACATTTGCTTTTGCTTGCCTTTATTCAA	31012	A_95_P029406	BP526310
31827	375	37	715	GCGAATTAGTTTCCTTACCCTCGCATAAGCCAAATACTGATCTGGCACCTACAGTTCCA	31020	A_95_P162332	EH621270
31835	375	45	385	TTGCCGGGATTGTTTATTGTTGTATCTTCCATGAGTTTGAACAACATTTTCTGCTTTGTT	31036	A_95_P142782	EB446216
31836	375	46	1549	AATTTACCGAAGCTTTTTAACCGAGGAACTTTGCCAAGTTGTCCACTGCCTTGACGCT	31038	A_95_P008371	AJ438263
31840	375	50	80	AGGATTCCAGATGTCACCAGCCATGATCAGAGGACTACTTTTTCTTCTCGTTATCACC	31046	A_95_P255384	EH614588
31841	375	51	1168	CTCCTAATAAGGGAAAATGTGAGTCAAGTTTAGAAGAAGTCTACTGTGAGGCAATAA	31048	A_95_P194907	TA16004_4097
31843	375	53	705	TTAATGTGATCTCTGTATGTTGTGTGTACTCACTCACTCATAATGTACTGAATGTCTTT	31052	A_95_P159067	EH617014
31845	375	55	368	GGTGCCAGACACCACTGTCAGGCAAGCCAACAATAATTTATTAATTTGGTTCTCTTTTT	31056	A_95_P087853	BP529898
31846	375	56	522	TACGGTCTGTGTGATCCATTTTCTTAAAGCTGGTATACAGATGCTTTTCACTAGTTCAA	31057	A_95_P253899	EH621297
31848	375	58	572	CCTATGGCGAACAATACTTTGAAACTGATTTTGTTCAGGTGTTATTACCTTTACACTAT	31061	A_95_P125247	FG634396
31849	375	59	334	AAGCACATATTGCTCAATGAGACATGCTTCTTTTAACTGTGGATCAAATATTCTCAGAT	31063	A_95_P212007	TA19737_4097
31850	375	60	810	CTTATGTGTCAAACTTGGTTGTCTTGTTTGGGGTTCCTGCTTTTTTCGGGCAGTGCACT	31065	A_95_P296183	EB450578
31852	375	62	309	GGTCGCGGTTCGTCACATTTTTTGAGTTCAAAGCTATCAAACAATTGAATTTTAGACTT	31069	A_95_P213877	TA20141_4097
31855	375	65	855	AGGAGAGAAACTCCATTGCTATTGAGATTGGTTATTGCTGTTTTCCCGTTCATGGGAT	31075	A_95_P228644	DW000428
31856	375	66	614	GACATGTCCACTGCATATTGGCACTAACATTCTTTCAGTTAGTATTTGTTGAAAGCAAA	31077	A_95_P047596	BP131697
31860	375	70	597	TCGAGACTCAATAAGATAGCTTCTTGTTTGGTGCTTTGCAACTTTTAATATTAAACCG	31085	A_95_P142272	EB445781
31861	375	71	858	AAGGTGCACTTAATATCACTCTGGATGGAGTTTACCATTCCCCTGTTGGCTCTGATGA	31087	A_95_P187972	EB679931
31869	375	79	600	TTGGTGATTGGAGGATAGTTCAATCAGGACACAAGTGTTTGATTTCTTTTGATGACTT	31103	A_95_P090358	BP530921
31872	375	82	1134	GAGCCATTTAAAGCTCTGTAATACCCTTCTGTATCTTATGTTGTGTCTGTTTGGTTTTAT	31109	A_95_P015541	TA13425_4097
31874	375	84	787	GGCAAGAAGACCTTGTACTCTTTTGCTTTAAACCACTTGTTGCTGATAGATTCATTTTA	31113	A_95_P016751	DV158928

31880	376	5	806	ACATCATTCTGTACTAAGGAGTCAATCTCAACCCTTGTCAGAGAGAGCACCCGGTAA	30958	A_95_P225657	FG133389
31881	376	6	595	CTGAATATGTGTCTTGTATCTCACTTTGCCTAATTATATTTCAGACCTGTCGTAATGAT	30960	A_95_P263131	FG640232
31885	376	10	876	TTAGATTGTGTTCTCTGCAGGCTTATGTTCTGGCATCTTTTATCCGTATGGTGCTTTGC	30968	A_95_P149792	EB679750
31888	376	13	787	ACTGCCACCACCAACACCTGTTATTAGAAAATCTACTCTGTTGAAATCAAGCTCTATT	30974	A_95_P127242	EB426760
31891	376	16	732	ACGAGATGATCAGTATTATGCTGGTCTTTTGATAGAGTCGGATGAGCACTGTCATTTT	30980	A_95_P162147	EH621003
31894	376	19	131	CCCCTGCTTTTCTAAGTGGAGAACAATTTTTGTGATCCTAATCTTTTGTGTAATTAAAG	30986	A_95_P147442	EB451870
31895	376	20	732	GTCACTACCTGAAAGACTTAAATATTACAGTTGGATTGGCAGAGCAATACTTCAGTA	30988	A_95_P145037	EB448579
31896	376	21	706	AGATAATTATTCATGTTGATCCGTTTGGGCTCTGTTGCTATTTAGGTTGAACCACAAT	30990	A_95_P293298	FG643559
31903	376	28	340	GCATGTAATAAGGACTCAATTTACTCTGGATTGCTTTTCTCCTTTCCACTTGATCATTA	31003	A_95_P088098	BP529960
31908	376	33	429	TGATCCCTGCAACTATTTTTTGGTGTTTATGGAACGAGAGGAATAGAAGATGCTTTG	31013	A_95_P070895	BP525562
31909	376	34	789	GGTTTTAATGGGCGCATTTGGTTTTGATGATAATGGACTTTCTATCATATTTTAGCGC	31015	A_95_P199882	TA17088_4097
31912	376	37	143	CTGTTGAGGCACTTGAGTGTGTTATGCGTGTATTGTTGTGTATGAGATTTGATATTTA	31021	A_95_P100728	BP535498
31915	376	40	218	CCCCTTTAGCTTAGTTCTCTGCTACCAACAGTAGTATCCCTTTTCTTGTGTTGTATTAG	31027	A_95_P159917	EH618459
31923	376	48	2844	TTCGGCCTCTTCCTATGTAATCTCCTGCCCTTTTTAATGCAAGTTTGTTTTAGTATGAG	31043	A_95_P007306	TA12480_4097
31924	376	49	463	TTCGACGATTTCATTGCGGATGCTCTTAGAGGTACTGGATTTTATCAGAAGGCTCAAT	31045	A_95_P199257	TA16956_4097
31927	376	52	368	GATTTTTCTTTAACTAGTAGCTGACATCCCGGGACTCATAAGAGGAGCCCATGAAAA	31051	A_95_P107197	CV018256
31929	376	54	376	CTATCTTAGCAATCTTAATGATTGGAGTGAAGAACCAGAAAGACCCGCGTGACAGCA	31055	A_95_P189417	EB680583
31931	376	56	735	CGGAGTATTTCATCGTAAAGATAAATGATGGGAAGAGTAGACGTATAACATGCATG	31058	A_95_P292453	EB427468
31936	376	61	890	GAATCTAAATGCAATGAACAAATTGGAAGTGCTGAAGCCCTGGACACTGTCATTTTC	31068	A_95_P235124	DV998904
31940	376	65	801	ACATGTATTTTTGTTAGGTGAGAGTCTCATGTGTGGCAACACATCTCAAGTGTTGGCT	31076	A_95_P268261	DW000289
31941	376	66	1773	CCCTTGGTCTTTTGTTTTCCAACTGTGATCAAATTTTAGGGTTTAATAAAATGGGGTG	31078	A_95_P012586	AY553216
31942	376	67	801	TCTGCAAATTATGCTTTACAAGGACCAATGTCATACAGTACCTTTGCTCAATGCTTTTT	31080	A_95_P216567	TA20734_4097
31944	376	69	830	CATATACAGAGGTTTAGGTTAGGTGGAGGTGATGCCACTATTTATGTGACTCAAGTG	31084	A_95_P289173	DV157904
31946	376	71	2075	GTTGTAAATAGGCTGCACTAACTAGTTTGTAAATCTGAAACCAGAGTGACAAAGGTA	31088	A_95_P017891	AF253511
31952	376	77	837	AAAGACTACTTGCGGATGTTATTCCGCCTTGCGATATTGGGGTTACTTTTGATGACCT	31100	A_95_P219852	TA21484_4097
31953	376	78	136	CAATAGAACAGCCATAGTTGTTGCTGGCCTACCATGACATACATAGACGTGGTTCTTT	31102	A_95_P051216	BP132591
31955	376	80	696	CACGTTTCTTGTGCACCTTTAGCAAGTGGAATATGTTTAAATCATCTTGATTTTTGCAC	31106	A_95_P001356	EB679961
31957	376	82	652	GGTGATGCAGTTACATGTGATCAGTTTTGATTAAGTTTATATTACGCAGTTGAAGAA	31110	A_95_P163507	EH622558
31960	376	85	418	GATGTCATGGACCAAGATGATGCAGATTCTGGATCAGAAAAGGGAAAGAGCTTCAA	31115	A_95_P164262	EH623408
31964	377	4	673	CATATATTGTCGGACTCCAAGCAGAAGCTCTGCAAGGCTTGCAATTATGCCATCAAA	31122	A_95_P146067	EB449929
31968	377	8	329	ACCCATCTAAGACTGTTATTACTAAGCTCAGGCTTGATAAGGACCGTAAATCTTTGAT	31130	A_95_P201929	BP526356
31969	377	9	539	TGGATCAGGAAGGTGCTGGCATATGTGTAGTAGGTGCTTAATGTTCTCATTTAGGAC	31132	A_95_P022171	BP534984
31977	377	17	834	TAGATACTTTGAGCTACGTTTCAGAATAGAGAGAGCATGCTATTCCAGTGCTAGCCC	31148	A_95_P244102	FG158775
31978	377	18	573	GCTCTCTCTAAAATTGCACTGAACTATCTATGCTATTCTTAAATAGTACACTGGTTCTC	31150	A_95_P248732	EB678067

31981	377	21	716	GGCGTATTCTGGATCTACTTTGTGTATTTCACTATTCATGATTTGTTTGTTCACTCACT	31155	A_95_P287883	FG153402
31986	377	26	984	CGGTATATGATACTGGAGAACCTTGAAGGCCTTTCTCTATTTATGAACAGTAAACCTT	31165	A_95_P203327	TA17831_4097
31993	377	33	337	CCACCTGAGCTGGAAAACATACCTCTATGCTCTATAATTTGGGTTTTGTAATATTGTT	31178	A_95_P006001	FG626563
32002	377	42	400	TTTAATGAAAAAGGACAACTGTAATTTAAGCTTCGCAACTGTTCTGAGCTATGGGCTT	31196	A_95_P164707	EH624005
32003	377	43	469	GGCTTGCTCAACTATCTTGTTGCATTGATAGGCTTTTATAAAGGATTCTCTACCATCT	31198	A_95_P023201	TA14829_4097
32004	377	44	823	CTAAATTTGGGTGAGAGACTGATTCAGGCCACTGTTAGAGGAGATGTCAGATCTAAT	31200	A_95_P309568	FG133349
32005	377	45	1991	CGTCTGTCTCTTTGTAACTTCTGTAATTGACAACATATGCTCTGAGATGTAAATAGAT	31202	A_95_P033026	AF223351
32010	377	50	675	GGTAGGCATTTCACTAAAAGCTCAGCCTAGAGTTGATCAGCTGATTTACTTTAAATAT	31210	A_95_P197377	DW004157
32012	377	52	311	TGCTGCTATCTGCATCCATTAATTTAATATCCCTGCTAAATGGTAGAAAATCCAGTTC	31214	A_95_P093613	BP532334
32015	377	55	3534	TATTCCGACTCTACCAAGCCAATCAATTCCCTTGGAAGGTATCTTGTTGACAATATAT	31220	A_95_P283518	AB361628
32017	377	57	47	GCTGGGGGTGGATATTGTACAGTCTCCGCTTAATTTTTGAATTAATGTTGTATTTATT	31224	A_95_P140307	EB444264
32022	377	62	1732	TTAAAAATAACGTGTGAGCATTTGCTATTCAATGGGAATGACAGCAGAGTTGCTTGC	31233	A_95_P025371	TA14706_4097
32024	377	64	600	TACATTCGCCAGTATCACAACATAAATATCAATGTAGCAGTGCAGACTGACAATGGA	31237	A_95_P155947	TA14223_4097
32031	377	71	1059	CAGTGACGTGAATTGATTCATGAAATTTTACGATACTGATGTACCCCGGATGTAATTT	31250	A_95_P006851	TA18546_4097
32034	377	74	467	ATCTCTAATGGGACACTGTGGCATCTAGGATGAGAAGAATTAATGAAGGAGAAGCT	31256	A_95_P132097	EB432535
32035	377	75	537	GTTCCTATTGTATCTATTGGATGTGAGAAATGCAGTATTGGAGGGTGTATTAATCTA	31258	A_95_P089168	BP530373
32040	377	80	1415	TAGGGTGTTATATGTTTCGTAATGTACGGCATGCTTAGGACCCAAGTACCTTCAGCC	31268	A_95_P027466	U66402
32042	377	82	893	GGGCACATATATGACCGTCAGGATCAGAAGTATATTGCATCAACTCGTCATTACCGT	31272	A_95_P290208	DV162216
32044	377	84	849	CTGTGGCATTGATTCCATACTATTTCCTACTTGGTTTTAGCTGTTACAATGTTCTCTGA	31276	A_95_P013451	EB450203
32045	377	85	578	TGTGATCCTGAAATGAATTTTGCTTACATGGTTCGAAAGGAAGTGGCCTGGGTGTTC	31278	A_95_P231274	FG644444
32062	378	17	910	TTTCGGGGATTTCAGTTTCTCCATGAATTTTTTGGACATGGAGAAGTGAAAAGGTCT	31149	A_95_P247692	DV999311
32068	378	23	600	TTTTGTAGCAACCATTCAATCAGTCAAATGTGCTTTAATCCCAAACTAGTTGGGTTGG	31160	A_95_P222077	FG640658
32075	378	30	739	GTTTACTCGTCTTTGTCAAGGATATTTGAGCTCTATCAACTTTGATACCAAAGTTTTG	31173	A_95_P088858	TA12020_4097
32080	378	35	211	GGCTTCGTTTACCCCTCATGTTACTGTTGATTCATCTGTTACTGTTACTATGTCTCTCT	31183	A_95_P106502	FG139571
32082	378	37	1036	GCTAGGCTCTGCCATGTTTTCCTGGATTTTGTTTTCTGTTACTTTAGAATAATTCAGAT	31187	A_95_P211717	TA19675_4097
32083	378	38	707	AATGGGACGGCATGGTGATCATATTGCTTGATTTTCAACCTTATTCTGAAGTTGAAC	31189	A_95_P221737	TA21883_4097
32085	378	40	494	TACAGTTCGTGGAAGACTGACTGCCAAGTTATCGAACAAAGAAGTGACAAATGTGA	31193	A_95_P264761	BP528728
32087	378	42	424	AGTTTGGGAAGTCTATGCCACTTGTGAGTTGGGTTCCTTTTGTGAACGAAATTCCGA	31197	A_95_P128002	FG172957
32094	378	49	574	TTGCTTGTCAATCATTAAGTAGTTCAATGAGTTCCTCCTTTTCAAGTGCTAATACTGTT	31209	A_95_P159532	EH617779
32095	378	50	270	GTAGGGGTACCAGAGGGTTCTTCTTCTCCTTCTTTATTTATTGTTTTCTGATTTTCTAT	31211	A_95_P026431	TA17965_4097
32096	378	51	712	CACAGGTTCCAGCCCATGTATGTTGAGCATTAGAGCTACATCTTTTCCTGTTGCTTCA	31213	A_95_P293398	FG194591
32097	378	52	335	CGATTGTGATGCATGTAGTCTTGGGTTCTTGAATAAATGCTTTTAATCGGGTAAATG	31215	A_95_P097028	BP533855
32102	378	57	769	GCAGTAAATTGTGTTTTTAGGGGGACTTGTTCTAGAATAATAAACTTGTGCGTTAAT	31225	A_95_P115672	DV157993
32106	378	61	1250	AAAGGATCCGGCATTGGCAATCCATCTCCACCATTGCCCAATAATCAAGGACAAAGT	31232	A_95_P196272	TA16304_4097

32109	378	64	1234	ACTACTATGCATTACCATCAGAACATTTTTTCTATAAATCTACCAGGCGCTCCCGTTTT	31238	A_95_P222477	AY029749
32113	378	68	282	ACAGGTGTTGATGATCCAGCCCATCCAAGGTTGTTGCATATTGTTGCAACTTTCAGG	31245	A_95_P103422	CV016495
32114	378	69	81	GGTATTCTGCTAGTTATGGCTTGTTCATAAGATTGTCTATATTGGGATTTACTGCTTT	31247	A_95_P095963	BP533412
32116	378	71	835	TCACACTCTATGTTATTCTGTTGATGCTCATGCCTCCGGCTATGTCATGTATGAGATC	31251	A_95_P309553	FG133319
32117	378	72	2111	GTTGTTTGTTAGCCATTTGAATTGCCATTGATGTTCATTTTCAGCGTTGTTCAATTGGT	31253	A_95_P013436	TA14936_4097
32128	378	83	743	TATTATAGAAACAGGAGACCCGGATGCATTTAAACAGTACCTGTCGGAGACGGACA	31275	A_95_P194462	EB425633
32133	379	3	35	TAAGAGAATATTTGGCATGTTGTACCCAAAGAAGAGCATTGTGTTTGGTGAATCTAC	31284	A_95_P034578	AJ719159
32140	379	10	691	GCAATTATGAGATCTGTCAATCTGTTATCTTCTGTAAGTCAAACTCATTATCACTGGA	31297	A_95_P249872	FG645304
32143	379	13	661	CTATAGCAGTCCCGTTGTCCTTTACATTTCAAATAACTTCTGAATGTAGTTACTGGTTT	31303	A_95_P268746	DW002885
32145	379	15	503	TGCGGGTTCAAATATGTATCTGGTTTTCACTGTTGCCTTATCAGGATGTACTTGAAAT	31307	A_95_P299203	FG635661
32147	379	17	730	TGAGAGAAGTCAAAGTCCACCAACGAATTGCAGCAACCTTTCTAATCCTTCTTCAGTG	31311	A_95_P152417	EB682758
32149	379	19	602	TGAACATGAGCTGGGCAGTATTTGTCAACCAAGTTGTTGAACTATTACTTTTTTGGTC	31315	A_95_P285473	FG636985
32150	379	20	493	GAGGGGGGTATGTTTTGATTTGATAAACATGATGCAAACAAAACAGTTTCTCGAGAT	31317	A_95_P029151	TA16757_4097
32156	379	26	499	CTTAGTGCTTTATTTATTGGCTTCTCCTTATTTAGATGGAGAACTGCTTGTGATTCTTT	31329	A_95_P197222	TA16515_4097
32158	379	28	508	GAAAGACCAAATGGTCCAAGCAGCAGAGAAAGATCAGATGGTCCTTTTAATTTCCCT	31333	A_95_P118837	DV161906
32161	379	31	714	ACTCAACAGTGCTGATGCATTCTGATCTTCGTCCAAATAGGAAGAGTTTTCGGTGCTC	31339	A_95_P221087	TA21747_4097
32162	379	32	348	CTACTGATGTCTTGGTAAAAGTATTGGAGCTTGAATTTCCGCAGATATGTATTAAATG	31341	A_95_P108342	TA14789_4097
32163	379	33	184	ATCAAAATGGAAGCAAGTTTCAAGAAAACTGCCCCGTAAAAGAAAGACTACTGAGG	31342	A_95_P087448	BP529800
32164	379	34	492	ATGCCATCAGTACTCAGCAGCATAAAACATTTCCTTATCTGTTTCGGTTTATGCATATT	31344	A_95_P132287	FG637879
32169	379	39	529	AAGTAGAGTTGCAACGACATGTGTACTGCCTGTGCATCTCACTTGCAGTTTGACAAG	31354	A_95_P134232	EB436351
32171	379	41	684	TACTCTGGAGGCTAGTTTGTTCAGATTGTTTTGTAGACCTTTTCTCTCGTTTGGATATC	31358	A_95_P135717	EB439244
32172	379	42	882	GATTTGTGTTTAAGACCATGGAATTGATGTTGATGTATAATATGTCATGGGAATGCT	31360	A_95_P181417	EB680718
32174	379	44	1117	GTTTCTTGGTTTATTTGATGCTCTGCATTAAATACATTGAAAAGGGATTTTGGTTCTG	31363	A_95_P007636	AB025029
32175	379	45	789	TAAATGTGAGACAGCAGCATATGTTGGAATATTATGTTTTATGTTATAATGGGTGTG	31365	A_95_P196352	EB447150
32179	379	49	698	AATGTCGTACCTACAAGCAAAGAGTGGGTACACCCTTGTAACTCGACTACGGATGAA	31373	A_95_P298878	TC73380
32184	379	54	758	TACATTTGACTTGGAAGCACTGCAGATGTTGGGACAGGTGGCTCAATGGATTTCTTC	31383	A_95_P305468	FG186405
32185	379	55	868	AATTTCAACAATCATTGGAATAGTCCATCTGTTCCCAGTGAGATGCCCGCTTATGCTT	31385	A_95_P150042	EB680100
32190	379	60	768	TTTTGGCATAGGACCGCGAATTTACATCTTACCGGTGAGTGATTCCACTTGTCATTCT	31395	A_95_P096663	EB681743
32193	379	63	337	CTTTTTTGGGATATGTATATGCGTACAATTACAATGCACAATTGAAGTGTCGGGTAG	31401	A_95_P132282	EB432743
32198	379	68	0	CCATTCTTGTACACTTCTGTCATGATACTGTGTGGATCGGAGCTGATCATGTATGCTG	31411	A_95_P258411	A_95_P258411
32199	379	69	513	CTTGAAGCTTAACGCTCCTAGTAATCTGCTGGAGTCAGTTATGTAACAAGTGTGTTG	31413	A_95_P037018	BP128888
32200	379	70	212	GCCGTCGGTGCTATGGTAGCAGGTATATTTGGCATGAACTTAAGATCCTATCTAGAG	31415	A_95_P038301	BP129237
32202	379	72	595	CAGAGCTAATATCTGTTTGTTGCTCTGGATTGAAACTTGAAATCCAAGGATGTATCAT	31419	A_95_P133967	EB435682
32204	379	74	544	TTTGGACAATTTCTCGTCTCGCTTGCAACTGGAGCAATTTGTGGTTTGCAATGTATAA	31423	A_95_P288714	FG635017

32205	379	75	866	AAACAGCAACTTTGAGATGCTACTGTTATTTGCTGAGTTCGTTGAACATCTGCATTAT	31425	A_95_P185667	DV157557
32207	379	77	254	CGCTCAATCAGCAACTACTGCTTACATTTTCTTAGTGGTTTCATCCACCGTACAAGTCA	31429	A_95_P103227	CV016408
32208	379	78	810	TGCTGAAAAGCTGGAGCAAGCTGAAAATCAACTGTCTCATTCACGTTTTGGCCCCTTA	31431	A_95_P126627	EB425942
32215	379	85	698	GGCGATACTAGGCTTCACAAAGATGTTCACTTGTAATTGTGACTAGTTGGAAAACAT	31444	A_95_P019616	DV999689
32219	380	4	825	TTTATAACATTGTGACATAGGTGCTGGCTGTTATTTTGCCTCCAATCATTTGTAACTTA	31287	A_95_P149132	EB678814
32222	380	7	841	CCTACTGCCAAATCTAAATGTTGCTGAATTAGTTAAAGCATTTTCAGTGAAGACGAAT	31292	A_95_P231374	DV158544
32223	380	8	667	TGTCAAAGAAATCGGAAGAGAGTGGTAAAGATGATAAATCCAGCTCCTGCTTGGCCC	31294	A_95_P264891	FG639353
32226	380	11	824	TGTAATGAAAATACCAGAAGTGATTAGGAGCTTTGGCAATGACATGATCATGGGAT	31300	A_95_P116542	DV159294
32228	380	13	467	TGGGGTCAGTTACAACTTTATCAGATCTTTTCTTCAAGTGTGTAGATACCATATCTTCA	31304	A_95_P219757	TA21462_4097
32233	380	18	437	AGCTGCTGTTGCTTCCCCTAATGACCTAGCGACTCTTAACTGTAATACATCTTCTCAAT	31314	A_95_P149637	EB679541
32234	380	19	896	CCCTTGGTAAACCTCTATAGGTTTCAGGTTAGATTTGCTCAATGAAAAAATGAATTTT	31316	A_95_P198292	EB424651
32236	380	21	155	AGAAATGGGGGTTCTCAACGATTGGCGAGAAGAAATTCGAAGCTAAGTACCCAATC	31320	A_95_P241780	AJ718633
32238	380	23	703	ACTCGTGGCAAGAGCATGGTTTCAGATTGATTTGAGCTGGTTCGAGATCTAGGTACT	31324	A_95_P125672	EB424754
32239	380	24	779	TTGGTAGCGTTTCTGCTCTATCCCTTATCTCTTGTACTTGTATATGTTCTTGACGACAA	31326	A_95_P140852	EB444670
32243	380	28	741	CCGCTTTTCCATTACCCTTTGTGCTGATGAACTTATCTGCATACCAAGTTATTTTTCAT	31334	A_95_P187757	EB683945
32245	380	30	760	ATGGTAAAATGGTAGAAAGTTGGAGGCTACATATTTTTCAGGGAGTCATGCTTCCAT	31338	A_95_P152387	EB441159
32249	380	34	632	TAAAAGCTTGGTATCTGTATTTCTCTGCTGAAATTGCAAGGCTCACAGCAGAGCGAC	31345	A_95_P029736	BP130716
32250	380	35	464	GCTTTCCTTATCTGTTATGTATATCTTCACAAGTACTTTGTCAATCTTGGCACTGTTGT	31347	A_95_P019471	TA14297_4097
32255	380	40	790	GGATCCTCTTTTCATTTTATTGGGTGCTCCCGGTTGTTTCACATGTTGTATATGGTTTC	31357	A_95_P153982	EB684144
32258	380	43	654	TTGAGTGTCGCATTGGACGTTTCCATAACATTTATGGCCCATTTGGGACATGGAAAG	31362	A_95_P015211	EB680314
32260	380	45	1495	GCTAATGTACCAAACAGCATTACTGGAGAGCGGTTTCCTGCTCAATGACCCAAAGGA	31366	A_95_P145662	TA13587_4097
32261	380	46	635	TGTTTTCTGTCTTTGTCAGTTGAAGGAGACAGTTGAACCTCTTTGCTCTTTCATACCAA	31368	A_95_P017266	TA15118_4097
32263	380	48	749	AATTACTTGGATCCAGAGCCTCAGCTGTTACTAGCAGAGTTGAATAAGCGAATGGCT	31372	A_95_P163632	EH622700
32267	380	52	1626	CACGAGATACTTTTCATTTGGTCTCTGGCATTGCTGTTATGGGATCATGTTTTTAAATT	31380	A_95_P207137	Z93771
32271	380	56	1383	GAAGCGAATTCAAGACGTTGAAGATTCTTTGAAAAATGTGTGGAAAGTTTAGTTCAT	31388	A_95_P025991	TA18698_4097
32275	380	60	947	ATTTCACTTTCCGTTGGGGCTAACGGTTATGCTCCACATTATCTCTATGATTCTATTGC	31396	A_95_P150297	EB680396
32277	380	62	798	AAAGAGGAGACGACTTCGGGAGTTAGAGCTCATCAAGACAAAGAGAGCTGCTCTAG	31400	A_95_P310613	FG137144
32278	380	63	559	GATCATCCTGATGCATCCTAATGTGCTGCATGTTGCAATCTTCAAGGGGAAAAGGGT	31402	A_95_P141102	EB444888
32279	380	64	893	TGTAGAAGGTGTCGACGTTTGTGACTCCCGAAATAATAATGTTGTTGCTGAGCATAT	31404	A_95_P290033	DV161758
32286	380	71	1120	GCCAGTTTGCTGCTCCGTTTGCTTTACTTGAAATTTTAATAGATAGGATATGCATATG	31418	A_95_P212022	TA19740_4097
32288	380	73	236	CCCGATCATGAAAGATTTTATCGCATATATGACGAGTATAGTTGCTTCCTTTCTATCA	31422	A_95_P114487	CV021623
32294	380	79	891	AAATGCTCTCCGTTTGTAAGTTTCCCTCTGTTTTTTATGAGTTTAACTATGCTCATAGC	31433	A_95_P198352	TA16759_4097
32296	380	81	877	CGAGTTTCAGATCCTTACGGTGGCTATGATATGATTGGCTTTGGGGATATTCTCTTTC	31437	A_95_P266926	DV161712
32298	380	83	755	TACCATAAGAAGCTCTGAGCGCAATGCAGAGACAGAAATCACTGAGATGTTGTTGC	31441	A_95_P299798	FG137368

32299	380	84	824	GACTATTCATTGGGGAAAGATGCAAAACAAAGTTCCCCTTGTTTATTAGTTTTAGCT	31443	A_95_P199117	TA16923_4097
32305	381	5	359	CGGAGCTAGTATTATTAGTGTGTAATTCATCCATTCATTCAAGTATTCGGTTGGTTAG	31454	A_95_P099203	BP534837
32306	381	6	241	TTGCTGCTCAACACTAAATCATGTAGCATTTTAACTGCTCTATATGTTCTTAGTGTGCT	31456	A_95_P111557	CV020253
32308	381	8	891	GTCTAGTTCACATCTTATCATAAGCATTCTGGTCCAGGAACTGCCATTTGGCTGTCCA	31460	A_95_P244857	DW005082
32315	381	15	634	TTCGTGGGCAAGATTATCAGTACTGTAACTTATATCCAATAGAAGTTAGAAGCCTTCT	31474	A_95_P125297	DW005088
32319	381	19	576	GGTGGATATCTCCTGCATAGAGGTTCTGTGGTGATTTTATTGCTTCGGTGCTCTATGA	31482	A_95_P041841	BP130198
32321	381	21	808	AACTAGTGATTGTTTATCTGCCCAGGCATTTAGAACCTTCTGCAATATACTGAGGAG	31486	A_95_P216167	TA20646_4097
32327	381	27	95	GGCATTTGGCAAAGACAAAGATGACACTTGATGTTCATTTGAGAAAATAAGTAATCA	31498	A_95_P145757	EB449498
32330	381	30	244	CCTTCGGCAATGACCTAAAAGCAAAAGAGCCCAATTTGGAGAGGAAGAGGAAGAA	31503	A_95_P198327	FG645435
32334	381	34	1015	AAAGATTGTGGCTTAGCAATTGATTTGTTCTTCGTTTAGTCCTTGTTTGGTTATTGAG	31511	A_95_P012396	TA13907_4097
32338	381	38	149	GTCTACGAATGCCCGAAGCATAATTGATATTAGAGTGTTATAATCTTTTCGGACAATT	31519	A_95_P004476	EH620214
32339	381	39	502	TGGAACTTGTTTGTCACTAGTTGCTGCTATGTGCTATTTGCTATCGTGGTTTGTTTCTA	31521	A_95_P073835	BP526313
32340	381	40	1066	ATCAGAATGCATTATTTGTGGCAAATGGAGAACATTGTTCATCAGAATGCATTATTTG	31523	A_95_P187967	TA14467_4097
32343	381	43	894	GCAGTTACTCGATTGCTTAGGAATTACTTGAAGCAGTTTGTGGTTGCACCTGACTTTG	31529	A_95_P225627	EB442771
32344	381	44	768	TGGTAAAGTACAGAATATTAATGAGCAGAAGTTTGTTTTACCACCTGATGTGGAGCG	31531	A_95_P284913	EB439011
32346	381	46	830	ATGACAATAGCTCAATGGAGAAACATGGGATACCAAAACCAGCCTGAGCACCAGGC	31535	A_95_P223692	DV161783
32355	381	55	721	TGGAATGATTATTCTGAAGGATGGAACCCTAATAAAGGTACTCCTGGGGTTATGCAT	31553	A_95_P148587	EB677948
32357	381	57	994	CTACTTTACTGTCTTTACATACTCTTAGGTTTAGGAGAGGATTAATGACAGCGTATTT	31557	A_95_P110887	TA13262_4097
32358	381	58	525	AATTTTTACGCGGCTCTTAATTCCCGCTGTGTTAGTGATGGATCTTCGGTATATACCC	31559	A_95_P072630	BP526013
32359	381	59	385	TAGTCCGCTTTGACTTTATTGTGAGCCCTTATATGGTGTTAACAGAATTATGATGGTA	31561	A_95_P112522	EH619918
32360	381	60	300	ATCAGAAGCTTTACAATGGGTTACATGTATGGGATCCGAGTATGAAGAATGGTGGG	31563	A_95_P070700	BP192703
32364	381	64	838	ATAGTTACTCTGATATGTGTTAGTCAATGCCCTTTGACTGTGTAGTTTGCTCGAGTCT	31571	A_95_P291618	FG169937
32370	381	70	1200	GCAACCCAATTGATACTAGTGCGTGTATGTACGTATTTATGTATGTATGTAAAAAGA	31582	A_95_P032431	AB072391
32374	381	74	772	CGCTCTCGTGTTGTAGCTATTTTTATTTTCTGTCATATGGAAGAAATCAAAAGGTCTG	31590	A_95_P149912	EB679921
32384	381	84	748	TCAAGTATGCAGAAGATGTCTGTGCAGGTGTTATATTCTGCAGAGAGCTCGTCAATG	31610	A_95_P138302	EB427721
32398	382	13	369	CTTGCAATCCCAAGTTGGAATTCTTCAATTCATGGGTTCATATCATGTAATTTTAGCTT	31471	A_95_P209967	TA19300_4097
32402	382	17	951	TGGCTATTCCCTGTTGGAACAAGAATTTTAAGCACATATGGATCCGTTGATTTACTCG	31479	A_95_P020576	TA18875_4097
32409	382	24	817	CCTAATGAAGCAGACGACCTTTATCTGCATTTGAATTTTAAGCCATTTGGAAACAATT	31493	A_95_P014546	EB426727
32412	382	27	689	CGAGATGGGTGGATTTTATGACTTGTATGGAAGCATTTCATGTTCTAATTGAAGTTTT	31499	A_95_P207522	DV160337
32414	382	29	822	ATGGCAAGAATATTGTTCTAATGTGTTGTTTATCTTGATCCCCACTTTGGACATTCTTT	31502	A_95_P142772	EB446197
32418	382	33	233	CTGCTAATGTATTCATTCTTTACCCCCGACATACTTACTTTACAAACCATGAACTATTC	31510	A_95_P127657	EB427216
32420	382	35	190	AGGCAAATTTGTTGCTAACACCTTTCCATTCAGCTCTCAAGGCATCATTTGTAACCTC	31514	A_95_P109612	CV019382
32421	382	36	879	TCTAGCTGCTCAAAGGAATGGTAAACTATCAGTGCAAGCTTTCCAGGTGTGTGTGGG	31516	A_95_P290163	DV162066
32424	382	39	186	AATTTCAACAGTGTTGAGGGGACAGCGCCCAGTGTACTTTTATGCTGCTACTGGTCA	31522	A_95_P046481	BP131408

32425	382	40	736	TTGCAATTGTACACTTGGCTTATTGTTTTATCAGTTTGCTAAAAGAAGACCCTCTTCAC	31524	A_95_P180782	TA12825_4097
32429	382	44	786	GCGACGGTCTATTTGACTTCTTCAACAATGATGAGGTTGTAAAGCTTGTCCATTCTTA	31532	A_95_P117572	DV160512
32438	382	53	613	CTTGTTTAGTATTTTTTGTCCAGTTGACCCACACAACCTTAAAAAACCTTCGCCCCGAG	31550	A_95_P316613	FG189664
32442	382	57	699	TAAAGCCTTGATGGCATTAACTAATGATGTATACTTTGGAGGTGTTTTACATTTCATG	31558	A_95_P123287	DW003169
32444	382	59	755	AGCTGATAGTGTTAGGTATCCTGATTGCTTTGATCCTCATCATTGTCCTCTCAGTTTGC	31562	A_95_P292098	EB426444
32446	382	61	578	CACGAAGAACTTGTACTGCAACACTTCTATAGTAATCTATTATGTCCAGTTGTTATCTG	31566	A_95_P111107	TA14464_4097
32449	382	64	832	TGTGCTTGGTAATACAGTTGAACCATGAGGCTTCAGACATGTTATTCTGTTGATTTTA	31572	A_95_P228704	EB427837
32450	382	65	419	AACAGTTCAGAATGAGAGTCTTCAAGAAGCATGTGCAGTTTGTCTTGAAACTCCTAC	31574	A_95_P075740	BP526806
32454	382	69	168	GTGTCACCTTGTATATGTGCTTAGAGGCTAGAGCTACCTAGTCTTTGTTCTAGTTACC	31581	A_95_P143737	EB446944
32455	382	70	814	TAGTAGTTGACTAGCATAAGTTTATGTAGCCTTCCTGCATTTGATCTTTAGGAAAATC	31583	A_95_P010426	TA12902_4097
32457	382	72	505	TTATTAACCATCCCCATGATAAAACTTGTTCTGGAATTCCACCCAATGAAGACGCATG	31587	A_95_P036158	BP128656
32461	382	76	575	ATGGATCGGAGACCATTTTTCTCTCCTTAGATAAGAAGGATAGTTATTCGTAACTAGT	31595	A_95_P209377	TA19176_4097
32464	382	79	411	TGGGGCTCAATTGGTCATATTGTTGCTTACTATATTCTTGCCACTTCAAGTAATGGAT	31601	A_95_P105257	DV999315
32466	382	81	1596	GGGTATTCTTCCATAGTTTTTGAATTAAAAGAATCCTGTTCAAGTTGCTTATATAGGC	31605	A_95_P017036	TA13973_4097
32467	382	82	393	CCAGGGCTTTACCTGCTAGTTTTTACTATACCAGCCATCTTTTTCGCATTTCGTATTCT	31607	A_95_P071045	BP525602
32470	382	85	1451	AACTTGTGTTGGTTTTACTTGAATTCACAAGGGGGAACACGAAAGAAGGGCTATTCC	31613	A_95_P021256	TA14913_4097
32474	383	4	1731	AGCTGTCAAGTAACTAAGAGATTGTCACAAATAATAAGCGCCTCTGTACATCGTGAT	31620	A_95_P006296	TA15721_4097
32475	383	5	719	GCAGCTCTTGTTTTATAATGGAGCCTACAAGTGCTCTTTCTGGGCTTCTCTTACAGCA	31622	A_95_P151682	EB681931
32476	383	6	587	TGTTTCTTGTGTAATTTTCGGTGTATATACAAATAAAGAACTCTACTGGAGGTTGTGT	31624	A_95_P011246	EB435218
32477	383	7	470	AAGGACGAGCACGACTGAAGTGGCTATACATACAAATCTATTTACGGATCTATATGC	31626	A_95_P079790	BP527848
32478	383	8	856	GTAAATTAATGTAATATTTTGCCCTTTGGCTGACATATGCTCAACTACTTTGCCTTCAA	31628	A_95_P228714	EB425860
32479	383	9	714	GTCAGATCCGTCCCTCGTTCTATATGAAGCTGATAACTCTATTATATATTCTAAGTCTT	31630	A_95_P139517	EB443279
32484	383	14	263	CCTGAAAAAGAGCGGAAAGAAATGAGAATGTTATATACTTCCTCCTACTATTGGGAT	31639	A_95_P107792	EH616159
32492	383	22	209	GTGTGGGTGTCATCTAACTAGCTGCTTCATAAAACATCTTCCTTGTGTATATATCTAT	31655	A_95_P201362	TA17407_4097
32497	383	27	416	ACCCCTTGCCTGGAATTATCTTGTGTGATAAGTGGAGTACTGAAGTTAGAAACTGCC	31664	A_95_P164997	EH624456
32502	383	32	525	CCTTCCCGCTTCTCCTGCCCCTATGTATAAATTTTATTCTTCTATAAAAACACACAAAA	31674	A_95_P050316	BP132368
32503	383	33	403	GGGGCGTGTGAAAGATGAGAATGGTGTACTTCCATTCTTTTGTTATGAAGATATTTT	31676	A_95_P006081	EB442374
32504	383	34	519	ATCAGCACTGTAATGCAGTTCTCTCTTTCTTATGCTAGTGATATATGGAACTTGGTTT	31678	A_95_P102732	CV016167
32506	383	36	1390	TCTGTTGCGCGGGATGTTTTGAAGTGTCGAGTCATCGTGCATACCCTTCTTGTTTTTG	31682	A_95_P189922	TA14891_4097
32507	383	37	386	ATACAAGTTTACTTGCTTTAAACTCTTGATCAGAAAAATGCTAATGATTCCGGCTGTC	31684	A_95_P042086	BP130267
32512	383	42	417	TGTGAATGTGAAGTTTGGGATTTACCAAATTGTCCCGAGTCAATTTGCTTACAGAAAT	31694	A_95_P091008	BP531176
32515	383	45	552	TTTATTGGTTTCTTGTGTCTGTATGGAGATAAACTAGCTCGTTGCCCTACTTGATTCTT	31700	A_95_P140712	EB444567
32518	383	48	5835	CATTTCTATTAGTGACGATCATCAAATTCTTCAACAGGTTAGTGTATCTTTAGCCAACT	31705	A_95_P222627	AB281587
32521	383	51	906	CACAGTATAACTACAAAATTATTTGAATGCGACTAGGCTCGGTTGGAACATGTCATAT	31711	A_95_P225952	EB680121

32524	383	54	175	TCTCCCAGAAACAGAGTAAATTGTAATTGTTGAGTGGTATAAGTTGACTTTTGTCCAC	31717	A_95_P100288	BP535304
32526	383	56	564	AAGATTCCTTTGTGTAGCATATCTGAGCCCTAGGAAGAGATTATCCCGTCTTTTCTGG	31721	A_95_P149662	TA17318_4097
32528	383	58	728	ACTGAAACATGATTAACTTTGTTATACTGATGTGTCTGAATCAATGCTGCATTGTTCT	31725	A_95_P151732	EB681978
32529	383	59	382	TTCTACATATCCTTAGCAGCACTCAAACTTTATTGCCTGCCTAAAAGTTATTGATCTCCT	31727	A_95_P124522	DW004332
32531	383	61	513	TTTGTGAGATACAGTTTGTGCTGCCTGATTAACGTAGAAATTAAATGACATGTAGCG	31731	A_95_P023591	EH624123
32532	383	62	815	GACATCAGGTGTTGTGCAAATTGGCGACGGATAATAAGAAGGGGAAGCCCCAACAT	31733	A_95_P228564	DW000863
32533	383	63	659	TATTCCTTATGGACGCGTGACATTGAGGATTATATAGTTCCAGTTTGCAGGGAGCTT	31735	A_95_P265781	FG643494
32536	383	66	576	TATCTGATTTCGGGCTGAGTGCATTGTTAGACTCAAAAAGGCAAGATGGTCTCCTCCA	31741	A_95_P152047	EB682345
32537	383	67	688	TTTCGGTGTGCACCCCCCTAGCTCAAGCTTCGCTAAAGTGATCTATCTTAATTGTACCT	31743	A_95_P164657	EH623919
32540	383	70	801	GAAAAAACTCGAGTATAACATGCCTCCGGATGTTCTGTACATTGCTTCTTTCTCCTTTT	31749	A_95_P146587	EB450655
32543	383	73	647	GTCGCTCTGTTCAAATTGTAGCAAGTGACTTGGATTTTTTATGCAAGTGGTGTTCAAC	31755	A_95_P188757	FG163849
32555	383	85	296	TGTTTGAACGTGCTGATAGAATCGGTGGTCTGATGATGTATGGAGTGCCCAACATGA	31778	A_95_P163997	EH623051
32559	384	4	300	ATGGTGCATTTGATGTGATATACAGTCCGGGATACTATCCTTCACATCCAGGACAAAA	31621	A_95_P026863	BP192559
32561	384	6	507	AACAGTACAGGAAAATACAAGCCAAGAAATGGAGGTTACAGTTTAATGGTTACTTTA	31625	A_95_P099343	BP534893
32563	384	8	856	ATGTTGCCCAGAAGATTTAGCTGATATTTTTCTTCAGCATCATTGAGCCGAGGGTCTA	31629	A_95_P253594	EB451249
32565	384	10	262	GATGACTCAATTGTGCGAATCAACGGTTCCTCTCGTACTAGGTTGAATTACTATTGCG	31633	A_95_P089353	BP530467
32569	384	14	834	TGACTCATAAGAAATCGCGGACTGATCTTGATCTATCTGCTCTGGTGGGTCTCATATC	31640	A_95_P256039	FG147527
32570	384	15	383	CCTTCTGTATATACCAACTAGTTGTATTCCTAAACCTCAAGAAATGAAAAGCAGCGAA	31642	A_95_P074260	BP526418
32576	384	21	834	TTCGAGCCGTGAAATCAGCCATTGATGCTTGTATGTATCAAGGTAGGCTACCTACAT	31654	A_95_P141547	EB445231
32578	384	23	824	AAACCATTGGCCCTATTTCAGTGGCAACTCTTTCCAGTGGTGAATGGATGATAGTGGA	31658	A_95_P229234	DV161417
32581	384	26	1503	GTTATTGACAATTGTAAGAGTGGTGAAAGATTTTTGCGACATGTTTTGAACCACAGCT	31663	A_95_P191342	TA15215_4097
32582	384	27	491	GTCCGTTAGGATTCATAAGCCGACTTAATTTGTTTGGAATTGAGCTGTTATTGTAGTG	31665	A_95_P001511	BP530317
32583	384	28	770	TCATTTCCTAAACCAATGGTATGAAGAAGGTTGCATCATTGTGCCCAATGATTGTTCA	31667	A_95_P216067	TA20624_4097
32586	384	31	792	GTGACATCAAGAGGCTTCTAGTGTAATACAATTGAAATTTACTTTCAAGTCTGGGAA	31673	A_95_P148852	EB678378
32589	384	34	654	GTGCAGGACGTAACATGCGGAAACCAACTTAGTTGTTCTTTTTCATGTAAATTTATTT	31679	A_95_P149577	EB449268
32590	384	35	1066	GATCTCTTGTATTGAAGAGTCATTGACTACTTCTTGCTACGATTTTCTAACTGAATATG	31681	A_95_P177032	TA11861_4097
32592	384	37	639	GGAATGTTAGATACACTCCACAGGCTAAGTAGATTGACCGTCTCTTTGCAATCAAACT	31685	A_95_P018881	EH617531
32593	384	38	1150	TCACTGATGCTGTCATTGCAAATCTGGACTAATTTCAAAGCCACTTCTATCTCTTTCGT	31687	A_95_P187457	TA14350_4097
32595	384	40	577	TCTCACAAAAATCTGAAGGCGTGGTAGAATTCATTGGCAATGCTGAAGGTCAAAGGT	31691	A_95_P042016	BP130245
32598	384	43	748	AAATTCACTTCTGAGGGTTGGAAGGAGCCAGGTAGATTGGTGCTTTTGACAGCAGAA	31697	A_95_P128402	EB428101
32606	384	51	375	GTTGGTCCTTTCGAATTGGCAGCTATTTCCTAATTGATAACATTAAAAAGCCTTGTTG	31712	A_95_P026436	CV016369
32612	384	57	841	CAACCAGGCAATTTGCTTGTTGATCTGTACTAGCACGAAGAAATCTAACACACGTTTT	31724	A_95_P013186	EB450017
32615	384	60	823	TGATGGCTGAAAGTTGGGAGTGTTTCGTCTTTAAGTTATTTGTGTAACATTTTCCTGG	31730	A_95_P208247	TA18926_4097
32616	384	61	0	TTGTATTCAATTTAATCCAGCTGTGTAGATGCTTTGGATGAACTCATGTACCATAGTCT	31732	A_95_P032231	A_95_P032231

32617	384	62	815	CCACCGTGTTTTTGTCTACAATCACTTGAATGTTTGTTGTTTTAGATAATACAGGTTGC	31734	A_95_P227839	EB426182
32618	384	63	461	TCTTGGGTTTTCTTCTTTTTTCTAATGCTAGAAAATGTCGGTTGGAGACCATCCTTGTT	31736	A_95_P190442	TA15016_4097
32619	384	64	0	ATAATTATATGGACCTCCTCCTCCACAACATGCTACAATTGTGCTTGTAAAACCAAATT	31738	A_95_P248767	A_95_P248767
32621	384	66	825	CTACGAGCTTGCAATCGCGTTGATTTAACTACAGGTAGTTTTAGACGCCATTGTTGTT	31742	A_95_P012261	EB678192
32622	384	67	782	GCTAGATCGGCTTGCTTAGTTTTTTAGGCTAATGTTACTTGCCTTGCGTTTATTCACTT	31744	A_95_P269166	EB451554
32627	384	72	774	GTTTTGTAAGTCAGTGCCTCCAGAAGCTGATGATTTGAACCATTGGGATAATTACTTT	31754	A_95_P163572	EH622605
32628	384	73	358	GCATAACTAGTTACTGAGCTGTAACACTTGATACATCGAGCTATAGTATGAAATAGT	31756	A_95_P131222	EB431369
32629	384	74	1334	CTGCTGTTTACAGTAGATCAGATACTAAAGTGTTTCTCATAACAAGCTTGAACAATCT	31758	A_95_P013701	TA12999_4097
32633	384	78	347	CATTTCTTAAAAAGCAAGGATGCTCGTGATGGTACTGAGCAGGCTCTGCTCGACGAA	31766	A_95_P104767	CV017162
32634	384	79	825	TATTCCTACGATGTTGAGATGGTGACATGATTGTTTCCTCCCTACATCTGCGTGACTC	31768	A_95_P309923	FG166468
32640	384	85	624	GCCTTTCATCCAGAAGGTGCTTGAGGAGCCATTCTTTAAAAATTGAGGTTCTAAATAA	31779	A_95_P195362	TA16099_4097
32649	385	9	620	GTAATACTTGCTGTTGGAATTGTGCGTGGGTTGGTTTTGCAAAATCTAATGTGCCTCC	31796	A_95_P162102	DW000310
32652	385	12	192	TAAGAAGCTTGTTTCTTGCTACAAAGTGAAGGCCTCAAGCTTGATGAAAGTTGAGATT	31802	A_95_P112572	CV020742
32661	385	21	834	CCCAGATAGCAAGCTTTTTACTGTTGTTGGGGATGATCTAGATGGTTTACTTGTTGAT	31820	A_95_P118392	DV161438
32662	385	22	231	ATTGATCAGTACGTCATTGCCTGTGAGTTCAAATTTTAGATAGTATCGACCCGTGTCA	31822	A_95_P078921	BP527639
32665	385	25	54	GCAACACTACTGTAGCTTTTGCCCCCTTACTTGTACCCTTCTGTTGTGGTTTTTATTTTC	31828	A_95_P098818	BP534656
32668	385	28	522	GAATCAAATGCTTTAATTGTTGTATGAACGTCTATCTATTAAACAGGATCTGGGCTCC	31832	A_95_P196807	TA16422_4097
32669	385	29	680	CGGGCAACTCTAAGAATGGGGTTTTTTATTTTTCTTTTCTTGGAATACTTTGTGCAATC	31834	A_95_P026771	TA14756_4097
32676	385	36	528	TTGCTCTTATGTATAGTCTCATTTGCATGTTGTGTGATCGCCCATGTATTTTCAAAATC	31848	A_95_P023141	EB452030
32681	385	41	688	AGGCGGGTTGCATAAATGCATGGCAACTGTGATTGTTCATGTTTATGAGTAATATAC	31856	A_95_P121777	DW001876
32682	385	42	351	GGCAGTCTAGAGTGGTTTCGCTGATTTCTGTAACCTTTTATATACTGATATGTACTTG	31858	A_95_P158572	EH616493
32689	385	49	1011	CTGAAGAGAGAAACATCAAGATGCGAGAGCATCAGACAAGCTTATAATACTCTATAT	31872	A_95_P107142	TA13160_4097
32691	385	51	543	GATCAGAGATGGTCGTTGGCTGCTGAGGGTAACAATTACAAGGTTTGGGAATCTTCA	31876	A_95_P273391	EB102906
32693	385	53	779	ATGAACTTGCTGAGAGGGCACTAGACGGGCCAATTAATGATGGAATGAAAGAGTAT	31880	A_95_P004061	DV160152
32699	385	59	694	ACCACAAATGTTACTGAAAATCATTATGTATATATGAGGGCTTCCTGCCCTTGATCTG	31892	A_95_P299213	FG639329
32710	385	70	595	TTGCTTTTAGAAATTATGCCCTTGCTCTTTTGAGTTCCCACTATCTCTCTCCCAGCATTC	31914	A_95_P220787	TA21683_4097
32713	385	73	522	GGAACCAAAGTTGAATCTCTGTACATAAACTTATCACGTAATGCTTATGCCAATTCCA	31920	A_95_P133567	EB435127
32714	385	74	668	TAGCCCGCAGCTGTTCAATGAACAATGTAATACTATCAATCTAATGTTTTGTAGTTGA	31922	A_95_P032706	AF049355
32715	385	75	310	TTCCTATGCTTGGAATTCCAGACAGAGCACGGATAAGTCTACCGTGAAAACAACAAG	31924	A_95_P112312	CV020620
32716	385	76	755	CCTGAATTCGGTATTGTGAACCTATGACGTGTTGAACTTTTTTGTTTTGTATTCCAAGT	6784	A_95_P000061	DW000215
32718	385	78	361	CGGTATCATGTTAGTCTGTAGATTTTGAAAACTCATTGAAGCCTGTTTCCCTAAGTAT	31929	A_95_P025301	EB680812
32722	385	82	1559	CTAAGTTTTAAAACTTTTGCCCTGTTGTTATTGGATGACTGTATTTTGCTTTGCTGGCA	31937	A_95_P188242	TA14527_4097
32723	385	83	610	CCGCACTTGGCTGCATCAATTTGTATGTTGGGGTTCTATCTATTAATAGTTTTGATTCT	31939	A_95_P190137	TA14944_4097
32726	386	1	774	GGGTAGTAGTTCTGGTTATCTGTTTGAATACTATAACATTGTTCGGTATTGTTTTGCT	31781	A_95_P248927	TA12662_4097

32729	386	4	1458	CACATGATGGGATCTCATAGAAGAAGATGAACCATAATTGTCTTTCTTTTCCTTAGTG	31787	A_95_P176892	TA11816_4097
32731	386	6	323	CTGATGGCGACGAAATAAAAAGCATTGACACTGTTGGTCCATATTGCCGGCGAAGTT	31791	A_95_P014151	BP532677
32740	386	15	452	GTGGTTCCTATTTAAGACAGATCCAATGATGATTGCCTTTTGTCCTTTATATACTAGTT	31809	A_95_P190232	TA14966_4097
32741	386	16	555	TCATTCATTTGTCTGTTACATCTCTCAAACTGAAGAGATATCAATGGACACAAAATGA	31811	A_95_P198012	TA16686_4097
32744	386	19	1190	TAATGAAGTGTGATGTGATACCCAGTGGTATTGTTAATGCTGCCAAACAGGTTCAACT	31817	A_95_P184567	TA13723_4097
32747	386	22	754	GGTCTGTTAACGTGTACACATGATTAGTTCAAGCCTATATATGTAATTGTTTGCCCAAT	31823	A_95_P205222	EB430967
32749	386	24	901	GAACTTAGCTAAGTATTTTGATATCCGAGGGATTCCAAGCCTAGTGGTTTTGGGCCCT	31827	A_95_P192072	DV161797
32750	386	25	755	CCTGAATTCGGTATTGTGAACCTATGACGTGTTGAACTTTTTTGTTTTGTATTCCAAGT	6784	A_95_P000061	DW000215
32752	386	27	465	CCTTTTATCTTATCCTTCTATTCTAGGCGAGGAGGGAAATTCAGAATAAATAGCCCCA	31831	A_95_P277633	AM811238
32753	386	28	375	TTGGCTGTTGTTTGGGATAAGCCTTGGGAGAAAGTTAAGAAGCTTACTTCTTTCAAAA	31833	A_95_P003671	EB425393
32755	386	30	511	TCCAGAAGCTCTCCGTAGTTTGAACTTTGAAGTCTGATATTTTCTATTTGTACTGAACT	31837	A_95_P068005	BP137025
32760	386	35	779	GTCACAGCAAGCATTTTTCTTTTTGGTGTAAAATATTGCAATTTGAACTGTGGTTTCT	31847	A_95_P117367	DV160263
32761	386	36	547	GGTATTTCCTCACGTCTTCCACCTTCAGTTAGAGGAAGATGTCAATGATGTTATCTTT	31849	A_95_P272826	EB678838
32767	386	42	575	AAATTCTGCTGGACAGGTTGCGCTAGACATATGCCATGTGTGTTTCTTTGTGCTTGG	31859	A_95_P039816	BP129660
32769	386	44	450	CAAGTGCTATGAACGAACGAGGTTCCTCTTTGTACACTTTATTATTTTTGCTTTAGTTG	31863	A_95_P211027	TA19523_4097
32771	386	46	1244	CGGCGTATTTGCCCTTGTAGCAAGACATGATAAAAGGCTTAAAAGAAACTAGAGAAA	31867	A_95_P248562	AF154648
32773	386	48	1274	TTTTTCAAGAGGTTTAGTATGGCGAGTCCCACAGTCCATGTGATTCCGCTTTTTGCTC	31871	A_95_P203492	TA17864_4097
32774	386	49	884	CAGAGAATAGATGTTTCATTGGTAAATGGTAATGGAATACTTCCCTGTTTGTTCCTTCT	31873	A_95_P178017	TA12123_4097
32775	386	50	642	AGAAAGGGCACAAACAAGTACCTACAGAGCAGCCTGAAAGATGATTCTTTCATCAGA	31875	A_95_P304963	FG179618
32776	386	51	158	ATGATGGGTCTGTCAATGAAAGTTTATTCTTGTTTGGAGGGGCAACCTCTTCTATTTG	31877	A_95_P133272	EB434602
32779	386	54	859	CAGCATTCTGAAGCCAGAGATTGTCATGTGAACAAAAATTGATTGTATGATACTTAT	31883	A_95_P122822	DW002770
32780	386	55	822	TTACCGTAACAGCAAAAGCAGCTGAGGACACTGAGTTTGGGGAGCTTTACCTCTTCA	31885	A_95_P208192	EB449876
32781	386	56	821	ACAACTAACGCTGCAAGACACCGTTTCGTAGCTGGAAGGTCCAAGATACTGCTTGAA	31887	A_95_P290788	DW001180
32783	386	58	934	TTGGAAGGTCTCTTGTGCATATAGATGATACATGAGATTATATAGTCCATGACTTTGT	31891	A_95_P221982	TA21934_4097
32786	386	61	852	CTTTCCCAACTCTTTCTATTATTCTCAACTTCAATTGCTATGAGCTTTATGGTTGTAGA	31897	A_95_P243442	EB449743
32794	386	69	780	TGTTTCGTATGATATACAGCACTCGGGATAGTGGAAAACATCTTCATTTACCATGACT	31913	A_95_P199447	EB679306
32796	386	71	717	AGCTCCAGTTGAGTTGAGGAATTCCTGTTGTTCCCTTCATTCCGCTTGACCTTTATTTG	31917	A_95_P148862	EB678383
32801	386	76	812	GGTACCTGCAGATTTGAAGGAAGAGTAATTATGAAATTGAAAATCTAGAGTGACAT	31926	A_95_P213072	TA19971_4097
32802	386	77	113	CCACGTATTGGTATCAAATCAATTATGCCTTTCAAACAATAAATTCGCTTACTGCCAT	31928	A_95_P158052	EH616104
32806	386	81	840	TTCGCACATTGGCACCTATGGACGTCACTATTACCCTCGATATGACTACGAGAATGTG	31936	A_95_P223872	FG143525
32811	387	1	384	GCACGGTTGTGGCTTTTGGCATGTTTTGAAATTAGTTAATCAGATGGGTTCTTCCAAT	31945	A_95_P084925	TA21634_4097
32815	387	5	391	TTTTCTATTTCTCATCCGGTGCTCGGTACTCGCATTGAAGTCCGGCTATATTCGGATTT	31952	A_95_P076860	BP527101
32818	387	8	935	TTGGCATACTTGCACTGTTGGTGTTAGTGGAGAAGGTTTCGTGGCTAGGGATATAGG	31958	A_95_P316268	AY772945
32819	387	9	416	TTTTGATGGAGCCTATTGAAGGATGAACTTCTTGTTATGTTAAGCGGCCGCATGAGG	31960	A_95_P270461	TC69261

32823	387	13	96	AAGTAGCTGCCATTCAGAAGCAGCTTGCTTCTCTAAATCTTCAAGAGGCTCCTGTAAT	31968	A_95_P251617	EB450323
32825	387	15	197	GTTCTCCACTTTCTGATGGATTAGGGTTGAGATTTGATAATGTAATTCTCCATTACAT	31972	A_95_P210857	TA19485_4097
32826	387	16	848	GTTGGCTATAAACATCTTAAGTTGGCATATCCAATGTGAGATTTGCTCTTCTCTTACA	31974	A_95_P008721	TC40562
32827	387	17	634	TCCTTGAAACCTGACTCCATTGAAGCTTGGTTCTCCTCCTTGTCAACATACATATCAGC	31976	A_95_P050616	BP132438
32831	387	21	493	CAGGTTGCAACTGATCGTTGTATTATGGGCTTGCTCTTTCTGATTGTGGTTGGGGTCA	31984	A_95_P045916	BP131262
32836	387	26	1255	CAAGGGAAACTCTTTTTAGTAAGTGTTAGTGTTCCAATAACCAATAAAAGGGCTAGT	31994	A_95_P027451	TA15950_4097
32837	387	27	427	CTAAAGCAATCCCCATGTCCCAGCAAATAAAATATTTTGAGCACTACATAGAGAAGC	31996	A_95_P316763	FG193947
32841	387	31	751	AAGATTGTATGAGTCGTATGGGGTATTTTGGGTGGCCTCAGCTAAAGCAAATCTTGA	32004	A_95_P125052	DV162505
32842	387	32	696	AAATCCCCTCCATCACATAGTACTATGGATCATCCTCCAGGTTATGATCCTAATCGTAT	32006	A_95_P301513	FG201996
32843	387	33	513	TTAGGGTTATTGGGTAACTAGGCTTATCTGGGAAATTTGGGAAACTAGTTTTCCTTCT	12052	A_95_P000101	FG167017
32845	387	35	153	GGTGATGACACAATTGGTTCCTCGTCGATTGACCTCTAGTAACTTTTTAGATATTAAA	32011	A_95_P134042	EB435830
32847	387	37	738	ATTTTGGTCTCAGTAAGTTTTTGAGTCATTCTCTAAAGGGGATTCGATACCCTTGTGG	32015	A_95_P144542	EB447964
32848	387	38	267	CATGTATGATAGGCCAGTTTGAGCTCTGGCAAGTATGTTGTACCAAATGAAAGAGA	32017	A_95_P152747	EB683096
32849	387	39	106	TATGCGCACAATTACAATGCACAATGAAGTGTCGGGTAGTATATATATGTAATTGAC	32019	A_95_P030571	EB426802
32850	387	40	335	TTTTACCTGCCAATGTCAATAGCATAATCACCACGGATGGTACCAGGAGCAGACTCC	32021	A_95_P063355	BP135757
32852	387	42	824	GTGTTCATCGGTCAGTTTGGTACGGTTTTGAAAGATTTCGGTTTCTGTATTTTCGTTTT	32025	A_95_P018121	DV159211
32854	387	44	829	GGTACAATTTACTGTCCAATGTAACCCTGGATAACTGATCAATACATCCTTTAATTTC	32029	A_95_P216412	EB677605
32855	387	45	633	TCCCGTTAAATTACTAATAATATCTGCAGACAGCTTTGGGTAATAAGCTGTCTCCATT	32031	A_95_P285043	FG640348
32857	387	47	550	TAAAGCTGTCAGCGTAGGCTTTGAAGTTTTGATAGAGAGGCATTCTAGAGATTTAAC	32035	A_95_P274428	AM787875
32860	387	50	767	CCTGGTTGTACAATAAGAAGATCAGTATGGGATCATAGTCCATCAAACCTATCAACA	32041	A_95_P146347	EB450375
32864	387	54	460	GAGGAGGAGGGATTTTTTGTTTCATTGGCTTTTTCATCCTGATAGCTGTAGTTGTAAC	32049	A_95_P144102	EB447262
32865	387	55	462	CACTAGTGCTTACATTTAAACTTGGAAGCGTGTTCATATGTTCTGTTCATCCTAAAACT	32051	A_95_P002136	FG635120
32867	387	57	1672	GAAAGATGCAGCCAAGACTCTGTTGCCAAAACCCCCTTTTTTGTTATGTCACATAATA	32055	A_95_P013491	TA12596_4097
32870	387	60	770	TCCTTACCAGACGATACAAATGTTTACTGTGGCCACGAGTATACATTGAGCAATTCA	32061	A_95_P146077	EB449939
32873	387	63	757	GTTCTGTCGAACTTGTAGCTAGACTTGTAATCTTGGAAGATTGTTGGGTCCTCGTTTT	32067	A_95_P222732	TA22098_4097
32874	387	64	753	GAGGAGCATCTTGTTGGTTGAATGCTGATACAGTTGTATATTTTTGTTGGAATGCATT	32069	A_95_P191222	EB450418
32877	387	67	708	CAATTATTGAATCTCTAGGTTCAAGGAGTGCTCTATTAAAGCATGAGGTTGCTTATGT	32075	A_95_P127397	EB426936
32878	387	68	497	AGTGAAAGGATCATTCAGCAGATGATCCAATCTAATGTGAAAGTGGGATATTACTTT	32077	A_95_P007916	BP534491
32880	387	70	147	AAACTCCAGTACCTTCTCCTGTATCAATATCAAATATCATAGAGAATGTTCTTGTTCTC	32081	A_95_P150177	EB680249
32884	387	74	563	GCGTTTGAACAGTCCTTACTCATACATCTTTCATTATGAATTGACGTTGTTTGTTGTGC	32089	A_95_P123852	DW003746
32891	387	81	406	AATGTCACCTAATGTACTTCGCTTTTGAGGTATATTGAAACTTTGATAGCCATTTTCG	32103	A_95_P000731	TA12957_4097
32894	387	84	491	TTTATGTTGTGTTAGAACCATTGAACTTTCAATCTATTGGATCGACCCCCTTGATCTTC	32109	A_95_P022766	TA15383_4097
32901	388	6	159	CATTGCGCACTTTGTCACCTTCTATCAGATTACCATGAATAAAAAAGTGCAAACAATT	31955	A_95_P134177	EB436159
32902	388	7	746	GAAGCATCAAATCCTAAAATCTCTGAGTGGTTTATCAAACGTTATGGTCCAAAGGTT	31957	A_95_P246692	FG197835

32906	388	11	848	TTTTGTATCCTGTGTGATTGCCTTGGTATGAGCTTGATGATACATATCATGAGCTTTT	31965	A_95_P293948	EB438840
32913	388	18	508	ACACCTCCTTTGTATGGAAAGCTGAGTGACTTCTTCTGGTAATGTTGATAAGACATCC	31979	A_95_P206467	TA18524_4097
32915	388	20	813	ATATGTAATGTGTGCACAGGCTCTTTATAGTAATACTTCTCTTGTAGAGGTTGTTGCT	31983	A_95_P148522	EB677870
32918	388	23	75	GGTGGACATCTTCATGCAATTTGTAATTTGTCCTCGTTCATCCTATTTCTCTGTATAAT	31989	A_95_P102702	CV016152
32919	388	24	809	GTTGCCTTAAAAAGCACGAAGACATTGAACATGTTAACATTAAACGACTACCAAGAA	31991	A_95_P220057	EB428295
32921	388	26	465	TATCGGCATGAGCCCAAAGTGCGATGGATCTATTCAATATGCTACGGATTCTCGAGG	31995	A_95_P058686	BP134534
32922	388	27	464	TAGCCACAAATGCTTGTGCTGAACTCACTTTACACTAAACAAACTTCTATTGTGCATT	31997	A_95_P273486	FG638324
32923	388	28	468	AGGTACTTTAAGAATTCAAGAATGTTTGCTCCGCTGCACCTTGATAGTATCAGTGGT	31999	A_95_P278213	AM803975
32925	388	30	718	TTGGAAGGTTTTTCGGGTGTTGAAAGAATGGTGGCTTGAATCTCAAGGACCACATTG	32003	A_95_P316233	FG197071
32932	388	37	643	CATCCTCCAACTTCAAATCATCTTAAGTCGTTCAATGATAAAGAGTTGCAAATCTTTG	32016	A_95_P062775	BP135601
32935	388	40	808	TAATTCATTGTGCTTGGGGCAGCGTCTTGTAGGCAGAGGGATTGAAAGCAGAAAAT	32022	A_95_P190577	EH615701
32936	388	41	1582	TTGACATTATGTATTGGCCCCAAGTCATCCGTGACACTTGATCTAAGATATGTTCAAT	32024	A_95_P189662	TA14836_4097
32940	388	45	834	TAATTGCTGAGCAATCACTTCTTGTTTTTGGAAGAGGTTACAACTATGCAACAGCTCT	32032	A_95_P221417	DV161551
32947	388	52	685	TTGACATTTACTATCCGTATAACCCGTCTGAGGATACAGAATAAAGTGCATCCACCAA	32046	A_95_P190717	DV162449
32951	388	56	837	AGACTTAACGATGGAGTTCCTATGGGTTGATGAGTTCTGGGTTCTTCTTGCTTACCAC	32054	A_95_P292493	FG172957
32955	388	60	705	AAGCAGTAGCTTGTTATCCCCTGTATGGCAAATTGCCTTTCGGAATCTTATTTATCCT	32062	A_95_P019901	TA21562_4097
32958	388	63	526	TGGATTCACTATCATATTGGGGGACAACCTCTGGAAAGGCTTGGTTATGATCAAGAG	32068	A_95_P092808	BP531984
32962	388	67	562	AATGGAGATGCTTCCTCCAGAGATCCAGGATGTGCTAAATGTTTCGCTTCTCACTCCA	32076	A_95_P215862	FG136377
32967	388	72	793	GTGGAGGCCAGCTATTATGCATTTTGGATCAACATATTAATTTGTGCTTCTATAATCC	32086	A_95_P116852	DV159654
32973	388	78	738	AGAAGAAAGGGGGCTATTCTATCACGGACAAACTCATGTTTACGTTATATATGAAGT	32098	A_95_P013076	EH621684
32977	388	82	853	AACCATTGTAATGGATTGAATTCTCCTTGTTTATCGCCATTAGCTCGTGGGAATTTCT	32106	A_95_P147447	EB451880
32978	388	83	656	ATCTTAAGGCCTCCATTTCCATGAAGGCATGAACAAACAATTCACTCGCAAGATAATT	32108	A_95_P193893	TA15769_4097
32979	388	84	711	GGGAAGATAACACCTGCAAAATGCAGATACGAAGTGATGTCTACCAAAATTGAGAT	32110	A_95_P126687	TA13868_4097
32982	389	2	500	GCCCTACTGTCACTTGCTTATTGTATTATGAATAATTCTTCTTTTGGGTTGACTCTCTA	32115	A_95_P163942	FS417555
32990	389	10	865	TAGTGTAACGTCAATCCATACTACACAAACTCATCTCACAATAGCCAAGATAGGTTG	32131	A_95_P203772	DW000646
33000	389	20	723	GCAGATTCTGTATCATACCTTCCAACAATAGTATTTGGGACATATTTAGGCTGGATTT	32150	A_95_P137727	FG144862
33006	389	26	1053	CATGTGGAGGAGACATTTTAGTGCCAATTAAGCATACCTCCTGATTATGGGACTTGT	32162	A_95_P012626	TA14649_4097
33007	389	27	1482	GACGAAGATTTTTGAGTTGGAGAAGCAGAGAATGGGCTCTGATGATTGTGTATAAA	32164	A_95_P016131	TA15330_4097
33016	389	36	892	CCATTTGAAAGTTGGAGACTTTGGATTAAGCAAACTAATCAGGGTTCAGAACTCCCA	32181	A_95_P225792	DV162248
33022	389	42	803	AGTTCTTCTCTAAAGAATGGGAATTCATTTGGATTTGGCGATTACTTTACAGATGTTG	32193	A_95_P292688	EB428119
33029	389	49	312	TCTGAGATGTCTGTGTTGTCGTCTCGTCTATTTATTGCTTTTAGAATTGTCATTGGAAT	32207	A_95_P094938	BP532942
33030	389	50	265	ATTCATGTAGCATATGTGGGTAGGGAGGACATAACAAGCGAACGTGTAGAAATGCT	32209	A_95_P077295	BP527212
33031	389	51	214	CCTAACCCCCACTTCACCTGTAAATTCTTTTGAATAAATAGTTCTATCAATGACTTGTA	32211	A_95_P062825	BP135615
33032	389	52	933	GTGTATTCAGACGGCTTTTATGTTTCCTATATTAGCCTTCTTTAATTTCCTGGTGGTAA	32213	A_95_P176787	TA11782_4097

33037	389	57	326	CGACTCTACAAGGGATCACATTAACTACTGAACTGCCATTCTAGTAAAACTTTCTATG	32223	A_95_P143447	EB446746
33043	389	63	562	TAGTTGATGGGACCATTTACCATTTTATGGAATTGAGTTTTGAATGGAAAACTGAGA	32235	A_95_P188062	TA14487_4097
33048	389	68	498	AATGAATTCTCCAGTATTTAAAAGCATGTTGAGTTTGAAACAATCAAGAGCACGTGG	32245	A_95_P077380	BP527231
33049	389	69	260	GTTTGTTCTCTGTCTCATGACATACTGATGCTTGCAGCCATGGCAGTTTTCAAATTTTT	32247	A_95_P099828	BP535083
33052	389	72	761	AAATCTCTTTCTTTTTCCTTCTTTTGCCCCCGTTTTATGTCTGTTTGCGCGGCAGGGAC	32253	A_95_P200647	EB438255
33053	389	73	817	GCTGATACACAAGTACCGCAGAGACTGACCAAGAATTTTTACCGTGGTGAGATACAT	32255	A_95_P119627	DV999078
33054	389	74	1020	GTGGCCAGTTACTACTGCTAACTTGTGTTTGTGAGAACATTAAATGTACTGATAGAT	32257	A_95_P013396	TA14491_4097
33055	389	75	1211	GCTGGGTGCTCTGTAATCCTAATAGCATGACTCATCTGTTTTTGTAATATTTGTATTTT	32259	A_95_P183712	TA13519_4097
33058	389	78	697	TTGCTGAAACTGCTGCAAGTTATTTTACTGATTTGCAAATTGTACCACTTTGGCTTATT	32263	A_95_P162132	EH620933
33060	389	80	923	CGATGAGAAGTGGTTTGTCGATGTTGATATTGAGAAAGCAATGCAACGTGTCCTAAA	32267	A_95_P118317	DV161328
33063	389	83	324	TTAGCCAACTGAAATTCAAATTCAGTTGATTTTTATACGTCTCATTTTCTCCTCGGAGG	32273	A_95_P072820	BP526059
33065	389	85	674	GCTCTACTGCTGTGACTGCAATTCTTATAAATGGTCGTAAGTTATGGGTAGCAAATG	32276	A_95_P143387	FG159719
33066	390	1	865	TGATATCAAAACTCAAATGTGCTGCATAGTTATGGTGGCGATATTGACTGAATCTGT	32114	A_95_P206492	EB451957
33070	390	5	972	TCTCCTATTTCTGGACATTTTTCGCAATGGTCAATTTCATAGTGGAAGTGCTTGTTCA	32122	A_95_P013571	TA12229_4097
33074	390	9	903	ATCTGCTGTACTGGCTGTGACCTTACATTCATGTTATTCTAGACATTAATAAAGTCAC	32130	A_95_P201352	TA17405_4097
33076	390	11	997	TATCACTTGAGAGAAGCGACCAAAGCAGCAAAGCCAGTACTTGGCAAGTATTACAG	32134	A_95_P117497	D26509
33077	390	12	815	CTAGTGACAATGGTGCCTGTTCTTTGTGTGGGCAAAATTTGTAGAATATGACAATGC	32136	A_95_P023641	DV157838
33080	390	15	715	TACGATCTTATAGATGATTTCCGAAGAAAGGGGGCTATTCTATCACGGACAAACTCA	32141	A_95_P112007	EH621684
33084	390	19	575	GAAGATATACCATTTTTGAAGGAAGATTCGAAATCACAAGTCTGTCATTTGTTGGTG	32149	A_95_P301988	FG137041
33089	390	24	672	GTGTTGATCTCTAGAGAAAGAGAAGTGAGAGATACTTAGGGCTTCATTTACATATTA	32159	A_95_P212987	TA19954_4097
33095	390	30	553	TAGCTGTTCTTTGCAGTTTTAAAAGTATGAACTTTACCTCAATATACGTACCCGTTCTC	32170	A_95_P191372	TA15221_4097
33100	390	35	1269	GTGATGTGAGTAATTTCTAGTGCCAGAAAGCAATAAGTTATGTTCAGTCTGTTCAAA	32180	A_95_P195087	TA16041_4097
33105	390	40	306	ACAAATCTGTAGCTGCTGTTGGTAAAGCTGGCGGTGACAAGTGGCAAACATTTGTCA	32190	A_95_P106127	EF051129
33107	390	42	795	CCACCGCCAATCAGCATAAGAGATTTTGACAGAGTGCTATGGAAACAGAAGCCAAC	32194	A_95_P149502	EB679377
33108	390	43	443	CTTAGAAAGCCTGCTTGTGCTTGTAAAACCTGCAGCTGTGTAAATTGCTGGGTTGTC	32196	A_95_P266036	BP532403
33110	390	45	1067	GCCACACTACTCTGTAAACTTTTAATGAGAAAGTTTGCTCTTCATTTATGATATCACCC	32200	A_95_P015901	TA14246_4097
33112	390	47	617	TTAGCAGTTTCCGGATTCAGTATGGACAGAGAGAGCTGTGCCACATGATACATGAG	32204	A_95_P283693	EB448436
33113	390	48	131	GAGGTTTTCTTCGTGTTCGTTGTTTCTTTGATGATTATGATTGGCATATGATTGTTCTG	32206	A_95_P101093	BQ843151
33119	390	54	751	TAGTTATTGGATTTGCAAGTGGGGAAGTACCTGTCATCCCAGCGAACATTGCTTTGG	32218	A_95_P151602	EB681839
33121	390	56	2100	GGTTATTATACACTTTGCCCATGATGATTTTTGCACTAAAATTTTGGCGAAACTTGAG	32222	A_95_P204512	L38828
33129	390	64	767	TGGGTACATCACCCCTTTTCAACTCTTCCTACATTAAGCAATAGAAAAAGCATTGTTG	32238	A_95_P212017	TA19739_4097
33131	390	66	108	AAGACAAAGAAGAATAACTCTCATTATCGTTGCATTTGGGGTAAGGTATGTAAGCCT	32242	A_95_P103822	TA12797_4097
33134	390	69	997	GGTGGTTTTGGCATGTCAGACAGTTGTGTATTTTGATCTGTTATGGTACTTATTTATA	32248	A_95_P220662	TA21655_4097
33135	390	70	536	GTGTCTGATGAATAGGACTGCGCCTAATTCTTGTTTCTTAAACCTTTAATGGAATCAT	32250	A_95_P003861	TA12993_4097

33136	390	71	783	GAATATCTAGTGATACTATTGTTGGTTCTCTTGCATTCAAGCCCTCAATTTGCAGCAG	32252	A_95_P183437	TA13457_4097
33138	390	73	605	TTCCTCTTTCTTGGATGTTGTTTGTCGTGGATCTTCACTGCCATATTTAAGTGTATTTG	32256	A_95_P297623	FG635703
33141	390	76	750	GATTGGGATTAGACTCTTAGTTGATTGACTGATTATTGATCAATGAACTACCAAAAC	32262	A_95_P119357	DV162518
33144	390	79	737	CTGGTTTGAGCTGTGAAGTATAGGGGGTTTACAACTATTATGCACAGGTCTGCAAAG	32266	A_95_P154142	EC391392
33147	390	82	752	TCGAACTTCACTCGTAGTTTGTATTCAAGCAAAGCTAATACAGGTTCATTGTTGGCTC	32272	A_95_P160632	EH619299
33148	390	83	519	GTACTCGCTGTACTTTAGGAAACTGAGTTAAACACAAGTTTATTGTATGGCCAAATG	32274	A_95_P201717	TA17483_4097
33149	390	84	763	TGTTTAATGGAACGTGGAAAATGGATTGCTTCCCGGCTCTTCAAATGCACACTGATTG	32275	A_95_P269061	EB425806
33153	391	3	688	GTGCTTGAGTAATGGTCTGGTTGTCGCTGAACTAGTTTGAGTTTGTTTTAAGACGTA	32281	A_95_P154082	EB684244
33156	391	6	393	CCTTCCGTCTCAAATTATTTGGCATTGTTTCTACAAATAGTTGTCTTAGATCATTTGGC	32287	A_95_P094668	BP532823
33160	391	10	616	TTTCAATGGAAATCGATTCAATTCTTCTCGTATGGAGCTCGATTGAGTCCGACCTTTG	32295	A_95_P299628	FG641339
33161	391	11	827	AACAGCTGTTCTGTAGTTGATATACCTGGAACTGTTTGCGTACCATCGCACAGTAAA	32297	A_95_P204277	DV159675
33163	391	13	760	GGTAGTCCAAATAATGGCATTGTGACTGGATCACCTTCTACGGCGAAAACAATTCAA	32301	A_95_P295798	EB448312
33175	391	25	823	ATTTGTAATTCATCCTCGTTCGTCCTATTTCTCTGTCTAATATAACGTGCAGAATGTCT	32324	A_95_P226959	EB451706
33179	391	29	770	TTGCATGCATTGATATCAAGCTGATGACGACAAACTAGATGTACATGCCTCCCCTACT	32332	A_95_P287983	FG162013
33181	391	31	285	TAGTGGCAAATAATAAATCTAGCCACTTGCCGAAAAGCAAGAGTTGGAGACTACAG	32336	A_95_P094778	BP532866
33186	391	36	231	GTTTCCTGAATGTTTTAGTGGTTTTTCTGATATCTGGTTTGGAGGATACTGGTTTTGG	32345	A_95_P121749	DW001844
33199	391	49	749	AAATCCTCACAGAGTTCAAAGGTCCATAAGCATTTGGGTGGCTGGTAAAGTACTGGA	32371	A_95_P244682	DV157497
33203	391	53	842	CGCATCAGTCTCTTGTAGTTTACTCGTGATGAATCATCTATTGTTCACATTTTATAAAC	32379	A_95_P194287	TA15859_4097
33204	391	54	788	AATGGGAAAGATGCTGTATCAATAGGGCTTGTCAATTACTGTGTTCCTGCTGGTGAG	32381	A_95_P149352	EB679198
33219	391	69	582	AGTGGTAACAAAGTGTGTTATATAACATGTTGCTGGATCCAATTTCTGGGGTTGTTA	32410	A_95_P160252	EH618948
33221	391	71	773	CTCGTGCTGTGATCTAGATGTTCTTAATAATGTGATGGAACTTGATATATTCTAGTCC	32414	A_95_P149127	EB678813
33226	391	76	297	TCTTCAACGTACCTCATGAGAGCCTCTTGAACGTTGGACAAATTTTCTATGTATAAAT	32424	A_95_P155327	EG650013
33228	391	78	647	TTTTGGTGCAATCTGGTAATTGAATATGATGTATATGGGAACCGTTGATACAATAAG	32428	A_95_P069310	BP137346
33230	391	80	242	TTTTATCTGCATCTTCCCTCGTAGAGTGGCGTCTTTTATAAGAAAAGACTTTCTCAGTG	32432	A_95_P143512	EB446788
33233	391	83	397	TGTATTGTATGTGTGTGCTCGTTAGTGAGACTCTCAAGATAGTGTTAGTGGTTTGAAT	32438	A_95_P179152	TA12438_4097
33234	391	84	189	CTGAAGAAGCTGCTGTGACAGAATCAGCTGTAGTAAGTCAGGAATGTGCCTCTAATT	32440	A_95_P240990	AJ718050
33235	391	85	790	ACACCTCAAGAGAAGCAAGAACAAACAGCATTTATAGAAGAGATCAGTAGAACTGC	32442	A_95_P247722	EB426856
33238	392	3	828	CCATGTAGAAGAATATTACATGAAGAGGAAGGAAGAGATGTTTCAGATCTATGATT	32282	A_95_P149977	EB424911
33247	392	12	557	TACTAAATGCAGCTAAGAATTACAAAGGATCCTGTGAAAATGACTTGACCTCAAGAA	32300	A_95_P287523	FG637100
33252	392	17	457	CAAGTGCGTGGTGCTGGTGCTGACATAATTTATCAGGCATCCTCTGGTTTTAGATGA	32310	A_95_P113532	CV021176
33253	392	18	375	TGAAATTGCTCAGGATTTCAAGACTGATCTGCGTTATCCAGAGTCATGCTGTGTAGG	32312	A_95_P110582	EB443620
33256	392	21	442	CGCGTCAGTTTTCCTCTGTAACATTTAACTTGTGGCTTACGTTAATACACTTAACTCCC	32318	A_95_P099633	BP535009
33258	392	23	350	CTACACTGTATTGTTGACCTCTGTAGAAATTGCAAATATGGCCCTTATTTAAAGTGTT	32321	A_95_P163722	EH622810
33261	392	26	1315	TCACAGATGACAATCAAAGAACGTGGTGGCAATAGGAAACACAGAGGCAGAGATG	32327	A_95_P196327	TA16315_4097

33265	392	30	573	TTTCCCCTTGGCTTGTGGACAGTATAACATGTGCCTTACCTAAATAGAGGCAGAATTT	32335	A_95_P188837	FG640417
33270	392	35	621	CCATCTGCAGGAAACTATTTTGATGAATACTACAGCTTTTTATCCACAACTACTCAGT	32344	A_95_P018871	EB435759
33273	392	38	806	TACTCTATCAAAGGGAGTTATTTTGGTATATGTAATTTGACAGTAGAGGTTCTTGGGT	32350	A_95_P191557	TA15263_4097
33282	392	47	575	TGCTCATCTGGTGAAGTCTGATGTATTACTGTTGTGTTTATGTGACCTAAAGTTAGTG	32368	A_95_P219262	TA21359_4097
33285	392	50	573	GTTTTGCGGATTTACGACTGGAAACCACCACTTCTATATTACCGTGCTCCTTACTTCCT	32374	A_95_P019991	TA12644_4097
33288	392	53	889	ATTTTTTCTGTCCTTGGGTAAATGGAAATGTTGCTGCTGCTGGCTGCAGTAGTGGCAC	32380	A_95_P213892	DV159446
33292	392	57	708	CAGGGAAGTTGACCCATCACATATTTCCTACACTTTGTTGTTGTAAATTTCCAATTTTT	32387	A_95_P188332	TA14547_4097
33295	392	60	803	TTGGTAGTATCATATACATTTCATCTAATCCGCTTCGTGATAATGCAATGGTTTGATG	32393	A_95_P013541	TA12651_4097
33300	392	65	238	GCTCTGATACTGTATTCAGACAATTCCAAATCATTTATCTCACTTTCCCTATAAGAAGG	32403	A_95_P093973	BP532509
33302	392	67	804	ACACGTGTCATTCGTTTCACTTGTTAGATCTAGTATGTAATTTCTCTAGTACCACATTT	32407	A_95_P290933	FG165317
33303	392	68	667	AAGGTGCTGGTATTCGCGACTATACTTCTCATATTAATCCTTACATCTAATCTTAATGA	32409	A_95_P029586	EB450630
33305	392	70	1348	GTTGGAATTCTTACTAAGTTTTCTGGTGCTCTGTCTTGCGTCAAAGGACGTCCATGCTA	32413	A_95_P007541	TC55092
33308	392	73	889	GCTTGATTCAGTACTTCTGAAATTTGCTTTATTGCCCTGAATATTAGTGACTGATTCAG	32419	A_95_P022701	TA15300_4097
33313	392	78	501	CAGTCTTAGTTGCCCTTATATTATAAACTTGATTCTTGTGGCACCATTATTATACGTGG	32429	A_95_P132327	EB432791
33317	392	82	1044	CAGGTTAATGTTCTATCTAAAGCTTTCTTGCTCCATATCAAGTGAAAGATTTCTCGTG	32437	A_95_P007681	CK720596
33320	392	85	818	AGGTCCATTGATAGATCTCCGAATCTTCAGTTCCTCGAAACCTTCTTTTATCAAAATGA	32443	A_95_P267856	DV162283
33323	393	3	783	TTTGACACCATGAAAGAAATTGGCGCTTCAGCAAATCATCTGCCGTGTTTCTCCTCAT	32448	A_95_P248197	FG160346
33329	393	9	847	CCTCATTGCTTAGAGACATGTAAATTTCACGTTGCAATGGTCAGTTTGTTATGAATAT	32460	A_95_P151507	EB681722
33331	393	11	2598	GGTCAGATTGAGTGGTGTTTCGGGTTATTGCCTATTTATTGTAAGAATTCTGTATTGA	32464	A_95_P194047	AB120519
33337	393	17	581	CACCGTTTACTCAGACTAATGTTTTGCTCATTGATATCACGAGTGTGTGTGTGTATA	32475	A_95_P100998	BQ843069
33340	393	20	780	TTCATCAAGTTCTACTATGTGAGCTATCTGGTCTAGTGTAAGGACTTTTGTGACTTTTC	32481	A_95_P157632	EH615687
33341	393	21	487	AGCTGTTATTCCACTTGTGATTTTTGTTCCCTTAGGGCTCCTTATTAATGTTTGTACTGT	32483	A_95_P001931	FG158502
33343	393	23	687	GCAGCATCTCAGCTGTAGCTTAGGTAAACACTTTGGCACAAAGATGTTGAAAAAATG	32487	A_95_P147332	EB451691
33344	393	24	838	ATTAGTAGAATGCAGTACACTCCAGGAAAGCTAATTAAGAATCTTGGGTCTTCGGTCT	32489	A_95_P184432	EB679902
33348	393	28	142	ATGGCATCTCCTCCCCTATTTGGATTTCTCTAAAGAACAGAGAACAAATCGAACCCCC	32497	A_95_P131172	EB431301
33355	393	35	884	GACATGCAGCTCTATTCTCAGTTGTCGTCATCAATTCTGTGATTTATGTAACTATATTC	32510	A_95_P229054	DV160959
33356	393	36	771	GATGGCACATTAAATCGTAGGACTAGCGTTCATTTGGCACTTTTTATGAAACAAAGAA	32511	A_95_P022981	TA15621_4097
33362	393	42	510	AGCTGTTAGCTAGCGCGTAACACCAGCATATTCTATGGTTTGTATCTGAGTGTTAGCT	32523	A_95_P048491	BP131925
33368	393	48	366	ATGGGAGATTATCCTGAACGTATTCTCTATTAATCTGACTTTCTTGAGAGGATTCCTGT	32535	A_95_P182717	TA13286_4097
33370	393	50	813	AATAGGGAACTTATTAGTGCCCGCCTTTTCTTGAATTTTTCGTGCATGGAGGGAGAAA	32539	A_95_P158042	EH616101
33383	393	63	1407	ATTGTTCTGGGGATTGTACTATGTCTGTTTGGAATATAATTGCGGCACTGCCCCTGTG	32564	A_95_P028806	TA18865_4097
33388	393	68	592	TTGTACTAGATCATTAAACATGCTGTCCATTCTGTTGTGAGACTTTGAAATGTCTTTCC	32574	A_95_P030341	BP534288
33391	393	71	269	TGTACTTCTGTACAACTCTTCACGTTTTGTGTTTCAAGATCTTTCGATGCTTCAATAAA	32580	A_95_P027576	CV019980
33395	393	75	727	TGTTTTAGGCTCCGAAGCACGTGAAATGCCGTGTAAACACATCTACCATACCGACTGT	32588	A_95_P139122	TA13961_4097

33396	393	76	290	GTCTGAAGGTCATGATGGCCAAGTGAGTTCCCTCTTCTGCAATTTACCCTTTTTACAC	32590	A_95_P058586	BP134512
33397	393	77	817	AGTTCCAGTATATAAGCCACCAGTAGTAAAGCCACTGCCTCCTCCAGTTCCAGTATAC	32592	A_95_P029951	EB425421
33400	393	80	711	TCAGATGCTACTGCAGAAGGGCCAACAGGAGGAACTACTTCTTATGCCTCAAACATT	32598	A_95_P302638	FG199999
33401	393	81	1494	CGGAGGTCATATAAGTTACACTTGATTCACTTGTGCTGTAATTTCTTCAGTCAATAAC	32600	A_95_P193732	TA15734_4097
33404	393	84	527	CCGCGGCACCGCTTGTCGGAAAATTATTACTAAATATATTTATTAATACTGTACGGAA	32606	A_95_P063795	BP135877
33410	394	5	685	TTCGACTTTGGAATTGTCTGTTTATCTTTCTCTACTGAATTGTTCTAGTGGAAATGCAA	32453	A_95_P014081	TA14640_4097
33420	394	15	618	ATATGTTTGGTCACGTCTTTCCGAGACAACGGCTACATTGATATTCTCCCCAAGGGAC	32472	A_95_P286838	FG642798
33422	394	17	124	GAAATTGAAAAGTGGTATAGTGTTCGTTTATAGTAGGATTGACTCTCTGGAATCTCC	32476	A_95_P099948	BP535139
33426	394	21	205	GTGGTTAATATGTCAAGCCCACATCTGGAATGAGTAAACTTCTGAAGTTTCACATTTA	32484	A_95_P140497	EB444396
33427	394	22	464	CGTCAAGTTCCTTTGTAACTTGTGCTTACACAATTAAAATGTAGTACATTAGAACTGC	32486	A_95_P027741	CV017334
33430	394	25	762	GTGTATTTGTTTTGCACTGATGATGGTAACTGAACATACGACTGCAATTCTTTTAATT	32492	A_95_P231639	DV999209
33435	394	30	779	ATCGGTTGAGCTTAAACATTGAGAGCTAAGTTATTTTGTCTGACAGTCTTTGCTTTTC	32502	A_95_P234614	EB440260
33436	394	31	404	TTTATCTGATGAACAGAAGTTTTGGTCTCCAGTGTGGACATGGAGTTCGCAAAGGTT	32504	A_95_P091993	BP531595
33439	394	34	174	GGTAATTCCCCCACTCAAGGTTAGGCAAGATACTTATCTCGAAACCGCATAATTTCTT	32509	A_95_P066330	BP136571
33444	394	39	1135	GGGGCGGACTTATTATCCACTTATTTGAATTGTGTCAGGGTTGTTTCTCGTTCATGAA	32518	A_95_P192472	TA15458_4097
33445	394	40	615	TACTGGAAAATTGCCTTGAGAACGGAAAAATGGGGGAATCTGCTCCTTTTGGCGGTT	32520	A_95_P161507	EH620230
33462	394	57	704	TGTGACTATGAGCACTGGTGTCAGAACTTGCCCCTTTTGTTCTTTTATATGCGCCTTG	32554	A_95_P029451	TA16734_4097
33467	394	62	472	GTCCCTAATGTCTCTTGGAGTGCAAAACTAAAAACTTTATAAAAGTTGATCCACTTGG	32563	A_95_P231659	TA21544_4097
33476	394	71	752	GATTAATGAGATTTAACGTGTGTCAAACATTTTACTAGTAATAGGTTCACGTACTGTC	32581	A_95_P012246	TA12837_4097
33477	394	72	557	CAGAAGTGGAAAGTAAACTAGTGTCTACTTATATATCAACTTTCACCTGGCCTTTTTA	32583	A_95_P162652	EH621646
33483	394	78	464	GTGCGGAAGTCTATGAACCTATTCTAGAGTACTTCATGAGATATTTTCCCCTTTTTTG	32595	A_95_P077370	BP527229
33484	394	79	198	AAGGCAATATGCCGCGACTTTGCCTCCGTATTCCTTTGAATTATGTCCTTTTTATGCTT	32597	A_95_P146462	EB450529
33486	394	81	901	GGTGATTGAGGCTACAGTGATTTGTGTGATTATTTGGAGTCAATTATTGATGAACTA	32601	A_95_P234674	EB679714
33496	395	6	448	CTGAAAACAGCATAATGGTGATTCAAGCTCCTCTCCCCTTGCAATCTGTGAACACTTC	32620	A_95_P261966	BP134254
33499	395	9	537	GCTTTTCCTTCAGAAGTGATGTGTTTCCATCATACTCCATGAAAATTGCATTCAGAAG	32625	A_95_P025926	EB683701
33501	395	11	780	ACTATTCTACGTACCTGCTATATGTCATCTTGTATCGTGTAACTCTGCCTATTAACTTG	32629	A_95_P136562	EB440327
33502	395	12	453	CAAGTATCCTTTGATAGTGATGCATTCTCAGAGAGCAGTCAAAAGCTTATAGAAGAG	32631	A_95_P106972	EB678624
33508	395	18	643	GCACGATGAGAGAATTTCCTTTTAGAAGGTTTTCCCTACCTACTTTTACCATATAGCTT	32643	A_95_P162302	EH621253
33514	395	24	784	ATAGATGTTGGAGAAGCAAAATGTCGTCAAGTGGTTAGCGGCCTGGCAAAGTTTTG	32655	A_95_P200907	EB679375
33516	395	26	1064	GAACAGTGTTCCTCTAGATATGGAGTACACTATTCATCTCACTCATTACTATTCATGC	32658	A_95_P024511	TC65064
33521	395	31	187	TTATTGCTTACTCTTTCACTTTCATTTCTAAATCCGGCTCGCTCCCGGCTACGGTTTGG	32668	A_95_P143862	EB447050
33528	395	38	914	AGCATTGTTTTATTCTGTAGACAGTCTGCGGAGCGTGTGAATATAAGAGATGATTAG	32682	A_95_P208857	TA19061_4097
33532	395	42	441	ACTCATTACACTTGCAATTGGTGAAGTGGTTTTTCTCCATCTTTTCTGATTTTTACCGT	32690	A_95_P260426	BP128766
33533	395	43	742	CTTGGATTTACCATTGAGTCAAAGGATTTCTCTAACAAAATGTTTGCGCTGTTCTACC	32692	A_95_P190302	DV160394

33538	395	48	495	CGTTCCTCTTTCATATTTTCACCTCGAAACTTAACTAGGAGCTTTCACCTCAAAAAATA	32702	A_95_P231519	FG644421
33542	395	52	852	GACAGTTGCGCCATTTGTAACTATGTTATCTTGCCATATATTCTTGGAAAGAAATCTA	32710	A_95_P272821	EB678607
33545	395	55	268	TTGGAGAGATCACAACCAAGCCACTGTCGACTATTAGAAGATAGTACGTGACACATG	32716	A_95_P004741	EH663814
33548	395	58	898	TTAAATTTAGTCTTTGGATCTACTATGCCGGTTGCCTCTTGTTTTTGGCCTTTTGGGCT	32722	A_95_P237019	DW001784
33550	395	60	923	TAAGATTTGTATCTAGATTGTGAGAGAACACCATCATTCTGTACAACTGGGTTTGCCC	32726	A_95_P207942	TA18857_4097
33551	395	61	734	CAAAAACAGGGCTAAGAATGCAGGAATAAGCAATGATCCTTCCCCAACAACTTTTGA	32728	A_95_P152962	EB683281
33552	395	62	1308	TAGAGTTTGTAGGATTTTACTGGGCCATCATTGTTGTTGGCGTTCTCGTAGAGTTGTG	32730	A_95_P026671	TA14564_4097
33555	395	65	510	GGTTATTTCGGTCCTACACGACCCCAACTCGTATAAAAGGGGTTCTAAATCTAATTTG	32736	A_95_P028211	EB434870
33557	395	67	850	CCTTTCAGTTTCATTTTGTATGTATATGTCACTGGTCCATATTGTTGTTGACACTCGGC	32740	A_95_P206787	TA18594_4097
33558	395	68	0	CTTTGTTGAACTTTTGCTACAAATGGAAGTGAAGAAAGTCTATCTATTACCTAGCGG	32742	A_95_P243282	A_95_P243282
33560	395	70	882	ATTGCATTGTTTGCCCTAATGATGGCCTTTTTGATCTTATTCGTATTCTAAGTCCGTTA	32746	A_95_P207852	TA18834_4097
33562	395	72	706	AACCCTGGTTGCTTTCGTCTTCGTTGAACTAACGAGTGTCTCTATAGCATTTCGAGCA	32750	A_95_P123467	DW003324
33566	395	76	391	ATTATTTAGGAGGCTGGCATGTTGACCGACTTTAGCATAAATCAGTTGAACAAATAT	32756	A_95_P094308	BP532663
33568	395	78	550	GTTTCTCCTGCTCATGTGAGGGGTACTTATGGGAGTTCGATCCAAATAGCAACATGT	32760	A_95_P145712	FG145527
33572	395	82	793	GAGCATCCTTTGTACTGTGGATAATCTGAACATGATTACTATTCTATCAAGGAACTGT	32768	A_95_P010561	TA12867_4097
33574	395	84	456	GATTCATTTAGTGGTTCTGTTGCTTCATGAATACTTCTCCACAATCCCACATTCTATGA	32772	A_95_P275633	AM794030
33577	396	2	801	GGTGAGTGATTCCACTTGTCATTCTTCACCTATGAATCCATGTCATTATTTATATTTGC	32613	A_95_P244332	EB681743
33578	396	3	631	GCCTACACCAGTGTGTAATTCGTCTATCCTGGGAGGAAATAATCTATAACCTTGGGT	32615	A_95_P261536	BP132658
33581	396	6	675	TTGACCTGTGTGAGACTTTGGAGAATATGGTCGCCCATTGATATCCAGAATGGGCTT	32621	A_95_P061635	BP135311
33582	396	7	740	CATCTTTGAAGGAAGGTTCGTTATGGACTTTTTGACAGTATAGATATTAAAAGTCTCG	32622	A_95_P188857	TA14662_4097
33584	396	9	796	CTCGCAGAGTTTAATCCAAAAGGTGGACCTGTATCCAATTTACTCAAGTTCTTGTGTG	32626	A_95_P137277	EB440987
33585	396	10	176	GAGGTTCATCCCTTGTAAATATCACCATCTAAAAAGGTGAAAGACCAATTCTTTGCTA	32628	A_95_P045361	BP131117
33588	396	13	927	CATTTCTCGGGATCATCCTATTTTCACAAAAATGTTGAATGCAACTGCGCGGGATTAT	32634	A_95_P186582	Y16644
33590	396	15	1103	GAGAGAAATTTTGACGTTCACCTGAAACTGTTACATCAAGTGAATATCCATCATCTGA	32638	A_95_P030831	TA13620_4097
33597	396	22	93	ATAAACACTGCGGTTTATGGTGTCAACATCTGTATGAATACGCACAACAGCAACTCG	32652	A_95_P106122	CV017766
33598	396	23	333	CGCCCCCCTTGGATTCATTTTTAAGCATGCTTTTATGGAGTTTTTGGGCTGGAATTTTT	32654	A_95_P062525	BP135537
33605	396	30	558	TAGTGTTACAGCTTTGCTGAGAATATGATTGGAGAACTGAAAATGACTGAGATACCA	32667	A_95_P024791	TC65629
33606	396	31	314	GTAACCCCTGCACTTGTTCTAAAATGAACAAATTACATCTTATTTAAGCAGAGATGGA	32669	A_95_P109182	TA11726_4097
33610	396	35	129	CTGTCTGTAGTTATCAAGAGGATTGCAAATTTGACATTCTGTAGCTTAAGTGCGAATA	32677	A_95_P004681	EH623011
33611	396	36	555	TATAGACACATTCTAAGTCAGTTACCAGTATTATTGATTGTCACATCTGACATTTCCCC	32679	A_95_P055586	BP133737
33613	396	38	427	GCTCACCATAAGTTTGAGCATGCTTGACACCTTTAGATGTTGGTTTGGTCAAGGGAT	32683	A_95_P078685	BP527577
33617	396	42	557	CCATATGTTGCAAGTGTACAGATGGGCGGAACATACGTATTGCATGCGAGAGATGT	32691	A_95_P220522	TA21625_4097
33619	396	44	680	CGCTGCTTGAGCACACAGATGTTGCAATTCTTCTTGACAATGAGGCCATTTATGACAT	32695	A_95_P259691	EB441978
33621	396	46	775	TGGAGTCGTTGCGAAGTACTTTGGAGAAAGTAACCCAAGAAAACAAACAAGCTAAG	32699	A_95_P287633	DV162026

33625	396	50	471	GAATTGATTTAAGCCTTACATTAGGTCAATAAAAGCGACCGTGCTAGAACCACGGGA	32707	A_95_P212432	TA19835_4097
33629	396	54	1629	AATCTGCACCGTATTTGTTATTGTTTTCAGCAGTTGAGATTGAAGTTTCTTGCATATTC	32715	A_95_P026006	TC63890
33634	396	59	373	TAATCCAGAAATTTTAATAGCTGAGAATCTGGTTCCATCAACAGTTGTAGACCTAGAA	32725	A_95_P219072	EB429767
33636	396	61	444	CATGTTGCACTCAATAAGCTCCCATCTTTCAGACTGTCATGTAGCAAATGTTCATCGAT	32729	A_95_P081805	BP528356
33643	396	68	430	CTCGAATCTAAAGCTTGTTTTCAGTTTAAGTGGGCGTTTGGACATAAGAGTTGTAAAA	32743	A_95_P021206	TA16556_4097
33647	396	72	641	GTGTTGTAGAGCTTATGATTCGGTATTACCAGTTCTAGGGAGTTGTATTATGATTTGA	32751	A_95_P216587	TA20739_4097
33652	396	77	311	GACCCCCTTTTGTTCGAGGAGTATTTGGAGTTGCTTTATTAAAAGTGTGCTAAAACTG	32759	A_95_P142507	EB445957
33653	396	78	513	AAGTATAGTTAAGCGAGCTGCTGCTCCTGCCCCTATGAAGAAACAAAAATCTAAGAA	32761	A_95_P085385	BP529267
33655	396	80	875	TAATCAGTGATGATTCACGATACATGACCGGAACTTCCATCTTTGTCGATGGTGCCCA	32765	A_95_P227899	EB425854
33659	396	84	479	CTTCAAGTTCTGACGATGATGATAGAGAATCCAGAAAATCAAGGTCTAAGTCCAAGA	32773	A_95_P055926	FG638526
33663	397	3	169	ATAGTTAGTTGAATGTGTTGCTGATGGTGGCAAGAGAGGGTTTATACTTTTGGTTGT	32780	A_95_P034384	AJ718656
33664	397	4	127	AGTCTTTTCCATTTCTTGATTTTTTGATGTAATAACGGGACTGCGGACCGGAACCTCG	32782	A_95_P132642	EB433192
33666	397	6	806	TTATCAGGAAATGAAGAAACTACTAACATCGAGAGGTTTGTTGCTGGTGCCGCAGCT	32786	A_95_P271561	EB680569
33667	397	7	933	CCTTGTAGGAAGTCATGCACAGATAGGTCGATGATTTGTGTTCTTGAAATTACATTAA	32788	A_95_P210552	TA19421_4097
33669	397	9	255	CAAATCTTTGCACTTTTGCCCAGTTAAATGGAGAAAACGAGATTAACCATCTTGTAGT	32791	A_95_P183887	TA13558_4097
33671	397	11	459	AACGATATGAAGTTTCTATTCATATCTTTTGAATGTGGACCTCTATCAGTTCGGATGGA	32795	A_95_P114012	CV021400
33675	397	15	403	GCACTAAGATCATTGAGGACGAAGATTAAGCTATCTATCAGTAGTGGAGAATGATTA	32803	A_95_P001426	FS435766
33678	397	18	1123	AAATCCCCTTGTTTGGATTCCTGGCTCCGCCTCTGTTAATTGTACTTTGTATCCATAGT	32809	A_95_P223477	TA22259_4097
33680	397	20	552	ATAAAGTTGGTTGTCTTTGTCTTGTACCACATTGTGTACAAGTCTCCTATTGGAAAAC	32813	A_95_P006086	BP129770
33686	397	26	491	CGGCTACTTTGAGCAGTCGCTTTGATAGTAACTGTTTTGACTATGTTTGTTAGTTGTCT	32825	A_95_P121557	FG639297
33692	397	32	589	ATTGTTGGTTTACTTCTTTTTTAACATTCATATTTTGGTCAACCCGTAACACGGGAGTT	32837	A_95_P153362	EB683645
33693	397	33	409	AAGAAAAACATTCTTGGATGGAAATTTTTCACAAGGCAGCCAACTGCATCAGGGGAT	32839	A_95_P213922	TA20151_4097
33695	397	35	622	GACAACGATAATCACGGCATCAGGATTATTGGAACAGTTTTAACATTAGTTGAACAAT	32843	A_95_P203637	TA17895_4097
33696	397	36	717	ATAGTTGGGTCAATCCCTAATATGCATCCTCTATCCCTATTCTCTTCTATCCAAGTTGAT	32845	A_95_P246102	DV999520
33697	397	37	950	ATATAATGCAGCCCGACCATTGGATCAAGACTTGCTGTTGAGTTGAGCCATCTTGCTT	32847	A_95_P212512	TA19852_4097
33703	397	43	316	ATGTGTGGGTATCGGTGGTTGGATGTTCATTCCATCTGTTAGTGAAGCAGTTCAATT	32859	A_95_P143467	EB446762
33704	397	44	0	AAATGTGCTAAAGTGCCTCTATCTTAAACAGGGGACTCAAGCCCTGTTAGTGAGCAT	32861	A_95_P303643	A_95_P303643
33707	397	47	659	TCAACTTCTTCGTGTTGAGCATGTTCTTGGATACTCTTGTTCCAAATCACCGTTTGTCG	32867	A_95_P221787	TA21893_4097
33712	397	52	462	ATTGCATTTAGTGAATTCCTCCAGTGAGGTGGTTTGTGAATATGTCTCTGGCCAGAGT	32876	A_95_P078755	BP527595
33713	397	53	755	TGTACGGAGTGAGGGTTGTAACTGTTTTCATATGTAGCATCTTTGCTGTTGCATTCTCA	32878	A_95_P179737	TA12574_4097
33714	397	54	728	GGACCAGTCGGATCATTTTTCAAAGACCCAAAAATTTCTTTCTTGAACACATTCGAGCT	32880	A_95_P273586	EH623052
33717	397	57	504	GCAGCTTTTGAGGAGCATTTTGCTTTAGTTGATTATATCCGACTTCATTCCCCATTCTA	32884	A_95_P290948	DW001994
33719	397	59	495	TACCTCGGGGCTTACTAATAATTTGACATTAGAGTTTGGCCCCGGCTTTATTTCCCTGT	32888	A_95_P031521	EB428123
33726	397	66	579	CTTTAATTTTAGTTTGTTGGAACTGTGTTGAATTAGAACTAATAATGGACTGTTCCGG	32902	A_95_P303368	FG635441

33731	397	71	618	CAACTTACCCTATTGTCTGACTTTAGGGGCAGTTTGTTTGAAATGTTACTTAGCTTCTT	32912	A_95_P005096	EB438050
33735	397	75	586	TTCTCTATCCCAACAATGTGGAGAAGCGTGGGTCTTAAAGTCAATAGGAAAGAAATG	32920	A_95_P064550	BP136082
33737	397	77	640	TTACAGACCTGGATCTTGTGGGGCTTCGTCTCCAAATCTGGTGGTATGTCAAATGAAT	32924	A_95_P160697	TA13067_4097
33741	397	81	135	CTAGATTTGCAATATGTCTGGTTAAGGAAGATACTTGGTTATCAGTGCTTATAGAACT	32931	A_95_P130212	EB430248
33743	397	83	554	TGGATGTTGAAGCACTTAACCCTTAGCTTTTTGTAATTTGTTGCTTCAGAATGAAAAT	32935	A_95_P303523	FG639260
33744	397	84	936	CTTCTGCATCTTGTAAAAATTGTAACATTTGACACTCTAAGGAGAAGGCAATATCAAA	32937	A_95_P015126	DQ676843
33745	397	85	437	GCATGAGGGACTCAAGTCTAAGATCCACGCTTATGATATAAAAATACCACATAAATG	32939	A_95_P074160	BP526396
33746	398	1	565	GTCCAGTTAGGGTTGCATTTGAAATTTGTGGTATGTAATGGACATCTATATCAAGAA	32777	A_95_P026886	FG636167
33747	398	2	786	GCTTGTTTGTACCAGAGTTTAGTTCTGAGGACAATTGAAATGTCTCTGTATTTCAAGA	32779	A_95_P232829	EB681870
33749	398	4	704	CAACTTGTATCTAAGGCAGCTAATCATATAGTCATGGATTCTATATATCCTCTTGCAAT	32783	A_95_P121262	TA14088_4097
33757	398	12	786	TGATAAGCATGTTAGCCTCCGCTTTCTACCATATCTGTTTGACATGTCATTAAATTATT	32798	A_95_P227299	EB425838
33759	398	14	841	TATGATTATCACTGATAAAAGTCCCGTTCTTCTGCATGATCGTGAATATCATCGTAGA	32802	A_95_P250272	FG146441
33762	398	17	464	ATATTACCGTGCACAGTCTGATGTAGATGGTCGTAAGAAATGTCATAACGTGCAAAC	32808	A_95_P114277	CV021525
33763	398	18	859	ATCATTTGTATTGCTGGGCTGTCGGCTCGACTATGACCTTTGTGAAAAATCCTGCGTC	32810	A_95_P272101	EB447618
33764	398	19	189	ATATTTGGATATGGCACCCCGGAGAGGGAATTGCAATACCCAGTTTGTGGATCAAGA	32812	A_95_P098603	BP534568
33769	398	24	374	AAGTCTCATGATGGGTCTCAGATACCAGGTAGCTTCTTTGAACCGAATGCACAAGAG	32822	A_95_P081960	BP528395
33771	398	26	817	GCTGCAGTTCCTGTTGTTTTGGTTGAGAATAGTGGGAGATGCAACAAGAATGAAAGT	32826	A_95_P200122	DV161462
33773	398	28	1166	TGCAATCTATTGCATCAAATTAATTTGGACCTGCAGTAGAAGTTGACTTTGCATATGA	32830	A_95_P026061	TA12472_4097
33774	398	29	370	TGGCTAATGGTTGGTGTGCTGGCACTTGGGCTTGTTCATCTGACTAACTTAAGGACAA	32832	A_95_P110772	CV019890
33776	398	31	796	TCTCTGGAGATGATTGTATTGCTGTTAAGAGTGGCTGGGACGAGTATGGAGTTGCAT	32836	A_95_P138702	TA14953_4097
33779	398	34	687	TTGTACTAATCAAAAGCCTTGGTGCAGAAAAAGTTCATAGAATGAAAAATCAGCACA	32842	A_95_P037706	BP129074
33781	398	36	436	GCAAGAAAACAAGCAAATTGCTTGGCCGCCTTCACTATTTACATTTACTCTATTTTGAA	32846	A_95_P001781	TA17156_4097
33785	398	40	315	ATACAAGCAGAGTGTTATTGAACAATAGAAGCGCGGCATACAGATGTTATCATCTGT	32854	A_95_P027531	EB431655
33786	398	41	702	AGCTAGTCGAGATGCCACCCTATCCATGTCATTTTGCATTGGCGTGTTTGAATTGGTC	32856	A_95_P268386	EB677398
33788	398	43	668	ATCTGAAATGAGTCCGGATACTCGTGTTAACTGTGTAGCACCGGGTTTTGTACCTACA	32860	A_95_P252294	EH616432
33792	398	47	850	ACAAAATAGTGATCCGCTCCTATCATGCCACCTCAGTGTGTTATGCTGCTCTCATCACA	32868	A_95_P300513	FG159785
33794	398	49	800	GATGTGATGCCTTCCTTGTACTTGGTTCATCTATGATGACCATGTCTGCTTTCCGGCTT	32872	A_95_P117017	DV159809
33797	398	52	328	TGGGAAGCATTTGTGTGAACCCTTTCTTTGGAGAAATCTTGTGAGGTTATTCTCTTAG	32877	A_95_P040866	BP129944
33800	398	55	719	CTCAAATTCCTTTAATAAGGTATGGCATCATTTTTGTAGGCCTTCCATTTTTGTGGTTC	32882	A_95_P117797	DV160754
33804	398	59	875	ATTTGGTAATAAAATCCACCTAGATGTTTGACGGTCTGTATAAGAAGTGTTAGTGAT	32889	A_95_P207052	EB425446
33806	398	61	973	TCAGGTTTGCCCAAAAGGGTCATGACTGTAACTTTAGAGTGTTAAACAGAAAGTATC	32893	A_95_P027431	TA16517_4097
33807	398	62	861	AAGAGACCGAATTCAAGAACAGATGAGGACCAAGAGTATAAAAGGGCTTCTATATG	32895	A_95_P013466	DV157572
33808	398	63	714	GGATGGATGTATTAGAACATTTCTCAATTATGGGTTGCCAATTCGTTTTTGAAATCTG	32897	A_95_P117112	DV159902
33812	398	67	719	TAGCATTGAGCAATGCCTGTGGAGGAATGCTGATGCTTTGAATTTGTTTATATAGATA	32905	A_95_P231199	EH624190

33813	398	68	454	CCAACATAGTATAGGTAAACTATGTATATAGTTTTCTAGCCTTCCACGCAGCTTTTTC	32907	A_95_P265901	BP532057
33816	398	71	599	TGATGGGTTCTGATCCATCATTTCTTGGAATGAGGAATGTGGAAAATGATCTAGTTA	32913	A_95_P044291	BP130840
33819	398	74	218	CATTTGGATGTTGTACATATTCCCACTTTATTGTCTCACAGAATTGTAGCTTGATCTGA	32919	A_95_P031811	CV020968
33820	398	75	0	CCGATGGATTTGTATCTGATCTGCTCCTGCTCACGTGACGTTCCTTTAACTGATTGTAT	32921	A_95_P242542	A_95_P242542
33822	398	77	937	CTTCAAGGATACAAAAGAATGTAACTGAGATAATAATAGAGACCAATGAACGGAGC	32925	A_95_P026196	TA18849_4097
33824	398	79	398	TCTGCAGCTTCAGGTTGCTATGCAATGATCAAAGAGCAAAGTTCAAGATTCTATATTA	32928	A_95_P104612	CV017094
33825	398	80	1197	ACGCATTCACAGGTGAAAATGAACCACGCCGGCTATTGCCAAATAAATTGCTTAATT	32930	A_95_P030001	TA14249_4097
33826	398	81	429	GGAATTTTGAACACTTCCTTTCAGCCTACAAGCACTTATTTCGTAGCTTTACTTTTCTG	32932	A_95_P113447	TA13685_4097
33831	399	1	362	TAGGTTCCAGTTTTCATTGCTGAGAGTAAAGATGTTACTCTGATTTTCTGATTGTCTG	32941	A_95_P219672	TA21444_4097
33838	399	8	572	AGAGTTGAATGGTGAAGTGGAGCGCTTAAAATCCGAGATCAAGTTGCAGGAAAATG	32955	A_95_P122212	DW002241
33839	399	9	277	CCCGGTTACATTAATATGAACCCTTTTCGTGTCAAATGAATTTTGATTGTTAGATGCC	32957	A_95_P022556	AM812473
33841	399	11	2103	GTCTGTTGTAGCTTTCAGTAAATTTATCCTCTTTCTATTTGACTGCATGGTAAGGAGA	32961	A_95_P032446	AB084669
33842	399	12	536	TGAAGGAACAATAGCAATATGATTACCATTAGAAGAAACAGGGATTTGCATTGATTG	32963	A_95_P088143	FG637946
33845	399	15	958	ACATTCTGACAGATTTGGGAAATAACTGTATCATTATCATTCTGACTTATTTGGGGTT	32969	A_95_P205717	TA18349_4097
33849	399	19	457	CATGTAGAAAGATACTTAGCTCTGTGATCTTGAATCAGATCCGTGACATGATGTATG	32977	A_95_P197442	TA16562_4097
33850	399	20	152	GAAAACAGAGTCCGCGGCTTGGCTATGCCTGAGTTTTGTACTAGTATATATTGATTTT	32979	A_95_P162057	EH620807
33851	399	21	437	GAATTGGATTGCTGGTTCCTTGATTTTTGCCAAAGCACCAGCTGCTTTCCCAATTTAG	32981	A_95_P156777	EH614792
33857	399	27	728	TGTTGCTGTTGCTTGATAGGAAAATTCTCCCCTCCACTGGAGGCATATGTCGTTTACT	32992	A_95_P144817	EB448343
33864	399	34	826	ACTTTGCAGTCTATGAATCACTAAAAGACTGGTTGGTCAAAACAAAACCACTTGGTCT	33006	A_95_P128722	EB428457
33865	399	35	386	GGTCTTAAATTATTTATCGTTGTCGGGAAAAATAAACTAGTACTAATCGTTCAGAGCA	33008	A_95_P098438	BP534475
33867	399	37	823	GCACCGGTCAATTGGTTCCGTTTCACGTCATAATTGATTTTGGGTATAAATAAAAAAT	33012	A_95_P028821	TA19898_4097
33871	399	41	764	ATATTTACTGTATGTATCTGTGCTGTTAGAATGTGTTCGATCGTTCTTCGGGGATGAC	33020	A_95_P237194	EB447792
33876	399	46	728	TGTTTCGTTTGTAAGTTGACACCTAGGCCCTTTCATCAAGTTTCTACTTTGTGAGCTAT	33029	A_95_P012366	EB683912
33877	399	47	875	GATTCATTTAAAGAATAAGATCATCCCGATCTTTGAGTGATGTATCGAGTATGCTTTT	33031	A_95_P022941	DV159900
33879	399	49	842	AGCATGTATTGTTGGAGTACACTTTCTTGAGTTCACATGATAATTGTGATGTCAATTT	33035	A_95_P025271	EB678939
33881	399	51	784	CCTTCGCCATATGAATACTAAGTAATAATAGCATGGCACTTCGAATTCGATATGAGA	33039	A_95_P241764	clpP
33886	399	56	166	GGTTCTTTTTTAGAGAATCGATGAAACTTGGTAATACCACCCTTGTCTAAGGAGATTT	33049	A_95_P259796	EG649566
33888	399	58	459	TATCACTCGAAGTGGAAGCTTGATTGTCTATGCAGGAGCTGTGATCTTGAAATGAAA	33053	A_95_P124782	DW004581
33893	399	63	293	TAATTAGGGTTGGGGTGCTATTTTGTGGTAGACAATCTCCTGGAGGACACAATGTGC	33063	A_95_P166822	EH664045
33894	399	64	842	TCATTCTGGTCAGGTTGGTAGTTTCAAGATGGTATCTGCTCTGAGCTCATTATCGTCT	33065	A_95_P294653	FG167397
33895	399	65	1510	CTATATTGAGTTTAGCAGAGCTATTTTTCTCTGGAAGGAAAGCTTTTTGCTGGTGAAA	33067	A_95_P189107	X79136
33898	399	68	611	CTGGAAAATCTCTTGGTGTGATTGGATTAGGTGGTCTAGGTCACTTAGCAGTGAAGT	33073	A_95_P131577	FG642025
33900	399	70	587	CTTTCTTCTAGGAATGAATGATTTCCTGGGAGTTTCTGGTATGGTGGAAATTTCATCT	33077	A_95_P194582	TA15926_4097
33902	399	72	138	CAATGAATGCAGAGCAAAGAGCCATGTTGGATAAGAGAAGGGAAAATGGGGGGAA	33081	A_95_P064900	BP136185

33905	399	75	647	CTCACCCATCCAAACCCAATACTTTTAGGGGTCATTTGTTTTGCAGTATAAGAAAATA	33087	A_95_P215652	TA20535_4097
33907	399	77	824	CGGAGGTGTAAATTTATGTTGTAATACAGAGAAGCATACAGATGTTGGAGTTGGGC	33091	A_95_P219187	EB424825
33909	399	79	879	TGTCTCTGTTAAATTTGTAGATGGTGGTCAAGCTGGAATGTATCCTGCAAGTGTAAG	33095	A_95_P227484	FG148811
33910	399	80	516	TGGATTCAGATGCAACTACACGCTCAGCTAATGATTGTGAAGAAGGCACAGGTTTAT	33097	A_95_P088193	BP529983
33911	399	81	1802	TCAGCCTCTCCATCAAATCAACAATTGTAATGAGTTGGAATAGCAATGATGATTAAAT	33099	A_95_P013046	TA12291_4097
33912	399	82	736	GTCCATAGTGTAGTGGCTGATGATATTAGATGGAACCTACAAGTTGTAAATATATGA	33101	A_95_P144427	EB447794
33916	400	1	259	CTGGATTCTAGAGGCTCAGATTCGTGACACCGGGTCCTAGTGAGATTATATTGTGTA	32942	A_95_P095023	BP532982
33917	400	2	818	GCCACATCTCCAGCCTTAGCTAGTGTGTATAGTAATAGGTTTTTTCTTCTCGTTCTTTT	32944	A_95_P117822	DV160789
33919	400	4	553	CATGTATACAGTCAATGAACATCAAATCAAGTGCTCCTGGACTGATAAAATAACATG	32948	A_95_P067645	BP136931
33924	400	9	751	AGATAGATGATATGGGTCTTCTTCCTCGTGTGAAGGGTCCTTCATTGTTAAGAGCAA	32958	A_95_P272511	EB450536
33926	400	11	253	ATTGCACGGACTCACATGATGCCTCCTTGGTTTTCCTATGTTGATGCAAAAACAGGA	32962	A_95_P034474	EG036055
33933	400	18	831	TTGGGTTAGCATTAAGGTGTCATCTTGATGATTTTAGGTTGAGGTCTACTCCTCCTGC	32976	A_95_P118817	DV161889
33937	400	22	576	AAGATGCTCCCTATACGGATTCATTTGATTGACAATTGCTAACGCTCATATTAAATAG	32984	A_95_P029716	DW002421
33944	400	29	747	AGCATCGGATATTTGGGTGGAAATGCTGATAGATGGTTGCTGGTTTCCTTGAGATGT	32997	A_95_P292033	FG163963
33945	400	30	551	CCAAGGCAAAGGATTTATATGTTCTATTGACTTTGCAAATCTATTTTCGCGACAATTT	32999	A_95_P261376	FG644419
33947	400	32	1450	CTCTTATTGATTTCTGTTGGTGATTCACAAATCTCAAGTATAGGTGTAGTTCAGCCAA	33003	A_95_P233929	AJ438613
33952	400	37	944	GCCTCACATTGTTTAAGTTGAGTTTTGTTGTGACGATCTCAAAATTTTGCTTCTTGTTC	33013	A_95_P012756	TA11902_4097
33953	400	38	477	TTATCCCAAGCCCAGACGTGCAGTGGAAATATAAATGTGATTTGTGCAATACATTGA	33015	A_95_P125192	DW004988
33956	400	41	773	ATGTTCAGTTTTGCCCTTCCAGTGCACAGAGTTTGCATGTGGAGATGATCTGCTTATA	33021	A_95_P262681	FG144321
33957	400	42	1980	TGTAGCCGAGACCAACTAGCTATTTGTGTTATAGTGGCAATATCAGCAAGTCTTAAA	33023	A_95_P192562	AJ289864
33959	400	44	426	GGATGCAGTTCTTACATCTTGTTATCTTATTAATCGTATGCCATCTTCAGCTATCCAAA	33026	A_95_P084300	BP528983
33964	400	49	199	GTTTATGCTTCCATAGATGCTATCTCTCTATCTATAAATACTGCTGCTCTTTTGAAGCC	33036	A_95_P140242	EB444197
33965	400	50	1065	GACCTTATCATTCACTTACACTCGCTGTTTGCAGAAATTATGGTTTTTGTTGGAATAA	33038	A_95_P305248	EU700060
33977	400	62	907	GTGCTGTCAAGATGTATTAATATCTGTGTTAAGAATGACCACCAGTACTTTCGCAATA	33062	A_95_P012226	TA15480_4097
33978	400	63	409	ATACGTATCATTGGACGATGATCTGCCTCTTGCTCAATTCGCTGTTGCATTTAAGTGG	33064	A_95_P001881	AJ719181
33979	400	64	802	GTCAAATGAAGAATATGCCACATCTCCAGCCTTAGCTAGTGTGTATAGTAATAGTTTT	33066	A_95_P151582	DV160789
33980	400	65	1110	GAGCCGTTTAGCCCTAAGAAATTTTTCACTTTTTTCAGAATCAGTGATTAGCCAAGAA	33068	A_95_P197967	TA16677_4097
33981	400	66	596	CTCATTTGTTGGGACGTACAAAAAGTTAAGGAAACATGTAAGGCGGGAGCATCCAT	33070	A_95_P146107	FG148780
33984	400	69	800	GAGTAGCACCACAGCTATTGCATGTGGATTTTAATTTCTTAAGAGTTTTTTGCTTGAT	33076	A_95_P259136	TA11961_4097
33990	400	75	690	TCAAATAAACATGTCTGTTGTGTGTATTTCTTGCCCCACGGAGAATTGTGATGTGTTT	33088	A_95_P009046	DW002310
33991	400	76	390	TGACAAGGTTATGTACATGCACAGAAATGTAAGGTCACTTATGCTTCAACTCTGAAT	33090	A_95_P131502	EB431801
33995	400	80	353	CTCCCATTCGACCAACCTCAATGGAGTGTGCAATAAAATTTTCCTTTTATTGAGAGTG	33098	A_95_P096193	BP533515
33996	400	81	705	TCTTAGTCCAAGAATTTGAACGCCGAATTGCATTCAACAAATTCCAGATTGCTAGTTT	33100	A_95_P296618	EB678339
33997	400	82	567	TTATAAAACTGTATTTTGCTCTGCAGTCCATGCTAGTTTGCATGTGCTCGGCAGATTA	33102	A_95_P054171	BP133370

34001	401	1	1704	GATGAATAAAGATACAATTTTAGCCACCCTTGGTCTTCTTATTTTGTTTGTCTTCCTCA	33109	A_95_P013881	TA14503_4097
34013	401	13	665	GCTTACAGATTGCGTTTATTGGCTTCTTATCTACCCGTTCCTCACACCCAATGATTACA	33133	A_95_P287003	FG195865
34017	401	17	727	GATGATTTTTCAGGAAGATGAAGGACTACGATAATGAATTCTCTAAAGTCTTGAGAA	33141	A_95_P122882	DW002824
34019	401	19	751	AGCAATCAGTTGTTTTGTGACCTTGACCTCATGCTTTGGATCAATGTAATGGGATTTT	33145	A_95_P014351	TA12865_4097
34020	401	20	784	AACCAGCAGTAATAGGGGATTATAAAACCGAAACAGATGAATTTGAAGTCCGTGTG	33147	A_95_P125642	EB424735
34021	401	21	876	GAACTCACTTCTGTGTGTATGACATCAAGTTCACCGCGAGAATCAGTTCAATCTTAAA	33149	A_95_P247437	DW001848
34022	401	22	759	GCCAAAATGTTGATATTCATAGGTAAAGGGAATAGGTAATCAGTTCAACCTTCTGAA	33151	A_95_P158862	EH616753
34027	401	27	542	GCTGGGGTTATTGAGAGAACATGTAGAGAATATAATACTGCACTTATTCTTAGGTTC	33161	A_95_P021246	EB436513
34029	401	29	119	TTCGGATTCTTTGTTCAAGACCATTGTTACCGGAAAGGGCCCATTAGAGAACCTTGCT	33165	A_95_P103857	TA11655_4097
34030	401	30	468	GAGAAGTGTATCAGGTTTTGTTTCCGCTTCAAATGTGAAACTACTGTGTAGTTATATC	33167	A_95_P124622	DW004407
34031	401	31	422	TCGGGACAAGTTTAGGTGGTTGTACATGATTTTCGCCAATATTAAACAATCGGTAAT	33169	A_95_P304488	FG644345
34034	401	34	423	CCATTTTTGCCCATTTTGAATAAGTGTATTCCATCTTTCAGAGGTCCAACAACCCTCAA	33175	A_95_P094898	BP532926
34039	401	39	658	GTCCTTAAAAGTCACCCTTGATGTCCATCCAATTTGAAACAATTGTTTTTTCCAGAAA	33184	A_95_P200697	EH623399
34044	401	44	39	AAAGGCGATTTAGAAGAAGCACTATATCAAGCAGGTGGTGTGCCTGAGCATGACAA	33194	A_95_P101268	CB337264
34050	401	50	463	TCTGTAGTCTTGAGTAAGAAAGAACCAAGGGTTTTGAATCTGCAATGATTGATGATG	33206	A_95_P000876	TA13391_4097
34052	401	52	158	TGATTGAACACTTGTTGTTACTCTTTGTTGCGGATCTGCCAGTCTACTATCCAGAAATT	33210	A_95_P062915	BP135643
34056	401	56	650	TCTGATATGCATAGTCATCTAAAACCTAGAAGTACTTGAGGCATACAGTTGCTTTGTA	33218	A_95_P187762	EB683945
34057	401	57	403	TTTCTGATTCTCGGAGGAAGAAAAAGGACAAAAATCTAATTTTGGGTTCAGAAGCTA	33220	A_95_P099123	FG146828
34058	401	58	400	ATGTTGTGGGAGTTGGCAATCATGTCTTTGGGTTATAGAACTGGCATCTGGAAAATC	33221	A_95_P080280	BP527966
34061	401	61	1220	TTCATCTTTGGTAATGCTGCAGTTGTGTTCCAAAACTCGAAAATCGCAGCACGAAAG	33227	A_95_P034638	TA14654_4097
34064	401	64	538	GTGAAGGTGGATCAAGGGAAGAGAGAAATCTCTCAGTATTTCATGTAGAGACATTT	33232	A_95_P071400	BP525694
34067	401	67	755	CCTGAATTCGGTATTGTGAACCTATGACGTGTTGAACTTTTTTGTTTTGTATTCCAAGT	6784	A_95_P000061	DW000215
34069	401	69	836	TGTTGATGATGGTATACGGCCAATGCCTCTGTTCAGACTGCAAGTTAAGCAGTGTTC	33240	A_95_P247557	FG160487
34070	401	70	918	GTTGTCATGTACTTCATTGTTCCCTAGCCAAGAAGAACAATTTTGTTTGTTAGTGTAAT	33242	A_95_P208917	TA19076_4097
34073	401	73	514	AGAATGTCTACTTTTACTTTCACTGTCCCGATTCTATTGCCTGGGAGAAATACGAAGA	33248	A_95_P278948	AM802231
34075	401	75	71	CATAGGAAGGATGCATTTAATTTCTGGTGTTAAATCTTGTTGGTCTATTATGTCACAT	33252	A_95_P103962	CV016775
34076	401	76	2263	GTCTCCAGGTTCTTCCTCCCTTTGAAATTCTAATGTTATGTCATTATAAATATGCCATC	33254	A_95_P195052	AY971376
34084	401	84	1153	GACCTCATGATTTGTAACTATTGAGGTTTCCTGGTGTATCAAATATTGGAAATATATG	33270	A_95_P030126	TA12717_4097
34086	402	1	584	GAATGTACTAATCAATTAATCTGTTCTTTGAGTTGTAACATGGGTAGATGGAGTCCAT	33110	A_95_P241280	FG634671
34089	402	4	680	TGTGCTTGGATGAAAGTAAATGTGGGTAAGGAATTCACTTACTTCTCTTCTTCGTTCA	33116	A_95_P164672	EH623932
34091	402	6	797	GCCGAGTAGATTATCATCTGGTACCAAGGGAGGCCATCTCTCTTTTCTTATGGATGG	33120	A_95_P269391	DV999189
34094	402	9	748	TGTTATAGTTGATGAGTCAAATTGGTGAATTATTTAGGTGGTAGTGGACTTGCTATG	33126	A_95_P254419	EH624379
34097	402	12	936	AGATTTCAACGTTTTGTGAAACTGATTATGTAGTATAATGATACACCATTGACTCTCG	33132	A_95_P001646	TA21639_4097
34098	402	13	527	CAACTGTTCGTTGTCTATGTGGAGCTGCAAACTGTTCTATATTTCTGGGTGCCAAGTC	33134	A_95_P086345	FG158351

34101	402	16	745	GCTGGGTGATTCCATGTGTATCATTGTTGCTTTGCTGAGTTCTCATATCTATTTTCCTT	33140	A_95_P011631	EB683371
34103	402	18	698	ATGAGACTTTGGTCTCAACATCATTATATCTTGATCATGGCATCGATCACTTGGTGAT	33144	A_95_P137857	FG640721
34105	402	20	526	GGCCTTGCTTCTCAATTTGAAGTATAGTTTATTGAGAAAATGGCAAATGCCAATTGTC	33148	A_95_P023571	DW004204
34112	402	27	1060	GTGATTGTCATCTATGGGATCGCGACTATAATCGTTTATAATAAACAAAGACTTGTCC	33162	A_95_P032271	A16119
34115	402	30	499	GGTATTGGAAGACAACATTATTTGTGTGGGTTAGCATGATGTTGTTTACCATGGAAT	33168	A_95_P262086	BP134553
34116	402	31	813	ATTTCTATGACTCATGAAAAACTGGCACCCTTTCCTATAAGGCAGTATGTATTTGGAG	33170	A_95_P117742	DV160694
34118	402	33	994	CAGTAGGAGGTTGTTTCTCAAAATAATGTATGCACAGATTGTATTTTTCTCTGTGAGA	33174	A_95_P010936	TA13191_4097
34119	402	34	902	ACTTCGGGAAGCACTGAAAATGGCAATCTTTTGCCAACTGATAGCAACATACCATTTT	33176	A_95_P247317	TA13860_4097
34121	402	36	512	ATGTAACATGATTTTCTACTGTTAAGAAATTTTTTGGAGATGGCGGACCATTTGGCTG	33180	A_95_P185437	TA13912_4097
34123	402	38	659	TCTACATGTTAGAGTATCCAACCATGGTGCATGCTTTCTACATTTTCCCAGAGCTACCT	33183	A_95_P150987	EB449923
34126	402	41	855	ACCGGCTCAGAAAGTCGAGTTATAGTTTCTCACAAGTTTCTCTCTTCTTCTTTTTTCTT	33189	A_95_P261696	DW000285
34127	402	42	957	GTACTTGTCTTGGTTTTATGATGATGAAGTTACTATTGCTCTAGTACATTGCTGGTTTT	33191	A_95_P194637	TA15939_4097
34134	402	49	477	GTGAAATCTCCTCCTCGATGCTTACTGCTTTTTAAAATTGTAAGCTTAATATTGTTCTC	33205	A_95_P000971	EH617048
34136	402	51	680	TTCACTTTTGTTCCCGTCCCTCCAAACTACATCTAGCTTTGGTGATCTGAATCCTTATTT	33209	A_95_P171331	EH665116
34138	402	53	554	GATGCTCATGTAAATTTCTCACGTTTAGTAGTTGTGAGCTGCAAACCCAGAATTTCAA	33213	A_95_P107962	EB678578
34139	402	54	899	AACTACTCTATCGTTTGAGCGCAACTCTTTGGATATCAGTTTATCCAAATAGTATCACT	33215	A_95_P181667	TA13037_4097
34141	402	56	108	ATAAACATGGTTGTACTCTGGATGGATTAGTATAGTTAACCACGGATACATTAATCAT	33219	A_95_P138767	EB442495
34151	402	66	626	TTCCTGTCAGCATCTGTGTGTTCTTGTTTATCTATGGGTGACCTTTCTAATAAAGTTAA	33237	A_95_P237654	EH617567
34153	402	68	231	ACAACAGTTCAAGGACTGAGGAAACAATTCACTTACAAAAAGATCCTCAAAGACCTG	33239	A_95_P158967	TA12804_4097
34164	402	79	642	GGCGACTTAGAATAATGCTTCTAGTTGAATTTGAGATAAGTTCACACTATATGGAAG	33261	A_95_P244572	EH621211
34165	402	80	784	TGGCCAACCAATTGAGAAGGTGCAACAGTACACTGAAAGGGATCGTTTTTTGTCTGT	33263	A_95_P243447	EB681076
34174	403	4	729	TGTGCATGCGAATACATGCATGGCTTTATCATCTTTCAGTGTTGCAAAGAACATAAA	33280	A_95_P248557	EH623509
34178	403	8	631	CTCTCTTTAACCGGTTATGCCCGCTGAATAAAGAAGGTAAACGGAAGTTCTGTGACA	33288	A_95_P121307	FG141428
34179	403	9	760	TTTGCCAAAGATTGTTGACAAAGTGGAAGCGATTGAGGCCATCGACACAAAAGGCT	33290	A_95_P115512	DV157751
34180	403	10	726	TCCCATTGATATTCTCTAAATAAATAAGAACGTGCATAGGTTATGCCTTTCCGCACTTT	33292	A_95_P115452	DV157667
34185	403	15	821	AGTCAGCACATCATAGTGGTACAAGAGTCATGGATATTTTCTATTAGTACTTCATAGT	33302	A_95_P001031	DV999190
34187	403	17	817	TTTTTAATATGCAGTTGAACCCGCTGTTGGCTTAAGACGTATGGAGAGCCAAGTGAG	33306	A_95_P296588	EB677957
34188	403	18	931	TCGAGATTCAGAAAATGGAAGAGAAATTTCATGGTGGTTTTTTCCCTCACATTTTGG	33308	A_95_P193322	TA15645_4097
34191	403	21	489	AGTTCTTTCTCCTGCCTTTTATGGCCATTAGAGCTTGGACTTTCTCGGCAATAAGATT	33314	A_95_P252899	BP525788
34192	403	22	412	AATTAGTCTGCTACATCCTTTCTCTGGTGTTGAGATCGAATTGCCGCATCAAATAGAT	33316	A_95_P076280	BP526945
34196	403	26	796	ATACCATTCCTGAGCAATTGTTGGAAAATGTCTCTGTTATTGTGGATCCGTCTGAAGC	33324	A_95_P232509	DV162021
34199	403	29	571	GTTTATCTCCACTTGGACATCACTCTCTTCACGGACATGTTATATACTTCTCAAATTAT	33330	A_95_P028911	TA11814_4097
34200	403	30	748	GGCAATTTCTCTCCTCATGTGACTGTAAATAACAAGTATACCCTGTTAATATGTCTAT	33332	A_95_P023856	EB426055
34203	403	33	636	GACAAAAGATGTTGATGCTTTTTGTGAACTGTGTGGTATGTCTAATGACATCCTGGT	33338	A_95_P243542	EB432106

34204	403	34	691	TATCTTTTGGTTCCTGTGCTGTCTAATTTGTGGTATATTATATTTCTGATTCGCGAGCT	33340	A_95_P001716	TA13252_4097
34205	403	35	92	TGTACGTAAAAGATTGTATGGCTTTTTCGACCTATGTTCAGTATACGAGTGGTTATTT	33342	A_95_P142217	EB445747
34210	403	40	525	GTATGTGTTCCCAGTTTGTGTAAGTATAATTGAAGACTTCCCACAAGTTATATCTTAT	33352	A_95_P178382	TA12233_4097
34211	403	41	63	CTCCAGCTTCTTTTTATTGTTAGTAGTAGTGTGAATTCTCGTGTTCTCAATTTGGATAG	33354	A_95_P033264	AJ344593
34213	403	43	365	CTCTTCAACCATCCAACTCAAATATGAAAGCTCTGGAAGCGCGTATACTGTGGCTTCT	33358	A_95_P081320	BP528224
34217	403	47	408	AACTGAGTGAAGTTGCAGACAATAGGAATGATTCCTCTGGTCCAACTGTGCTGGATC	33365	A_95_P299383	AM793808
34221	403	51	603	GGACTGCCTCTCTTTTTTGTATCATCTTAATGTGCAACAAGTGGTTTAGTTGTTAAAG	33373	A_95_P286658	FG637905
34228	403	58	773	GGGTCATTGCTTAATAGAGCCTAAAGCCATCTTTTCTGGAGCTATCAAACAGAATTTT	33387	A_95_P221952	TA21928_4097
34229	403	59	759	CCCATTTTAAATAAAAATTGCGGCTGATTGAGGTGGTTAATGGGGAAGGCAATGCA	33389	A_95_P149512	EB679387
34230	403	60	683	GCTCAGAAGGAGTATGCCAGTGACATTGTTGTAATTTATACTCAGTACCATCAATATT	33391	A_95_P316938	FG201409
34233	403	63	536	TTCATGTACTGCTTACGAGGCACAAAATTTGAGAGGAAGAACTAATCAATAAGTTTC	33397	A_95_P129547	EB429518
34235	403	65	662	AGAGATCCATGGAATGAACAAGAAAACCAAACAACACGGCGCAACATAATACAACG	33401	A_95_P316118	FG201375
34236	403	66	757	GTACTAAGTGATTCAGCTGTAAAGAGGTGTGAGAATGTATTCAAATGAATTATTGCT	33403	A_95_P180097	DV162548
34237	403	67	714	GAAGAGAGTTGCAAAGAAAGCCTTGACGTTTGGGCAACAAGTGACCCTAAATATTG	33405	A_95_P150897	EB681051
34243	403	73	165	CTCTCGCATCGATGAAGAACGTAGCGAAATGCGATACTTTCATATTTTTCTTATCTTTT	33417	A_95_P031906	TC76829
34246	403	76	542	TCTCCGTAGTTTGAAGTCTGATATTTTCTGTGCTCTCTCTAAAATTGTACTGAACTATC	33423	A_95_P017721	EB678067
34252	403	82	323	TTCTGTGTCTCTGGTAGGTGAGTTCTCCAGTTTCTTCCTCCCGTTTGTAAATTCTAAAT	33435	A_95_P102552	CV016071
34256	404	1	836	CCTGACTGGCTAGAGTAACATGAATTTTGCTTGCATCTGGCTTTGTGTAAACTTATCT	33275	A_95_P277918	EB683280
34264	404	9	1215	CTGGTATCCTGTAAGAGACAATTTTGTTGCTAGACTCTGATTTTCAAATATTTTAGCA	33291	A_95_P212107	TA19758_4097
34268	404	13	864	GTCCCTCTCTGCCATGTTATTACTGTTGGTGATGAAAGCGATTTACAATTTATTTTAAC	33299	A_95_P007711	EB424607
34269	404	14	183	CCACTTGCATAAAGAGCAGAGGGTATCTATTTAGTCATCTTTGTCCTGATGGGCACAT	33301	A_95_P166772	EH664032
34271	404	16	403	CTGAAATCTCCGGTATTTTGTGAATTATGGATTGTATTGGTCAATAACCTGCAGAGTT	33305	A_95_P029886	FG645607
34276	404	21	243	AGCCCTACACTCTGTTCAGTCACAGAAGTGATTGTTTTGATTCGAAAAAAGGTGACT	33315	A_95_P088848	BP530243
34281	404	26	258	CGACTTCGTCAGGAAGAACTAGAAAGACTTGCAGAAGAGAAGAAACGTTTGAAAAA	33325	A_95_P132212	EB432657
34282	404	27	775	TCAACAAAGAAAGAACCTGCCGAGAAAGCTAAGACCAAGAAACCTGCAGTCGCTAA	33327	A_95_P234344	EB450381
34284	404	29	1179	ATTTCAGGATGTACTATGCTTGAGACGCTGGACGTACGCTTTTGTCCCAAGATTTGTC	33331	A_95_P018501	TA19010_4097
34285	404	30	1280	GGATGTTTATTTGCTGTATTTGCGTTTCTATGTACTGAATTATGATTGGCCTTAGATC	33333	A_95_P195657	TA16165_4097
34287	404	32	259	CTGGAATACCTGACAGCAGAGGTTCTTGAATTGGCTGGTAATGCAAGCAAGGATCT	33337	A_95_P021426	DV158629
34290	404	35	1217	TTAAAAGTTTTGACAAACTTGTGAGTTCATACTGCAATCTGCAACTGCCTAAGCCTTT	33343	A_95_P015221	TA16816_4097
34293	404	38	854	GATACTTGAGATGTATTTTAAATGGGTATTAATCAACTTCCTCACCATCGCTGCTGTTT	33349	A_95_P296123	EB450072
34295	404	40	391	CCTTCGTAGAATGAGAGCATCTATGATGCTTTTCTACCCTTTCTTATTTAGTTTGTGAA	33353	A_95_P098403	FS433680
34296	404	41	302	CATTGGTGACTATTTCAGTATGTGCCTTCAACAACTTTGATATCAATGCATTTTGCTGT	33355	A_95_P091608	BP531435
34309	404	54	788	ATATTGCACAATGCTGTTGGAGTCTTGGCAGTGTTTGGAATTGCTCTACTTGTTGGTG	33380	A_95_P201137	EB450512
34310	404	55	433	ACCACCTTTGCTTGTTCCTTGACTCTTGAGTGGCTTCCTATCTTGAAATATAACAATTT	33382	A_95_P219587	TA21427_4097

34311	404	56	748	CCTAATCCATCGGACTGAGGATGTTATGGTTATCACAGATTTATAAGATACTACATTA	33384	A_95_P115927	EB439621
34313	404	58	815	TGAGGGGGTTCCAAAGTATTGTAAATTACTTGGTCACTCCATAGTACAATGCATGGC	33388	A_95_P119647	DV999105
34314	404	59	171	CCTTCTTTTTGTCATATACAAGCCACAAGGCATCAAGTTGCTGTATTGAATTATTGAC	33390	A_95_P097338	BP533992
34315	404	60	1085	GCAGGAAGGCATTGTAGAACCTCTATATTTGTTCTGGTACAAAACAGTCTAACATGT	33392	A_95_P137482	Z93770
34319	404	64	584	AGAGGGCACGTGGAAGAAGAAAGAGCAGGGGTTACAAAGTTTAAGTTGATTTTCAT	33400	A_95_P101003	TA12021_4097
34322	404	67	439	GGGGTAGAAATTTATGCTTGCATATTGTAAGTTATGTAGCTTCAGATTCCATATGGA	33406	A_95_P024581	BP525841
34323	404	68	867	CCCAGTTATCCTTCCTCGAAATTGAGACACGTGGATTGGGATAAATTAGAGGCTGAA	33408	A_95_P185232	TA13868_4097
34325	404	70	725	GCACCCTTCTGTATCTAGCCTTGTTCATAGTTGTAGTATCCCTTTGTTCAGTTTTTAAA	33412	A_95_P235119	EH615107
34327	404	72	786	CGTGCTGTTACGTTAGAAACTTGTCACTCTTTCCACATCAAAGTTAATATATTGACTTA	33416	A_95_P012176	EB438154
34328	404	73	768	GTGTCGTAGTTAGAAAGTTTTTAACGTTCCATGGGAGAAATTACGCATTTTTTGCTTT	33418	A_95_P250587	EB677940
34342	405	2	781	AATTATGGATTTTGGAAATGCACGTCTGCAGAGGCAATTTGTTCTCGTCGAGCCCTA	33445	A_95_P250417	FG140098
34347	405	7	854	TCTAGACTCGTGACACCAGATTGTTGGGACTTGTAGTTTATCATTATTTAGACTTCCG	33455	A_95_P219547	EB681712
34351	405	11	300	TACTCTTGTTCCCATTATGAGAATTATTTTCCTTGCACCTTAGCTAACCCCAATTAAGT	33461	A_95_P025831	EB446783
34359	405	19	688	AACTACGATGTACTTTGCTCCGCTTCCCAGCAATGCCTCGATTAGTTTGCTAACTTGA	33477	A_95_P303828	FG200649
34367	405	27	764	GGTCCTTGGTATGCACAGTTAGTAGATAGTATGTGAAGGTATTTTACATTCTTTTGTA	33492	A_95_P117587	DV160534
34368	405	28	1206	GTTGTAGGAGGGTAGACATAGAAATGTAACGTATTTTAGGGAGGTTATTGTAATTCT	33494	A_95_P014446	AB107692
34374	405	34	914	TTGTCCTTTTTATTTTGAGGAAGTTGCCTCCAAAGCGAGGGATCACACAGTACCACCC	33505	A_95_P010151	AB193040
34375	405	35	323	TCAGGAGTTCAGATGGTGGGATCAAATTGATCAGTTTCTCCTCCTTGGAGCAGTTCC	33507	A_95_P147177	FG159920
34380	405	40	361	TTGCTGAGGCAGACAGTGAAGTTATAGTGTTTATTTCAAGTATTCAGCTCTTTGTTCA	33517	A_95_P068100	BP137050
34381	405	41	350	GTGGTTAGTCCGAGTACATACATGGTTATTATGCTCCCATGGATATAAATATTGTACC	33519	A_95_P026851	TC69357
34383	405	43	803	TGTTCCATACTTAGCAGAGAATGCATCAACCGACGGGAGCTCTTCAATTGTGGAAAC	33523	A_95_P234399	EB425505
34386	405	46	627	TCTTGTGAACTTCTACAAGAGGACTACAGGGCTTGATCCTGTGATAGAAGTGAAGAA	33529	A_95_P127282	FG157369
34389	405	49	777	TTTCCACTAACCACTCCTCATTTGTACAATGCCATAACAGATAATTGCATGTGCTGGC	33535	A_95_P143842	EB447026
34394	405	54	229	AGAGGCAAGTGTTGTAATTCTTCAGATCAAGTTTATCCCTTTTTCTCGCTGTTTACATT	33545	A_95_P093303	BP532213
34395	405	55	565	AGCCCGTTATCTGCAGCCTTTCGAATACCTTACGTTCTGTTCTTTGTTTAGACCTACTT	33547	A_95_P268756	DW002932
34399	405	59	510	AGATGCAGGGATTTGTATACGAATTTCGAGAGATGTATGATGCTTGTGTATATGAGA	33555	A_95_P160617	FS435443
34403	405	63	790	CTCCAAGGTTGTGTTCTAGTTCCAATATTCTCTAATTAGTTTGTGTTGTATGCTAACCA	33563	A_95_P028756	TA19504_4097
34405	405	65	605	GCTCGAGGTTGCTGTTATTTACACAAATTCTCAGTACATTATTACATCTCAACTAAGA	33567	A_95_P027461	TA18771_4097
34406	405	66	769	ATAGTAGTAGGGCATCACGCCATTAAAAGTGTTGGGCATCATGGCGACACTCAAGT	33569	A_95_P316188	EB425136
34407	405	67	152	GATATCCCGGTTCCTTTTAGATGAATTGATGAAACTTGGTAATAGCACCCTTTATAAG	33571	A_95_P154352	EG649542
34408	405	68	765	GGAATGAGTACTGTTGTGGATTGTTCTTTTATTTATTTGAAGCACTACAGAAGTGGA	33573	A_95_P148492	EB677831
34409	405	69	1094	TATTGTTTAATCCACTCAGGTCAGTTACCGGCCTCTAGCGTTCCTTATATTTATAAATG	33575	A_95_P192457	TA15455_4097
34410	405	70	656	ATTCCATTGGCAAAGGAAGGTGTTTTTCTGTTGTCTTTAGGCTATATAATCAGTCCGG	33577	A_95_P302013	FG640485
34413	405	73	1029	GATGCTCCAGTGAAACTCTCTTATTTCGTGGAAATGAATTCTTGTTTTTACAGAGCAA	33583	A_95_P251777	AB119466

34420	405	80	1773	AGCTGATCACTCTGTGATTCAAGTTATTGAGGAGTCTATGCGATATACTAATATTGCT	33597	A_95_P290233	AB454418
34421	405	81	998	CAATTTTGGGTTAGTGTTAGCTTCTCCACCTGTGTATATATAGCTCACCATCACCTGTG	33599	A_95_P209977	TA19303_4097
34425	405	85	621	ATCCTCCCCGTCTTTTTGTCCTGGTTGCTGGAGTTTGAATTAATACTAACAATGATTTT	33607	A_95_P210997	TA19516_4097
34432	406	7	471	AGTTGAAGATTTTTGACTCTTTCTTCTTGTTCGGTTACTCACTGAATTCTTTGGCTTCT	33456	A_95_P021626	TA13926_4097
34434	406	9	784	CGCAATATTGCAGTGTATCAATTAACGATAGCAGCTTTTAGAGGATTGTATGATTTG	33458	A_95_P200477	DW000158
34435	406	10	604	ATTCATATCGGCTGTGTAATATTGCAAGTTCTAATGGGTATGTACTTTGTCAACCATT	33460	A_95_P182452	AF153278
34436	406	11	840	AGTTGTTCTGATTAAGCCTTTGTCCCGTCGTTGTAAAAGGTTTATACCTGATCAGCCC	33462	A_95_P021386	DV160093
34451	406	26	1154	TGATGCTGTTGAAGTTGTACCGACATAATTTTGAGAAGTGAGCCTTTTTCCTTTTTTCT	33491	A_95_P195792	TA16195_4097
34453	406	28	836	TTGAAGGTACTATCACTTATCTGTCCTCCTCATAGGCTCTGTGTATTGTCACTATCGCT	33495	A_95_P273271	FG135498
34456	406	31	1374	CCAGCTCCGTCATATGCCACACCATAAAATATGAATCTTTTCTCGAATTTTGATTTTGT	33500	A_95_P199967	TA17109_4097
34457	406	32	750	TTGCTGAGTGACAGAAACCAGAAAATGTCAATTCCAATGTCTCCCAGGAGGCATCAT	33502	A_95_P129917	EB429852
34463	406	38	841	GCGAGATTTTCTTTTGCAGTGTCTTTTTGTCTACCTGTTTATACGTTTAGCATCGTTTG	33514	A_95_P021901	EB446106
34464	406	39	1578	CCAGGAAATGAAGATTTCCCGAATTGGGGACAGTTTCCGCATCCAAACAATTTCGTT	33516	A_95_P237479	U66401
34469	406	44	420	GTTTATCGCTTCCGAGTAATACTGAAGATTCAAATCTAATTAGATGTGGCTAGTTTTG	33526	A_95_P180657	TA12797_4097
34470	406	45	125	GATTATTGACTATATAATCAATGTCCTCGCCGATAAAATTTTCCCGAATACTCTTGCG	33528	A_95_P167266	EH664155
34471	406	46	1631	GGGGGATATTTTGATGTGTATTTATGCATGTCCTTTTATGGCAGTGTTTGCTTAATTT	33530	A_95_P194142	TA15830_4097
34478	406	53	476	AGAACAATAATGGCAGGATTGAAGATATAGAGAAGACAACATGGGGTGCCTTCGTT	33544	A_95_P282868	AM831732
34479	406	54	697	CATTGGATGAAAGTGGAGAGGATCTCTGGAAGCTCACAATATCTTCTACTGCATCTG	33546	A_95_P219987	TA21512_4097
34480	406	55	392	ATGAACGTCCTGCTTAACTGGAGTTTGTTACGTCCAAATTTCTAGTTTCTCAATACCTT	33548	A_95_P309248	FG645376
34482	406	57	593	AGTTTGGTGTTTGAGGTTCTGTCAATTCCCTGTTGCAAAAACATTTAATATGTGATCA	33552	A_95_P109387	TA12024_4097
34487	406	62	759	GAGTTTGGTATTTTGTTTGCTTGGACAGTTGGAATCCTAGTTATACATCTCAATGTCTT	33562	A_95_P182427	TA13214_4097
34489	406	64	818	AAGAGAGCATTTGGGAAAAGATTACACTCAGGTTCCATACATTTTTGCAACTCGGAT	33566	A_95_P147272	EB451579
34490	406	65	575	GGAGAAACTGGTGATTGTAATATGGTACTCTTTCTTATTCAAGTTTAGGTTCTCTCCTT	33568	A_95_P004091	EB451750
34493	406	68	677	GGGGATCTTTAGGGCCAAAGTGGCTGAATTAGAGGTAGATGAAGATTGTGTTTTTA	33574	A_95_P118922	DV161997
34494	406	69	786	AGCACCTTAAAGTTTTGATACGTTATTCGCATTGTACCTGAGCTATTCCTATTTCGGTT	33576	A_95_P145772	TA11948_4097
34503	406	78	341	CAAAATGTTCCTGGAAATGGATGCTGAACTGTTCGAAGATTGCCAGAAACAGTATGC	33594	A_95_P111967	CV020454
34504	406	79	720	TGATGTCATAACTGTGATAAAATTCACTTATCTTTCGTGCTCACCACCAGTGATGACTT	33596	A_95_P223652	TA22299_4097
34506	406	81	741	ATTCCTCTTACAGTAGAAGTGGTGGAGGTGGTGTGAGTTACTATGAAGGAGGTAAC	33600	A_95_P148537	EB677889
34508	406	83	725	TGGAGATTAGTCCCGTGTGACTGGAGAGTGCCACCGATACTCAAAGGTAAGTTTTAT	33604	A_95_P136497	EB440258
34513	407	3	777	CTGAAGTTGCTGATTGCTGAAACACTAATTATGCTGAGATTAGTTATGATGTGACTTT	33612	A_95_P204577	EB438260
34515	407	5	512	AATTTGCTAAGATTCTGTCCAGAATTTCCTCTCGATCCCTGTCTACGGAAACGGGAAA	33615	A_95_P282638	AM835801
34516	407	6	648	TTCTGCAAGATTGGGCCTCTATTCCTTTTACTATTCAGTCGAAAGAATTGTGGTGAAA	33617	A_95_P052111	BP132834
34518	407	8	727	CAGTTTGAAGTATTTGACGTGGAACTGCTAGGCATTCAAGACTGCAAACGGAGGAC	33621	A_95_P293683	FG645494
34520	407	10	356	TTAGCTAGAGTTGTTGCTGTATGAAGTTACTGGAGGACACTGATGTTCCCTTTCAACC	33625	A_95_P004961	EH665674

34526	407	16	305	AATTGATGAGTTATGTGAAGAATGGGCCCCAGAACCACTTATCCCTTCCATCACTGAT	33637	A_95_P087248	DV162026
34528	407	18	730	GGGCCTTATCTTGTCGGATATTGGCTTAATAGTGGAGCCCCATTAACTGTTGTATCTG	33641	A_95_P015236	EB680043
34532	407	22	839	TGGGAGGATGGCAGTTATAAGCATGAGAATTCTACATTCGAGCTCACCATTAATCAT	33649	A_95_P126122	EB425359
34535	407	25	657	TCCCGTCGGAAAATTGAGGCGAATTATGAAAGAGAGTGGCCATGATGTGGAATCTG	33655	A_95_P024086	EB449027
34540	407	30	779	AGTACTCAACTCAGAAGGAGAATCAGTTGATACCAATTAGAAGACCTGGTTCAAACA	33665	A_95_P125812	EB424907
34543	407	33	783	ATGTGCCAACTGTTATTGGAGATGACATTGAGATGCCAAGACAGTGGGTATGTGCA	33671	A_95_P284088	EB679092
34546	407	36	660	GAAGTTATTGTTCTTGTTTGCGATTCACTTCAGTTCCTCGTCGCTGAACTTTTCTTGTC	33677	A_95_P285638	FG634274
34547	407	37	1864	TAGTGACTAGCCTGAACGCCATACCAAATGTTAGGGCAAGCTCTCTTTGGTCTTACAT	33679	A_95_P113127	AF223573
34552	407	42	891	CCTCTTAGTTTCAAAGACAATCTGCAGTATTGTAATTGTACTTGTTTCTGTTGGTTGTG	33689	A_95_P016741	TA15939_4097
34554	407	44	823	TGCAGAGCTAGATTCGGGTGGATTTTTATTGTATTTTATTCCTTGTTAAGGAGCCAGT	33693	A_95_P291573	EB426455
34559	407	49	594	ACCCCCTTTATCTAATGCTGAATCGACGACCTATTCTAAGTAAGAAGAGCTTTTTGGAT	33703	A_95_P191082	EB429462
34561	407	51	840	TATGCATTGGTGCGTTGACAGTTTTGGCAGACTTAATGGGAGCAATTGGATCAGGA	33707	A_95_P288338	DW002516
34562	407	52	158	ATTCTAGGAGAAACCTCCTTTTATTATCACCACGTCTGTGTGGTAATATTGATTAAAG	33709	A_95_P288518	BP533050
34564	407	54	410	CTTACCCCTACCTTATGACGGTAGAGTAGGTTGTTTCTGGAATGATCCTCTTCTGTAG	33713	A_95_P056831	BP134057
34568	407	58	760	GAGGCTGGATTTATCGAACAGGTTTCAAGATGCAATTAAGGAAGTAAGCAATAAGCT	33721	A_95_P128647	EB428386
34575	407	65	94	CATGGGGATCACCTATCACATTACTTTTGAGCTTTAACTTACTGCATTACTAGATGTTA	33735	A_95_P134757	EB437526
34576	407	66	517	CCCTTCACCAGATTTTTGTTTCAATAATGTTGTCACAGCACATAGCAGACCATTATCTA	33737	A_95_P078160	BP527443
34581	407	71	798	GTTGATAAACTATAATGGGATTCAATGACCAAGTGGAGTGCCTCATGAAACTTGCAT	33747	A_95_P272811	EB679048
34582	407	72	789	CTTGGATCTCATGAATGCATAGTAGAATACTGTTGTCTTTGCTTATGTTATCGCTATGT	33749	A_95_P231674	DV159157
34583	407	73	1557	TTTTATCAGTTTGCTAAAAGAAGCCCCTCTTCATTAACTTCTGCTTTCTTTTGGTGGTT	33751	A_95_P180777	TA12824_4097
34584	407	74	505	AATTGTAAATGTTGATTGTAGTCCAGATATGTTATTCCACCGTGGGGGTTTTCCCCTG	33753	A_95_P024546	BP530731
34586	407	76	474	ATTTGCCTAGTGTGTATCTCCCTGTCGCCAAATGAGAAAAGGAACTTGTTCTTTTGATT	33757	A_95_P041556	BP130120
34599	408	4	521	TTAGCATAGTTGAAGAACCTAGATTTTGCTTTTAAAATCTTGCTTGAGGCAGACATTG	33614	A_95_P123972	FG645200
34600	408	5	611	CAAGCAGCATGAGACATTTTTCTCTGTTAGAATTTGCTATTTCCCATTTTGCTCTAAAA	33616	A_95_P016436	EB429008
34602	408	7	326	CCTGGGAAAGGTTCTCTTTTACAACTTGTGGAACCCTACTTTAAAATGGATTCATGTAT	33620	A_95_P099498	BP534952
34603	408	8	369	GACTGAAAATTCCATTATGTGGTACTGCAAGTTCCTGACGTTGAACAACAACACAAA	33622	A_95_P099703	BP535033
34606	408	11	733	GAAGCTGAGGGCTGTAGTTTCAGTTTGTTTGCTTGAATTAAGTAGTATTAATTTCGTT	33628	A_95_P150592	EB680711
34609	408	14	708	GTGACCGTGTACGCCCGTGCTTGCATGTGTATATGTATTATTTATCAACTTAATTTTTA	33634	A_95_P296803	EB679782
34610	408	15	491	TTTAAGATGATGATGACGAAAATGAGTGAATGAGGGGGCTTTATAAGCATGCACCT	33636	A_95_P156102	EG650409
34616	408	21	841	AGTCATCAGATGTCTGATAAATATTGCTACTACTTAAACCAGATGGCTGCACAAATCT	33648	A_95_P254084	EB447452
34617	408	22	952	CGTTTTTGCTTTCACCTAAATGTATTTAGGAATTAGGTGCTTTTGATCATCATCTAGGT	33650	A_95_P221457	TA21823_4097
34619	408	24	802	TTGTCTCTGCACAAATAGAACGATCTTTTGTATTTCTACGGCACAAGATGATGTGATA	33654	A_95_P126147	EB425394
34626	408	31	797	CCTGTTCCAATAACTATACCAGCATCTGTTACGATGCATGATTTTGCTATTACTGAAA	33668	A_95_P009231	TA14042_4097
34627	408	32	280	GCTTCTAAGACAATCTGCAGTATTGTAATAGTACTTGTTTCTGTTGGTTGTGTTTAAT	33670	A_95_P176312	U91562

34628	408	33	827	AAGAGTGCGTTGAGGATTGCTTCCTTAGCAATCAATCCAAAGGACTTGAAATCTCAT	33672	A_95_P127847	EB427398
34640	408	45	623	TGGGGGAATTTTTGTTTGTAATGTATCTTCTTTAAGCTTTCTACGGTGCATGGTCCAG	33696	A_95_P017031	BP530168
34646	408	51	795	ATGGCAAGCAGATCAAGTCCATAAAATGAAAAGTTAGCCATGACTATACAACGTCTT	33708	A_95_P239629	FG172966
34647	408	52	563	CCAATGGTTTTGTGTTATGTTTCCGGTGGATTCCTTTTCCCCTGATTCTTTTAGCATTC	33710	A_95_P095938	BP533405
34652	408	57	741	CATTGATACATGGCTGTTGAGACATGGATCTTGTCATTGTGCAAACGGACTTGTTATT	33720	A_95_P161407	EH620156
34653	408	58	709	AAATATCGCCAAGTACTTTGGCAAGGGAGAGTTCTTAACTCCCAGTTCACAGATGAG	33722	A_95_P305318	FG151267
34661	408	66	358	ACGTACAAATCAATCTTTTCCCTCTCAGCGAGGTTAACAACCGAAGCAGGAAATGGT	33738	A_95_P080175	BP527942
34664	408	69	846	ATGAGCTTGAAGGAAAGTTTGCAATGCTGGAGACCTCTTCCGTTGATGATGATCTTG	33744	A_95_P268301	DW000560
34665	408	70	853	GGTGATTGAAGGCAAAACTCCCGAAGAAATACGTGAAACTTTCCATTTGCCTGATGA	33746	A_95_P119782	DV999342
34671	408	76	1050	CAGTTGCCTGCAATACAGCAGTTGTATATGGTGTTTCATTGCATCATTAGTAAGTAAT	33758	A_95_P178702	TA12323_4097
34672	408	77	600	TCTAGCTGAGTCTGTCGAGTCTTTTGTCATCGTACTTCCCATTTGTATTTGAAAACCAA	33760	A_95_P214682	TA20315_4097
34673	408	78	801	GGCTATCCTGGAACACCTCCAGTTGTTAGACCGATGGGTATTGGCTTAAAGGATAAT	33762	A_95_P150022	EB680067
34674	408	79	911	CTTCCTCCTATCCCCTGTCTGGGCTAGAAATACATGAGCAGTCAAAAAGTAATACATG	33764	A_95_P272741	EB677789
34678	408	83	748	TAATTCGGATAGGCCTTAGTTCTTTCTTGGCCAGTATATGGAAATCATGTGTTTTGCC	33772	A_95_P028201	TA12622_4097
34687	409	7	428	GTTTCTTAGAGGATGCACTTGAGGAGGAAGAGGATACAGATTACTATGACTCTCGA	33789	A_95_P122542	DW002519
34690	409	10	407	TGTATTCTTTTCTCATTGAAAGGACACTGTAGATTCAATTGTGACCGATATGCTAGAA	33795	A_95_P281898	AM802407
34693	409	13	1851	CAGCAGTCAGATCAATTCTTTGGTTTTCTAACTCATTATGTATTGAGGTCACTTTTGTC	33801	A_95_P033379	AJ577852
34700	409	20	425	TTGGTGAATATGACAGCAGCAGTTGTATCTTCGAATAATGAAATATAGATCCCGGTC	33815	A_95_P130187	EB430226
34702	409	22	554	CTCCTGGTAATCAAGGAAACTCCAGTTTATGTTGAAGATACAACAGAAAGTAGAATC	33818	A_95_P051766	BP132737
34703	409	23	511	TGATAGGTTTTCCGTTCGAGCTTCGATGGTGGTTTGGCCTTTATATCTAGGCTTTCGA	33820	A_95_P048031	BP131803
34704	409	24	791	GGGGTTAAGACGAGCTTGTGATGAATAAGTGAAATAGATTATAGCCATACTTGTACA	33822	A_95_P296503	EB677464
34705	409	25	706	AACATCCTCTGGGTTAACCCTGATTGTGGCCTCAAGACGCGCAAGTATACTGAAGTT	33824	A_95_P199347	TA16975_4097
34711	409	31	786	ATTAAGAACATGGATCTTGAGATCAGACGCCGAGAATCAACAGGTTCTGGGGCAAA	33835	A_95_P217957	TA21062_4097
34714	409	34	738	TGGGAGGTTCATGGTTACTAAGCAAGCGCTAACCAGCTCAGAGGCTATCTTTTCTAT	33841	A_95_P149632	EB679531
34715	409	35	856	CTATGGACCTATGGGAGATATATAAACTATCTTTGAAGTAAATAAGCATGTAACCAG	33843	A_95_P008566	DV157490
34717	409	37	378	AGAAGATGACAACTGGAGTTCCACATTAAAAGGAGTCACGATTTATAACAGGTACG	33846	A_95_P068485	BP137140
34719	409	39	854	TCAATGTCTGTTGATGCAGTTGACGCTAGCACCTGTGATGTGAAAAGTAAGAGTGA	33850	A_95_P118882	DV161964
34720	409	40	721	TAGACATGATCTATGCAAGAAGAAAGGAGCGTGAATATTTTGCTACCAGTCCGGACT	33852	A_95_P150817	EB680938
34721	409	41	904	GACTGGATATAGGATATTTCGATGACTCTTCGTATCACTGCTGAAATGGTTTGATATA	33854	A_95_P009346	TC40810
34725	409	45	402	TCTGGATCTGTTGCTACCCCAGCCAAATCTGTGGTGTCCAAAATTGTGGACTTAATGT	33861	A_95_P027191	BP531259
34727	409	47	438	TGACTTTTATAGAGAGGTCTGACTGTACTAACATATTTGTGGAATCAATGCCCTTAAC	33865	A_95_P098483	BP534494
34732	409	52	758	AACTATGAAGCCAGTGGAATGTATGACTGGGTTGACAGGAAATCCTGTTCATACCGT	33875	A_95_P138352	EB442107
34734	409	54	879	GAGTGACGGGTCTCTTTGCTGTGACCAAAAATTTTCATACATTCTTGTACATATTATA	33878	A_95_P190547	EB425754
34741	409	61	588	GCATGTTTTGTGTTAGTTTCGTCTGTTAAGATGTACAATTGTCTGAAACTCATGATGT	33892	A_95_P186437	TA14128_4097

34742	409	62	720	CTGCTACGTGATCTCTCATATATGTGAAGCAGTCCAAAGCTTTAAAACTTGAGTATTT	33894	A_95_P000471	EH619487
34744	409	64	443	TGCCCCGCATGATTGTTGTTACGACAACACATTGGCTAAAGAAAGAATCTGTTTTTAA	33898	A_95_P025541	TA13897_4097
34753	409	73	752	AGAAATTTCAATCCTAAAAGGGTTTTAAGGGGGGCCTTGGGACAATTTGGGTTTAAC	33914	A_95_P099958	BP535146
34754	409	74	403	TACGAGGAATTTACGGCGTTATGATGGTTAATTCCAGATTGAGGGATGGAACATGCC	33916	A_95_P060055	BP134901
34756	409	76	612	CTTGTAATGACAATACTCAGTAGGTAAGCTGTACAAATCTTGGGTTGTGTATTATCAT	33920	A_95_P236914	BP128992
34757	409	77	688	GCTTCCTTAGGTTTTTTGCATTATCTGGTTTTAGCCCTTTTATTTTGAGACTAGTTCAG	33922	A_95_P101013	DV160879
34759	409	79	773	GTAGATATTCTGGAATCTCACTTTAAGGATCTTCTTAAATATTGGAACTCTGATCCTC	33926	A_95_P117532	DV160450
34760	409	80	385	GGTGGAATGAAGCTGTACATTGCACAAGGGGAATTAATCTTTCTGCTACTACCTCTTT	33928	A_95_P132702	EB433334
34761	409	81	367	TTTCGCGGCTGAGGAATTGGCTCCTAGCGGATCCTAATAATAGAGAATTTTGAATAA	33930	A_95_P161142	EH619888
34762	409	82	679	GTAGTTTGGATTTGCTTTTTCTCGATGAAGTGCTAAAGCAATGCTTTTTGCGTTTTGCT	33932	A_95_P182602	TA13257_4097
34765	409	85	710	GTTCGTCGAGGTTCGAAAGTTCCTGTTCTTCGCCCTTTGTTTCATTTCATGTATTTCTT	33938	A_95_P207992	TA18868_4097
34768	410	3	779	AGCTCTTTAAAACCAGCCTCCCCACTGTTGAGACAGAGGAGTCAAAATTTGTACAGG	33782	A_95_P141402	EB445134
34775	410	10	435	GACCTCAGATTTTCTGGACACTATTTAATTTTCAGCCATAGTCATATATCTCAGTCCAC	33796	A_95_P202352	TA17615_4097
34776	410	11	445	CGTAGATTACTGGATGGTCTTAGAATTTGTGGTTACATCAATGGTAATGCATTGCTTT	33798	A_95_P012881	GO944065
34777	410	12	76	CCAAGTTGCTGACTCTGAGTTAACTGATAAAGTGGAAAAGAAAGATAAAATAGAGT	33800	A_95_P130362	EB430388
34782	410	17	139	GATTGTACCTCTGGTTTATATCTGTTTTGATTTTTGCCATCAGTTTTCATGCAACCTCA	33810	A_95_P109847	CV019475
34785	410	20	366	TTGAGAAGCTGTCTATTATTAACTGAAACCCGTGTTTGTTTGCTGGTCCTGCTTATCTT	33816	A_95_P107192	CV018252
34789	410	24	856	TCTTGATGCAGCATATTGATGATTAATCATAGTATCCGTCTCCTCAAAGTCCACGCAA	33823	A_95_P125652	EB424738
34794	410	29	486	TCACCAACACCCTTGTACCTCAAATCTTGTATACAAATAGGATAAGTTGTAACGAGGT	33832	A_95_P213792	TA20124_4097
34798	410	33	116	GGGAAATAGTTTCCTTAATGTACCCTTTGTCTACTTCTTAGTACTAAAGAACCCTTTAT	33840	A_95_P100743	BP535504
34799	410	34	352	CCACCTAAGATATATGGAGATTATCCTGAACCTATTCTCTTTTAAGCTGACTTTCTTGA	33842	A_95_P189317	TA14763_4097
34800	410	35	409	CAGTGGCACTTCCTGATTGTAATACCCAGATGCAGCAGTTTGCTATAAGATCTATCTC	33844	A_95_P075045	BP526624
34801	410	36	839	CCTTTATTATCACAGAGCCTATGTTTGGGCAAGAATGGATTTTGAAATCACTGTATTC	33845	A_95_P001126	DV158629
34802	410	37	849	ATAACGACGCTGCTTTGTAGTCTTGCTAGATTTCCTGGAATATATTTTTCTTCGCAAG	33847	A_95_P186687	TA14179_4097
34803	410	38	658	TGCCCTTGTGAATGTATAAACACATACCATATATAAAAGCGGGAATAGCGCAGAAAG	33849	A_95_P203287	TA17822_4097
34804	410	39	867	GTCCTGTCAGATAGAAAGAAAATTAGACCCCAAAGAGCCCTTCTTTACTTTACTACTT	33851	A_95_P214792	TA20338_4097
34805	410	40	839	CTGGGGTCAAAATTAGTCAGATAAGCTAAAGATTGATGTACCATCTACTATGTACTGT	33853	A_95_P231264	TA18923_4097
34808	410	43	1276	CTGGATATGTTCTCTCTTGTTTTGTTTTGCTATCAGTGTATAATTATATGTTGGACCCT	33859	A_95_P010946	TA13063_4097
34811	410	46	336	TCGCTGTAACAGCTGATTAAAGGCAGAGTTACTGAAAATAAATGCTCGAACGCAATA	33864	A_95_P161612	EH620282
34812	410	47	543	TTGCAGATGAGTATGGGATTAAGTTTTTTGAAACTAGTGCAAAGACAAATCTTAACG	33866	A_95_P248317	DV999323
34815	410	50	551	GCATTTGTCGTGTTTAGCTGTGGTTAAAGATGTAATTTTTCTTTTGGTCTATCGACGAT	33872	A_95_P213312	BP534527
34816	410	51	869	CTCATTTGTAATGTGAAAACACTAGTACAATATTGGCTTTTGTATCCTAGTGGAGCTA	33874	A_95_P009656	TC41004
34821	410	56	465	AACCCTGGCATCAACTATGAGTTAAATTGTTCTTCAGTAGATTGTTCAGTATTGAGTT	33883	A_95_P140122	EB444081
34825	410	60	656	AACCTGTGGCCAATACTCATTGTGCAGTAGCATGAAAGCACTCCAGGATCAAATCAC	33891	A_95_P161462	EH620204

34831	410	66	796	GCACTCAGATTTGACACTTCTTAATTGAGGATGAGTTGCTTTATCATCCAATAGTTTA	33902	A_95_P031716	EB430603
34835	410	70	785	GTGCTTGCCTGGCGTTCCTGATGTATGGAACGAGCTGCTATTTCAATTTTTGTGAAAA	33909	A_95_P216172	TA20647_4097
34837	410	72	723	CAAAGGAAGCAGAATTGTTGAAGGGAAACCCTCTATTAAACCAGCCAACATCTTTCA	33913	A_95_P115857	DV158249
34838	410	73	753	ATTGCTGTTGTTAAAAGAAGAATTACTTAACAGGTGGATTTCCTTTCCCCCACTCTTTA	33915	A_95_P192652	EB429570
34845	410	80	855	AACTTGTGGATGGGGGAGAATCACAAGACGTCATTTTATAAAGATGCTATGAGCTGT	33929	A_95_P226169	FG164977
34848	410	83	243	AGGACTAAGACACAGGCATGGCGTTACCCAAGATGCTTAAAGTGTGTATCACCAATC	33935	A_95_P091408	BP531341
34850	410	85	642	GTGCAACAGATGCTTTTCAGTGTCAAATGGAATATGAGTGCTATGCAGTTAAACATT	33939	A_95_P293253	FG641774
34851	411	1	340	AATCAATGAAACCCCTTGTTTCTACCTACGGTGTTTTCAATCTATACTCTGTTTTACAT	33940	A_95_P089853	BP530686
34852	411	2	285	TGTGGTGCTCAAACGAGTTTGAATGTTAAGACTTCTATTAATCGATAAAGGGCCTGA	33942	A_95_P096788	BP533762
34856	411	6	1359	GCAGTGGTAGAATTAGAGTTTATGGTTTGATTTGATGTGAAGATACTTCCACTTATTG	33950	A_95_P194042	TA15807_4097
34857	411	7	562	AACAGAGGCTCTGAAAGTGATAACTGATGTCAGAAAATCACCCAGTTCTCATCCACT	33952	A_95_P160407	FG642013
34858	411	8	793	CTAACAACTTGGGCAAGATGGGTTGATCAAAATGTTGATTCTTCCAAAACCAAAGTT	33954	A_95_P126712	EB426048
34861	411	11	845	ATATTCAGAATATCAAGCGTCTGGAGCTTGCATCTTGAGCCAGCAGTGATGTCGTTC	33960	A_95_P258566	DV999762
34863	411	13	836	GATGTGAGTTCAGAAAGAAAGAAATGTCTGTAAATTGAGAGGATCCCAATTTTTCCC	33963	A_95_P217462	TA20937_4097
34865	411	15	911	ATGGAACTGAGGTAGTGCAATTAAGGCGGAAATATGGTAACTGGAATGTAAATGAT	33967	A_95_P231739	DV161448
34866	411	16	396	AGCGAAATTTTTGCCTTGCAATATGCATTCGCTACCAGTTTTTGAAGAAGCGATGTTA	33969	A_95_P309073	FG644639
34868	411	18	92	CCCCTGGGAAGTCCTCGTGTTGCATCCTTTATGTCTTATATAATATTATAAATAGTAAT	33973	A_95_P202282	TA17601_4097
34869	411	19	764	TCGAGAATATGGACCTGAAGCTGATATTTGGAGTGCTGGGAGTATCCTGTACATTCT	33975	A_95_P285493	FJ026805
34870	411	20	827	GTGTTCCTTTCGTACTGTGCACTTATTTCAAGTGCGATGTTTGTTTTGATTGTCATTTA	33977	A_95_P217927	EB438730
34872	411	22	603	ACAGAAAGTTTGAGTTAGCTTTAATGTGTAGTTCACATGTAACTTTAGGAGTGAGAC	33981	A_95_P025586	FG635985
34876	411	26	781	CAAATACTTAATCCAGAAACTGCCATTTTAACTTGTAAGGAAGGGAAAGGATTTCAA	33989	A_95_P267081	DV158186
34881	411	31	739	TTGGATCCATTCTTAATAGCAGCAGGGGAGCGTACTGAGGTTGATGATCGTTTCTTG	33999	A_95_P147122	EB451368
34884	411	34	797	TATTGGTTAGCCGATTTGCCTCAGAGGGTCCAAATGGTGGTGCTGTAACCTTTAAAT	34004	A_95_P295298	EB445287
34885	411	35	117	TGTAAAGGAAACTCCACCTCCCCCTCTAAATAATCCAAGATAATCGCATGCTGTGCAT	34006	A_95_P052506	BP132941
34892	411	42	380	TGGGATAGTGTACTTGATTATGAGAATGTTGTGTTGTATATGTCGAGCGACATTTTA	34020	A_95_P092898	BP532038
34897	411	47	834	AGCTATTTACTATGGAGCAGCATGCATTGAAGCTGCAAGGAGGATCTCATGCACTGA	34030	A_95_P248132	FG174240
34899	411	49	609	TGATGATCTTGGTCTAAAGGTAAAGCAGCTATATAATGCTGTTGTCAGAACTATGGT	34034	A_95_P195017	TA16027_4097
34903	411	53	297	TGGGCAGTTCATGACTTTTTCTCCATGAGGGAGAATTAGATTTAATGAATTCACATTT	34042	A_95_P094268	BP532632
34908	411	58	831	AGAGAAACCTAGTTGTTGAGCTATAGGCATCTGCTATAGGGTCTCTGTAAGAAGGC	34051	A_95_P119397	DV162575
34914	411	64	360	GGTTAAGCAAGCTTGCAAAGCAAATACATGCTTTCTATGGCTTCAGAGTCTGTCATC	34063	A_95_P114817	CV021769
34926	411	76	1194	CGGAGTTATGCGTAGATTCGATTTTGTAATCCATTACAAATGTTTTCTTATGTTACAC	34086	A_95_P195957	TA16232_4097
34927	411	77	823	TGCACTGGTCGTCCCTGTTTTGTGTATTTGGTTTGGCCATTTGTTGCTGTAATTTTATT	34088	A_95_P223952	EB448995
34931	411	81	371	GTTTAGTGTAAGGACATTACGAGTTGCTTGAATCGAGTCTTAAAATCTTAAGCTGTTT	34095	A_95_P207007	FG640440
34933	411	83	643	GGAGAAAAGAAGAGCTTCTGAAGTTGTACTCCCCTTTATCTCTCCTCCATCACCTACA	34099	A_95_P295823	EB448367

34935	411	85	442	GGTTGTCTCGAATTATGATAGAATAATATTGAGTATTGGTACAGTGTGTGTGAAGTA	34103	A_95_P147842	EB643469
34939	412	4	394	AGAGCACCAAAAGGGTAAAATGCGGTTTGGTTTGATTTCTGCCTGTGGCTACTTACT	33947	A_95_P074980	BP526609
34942	412	7	763	GAGAGAAACACACAATCTATTCAAGGCATCATACAAATGCTGCAGTGGTTAATTTTT	33953	A_95_P267981	FG638814
34945	412	10	474	AGTTAAGAAGCCTCTGATCCCCTTTGGACGTGGCATTACTGACCTTAAAACCATTGTT	33959	A_95_P260341	BP128500
34948	412	13	482	AGGAATCTAGTCTAGAGGAAAGAGAGCACGCTGAGAAATTGATGGAATTCCAGAAC	33964	A_95_P003381	AY083924
34950	412	15	831	TCTACAGTTGGATTAGTTTTCTTTTGAACTTGAGTTACAAAGGGTGTCCGAGTCGGTT	33968	A_95_P257896	EB425483
34955	412	20	580	TGAGTATTGAACCTTTTTTGCTATTAGCTTGAAGAAGCTTTCGCAATCATGGTTTTCT	33978	A_95_P222237	TA21989_4097
34957	412	22	806	GGTAGAGTTTAACAAATCATATCTGAATGACCAGATAATAGCAGTTGAAGGGTTGA	33982	A_95_P216937	EB426706
34959	412	24	839	GAAGGAGAATGACATTGATTACAGCTACTCAGAAGTGTCAAAGTTTGCTACTTTCCG	33986	A_95_P252509	EB445917
34961	412	26	355	AGCCTGAGAAGAGCTCCAAAAAGGTGTTGGTGAAAGTGCCTTGCAATGAACAATAA	33990	A_95_P157697	EB451576
34962	412	27	313	ATTGGACCAGAATTTGGCTAAGAATTTTGGCCGGTTAACGTAATTGGGGAACCCAG	33992	A_95_P107802	CV018537
34963	412	28	535	CCCGGCTTTATTTCCCTGTAACAATGGAATCGTATTATGGAACACTTTGAGTATTGTT	33994	A_95_P292693	TC56980
34968	412	33	0	TTAATAGCCCATGGTTATCCAGTTTCAGATTATGCCCAGCTTGTCTGATTAGTGCTCA	34003	A_95_P311143	A_95_P311143
34970	412	35	322	GGGGTGCAAACGGCCATGTGTAAAGTACAGATGTATTACGATTTAGTAGTGTATTAT	34007	A_95_P163212	EH622198
34973	412	38	771	AGTTGAGGTGTTAAAATGGAAAATGTGTAAGTTTGTTTACCGAGTTGGCAAACTGGT	34013	A_95_P145272	EB448879
34977	412	42	792	GGACTGCTAACACTGAAAGATACAGTAATGTGTTGTTGGACTTTAATGACATTATTG	34021	A_95_P163832	EH622877
34982	412	47	943	GGTTTTGTTACGCAGACCTTTATCACAGCAGAGTTTACAAATTCTCATAATCGATTTT	34031	A_95_P014121	TA13331_4097
34983	412	48	321	GCCCTTTTGGCTCCTACATTTTGTTTGTCTCTTGCAATAAGTAGACATTGTAATTTTAG	34033	A_95_P083860	BP528874
34989	412	54	407	GGAAGAAGAGGGTAGAGTAGAATTGTTGTATGCTTTATTTCCTACGAGCTTGAACTA	34045	A_95_P001956	BP132869
34990	412	55	1014	CAGAACTGAGCTTGTATTATGTCCTGATAAATGACATGGATTCTTTGAGATGTTCCTT	34046	A_95_P193642	TA15715_4097
34993	412	58	744	TGGTATATAATGGCACGTGAGTTGTCCGTGCAGTATGTGATAAAGATCTATCCTCTT	34052	A_95_P215337	EH617089
35001	412	66	361	GAGTGTTAGCTAGCGCTAACACCAGCATTATATCAATTTGGTTAATTCTTGTGTATGT	34068	A_95_P006701	TA19034_4097
35007	412	72	707	AAGCTCCCTAAACACCCTACATTGGAGAAAACATTTCTTTGTAGTATTACACTGTTAT	34079	A_95_P005141	DW004395
35009	412	74	441	ACACCCCTGTCAGGCAAGCCAACAATAAATACTTAATTAGGTTCTCATTTTGTTACTT	34083	A_95_P307333	FG638242
35010	412	75	1640	AGCAAGATGTGAAACTTGGGAATTCCCCTATTAGTTTTCATCTTGTCAATGTTGACAT	34085	A_95_P205422	TA18285_4097
35014	412	79	420	CTTTAATATCTATGTTCTGGTGGTGTTGCTGATGTTGATTATCGGAGCGGCCGCTCAA	34093	A_95_P276833	AM831626
35020	412	85	767	TTGCAAGTTTGATCACCCAATGACGGTATTCACTTATAGCATCTCAGCATCATCCTCC	34104	A_95_P196437	TA16338_4097
35024	413	4	2193	TTTGAGATATTCTTGGATATTGTTCTCTACTGATTGAATAAACTGGTCCCAGTATTTG	34110	A_95_P023156	TA14847_4097
35026	413	6	614	GCAGCTGTTCTTGATTAGTATGTACAACTTCACAGTAATCATACAAAAGAAGAGGAG	34114	A_95_P031541	EB445400
35027	413	7	2267	GTGAGATATGTAGATAGTTGAGATAACACCTTTTGTACAGCAGTTCGTTACACTAAT	34116	A_95_P192237	TA15408_4097
35029	413	9	1186	ATGACTGTAGTTACAATGACATTCGCTGTCCTCGGATTCTTATCCCCTTCAAATCGGG	34120	A_95_P025491	TA17818_4097
35030	413	10	631	TTCAGTAAATTTACAATCAGAGGAAACATTCGGGATGCCAATTGAGGACACAGTACC	34122	A_95_P062070	BP135419
35040	413	20	872	AGGGGAAAGAATTGGTCATGACTATTGGCTAGCTAATAACAGTACTATTGGTAACA	34142	A_95_P206267	EB424670
35041	413	21	178	ATGTATGTATGGTTGCAGCTTTTCTATATTGTTTTCAGGTGAAATCCTTTTGCACAAC	34144	A_95_P145687	EB449432

35042	413	22	354	AATGTCAGCTAAATTCAGGATCAGGAGTGGCATTCCTCCAGAACAGCAAGGTTGATC	34146	A_95_P170756	EH664976
35043	413	23	310	CATTATTGCTCCACGGTAGAATATGTTTACATTGGTATGCCGGTACACAATTGTATCT	34148	A_95_P058011	BP134362
35047	413	27	1005	TTACTACCAACGAACTAACTGGGTATCGAGGAAGCAAAGAAACAATTTTGTCAAATG	34156	A_95_P015121	TA14613_4097
35049	413	29	825	CCCACACCATCACCACCAAGAAACAATGATGGATGTCAGCATGCTCATTTGAGATCAT	34160	A_95_P303938	FG153238
35050	413	30	706	GAGACTTTACGGGAGGGAAAGAATTCAAGGTTACGAAGTGCCTTTTATTTTATTTAA	34162	A_95_P213912	TA20149_4097
35052	413	32	323	GCTATAATCGAAACCTTTAATAAGGTTGTTTACTATCCTGTCGCTCTAGGTTGTGTTA	34166	A_95_P095678	FS436463
35053	413	33	842	GTGCCTTATTGTGTATAGTGTGTGAAATTGAAGTGCAAACTTCATCTCTTGTTTATAT	34167	A_95_P015691	EB439026
35056	413	36	616	AGCAAAGACAACGATAATCACGGCATCAGGATTATTGGAACAGTTTTAACATTAGTT	34173	A_95_P025256	TA17895_4097
35060	413	40	1332	ATATAGATCTGGACTTGTGCTAATGGAGCTAATACGATTGGTTTGGACTTACAATAG	34181	A_95_P026301	TA15688_4097
35062	413	42	214	CATGCTAAATTTTGTTGGCATGTTTAGTAAGTTTTGTTTTCATGATCTTTCGGTGGTGC	34185	A_95_P029811	DW000198
35065	413	45	895	TTTTCAGCCTGATAAAAACTCCCTTATAGTCACCATTGGAGATCTCTTACAGACATGG	34191	A_95_P135267	EB438588
35066	413	46	370	CGAGAAACCGAGAAAATTTCATAAGCCTTTGAAATCCTTTCTCTTGGGTTCCACTAAA	34193	A_95_P095423	BP533190
35068	413	48	812	TTTATTCTAGTGGTGAGCTGGACAGAGTGCAGTTGTATTGTGAGAGCTTTTCCACCA	34197	A_95_P251472	EB678121
35071	413	51	716	GTAGGCAGCTCGCATCCAGCTTTCTTCGTCTTCAATTCATATATATTAGTATTAATTTA	34203	A_95_P209612	TA19228_4097
35072	413	52	699	TAGGATATTTTGAATGTGTTTTTACCTCTAGCTTTGTCAATGCTATTGGCAAATTGGTC	34205	A_95_P268766	DW002962
35086	413	66	829	CCTAAGTGTTGCAGCAGTTGTGATAGATTGTTTGCAATTGCAGAAGAATGATTACTA	34233	A_95_P267046	DV157983
35089	413	69	0	GCGGAGTCATGTATCTCCTTTTTATTGCAGTTCATGCGAAGATAAAGAATACAATAA	34239	A_95_P008766	A_95_P008766
35090	413	70	287	GGATCAGATAATGTTGCTCTTGTACTGGATCTATAAGGTGAAAGATTGATGTAATTT	34241	A_95_P041106	BP130008
35092	413	72	273	CTAGGGTTCTGGAGGTGATTCTTCTCATGTTTCCATTTTTCGTTAAAAATAGAGTAAT	34245	A_95_P156337	EH613699
35096	413	76	789	TTTGGGGGCGGGATGTTGATGACATAATTTGATGGTTATATAGAATTTTGATCTGTC	34253	A_95_P267436	DV160203
35104	413	84	353	CTGCGGTTCTTCTAATTTTCTTGATTGTTCTATTAGCATTCCATATTTGAGTGATGAGC	34269	A_95_P077605	BP527294
35115	414	10	791	TTTCAAAGATGTTGCCCGTGTGGACTCTGTTTCTGCTTAAGATTTTAGATGACCATGT	34123	A_95_P117897	DV160864
35116	414	11	837	GCCCTCACCAGTGGAACTTCCAGAATAGAAAAGATTTAATTTGTGCAAACCAAGGTG	34125	A_95_P196297	DV159106
35120	414	15	329	CAAATGGACTTGAGCATATTGTTGAAGTGATTGAGGGGTCAATGGAAGATATTACTC	34133	A_95_P085755	FG134245
35122	414	17	489	TCCTGACACTCCTTAAGTTTCTCTCCTGCACGTGTCTCCTGGCACAAAAAAGAAAAATT	34137	A_95_P035973	BP128611
35124	414	19	789	ACTGATCTCTCAAATCATATCATCCTTGACCACCTTCATTACGGTTTGAATGGGAGCC	34141	A_95_P162452	EH621397
35132	414	27	2084	AATAGATAGCAGGGCATATTTGCAGCTCCAAACTGGGTTTCGTTGAATATATTTACTC	34157	A_95_P011311	X83524
35138	414	33	1419	CCTTGTTGAACTAGAACCTACATCATGTTATCCTTTTGATGGTTTTGCGGAGTTATTA	34168	A_95_P012552	TA13054_4097
35139	414	34	1009	GTGGGCAGCAAGTTGGCTATATCATGCAACTGGAGATCAATCATATTATGATTATGC	34170	A_95_P201147	TA17362_4097
35141	414	36	583	GAGACTACTAGTTCTTCTCGGCATCAGTTGCAAATTTGCATTTTAGTTCCAAATTTTGT	34174	A_95_P034324	TA13389_4097
35143	414	38	818	GTGGATCGCACTGTCCCTGGAAGATTGAAAATAACTCTGTCTTTTTGGTGGCTGGTA	34178	A_95_P205967	EB439676
35145	414	40	711	AATTCCCAAGTTTGTTATGGATGAATGCTATGACATGGAGCTCTATGAATGGAAGGA	34182	A_95_P257876	TA12452_4097
35149	414	44	655	ACGGCTATCCAACTGGTTTTCAGTCTAGGTTTAAGAGGAGTGCAGCTTTTGCTCCAGT	34190	A_95_P284343	FG190019
35151	414	46	694	ATGTTCTTGCTCTCGTGCGATCCTCTCATGGACAGATAAGTTTGTTCAGTGAGTGTTT	34194	A_95_P164922	EH624378

35152	414	47	845	TTTGGTGCTGCTGCTTCTATGTTGTTGGGTTTTGGTGCCTGGTATTGGTATTTCACCA	34196	A_95_P150122 EB680202
35157	414	52	372	AGGTTACATACTATAGATAAATCAGCTCTATCAAGCTTTGATAAGCAGCATTTTGGCA	34206	A_95_P124812 DW004608
35159	414	54	417	ATGAAACACTTAGATTCTGGAATGTTTTCCCTTCTCCTAAATCTAAGAACACCGAGAC	34210	A_95_P059740 BP134816
35161	414	56	851	AAGGGCCAAGGATGGAGGTAAGAAGTTGATGGATTTGGGACTACAATTTATTGACA	34214	A_95_P231554 DV159738
35163	414	58	675	GCAGGTGATTTTTCATTGAGTTTGATACCTGACTGGATATTTTAATGGGTTATATCTG	34218	A_95_P205342 TA18263_4097
35170	414	65	2517	GATTGGCATCCTTGTATTTACCTTTCGGGGATCACATTTATGTTAATCTTTTATTCCTG	34232	A_95_P177082 TA11872_4097
35171	414	66	442	TTACTGCCGTATTTATGTTAATGCACTTTCTAATGATACGTAAACAAGGTATTTCTGG	34234	A_95_P211867 ES659053
35176	414	71	518	CTTGGTTGGATGCTGGACCTCTCAATATTCGTTCAAAATTGCCCCTGGCTTTTATGTT	34244	A_95_P049106 BP132084
35177	414	72	838	CAGGAAGTTTTAGTTATGTCCTAGTTTATGTTAGCTGGTCTGTATAGCAGCTTTTTGA	34246	A_95_P289868 EB451794
35180	414	75	783	TTCAAGCTCCCTAAAGTGGTGGACAAGGATACTACAATGAGTTAACTTTGATCCTTG	34252	A_95_P135872 EB439421
35182	414	77	630	GGAGATGTGATTTCAATGCCTGCCTTGCAACATAGTGGAAGTTCTTCAAAACCATTA	34256	A_95_P047651 BP131711
35190	414	85	823	TTGGATACCGAAATCATTGTTGCTGCTGCAAGGGACACAAATACAAATGCAACCGCT	34272	A_95_P027016 EB437209
35194	415	4	877	GCTAGACAATAATCCCCTCAGACAGATACCATCCTCTGCATTTCAAGTTGTATCCAAG	34279	A_95_P260521 EB428364
35198	415	8	902	TTGGAGTAAAGCTCGCTCAATTAATGCACAGTTGAGAGTAAAGAATGTTGGGATGC	34287	A_95_P115517 DV157766
35201	415	11	86	GCTTGAGGGTTACTTCTGTGTGATGTTTAAGTTCATTTCTACTGATATGTTCACATAT	34293	A_95_P003726 EB434979
35202	415	12	670	AAACAAAAATTTGACAGGAACTGCTAGATACGCAAGCATGAATACTCATCTTGGCAT	34295	A_95_P137352 EB428048
35207	415	17	1260	AATCTGTCTGCATAGATGGGTATTTTAAACAAGATGTACCAAGACAAATCGATTGCG	34305	A_95_P201527 TA17444_4097
35208	415	18	503	ACATAACAAGAAGCCCGAGATCGAGTGTTGAGGAGAGTAAAGAATCGATAACCTAT	34307	A_95_P124392 DW004227
35210	415	20	530	CACAATTAGAAGAGAGTTGAGACAAGCTGCGAGACCAAGAATTATGTTGGGCATTA	34311	A_95_P010181 BP133122
35215	415	25	677	GAGTCCTTTAACAGCAATTTTGGAGTTGTCATACACAGTAATGATTTGTCAGATGAA	34321	A_95_P146852 EB451002
35217	415	27	469	AGTTCAGGGATCCTTCGAGGATGGTATTGGACCCGGAGGCAATATTATTCATGTCTT	34325	A_95_P031426 BP529158
35218	415	28	352	CTGTTAGCTGTTTGGAATGACAAAGCCTCCACAATCCCCATTTACACCAAAGGTCTAT	34327	A_95_P111627 EH617531
35219	415	29	796	TTGTTGCTAGAGAATGAAAGATTGGCGGGGTCTAAATGAAGGATTTTGTAGTTTTTG	34329	A_95_P124082 TA15549_4097
35222	415	32	541	TGCTTCTAGTATAACTAATGTCTTTCATGCTGCTTGTTTTTGCAACCATGGAGGACTTT	34335	A_95_P139737 EB443648
35224	415	34	841	GTCTCAGCTTGAAATTAATGAAGGATGGTTCCTTACAAATGAACAATGAGACTAGAT	34339	A_95_P267901 DV162604
35225	415	35	297	AATGGTTGCTAATGTATTAATGTAGGCTGAACCAAATCTTCAAACGTGAAGTTGTTG	34341	A_95_P080795 BP528099
35229	415	39	1247	ATGTGCTTTGTTTACTGAGGTCTCAAAGATGTTCTATTCTGTTTCTGTTCGCTGTTTCT	34349	A_95_P001736 AB032546
35230	415	40	785	TTGTAATCCAGTATCATTTTTTGTGTGGATGTCTTTTGAAGCGTTTTGCTTGGAGTTG	34351	A_95_P271421 EB443290
35234	415	44	676	CTCAACAATCCAAGAGAGAATATAATTGTTGACTAGAATGATATATAGGTTGCCCAA	34359	A_95_P183622 TA13500_4097
35235	415	45	842	TAATTCCTGAATGAGATATCTAATGAGTGCACGGAATTACTTCCCGAGCCCAGACTG	34361	A_95_P289213 DV158089
35236	415	46	1300	TGTCGAGACTCACCCATTGTCTAGTTTGGTTTGAATTTGGAGATGCACAAGAGAGAG	34363	A_95_P207152 TA18678_4097
35244	415	54	628	TAACACGAAGAGAATTATCCCACATGACCAAATATCCACTTTTTCTCCATCGTATCCTT	34378	A_95_P316723 FG192477
35247	415	57	595	AGGACGTTGTAGGAGTGGATGTTGTTATGCACGTAAGGGCTAAAAAAGATGACGG	34383	A_95_P137772 EB441552
35248	415	58	797	CCTTGGATGTCCATAGATAATGTGCCTCGTTAAAACCTTATTAGGAAAAAATCCTATG	34385	A_95_P120152 DV999904

35255	415	65	323	GTTAGTAGGGGTGTGTATGGATATCTTTTCCCTAAAAAGTAATCAAACCAAATAAGTT	34399	A_95_P214292	TA20231_4097
35261	415	71	837	TATGGAGGTTCTGTAAATGGAGCTAACTGCAAAGAGTTGGCAGCACAACCTGATGT	34411	A_95_P217862	EB426276
35263	415	73	475	TGTCACCTGGTGTAGTCTTAGAGTTTGTAACTGAATGGCAAATTGGAGAACTTGTTGA	34415	A_95_P257344	EH623258
35267	415	77	72	TAAAAGGCGACCTTGGATTGGACATCACCTTTTTGGAGTCCTTTTGGAGAAATGTGCT	34423	A_95_P116807	EB681743
35268	415	78	811	TTTTATTGGTTCGTGACCTTAGAAAACGAACCATGGCAGTTCTCTTCCTTGTATCAATT	34425	A_95_P126282	EB425543
35269	415	79	824	TCCATATAAGTTTCGGCTAGGCGACAAAGACATCATAGAGGGATGGAACCTTGGTCT	34427	A_95_P272661	EB680239
35271	415	81	882	AGATGTACCCGCTTATACTTGCTTCAGGAAAATCAAACGTCTGTAGCTTCACCATAGA	34431	A_95_P271396	EB443151
35273	415	83	795	CATAGGAAAATACATGTAGATCCTTCTTTTTTGCTCTTCCCTTGTTAATATTAGTCCTC	34435	A_95_P149832	EB679803
35277	416	2	428	CGAGTGAGATTGTATATGCAATCATCATTTACCAGATTAGATGGTTAGGCTTCTCGTT	34276	A_95_P072945	BP526087
35278	416	3	540	AATTAAAGATGTAAAATGTCGATGGCCTATCGGAAACAGCTTCTCTACCCTTCTAGG	34278	A_95_P161147	TA15777_4097
35282	416	7	801	GTACACACAGGTTCAATGCATACTACGTGCTCAGAGTTCTAAATTTTTTGTCATATAGA	34286	A_95_P267536	DV160564
35283	416	8	334	GTTCATCTGTTTCATTCTAATTTTTTGCTTTACATTCCCTGAATGAATCAAGGTCTTGG	34288	A_95_P103312	CV016454
35284	416	9	806	TTTCAGTTGGCATGCGGTTCTTTTGTGCTTGTGTCATTCTACTGCAACTCTCACTGTTG	34290	A_95_P202842	EB426615
35287	416	12	879	GGACCCGGAAAATATATTACCAATAGATGGATCTGCACCGTCAGACCGATCATAACA	34296	A_95_P165392	EH663669
35292	416	17	631	CAACGTTTTAGCCTGGTAGTCGATATTGATGGATTGCATAGAGTTCTTTGTTTAATTT	34306	A_95_P020286	DW001539
35295	416	20	794	TCTCAATTCCTGCCATCCTGAAGTTGGCTGATACCCTTTCACTTGAAGTACAAGCTGT	34312	A_95_P185957	TA14025_4097
35297	416	22	721	TGTGAATGCTCTTAGGTGAAGGCAAAATGGTGCTTCACATGTCATAATTCTTTACACA	34316	A_95_P209072	EB681340
35301	416	26	629	ACTATGTCCAATAAGTTTGATGCTGCAACTCATCCGCAATATTCAGTTTTCCTTTGGCA	34324	A_95_P017701	EB436446
35302	416	27	1269	GTAGTTTTGGATTCTAGTTTAAGTTAAAGGATATGTGGTGTTTTGAGTGTGCTTCAAG	34326	A_95_P012956	TA14617_4097
35304	416	29	0	TCTTCTTCTTATGTTTCTTCCTTTAGAGAAAAAATAAACCAACTCCCCCCGGCCGTAAT	34330	A_95_P009041	A_95_P009041
35307	416	32	798	ATCTGTGTAAGTTATCTCCTTCTGACAGCCAATTCTATGTCATATTCTACAAAGCAGAA	34336	A_95_P021301	EB679795
35309	416	34	440	TATGGTATGTCTTTCACTGAGGCAGGTTAAAACAGAAGCTTTGGTTGAGTACAGGTCT	34340	A_95_P092933	BP532056
35310	416	35	378	TTCATCCTGAATTTGCTGCAGATCCTCGAAATGTACGACTTGGCCTAGCTAGTGACAG	34342	A_95_P097513	BP534081
35313	416	38	515	GTCAGCTTCTATTTTCTAGCACTTTGATAATACTATTGTATCAGTGTTGATCTTCTCAG	34348	A_95_P157672	FS433102
35319	416	44	602	GATGGCTGATGTTTCAGCCAATTTCGTTAAATCTTATAGCCACCTTTCCTGTGTTATGC	34360	A_95_P213522	EB443490
35321	416	46	873	TTAATTTCTAGTGATTGATGGTGTGGGAATGCCTGTAATGGTAGCGAGGCGTGTGTG	34364	A_95_P200802	EB449689
35325	416	50	829	TTGGCCAGGCTTTTAACACTTTGCAACAACTTCCTGTCCCCATTAAAGATGCTGTTTCC	34371	A_95_P235354	EB681365
35327	416	52	701	TAAAAAGGCAAAATTTGCAACACCTCAAAAGGCTGATGGTGAGAAAGGTGCTGTCCA	34375	A_95_P269041	EB428281
35328	416	53	608	TGGACAAGATTATCAGTACTATTAACTTACATCCAATAGAGGTTGCTGTTTGACTATCT	34377	A_95_P179477	TA12516_4097
35331	416	56	844	TTAGTATGCAATGTATATGTGAATGAGCTTGCTGTAACTTAAGCGTGATACCTATCTC	34382	A_95_P270721	EB443132
35335	416	60	824	GAGCTAGAATTGAAGACGTACATGTGTTCCAGTTGTAGCTGCATCTTATTCATGGTA	34390	A_95_P120112	DV999849
35336	416	61	506	TCCCCTGAGAAGCTGTCGTAGATTTACTTAGTTCAAAATATAGGATCTATGTCCAAGT	34392	A_95_P269116	DW004091
35344	416	69	1054	GATTTATCTACCATGATACGTCGTCAAAGGCAGGCAATTGATGAAAAGATAAGGGA	34408	A_95_P219347	TA21376_4097
35349	416	74	544	ATGTGTGAAATCAACACTTAATGTACTCGATAAGGTTCGTGCTTCACATTATTGTTTCT	34418	A_95_P024916	TA20830_4097

35350	416	75	420	ACTTGAGTTGATTAATAAAAGAAAACTGATTAGGCGCAGCTTTATCTGTTGGGTCAT	34420	A_95_P097178	BP533913
35351	416	76	652	GCTGGTGGAAGAAGATTTATTTTTTGGGTTACTATTAGAATAGAACTTAAGGACCTT	34422	A_95_P257861	DV158996
35360	416	85	818	TCCTTTCGCACATCCATTATTTGGTGTACGCTAGATAGTCCTTCTCTGGTTGTATTTTTT	34440	A_95_P025081	DV159714
35373	417	13	859	GATGCTAATTTGATTTTCTGCTGATCTTCATTCTTTTTGGGAGCATAGTAGGTATAGG	34465	A_95_P182217	EB448209
35375	417	15	382	ATCCAGTCAATAAGCTCAGCAAGATTATGGTACTTTTATGCTTTGCAAACATCTTTAC	34469	A_95_P064090	BP135954
35378	417	18	160	CACCCCTATCCCCTGTCCTTTTATTATGAGTCAAATTTTGTAACTGAAATTTGACATTT	34475	A_95_P181772	EH613905
35383	417	23	315	GGAATTGATCGTTGGTTATGTTTGGTCTGAGTCTAAGAGTCTTAAGTATGTATTATG	34485	A_95_P133202	EB434505
35384	417	24	679	CAGGAACTTCAGGTTTAATATGACTGATATTCTTTTAGAAGGTGAAGCATGCAACCC	34487	A_95_P013241	EB682934
35386	417	26	880	GCAAAACGTTTTCTGCATCCTGACATTGTAGCACCTTATGACTATATATTCATCTGGG	34491	A_95_P227529	EB428349
35388	417	28	669	ATGTCTGGAATTCAGATGTAAACAGAGTTCCGGTGGAAGTTTTGAAGCTTGGGGCA	34495	A_95_P284843	FG199640
35391	417	31	1397	TTTCAAGTTAATGCTCTACTTCCAAGACTGAACCACCAAAACGACTGTCTCAAATACC	34501	A_95_P007806	TA13797_4097
35392	417	32	566	TGTTTGTAAGAACAGTGCTCATTTTGTTTGCCTACACTGTATGTTATTGTCCGAACTGT	34503	A_95_P212307	TA19805_4097
35393	417	33	1223	CTTGTGTTTTGTATGTAATGTTTGTTCTTGATGTGATTGTGATGGCCATTGTTGTTCGT	34505	A_95_P023056	TA15890_4097
35396	417	36	682	CTTCGGAAAGCTAGCAGGATCCTCATTCTGATGTCAGAAGGGTAATTAATTGATGCA	34511	A_95_P141887	EB445505
35397	417	37	320	TTGCTCTGGTGTTGTATTCAGACAATTTTCAAGTTCTTCAGATGATGTTCCAGTTTTAT	34513	A_95_P307638	FG638976
35401	417	41	616	TCTGTTTTTGTATCTTGTCTGTAGTCGAGTCTGTTAAAGGCGTGTTTGATGTGAATTTT	34521	A_95_P015871	TA12007_4097
35402	417	42	754	TGAATCACATCAAGAGAGCACCGAGAAGGTTATGGATGATCCCTGGGGATCTGTTA	34523	A_95_P268546	DW002999
35403	417	43	145	CCCTCCGAGCAGGCAGATTATATAGCTTAGATATACAGTAATAAGGATGTATGCTTTT	34525	A_95_P141997	EB445585
35404	417	44	742	TTGCATCAGATGGCTTATGGGAACATCTCAGCAATCAAGAGGCCGTTGACATTGTGA	34527	A_95_P146552	EB450614
35405	417	45	575	AAGGCTTACTTTATTAGCCCTCTGTTTCTGTCGTCTATTCGTTCTGTTCTGGAGAAGTT	34529	A_95_P023296	TA15396_4097
35408	417	48	771	GCTTTTCTCTTAGTAGCAATATGTACTTATTTTTGTCTTGATGGGTAAGTAGCTCCTGA	34535	A_95_P010401	TA13834_4097
35409	417	49	1017	GACCATGGAATTGATGTTGATGTATAATATGACATGGGAATGCTCGTTAAATGGTTG	34537	A_95_P181422	TA12976_4097
35411	417	51	686	CTTCATGTGGTCCAGTTTCAAGTAATTGAGCTTTATCATTTGTTAGCTTCACTATCTGT	34541	A_95_P000411	EH618900
35413	417	53	641	CAAGAACGGACAGTCCTGATGCCTATGATTGTATTAATTTGATTACTAACAGCTTGAA	34545	A_95_P124572	DW004363
35416	417	56	761	CCCAAGGCTAGGATTCGTTAGATCATGTTATGTGTACACAAGTTATATTTGTATGTAA	34551	A_95_P128342	X51426
35418	417	58	680	GGTTCTTTTGGAACTTTTGTCTTTTTGGTGTTTGATGAATGACTTTTAGACAGCTCTGT	34555	A_95_P148832	EB678367
35422	417	62	238	CCTTATTCCTATTATTCCCTTCCTTACGGCAAAACCGGAACAAATGGTTGACAGTGCA	34563	A_95_P070190	BP192547
35426	417	66	413	ATTCAAATTTCAAGGTCATTTGGTCTTACTACCTAACTACAAATAGGGATCGATAGTG	34571	A_95_P132202	EB432654
35428	417	68	304	AATGGACAAGTATCCACCGGTACCATTTCATTAAACAAGTCGAATGGTTCCTTCGAC	34575	A_95_P162153	FG642918
35430	417	70	856	CTGCAGCAAATATTTATCTGCATTATTAAGGGTTAATCATGTTCTGATTTCCAACTGCT	34579	A_95_P183632	TA13502_4097
35433	417	73	831	CCCTCTCTGGATTTCATATATCTGTGCATTGTGATGTAATACTATGTACTTTACAGTGA	34585	A_95_P021291	EB426312
35438	417	78	660	GCCACTACCTATTGGCATGGGTTTTTTATGATGTTCATCGATTGTATCAGTTAGTTAG	34595	A_95_P153597	EB683838
35441	417	81	897	TCTTCGCCATCTGATGGCAAGCTTGATGTGTCAAAGGCTTTTCTACTGTCGTTGTGAA	34601	A_95_P011651	AB079023
35443	417	83	395	AAATATTTCCTTCCTTTGTCTCATATCTGAAGAGCAAGGATGCTAGTGACGGTACTGA	34605	A_95_P109977	AY074787

35449	418	4	734	GTGATTTACTTCTTCTTGCTGAAACTGTCTTCTAACATAGTTTCTCATGCATGTCAGAT	34448	A_95_P117472	DV160392
35452	418	7	1337	GATTGTCTGTCTTCTGTTGATTAAAGCTGCTGTCTATCCCAATGAACATGTTAAATTTG	34454	A_95_P074840	TA15200_4097
35453	418	8	811	GTCAACAATTACTGCGCGAGCTACATTTGATGTTTGATAGTTCTTGCAGGATAAATTT	34456	A_95_P126997	EB426416
35454	418	9	372	TGAATTTCTAAGAGTCAAATGGTTTACACAGATCAGACATCCAGTCCAAAAGGCATG	34458	A_95_P154607	EG649670
35456	418	11	538	TGATAGAGAAAAGGGTGACGACGACAGTGATGTTATAGTCTGCCCATGTATGTATTG	34462	A_95_P035183	BP128398
35459	418	14	717	AACACTTTCTTGATGCTCTTGACCAGATTATGAGCCCAAAGGCCAACAGAACAAGCC	34468	A_95_P164417	EH623650
35461	418	16	191	GCACGGGGACAAGAATTTGCTTGTCATAATAATATGCTGATTTATGCTTTTTTGAAAG	34472	A_95_P032171	EB436705
35463	418	18	1111	ATGTAAAAGAAATTGAAAACAAGGGAATTACTATGTATTGTGTGGGAGGTGTCATG	34476	A_95_P141752	TA13567_4097
35464	418	19	557	AAATTAAATACTCCTTTCTTTTCTAAATCGCCCGCGAAGACCAGACGTCGGAAAAGG	34478	A_95_P038141	BP129188
35466	418	21	634	TTTGAGGCGCGCATACACAAGGGGAATTCCTTTCTTGTCCAATACAAAATTTAATATA	34482	A_95_P134777	EB437551
35467	418	22	832	TATCCTCCTCCTGGCTATCAGAAGTGATCTTTCGAAGGATTTGGTGCGTCATTCTATT	34484	A_95_P147202	TA15797_4097
35470	418	25	472	TGTGCACTTTGCAGTTTTGCTGTATGTGTCGACTTAATTTTATCCATGTTGATAATGA	34490	A_95_P125337	DW005129
35476	418	31	598	ATAATTAGGTTGGAGCTGAATTTCTACTAATTTGCATTCTGAATGCCTTGATGCATGA	34502	A_95_P019976	DV162200
35480	418	35	691	CCAGTTATTGGTAGTGCTGTGAAGGGCACAAAGGTTAAGTTATTGGACATAACAGCT	34510	A_95_P280038	FG194561
35482	418	37	106	AAGGATGTTGAAGTGAAAGGATTCAACCCAGGATTAATATGTCTATAACTAGTTGTA	34514	A_95_P107057	CV018193
35484	418	39	491	TGAGTTTGGTCGAGACAATAAATGATAATGAGTGGCGGCCCTCTGTACTTTGGCCAT	34518	A_95_P010846	DW004048
35488	418	43	395	GATTTGTTTCTTGGTGGAGAAACCATGTAAGAGGGGAGTTGCCCTTTCTGATTTGAA	34526	A_95_P102997	FS417555
35490	418	45	857	GGTCTTCATTGCGTTGGTTGTTATAAACTCTCATGATCAAATCTTGTATCTATCTCTTC	34530	A_95_P008091	DV162582
35491	418	46	355	TTCTTGGTTTTGGGGAATATATAGAAGAAGTATATGCTGCATATGAACAACACAAGC	34532	A_95_P146258	FG643952
35495	418	50	833	TCTCCAGACTTTGGATAAGAGAAAACACAAAGTGGATGGACCAATCTTTATTATTCTT	34540	A_95_P252444	EH615331
35497	418	52	798	GATGAGGCTAGGCAAAGGAGTGAACAATTAAATATGCAGGCAGATGGGACTTCTTC	34544	A_95_P209187	AB379974
35498	418	53	406	TTGACACCAGGGGGAAATTATGTGTCTATTCCTCTGTAGTAAGGAAGAGTAATGGA	34546	A_95_P105447	CV017464
35502	418	57	1233	CATTACTCAAACGTTTGATTTGCTGGGATATACCCCAAAATTGTCAACTTTTGTGATC	34554	A_95_P207332	TA18717_4097
35505	418	60	494	ATGCTCAATGAGCTTCTTAGTTTGTAGCTACGAGTATTGAGTAAAAAGTTGTAACAG	34560	A_95_P142397	EB445877
35507	418	62	124	ACGATGTTTGGCTCAACTGCATATTATCATGTGAGCGGAGTCAAAATTGGATCCAAG	34564	A_95_P042886	BP130471
35509	418	64	498	GCTGTGTGAGACATTATTTACAATTTTGTCTGCTGAAATCAAATCTTTGCACTTTTGCC	34568	A_95_P233784	FG640626
35510	418	65	1525	GTTGTTCTTCAGTTGCTGCATTTTAGACATTCCAGTACTAGTTTATACTTTGATGGTGT	34570	A_95_P257911	AB052822
35511	418	66	1031	TCGCAGTTGTTCGTCTTTCATAAATCCAAGAATTTCACCTCTGACTATGAAATACGAA	34572	A_95_P193342	TA15649_4097
35513	418	68	353	GGATGGAAAATTTGGAGAGGAAAATTAGGGTTCTAGGAAATGTTCTTCTTCTTCCTT	34576	A_95_P088638	BP530162
35514	418	69	1125	CACTATTATGTAGAAGACTGATGAATGTGTTTGTCAATAATGCAGCAGTATACCACT	34578	A_95_P222922	TA22136_4097
35516	418	71	847	AGCAGTAGTTTGTCATCTTTTTCTATTTCAGCTCTCTGCGTGCTGTACCACTGTGGGA	34582	A_95_P298508	FG160952
35517	418	72	508	TATGGAGGATTTGCTGCAGCACTGAAAGACTTGAAAGTCTGGGTTATGAATGTAGTT	34584	A_95_P034059	TA15455_4097
35519	418	74	853	TTTGGTTGTATGTGTTCTTTTGTGTCTCTTGAATGAAAGAGCAAGGCAAATCGCGTTA	34588	A_95_P196737	DV157807
35524	418	79	401	GTTCGGTTCTACATTTAACGAGTTGTTGTATAAGTTGGAGGGTGATTGTTGTCATCAT	34598	A_95_P023566	CV019069

35525	418	80	312	CTGGGATAAGGTCAAACTACAAAAGGATACATATATAACTACATACACTGTAGAAAG	34600	A_95_P089208	BP530399
35531	419	1	553	TTGGGTGTAACTTGTGAATTTTGGATGTGATTTGAGTCTAGAAGTTTGTTGTTTGAG	34611	A_95_P073145	EH618900
35535	419	5	1035	TGAAATCAAGGGTGTACCAGAGACGTCAAATGTAAAGAGAAATTACCAGTTTTGTTT	34619	A_95_P217892	AY141105
35538	419	8	838	TGCATCTATGTTTCTGGTTTAGTTTAGTTTAAAACCTGGTGACTTGCACTGTTTTTTGG	34625	A_95_P217282	TA20899_4097
35539	419	9	563	AAAGGAAAATGTTATTGAAAAGCTGGAAACAAGAATTGGGTTTCTGATTTCTGACCC	34627	A_95_P121297	DW001304
35542	419	12	471	GGTCTGCATATGATGTTTTCAGGGTGGTAGAGTTGACTAATGTTATCATAGGTTTTTC	34633	A_95_P101838	CN824878
35544	419	14	836	TAGGTAACCTTTCAGAGTTAGCAGAAGACGAGGCTTTGTAATGAAGTGATGAACAA	34637	A_95_P149337	EB679186
35553	419	23	636	AAGATGGGAAGGTTAACCACAGGGGTGCAGTATGAATCACAGTTTGGAAACACAAA	34654	A_95_P129202	EB428919
35557	419	27	151	TCGGGGGTATGGTACGTTGATGCTGCAGAATTAGAAGATAAAATTATTGGAGAGAA	34662	A_95_P031221	EB444185
35560	419	30	527	TTGGAAATGCTCTGATATGCCTCACAAAAGAATAAGTTGTAATGATGCTGAAGAAAG	34668	A_95_P063560	BP135813
35562	419	32	764	GGACACTGCTTCGCCCCTGATTGAAATCTGTATATAATTTCCGGTATGCTGTAATTGG	34672	A_95_P144797	EB677519
35563	419	33	764	ACTTTCCCCAAAGACGCTCTTGAGATAACTGCATGGACAGAAGATGGTCTTATAATG	34674	A_95_P246002	EB426543
35568	419	38	356	ATGATACAAGATGTTGACGATATGCTTGGTTATGACATCCCTGAACTTCTCAAGAATT	34684	A_95_P269886	TA19780_4097
35573	419	43	244	GCTCATGTACTCTGTGACACCCGAATTTTAGGGGAATATTGTATTGAGTCGCGGTAT	34694	A_95_P222272	TA21997_4097
35582	419	52	658	CTTGTATGAATAATCTAGGGCTGAAATTGCCATTGGTGTGTTTTGATATCGTATGTG	34712	A_95_P262896	FG638854
35586	419	56	775	TTCTTTGAACTGATGTCGATGTCTGCAGCTGATATGTAAATCCTCAAAGCCAGCCTCG	34720	A_95_P284893	FG134869
35587	419	57	848	ATACTGAAACAAACATCTAGTGTCCCACCCAGTCTTGGACCAATTGTAGTCCACTGCA	34722	A_95_P013311	TA16511_4097
35589	419	59	968	TTGCTTGCCTTTCTGTCTTTTGGGTGCAATGTAAACTTAAGAAGCGTCTGGTTCTCTT	34726	A_95_P187617	TA14386_4097
35591	419	61	157	ATGACATCTCTGTTGAGGATTACATCACAGCAACTGCTTCCAAGCCATCCGGTTTCAC	34730	A_95_P104967	CV017244
35593	419	63	454	GGAGTATCCACCTTTCTCTTCTGTTGCTTCATCTTGTGCCTTCTCCTATTCTGATTATAG	34734	A_95_P279898	AM818654
35595	419	65	203	GCCTCAAGGTCCAACACATCCACCGAGGACAAAGCTTTCCATGTTTTCTCTCTGATTA	34738	A_95_P103562	CV016579
35596	419	66	642	TTGGACAATATGTATCTTCAGCGGGCGAGTTTGGATAAGCTTATTATTTATAACTTAG	34740	A_95_P115592	DV157844
35597	419	67	1670	CACAAGGAGCATATTCCACTTGTAGTATCTTTTTCCCTATGCGATTTTTAGGTCTATTA	34742	A_95_P283429	AY639146
35602	419	72	236	CGCAGTTAACCAAGTTCTTTATCTCGGTGTCAATTCTCAAAATACTGTAAAGTTTGTT	34752	A_95_P164837	EH624205
35604	419	74	152	CTTTTCACTGGGATTGTCATACTTAGTGTAGAAATTTAGGTAGGACCTTCAACTTTTT	34756	A_95_P077395	FG623741
35607	419	77	1180	GGAGACCGTTAATTCCCCTTGATAATTTGGTTTCAGATTGGCATTGTATTTATTAGTA	34762	A_95_P193112	TA15601_4097
35616	420	1	424	GATTGCCTTTAGGTATTTGTGGTGCGATCTAAACTTTTTTATAATGTGTCGACTATAT	34612	A_95_P189847	TA14875_4097
35617	420	2	428	CTTTCAGTGAGGTTGCACTTTTACTACGGGCATCAGACTCTCTAATCCATGATCTGTG	34614	A_95_P068220	FG154845
35625	420	10	790	CTCAAGATCATCGGGCAGCAACGTAGTAAGGTTGTTGGTTCATGATATAATGCCCAA	34630	A_95_P292068	EB426307
35628	420	13	659	AAGGAATCCTTAATTTCTGTTCCTCTTATTCTCCACCAATAAAGTTCTGCTTTGGCAAC	34636	A_95_P235729	BP136083
35632	420	17	885	TCTTATGCATGAGAAAGTCTTTGTTCAGTATATGGAGATACAACCTGAAAGTCTTTCC	34644	A_95_P250792	EB678124
35633	420	18	242	ATTCTTAATATCATGAAACTGCCCCCCAAAGCCACACTTTCTGGGGAGGCTTCTCTTC	34646	A_95_P097648	BP534136
35640	420	25	473	AGAGCTGCAGTGATTGAGTTGCTAGAAATTGATCTTTGGAAACATTAATTTCAGTCA	34659	A_95_P204242	TA18024_4097
35646	420	31	638	TCATGACGAAGAAAAGTGGAATCTCAACATGAAAACTGCTTCGAGCTTCAGCTCTCT	34671	A_95_P244497	FG640490

35648	420	33	953	GGTGTATGGTGTGTTTAAAACAGCCTTGGATTTAATACCATGTAATCAAGTCCTGACT	34675	A_95_P181977	TA13107_4097
35652	420	37	401	GCTCAATTCTTTTGAATACTGGAGCTGTTGTATCTCATTTGTTTATGAGAGTTTGTTCT	34683	A_95_P256774	AM817228
35653	420	38	551	ATGCTTGAGGTTTTCCAGTCACATTGACATTGCTCAGCTTGTAATAGTTTAATTTACA	34685	A_95_P020716	DW005235
35654	420	39	179	TCATGGGGCCTGCTGTGCTAGGTAGGCTTTGTTAAAAACATAAAGGTGTCCCTTTGTA	34687	A_95_P103222	CV016404
35655	420	40	282	TTCCCTTGTGCTTGTATATAATCAAATTTTTTGGCATCCCTCAAGTGAAAAGAGTTGC	34689	A_95_P125542	EB102913
35659	420	44	738	ATGCAGTCAAGAAAAATAACTTCCCCTGAGGAATAGGGGAAGATTACTGAATGTGG	34697	A_95_P187472	EB449629
35660	420	45	405	GAGCCCTTATATGGTGTTAACAGAATTTTGATGGTAGGATGCCAAATTTGGTTTATTT	34699	A_95_P000931	EH619918
35661	420	46	368	CTTTGTGCATACCACAACACAAAGGGCATCAGCATTATCGTCTATGATTTGAGGCTG	34701	A_95_P061250	BP135214
35662	420	47	199	TCTGCCGTTCAAGCCACAAAGAGCAATGTAGTGAACTTGTTGGCTTCTTATGGATAGA	34703	A_95_P114477	CV021619
35663	420	48	376	ACCAGAAACTAGGTTCAGGCTTGGAATGAAAACTTTTCTTATGAAGTTGAAGATGTTT	34705	A_95_P055131	BP133617
35664	420	49	563	AGTCTGCTTGCTTTCATATACGTGTGGTTTGTAAAGCAACTTTCAACCGTAATTTTTC	34707	A_95_P001241	EH617784
35668	420	53	520	GCGTGGATGGCAGACTTGTGAGAATCTTATGCCTATTAATGATGTTTTGAATTGAAAA	34715	A_95_P202677	FG644444
35671	420	56	344	GGCATGTTGCTCTTCATCTTGATGGTCATTAGATTTTGAAGCCCCTATATTGTTCCTTTT	34721	A_95_P132787	EB433498
35674	420	59	493	CCAGCGGAAAAGAGATCAATCTCATGCAACAATTTATTCTGGATCTTTAAAATCAGA	34727	A_95_P291118	FS418200
35676	420	61	853	TAAGAAGATGGTGATTATGGTAGCAGTGCACGCGACATTTTATTGCGATTATATTCTT	34731	A_95_P247862	DV999990
35679	420	64	661	CTCTTTCGCGTGTCCAATTTTGGTGCTTGGATATTTGTTCTTGTTAGCTAATATTATACT	34737	A_95_P024251	EB445181
35680	420	65	404	GCGCACTGCACATTAGATCCCTGAACTAAGCTACTTATCAACACGGACAATCATTAGT	34739	A_95_P092303	TA15396_4097
35682	420	67	163	TCAAAGGTTTATGCCATAAAAGGTCCTCGGGTTATGCCAGGGAGGGTCATTAGGTTA	34743	A_95_P159062	EH617013
35684	420	69	847	TTTTCTGCTGATAGGAAACTGCTGCTATGCACAAATCAAGACTTACATTATCCAAGCTT	34747	A_95_P272181	EB448123
35687	420	72	401	TTAGGAAGCTTTCTAAGTTGCCCATATCAAAATGAGGAATATTTTCTTCCTTGAGAACT	34753	A_95_P148557	DW002260
35701	421	1	1008	CCTGGTCAACCCACATGTCAATACTACATGAAAACTGGCGATTGTAAATTTGGATCAT	34780	A_95_P018201	TA22281_4097
35703	421	3	732	CAGGCATGCAGCTGCTGTTTCGGAGCTAAAACTGTGAATTTCGAGTTAGAAGATCTT	34784	A_95_P162692	EH621679
35704	421	4	388	TTTAAAACTGCAAACATTTCAGTGGAGACTCCAAAGGTTATGACATCACTAGGACCT	34786	A_95_P187812	TA14431_4097
35705	421	5	781	GTTTGCTGCTTTGCCCTTCATATTGTGGCTATCCTTTACAATTACAAATGCTATCATTAA	34788	A_95_P181252	EB429556
35706	421	6	506	TAACCATTGAGAATACAAGGTTATAGATCCATGATTGTCATCGAGCGAGTTTTTAGA	34790	A_95_P212602	FG634406
35710	421	10	1229	GTGAACAGTACATCTGTTATCTGTATGTAATCACAACGTGGAGTGACCATGAACAGCT	34798	A_95_P220397	TA21598_4097
35713	421	13	428	GTGAGTGTAGCCGACATGAGATTTACAGATTGGTTATTATGTATTCTTTTCTTCCTTTT	34804	A_95_P143342	EB446673
35719	421	19	999	GGGGTTGGTTAATGTTGTAACACCAATAAGTTTCGGCCTTTTTGTGTGGAGATGTTTA	34815	A_95_P007261	TA14332_4097
35726	421	26	325	AAGCATTGCTGCTTTTGTCCCCAAACGCATGGTTGTTTGAACTACATTGAGGAAAAT	34828	A_95_P114744	CV021739
35732	421	32	768	ATTATAACCAGCGTGGTTTGCTGCTTTTGGAGGGGCAAGGTATTTATCGACTGGGTG	34840	A_95_P262366	EB678611
35733	421	33	894	AAATGCGGAGTTTGATATAAAAAAGGAGGCTGCATGGGCAATCTCAAATGCCACAT	34842	A_95_P290063	DV161885
35737	421	37	5062	GCAAAGTGCAGTTTAAGGTTGTGTTGTATATGAACTATGAAGTGTTAAAATTGTCAA	34850	A_95_P205872	AB180675
35738	421	38	781	ATTCTTGCTGAGAGCACACTCAAAGAATTGTTCCAGTTTTGGCCCAGAAAGATGAGG	34852	A_95_P292728	FG157460
35743	421	43	1640	TACAGCACGTTTTTGCCTGTAAAATGCCGTTACCTGTTGATTTCCTCTCTAATGAAAAA	34862	A_95_P239749	AJ133453

35748	421	48	1455	GATCACGAAAGCATTTCTGCTGTGTTTATATGTACATTTTATTGGCGTCAGTTCTATGT	34872	A_95_P200242	TA17167_4097
35757	421	57	1150	AATTTCAGAGCCTCGGGGAGCTTTCTATCTATTTATTGATTTAAGCTCTTATTATGGA	34888	A_95_P147472	TA15308_4097
35759	421	59	855	GTATGGCAGTATCAAATGCGAATAGCTGGTTGCTTTCAAGAACATCCTTTGCTTGTTT	34892	A_95_P267116	DV158456
35763	421	63	789	TGAGTTGGGATGGTTTTCCTTGTTCTATCACGTTTATTTCGCATTTAAGATTATATTGC	34900	A_95_P011206	DW000282
35766	421	66	547	TTCCAGTCAGATACTGTAAAGCAGAGCCCCTATGACTGCGATGGAATATTCACAGGG	34906	A_95_P044146	BP130798
35771	421	71	1042	CCTTCAAGATCATTATATTGCGATAGGAAATTGTTATCGAGCTACTAGGAGTCTAGAT	34916	A_95_P008486	TA13784_4097
35772	421	72	839	TGCTGTCATGTGCTGAGCTTTAATATGGTGTGCTGATGCAATATATAGTTTTCTTTGA	34918	A_95_P183847	TA13550_4097
35774	421	74	1754	TAAAGAAATCAACATCATTTGGTTATCGCGTTGGAGAAAATTTACCCCTATTCCTGGG	34922	A_95_P026211	TA14910_4097
35778	421	78	794	TAACATTTTCTTGATTTTGGTTGCCGATTCGAGTTCCCGTCCAAGGTTCGTCACATTTT	34930	A_95_P147002	EB451245
35779	421	79	474	GATACTGATAGGGTCGATCATTTTAGCTTATAAGCTAGTTTTCGTAGCTTAATGCATG	34932	A_95_P028861	BP530047
35780	421	80	322	CTCTTTGCCTTCTGTGAGTGAAGATTAAATGTCTTATACAATGTGGTTGTTGAAGATAT	34934	A_95_P134867	EB437747
35781	421	81	729	TCATGGTTAATCTATTTGGTATGGTTGTGGATCTCTTTTAGAGAACCTGCTCAAGAGA	34936	A_95_P137102	EB440833
35784	421	84	693	TAAGAAAATTTAATGACAAAAACTTTAATGCCCGGGAAATGGTGGCGCTAGCCGGT	34942	A_95_P004536	FG164960
35786	422	1	557	TTTCACTAGCCAGGCCCCAAATGTTTATTACAAGCTTATTACAATGCAGAATGCTAAAT	34781	A_95_P062550	BP135544
35791	422	6	1149	GGAACTTCCTCTTTAGGTTGGATGTAATCACTATTTGGGCTTTCTCTTAATTTCATTAT	34791	A_95_P181007	TA12876_4097
35795	422	10	536	GTGAACCAACTTTTAATTGCTGTATGTTTGCAGCAGCAGCTATTAATATAAATTGGTC	34799	A_95_P211432	TA19609_4097
35808	422	23	403	CAAATTCCATCATTGTACAGAACCAACATTTTCCTCAATGGTGAGAACTTGCATTAAA	34823	A_95_P026601	TA21385_4097
35810	422	25	755	GAGTATTGTCTCAGATCGTTACCGAATTCAATTCAAAGTTGTCACTCATTAAAACTAG	34827	A_95_P013761	DV157504
35812	422	27	656	GGAGCAAGTCAAAATCAGTGAAGTGCGAGGATTATGTGGCTTTTCAATTTTCTCATAT	34831	A_95_P183452	TA13460_4097
35820	422	35	596	GGTTGAGTTGCCGTTGATCCACAAAAAATCTTGATGAATCTATGATTCACAAAATGAT	34847	A_95_P032131	DW005237
35823	422	38	157	TTTCTTATTGTTGATATTGTTGCTTGCTTCCTTGTCACTGTTCGTTGAGCGAGGGTCTA	34853	A_95_P128902	FG134537
35829	422	44	624	TCTTTATGTCGTTCCCTTGAATTCTACTCCTCAAGCTTATCCGGAGCCTGATGCAGCAA	34865	A_95_P233479	FG641901
35830	422	45	743	TGTACGTTTTGTCTCTGTTGTAACCTCTCTCAAGAGCGATTGAGAATCTCGAGAACTTT	34867	A_95_P222792	TA22110_4097
35840	422	55	854	ATCATGTCGTGAGACTTGAGAAAATTGCAGTTGTGAATCTACTTCAACACAGGATCAA	34886	A_95_P278618	FG155234
35845	422	60	225	GGGTCGTTCCAACGATGTACCTACCAAATGTCTATTTCATTTTTCTCCTGATTTGTCTCT	34895	A_95_P208467	TA18975_4097
35848	422	63	565	AGGCTCTTTTGCTCCATGATTTGCTCTGATCCCAAATAGATTCACACCGTTCAAGATTT	34901	A_95_P004881	EH665149
35851	422	66	786	GCAGGGAGTAAAGTTACTTTGATTCCGATATTGATTGGAAAAGACCAAGTAAAATCG	34907	A_95_P122277	DW002296
35855	422	70	515	TATGACTGAGGCATAGTTGTTGTTGTTGCTGTTGTATCTTGAAGTTTCAAATGACCATA	34915	A_95_P278308	FG638668
35859	422	74	455	CAATCAGCACTAGTGTTGATCCTGCTTCTGCACTTATAGCTTCATACTAAGACTATGTA	34923	A_95_P029981	BP129737
35861	422	76	692	ACTGGTGTCGAACAATGTTCAGTACTTTCATCTAATGGCTAGTTTCAAGTTGTTGCGG	34927	A_95_P177902	TA12100_4097
35863	422	78	739	GGGGTATGGGGAGTAGGAAATAATGTAATCTAAGAAGTTGTGCAAAATGAGGTGA	34931	A_95_P135542	EB439036
35864	422	79	313	TTATGGAGCATCAAGTGAGGACAATTGCTCGTAACTTGCCCTGCACATCCAACAATGA	34933	A_95_P111397	CV020187
35867	422	82	1038	GATGAGCTGCTCTGATTTGCCTGTCATACCAATGTAAATTGGTCATCATATAAAGAG	34939	A_95_P248992	Y09109
35868	422	83	758	ACTTGATGCTTTGATTCCGAGCACATCAAAGAAAGACGACAAATCAAAGGGGAAGA	34941	A_95_P116262	DV158884

35881	423	11	570	TCATCAACTCTTCTTTCTTGGTATGTACGATGGTACAATGTGGCATCACCATTCGAAG	34965	A_95_P117407	DV160328
35884	423	14	457	GGGGATTAAAGTGCAGAAAGAGCTGGATTAAATGAAACTATTGAACGGTATTTTTG	34971	A_95_P130167	TA17452_4097
35886	423	16	857	CCTCGGATAATTTTAATCTTTGCCTCAATATATTCTGCCTGGTTGATTTTGTTGGTGAT	34975	A_95_P011001	TA15296_4097
35887	423	17	698	GACGTTCGCAGACCCGATTTCTCCTTCTATCTCCACTTATTATTCCGCATTTTAGACAT	34977	A_95_P223282	EB679603
35889	423	19	935	CCAGAGGGGAACGTACTTGTTGATGGTCAAAGATATACTGTCGTTGCTCTTCTTTCTC	34981	A_95_P020316	TC56111
35892	423	22	969	GTAGATAGATGTATGTGAGCTTGGTAAATCTTGACTTGCAATGTGGACTAAATGTTA	34987	A_95_P012811	TA16106_4097
35894	423	24	498	TATAGCATTTGGCCTGTGGTACTTATTCCTTATAATTTACCACCTTGGCTATGCATGAA	34991	A_95_P055881	BP133816
35900	423	30	479	CTGCTGCAGAGATGAACTAACTGATTAGCAGTAACAGTTTGCTGTGTTTGTATTTGTA	35003	A_95_P021866	BP526432
35907	423	37	579	TTGCAAGTCTGGTTAGCTTTAGCTTTTGCCCCATATATACCCTCATTTATGAAGTAAGT	35017	A_95_P031476	BP134683
35909	423	39	798	CTCAGTTTAGTAATGGTGGTGTATTATCGTGGAGTATATCACTTATGTCAACTTCTCT	35021	A_95_P116072	DV158614
35912	423	42	88	TTATCAGTTCTGTCAATGGCGAAAGCCGGTCTCGTAATTGTGCCTTCTTCTCTTCCTCT	35027	A_95_P206377	EG649505
35913	423	43	692	CGCATATATGCGCTATTCCGTCTATTGTAGTTGTTGGAATTTTTCGTCAATTAAAAGC	35029	A_95_P254479	EB447363
35914	423	44	275	TGCAACCATCATCAGCTATCTACAACCCTTAAAGCAATGGAAGTGTTGAAATTCCATA	35031	A_95_P026611	BP535378
35919	423	49	355	TCAAATGTATTCATCGTTCAGTTTCTGATGCCTTGTTCACCTGTAACGAGTCCCCTCTG	35041	A_95_P155952	EG650341
35920	423	50	862	GTGTCCCAATTTTCTCATCCCTTTAGTTATAGGGAAAATTGAATTTGTTCTGTTGTACG	35043	A_95_P008941	EB683385
35924	423	54	726	ATGTGCACTTATTTCTTTGCCGGTTATGCTTGTGTACTGTAATTTAGATGCGTTGCTA	35051	A_95_P148162	FG645393
35926	423	56	933	GTGATGATTCCCTTGAATTTGCATCTACTATGTGTTGTTAAAATGTAACCGAACATAC	35055	A_95_P184887	U64924
35930	423	60	598	TGTTTGAGATCGATGTTCTGAGTTTCCTGATACAAGTACATGCTAGCTGCTATGTTTA	35063	A_95_P181447	TA12982_4097
35932	423	62	596	GAGTCAAACGGCTATGCAAGTGCTGAATGCATTCCATTATTTCTATATCGTTGGAGT	35067	A_95_P027621	TA13998_4097
35933	423	63	248	TATTTTGTTTTAATCAAGAAGTGAAAAGGTTGTGGCTGGATAGGCCAGCTGGATAAA	35069	A_95_P235824	BP135456
35936	423	66	796	GATGATGGTCTAAGCTTTATTGTTCATCTGTAGTTTTAGCATAGATGGTTGTCTTTTG	35075	A_95_P020446	DV162700
35940	423	70	672	GCAGTCGAAAGAACTTGGTTCAATTGGGCATAAACTTCTTTATTGGATTTTTAGAGA	35083	A_95_P001266	FG176960
35955	423	85	201	GACAATCGGTCCATGAAGTTATAGAACTCGTGCTTGTTTTCAGTACTTTCTTTGTTTT	35113	A_95_P219227	TA21352_4097
35956	424	1	416	TTACGCTTTACTTCGCAGGGTTGGCTCTTTATGTTTGGTTAATAAGGCGATAATAAGA	34947	A_95_P143027	EB446412
35972	424	17	691	AGGTAAAAGAGCAAGAGACGTGCAATCATCGTATAAGAAGAGGGAGGAACTCTTTA	34978	A_95_P219027	DW001900
35975	424	20	1257	GTGGAACTGTCTCTCTGCAGGTATTCTTTTTGAGGGGTAAATAAATAACTAATCAACT	34984	A_95_P013626	TA16452_4097
35977	424	22	308	GCTGGCACTGTATTTTGATATTGGGATCTTTATCTTGGTTGTTTTGAAGTTTTGGCAG	34988	A_95_P006097	FG623522
35978	424	23	812	ATGGTCCAGAAGAAGTATCCCCCAGAATCCATCCACAATTCACGGATTGTTCCACTG	34990	A_95_P012316	EB448393
35981	424	26	375	GGCCTTGAGTTTCAAGAGCTATCATCATCTGGCCTACTATTTCAACATCCTCCTTTTGG	34996	A_95_P098308	BP534409
35993	424	38	550	CCAAGATCATGTAAACATTGGTGCAGTGGACCGAAAGCTTGAAGTTGGTCATTGTTC	35020	A_95_P036238	BP128679
35994	424	39	443	GAATCCTTGTCTATGTGTTTGCTTGGTCTTCTGTTGATGCCATGAGTATAGGATTTCTT	35022	A_95_P084585	BP529058
35995	424	40	419	CTGGTGAGAACTTCTGCGTTTCTGAATTATATTTTAGAAGCAGCGTCTGTAATAATAT	35024	A_95_P028491	TA12914_4097
35996	424	41	757	CTAGGAGCCGACTGCATAAATTATCCTTCACAATGTGCTTAAGAATATAAAAAGGTA	35026	A_95_P146517	EB450574
36002	424	47	202	AGAAGCTGCTGCTTTGAGTGCTAAGTATTGCTGACACTTAAATGGGGCAAGCTGCTT	35038	A_95_P032296	AB001548

36011	424	56	778	ACAATTTTGTGCTATATTGCCCGGCTGTCACAACAGAAGTTCTGAGTCCATGGGAGA	35056	A_95_P256149	FG172775
36019	424	64	528	GGACAATGTAGCTTTGGTTTCTTACTAGTCAGGTTACCTTTAGCTAATATTGGTACCT	35072	A_95_P301648	FG635137
36021	424	66	459	CTCTCAATTCCACTAGGTCGAGAGTTCAAGGCTGGTAAGAGAAGGAGAAAGAGAAG	35076	A_95_P059640	BP134791
36024	424	69	313	TCTCCTTCTGACCTTGGCTCTTGAATATCAACACATTTGGTTCCACAACTACTGAGATT	35082	A_95_P066435	AM791244
36025	424	70	911	GCCTCCTTTATGACTTACATAGCCGTGATTTAAGCAGTAAATCACTAAATCTTGATTG	35084	A_95_P015756	TA14117_4097
36029	424	74	2459	GGAGGTTGGAGCTTGAAAACATGTTCGTTCATTTTCTTTTTGGGTAGAACTAATCAA	35092	A_95_P032651	AF022727
36031	424	76	1603	GCACGATCGATGAGGTGGGGTACTTCGAGTTGGTTGTCAAGATATACTTCAAAGGA	35096	A_95_P247817	X06134
36046	425	6	551	ATATAGCCAAGCATATGAGGCAACACTTACTGTAGCTTCGTGCCTCCTTAATTGTACT	35125	A_95_P233719	BP134784
36048	425	8	731	GTGTGCTTTCTATGGATTGATTGAAGCATCAAGACATATACCTAAGATGGTTAGCAA	35129	A_95_P107867	TA11779_4097
36051	425	11	558	GGAGGCTTCTACATTGTTTCATGTTTATCATCTTAATCGAAGCTTAGCGAGTTAACTT	35135	A_95_P026291	TA19839_4097
36052	425	12	104	TTCTGGTAATTGTCAAAATGCCTATCGGTAATGGGGAGGATGTAATCCTGTTTATCT	35137	A_95_P117627	DV160551
36054	425	14	1075	ATTTTGAGTGCAACTACCACAGATACAGGGAACTGGCATTAGAGTGGCTTATTATTA	35141	A_95_P198112	TA16709_4097
36055	425	15	230	TTTACTTTGCTCACCTTCGCAGGTCAGATAATTTCAGTTTTTTCACATCAGTTCTTTTG	35143	A_95_P154627	EG649678
36059	425	19	3048	GAGTAGTGACGAGTTATACTTGTAAAGGCATTTTGAACTATACGAACTCCAACAAAA	35151	A_95_P009241	AB095098
36065	425	25	709	CTGCTGTTGCTTAGGTAAATCCCGATGTTAAACCAACCGAAGAGATTAAAAAGAAGA	35162	A_95_P270871	EB450283
36067	425	27	611	CAAAATCAGCGCGGACTTGATGCATTGCCTGGAATGACTCTTTTATCCGCATGTTTG	35166	A_95_P157172	EH615204
36069	425	29	190	TGTATTGATTTGCCAGTAACTGTACTGTCATTGTGTAATGACATATTCTCGCTAAGGC	35170	A_95_P109872	CV019482
36074	425	34	1725	GAAAAGAGACTTGCTGAAATGGGGATTGAATTGGAAGATGATGGACCGGTTTGTCA	35180	A_95_P007426	AB102808
36077	425	37	704	GTGTTTAACTGTGCGTCTGCGCGCAGAGTTTAAAAAAGAAAGAAAGAAAGACCATG	35186	A_95_P215542	TA20509_4097
36079	425	39	215	TGATCGCATGTTGCAGTAACATTTAGTTTTCCAAACACACGCCATTGAGGAATCTTCC	35190	A_95_P112852	CV020882
36080	425	40	2222	CGTCAGTATGATGCTTCAGTGAAGATATGGTTGTAACTTGTAACCAAACAAAAGAAA	35192	A_95_P239839	AJ627182
36086	425	46	1344	AAGTCTTAAATGTATCCGAGAATGCTTTTCTAAGAGTAATTCGAAGATGTATTCGACT	35204	A_95_P208957	TA19085_4097
36088	425	48	75	TACTTGCTGGGTCAGCTGATTTCAAGACAGAGCTGAGCCAGTCTGATATGTTTGATC	35208	A_95_P138607	TA13824_4097
36092	425	52	414	CGACTGAAATTAAATATTATCATGTATCATACTTCAGTGGATTGGATTTTGGGCATGC	35216	A_95_P132217	EB432660
36094	425	54	873	GCTGACCCTGCAGATTTGTTGGATGCTCCAGAAAAGATGGATACAGCTTCTTATCAT	35220	A_95_P010761	TA14812_4097
36098	425	58	785	GTAGGTTCCAATGTTGTAAATAGACAGGTTTGACTTGCTAAAGCTCCATTCGACAATT	35228	A_95_P219022	TA21308_4097
36099	425	59	1573	CTATTGCCTTATATGTCGAAAAGTGTGCTGCAAAATCAATCTCTTGCCAATACAATTT	35230	A_95_P224137	AY433959
36104	425	64	836	CGATGTTCTAATAATGTAAGATACACGGAGATATTTCTTTTCATAGCAACTCTGATCC	35240	A_95_P143632	TA16928_4097
36106	425	66	477	ACCGTTAAGAATTGGGGTTTGATTGTTCTACTTCTATCTAATGTATTTCTCTCTACTTC	35244	A_95_P018181	FG641597
36108	425	68	499	ATGAGCTTTCTTCTTATTATACAAACGACCAGATAGCTTCTAAGCTACTAAATGGTGG	35248	A_95_P111372	EB437086
36110	425	70	546	TTAACGATTGTAAATCAACTGAGGTCCTTGAAAGCAATAAACTCCTCTTATCTCAGTA	35252	A_95_P180762	TA12821_4097
36111	425	71	276	TAAGGTAAGGTTTAGCCCGGTTTGTGTTATATGGGTAACAATACCGGTGCTATTGTC	35254	A_95_P123662	DW003532
36113	425	73	143	CCATTCCCTATCTTGGAATTTGTTGGAATCAGATGTATTTGGTGAATTTGGTTGATTT	35258	A_95_P129247	EB428957
36116	425	76	121	GGGACCCCTATTGTATCGACTTCTGCATTCCCTATGGTCAAATGATGAAATTTGTTGC	35264	A_95_P100548	BP535422

36122	425	82	663	GCCTACCAAATGAGGTAGTGATCAATTCAAAAATTTGGGGAGCTAATTAGTTTTTCA	35274	A_95_P288388	FG186056
36126	426	1	1537	GCTTTGGAAGACTACATGCTATGCTTATACAAGTATTATGTTGCTTGTCTGTTTGATA	35116	A_95_P006356	TA15030_4097
36137	426	12	273	CACTGTTAGTGTTGAAAGACACCTTACTCCAACTAGATTACCTGATTATGAATCTTAT	35138	A_95_P216987	TA20828_4097
36138	426	13	810	CATGCATTGGAATGGTCAGAACCAAAGGCAGCAGCTGGGGAAAACAATTTGCTACA	35140	A_95_P291993	EB425909
36147	426	22	1534	CAGCTTGTAATTCTCTTGTATGCCATAAGAATGCAAGGATTTGCTAATTGTGATTTTC	35157	A_95_P007446	TA13801_4097
36148	426	23	156	CAACTGAGTCTTGAGATAGTGACGAATGTCGGACTTATATTTCAATTACAAGTGTTAA	35159	A_95_P004556	EH620851
36152	426	27	821	TCCATTGCATACCTTCCCTACGGGAACTGGATATACGTGGTTGGTTATTGGAGTACTT	35167	A_95_P269981	EB428526
36153	426	28	992	CTACTTCAAGATAAAATGACGTTCCGTTTGGTACAAGAATTGCTGATTAAAGTTGAA	35169	A_95_P021161	TA20789_4097
36156	426	31	617	TCTTCATGTTGTGCTACTCGACCATGAGACATTGTACATATTATCTCTTGTATCCAAAT	35175	A_95_P159142	FG163977
36158	426	33	1232	AGAACCGGCTAAACTTTCTTTTCCATGTTTGCTTTAGTTTTTGCTTTGGATTTCTAATG	35179	A_95_P013636	TA14494_4097
36160	426	35	807	TCCATCAGACATGGCCAAGTCTCAAATATGTGCTGGATGCTGACTATTGTGATATTG	35183	A_95_P281708	TC50226
36161	426	36	1375	ACTCTTATGTTTTGAACGGCTTAAGTATGATTTCCATGTTATATTATGCTATTCCGCTG	35185	A_95_P026456	TA14848_4097
36163	426	38	440	ATTTTAATATAGGTATTTGAAGCTATTCAGTTGAGAGTTTCCGGCGATGGCGTCAGA	35189	A_95_P190042	FG144865
36167	426	42	378	GTGTACGTAGAAGCACGAGATGAATGGCATAGGATGTTGAATGAGGATAGAACTTC	35197	A_95_P114182	CV021486
36171	426	46	1369	GGGTAAGGAGTTGATTGTTGGGTCATCTTATTCTCTTATTTCTCTATTTGACTTTCAAG	35205	A_95_P110472	TA12248_4097
36177	426	52	809	GAAAACTCCTACGAAAGAAATGTTCAGCCACCTCCACTATCTGACAAGACCAGAGAG	35217	A_95_P191697	TA15294_4097
36178	426	53	699	ATAAATGCTCAAGCCTTATCTGCATACCTGCAGTTTCAGTCTGTATCTAGGGGTGTTC	35219	A_95_P296038	EB449538
36183	426	58	360	GAGGCACCATTTACTCTACCCATGTCATTCTATACTTTCACTAGTTTCAACACATCGTT	35229	A_95_P078150	BP527440
36184	426	59	443	GTGGCTTTGTGTTGTCAGCATGGATCGAAAAGGCATGATGGCGAATGTTACTTCAGC	35231	A_95_P155612	EG650166
36186	426	61	940	TTTGAGGATGGCTGCTATGTTCTGGATAAGATATTTGGAATGTAGAAAAATGGAGA	35235	A_95_P223127	TA22184_4097
36187	426	62	404	CTTTGCTACGTTATAATTCTGTGTGATGGTAATAAGAAGCTTTCTGAGCTGCTACTTG	35237	A_95_P018061	TA13981_4097
36189	426	64	1049	TATATAGAGGGATTCCTCTTAAACACTTTCTGCAATATGCTGGCTTACAACTTTTGCTC	35241	A_95_P197242	TA16519_4097
36191	426	66	430	CCTTTCCCTCTACTTTTGTGTTGATTTGAGTATGATGAGAGTTTGGGATACAAAATAG	35245	A_95_P143997	EB447197
36193	426	68	285	AGTGAGTTTTTATTCGGAAGGTTCGACGATGCAGCTCAAGTTAATACCTGGAAATTC	35249	A_95_P167971	EB439337
36195	426	70	759	TTTATTGCTACAAACCGTGATGCTGTTACCCATCTTACAGATGCTCAGGAATGGGCA	35253	A_95_P126552	DV999727
36199	426	74	713	CCAAAGCCCCGTTGTTCGAGCTTTCGTATGTTTGTTTCAGTTATGGCTTCTGCGTTTTG	35261	A_95_P222102	EB439875
36205	426	80	877	TTACCAATATATGTCGGGATTTACTGCCCGGTGGAAATATTATTTTATCTGGTCAATC	35271	A_95_P201057	EB427795
36206	426	81	527	TGTTCTCAACGATTCCCTTTTGTAACCGGTTCCTAGCTCCATTTGAGTTCAAATTTGGC	35273	A_95_P108367	BP530524
36207	426	82	401	TACCTATAGTTCAGATATAGCCAGTTATGGTGTTATTTTGATGGACTTTCAGCCATTG	35275	A_95_P024986	EB433044
36214	427	4	694	TGGCTTGTTTTGCTAAAGGGATATAATTTGAACTATGTCTAAATAAGATAGCACCCCT	35288	A_95_P121612	DW001701
36219	427	9	903	TCTGACTTGCATTGCATCATTTGGCGATAACTGTGTTTTTGAGGATGGCTGCTATGTT	35298	A_95_P269026	EB438854
36221	427	11	788	TATATATGAATTGCTATTGCCCAGGTTGGGTGAGACTGCAATGACGAGTGGGCTGA	35302	A_95_P294713	FG166045
36225	427	15	237	TAAATTTGGACTGTATGAATGATGACACAGTTGATGAGACCTCGATGATTGCTATAA	35310	A_95_P158987	EH616877
36234	427	24	750	TAAAGGTAATATTTGCCACAAGGGATATTTGTATAAACTATGTTCAATTCGCTTGCCC	35327	A_95_P028616	TA16788_4097

36237	427	27	860	TAGCCTGGAATTTAGGCACACATAACAACTTTAATTCTTTTTACTTTCTTCAGCGAGTT	35333	A_95_P020221	TA17157_4097
36241	427	31	239	AGTCGACCTTGAATCTCGCTTGGGAAAGACTCAGGTTAGCAACTCTATTATCCTCTCC	35341	A_95_P079810	BP527852
36244	427	34	772	CCTATAAAGATAGCACCCTTATCACGCAGTTATTGAGGGACAATCTCACTCTCTGGAC	35347	A_95_P290508	DV999880
36247	427	37	1210	TAAGCATAGTATCAGTAGGTCATTATTCCGATTTTCCCCTCATTGGGGAAGGGAGGA	35352	A_95_P219412	TA21389_4097
36250	427	40	577	TATATTTAGAATTTCTTGTTGAGTTGGTATTTCGAGATCTTCTGGATTTTGGCTTCGGT	35358	A_95_P253964	TC53391
36252	427	42	432	TTTCTGTGAATTATCGCCTTGCCCCAGAAACATGACCTGCCCACACTTTTATCAAGACT	35362	A_95_P158797	TA13475_4097
36253	427	43	333	CCTCGACAAGTTTTGTATTTTAAGTGGTATGCAGAGTCTAATTCTGGTAATGACAAGT	35364	A_95_P132012	EB432445
36258	427	48	703	TTCAACAGAAGGAAGAGAAATGGCTATGGTCTTGGTAGGAGAAAGATGAATGTCCG	35374	A_95_P127762	EB427332
36266	427	56	832	GTAACTTAAAACGGAAGGAACTGGATTGAGGCAATAAGTGATTCTGGAGAACAATT	35390	A_95_P010351	TC41609
36271	427	61	242	CACGGGTGCATGATTCAGTCTGTGACATTACTTAATTACTTAAGTTGCTTGAACATTT	35400	A_95_P027411	EB450337
36282	427	72	835	GATGGGCAGCATTTTGAGATTTTAAGCGTATGTTTAATATGGCTGAGATAGTGAGAT	35422	A_95_P224352	EB450269
36284	427	74	835	ATGTACACTTATTATTACAAGGCCTCCCCCTGGAAACAGAAAATTGAGCCAAACCTG	35426	A_95_P230274	DV158655
36287	427	77	397	TGGGTCTTGGCAAAACTATTTTGTATATGCCGAGTGGTACTACTCTTGGCTATTTATA	35431	A_95_P065195	BP136266
36297	428	2	786	ATACCAGATTGGATTGTTATGTAAGAGGGAAGGTTTAACTTATGCTGCACCTTTCTGT	35285	A_95_P180442	TA12746_4097
36304	428	9	842	AAATGATGAGGACAAGCTTCTAAAAGCTGTGGCAAAGCAACCCGTGAGTGTTGGGA	35299	A_95_P220062	TA21528_4097
36307	428	12	254	AATTTGTCTGAGGAACATAGGTTTTTGTTAGTCTACCATCTCTCTCTCAGTATAGCAA	35305	A_95_P034259	AJ718327
36308	428	13	829	TTCCAGCATTCTACAAGACATGTAAACTGCAAGGACATGATGTCGAAAGGTGCAAG	35307	A_95_P125802	EB424899
36311	428	16	755	TATTTTTATACACTAGACATGGCTTGGTTCTACTGGGAAATATTGAACCCAGGTTTTC	35313	A_95_P161112	EH619844
36313	428	18	507	CTGACAGTACCAAAAAATATGAAGCCGCCAATTTATGTGTATTATCAGCTTGACAACT	35316	A_95_P127307	EB426825
36315	428	20	641	GGTGAGACTTGGATTGTAAGTTCGTTAGATAGGATTATGCAATTGTTTGTTGATCAT	35320	A_95_P271066	EB439373
36316	428	21	494	GTAGTAAATCTGTAGCACAAATAACAGGGTGAAATTGCCTACGAGTATGGTTACAGT	35322	A_95_P263196	AM819871
36320	428	25	91	ATGATAACAACTCATAAAATCTAAAGCTTGCTTCCAGTTCTAATAACGTGTCTTCCCT	35330	A_95_P091138	BP531223
36327	428	32	107	CTGATACATTGCAACAGACCAGTTATTTGTGCTTATCTAGAGGTTTGTTCCATTTGAT	35344	A_95_P178632	TA12300_4097
36328	428	33	743	TCATCGTTTGTCTTATATTTGAAACTACTAACCATCTCTTGGAAATATCAGGTGGCTT	35346	A_95_P223847	AJ250174
36347	428	52	466	AAGCTTAGGACCTAGATAAGTCTTCATCTTTGATGGGTGATAATGTGGAGGTTGCAA	35383	A_95_P154017	EB684179
36349	428	54	751	ATATAACCCTCGAATTGCTCCATCAGTCTATGAAAGCTGGGCAGATCTCTGGTGAAT	35387	A_95_P297873	FG132806
36352	428	57	808	AAAGAGAGAACTTGTCGTAGTACTCTGAATCTCCTCTCGTGCACGTTGTCCTTTTCTT	35393	A_95_P126447	EB425766
36353	428	58	288	CTTGTCGAAAACTATCTATCAGTGTATGGATTCACAGGATTATCAAATGGAGTAAAG	35395	A_95_P026276	AM799412
36355	428	60	475	GTTGTACTCACTTGAGGTGATTTCGAGCAGAAATAATTAAGAACTCTTATTCAGGTCC	35399	A_95_P299813	FG633507
36358	428	63	366	TCAGGGTTTATGTTAGCGTGTGAATACAAATTAAGGGATGAATGAGAACATCATTTT	35405	A_95_P133842	EB435538
36360	428	65	326	CTCGTATGTCATTACAACAGACTTTGGTTTGTAATAGTCAGAGCAATAATCTTCTGGC	35409	A_95_P075720	TA19140_4097
36364	428	69	829	CACCGTCATTGGTTCGGATGGAAACAATATTCAGCCTCGATTCCTAATACATTGTTAG	35417	A_95_P017111	DV157821
36365	428	70	612	TCATAGAGGTTGAAGTGTCTCTCTCCCTCCTCATTTTCCCCTTTCATGAATCCGAAAAA	35419	A_95_P253019	EH618843
36366	428	71	818	AAATAACAAATCTTTGGATTTGTGCCCTCATCTTTTTCTCCCCCTGGATTACTTTGAAT	35421	A_95_P117402	DV160325

36369	428	74	1012	GAGGGAACTCTTAAAAGTCCTACTTATGTGTATATTAATTAAAGACTACGTTCGTTTC	35427	A_95_P191692	TA15293_4097
36371	428	76	1580	GAAAAAGATAGGTTGTAAAATTGCATTGGTTTTGCAGTTGTCGGCTGGATTGGCCTT	35430	A_95_P009401	TA14843_4097
36375	428	80	528	TTTACTCCTTTATTCTTCAGCAATTTGAAAACCCTGCAAACCCCAAGGTACACTATGA	35438	A_95_P170391	EH664892
36377	428	82	397	CCTCTGGTTTTAAGTACTATTTCTTATAATGGGTAATCAGTGCTGGCAGGCAATTTTT	35442	A_95_P098258	BP534390
36378	428	83	890	CGCTCTGGTCATCCCAATGTATACACAATTTAGTTTGTGGGATGGTTTATGTTATGTT	35444	A_95_P221022	TA21732_4097
36384	429	4	672	AATTGACTACTATGCGAAAAAGAATATGGTAGTGAACCTTCCTGCAGAGGAACCACC	35455	A_95_P127012	EB678753
36386	429	6	715	GGTTTACTAGCATCGGCCTATGTAATGGAATTTTGTTATCTGTTTTTGGAATTGTTTG	35459	A_95_P191317	DV159804
36389	429	9	630	AATTTTGTTCAGTTCCACAGGAATTCTCAGTTGCTCCTTGTTGGTGGGTTGGATAAAA	35464	A_95_P118507	DV161596
36391	429	11	839	TTTCATTCACAGGGCACTGCTGCTGTTGCATTGGCTTCATATTTCTGCTGCTGTTACTC	35468	A_95_P225652	FG166616
36397	429	17	583	TTGTCTGGTTTTTGGTAATACCTCAAGTTTTCACTTTGGCTTTTTGGCCATGGAATTGC	35480	A_95_P263251	FG643630
36399	429	19	675	TTTAATGGGCTTTCTGTGTCAATGTCATTGCCAAAATCATCTTGTTCTTGGTCGGCAA	35484	A_95_P261336	FG645254
36400	429	20	727	TGGTTGTACCCACTTTTTCTTGTTTCCTCTTATTTATCCGAGCGAAATTCATTGGAAAA	35486	A_95_P149107	DV158658
36402	429	22	0	TCTAGGAAATTTTTCCTAGAAATGCCTATACATCATCTAGCATGCCTTTTTTGCGGCC	35490	A_95_P259766	A_95_P259766
36411	429	31	482	TTTTGCTTCAGGGCTTGAACTTATTCGGCAGAAGCTTCAGATGGAAACACTGCAAAG	35508	A_95_P072460	BP525966
36413	429	33	872	AAGCAGGACTGGCGAATTCAGTGGTTATACAAAAATTTTGATGAGGTGCAAAATCA	35512	A_95_P215417	DV159723
36423	429	43	0	GCTCTGACAATTGGTCTCGAACTCGAAATAGACTTGCTAGTATTGCGTATTCTGTTTT	35532	A_95_P027241	A_95_P027241
36428	429	48	707	CTGTAGGACCATTTCCAGATGTAATGTTGCATGATGGTAGTAAAGGTTATTCCAATTT	35542	A_95_P119607	DV999054
36429	429	49	521	GGAGTGTACAGTTGAATAAGCTGGGTTTCATCAATAACTTTTCTTGTAGCCATGTAA	35544	A_95_P152812	EB683154
36431	429	51	727	CCAGGCTTTGGAATTATAGAACTATGGCATATTGATTGATAATGGAAAGAATATGCA	35548	A_95_P182167	TA13147_4097
36432	429	52	597	TGACGACGTTAACAGTATACGTAGTGGAATCTGATTCACTACTTGATCTGTGTATGAA	35550	A_95_P159127	EH617079
36439	429	59	524	CTGGGAACATAAGTGACTATTTGGCTGCTGATACATGTATTTGCTCAACCTTCGATAT	35564	A_95_P018606	TA16671_4097
36442	429	62	115	GTGTTAGTACAATGTACTCTTGTGAAGGTGTTAGTGCTATCTTTTCTAGCCACTTCAA	35570	A_95_P031556	DW001061
36444	429	64	839	GTCACGAATGGTGGTTGATTTACATATCTCATACTAATATACGATATAGTAGTACTGC	35574	A_95_P226589	EB451471
36448	429	68	455	CGATCATTCAGTGGATTTCATTTGGTGTTACTTGTCAAAGGATACATGGAATAGGTA	35582	A_95_P040316	BP129793
36449	429	69	616	ATGCTGATATTCTGGAATTTCTGGTGGGAGATGGGAAGTGGAAAAGTTGACCGGTT	35584	A_95_P057861	BP134324
36456	429	76	736	AAAGTATTGGAAGTGAATGTTGAGAAAGGGATGCAACACGGTCAGAAGATTGTTTT	35598	A_95_P138602	EB442337
36458	429	78	287	TTGTTTATGATTGGGAGAGGGATCTACAATATGTCTCATGGGCATAGGTAAGAAGG	35602	A_95_P085545	FG637879
36464	429	84	605	TTACTACGTCTTTCTTGGGTTGCATAATTGTCAAAGTTGTTGATTTTAGCCCTTGAATG	35614	A_95_P234724	FG638771
36467	430	2	505	ACAAAAAGCTGTATTTCTTCCTTTCTCTCAATCAAGTTTCATGTGCATAGGTGTGATT	35452	A_95_P052336	BP132898
36468	430	3	685	CTGGTACCTTTTGTTGTTTTTATTGTGGATGTTTTGGTAACAATGGAACTGTTCCCTG	35454	A_95_P120327	DW000159
36470	430	5	551	GCTTGTGTAATCCTTGTTGGCTTTTGGTTACATGATGCTTGCAACGGATTAGAACCG	35458	A_95_P004346	EH617829
36471	430	6	168	ATGTCCTGTACGATTGTTGATACATGGAACGATAGTTGCTGGACTATTAAATTCCTGT	35460	A_95_P145597	EB449365
36478	430	13	481	AAACATTGTCGATCTTAGGATCACGTTGTATGTGAACTATTTGAAATTCCAGTTGCTG	35473	A_95_P160752	EH619425
36483	430	18	779	CAACTATAGTGAGCTGTAGCTTCAGCAGAGTTCCATTTCGTCAGTTCTGCAAATTTGC	35483	A_95_P012281	TC48787

36484	430	19	610	CGTACTTGAAGCTCCAAAATTTGTCCTTTCTCCACCACCGGAGTTTAAAGGGTCCTAAT	35485	A_95_P037348	BP128980
36485	430	20	750	TTGCCTTTGGAGTTTTACTATTGGAGCTTATTACTGGTCGTCGTGCAGTTGATTCGTAT	35487	A_95_P211592	DW000813
36492	430	27	322	GCCAGTGTACCAGTTACTCAATGGCAGTGTATTTGTTTTATAAAAAGATTTGCTCGG	35501	A_95_P212583	TA19867_4097
36495	430	30	260	GGAGGTTGCACCTAATTGATTTGCTGTTAAACATGTTTGAATCGGTGTAAAATGTTGT	35507	A_95_P028181	TA15647_4097
36500	430	35	382	TTCGGGGGGTTGAAAGATTTCTGGGTATAAAAATTTAGGAGAGATAGAGTTTTCCG	35517	A_95_P308853	FG643714
36501	430	36	2	GAAAACTGGATACGTGAAGTTGTCAAGCTTCTCTCAGTCTGCTGCTATGGACATGGA	35519	A_95_P045706	TA16788_4097
36509	430	44	840	GGCATAATTTACCTTCATATTTCAAGTCACTTCTCTTATTAATGCATCTCGGGAGAATA	35535	A_95_P017711	DV160640
36510	430	45	576	GGTGTGATCATGTGGATTCGTTGATATGTGACTATCGAATGGCTGCTTTGTTCCAAA	35537	A_95_P307558	FG638728
36511	430	46	207	AAAGCAAGACTTGGGTATTGTTCCTCCCAATTCAACTGTGTATTATGAGGTTGAGCTT	35539	A_95_P211978	FG197884
36513	430	48	1303	GAAAAAATGTACAACTGTGGGGAAGTAACAGTAATATGTACACCAATGGAGCTTTT	35543	A_95_P008496	AB031321
36520	430	55	882	AAGCCTCTTTCTTTTTCCCTTTTCTGTGCTGGTGCTATCTCATTAAACTGAGTAAGTCC	35557	A_95_P024416	DW000175
36522	430	57	810	AGGCTCAATCTTTATGTGTAAGTCTTTCCTTCAGAGTTACTGTCCTTTCAATTTGGTCT	35561	A_95_P015351	TA15727_4097
36530	430	65	709	TTATAGTGAGGTGGTTCCGGATAGGATTGATCGGGAGATGTTCTGGAGCCGATACTT	35577	A_95_P150287	EB680392
36532	430	67	384	TTAACCATTTCAACATTTGATCTGTGAAACTGAAGAAGCTGTTTTACGTCTTTCCTCTG	35581	A_95_P105657	CV017557
36533	430	68	584	CCGTCTTTTGTCTAGTTTATTGGTACTACTTCTTGTAGTAGGACGTAGATTTTAGTTTT	35583	A_95_P002516	FG170570
36534	430	69	670	TTCTCCATTTTGTGTGTGACTTGTTGCAGGCTCGTGGTTAATTATTGCGCAATGGATA	35585	A_95_P019881	TA13383_4097
36536	430	71	848	AGTAGTCACACGAACTGAGATCGATATGCAGTATATAAAAGCAGAGTACCAGAAAA	35589	A_95_P196347	EB426369
36537	430	72	211	AGTATGCTACAAAACCATACGATGCTAGCTCCGGTTTGCTAGGAGAGGTGGTGATTG	35591	A_95_P131797	EB432206
36542	430	77	812	GAGAACTTTGATATGCCCTTTTATCACCCAGAGACCACTGAAAGTCAGTGTCAGCAT	35601	A_95_P305933	FG147814
36546	430	81	635	ACCTCTGCTGTTGTCACAATAGTTCCAAGTTTATCAGCAATGCATATTCATTCTCTTTG	35609	A_95_P219152	TA21337_4097
36548	430	83	340	AAACTAGTCGAGGCATTTTTTGATTACAGATGGAAATTCTAGTTGATCATTTGGTGAT	35613	A_95_P094723	BP532846
36557	431	7	633	AGTGGCACAATGAAGGATTTTGGGGTCGTTGGTTCAAAAGAGATCATTCTGGTCAA	35629	A_95_P252594	FG185511
36560	431	10	1153	GGTTGTAAGCGTTTTTGGCTTCTTGTAGTTCTTTATCATGTGCTATGTAAGTTATGTG	35635	A_95_P010226	TA14416_4097
36561	431	11	774	GTTGCCATTACATTCTGCTTTAGTATCCTCCAATTTGGCTGAAATATAATAGTAGAGC	35637	A_95_P185687	TA13967_4097
36562	431	12	471	TATCCGAACGTGGAATTATTGCTTTTCGTAGTCGCTTTGGTTGTGATTCCTGGGAGG	35639	A_95_P160802	EH619499
36564	431	14	481	TATGGTCACTTGCTTTTAGTGGTGAAGGTTCACTTCTTGCATCTGGCTCTGCTGATTG	35643	A_95_P034568	EB679195
36567	431	17	180	AACTGAGACAGCACAGTTGTTTTTGAGCGCACCTAAAGATGAGGACATTTGTTCGCC	35649	A_95_P106082	CV017751
36568	431	18	500	CCACATCATCAATCTAAAGGGATGTCATCCCTACGGAGATAGTAGACTATTTGATCTA	35650	A_95_P036813	BP128829
36569	431	19	515	TCGAGCTCTTGTCAGCTACTTCTCAAACATGACCAGAGGACTGTTAGGACAAATTTG	35652	A_95_P264351	BP529347
36570	431	20	561	TCTACCATAACGATTTTGTGGGATCCTTTACAACTGGAATGCTTGTATCTGCAGTTTT	35654	A_95_P047361	BP131638
36571	431	21	1084	GATCTCTAGTCTTTTCTTCCCCTATATTAATAAAATCAGCGGGGCAGAGACTTTCAATT	35655	A_95_P206017	AF081794
36573	431	23	321	TGCAGGGAGTTCTCTTTTCTTTGGCTATTAATTGCACGTAATCTGAAAGGGTGGGGA	35659	A_95_P160877	EH619576
36575	431	25	664	CCTTGCTCTAAATCCCATTTGTGTACTAGTTGATTGTAAAACTGTAACCATTCATGATT	35663	A_95_P288008	EB437505
36576	431	26	590	TTGCGGAATGTAGCCTTTCTTGTCACGTTTAGTAATGATTAACACGTGGATTAACTTA	35665	A_95_P314228	FG166441

36579	431	29	725	CTCTGTATTGTGGACAATAGCACTATCGTATCTTTACTCAAAAATGAATGTCAGTAAG	35671	A_95_P144652	EB448124
36580	431	30	722	CCGATCTTCACAGGAAGATTTTCCAATGCAAGATTAGTAGCAAGTGGGTTGTCAATC	35673	A_95_P149907	TA13110_4097
36581	431	31	510	TTAGAGGAGACTAATTAAGTTACCAGTGTACAATTTTCGACTGTACAGAAGCTTGGA	35675	A_95_P266906	AM840784
36582	431	32	414	TCGAAGAAAGATAATCTTTACAAAGACGCAATGGAAACAGCCTCGCAATCTGGGGA	35677	A_95_P032521	AB120536
36584	431	34	290	CGGTCTGTAAATACACTATTTGCTGCAGTTAGATATCGTGGTGAGATAATTTGTGCCC	35681	A_95_P080255	AM830869
36585	431	35	647	ACTTAACAAATTGGCTGGTTTCTTGGCCCCTTTCTCTTAATGTACATATGTGTCAAAA	35683	A_95_P160377	EH619077
36589	431	39	118	CTTGAGAAAGAATAGAGCCGTTGTAGCTTATTCAAGGATCATTACTTTCAAAACAAC	35690	A_95_P112887	CV020905
36591	431	41	532	TGTGGCTCTCCACACGCTAATAAATGGATTAGGAGTTCATATGAATACTTGTTTGTTA	35694	A_95_P255949	FG635710
36595	431	45	831	ACAGTGACACAAACAGTGATCGATATGATGAGCAGCTTATCAGATTACTTTAACAAT	35702	A_95_P208137	EB679127
36598	431	48	630	AATTCTTGTTTGTTGCACCGATGCATCACTTGGGAGCAACTTTTTCAGTGTAGCTGTT	35708	A_95_P007376	DW003514
36602	431	52	956	GCCCGACTTGTTTATAAGGTTTAACTCCTTTTTGTTGTACTTGATCATATCAGAAGTTT	35716	A_95_P015996	TA19056_4097
36603	431	53	400	GTGGTCTGTTGCTCATTTTAAGTTAACATACTCATTCATGGGGATTCATTTTAACCAG	35718	A_95_P089008	BP530299
36605	431	55	1493	AGTAGCTTCATCGAGAATCTGAAATGACAGACAGCGGCTTGAGACGTAATTCTGGC	35722	A_95_P191987	TA15356_4097
36614	431	64	714	TGGGATTGTTGGAGATGTATTCCCTTAACTATCTAAGGAGAAATACTCATAGATATA	35739	A_95_P218617	EH615151
36615	431	65	564	GAAAAGTTGGTGGTTTTGTTTGACGTTTGCCCACTCTTTGGATTATGAATTTTATTGG	35741	A_95_P142077	EB445642
36617	431	67	622	GTTTGTAATCATAACAATACTTGGGTTCTACTATCTCTCAATTAGTAGGGATGATCGT	35744	A_95_P027511	TA13972_4097
36618	431	68	386	CAACCCTACTTTGAACTCATGGACAATACCATTTTGGTGATTGGTTGACTATATATTA	35746	A_95_P100753	BP535507
36621	431	71	1670	CTTCTCTGTAAATACAGCTGAAAAGCACACATATATTGTCTGGAATATATTGAGAGC	35752	A_95_P009776	AB075950
36622	431	72	851	GTTTTGATTATATATTCAACTTAGTTGTTTTGCGTCGCATGGAATGTAGTGAGTTGAG	35754	A_95_P177312	TA11946_4097
36628	431	78	1168	TATGTTTGTATGGTGTTCATGTATGCGGTCCTCTTTCTTGGCCTAAATGCATGCTTTT	35764	A_95_P203177	TA17798_4097
36630	431	80	326	TTTCAGAGGCAATATCAACTGCTGTCATTCAATGTTAGTTGGTTGGGCAACCAGCTG	35768	A_95_P094238	BP532614
36632	431	82	265	TCAATATTACCAAGTTGCCTTTGCTGCCGCAAGAGGTTTGAAGATGCTGTTGTAGAT	35772	A_95_P099253	BP534854
36636	432	1	839	ACGTATATGTGGTTAGATGTCATATCATCCTTACCTCTGTACTGCAGTGATGAGAAGT	35618	A_95_P245367	EB449740
36642	432	7	454	CACAGATTGCTTTTTCTACATTAAGTTTTGCATGTATGCCACATCTGCTTATGTATGGA	35630	A_95_P221007	TA21729_4097
36644	432	9	792	AACTGGTCCTGATGAGCAGAAAGGAGTTTGCATGATGCGTTGTGTGTTGTAGATGTT	35634	A_95_P272461	FG135963
36645	432	10	1194	GGTTTCTTGTAATGATGAAAGACAATGCATCAAGGCACTTAATAAACTAAGCTTTCTT	35636	A_95_P013771	TA13849_4097
36646	432	11	860	ACCTACAAATTTTGTGTTTTTGATTCGCATGCTTGAGCGATGTTAGAGATCCTACGTG	35638	A_95_P227709	EB677603
36647	432	12	821	CAAAATGGTTCAGACAACACTGTACGCTGTTGATTAATTGGTTTAAGACCATCTCGTT	35640	A_95_P017176	TA13237_4097
36648	432	13	379	GTACAAGAAATTCGAGTTGTCTTTAGGTCTTGCGGTATAATCTCTTCAAGAGAACAA	35642	A_95_P037478	BP129016
36650	432	15	718	CTCTAGGACAGTAGAGTTCCATCTCCTTTTAACTATTCTGGACAGATTTGCAACGAAC	35646	A_95_P273651	FG635928
36658	432	23	440	GATGGACCTTCTGTACAATGTTAAAACTTTAGTATTTCTGACGTTGATATGAGCTACC	35660	A_95_P067335	BP136841
36660	432	25	335	TTAGCAGTAGACCCTCTTTCATTGTATTTGGTGATGGAATCAAATTTCATGCTTTTAG	35664	A_95_P116457	FG629295
36665	432	30	281	CGGGGACCCTAGATGATGCTGATAAGGTTTTGGTAGATGTTGGCACTGGATATTTTA	35674	A_95_P121912	EB679221
36666	432	31	174	CAACCTCCAAAAGCAAATGAAGAGGATCCCCAAACACATGTAAAAGAGAATATTCA	35676	A_95_P089453	BP530511

36668	432	33	771	GACCTAATTGATGTTATTGAGGGAAATCGTAAATACATGAAGTGCATATACGTCTAC	35680	A_95_P128217	EB427742
36674	432	39	528	GATTTCTTCTTCTAGCCTTCAACCAGATATCTAACAACTGTGGTATGCTTCACTACACA	35691	A_95_P127642	EB682835
36678	432	43	491	GTAGGACCAGCAGTTCATTTATCCTTCTCTTGTTTTCCTCAAGAGGAGATAGCTCATG	35699	A_95_P106657	CV017995
36681	432	46	279	TAGTCATGTTTTTCGATCCAACTAAGGGTACTACTATCCAAGTTAACTCGAAGACCAG	35705	A_95_P043376	BP130599
36682	432	47	882	GATATCTATACAGTGAACTGTGGCATGGCATATGGTCAAGCAGCAATGCTTCTGTCA	35707	A_95_P015746	EB427484
36683	432	48	832	TTATGTAGTCGCTGGTTGATGTACTGTGTGTAGAAACTGAATAAACTCTTTTGGTTAC	35709	A_95_P185332	EB677878
36684	432	49	743	CCTTGCAAAACTGTTTAGCTTCTGTTCTGAGATGCATAAAGATGTACTGAGACAATAT	35711	A_95_P121497	DW001581
36685	432	50	913	AAGGATGTTGGAGATGCATTTTGCATTCCATAATCGTTTGTCTGCTTGACTTTTAGTT	35713	A_95_P193907	TA15772_4097
36688	432	53	1408	TGATGTTGGTGCTGCAAAAGAGCTTATGGCTCATTTAGTGAAGCTGCAATCTTCCCT	35719	A_95_P186857	TA14218_4097
36690	432	55	349	TTCACATTAAGCTTCGGGCATAAAAGGAGAGCAACAAGACTAAGACTCCTGGTCCTG	35723	A_95_P114887	CV021807
36694	432	59	755	GTGCTGGGATTGGTTAGAAGCCACCGCTATGGTCCTTCCAACTTTTTATGATTGTTTT	35731	A_95_P018126	DV159856
36696	432	61	1781	CCCCCTTCTCTCTTAATTTGGTAAACAAACAACCTACAAATTAATGTTTCTCTTCTGCA	35735	A_95_P189512	TA14804_4097
36698	432	63	614	CTCTAACTAGCCAGGTCCCAAAGTTGTCTAGTCTCTTGAAGTCTATGGGGAAACATA	35738	A_95_P042771	BP130441
36699	432	64	327	TGCTCTAGATTCTGCTGCTGCTCTTTAAGGAACATATATTTGTACCAAGTTATTCAGT	35740	A_95_P111742	FG638507
36709	432	74	153	GGCTCTGAAGCTCTTTTTGTCGTTAAATTTATCGGTTATTGATGAAAAACTTGAGCTT	35758	A_95_P107902	FS383363
36711	432	76	520	GATTTTGATAAGCTTGAGGAAAGGGCTCTTGATTTCCGTCCTAAGATACTTATATGTG	35761	A_95_P073540	DV161209
36713	432	78	579	GTCATTCGGTGGTTCCAAAATTAGTGTTTATACCAATGTTGATGCATTGCATCTAATT	35765	A_95_P025556	EB436800
36715	432	80	822	CTTCAAAATGTGTTTGACAGTGCACGTGCAAGGGAACGAGAGAGAGAACTGCATTA	35769	A_95_P150442	EB680516
36720	432	85	1309	GTTATTAAGTGTTTGTTATAATTAAGTTTTGGACCGTATGCTGCTTGATGGGTTCGTT	35779	A_95_P009071	TA11879_4097
36724	433	4	443	GTGTCCCAGCTTCATTTGAATCATACGCAATTAAAAGAGAATCATGTACTGATAATG	35786	A_95_P113242	CV021072
36725	433	5	713	ATTGGGTTTAATTCCTCAACAATCTATGATATTGGGTGGTGAAAGGAACAATGGATG	35788	A_95_P142647	EB446082
36726	433	6	812	TCTAAATGCTGTCAGATCCTTATTGCAGAGTGCCAGTCGATTGACATTGACTGCATG	35790	A_95_P309453	FG149083
36733	433	13	621	GTAAATGGACCGACAGAGGGTCTCATGTGATATATTCTCAGCATTCTTACAGCTCTA	35804	A_95_P159102	EH617057
36739	433	19	527	TTGGCTCTGATGGAATTCATGTGGGAGCTTCATAGCCCCTCTCTAATTGTACTTTCTTT	35816	A_95_P122272	DW002294
36741	433	21	357	AAACTAACTAGTCCTGAGAGTCAAGAAAAGAAACATGCACCAGACGATCAGAAACT	35820	A_95_P071800	BP525796
36747	433	27	703	AACTGTTTATGATCACGACACGTTCAGCATGGACGACAAAATGGGAGATGCAGAAT	35831	A_95_P304998	FG185820
36749	433	29	954	ATGTACAAGGAAGAGATGAAGAAATTGAGCTTGTGATTCCGCCAGTCTTTGACAACT	35835	A_95_P015536	TA18756_4097
36750	433	30	1356	ACCCTCAAGTTAGTGAGCCTGTAAAACAAGTTTTATTGCTAGGGACTGAATAAATGA	35837	A_95_P106272	TA14079_4097
36752	433	32	80	CCCTTGAGATTCTATCTTTTGTGCCCTTGAGATTCTATCTTTTGTGCTTATGTACAACA	35840	A_95_P140437	EB444343
36753	433	33	562	TTTGTTGCTTGGTTGTCATAATCACACATCGCTTTAGAAAAGAATTTCTCTGGTTGGT	35842	A_95_P195417	TA16110_4097
36754	433	34	668	GAACTGTTATGGTTCTCTTATAATTTTGCTAATTGTAATATGGTGCTTGTGCGGATGT	35844	A_95_P293598	FG635844
36759	433	39	0	TTAGCTTCTGTGTTCGAACTTTGTACCTCTATATGTTTATGACTAGGTATAAAGCTGA	35854	A_95_P273938	A_95_P273938
36760	433	40	921	AATTGTTTCTGCTCTTACAAGCTGCGTATCTTAAAAATACACAGGAGTACTTATTGTC	35856	A_95_P135512	EB438996
36763	433	43	669	AGATGTACTGGGATGTAACTATCTTTCAAATAGTGAATGGCCAAGATTTCTCTTTGGT	35861	A_95_P254544	EB437757

36767	433	47	721	AACCAAATATGGAAATACCATCTCCATCGCTTTGTGTCCTTATTCCGACATGGTCCAC	35869	A_95_P283788	FG187360
36776	433	56	745	ATGCAGACATGCCTTTTTCCTCTTGATGTTCACATGTAATATGTTGAGTCTATTTGAG	35886	A_95_P245382	EB677364
36779	433	59	704	CTCAAATAGAACGATCTTTTGTATTTCTACGGCACAAGATGGTGTGATACATTTATTT	35892	A_95_P131022	EB431153
36783	433	63	323	GCATTCTGCTTTCTCTTGTATGCTTTTGGATTGTGTTTTAGATCAAGAAAATTTGTGCC	35900	A_95_P014726	FG622502
36787	433	67	780	TCATTCCAAGTGTTAGAAGGAGAGCGTGGTGTAACTGGTAAAGTTGATGCCATATG	35908	A_95_P145242	EB448829
36789	433	69	458	AGTATCCTTGCAATTATCTTGTATTGCCAGAATGCTTCAATGCATTAGGAAAGAAGA	35912	A_95_P209877	FS405773
36791	433	71	757	GATCTGGTAGGCATTAGAAGCTACTTCTGATCAACATTTCATGCAGTTGTTTTCGAAA	35916	A_95_P122322	DW002321
36793	433	73	0	ACGCTAATGTGATTTGCATTTTCTTATCGTCGAGGTAATTATCATTTGCACCAAACAA	35920	A_95_P315603	A_95_P315603
36796	433	76	403	GACACCAGTCTTGGGTAGATTTGTTATGGATTGGCATTAGCAGTATTATTAAAACTTT	35926	A_95_P002276	BP533488
36799	433	79	1513	AAACGCTGTTCCCTCTCGAGGATGGGAATAACAAGCATATTTGGGGCTATATATAAA	35932	A_95_P178727	TA12329_4097
36800	433	80	701	CCTGTTTCCTTTAGTCTTTGTCGAATTGGTTCATTATGTAGACATGTTTTATGAATGTG	35934	A_95_P116522	DV159284
36804	433	84	469	GACTCAAAAGTATGCCATGGGTTAGTTGCTGAAACACAAGTATTAGGAGGTGCTCCT	35942	A_95_P178067	EH619487
36806	434	1	822	TCTATGTGAGTTTGCGTCTTTTCTTAGGGTTTGTTGGTAATAAGACAAATTGGCAATT	35781	A_95_P228709	EB443398
36807	434	2	512	TGTATTGAAGTATGTGGTGTATGCTGATAATGGATACTCAAAAATTGGGAAGTGGT	35783	A_95_P107732	TA12078_4097
36808	434	3	1071	CTGTAAGTGTGCTTGGTCATTGAAACGGAACTGTATTCATTCATTTTTGACGATATAC	35785	A_95_P022026	TA15152_4097
36809	434	4	671	TGAGGTAGCAAGTATTTCGTTGAGTTGGATTCGTAAGTTGTCTTTGTTTTTGATGATT	35787	A_95_P021461	TA14285_4097
36810	434	5	729	ATACCAAGATAGTGAGACCTGCACAGGTGTATACTGGTGTATGGATGCGTCACTATA	35789	A_95_P209767	TA19260_4097
36812	434	7	788	CTCATATAGATGGTTAAGAGTGCTATGACAGTTGCTAAATGATCATTTGCTTTGCTGA	35793	A_95_P016406	EB678695
36813	434	8	289	AAGTGTACTATGTGAATGGCGAGTTTCTTCATCCTATTGCGTTGAAGTATGTAGAATT	35795	A_95_P145997	EB449808
36816	434	11	495	CGTGGAAGAACATTCCATGCACCATGTGAAATCTCGTATTAGTTTTGATTTGATTTCA	35801	A_95_P032036	BP530801
36818	434	13	922	GCCAGTAAGGACCTTGAATCAATTATAGTACTTTTGTGTAGCACTTGAGACCCTAATA	35805	A_95_P185872	TA14008_4097
36819	434	14	236	TTACCAGGCTGATCAACAGGAATACCACCATACCTACAAAGAAAAGCCAGGTGTTCT	35807	A_95_P241385	AJ718290
36820	434	15	0	AAGATGATGGAAAGGCTGTGGGGTGAGAACTTCTTGACCTGCACAAAAGTGACACA	35809	A_95_P311248	A_95_P311248
36821	434	16	788	GAAAGTATGCAAGAAGCAATGCATCGATCAAATTTGGAGATGAGTGGTGCAGAATA	35811	A_95_P121067	DW001078
36823	434	18	258	GCTTTTCGTCCGGGGACTAATAAATATGTTGTGGATTAAACTTTTGTTGAGATTTCTA	35815	A_95_P069945	BP192481
36830	434	25	1172	AAGTTCAAAGAATAAGACTGTCGCAGATGGACTCACTTGGACCCACGTACATCAGAC	35829	A_95_P034808	AY729656
36834	434	29	428	TACTAACAATGTTGGTTGGTTTCCCTGTTTCCTTCAGATGTACAATAGCTAATTGACA	35836	A_95_P002146	TA15963_4097
36841	434	36	1819	TTTTGTATTTGCAGTGTTCAATACAATGTGCAGATATACATCTCACTTCCCATTCTGAT	35849	A_95_P239384	AY220479
36843	434	38	197	TGTCTGACATTCGTCTTGGAGCTGGTGTATTAATCTTGAAGTGGAACAGTTTGATCTT	35853	A_95_P133807	EB435495
36846	434	41	3187	CTTTTTCCTAGTGAAAGTGTAAGACGATGGCCTATATTATTTCCTGTTGCTTATCATGT	35859	A_95_P007901	X79794
36847	434	42	836	TGAGTCAATTTTGGAACTCGTTTGTGAGATCTGCTCGGAGCCAGTTGTTGAAGTCTT	35860	A_95_P149227	EB678942
36848	434	43	818	AAAGTTGAGACAACTCCTGTCAAGGAGAAGTCTAAGGAAACTTCACCACCTCCTCCT	35862	A_95_P245297	DV159622
36849	434	44	87	CCCTTGAAGAAGGAAGGGAGCTCGCATTCATGTATAAATTTTGTAAATTTTCTACAG	35864	A_95_P142942	EB446355
36850	434	45	627	CGTTCGCAGACTCGGAGTCACCCTCTGTCCTTGTTTTTCTATTGCATACTCTTTATTTA	35866	A_95_P065750	BP136415

36851	434	46	326	GGTTGTTGGATATTTGGTTTAAGGCATAGCAATGCATTTGCATGGTGCATTTTCTTTT	35868	A_95_P002216	BP531361
36858	434	53	568	ACCACTCTGTACTTTCTGACAAATAACCCATGTTTACACTGCTGTGCTGAGACGAACA	35882	A_95_P049406	BP132154
36861	434	56	307	ACTGATGGGGAATCAAATCTGAATATCATTGCCATCCAAGCCCAAGTGGTTCCACTTT	35887	A_95_P106602	CV017969
36863	434	58	617	CTCTTGACACTAAAAAGAGAGTATTTTTCAAGCTTGGGTTCTCTATTGATGAATCTGG	35891	A_95_P047386	BP131645
36864	434	59	589	GGTGAGCCTCGCTTATCCATATGCTATCAAATTTTGTCCATGTTTGAGATATTTCTTTG	35893	A_95_P140037	EB443965
36866	434	61	851	AAATTCAAAAACTGGAGGAGAGCACAATCTGGTTGCATGGGCAAGACCCTTGTTCAA	35897	A_95_P290018	DV161730
36867	434	62	898	GTTATGGTGGCATTGCACCTTGTTTACTGCATCTTTCATTTTGGTACAGAATGTTAAAT	35899	A_95_P007881	EB446591
36869	434	64	297	GCTGGTGGATATCTGGAATTAGAGTTTTTAAATTTTCATCTCCCTTCAGCTAAATGAT	35903	A_95_P111382	DW003761
36870	434	65	442	AGTAGCTACTAGCTAATGAGAGTTGAGATGGAGTTGGAGTAGTACTTATCAATAAG	35905	A_95_P029096	TA14334_4097
36873	434	68	1033	GTTTCTAGGGGTACAAATTCGTTTACCTCTAAGTTATGGTGACTGTTTGGATTTTTGT	35911	A_95_P193172	TA15614_4097
36874	434	69	699	ATGTACATTGCTAACATGGACCCATGATTTGGTGAGGTAGGTTTCAAAGGTTAGTGT	35913	A_95_P291123	DW002771
36876	434	71	576	AAACTGGGTGTCATTGTGGTGTACTCATGCTACTCTTCTGCACATGTTTTCGTATGCA	35917	A_95_P288198	FG634947
36877	434	72	813	AAGGTCTTCTTTCACAAGGAGCATTTTATGGTGTGTTTGATGGCCATGGTGGCGTTG	35919	A_95_P119552	DV998906
36880	434	75	549	TTTGTCATCTCCTGTTCCAAAGATATTGCTGTTAGCTGGGACAGACAGACTTGACAGA	35925	A_95_P146152	FG164293
36882	434	77	591	ATGCTTGTGTAGAGAGGGGGGAAGAACTCATTTGCAATGTGGATTGTGACCTCAAA	35929	A_95_P020471	BP133283
36885	434	80	1266	ATTCCAGATTCTCCTGGTCCGCAAGTTGCCTCACATATGCCTCAAGATTGTTTGGTATT	35935	A_95_P286393	EU700061
36887	434	82	847	TCCTTCTGGAGTAGTGTAACTGATGATTGTGCTAGTCATGGACAGAAATTTCACATAC	35939	A_95_P266291	EB424707
36890	434	85	460	TATTGTTTCGCAACTTCAACAAATCTTCGATGCTGACTGGACTTCGCCATATGCAGTG	35945	A_95_P260966	AM811421
36893	435	3	793	TTTTTCACTTGTTTGGGTCAAGATTAATCCATTTGTCTCCAAAGATGATCCTGCAGCTA	35950	A_95_P118012	DV161028
36895	435	5	422	GTATGAAAGGAAGCTGATTTGGGCTGTAACACGAACTTATCAATATATATCTCCTCTT	1861	A_95_P000051	FG625247
36900	435	10	680	CTTCCCGTCATTGGAAATTTCACCATTCCTCTCTCTTATAGCGGCGAGTATAAGCTTCC	35963	A_95_P136547	EB440322
36901	435	11	523	GCAAGCATCCAATTGTTTGAAATTTAACTTAGTTAATGAATCAGTTTGCCTGGCTTAT	35965	A_95_P124372	DW004214
36909	435	19	672	ATTAGAAATCCATAAAGGTGGAAGCTTGGCTCGCCCCCACTAGCAATTATACCCCAG	35981	A_95_P316278	FG195029
36910	435	20	1318	ACGGGTCAGGTCTGATGAGTGTACCTGATTATTTACACTTACATGTGGCTTTATAAAT	35983	A_95_P217572	AJ271748
36913	435	23	1231	TCGAGGACTCCACGAAATACATGTACCTTTTGGCCTGTGCAGATTAATGTATCTGTTT	35989	A_95_P190452	TA15018_4097
36917	435	27	269	AAAGGATTAGATACAACGGATAATGATGCTGAGGAAAATGAGGATTTTCATGGGCG	35997	A_95_P159122	EH617074
36922	435	32	1243	GATTGGGAATCGTAATGTGTACAAAGGATGTTGCCTTTCTTGATTGTCTATCATGTAA	36006	A_95_P114002	TA13144_4097
36924	435	34	971	TTGGTGGAATCTACTGCGTATCATGCCATGGAAATGGATCAAAATTGTGAATGAAAG	36010	A_95_P018156	TA16444_4097
36928	435	38	482	AAGGGCTGATGTTGCTCCATCTATTTCTCCACAAGATCAATAATATCTCTCTCTCTTCT	36018	A_95_P306423	FG635180
36931	435	41	184	ACGAGAATGGGGTGAAGAAAGTAGTGGAATACAAGTTTCAACGCTGACAGGAAAC	36024	A_95_P106432	EB450504
36932	435	42	757	ACGGCCGAAATAAATGGAGCTGATGTTGTAATTAGTCTCTCGTTATTCAAGAAACTTT	36026	A_95_P190937	EB677483
36933	435	43	757	CTGCAGAACTTACTCTGTCATATTCTTGTAGTATATGAAAGCTTCACAATTGTACTTGT	36028	A_95_P211537	TA19634_4097
36936	435	46	429	TTAATGAAGGTGCATGCGGCAATGAGTGCAATGAAGTAGTCTCCTGTGTATGGGTTC	36033	A_95_P187672	TA14398_4097
36937	435	47	724	GTTCTCTCCTGATTTCCCAGCACACTCAAGTCTTTTCTTGATTTCTTAACAGTTAAAAT	36035	A_95_P273841	TA12752_4097

36939	435	49	473	GACCAGCTCGGCTGAACTTTAATCGCCACTGCAACTTGATATGAAAGTCATTACTTCC	36039	A_95_P234814	FG640961
36941	435	51	572	GAAGATAGGTACTGTAGGCGGAGTGATGCCTTATGTTGCCTGGTTGAAGATATATAT	36043	A_95_P059421	BP134736
36944	435	54	819	ATAGGAAGATGAGTTGCAATAGATTCATTTCCTTGTAGACTGATACAGATATTAGTC	36049	A_95_P125027	DW004831
36946	435	56	469	CGTGATCAATAGTCGGTTTGTACAAGCAATTTGAACAGGGTTTTCTGTGTTGTTTAAA	36053	A_95_P030061	BP526699
36947	435	57	455	CTAGTTTTGTGTAAGTTACATTTGGTACATAGTCTTCCAGTTATGCTCTACTTTTGTCC	36055	A_95_P097638	BP534127
36950	435	60	528	GTTTTTATGTCAGCAACAGAAGCCCAAGCTTATGGAATTGTTGATCTTGTAGCGGTT	36061	A_95_P006906	U32397
36953	435	63	523	AGGCATGACCTGTCATCATCAAAGCTGAAATATGATTTCTAATGTATAGGTTAAACA	36066	A_95_P047661	BP131713
36955	435	65	240	TGTTCGCATGTTTCGTTTTATGTTATCTGTTGTGAATAAAGATTCCGAATTCTGTTCTG	36070	A_95_P105417	CV017455
36957	435	67	507	CAAGTCAGTGCCTTCGTAAATTTTGGGTTCTAGTACTAGTACAACTAGTTCTTGTTATT	36074	A_95_P038766	BP129365
36966	435	76	790	TTTTACTGTTCAGCAGACGATTGGATGGGAAACTCTGAAACAGCACTCCACCTGTTTC	36092	A_95_P234404	FG172576
36967	435	77	636	TTCTAGTAACTCATGTTTCTTCTTTCACATCTGTCTTCTGGTTGGCCTTCCAATCCATG	36094	A_95_P159677	EH618121
36968	435	78	379	GAGAAACAATAAGTCACCAAGGTACTACGATGGTAGATACTGGAACCATGTGGAAG	36096	A_95_P110452	CV019738
36973	435	83	156	CACAAGAAGGAGAACATGAACAAAAGAGCTATGACCACTGGAAAAATTGAGCAGAT	36106	A_95_P033844	AJ717804
36976	436	1	813	GGATGACTGTTGAACTCCTCATTAGCTCTTTAATTTATCCCTTCTTCCAAACTTTGCTC	35947	A_95_P010331	EB439699
36981	436	6	571	GAAAAATCATCTTATGCTGTATAATCTGTTCTTGATATACAAACTCGTAGACCTAGCC	35956	A_95_P025816	TA20291_4097
36982	436	7	875	CGGAGATCCCAATTCTTTACTCCGTTTTGCCTTTATTGAATTTATTGATGAAGAAGGA	35958	A_95_P126052	TA15544_4097
36989	436	14	697	GGGGGATCCATCATTCTTTGTCTCAATTACTGCATAGTTATTAGATATTATGATGAGC	35972	A_95_P143987	EB447187
36993	436	18	1726	GATTGCCAAGAATTTGCTCTGTTGCAGCAACTTCCCTAATTGAATGGTAGTACTTATG	35980	A_95_P176512	Z93768
36998	436	23	675	CAGGTTTTATTGGTGTTTCCAAGTACACGTCCAAGGAACATAATTTTGCTTTACCTTTT	35990	A_95_P019056	EB429308
36999	436	24	451	AATGCCTCTTCCTTCCGCCATTAATCCATCTCCTCTTCTTCAATCTTGAAAATAATGTAA	35992	A_95_P280563	AM820707
37000	436	25	396	GGATTGGCCAGATGATTTGATCACCGTGATGAATCAATTTAGATGGGTTAAATGATT	35994	A_95_P133407	EB434850
37001	436	26	653	CCTGTGACCTCTACAGCTATACAAATGGTATTTGGTGATACAGTGGCGATTGCTTTAA	35996	A_95_P275013	FG201694
37004	436	29	797	CTGAATCAAGCTGATGGAATGTGTCCATTGTAACAAGATTATATCCATTGAAACTTGT	36002	A_95_P012256	TA16431_4097
37007	436	32	622	AGGCATGGAGCACAATTTTCTGATATTAGTGTCTTTTGTTATCTGACATTGTGTCCTCT	36007	A_95_P186157	EH618496
37009	436	34	809	AAAGAATATAAAGGATGCACGGTCAGCTGCGAAGCACCTTAACGAACAAGCCCTTG	36011	A_95_P228479	EB679608
37010	436	35	377	ATGCAAAAACTCTTGGCGAATGGGCTGGTTTATGCCAAAATTGATTCTGAAGGGAAA	36013	A_95_P004996	EH666031
37011	436	36	935	CATACTCTTAGGTTTTGGAGAGGATTCATGGCAGCTTATTTCTTATGTTAACATCATG	36015	A_95_P025391	TA13263_4097
37015	436	40	401	TGTGAGACTGGCAAGTTGTGTTAGTGGATGGTTTTAATTCTGATTTGTGTAAATAATT	36023	A_95_P188872	TA14666_4097
37018	436	43	688	TTTGTGGCAGTACAGGGCAAGGGTACTCTGCTTTTTGATAATAATACAGATCTTTCCA	36029	A_95_P269056	DW003891
37020	436	45	1120	TCAGTTGAGGATCTTACAAAGCCATTTGTTTCCATGTACTTTGGCGCGGGCTATTTGG	36032	A_95_P208552	TA18993_4097
37030	436	55	293	GAATGTTTAGCTTGATATTTCATCTTACCTAGGAGGTGGGGATATTCTTTCTCAAATG	36052	A_95_P114082	CV021434
37034	436	59	205	ACATACTCTTCAGCGTTTGGGAGAGGATTCGTGGGGGCTTATTTCTTATGTTAACATC	36060	A_95_P104827	CV017187
37036	436	61	654	GTGTTTGCAACTCTACTGAGTTTGCACTTATTATACATTAATCTTGAGATGGAGAGTA	36064	A_95_P250282	FG644533
37037	436	62	1836	GCTGCAGAGAAGTCCACTTTCCTTTCTGTTTTTATCTGAAGGAAAGAATTATATTTCT	36065	A_95_P022346	TA15836_4097

37038	436	63	696	CTGAATATATCTGTATCATATTTAGTGGGGAGAATGGCCTCCTTCAGGGTGTGAAAG	36067	A_95_P234949	EB446680
37040	436	65	1739	TCTTGTTTCTGTGCCATGGGGGCTATAAATAACATCACAATTGTTTCACTGGGCCAAA	36071	A_95_P187652	TA14394_4097
37041	436	66	852	CTGACGACATGCAAAGGAGCTCAAAGAGACAGTCGGTGCATGTATGATGAAAAGTG	36073	A_95_P268031	FG139523
37044	436	69	873	TTGGGGTCTTGCTTCTCAAATGGTATATATAGATAGATCTTTCTCTTCCCTCTGCATTG	36079	A_95_P228499	EB449516
37053	436	78	766	GCTTCTTTTGGTTTTGAAAAGCAAATGCAGTTTTTGGTTGTTGGATTCTTTAGGGATA	36097	A_95_P116492	DV159243
37055	436	80	1521	CACTTCAATATAGAAAGATGGATTTTGAAGAATTCTGCGCAGCTGCCTCAAGTGTTC	36101	A_95_P024196	TA17300_4097
37056	436	81	868	CTCTCTGAGTGACGGGTCTCTTTGTTGTGACCAAAAAACTTATACATTGTTGTACATG	36103	A_95_P269586	EB425527
37058	436	83	883	ACTTCGAGATGTGCTATAGTTTTCCTCTAGTATATTATTCGAAGCCGTCATCTTCTTGT	36107	A_95_P115522	DV157776
37059	436	84	869	TAAGATGAGTTCTATGTTCTCGTCCCTGATTAGCAAATATGGGTGGGGATCCATCTG	36109	A_95_P272761	EB677959
37062	437	2	721	GTTGTACTAAGTTTTTGCCAACACAACATTAACCGTAATAAAACATACTCCCGTTAGC	36114	A_95_P159722	EH618175
37063	437	3	431	TACTGTGTGCTTCTGGTTCACTGCATCGCCGAGATCCAAATTCATTTCTTATCATTGTC	36116	A_95_P030201	TA18314_4097
37065	437	5	858	ATGCTGCTCTTTTGCACTACGAACATGGAGGGAGGAGCTATCTCTGCATTATGATCT	36120	A_95_P269826	FG167698
37067	437	7	855	CAACAACCTTCTGTGGCTTCATCTTGAGAAATTTGCTGTACTATGTAAGCTAAAAGAT	36124	A_95_P213707	EB425095
37070	437	10	737	GTGAGGCTATTGGTTTTTTCTGCTGGTTTCTCCAGAGTTCTCCTTGTATGTATATTAAA	36130	A_95_P216467	DV160776
37075	437	15	888	ATCCTAGGGGCATAACTGCTGCTCATAACTGTACAATGATGGCTGTAGCACTTATTG	36140	A_95_P144362	EB447728
37081	437	21	460	AAATGGGAGGTGCCTCTGCCTAAGGTAAAGTTGGAATAGTGGTCTTATTCTCATCTT	36152	A_95_P147752	EB643436
37084	437	24	248	CCGGTAATATTTGATAGCACTTCAACGTCGAACATGGAGCTAGTAACTTGCTCAGTT	36158	A_95_P036833	BP128838
37097	437	37	743	TGTTATAATCTCATTATGTGGGACAGCTAATGATCCTGGTTGAGTTGAAAGTCTCTTA	36184	A_95_P183232	TA13411_4097
37104	437	44	1565	CCTTTCGTGCACAGAACCAGGCATTATGAAATCATTTTCAACTCTTGGCATAAATATT	36198	A_95_P202292	TA17603_4097
37106	437	46	1649	GCGAGTATATCAGTTATAGATAGCTATCCTTTTGATGTCTTTCAACAAACTCTATCCTT	36202	A_95_P246857	Z48977
37107	437	47	925	GCACTTGGAGTTTGTGAAACAGCTGCAACACCACTCTTATCTTCCTCATGTGTCAATA	36204	A_95_P009061	EB425363
37111	437	51	129	TTGCAACCTTTGGCTTTAAAACCAGCGGATAGGGATTGATCCATGTAGGTAGAAATG	36212	A_95_P051371	BP132629
37112	437	52	795	GGACAGAGTTTACTATTGCAGTTAAAGACTCACCTGAGTTAGATGCCTCTGCCTTAG	36214	A_95_P272466	EB450354
37124	437	64	1593	GCACCTTGGATATTTACTAGCTTGAGTTGTTACTTTTTTCAGTGTAATTACTCACTGGT	36238	A_95_P009126	TA16001_4097
37136	437	76	831	GATAGTGTTTATCGGGTTAGTTATTTACAACCATAGAACTATGGCAATTAGTGTTGCT	36262	A_95_P212557	TA19861_4097
37139	437	79	223	TGGAACTACAGTGGCATCTTCGATCAACTTGTACTAGCTGTAAGGAAATAAAACTAT	36268	A_95_P006466	BP530900
37140	437	80	499	GCTTCATTTAGTCCCTTGTAGTCATAAAACCATCATTGATATGAGTCGTATGTAAGAT	36270	A_95_P002761	TA18656_4097
37142	437	82	529	GCTCCTTTTTCTTGCTGTACAGATTCCAGAACCAACTCCTTGTTTATCTCCCTTCTAGT	36274	A_95_P270171	EB683413
37143	437	83	256	AGTTGTGATCATTTTTTGGATTGTGTCTGCTCCTTAGTTTTAACATGGGTTTCTTTTGC	36276	A_95_P144152	EB447311
37146	438	1	536	GCAGCTAAGCTTGAACGTGCTTTGGAGCTTGAAAGGATGTCAAACTTGGAACTGCA	36113	A_95_P064730	BP136135
37150	438	5	1069	GGAGTTGGAGCAGCTGCCTTGTTGATTTGAATTATCTGAGTATAAGTTAATTGAGTT	36121	A_95_P203257	TA17816_4097
37164	438	19	780	CAATATATAGTTTTCTTTGACCCGGCAGCTGAGCTCTCAAGTATCATTCTGCAATATC	36149	A_95_P011281	TA13548_4097
37165	438	20	445	TTCCTACAAGGGTGTATTATTAATAAAAGTGAATTGGCAAATTACATGCACCTTGCCA	36151	A_95_P068985	BP137263
37168	438	23	575	GTACCTTAGAATGGAAAGAAACGTGGTGGGAGAAAAGTGATTGGACCGGATACAA	36157	A_95_P137562	FG144128

37171	438	26	808	TTTGTGACATTGCTAGTGATTGTATCTATGAATGTGTTGCTATGTTCCGTCCATCTTG	36163	A_95_P220742	EB440189
37177	438	32	1573	TGCTCTGTAATGCATGATGATTTGGTGTTTCGAGTTAAATCTAAGAGACTGTAATCTC	36175	A_95_P009076	TA14034_4097
37178	438	33	586	TTCCCCCTCCTCTGTAGTGAATATAATGGTGTGTAGTTATATGATTTTGTGTAGAATT	36177	A_95_P117762	DV160709
37180	438	35	460	CTTGAGGTCTCAAGTGCACGAAATACTTTATAGTGTGCAGTTAAGATCACTGCGTTC	36181	A_95_P073110	BP526131
37188	438	43	2095	GGGCATATTTGCAGCTCCAAACTGGGTTTCGTTGAATATATTTACTCATAAAAGCAAA	36197	A_95_P240014	X83524
37194	438	49	368	GTCGGTGAAATCAAATATTTGCACTTTTGCCCAGTTAAATGGAGAAAAAGAGATTAG	36209	A_95_P183882	TA13557_4097
37197	438	52	1114	TGGTCTGATTATGTAATTTAGACCTAGGTTTGCTATGTACTGTGTACTTAGGCGGCCG	36215	A_95_P238834	AJ414051
37198	438	53	1585	CAAGGGAGAGTGTACCAACAACTGAAATGCTTAATACATCAAGTACGAACTTAATTT	36217	A_95_P210082	AY570725
37199	438	54	730	TATTACGAAATGCTGGTTGTTGAACTTTCTTTTCGCAATGTAAGCATGTTGTTTCTCCA	36219	A_95_P151607	EB681849
37202	438	57	837	AATTTTTGGTTGTTGTCTTGGTTCTCTCCACTCTCGGGGCACTATGCTGCTCAAGATC	36225	A_95_P219112	TA21329_4097
37204	438	59	486	GCACTGATATTATCGACCAAATAAACCGCACCTCAAATTTGTATAGTCAAGACCCTGA	36229	A_95_P124157	DW003998
37207	438	62	612	GTTACCAAATGAGAACACATCTCTGTTGGAACTCAGCATCAGTTGGATCCTTTGACCA	36235	A_95_P053496	BP133193
37215	438	70	689	CTGGGAAGTTCATCCTGGTCTAACATATTGAAAACATGACTTGTTCTTACTGTCAATT	36251	A_95_P118127	DV161142
37216	438	71	1322	GAGTGATTTTGTGTGTGTATAAGAGCAAACGATTGAATAAAGGGAATTTTACCTCTC	36253	A_95_P239369	AF211536
37217	438	72	446	GTACCTCTAACGATAGTGTTAATGGTGCTTAAAGCTGTTCTTTTCTATGTACTCTGAT	36255	A_95_P022966	DW003209
37223	438	78	234	CGGCTTGGCTCTTGCAGCATTTTTGGTAAGAAATTCAGAAATAGCTAGATTTACAAG	36267	A_95_P218427	TA21172_4097
37225	438	80	763	AAAGGTCCTCGCCATCTGAAAAAACTAAGCTTCAGAACGGAAGTACATCCTGGGAA	36271	A_95_P215762	TA20559_4097
37226	438	81	1273	GATCTGATGTCATTGGAAGATATTGATGTGTAAGCTTCCTGTCATGATTCTGTAATAG	36273	A_95_P210812	TA19475_4097
37227	438	82	521	GAGCCTTTACTTGTTTTCATCAGTTTACTGCAAAATCTTGACGACCAGTGCAGCAAAA	36275	A_95_P288823	FG643580
37233	439	3	519	TGGTTTCAGTGTCTCATCAACTTTGTCAAAATATGCCTGAGGTTTTCCAGTTACATTG	36286	A_95_P103447	DW005235
37234	439	4	1618	GTAGAGGAGCAATATTGAGTTTTCTTCAGGTTATGGCTTGATTTGTATTTTTGTATCT	36288	A_95_P018326	TA14549_4097
37248	439	18	854	AAGCAGTGGTGTCAGAACTTGCGCCTTTTCTTCTTCTATATGCGACTTTCATTCTCTCC	36315	A_95_P296728	EB679151
37249	439	19	674	CCATGCGTATCAGAATCTGGTTCTGACATATACAGTAAGCGAGAAGTGATACAAAAG	36317	A_95_P136867	EB440575
37251	439	21	580	GTGCCATAATAATTCCACACAGGTTCCCTGTTTTGTTTGCAAGGAAATTCTCAAGAGG	36321	A_95_P260726	BP129674
37254	439	24	267	AATGCATTAGGTGCATAAGTGCATGTATGCTTTAGACTTGGTAACGTGTATGTATAG	36326	A_95_P098998	BP534725
37256	439	26	398	TCTAGTGAAAAAGAAAAAGATGGGAGATATTGGCATTTTGAGGGGGAGGGGGCCC	36330	A_95_P164982	EH624444
37259	439	29	918	CCTACCAGAAAAGTATGTCAAAATTGTTTTACGGTGAATTGCTCTATACTACGTTCCA	36336	A_95_P148702	EB430421
37264	439	34	859	AATTTGGGGTTTCTGGAAAGGTGTTTTTCCGACGTTAATCATGGTAAGCAATCCTTCT	36346	A_95_P232374	DW000853
37266	439	36	692	TATGTGGGGCTTGCGGTGAAAACTATGCATCTGACGAATTCTGGATCTGCTGTGACA	36350	A_95_P275648	FG643795
37267	439	37	678	GAGTTTTCTAGTCGGAGCAGAGATTTATATGCTAGTAGAATATACAGAGACTTCTTG	36352	A_95_P014521	DV162558
37268	439	38	861	AATGCTGCTATGTTTGGTATGTACGAAGCACTAAAGCAGTACTTTGCAGGAGGCACA	36354	A_95_P150527	DW000396
37270	439	40	508	TTGTACTTAGAGGCTCATGACTAGTGACACCAGATTCGGGCTTTATTAGTGTATCTTC	36358	A_95_P147757	EB643437
37271	439	41	467	GGGAGATGAAGATGAGTTTTACAAATTAGTTATAAGATCTCCGCAAATTGAGTGTCA	36360	A_95_P274493	AM793040
37276	439	46	712	GGAGTCTACTTCGCATAATGTTGACTTTTCATGCCTTGATGTTTTTATATAAAGGGTA	36370	A_95_P271641	EB444516

37279	439	49	757	GAAAATATTTTTGCCAATCAAATGCTCTTTGGGAGTGATGGAGAATGTGCTGGGTTT	36376	A_95_P145457	EB449230
37281	439	51	278	GTGAACAAATTAAATCTTAATTAAGCAGAGATGGATGGGTGTTAGCCTTTTATGGCTA	36380	A_95_P002471	EH620447
37286	439	56	480	GTGTACCAATGTATGTATGTCTGCATCTATATGAGAAAGGGAGTTGTATTTGACTAAT	36390	A_95_P122762	DW002723
37287	439	57	531	GAACAGGTGCCTAGTGACACCTTTTTAAGACTTTGTAATGTGATATGACTTTTGTGTT	36392	A_95_P108357	TA13937_4097
37289	439	59	868	CGTAGAATTGAAGCTGTTTTCCGCCAGTACGGTTTCAAAAGATTTTATGCAATTTTCTT	36396	A_95_P204797	DV999368
37295	439	65	475	ATATTCTGCTGGTTTCTCATATTTCTCTAGCTGTGCTAGTGAATCTTGAATCCGAGTTT	36408	A_95_P047411	FG644329
37301	439	71	532	AGTTATCTAATGACATTGTGTTCTATGGTTCTTTGACTCACTTTGCTCTCATTTGGTAT	36420	A_95_P180857	TA12842_4097
37303	439	73	1729	CTCGATGAGAAGTAAGATTTTCGTCGGTATAGGAGAAATATATCTGCATGTAATAAT	36424	A_95_P191672	AJ001769
37305	439	75	815	TTGGTTCTCTTTTAGTGGGTCTTTTCTGGGCATTTTTAATATTTGCTGGAAACCTGTTT	36428	A_95_P018571	DW004647
37306	439	76	862	TTTACTCAGCACTACTACGGCTTCTGCTGTAGTATTGGGTCTAGTTCTCCCGTACTGAT	36430	A_95_P287508	FG169764
37307	439	77	932	TTCACAATTGCCCTTGATTTGGGATGAAGTTGGTTGTATTGTGTGATGCTGTTGGGGT	36432	A_95_P023341	TA13320_4097
37308	439	78	457	CGAGTTTGAAATCGATATGGATTTTGGACTTCACCTCTGGCAATTCTTGTATAGTAGT	36434	A_95_P261596	AM829948
37309	439	79	179	GCTCGTAATTTGTTGTTGTAGACGATTCACAGTGCAGCAATAAAGGTCAATTTCTGAG	36436	A_95_P095393	BP533176
37310	439	80	99	ACTTCATTGATGATAGTGGTGTGGATCCAGCTGACAGGTATGGAAGTGACAATGAA	36438	A_95_P128732	EH665155
37312	439	82	745	CCAATTTAAGGAAAGGATTTTGGTTGTCCTCAACTTGGGAAAACATATTGACGTTGAT	36442	A_95_P115887	EB678058
37314	439	84	62	CAGAACATTAATTGCGAGTATCATTCTTTACATCAGACTTATTCACCAGGCCAAAAAG	36446	A_95_P032136	CV020812
37325	440	10	1048	CACTTGCAATCATCATCATCATCTTTGTGTTAAGGGAGGAATGTTTAATTTAAGAACA	36301	A_95_P211702	TA19672_4097
37330	440	15	490	TTCGCAATTCAACTATGGAGTTTGATCGAGTTTGCCGTGGAGTTGAAGCTGTCTTTCG	36311	A_95_P084125	BP528938
37335	440	20	458	AATATGATTCTTGAACTGCAGAAGCTTGACAAAGATTTCCATGGGGTTTATTTAGAGT	36320	A_95_P279118	AM793251
37337	440	22	756	TGTGGAATAATCTGGAAGTGGATGCTAATGTTCCAAAGTTTCAATAATGGAGTTCTG	36323	A_95_P019806	TA19050_4097
37338	440	23	728	AACTGTTTCTTAATGTTATAATCTCATTATGTGGGACAGCTAATGATCCTGGTTGAGT	36325	A_95_P234659	EB439771
37339	440	24	91	GTTTTGCTGTGCACAGTTTGTAACTCTTAGGTCTGTCTTCTAAATTATGTGTTACTTAG	36327	A_95_P140512	EB444408
37340	440	25	829	GACAACACCTTTTTCTGCTTTCTTCGTACCATGTTTCTTGCTTTTCTTGTTGGTGATGCA	36329	A_95_P200057	TA17127_4097
37344	440	29	596	TGGGCACTTAAGGTTCTGCTGTAGTGCGGCATTGTTAGGATTTAGTTGAGAGAAGAT	36337	A_95_P058536	BP134498
37348	440	33	266	AAATTTGCTTCCTTGTTGATCTGCCATTGCGCTAGTTACAAGCTGAATCATGGTCGCT	36345	A_95_P241865	AJ718686
37350	440	35	627	TTTTGAGGCAAAAAGCCGGAGTCAAATAGTTGAAAGAGGTGGATGTCATACTGGTTT	36349	A_95_P260676	BP129537
37351	440	36	773	CATGGTCAGGTTATGGAGAAAAAATTACTGACGATGGCTCGAGAGCTTGAAAAACTT	36351	A_95_P149417	TA16716_4097
37352	440	37	1338	GCCAGTGTTATCAGTTTGAAAAATGATGGATTTTTTGTATTGGGATCAAAAGAAGAG	36353	A_95_P190242	TA14968_4097
37355	440	40	663	GCTTTCTTTTCTTGACCGTGTTTATGGTTCTAGCACTAAATGATGTACCATTTGGAAAT	36359	A_95_P129862	EB429802
37356	440	41	769	TCTTAGCAATCAAGAAGCAGTTGATATCGTCCAAAATAGCTCTCACAGCGGAAGTGC	36361	A_95_P117857	DV160831
37357	440	42	675	GACCCGAATATCTGAGCTGCATATTGTTTTCCTTGTTATATTTGCAATTGGTTGGATTT	36363	A_95_P190862	TA15105_4097
37369	440	54	762	CTTCAATGAGTTCGCACCTACAAAAGAAGTTGTTTTGGATCATCTCTTATTGAGTTAT	36387	A_95_P247262	EB679649
37372	440	57	890	TGTGTTATCATATATGACATTAGCAAGCCAGCTTCGAACCGAATCACGATTAAAGGA	36393	A_95_P013676	DV162033
37375	440	60	471	CAGCAGCTTTGTTCTAGTTCTTCTTCTTAAGGTCTTGATATTGTAATTTCTCATTGCAG	36399	A_95_P002496	TA12411_4097

37390	440	75	837	ACTGTGTCCATTGGTGCTTGCCTGGTCCTATTGATTCTTGGGCTGATTTCTTGTTTCAT	36429	A_95_P146037	EB449864
37400	440	85	413	CTTGTCTAGCGGAATAGAATTCTAACTGTTTGTGCTAACAGAAAATAGATTCTTTGAC	36449	A_95_P207397	TA18732_4097
37403	441	3	796	GAGACTATAAAATGATATGAGTGGTGGCTCTCTGTACTTTGTTCATGTTTTAGTCTAA	36453	A_95_P018426	TA13873_4097
37407	441	7	910	CGATTCTTGTTGATAGAACTGGCTATGCTGGAAAAAATGAAATTAGTCTAATGTCTCT	36461	A_95_P017006	TC45123
37410	441	10	491	GGTACACACCAAAGATTGGTACCCCTACTTGTTGGAACGATCAAATTAATTGATTTAT	36467	A_95_P164442	EH623689
37412	441	12	764	CTTGTGCATGCTTTTATCGGTGATTGGGATTGTACTACTTGTTGCAGTTATATATATG	36471	A_95_P117197	DV160019
37414	441	14	833	CCTCTCTGAAAAGTGCTAAAAAACAGAGAGCAGCTTGATTTCTTGTATTATTGACTAA	36475	A_95_P195692	EB425651
37416	441	16	821	TCCATAGTTACAAGTAGGTCAATTTTGGATGAGTGTTCTTTCCAGTAAGTTTTGTCGC	36479	A_95_P008246	EB679495
37421	441	21	529	TACCTACTGGTGATAGGGTTCTTTTGCACTAGTATTGCTCGCCTTTGTAAGCTGAATT	36489	A_95_P193178	TA15615_4097
37422	441	22	183	AATATGGGAGAGTACGAGATGTGGATATGAAGCACGACTATGCATTCGTAGAATTT	36491	A_95_P161817	TA13397_4097
37424	441	24	352	ACGGAAACTGTAAAAGCTACTACGAGGTTGATAGATGGATGTTCCGTTTATGAACTA	36495	A_95_P043446	BP130617
37426	441	26	435	TGGCCCTTCGAGCTTGTGATATTGTTCATTGTTATTACATGTATGACCAATTTCTCTTC	36498	A_95_P108337	TA13278_4097
37429	441	29	202	CTTTCTGTAAATATCCCAAAAGTAACCTATCCGTAGGGAGAAAGGAGTACAAAATTG	36504	A_95_P131362	EB431540
37440	441	40	412	GTTGAAGTTGTTATTGAGTTTGTAAGTCTAGATTCACATTGTAAACATTCACCGAGAG	36526	A_95_P013151	TA15069_4097
37447	441	47	869	CCTTGATAAGTTGAAGGACTCAAAGAAGAGCGATGATGACTCCAAAAGCAGCATGC	36540	A_95_P290053	DV161861
37448	441	48	589	GGACATCACTGTTTCCTTTTCTATGTTGGTGTGTTTATTGAGTAAAAGGAAAGAAGTT	36542	A_95_P112367	EB437303
37449	441	49	317	ATATCCCTTTCCCCTCCTCTTGGTATTTAATGTAGAATTGGTTAGAGCAGGACCTTATT	36544	A_95_P089893	BP530701
37453	441	53	163	CTGTTTACACTGACCAGAAGATAGCTGTTAGCTGTGACAACACGACTAAATCTGTCTC	36552	A_95_P131897	EB432316
37459	441	59	341	GTACAATATAGCTGAAAATGCAGAGGTGGTGATGTCTAGATATTTTGTATGCACTAA	36564	A_95_P131687	EB432061
37461	441	61	905	TCAGGAAAATCAAACGTCTGTAGCTTCACCATAGATTTGTAATGTATATGGTTGCAG	36568	A_95_P211382	TA19598_4097
37463	441	63	761	TAAGCAGCAGCTAAGGTCCATCTCTTTATTCTCTTATTACCTCTTCAATTTGGTGATAT	36572	A_95_P218992	EB678537
37464	441	64	848	TCTTGGTTCGTAAATTCAGTAGCGGTCAACCAATCAAAATCAATAGTGTTCCTTCAAG	36574	A_95_P289658	DV160388
37466	441	66	1518	TTTTCAGATATTCTGTAGGCTGACCTTGAAATTGTGACGTTTACCGGTTTTTCTTGGCT	36578	A_95_P031821	TA18075_4097
37467	441	67	948	GAGGCTGGATGGAACTGCAAATGATCAGTCTGTTTTGGATTGTAAAACTTAAATCTT	36580	A_95_P018616	TA16502_4097
37468	441	68	142	GTGACCAAGATCATATGTCACGACTGAAAAACATTACTGCAAAAATATATCACGATT	36582	A_95_P096108	BP533477
37478	441	78	563	GTCTAGCAGTTATAAGCGGAGAATTTTGTGAACTTTTTTCATTTGGATTGATTGTACA	36602	A_95_P062785	BP135605
37482	441	82	143	GGTTGGTAGTGCTTGTATACCTATATGTATCTTCTTCATGTAACTCAAGTCTTTTCCTC	36610	A_95_P033664	AJ632885
37488	442	3	0	TTTGTAGGCATATGGAACTCTTGTGCTAGTTGTAGAAATGTATTTTCAAAGTCTTGCG	36454	A_95_P027056	A_95_P027056
37492	442	7	458	GTATACTTAAGTTGATCCTGCTGGGTTGAACTTTATTCTTACAGTAATCATGAAATGC	36462	A_95_P103782	CV016686
37493	442	8	494	CTATGCCTCACAAGGAAAGACTTTCAGTCATTGCTGCTCTGCGATCCCAGAAAAGAG	36464	A_95_P146537	EB450598
37499	442	14	578	CTGTAAAGTAATAAATATCTATTAATGTGTGGTATGGTTGACAAGGGACCCTGCTGC	36476	A_95_P124582	DW004371
37506	442	21	825	TTAGGAGATAGCGGATTTATGTTGGTTAGACATGGATATGCCGCATTTAAATCCCCT	36490	A_95_P019666	TA20369_4097
37507	442	22	750	CCGTTGAGTTCTTTCATCAGATACATGCTGAAGATTTCTTGCTTTGTAAGAAATTCAC	36492	A_95_P013196	Y09109
37508	442	23	820	CCCACTTGTGAGAGTATACCGGGTTTATTACTGTTGTAATTGATGCTAGTTTATAGTA	36494	A_95_P219772	TA21465_4097

37511	442	26	609	CACTTTGTAAAGTACCAGCTTCCAGCTTTGGGTGATTCTGGTTTAATTCTTTAAGAAA	36499	A_95_P051141	AB195174
37513	442	28	462	CTTGCAACATTGTAGCTGCGTGGAAAATTTTGAGCCATGATCATTATGAACTTATTGA	36503	A_95_P214777	BP131286
37514	442	29	1362	ACTGAAGCTGATCCAAGATGCCCCCAATGCAAGAGCACTACTACTAGGAAGATGACT	36505	A_95_P239544	AY776171
37515	442	30	577	AAGTAAGATGATTCTGGATGAGTGGAAGAGGCTTTACTCCAACACCAAGACCAACTT	36507	A_95_P144357	TA12453_4097
37517	442	32	838	AATTTCGACATGTGTGTCAAGATTTAATGAAGGATTGGAGTCCTAGGTTCAGACCAT	36511	A_95_P313173	FG155239
37519	442	34	366	AAAGATTCAAAGAAGCAGCAATAACATGGCACATTGTGGTCTGTATTTGAAGTTTAT	36515	A_95_P087153	BP529724
37520	442	35	823	CAGACTCCACTTGTGGTAATATACTGGGTTTGTTGTTGTTGTAAATGTTAGTTCA	36517	A_95_P194597	TA15929_4097
37521	442	36	493	GCATTGCACTGTAGCACCAGATTGATGAAAATTGAAACCGTGAAGTTTCTGATGATT	36519	A_95_P099048	BP534747
37522	442	37	825	AATAGACGAACGCAGAAATTTGAGCCCTATTGAAGAAAATGGCCGCAGTCACAGCA	36521	A_95_P232239	EB677939
37531	442	46	674	TACAGGGAACTGGCATTAGAGTGGCTTATTATTATAAGAGATCTCCGAGTTCTGTGC	36539	A_95_P129592	EB429581
37533	442	48	944	CAATTTAGCAGTTCTCCTTTTGGGGAACAACTCTTCTAAGTGCATACTATCAGTTGAT	36543	A_95_P204432	TA18065_4097
37534	442	49	240	TTTGTTAGGGCTTCAGATTTGAGTGATGATGATCTTAAGACGTATGCTAAAAGAAGG	36545	A_95_P109997	FG635113
37538	442	53	867	GAAGTCACGAAAGATAATGAAGAGCCTTTGGATGAAGATGATCTGACCTAAACTTTC	36553	A_95_P204252	DV999565
37554	442	69	391	TTGGGCACACAATGTTCAGCACTCAGTCAGTGTTCTTGTAAAGTGTATAAAGAATTCT	36585	A_95_P141742	EB445392
37564	442	79	845	TGCAAAAAGGTCAAATGAGTGATTGGAGCCAGAAATGCTGATGGTTTGCTGCAGTT	36605	A_95_P116002	EB643439
37565	442	80	717	GACTATTCAATTCTAGTTAGCGAGCACATTGTGGTCAATCACAATAGTTTGCATTTGT	36607	A_95_P111302	TA15727_4097
37570	442	85	467	GTGGAAAATACAACATTTAGTATGTATCTGAAAAATGCGGCAACATATTGTGAGCTG	36617	A_95_P264526	AM800056
37577	443	7	703	CCTTTTCTCATGTAAAACATGAAAAGTTGGTTAAAGCTGACTAGCTGAGATTGGTTTC	36630	A_95_P192577	TA15482_4097
37581	443	11	882	CCATGGAAATTGTAATTTGGCATTGTAAATTATTCGCATGGATCTTCTATCTGGCTTC	36638	A_95_P011551	TA13838_4097
37587	443	17	1164	TTCGTCATGGTAGAATTGGGTAATGTAGAGTTAATGTCCACAATTGTTCTCATTGATG	36650	A_95_P229649	TA14879_4097
37592	443	22	725	GTATGCAGTGTTATTCCTACCTTACGAAGGTAGAGAGGTTATATTTTTCTTTTAAACG	36660	A_95_P152707	EB683051
37594	443	24	614	AGCCTGTTGTAGTTAAATACAGGCCCATCTGAATCTGTAGTTATAGAGTGATAATTCT	36664	A_95_P262596	FG638898
37601	443	31	523	ACTTGTCCTATTTGTAGAAATTCTCCACCTTCCCTTCTCCTTTGGTTGAGGTATTTCCTC	36678	A_95_P035478	BP128480
37607	443	37	914	AACATGAATGCTCAGGTAGGTCTTACAAGTCCCGGCTTTATCGGTGCTGATGTTTGT	36690	A_95_P247197	EB680319
37608	443	38	762	CTGCCTTACTCCACCGTATATTTGGAAGTTGAGAAGCTTAAGAAGTCTTTTGGAATTT	36692	A_95_P292143	EB426653
37609	443	39	816	GACAGTGGATGACATGGTCAAGCAGAATCAACGTCTCGTAGTCTTCACCTCTAAATC	36694	A_95_P127407	EB426943
37610	443	40	663	GTTCTTGGTAACCATCTTGTTTACTTGGTAACATTTATTGGTCACTTCTGTGTTGAATG	36696	A_95_P122202	DV162480
37613	443	43	823	GGAAGGGAACGATAACTTCTTGTAACAGAGATAGATTCAAGTTTCTTTTGCATATGG	36701	A_95_P187092	TA14270_4097
37618	443	48	900	GAGGCTGAGATGGCATATTAAAGAAAATGCATCTTACATGTAGCCTTAAACTGTTCT	36710	A_95_P186902	TA14227_4097
37623	443	53	1420	CTTATTATGTCTGGAAAAGGACTGTATCTTGTTACAATTGAGGGATTCATTGAATCGT	36720	A_95_P190887	TA15110_4097
37624	443	54	1800	CTCTACTTCTCTCAGTTCTGTTGTGCAGTGTCTGAATTATCTATCTGTTAGTTCCCTTTG	36722	A_95_P192843	TA15543_4097
37626	443	56	836	AGTGCTCAGCCTAGCTAGAAAATATCTTGTATTTATGGTGTTTGAACTGTATGATCTG	36726	A_95_P251242	TC58481
37628	443	58	309	CCAAGTCCTGTTTTGACTTTCGCTTCCGGAATTTCTGTTCGGAATTTTGGTTAAACATT	36730	A_95_P213167	EH613891
37630	443	60	1402	CCTTGTTCCTGATCGCCATGATTTATCCAAGAACTTATCAGAGTCTGCTGCTCCTCTTT	36734	A_95_P192447	TA15453_4097

37636	443	66	1731	CGCTATCTGTCATGTCATTATATTTTTCCAGTTATGTTACCTAGTTCTAATGTGTGTAC	36745	A_95_P016256	TA14638_4097
37639	443	69	138	GACTTTGTTAGAGATTGGTGAATTCCAATACCATCTATGTTTATAATCGGATTGTGAG	36751	A_95_P162662	EH621663
37645	443	75	518	TTAGTTCCCATGATGTGAAATTACAAAAGACTTTTGCTATGCAAGGTGACAGAAGAT	36763	A_95_P027896	TC70724
37652	443	82	878	CTGCGAAATTGTGCCTTTTGTTTCATCAATTGTATGGTAATGTTGGGATATTTACTTTC	36777	A_95_P115507	TA15437_4097
37655	443	85	543	GGTGTGTGAATGGAGAACAACTTTTTGCTACGCGCAACCAATGTTTTGATATGAAAT	36783	A_95_P252719	EB436472
37656	444	1	415	TGGGTTATCTTGCATTCATTTTTAAGCTGGCTCCTCAAATGTATGATTTTCCATGAAGT	36619	A_95_P109497	CV019339
37659	444	4	261	TGCTTGTTAGACTTAGATGGCTCTGTAATCTCTGAAGTTTCTTTTTACCTGAAATGCTT	36625	A_95_P099363	BP534899
37664	444	9	632	TTTGAATGATCGAATCATTAATTTCATGAATCTATGAGGCTGTGTTATTTGCCTCGGT	36635	A_95_P020696	TA13064_4097
37665	444	10	776	GGTCCAAGGTTGAGTGGAAACATGTAATACATGTGTACACCACCAAATCTTTCGTAA	36637	A_95_P248637	FG163565
37666	444	11	488	ACCGCACAGAATCTGCAAATCATGTAGAGAAAGGTTTATCTTTTCCAGGCTTATGATT	36639	A_95_P147787	EB643451
37668	444	13	661	GACCAACTTGTTCAAGAATATTCTTCAGGATTCTCGGACCATTGCAAGTTAGATTTTC	36643	A_95_P005186	FG639256
37669	444	14	877	ACCATGCACGCTACGTAATGCATACTTTGAACAGCTCGTCAGCATACTATGGTACAG	36645	A_95_P232819	FG159402
37670	444	15	1399	GCTTGAGGGAGAAATGAGCAAGCCAAGGAACCAAAAATTTTGTAAATATATCATTCT	36647	A_95_P239129	AF520810
37677	444	22	816	CAAGCTACACAATAGTTTATCTGAATAGCAGATAACACCCTTTTGGAATCCTCCAATG	36661	A_95_P010491	TA18174_4097
37679	444	24	431	TGATGTTAACGAGTTGAGAATTGGGTTGCAGAAACTTGGCCATCAAATTCCTGAAAG	36665	A_95_P034853	DV162604
37686	444	31	248	TTTATTCGCTATTCTTGTCGTTGAACTAGGAATTCTGAATTGCTGAGCTCGCCTAATGT	36679	A_95_P006541	EB429322
37696	444	41	420	TCACAAACCCGATAACGGAACCAACAGGATTAAGCTGCCTTCAGGATCCAAGAAGAT	36698	A_95_P022451	X62500
37707	444	52	778	CTAAAGCCATATGTTGTGGCAGACCCAGAGATTCAGGAAGAAGAAATTGATGGTGT	36719	A_95_P157642	EH615696
37711	444	56	212	TAAGGCAATTGCTGCTGCATTATTGTTTTCCTATGGTAATTGACATCTGAATTGGTGC	36727	A_95_P092373	BP531775
37714	444	59	819	TATTTCATAGCTATCTATTTGACAATCAGACCACCTATGAGCTCGTCGACGACGGCGC	36733	A_95_P289178	FG136073
37717	444	62	430	GAGCAGGCCATGAAGAGAGATGTCAGGATGAAATACTTTCTGTAAACTACTTTTTG	14301	A_95_P000096	EH619820
37721	444	66	418	GTATTTGTAAAGACCATTTTTGCGTTTTTACTTTATTCCCGTCTGTCCCATATATTGGA	36746	A_95_P188142	TA14504_4097
37722	444	67	243	GTAACTGTTGATTGTAAGCCTTCTGCAAATCCTGTCAATTTGACTTCTATGTATTCTAG	36748	A_95_P118897	DV161972
37723	444	68	99	TTGGTTTGTGAATACAAATGAAACAATGAACGAAGACCTGTGTCTATTTTCTTCTCGT	36750	A_95_P103382	CV016480
37727	444	72	410	TTATTGGCATGATCACTCGAAAGATCTGATACTTAAGGATAATGATGATCCGGCGGC	36758	A_95_P035293	EB678111
37728	444	73	1216	TAAAACTTGAGAGAGTTTTAAGAGCTCGTGCAAGACGAGGAGTCAATTGCCATGGT	36760	A_95_P017281	DQ213015
37730	444	75	827	TGTGACAGTTACCAAGACACATCATACATCTATGCCTTCTGCCAGTGATAAAATTCGT	36764	A_95_P151782	EB682029
37735	444	80	786	GAGTTTGGTTAATGAAACTGGTCACCAGATAAATGAATGCAAGTTATGCATGTTGCA	36774	A_95_P020561	TC56361
37736	444	81	841	TTACAGCCACTGTTCTTTTGGCTCGTGTAACTGTTGAACATTTGAGAGGTTGAAATAT	36776	A_95_P121977	DW002045
37737	444	82	432	ATAGTTTTCTGGCGAACTCCTTCCCGCTCGTTTTGTTACTGTCACTGTTTTCGTGATGA	36778	A_95_P107967	EH617488
37738	444	83	569	AAGCAATTACCCTGGAAGCAAGCAAAAACCCTATGAGAAGGCAAGTCCAGACTCCT	36780	A_95_P221522	FG140103
37740	444	85	767	GGCTGTGAAGTGCTTGTGCTTATTCATCATTGATGTATTATTGTTCTATTATAGCAAG	36784	A_95_P135012	EB438104
37742	445	2	544	AAGTTATATGAAGGTTATGTGCCCATGAGATACAAAGTACTTGAGGAAATGAAGAG	36787	A_95_P073855	BP526318
37744	445	4	1795	GTACTGGTAGTTGTTGCATAAGCTTGTTTTGTTCTCTGTTCATGATCTAGTTACTTGAT	36791	A_95_P115102	DQ340760

37745	445	5	637	TGTTCATGTAATCGATGACGAAAAACAGTTCAGCAGCAGTTTTGGCATCAACGTTAT	36793	A_95_P132427	EB432888
37748	445	8	255	ATTGTACCCTTGGGATCACAATGATATATTACGGATCTTCCTAAGAGGCTGCTTTCCA	36799	A_95_P103637	CV016612
37750	445	10	351	AAGCTCTTGATAGATGGCATGACTGTTGGAAAGGTGACATTTCACCTGAGGAATTGT	36803	A_95_P108322	CV018791
37751	445	11	310	ACCAAAGCCAAGTCTTTACTTCTCCTTCTGCTACTTATGTTGGTGTTTTATGATGGCCA	36805	A_95_P163262	EH622349
37752	445	12	925	CAGATAGCATTCTGGATGAATAAGCGATGATTAAGAAAGCTCAAAGCAGTTACTGAT	36807	A_95_P204892	TA18163_4097
37753	445	13	884	AGCGGATAGTCTGCCGGCACATTAAACTTGGAAGGCAACAAGAATTGCCCTAAAAA	36809	A_95_P197287	TA16528_4097
37757	445	17	773	CAAGGTTGAGGTGGAAACATGTTAATACATGTGTACACCACCCAAATCTTTCGTAAT	36817	A_95_P016016	TA12459_4097
37762	445	22	243	GACTAAGAGAAGTAGATGTCTGTCCATTGGTTGAATCTATGTATTCCTTTACTTCGAA	36826	A_95_P112782	CV020832
37765	445	25	424	ACACTGGTTAAGGCTAAGGCTTCATCGAATTATGTATGTAGAATAAGTTATGCTGTCT	36832	A_95_P090053	BP530782
37768	445	28	125	CAGGGAATAAGAGTTTAATCCATGTAATGCTTCTTGCTGTTCAATTCATAATTTCTTG	36838	A_95_P031141	CV021164
37776	445	36	809	CGGTTTATTTCACTGTGTAAGTTCGAATTCGTGCAAATTTCTTAAATTGTGGTTTTCG	36854	A_95_P180867	TA12844_4097
37782	445	42	888	GAGTATTCAGCTACACAACAATCTGGTAGTAAAGTAAGTAACATGCTAAATTTTGTT	36866	A_95_P100053	TA12097_4097
37790	445	50	317	AAGCTTGGGGTGGACAGTTTTTTGGATTTTGCTTTTACAAGATTAAGTGAGGCACAT	36882	A_95_P077905	BP527378
37801	445	61	1620	AGACCATTTTCTCTTGAACAGCCTGCCACATAAGTTCATGTGTATAGCCAGTTGCGAA	36903	A_95_P028961	TA12364_4097
37802	445	62	1046	TACTTGCCCACCAGTTCTGGGTAGATCATGGATTTTTGTGCGAATAATTTTGCTGGCT	36905	A_95_P182587	TA13253_4097
37803	445	63	897	ATGTGCGGATAGCGGCTGAGACTTAATAAATTCCTGCATGTAGTTATAGTGATGTGT	36907	A_95_P191122	EB678173
37805	445	65	469	ATTCATGGCGACTGGAGTCTTCTTCATTTTCATGGCATTTACTTTGTTCCTCCCAGTGA	36911	A_95_P037821	EB438528
37810	445	70	707	GCAGCACTCTTGTATCTAGCCTTGTTCATAGTCTGATATCCTTTCTTTAGCTTTACTTGT	36921	A_95_P000576	EB446879
37811	445	71	696	AGAAAATCAGCAGTTGATGAGGTCCAAGGGGCTGTTACCTTTCTTTGACAGTGCTTT	36923	A_95_P156982	EH615040
37816	445	76	400	ATAGCTGTGGTTTTTATTTAGCTGGAGGCCCGTTCGCACTGATTGCAGTTTTCAACAA	36932	A_95_P132507	EB433000
37818	445	78	826	CTCTTGAATGAAAGAGCAAGGCAAAAACTGGAATCTTCGCGTTATGTTAAATATCAT	36935	A_95_P014296	EB451505
37822	445	82	1360	GGCAAGGAGTTGATTGTTGGGTCATCGTATTCTTTTATTTCTCTATTTGACAAGTTTCT	36943	A_95_P003696	AF154640
37823	445	83	828	AATTTTGGAAATTCAAACGTGAATTGTAGTGTCCATTTCTGCTGCCCCCGGCCGTAAT	36945	A_95_P117592	DV160535
37824	445	84	882	TGGTTTTGGTAACTTTGAGTGTTCCTGAGATTTTGAGTTGATCTGATACTTACTTTCA	36947	A_95_P177372	EB677529
37828	446	3	150	TTAGCTAAGCCAATCAGGCAAAGGGTGAATGGTTTGAGGATTAACTTAAGCTTGATT	36790	A_95_P043926	BP130747
37829	446	4	244	TTACTCACAGCATGGATGGGTGTTAGCCCTTTTATGGCCTAATATAAACAAATAAGCT	36792	A_95_P032021	CV018753
37830	446	5	561	CTTTAACTGTAAGCCTTCTACATTTCGTAACTAATTATGCAACTCCTTCGGTTCTAGTT	36794	A_95_P133417	EB434863
37838	446	13	0	ACTGACAGCTTTGTCCAACAGTTCAATGATGCCTTTGTTTTAATATATACTATTTCCCG	36810	A_95_P015081	A_95_P015081
37839	446	14	878	AGAGGTCGAACAAGAGCAAAGATGTTGTTGAAGGAAATGTTTAGTGGTACAAGGC	36812	A_95_P189247	TA14749_4097
37840	446	15	1155	GCTTATGGTCCTCTTTGTTTTATTGCGTTGAGTTGAGCTGGTTACAGTTTTTATCTATC	36814	A_95_P012106	TA12528_4097
37841	446	16	1355	GGATGTCCCTAAATTGTACATTTTTAGGTATTTTGAGCCATGAACATAAGTATTGGAG	36816	A_95_P101283	CK720588
37843	446	18	396	CCAACTAGTTGTATTCCTAAACCTCAAGAAATGAAAAGCAGCGAAATACTGAACATA	36819	A_95_P014601	BP526418
37845	446	20	666	ACGCGTTGTCATGTGTCTTCCCTCCTCTTTGGCTGAAATAAATTTCTTGTTTGGGGCTA	36823	A_95_P261621	FG639495
37846	446	21	1074	GTTGGATCCAAATCCAAATTCAGAATCACTACATCTAGATTATGGAGTCACTTGGTTT	36825	A_95_P182417	TA13212_4097

37848	446	23	651	CAAAGGTTCTGTAAAGTGCCTTCATCATGTTTTCTCTTCAAAGGAGACAAATTTCTAT	36829	A_95_P216717	EH623168
37849	446	24	569	CTCCCAGTATTCATTTGCTATTGATGACTGGTTGTGTGTTTGGAATGATCATATTTCTC	36831	A_95_P001696	FG641355
37850	446	25	118	GTTTTGGATTAGTACTTTTTGTGTTGTTTAAAGACAGCTTTTGCTGGGAGGTTACTGA	36833	A_95_P098373	BP534443
37853	446	28	725	TATGTCCTGAATAATAGTCTCACATCGGAGCTGTTCCTAGTAATTCCCTTTATTTCCAG	36839	A_95_P234264	DV999602
37855	446	30	933	GACATATACTGTACTGTAGTCTGGAGCGCAGTTGTTACAAATTATCTATAAAATGGT	36843	A_95_P019011	TA21205_4097
37861	446	36	667	GAGCTGCAAACCCAGAATAACAAAAATAAATGTCAGACTTCGAGTCGAAATTGAAA	36855	A_95_P111222	TA12934_4097
37865	446	40	787	CCGTTTCACAAGACAGGTGGTGTAAAAACTAGAATGAACAATTTTCTCCAGAAATTA	36863	A_95_P224672	EB447540
37866	446	41	786	TAAGATTCCTATGTATGTGAAGTACACTAGTTGAAGGGAGTAAGGTTTTTGTTTGCTT	36865	A_95_P216322	DV999287
37868	446	43	853	GGGCTATATTGTGGCAATTGTGGAAACGAGTTTATATTAACTGTAAATTTCTCATGGT	36869	A_95_P121567	DW001655
37870	446	45	961	ACATCATGCATGCACCGCTTATGAATCAGACTTTTGGAAAAGAAGAAATAAGACACG	36873	A_95_P189597	TA14821_4097
37872	446	47	869	ATGTTGTGAGATTGGCATATTGGCATTTACCTTTTCAGAAAACAATTACTCCTATGTA	36877	A_95_P249052	EB677619
37873	446	48	449	TAAGCCCTCCTGTTTATGAAGATTAGACTTGGTTTCATAGTAGCTGTTCTTTGTTTTAG	36879	A_95_P213897	FG640780
37874	446	49	750	TCAACGAAATGTGGTCATATCTTCTGCAAGGGTTGCATCAAGGCTTCTATAGCTGCTC	36881	A_95_P294103	EB439586
37884	446	59	541	GTACCCATTGGTAACATTGGCAGCATTCTGTAAATCTTTATCATATTTGCAGACTTCAT	36900	A_95_P210772	TA19467_4097
37888	446	63	541	TTGGGGGGCGCCAATTTTGGAAGCGGGAATACTTTAAAAAGAAGGAAAAATACAAA	36908	A_95_P090593	BP531011
37889	446	64	198	GCTGCACATAGAAGGACCTTCTACTAATCTGTTACACATGACATAGATCATCAGTGCT	36910	A_95_P108312	CV018789
37890	446	65	341	TGCCACCTAAAGTCTAATGGGATCTAAAGTTAAGGTTTTCATGTTACCCAAGCAATAT	36912	A_95_P110877	CV019945
37904	446	79	851	CCGAACCTTGCAGCTTTGCCAGCTACTGTTAGCTAGTATTATTTCTTTATATGTAATGT	36938	A_95_P010826	TA14366_4097
37906	446	81	143	ACAGTAATTGAAATGTTTTAACCTGTGGATACTCTTTGAGGCGCTAGTTCGGTTATAT	36942	A_95_P091843	BP531525
37909	446	84	164	TATGTAAGAGAGAAGGTTTAAGTTGTGCTGCGCCTTTCTGTCTAACTAAATTTTGTCTT	36948	A_95_P011536	EB442973
37910	446	85	942	GCCAACTTTTTGATTTCTTTAGGATGCTCTCGTTCTTCTTCACAACAGTTGGTTATTAT	36950	A_95_P177997	TA12119_4097
37913	447	3	423	AAATTTTGTTAGAAAAATGGCCTTCGGGGCTTTGGTCAAGAAGTAAGAGCACATCGC	36955	A_95_P096288	BP533557
37915	447	5	642	GCCGCCAAACAACCCTTTACTATGTCATCAATGTAGGTAAAGTCTCTAGCAACAGTCC	36959	A_95_P307818	FG193417
37916	447	6	940	CTCATTTTTCTTGGATTTTTTCTTTCTGTTCCCAGTGGAAAGATCAGTTGGAATTATTG	36961	A_95_P186517	TA14144_4097
37918	447	8	257	GTTAATAGTTTGGTACTAGCTTTAGCTTAGACCGTGATACAGTGTTGTGTGGCATGC	36965	A_95_P132237	EB432682
37920	447	10	333	GCTTTCAAGTTTAAGCACCAACTTAGCAAGCAAAAGCTAAATCTACCATATTCCCTTC	36968	A_95_P220287	TA21576_4097
37932	447	22	1256	CGTTACACCCCATGTTTTTGTACGTGAAAGTACGTCGTAAGTCAATTGATGTAAGCTT	36992	A_95_P017391	TA12092_4097
37946	447	36	790	CCTCAGACATGCGCTTTCGATGAATTGTCCTATGAACAGACATTGGTGCTTGTAATCT	37018	A_95_P294753	EH621359
37948	447	38	710	CCTTATATCGACGATAATAGTGAGTAAGGCGCCAATAATCCTCTACGGTATCAGCACT	37022	A_95_P316153	FG189707
37949	447	39	796	AAGTGTTTTGGAACTTCTCCAACGAGTTGATGCAGTTGATTCATGACACCTAGATTGA	37024	A_95_P146127	EB450036
37951	447	41	717	TCAATGTCAAAGATGTCACCATAAAAGCAGTTGGCATTTGCTTGTATTTTCTGCATGT	37028	A_95_P271471	EB452098
37953	447	43	342	TCAGATCTGTGTAAAATGGGGCAAAGAGAAGACGACAACACGCCATGGCTGCAATA	37032	A_95_P081610	BP528303
37954	447	44	462	CCCGAGAAGCAGGTTGGGTACATAGTCACATCATGTTTGCTCAATGAGAAACCACGA	37034	A_95_P158397	FS382929
37960	447	50	809	AGTTCAAGTGACAACAAGTGCGTCAGATGCTGATAATGTGACCGGATCTACTGTTGA	37046	A_95_P011176	EB427793

37961	447	51	360	TGGATCCAAAAGGGATTCCATTTGATGATTGAGCCAATAAGATAGGCGTAGAATAC	37048	A_95_P162192	EH621079
37965	447	55	713	TTGTCAACTCCACGCAATTGAGTAACAATGCCATTGACATTGTAGCTAAGATTTCATC	37056	A_95_P315008	FG198981
37969	447	59	870	ATTGCTATTGGCATCAATCCAGAATACAAAGTTCTGGGCAGCACGTATCCATGGATT	37063	A_95_P116682	DV159444
37970	447	60	500	TAATAATACTTTGATTAATGTTCCACCACAAGAATCTGCGGGCGAAGAGCATGACGA	37065	A_95_P142767	FG171206
37972	447	62	695	CCGCAAAAATGCCAAGTGATGCACACTGTTTCGTTCTTGATATTTTATAGTGAACTTT	37069	A_95_P148672	EB678096
37978	447	68	534	TGCGTTTGAGGTTTGCACCAGAACCTAGTGGTTATCTCCATATTGGTCACTCAAAAAG	37080	A_95_P077600	BP527293
37981	447	71	542	TCTAATTGACTGTCATATGTCGCTTACGTTCTGCATGCAACACATACCTGCTGTAAGA	37086	A_95_P111852	DV159141
37983	447	73	839	CCTTCATGTTCGCATACGTCGCAATTTTGCGTTTGTGCAGTTTGAAAATCAGGAGGAT	37090	A_95_P289728	EB677597
37985	447	75	295	TTTCTAGGCCGCATCTTGGAGGCTCTATTGTACCATCATCCCCATCCATTGATACATCT	37094	A_95_P087618	BP529837
37986	447	76	851	TATTCTTGACCGGTTGATGTGGAGTACTCAGTTCGAAAACTTCTTGGCGACCAAGTG	37096	A_95_P120607	DW000571
37988	447	78	853	GTATGTGAAAACTGATACAGGAAGGAGATTTCTGATCCAAGCTTTTCTGATTCATTAT	37100	A_95_P008906	DV162712
37991	447	81	419	GCATCGTGCATTACGAGTGATTGGTCCTAATTATCCCTGGCAGTTTTAATTATGTAAC	37106	A_95_P112352	EB678288
37993	447	83	745	TATGTCAGCAAGATGTCACTGCAGGTTTATGGACCAATGGATAGATATCTGTCCAAA	37110	A_95_P236529	EB678502
37995	447	85	384	AACTATCAAGTTGGGAAACTGCTTGTATTGTATGTGTGTGCTACGTGTGTGAGACTC	37114	A_95_P106462	CV017912
37997	448	2	265	CCATGAATCTGTTGTAGTAAGCCTGGTTGTTGTTGTGCTTGAACTTATTTGGTAATAT	36954	A_95_P140567	EB444457
37999	448	4	480	CATCCTCACAGCGCCCTGCTTTAATTCCATTCCATTCTGTGGAATTACGGTTGATTGAT	36958	A_95_P062220	DV160093
38002	448	7	228	GGTGTTCATCAGTCGGTTTGTACAACTTTGAAAGATTTTGGTTTGGTATTTTCGATTT	36964	A_95_P160412	EH619099
38005	448	10	396	AACTGTCTGAATCACTACCATTTCTTGGAAATGAAATCCTCTTCCTCTGCTTGGCTGA	36969	A_95_P308933	FG644095
38008	448	13	749	ATACCCTTGAAGTGACTGACAACTCACCTTCTGATGATTCTACTGCACTTATTCGCAA	36975	A_95_P138327	EB442057
38010	448	15	297	TATAGGTAGAGAGTATATGCATTAGGCTCGTCACAACGATGTACCTACCAAATGTCT	36979	A_95_P095758	BP533324
38011	448	16	466	GGTGCATCTATGTTGAACTTTTTGTTTATGGCATCACCGGAACTACTTCGATATCATG	36981	A_95_P129717	EB429676
38019	448	24	367	TTGCTTTAATCTCGTCCGTCGAAGTATGATTTACCTATACGTAGGTTCTTTTTACTAT	36996	A_95_P143542	EB446803
38029	448	34	843	GACACAATTAGAAGAGAGTTGAGACAAGCTGCGAGACCAAGAATTATTTTGGCATT	37016	A_95_P197352	TA16543_4097
38030	448	35	822	GGAAGAAGCTGCCAGGCCATTTTAGTTTCGATCACAACCAATGCCGACTATCTAGAA	37017	A_95_P200262	DV160352
38034	448	39	467	AAGACGAATTCAAGGGCTTCTTCTCCAAGTATGGGAAGGTGGTTGATTGCGAGATC	37025	A_95_P161602	EB437757
38035	448	40	463	CTTTGACAATTGTTAGACTTGTTGGAGACTCTCTTGAAGGTTTTAGCAACATAGTTTG	37027	A_95_P123237	DW003102
38038	448	43	292	TCTGTTCGCTGCTTTCTTTTATGTTATCTGTTGTGAATACAGATCCGAATACTGTACTA	37033	A_95_P109652	CV019402
38039	448	44	883	TTGAGAAACGTGGAAAGAGTTTACTTTTCGAATTGGGCTCATGTAACCTATTCAGAT	37035	A_95_P092873	TA21639_4097
38041	448	46	619	ATCCTATGCTATCTTCTTAATACAGGCTCAATGTTTTTAGTCTATTCAGTAACATCTCC	37039	A_95_P216512	TA20722_4097
38043	448	48	744	GAGGTATCAATCTTCATCTGATTTAATTTCACTTGAAGGTTGACAAGAGCTCAATGTT	37043	A_95_P149837	EB679804
38044	448	49	849	GCAGAATGTCAAAGGCTAAAGGTGAAAGTTCTGCTCAGAAGCTTGACGTGAATGCA	37045	A_95_P180907	EB681339
38046	448	51	58	ATGCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAA	37049	A_95_P200752	TA17274_4097
38047	448	52	808	TCTTCAGTTAAAGGGAAGCAGACAAAATCTGCAAATGCAAAAAGTGCGATGGCTTTA	37051	A_95_P138247	EB441985
38054	448	59	801	AATGCAAGTTTTAATCTCCTTGTCCTGATTTCTTTGGGGATGCAATGCTAATAGGTTT	37064	A_95_P121757	DW001847

38063	448	68	753	GAGCAGAAAGATGTCGAGGCTATTATTTTATACTGTTGCTATTCATTATATGTCAACT	37081	A_95_P006641	EH622482
38069	448	74	609	CGCGCCAAGCTGGTTGGCAAGGAGAATAAAGATTTAAAACAAAACTAGTGAATAAG	37093	A_95_P266006	DV160091
38072	448	77	522	CTACTGTTACTTTTGAGAGAACATTATTGTCACTTCTTGGAGGCCATTTCTTGGCCACT	37099	A_95_P220122	DW002840
38073	448	78	863	CTTTATTTATGTCTCCTTGTTTCTGGGCTGTACTTTTCTCAAATGAAGCTCTACAGAAC	37101	A_95_P246517	EB431617
38077	448	82	703	GATTTTAATTTCATATTGTTGCAGGTAGGGGTGTACATGGACCGGGTTGATTTGGTT	37109	A_95_P250762	DV158979
38085	449	5	471	TACTTCTGAGGTTTTATTGGTTGTAAGGCAACGCGCTTTCAGATATTGCCATGTACAA	37124	A_95_P091088	BP531203
38088	449	8	745	TCCTATATTCCAACGATATGGAAATCTTGTACCTCTGAAGCGGCCTGTACTAACAGCT	37130	A_95_P030961	EB428717
38091	449	11	454	ACGAAAAACAAAAATGCTGCGAGTTCTATTTCGCAGCTTGTCCACTGTTATAATAAG	37135	A_95_P155522	EG650116
38093	449	13	1254	TTTAAAACTGGAATTGGCACAATATCGCGAAGTGGCCGCCTTTGCTCAATTTGGCTC	37139	A_95_P147867	TA12737_4097
38094	449	14	202	CATGTAAACCCAAAATTTGGCCATAATAAATCTACGCGAACTCCTTTCCACTATTACT	37141	A_95_P030756	TA12193_4097
38096	449	16	571	GTTAGTGAAGATAAGAATCATTTCGGACATTAAGCATAAAAAAGTTTCCTCTCTTGG	37145	A_95_P050596	BP132431
38098	449	18	434	GCCATATTGGCCCCGATCTGTATGTACATACATATGTCGTCAAAACTCGACATACTAC	37149	A_95_P083585	BP528795
38102	449	22	283	GCATTCATAGACATAACTTTGCCTCATGGCCAAAGAAAGGAAAAGATGGTATGAAA	37157	A_95_P130492	EB430526
38104	449	24	345	GCTGGAAATGTTGATCAGTCTGATGGAAACTTTCTTGATGATGACCAAATGGCTGAT	37161	A_95_P107637	EB442583
38105	449	25	331	ATACAGCTGCTGAAGGGCAGAATTCTCCTGTAAGATTAGATGTTTATTTCCATAATCT	37163	A_95_P074395	BP526460
38108	449	28	740	AGATGAATCACGTATTATGCTGGTCTTTTTGATAGAGTCGGATGAGCACTGTCATTTT	37169	A_95_P201167	EH620891
38109	449	29	0	CTGCATATTCATGTTTCTCTGCCTCCAGAGCTTTGTGCTTTTCCTCTACTTTGTGTAAT	37171	A_95_P271221	A_95_P271221
38110	449	30	637	GTAAGGAGTTTTGGCTTTGGTAGCAAAAACTGCCTAATAAAAAATTGCTAGGTCCTT	37173	A_95_P005311	TA13278_4097
38112	449	32	1178	GTTAGTACCTGTATCTAGTGGGCAAGAATGAATACCTCAGTATGATTAGTACTTGTA	37177	A_95_P196912	TA16447_4097
38113	449	33	602	TTTGTTGGTTTTGTTGCTGACATCATATTCGAGGTATCATATTTGTACAGGGTGTTTT	37179	A_95_P121622	DW001740
38114	449	34	803	GGTTGTACTTCTATGTATTCTTGTCGGTTTCTGTACATTGTAGCATATTGAAGGTTGT	37181	A_95_P019501	AF197567
38122	449	42	0	AGGGTGGCTCCAATGTCATTTGCTTTTGCTGACTTATTGTTTAAGAAAAGACAGCTCC	37196	A_95_P307653	A_95_P307653
38124	449	44	402	CCAAAGTGCAATAAATGACTTGAATGGGAAATGGCTTGGAAGCAGGCAAATCCGCT	37200	A_95_P137732	FG148931
38125	449	45	610	TATTACAGGAGAGCAAATACATCAGCAAGTTTCGACAGCATCGCCGGTGAGACAGA	37202	A_95_P153017	EB683331
38126	449	46	724	GCTGGGATCTTGGTGCCACTTTTCTTTATGCTTTCTACAAAGTTTTCTAGCCTGGAAT	37204	A_95_P164022	EH623128
38127	449	47	74	AATTAACAATGGCTTCCTCAGTTCTATTCCTACTAGCAGCAGTATGCCACCCGCAGCA	37206	A_95_P176672	TA11710_4097
38133	449	53	760	CCTGCAACTTTTATTCAGGAGCATTCTCAGATCATTCAGAATACAAAGATGATTCTCT	37218	A_95_P303558	FG175635
38143	449	63	797	ATTGGGTTAATCTAACGGCTAGGATTGATCTATATTTGGAAGTTTTATCGAGCTGTCT	37238	A_95_P000636	DV999134
38145	449	65	592	ACAGTGAATAGATGCAAGCAAATGCTTGGATAGGATAGTCCCTTTTTTCTTTCTTTTG	37241	A_95_P308123	FG641059
38147	449	67	374	ATATCGCCAATATACTTTGGTCTTTTCTGTTGGATGGAAATGAGAAAATCTTTCTCGT	37245	A_95_P186832	FS429988
38151	449	71	516	GCTTCATGTAAGTTTAGCCTCAGCCCTACAATGTAATTTTCCTGTAACATCATTCTTAT	37253	A_95_P217032	TA20839_4097
38152	449	72	718	TTGCTCAAAACAAGAGGCAAAACGCTTGGCAACAATTTCAATCAACTAAAGGTCAGA	37255	A_95_P265096	EB679658
38156	449	76	1556	CTTTGAGAAAGTTCCTATACTCTGAAGTTGTTGATTTGTGTGCAAATTCTTGGTTGAT	37263	A_95_P191767	TA15308_4097
38163	449	83	565	CATCGGGATGGATCTTATAATTGTTTGTTGATACTTAGTTGGGATGTTTTCACAGAG	37277	A_95_P068605	BP137171

38170	450	5	109	GAAGATATGGGATTGCAATTAAAATTCTTTAGTTGCCATCAAGCGATGGCCAGTTTG	37125	A_95_P104957	CV017238
38172	450	7	474	TGGACTACAAAGTATGCTATGGGTTAGTTTGCTGAAACACAAGTATTAGGGTAATAA	37129	A_95_P112027	CV020487
38176	450	11	504	ACGTGAATCACTCCAATAATCATTTGTACTCAAATATTGGACCCATTTTTCGTGAACAT	37136	A_95_P143347	EB446681
38179	450	14	278	GCCACAAGCAGTAAATAGTTGATACATTCGTTAAGGTTGATTTTACAAGTACTTGTTT	37142	A_95_P219352	TA21377_4097
38180	450	15	938	GGAGTATTGGGGAGTTAGCAACTATCTTGATAGAATGAAGTTCAGCTTTCTTGCTTCT	37144	A_95_P181107	TA12902_4097
38182	450	17	531	CAACGCCCTAGCCGGTGTATTTTTGTACTCAAGACTTGCGAGTATTTCCTAATTGAAC	37148	A_95_P153452	EB683715
38184	450	19	896	CATGCCCAGTTGTGCTGGTCCATTGTAATATTCTCAATTTTGGGATCTATTAATGCAA	37152	A_95_P243937	EB678959
38186	450	21	744	CTCCCTTCCTAATCACTGTCCCTGTTAAATATGGTTTGTAAACTTTGATGGAATTTTAG	37156	A_95_P262031	FG166722
38188	450	23	253	AAACGCAGAACATTTTTACAAGTATTAACTTGCAATTTGGCCGATGTGTTATTGTGTG	37160	A_95_P015156	EB446995
38189	450	24	1208	CCCTTTGTGCTTTAAAGATGTAGTATGGGACTGGTTTATTATTTGGATTCAATGACTCT	37162	A_95_P179647	TA12556_4097
38194	450	29	838	AGTTTACATGGAGGATGTGAAGTACTCTCAGGAGAGAAGTGGTCAGCTACTAAATG	37172	A_95_P145487	EB449248
38198	450	33	817	CGGTATTGTTTTGCTTCAACTTTGTCTTCTTTAAAGATGTTAGCAGTGATTACCATAGC	37180	A_95_P180112	TA12662_4097
38208	450	43	662	TGATGAAAGGTCCTGTTTCTCTCTTTTCAGTTTGCCCTTTATTTATGTGGCTGTTTGTC	37199	A_95_P203272	EB445782
38212	450	47	154	TATTTGTATCTGCTTTAAAGTGCCCATCTCTATTCCCTGTACGGCAACCAGGTGTCTG	37207	A_95_P160842	TA17380_4097
38216	450	51	276	GTTGTGTTGATAATTCCCTTAGGTATCTGCTTGTTGCTTATTTGATGTTGCCAATAAGC	37215	A_95_P097133	BP533889
38218	450	53	866	ATGCGTGGCGTGATGTTTGTAGTCTGTGCATTATTACTTTTAACATAAATTTAACCAT	37219	A_95_P130437	DV158046
38223	450	58	792	GCTCTGAGAATATGATCATTTGGCGGAAGATTTGGAGTGTTGATGACAATGGGTTGA	37229	A_95_P225002	FG133315
38224	450	59	839	CTGGAGTTCTTTGAAACAGTTTTTATCTGTTTACTGTGTTGTGGATTGTTTGTTGTGTG	37231	A_95_P184877	EB424704
38232	450	67	510	CTGACTCTTTGTATACACTTGAACCCACCTAAATATTCAGTGATCTCTCTATTAGGAAT	37246	A_95_P263611	EB436961
38235	450	70	185	ATATTAGAATTGGGGTGGTCGAAACATGGACAAGAATGAAAAGCAAGCTCTGTTAG	37252	A_95_P051466	BP132651
38260	451	10	876	TGTTAGAGCCCTTTAGTTACTGGATTTGCTTTATTACGTGTACAATTAAATGAGTATG	37301	A_95_P208367	DV157686
38263	451	13	803	AGTAATGCTGGTACCTGGTAGTAGGGATTGGCAAATCAATGGAACGCATCGTATAAA	37307	A_95_P268966	DW003673
38266	451	16	1764	AGAGCTGTTGGCAGCTCCCTTAACTCAGAAACTATTCAGTAATTCCTTTTCTGGAAAA	37312	A_95_P251697	X92967
38270	451	20	476	AATGCGTATGGTGAAGATGATGACTCATATAGAGACAATAATGATGATTCATGCTAT	37320	A_95_P262891	AM783645
38279	451	29	560	CATATGTTCTATCATAGTGTTATCTAGATGCTTGTGGTGTTAATTTCTTTCCGATGCTT	37336	A_95_P060885	BP135115
38283	451	33	494	TTCCCAATTTCGGATTCTGTTCCAAAAAATGGAGTCGGATTGAACGACCTTGTCGCTA	37344	A_95_P077885	FS406615
38284	451	34	796	TTCTTGAACTTTTGGATGGAAAATGTGGTTAGTGCTGTGCAAATTGAGAAGCACTTG	37346	A_95_P267416	DV160102
38287	451	37	686	GGGTAAATGGTGATCTTGTATATCTGATTTTCAAGTCTTTTTCGAGAATTTTGGATTC	37352	A_95_P123807	DW003714
38288	451	38	313	AATGAAGCATGAGCGGGCACGGTTGGAGGAAGAAAATTCAAAACAATTGGAATTAC	37354	A_95_P147747	EB643433
38291	451	41	288	AAAGGTTTGAAAAAGAAGGTCCTCAAGTCGCTTCCGAAGCTCAGTTACACGACGGAA	37360	A_95_P002131	FG642019
38293	451	43	910	ATCCAGCGATAACAATTTTCATTTGCCTTGTATGGATGTGCAGTGTGTCAACTGGTTTT	37363	A_95_P247907	EB430441
38297	451	47	814	ACAGTCCAATCCGATACCCATGTCACATACAGCACCTGTCTCTGATGTGAAAAAGAA	37371	A_95_P285098	DW001320
38306	451	56	885	ATTCTAGAACCTTACTGCAGACTGCTATTGGCTGTGTCACAACCTTCCTTCTACAATGT	37389	A_95_P268161	DV999672
38312	451	62	545	GAAGCCAACGACTGATTACCTTTTTCCCTTTCCTAAATGTGAAAAATGGAAATGTAAG	37401	A_95_P134327	EB436553

38315	451	65	513	GATATAAAGTTGGAAAGGACAGAAGTTGGAAACCATTTGGAGGAATTCTAGTATCTA	37406	A_95_P045511	BP131163
38318	451	68	758	GGGAAGCAAACGTGTAGAAGGTATCATATCACTCAGTGACATTTTCAAGTTCTTGCTT	37412	A_95_P303513	FG194435
38327	451	77	896	TGGATTTGTACTTGCCCACCAGTTCTGGGTAGATCATGGATTTTTGTGCGAATAATTT	37429	A_95_P250362	M77225
38328	451	78	416	CTCATCATAATTTCCCTAGTTGAACTATTTCCCTGTGAAATTCTCTACTAAGACGTAGT	37430	A_95_P074065	BP526376
38330	451	80	740	CCGCATGGTTTAGTATTTTGCTTCTAGCAATATTTGAGCAGACTTAAATTGTTTCAACT	37434	A_95_P017631	TA12941_4097
38337	452	2	175	ATGTTTGCCGTCACATTTTCGGGTTCTACAAAGAAGTTGAAAGATCTGCAGGTTCATG	37286	A_95_P115653	TA17337_4097
38338	452	3	601	GTTTTCTTTCCTAGACTTCCCAGATTATTATGTAGAGGGGATGTATCCAATTTTAGTTC	37288	A_95_P123677	DW003542
38345	452	10	875	TTTCTCAGATGCTGTCTCAGTTGTATGATATAGTAATTGATGTGGACGGCATTTCTGA	37302	A_95_P244812	DV161814
38346	452	11	640	GGTAAAAATGAAAAGCTACATGGTGGGGACTCTGAAAATGCGCTGGAAAGGGATT	37304	A_95_P144777	EB448318
38353	452	18	733	AAGGCCATCAGGAAGTGGCAGCAGCACAAGGGAGTAAACTGATTGTGTTTTAGACC	37317	A_95_P117097	DV159885
38354	452	19	893	AATGTTTGAACCAGGGTTAAGCCCAGGATATGGGGGAAATGCAAGCTGCTGTTGAA	37319	A_95_P201972	TA17534_4097
38361	452	26	827	GTGGAGATGTTTGCAAAGTAGCTTCACAAATCTTGTAGTAAGCTTGAGAAGTAATTA	37332	A_95_P010736	TA13597_4097
38369	452	34	790	CAATAAAATGATGGCCAAGCAAAAGCGACGAGAAAGGGAATGGGCTGGCAAATCT	37347	A_95_P093403	EB444132
38372	452	37	145	GTTGGTATCTTCTCTCAAGTCGCTTTGAGCTATGTAAGGCAAATAATTTGGTTATTTT	37353	A_95_P029266	TA19409_4097
38373	452	38	542	TTCATCTGGTGCCTTTATGTTGAATAGGCTGTTTGTTATTAGTGGTTCAATGCATTGAA	37355	A_95_P263266	FG635677
38375	452	40	509	ACCACTAACAATGATGCTGATGCTGCTGACCCCAAAGTTGCTGGACTGATTAAGATT	37359	A_95_P102352	CV015989
38379	452	44	169	TTAATGCAGCCTTAGAACAGTTGGACTTCCCTGGAGTTTGCAGCTTTCTACAGAGTTC	37366	A_95_P078535	BP527538
38381	452	46	819	GACGAGTAATGCAGAAGTTTAAATCAGCTTTGAGCTGGTTGATGAATATACTTTATTT	37370	A_95_P207502	TA18755_4097
38382	452	47	573	ATCCCTACCCCGACCATGTATTTCACTTTTTACTTAGTACGTGATAGAAAGTGTAATTA	37372	A_95_P027876	TA17866_4097
38384	452	49	1451	TGAGGTTCACAGCAATGAAAGCAGCATCTCTGCCGCTGCAACTTTTAGATGGTATAA	37376	A_95_P206392	TA18506_4097
38388	452	53	657	ATGCATTGTAGTCTACTAGGCATGCCTTCTTGTTTTTAACACTTGGATTGTATCCATAT	37384	A_95_P000446	EB432747
38389	452	54	404	ATGCCATAAAACAACTCTTAGGCCTATATATTAATTTTCTCTGAAACGGCAAAACGGC	37386	A_95_P213612	TA20085_4097
38391	452	56	411	CTGCCAAATGCTACTCAAGTTTATCTCTAACCTCTTTCTTGTGAAACTAACTTAATGTG	37390	A_95_P086798	BP529632
38393	452	58	645	ACTGTAGTGAGGTGAATGGAAACCTAGAGAATGTAGATATTTGCTGAAATAAGGCA	37394	A_95_P021096	EB432538
38395	452	60	610	GATGTTCAATTGGAAAGCACTCTGAGCCGTGTTTTGGTCGAGCAACTTAGAGAAAAC	37398	A_95_P159432	EH617629
38410	452	75	750	CTGCCAAGAGTATTGGATTCCTTCATATGAACTTTGTGTATGTTTTTTCTCTAGTATCC	37426	A_95_P162247	EH621149
38419	452	84	246	GTGGTTCAAAAGAAAGTCGATATGTATATCCCATTCGTTTTTTATCATCCTTGAGTCAT	37443	A_95_P155027	EG649864
38426	453	6	1077	AGTGTCTCGAAAACTCTATCTAGTGGCACCATCTGAATGACTATGTAAATTGAAGGTT	37456	A_95_P192552	TA15476_4097
38427	453	7	1181	TTTGATTTAAGCTGACAAAGATGCTAGCAAGATGAGTTACGTGGCAGTTCTTATCCC	37458	A_95_P210792	TA19471_4097
38428	453	8	367	AATTTGTGGGCTGTGATGGAAAAGAGACATATAGTCCCTGACCTTTACATACAGTTAT	37460	A_95_P071905	BP525820
38430	453	10	845	CATCTCTCCCTATCATTGTATAGGTTGCCTTCTTATACTTGTATGTCTCTCAGCGGTGG	37464	A_95_P231309	EB439273
38433	453	13	889	GTGGAATAGTTGAATTGGCTCCAGGTTACTTGCCTGCTGTATACAACATTATACGAAA	37470	A_95_P128302	EB427893
38442	453	22	871	TGCTATACACTCAGTTATGGTATTTGTCTGTGTAAAGTATCTTCCTGTTTACACAGTTC	37487	A_95_P205072	DV161430
38445	453	25	723	CCAGACTGCTATTGTATTGTAAATTAAATTATCTCTCGATTGAAAGAGCAGCTCATGT	37493	A_95_P013811	EB429285

38448	453	28	403	ACTGTTGTACTTCTTGGAACCAGTGACCCTTTTCAGCAACAAATGTTTTTGATTAATG	37499	A_95_P248142	FG645407
38449	453	29	914	GCGTTCAAACTTTTCTCCTGTTTGTTTTTGGGGTTGTGTTCGACTTTCTATCAAAATTT	37501	A_95_P000306	TA11800_4097
38451	453	31	465	GTTCTTAGGGTTTACACCTTTTGGATATCTAAACTCTTGAATTTCTGTCTAAGCCACGA	37505	A_95_P127392	EB426935
38455	453	35	873	AGTTCAATTCGATGTTAGAGTGTTTGAGCCAATACGGGATGTAAAGATAGATAACCC	37513	A_95_P013406	DV999136
38460	453	40	1443	GGATCAAGCCTTGTCCTTTGTTATATTCTATTGTTTCTTCATTTACCTTCTTAGAGCTG	37523	A_95_P205647	TA18334_4097
38462	453	42	1187	CCAGTTTCCTTGATGGCAGTGTAATGCTTAAAATGGTCATCTATTTATGCATTTCTACT	37527	A_95_P201022	TA17336_4097
38463	453	43	657	GGACAAGGAATCATGGGATATGAATACTCAGGAGAAAATTGAGGCTGCTGGCAAG	37529	A_95_P102002	CN949739
38470	453	50	1148	AGCTTCTTTTGCACCTTGTGGTGACAGCTTTTTACTGTTTGTTTTGTTAATAATATCCT	37542	A_95_P141307	TA14854_4097
38476	453	56	525	CGGACTGCCAGTGATGTATTTATATTTGCATGTATTATCCGAAATTCGGACTGGTTAT	37554	A_95_P121872	DW001963
38478	453	58	680	ATTTGCTAGTTTGATGACCAGAATGCTACAACAGCAGGGACAAGGCACTTAAATAAT	37558	A_95_P151382	EB681594
38481	453	61	1529	AGCGGACTTCTTGACATTTGCCAAAAATGCTACTTCTGTTTCTGGTGTGATGATCAGC	37564	A_95_P018211	AB120519
38487	453	67	772	GCACGGTGATGGTTTTTGACTTTGCAAACTGAAGCTGATTTGCTCCGAGTTGTTTTTC	37575	A_95_P123862	DW003750
38488	453	68	333	CAATCAGGTGTTGAGGGAGTGAATTATTTGGAAGTCTTAAATCTGTAATCCAGTGAA	37577	A_95_P093923	BP532482
38491	453	71	735	ACGAAAAATCCCATTTACTGACAAGGATAAAGAGGAATTGATGTTGCGCACTGTGGT	37583	A_95_P127412	EB426949
38495	453	75	92	TTGGGTGGTTCTTATATTGAACGTACACTTCCTTTATTAATGTTTGTGGTACTTCTTGG	37591	A_95_P216277	TA20669_4097
38503	453	83	460	CTATATGGATTTGGTGGTTAAATTTCTGTATCTGGGTTTTGGGTGTTTTGTTTAGTCT	37607	A_95_P000976	CN949751
38505	453	85	250	CCCTTTGGCAAGTCTGCACTGTTTCGATACTTGAAAAGCAAAGAAAGATAAATATCTT	37611	A_95_P088748	BP530198
38511	454	6	535	GTTCTGTATCTTTATTGGAAACGGATCATGAAGAGATCAATGGTAAATTGAAGTGTC	37457	A_95_P071355	BP525684
38513	454	8	1249	AGAACACTGTACACGTTCAAGAATGGAACATGGAGCTTACTCTAAAATCACGATAAA	37461	A_95_P228129	EB643449
38515	454	10	677	GTTTGTAGATTTGGTTTTACAACTGAATGGCTGCAATGTAGTGGGTGGCAATTTTTC	37465	A_95_P187547	EB679266
38524	454	19	842	TAAACTTGTTGGAGAAGTTAGTAGGCTTGTAGTTGCAGAAGCTTGCATACAGGCGCT	37482	A_95_P217997	EB679873
38526	454	21	765	GAGCCTGTGACAGCACAATCAGGAATGTTACTTCTGTTATTTTAATTAATTGTTTGCC	37486	A_95_P011616	DV159148
38538	454	33	674	TCCACGTGCCTGGTATGATGAACTGAAAGCTTATCTTTTATCTTTTGGTTTTCATTACT	37510	A_95_P128867	EB428602
38539	454	34	716	ATTTACTAAAGCTCAAGCATGAAAGACGCTCCAGGACCATCTAGTCAGGACCACTGC	37512	A_95_P146142	EB450046
38540	454	35	447	TCATCTCGATCTCTTTGTGTAGTACTTATGCCTCATTGATTGCTTATTAAAGGGTTTCA	37514	A_95_P062940	BP135650
38541	454	36	840	GAAAGGGAAGGATGCACAGATTCAACTGTGATATACGGAGCATGACAGATCTCATA	37516	A_95_P150302	EB680397
38545	454	40	278	CTTGGACAAAAATATCCTACCTGTTGATGCTAATTGTTTTGACGAAATTACATGGGTG	37524	A_95_P074180	BP526400
38548	454	43	781	GAGTTTTTATCAAGTTGAAAATTTGAGCGCATCGAGAAGGATTGACTGCTCTTGATT	37530	A_95_P115477	DV157710
38549	454	44	1377	ATCACTGGATGTAGTGCTAGGATTTTTATCTAGGAACGACTTTCAAAATTATCTGTCT	37532	A_95_P198137	TA16714_4097
38553	454	48	411	GCTATGGTTTTCCACTCACCCATCGGTCTTGTTTTTACATACAGAGACTGAAACTTCC	37540	A_95_P094558	BP532774
38554	454	49	279	TTGGGTACTTGGGGCTGAAAAATGTTAGGTTTCTAAGTTTTTGCTTGTTCAATGATGT	8937	A_95_P000091	AJ717873
38555	454	50	894	GATATGTGATTTTCATCCGAGATAGCGAATGATCCATCCCTCAATTTGTAGCCTTAAT	37543	A_95_P250922	EB679010
38557	454	52	172	GCTGCATTGCATTGACAAGCTCCTGTAATATATGAATGTTCGTTTTGGTTTAAAAATG	37547	A_95_P178567	TA12282_4097
38560	454	55	326	GCTATTTTGTGAAGGGAATCTGTGTGGTTCATTTTTGGCTTAGGTATTCAAATTTTTG	37553	A_95_P088358	BP530024

38561	454	56	703	AAGACAGAAGCTGTGAATGAAGATGCCCCGACGGGCAATAAAGAAGAGAGTGATC	37555	A_95_P124232	FG147854
38563	454	58	799	ATAAGCAGTTGAATGATAAAGAACGGGTAGCTGCAGCATTGGAAAACCCTAACCTT	37559	A_95_P134447	EB678124
38565	454	60	828	GCAAAGCTTCCGAGACTGAGATCATGAGAGATTTTTTCATGTGTATTGTATGTTATCT	37563	A_95_P030016	EB677612
38566	454	61	227	TTGGTACTACATTAGAGCTGCTTCTATGGCAAGGCAAGATTTATTTGCAGGGGCGGT	37565	A_95_P108422	CV018824
38569	454	64	1277	CAATAAGGATGATTCTTTAGTTTTCATGCTAAGAAAGTGGTTCAGGCTAATACTCTTG	37570	A_95_P179482	TA12517_4097
38571	454	66	810	GAATCATCACGAGGATCTGACAATAGATGGAGGCACAATCAGCATTTCAAGTCCTTA	37574	A_95_P264081	EB426755
38575	454	70	902	GGTTTGCAGTGTAAACTAAGGTGCTTCGTTGATGCTTTTGTTTTTCCAGAAAACATAA	37582	A_95_P214042	TA20176_4097
38576	454	71	0	CTCAGAAATTATTGGCGGGCACTTAAAGAAAGATAAGTTTCTCTGTAATTTGTAGTCT	37584	A_95_P016896	A_95_P016896
38577	454	72	789	CTCGTTTGTAAACAGCTAAGCTAATATGGTCTCAAGTCAGTTTGGTCGATTACATAAA	37586	A_95_P020001	AF072519
38581	454	76	737	GAGTATGGATCACAGAAGATAAAGAGGATGGAGGAGTCATTGGGAGTTTGACAAT	37594	A_95_P160512	EH619204
38582	454	77	737	GAAAACGAAGTTTCGAGAGTAACATGAAGCATTTGAGTGAGCAGCCACCTGTAAAC	37596	A_95_P156657	EH614430
38583	454	78	566	TGCTTGGAATTGGAGCTATATGGATGTGATTGTGAATTAAGACTGGTTTGCATTGAA	37598	A_95_P023321	BP534049
38584	454	79	700	ATACTCTTGTCTCCTTCAGCCTTAGAACCGAGACTAACTACAGTTTCTCATCATTTTTC	37600	A_95_P223667	TA22302_4097
38585	454	80	507	TAAATATGGGAAAGAATTCGTCGCTGCTGCTACAGAGCTCATGCCAGAATGTGGTGT	37602	A_95_P145127	EB448669
38586	454	81	854	AGTGTAAGGTTCAAAGTTGGTAGTCCTGGCTGACTATGATAGGAAAGCATGAATCT	37604	A_95_P018386	TA13793_4097
38588	454	83	454	TTCCCAGTCAAGGTTTCTAGGATCAACATACCAAGTGTCCAAACATCAGTTTTCCTGT	37608	A_95_P275328	AM827537
38590	454	85	700	GAATCAGATGTAGTTCAAGCATGCCGAAGATTGCTTGGTGAGCGACAGAGTCCAAA	37612	A_95_P202517	FG135146
38592	455	2	222	ATGATCGTTGCTTTGCCTCTGGGCGTTGTTCATATTGTATTGAAATCTTAATTTTCCAT	37615	A_95_P093348	BP532227
38601	455	11	300	TTACTTGAAAAGGAATAAGTGGGCTTCGTATTATGCAAGTCATTTCTGGGATGAGAT	37633	A_95_P089393	BP530482
38604	455	14	441	TTTCGTTAGCTAAACCAGATACTAAGTACTATATTTGATATTGGGAAGAGGATTTGTC	37639	A_95_P134462	EB436799
38608	455	18	488	GTGGTCTTGGATGTCTTTTGGGCTTGTAGTTACTGCATTGTGACAGTATAATCAACTG	37647	A_95_P281078	AM811486
38609	455	19	799	CATTGCTTTTTTGTACTAATGAAAGAGCTATAAGCGAGGAGGGAATGCATTGTAATA	37649	A_95_P139447	EB443206
38617	455	27	527	TACCGTATTGTGATGTAACGTAATACTGATGAGATTTGACTATGGTGGATCTCTTTGA	37664	A_95_P121572	DW001658
38620	455	30	356	GACTCCATTAACATCCTATTCTTGCTTTTGGTGTGGATGGAACATGTAAATGAGGTTG	37670	A_95_P078360	BP527496
38624	455	34	740	TATGTCACTGATATGGTGCACAAAGCTCAAGATATTGCAACCAAAAGGGGGAAGCTT	37678	A_95_P295573	FG197647
38626	455	36	930	GAGTTTGAATGTTTCGGTTTGTTTAGCAATACCTATTTTATTTTGCGAACTGCCCTTTG	37682	A_95_P233984	DV157889
38629	455	39	469	GGACAAAAGTTTCTTGTAAATGTAAAATATCCTGCAGTAATCCCCTTCTCTTGAATTT	37688	A_95_P050001	BP132294
38630	455	40	620	TAACTACTTTCTTCCTTATTGTGACTGTTGGACGCTATAGCTATTCTATGAACTCGTTG	37690	A_95_P016591	FG144478
38631	455	41	594	ATTGAAAAAGCTCTACATTGGGGGATCTGAGACAGAGCATTACGTGGAGGACCTAA	37692	A_95_P041586	BP130129
38633	455	43	882	CAAGCTTTCCTAACATATATGTGGTAGATGCCATATCATTTGTACCTCTGAACTGCAG	37696	A_95_P189797	TA14864_4097
38644	455	54	848	TGCTTAGGGCATACAATGTTGATTTTTACATGAATGGACACGACCACTGCCTTGAAC	37718	A_95_P216917	EB425136
38645	455	55	630	TTGTGAAATGCTCATTGTTGGAGAGGTGTTAACGGGAGATAAAGTAAATACAATCTC	37720	A_95_P263831	FG636095
38648	455	58	338	GAATAAATTGACAGACCTGGCTTTGCCTATGTGAATGTATTGTTATCCCTATAGTTTG	37726	A_95_P031401	EB435730
38652	455	62	455	AGGTTCCTGCTATGGTGAAGTGAAAGATCTTTCACTATAGTGGGAAGAAGACAGGT	37734	A_95_P028346	BP525606

38656	455	66	890	CCTTTGATCAGACTGTTTGGTCAGCAATTTGGAACAGCATTTACTACACAGTTTTGGG	37742	A_95_P008046	DV161189
38668	455	78	866	ACATAGTTGGGGTTCTCTCCTTATTTGTTCTTATTAGCTGTGATGATGTGATATGCAT	37766	A_95_P233959	DV999223
38670	455	80	1317	CAATGTACCAGTTTTTTGAGTTCTGTAGTGAGTTATTTTCAGAATAGACAAGCAGCG	37770	A_95_P026896	TA14217_4097
38677	456	2	976	CTATTTCTGGACATTTTTCGCAATGGTCAATTTCATAGTGGAAGTGCTTGTTCAGCTTT	37616	A_95_P178362	TA12229_4097
38681	456	6	749	TTTCATTGCTGTTGTTAAAAGAAGAATTACTTAACAGGTGGATTTCCTTTTCCCCACTC	37624	A_95_P230384	EB429570
38683	456	8	412	AGTCTTTGGACTCTTGATTTTTAAGTGAAGTTCTCTTGTTGTTGACAGGTGCTTTGGTT	37628	A_95_P214567	TA20289_4097
38684	456	9	392	AGTCTGTCATAGTGTAGTTGAGTCGTTCATGTCTTTCATTATCGTATTTCCCTTTGTAT	37630	A_95_P095763	BP533329
38687	456	12	844	GAGTGGCTCCTGAAAATTCGTCGAATAATGCAACTATGAGCATAGATATGGGCCAG	37636	A_95_P253024	FG142932
38690	456	15	617	TCCTTATGTTTGTAAGATTAAATGGTTTTGAAATTCTGTTGGATGGGTTCTAAGTGGG	37642	A_95_P258186	TA12136_4097
38693	456	18	818	GTACCAGTTATGAAGTCTCCAGACTTTGGATAAGAGAAAACACAAAGTGGATGGAC	37648	A_95_P157277	EH615331
38697	456	22	232	AATATTTTGTACTAACATCACTTTCCCCACATCCACATGCTCTGCAAAGATAGAAAAG	37655	A_95_P038341	BP129248
38698	456	23	492	ATTTTAAAAGAAAAGCACAACAAAATGAAATATCTGCTCGGTTCTACACACGCCGGG	37657	A_95_P284373	FG634129
38701	456	26	370	GAGATATTGTTGTGGTGTTTTGTTTTTGAACCTTGCTATTGGGTGCACTCTAATTCTAT	37663	A_95_P092713	BP531941
38705	456	30	239	GACCATTGGGTCTCAAGTCATCATTGCAGTTTTTTATGAAAACGTAGTAATTACAAGG	37671	A_95_P163317	EH622329
38709	456	34	1445	GCTAGCTAATTATGCACTTTTAGCTTACTCGAGGGAAATTTCGATACAATGTTGATTC	37679	A_95_P154222	EF051137
38710	456	35	193	ATCGATGAACTTGAACGAAGCATCAACGATTTGAGAGCTGAAATGGGTCAAGATGG	37681	A_95_P109797	TA16250_4097
38711	456	36	856	AAGATGTTGGAGCAGCCATGCAATACCTTCAGTCCAAATCACTCTGCATCATGCCCAT	37683	A_95_P291058	EB680364
38712	456	37	821	GAGGGATCCGGAACTCAGAAAGAGACAAGGATGAACTCACTGCTATTACAGTTGCA	37685	A_95_P115402	DV157585
38713	456	38	725	CAAGTGTTACTGTTTAGTTTGTAAGACTAGTGTTTTCCTGAAACATCAAAATGGATTC	37687	A_95_P020891	DV158794
38715	456	40	484	TAGCAGGTTTATTTCCGTATCACTCTTCTTTATTTGAACTTGTTTGGGTGATTTGAGCT	37691	A_95_P280228	AM822222
38718	456	43	961	TATGGGAGTCTCTCCTCTGTGATTATTAATATCAACTATGACGATATGATAGACAGAT	37697	A_95_P031601	TA16934_4097
38720	456	45	109	GCTCTACGATCGAGACTCATAAGATTGAAGTGGTTAGCAAAAGAAGAACAAAGAGA	37701	A_95_P120312	EB449849
38721	456	46	136	AGGTTTGGCCTTTATTTGGTCATCTTTTCTTCTATTGTTCTTGCTGATAGGTATGTAAT	37703	A_95_P048611	BP131960
38722	456	47	777	CGTGATCCTAATGAGCACAGCTACTGCAGTCAATATGACCTCTACCTTTGTTTTTTGCC	37705	A_95_P119772	DV999332
38728	456	53	822	CAGAGTGCAGCAATTGAAGCAGTTGATCGCTCAATATCAGAACAATTAAAACCGCTT	37717	A_95_P249727	FG155326
38729	456	54	840	GTTTTCACCAACAACAATCTCTCTGGTTGTGTTACAGACGAAATCGCTAAGCTCAAGA	37719	A_95_P128677	EB428428
38733	456	58	210	GTACTATTATGAATGACGACGACGAAAATTTATACTATGACTAGATGCCACTTGTGTT	37727	A_95_P114282	CV021526
38744	456	69	1004	GCCTTTGTGTGTATGAGTCTGCAAACTTTAATGAACATGTTTCTGTTGCATTCCTTATA	37749	A_95_P186892	TA14225_4097
38747	456	72	418	GTGTGGTAATGTCTGGCATGGTTTTGTAAATTGTGACAAAATTTGAAGACGTAAAGT	37755	A_95_P309168	FG645001
38750	456	75	203	GAAGGTGTACATATATGATGTAGATGCCTGGGTGTGGATCTAGTTTGTAAAATTTAA	37761	A_95_P147132	EB451376
38753	456	78	663	CTTTAAATATGTTTTGAGACATGGTGTTGTTTTTCCGCCGGAACAGCTGCAGATCTGA	37767	A_95_P202532	DV160679
38754	456	79	752	GGATAGGGATTGATGAATGGTTACGCATCCCATCAGTTCAGATGTCTCTCATGCCGA	37769	A_95_P289823	FG177300
38759	456	84	519	TGGTGCTCCCATTATCTTCCAAAAGTTGTAGTTGACATACTTATATACATGTTCAGGTT	37779	A_95_P274383	FG634502
38760	456	85	774	GAAGATGAAGAGGCTGTTGCAGTTCATCAGAAGAGGGGTAGAAAAGATTCTGTTTT	37781	A_95_P244272	DV158739

38761	457	1	395	AGGGCTCCCTTTTGGGCACTTGACTTTATCAGAATTGACAGAGCTACTTTTTCATTTTT	37782	A_95_P269861	FG625527
38762	457	2	699	AGTCCTGAACTTGATGCGAGCTCTCATATCTATCTCTAATAATATCTTAAATGCCTGT	37784	A_95_P185387	TA13901_4097
38765	457	5	1069	ATCCTTTCCCTTGGTGGATCATGCTTCCTTTGAGTTCTTTAGTTTGTATCAATAGAATT	37790	A_95_P163012	AB281271
38767	457	7	211	GAAAAAGAAGTCCAGTAGTAGTTCCTTATTTTACGAAGCTCCCCTCGGCTACAGCATT	37794	A_95_P004020	FG141290
38773	457	13	1060	TCAAACGCTAAGAAAGATGTTATTCTATTTTCAGTAGAGTGACGATCTTGTCAACAA	37806	A_95_P182247	TA13167_4097
38777	457	17	901	TATTTCCAGTCAATTCCTGGAATCCAAATGGTTGCCTGCTCAACCCCTTACAATGCCA	37814	A_95_P187212	DV161194
38779	457	19	606	AAAGCATGTTTGCTGCTCTAAGAGTTCACTTTTACTCTCATTGAAGTTCTTTTGTTTCC	37818	A_95_P157712	DV158956
38782	457	22	773	TTCCTGAAATTGCTGGACAATGTGGCTATCTCTTCCAGATTCTTTTCCAGATGGCTGC	37824	A_95_P013101	FG134922
38793	457	33	2213	TCATTTTGAGGAATCAATGAAGTATGCTAGGAGGAGTGTTAGTGACGCAGATATTC	37846	A_95_P101888	DQ515925
38796	457	36	763	AAAGATGGTTATGAATTCTTTGCCGAGAGGCAGCTTGTCACCATTTTTTCAGCGCCCA	37852	A_95_P201437	Z93770
38801	457	41	383	TGATGTACTGGATAAATTGTCGGCGGCTTTATTTCCTTTTACTTTTATGACGTGAACT	37862	A_95_P108642	CV018933
38802	457	42	1095	ATAAATGAAGCGTTCTCTGTGGTGGCTCTTGCCAACAAAAGACTGCTCAATCTCAATT	37863	A_95_P012216	AY748246
38804	457	44	398	CATGGAATTAAGCCAACAGGTGTTGCTGTGGTTCTACAGTGTTCACATATTCATTTCC	37867	A_95_P138227	FG167397
38807	457	47	819	GTCATTTCTTGAGGCTTAGTTGTTGTCACTTGATTATTTTGAAACTCCATTGCATTCTT	37873	A_95_P148477	EB677823
38808	457	48	323	AACTTGCTGCTGCTGCTGGTGATACTGTATCAATGGGGAGAGGAAGCTATAACTCTA	37875	A_95_P154207	FG163331
38809	457	49	612	GATTATGGCCTTTTTGCTCTGCGACTGTCATATATATTCGTATATGAATGTTGCAGTT	37877	A_95_P029206	TC72615
38811	457	51	406	TTGCTGACTCGTACGAAGTCATTTATTTACCATTACCTTCATGCTCATGTCTGAGTAGT	37881	A_95_P094138	BP532581
38814	457	54	868	GAGTTGGTTAGTATGCCACCACTTTCCTGATGAACAGATTGTGGTATCGGTAAAGCT	37887	A_95_P008266	EB447962
38817	457	57	620	ATGGACAGTTTTTGTGATGTTGCTATCCAATAGAAATGAACCAAACTCAATTGTCTCC	37893	A_95_P201782	TA17496_4097
38819	457	59	589	TGATGGTACAAGTGATTCCATACTAAAGCATAAACCTATATGGGCTACTTATAGCCA	37897	A_95_P118132	FG158775
38824	457	64	422	GTATGAAAGGAAGCTGATTTGGGCTGTAACACGAACTTATCAATATATATCTCCTCTT	1861	A_95_P000051	FG625247
38828	457	68	228	ATTGGTTCTGTGTGCCTAAAGTTGAATATGATTCTAACGGGTTTTGCTGCCATTTTT	37914	A_95_P015826	CV021776
38829	457	69	846	TCTTTGGCTAGCTACGACCTCGAGTGTATGCATATTCTTGGATGAAAGAGATGTCAC	37916	A_95_P274568	FG163833
38834	457	74	193	ACTTGATGACCAGCCGAGTATAAGAGATCCAGATTATCTACGAACAGGAGGACTGT	37925	A_95_P107607	CV018461
38842	457	82	820	GTGTGATCTTGCTATATATATCAGCATGGCTCGCTGTATGTCTCTGTCGTGTATATGA	37941	A_95_P268601	FG144509
38844	457	84	622	GATTTTGGAGCTTACTTACTCTAACAGTACTAATTAGGGGGGCTAGGGTTATTGGAA	37945	A_95_P285108	FG148198
38845	457	85	357	TGGAGGGGTTCTGAGGAAGGGGTTTAAGTGCCAGTAGTGGTGTTATGCTTCCTTTTA	37947	A_95_P065650	BP136391
38848	458	3	788	CAGTCAAGTTATATTAATGATACCGACTCTGTAAAACCCTGCTTTTCAGAGGGTTTTA	37787	A_95_P186092	TA14052_4097
38850	458	5	290	GAAAACATATCCTGATGGTGCATTTGATGTTGATATTACAGTCCGGATTACTAATCCT	37791	A_95_P070555	BP192664
38853	458	8	1004	CCTTTTTGCACTGAGAACTGTCCAAAATCATTAATGTATCGACATTTGTATCTCTTCTT	37797	A_95_P117072	TA16244_4097
38856	458	11	743	GGTACGGTATTCGAAAATTTAGCATATCGGGAGATTTTATTATGCTCAAGAGTTGAA	37803	A_95_P219912	EH617181
38862	458	17	1113	CCTTGGAGGAATCGAGATTCATGGTTCATTAAATATCTTGTCTCACTATTCTTTATCTT	37815	A_95_P016541	TA16072_4097
38867	458	22	685	CTGCGTTCTTTTCTTGACTGTGTTTATGGTTCTAGCACTAAATGTTTACCATTTGGAAA	37825	A_95_P148482	EB677824
38873	458	28	303	CTATGCTGTGTGAACTCAATTCATTTTCGTTCATTCCATGGTTGATGGTACCTCTGAC	37837	A_95_P092488	BP531833

38874	458	29	495	TTTTGGGTTTGATAAACCCTGGTGATGAGGTTATCCTGTTTGCTCCTTTCTATGATTCT	37839	A_95_P127292	EB427335
38877	458	32	472	AGGTATAGCCAACAAAACTTAAATCTTCGGGAATCAGACGCTTCTTTCTATGAGGTC	37845	A_95_P264706	AM833236
38880	458	35	518	GACTCTACAAATCTTAGTTTTGCTGGTTATTGGGGATGTTTCACCAGTCTCTGAATAG	37851	A_95_P215927	TA20593_4097
38885	458	40	865	TTGATCTCCTGTTACCCTTGAACATAAATTTTCTTATCCCTAAACGTGTAGTTGTACCA	37861	A_95_P008841	EB427847
38889	458	44	246	TTTCAGCCATGTAGATATGCCGGGTATCCCAAAGGAAATCGCCATGCACAAACTGAA	37868	A_95_P192887	BP130642
38890	458	45	509	ACTCTGTATCCTATTCTATTCACGCTATACTTTACTTGGGGAGTTTTAACTCGTTTTTA	37870	A_95_P133612	EB435249
38892	458	47	532	CAACTCTTTGGCGTGCTGCTGCGTCCATATTCAAAGATGAGAGTCTATGTAAATCTAA	37874	A_95_P039396	BP129535
38893	458	48	753	CCAAATTGGTACCTGCATTGCTTTGTAAGGTTAGATATCTTTCAGTTCTAACTTCTGTA	37876	A_95_P190592	TA15048_4097
38894	458	49	233	GCAATTGAAGATCAGTTACCTTCTGTTAATATTAGTGCAACCCCTCATGTTATTGACA	37878	A_95_P155282	EG649993
38898	458	53	649	GAAAAAATACATCAAACCGTGTCACTTGTGCAGATAATGAAAGTTGCTTTCAATACG	37886	A_95_P149457	EB679293
38905	458	60	309	ACAACCATAACTTTTTCTTCTGTGGAAAAAGTGGTGTTGGTGGTGTTGGCGGCGGAA	37900	A_95_P038926	BP129406
38906	458	61	802	GCAGAACAGTGGATTAAGTCTATCATTAGCTGGATCTGATGGACGATTTCGGGGTTG	37902	A_95_P225892	FG143737
38910	458	65	1077	TGGCTGCAGCACACAGCTTATCATATTCAGACCAGACTTGATTATTGTGTAATTAACA	37909	A_95_P019406	TA14241_4097
38915	458	70	460	ATAGCAGAGGTTTGTGTATTAGCCAGCCTATTCATCCCATTTATTATTATGTGTACTTA	37919	A_95_P089863	TA17504_4097
38919	458	74	270	TCGGACTTTCGATCATTGCTTAATTAACGGTCGTCTCGGGACAGTGATCTCATTTCAT	37926	A_95_P063210	BP135715
38920	458	75	805	CTGTTCTCCACAGCTTCCCTATTTGCTAACTTGGTTTAAATAATTTTCTGTGTCACTCAA	37928	A_95_P150842	EB680967
38921	458	76	310	TTTCCAGTCGAGGTCAGTGTCGAGTCTCAGATTCATGTAAGGTTTCATTTTTGGCCTC	37930	A_95_P099133	BP534804
38925	458	80	835	ACCTCTCGGGAGCTATGCTTCTTTTCTCAAAGAGAAGAATGAGAAGAGAGTCTCAAC	37938	A_95_P218002	TA21073_4097
38926	458	81	540	TTCCTTTTTTCTTGCCAATACGTGAAGCTGAAAATGAGTTTCTCTCGTCAAATGCATAA	37940	A_95_P040806	BP129928
38932	459	2	357	AGTTTGTAATGCTTGTCCCGGTAATGTTCTCCAATTTTGAGTTTGTGCTACAAAAGCA	37951	A_95_P143572	EB446834
38933	459	3	200	CTCGAGTTGTAACTGAATTATGCGGAATTTGTAGTTTTTATGTTTGTGTTTGATATGC	37953	A_95_P128757	EB428492
38937	459	7	422	GAGCACTTACTAACTCACATACAAGTAGGCTTTGTTCTAGTCTTGTAGGAATTAGTTT	37961	A_95_P266936	TC69181
38938	459	8	813	CGTAGTCTACATAGTGGTTGGTTTGTAATGAACAATGGCTGGTGATGCACAATGTTT	37963	A_95_P146362	EB450395
38941	459	11	449	TCAACAAATGTCGGTACAAGTTCTTCCATTTAGCAATTATCTTTACTCCTTTTAACCCT	37969	A_95_P264551	AM830869
38944	459	14	765	CGGTTTTGCAACTGTCATATTTCCGTTGGCTGCTAATGTAATGTATTTCTAGCCAAAA	37975	A_95_P115827	DV158198
38948	459	18	417	AATGGTCAATGGTACAAAAAGATGATACGTTGTTTGCACATTTCAGGTTTAGTTCCCA	37983	A_95_P005656	BP133446
38950	459	20	0	AGTAGCATCTGCATCATCAGATGGATCATACGTGTTGGGATGTCGCATGACTAGAAG	37987	A_95_P260221	A_95_P260221
38951	459	21	935	TTTCTCTTTGCATATGCACTTGGAGCAAATTTGGAGTCTTAATGCAAGACTCGCCCAT	37989	A_95_P223152	TA22189_4097
38956	459	26	827	ACATCAATCACAAAGGACGCAACACTTACATCTGAACATCCAAAATTGATGGTAAAT	37999	A_95_P120032	DV999704
38957	459	27	759	GCATTCAAGACTGGAGTTGTTGCTATTGTACGCTTTTAATAAGAGAGTAACGTGTCT	38001	A_95_P136142	DV157807
38958	459	28	302	ATGCTTCTGCATCTCAGTTCATTCTCGGGGCAACAAATAACTTTAGCACTATGGGCTG	38003	A_95_P106492	CV017920
38961	459	31	1012	CCTTCGTTCTAAGTTCATACATTCTTATTAACCCTTTTCAAAAATGATGATGGGTACCC	38009	A_95_P258571	AB286178
38962	459	32	886	TGAAACTGCAATTGAGGACTGGATTTGGTCAGTTGGATGCAACCCTCTATCCATCAC	38011	A_95_P228824	DV161409
38963	459	33	453	AGTATGGTGGGACTGTGTTGCTAAGGAGGAAGAGATCATATATACATTGCTGTTTT	38013	A_95_P032086	EB445389

38967	459	37	907	GCGACTTGTTTCAAATTTCAGTGGCTTTGTCTTTTCTCTCATGGGTTCCTTCTTGCTAT	38021	A_95_P222352	TA22015_4097
38974	459	44	455	CACCTTTGAACTCATTCACAGATCTGCAGCGTGTATTATATGCAGTTCGTTCTTCTTCA	38034	A_95_P026296	BP528192
38979	459	49	772	ATGTGATCAGGAGAATGCTGCAGACTGGACATCCAACTATGCTCAGCTGATTGGAA	38044	A_95_P226204	EB450391
38980	459	50	113	GTGCTAGCCAAGGAGGAGCTCCAAAACATTATATTTATCTTTGTTCTTTTGTGCATTT	38046	A_95_P107602	AM800292
38984	459	54	776	CTGAAGGCAACTAACGACATCAGATTCAGATGTCACTATAACTTACAAGAATATTTG	38054	A_95_P123137	DW003043
38985	459	55	417	CAGGTGTGCAACGTGCAGTTATTCTATTCTGTACCAACGTTCAAAGTGGTCTCATCTC	38056	A_95_P073955	BP526350
38987	459	57	768	CAAAATGGATAGAGGAAATGAACAAGGTTGATGGTTACAAGCAGACAAAAGTTGAT	38060	A_95_P249167	EB679935
38993	459	63	757	GGCTTGAGTGGGTAGGACTGCTAGATGAAATTACCTTTCATTATCAAATATCCAAATT	38072	A_95_P216627	TA20747_4097
38994	459	64	1023	GGCATTGCTGTTGAATTATGTGTTCCAAAAGTTTCTAGCCGTTTAATGATCTTTGTTA	38074	A_95_P030936	TC74235
38995	459	65	778	TTAACTGCTGTTGGAACCAAGGGCACGTTACACCTTCACGACTTTATCATCCCTTTTG	38076	A_95_P148707	EB678167
39003	459	73	919	CTCCTAAAGTGTAATTATGACGTTGCAAAATTTTTTCCCTCTCCTTGAATACTCATCTG	38092	A_95_P245952	EB680458
39004	459	74	621	AGTTTTTTCCTAAAAAGACAAGGGTAAAGTGTGAAGGGCTTATTGGTCTCTTTGGAT	38094	A_95_P220152	BP133134
39006	459	76	458	GAGGTAAGGTATATGTCCCCTCCTTGTATTTGACATGTTAATATAATCTACAGGTCTG	38098	A_95_P213272	TA20012_4097
39009	459	79	513	GGATAGGGGTAAGGTCTGCGCATACACTATCCTTAACCCAAATCCTACTTGTAGGAA	38104	A_95_P105772	CV017611
39013	459	83	835	GTAAATATACTCGTCGCTCTTTATCTTGTATCACTTTCAAGGTCTTTTCCCCTGCTCCCT	38111	A_95_P313153	FG155155
39017	460	2	571	ACACAGGGCGTTTCCATTTTCTCTGACTTGAAACTCTATAGAGATAATCTTGCTAATG	37952	A_95_P046021	BP131287
39018	460	3	404	GTCTTTGAACAAAAAGACCACTTTGATTTCTTCCTTATAACAGATCCAATGAATGGAG	37954	A_95_P036418	BP128726
39019	460	4	666	GCTGTGATGATTTTGTGCATAATCTTTTACAATGTGGCTCATAGGCTTCCGGTAATTA	37956	A_95_P136807	FG157644
39023	460	8	808	ATAAAGCAATTGGAGAAAATGGTTTCAAAGTTGTTACCCTTCTCCGTTTGAGCCCTTT	37964	A_95_P130617	TA17898_4097
39027	460	12	818	GCTGTTTGTTTTGTTGCCTAGTGTTTGTAAGTTAACATGGTCTACTCATGCTTGAAAT	37972	A_95_P247472	EB426399
39029	460	14	0	CCGTTCAAGCCATATCTAAGCTTACCACCTACTTGGCTCATTGAGTTGAAGATCTTGA	37976	A_95_P315623	A_95_P315623
39031	460	16	577	TATTCAGAAGTTTTGTTAATTCAACTGTCCCTTAGTGTACCCTAAACCTGTTTCATTCT	37980	A_95_P143602	EB446852
39035	460	20	213	GCATCTCTTGTTCCTCCGTATACACAGATTGCTCGTATAGTAATTGGAATGATTTTGC	37988	A_95_P209392	TA19180_4097
39039	460	24	762	AGTGTCATAAGCCGGTTAGTTGAGGAGTTTGAGCAGAGGAGTCAAGTATTTGGTGA	37996	A_95_P135347	EB438738
39043	460	28	799	ACAACATACCCAGTAAATCACACTAGTGAGGTCTGAGTATTTTTCATAGCTTACTTTG	38004	A_95_P119832	DV999443
39048	460	33	398	GCAATTTGCTCTTGAATTTGATGGAAAACTATTGCTGCGCCATGTTAGGCGCTTTCTG	38014	A_95_P029056	EB443749
39051	460	36	781	ATGTGCAGATGGAGGGTCAAAGCATTTAGAAGATATGAGGGAATTAGGTTGGAAG	38020	A_95_P253059	EH621755
39054	460	39	345	TTTTGTGCATCAACTGGCTGAATTGATCAAGTTGGGATTCATCCTGGGAATTCGATG	38025	A_95_P083820	BP528864
39057	460	42	725	GAAAGAGCACACTTCTTGAGGCGTAAATCTTTGAATGCGATGTGTTAACTTTCCTCG	38031	A_95_P273656	FG186025
39069	460	54	446	TCTAGATTGAATACATAGCAGAGGTTTGTGTATTAGCCAGCCTATTCATCCCATTTAT	38055	A_95_P201822	TA17504_4097
39072	460	57	432	TGGCGGCTTGTAAATATTTGGCCTGTCTTGGTAATTTAAGTGCTATTAATAGCACTAT	38061	A_95_P162047	EH620787
39074	460	59	583	TGATTGATGCACTTGGCGACAGTTTGAATTTTATGGAATTGAATGAGTCCTATCTTGC	38065	A_95_P141082	EB451357
39078	460	63	581	AGTGCCTTTGGATGGAGATTTTATTAGCTAGTGTACATCCCTGCGTCTTGTTCATTTTT	38073	A_95_P201732	FG168935
39079	460	64	534	CCCCCTGCAAATTCCATCCAAGAGAAAGTGCAACAGAGAAATTTCCTCGAGATGAAT	38075	A_95_P140542	EB444438

39082	460	67	386	TTCTGAAATTGCAGAGGCATTGGTTCGATCAAGCCGCTGAGTATTGGAAACAGGCTA	38081	A_95_P047176	BP131588
39084	460	69	365	TCACATGACGCTGAACATGATTTCACCGGAGACTCACTCAACAGTGCTTGAAGTTATA	38085	A_95_P074185	BP526401
39087	460	72	589	ATGTCGGAAATCCATGTTTGGATCCTAACCGCGGTTTGTTGCCGTTTCAAGAGGATT	38091	A_95_P031711	BP133329
39103	461	3	179	GTCATATTTGACTCAGCTTATATGCGGACATTATGATGTATGTGCTACTGATATTTCCT	38121	A_95_P132902	EB433714
39108	461	8	541	TAGCATGACACCCTGAGAAGTACTGGATTGTTTCTTTTATCACGAGAATCTTAATAAA	38130	A_95_P029731	BP136973
39110	461	10	839	ATATAGACGATGTTCTGATTCACAGGCACATCTGCCACCTCGCAGGTCATTGTCTGAT	38134	A_95_P283048	FG152355
39112	461	12	647	GACATATATGTGACTGTTACCAAAATCTGGGGTGCTTTCTCAATATAGGCTAAATTGT	38138	A_95_P026706	TA20202_4097
39113	461	13	600	CCGGGCTGCCCATGTCAATAAAATTATTTGTTGAGATTTGCATCTTCAGTATAGGTGC	38140	A_95_P001226	FG644966
39114	461	14	660	GAAAGATTAGAAGTGCTTGCAGAGAAGCACAAACGTGGAGAAGCAGCAAGATTTAT	38142	A_95_P250227	EB680783
39115	461	15	737	GAACATCTCTAGACTACGATATTGTCTCTTTCTTTTAGGTGTGATTGTCATGATCTCTA	38144	A_95_P014711	DV162480
39126	461	26	689	CGCTCTCTTGCTTTCTCTTATGCAGCTTTCATTCCAAAAGGTTTTAAAGAAAGAAACAT	38165	A_95_P307553	FG638693
39130	461	30	1427	AATAAGGAAAGAGAGTTAGAGAGAGAAATGCCTTAGCAACGCAACGCAACGCAAC	38173	A_95_P189082	TA14714_4097
39131	461	31	280	CCACCTTGGGTTGCAGTGACTACATAAAGCAGCGATGCACATACTTATCCAAACAAAA	38175	A_95_P039846	BP129666
39134	461	34	299	GCCCAAAGATGGGCAAGAATTTGGTTGTTTTCTCCTTTCATATGTAATGAATGTATTA	38181	A_95_P162702	EH621693
39137	461	37	423	GGTTTTACATTGCCATTGTTGTCTTATTTGGTGACAAGATATTACGGATCAATACCCC	38187	A_95_P033324	AJ344616
39143	461	43	465	GGAGATTGATACTTAACCTGTTATCACAATGGTAATACGTCCCAATTTCTTTTAGAC	38198	A_95_P095983	BP533417
39147	461	47	778	CCTGTAATAAGATTTTTCGTTCACTTTTTCCTGCCAGTGTTATCAGTTTAAAGTTGGAT	38206	A_95_P190247	TA14969_4097
39148	461	48	1310	AGGGTGTTGTTCAGTGGTACCATTCAACAATAGCAATGCCATTTTTGTTTGTCGAAAA	38208	A_95_P238099	AF191497
39152	461	52	529	GCTACTTCTCAAACATGACCCAGAGGACTGTTAGGGACAAATTTGCTCGTCTAACCCA	38216	A_95_P222452	TA22036_4097
39153	461	53	573	TTCAAGTGGACTAACGTACAGAAGATCAGCCAGATCTATGCTGACTGGATTGAAACG	38218	A_95_P235734	BP131939
39160	461	60	852	GTTTTGCCACTACTTTGGTCAGCTGCTTGTACAATTTCAATATTCAATACATTTCCAGT	38232	A_95_P110122	TA12996_4097
39162	461	62	861	ATTGGCAGTGTCTTTGATCCAAGTACGAGGGACCACATACAGAGGCTAAAAAAGAT	38236	A_95_P247687	EB441414
39163	461	63	753	CCATGACGTTAATGTTTCTTCACAATCTATTTACTTTCTCGAAGCTCCTACTATGTCTAA	38238	A_95_P187312	AB079020
39167	461	67	767	TTCCATCGCAGAGTGTTAACTCCAGATTTTGCTCGAGGTCATTGAGTTGATTATCTGT	38246	A_95_P149332	EB679168
39168	461	68	735	CTCCCTCTGTTGTAATGTAAATGTGGTGAATTCTACATTCAGGTTTTCATCATTAGTGA	38248	A_95_P117362	DV160260
39169	461	69	856	TTTACCAAGGTCATCATGGTGATCGTGGTGTATATCGTGCCAATGTGATTTTGCCGG	38250	A_95_P228909	DV161164
39170	461	70	339	ATAGTTGCTCTTCCTCTTTGGAATTCACTGTCAGGCTATCCTTCTGCTTGTATTTACTT	38252	A_95_P081525	BP528277
39174	461	74	487	GTGGGGAGAAAGGAACAAGATAGATCTGATTGTGAACTGGTCACACCCTGGTTTAA	38260	A_95_P087708	BP529862
39181	461	81	399	ACACCGTAGTAGCTTTAAATTTCTGATGAACTTGGGATGCTGTATTCAAATACCTTTGA	38271	A_95_P022811	TA18295_4097
39182	461	82	751	GTAACTAATAGAGATACAGTGAAACATACAAGTCTCTTCTTAGGAGCTTATGAAGAG	38273	A_95_P253449	EH621440
39183	461	83	711	CTCAACTGTATTACTAAACTTTGCCTTCCGTTGGAAGTTGGCAACAAAAATGTTAGCG	38275	A_95_P211117	DV158613
39184	461	84	574	TTCCTGATAAGCAAGCCTACAGGTGCCTGCTTTGTTCTAATATCCATTCCGTAATCAT	38277	A_95_P005331	BP130890
39189	462	4	346	TATCTCTGTAAGGTTCAGCGATGTTTTTGAAGGACTAAGCAGTGAAGGAAGCCTTTTA	38124	A_95_P098958	BP534709
39198	462	13	379	ACTCTGACTGTAGCTAGGACGTAAATCACATCTTCCTGACTCTCCCTCAGCTGATTTTT	38141	A_95_P259791	EG649515

39203	462	18	460	GAGGGAGAGGAGATGAACAGATCAGTTCTTTGGGAGATACTGTGGATAAAGTACA	38151	A_95_P073405	BP526206
39204	462	19	696	TATTGGTTGATCGGGAGTAATTTATCTTCGAGAAATGTTGAGCGCCTCTGCAATTTTA	38152	A_95_P186842	TA14213_4097
39205	462	20	253	TTCATTTGTCGTAGTAGTCATTGGCTCATCTCTGTTCCAAATAATAAGGACCGCAACC	38154	A_95_P114067	CV021429
39206	462	21	656	CTACCAAGACTCCGTGATTATTTAGAATCTTTAAAGGGTTCTGGTGAACTTGTGCAAT	38156	A_95_P284653	FG641345
39208	462	23	399	ACATTGAAGAAAACGCGTTCAGGCCTGGTGTAAACCAATTGGCTTGCACAAAGTGCT	38160	A_95_P091213	EH665799
39212	462	27	269	CATACTTTTAGGGATTCCACTGAGAAGCTTCATTCTGCAAAGAGGGAACTTGCAGCT	38168	A_95_P217787	TA21018_4097
39214	462	29	654	TCCTATGGCCTGTCCCCAGTTAATTCCTACCCTGCTCGGTGTATTGATGTTGCATATTA	38172	A_95_P053931	BP133312
39218	462	33	134	GTTCTCGACTTCAAAATTTTGTAATACAGTCTACTATCAGGACAATCAGTAGTGCAAT	38180	A_95_P133077	EB434145
39219	462	34	919	AAGGATGCAACTGAGAGCTCACATGTGTATGAGCTATACGCAATAAGCAACCATTAT	38182	A_95_P261411	DV161227
39223	462	38	776	TAACGGGGAAATTCCCGTCCAATTTCTTGCAACAAGGAAAAGGAAGTGACACGGAT	38190	A_95_P026161	EB425857
39224	462	39	988	GTTCTGGTAGATGCTGAGTCTGCAGTGTACTCGTTATAAATGTTTAATGATCTATTGG	38192	A_95_P185057	TA13833_4097
39225	462	40	881	GATGCAAAGCTCAATTTTGACGATAATGCTGCTTACCGTCAAAAAGAAATCTTTTCTC	38193	A_95_P008511	TA13724_4097
39227	462	42	387	ACAGGGGCGGTCTTTCTACTGTATGAATAAATAACATAGATATTTCACTATCATTGAC	38197	A_95_P134827	EB437665
39229	462	44	731	TCTCAGTCGAATATTTGGAGCAAAACACTGTATCCGTTGATTCCTCTACTCTATTAAA	38201	A_95_P313183	FG155257
39231	462	46	620	GCTGGGCCAACGTTTATTGTATTGACGTTTAGGCTTCTTATATCAGTTTGCTGTAGAT	38205	A_95_P222337	TA22012_4097
39235	462	50	450	CCTTTTGGTTCTATCGGAGACCCGTTCATGGACTCGCACATGACTGGATTTATAGAAC	38213	A_95_P123907	FG139259
39237	462	52	112	CTCGATCACAGCCATTAATCTATCAGATGGTGTTTTTCTCCAGCATTTTACTGATAATT	38217	A_95_P164467	EH623707
39238	462	53	563	CTTCTTCTTCTTCTTCATATAGTTGGTTTTATTAGAATATGAATGGCTGTGGCATACTG	38219	A_95_P016831	AB015760
39244	462	59	2122	GTGCGTGCTACCCAAACAAGATTAGTAGTTGAAATAGGTTTGATTCTTGTATATATC	38231	A_95_P017546	TC47444
39251	462	66	278	ACTTCAAAGGTCATAAGAATGGTATAAGGGGAAGATTGGATTAGTTTGGTAGATCG	38245	A_95_P033959	AJ717944
39252	462	67	268	GTTAGTGTAATCTAACTTTCATGCGAATCCCAACATAGTGTAACAAAAGCTCGATCAT	38247	A_95_P141927	EB445533
39253	462	68	677	AGATTGCCAAAAAGGCAGGCTGCATTCTCTCTTACGACCCAAATCTAAGGTTGCCCT	38249	A_95_P292118	FG201107
39254	462	69	586	TTTGTTGACTTGACATTCCCTTTCCCCCTCTCTGCAATGATGTTCTTGAATTCTCTGAT	38251	A_95_P162232	EH621123
39259	462	74	1742	GGCCCTAAGTTGATTGTCACTGGATATTTAGTTTCTATAGAAAGATAAACGTTTCAGT	38261	A_95_P013386	TA12466_4097
39260	462	75	533	TTTTGCTGGGTGAGGCTCAGAGCATTATTGCTCTCGATCTCTTTGACCAGTTGGAAA	38263	A_95_P052801	FG199640
39263	462	78	390	AATTCATACAGATTGTGAAAAACTCTTATTACTGATCTTGAGCTTCCTGTATCTGACT	38267	A_95_P105862	TA12574_4097
39269	462	84	766	GAATGACAGCGAGTGGGCTTTGTTTCTAGAGAAGTTTGAAGAGCTGCTTTACCCAGC	38278	A_95_P149567	EB679467
39270	462	85	704	GCTTCAATTGTATGAAAGCTGTCACGTTGGGTTACCAGTACAAGGGAATTTTATCCTT	38280	A_95_P143717	EB446936
39271	463	1	620	AAGGAAACTAGAGCGTTTTTGCTGTTCTAATTTCACTATGGCATTATCTTTCCGCCTG	38281	A_95_P303388	FG134173
39273	463	3	209	GCTCATTCAAATCTTAAATGAGTCATCTGGGGATTCTTCAATCGAAAAATTGATAGG	38285	A_95_P210392	TA19387_4097
39278	463	8	849	GTTATGTGTCATTCTTGTTCACATGGCTAACATCCATGGAAATTGTAATTTGGCATTG	38295	A_95_P236239	DV160810
39280	463	10	1691	CTAATTAGCTTCACATTTCCTTAAGATTTGAGTAATCTACTTGGTTTTGTCGGGTTGA	38299	A_95_P192752	TA15522_4097
39283	463	13	551	GTTGTTCCTTTGTTGTTTGTAAATAACTTTGCATCCATGTGAGATGTAGTAGGAAGTG	38305	A_95_P209772	TA19261_4097
39284	463	14	453	TTGCTCCTTGCTTTTTATAAGTGCCTCATGGATTTATGACAAGGTCAGGTATCAATAA	38307	A_95_P139812	BP534904

39293	463	23	855	GCCAAGTGTAAACTTTGCAATTTGTTTTTGGACAAGTTTATTGCGTTAGACCAATGGT	38325	A_95_P248497	TA13181_4097
39294	463	24	648	CTGACTTGATAGCTCGAACGGCTTATGTATTTTTATTTTGGTGTGTTTATGAAATCAG	38327	A_95_P159347	EH617446
39298	463	28	561	CCAAAGATGCGAAACAGTATGCATCGAGGATGAAGATTGTGCATGCCCAATGTGCA	38335	A_95_P060025	BP134894
39299	463	29	417	ATCCCAGACCTTCATCAGATCTAAAAAGGGTCTTAAGGTTCTTGTATATGTTATCATT	38337	A_95_P033644	AJ632880
39301	463	31	839	ACTCGAAATGCATAGATTCAGTGAAAGCCATGATGATGCTGTGAACTCTTGTGGTTG	38341	A_95_P313143	FG155134
39302	463	32	718	CGCACCAAATCTCAAGTTGCTTTCTTCTGAATTATTCTTGTGACAATCTGAGTCTTTTT	38343	A_95_P217707	TA20994_4097
39306	463	36	833	CTTGTATTAGTAGAATGCAGTACACTCCAGGAAAGCTAATTAAGAATCTTGGGTCTT	38351	A_95_P141147	EB679902
39307	463	37	585	GAAGAAGAGGTGAAAAACACTTGGCAGACAATGCCAATTTTAATATCATTCTCTTAT	38353	A_95_P244232	FS411833
39310	463	40	469	GACCGTGGATGGAGTTATTTAGCATGCAAAAATTGCGCAAAGAAAGTAGACAGAGG	38359	A_95_P080650	BP528056
39322	463	52	780	AGGAAGCAAATAGGGTTTCAGAACTCCAATTTCTCCATGAGCTCGTGACTAGGTTAA	38382	A_95_P136067	EB439639
39323	463	53	557	GTTTCATCTGAAGCCGTTCTTGAGTCTATGCTGTCGCAAAAGAGGTCGTTGTTATCTT	38383	A_95_P042181	BP130292
39334	463	64	630	TATTTTCCAAGTTTCAGTGGGTTGGGTATAAATCAACCACAACACCCTTTTATCAGAA	38405	A_95_P228379	FG638986
39337	463	67	856	ATGGTGCCTCAATAGAAGTTGCACAGTATAATCCACCATTTACTCTTCCGTTCACACG	38411	A_95_P196732	DW000294
39340	463	70	866	GGTTGATGATGAAATGTGTCTCTCCTCCCCATCGTCAGATCTGAAATATGTGACTCTT	38416	A_95_P254954	FG160502
39344	463	74	102	GGGAATCTGTCGTGTTAACCTAGTGTACTTGTTATACATTAGCCATTGACTCGCAAAA	38424	A_95_P257359	EH623173
39349	463	79	387	AAAGAGATTGTTGGATCTTTGCTTGGATCGCATCCGCAAAGCTTGCAGACAACTGTA	38434	A_95_P170366	AJ421413
39350	463	80	535	ATGGGCGATTATAGGAGCCTAACTAATTTCAGTTAAATTAGTTGTTGGTACTTGAGT	38436	A_95_P209562	TA19217_4097
39351	463	81	832	TCGGAGTTGGAATTCAAATACTTCAGCAGTTCTCTGGAATCAACGGTGTTCTCTATTA	38438	A_95_P282263	EB682554
39356	464	1	782	TAGGATGATTTTGAGATCTTTCAGTGTTGTACTCTTCCCTGCTTTAAAATGATTGGGT	38282	A_95_P000616	TA12414_4097
39358	464	3	646	AGGAAGCTAAAAGTTTTGCGGTTGGGAACAGAGCTCTTGCTGCTCTGTTTGTACATA	38286	A_95_P144917	EB448475
39362	464	7	267	CGAAGCAGTTGAACCATATCTAGAGCTATAGTTCCTATAGTATCTTGAATATATGGGT	38294	A_95_P070585	BP192672
39363	464	8	714	CTCAGAGCAGCTTATTTTGACGACAGGCTTCCATTAATAATTCATTCTGCAGATTATG	38296	A_95_P123612	DW003482
39364	464	9	215	TCAAGTGGTTCCTTGATGCCCAAACATGTCAACTGGTAAAGATCTCACTGCATCATTT	38298	A_95_P089678	BP530599
39376	464	21	1026	ATTTATGAGGGGCAAATTGTACATTCGTTTCGTCGTTGAATTCCCAGATTCATTGAAC	38322	A_95_P093233	AJ299254
39379	464	24	1096	CAAGTTTATTATTTTCTTGGTAGATGGATTGGCCATTCTTATGGTCTTTGTTTGAGTTG	38328	A_95_P014131	TA16725_4097
39380	464	25	1233	GAGAAATGAAAATTCACACCGTCGCCCCAACTTGTTTAAGACTGAGGCGCAATTGTA	38330	A_95_P018136	AF390556
39387	464	32	812	GGCTTCTGTATTGTTTTTAATGTAACTTGACACCAAAGTGGGAATAAAGATATGCAG	38344	A_95_P011406	EB425761
39388	464	33	315	GTTACTTGATTGAGAAACATCCTGTACTATTTCTAATGGTGATTCAGGAAGTTCCCTT	38346	A_95_P142912	EB446307
39394	464	39	765	GGTCACTTAGTATTATTCTCTTCTAGGCACTAGTTTCAGGTCATATTTTAGTTTTATGG	38358	A_95_P227334	EB451548
39397	464	42	787	AATGGATAGCATTCAACACTAATGACAATGCCATGATCAACACCCTGAGTGGCCGTA	38364	A_95_P125952	EB425138
39398	464	43	890	GTTGCACTATTCCTGATCCTTCCTACTATCGAAGCTACCTTACTTTCCACAGAAAACAG	38366	A_95_P009156	EB677644
39402	464	47	823	TAATAACTTGCTCTCTCTTCTAAATTCTCTGTAGAAAGTTCACTTACCCAAGTTGTGAC	38373	A_95_P151482	EB681683
39404	464	49	379	CAAGCAATGGATGAATTGTGTATATACAGACCTATACAGAAATATGCTATAATCGAG	38377	A_95_P136997	FG638503
39408	464	53	697	GCTGCTGTTATTATCGTTGAATCTCTTCTCCCATCTCAAGAGCTTTGCTTGATATTTTC	38384	A_95_P301348	FG186234

39409	464	54	1523	GTGATTCCAAGATCTGGAGCTAATTTGCTAACCTCAAACTCATATTGATTCTTGTAAG	38386	A_95_P196037	TA16252_4097
39413	464	58	604	TGCCTCTGCTGTAGTTGAATCTATGTTCATATATTTTGTTTAATCTGTCGAGAACATA	38394	A_95_P211257	TA19571_4097
39415	464	60	731	CGGGGTTTGTCCGTCGGTTTTGAAATACTTGGGTTCAGTATTTTCTGCATTTTTAAAA	38398	A_95_P002721	EB678636
39417	464	62	572	GTACCTGTTGAAGCTGTTGACTTGCCAGGATACTTGGTTTTGGGTGAATTCGGAAAG	38402	A_95_P069750	BP137474
39419	464	64	838	TTCAAAACAGCAGGTTTGTAGAATCAGTGTTAGATGTTTACTGGGAGCTCCCTCCTG	38406	A_95_P296223	EB450843
39421	464	66	342	GCGGATCCATTTCACCTATGGGCGTAAGAGGATAATATGGTGATAGTAATCTTAATG	38410	A_95_P134142	EB436062
39440	464	85	462	CTTCTCTAATGTTCGCAAGTTTGGCAGAGAGTGTCACCTTTCAAGATATCATCCCATG	38446	A_95_P209812	EH616377
39441	465	1	1890	AGATCAATAGGTGCGCTCCCAAACAGGATTAGTAGTTGAAATAGGTTTATTCTTGTG	38447	A_95_P019851	AJ002314
39443	465	3	500	ACCTGATTCCTTTAAAGGATATGTAGGCAGCCTCATAGTTTGGTCTAACCAAATAAG	38451	A_95_P308058	FG640649
39449	465	9	853	AAGCTGCTTACAGGGCCATTCACGACTTCTCTAAGCCATTGATCAACATGATGAAAG	38462	A_95_P226224	EB442821
39452	465	12	619	GGTTTCAGAGACCAACCCGTTGTTATTTACATTAAACTATACAAGGTTCTCTGTTTTT	38468	A_95_P194587	FG637891
39455	465	15	638	TCAAGAGCATGCTTGACAAAGATGAGAGAGTCATACGACATCTAGTGATGAAGCAG	38474	A_95_P145512	DV160165
39456	465	16	537	GTTTGGGTCTAGACTCTTGGTCAAATTTTGTTTCTAGATTTCGAAATCAGGAAAATAC	38476	A_95_P163337	FG643534
39458	465	18	328	GGGCTAGGTAGTGGTATTATCTTTGGACTTCCGCATGTTTAACTTACTGTTTTAGACC	38480	A_95_P222802	FS433138
39461	465	21	838	CAAACGGTGATGATCATGTGACTCTGGCTGCTGTAATATCTTCCATTGTTTTCCAAAT	38486	A_95_P269546	FG161244
39467	465	27	524	CTGCATTTGCTCTTGTTATTAAAAACTATCTGGATTTCTGCTTCAGTAGAGGCCTGCA	38498	A_95_P131652	EB432004
39468	465	28	682	GTTTAAAAAGATCATTTACGTTAATGTATGGTGTCTTGGACTTGGGGCATTATAAAT	38500	A_95_P182257	TA13169_4097
39477	465	37	389	GGACATTTTCTTCTTCTTCTTGTCGGAGTGAAACTCCTTCTATGTGTTCTACTTCATCA	38518	A_95_P159547	EB682721
39478	465	38	594	ATGGCGTTCGCAGACCCGTTTTCTCCCTTATCTTCTGCTATTTATGATATCTTCAGACT	38520	A_95_P303343	FG644449
39480	465	40	210	ATAACTTTCCAGGCAGAGTTGGAACTGGTTGCTGATTAAGAGTCTTAACTGACCGGG	38524	A_95_P094803	BP532877
39486	465	46	408	CTTTTTATAAACAAGGTTGAAGGGGGGTGGGGGGTTTGAGTAAAGAGTCAGGTTTA	38536	A_95_P072205	BP525899
39491	465	51	815	GAGAAAGGATCTGCTTAACAGGTTTAATCCGTTCTCTTCCCCTATTGTTTGCGATGTT	38546	A_95_P154007	EB684167
39495	465	55	388	ATACGTGTAAGATGGTATTGAATTGGTTTTGTATGCATGGGGTTGCTCGTGTACACT	38553	A_95_P142362	EB445845
39500	465	60	688	TAAAACGGGTAGCATATTCTGCTGTTGTGGTTGCTGCGTGTATCTGAGCATTGCATA	38563	A_95_P301263	FG174837
39503	465	63	772	TCCACTGGTTTATGATATCAAACACCTGATGAAGTTCTGTAATAGCCTTCATGGTGGC	38569	A_95_P117617	EB679871
39504	465	64	1779	AAATTTCATTGTATTCTTCGTTTCGAGGCCGATTTAATAGATGGTCGACAGTGATTTT	38571	A_95_P008811	TA15510_4097
39505	465	65	1141	CTGTGATAGCAGCTGTTATTCGATATGTTTATGTCATCTTAAGATGACTTCTGGCTTG	38573	A_95_P026306	TA14719_4097
39506	465	66	731	CTTGACAAGGTCTACGTTGTGAATGTCCTAGGATACATAGCATATAATTTTGTAATAG	38575	A_95_P217262	TA20894_4097
39512	465	72	471	GTGGTTAAATCCGCCTTTAGGTGTGAGATACATTATGTTTACTTCCTACAAGGGTGTA	38587	A_95_P235479	FG644993
39514	465	74	189	GCAGCGACAACATCATAATTTAACACATACACACACACTTTCTACCGATTTCACAAAA	38591	A_95_P097763	BP534188
39516	465	76	201	ATTGTATTCTAGGTTTAGCGTGAAGGTACCTAAATATTGCGAGGCAATTTGAAATTA	38594	A_95_P109747	CV019433
39518	465	78	774	TATGCAAAGTTTGAGTTTGTCATATCCAAAAATGATGGACGTTGCAGTACCAGCTAA	38598	A_95_P272496	EB450503
39520	465	80	744	GTATTGTAACATTTGCTGTGATCAAATCCAGTAGGATCAAAAGCAATGGCTAGATGG	38602	A_95_P263776	EB451244
39523	465	83	109	CTTCTCCTTCTTGCTCGTGATTGCTTCTTATAAAATTTAAGTAAAAATACATAGCCTGG	38608	A_95_P098783	BP534638

39527	466	2	759	ATATCTCATGAGGTACCATTATTGTGATATTCGGATCGTTGCTGCTTGTCGGGCTGCA	38450	A_95_P273316	FG142451
39528	466	3	821	GCAGTTTCCAGTTAAAAATCTGAATGTCGACCATCATCATCATAGTATGGAGCTAATT	38452	A_95_P242437	DV999851
39530	466	5	422	CATGGGATCCTGTAAGATTATACTGACAAGATCTCCATCGTGTCTACACCAACTGCTG	38455	A_95_P098698	BP534604
39532	466	7	0	TTAGGCTCTTCATCTAGTGGTTTGTGCTATTAAGAAATTCTTGCATAACTTGTGGCTTT	38459	A_95_P308298	A_95_P308298
39533	466	8	1689	TGTTTGCAGTTATCTCGCTGTTTCTGGCACTCACTTGGGATAACTTTTAACAGCATTAT	38461	A_95_P026606	TA13264_4097
39534	466	9	985	TGCGGTGCGATCTAGACTTTTTTATAACGTGTCGAGTATATGCTTGTGTTATTTATCC	38463	A_95_P189852	TA14876_4097
39541	466	16	602	TCACGGGCTAGAAAGCAATGGTGTTGACAACTAATTATATGGTGTTAGTAACAAGA	38477	A_95_P123172	DW003067
39543	466	18	491	AACTTTCTCATGGGTCTTGGCAGGAAGGCAAATCAGGTGTACATTATTGATTTTGGA	38481	A_95_P122207	DW002236
39544	466	19	764	TTGAAACGCCTGAACTCTCATTGACATCTTTACTTTTGGGTCTGTGCTTCTGATGCAGT	38483	A_95_P253939	EH622184
39546	466	21	436	ATGGGATGAGGCTTAAACCGTCCTCCTTTAACTTTAATGAATAGATGCTGTGAATCAT	38487	A_95_P023116	CV017227
39551	466	26	138	TAAAATGAAGATGTTTGTTGTTGCTGTCGTCATCATGATGATGGCTATCTCCGCCGTG	38497	A_95_P000818	FG633313
39553	466	28	538	GGGAATGCAACCCTTTAAGTTGTACCAACGTAGAAAGTCTTTATGTTTTGTGGTTAA	38501	A_95_P024796	EB431293
39554	466	29	256	TGGTCTTAGTTTCATGAAGACCTTAATGTACCTGTGATACAATGATACCTGTAATCCT	38503	A_95_P027636	EB445660
39560	466	35	425	CTAGCATTTCGAAGGTTGATGATGCACGGGAAATCATAGGTCAAGTGAAGGAGAAG	38515	A_95_P164347	EH623536
39567	466	42	835	AAAGCTCGAAAGCTATCAAGTGCATTATCTGCTGCTAGCTCAGCTTGTGATCATATA	38529	A_95_P130787	EB430890
39571	466	46	587	CAGAGTGTCCTAAGATTGTGGAATGGGCATCTTAGTTTGCAGCTACTCTTGACAAGC	38537	A_95_P161997	EH620702
39574	466	49	761	TAAAGCCACTTGATCTCTTACCGACAAACGGTCTGTTGATGAATCGGATATTAATATG	38543	A_95_P159967	EH618564
39577	466	52	775	GACTATTGGAGACCAGCTGCTGTTTTCTTCTTGATCTTGCTCGACCCTTTATTTGGTCT	38549	A_95_P001401	EH620962
39580	466	55	822	CAAGCTTTCCTTTTGCATCCCTATGTTTGTTGTCTTTGTGAGAAATAGAACAGAAGTAT	38554	A_95_P183872	AB049816
39582	466	57	490	GATCCCCCTGTAATAGTCTTTTAAGGTAAATTCGTGTTCCACAATTTATTTGTGGTGT	38558	A_95_P182972	TA13347_4097
39587	466	62	883	CTATTGTAAATTGAAGTATATGCGGGTGGCATAGAGGTGAACTACTGTTGATCACAT	38568	A_95_P268106	DV999551
39588	466	63	510	GAGAGGAAAGAGTGAGGTATTTTATTTGTTCATGTCACAAGGGCCTTTGCCATGTTT	38570	A_95_P164017	EH623119
39591	466	66	319	GGGCCAGAGTTTTTGGTCTGACACATAGGCTTTTGAATTGATCGTTGAATTTACTGA	38576	A_95_P142887	EB446289
39592	466	67	502	ATCTTTTCGTTGAGGACCTTATCCCGTCGTTAATTTTTTCTTTTGGAGGGGATGGGGG	38578	A_95_P282003	AM792648
39593	466	68	563	TAGAATTTCCTGTCAGATACCTGAAGGAGGACAAACCACATGGTTCAGCTGGAGGA	38580	A_95_P157567	EH615620
39597	466	72	457	TGTATGTCCGATTAGCTCTTTGGTTTTGGAAGCTTTGGATTATAAATTTTGCATACTCT	38588	A_95_P212522	TA19854_4097
39598	466	73	797	ATGTTTTACGCATAAGTCATACAGGGAGATGTAGTTTCTTGGTAGCATTTTGGGTGCT	38590	A_95_P297303	FG140103
39600	466	75	1478	ATCTTTCGAACTCTCCATGTGTCATTTCATGGAATGTTGATGTGGAATTGTTTCTAAT	38593	A_95_P178327	TA12217_4097
39605	466	80	841	CTCATATTTTATATCATGGGATTTCATGTTGGATGGATGGACCAGTGTGTATGTCAAA	38603	A_95_P016766	DV160218
39609	466	84	593	GTTTGATTGGGATCTTACGCGTGCTTAATTTATGAATTTGAATATGGTCTCACACTTTT	38611	A_95_P152852	EB683190
39610	466	85	1193	AACTAAGGGGTCTTATTCATGGTTGATTTGCTTCTTAAGTTATCTTTGCTGGTGTATC	38613	A_95_P153747	AF352797
39612	467	2	522	CATAACAACTCAGATACAATATGGCAGGTGTGGATACTACCCAGCTGCTTGAGAGGT	38616	A_95_P054631	BP133489
39617	467	7	657	GCCTATCCATGCTTTAGTGTTGTTAAGGGTTTTTATGTATTTTCATCTATGGCTTTAGC	38626	A_95_P140022	TA17508_4097
39618	467	8	139	GAGACTCTATGGGAGCTTGATCGGTTTGTGACCAATTGGAAGAAGATGGTGAGCAA	38628	A_95_P034379	AJ718638

39619	467	9	1463	AGGCGCCTTGTGTTTGTTAGTTTATCTGTGCAGTATCTTATACTTGGCTATCCGAAAA	38630	A_95_P117102	AB505625
39621	467	11	1391	TCGGTGCTTCTACTGAAAGACCGAGATGTAGTTGTATTTATCTACCGATAAATGTAAT	38634	A_95_P025821	TA15595_4097
39622	467	12	944	GCTCTCTTATGTAGAACTACTAGTTAGTAGAAAGGTGTGAACTGATAATGTGTAGTC	38636	A_95_P199712	TA17052_4097
39627	467	17	835	TTGTAATTCTGGCTTAACTGGGAAGAAAACTGGAAAGGCAATCATTCTTTGTTTAGTT	38646	A_95_P230679	DV157898
39628	467	18	528	AGAACCATTTCCGTTGTCTACCAATAGCTGGTTTTGCTATATTTTCCATCTGCTGTCGA	38648	A_95_P290518	TA13817_4097
39632	467	22	693	ATGAAACCACGCTCAAAGGAATTGAGAGTTTACATTTCGATGAGGAAGATAGGGGT	38656	A_95_P210717	TA19455_4097
39636	467	26	347	ATGAACGAAGTAGATCGCCATGTACCTTATTTACTGAAGCAGACGTCATGCCAAGCT	38664	A_95_P158407	FG645271
39638	467	28	311	AGAAAAGACAGTTCTGGGCATCGGCTGAAGGAAGCTTCACAATTTGATGAAATGGT	38668	A_95_P131227	EB431373
39639	467	29	572	TAGGTTGTTTTTCGGATTGGGGTGGTGTTGGCTGGTATTGCTTCAAATACAGTGTAA	38670	A_95_P151417	EB681616
39641	467	31	690	TAAAACAGCCACTTTGGGTCATTTTTGAGACTTGGTCCAGTTGACCCCCACAGCCTAA	38674	A_95_P159387	EH617554
39643	467	33	1065	TCGTTTGAGATTTGCACCGTCCTTTTCTTATTTTATAGATTTTTTGTGAGGGCAAAGTA	38676	A_95_P180647	TA12795_4097
39644	467	34	1348	TTGGTGGACAGTGTTCGACTTGTTAAAGCCTTGCAACTTCTGCTGTAGTTGTGGATA	38677	A_95_P211582	TA19646_4097
39648	467	38	927	TGATCCTATGGTTCTTTGTTCTATTGAAGAGTCTGGAGAGCATATCATTGCTGGTGCT	38685	A_95_P239779	EB442830
39650	467	40	271	AGATGTAATTTCTAAGATTCGGGGATACGGATCCTTGTACAGATACGGGTGCGGGT	38689	A_95_P088643	BP530163
39652	467	42	776	TTAAGAAAAATACTGCTGATAGTGTTCCACTGGAGCATGTTACGCGTATCTTCCCCAT	38693	A_95_P289343	DV158833
39657	467	47	893	TAGTGTGTGTTCACCATGGTAGTTTACCGACCCTTTCCTAGTTTCTACTTTTGTGGATT	38703	A_95_P149347	EB679195
39658	467	48	866	CCTTGACTATAGAGTAGATTGAGGTACGTACATTTGTTAGCACTATTTTCTGAATGTC	38705	A_95_P203982	DV158120
39660	467	50	209	CTCTTTTTGACATGTAGGTTTTATGTACAAAATTCGATATTTCTTCCCCCTTGTTCGAA	38709	A_95_P130657	EB430725
39661	467	51	356	CGACTGGAATGGCAGTTTTATGCACTAGCTTGAATTCAAAATGGATTCAGATATAAA	38711	A_95_P232609	BP530829
39664	467	54	376	GTTGATGCTGCACGTAACTGTGTCAAGTTATTGGAAGAGAAAGGTATAAAAGTTTAC	38717	A_95_P205822	TA18372_4097
39666	467	56	136	GCTTGATTGAGTCAGCATAATAGAGCTTAATAAATAAACAGCTGCCAAGTTGCAATG	38721	A_95_P159757	EH618204
39671	467	61	727	AGCAGATGTACAGATGATAACGTGTTGTTTAGCAAATGAAATCAGAATTAGGGTGA	38731	A_95_P135662	EB439191
39674	467	64	814	TTGAGAGTTAACTATTGTGTATGCCGAGCGACACTTTTAAACATTGTTTTATCGTTCT	38737	A_95_P136007	EB439571
39677	467	67	969	CGAGAGATGATATTGACATGTGGTGCAACTTTGCTTATGAAGAGAGCTGATTTAGAT	38743	A_95_P207147	TA18677_4097
39678	467	68	2086	TTATGGCGGCACAAACATGGTTGATGATTGATATACATGGTTGCAGTTGGTGTTAAA	38745	A_95_P237879	AF096299
39679	467	69	1188	TGGCACTGTTGATTTCATCTTTGGTAATGCAGCAGTCGTGTTCCAAAACTCAAAAATC	38747	A_95_P019251	TA14653_4097
39680	467	70	443	GAAAATGTGTACTGCCGATCCTATAGAAATAAATGCTTTCCCAAGATACGAAAAAGC	38749	A_95_P130707	EB430778
39686	467	76	733	GGGTTTCTTTTTTGGGATGGTTCTGCAAATCAGTGTACCAAATATTCTGGACATATAT	38761	A_95_P122812	DW002768
39687	467	77	1037	ATTTGGCTATCATGCACCGGAATACGCTATGACTGGACAACTGACACAGAAGAGTGA	38763	A_95_P019091	TA15002_4097
39689	467	79	1755	GTCCTTATGGAGCTTTCGTTTCAACCTTGTGCAAGCATATTGGATCAAATAATGTTTT	38766	A_95_P010316	AJ344535
39691	467	81	351	TCCATGTAACTCCCTCAACCAATGATGTAATTCTTGACACGATAATGAATGAAGATTA	38770	A_95_P306588	FG635682
39694	467	84	189	CCTGATCTTATTGCTTGATATAAGCATTATTATTAGGGGAAAGTGGCTGAACAACTT	38776	A_95_P097198	BP533925
39701	468	6	786	ATATTGAATAAAAAGAGAGTGACAAAAGAGGAGAGGGCCGTGGGTCAGATTTTTCT	38625	A_95_P187597	TA14382_4097
39702	468	7	870	CAGTGACTGGGAAAAATCTGGAATTGCAAGAAGGGAAATTGATTGTGCAGAATTGG	38627	A_95_P236289	EB678675

39704	468	9	413	AGAAGGGCCTAAAATTCTGTCCAGTTCTGCACAGGAAGTGCAGGCTGAAGAGTTTGT	38631	A_95_P075235	BP526673
39706	468	11	709	GGTGGCCAAATTTTATAGCAACAGATCGAAACTTGGGTTCAATGATTATTGTCTCTCT	38635	A_95_P124322	FG137969
39709	468	14	338	AGAGTGCCGGCTTAAATAATTTTAGTGCTGTTGTAGCGAATTAACTTGATTCTACTGT	38641	A_95_P140302	EB444262
39713	468	18	166	AAGCTCGAATGGTACTACCAATTCTCCTGATGATGAAAATGGGCATGAACTGGTGGG	38649	A_95_P154537	EG649632
39715	468	20	803	ATTGTGGAAAGCTTTCTGGCATGCCTAGTGTTCTTCACAATGGTGGCAGAACATTTGA	38653	A_95_P224042	TC50531
39716	468	21	855	ATTGAACCTGAACAGTGAGACACATATCTTGTTCAAGTTCTGGTGTACAATCTTTCAAT	38655	A_95_P230469	DV158286
39720	468	25	899	CACCTGTCTTATCTTATGACAATCTGAAGACGGGTGCTGCTGCTGTTCTGTAATTCTGT	38663	A_95_P186932	TA14233_4097
39722	468	27	850	CGTTTATACCTGCTTTGCGTTGGATATATAGATGTCTGGATTCAAAATTCTGCAAAGTA	38667	A_95_P211652	EB435434
39724	468	29	724	GGGTGAGCTTGATGACACTGCTGCTTTCAGAACTTCAAAATTGGGGAAATATTGAAT	38671	A_95_P160997	EH619706
39725	468	30	727	GAGGATTGTAACCTCATGGTTTCTCAATGTTCCTATTTTCTTCCCTTCCCTGTTTCAACT	38673	A_95_P204957	EH619176
39729	468	34	984	TCTGAGGACTAAATCAGGCAACCTATTTATCCTGTTCATCTGGACCCTTGGACTAGAC	38678	A_95_P252024	AB195470
39730	468	35	256	TAGAGTTTGCACACCTATGGAACAAAGCTGTGGATCAGGCATTAGGACCTGTCATCA	38680	A_95_P111847	FS407121
39736	468	41	465	AGTCAGGTGTTAAGACGAAGAACAGGCAGGCTTCAGACTTCATGCTAAGAAATGCTA	38692	A_95_P109502	TA13168_4097
39738	468	43	1117	CACTCCTGACTAGTAGTTTTCTTGAGATTGAATGTTTGATGAATTAATCGTTGTCTTTC	38696	A_95_P198677	TA16830_4097
39741	468	46	828	CTGAGTGAAAAAGGCATGGTTTATGTTAAGGGCTTACTTGAAAGATGATATTACTTG	38702	A_95_P010786	EB425106
39742	468	47	855	CTGAACATCTGTTGCGTCTTTTTGTAAAGTTGCCTGAGTTACTTGCATATGTAAAAATT	38704	A_95_P220862	DV159376
39743	468	48	336	CAATACCAATCACTTCTTTCGGGTTGATAAGGGTTTTGTTGCCCAAGTGGCTGATGTT	38706	A_95_P214442	DV162682
39746	468	51	725	CTTGGGATCATCATTTCTTCCACAAGAAGGAGAGAGACCCAAATCTGCAGGAAGTGA	38712	A_95_P137567	EB441291
39747	468	52	193	CCTTTGATTTTCTCATGCTTATGTGGGAACTTGGTTCATTAATTGACTGATTCCAATCA	38714	A_95_P271476	EB443565
39748	468	53	343	CGATTCCAATCCATTGCCGGATTCCTTTACTTGTATGTTCAAAGTTGAAATTATTGAAA	38716	A_95_P093123	BP532151
39750	468	55	779	ATCTGGTGACATGTATTTTGTACAAACAGTATGCACACTGAAAATATGTCCTACTGAA	38720	A_95_P027006	EB448130
39752	468	57	689	TTAAATTCAGTAGGAGTTTCCAAGCATAGAGCTACCCCTGGTGCCATAGCCATTAACT	38724	A_95_P290768	DW001157
39753	468	58	643	GATTAGGCTGTATCTATATATTCTGGATGTAAACGTGTATATTCATCCAGCCCTACTAT	38726	A_95_P265166	FG642019
39756	468	61	756	TTTGATACTTTTACGCGATCCTGATGAGGAGAATGTAGTGGATGCGTTAGCTATTGGA	38732	A_95_P160637	EH619303
39757	468	62	822	GCAACACATAGCATGCCCGATGCTTTCTGTTGATTCTTGAGTGTATTTGTATTATAATA	38734	A_95_P027051	TA16619_4097
39758	468	63	666	ATTGTGATAGAGAGACGGTTTTCCCTTTTTGTTCTGATCAAAATGATGGTGGATATTA	38736	A_95_P013891	TA14396_4097
39763	468	68	437	ATTGAGTTGAGGAGTGTTAATCCAGCTGATAGGTCGATCTGTGCTTTTGCTGTTGCTG	38746	A_95_P076565	FG142037
39767	468	72	859	TTTATGGTGGCTGTTGGTGCTGCTCAAGGACTTGCTTACTTACATCATGATTGCAAGC	38754	A_95_P118092	DV161102
39768	468	73	658	ATTAGATTTGAGCATTGCTTCTAATTTCAGCTGTTGTGAGAGCACCGCTTGCTAAAAG	38756	A_95_P130457	EB430499
39771	468	76	597	CATGAACATGAGGCCAAATTTGTGTTTGCAGATTTGATTGATGTACTATGGAGGTTAT	38762	A_95_P002911	TA14681_4097
39776	468	81	813	GCATCTGTTTGGTTCGACTTGCATTTTGACCGGCTTCTAGAATAGCGAAAGAAAATCA	38771	A_95_P117122	DV159907
39777	468	82	649	GTAATTAGTGTTTCAACTGATGGTACACCCCGCACTGCAACTATAAGATCTACGGCTC	38773	A_95_P041636	BP130144
39778	468	83	712	TCAGGAACAAGTGAATTGATACCTTAGTACTTTCTGGCAGGATTAGAATTACACTTTC	38775	A_95_P133802	EB435494
39781	469	1	661	GAAGTCTTGAGAAGCAACAACACTGTCCACTTTGAACCAATAACACCAGACCAGATCA	38780	A_95_P131822	EB432235

39782	469	2	709	GCTATTCTATATGCAGTTGTCTCTGTTGTGTCATTTTAGGTTTCCGTGAACTAAATCGC	38782	A_95_P117522	DV160446
39783	469	3	229	GTTGTAGATCGATGTTATTAACTCTGGGGCTCAAAATAAAACTGAAAGAAACATTCC	38784	A_95_P099758	BP535053
39784	469	4	774	GAAAGACAACGTTACCTGTACGAATTTGGAAGTTGGTTTAAAGTTTTGATACCTTGTT	38786	A_95_P136402	TA11945_4097
39786	469	6	430	TGCCAGCATATGATCTTACAATATATTCAAGGGGCTGCCAAAATTTTGGCCTTTTATG	38790	A_95_P080505	BP528020
39789	469	9	599	ATAAAGCAAACCCCTTAGCTACAGTGCTCAGTGCTGCTATGCTTTTGCAATATGGCCT	38796	A_95_P201552	TA17449_4097
39790	469	10	741	GCTATCTCTGTGGGCGATGACCTGTTTGTATTTGTATATTTGAGCTGTTTATAAGATA	38798	A_95_P013091	TA13965_4097
39791	469	11	807	TGATGTATGTATGATTGCACCTTCCAAATTACTGCACTTGGCAAAAGGTGGAGCGGA	38800	A_95_P198617	TA16817_4097
39794	469	14	793	TAGTGTAGATAGGATCTAGATCTCTACTTGGGCTGCATAAGTTTCTACATTAACCGTT	38806	A_95_P176928	EB448154
39795	469	15	1366	TTTAAGGCCCATGAGTTAAAGGGTGTCTCTGCAGAGACTCTATTGAAGTTGGTTCCA	38808	A_95_P200197	TA17158_4097
39816	469	36	2248	TGTGAAAGGCCCCAGTTACTGGTTTCTGTAGGTCTGAACTATTAGCATTGTGGCATC	38849	A_95_P024731	TA14441_4097
39819	469	39	459	TTGTCAAAAGCTCAGTGACCTTCAGTTCTTTGTAGGTGAGAGCATGGCTGATGATACT	38855	A_95_P104027	CV016812
39828	469	48	955	CTGGATTTTTTCTTCCTTTATGAATATCATTGTCCGCTAGACGGTCTTTCTAGTTGGCT	38873	A_95_P020911	TA13732_4097
39833	469	53	206	CCACTGACTTGTTTTCTTTTTGCAAACATTGTTATCCAGGTTTCAATTTTGCATTCTGG	38882	A_95_P093038	BP532117
39837	469	57	904	ATCCCCTTCAAGTATCATTGCTCAATTATGAAATGTAACAGTTGATAACGTTAGAAGT	38890	A_95_P198927	TA16884_4097
39839	469	59	0	GAATGACAAGGGTGATACCTTAGTGCTTTCCTACTACCACACTGTTAGCCGGTGACA	38894	A_95_P259486	A_95_P259486
39840	469	60	816	GGTCTCGAGTCAGTTTGGTCGATTACATAAATTATCAGTTATCACTATTCATTTTGCTT	38896	A_95_P238034	AF072519
39845	469	65	57	GATTTTCAGAGAGTATCCAAAGCCATAACTTCTTCTCTTCTTCTTCTTCTTCCAAATAG	38906	A_95_P001611	EH618769
39846	469	66	565	CAGCAGCTGGCTGTACTATTAGTATCTTAGATATGCTCTACTTGACTGTAATTTTAAT	38908	A_95_P269201	FG639102
39847	469	67	411	GTAATATCTGTTGTATTGCCAGTGAGAGTGTTCTCACCAACTATATTGTCCAGTTCAAT	38910	A_95_P196637	EH620951
39857	469	77	560	TATTGAGACGAACACTTTCGGATGACCGACGTCAGATTTTTCCCTTGGCTGAATGAAT	38930	A_95_P122237	DW002265
39860	469	80	730	TTCCTTCTGCTGGTTTCTCCAGACTGCTATTGTATTGTAAATTAAATTATCTCTCGATT	38936	A_95_P190827	TA15098_4097
39865	469	85	790	TCTGATTATCCATTGAGTGCTGCATACTGCATATCCATGATCACAAATGCTGTGGAGC	38946	A_95_P126077	AF154642
39866	470	1	795	CTATTCGAAGGTTCGATGTATACTTTCGTATTCCTGTGGACTCCTGCTCTGAGCCCTA	38781	A_95_P013446	DV161541
39867	470	2	855	GACACTGGATCACGTTGATTCTGTGCCATCAAAGTGTACTTTAATAGTCTACTTTATAT	38783	A_95_P017726	TA12593_4097
39869	470	4	676	GCTTCCTCCTCATCTGAGTTACAACGCAAAACTGAAAGTCGAAAATTCCAGTGTTCAT	38787	A_95_P018451	TA16251_4097
39870	470	5	563	CCCCATTGCTAATGTATTTCATTTTGTACCTTTTTTGTAACCAGGGAACGAATTGAGGT	38789	A_95_P306478	FG635368
39872	470	7	109	GTTCATTTTTCGTTTGTTGTTATCAAATCAGAAGGTTCTTGGCATTACTTTGGGACGTT	38793	A_95_P154737	EG649739
39873	470	8	739	GAATGTGAACTTTGAGGTCTTCCATAAAGATGATCTTGTTCTCTCTGGGGTTTTGGAA	38795	A_95_P137432	EB441171
39876	470	11	823	ATACTGCAGCGTTTGCACCATTATTCTAGTTGTGTTATGGCATGTTTTTGGAACTTTG	38801	A_95_P009581	TA13726_4097
39883	470	18	169	CTCTGACTCGCCATGATGGCAGCCACTTGTCTTACCATATATTATTTTACTAGTTTCTG	38814	A_95_P109417	CV019297
39899	470	34	255	TGTCTTCTTGTAGTTGGCTGAGACCCCGATTCTAGTCTTTAGTAGCTCTTTAAGGTATT	38846	A_95_P210732	TA19458_4097
39901	470	36	702	ATTTTGTTTTCTGTTCTGAGGGATGTTTTCTGCAGACTTGCAAAAGATAATGCTTCCTT	38850	A_95_P000941	TA13754_4097
39908	470	43	230	CAAATCGGAGAATGCCGACAGGTATTTCTTGGATCTCATTAACTTGTGAAGTGCAAA	38864	A_95_P100708	BP535491
39921	470	56	804	GTTGCTAACGGGACTCCATGTATAATAGGAAAAATGGTTACATCTTCAATCCTTATTC	38889	A_95_P021766	DV162599

39925	470	60	379	GCCAATATACTTTGGTCTTTTCTGTTGGATGGAAATGAGAAAATCTTTCTCGTGTTTA	38897	A_95_P025266	FS429988
39929	470	64	388	AAATTCACATCACCATATAGACGGACAAATTCACATCACCATATAGACGGATCAATC	38905	A_95_P063460	BP135786
39930	470	65	805	GAGCAGTGTCAATGCTTGGACATGTAACCAGTTTTCTGCTTATCTTTCGTATTTATTTT	38907	A_95_P235224	EB449888
39932	470	67	852	AAACATATCAGCATATAGATGCTCGTCCAAGCTAGGTTTGATGTGTTGCACCGAGCT	38911	A_95_P246627	FG167264
39933	470	68	813	AAACTCCTCCGAAAGAAATGTTCAGCCACCTCCATTATCTGACAAAGACCAGGAGGA	38913	A_95_P013266	EB437021
39936	470	71	587	AGGCTTTTCTGTGATGACTGTATAATACTACGACTGTACCATAGGTGTGAGGCTTTA	38919	A_95_P141717	EB445374
39937	470	72	968	TTACTACCTATCCTTGTGAAGCAGAATAACGCCATTATGGTTTTATGCTCTTAGCTGA	38921	A_95_P191072	TA15151_4097
39939	470	74	811	AATCACTAAGCGAGCAGGAGGACCTAATTGTTTGGATGCGTACTGCTACTCTTCCAA	38925	A_95_P197962	TA16676_4097
39942	470	77	647	GAGTGATCAGATTTGTGTTACTTTGACCAACATTTGTGGTTCCAGCAGATTTTAAAGA	38931	A_95_P123372	DW003223
39943	470	78	445	TTGCTGTGAAATTAGTTGAGCTTGTATTACATAGGCATTAGCTGTGTTCTGGATGGA	38933	A_95_P006146	BP533450
39950	470	85	643	GGATGTGAAAGATACTACAATCAGTACTCTTGCAACTGAGGTACTGGGAAACTGCA	38947	A_95_P158757	EH616613
39951	471	1	658	CCTCCGTCTCGACGTTTTGAGATCCGTTTAATTTAGTTGAGTGTTATATTTGATTTTGA	38948	A_95_P248227	EB444101
39966	471	16	611	ACCAACTCTTCCAATTGGCATGCCATTGTTGACTAAACATAAACCAACACTGGGTTTT	38978	A_95_P101023	BQ843094
39970	471	20	843	TATTAGTAGAATGCAGTACACTCCAGGAAAATTTATTTAGAATCTTGGGACTTGGGG	38985	A_95_P184442	TA13697_4097
39974	471	24	220	CTCTGCTTGTCTCAATCTTCTCTCTGTTGAGGCAATGATTTCGTTCCTGGTAATTTGGT	38993	A_95_P158497	EH616430
39983	471	33	2080	GGCTTTTTATGGCGGCACAAACATGGTTGATGATTGATATACATGGTTGCAGTTGGT	39010	A_95_P023976	AF096299
39992	471	42	736	TTCAACATTTGACAGGCTGAGGACTTCTTGAATATTGGGTAGTCCATACGTTGGTTG	39028	A_95_P253579	DV160140
39995	471	45	1438	GGAGCTACTGCAAAATTTGGCGCAAGCAACAATTTGTATTTGAAAAAGTTATGGAGT	39034	A_95_P245137	TA13335_4097
39996	471	46	681	GCATATTCAGGTGCACAATAACCATATGTTCCCATGACCCTGGTGGAGACATGACTC	39036	A_95_P284813	FG194107
40003	471	53	847	CATCTGTTTTAGCACCTGTAACTCTGGAATACTTATAGGCAAAGAAAGAACTACTTAA	39050	A_95_P117087	DV159878
40004	471	54	495	GCACAATTGGATTTAGTATTGGCAACATTTTGCTGGATTCGTTTGGAGGATTAACAA	39052	A_95_P261266	BP131465
40006	471	56	586	GGAGCTAGTATTAAGTGTGAGCTATTTATTCTACGCTTGGATCAGATGTTAGAGGCC	39056	A_95_P084425	BP529013
40013	471	63	86	ACTGGAATACTCCACTCTGGTGTTTGGTTTTTGAGAAAAAGAATTTCCATGGTCTTTC	39070	A_95_P026561	EB443859
40022	471	72	378	ATGCTTTACATTCCCTGATGAATCAAGTCTTGGATATTTGTACCTCGAGTATTATCTCT	39087	A_95_P112787	EB447241
40023	471	73	336	TTGAATGCACTAGATGGGTGAATGATGCTGTGGATACCAAGGAAGTAGAGGAAGTA	39089	A_95_P127667	TA16745_4097
40029	471	79	832	TCCTTCCAATGTGAAGAGCAATTGGATATATGTGTATCATTGATCAATGGTTACATTG	39101	A_95_P225442	DV999954
40032	471	82	211	GACTGTTGCGATAAATACATAGCAAAGTTTTGTTACCCCAAGGTGGGCTATGGAAGC	39106	A_95_P050106	BP132317
40033	471	83	1469	GTTGCAATATTGCACTTAAAAATCCTATTCCAAGGGGCACACACAACATTGATTGAA	39108	A_95_P185837	TA14001_4097
40039	472	4	82	TTTTTGCAGCAGCCCTGGGTTCTGGCACACAGTTGTTTACCTTGACAATTTTCATATTC	38955	A_95_P199087	EB438068
40041	472	6	939	GCTTGTATTTTATCTGAAGTTGGGCTTCTGTCTCTAGTAAGGTTCTTTGGTCCATGCTT	38959	A_95_P181547	TA13006_4097
40042	472	7	400	GTAGTGCATGAAAAAGGCCAGCCACTGTGCATTCTCTTATGTTTCTATTGAAACAGA	38961	A_95_P160507	TA14660_4097
40044	472	9	892	CCATAGATAAACTTGTTGTTAAGCTGCATACTGATATATTAGGGTCGAGGGAAGCGC	38965	A_95_P272081	EB680173
40050	472	15	1468	GCTTCTCTCTAGCTGTGGTATCTTTGGCTGTTGCTTTAACAACTGTTTTTCTCTTTAAC	38977	A_95_P197672	EU375459
40051	472	16	623	GCTTCTGAAGGTGAACCTAACGTCTCATAATGGTCACTTTATTACTATTACTTAAACC	38979	A_95_P029371	BP530123

40053	472	18	559	GAGGTTTGCTCTATTGCAAGATTATCTTCATTGTCTTTGAGGAAAAGCATACGATTTG	38982	A_95_P219322	TA21371_4097
40055	472	20	512	TTGTTGCTTTTTCTTGTTTCAATCTGGTGACAATGTTGCTGTGCCTGGTTCTATAATAA	38986	A_95_P184257	TA13651_4097
40059	472	24	691	TCAAAGATTCTGAAACTCAACAACTTCATCATTGTTCAAACATATTGACAGGGTCCGT	38994	A_95_P287403	FG636812
40062	472	27	328	AGGCAGCTCCCCTGGCTTCTAATTAGCACTGGAATTCATCGACTCAACTATGTTTATT	38999	A_95_P070020	BP192499
40067	472	32	495	TTTGATGTCACGTATTCTGACCCTTTGTATATGGCGTGTTTGAGGTTCTTTCTACTAAA	39009	A_95_P172031	EH665275
40068	472	33	407	GAGCGACAAGAATGCTAATATTGGCTGGCATGAGCTAGATATTCCTCTGATTCATGT	39011	A_95_P064345	BP136023
40069	472	34	458	TTTCTAGTGCTCCAACCCCGTCTGGGATCTATTTTTACAATTGCCTAACCAATCTCCAA	39013	A_95_P039281	BP129507
40072	472	37	608	TTTTGTCCCATTTGAAGATGTTCCTGTGTAAAGTTGCAGATAGTTATTTATTCGGGTG	39019	A_95_P064925	BP136190
40079	472	44	662	AGTTGGCCGTTGAATCTACACTCATTTGTTTCTTCTGATTCTGTTAAAAGTTATTCGTA	39033	A_95_P211912	TA19718_4097
40087	472	52	949	GTTGTTTGCCTGTGAAACAAAATGTAAAGTTCCGAGATCTACTGATGACCATTCTAAA	39049	A_95_P018281	TA17065_4097
40088	472	53	343	ATCTCGTTGTATTTGCCTGGTGGATTGGTGATTAAAGTGGTGACTGGAGTATTCGTG	39051	A_95_P103597	CV016595
40094	472	59	903	TTGACAGGTCATACAAGTGTTGTTATGTCTGTTCTATGCTGGGATCAGTTTCTTTTAT	39063	A_95_P228869	EB678232
40099	472	64	691	GAGTTTGAGAAATAAAAATCAGCCCAACAACTTCTTACTTTACGGATACTTCGCATAC	39073	A_95_P301798	FG192435
40104	472	69	730	TTTTTAAAGATGTTTCAAGCGGTGGTAGTGGTGGTGGAGTACTAAAGAAGAGGGAC	39082	A_95_P210727	U64926
40110	472	75	358	GGTTCCGGCCCATAATTTTCAAAAAATCCAAAAGTATTTTCCTTTACTTCCTCTCTAGA	39094	A_95_P004731	EH624481
40113	472	78	124	TTTCATCATGTATTTGGGACCTTGAGTCAAACTGAAAGTTGACTCATTGATTTGCATT	39100	A_95_P210647	TA19440_4097
40116	472	81	857	GTTATCAAACATTTGTTCGTGAACTGAGAGACATGAATCTAATTTCATGCTGCTTTCT	39105	A_95_P131167	EB431296
40117	472	82	691	CAGGGAGACTGTTCTTGTCACAGTTTTGGTCCTGTCATCTTCTTGTTTTCATTATACAT	39107	A_95_P148712	EB678176
40119	472	84	1357	CCTTTAGGGTTGTCTTTAGCACGGAGTTCAGTTGTCTTGTACTGTAAGTATTTTTATTT	39111	A_95_P203472	TA17860_4097
40124	473	4	837	CTTTTCTTATATATGCTTAGAAAGGGGATAAAGAGGTTTCTCTTCTATCCTTGATCCAT	39120	A_95_P217242	DW004715
40127	473	7	192	GGTGCGGAAGAACTTATTGTTGTATGAAGTATCAAAGTATGTTAGACTTGGTGAAAT	39126	A_95_P128012	EB427574
40130	473	10	879	GAATTACTTTTCCGACACGAGAGAATCCAGAAAGTATTTATATGTAGGACCAAGGGA	39132	A_95_P232789	DV159931
40135	473	15	1257	ATACCTGTGAGAAACACACATGTCTATGCATTTGCAGAACATGGAAATGATCTTGGG	39142	A_95_P188272	TA14533_4097
40137	473	17	496	CTCAAAAGTAGGGTTATCATATTTCTTTCGTCGACTTTAGCTATGAAACATGTAAGTG	39146	A_95_P035083	BP128353
40148	473	28	711	CCCTCACGCCTTTGATGGTGAAACTTTTTGAAATGTGGCGCATTTTTCTTTCTTAGTTC	39168	A_95_P204357	TA18048_4097
40150	473	30	1603	GGTTGGCCAAGAAAGTTATGTTATTTGTATTCTTGATTATAGAAAGATACTCTGTCCA	39172	A_95_P007501	TA17352_4097
40151	473	31	499	TGTTGCCTTCAGTTGCTAGTTGCAAATTTCATTGTTGTAATTGATCTGCTGCAAATTTT	39174	A_95_P131477	EB431768
40153	473	33	927	CCAAGGCGTCAAACGAGCATGCGTTCATTGGATTCTCGCTTAAGCATTGGCTAATTTT	39178	A_95_P209282	TA19155_4097
40156	473	36	440	TCATACCTTGTTGTCAATGCTGATGGAAGTGAACCCGGAACCTGTAAAGACAGGGAA	39184	A_95_P138107	FG136993
40158	473	38	641	TCTGCTACGTACTGTTATCTATTTCAGGGGACCTTGTAAACAATGGATTTTAAAGTGG	39188	A_95_P162617	TA15941_4097
40159	473	39	565	CTGGATCTATTTTCTGGATACTTTAGCAATGACAATGTGAAAGTTGGTGATCTTATTG	39190	A_95_P004716	DQ648018
40168	473	48	214	CTACGCCACAAACTTTGTCCCCGGAAAATGAATATCATAAAACAATCTTAAAATTTGA	39208	A_95_P005136	TA11655_4097
40170	473	50	1802	GCTTGTTGATCTGTACCAGCACGAAGAAATCTAACACATACGTTCTTTTCATGAAGAG	39212	A_95_P188852	TA14661_4097
40171	473	51	782	CAGAAAGCCAGAGCTAACTTTTTCTAGTCTATACACAATATCAAAGGAGTTTCTCTTT	39214	A_95_P293903	EB438474

40172	473	52	542	AGACGCAATTGTCACTAGATACTATTCTTCTTTCTTCTCTACATGGTGTTTGAATCAAT	39216	A_95_P307823 FG639648
40174	473	54	93	TTTCATTAACTGGATTGAGATTTTTCACCGTTTACGGACCATGGGGTAGGCCAGACAT	39220	A_95_P088228 BP529991
40175	473	55	830	CATCAGAAATGGGCAAAGTCTCAAATATGTGCTGATGCTGAACTTGGTGTGATATTG	39222	A_95_P310098 FG135000
40178	473	58	887	CAGGCATTGCCCTCAGACTCTTTCGGAAGTCTCCTGTTTTACTTTTCCTATTTATTTTGT	39228	A_95_P230239 DV162407
40179	473	59	393	TAAAAGGAAATCGGACTTGGAGTCTGATAGTGCCAGTGACACTGATAGTGGATATGA	39230	A_95_P155112 FG139357
40180	473	60	916	GCAAAGCTTATTCATGAGAGAGGTGGCAAGGTAATTGCAGTGAGTGATATAACTGGA	39232	A_95_P194207 TA15843_4097
40184	473	64	390	ATGGTCCAATTCTGATCGGTAATAAATACCGGGACTTTGCAATATTTGATTGATCACA	39240	A_95_P278918 AM842139
40188	473	68	192	CCCAGCTTTGGTTGTTAGCTTTAGTCACTTATAGTTGTTTTATAATATTCTTTCGAGGCT	39248	A_95_P097228 BP533941
40189	473	69	522	GTGGTGAGATGATTTTGATAGTTTGTTTTCTTGACTAATATTAAGTTGGCTGGTACTCT	39250	A_95_P019606 TA15061_4097
40192	473	72	637	TTACAATACCAGTTGAGGACTTCATTGAACTTGTTGGCTCTAAATGGAAGTGCAGAAT	39256	A_95_P186532 TA14147_4097
40200	473	80	511	AGTCAAAACCATCTTTTGCATGGAATTCTTTTTCTTGGCCATGCCTTGGGGAGTCCTT	39272	A_95_P031706 BP535041
40207	474	2	573	TCTCTCTCCTCTTCTCTAATTTGGTCTTTCATTTAGGCTAGAATGTACAACTTCTGTAA	39117	A_95_P195662 TA16166_4097
40212	474	7	884	CGTGTGGCACAATGGGTAATATTTTCTGCTTGGATGTTTTATTATGCAATCATGCTGTA	39127	A_95_P011886 EB447549
40214	474	9	876	GTTAGCTGTTGCCAGCTTTTTGGAATTTCCTTGTTGGTTCCTGAGGAGTTTAATCTTAT	39131	A_95_P231869 DV162468
40217	474	12	559	CCATGGGCCACTGAAGAAGACTATGAAGTACAATAAATATAGCTATTAGAGAAGTC	39137	A_95_P119682 DV999152
40224	474	19	833	AATTTCTTATCTTGCAGTGATGACTCTGGGATGTTGTGACGATGAGAGCTGTGTCGAT	39151	A_95_P250427 FG157464
40226	474	21	751	CAGTAGTTTGATGTGAGATACTATATATTTTTCAGCCTTTTGCGAAAACCCATTCTTG	39155	A_95_P297573 FG171924
40227	474	22	825	AGTGTTTCCATACATACAGTGCCATGGTATGAGTGGCTGGAAAATGATTTTTGTAAT	39157	A_95_P214662 DV998978
40230	474	25	479	ATGTCCAAGAGTTTTTGTCGTCTTTAGATATCAAATCATTCTTGTCTAGCATTTCTGGA	39163	A_95_P122112 DW002152
40232	474	27	222	ATGGCACAAGTGTCCCACTTAGTAGTATACTGGCCCAAGTGCAGTTAGAGGCTATTTT	39167	A_95_P174722 EH665915
40240	474	35	195	GTGAAACTTTCCAAAGAGCTTGTTGGTATTATGGAACTTTGAAGAGATTCTGTCATAA	39183	A_95_P140812 EB444643
40243	474	38	491	ATGTACAAACTCGCCCCTCCCCTGGGGTTGATGGAAGATAAGTAGATTAGTCTATGAA	39189	A_95_P039511 BP129566
40249	474	44	963	GATTCTCTGGGATGCCTGGAGGTTGAAAAATACAGCCTTTTCGTTGAGTTGAACTCAT	39201	A_95_P198082 AY740530
40252	474	47	469	AATGCCCATTGAAAAGATTGATGTGCTTAAAGTTTTCAAAGTATGTATTCCAACTCGG	39207	A_95_P224837 FS406426
40258	474	53	531	CCAAAAGATGCTGAGACAAGTTATAAGACCTGCTCTCGAGGAAATTGTTTGGTCTTG	39219	A_95_P266871 BP535412
40259	474	54	794	GTGCAGTTTTGTTTGTTTGCTCACGTTTGATTTATTAAAGCCTTTTGTTGTTGACCAGT	39221	A_95_P190697 EB680692
40260	474	55	324	ATTGTGTTGCTATGGAGCTCAGGGTTGTAACTTAGTTTGTAAATGTAGGCAAAGCTA	39223	A_95_P139612 EB443417
40263	474	58	614	GATGTTGGTTTAACGGCTGTCCCTTCAGATGTCTGGAATTCACGAGACATCTCAAAAT	39229	A_95_P037686 BP129070
40264	474	59	1577	GTTGCCCTCCATTTTATCATTCTTCCTTCTGGAAGCATCTTGTATTATTCCACTGAGATT	39231	A_95_P016891 TA14279_4097
40265	474	60	623	GTGATTAGTCTTGAGACTAGTAATTTGCTGATACATTGCAACATACCAGTTATTTGTG	39233	A_95_P105577 EB446038
40269	474	64	466	TCAGTTGCTTGTATGTTTTACATTTGGTGGAATTTAATTAACGGTTTGAATCGCTTGCT	39241	A_95_P103502 TA11915_4097
40272	474	67	363	GCTCCAATGTAAGGTTTTGCAGGCTTGAACCAATGTTTAAGTAGTTTCAAAAGATTAT	39247	A_95_P092338 BP531754
40277	474	72	1098	TCTTTGAATTATGCCCCTGATTTGACGGGGGAACTAAAGGTGTGCTTTAAGTTTGAC	39257	A_95_P188132 TA14501_4097
40281	474	76	491	GAAGTTTATGACAGGCTTGGATGCTAGACGAATAGCAAAGCTCCCTGAACACAGTGA	39265	A_95_P047271 BP131613

40288	474	83	901	AGAAATGACAGGGCAAAATGTGACTGAATGCATTGGCGGATCACGAACAGTAACCT	39278	A_95_P259206	EB679951
40291	475	1	425	TGGCAGTGTGCTGAAGGTTAACTACTTCATGTTGTGGATTAAGGTTTATGTGGATAT	39283	A_95_P002201	DW002911
40293	475	3	374	GTGCAGTTAAACTGGAAGAAGTTGTAGGCCTAAAAGAACCAACATTGGTTGTGTAC	39287	A_95_P052566	BP132956
40298	475	8	1154	GCCAGTATGCATTCGTGCTATACCTGCATTTTATGCCAGTTTTAATATATGAATATCG	39295	A_95_P201227	TA17378_4097
40300	475	10	154	GTTGTAGTGAATACTCAAAATCCCTATACTTTTCATGACAGATATAGTGTTTGTCACT	39299	A_95_P142082	EB445644
40305	475	15	606	GCTTGTTGTTACTTGTATTTGGGAATTGTGGTAGAGAACATTCTTGTAGTTTGTTGTA	39309	A_95_P189862	TA14878_4097
40307	475	17	947	GATAACCACTCCTGGTACAGAATTAAAAAATTTGAGCAATCATAGTGTACTACTTCCA	39313	A_95_P082255	TA13610_4097
40313	475	23	366	TGTTAGCCTTAGCACTTTACTAGCTCTATATCAGAATGGGCCTTCAGAGTTAGCTGGT	39325	A_95_P080465	BP528009
40316	475	26	789	CTTTCATCGATAGGTAAGCTAGCCCCTGTATGTCATTATTCATTTTCTGAGCTCAGTCT	39331	A_95_P135957	EB428177
40317	475	27	671	AGCTACGGGTTACCAATTGTAAACGTCCAGTTAACTGTTTCTTATTCTTCTTTGCCTAA	39333	A_95_P182872	DV160305
40319	475	29	665	CTTCTTCCGGTGAATGTGATCCATTACGGGATGGTGAAAATTGTCCCCAGTCAATGTT	39337	A_95_P019326	TA17466_4097
40320	475	30	705	TTGTTAATGATCTTGGGCACCATTTCTCTGAATCTCTGAATATTGAGGATGGTGAAGA	39339	A_95_P017861	EB440968
40321	475	31	859	ACATTGGCTCGAATAGTGTGATGTTCAAGCTGATATGCCAGGAGCTATGTTTCTACA	39341	A_95_P197342	DV157504
40322	475	32	838	GTAGCTTTGTAATTTATTTCATCTTTGTTTGGCTGCCAATCAAAGTAGAAACCGTATG	39343	A_95_P179097	TA12426_4097
40326	475	36	1700	AGGCATCAAGAGGATTCATGTACTTTAAATGAATGAAAACCAAAGAATTGCCGTCCT	39351	A_95_P177577	TA12012_4097
40330	475	40	413	TTGTAGTTTTTATCTCATTCTAGCAGAGGTCTGCCCCAGGTGTCGGGGCAAATTTAGT	39359	A_95_P082015	BP528409
40332	475	42	290	AAACGTTTGCCCGGACCTCATTTTGATCCTCCTACAAAAGATGAAGTTAGAGCCCTG	39363	A_95_P108217	FG634551
40337	475	47	771	CAACCAAACATGTAGACTGGTTCTAAATCTTGAAAATCCTCCTAGGAGACCACCTTGT	39373	A_95_P267306	DW000135
40339	475	49	1176	GTTGTCATATTCATCATACTGGCTATTATTCTTGCACAGCTATCTGGAAACCGATCTTA	39377	A_95_P007126	U60057
40346	475	56	543	GTTCTCTGTTGCTGTTGCAATTCGAATCTGACTTGTAATTGCTTGTAAATCGAATCAA	39391	A_95_P036093	FS433957
40347	475	57	1277	ACTGTTTGCCCCATTGTAATAAAGACTTGAGATGCTTTGTTATCAAAGAAAGCACGA	39393	A_95_P145117	TA14320_4097
40348	475	58	1020	CTTGCAATGACAAATCTTATAGCAGCATATCAACGAAATGAGATCTTGGAGTTTGAG	39395	A_95_P192737	TA15519_4097
40349	475	59	865	CTGTTTGCAACTATGCAGATTTACATCATTTGTGAGTGCAAGAACTGCTTAATTATCA	39397	A_95_P232614	DV999247
40352	475	62	523	TTTAAGTGGAGAACAGTAGAGCTGACCATTTATCTTCCAGATCTCGAACCATGCACC	39403	A_95_P073765	BP526296
40355	475	65	1099	ATTGCAAGGGCAAATTGTCACTCCTGACTAGTAGTTTTCTTGAGATTGAATGTTTGAT	39409	A_95_P245432	TA16830_4097
40360	475	70	391	TGCGGCTGTTCTATTTCCTCTCTACTGTTCGTGTGTGTGTGTGTATCTGGGTATTCTTG	39419	A_95_P080460	BP528008
40363	475	73	874	TCAATTTGGGATAATTAGTCTAGTTCACATCTTATCATAAGCATTCTGGTCCAGGAAC	39425	A_95_P008716	DW005082
40368	475	78	685	CTCTCTTCTGTTGGTCCTATGAGACCGAATGAAAAATGGATAAACATCTGATATTTTT	39434	A_95_P027596	FG163977
40380	476	5	434	GACTCCTGTCCAAATTTTGAACTTAAATGATTTATAGACCTGCTTGTTTTCCAGCGGC	39291	A_95_P266796	AM828280
40383	476	8	891	CCATGGAAGAATGACTTGTATTTGCATGATAAAATCCATTTGTGAACTATTAGAGTG	39296	A_95_P249437	EB425035
40385	476	10	301	TGGACTTGTGAAGTTTTATCGCAGGATTAGCTAGTGGGTTATTATCCTTCATTTGTTA	39300	A_95_P129927	EB429857
40387	476	12	668	TCCACAACTCTTCCAAGTATTTCTTTTGCAGAAATTCATTGAAGCTGGTTTCGATTCCC	39304	A_95_P220102	EB678030
40389	476	14	790	CTTCATAAGCACCTGTTTCTTGGTCAAAGGCTAGTTACTAAAGAGGAAAAGATTCTTC	39308	A_95_P163352	EH622376
40396	476	21	811	AAGGCGAAAAAGGCGTTAGAAAAATACTATTCCGACGGGAATTATAGGCTTTTACA	39322	A_95_P139132	EB442824

40397	476	22	421	GCTCCAAAAAGTTCTCCTTGTTGACTTTTCAGTTTACACTACCAAATTTCTTGTATTGC	39324	A_95_P088528	BP530110
40403	476	28	749	TTCTTATCCTGTTGCACCTTCTGTAATCCGTTTATGTGTTATGATGCTGGCTGGGTGC	39336	A_95_P017976	EB424751
40404	476	29	1975	CTCGTGTCTTAAGAGTACATTTTGTATGCAACTGTCCTATTGAGACATTATCATTTGA	39338	A_95_P011396	TA15759_4097
40407	476	32	716	GTGTTGCAGACTCATGGGAAGTTCCTTTTGTAACTCTTTACATGAATAAAACTTCCTT	39344	A_95_P013286	DV158510
40424	476	49	627	GCTCCAAATTTGGGTAAAAATGTGCAACCTTTATCCATGAATTTATCATGACAGTTCT	39378	A_95_P245342	DW002215
40425	476	50	304	AGAGGCAACACTACCGTAGGTAGCCCCCTTACTTGTACTTTTCCTTTATTGTTTCTTTT	39380	A_95_P004651	EH622738
40427	476	52	841	CTGGCCATTGGATTGTCAACTGGTTTTCTAGGAAGCCTTACAACTTTTAGTGGTTGGA	39384	A_95_P216127	EB681526
40430	476	55	521	ACATAGTTCTGCAAACATACTGTAAAGAGGTAGCTGGTAAGGAAAGTGTCTTACCTT	39390	A_95_P273963	AM793740
40431	476	56	701	TAGGGGAATGTAAGTGCATGTGTTTGTTATTGTCATGTTGAAGTTTTGCACTTGATTT	39392	A_95_P208492	DV158298
40439	476	64	621	TTTATTTCTGACCAAAGATGATACATTTGTGACTTATTGATCAGTGTAGTGGTTCACC	39408	A_95_P122837	DW002778
40441	476	66	700	AGGCGAAGTTTCACCTTTAGTAGATCCCAAGTTGAAGCTTTGTCCAATGAAACAAGT	39412	A_95_P068570	BP137159
40442	476	67	848	AGATGGGAATTGGCTCGAGCATTTGACACCTTAAATGTATTGCAAGTGGTGAGGTT	39414	A_95_P218077	EB439797
40443	476	68	661	GATATTTGTTTCTCCTCCTCATTCAATGCCAAGTGATGCGGCTAGCGGATCCATTTG	39416	A_95_P270196	FG636806
40445	476	70	77	GTATGGAAGCATCTTGTATAATTTTGATTGACCTGCTGTTGGGGCTATAAAATTTTCC	39420	A_95_P129232	EB428947
40447	476	72	497	AAGCCTCATTGGTTCGATAAATAAGCTCTATGTGACAGGTTTTCTTTGTTCAAATAGA	39424	A_95_P063955	BP135917
40450	476	75	451	ATGCCCCTTGAGATAGTTTTCTTTATTCGTTGATGTATTACACGAGGTTTACTCTTTGT	39429	A_95_P088908	BP530268
40457	476	82	180	AAATATCCCTGACGTAGTTTGCTCACTTATTTCTGACTCCTCTACAGGCACCAGATCTA	39443	A_95_P109712	CV019423
40464	477	4	718	CATCTTAGCCACTTGTTCCAGCTTCACCCCAGTCAGAGCAAAGTGTTCTTTTGCTACA	39455	A_95_P253199	EH619700
40465	477	5	1907	TTTCGAGGCATCTCAAAGTGTCATATCATGAGATTAAGTTTTCGTTTGGTGGCTAAAA	39457	A_95_P069920	X70651
40468	477	8	732	CATGATCATTATGTTGGATACTTTGATGGAGCAGTAGGATAATGTCATTTGTAGTTG	39463	A_95_P116507	DV159272
40469	477	9	513	CTAGCTCTATCCCTATCTCTCTTTACTGAACAGCTAGTTAGCTGTGTTATTTGATCTTT	39465	A_95_P074560	BP526504
40470	477	10	1289	AATATTGTACCAGAGCATTCACCAATTGTTAAGTTGCAATACAGCAATTGGTGGCCA	39467	A_95_P028041	TA14403_4097
40473	477	13	739	TTCCTGATCTGTGTTACTACTTAAGACAAAGGGGTTGCTCTGATGGTAAGCAACCTC	39473	A_95_P147497	EB451962
40476	477	16	506	GTTCTTTCCTTATTTTCTCTAGCTATCTGCTGAAGTATCTGATGAGCCGGAACCCTTGA	39477	A_95_P086435	BP529536
40480	477	20	312	ATCGAAAACTATTGATCAGTGTATGGCTTCACAGGATTATCGAATGGAGTAAAGGAT	39485	A_95_P188102	TA14495_4097
40482	477	22	568	TCGTGTTCTGATCTGATTAATCGTCTTGTAACTGTTTACAAGCTGTGGCTATGTAAAA	39489	A_95_P003611	FG642155
40486	477	26	857	GAAGTGTAAGTTCTCGCTTGTATCAACTTGTATCTGTAGAAAACTTAATTAATCTGCA	39497	A_95_P190932	DV159857
40487	477	27	509	TACCTGCCTTTTATTTTATTAACGGTCAGCATTATGATGCGTACTTGTTCATCTACTAT	39499	A_95_P076315	BP526954
40490	477	30	741	ATGAGATGGTACGCTACTCAACACATGCTTGAGAACGGTAGCTTCATTCTTGTTGGA	39505	A_95_P292378	EB428451
40497	477	37	232	ATTGTGGTTGCATAACTGTGCTCATCTGTCAAGGAACCACATCATGGCATCTCTGTAT	39518	A_95_P102842	CV016229
40500	477	40	325	AGAGGAATGTCCAAAAGCATTCAGATAAGAAAGGTGTTGGACAAAACAGTGGTGTA	39524	A_95_P116362	FG634672
40504	477	44	864	CTAGTGACAATATGCAGTTGCTTTCATCTAATTCTTCTCAAACTTTTACTACCCTGTTC	39532	A_95_P196382	TA16326_4097
40506	477	46	568	TTTTATCTCCGTGATATGCGTCAGCTGTCAGGGATGTTGCCAAGTATTTCCAACAGCA	39536	A_95_P039136	BP129464
40507	477	47	394	TTGGGGTCATAATATGGGAACTATTCACACTCAAAAAACCATGGGAAGGTGTTCCAT	39538	A_95_P085820	BP529385

40510	477	50	813	AGTATACAGCCAGTGAGATAGATGTTTCTACGAAAGAGTCAGACAGCGAGCTCTCCT	39542	A_95_P310093	FG134997
40511	477	51	408	GCTTGTGTAGCAAATGTGGAATATTTGCCTATGGTATATCATATATTGCCAAGCGCTT	39544	A_95_P006221	TA15867_4097
40518	477	58	286	TTGCGTATTAACAAGACTGTGTCATGTGCTGGAGCTGATAAGGCACCAAACAGGCAT	39557	A_95_P106107	CV017757
40520	477	60	1064	GCGTGCCTATGCAATGTCCTGTCCATGCATAATGAAGTTTGAATTCTGCTAGTTCATT	39561	A_95_P132737	TA12370_4097
40522	477	62	102	TAGTATGTTGATCGTATCCAGCCTTCAGGTGAAGCTCAATACCATGCTGCTCATTTCT	39565	A_95_P137972	EB441688
40532	477	72	170	TGTAACCTATAGCAGAGATACTCAGGAGATATGGCTGAAGAAAACAAAGCATTGGA	39585	A_95_P128052	EB427609
40534	477	74	756	ATTGTACCAAGGGAGGACTTGAAAGATGAGGTGCTTGCATCAATTCCTAGAGGAAC	39589	A_95_P028541	EB444615
40535	477	75	420	TTTGAAATTTCAAAATTCAACATTCGATGCCGAAACCCATCAAATCACGTCCGATGTG	39591	A_95_P038666	BP129332
40539	477	79	743	TTGAGAAATTTCTGAAGGGAGCTTCCAGTGTTGATCAGCATTTCTACTCAGCACCCTT	39599	A_95_P151227	EB681454
40541	477	81	545	AAGCCAGGCTTAAGGCCTATTCAGCTAACCTGTCAGAGTCAACAGCAAAAAGAAGT	39603	A_95_P064390	BP136039
40545	477	85	132	AGCCATGATTTCTGGGACTTTCTCTATAATCCAGCAATCGCTCGCATTAAGATGCTTT	39611	A_95_P242507	DQ460155
40546	478	1	483	GTAGTAGTAGCATATATTTAGAACTGTTTGGTGATGCTTTTGACCATGAGGGTTGAG	39451	A_95_P001346	FG623263
40552	478	7	558	GTTAAGGCCATTCCTCCTGATAGTTATACCAAATTGACCGTCTTGTTGTAATAGTAATT	39462	A_95_P124172	FG633796
40556	478	11	1640	GATGAGGATAGAAATAGGATTATGGATGCTCCTGACCATGTACACTTAAAACATATC	39470	A_95_P133287	TA12715_4097
40558	478	13	305	TGCAAGTGAGCTTGAGGTCTTAATGATGCATAACAAGAACTTACTGTGCAGAGATTG	39474	A_95_P109982	DW001669
40559	478	14	903	TGGGTTTGTGAAGTTGAGCCAACAATCACATGGCGAATGGATAATGAAGGCGCTAA	39475	A_95_P016041	TC48562
40560	478	15	894	TTTTCAAAATTTCGCGGCCCTGTTTGTGTAAGGTCAACATAATCGCGCCCCCCTTTTG	39476	A_95_P099848	BP535091
40562	478	17	94	TTAGGGTTTAGAGAATCAGATCGGTGAAGAGAGACAGACATGTCGGATCAGAGATT	39480	A_95_P049811	FS419162
40565	478	20	929	CTGATTTGGAGGTCAGCTTTTTGGTTAAGTTATGTTGGTTGTTAAATATAGGAACGG	39486	A_95_P217047	TA20843_4097
40569	478	24	469	TCAGACCTTTTTCCTAGCTGAGCGAGATAGCATTTTAATTGAGGACTCTTTATTTACTT	39494	A_95_P123947	DW003808
40574	478	29	485	AGACATTGAATGCTTCTTATCTGATTCTCAAGAGAGCCATGTTCCGCGGAAAGATGA	39504	A_95_P145252	EB448852
40578	478	33	512	GTAGAAACATTTTCTTCTTCTTCTTTTGTCGCCTGGCTTCTTCAAAGCCATTGTATGTCT	39511	A_95_P222722	TA22096_4097
40579	478	34	700	GTTAAAGCATTAGATGCTGTTTGAATGTAACAATAGACGTACTTGGGAAAATTGTGG	39513	A_95_P022581	TA19428_4097
40585	478	40	182	ACCAATACCAATCTTTTGTCCATCATCCAACAGATATATGACTTAAATTTGTGACTGCT	39525	A_95_P100058	BP535194
40588	478	43	529	CTACTTAGTTTGGAACTCTTTGTGAAAAATGCTTATAATAACTGCCTCCTCTCATATTG	39531	A_95_P162627	TA13077_4097
40591	478	46	309	AAATTATGTCGATCGAGCGGTGAAAGATGATGATAAGGTAAAGGAGAGCGTTTCAC	39537	A_95_P103042	FG143585
40596	478	51	675	GAAGTTCATACATTTCCGGGCTTCTCCTAGTGATAAAAAAGCTATTTAACACATTGTT	39545	A_95_P134572	EB437111
40599	478	54	166	GAAGCTTTTGCCACACGCTCGCTCTCTTTCATCTCTAAAGAGTGCAGAGTGAAAAGAT	39550	A_95_P061425	BP135256
40602	478	57	303	ATTTCGCCTTTATTCGGCCCTTTAAATTAGTTCTTGCTTAACCAGGTATTCACTTGTGA	39556	A_95_P190787	TA15089_4097
40603	478	58	788	TATACCAGATTGGATTGTTATGTAAGAGAGAAGGTTTAAGTTGTGCTGCGCCTTTCT	39558	A_95_P180437	TA12745_4097
40606	478	61	545	AGAAGAAGGTTTGTTGTATATTCTTGCATATTGAGGGACCTTTTAAGGGAAAGTACA	39564	A_95_P132052	EB432481
40608	478	63	741	TAAGCACTGATGATGTCTACAAAAGTGCTGAGGTTGTCAACCTTGTTACCCAAGAGC	39568	A_95_P182047	TA13121_4097
40609	478	64	151	CCAGACTATCAAATGGAATTTCACCAAGATTTCTGATTGATAAGGAAGGGAAAGTTA	39570	A_95_P055691	BP133768
40611	478	66	732	TGCTTATGTTTACTCGTCTTTGTCAAGGATATTTGAGCTCTATCAACTTTGATACCAAA	39574	A_95_P014306	TA12020_4097

40618	478	73	735	AATAACAGCTACCTGTTCTCTATTTTTACTGATTGCAACTGTCTGTTGATTTACAGATG	39588	A_95_P183657	EH622517
40620	478	75	744	TTCATATTATTGTATCGTGTTATGCCATCAATTGATTGTGTGCGGCTGTTGACTTGTGT	39592	A_95_P142597	EB446030
40624	478	79	813	AGATTTAGAGTTAGCTACGATGAGAGTATGACCTTCAGAGCAGCAGCTTCTGCTGCA	39600	A_95_P275718	FG144926
40626	478	81	868	GATATACTCTAATATCTTAGAGCTGGTAACTTAGAGTTGTGTATATGTCGAGATACTC	39604	A_95_P149452	EB679292
40629	478	84	624	CTTGGTATTGTTCCATTGAAATTGTGTTGCAAAAGGTCAGGATTGCATTGAAATCTAT	39610	A_95_P117872	DV160841
40631	479	1	837	GCCATTTTAGTTTCGATCACAACCAATGCCGACTATCTAGAATCAACATTTATTGTTTG	39613	A_95_P233624	DV160352
40634	479	4	763	GCACAAGTATCATATGCATTTCATTCAGAAAGAAGATGCATCCAGAAAATTCAAAAC	39619	A_95_P251427	FG147735
40635	479	5	462	GTTTGACAATTTGTACAACAATGATATTACTGCAATTGTGGTTCATGCAACAAGAGCT	39621	A_95_P145817	EB449557
40636	479	6	284	AATTGTGTACAACTTGCCCCTCGTTAACCAAAGTTTACACTATTGATTCTGTTTTCTGT	39623	A_95_P143242	EB446589
40637	479	7	892	AAGGTGTAAACGCTTCACTACAATAACAATGCTGTGTAAGATGTTTGGTGGATTGTC	39625	A_95_P025326	TA20015_4097
40639	479	9	352	ATGAGGGTTTGGATTTTGATTCCCATCTTGATTCTTCTTCATTCTGTTTTGGTTTGAGT	39629	A_95_P001206	EH618849
40641	479	11	0	TGGTCAAGATAGTCGCTTAGTGCTATGGTGATTAAAATTTGACATGGTGGCATTAAA	39633	A_95_P239614	A_95_P239614
40642	479	12	1510	GGTGGTCTCAAGGCCAGAATAATTTTCCTCTGTATTTTCTTGGTGGGTCATTTATCTT	39635	A_95_P092018	Z93769
40647	479	17	689	CTGTTGCATTCCTTTGTTTAAGGGTAATATGGATTGTTGCCCAAAGACTCATGTACCA	39645	A_95_P151777	EB682025
40650	479	20	391	TACCATACCCGAGTTTGTAATCTTCGCACTATATTGAACATCTAGTTGTAGCAGTTTTT	39651	A_95_P001851	AJ718707
40651	479	21	796	GCTGTGTAAGACGATGGTCGAATATATGTTTTAGTGCTGTCTGTTTTAGGTATATTTT	39653	A_95_P010866	TA12119_4097
40652	479	22	0	AAGATATCTCTGTCACTCTGTGCACAAATACTCGCTTAGCAGACCGTTACATGCACTG	39655	A_95_P294883	A_95_P294883
40660	479	30	1542	GAGTGACATCTGTAAATAACAGAATGTTGGATACAATGGCTTTGTGAAATACTCTTCT	39670	A_95_P183327	TA13434_4097
40662	479	32	246	GGTGTTACCGGAAAAGGTGTACCTTATAGCATTTCCATTTGATTTTCATGACATGAAT	39673	A_95_P028656	EB430793
40663	479	33	699	GGAAGACTGGGTTGACTCTTGGTCTTTTCCTGGACTCTTTCAAATATTAGAGTGGAG	39675	A_95_P298953	FG194724
40664	479	34	87	TATCATATTGGATGTACATCTCAACCCGTCAGTAACCCGTCAAGCAATAGGGCGTGC	39677	A_95_P088553	BP530122
40669	479	39	581	TGGAATTATCACTAGTATTCATGGACCCACTTAAAAAGAGGGATTTGGCTGGAACTT	39687	A_95_P019526	TA17909_4097
40670	479	40	750	GCCTTACAAAGCAGGGATTTTGGGAACTATTTTAACATCTTTAACTCTTTTAACACTG	39689	A_95_P264106	EB439549
40674	479	44	538	AATTAGGACGTTTGGGGGATTATTGTTTTCAACGGTGACGATGGTGTAAGTTTACGG	39697	A_95_P061075	BP135171
40678	479	48	293	GGTCCCAATTTGGTGGTGACCTTGGATTGTTTTGAATAGTTACTGAATATTTTGTTCTT	39705	A_95_P151767	EB682017
40684	479	54	619	AGTTTAGATAGCTGGCCTCCGTTAGAATTCTCACGCTGTTTAGTTAAAAATATGGATT	39717	A_95_P152832	EB683169
40685	479	55	792	TAGACATATGGACATGTGGAATCATCTTGTTTGTATTGAATGCTGGATATTTGCCATT	39719	A_95_P128872	EB428605
40686	479	56	0	GATGAATGTTAGCAAGGGGGAAATGTAATGTAACTTGTACTTTGGTTGTCAACACAA	39721	A_95_P242762	A_95_P242762
40687	479	57	917	GGTATTTAAGTTCCTTCACTGTTACTCTCTATATCTTGCTGTCAAAGTTGTGTGGAATT	39723	A_95_P249932	EB677695
40688	479	58	571	ATAGAACAAGACTTATCGCTCTCTTGATCCTGTCCCCCCTTCCTTTCTCTGATTAGGAA	39725	A_95_P131597	EB431943
40694	479	64	185	ATACTCCAGATAACAGCTTTCTTGGTGCTCGTGATGCCATTGGAATTACTTCCCTTTAT	39737	A_95_P311148	FG167536
40702	479	72	516	ATTATACTGTGTACTTGGATTGCTATTAGTTTGGTTGAAGCAGCAGCCAGAGTTTTTA	39753	A_95_P018941	BP131365
40703	479	73	328	CTGATTTCATGTAACTGTACAATTCAGACGAAAATTGTGTGGATATAAATGTGGGCTT	39755	A_95_P209532	TA19210_4097
40704	479	74	824	ATTTGTATCCTCAGCAAATTTATGGCACAAATGGCTGGTATGGCTATGGTATGCCCA	39757	A_95_P241664	FG166039

40705	479	75	631	CAGTTAGACGTATATAATGCAGCCTCTTTTGGATGGTCTTATTGGACACTTAGTGTGA	39759	A_95_P065735	BP136410
40712	479	82	284	CAGTGAACAAATTAAATCTTAAATTTAACAGAGATGGATGGGTGTCAGCCTTTTATG	39772	A_95_P114032	CV021413
40714	479	84	633	AACATGACATGGGTGACATGATCAACTCTCTATTTGCTATGGAGATTAACTAGTTTG	39776	A_95_P014791	FG637726
40715	479	85	895	ATATCAAGGACAGACGGTCGCACCTATTACCTTTCAGACCAAGTTTCAGCCACATCTC	39778	A_95_P291693	EB680171
40720	480	5	738	AGCATTTGATGGTGTACAACTCTTGACTTGTATTTTCCTGCCATTGCTTTGCCTTCTTT	39622	A_95_P195702	EB678808
40729	480	14	834	CCTAATCTCTACGAATCTGTGCAATACAGCAGCTGGTATTGCTGAGCACTGTGTTATG	39640	A_95_P310728	FG149203
40733	480	18	660	GTTGTGTTCTCCTTATATGTCCTTTTGTTCTATTGTACTCAAATGACATATGCAGACAT	39648	A_95_P043456	BP130619
40735	480	20	268	AAATGTTCACAGCATGTTTTTGCTGACATATCTAATTATAAACCCAAAGTTTCCCTGC	39652	A_95_P160152	EH618800
40738	480	23	1043	GGTGGTGAGGGGTGGGTAGTACTTTTAAATTATAATGAGATTATTCAGTGCTTATTT	39658	A_95_P028166	TA17665_4097
40748	480	33	812	TATCTTCACAATGAGCCAAATGTTATAATCCACAGAGATCTAAAGCCCAGGAATGTT	39676	A_95_P138162	DV162248
40754	480	39	621	CATATCCTAGCAAAGTGTACAAAGAATCTTACTCCTACCCCTTGGCTTCTGGTGCTGG	39688	A_95_P299108	FG635787
40758	480	43	151	GCTGAGTTCTGTCATTTTGTGCTCAGCACCGGTATATTAACATAGACAGATTGTCTTT	39696	A_95_P104247	CV016907
40761	480	46	793	GCTGTATAATTCATTGACAGAGCTAGCTGGAGCAATTTTCGCAGCCATTATATAATAT	39702	A_95_P194952	EB446333
40762	480	47	714	AATGCAGGGCAGAGGCAGCAAGAAAAGGTGATTTGTCACCTATGCATAACGGAAAA	39704	A_95_P115737	DV158063
40764	480	49	358	CATTGGTTAAGTGAAGCAGCTTTATATCTCAGTAGATAGACCAGTTGCTATCTGTTTT	39708	A_95_P089778	BP530650
40765	480	50	474	CGTTGTGTATACAAGTAGTTGTGTGGTTTGTAACATGAGCATCTCTGCTTCTGGTGTT	39710	A_95_P106877	EH620447
40768	480	53	862	AGTCATTCCCTTTGGCCGTTTACTTATCTCTTATTCCCATCATCGGTGGCTGTGGTCTT	39716	A_95_P199977	TA17111_4097
40770	480	55	499	TCCGCTTTGTAATGACCGAAAGATATTTCCTTTGCTGTTACTTAGAATGATACTGATA	39720	A_95_P071600	FG641857
40774	480	59	599	CTGCATGCTGTGGTTGAGGGTTATACGCAACTGTAAGGTTGTTCAACTGTCTTGAAC	39728	A_95_P044041	BP130775
40775	480	60	802	TGTATCCTATGCGTGAGTGATCCAGCATCTAGTTACGTCTGTCAAACTGTTCCGAAAC	39730	A_95_P265821	FG148043
40777	480	62	877	CCGGTCCATGCGTGAAGACCCTCTTCCTGATATGGATCCAAATGAAAAATTTTATGCT	39734	A_95_P224522	EB441919
40780	480	65	227	GGCCTTAACTTTTCGCAAGCTGTACAGTGCTTGTTTCTCTTTTCTCATTTAGTTGTTTC	39740	A_95_P132862	EB433652
40782	480	67	371	TTGTATCTCAAAACATTGTCCATTGTACTTTCTGCTTGGTCGTGTTATACTGGAATTG	39744	A_95_P106072	FG625538
40787	480	72	822	GCAATTAGTGTAACCTACAGCGTCTACATGAAAGCAGGAAACTCTCACGTTAGATCT	39754	A_95_P273026	EB680914
40789	480	74	460	TGCCTTCTTTGCCAAAATACGTTTAAGCATGTAACAGGCTATTAGCTATTTTGAGTTT	39758	A_95_P124722	TA16894_4097
40797	480	82	890	AATATGATGGGAGGATTTACCAGTCCTTTTGTTGGGTTGAAATAAGAATATTGCGAC	39773	A_95_P011196	TC42564
40800	480	85	1037	CTGCTGCTGGACAAAAACCCTTCATTCCATCTTATAGGTTATTTGAAGATCTTAATGT	39779	A_95_P023961	TA14913_4097
40801	481	1	349	CAAGTTCACCTAACATACTCTCTTATGCAGATTTCTATCAGTTGGCTAGAGTGGTTGC	39780	A_95_P113642	CV021236
40809	481	9	823	CTATATCTTTACCCACTTCATGCACGCAGCATATGATATTGGACTTTTTGACTTTTTGC	39795	A_95_P222497	DV158650
40811	481	11	478	GGTAGCAAAACTCTGTAGAGCTTATGACTTGTACTACCGGTTTTGGGAATTGTAAAT	39799	A_95_P308903	FG643908
40813	481	13	1111	CTGCGGTGCGGGCTGCAATTAAGGTGAAAGCATCAGTAATTATTTGCTTCACTTCAT	39803	A_95_P021596	TA17748_4097
40816	481	16	437	ACTTTGTTAGTTTGTTATGTCTTGAAAAACTTGTTAGTGGCAAATGCCTAGCTAGCTT	39809	A_95_P076270	BP526941
40820	481	20	499	CGGCTCTTTCGCTTTGTACAGTAATTCAGATGCATCATGTTATAGAAGCAGTTAGTTT	39817	A_95_P072770	BP526045
40821	481	21	780	AGAATTGAGAGCCTACAGAAACATAATTTTGGAGTTCCTTTTTGCTAACAGGCAATT	39819	A_95_P026736	TA17743_4097

40822	481	22	707	CATGGTAATGTACATGTATTGTGTAGGTGAGTTAATGTCAAAGCTTTGGTAGGATAT	39821	A_95_P013946	TA16897_4097
40825	481	25	231	AGTAAGGAGCATAGTCTGTCAAAATTGTGATGGAAATGGTGCAGTGTCGTGCTCAC	39827	A_95_P107842	CV018551
40832	481	32	601	TATCTCAGACGAGGCGAATTGATGATTCTAGTTCGGATGATGACACTCCTTGAGTAC	39841	A_95_P043956	BP130755
40836	481	36	729	ATGATGCGTTATGAGATTCTGGGTTTAGTAAAAGGTCTGACGGCTGCACCTAAGAGT	39849	A_95_P145802	EB449549
40843	481	43	524	ACAGCTATGTCTCAATCCCAGGTATTTTGTATTGCGAGGATTCATCATAAACAGAATA	39863	A_95_P070820	BP525545
40845	481	45	729	GAAGAACATTAAAGACTTGTCAGCATGCTTTCTCACATTCCACACCTTTCTTCTTCTTT	39867	A_95_P300223	FG197293
40849	481	49	373	TTACTGGTTACAGTTAGGAATTTTATTGGTGCTTCTTCTTGTAAGTTCTGAAGAGAGT	39875	A_95_P069700	BP137460
40853	481	53	468	TTGCCTCAGTTCGGATTGTTCTCTGCAACTCGGGAACATGAAGTTGGAATCGCTAGT	39883	A_95_P198567	TA16807_4097
40860	481	60	398	AGCTAGTAATGGGCATCGGTTATCAGCTGTTGTACTTTAAGAAATCCTCTCAGTTTAC	39896	A_95_P211202	TA19559_4097
40868	481	68	864	CATTTTTTGCCAGCAAATCAAGCCATTTTGTTGTTCCAGATCTGGCATTAATCCTTGCC	39912	A_95_P020406	EB683273
40871	481	71	171	CAGGGAATGATATGACGGATTGTTCGATGGCGTCTTTGTACTTGCTTTGTTCGATGA	39918	A_95_P092888	FG624161
40872	481	72	432	GCGTGTAAAAGCTAGCTAAAGACATATTGTCTATAATTAGTTGAGCGTCAGTTGTTG	39920	A_95_P123977	DW003836
40876	481	76	550	CACCAGAAAGATTTCAAGCACACAGTTATGTATTTCACGGCTTGTTTGCATATATGAC	39928	A_95_P304663	FG643471
40878	481	78	620	CAAATTCCACAGCTGCACATTTCTGATCATTTTTACTTCTATGTTAATGATTAGTGGCC	39932	A_95_P028786	EB445150
40880	481	80	261	GGTCTTAACCTTCAAGATGATAAAATTCTGACATATCGAATGGCACATCTTCGGTTAG	39936	A_95_P109247	CV019208
40882	481	82	363	GCAGAATGGACAAGTATTTCTTTGTCATCAATTGAGCGCATGCCTGAGAAATCTGCT	39940	A_95_P082190	AM833236
40887	482	2	811	GAGATCCCATATAGCTTTGCGGATATTGAAGCACTGCAATTTATTGAAGTGATCAAA	39783	A_95_P296288	EB451171
40896	482	11	422	GGAAGCTGATTTGGGCTGTAACACGAACTTATCAATATATAGAATACAAGTTGGCTT	39800	A_95_P003461	DW002887
40897	482	12	257	GTACTGGAAGAAATGCTTGGGTTACATGAGATCAATTGGATGTTATTTGAATGCTTA	39802	A_95_P212692	TA19890_4097
40906	482	21	559	TGCTAACTCTGTATTTGGGCTTTCAAATGTGTGTACTAGATTGTCTAGATAATGATTC	39820	A_95_P213862	TA20138_4097
40907	482	22	725	TCATCCTTCTAAAAGGTCCGCTAGGTAACTGTGTCTTTACCGGTGATTATGACCAGAA	39822	A_95_P193022	TA15582_4097
40915	482	30	223	TTTCTTGTTGAAGATGATGGAGGTTTCAGTTGCTTTGAAACTGGAAGAAATTTGAAT	39838	A_95_P213477	TA20057_4097
40916	482	31	591	CCAAGGAGTTTGAAGGCGTTTAGTGTTTTATTTTCTAGTCGTTATTATATGCGTACAA	39840	A_95_P306623	FG644296
40918	482	33	155	GTGGGATGTTACCTTTGGCTATGTAAAATAATAGAATTTGTGACTGAGCTTCCTTATA	39844	A_95_P114167	CV021477
40919	482	34	802	TATAATGATGAAACCTAAGCCAGCTAAGCCGGCAACTCCTGAAACAACTTCACATGC	39846	A_95_P070315	FG132790
40920	482	35	408	TTGCTTTACTAGGAGAAACTAGTAGCAACAGTTAGCTGCTTTGAATAAAATCTGTCAT	39848	A_95_P214212	TA20212_4097
40927	482	42	890	GAGTACAACCTCAACCACAACCACAACCATTGTAATGGATCGAATCCTCCTCTTTGTT	39862	A_95_P217437	EB428317
40931	482	46	684	CACCAGCATCAGCATCATCATCATCATCATCATCATCATCACTATTCAATTATAGATGT	39870	A_95_P312863	FG163611
40935	482	50	85	GTTTGTCGGTATGTTAATTATAATGTGGCTTTTTGGTCATTTTCGATCTGACATGGTA	39878	A_95_P108747	CV018987
40936	482	51	1421	GATTCTAAGTTTTGCAAGCTTTGGTTTTCCTTGCCCCGGCCTTTCACTTCATTTCGTTC	39880	A_95_P259281	AB300776
40946	482	61	1538	CAAAGTAAATATGGATAGTTGAATCAAACCCTTTGGTTTCCAGTTAATGTTTATGAGC	39899	A_95_P143907	TA14706_4097
40951	482	66	752	ATAGTGAAGTACTATCGTGCAAAGCAGCTTCAGAGGGATCAAAAGACTGTTGCGGG	39909	A_95_P199782	EH622406
40952	482	67	559	CGTCGAAGGTGCGCACAGACCTATTTGTATTTATGTTTGAATTTTATGACAAAATTGT	39911	A_95_P153382	EB683672
40953	482	68	451	GTCGTTCAAGCGTAATAAGTGGTTTCCTCTTAAGTTGGAGTTTTGGGATAAACCTATA	39913	A_95_P006131	BP530922

40956	482	71	765	CTTAGTAGAGGGCAAATTTCTCATGTAGATATTTCGGAAGCTATATGGAATATTTGCT	39919	A_95_P154107	EB684261
40961	482	76	1137	CTTGTCATAGTTTGGTTCTATATATTCGGACTTCCTCAACCAGTGATCTTATTGTTTAT	39929	A_95_P189972	AF113545
40964	482	79	863	ATAAGTGTAGCCATCAGAGATATTGAAAAGGGAGCTTTTCCCAAATGTTGCTTGTTG	39935	A_95_P285798	DV161389
40967	482	82	224	ATGTATGACTATGTAACTTGTATTTCGTCTGGGAATGGCAAACTGAGTAGCTAATGG	39941	A_95_P104132	CV016863
40975	483	5	187	ACATGATCTACCAAGCTTCCTATTTGGGGAATCCATGGGTGGAGCTATAGCTTTGAA	39956	A_95_P087698	EB428319
40977	483	7	831	AGGGATTATTTCCGGTATTTGAATTCAGAATGCAATAACATGGGTTATCTACTACTTC	39960	A_95_P125822	EB424909
40981	483	11	229	TTAGCATCAGTTTCACCTTTCTTATTTTAACTATGGGCATATGCTTATTTGCCAGTCAG	39968	A_95_P111717	CV020345
40982	483	12	728	AGATCTATACAGTTCTGATATGGTGCAGGTCCTGGCATTCTTAGTCGGTTGTCAATTC	39970	A_95_P252164	EH618097
40984	483	14	501	TATAAGTGTCGGATTTTGGACCTCAACCAAAGAAAGAGAAAGAGAACAAGAGTGGG	39974	A_95_P111187	CV020089
40986	483	16	430	GAGCAGGCCATGAAGAGAGATGTCAGGATGAAATACTTTCTGTAAACTACTTTTTG	14301	A_95_P000096	EH619820
40988	483	18	432	ACTTTCAAAGTTACCCACATTGTAGTTCCTTTCTCCTTACAGTAGACTATTTTCTTGCA	39981	A_95_P213182	TA19994_4097
40989	483	19	353	GTTGTTCGGATGTCTACAATTCTTACGTCCCTCCGATAGGAGGATTATAATTAATTAT	39983	A_95_P209382	EB428350
40994	483	24	2788	GTTCTATCCCCCTCCCTCCCTTCTGAAAAGAGATAGGAAAAAATTCTATTATTTTTAAA	39991	A_95_P007291	AF115482
40997	483	27	694	TGACTCTTGCTCAAAGTGATGTCTATACTAATAGGTTAATCAAACTTATTGCCTAGCC	39997	A_95_P126002	EB425203
40999	483	29	856	GGACTTGTTGAAGTTCATCTTGAGAGGCTTCAGGTAAGTGACACTGGTCTTGCTGCT	40001	A_95_P223367	TA22237_4097
41002	483	32	847	ATCTGACCTGATGACTGCTATGTACTGCTCATATGCTAGATTCTTGTGGGATGCTGAG	40007	A_95_P242322	FG162154
41006	483	36	761	TTCAATTATGGGTATCTCGCTCTACTGCTATGCTGCACCACATATTTTTACACCTTTGC	40015	A_95_P259581	EB449659
41010	483	40	596	GCTTGTTGGAATCATGTTTCGGGTGTAACTAAGATAACTGCTTAGTGACTTTAATTTA	40023	A_95_P026091	TA15357_4097
41011	483	41	1498	GTACAGGCATGCTATATGGTGTGCAAGTATTCTATTGTGAAACAGCAAATTATGATG	40025	A_95_P206977	TA18639_4097
41013	483	43	796	ATATACAGCGGGTTAGCCAGGAGATTTTCTGGAAAGATGCTATTGGAGGCTGCCAA	40029	A_95_P120877	DW000845
41016	483	46	585	TGATACTGAGAATAATAAGCTGCCCATGCTGCTGCATTAGCATCTGCTGCTGCTTTAC	40035	A_95_P315883	FG189354
41028	483	58	360	CCTTTATTGTCCGTCCCCCTACTGCTCTATATGTGTGTGTGTGTATTTCTGTGGATG	40058	A_95_P049316	BP132133
41031	483	61	2838	GGTCTTTGCAAGTCTTCATAACAAGTGTATAGTTTTTGCAACTTTATCACCTGCTAAAT	40064	A_95_P019156	AB032535
41034	483	64	269	AACAAATAAGATCTTAGTTACTCAGAGATGGATGGGTGTCAGCCTTTAATGGCTAAG	40070	A_95_P103317	CV016457
41042	483	72	480	CATTAGTAGACTTGACATTCGCGTTGGTCTCATAACGAAGGCACAAAAACATCCTAAT	40086	A_95_P074855	BP526578
41044	483	74	1298	CTGGATAGTGATTTAGAGCTTTCTTGTAGCTTCTCCAATTTGTGTATGTACTGTAAAA	40090	A_95_P205357	TA18266_4097
41047	483	77	800	CTTTGTATAGAATGGAAGTACCTAGTAGAGTATGTCGTTCATACTGTAGTTTAACTTT	40096	A_95_P021116	EB438023
41050	483	80	807	TGCCAAAGGTGAAGCTAGAGGTATGGCTATAAAAGCAAGAATAGCTGCTTACAAGA	40102	A_95_P120827	DW000794
41054	483	84	646	CCCCACGGTGGGCGCCAAACTATTTACATTGAAATATGAGTAACAATTAAACTTATA	40110	A_95_P118402	DV161455
41055	483	85	741	GTTCTTTTATATGCGCCTTGCATTCTCTCCTATCTGTGATGGGCAATAATTTGATGTAT	40111	A_95_P198237	TA16734_4097
41056	484	1	506	TGAATTTGAAGTTGGGCCTAACTAATTGTCAGCCTAACAACAGAGTCCATACCCTCAC	39949	A_95_P112172	CV020555
41057	484	2	859	GTGTATACGAAAGACTGCTTCAGATGTAATATTGGGATGATTTCTGCCAGCTTGACCT	39951	A_95_P216642	TA20750_4097
41060	484	5	1580	GTCCTACTGTTGTAACTTTTATGTGGTTAAGGGTGGACTGCTTTCTATATGAACTATT	39957	A_95_P012796	X77763
41062	484	7	498	GTCTGTCCTTCGGCGTCTGTTTCACTATATACATAAATTGTAAAATTTTACCCGTTTGC	39961	A_95_P194832	TA15985_4097

41064	484	9	214	TGAGCTCTGTTAAATGATCGCATAGAATTGAAGCGACTAAGTACAGCATGTTTGATA	39965	A_95_P154787	EG649759
41069	484	14	521	ACCCATTGTTCTGGGGTTGTGATTTAGCCATGAATATTGTTGTTTGATATTAGCTTGA	39975	A_95_P308783	FG643588
41071	484	16	417	AGAGTATGTAAACCATGAAACTAGGCAAGGGACTTTTAGCCACCAGATTCTGGTTAT	39978	A_95_P093673	BP532365
41075	484	20	490	GGATTTCAAGAAACATTTAGAAACAGATCACAGACTTGGTTTAACATTCAGTGCTTA	39985	A_95_P122547	DW002533
41088	484	33	636	GAGTCCAATTATACTGTAACTTTTGACTCTCCCGATTCATTTCTACTTTTAAGGTATTC	40010	A_95_P207547	BP129575
41089	484	34	868	GTTTCTAAAGTTGAGATGGCTAATTATAATCCGATCAAGTTGGAGTTTTTGCCTCTCA	40012	A_95_P127887	EB427450
41095	484	40	220	GTATTCCGCCTCCACAGAAACTAAGTGTAGTATGGAGGTTTTCTTCATTTTACGTTCC	40024	A_95_P063920	BP135907
41096	484	41	185	ATAAGAAACGCGTCGATTCTAAGCAAAAGCGTGCCGTTTCCTCTTCCGTTAAAGCAA	40026	A_95_P201292	FG136640
41101	484	46	324	GACTTATAAATGTGAACAACTACATCGAGTATGTAAAGGAGTAAGGATCTCCGAGTT	40036	A_95_P131707	EB432091
41102	484	47	801	CTCTACATCTTTTGACATGTTGGTTGGTTCTTTTTGGGATTATATCCTTATAACGCCCT	40038	A_95_P020011	EB428986
41104	484	49	813	TCGTTTCTTAGTTAAAGTTATGCTTATGAAACTGATGAGCTACAGGTCAAGTTCATCA	40042	A_95_P266841	EB451993
41105	484	50	2129	GATCGTGATAATTATGGATTTGTTCTTAGAATTGCTATTAGCGTGCTGTCTTTGGTGT	40044	A_95_P009436	Z28373
41107	484	52	605	TCACTTCTAAGGATAGGGTCTTGGGAATATGCATCTAGATATGAAGGTGATTTGGTG	40048	A_95_P127677	FG162856
41108	484	53	908	ATGATGAACAGTGCATGTATAGCTTGTCATGCTGGAAACTGGCTGTACTGCCGAAAG	40050	A_95_P008706	TA14965_4097
41113	484	58	774	GCAGGTTAATTTCGAGGACACATGCAAAGGTTTTTTAGAGGTTGCAAAGGAAGCTG	40059	A_95_P262771	EB442083
41114	484	59	521	ATGTTGAAGGGAATGTTCCTGCAACATTTGGACACCCCTTTTGGTCTTTGTTATGTGA	40061	A_95_P134487	FG641157
41117	484	62	447	GTGTTCTAGAAGAACGAATATTGAGGTGTATCCATTTCATGAAGAAGTTTGTCTTCT	40067	A_95_P002151	EH620847
41118	484	63	479	GTCATACACAGACTAATAGGATGTAGTGGAAGATTGTCACGACTTGATTTTGCTTTT	40069	A_95_P140287	EB444249
41120	484	65	842	ACGACTTCCAAAATTTGCTACCCTTTGCAAATTCAGTATGAAACTGGTCTTTCAGAAT	40073	A_95_P190357	TA14998_4097
41123	484	68	189	GACTGTTGAAACTGCTCTCTTGAGCCAAATGGTTGTTGTTGTTTATTGATGAGTATTT	40079	A_95_P204867	TA18158_4097
41125	484	70	712	GCATTTCTTCAATATCCCATTGAGCTCCTGCTTTGTTTGATAATAATATCCTTCCACAA	40083	A_95_P315608	FG197573
41128	484	73	464	ATAATATTGCGGGGCGTAACATCATTCCCCCCTTTGGAACATTCGTCCTTGAATGTTG	40089	A_95_P034993	BP128316
41132	484	77	836	CGCTTTGATATGTGTGTTGGACCGGATAAAGAGGACGGATACTATATATGAATAATA	40097	A_95_P251147	EB424811
41137	484	82	630	GATGCAAAAGTGTTCTTACGGTTACTTTCTCCACATAATAGATTTTGTCCATCTTCTCT	40107	A_95_P134087	EB435916
41141	485	1	660	TTAAGGGGTTCGCTTTCAACTAGATGTTATTCTCTGTTTCTTTTCCTTTGCTCTGCTAA	40113	A_95_P186027	TA14039_4097
41146	485	6	869	AGTGTATTAACATGGTTCTCCCACATGACGGAGTCGTTCCTCGGTGAAAAGTATAGC	40123	A_95_P231549	DW003993
41148	485	8	758	GGAACAGTTGATCGCTTGTTTTGTAAGAATATTTGGGTACAACGATGTCATTTTGAA	40127	A_95_P229679	DV159989
41153	485	13	875	GGAGATATGATTCGCTAATGTGTTTTGAGAGGTACTTTCACTGATTAATTGAAGGAA	40136	A_95_P153812	EB443735
41154	485	14	225	AAGACAATAACAATGCTTTGTACTGTGAGAGCTGGCGGTTCACCGTTGAGACTAATG	40138	A_95_P111337	EB679494
41157	485	17	498	GTCTTCAAGGGTTCCTTGGTATTCAAATGCTGATAGGATGGTGGTAACTGGTTCAGG	40144	A_95_P111092	CV020051
41163	485	23	990	CTGAACAATGTGTGTCACACAAATAATATTAACCGGCTGTTTGAGCTTTGGGCTTATC	40155	A_95_P027681	TA15280_4097
41166	485	26	795	AACTTCCATGAATCTGTGCACCTTGATAGTTTTGATGTGGACAGGACCCTGACTCTG	40161	A_95_P011746	TA16057_4097
41167	485	27	776	CTTGCAGGAGTAGGTAGTATTAGTTTAGTTTGATTGGGGATTTGACAATTGATGTTT	40163	A_95_P200307	EH613966
41170	485	30	1088	AAGAATAGCTGTATAAATGAAGGGCGGGTAGAATAAATGTGTTGGTACACATTTGT	40169	A_95_P021141	TA19071_4097

41171	485	31	345	AGAGGACAAGTGCCAAATGGTGTTCCTCAACTCAATCATCGCAATGTGGGAGGTCA	40171	A_95_P033869	FG145583
41172	485	32	256	GACCATTTTGTTGGATTAGGAGGTGCAGTTAGCCAGTTTAATACTCCTAGATAGATG	40173	A_95_P154722	EG649733
41177	485	37	472	CTTTGTTAGACAAACACCCGTGAAGATAAAAAGTACCCCTACTGTTACTGTTTTGGCG	40183	A_95_P025141	TA19964_4097
41178	485	38	333	TGTAACATAGATGTGTCACTGTTGAATCTAAACAAACTAGCTTCTTGCCTTTTGCTTG	40185	A_95_P029876	TA13556_4097
41182	485	42	183	CCAAGGGAACCTTTATCCCATCCTCTGGTATCAAAAGAATTAAGACTTTTTTGTATGT	40193	A_95_P142872	EB446286
41185	485	45	642	GAGGGGGAATCCGAAGATGAGTGATTTTATGTTAACTTTGAATGTTACATTTTGGTG	40199	A_95_P121492	DW001579
41188	485	48	439	GTATCGAGATGTAAAGGAGAGTTCTTTGGATGCTAAACCTAGGGATGGTCTTGGTTT	40205	A_95_P040791	BP129923
41203	485	63	1705	CTACTTCCTTATTTTCAGGGAATTTGATATACGTCAATCAGCCAAATTTCAACTGATTG	40235	A_95_P181462	TA12987_4097
41205	485	65	347	GATGGAATATTGTCGGATCTTCATCACCGATCTAACTCCTCATCTCTCTAACTTTGTCT	40239	A_95_P103212	CV016396
41206	485	66	512	CATTAATAGCTCTAATTCTGAAATATGTGTGCATATGCTTATCGTCAGCTTCCCTTGTT	40241	A_95_P035413	BP128466
41207	485	67	744	ATCGATGATGCATTAACACAGCTTCAAGAGCAAAAGCAAGGAAAGTTGGGAACTGT	40243	A_95_P151017	EB681225
41211	485	71	628	TCTTCCCTCAATAAGCTGTCGATTCTGCCGGTGGATTTTGAGGGAAAGACAAAGATG	40251	A_95_P003526	EH613915
41212	485	72	1613	ATAGATACCACGAGCCTAACTCGTGGCGGTTGAGTAAAAGGAGAGCTTGATCTTTTT	40253	A_95_P017996	TC53168
41216	485	76	9	CGCCATAGATAAGTTAAACGGTATGCTCATGAATGATAAGCAAGTATATGTTGGGCA	40261	A_95_P115677	AF190657
41217	485	77	641	GCAGTGGATCTAACAGTTAAGATAACTGGGAATCTAACAATAGATGTATTCGTCAAG	40263	A_95_P139962	EB443904
41225	485	85	264	ATGAATTGTACCCTATGTCACTTGTTCTGAAATCTGAATCAACTGTTGCAGTTTTAAT	40279	A_95_P143417	EB446723
41226	486	1	343	AACCCCCTACCTTAGAAGGTCTTGATTTACTTCAAGCTAAGAAAAAGCGCGCGCCTA	40114	A_95_P158532	FG164661
41234	486	9	351	GTGTAAACTTGAATTGAGGGATGCCCTCTCTATTTTTATTGCACTGTGTTTAATTCTG	40130	A_95_P219702	TA21451_4097
41243	486	18	505	CTTTGTAACTGCAAGTGATGGAAGGAAGTTTGAGAAATTCACTTGGGGAGTATCAG	40146	A_95_P079470	BP527773
41251	486	26	999	CGATGATGTTGTCACTCTCTTCCAGCTAAATAAGATAAAGACTTGTATTCCTTTTTTCC	40162	A_95_P017821	TA11931_4097
41254	486	29	768	TACTTGCAGAGACTGAATTTTTCTTTGGCCTTTCTATGGGATTGATAAACTGTTTCCT	40168	A_95_P204392	DW002350
41256	486	31	670	TTGCCTATCTCGAGGAAAATAGTGGTAAAAGTGGTCCAGTATTCTCCTGGTCGAAAG	40172	A_95_P311938	FG151562
41259	486	34	1966	ACACCTTTTGTATTGTTTGGCTTTAATTTATTAGTGTGCTCTCGTGCACCTCTCTCCTA	40178	A_95_P020586	D26602
41271	486	46	866	GATGGAGGGATTTTTGTGCTTGTTAAGGAAGGGAGTTCTCTTCTATATTAGTAGAGA	40202	A_95_P272291	EB449818
41272	486	47	306	CTGTATTTGTTGTTCTCTGTGTTTGATTGAAAGGAGTTGATTGCTGGATGATCTTATT	40204	A_95_P069970	BP192486
41274	486	49	670	GGCTATGTACACTTGCATAATGCATACAATTGTGCACTTGTTGGAATTTTCTTTAGTC	40208	A_95_P119857	DV999465
41275	486	50	297	TGAAACCTGAGATGAATACAGAATCAAAGGTGCATATTGCTTGGTTCCGTAGGCATA	40210	A_95_P088703	BP530184
41278	486	53	695	ATCAGAGGAAACATAAAAGGGGTTGTTGGTAGCTGGCCTGGGATCATGAATTGTCT	40216	A_95_P301848	FG639980
41282	486	57	1153	TTCTATCTAAAAGGAGTGAGAAGAAGGTAGGGTATCCTACCCATCTCTCACCAGTAT	40224	A_95_P121427	TA12896_4097
41283	486	58	1559	TCTTATGTGAAGGCAACCAAAATTCTTTGCGCTGTGTTTATTTTGCAAGGGATACTTG	40226	A_95_P194782	TA15973_4097
41285	486	60	203	CGAGCAATCTTGTTTGAGAGTGTTTCTAATGACTTTGTATTTCTAATGAGCAATTCGT	40230	A_95_P133317	EB434718
41292	486	67	1590	CAACTTCTGTTTTCTGATTTGGAGAAATTAAATGGGTGGAGCTTTTGCATGGGTTAA	40244	A_95_P238409	AJ344537
41293	486	68	784	GCGTGCTAGCTTTATATAAGTCATGGAACACACTGTCTCGCCTGGTTGATATCTGAA	40246	A_95_P012696	TA13030_4097
41294	486	69	0	ATCATGGACTTTTTCTCAGATCATCTGTGAGTAACACTATGCTGTGGAGCTGGCATG	40248	A_95_P296713	A_95_P296713

41295	486	70	793	CATGGAAATGAAAGGATCCAATTATCAGCATCTGCTATTCCTTGTTGAGTTAATTTCTT	40250	A_95_P009151	TA11962_4097
41296	486	71	765	GTATCCAATATTATGAATCTGTCATTGGAGAAGTCGCAAGCTCACTGGAAGGGGCGA	40252	A_95_P150687	EB680821
41302	486	77	770	GGTGTTAAACACGAATATACTGCAACGAATCCGATTATCGGTTTTCAATAATGAAAT	40264	A_95_P246602	EB677971
41303	486	78	937	GAATTCAAATTCTGAGGTTGTTATCCTTTTCCAGTTCCATCTATTTTGCGAAGGCTTAA	40266	A_95_P192372	TA15437_4097
41304	486	79	482	ATAAGGAGAACTATGCGGCCTGGAGATGCTTTGTGGAGCATCTCATCGGATTTTCAT	40268	A_95_P277968	AM789925
41308	486	83	283	CTTCCTCGAGTACTGATGTGACTGATGTTCTAACAGTATCAACGAGTTCTGTGATATT	40276	A_95_P095783	BP533340
41310	486	85	658	TTGGTCATTGAACCTCTCCCTTCCTGCTTGGCTACCCATTGGATATCTTTATTCTTCTTA	40280	A_95_P040126	BP129741
41312	487	2	819	AACACCATGGATATTGCACATGACGAGCTGGCTTTACTATGCTGGGATGCTAGTATG	40283	A_95_P294528	FG139458
41313	487	3	355	AACTGGAGGCACAACTCTCTGAATCTTCTCCCCTTTGTTAATGGACATATTTAGTATGT	40285	A_95_P108417	EH623004
41315	487	5	864	TTTTGGTGCATGCTCTCAGTGCGCTCTTCTCTTGTCAATATCAAACTGTCGAAGTAAG	40289	A_95_P304038	FG167416
41317	487	7	446	CTTGTCGGCTGGTTTTTGTTGTATAGTCTTTCATGGTAGCGTGGTAGCTCGTACCTTAT	40293	A_95_P126617	TA15684_4097
41320	487	10	707	TAATACTGGGAATGGTGTCCCAACCAATGTTGCAGATGCCAAACATTCGGCAATCTA	40299	A_95_P216707	FG159163
41333	487	23	639	ACACTAGGAATTAAGGCCACATGCTGTAGCACTCTCATTCTTTATCCGCATGTGTGTT	40324	A_95_P303538	FG638377
41335	487	25	858	AATAGCATTTCAACTACAAATGTCGACCGCAGGGTGCTTAGTTTCTCCACTCAGCTGA	40328	A_95_P195607	EB438394
41340	487	30	874	CTGCTGAGTTGTGTAAAACTTAAGACATGTCTGTATGTGGTGTGTTTATAATGTATAA	40338	A_95_P010146	DV999957
41343	487	33	49	TAGGCAATCCCCATCAGATTCGATCATAGCCATAAACAAATTGAGTGAAAAAATAAAT	40344	A_95_P031846	BP535438
41345	487	35	850	GCTCTTAGCTGAGGCTGATATTAGCTAGCAAGCTTTCTATGCACCTATTTACTGGACT	40348	A_95_P008421	TA15150_4097
41346	487	36	837	TGACAATAATTTGATGTGTCTTGATGCTCCAGAATGTTTCCGGGAGCTTGCTTTTGGA	40350	A_95_P246362	DV158308
41348	487	38	495	ACAGATTTGCTTGGGACACTTCCTCCCGAAACAGTTGCAAAGATCAGAAATGAAAAG	40354	A_95_P029821	EH663694
41349	487	39	181	GAAATGATATTCCCCTTGCTTTTGCATAAATTTTGGCATAATCCAGTTGTGTGTTGTCT	40356	A_95_P079305	BP527730
41352	487	42	731	AAATTAGGGTATGTAAAAATGCAGTATGGTGATGTGGAGGGCGCGAAAAAGGCGTT	40362	A_95_P023716	EB439602
41355	487	45	164	ATTGTTCTGCTGCATGATCGCCTGCTAGAAGCAGTCAAGTTTCTTGATCTAGGTGATG	40368	A_95_P050141	FG623870
41362	487	52	438	GGTCTTATAGTGAAGAGGTATTTATCAATGTATGAGGACGATTTTAAGTCATCTTGA	40382	A_95_P221112	TA21752_4097
41364	487	54	2235	GCCATTTTTTGAGAATGGCAGTTCAATGTAGGGTATAATTTATTGGCTCTTTTGGTTT	40386	A_95_P034718	AY519499
41365	487	55	573	CAAAAGGGGATGCTGTTAGCACTTGTCTTTTGAAAAAGGTGTATTCATAGACTTGAAT	40388	A_95_P021881	FG634262
41370	487	60	574	GATATCCAACTTTTTTCTCTTTAATCTCCTGGGACCTTTTCCTGCAACTCAAACATATG	40398	A_95_P290923	DW001932
41377	487	67	866	CTCAGCCAGAGTTTGTCAGCTTCAGAAGTTTGGAAGTCACATATGTCACTATAATAA	40411	A_95_P265016	EB678047
41384	487	74	838	CATCATCGTCTACTCTGTTGGATGTTGTGCCTTCAGAAACACCAGGCGTGACAATTCT	40424	A_95_P126277	EB425538
41387	487	77	726	ATGTCTCCTGTACTGCAATATGATATTCTCCTCTCCTTCATAATAAGAGCGTGTTCTTG	40429	A_95_P022001	DV158073
41388	487	78	91	TTCATTTTCACTGTTCTTGAGCCGAGTGTCTTTTGGAAACCTCTCTACCTCCCTACCTT	40431	A_95_P034608	AJ937840
41390	487	80	0	CTCGCTTTTGGTGTACTCGTTTAAGTTTATCAATGCCCCAAACAAAAAGTTGGCGAGC	40435	A_95_P231244	A_95_P231244
41398	488	3	635	TTCTCAACTGTTTGGAAGCCCCGTTGGATGTTGACATTAAAGGGTGGTGGAAAGGTT	40286	A_95_P160882	FG146492
41402	488	7	1943	GCCAAATGTGTACACGAGTTTGTGCAGTTTAATAGTTTATTGAGATCCAAAATTAGTT	40294	A_95_P030136	TA15301_4097
41405	488	10	666	ACCAGGTATGAGGGATTTTACGGCCCTGCAAGGACTGTTGCAACATTTAGCTTATCT	40300	A_95_P129207	EB428925

41406	488	11	1782	CCCAAAGTGGAGCCGAAATGTTGAAAAATTGCAAATGTTTATTTATTTCTCCCTCATG	40301	A_95_P016106	TA13404_4097
41407	488	12	1142	ATGACGTTATTCTTTGGTTAATAATGACGGCCCTATTGCGCTGTCCAAAACTAGAGTG	40303	A_95_P237959	AF098636
41411	488	16	408	CACTAAGAATGCTGTTCTTTCGTGTATTTTGGTCACTCGGTCATCTTGGGACTCTCCTA	40311	A_95_P088248	BP529995
41412	488	17	526	ACTCAGTAAAGTCGTTTCGTATCTTTGGCTGTTTTCTCAGGTGTAGCTGTAATTCAAA	40313	A_95_P141452	EB445175
41413	488	18	526	ATTGTAGTAATGACGCTGGTTGATACAACCTTCACAAGTTTTTACCATATTTATGCTG	40315	A_95_P033564	AJ632843
41415	488	20	600	GCGTGTTGAATTCCGGTACATGTGATGTTTGTGTTACATACAAAGTTTATCTAGTAAA	40319	A_95_P039571	BP129587
41418	488	23	555	TTAAACTAGAAATGTTGGAGAAAGAAGTTCCTTGGTCGCTGCATCATGTGGGCTCTT	40325	A_95_P051806	BP132745
41424	488	29	530	CCAACGGTAGTGTCTCATGATCAGAATGCACCCCCAAATATTCAACATCAATTTGGAG	40337	A_95_P275738	AM782816
41429	488	34	411	TTACTGCTTCAGCTCCTTATCAGCCTCTTGGATTTGGTACTACTGGTGGTAAGCAAAT	40347	A_95_P150222	EB426566
41431	488	36	261	TAAGCTCTTGCATAGTTGGTCAATCTGTCAATTGGATCAAACATAGTCATTTTGTTAA	40351	A_95_P089753	BP530639
41433	488	38	381	GGAATCTGTGAATAGAAGGTGGAATGGTGGATGTGGTGTTTATTTGATTAGACATTT	40355	A_95_P094828	BP532890
41435	488	40	547	GATTCTTGTTGATTTCTCTTTCCTTGTTTGTAATGCAGTAGCTTATGCTTGTATAGTGG	40359	A_95_P003126	TA12166_4097
41441	488	46	713	CTATAGAACGTGTGCTTTCCCTTATCTTCTTTAACATTTAAACTCTGCCTCTGTCTTAG	40371	A_95_P180547	DV160233
41442	488	47	1266	GGTCCAGTGTTGGATGGAAACCTCCATTTGTCGAATTGAATAATTTGAGTTTAATTTT	40373	A_95_P011586	TA14882_4097
41452	488	57	482	CACGATTAGTTTGTTGGTGTCACCTGCAGATTTCGCTTGTTAGTTTAAATTTTGTTTAC	40393	A_95_P187842	EB678761
41453	488	58	213	CAAAGACTCCAGCTTTTGCGTAGTTGGTGACTTGTACAAATAGATATTGTATATCTGT	40395	A_95_P096323	BP533575
41454	488	59	864	ATATGAGCTGTTATACACGGGAAAGTTGCACTTGAATGTGGCAATGGAGTATTATAG	40397	A_95_P217287	TA20900_4097
41455	488	60	905	GCCTCTTGTTCAGGGTAGCCTTAGATTTATAAAAGCTCTGTTTATGTATTATTCAAAC	40399	A_95_P139412	EB443156
41456	488	61	481	GTTGGGGTTTCGGATGTTAATGGTTACAACAGACAGTAAAAAAGAGAAGTTATATTT	40401	A_95_P143292	EB446641
41464	488	69	242	CTTTGCGAGCATCATTTCCATCTGAGAGTTTCTTCACTTGTACATTCAAATGTAATATT	40416	A_95_P131262	EB431415
41465	488	70	874	CGTATATTTACATGGGCAGCAGTTGGACTCACAATTGCTATACTTGTACTTCTGTTAA	40418	A_95_P194902	EB426141
41468	488	73	835	AAACATTGGCTTGGTACAAGCGGAACTAAGGTCCATAGCAATGTTCAATCTTCAAAC	40423	A_95_P183087	TA13376_4097
41470	488	75	879	GTCCCTTTCTGCAAAACACTATGATATGGGGAACTATTGTGTCTATGGCGCGGCTAT	40426	A_95_P201992	EB432490
41474	488	79	632	TAATGTGAAACATCCACGAAAAGAGTCGATGGATGGATGGAAATAGAAATGGGATT	40434	A_95_P157027	EH615077
41476	488	81	835	TTGGAAGCGGTACATATTGCAGCGAATAAGAACACTGTTCCTGGAGATGTATCTGCC	40438	A_95_P246752	DV999084
41480	488	85	3027	GCGATTGTGTATATAAAGGAAGAGTAGTGACGAGTTATACTTGTAAAGGCATTTTG	40446	A_95_P134537	AB095098
41481	489	1	1424	CAGTTTACGTGCTATGTAATGATAGACTTGGTGTCATTGTGCTTTATATTCCTCTAGG	40447	A_95_P180982	TA12869_4097
41483	489	3	515	ACAATCAGGTATGCTTCAAGTCCGTGTATAATTTCATTTAGGCTTCGCTCTTGGTTTG	40451	A_95_P043406	BP130608
41486	489	6	731	TACTAATACGAGAAGAGGAATAGAACAGAAGATTCAGATGACTGATTCTTCTTCCAG	40457	A_95_P149857	EB679817
41487	489	7	687	ATACATGGGAAGAGCAGTCAGAGATAGATGTGGCTTCAGGATTTTACGTTCTCTTCG	40459	A_95_P287398	FG199342
41490	489	10	1245	CATGTAGTGGTGAGAAGTGTCAGGTATTCTGCATTTTCTGTCTTTTTAATTTAGCTTT	40465	A_95_P030926	TA16714_4097
41494	489	14	1021	CCAATAAGTTTCGGCCTTTTTGTGTGGAGATGTTTAGTAATAATACTCCCATCCTTAT	40473	A_95_P187372	TA14332_4097
41495	489	15	198	ACAGCACATTGCAGCCTCGCTTTTATGATCGATTAAAAAGGTATGAAAGTGTTCCAA	40475	A_95_P134697	EB437371
41501	489	21	930	ATAAGACGAGAAGTGTCCAGACATCAATATCGTTGTGCACATGCTCATCGATAGAAT	40487	A_95_P292093	EB426389

41502	489	22	717	AAGGAATTGACGGTGGAGAAAGCCGTTCAGAATTGGATCCGAAAAGAAGGAGACA	40489	A_95_P292868	FG194353
41503	489	23	915	CTTGGCAACAAAACTATGCTCTTGTAATTGCTTTGTATTTGTAAATGCAGCTCAAGAC	40491	A_95_P220242	TA21567_4097
41508	489	28	325	CTAGATGAAGATTGCCCGTGCTATTGCACAGGCCCAACATATTAAGCATTCTGCTTGT	40501	A_95_P099323	BP534885
41511	489	31	1487	CGAAACTTTGTGGTTTTGAGTAATGGATCAGTGACCTTATCACCTAAATGATAAAAA	40507	A_95_P191667	TA15285_4097
41513	489	33	811	ATTGCGAGAGGGAGATATGGCTCTTCTTGATATGGGAGCTGAATACCTCTTTTATGG	40511	A_95_P128277	EB440534
41519	489	39	556	TGCCGTTTTTGACAATAGTAGTTCCAATGCAATAGATCTTGTTTTGTTGGCTATTGAA	40522	A_95_P177067	TA11869_4097
41522	489	42	953	GCTTTCAGGCAAGCAGTATGTAGTTTAGACTTGCTAGACAAATTTTTAGGTTTGTGTT	40528	A_95_P007641	AJ012662
41524	489	44	637	TGTATGAGTGTACCTTGGCTGTATTTTAACCAAGCTTTCCCCCTTCACTCTTTCCATTG	40532	A_95_P157532	EH615585
41527	489	47	371	GGGACTATAGTCGGATTAATTCATTGTATGGTGATTAATTTACAGAGTGACATTGTC	40538	A_95_P109117	CV019156
41528	489	48	794	AATTGTGAATGAAAGCGGTAGTTGTAATTTCTAGGTTTATTTTCAATTCCCAAATCCC	40540	A_95_P126207	EB425456
41529	489	49	724	GCTCGTAAAATTGAAGAGCACTGCCGAAAATATGAGCGTCTGAGACAAGAGAAGAA	40542	A_95_P014186	TC65246
41531	489	51	712	GTACAAGCTGTGAGATCAAGCAGTTGATTCCTAATTTATGATTAAGCATTTGGTACGT	40546	A_95_P222612	TA22071_4097
41532	489	52	1674	GTGTTACTGTCAGAGTTTGTCATCCGATTTCTGAATGTTAATAGACTATTTCGATTAT	40548	A_95_P014536	X63195
41535	489	55	828	GCATTTTTTGGCTATCTCTTTGGTAAATGCTTAAGGCGGCAGAATCCTTTTCTTGAGG	40554	A_95_P017306	EB680102
41537	489	57	514	ATACTATACATTTCTCTCTACCTTCGTCGACCCTGCAATTAGGCCGTTGATCGGATCAT	40558	A_95_P148692	EB678140
41541	489	61	802	GAATGATGATGATGTTATGTTTGTTGAGATATGGAAGGCCATTTCTGGAGATACTAC	40565	A_95_P246522	DV158084
41544	489	64	173	TATTTTATACTCAGATTGGACAGTCTCCTTTCACTTCTGCTTCAAGGGCGGAACTCGTT	40571	A_95_P092573	BP531866
41545	489	65	777	CACTCTATCGTGCTGTATATGATATACCAAGTTCTTGATGCTGTTCTTTTATGAATGAT	40573	A_95_P257374	FG144896
41546	489	66	484	GACAAAAGAAATATGGTTGCACCCGCTTTTGGTGAAGATCAAAGTGGAGGCACAGT	40575	A_95_P266101	BP532651
41551	489	71	1210	TGTCGACTACTTACCTAGGATTGCTCATGATGGATGGACTGGGGATGCCATTCTCTA	40585	A_95_P209247	TA19148_4097
41554	489	74	364	CCCGTAGTTCCTCTAGTATTATTAGCTGATGCTACAAAGTCCCAACAAATTAATATCAT	40591	A_95_P152647	EB682973
41561	489	81	329	CTTGTAATAGGTGGATATTCTGTATTAGAGGCTCATATTCGTGACACCGAATTCTATT	40605	A_95_P094093	BP532557
41562	489	82	803	CCATTTCCAGCTAATGCAGGACTTTATGGTTGTCCAACAACTGTCACAAATGTTGAAA	40607	A_95_P014776	TA18567_4097
41564	489	84	796	GAAAGAAGGAAGTTCTTACCACAAGATGAAGATCATTGATCGCTGCTTCTCTCGAAG	40611	A_95_P126747	DV162062
41566	490	1	688	TTTAGAGGAAGGACTTGCCATGATTGATGATGGTCACAGAGATGGCAGACGTAGAT	40448	A_95_P143672	EB446908
41568	490	3	709	TGCTTTACAGCTCTTTTCGTGTGGTTTGGTTGAGGAGGGTTCTGTACAAGGTAAAGC	40452	A_95_P136137	EB439760
41571	490	6	1381	CCTCAAGTGTCAAATTGTTTCATCAAAGCAAAGTATTGCTTCACTGTTTCAGAAGCTT	40458	A_95_P007766	TA12022_4097
41586	490	21	198	CCCGACATTGACAAACTTCTTTGATATACCAATTTGGATGTAATCGTGGTTCATTCTTA	40488	A_95_P306578	FG635672
41603	490	38	785	GTTGCTAAGACCCTTAAAGCAGAATGATTAAGAGTTCTGCTTCATGTAATTCCAGTAT	40521	A_95_P015641	EB684169
41610	490	45	697	GGAATGAAGCTGATTTTATCAAGGTTAGTGATGATGAGGTAAATTTCCTGACACAAA	40535	A_95_P128327	EB427949
41614	490	49	382	CCCATTTCCGAAAACCATTTCCAGACATAAACACTTGGAATGTCAATTTCTCAATATAT	40543	A_95_P186722	TA14187_4097
41615	490	50	858	GTATTTGTTTATTATCTTGTGTCACATGAGGCTCCTTGGCAGTCAAGGTAGTTTAAAT	40545	A_95_P194267	EB449400
41616	490	51	23	CTGCTCTTAAATGACAGAGGCAGAGTTATACAGCAATGACTTTTGTCATTGAAATCAT	40547	A_95_P031671	EB431956
41618	490	53	995	CCTTTATGTGATTTTATTTGTACTGGGTGATTGATTATTATCGTGCTTGCGTGAATGC	40551	A_95_P016361	TA13241_4097

41621	490	56	659	GGTAAGAATGGACTGAAGCCATCTCATCGACATTACCAGGCTCATAATCAACTAAAC	40557	A_95_P037836	BP129106
41629	490	64	1587	CATCGATTGGCTTAGTACGGTTTTGAAAGATTTTGGTTGTGTATTTTCAGTTTCGGTTT	40572	A_95_P008481	X84226
41637	490	72	730	CCATGTGTATACATTACAACTTGTTTGGATGGTTGTTACCCATTGTATCGTATTGTATT	40588	A_95_P011726	DV160318
41641	490	76	120	CGTCAACCTAACGAGCTAGTGAAAATGGTGGATGTATGTAGATGGAATTCATAATAA	40596	A_95_P099013	BP534731
41651	491	1	687	ACACTCATTTTGAGCTGGCCAGCTTTGCGAGATAATGAAATTTTCTTGAATTTGGCTT	40615	A_95_P258366	EB679246
41653	491	3	1188	TCCCATCCCCCATATTGTTATAAGGCATTTAATTACCTTCTCTTCATCATTTGAGAATA	40619	A_95_P002186	AY695053
41654	491	4	521	CGTATACGGGAGACTTTCCCTTTAGTAGTGAAATTATTTACCTTTTCCTGGTAAATTTT	40621	A_95_P299453	FG637388
41658	491	8	445	CATCTAAATGGACGAGAATGTTGCTGTGGCTTTGTTTTTGAAGTGTCCTAGTTTTTGC	40629	A_95_P008726	EH617354
41660	491	10	792	GGAAACTGTTGGAAGTCTGTTCCTTGTTTTTTGTTCTTTCCCTTGTCTTTCTGTTGTTG	40633	A_95_P186672	TA14176_4097
41661	491	11	1439	ATGGAGGAAATTTTTTGCCTCTCCATACCAAAAAAGATTCCACTTGCTGCCTGTGATT	40635	A_95_P007046	TC45426
41663	491	13	412	GTTTAGACTGGTAATCTTCGATCGAGGGGTTTGAATCAGCTACGCGTGATGGTGGTA	40639	A_95_P004851	EH664946
41665	491	15	167	GCTAGAGGTACTTGGGAGATTTATCAGTCTTAAAAATTTGGTATTGGATTGTTGGAA	40643	A_95_P192052	TA15370_4097
41666	491	16	821	GCTAACTTGCAGGGTGTGGAATTGAAGACTCAGGATGTTGCTAATGCTGTGCTGTTT	40645	A_95_P226994	EB425577
41668	491	18	884	AACTCCAGTACTGTACCTGCTCTCCTGCTATTCTTCTTTATGCTTTTGTAGAGGTTTT	40649	A_95_P019691	TA13952_4097
41670	491	20	238	TACCGTTAAATCTTCAATATGAGCTTCTACGAGGACCTCTCTACTGGAGAAGTGGTG	40653	A_95_P113487	CV021161
41674	491	24	514	TTGGGCTAATGGGCTTGGGTTTGTAAATCTGTGTATTCCAAAATAAGAGAAAGTGAA	40661	A_95_P308698	FG643338
41675	491	25	304	GACTTCATGAACTCATTAGAGACTCGAAGGGACTGAGGATATATTATGTTAATACAT	40663	A_95_P027426	EB429409
41679	491	29	208	AGAGACCTGGTCATTGCTGTGTGTGTTTGCTTATTTTATCAAAGCACTGTATTTGCTT	40671	A_95_P112182	CV020560
41682	491	32	684	CAAGCACAAGCACTTCACGGAGTAGTGATGATTGCTCAAGAGATATGATCCTTATCG	40677	A_95_P015151	TA12653_4097
41684	491	34	592	GAAACTGATTTTGTTCAGGTGTTATTACCTTTACACTATGGAGTTTTTGCGGAATTCT	40681	A_95_P228074	FG634396
41688	491	38	754	GATAGAGCCTGCTGGAGTGAAATAATGCAACTAGTTGCGTTGAGTCTGGTTTTACTT	40689	A_95_P304688	FG136427
41692	491	42	298	CTGTGCACCTTGCAATTGTTAAGATAATTCTCTTGTTGATTCCACAATACATGTGTGT	40697	A_95_P176542	TA11634_4097
41698	491	48	606	GCTGTATAAAGCATTCTGTTTTTATGTAGAGTTCAAGAAACGACGCACTTGTGAAAAT	40709	A_95_P252434	EH621105
41699	491	49	730	CATACTGGATGTATGTTCCCAGCTTTGGTTGTTAGCTTTAGTCACTTATAGTTGTTTTA	40711	A_95_P291303	DW003703
41703	491	53	381	TGCACCATTTGTCTGTAGATTTACATTGTTCCATTGGTGTTTGGTCAGTAGATTCTCCT	40719	A_95_P220697	TA21662_4097
41704	491	54	1421	GTTGTTGAGGCACTCTTGTCGTGTTCTTTCTTTCTTGTTAAACCAAGTCTTTAATCTCT	40721	A_95_P203137	TA17789_4097
41712	491	62	1219	TGTTATATTCAAGTGACGCTGCTAACTCCCCGAAACTGGAGAGATAGCTCTATTTGTC	40736	A_95_P025051	TA14701_4097
41715	491	65	363	TTTCATTTGGTGGTACAAATTTGTAGTCTCGCAATCCAGTCGAAGTCAAGCACTCCCT	40742	A_95_P210032	FG625993
41718	491	68	739	GATGTCGGGCTATGTTTATTCCGCAAATTGTACTGTTTCACTATTTTCTTTGGGATTTA	40748	A_95_P207947	DW000106
41723	491	73	665	TGGTGCTTGCTAGATACATGCAGGTATTGTCTGGAGACTTCTTAAAAAGCTATAAGA	40758	A_95_P306008	FG633724
41731	491	81	914	CTTCCCATGCAACCTCTGTTGTTACTTATGGAGTAGTTTGTATTTATGCCTTTTATTAA	40774	A_95_P023896	TA14103_4097
41736	492	1	504	TCGTTTTCTGTCGCAATTTCTTCATTTAGAGTTTGTCATCAAAAGTTGTATTTGCCGGT	40616	A_95_P139572	FS411114
41737	492	2	1237	CAGATATGCTTGGTTTCGTTCATATGTTTTGGTTAACCTCTGATCTGATATGCTTGTTT	40618	A_95_P205092	TA18206_4097
41738	492	3	493	AAAGAGAATCTCTTGCAGAATGTCTTGAGTGCTATTCCCTCAGACCTCAACAGAGAT	40620	A_95_P079780	BP527846

41740	492	5	1497	TGTCAACGAGATTCTCATGCTTTTGCTGTAGAAGTGGATTAATTTATAATGGGTTCTC	40624	A_95_P002621	AF012823
41741	492	6	815	TGCAAGACCACTCTGGCTGATATTTACTTCATTCAATAGCACATCCCACGTTGCTGCG	40626	A_95_P192612	TA15489_4097
41742	492	7	537	TCAAGCTACTAGATCAATGCCCATGTATATATTTTTCCAGCTATTGGGTGGTTCTATTT	40628	A_95_P139617	EB443423
41744	492	9	731	GTTGAGGACTTCTGTGACTGTCAGTAAAGTTTTTAACTGCGACATAACCTAGATTTAT	40632	A_95_P159907	EH618453
41745	492	10	723	GGGGAGGCTAGAGAGCCTTTGCTTTAGATCCCAAAAATTTTAATAGAAGATTTTATG	40634	A_95_P203467	TA17859_4097
41749	492	14	786	TTCATGTTCCTAACCTTTCTGGCTCTTCCTCGGCGACTGCTTGACAAATATGCTCTATG	40642	A_95_P287118	FG166026
41758	492	23	320	TGCTGTCCTTCTATTTGGCTGTTCAAATAACCGTGTAAGTCTCCTAAATAAACAGAAT	40660	A_95_P090393	BP530935
41759	492	24	616	TGTAATGCTGTCTTGCAATTACGTTCTTGAAGTTTTCCTCATCAAACAAACTGCAGGG	40662	A_95_P248567	FG643712
41763	492	28	850	CAAGGACAACGGGTTTTTGTGAAATGCCACTGTATCATTTTTTCTCAACTTGAATTCA	40670	A_95_P179877	DV158142
41767	492	32	433	CCACTCAGGTTTTTACGACGATCACTAATAAAGCCTAAATCACCAGAAAATCTATTAA	40678	A_95_P076265	BP526939
41769	492	34	314	ATTGTACATGGTGTCTTTTGAGAAACACAACCCTGTATAGGACTGATCAAAGTGCTA	40682	A_95_P188213	TA14520_4097
41772	492	37	757	AGATATTGATGGGCATCAGTTGAATTGTAGCTAGCTATTGATGGGAGAAAGGGGGA	40688	A_95_P308458	FG158665
41775	492	40	578	GATGATATTTCCCAACACTTGTCTAACAATGTAAGAATCTTAAGCTAACTTCCATAGT	40694	A_95_P008321	EB683976
41778	492	43	702	CCCTTATGATGTGTGGAATGCAACAGGTTAATGTTTGTTTTCCCCATATTTATCTCTG	40700	A_95_P300923	FG185895
41799	492	64	1429	CGATCTTGCCGTTACCCGATTCTCAACATATAATACTGTTAATATCTCATAAGATCATA	40741	A_95_P205667	TA18338_4097
41800	492	65	461	GGGAATAACCCATAAATATCTGGAGTCTGGTGTTCAACTTTTATGTAAGCATTTTCTA	40743	A_95_P088623	FG639451
41801	492	66	684	GAGCAGTGACTGCCTACAAATATTGGCAAAAGAGAAAAAAGCAACAAGATCAAGCT	40745	A_95_P127067	EB448422
41802	492	67	268	CTTGTGAGTCAACTGGAATTTCATGTGTCTTAACTGATTGGACTTTTACTCTGTTTCAT	40747	A_95_P129752	EB429706
41803	492	68	735	ATGCATTCTGGTCTATTTTCATTGCTGCTGCTGTTATGGGCCTTGTGATTATTGGGCA	40749	A_95_P189142	EB424654
41805	492	70	468	CAGCACGTTGATTAGGGTTGGTATCACATTGGTGCTCTTTTGGATTGTATGTATTTCT	40753	A_95_P085945	BP529418
41806	492	71	516	TCTCAAGCTTGGGTCAAATGGTATGTTTTCTTTTTTGCATGTCTTCTCAACTTTGTTAC	40755	A_95_P231959	FG643750
41807	492	72	308	TGGCAGCCTTCTATATCATTTTTGGCAGCTCTACTAGGAGCTATATATTCTAGCTAGC	40757	A_95_P108372	CV018807
41810	492	75	756	AGGAATGGTTACCAGGCTAAATTTTAAAACGGAACAACGCCAGGCCCTTACCAACAC	40763	A_95_P094188	BP532594
41817	492	82	678	CACAGGGAGACCTTAGGTTGAAGATTGAGAATCTTGCATCCTCACTCAAGTTTCCCC	40777	A_95_P220932	EB441014
41819	492	84	599	CGGATTCGGAAAATATTTGTTTCTTGTAGAGTTACGTTGGTGTTAATTGTGAGATAA	40781	A_95_P061130	BP135186
41823	493	3	692	TTTTGTGGTGAAATTCCCCAATGTAGTGGTGTTCATGAGGTATCCAATTTACAGTCGA	40788	A_95_P028146	TA17198_4097
41829	493	9	284	GAAAGGAGGTGTATTTGTACATATCCTTCACTGGCATAAGTTCAGTCCCATGTGGAA	40800	A_95_P035713	BP128546
41830	493	10	672	TAAGAGGCCAAGTATTGAAGAAATGGAGATGTGTGAGGAGTACACGTGTGTGATTT	40802	A_95_P306618	FG635755
41832	493	12	714	GTTCCACTTGTTGCTGCTTATGTTTATCGCAGGATGTACAAGAACGGCAACACTATAC	40806	A_95_P128837	X84226
41837	493	17	656	CATAGTTGGAGTTGCTAATGATCACTGCAGCAAGCACCTCCTGTGGTTAAAATCTTTT	40816	A_95_P293513	EB435122
41843	493	23	809	TGTATTGGTGAATTCTGTTCTTGTTTTCCCCCTAAATGGTTTTATGGGGGCTTAATTGT	40827	A_95_P194092	EB425719
41844	493	24	667	TATAGCTGCTGTTTTCACTATGTGCTTCTACAATTAGGATATTTAAACTTGCTCCAGCT	40829	A_95_P303093	FG644018
41845	493	25	186	TGACATACATGGTTTGATCTTGGTGCCATTTAGCTTCTTGCTGGCCTTGTAAGTGCTG	40831	A_95_P033914	AJ717885
41846	493	26	441	GAGGGAGCAATCTTTAAGGTTGACCTTGATATATTTGTATTCATTGCACATACGGAA	40833	A_95_P008306	EB434574

41849	493	29	494	TTTTTTCCCCCAATTAAAATGAGCATAATGTGATGATTACCCTTTGTGATGCTCTAAG	40839	A_95_P286478	FG638507
41851	493	31	407	TTGCCAGTAGATGGCTAAGCGATTCTTCCATATTTTACTTTTGTCCTTTATCTTGTTGG	40843	A_95_P274968	AM839082
41852	493	32	732	GATATCACACAAGAAACTATCTGAGCTAGGGGTTACCCCAAGTTCTTGGTTTCCAAG	40845	A_95_P162487	EH621443
41854	493	34	712	ACATAAGATTGATGAGAATGTAGCAAGGGAGATCATTAATCATAAATCACTTCGACA	40849	A_95_P139097	AY081175
41856	493	36	706	ACGTCTTCTGCGTGATCTGCGTGTTATGGCCTAATTCAGACAATGCTTTCCAGTGATA	40853	A_95_P156557	EH614280
41860	493	40	734	GCCAGTGTAATTTTTAGCCATTATTGTATGTACCACTAGTTCCCTCCATAAAAATCTTG	40861	A_95_P012581	TA14608_4097
41863	493	43	618	GGCTATTGTATGTTGCCAATTGTGATATTATCCGCGATTTCACTGTTTTTGCCTGGT	40867	A_95_P305623	FG633903
41867	493	47	1125	TGCTGCACCTATGTTAGATGGGTTGTTGACATCCATTTGTGTTAGGTGGTAATTAAA	40874	A_95_P020151	TA15207_4097
41870	493	50	622	CCTTATATCCATTGGCATGTCTTGAATGGTATGTCTGGTAAGGCAAAGAACTGGATTT	40880	A_95_P246137	TA12645_4097
41878	493	58	523	CTCCTTTGTAATCTTGTACCATCTCAGAAGGATGATTATATGAAATGTTTTGTCTGCTT	40896	A_95_P123967	DW003823
41880	493	60	624	AAGAACATCTAGAGATTTTGGAGTCTGTCTCAATGGCGGTTAGTAGCTTGCTCGAGT	40900	A_95_P278608	FG639919
41882	493	62	741	TCTGCAGCACTCAACAATTTTACGCAACATGTAAAGTTTCTCCCCTATATTATGATCTC	40904	A_95_P207347	EH615646
41889	493	69	323	ATGTTTGACGAAACGATTTGGAGAACGTTCGTAGAAGTAGTAGATTGAGTTTGAGG	40918	A_95_P124842	AM824464
41895	493	75	445	GGCTTGGTAAAGTAATGTGTATGGGAGTAACAGCTGGAGCATGTGTGCTTACCTTGT	40930	A_95_P152107	FG135146
41900	493	80	549	GCTTAGAAATCCTAGGTATATTATCCAAAATTCTGACTGGGTTAAGGATTTGTTGCAT	40939	A_95_P241320	FG193095
41901	493	81	825	ATATATTGTCATATGCCGTTTCCCGTCCATGCCGATTATTCTTCTCTCTGATGACTGCC	40941	A_95_P287658	FG155231
41903	493	83	827	AGACTTGTACTGTATGCTTTCCGGATAATGAGTCAAGATTTGGGTTTTGGTGTTTGCT	40945	A_95_P200812	TA17289_4097
41912	494	7	718	CGTTCTATGGTTGTCAATCATTTCGAAGTGATTTAGCTAATAACCTTCTTGTTACTTGT	40797	A_95_P211457	TA19614_4097
41916	494	11	1000	GAATGTAAATTTCCTAACCTTCATAAATGGAAGAGGAGGTCCATTTGTTGGCATCTGT	40805	A_95_P204172	TA18009_4097
41918	494	13	0	GCAAACAAGACCATTTAAGAAACGTGTCACCTTTTTGTTTCTTCAAGATTAACCTGTA	40809	A_95_P027131	A_95_P027131
41920	494	15	273	ATGACAAGGAATACGTGGATGCTATAATGGAAGCAAGTAATTGGGGAATGACATCA	40813	A_95_P070045	BP192506
41926	494	21	474	AATGAGAGTTGAGGTGGAGTTGGAGTAGTACTTATCAATAAGATTTATGTTTCACAT	40825	A_95_P187387	TA14335_4097
41927	494	22	879	CTGCTCAGAAGCTTGACGTGAATGCAGCATCTATAAGCAGTCCTCAGAAAACTAAGT	40826	A_95_P012241	EB681339
41928	494	23	523	CACAATTAAGAGGGTGGGAAGCATAATTGTATGTCTCTGTTGCAGCTAAATGTTCTCT	40828	A_95_P100663	BP535477
41929	494	24	190	CAAGTACAATTTCCGGAAGTTCAAAATAAAGTATCATTGATGTTGCACAATTTCTGGT	40830	A_95_P154767	EG649751
41930	494	25	478	TCTAATTTGAGTTATCCCAATTGGAATGTTACTGCAATGTTATTTCTATGCGGTGGTT	40832	A_95_P021521	TA12506_4097
41933	494	28	475	TTGACATTATTGGTTAAGCTTCAACCTAGGTAGAGGAATAAGAAACCGAGACTCGGA	40838	A_95_P057936	BP134343
41934	494	29	256	GAACTTGCCGGGGTTGAGGCATATGTGTTGTTGTACACCAGTAATGAAGTAAAGAC	40840	A_95_P098203	BP534363
41941	494	36	755	AAACTTTAGCAATGGCCACTAAGCAAGGATAACCTTTATCTTATGCTTGGTTAGTGAC	40854	A_95_P223642	EB450831
41943	494	38	676	GCCTCCTTTTGCTGTTATGAAGTCTTGGTTTAATGTGAAGCTCACGTAAATTGATGCA	40858	A_95_P026441	TA15577_4097
41944	494	39	204	ATTAGCGCATGAGGCACAAGAATTGATTCTGTATATGCTCAGTCTTCTTCTGATGGA	40860	A_95_P105582	CV017530
41949	494	44	764	GTATTTTGTTTGCTTGGACAGTTGGAATCCTAGTTATACATCTCAATGTCTTTTATGCC	40869	A_95_P012891	TA13215_4097
41955	494	50	816	TATTTGGAGATCAGAGACTTCTACTGGGATTCTTCATTGATAGTGCGTGCGGTCATG	40881	A_95_P310028	FG161371
41958	494	53	192	CTGTGCTGCTTCATATGCTATTGGCTATTCCGAGAATTCTATTTGAAAACAAAGAAGA	40887	A_95_P033274	AJ344596

41960	494	55	240	ATGCTTACTCATTTGCCAGACACCATTGGATTTGAGCTTATAAATCTCAAGAAACTAT	40891	A_95_P092438	BP531801
41966	494	61	732	AAGATCCAATTCCAGGTTTTCTGATCTCAGACCATAATGCCTCCGCTGCTACCTTGAC	40903	A_95_P137862	FG137204
41967	494	62	371	GTCTATCATTGGCCAATTGAAGGTGATACTGAGCCTGTAAAGATGTTTGATAGAACA	40905	A_95_P085095	BP529195
41969	494	64	539	ACTATATGCTAGTGAAGATGTAATTGTTAAGCCTGCTTCATAGTGTACGAGCTTCTGC	40909	A_95_P001286	FG628825
41970	494	65	702	ATCTGTCTTCTTGGCTTAGAGTTCTCGAGATATTCGACTTTATGATGCAGTTATTAGG	40911	A_95_P304013	FG636664
41972	494	67	381	ACATGGCGATCTTTTTCCTTTCTTGAACCCAGTTGATTCCTGCTATGGCTCTTTCTTCA	40915	A_95_P281183	AM789543
41975	494	70	457	GTTTCTCCATCTGATATATATTTCTGTAGTGTGATTTGGGGTGTAACAGAAACGTATC	40921	A_95_P005456	TA11650_4097
41982	494	77	444	TATGCATGGTTGAATATCATCTGGAATGATCCTTGGATTGATGTGTATCTGAAAATCT	40934	A_95_P135912	EB439462
41994	495	4	1412	GGCAGTAATGCTGCTCCAAATTTTGCAGTAGCACATTTTGTTTTTCATTTCCTAATTCT	40956	A_95_P239959	X79004
41998	495	8	248	TTGCACGGGTTTGGAACTGTTCAAGCATTGCTTTTTATTCGAAGATGTTCTTGAATGT	40964	A_95_P133777	EB435463
42004	495	14	172	TTTCCAGAAAAGATAGCCGGTTATTCCATAGCTTCCGTCCAAGAAGGGTGAGGTAAG	40976	A_95_P093988	BP532514
42005	495	15	2327	GTTTTACTGCTGTAGGGTATTATTCCAGGCTCATTTTGTTATGACGTTTTAGGTTAAT	40978	A_95_P013031	TA11872_4097
42006	495	16	906	GTGAGGCGCGACCTAACAAAATATTGGATTATCTTTCTTTGGTTACGTTTGATGTTAA	40980	A_95_P004011	EB447510
42009	495	19	879	GCAAGTCAAGTGGACATAGTAGTGGTAGAAGTGTACATGAAGCTAGGTCTGGATAC	40986	A_95_P225292	EB425084
42014	495	24	783	TAGGGCTCGATATTCCTGTAACATATACTGATGAAAAATGAATAGCAGCTTGGTATT	40996	A_95_P293698	EB437163
42015	495	25	232	CTATTGACATACTGGTGCTGGAATTGTGAAAATGAACAGCTTAGTTATTCTTTAGCCA	40998	A_95_P159147	EH617100
42017	495	27	699	GTGCTGTAATTGGTATTAGCCTGCTTCTACCAGTTTATGTTTAATCTTAAGACTATGG	41002	A_95_P000171	TA11676_4097
42019	495	29	726	CTTGCAAAGTCTTACATCTTTGAAGGAAGGTTCGTTATGGACTTTTTGACAGTATAGA	41006	A_95_P016386	TA14662_4097
42021	495	31	330	GATAAGATATTGGAGTATTAACAATGGTAGCTGCACAAGAGTGTTCAAGGGTGGGA	41010	A_95_P032031	TA16107_4097
42022	495	32	622	ATACTACAATTGAAAAGGCCTTCTGCCTCCGTATTCCCCTGGTCCTCTTTCTAGAAGC	41012	A_95_P098503	BP534506
42030	495	40	685	GCAAGACAGACCATATTATCCATCAATGGATCCACAAAGGATGGGTGCCCTAGTTCA	41028	A_95_P135572	EB439075
42031	495	41	744	TAAAATTGTTGTCTCATTTGCAAATTTCGATAGGACCAGCCAATTATTATCCCGAATT	41030	A_95_P212822	TA19917_4097
42032	495	42	798	TAATAATCTTGTAAGACATGGACCACTAAAGCTAGTGACGGGTGGACACCTCCGCAA	41032	A_95_P156427	EH613927
42034	495	44	187	TTTTGGAGTACGAATTGGCCCATGATGATGTGGATGGAGAGTGCTGCTTGTTATGTC	41036	A_95_P008761	EH663687
42038	495	48	385	ATATAACTTGAAGCTATGTGCTGATAGAGAGACTTACGAAGCCATGGATGCACTTGC	41044	A_95_P100248	BP535291
42041	495	51	980	GTCTTGCTGTCAATTGAAAATTTAGCCTAAATGGCATTGCTGAATAGGACAAAATGG	41050	A_95_P186827	TA14210_4097
42042	495	52	710	GTGTAGTGTCCTTGAAAAGGTCAGATCACATTGGATCTATTGTATGTAATCTTACTTT	41052	A_95_P126442	EB425762
42050	495	60	747	AAGCCCCTTCCCGGACGTTACGAATGGGTGAAAGTAGATTGCTTGATATGTCCTGTA	41068	A_95_P217372	EB681505
42054	495	64	814	CAGCTAGTTTTAGAAAATGAAGACATGAGCACCTGGTACACCAAATCTTTGATATAC	41076	A_95_P269506	EB424994
42055	495	65	687	TGAGGCCGTGACTTTGTCAATGTTATTATTGGTGCTGAAACTTTCTGTTGCTTTTTGT	41078	A_95_P204927	EB446634
42060	495	70	399	TTATACATGTGGACACCTTCTGGTGCTTATTGCATAAATGTTCCATTGCCTCAATTTGC	41088	A_95_P096063	BP533456
42064	495	74	414	TTGACAGTAATGTGAGTGAGCCTCAATGGTGCCGAATGAATTTTGTTGTTAGATGCC	41095	A_95_P005901	AM834148
42066	495	76	560	CTAAAGGGGTTTTTTCTGAGACTCTGAATTTTGTTGCAGTATTTAGTGATAACATTGT	41099	A_95_P118572	TA13353_4097
42067	495	77	766	GATCTTCCCCACCCATCTCATGGTGTCGCTTTGCAAAATGTATCCCATGAGGAGAAAA	41101	A_95_P310803	FG138225

42071	495	81	170	GGACACAATTTGGAAGTATGAACCATTTTGATGTTAATGGCATGGGCTTACTTTAAA	41109	A_95_P130392	EB430438
42072	495	82	798	CCTTGGTTTTTTGTTTTTCCCTTGTTATATAGAGGAAAGAAGGATGATAGAGTCATCA	41111	A_95_P126372	EB425717
42073	495	83	1453	CCCAGTGTAACAAACAGATGCCTTTTTGACACATTCAAGCGAACAATGATTATTTATT	41113	A_95_P217757	TA21009_4097
42074	495	84	434	GAGGACGAAAATTATGTATGTACTCGAGATTTTGATCCCAGCATCAGTTGTAGTTTA	41115	A_95_P152602	EB682928
42076	496	1	370	GTTCATATTGTTGATGTTCCCAGGGCATTCTCGTCTACGTCTGAAACTAGATGAGTTT	40951	A_95_P085560	FG633961
42081	496	6	424	GACATGTAGATGTATTAATGACTCTTCCGGTCCCTTTTCTCATCTGTGAAATTTATTAT	40961	A_95_P162672	EH621667
42082	496	7	778	TTACTCAGTTTTCCAATGCTATTCAACATGCTCTCAAATCATCTTAAACCGTCATGAGA	40963	A_95_P228409	EB678357
42086	496	11	348	AGAAGAACCCCCCACCTCTGGTTCTTTTTCTTTTCTTTTGTTGCATATGCAGGCATCCT	40971	A_95_P095233	BP533088
42088	496	13	387	TAGAAGGGCAAGAAATTCACCAGAGCAACATTGGATGGTCCCCTGTTTATGTTGAGT	40975	A_95_P146907	TA19979_4097
42091	496	16	417	TAGAGAGATGAAGCCTAACGTGTGGTTCGAACGGAGAGTTGTATTCCTACACTCTCT	40981	A_95_P071560	BP525733
42096	496	21	844	TGTTATACTTTTTGGTGGCAAAACTCTAGATCATCATGGTAATGAATGTTGAGACCAT	40991	A_95_P269606	EB425595
42097	496	22	570	GCAACATTGATAATAGTTGACTTGAAATGAAATGACTGACTACCACATTGTGGAGGC	40993	A_95_P125422	DW005212
42099	496	24	161	GAAATCCAAAGGCCCCGATTCTTCTTCTACCAAATAGTACAAAAATTAAATAACTACC	40997	A_95_P033549	AJ632828
42100	496	25	804	GAAAGGTAACATTAGTCTTCTGGATCTATGGTAATCCTGTATTAATTTTCTCATTGGG	40999	A_95_P116137	DV158711
42101	496	26	558	GAGAGAGAGACGATGATATTCATGATAGCAATAGGCAGATCTTACGAGTACCTGCA	41001	A_95_P052551	BP132952
42108	496	33	755	TGGAGTAGACTCTCAACATTTTTTAGAAGGAAATAGGCTTGCACACTTAGCATGTCC	41015	A_95_P237979	AF153278
42109	496	34	854	GGCTAGCTTGTTGTCTTTTGGTTTAACCCAGTAGTTAAAGTGACCTCAAACGAATTTT	41017	A_95_P224382	EB449788
42110	496	35	745	GATATTCCAAGAGCATTCCTGGTTGTGGTTTTAGTATATCCTTAGTGCTGCTATGAAA	41019	A_95_P001676	EH618501
42111	496	36	645	GTATGTCCACGTCGTGGTTGATGAATTTTGAATTCTCTTGCATTAAAGATGTTTTTGC	41021	A_95_P308478	FG642544
42122	496	47	808	GTCAAGACTGTTGGAAATTATGCTGCAGTAAGCTATCCTTATGGAGCTTTAATTTATT	41043	A_95_P011516	EB682378
42124	496	49	672	ATCTAAAGGAATAAGCAACTTGAGTCGTATAAATTCAATGACAGAGCGGACAGAAG	41047	A_95_P144682	EB448178
42125	496	50	334	ACCGACTTATGGCCCAAACCTCAGCTTTTAGAGCAAAACTTGTCCAGTCTCATTATTG	41049	A_95_P085510	BP529304
42130	496	55	876	AACTCAGCAAGCATCCAATCCTATACACACGGTGGCTAATAGTTTGAGCCTTCCAGG	41059	A_95_P011531	DV161576
42134	496	59	847	CAGAGAGATGAGCATTCTGATCTTCGACGTGCTGCTCGTTCGTTATGCATATAAACCT	41067	A_95_P251277	FG136377
42137	496	62	343	GGGTTAGTGAGGTTTGGAATGAAAAAAGGGCGTGACACAAATTATTCCAAATTTTAA	41073	A_95_P068745	BP137204
42138	496	63	679	CTTGGTGGAAACATATATGTCCTGTCTTTATTCCATGAATTTGGGATATCTTTTGCTG	41075	A_95_P210667	EB678572
42142	496	67	1169	TGAAATATTACCGTCGACAACTGATGCTCGATTCATGAGACGACTGGGAATTCCCAC	41083	A_95_P201247	TA17382_4097
42143	496	68	717	GTCGTCTTTTATACTTTCAATCCATGTGACATTGAAGCGCAAAGTATACTGAAGAAAG	41085	A_95_P003291	EB437101
42145	496	70	684	GGCTTCCTTTGTTCTCATGTCAATGATGATTGAAGTGTCATCAACTATGAATTGTGTA	41089	A_95_P215287	TA20451_4097
42153	496	78	466	CTTGTTACATCAAGTCATCCAGGGAAAAAGCTAATTTAGTTTGTGGTTATTCCATCAA	41104	A_95_P024111	EH623214
42158	496	83	938	CGGTGCTTGGGATTGTAATTCTTGTTGTGGCAATATATATGTTGATCAAGTATCTGTA	41114	A_95_P011086	TA15475_4097
42159	496	84	772	CATCAGTCATTTAAATTTGGTGGGATGAACTGTTGCTTTATTGGTCAACTTAGGTCTA	41116	A_95_P148302	EB677571
42163	497	3	773	TCCCTCAAAGCTGGGGAAGGTTCTTAAAGGAAAAGAAAGTAAGAAGAATGATTGGA	41121	A_95_P230199	DV158861
42169	497	9	1615	GGTGGCTCGGAAGTTTTGTTTGTTATGTTGTCTTAAGATACTGAATTCCGAACTTAAA	41133	A_95_P237919	AF120093

42177	497	17	284	TGAACTGTAAGAACTTGGAAACTTGCTGAAAGGCGAAAGCTGTTATAAATTTGGGTT	41149	A_95_P203307 TA17826_4097
42179	497	19	605	TGTATATTAACGATTGTAATTCTACTGAGGTCCTTGAAAGCAATAAACTCCTGTTGTC	41153	A_95_P020626 TA12820_4097
42188	497	28	380	GAAGTTTGAAATTCCCTGGTCAAGCTCCATGTGATTAGCATGTTTTTGCAATATTCTA	41171	A_95_P072675 BP526024
42189	497	29	734	GGAGGATACTTTAGCTCTGCTTTCCTTGTTTCCTTGATTTATAAAATGTCTAAAATTGG	41173	A_95_P191422 TA15234_4097
42191	497	31	377	AGAATGCTCCAATATAGGAATACTATCTGAGGATTTCTCTGTATCATATGCAAAGGAT	41177	A_95_P079350 BP527740
42198	497	38	526	CATTTTTCAAGTTTGAGTTTTGTCGAAGTCGTCGGTGTAGCTTCGTGGTCGAATTAGC	41191	A_95_P028366 TA19522_4097
42200	497	40	494	TTGGAATGACTGTGAACATGCCGGTAAAGAATGACTCTTGTTAATGTACTTTTTTCAA	41195	A_95_P211772 TA19686_4097
42201	497	41	766	CCTAACATTAAGATATGTGCAATGCTCCTTGTCTGCTTGTTTGTGTATGACATATTTTG	41197	A_95_P127902 DV161576
42202	497	42	1019	TTTCCTAACAGTTCTCCCTCTATGTGAAAGTAAACGAACTACTTGTAAGGTTATCTAT	41199	A_95_P141067 TA12884_4097
42203	497	43	108	GTGTTATTGAGGAGGAAACAGAAACCTGCACCCTACATCTTCCAAAAAATTGCCCAC	41201	A_95_P038326 BP129244
42207	497	47	144	TTAGAGAAGAAAATAAGGGGCTTCAGGCTCAACTGAGGGATACTGCTGAAGCTGTA	41209	A_95_P034334 AJ718475
42211	497	51	671	GAACTAGTTAAATGCGAATTATTTGGAACCTGTGTGTGCTTAAGATGTGATAGTTCT	41217	A_95_P012856 DV160997
42212	497	52	734	CTGCTTGCTGAATTATTCTATTTAAGTGCAATCCTCACTGTGTTTTTCTGTGGGATCGT	41219	A_95_P155152 FG139568
42221	497	61	491	TCTGTTAGAAGCATACATGACATCTGATTGTGTTTCCAACTTTATAATCTCTCTTCAGC	41237	A_95_P035328 TA17207_4097
42231	497	71	409	GGGACTAAGGCTGTAACCAAATTTACTAGTTCTTAGATTTGAGATTTGGTGGATTTTA	41257	A_95_P002361 TA13470_4097
42236	497	76	866	ACTGAAGCCTACAAAGGTCAAATTGTTGGAGTCATTGTCTGTAATGGTGCACCATCA	41267	A_95_P227524 DV161230
42243	497	83	767	GCAGTTTGTCCAGTGTCGTACTGTTATATAAACGAATTATTATCTGAACAGGATTTGT	41280	A_95_P188127 TA14500_4097
42251	498	6	1898	GCACTTTTTATCCTTTAACTTTCAGTTGCTGAAGGATAGAGGGTGCTTAATTATCTGC	41128	A_95_P198092 TA16705_4097
42252	498	7	785	GGCGAGTTGCTTAAGTGGTTCACTCGGTTTTTGGCCTTTCTTGTTCCTTTTTTCCTTTTT	41130	A_95_P223457 TA22255_4097
42253	498	8	509	TTGCAATCCTTAAGGCGTTTGGAAGCTAAGAGGAAAAGATTGGAGAAAATGAAGAA	41132	A_95_P107307 FS413389
42255	498	10	687	TGAAGCGTCAGATCACACACATGATTAGATACAAGTATGATCCATTCAACATTGGGA	41136	A_95_P306873 FG636650
42256	498	11	423	GGTATGACCATGAATGGGGTTACAGCATCTCGATGTGATTGATTTGATCTGCCATATT	41138	A_95_P105952 CV017701
42261	498	16	521	ACGGCGACAAAGGGCGTTATGCCTGTTTCTTAAATAAATATTTTTCTGAACACTCAAA	41148	A_95_P156392 EB678300
42267	498	22	613	CGCCTGTTTTGTAAAACTTAAGACCTGTCTGTATGTGGTGTGTTTATAATGTATACCTT	41160	A_95_P009761 DW005003
42271	498	26	657	GCGGGGAAAACATTGATACGTCTGACGTGTTTTTTCTGTAATAGTAGTATTTACCATT	41168	A_95_P211937 TA19723_4097
42276	498	31	832	CGCTGCATATAAATATGGTAGTGTCTAGTGTTAATACTACAGCCATACCCCTATTTTCT	41178	A_95_P013536 TA14508_4097
42289	498	44	641	CAACTGGGGGATAAAATTTTGTAAAGAGTTGGCAGGCTTTTCCCGTTATTTTGTCGA	41204	A_95_P148127 EB677332
42297	498	52	921	GGGGGTATTTGCCTCAAATTTTGCAATCTTTGAGTTGGTGATATTTGTTATAGAATGG	41220	A_95_P212172 TA19776_4097
42299	498	54	707	CTAGCTAATATGTGGATTGTTATGCTTATGGTTTGTTAGTTCTGCTGCAATACTGTTA	41224	A_95_P255454 DW005098
42300	498	55	754	CAGGCATGGGTTATATTCTTGTCACTGTACTATTAGGTTATTTTTTCCATGTACTCTTG	41226	A_95_P292368 EB427237
42302	498	57	785	CTCTGGTTTTACTGATAAGCTTTTGTCATTGAGCACTTGGTTATATATAATGGAATGG	41230	A_95_P183032 EB440103
42311	498	66	426	ACCTCGAAAACCACCCACAAGTGTAATCTATAGGAATGGACTGGAGAACATTATTAA	41248	A_95_P122877 DW002822
42313	498	68	416	CTGTTTTTCGTGACTAAATCAGCATATTTTGGTTATCTGGAGGAAGATGAGTTAAATT	41252	A_95_P071945 BP525831
42314	498	69	497	GGTAGGCCATTTGTGGATGCTGTTCAACCCTTGGAAACAAAAAGCTTTTACATTTGAT	41254	A_95_P189362 EH622255

42318	498	73	757	TAGCAGCCATACAGAGCTCCTAGTTATTTACTCACAATGAAGTTTCTTCTTTGGATTT	41262	A_95_P209707	TA19247_4097
42319	498	74	339	CCGGGGTTGACTTGGATAATGAATGAACCCTTATAGGACCATCTTAAAAATCTATTTT	41264	A_95_P139687	EB443547
42322	498	77	0	CAAAATCCAGTGGGTGTTTTCTCTGCCACTATGCACAGAGCCCTGAATACTAGAAGT	41270	A_95_P314098	A_95_P314098
42327	498	82	507	CCGTGGCAGTTCATGATCTTATATGGGGGTTTATTTACTTGCTGGTCAAAATTTGTAT	41279	A_95_P291393	DW004030
42328	498	83	1274	CATTATTCAGAACTAAATGTAAATCAGATGGTCATGCCATCAGCACTTATTTGCTATT	41281	A_95_P015146	TC42598
42329	498	84	159	GCAGGTTTTTGTGTATCTTGTTGTAGTTCACATTGGTAGCTTTTCATTGTTTCTAAATG	41283	A_95_P089248	BP530419
42336	499	6	777	AGGCTTGGATTTTTGGTGGATTTTCTATCACATTCAACAATTACTGGATTTATGGGAG	41293	A_95_P127572	EB427794
42338	499	8	731	CTGAGAAGACTACTGAGAAAGAAATCAGTGATGACGAAGATGATGAGCCCAAGAA	41297	A_95_P246497	EB430190
42340	499	10	212	TGTTGAGCTTTTTGCCCAGCTTGATGTTGTCATAATAAACAAGCTTGCTAGGTTGCGC	41301	A_95_P164383	EH623606
42341	499	11	765	ACAGTGTGCTAGATATTAGATAATGCTGTGCTGTAAAAAGCGCTTTTATCATCAGTT	41303	A_95_P226134	FG186345
42342	499	12	501	TTGAAAGTCCACACAGGCCAGCAAAGTTGCCTGTATTGGAGCAAGCCAATAAACAT	41305	A_95_P054371	BP133418
42345	499	15	793	GTGAAGACCTGTTAGTTTTATGTAAATAGTGACCATTAGACAGACCATGTAGATAGT	41311	A_95_P115772	DV158104
42349	499	19	668	AGGCCTTAGTTCTTTCTTGGCCAGTATACAAAAATCGATCCCAAAGAATCAATATCAT	41318	A_95_P159527	EH617777
42352	499	22	649	GTTGCACTAGTTGGCCAGTTTGACATTAAACAAAAACCTTTGTGTCTTTTCGAGTCCT	41324	A_95_P107872	TA12059_4097
42361	499	31	490	TAAGTACATACGATACATATATAATCGGGTGATACTTGAAAATGCAACAGTTCGGGC	41341	A_95_P034309	FG133389
42362	499	32	1020	CATATTTATGTTGAATTAGGGGCGTTCTATCGGTTGGTGTGGTACGGTTTTAAGTTC	41343	A_95_P179512	TA12524_4097
42368	499	38	827	TGTATGTTGATGTAATTTGCTTCCTGTTTTGCCACTACTTTGGTCAGCTGCTTGTACAA	41355	A_95_P250097	EB449449
42372	499	42	889	GGGGTTTGATCGGCTTATAGATTGTTTGATCCGTCATTATTTTTGGAGATTAACAAAT	41363	A_95_P289203	DV158051
42375	499	45	340	GGTCAACATAATGGTTCATTTTGGGAAGCATTGAGTTGATGTTGTAGATTTGTCATG	41369	A_95_P107567	TA12386_4097
42377	499	47	829	GCCATCACGAAAGACTAAAAATAGAAATTTACAGTGACCCCAATAACATGATAAGGA	41373	A_95_P272776	EB678072
42383	499	53	498	TCCATGGATTTCTACGGACCAAAGACACACCCCGTGATGTACTTGGCTATTTTGATAG	41384	A_95_P276528	TC57333
42384	499	54	821	AGAGGATTCGTCTAATGAGGTTATACAAATGTTAGAACGGGAGATAATTGAGCTAA	41386	A_95_P149432	EB679278
42385	499	55	782	CTCGTTAACTGAAGCTTATCTTTGACTGCATAAATTTTAGCTTGTGAACTCGGGTGCT	41388	A_95_P271961	EB446465
42388	499	58	1289	AAGTTTGCCTGCTTTCTAAGATGTAAATCTGGTTTCCATGTCCATCTATCCTTTTCCTC	41394	A_95_P222262	TA21995_4097
42393	499	63	915	CTCGGGAATTCGGAATAGTTGTAGAATGAGGAAATCAAATATAGGAGCGTCCTTTG	41404	A_95_P178142	TA12161_4097
42402	499	72	106	TTGATTTCAATTCAATTGCCTTCTTGTTTGGATGGTCGTCGTCTTCGATGGGGCAGCA	41422	A_95_P107132	CV018222
42403	499	73	733	GACCTAAAATACCTAGCCTTTCCTGCTGTTGAGTATTCTATTCAATCTCTGTATATGTA	41424	A_95_P290293	DV162581
42404	499	74	682	TAATTGGTCGTTGCAACAATCACCTATACACATTCAAGTACTATCTACGTTTATCTTCT	41426	A_95_P185542	TA13937_4097
42407	499	77	611	TTTTCGTTTACTACTGTTCTTCATACTTACTTCCGCGCGTCTGTAACAGGTGCATCAGT	41432	A_95_P082465	TA15194_4097
42412	499	82	756	CTCAAGTGCTGTAAATTGAAAATGTTCTACCTTCTATGTGACAATTAAAGCTGATCCG	41442	A_95_P290298	DV162605
42417	500	2	770	TTAATGTACTTCTTAAGAGGAAGTCTCCCTTGGCAGGGGCTGAAAGCAGGCACTAAG	41286	A_95_P016601	EB428048
42419	500	4	892	CGATTGGGAGTAATTCAGCAAGTACTTCTGAATAATGAGGTGAATTTGATGTTGTAA	41290	A_95_P210517	TA19414_4097
42437	500	22	137	TCCGATAGTTGCTCTAACACGTATAAGATGCCCAGTGATGGTATTATTGTTTTTTCCC	41325	A_95_P109312	CV019240
42441	500	26	761	CGAGAAGAGAGAGATGATGTTACAAAGAAAGCTGACATCAGTGACTTTTACTTCAAT	41333	A_95_P149022	EB678686

42443	500	28	495	AGAAAAACCCATCTTTTGGAACCTATGTGTTACTACTACTCCCTCCCCAAAAAAGGAT	41336	A_95_P035813	BP128573
42444	500	29	772	AACTGCTGCTGTCAATCCCACCCATTTCTTAAGTTAGCTGATGCACTTAACCTGAAAG	41338	A_95_P163472	TA12252_4097
42446	500	31	535	GGACATGCTCTTGTCGAAAAATGCCGATGTTGTATTTTTGCAAGTTCAAAATTTTCAA	41342	A_95_P122257	DW002283
42447	500	32	475	ATTGCCATCTCATCTGTACAACATTATTTGTTGTAATTATCCTGTGTATAGGTGTTGCC	41344	A_95_P314963	FG178196
42456	500	41	207	GGAATCGTAATGTGTACAAGGATGTTGCCTTTCTTGTTGTCTATCATGTAATTTATAG	41362	A_95_P028746	CV021398
42459	500	44	833	GTCTGGACCTGTAATGTACTTACTGTATTACTGTAATACATATGAAGAAATTCAGAG	41368	A_95_P023151	TA19042_4097
42461	500	46	519	CTGACTATTAACAGCCAACCTGCAGTTAATGCTGAGAAGTCTGACTCTCCTTCTGTTG	41372	A_95_P142477	TA16719_4097
42464	500	49	1056	GATCCTCTGTTCCATTTGCAAAATGAGGTGCACAATTTCTCATGATGTGAAAAGTTAT	41378	A_95_P207177	TA18683_4097
42465	500	50	722	CTTCTCTTGTTTTAGCTTTCTAGGAATATGGTGAACGAAAGGATGTTCAAGATTTTCT	41380	A_95_P163002	EH622003
42478	500	63	669	TTCGACTGTCATTTTGAATTTTACGCATATATGCGCTATTCCGTCTATTGTAGTTGTTG	41405	A_95_P207582	EB447363
42483	500	68	827	TAATATCTGTACTCGTGGATGAGCTTCTTGTAGTCTTAGAATCATATGCTACGGGGG	41415	A_95_P190347	TA14996_4097
42493	500	78	701	GGGAAGTGTGAGAGGCTATCAGTACAGATAGTTCAGTTGATGAACTCAATTATATA	41435	A_95_P163022	EB425650
42494	500	79	625	TCTCTTTAAAATGTGGTTCTCATCTTAGAATTTATCAAGGCTGGAATGTGGTTTTGTA	41437	A_95_P236269	BP133465
42499	500	84	788	CATATGTGTAAAAGAGACTAGCCGCACTTAAAAGCCGAGTACTCTACCGTTGAGTTA	41447	A_95_P022061	EB426325
42502	501	2	1468	GAGGTGGATCGCTTGTATTGGTTCTGTTTTAATTTACTGAAGTCATAGTGGACGAAA	41449	A_95_P238419	U94192
42505	501	5	966	ATGGGGAAGATAAGTTTTTGTTTTGCTCTTTGTACAACTGGTGATTACGAAGTCATG	41455	A_95_P199162	TA16932_4097
42506	501	6	477	AAGGCCGTTTTGTTTGTGCTTCTTTTCAGTTGGTTAAACAATTTTACTGATGCTTTCAC	41457	A_95_P123837	DW003728
42510	501	10	378	CCTGATGCAAATGCTTTGTGGTGGTTGATTTATGGTTCATATTGTAAATCCAGTTATT	41465	A_95_P033779	AJ632969
42513	501	13	524	GACTTTGCTCTTATTTATAGTCTCATTTGCATGTTGTGTGATCGCCCATGTATTTTCAA	41471	A_95_P147547	EB452030
42515	501	15	1470	CTAGAAACGCTGTTCCCTCTCGAGGATGGGAATAACAAGCATATTTGGGGCTATATC	41475	A_95_P021121	TC41439
42517	501	17	871	TTGCAAAAGCTATTCTGGAGAAATCAGAAGGGAAGGTTCGGTTAACAGGTCTAGGT	41479	A_95_P233874	DV999224
42518	501	18	636	TGGTAATGGCACTTCCAGCTGGAAACAGGGATGATCTGCCATTGACCAATATGAGTA	41481	A_95_P053141	BP133098
42520	501	20	460	AACAGCAGCTACGTGAACTTGCTATGCTTAATGGTACTCTTCGTGAAGAAGGTTCTC	41485	A_95_P200797	EB449689
42522	501	22	543	CAAAAAGCGGAAGACATCAACAGGTCATACATCACAGGTTTCCAGAAGGATGAGAG	41489	A_95_P199787	DV159856
42524	501	24	590	TGGGGAATAGCCAATCATTCTGGGCAATTTTAACAATATGGATAGCTTTGGTTGGAG	41493	A_95_P020991	EB681060
42536	501	36	418	GACCCTCATACTTGAGATTTGATCGTTCATATCTCAGTTGAGTTTTAATAGATGATCT	41517	A_95_P072055	BP525859
42537	501	37	0	ACCCGTGGCATCAACTATGAGTTAAATTGTTCTTCAGTAGATTGTTCAGTATTGAGTT	41519	A_95_P027991	A_95_P027991
42539	501	39	724	AGCTGGTTTTGCCTGCTCCGCTATGTTATTTTGTTGAGAAAATGCCCAAAATTTTTCC	41523	A_95_P219492	TA21407_4097
42541	501	41	699	CGTTTCTGCCTCTTGTAATATTCTCTATATTGTCCCCTTAAATACTTGTTATAGGGGTC	41527	A_95_P147432	EB451842
42543	501	43	812	CTGTTCGCTTCTCTTACGGAATTTCTAATGCTAAGCTAATAAGATACTCGTTATGATA	41531	A_95_P201537	TA17446_4097
42544	501	44	267	GGCACCGGGAGCTACTGTTTGAGATCATTATTCTTTAATTTCGTATTTGAAGTAACAA	41533	A_95_P140592	EB444477
42548	501	48	194	TGCGGTGTACTCTTTAGACATGATGTTGAGTTTTGGGCTTCTTTAAACTATAATTTCTT	41541	A_95_P102387	CV016003
42549	501	49	440	CTAGACAGCCAGAACGAAAGTCCAAATCATGTCAGTGACAAACGTGCTTGAAATAG	41543	A_95_P112587	CV020746
42552	501	52	203	GGTTACAAGGATGTTCGCAAAGAAAACCACCAGATGTTCGAGCAGCTACTGATTGA	41549	A_95_P164977	EH624438

42553	501	53	1322	CATATTACGAAATGCTGGTTGTTGAACCTTCTTTTCGGCAATATAAGCATGTTTTGTTT	41551	A_95_P014476	TC56514
42554	501	54	709	TGGGATAAGGATGTGCCTGTAGCTTTTGGATATTTGGGTGATATACTTCAGAAATTCA	41553	A_95_P170511	EH664919
42557	501	57	547	CACAGAGCAAGGCCAGGAAAGAGTTTGTATTGTCATATGAAATCAATAAAACATGTT	41559	A_95_P101763	TA14806_4097
42562	501	62	782	TGTGCTTGTGCTTCAGGGTTAGGTTGTTGGTTCTTTAATATGTAATATAAATGCCATT	41569	A_95_P253239	DW003641
42564	501	64	697	TAAAGGTTTACCAGTGGAGGTTTCTGTATGATTCGAATAGGTCTCCCAGTCTATAATC	41573	A_95_P239694	DV159666
42566	501	66	754	GCTTTTGATACTTGTTTTCTCTGTCATGGACTTGCTGTTATTGAAGGGATTGAATTTGA	41577	A_95_P014746	TA12923_4097
42567	501	67	445	TGCCAGTTCAGTGTTTACTCCGAAAGATAACAGTATTGAAAACTATAGGATGTAGTCT	41579	A_95_P040311	BP129792
42568	501	68	1703	CCCCCTTTTTTGTTATGTCACATAATAAGGGGGGTAAATGGTGATCTTGTATATTTGAT	41581	A_95_P179842	TA12596_4097
42569	501	69	1299	GAGTGAACTTTGCTATTGTTTTGCCTCAAAGAAAGGCTCTTTATTATGTACAGAAGCT	41583	A_95_P180412	AY286010
42573	501	73	630	GCGTTCCCTTTATCGTTTATCATGTAAGAGCTATTTTATTACTGTCATAATCGGAAGG	41591	A_95_P018981	TA15283_4097
42583	501	83	450	GACGTAGTGCAGGAGTATCTGTTATTGAATCATGTGATCAATATTAGTCTCTCTTAGT	41609	A_95_P110867	TA14944_4097
42587	502	2	172	AATGCACTTCAAATTTTCTAAACAAGCCATAGACTTTACCCTGCCCATCTAGGACCCGA	41450	A_95_P154572	EG649650
42592	502	7	1220	ATCCTCAAAGCTAGGAAACGAAGCTGCAAAACATGTATGTTGAATTCTCCAAATTTTG	41460	A_95_P005986	TA15194_4097
42605	502	20	896	AGTAGAAAAACTTAGATCTGAATTTTGGCGGTCTAAATGATTGGAATGATTGATCGCA	41486	A_95_P190382	TA15003_4097
42607	502	22	809	GTATTGGTACTGGGTAAGCTGTTTACAGTTTGTATCTGAATAAAGGTACTGTGCATC	41490	A_95_P024161	TA16385_4097
42608	502	23	702	GCACTTGTGACACCAGGTTCTGGGACGATTATAGGATACTTAGTGTTGAAGACACAA	41492	A_95_P266686	EH616930
42609	502	24	186	CAACGTATTGCATTATTTATGCAACCTGATTGGGACCAAAAGCTTAATTTTCCCGAAG	41494	A_95_P051316	BP132613
42610	502	25	616	ATCCTTTTCGAGACCAAGTTGTTGTGCTGATAGGGAGTGCTGCAAGTGCTACTGATAT	41496	A_95_P129117	FG170823
42611	502	26	979	CTGTGGGGCTGTGATACAAGTTCTTATCCGTATATTTGTACTTATCATCTGATCTATTT	41498	A_95_P201087	TA17349_4097
42614	502	29	547	GTGTAAATGACCCAGTCACCGCAGTGGAAAAAACAGAAGATACCTTCATTGCTGAAT	41504	A_95_P164237	EH623373
42619	502	34	268	AACAAGTTGTTTCTGGTATTAAATATTACCTTAAAATCTCCGCAACTACTTCCTCAGGT	41514	A_95_P156542	FG642287
42622	502	37	441	GTAATCATCTTCTTTCACAGCCTCCATTTCCTGAGACGGTTTTGAGACCTGCTCATCTG	41520	A_95_P090038	BP530775
42623	502	38	692	GTTCACTCCTTTGCTGATGGAAGTGTTCTGTCACCTATGGGCTATAAAGAAGTAGAAT	41522	A_95_P209987	EH621158
42625	502	40	420	TTAGTGGTTTGTCCTAATTGTGAAACCTCCTGCCATTGAGTCAATTTATTATGTGAAA	41526	A_95_P024451	TA12436_4097
42628	502	43	819	TATTAGTTTATGGTCCTGTGAGATGTCACATGGGTTTCCCAGCATGGAGAATCCGGTA	41532	A_95_P119837	DV999447
42631	502	46	380	GCATGTACTAGAAGTGAATTGCTAGAATTAAACGATCTGTGTGTTTAGCTTTGTTTCA	41538	A_95_P006046	FS412805
42632	502	47	790	AATATATTCCTGGCACGTGAAAACTTATTGAAATAAATTTTGCTCAGCCATAGTTGTG	41540	A_95_P187202	TA14293_4097
42633	502	48	870	TTAGTTTTGTTTTATCAACGCTGGGTACTCTATATATAGAGACATGTTTGGGGAATTG	41542	A_95_P258546	TA12203_4097
42634	502	49	475	CCAGAAATCTTACCGTTAGATTTCTTCTATATGCTTCTTCTTTACTGCTGATGATGTTGA	41544	A_95_P001636	TA21482_4097
42638	502	53	562	ACGAGGGCCAGTTTTCTTGTCAAAGCCCTCTTTTGCTTTAATCTACTGATTATTATCTCT	41552	A_95_P138937	FG623478
42639	502	54	962	GGGATATTTCTGAGGCCAAAATATCTATTTTGATCGTAGACTGTTATGTTCGATGAGA	41554	A_95_P014396	TC45811
42641	502	56	193	GGAGGGTAGAGAAGGGGAGAAAGAAAGCAAAGGGCATCTCTCATATTTTCTTGATA	41558	A_95_P037961	BP129142
42642	502	57	283	GCACGCAATTGTCATTTGAATAGATCTATCTCTTTAAGTTTCTCTCCTGATCATCTTCA	41560	A_95_P047911	BP131775
42643	502	58	1181	GGGTAATGTAGAGTTAATGTCCACAATTGTTTTCATTGATGTAAAAGTAACTGTGGC	41562	A_95_P189867	TA14879_4097

42647	502	62	93	CTTTCTTTGGAGTGATCTTGTAACGTTATTCTCTTGGGGTATTTGTGACTATTTACTGT	41570	A_95_P138977	EB442685
42654	502	69	686	CTGTGTGTGCTTAAGATGTGATAGTTCTGGGTACTTGCATGTCCAACTTATTATTTGG	41584	A_95_P121707	DW001811
42655	502	70	449	TAGATTGGTGGTGTATAGATACTCATGAACTCAGTGACACCCCGATTTGGGTTCCAA	41586	A_95_P271791	AM839972
42657	502	72	461	TTGGATAACTAGATTTGCAGGTGCACTTGGCTGCAAAAAAGGAAAGGCTTGTTAATA	41590	A_95_P176322	U95924
42663	502	78	753	ATCAATCCCCTGAACTCGATCAGAAATTCCCGTTGTCAGTGGACCCTTCTTTTGAAGG	17966	A_95_P000116	FG157904
42674	503	4	585	TCGCTCTGGAAAATTGCCTCAGTAAGTCATACTAGTACAATGTTATGTTAGCTTCTTT	41616	A_95_P053776	BP133272
42675	503	5	632	AACCAGGTGATTGGAATTGATTTGCTCTCCCAATCCCTGCTGCCAGCTATTGTTGAAC	41618	A_95_P127987	FG132900
42676	503	6	314	GTGGCTTTGCTCATTGTCAGTGTTGTACTATTAAGTAGTCGATATTTATGTTTGCTTAA	41620	A_95_P050986	BP132534
42678	503	8	563	GATGTGGGGCACTCAGTACAGGTTCTGGAATTTTACTTCTACACACCCCGAATCTAG	41624	A_95_P157772	EH615809
42679	503	9	774	AAGCAGTATATCCTCGCATAACCAATCTTTCTACGGCGTCACTTGAAAATCCTGCTGT	41626	A_95_P129877	DW000183
42686	503	16	853	GCTGCTGTGGCAGTGAAGTTGAATAGTTTTGCTTTTAGAATTTAATCTTAGACTTGAC	41640	A_95_P039176	TA16262_4097
42687	503	17	459	ATCAGCTTGTATTAACTGCTACATGGGATTTCAAGTTATAATTTCGGAAGTGGCATTC	41642	A_95_P132632	EB433185
42689	503	19	543	ACTGCTACTGTTAATTCTGCTACTGTTAATGCTGACTGTTAAGTGTTAATTCTGCTACT	41646	A_95_P223107	TA22178_4097
42695	503	25	803	GACGATAGTGAATATAGGTCCATTGATAGATCTCCGAATCTTCAGTTCCTCGAAACC	41658	A_95_P119212	DV162283
42696	503	26	352	TGAAATCGCCTGTGATCTGAAAGAACATGTAATCAAACCCGTGATACCCGAGAAGTA	41660	A_95_P141592	EB429936
42700	503	30	816	GAGTTGATGAAGTGTCTGGACCTGTAATGTACTTACTGTATTACTGTAATACATATG	41668	A_95_P244337	EB429106
42703	503	33	594	TATTTATTTGTTTGTTTGGGTTCCTGTATACAAATAAGAGATACAGAAGACCATGCGG	41674	A_95_P030866	DW001385
42706	503	36	341	ATCTTTACTCAAATTTTACGCGGCTTGTCTGGTGCCAAAGTCACTAAACCGGGGAAG	41680	A_95_P018046	EB682350
42720	503	50	1101	GTGGCTATGTATAAGACGATCGATGTTATATGTTGCTCTAATTTGACTATTAAGAGT	41707	A_95_P019591	TA15680_4097
42721	503	51	883	CAGTCCTCGAGTGGTAATATATGTTTTGGTGAAGAAGTGGAGAAAAGAAAAGTAAG	41709	A_95_P263116	EB424976
42722	503	52	672	TTTTAGTAAAAGTGCTGTTAAGCTCATGTCGCTCTTGCTCTGCTATGGATCCTCCGGA	41711	A_95_P150997	EB681180
42726	503	56	2814	AAGAATTGACAAAAATTACAAAGTGAAGTTAGCGACTAATCTAGGGCGGGTAAACC	41719	A_95_P239564	AB196790
42733	503	63	799	GTTTGCCAGTTTACCTGAGCCTTTCTCTAGTTTTTCCAATTTGCCTGGCTTGTTTGGTT	41733	A_95_P010856	EB677495
42736	503	66	286	GACGAGTTAAATGAACTGGAAGCTAGCCTTTCAAAAACATCGTTACAAATCAATGAA	41739	A_95_P095153	BP533043
42737	503	67	860	CCGGCATTCTGCAATGCAATCTAGTTTTCCATTCGTAATCATATTATGTATATACATCG	41741	A_95_P009556	DV162646
42741	503	71	520	CATACAAGAGACCGGAGATCTGAAAGTTTCGGCTCTAGATTTTACTGGATCTGATCG	41749	A_95_P045986	BP131279
42743	503	73	274	CAATTGGTTGGGACAAGGTAGGAAAAAGCTTGTATAGATTGTATCTTTACAGATCAA	41753	A_95_P033659	AJ632883
42745	503	75	736	TCAATTTCTCCTGTACCCTTAAATTGTTGCAATTATGTGTCCAAGTTAAACGTCAAGG	41757	A_95_P140917	EB444726
42751	503	81	247	TAGGGGATTGGGAATGAATCAATCTGGTTCTTGCTTTTCGAAGGTAAACCAAATAAT	41768	A_95_P033429	AJ632731
42757	504	2	533	CTTGTACTGTGCTATTGTCTCCACCATTAATACATATAGTGTTGCTAGCAGATTTTCTT	41613	A_95_P059665	BP134796
42765	504	10	785	TAATAAAAACAGACCGACTCTGGTTGCAATGATGTATTTATTTCTGTTGTGAAACCTG	41629	A_95_P248762	EB677818
42766	504	11	295	AGGAAAATTGTTGACTGAGGATAAATCTTTTCACAAGTGTGTATAGCATATTTTGCT	41631	A_95_P033449	AJ632753
42767	504	12	816	GTCAAAGTCTGTCGTAGTGTAGTTGAGTCTATCAGGTCTTTCATTATCGCACTTCTTA	41633	A_95_P194472	TA15904_4097
42770	504	15	895	CCTGCCCATATATATGCTCTAAGAGGTTGGATCATGGTGTCTTATTAGTGGGTTATG	41639	A_95_P009136	EB678171

42772	504	17	353	CAAGACCATTTAAAAACGTGTCACCTTTTGTTTCTTACTAAAGGACGACGTACTTAGT	41643	A_95_P150627	EB680762
42775	504	20	654	AATACAGACCATACAGCCATGCTAAAAATTTTACAAGAAGTTGAGCTTGTGATGAGG	41649	A_95_P216662	TA20754_4097
42785	504	30	523	TTTCTCTTTTCGCATCTCCTTTTCGTGTGCCTTACATGCTATTGAAGAATGTCATTGGA	41669	A_95_P069670	BP137451
42786	504	31	107	AAGCAACGAATCGGATTCCAAAAATTAGGTTCGATTACCTAAAAAGCTCAATTCGCC	41671	A_95_P215242	TA20442_4097
42787	504	32	195	AAATTTGCGCTGAGGCACAAGCCTTGATTCTGTATATGCTCAGTCTTCTTCTGATGGC	41673	A_95_P113522	CV021173
42791	504	36	844	CGACTTCATGAAGAAAGTTCCTGAAACACAAGTGCAAGCTACATAAAGCTCAATTGT	41681	A_95_P232404	EB678937
42794	504	39	70	GCGGCTAGTTTTTAAAATTTGGCCCTGTTTTTTGTTGGATTAATACAGTTCTCTGAGA	41686	A_95_P235709	EB446851
42797	504	42	1192	ATGTAATGCTGATTTGCAAACAGTTTGAACGGCTGGACGCTGGCAACTGTGGAAGG	41692	A_95_P283483	EU161633
42798	504	43	744	CCTCGTCTTATTGGCGCAATGGCTTATTCATAGTAAATGATCATGTCTTTATACTGTTT	41694	A_95_P192687	TA15507_4097
42800	504	45	784	AACTGCTCAAGGATCTTAAGCTACTGTTTTTTAACCTTTCTTTCTTCAAAGTCTCCTGT	41698	A_95_P262821	DW004791
42801	504	46	746	GTTTATTTATTGCTACAAAAATGTAGAATTTGTTCACCGTTGCAGATTCTGTGTTGTG	41700	A_95_P189127	TA14724_4097
42805	504	50	427	AGAAGTCTAAGTCCAAATCCTCTCTCTCCAATCTGTTGATTACTAAAGAGGAAGGGTT	41708	A_95_P176012	EH666226
42810	504	55	146	ATTCCATCTTTGGCCCACTTGAGAGGAAACCAAGTAACTTCAACAGGAAATTGAGTT	41718	A_95_P090208	BP530859
42811	504	56	817	CCATATACAATGATGAAGTTTGCGTCCTTTGAGACTATTGTGGAGATGATCTACAAG	41720	A_95_P012351	TA12330_4097
42812	504	57	502	TCAGGATTGGGGCATAGTTGTTGAACATAATGAAATTTTGTGCATATCAAGGGCCTT	41722	A_95_P033579	AJ632852
42817	504	62	744	TAACTTACTGCTGCAACTTTACCACCTGTCTGAGAAGTATATACTGTAGGTTCGCGTG	41732	A_95_P201142	TA17361_4097
42825	504	70	1164	ATATTCTCGAAGGAGGTCGTTCGTCGAATCGAGATCGGTCCTGGTGGTTTATTTTTTA	41748	A_95_P015581	TA17510_4097
42826	504	71	324	CCTATTGGTGGGTGAACAATCCAACACTTGGTGAATTCTGCTTCACAATGATAGGAA	41750	A_95_P091428	TA12368_4097
42833	504	78	241	GCTAATTTTGCTCATGGAACCTTTTTCTGTACGACTATTCAGCTGTGTCTTTGCTTTAA	41764	A_95_P002711	EH621391
42835	504	80	400	TCATTTCGATGTTTATATGCGTGATTTGAGGCCTCGAGTAGGTCCCTATTAGTTTATG	41767	A_95_P094533	BP532765
42843	505	3	731	TGGCATTTAAATTTTGTTTGGAAGGCAGAGGACAGTGTTAAAACTGTTTTTGAGTTT	41775	A_95_P285953	EB445825
42845	505	5	504	TGCTGCATTGGCTGATTTTTGGTTGAAAAATGGCGATCGGAGATAGAAGGCAACATT	41779	A_95_P275878	AM788334
42848	505	8	177	GTCATACTACTTCATTTAAAATGCTAATGAATAAGGCTTCGTAGCTGAAGGTCTAAA	41785	A_95_P129842	EB429794
42850	505	10	1026	TCATAGACCAAGATATGGTTTTTGCAGCTATTTATTATAGACCAAGATACATCTACTG	41789	A_95_P177182	TA11901_4097
42853	505	13	803	CCGAAACCCTGCCACCAAGAAAAAGGATTTAGTTTTAAGTTGTAAGTGTAATTTAAC	41795	A_95_P296658	EB678639
42855	505	15	802	CCATTCGTGGACGCCATCCAATTAGCGTTTTTCTCCATATGCTGAAAAACTCCTCGAC	41799	A_95_P010666	EB425633
42858	505	18	488	GCTATGAACTGAACATTTTCTGCTCTCTGTTAACATTGTCAATACAGAGGATAAAGAA	41805	A_95_P003051	EH620495
42859	505	19	1297	TTCATGACCAAAGAGTACCACATCTACATGACATCAGATGGACGCATCAGTATGGCA	41807	A_95_P023461	TA15086_4097
42864	505	24	504	ACTGCTGCTCATTGCATCTATAACTAGGTAGGATCCTTTCTGTATATAAACACAATTA	41817	A_95_P123847	DW003734
42867	505	27	1844	TCTTCACCATCAGACGAGTCAGAAAGATGTAGTGAAGATTTTTGTGCATCATCCTTAA	41822	A_95_P214537	AB023572
42870	505	30	279	TGACTGCTTCTTGTCGAAAACTATTTATCAGTGTATGGATTCACAGGATTATCAAATG	41828	A_95_P188107	AM799412
42871	505	31	677	AGGTTGGGTTATATTGTGCTGATATTGGGATTTCGCTAATTATACAATTAGCTAGTG	41830	A_95_P290998	FG635425
42872	505	32	482	ATGTTGATTATGATCCACTTGATACCTTAAGCCCTCAGCTCGGCCAACAGACCTAACA	41832	A_95_P277483	AM786721
42875	505	35	313	TGTGTGGTTTATTTGTGCTAATGCTGCAGTAACTCTTCAAGTTTGGTCTTATGAGGTA	41838	A_95_P095778	BP533336

42880	505	40	685	TCAGAGCAGGACGATTCTTATTGGATGCGCTAAAAGTTGTTTCTTCGGGGACAGTTG	41848	A_95_P299863	FG182558
42882	505	42	737	TTATGCCTTGCATCACCTGAATAAATATGCCCGAGACAAGATACCCTTCATAGGCGT	41852	A_95_P126697	EB426022
42885	505	45	783	GCAGGCTGTTGATATTCAGCTTGGACTTGCAATTGACAGTACTAAAGCAACACTGGC	41858	A_95_P027356	DW000734
42888	505	48	1033	GGTGGTTACCTCATTAAATGGAGCTATTCATTCAGCTCTATCATGAGTTCTTTTACAA	41864	A_95_P205692	TA18343_4097
42890	505	50	483	ACTGGTTTTTCTATGTTGTTTCGACATCTAGAAAGAATAGGACGTACCGAGTTATGTT	41868	A_95_P244132	FG644144
42892	505	52	1354	GTTTGATTTATACCGAGTAAGTTGTCGGTAGGTATACCTGGTGTAATCTGATATCTCA	41872	A_95_P024406	TA16640_4097
42896	505	56	767	GACTCTCTGATCAATATACTTCACAGCACACAGCTGTACAGTATGCTAGCATTATGGC	41880	A_95_P290888	DW001774
42900	505	60	792	CGGGTTTAGCAAACGCAGTGTTTTTGAGGTAGAATTCAATATTATTTGCAAAGAACA	41888	A_95_P013116	TA18258_4097
42902	505	62	1020	TGATTTGAGTGAGTTTCTCGTGTTTCTTATTCTGACTCTCTCTACCATTTCTTGATGGG	41892	A_95_P154217	EF051135
42903	505	63	556	AGACGAAGAGATTTGTCGTCTTGAACGGGAGCTTTTTATAATGGGAAATATTTTGGA	41894	A_95_P301173	FG180856
42906	505	66	839	TGTGACACCCCGATTTCGGGCTGAGTTGGGATGGTTTTCCTTGTTCTATCACGTTTAT	41900	A_95_P135597	EB425297
42907	505	67	517	GTTGAGAAACTGAAGTCTGGTGTTGTGAGGGATGATGATCCAGATTTCCGATGATCC	41902	A_95_P222997	TA22151_4097
42909	505	69	553	TCAGTATCTCCTTATAATATCAAAATATGTGGAGTGGTTTCTGCCCATTTGCTTCTCTT	41906	A_95_P018631	TA13260_4097
42913	505	73	256	CATAAGGAGTTGGCCTTTAGAGTAACTACTAAGATGTATGTTACCAGAAAACGAACA	41914	A_95_P132792	EB433504
42933	506	8	665	GGTCGAAGTTGCATCCGACTAAAAAGGGCGATTTGGAATATGAAATTATGTTGTTTA	41786	A_95_P027141	TA15716_4097
42934	506	9	846	ATTGGGATCCTAATGCATTGCCTGAGATAAAAAGGATTAATTACCGCGATGTGGTGG	41788	A_95_P244112	EB679225
42936	506	11	299	AAGATGTGTCAGATTTTGGAAAGAGAGGGTGGGTGATTTTGTTGGTGCCGCCCACA	41792	A_95_P164792	TA18036_4097
42942	506	17	988	ATTGTTGCAGAAACCTGTTCTCCCTTTACTGTCTTGCCTGCCTTGATGAACGGATATC	41804	A_95_P202452	TA17639_4097
42945	506	20	402	AGGTGGCTACTATGTAACGTAGATTGGATAAGTACTTTGGATGCTTTTAAAATAAAG	41810	A_95_P163112	EH622100
42946	506	21	314	GCCGGCACAGCTCTTCATAGTGAAATTTATAACCCCTTTTGTGTTTACAGTATTTTAA	41812	A_95_P025641	TA16984_4097
42947	506	22	234	AGATGGTGCCTTTCGCTGGTTGGAGTATGCCTATCCAGTATAAGGACTCAATTAATG	41814	A_95_P032301	AB001553
42948	506	23	388	TAACGACTATTACAGCCCGACAGTAGCTTCCATCATGAAGAAACGGAACAACTTGGA	41816	A_95_P146717	TA17708_4097
42954	506	29	631	AAAGGGTGTGTCCATGACTGAATTTATTCACCCCCAGAGCAAGTACGAGAGCCCATT	41827	A_95_P037901	BP129126
42962	506	37	280	GACTCATGTGTCTGCTGTGTAAAACTATCTAATAACAGGAGATGTAAGTTTTGCTAG	41843	A_95_P143847	EB447033
42964	506	39	777	GAGGATTGCAATTGGACAGGCACCTGAGCAAGAACTTGAATTTTTCAACAACAGTTC	41847	A_95_P222092	EB444939
42971	506	46	698	CATGATCTTGGTTTATACTACTTGTTACCTTAGTGTGTGTTTGTAATTTCAACCTCTGC	41861	A_95_P018021	DV162334
42972	506	47	152	TGGATTCAGATAACGTGCGTCAAGTGCAGTGCATCAGATTTCATTGCCTACAAGCCT	41863	A_95_P111077	CV020039
42973	506	48	434	ACCTGCTGCTGCTTCTTGAGACTTATAGAAGGATTTGTGAGCCATGCCTTCCTACTTT	41865	A_95_P111407	CV020189
42975	506	50	507	TGGAGGTTTCTGTTGAACAGCTTTGCTGAAGAGAGCTTGATATTTATTTGGCAGTTG	41869	A_95_P121992	DW002063
42978	506	53	1156	TGATAGTTCACGTGAAACTTCCTGGAAGAGAGCAGCAGATTTACTGGTGGATGTTGC	41875	A_95_P221322	TA21796_4097
42981	506	56	2276	GTAGATAGTTGAGACAACACCTTTTGTACAGCAGTTCGTTACACTAATACATTTGATT	41881	A_95_P142732	TA15408_4097
42982	506	57	365	TTGGAATGATGAATGTCTGGGTCCTTGTTTGTGACTGATGGAATTATCCTGCTTCTAA	41883	A_95_P157692	BP534468
42986	506	61	747	TAATGGAGGCAGCAACAAAATGTGGTGAGTACCTTGTCTCTGTCAGTCAGTCATCAT	41891	A_95_P019301	EB450257
42996	506	71	856	GACACTGGATCACGTCAGATAACGGAAAAAATAATTGGATCGAGATTCATAACTATA	41911	A_95_P089933	EB427992

42998	506	73	1672	GAAAGTAAGACCAAATTGTGTTGAATAAGAGTATGGTTGGTGGTGTGGTATGATAT	41915	A_95_P255244	AY639864
42999	506	74	604	TAGTATTGGATCTGTGGTTTGTACCCCTGCTGATCTTTTTCATTTCCTTCTGTTGTTGT	41917	A_95_P129642	EB429605
43006	506	81	886	GTTGTATGCCTTTGAACATTACAGGGCCTTGGCAATTGAATGACTTCTTTATTGAAGT	41931	A_95_P023596	TA15548_4097
43008	506	83	114	GTCCGACAATCCTAAGATCTTAGTATTCAAGTCACTAGCCCTTCACAGTTCAAGATTT	41935	A_95_P147782	EB643450
43016	507	6	335	TCTGTACATTGTGTAGATTTATGTGCAGAGGGTGAAAATGCCAAATCATTTGGTTTTT	41943	A_95_P214012	AM816159
43024	507	14	735	GCCAAAGTTGATCACACGTCTGAAAATGTAATCCATATATTGAGATTCCACTGGTTAT	41959	A_95_P003866	EB443493
43027	507	17	810	CAGGATCTACAGAAACCATGAAAGTTAAGTTTTCCATGACACAAATCGACTGCACAC	41963	A_95_P218332	EB448847
43028	507	18	380	CGATGTTCTTCAGGGTGCTAAACAAACGACAGATTTGTGAACCCATTTCCACCAAGT	41965	A_95_P103132	CV016360
43031	507	21	498	GCGATGAGTTGAAGATTTTGACTTTCTTCTTGTTCTGTTACTGGCTGAATTCTTTTCTT	41971	A_95_P000956	FS411112
43035	507	25	798	GGTGCACCAACTAATACATTTGCTTATTACTTCCACTGACGCTCAATATACAAGTCTT	41978	A_95_P272346	EB450818
43037	507	27	574	TGAAACCGTTAGCAAACCTAGTGACAAATCAACCTCATCAGATGATTCTAGTAAAAT	41982	A_95_P153897	DV999293
43038	507	28	676	AATTTCAAATCCGACGTTGACGGTTTCGAATATTCCCGAGTTGTGTAGGATAGCGCA	41984	A_95_P292258	EB427017
43040	507	30	89	TTAGTGAAGTATGGGCTCATGTGCTGCATGCAGTGCTTCCGCAGTAATGCCAATGAA	41988	A_95_P114622	CV021691
43043	507	33	385	AATGGCCTTTTAAGAATTGTTTGATGGCAACTAGAAGTTGCCAGCAGTTATATTATG	41994	A_95_P063480	BP135790
43050	507	40	217	CCATTGGAGACAATAAGGACACATTTGATGGTTGGAAGTAGTGGGCATTCTTCTACT	42007	A_95_P200177	DV160992
43051	507	41	915	CGCGGACATGTGCAGTTTTGGGCTTCGGGTTTGTTAAATTCTTTGATTGCTTATTCCC	42009	A_95_P269386	EB449208
43053	507	43	789	CAGAAACTTCTAAGAACAAATCCAAGAAGAAAAAGGGTGGGCGTACAGTTCAAGAA	42012	A_95_P016631	TC50971
43054	507	44	807	GAGGTGATAACGTTGATGAAATCAAATCGAAGCTTGATGTAGCAAACAAGGCTGTT	42014	A_95_P288993	TA14249_4097
43056	507	46	183	CATGTAGGCTAAAGCAAACTGTACCATAGGTTCAAAGTGTCTAGTTCGTTCAAGTTC	42018	A_95_P139672	FG155763
43058	507	48	324	CTTCTCTTAAAGACAAAAATATGCTTTGCAATTGGCAACGGCAGTTTACTGTTGTTTT	42021	A_95_P010076	BP534433
43066	507	56	576	TGGGTACTGTTAAACAGTGTCTGGAAATCCGTTACTTTATATGACTATCTTTACTAAT	42036	A_95_P063345	BP135754
43068	507	58	1020	ATACTTCTTTCAGGGTAACGCAATCCCATCCAGAATTGTCATCATGGTCTGCAGGTAG	42040	A_95_P186737	TA14190_4097
43069	507	59	446	TAATGGTAGATCCAATGCTGAAAGGGAACTACCCAAAGAAGGGACTGTACCAAGCT	42042	A_95_P052546	BP132951
43072	507	62	734	GCACTTGCTTGTAAGCTTTGAATTCCAAGTTTTGAACCCTGAATTAGCAATTGCTTTT	42048	A_95_P200817	EB681013
43078	507	68	646	CTGATCTTGACAGTGGGGGCAATATTCTTACAAATTTATTTCAATTTCAACCGGTTAT	42060	A_95_P288628	FG643167
43082	507	72	434	CAACTCTTGAATCATATTTTGCATTATGATTGAACTGCTTTGCTTCTTTTGCACTGTCC	42068	A_95_P178652	TA12304_4097
43085	507	75	853	TGATCTTTTGTTCAAGGGAAGTCCTCCAGTTAACCTGTAAGAATGCCTTGTGGATTTC	42073	A_95_P266441	DV157831
43087	507	77	247	GTAAGGGCAAATTTTCCAAATGATTGTAATGTGAATATTTTCCCTGTTCACATGAAGA	42077	A_95_P194217	TA15845_4097
43089	507	79	1175	AAGATCCTATATTCTGGCGCGAAAACATAAATAGTTTTGAGGAGAATGATTTCCAGA	42081	A_95_P210227	TA19354_4097
43092	507	82	236	TAGCAAACAAGGACAAACCTGCAATCCTCAATGTCAACATCGGGACTACTGTGAAAG	42087	A_95_P136927	FG143157
43098	508	3	349	GATAAGATGTAGGGCTCTTGTAACTGTGGACTAATGAGCACATGATTTTAGATGTCA	41938	A_95_P113927	CV021368
43099	508	4	813	AAATTTTGGCATCTCGTGTCAGTGTCGTGTTAATTCTGTTCCACTATCCTATGACACTT	41940	A_95_P267281	EB681840
43103	508	8	479	TTTGGCTTTGGTTCATTCTCTTGTTAATGGTTGAATCATTTGAAGGTTGTGCTTGGAA	41948	A_95_P029101	TA21080_4097
43117	508	22	388	TCGGAAGACATATTCCCAAACTATACATCCTATTCCAGATAAATCATTATGGAAGGA	41973	A_95_P153577	EB683819

43120	508	25	776	GTTGGAGCAAGCTGACCTGATCCGGATGAAATTGAGCTTAGCACAATAATATAAAG	41979	A_95_P289608	DV160210
43124	508	29	349	GTTGCCAGCTTTACCTTTTTTATATGTATCACCATGCAATATTAGCACCCCTTACTTTA	41987	A_95_P081405	BP528243
43126	508	31	1825	TCCTGGGATGTGGGAGAGGCCTTATGAGGAAAACAAAATAATGTCGTAAAAGAAAA	41991	A_95_P024981	AB017967
43127	508	32	906	TGCTATGGAAACAGGACAGTTTGAGAGGACTGTTATAATTGCAGAGGAAGGGAGTT	41993	A_95_P233659	EB441391
43129	508	34	464	ACAAACTCCTTACACAGATCAAGGATGGGTAAGCTGAGGGAAAAGAACTTGTCATG	41997	A_95_P114557	CV021663
43136	508	41	519	CCCACCTAGTGGTTAAAGACATATATATACTTTCAGTGAAGATGGAACAAATGCCTG	42010	A_95_P022681	EH621211
43138	508	43	574	GTGCTCTTTTTCAGGGTCTCAGGATACTTGATGTCTGATAAACTTGAGATTCCTCGG	42013	A_95_P047106	BP131572
43141	508	46	700	AAAGATGACGCACAATTATCCAGTGGAGGAGTCGTGCAAAATTGCAGCAGCAGTAG	42019	A_95_P191662	EB441414
43150	508	55	804	TTTGATGATTTAGCCGTTGGAAGCCTGAGAAGGCAAGAAAGTGAGCCACAAGAAGG	42035	A_95_P260851	EB451879
43153	508	58	587	AGGGTGGTTAATTAAGTTCAGCAGTGCAATAATACGTTTCTGCTTTTGGAATATTGTT	42041	A_95_P153182	EB683490
43158	508	63	629	ATTTATGGCCAAGCATGGAAATACAAGACAAAGACAATGGTTCGTCGGATAAAGCT	42051	A_95_P128977	FG643286
43169	508	74	922	CGTACTGTATCATGTCAAAGACTGTTTATTTTCGCATGGAAAAGGAAGATATTTTCAG	42072	A_95_P220977	TA21723_4097
43172	508	77	907	CAGGGCCTTGGCAATTGAATGACTTCTTTATTGAAGTTAAAGAAGTTGCATTTCCCG	42078	A_95_P192867	TA15548_4097
43177	508	82	96	AATAGAAACTTAGCATGCATCAAGCTATGGGTTTAGAGAAATCATCTTTTGGTTGAG	42088	A_95_P119152	DV162228
43178	508	83	701	TGATTATCCAAAGAGGACTTATGACCGTGAATCTCGGAGAACCTCTGATCATGAATC	42090	A_95_P136422	EB440185
43185	509	5	809	GTTCTGGTTTTGAAGTTTGTTTGTGTGGTCAAAGCTGGTGTAAAATATCAAACAGGA	42094	A_95_P236639	DV158457
43188	509	8	524	AATTGTACTCAGCTTGAAAAGAAAAGAAGCCTCAAGTTGATAACGTCATCATGTTCG	42100	A_95_P021501	TA20971_4097
43197	509	17	589	TCTCTTTCATGTTAGGTTAGCTACTATGTAACATTTTTCTGATGGCAGAATCAGTTAG	42118	A_95_P134457	EB436785
43208	509	28	469	CAATGGAAAGCATAAAATGGAGGGTTCCACTGTCCCTTTGGTAGTCAAATGGGCAG	42137	A_95_P136682	DV161271
43211	509	31	1321	GCAGGTAGAAGGAATTAGAGTCTTCCCCTGTTATCAAGGGTCTGTAGTGCTGGATTT	42143	A_95_P211687	TA19669_4097
43215	509	35	848	AGCTATATGGTGAATCTGCACATGTGCTGGCTAATCGTCCTCTGTATCATCTAAAGCC	42151	A_95_P230749	DV157786
43217	509	37	267	GCCATAATGTATGAAATTTGCTTGTCCGGAGTCTTAGCTGACATGTAATAAAACGTT	42155	A_95_P131682	EB432060
43220	509	40	254	AAGGCGGTGTTATAGGATGATTGGAGGTGTTCTTGTAGAGAGAACTATCACGGAAG	42161	A_95_P105062	EB678453
43223	509	43	712	CGATGTGACCCAATTCTTTATTCTTCCCTGTGAATCTATTCATCGTTCAGTTTCTGATG	42167	A_95_P297813	FG637808
43225	509	45	669	CTTGCAACTAATTTATCCCTTTTCCCACAGTTCATGTATTATTTAAGGAGGTCTCAGTT	42171	A_95_P128462	EB428168
43227	509	47	851	AAGTCAGATAATAACCAAGTGCCTTTGGGTCTATTAACTAATCCTACTCTACTCGTTT	42175	A_95_P013656	EB438344
43232	509	52	722	CGCAAAATGGGATATGGAGAAGGCTTTAAATGGCTCTCTCAATACATTAAATAACAG	42185	A_95_P177642	EB683024
43236	509	56	721	GGGAAACTTGGTGTCTCAGTTACTAATAAGTAGGATTATATGTTCTTTTAGGAACCTT	42193	A_95_P256799	EH622195
43240	509	60	1327	CTGGGCCGATATTGTTACTATGCGTTACTTCATACATTTTGACAGTGACATTTTCATTC	42201	A_95_P003411	TA12011_4097
43245	509	65	811	TCCCCAGACCCCACTTGTGAGAGTATACCGGGTTTATTGCTGTTGTAATTGATGCTAG	42211	A_95_P291478	TA21465_4097
43247	509	67	338	TTTGACTGCGCCAATCTGTAAAATGAACTTGACTTCTGATGGATCAGGTGATCACCA	42215	A_95_P164432	FG151495
43250	509	70	3272	TGCAATCATCCTGTTTGTTGTTTGGACCATGTATGCAATTACCATGGTACCCGGATCC	42220	A_95_P011806	AB041352
43253	509	73	789	TATCTTCTCCAGCCTTGTCTAGGTGGTGACTCGAAGACATTGATGTTTGTCAATGTCG	42226	A_95_P266131	EB450896
43254	509	74	606	GTTATGTTGATTAGGATACTTTCTGTTAGGTTCATGTATGAAGTAGAGCATAGGATG	42228	A_95_P219432	BP129744

43255	509	75	961	TTTTTCTTCCTTTATGAATATCATTGTCCGCTAGACGGTCTTTCTAGTTGGCTGGTATT	42230	A_95_P184612	TA13732_4097
43256	509	76	755	CCTGAATTCGGTATTGTGAACCTATGACGTGTTGAACTTTTTTGTTTTGTATTCCAAG	6784	A_95_P000061	DW000215
43268	510	3	614	AAGTCTGTGATCTTTTGAACAGTGCTGGCATGTTATCCTGGCTATTCTGGTGCACGCA	42091	A_95_P044166	BP130805
43269	510	4	302	GCAACAGTTAGTCAGGCACTAAATTGAAGGAAAGCCTGTAATGTCCTTTTAATATTT	42093	A_95_P008801	CV016523
43272	510	7	856	TATGACTGGTGGCCCAGATGTTACACTATGCATGATGCAGAGCTCATGTTGATTGAT	42099	A_95_P287958	FG167284
43273	510	8	1547	GTTTTCCTGTTGCATAGGACACTTGGAATTTTGTTCATCAAATTTTCACCAGCATATAC	42101	A_95_P187612	TA14385_4097
43282	510	17	883	TAAGCGTGATACCTATCTCCTTCAGGAGGGTTAGATTGATGAAGAATTTATAGTTTT	42119	A_95_P213457	TA20052_4097
43284	510	19	516	ACAAGTCCAAGTCTCTGCTGATTCCCAGTTTACACTTAACAATGTGAATTTCTTGTAT	42122	A_95_P102862	CV016239
43285	510	20	544	AATTGCTTGTACGCATTCATGCTTCTGTAAAGGTCTTGAATTTAATGTCTTTTGGACC	42124	A_95_P005976	TA13055_4097
43287	510	22	245	TTGTACCTGTAAATGGGGGGAACGGACAATTAGTGCAAATTATGGAAAAGGGGAA	42127	A_95_P029751	EB437829
43290	510	25	833	GTGCCACAGGGGATTACCAACTACAGACAGTTGGTTTTCCTCCTAAAATCCTTAGTG	42132	A_95_P216777	EB441412
43295	510	30	370	ATCTTACCGATCTTCCGTTGTATACCAGATTGGATTGTTATGTAAAGAGAGAAGGTT	42142	A_95_P180432	TA12744_4097
43297	510	32	190	TTAGATTCCGTTGGATGGTTTAGTGATGTAGCTGGTCAAGTTAAATTATGAGGGAAA	42146	A_95_P164392	EH623619
43300	510	35	668	CTCCCTTCCGAATTCCGATGAGCCAATTGGAAATTTTTTAAGTTTCCTTTAAGGATAT	42152	A_95_P149157	EB678854
43304	510	39	868	GCAGGTATTCTTTGTACAGTTGAACTGCTGCATTTTCAGTCCACTTGTTCTTTGTTCTG	42160	A_95_P200327	TA17184_4097
43311	510	46	1244	CACAAAGTAGTGTAAAGTGTATATTTGCGTTTGGTGTAATGCATGAATTTGACTGTG	42174	A_95_P026271	TA17612_4097
43313	510	48	889	GCTGACATTTTGTTCTCCTAATATAATCAGATTGGTGCATCATACTATAATGAGGTAG	42178	A_95_P011711	TA15348_4097
43315	510	50	175	GGCCGTGAGGAGAAGAATCAGGGGATTACATATTTTAAACTTAAGATTGTTAAAAG	42182	A_95_P208907	BP534683
43316	510	51	439	AGTGCATTAAGTTCATGTCCACATGTAAGCTGGCTAAATTTGACTGTGAGGGCAGAG	42184	A_95_P067300	BP136833
43323	510	58	762	CCATGTGGAGAGTTGATGTTTAGGTGAGAACAGAAATTTCATGTATGGTATTGACAA	42198	A_95_P207612	EB681605
43324	510	59	642	AACTTGATTTATTGTACTTTGTATGAGTTGCAACAGTGTCCATTTGTAGTGCATCCTG	42200	A_95_P130628	EB445989
43328	510	63	874	CCTGTCTAGAATGCAGCCCCCATTTGTTGATAACACTTTAAAGTTAATTTTAGAGGTT	42208	A_95_P204792	EB424701
43332	510	67	2679	ACATTGTTGTACACATGTTGTTTCTATAGTTACTCGATTAGCTCAGGCACTTGGTGAA	42216	A_95_P033216	AJ344534
43335	510	70	581	ATTCTATCGGGCCTTTGGAAAGAATAAAGAATACAAAGGTTGCAGTAAGTTTTAAGG	42221	A_95_P018846	TA14369_4097
43340	510	75	1072	GTATATGTATTTCTTAGTTGTCTTTGTGACTCCAGTCTTGTAATGGCCTCTAACCATTT	42231	A_95_P223192	TA22197_4097
43342	510	77	896	CGAGTGGTACAATATTTCCTGTTTCGAGGCGTAATTAGCTCTGCCATTTTTGTTGTTG	42233	A_95_P248517	EB446238
43345	510	80	1039	TTTTATTGTATTATTGGAGTCCAGACGATTTCCATGTTCATAGGAAGCTTTCTCTTTCC	42239	A_95_P198247	TA16736_4097
43346	510	81	1087	GTAAGAGGATGATATTACCACATAATAAGAGATCGAGAATCATATGCTACTCACTTC	42241	A_95_P189587	TA14819_4097
43347	510	82	757	GCTGCTGGGTGGAAATCGTTTTGTAACAATAGGAGGATTAACTAGCTATAATGTTAT	42243	A_95_P126847	EB426204
43357	511	7	715	GTACCTGGTTTAGAGTATCATTCATCTACTGTTGGCCGGCTATTCAAAAGTGGGTTTG	42251	A_95_P265866	FG637902
43359	511	9	782	AGTAATTCACACCATCAGTTTGCTGCAGCGAATCCAAGTTTTACGTATTCTGCCAATT	42255	A_95_P135937	TA18135_4097
43366	511	16	436	TCCAGGAAGTTGAGATTAGTGCCTAGAGGGCAAATTACACTGATATATTTCCAACTT	42269	A_95_P041401	BP130085
43367	511	17	713	GTTATTTTAGGGGTTATATACTCTGCATCAATTGGAGGAATGAGTACATTAACAGGG	42271	A_95_P138802	EB438454
43371	511	21	521	ATCAGCCTTGTAAATCTAAGTCTTAGAGGCTCATGATTTGTACTACCAATCTTTGGGA	42279	A_95_P282483	AM801773

43375	511	25	880	TCTCCCCTTTTGATATTTTCACTTCACTGGGTTTCCTGGTCAAATTGCAGTTTTTGCAAT	42287	A_95_P245997	EB428320
43378	511	28	531	TGGCACTGGAGGTTTTTTCTTTTTCTTTTATGGGGAAAATAACAAGCAACATGAGACA	42293	A_95_P025251	X82120
43380	511	30	845	AGTCCCAGTTTTGTTTTGGGAAGCACTTGTAGGTTGTATAATCGATTATTCGGATCCA	42297	A_95_P290543	DW000090
43382	511	32	274	CTTTTCTTCTCCCTTTGTTTCATGTGTTGATTGGTTCCGTGAAGAATTGGATTTCGTGG	42301	A_95_P121232	DW001254
43386	511	36	241	CATAAACAAAAGATTATGTAACTTCATCTTTTTCCCTCTGATTTCCCCGGGCAGGTACT	42309	A_95_P083115	BP528678
43388	511	38	1191	GGGATGCTGCGTCGTCAGTTGTTTACTCTTTAATTGTACTCTATTTTTATGTCCATGTTT	42313	A_95_P000546	AJ299256
43389	511	39	1046	CAGTCAAACCTGGTATTGTGTAAGCTTGAGTTATTATAAGAAAATTTAGATGGGTGT	42315	A_95_P010876	AB119477
43390	511	40	152	AGATTCCTTCCAGATATTTTACGCGCCTTCAGACTTCTCGATTGCATTTGCGTCAGCAT	42317	A_95_P104637	CV017107
43391	511	41	493	AGGAGGTCTTTTGTGTATTGGCAGTTATGTAAAACAGTAGCTCATTTGAATGCTGTAA	42319	A_95_P307893	FG639932
43396	511	46	1216	ACCCCATACGAGGAGTGAGCATATCTTTTTCCAGGAAATTACAATTTGAGCATTAAA	42329	A_95_P214472	TA20270_4097
43397	511	47	812	GGAGTATGCTAATTATTCCCCTCAGATTTTCAGTGATGAAAATCCTCATGCTTGCTCT	42331	A_95_P145447	EB449196
43399	511	49	677	GAAACAACCAACCAATGCATCCCCACATGTCATTTATGCCGCAACAAGGGATGTATG	42335	A_95_P138182	EB441931
43400	511	50	383	AGAATGAAGAGTTTGTATTTTTTGACTTGTTGAGAGAGGAGCTACACCACCCTCTCCA	42337	A_95_P304743	FG637992
43406	511	56	4127	GCTTAGGGAGTCCTAATCCTCATGTTGTATAGAGCTATATGTGTATATTGTACTTTACA	42348	A_95_P009926	U52078
43407	511	57	745	GTTTGTTCGTTAGCAACTTGCTGGTGGCACATTTACTGTTATGATAGATTGATTAATA	42350	A_95_P291038	DW002249
43414	511	64	663	CTCACCCCTACCATTGTGATCCGTTCCTAAAGCTCCTTGTGCTTTTGATTACTTGTTTT	42364	A_95_P181197	TA12922_4097
43416	511	66	882	CGCTTTGGCTCTCAAGCCATAGACTTGTTATCTTAAATCCATAGACATGAGGCATTGC	42368	A_95_P009161	AB286178
43419	511	69	1245	GGGGTCTGTTTGGTTCATGATTTAGAATTTGTGTAGTTTCTGTTAGTTGTCATCATGTT	42374	A_95_P010476	TA11987_4097
43421	511	71	1021	GGGGACCAGTTTTTGTATCTTAAACTGATTGTGCAACTTTCTTTTTTGTGTTTAATCTG	42378	A_95_P011386	TA15755_4097
43424	511	74	1426	CCTGTGTTTAGAACTTCCTTACTGTATCTGCTTATTGCTATCTTAGTGTTGTCAATAAGA	42384	A_95_P016201	TA14791_4097
43428	511	78	896	GTGTACTATTTCGTTTTCTCTGACAGACTTGTTTGCATTATTGAAGCTGTCTTGTTATCT	42392	A_95_P146172	TA14739_4097
43432	511	82	102	TAAGTGGGCCGGTCCCGGGCCTAAACGGGCCCAACAGAAACTTTGTATTTTTAATTTT	42400	A_95_P147362	EB451742
43444	512	9	654	AATATTTCGTTTTCATATCTTTTCAAAATGTATCGCTCTACCCCTACCCCTGCTATAGC	42256	A_95_P204287	TA18033_4097
43455	512	20	998	CTTGCTAGTAGTAGATGGTTAGGCGTATCTGTTTGTGCAAATTTCAAACAAAGTGATA	42278	A_95_P193032	TA15584_4097
43456	512	21	255	CGTGATACAGTGAAAATGTTTGGCGCAGTTCCAAGAAAACGAATGAAAATTTCTGAA	42280	A_95_P089443	BP530508
43463	512	28	130	ATGGTTAGTTATAACTAATGAGACATTCCTCCGCTTTCAGGCGAAAGTGAAGATAAAA	42294	A_95_P140427	EB444336
43470	512	35	706	CTTCAAATGATGTTGAAGTGAAGCAGATGGTTTAACTGTTGTTGAAGTGAACAAACT	42308	A_95_P186227	TA14080_4097
43471	512	36	325	CGGGCTCCGCCTTTGTGTATTTCATGGATTGTTCTACTTTCTTGTATGGCTTCCATGAT	42310	A_95_P210797	EB424986
43473	512	38	259	TGCCATTTGTAGGAGGCACTTATATTGGACAATCCCATGGACTGTAGCTTTATGGTAA	42314	A_95_P097148	BP533896
43474	512	39	713	GGTTCAGTTGGAAATATTATTTATGTTAATAATGAGAATTCGTTGCCCTTGTCACAAG	42316	A_95_P127032	EB426449
43479	512	44	715	CTGTGAGATGTTCTCTTGTAATATTACATTTTCAATGCTAAATTGTGTGAGAGTCTGCA	42326	A_95_P115587	TA12160_4097
43482	512	47	897	GAAGAAGCTATCTGGTGATGATGTTGGAGAACTTCACTACAATTACTATCCCGTTGAA	42332	A_95_P250712	EB451424
43484	512	49	896	CCTCCGATTTGAGACCTCAAAATCAGATGGTAAACTAACTTCGCTAGACCAGTACAT	42336	A_95_P226409	DV159465
43488	512	53	850	ACGATTGTTGTGATGGCTCTATTTAGTATACATACAAATTGGTGAAAATATGGACCA	42343	A_95_P011236	DV158061

43499	512	64	397	TGGCATTTATAAATGTGCTTAAGCTTGGCTCTCAACAAAAAATCAGATAAAGCTGGG	42365	A_95_P092848	BP532013
43500	512	65	585	TTCCGACGAAGACAGCCAAATATTTCTCTCTGACTGCATCGCTGTTATCTTCTCTTTAG	42367	A_95_P206602	TA18553_4097
43504	512	69	681	AAACCACATTCTAGATGGCACATTAAATCTTAGGAGTAGCATCATTTGGCACTTTTTA	42375	A_95_P115847	DV158226
43508	512	73	389	CACGGGCCTTTTCTGGATTTATATTTTTTGGACATGTTAAGAAAATAGTGGCATTTCT	42383	A_95_P002316	FG643424
43509	512	74	1181	TTGCACGCTTATCACTGCACCTGGTCGCCATTATATGCTTATGGACCATTACTTGGGA	42385	A_95_P194697	TA15953_4097
43510	512	75	123	GTGAGACACATATCTGGCTTTCTCGTTTTCCTTTCACCAAATTAAAGTAAAAATTAAG	42387	A_95_P150927	EB681077
43515	512	80	794	TTAACTGTCGTGAAGTGATCATCTATATGGACGAGAGCGAGAAACCTCCAGTTGGAC	42397	A_95_P146057	EB449908
43530	513	10	546	ACATCGGCTTGGTACAAGCGGAACTAAGGTCCATAGCAATGTTCAATCTTCAAACTA	42414	A_95_P123272	DW003141
43531	513	11	804	AACAGCAAGGCAAGCAGATGAGCTACACTTTCCGTTGGTCAATCAGCAAGCACTGA	42416	A_95_P125807	TA15758_4097
43541	513	21	678	ATGGAATTTCATGAGCTCTACCTTGTTGCATTATGTCATTCACATTATTCAGCTCCTCT	42434	A_95_P019001	EH615127
43542	513	22	874	CTTTTGATGTACCGCCCAAGGGACAAAAGTACATATCTTGTGCAAAAGCAAAAACAC	42436	A_95_P019271	EB682461
43545	513	25	731	TGGCGTATGAGGATGTTTTAGTTCTCATTTTGGCTATCAGATCAATTCCATCTTTTTTG	42442	A_95_P248972	TA14912_4097
43546	513	26	581	GCATAAAAGCATTGTTGGGTTGATTCTGGTTTCTCAATAATGGGTTTGGATCGAGTT	42444	A_95_P144437	EB447800
43547	513	27	785	TCTCGACAAAGTCTCTGCATCTTTTCCAAGTCCTTGTTTGCAGGTGCAATAGAGGATC	42446	A_95_P125867	EB424988
43551	513	31	565	ATGGCCGCAACAAACTTATAAAATTTGATTGGATTATCAGTCAAATACGTCTCCAAAT	42454	A_95_P185692	DV160583
43553	513	33	817	TTCGAGAGGTTCGACTACTTCAGTGGAGATCTTCTTTATGTGAAAAGATCTATCATCC	42458	A_95_P229734	FG166470
43556	513	36	1147	ATTGTTTTCTATCAGACCGATCCACACATCTTCCGATCTGCTCCAAAGGATGAATGAG	42464	A_95_P011081	D26509
43558	513	38	1328	ACGTGCTTAGAGATAAGGAGATCATCCAGCAACGAGAGGCTTCCCAAATTTAATCTG	42468	A_95_P178237	TA12191_4097
43564	513	44	478	GTGTACATATACAGTTCTTGTCACATCAACCAATAAACCCAAGCCCCACTACAGGCTT	42479	A_95_P153927	EB684087
43570	513	50	335	CTGCCGTCGATATTATGAGTTCTGAAGTGCCAAATAAATGAATTGGATTGCTGCAAA	42491	A_95_P308323	FG642078
43572	513	52	770	AAAGAACCAAATATATCCAGTTGGATTGTTATCTGGTTCATACCAAGCTTGTTGAGG	42495	A_95_P298493	EH621931
43574	513	54	734	CTGAGAAAAGAAAGGAGTTAGAAGATGAAGGCTACAGGATTCATGGGAGCTCTGG	42498	A_95_P017651	EB449886
43576	513	56	610	GGCGTAATTTACCTTCACATTTCAAGTCACTCTCTTATTAATGCATCTCGGGAGAATA	42502	A_95_P122962	DW002857
43580	513	60	273	GTGATGATGAAGTATTTGGAGCAAATAATGAATATGGTTCTGCATGCTTTCCAAGAT	42509	A_95_P159707	EH618154
43583	513	63	799	GCGGTATATATGCTTATTTCTAAAGTAAGACTCTCACTAATGGAGTTACAGGGTAAA	42515	A_95_P220492	TA21619_4097
43588	513	68	851	TCTTGTTCCAGGTTTCTAGTGAAACAGTAAAAGGAGTATTCTCTACTATATTGTCTAC	42524	A_95_P125277	TA12032_4097
43595	513	75	901	GGTTCAGCCTAAGCTTGCATCATGCTTTCTTCTTTTGTAAACTAATTCTGCAAAGTTAA	42538	A_95_P183722	EB428087
43597	513	77	750	ATGTACTAGTTGATGTCAGCAGTGTCAAGGCATAGTGTGTTCGTTGGTTTCCAAGAG	42542	A_95_P248827	EB681443
43601	513	81	697	GTGGTGTGATTATGTGTCAAACTTATCAGACTGCTTTGAAGTTCTTGTTATCATATCT	42550	A_95_P013831	TA18221_4097
43602	513	82	694	CCATCAAAAGGAAGGAAATACAGCCCTTCACCTGATGAAAGAAGTCCACAAGAGAG	42552	A_95_P137717	EB677939
43610	514	5	304	AGAAACTGAGACAAGTACTACTTCATTGAGTTACTGAACCAACAAAACAAGTGAGA	42405	A_95_P034898	BJ999155
43614	514	9	618	CAACAAAGTGTAGAATAGCATTAAATGTCGTCCTCTCCAAGAAAAAAGAGATGCTTT	42413	A_95_P120817	EB677535
43617	514	12	1169	AATTAGTTGGGCCGCAAACATGTGTTTGCTTGCTGTTCCTCTTTGTTGCTACTGCTGT	42418	A_95_P015366	TA15691_4097
43619	514	14	890	TGACCAGTTTCGAAGTGATGGTGTTGTTACCAGAGGAGAGGCCTATGGAATTCGTA	42422	A_95_P019351	DW000724

43621	514	16	739	GTCTTGGATCTATGTATTGGTATTGAGAGTTAAACATGGTGTATATCGAGCAACACC	42425	A_95_P218392	EB439521
43622	514	17	453	AAGTCCCGAAGACTGAGTACTCAATTCCAGATGCTTCATCCATTCAAGCATTCATGTC	42427	A_95_P127162	FG195316
43623	514	18	275	ACACTAAAGAGGGTTTTTCCGACACTCTGAATTTCTCTTGACAACAGTATGCATTCTG	42429	A_95_P054766	BP133530
43626	514	21	476	TTGTATTAATAGTGTTTCGGTTCTGAGAACTCGCATTGAAGGAGGTGCCAAAGCTGT	42435	A_95_P097298	BP533971
43627	514	22	262	CATTGTAGGATTGTTTTGATTATTGCACTCTTCATAAATACATGAAAAGAGTGTGGGT	42437	A_95_P130847	EB430953
43631	514	26	826	TTAGTGCCAAACTGACTGGTAGTTGGAGGTGACCAAGACAATTGTCTAACATATTCT	42445	A_95_P018436	DV157755
43641	514	36	247	CTGTCATAGTCTGTTGGTTTCATTGTTTGGTTTAATTCGATTTTCCGGCGAGGTTGTCC	42465	A_95_P163067	EH622075
43647	514	42	644	TGTAATGTGTGGCCTACGCTGCATTGCCAATGAAATAATTTGTTTTACATGTTTAGAG	42476	A_95_P192247	TA15410_4097
43652	514	47	816	GAGCCGTACAGAGAAAGAAGTCAAAGCTGATTACGATACAATGAATACGTTCCCAG	42486	A_95_P243822	EB682813
43653	514	48	1097	CCCTGTGGAACATCTATCCCCTCTTCCTAATTGGAGAATGTCACAAACTTCATTAGGG	42488	A_95_P190252	TA14970_4097
43656	514	51	831	CCATTTAATCAAACTCTTTCTCACTGAAGAAGTCCAAGTTGGTACTAGTTTTATGATC	42494	A_95_P218047	TA21086_4097
43657	514	52	539	CCTCAATTCTCTCCCTAAGCAAAGATATGCCTTTGTTCCGTGTTTAGGTTAATTATCAT	42496	A_95_P213437	TA20048_4097
43661	514	56	427	GTGACACCCGAGGTCAGGCTTTTATTTCCGCATTTTGGTTTTTGATTTTATATCTTTTT	42503	A_95_P275103	TC71239
43665	514	60	432	GTCTATTGTAGGGAAAACCTAGTTTAATCCGAGATGATTGCTATCATTATTGCCTCTC	42510	A_95_P201037	TA17339_4097
43667	514	62	511	CATGTAATTTTGAGGTTAATGACTCCTGTTTTGCTAGTTTGTGCCTTATTTTTGAGCCA	42514	A_95_P000946	TA13775_4097
43673	514	68	138	GAAGCTCAGCCACCGAGATTTGTTTAAACCTTCTATTCTTTCATTTGATTCCTTTTTCA	42525	A_95_P094718	BP532843
43674	514	69	397	GCCTTTTATCCGAAATCTCCAGAAAGGAAAACTATTGTAGCTTGAAATTTCTGTTGAT	42527	A_95_P134677	FG139988
43678	514	73	833	TACAGATCCTGGACTTCTATTACCTCGGGCCAATTTGAAATTTTGGGCGGGGATGCT	42535	A_95_P310418	FG155139
43680	514	75	814	ATGCTGTCAAGAAATCTGTTATGGGACTATTGCGGCTTGTAAAGTTAAAACAGCCCT	42539	A_95_P216957	DV999409
43685	514	80	533	TTGTAAAAGTTATTGCTATTGTGATGTTCTGAACCATGGATCTCTGGAAACAAGTTTC	42549	A_95_P150257	EB680347
43686	514	81	936	CACAGCTAGATCCTATGTTCTCTCTCCTTATACATGTCTCTAAAAAATTTTGCCACAAC	42551	A_95_P198472	TA16784_4097
43696	515	6	903	AATTGGAAGCGTCACAATTTCTGGTCACAAGTTCTTGGGATGTCCAATGCCTTGTGG	42555	A_95_P222867	DV159323
43698	515	8	922	TGTAAATTTCGCTACATGATCTCTTGTATGTTTTCAGCCAATGTTTCAGATATCATCGT	42559	A_95_P193262	TA15633_4097
43703	515	13	768	TTAGGAACAAGGACACAAGTTAGCCCTCTTTGTATCCACTTGGATTATGCCCTCGGAT	42569	A_95_P157057	EH615096
43708	515	18	404	GTTTTTCATATCTCTATGTTGAAAAGGTGTGTTGGCGATCCTGCCCAACAGCTTACTC	42579	A_95_P064010	BP135931
43712	515	22	628	ATCGAATCATTAATTTGATGATCTGTGAGCTGTGTTATTTGCCTCGGTTCTGCCAAAA	42586	A_95_P244242	EH615092
43714	515	24	195	GAGCTTTAAGATGTGAATTTGTACGGTAAACATTGAAGTTCTCCTTCCAGTGTTGCAT	42589	A_95_P092203	BP531691
43719	515	29	1161	CCTTGTGGTGACAGCTTTTTCACTGTTTGTTTTGTTAATAATATCCTGGTGACAGTTTT	42599	A_95_P008376	TA14854_4097
43722	515	32	451	AATTTTGAAGTTTACACTTTACTGGTGCTGGTGGGAGTAAGCTTTTATCCCTTGGTTC	42605	A_95_P174452	EH665844
43723	515	33	296	TTCTGGGGTGTACTTTGTTAGAGTGCAGTCCTTTTGATATAATTTGCTCAGATGTTCC	42607	A_95_P133362	EB434811
43724	515	34	1036	CCTCTGCATACTGGTATTATGGATTGGTGTTCTGATATTGAGATATCTATTGTTGGTT	42609	A_95_P143712	TA14032_4097
43725	515	35	672	GGTGGATCGAACAGTTAAGATAACTGGGAATCTAACAATAGATGTATTCAGAAGGA	42611	A_95_P225467	FG643186
43726	515	36	1169	GTGGTTGAGAGCTAATTCAAACCTGAAGTATCTTATCTCGATTTTGAAGTATATGTAC	42613	A_95_P189552	TA14812_4097
43736	515	46	719	TTTCCATCGCTTAGCATTTTCAAGCTGTCAAACAATCATATTTCAGATTTGTTCAAGGT	42631	A_95_P154047	EB684209

43737	515	47	963	CTATCCCTTGTTAACTCAAAAAAGGGTTCCGATTTCTTCAATGGCTCTGACTTGTACCT	42633	A_95_P011566	TA15971_4097
43740	515	50	610	GTGTTTTCTTTTTTCAGCAGAACATGCTTAGTCTTATGAAGTTACTTTCTTGGATGATG	42639	A_95_P124247	DW004103
43751	515	61	861	GGTGGCTTTGTCAATGGAACCATCATCACTACATTATCCTCATCTCTTCAACCTCGATG	42661	A_95_P115557	DV157809
43752	515	62	364	TGTGTTATAACCTCTCAAACCTCTTTTCTGAATTAAAATCAATCAGGGGAGTTTGACA	42663	A_95_P086693	BP529607
43759	515	69	705	GATACTTTATGATCTGCGATATTTTACATTTCCTACTGAAGACATGTTTCTTTCCCCCT	42677	A_95_P150637	EB680772
43761	515	71	828	AAGGATTCGTTTCAATTCTATGTATACATCTCCCTGATCGGCTCGAGCTACTGCCTCT	42681	A_95_P288983	FG160073
43768	515	78	1396	TGTCAACTGGTTGTACCAGTATCAAACAATCAGATAGTGGCAGTGTATGGTATAAAT	42695	A_95_P130772	TA12620_4097
43784	516	9	1194	CCTTGACAGTTAGAACATGAAAGCAGAGATAGTTGTTTTAGCAACAAAGTTTGTTGTA	42562	A_95_P014806	TA18534_4097
43785	516	10	909	GGTGCTAGAGAGAGGAAGTGATCGAACCTTGGTCACCATATGAATCTCTGGATATTT	42564	A_95_P234309	EB444751
43786	516	11	715	CAAAGGACTATTGTTTCTGTATGCTTCCGGTCTGTGAGATTATCTTTGCTGGACTTTTT	42566	A_95_P020761	EB684204
43790	516	15	234	TCTGAGGACTCGGTTTACGGCCATTCACATGAAGAAAAACCATTGCTCGAGGGATAT	42574	A_95_P058016	BP134363
43794	516	19	659	GGCCAGTGCGAGCTTCCTAGAAATCTTGATATTTATTCCTATGTATAACTATCATTCTT	42582	A_95_P220747	EB437995
43795	516	20	654	GTGATCTCACAGATCACCTCATGAAGATTCTCACAGAAAGAGGCTACTCTTTCACCAC	42584	A_95_P128147	FG139197
43798	516	23	628	AATGGATAGTCAGGTCACTTTACGTTGGACTCTGATGAAACGAGATGAAATGGGATA	42588	A_95_P039196	BP129484
43799	516	24	1324	GAGAACTGAGAAGTGAAACTCTTACTGGAATTACAGATGTAATAATACAATCCTGTG	42590	A_95_P199547	TA17018_4097
43800	516	25	1207	CCCTTTGTAATGACCAACAAATGGCCATAGTATAGTTTTCAATTCTTAAAGATAACCT	42592	A_95_P180632	TA12792_4097
43801	516	26	403	AATCATGCTCAAGAAACATATTCTGATAGAGTTCTATTTGAAGTTCCGTCTCCTAACCA	42594	A_95_P075470	BP526737
43802	516	27	2443	TATACAAGTTCTCGGACGAGGTTTTTGAACAGAACTTCGATAGGCGAGAGGTGTAA	42596	A_95_P012761	TA12579_4097
43811	516	36	863	GAGAGCAATCTCTTCATTGTCGGTGATATTTTTAGCGGGTCTTTTTAAGTTTCATTTTT	42614	A_95_P232414	EB425093
43812	516	37	0	ACATATTTCAGTTTACTCAGCTACTCAGAGTGTCTGCTTTGCTGTCGTATCCCATCTGC	42616	A_95_P298003	A_95_P298003
43814	516	39	713	TGGAGGCTAGTGATGACAATGATATACCGGCTCTGGAATCTCTTGATGTGGAAAGCT	42619	A_95_P014661	EB449721
43816	516	41	397	CCAACCACAGTTCACATTGTATATGAAGGTGGAAATATTGCATATCAGTGAATTATGT	42623	A_95_P221127	TA21755_4097
43817	516	42	723	CTTCAAAGTTGTGGGTATCTAATCAACAGTTGTAATAAAGAGAATCCTGTTCTTGTCA	42625	A_95_P014176	EB437412
43821	516	46	806	CCTCCAGTACGTGAAGTGTTTTCTTTTGTGCTTGGTAATACAGTTGAACCATGAGGCT	42632	A_95_P128287	EB427837
43827	516	52	850	TCTGTTTTGAGCTGTAGTAGATCTTTAATGTGCTGCTTCTCATGACTCGTGCTTTACCT	42644	A_95_P284858	FG163875
43828	516	53	358	AATGCTTCACATATATTCCCTCATAACACACCGATTACAAAGGAAGCCTACTATTATA	42646	A_95_P006901	AY061820
43829	516	54	508	ATGGAGCTATCTGTTTGAGAATGTCCCGATGCTAAATTAAGTATACATCAGTTGTGAA	42648	A_95_P024591	FG631924
43831	516	56	542	AGTTCCTGGAAAAGAAGCAAGGGAGGAATCTGTAATTTAATGGGAACTTGCCAAGTT	42652	A_95_P089758	FG153402
43840	516	65	771	ACAGAGATCAGGAAAATTAGCAAGTTAAGGCACAAGAATATATTGCAGTTATTGGCA	42670	A_95_P238764	AF252414
43848	516	73	192	AAATCGATTAGGAGCTAATCCACTGAGAGTTTGCCATGTGTATTAAGCTTTCTACTAA	42686	A_95_P078670	BP527574
43849	516	74	382	GTGTCTCATGTTCTTTAGTTTGGACAATCCAGTTGAGGCTATCAATTATCTTTTGCTGG	42688	A_95_P134157	EB436084
43850	516	75	901	ATGTCTGTCTTTGTTTCACCTGTACCTTCTGAAGACTGGCATGTGGTAATTATGTGTGT	42690	A_95_P188947	EB447633
43865	517	5	676	CTAAGTGCCTATTGGTTCTATATTTGGCCTCAAGTCCTTGATGTTTATGTTAACTGAAA	42704	A_95_P194602	EB446340
43866	517	6	555	ACTGGGACTTTTGGGATTCATTATCATGTCTATAGGAACTTCCACAATAATACAGCAT	42706	A_95_P187407	TA14340_4097

43867	517	7	93	GGCTTGTCGTGTGTAGTAGACAACATGAATTCTGATTGGCTATGACATTGAACGATT	42708	A_95_P139397	EB443139
43868	517	8	794	CATTCTAATGCTTAATGCCACAAGTCAAACTCAGTGAATCATGTCATCAGATTCCTAT	42710	A_95_P294053	EB439288
43869	517	9	208	CTTAGACTCCATTCAAGTTACAATTTATTTGCCTCCGGTGCTGATATCAAATCAATCAT	42712	A_95_P138397	EB442167
43871	517	11	1190	CATACTGGCTATTATTCTTGCACAGCTATCTGGAAACCGATCTTAGACGATATTTTGG	42716	A_95_P140172	U60057
43876	517	16	790	CTATGTTCTTAGCGCAAGGCTTTGTGCTTTCTTTGAAGTGATTTACTGATGTTTCTTCT	42726	A_95_P284533	DV157765
43877	517	17	1164	ATGAATTCCATGACCATCAGTTAAAGGTGGCGTTGCCTTCACGACCAGTGCAAACAA	42728	A_95_P022826	TA14385_4097
43878	517	18	729	TGGTTCTCCATCTTTAACTCCTTCATGATGGTCATCTTTCTTACTGGTCTGGTGTCTAT	42730	A_95_P162428	EH621378
43884	517	24	398	AGTGAATCACAACTGAAAGAAGATGAACAACTTGCCACGAGCTCTGCATGGAGAGC	42742	A_95_P041501	TA16023_4097
43887	517	27	56	TTGAAGTGTGAACAACAAAGAAAAGATAAGTCCAGTCGACCTCCCCCTCTAGCCTCC	42748	A_95_P045911	BP131261
43889	517	29	579	ACAGATGTTGTATTATTATGACACTCTTTAGTAGATGGTCATGCACTTGTGACATCGG	42752	A_95_P121507	DW001586
43890	517	30	587	TCTTTTATTGCTTGTTGGAATCATGTTTCGGGTGTAACTAAGATAACTGCTTAGTGAC	42754	A_95_P191992	TA15357_4097
43894	517	34	655	TGACTTTCCCCTCAGAGAAATACATGAGGTCCTATATACCAAATATTTCGTTCGGAAA	42762	A_95_P299623	FG190948
43896	517	36	816	GTACCCTGCTGAGTTAGTATTTATGGCCCTGTATATATATATATAGGTACTGCATCAT	42766	A_95_P022776	TA21613_4097
43899	517	39	1026	AGGAGAAGGCAATATCAAACGCTATTGTTAATCTAAGTTTTTCATGTTCTTCAGTGTC	42772	A_95_P176577	TA11646_4097
43902	517	42	682	TGTATGAATTATTTGGAGATGACACACATGCTAGGTGACGGGCATGTGGGTGTGCA	42778	A_95_P306438	FG643392
43903	517	43	765	ATCTGAATTTGTATTGAAATCTTTTTTCTTGCGGCGAATGGATTGCGTGTGTGACTTT	42780	A_95_P178422	DV160879
43904	517	44	350	TAAGAGTGCTTTGCTGTCCAATAATGGTCACATCCTTTCAGTTGACCTCTTAAACCCT	42782	A_95_P093498	BP532290
43909	517	49	773	TACACATTTACTTTTGTACCCTCCGATGGTAATGTTCGGGCCTTCTCCTTGTGTGTGA	42792	A_95_P199492	EB678882
43917	517	57	461	TAAATTTTACCATTCCTGCAGGAGTCTAGCAATAGTTGGCAGGATGGAGATTTAAAC	42807	A_95_P264286	AM840522
43918	517	58	861	AGGATTATACGTCGGGCTCTACTCTCCCTCCAGTCTTCATGTTGAATTCGTAACATGC	42809	A_95_P229244	EB425232
43924	517	64	1483	CTTGAAAGGAAACTGTAATGTATGCTCAGTATTTTTCCCTCCCAGAACTATGAAAGA	42821	A_95_P025186	TA14118_4097
43925	517	65	808	GCTCTGTAAAGTTGAAGTTGATGCACATTACTCTTGGTTGAAAGAAGGAAATCCTTG	42823	A_95_P265871	EB678199
43926	517	66	414	TGGCAATAGATCTTGACACTACATTTTGGCGTGGGTGTTAGATTTTGGTTTATTGATT	42825	A_95_P212682	TA19888_4097
43927	517	67	330	GAGCCCAAACAGGGTGGTCAATGAAGTTCTCGCTAAATAATTGTGGATTGGATATTA	42827	A_95_P104437	CV017014
43959	518	14	496	TACAAGAAGTTGAGCTTGTGATGAGGCTCACGGGAATCTGAAGAACGTGGCATCAT	42723	A_95_P207322	TA18715_4097
43963	518	18	730	TTTCCTTTTGGTTACTAGGGGATTCTATTACTGATTTATGGGATTTGACTCCAATGAT	42731	A_95_P201667	EB678092
43965	518	20	902	GATGTCTTATGTGGTTTTGGGTGGTTTCTACTGTTCTGATATGATGACTTTCATCTGA	42735	A_95_P258576	TA11956_4097
43973	518	28	1144	TGTAAGAAGCATACTTTTATCGGTCATCTGAATGGTAGATGTAACGGTAAAGATTTA	42751	A_95_P210292	TA19367_4097
43975	518	30	409	GAATGTTATCCTTTTGGTTGCCACTTTCTTTTTAATGTAGCCTTTTGTTGAGTAACTGG	42755	A_95_P098498	BP534502
43977	518	32	781	ATTCAGGCTGACTTGTTGGGTAGTCCGGTTGTAAGACCAGCTGATATAGAAACAACA	42759	A_95_P214882	TA20359_4097
43978	518	33	736	TTGACAGTAACCAGAGTTTTCGTGACTGTGAGATAGGAGATGGGGATATAATTTGCT	42761	A_95_P269996	EB428655
43979	518	34	494	TCTATCTCTCCCTTAAAGCTCATGGTGAAGGCAATTTCGGTACCAAGCTCTCATTCTT	42763	A_95_P073670	BP526271
43980	518	35	575	TGCATTGTGTAGTTCATGATTGGCTGTTCTGTATTAACATACAAGTTCAAAACATTCC	42765	A_95_P193182	TA15616_4097
43983	518	38	664	GATTCGATTTTCTTCTCGGCAACCGCTATTAAGGTTGTTTTTCCCACTGTATTGTTTTT	42771	A_95_P214602	TA20297_4097

43992	518	47	868	AATTTGTAACCATTTTGGGGTCGTTTTTGTGAAATGTCAATATGGGCGGCTTTGATGA	42789	A_95_P227774 EB425751
43995	518	50	1505	TGTTGCTGTGATGAAGTAATCTTTAACATACCAAGAAAGCCCTATTGACAACGCTAGT	42795	A_95_P191102 TA15157_4097
43997	518	52	737	TATGTACCAATTGTTCCAAGGCGGGTGGGACTATTGAACCAGATGGCGAATATCCTTA	42799	A_95_P195517 TA16135_4097
43998	518	53	831	TTCCCTAGGATGGGATGGATTGTTTTCTGGCGAGGTCTAAGATTCACGTATGGTCGAA	42801	A_95_P017276 DW003721
44001	518	56	1828	GCTCTAAACTGGTGACAACTGATATCATGACCCAATCTGAATTTCTTTTTATATGGTTT	42806	A_95_P184617 TA13733_4097
44002	518	57	787	TAGTGATACTATTGTGGTTCTCTTGCATTCAAGCCCTCAATTTGCAGCAGTTTCATTAT	42808	A_95_P162027 EH620774
44008	518	63	0	TTGATGGATGTCTTCTGGGGGTTGGTTTGTAATGACTCAGTGAATTGGGTCACGTTT	42820	A_95_P019226 A_95_P019226
44021	518	76	698	GAGACAGAATAGTGTCCGATTTTCATGTGTGAAATGCTTTCTTTATTTGGCTGATGTA	42846	A_95_P093178 EB438892
44022	518	77	768	AAATTTCTGTGGCTGGTGCAACATACAAAGCAATGGAGCTTGTCGGCTCGACAGTTG	42848	A_95_P120657 FG141669
44041	519	11	592	CCAAATCCAAGGTTGATAGATGGAATTCTGCTTACCAAGTTTGACACCATTGATGATA	42865	A_95_P200837 DV158412
44049	519	19	709	ATGCTGCTGATCAAAACAGAAATGGTTTCTCCACAAGGCACAAGAAGCTGGGTTTAA	42881	A_95_P152447 EB682780
44050	519	20	1469	GTTTTCAGTTAAACACTTTAGTTCTCTTTACCTATGTTGCCTTCTGATCTTCTGGCAAAA	42883	A_95_P008871 TA13572_4097
44053	519	23	547	ACCTTGTTGAGCAGGAAAATCAATTAACACATGAAGTCTCTCTCTCAGATACAATAGA	42889	A_95_P040486 BP129843
44054	519	24	553	TCTTTATACGGGCTGAAGTGTAAACTCATAACGACATTTTCATGGCTGCCATAATTAT	42890	A_95_P099288 BP534870
44059	519	29	761	TGAAGAAGGGGAGAAACTGTATTTCCTGCTGCCAAGGGAAATTTTAGTACGGTTCCT	42900	A_95_P252754 EH618717
44062	519	32	326	TTGGTCAAACTTCTTAACACCGCAAAGCTTGTTGCTAAACAAGAAGGGTCTGCTCGA	42906	A_95_P108477 CV018851
44063	519	33	496	GCACGGAGTCATTACTATTGAGCCTTAGACTATGATGGACATCTAGAAGAAGAACAA	42908	A_95_P307283 FG638101
44065	519	35	244	CATCTGGAAACGACAATAGCTCCTCTTCTTCCGGTGATAACAATAATAATAACAATAA	42912	A_95_P001316 EH616009
44067	519	37	379	GTCATAGACTAAATGGGCTTAATTGCGTCATTGGCAATGATTTCTATAGGGATAAGAA	42916	A_95_P143662 EB446899
44072	519	42	278	AAGTTCGATCTTATGTTTGCCCAACGTTCTTTCGTGCCCTGGTATGTTGGTGAAGGTA	42926	A_95_P106932 CV018133
44073	519	43	418	AAGATTACCAGTACACTAGATATGAGGAACAGAAGGAATAAGACCAGTTCATCAGA	42928	A_95_P089088 BP530342
44074	519	44	508	TGCGTTTGATTGCAAATCAAATTTTGTTCGATATGGATTTTGGCCCATCCTTGTGTTTA	42930	A_95_P196717 TA16400_4097
44078	519	48	740	TTAGCACCTGACTGTTGAATTTATTATTGTTATTGTTAGAAGAAATGGTGAGAGATG	42938	A_95_P273161 EB681926
44079	519	49	255	GAAATGGATGAAGCTCATCGTAAATGCCTTCGAGCTGAAGGCTTCAATGTCTGAAGC	42940	A_95_P095663 EH623842
44081	519	51	547	GGAAAGGAAAATGTAATTGAAAAGATGGAAACAAGAATTGGGCATTTGATTTCTGA	42944	A_95_P005326 TA14182_4097
44085	519	55	187	CAGGCGGTGCAAAAAGAGGAGTGCCAAGGAACAACATGATAATGAATAATTATGGA	42952	A_95_P159232 EH617186
44091	519	61	317	GTTCGGTAGGAGCTTATGCTGCGATGAAACATGTTGTGTTTTAATTTCAATGAAGTTT	42964	A_95_P001066 FS411872
44097	519	67	484	CGATTCCCTCAATACAGCTTAACTCCGTCAAGCCTGTACGAGTAGTGAAGAAGTATA	42976	A_95_P282203 AM792645
44102	519	72	686	GGTTCTGGCTTTGATTTTTGTAGTCGCTTCTTCTGCCCAAGTTCTGAATTCAATGAGGA	42986	A_95_P159517 EH617764
44106	519	76	382	CGTCTGCTTCCCGAAGATGATTAGAAATGGTGACTTGTCATAGAGAATGTTGATATA	42994	A_95_P132172 EB432641
44107	519	77	1462	ACTGTTCTAGGAGACCATTTTGGAGTCCCTTTTTAAGTAGATTTTCTTTCTCTTTTGTT	42996	A_95_P028716 TC71857
44122	520	7	887	AACTATGTGAGATACGACTTCATCCTCGAGGTGGGGTTAATCTTATCGTAGTTTAGTT	42858	A_95_P013176 TA12893_4097
44127	520	12	866	CATCCTAAGTAATTCTCCGTGCTGTCAATTAACATGTCTGGATCTTGTGATCCCTGACT	42868	A_95_P184867 EB439049
44130	520	15	776	AAATCGTTCGTGAAGCAGACATTATTATTGCTGCCGCGGGGCAAGCTATGATGATCA	42874	A_95_P021351 FG169533

44132	520	17	234	CTAGGTGGATTGGAAAGATAGTTATAGTATCATTATTGTGGTAGCGAGATAATGTAG	42878	A_95_P219922	TA21498_4097
44133	520	18	533	TCTTAAAATTGTTAAAAACAAATGCGCATCAGGTGACACTCCCTGCACCTAGTTGTCT	42880	A_95_P101723	CN498901
44140	520	25	500	GTGTGGGTAAATCAGCTTATACTGATTTCTTTTCTCAATGTTCAATGCATTTCTAGATG	42893	A_95_P001151	FG640488
44143	520	28	812	CTGAATAATAGTCACTCGTGTTAGTCTGAGTTTTGAATTGCCAAATGCGAATAGTATA	42899	A_95_P181912	EB425536
44145	520	30	375	CACATGTAATTTAGACAACTAGCATAAATGAAATTTTACGGGTTACCTCTTGAAGCGT	42903	A_95_P306853	FG636547
44147	520	32	859	ACTGATGGGGATGATGCCCCTACTGTTGCATTGGAGGAATTGTTGGCTGATCTTGAT	42907	A_95_P233644	DV161350
44150	520	35	796	TTGCATGGAGATTTGATGCTAAGGCTGCACTTACTTTGGGGATTTGAAGGAAAATAA	42913	A_95_P228674	EB449849
44159	520	44	1209	GCTGGCTGCTTGCTAAGCATTTTCCAGATTTGCTGGCAATTTGTATTCTATTTTTTAAT	42931	A_95_P008401	TA13254_4097
44165	520	50	449	TGACTCCAGGTTTTGGGGTATTGCGGGACATTTGTGGTTGTGTTTAGACCCTATCTTA	42943	A_95_P061125	BP135184
44169	520	54	777	TTTGCTGGCTATGCTGCCGGTATTGCCGCATATCTAGCAACACATAATCTCAACATCT	42951	A_95_P235924	EB450449
44172	520	57	175	GCATTGCATTGACAAGCTCCTGTAATATATGAATGTTCGTTTAGGTTTACAAATGCAA	42957	A_95_P110642	TA12282_4097
44180	520	65	811	GACATGATTCTCTCATTTCCAGTAGGCATATGGACTGATTTTTGTGGACTTCTATTAAT	42973	A_95_P126127	EB425373
44183	520	68	92	ATATGAAAGTATCGCATTTCGCTACGTTCTTCATCGATGCGAGAGCCGAGATATCCGT	42979	A_95_P118517	DV161600
44187	520	72	434	TGTACAAGACCGATAAAAGCAAGTATGAAGCCACTGCTCGGAGCTGGACTCAAAAA	42987	A_95_P108802	CV019009
44190	520	75	872	GGAAGCATCAAAAGATTGCTGTTTGTGATCATTATATTCTCCATCAATCAACCATCTTT	42993	A_95_P217082	EB424688
44194	520	79	841	GGTCGCTCCCTTGCTTTTGGCTCAGCAGATCACAAGATATATTATTATGATCTACGTA	43001	A_95_P268306	DW001336
44195	520	80	355	GGAACTTTACCTATGTTGTTGTGAAGCCTATTTGTATCCTTAAGGCGTTGGCCCTTTT	43003	A_95_P140637	TA14595_4097
44213	521	13	488	GGTGGGATGTTACCTTTGGCTATGTAAAATAATAGAATTTGTGACTGAGCTTCCTTGT	43016	A_95_P000586	EH616662
44216	521	16	844	GGGTTTAGCTGACAATGACATGTTTGGACATAGTTTGTGTTTATTATGATCATTTCTA	43022	A_95_P192497	TA15464_4097
44220	521	20	524	GTTTGTTGCTGTTGAGATTCCATTTACTCCTCGTGCAAAGCGTGTTCTTGAACTCTCTC	43030	A_95_P196062	FG137301
44221	521	21	1019	CTGTGAACTAGTGTTAAGACTTCTAATAGCTGTTAGAAGAGACTTGGATTTATATGA	43032	A_95_P185812	TA13996_4097
44232	521	32	627	CCCGTTTTAAGGACTGGGTGTAAAGATTTTTGCTGCGTCCCAATATCTACAGCATGTT	43054	A_95_P182657	TA13270_4097
44235	521	35	406	GGTCTGGTACCAATGTTCTGTGATCTGTTTATATGCTTCTTCAGGATTTGTTGTATACT	43060	A_95_P132362	EB432837
44239	521	39	291	TGATCCATGGTTTGAACAGACACTACTACTCAATAACCATACAACATACAGAAAGAA	43067	A_95_P112702	CV020789
44242	521	42	480	CAAACTCTGTGCTGCATCTTGTTCGTCCCAGGATTAAATTTGTTGCCTAGGCACAAAA	43073	A_95_P076925	BP527119
44245	521	45	748	AAGGTGTAGAAGTTTTATACAATTCAGCTTCTGTAATGCTTGGTTGTCATATTAATCC	43079	A_95_P230209	DV158827
44246	521	46	1919	TCAGCTTGTCGAACAGAATGATGCTGTGGCAATGAAGACTGCAGACACTGAAGTAA	43081	A_95_P176262	U01961
44247	521	47	479	TACGGTACACAACTGAAAACCTGGTTATTGTAATCCGAATATGAAGCATGAATACGA	43083	A_95_P089258	BP530424
44253	521	53	624	GTTGAGGATCGAAGACAATGGATGTCAACATAATATGTAGAATTAGCTGATTGTACG	43095	A_95_P262351	EB450487
44254	521	54	513	AAGAAGCGGGCAAAAGTTTTCCTTTATTCATAGGCTTTGGCTTGAACGAGTCTGCCAT	43097	A_95_P150162	FG163431
44259	521	59	872	ACCTGATGAAAGCCAAAAATTGAAGGAATGGAAACTCTCTAATTGGCTTTTCACTTCT	43106	A_95_P069935	TA12296_4097
44265	521	65	321	CTGAGACTCAAGATTTTCCATATCTTAGATGTTGATATAGGTGAGTCTGAAAGCATG	43118	A_95_P155267	EG649990
44267	521	67	799	TAAGAACCCCTGTCATCATCGTCAGTATATGGCAACAGTTATATCGAGCATAGTTATC	43121	A_95_P144447	EB447804
44270	521	70	701	GCTGCACAAGCGTTGGGGAAGATTCCAATTGATGTGGAGAAGATGAATATAAGCTT	43127	A_95_P189232	EB441756

44273	521	73	1258	CACTTGTGACAGTGGATTTATAACAGGAATTTCAAGAGCTGTGCTGCTTGTTCATCA	43133	A_95_P180292	TA12709_4097
44275	521	75	482	TTGTTGGTTTCAACTTTCATGGGTGGTGCGGCCATTACAATTGCCCTCCAGCAACTTA	43137	A_95_P083935	BP528893
44280	521	80	678	CCGCTCACCAAATCTCATGTTTTCTCGGACAATATATGAATATAGGATCAATTGATAA	43147	A_95_P271941	EB446273
44293	522	8	170	CTCTCATGTTTCAAGCGCAAGCAAAATAGGATACTGTAAATTATTTATAGGGCGTTTT	43007	A_95_P142992	EB446386
44296	522	11	505	CCTGCTTCAACTTGATGTCATGGATAGACTACCCATTTGTCTCAAACATCTAATTATTG	43013	A_95_P177762	TA12067_4097
44300	522	15	894	AATATGGAATTTCTCTTTGGACTTGACATGCTTCGCAAACACCAGTGCATGATTGATC	43021	A_95_P253504	DV158761
44306	522	21	606	CAGCAGTGTTATGTATGTGAAAGTGTCACTCTTATGTTAATCACAGAAATCATGCTTT	43033	A_95_P232699	FG645464
44307	522	22	471	GTTGGCGAAGTGTGTTCATGATATTCACAGCTTCTGCAGATGATGATCTAGAGCCAA	43035	A_95_P074910	BP526590
44313	522	28	896	TGGCGATCTCCATACTGGTTCTTTGATGGTCACTCACAATTCGACCCAAGTAATTGAT	43047	A_95_P196302	EB428815
44317	522	32	1745	CATGACTCTGTCAAAGTAAGGTAGGACAGTGACTCATTGTAGAAAGTTGAATTTTAT	43055	A_95_P239499	AB022693
44322	522	37	327	GATGAACTTAGGTAATCAGGTTGACTTGGCAAGATTATGTTTCTCGCCCTGATCAAA	43064	A_95_P090175	BP530836
44323	522	38	910	TGAAGGAAACAAATGCTGTATTATTTGGCTTATTGCCTCTGTATTATCATTGTCGAGA	43066	A_95_P011481	TA13633_4097
44324	522	39	519	GCAGCTTCAGCTTTCTCGGAAGATGATGCTAAAAAATTGGAGAAGGAAATTGATGA	43068	A_95_P134477	EB436843
44329	522	44	346	GCAGGTTTCTTGTGTGCCTTTAGCAAGTGGAATATGTTTAAATCATCTTGATTTTTGT	43078	A_95_P210242	TA19357_4097
44330	522	45	866	TTGATTTTTACATGAATGGACACGATCACTGCCTTGAACATATTAGCGACACCGAAA	43080	A_95_P227769	EB425136
44333	522	48	797	TGTTGTTCGCATGTGTAGTAACAATGTCCCGTGCACATGTCTGAGCTTTGAGTACTTC	43086	A_95_P190812	TA15095_4097
44335	522	50	227	CGGTTTGTTTGGGGTAACCGTTTTTGTGAAAGGTCAAAAGCGGTTTATTAATTTATTT	43090	A_95_P130542	EB430594
44338	522	53	931	TAGGTGCATAGTAGGAATTCCCTAGAAAGTTGGGGTCTGTATTAGGAGTCCATTATT	43096	A_95_P183837	TA13548_4097
44340	522	55	789	CAAAGAGAGTAGCTGATGGAACTGAAGAAATCAAATATACAGAGCCCAAGCAATTA	43099	A_95_P229004	EB681088
44341	522	56	2787	ACACCTGTCTTTTACGGTGTTAAGAGTGTTACTGCCGTGTTTTATTTAAAGATATCTTT	43101	A_95_P015026	TA12219_4097
44344	522	59	278	GTTGGTAGGGGTTTATGTTGGTTTGTGAATACAACAAATGAAACAATGAATGAAGA	43107	A_95_P132937	EB433802
44352	522	67	963	GTTCTGGACTGTAAAAATAATTCTAGGGTGGTTGCTTCAACCAACGTCTTTGTCAAAA	43122	A_95_P244772	AB286176
44353	522	68	216	TTGTACGGTCTTACACTGTGGTTCTTCGGTTCTTGTTTTCTGCTGTGTATGTCTGGACA	43124	A_95_P105457	CV017467
44357	522	72	561	AAGGTGGTGCTTTACCCTGTAAATCCTTGATTTAGCGGCAATTGAGTACATTTATTTG	43132	A_95_P201427	AY329066
44361	522	76	1038	GGAAGGCCTTTTATGTTCTTTGTTGCCAATCATCTTTCTTGGCAGTTCTGCCCTCTTTT	43140	A_95_P112932	TA16625_4097
44390	523	20	1182	CTATTATTTTGCTACGTAGTAGTATATGACTTACCTGTATCCGTAGGTGGTTAAGCAG	43172	A_95_P199917	TA17097_4097
44391	523	21	692	AATTGCCCACCAGAAGAGCCGGTATATTTTTGATCTCTATCACAGGAGGAAGGAGAT	43174	A_95_P287988	FG184919
44392	523	22	0	TCTGCCAACATGAGTCATAAGGGTGTATTGGTATCCATCTATTTGACAGTTTTGGAAC	43176	A_95_P309113	A_95_P309113
44397	523	27	1261	CATCTGCTTCGAAAGGTGCATTCGTTATACAAAATTGTGAGATCAAAGCAGAACCAG	43185	A_95_P013951	AY772945
44403	523	33	775	AGGTGAGATTGTAATATTGCACAATGCTGTTGGAGTCTTGGCAGTGTTTGGAATTGC	43196	A_95_P031091	EB450512
44407	523	37	473	TAGGAGTCCTTTAAATAGTACAGAACTGAGTTGAAGTTGGTCATGTCTGAAGAATTA	43204	A_95_P133122	EB434344
44409	523	39	740	TGGGTCTGCAGTTAATCTTAGTGGGTGTTTGTATTGGATGTCATATAATATTGATATG	43207	A_95_P287073	FG162850
44421	523	51	605	CATTTCCATGCCGATCATTATATTGGCTTGACGAAAGTATGGTCACATGGCCATATCT	43231	A_95_P220517	TA21624_4097
44422	523	52	478	GAGCGTTTAGCTTTTTTCGAAGATGCCATCGGAACATTTTTTATTGTTAAACAACCAG	43233	A_95_P096923	TA13055_4097

44425	523	55	183	ATTTTAGAACATGTCAACCGCAGAAGAGTCCACTTGAGCAAACAGCACCTGCTGTTG	43239	A_95_P104202	CV016886
44427	523	57	503	CTCTTAACCCATCATACCCTTAAGTACATGTGTTATGTGTGCTAGTACAATTACAATG	43243	A_95_P221332	EB680130
44429	523	59	641	TATCTTAGTGATTACTAATATTTAGTCCATAGGCCATTAGAACTTCATCCCCCCTCTCC	43247	A_95_P116337	DV159031
44430	523	60	203	GATTTGTGTATGAGAACGTTGCTGTGTTTTCTGCAACATAATATAATTTGCGATCCTC	43249	A_95_P096058	BP533454
44437	523	67	832	TGCAAAGAAAACCATTAGTGGGGAACAACATGGTGAGGTTGGTGGTGAAATCTACT	43263	A_95_P289068	DW000214
44439	523	69	441	CGATGGCTCGAATTATGGGTATCAAAACAATCCGATGAATGGAGACAGTTCAACGC	43267	A_95_P073660	BP526269
44443	523	73	142	GTTTGTGTACTCTCCATCTGTAATCTCACTATTTTGATTTTGAAGGTGAAGCATTTGAC	43275	A_95_P095748	BP533319
44447	523	77	859	CTGTGTCATGCGCGGTGGCATTGGAAGCTCTTAAGATCTACAAGGAACGAAATATTG	43283	A_95_P225682	DV161260
44464	524	9	526	GGATGTTATAATCAGCAAGAGTACGTCCATCTTCGAGCTGCTTTCCGGCAAAAATCA	43152	A_95_P247252	EH614418
44466	524	11	1055	TTATTTCGAGTTGATTTTTTGGAAAGGACTCTCAACTGTGTCTCCCATTCTCTTTTCCA	43156	A_95_P196127	TA16271_4097
44472	524	17	728	AGATAGAGATATTGACCGAGCTATTGAATTCATCCATGGTAATGCATCTTGTGGTAA	43167	A_95_P017836	TA17610_4097
44478	524	23	492	GATTGTGCTTTGTTTCTGTTGGCCAATGTTGGCATGAAAATTGTTGTGTGGTTTATTT	43178	A_95_P206002	TA18412_4097
44480	524	25	239	GCAATGGATCATGGTGAAGCATTTTGGGGCAAACTGAAAGCAGCTGCTGAGAAAAA	43182	A_95_P005756	TA16206_4097
44484	524	29	689	AATCGACAACTTTTGGCTTCTGTATTTCGAGCTTTTCTTAAGGTGTAATCTTCTTCTTA	43189	A_95_P015966	TA14464_4097
44487	524	32	2618	GCATCTTTTTGTAAATTCTATGCTTTGGTGTTTCTAGATGTGCAATACTTTCCCTGGAA	43195	A_95_P250117	AJ344533
44489	524	34	430	CATACCTCATCACAGATACCTACAGAATTAGGACGCATACATTGTAATAGCAAAGAA	43199	A_95_P022571	BP531559
44492	524	37	1880	GACTAGTCCAACGTGTTAGAGGCTCTCGGAAAAGTTAGCTTCGTAAAGGTGCATAG	43205	A_95_P083590	AF435451
44495	524	40	658	CTTAACTAGGCTAGGGTATCTTGTTAAACTTTTGATTTGAAGTTGATCCTGAACTCGT	43210	A_95_P119597	DV999026
44499	524	44	495	CATCATGCATATATTCAACCTGGTGCTTTAGTAAGGGGAAGAGGACACAATTTGGAT	43218	A_95_P073650	BP526267
44500	524	45	687	AATCCTTCTTGACAATGAGGCCATTTATGACATTTTGCAGGCGGGTCACTGGACATT	43220	A_95_P283433	AJ421412
44501	524	46	516	AATATGGAGCAAATGTTGATGGATACAGCCCCATCTACAACACAGATGATTGGTCTC	43222	A_95_P002486	EB438907
44502	524	47	306	AGGCCACACTCATGATTGATCTTGGCACAGGAAAACAATAACAAGATCAACTGGGC	43224	A_95_P112207	CV020574
44503	524	48	142	AGTCTGTATTTTAAAGCATCGGGATGTATGGTTTTGCCCAAAAATAAGTCGTCCTGT	43226	A_95_P140062	EB444024
44504	524	49	953	CAAGCAAGAGAGCAAGCAAGATGTAGTTTAGACTTGCTAGATAATTTTTTAGGTTTG	43228	A_95_P032676	AB025029
44505	524	50	583	TGTTCGCGGTTTCTATCACAGATTTGGAGTATTTTCAGTCGAGTTAGGCGGCATCAG	43230	A_95_P054866	BP133550
44506	524	51	1132	TTGTGGAATAGCCCTTGTAATGAATTGCTCTTCAACATCGCATGTCTGATTTATCAAA	43232	A_95_P012781	TA14792_4097
44508	524	53	784	CCTTGCTAATGAGTGTAATCCTGAAGAAGCCACACACAATTGATATTTCACTTTATTG	43236	A_95_P215817	TA20571_4097
44514	524	59	787	TGACAAAACCTGGAAATAACAATCATGTACAGCCATCGGATAACATCGGTCAGCCCC	43248	A_95_P128182	EB427714
44515	524	60	357	ATGGAGGATGTTGGATAACTATTTGCATTTCATCTCAGTTTGACTGTTTTCCCTGCTA	43250	A_95_P308618	EB683967
44517	524	62	611	AGGTTACTAATAATTCATGCACGGATATTCACATGATTGAATGCGGGATGCTTCGTG	43254	A_95_P069565	BP137419
44518	524	63	97	GAGAACTGAGAAGTGAAACTCTTGACTGGAATTACAGATTTATTGATACAATCCTGT	43256	A_95_P104832	CV017188
44519	524	64	813	GTCTCTGCATGACATATATGTTACGGGTTTGAGCCGTGAAAACATTCACTAATGCTTG	43258	A_95_P203522	DV157966
44522	524	67	753	TCTAGTTTGAGGTAGGACTGTATTGTATATTAGCAGGCATTTGACTCAGTTCTCCTTT	43264	A_95_P086510	EB678998
44524	524	69	482	TAACGAGCTTGTCGTAGTACAAATGTGGTGATTTACTTTGTTTTTGAAGTTTGAGTGT	43268	A_95_P228429	DW002260

44530	524	75	113	AGTTCTCATGGTACAGTCCTATGGAGAGGGCTTCCTGTGCAATAATCTAAATGACCAT	43280	A_95_P143332	EB446661
44531	524	76	815	CAAAATCCATTACAATGAATGTCCGTGTCATGTAGGCTGTACCTTGTAAACTTAATTT	43282	A_95_P222117	EB424966
44548	525	8	665	GTGTAAATTGCAGTAACAGGCTTTTACTGAATAGATAATACACTTCTTTGTGTGACCC	43288	A_95_P273686	EH618465
44551	525	11	561	TGATCAAATCACTCTTTAACACAAAAAATGGAGATTGTGGGAACTGCTAATTCTTGT	43294	A_95_P122752	DW002719
44555	525	15	995	ATACTTTGTTCCTGGTACTAATATACTTTCGTTCTGGTGGGAATTTTTGTTCCCCTGCG	43302	A_95_P213392	TA20036_4097
44559	525	19	767	AGAAGTGCAGAACAGACTAGTAGGATCACCAACTGTTGGCCCAAGTTCAAGCAGTAT	43310	A_95_P281653	EB682384
44564	525	24	912	GGTACTGTTAAACATGTCTGGAAATCCGTTACTTTATATGACTATCTTTCTAATGCAC	43320	A_95_P190582	TA15046_4097
44566	525	26	463	AACGGCTGGTCCAATACATTTAGAATTGAGACGTAGTTATTATTGTAGTTTGTAGCAT	43324	A_95_P001301	FG641987
44570	525	30	628	CAGTGCGAAGTGTGAAGTATGAGTGTTTGTCAAATGTTCTTGATTGTAAAGAAAGCA	43332	A_95_P152667	EB682983
44575	525	35	1735	TGATTTTCTTGTACTTCGGCATCAAGAATGGTGCGACATTGTAACAAACATGCAACT	43342	A_95_P018096	AF215852
44576	525	36	1681	CCTACTGAGAAAAGACAGACGAGGCACACACTCAGAAATAAAACAGTTATGAATTGT	43344	A_95_P191382	TA15223_4097
44578	525	38	719	AATTAACTTAGTGAAGTTTTGGTGATCCACCATGCAAACTGCCCTTGTACTCGAGGTC	43348	A_95_P160502	EH619193
44580	525	40	870	GAGATGGTTGGACAGGTTGACTTCAAGAGAAACATGGACTTTTGGCAGCTTGATAA	43352	A_95_P260091	DV162086
44583	525	43	468	AAATCAAAAAGGCAGCCTCATCAACTGTCAGACCATGGATTTGGATGTTGTCTCTCCT	43358	A_95_P078875	BP527628
44584	525	44	532	TTCCTTTTGAAATCATTGTGTCAATTTAGCTGACAGTGTTAGATCCCATTTATGCCATT	43360	A_95_P207807	TA18823_4097
44588	525	48	160	AGCAGCCATTTTTAGCTTCATCCTAAGAGAAAGAGAAACATCCACCCATCTCTAACCT	43368	A_95_P103652	EH664439
44590	525	50	848	GGATCTTGTAACCTTCACTTTTTGGTGGATTTTAAGTTTCAATCTCCATTATATCGACA	43372	A_95_P267471	EB425928
44595	525	55	0	AGTGCAGTTCCTAACAAAACTCCAACCACTGGTTTTTCATCTGGATTTCCACCTAGACT	43382	A_95_P316888	A_95_P316888
44602	525	62	597	AGAAATTTTATAAAGCCCTGCAGCAGCCTTGTTAAGTGAGAAACACCATGGAGTTCT	43395	A_95_P051021	BP132543
44603	525	63	392	AGATCTATCGCCTCACTTACTATGGCAAAGGGAGAATGCCAGGATTTGGTCAGAATT	43397	A_95_P061765	FG645308
44605	525	65	758	GATTCGATCAACTTCAATGTCATTGCTATTTCAAAGAGTTAAAAGTGATGCACTCTGA	43401	A_95_P117567	DV160506
44613	525	73	435	TCATATATTTGTGTCCTGAGCCTTATCCTGAGGAAAATTTGGAGTTTCTTCGAATTAA	43416	A_95_P001396	FG642013
44618	525	78	709	TTCTTGCTGCTCGGATTACTTGCTCCACTGTGTGTTGGAGGCAATTAAATCCGCAATG	43426	A_95_P179257	FG163565
44640	526	15	789	AACTGAACATACGACTGCAATTCTTTTAATTGCTAGATGCTGAAATTAGTCGCTGTCA	43303	A_95_P191807	TA15316_4097
44643	526	18	397	AAATACCAGTTGAAATAGAGACTCCAGATCACCACTACTATCATCTTGCCTTTTTCACT	43309	A_95_P050256	FG641345
44648	526	23	1566	TCAGCAACTATTGCCTTATATGTCGAAAAGTGTGCTGCAAAATCAATCTCTTGCCAAT	43319	A_95_P034703	AY433959
44649	526	24	734	GACGGTTCAGGCTTGAGTATGAGTTTGTTTTGTTCTAAAGTTGTTCTTTTTAGGATTT	43321	A_95_P070135	DV159788
44652	526	27	797	AGAAGCTGAAGTTTTCTGTTACTATCTTCTGCTGCTCAGCATTTTAACAGCACTATTTA	43327	A_95_P180142	DV157719
44654	526	29	552	CAATTCCAGAATACAGATTCGTAATATTAGATGGTTACGATATCAGTGCCATTGGTT	43331	A_95_P138742	EB442458
44657	526	32	524	AATGAGAGAAGCAAGTAAACTTGCCTCCCCGACTTGACTTGATGTGTTCTGGTTATT	43337	A_95_P197082	TA16484_4097
44661	526	36	209	AGACAAATGGGAAGAGAAATTTTTTGCTGGCATTGGTTCACGACAAGGGGAGACTT	43345	A_95_P155092	EG649893
44667	526	42	867	GTGTAACTTCATGTTTTAACTCCAGTACTGTTCCTGGTCTCCTGCTATTCTTCTTTATG	43357	A_95_P007986	DV157830
44675	526	50	1842	GATCCAAAGCCTAGAGTAACACTACCTCACCACAGAAGAAGGATGTCTGATCTACTC	43373	A_95_P017461	AB003037
44681	526	56	216	GCAGTACATGAGCTAGGATGGGAGTAATTTACATATTGGTTAAAGATTGTACAGCTT	43385	A_95_P129722	TA18797_4097

44682	526	57	224	TCTCCCAACATATTATCCTTTTTGGACTGAGAACTTCTGTTCTGGATAATTAATGTATC	43387	A_95_P139742	EB443650
44683	526	58	587	AATGCATATCTGATGAAACAATGAAGACGTAAAACGCAGATGTCTTTCCTCATTAGA	43389	A_95_P017796	BP136685
44685	526	60	713	TTGCTCTGCTGTACTAGCCAAGACTTGTTCTCAAATGGAGGGCCCTTATATAGAATAC	43393	A_95_P127692	EB427243
44687	526	62	828	TGTCTGAGCTTTGAGTACTTCTGGGCATGCGAGTGCTCTTTAGTAATATGTTGGTTTT	43396	A_95_P012786	EB446058
44690	526	65	783	GTGACTGAGGACTGAGAACAATTCGAATAGTAGTAGATGGTTCCAGTTTATTATTTA	43402	A_95_P193352	TA15651_4097
44691	526	66	545	GATGGAGTATTTGAACCTTGGGATTTATTGCTTTGAAATACATTTGAGATGTTGACTG	43404	A_95_P108832	FG152141
44692	526	67	807	CTGGCTTGCAGTGAGAAGTGATAAAATTCTGAAGACAAAAGGCATTTAAGAAAATA	43406	A_95_P188547	TA14596_4097
44693	526	68	979	GGGTAATTATGTGCAATGCTCTCAACAATTTTGTACGTTTATGGGTATGATGATACCA	43408	A_95_P195512	TA16133_4097
44694	526	69	872	CATTTACCTTTTCAGAAAACAATTACTCCTATGTAGCTTTGTTAATCGCGTGTGCTATT	43410	A_95_P206142	TA18443_4097
44696	526	71	822	GAGGATCTGGTCAATCTCCAACTGGTACCACAGGATATGGGAATCAAGGTTATGGTT	43414	A_95_P244767	DV161566
44699	526	74	440	ATTAACGAGTTGCCTTGGCACAAGGTGGGAGTGAGAATAACCCGGATTATCGAGTG	43419	A_95_P173287	EH665571
44700	526	75	2152	CAGGGCTCTGTCCTTTATAGACAAGTATTGTAGTTTCTTTGTGATTTAGTTGATGTTTT	43421	A_95_P127302	AY248907
44719	527	9	788	ATGCGAAAGGCAATCGCCAAGTCTTCTCACACTTTAGATGAGTCTCTTCGAGCAAGT	43427	A_95_P070295	TA18690_4097
44720	527	10	514	GAAGCTCGTGCACTTGTGACTCCAGTTCTGGGATGGTATTTAGATATCGCGATTTTTA	43429	A_95_P207747	EH622203
44721	527	11	1002	CGATTGATGAAGCTTCATAAATTTGGATCTTCATAGGGACCAAGAGCTCCACAGAGC	43431	A_95_P203352	TA17836_4097
44722	527	12	655	GGTTGGCTTAAGCAATTATTGCAGCAATAGAGATTTTGAAAACTAGTATCCAGTTTTG	43433	A_95_P002346	TA12017_4097
44727	527	17	721	AATATCATGATTGCTTTGTACGAGTGCGGTTTGGTGACTGATTGCGCTACGGGAGAA	43442	A_95_P126497	EB425818
44730	527	20	861	AGCAGTACATGCTGCTGTACCATTCATTGGTATGCTCAGGAAGTCTGTGTTGATGCC	43448	A_95_P224747	EB425191
44738	527	28	781	CGGAGTATTACCAAGGACAAAGAACTATAAAATCTTTTTACGAAGTAGGAGCATGTT	43464	A_95_P126647	EB425991
44745	527	35	881	GTGTCCTTTTTCACGTATATATAGATAGAGCAAGAATGAAAATGGAGACACCTTTTC	43478	A_95_P198837	EB678922
44748	527	38	813	CATGACAATTAACATATGTTGGTTTGGGGCTTTAATAATGGACCCTTACTAGCATAAT	43484	A_95_P199517	TA17011_4097
44751	527	41	671	CGATTTGGCGAATTGTGCAAGCAGTTGCTAAGTGTTATTGTATATATATGCTCTCTAT	43490	A_95_P286133	EB446708
44753	527	43	809	GAAGCATATCAAAGAGGAAGTGCAGATAACATCACCATTGTGGTTGTCCGTTTTCTG	43494	A_95_P025976	TA18770_4097
44754	527	44	632	GGGAAAGGAGTAACTTTATTTTCAGATTTGACCGCAATGCGAATGCCAATATTTACT	43496	A_95_P155377	FG633779
44758	527	48	319	CAGAGCCTGCAACTTGAAAAATTTGTGGGAGCTAATGTTCTTAAATGACAAATTGTG	43504	A_95_P143157	EB446501
44760	527	50	706	TACTTACACCATGGCAAGCCATTGAAAGGAGTTTCCCATTCTCTCAAGAGATATCATA	43508	A_95_P316163	EB424895
44761	527	51	322	TCAGTACTACCAGTCTTGGGAGGTTGTATCTTTATTTTTGCTGTTGGTTTCGATTATCT	43510	A_95_P308918	FG643982
44765	527	55	777	CGTTGTTATTACCTGTTTTGCACATTTAAGTATTTCAGATATGTCGTTGTCTCCTAACA	43518	A_95_P199352	TA16976_4097
44767	527	57	421	TCTTATTTCACACCTTATTTGGTCAATTTCGCTGTTGCTGCTGCTGTCTGTCTCATCGC	43522	A_95_P093033	BP532114
44779	527	69	517	AATGTAGTGAGGGTGTTCGTTCTTTTCCTTGCCGCCTGGTGTTGCTAATCATCTTCGA	43545	A_95_P307053	FG637202
44782	527	72	780	ATTTGCGACACGTGACATTAAAAGGCGAGCATCTGACCTACGATTATCAGTCGTCAT	43551	A_95_P241475	FG147699
44783	527	73	824	CTAGCACTAGCGCTCCAACTCCTGAGTGGCAGCAAAAGATGACAAATCGCAATTAAA	43553	A_95_P234424	DW003168
44784	527	74	902	CTACTCCTGCTTCGAATACTTAGTGCTTTCAATTGAAAATGAATTGATCCAGTGTTTTG	43555	A_95_P009006	X95752
44806	528	11	656	AAATTTGAAGGTCCGCCGTCTCGCTCGTTCAAAGATGGATCCTGATGAAGAAAGGA	43432	A_95_P103977	EB425907

44812	528	17	849	TGCAATAATGCTTTTCGGGATAGTGCATTTGGTTTTCTGGATAGTGCGTTTGGTCATG	43443	A_95_P263871	EB425395
44815	528	20	877	TTTTGACGCCATTGTTGTTTCATGGGTCAAAGCTAAAGAATAATTGATAATTCCCCGT	43449	A_95_P177212	TA11913_4097
44820	528	25	825	TCTGCTTGTTGTTCGTTGATGCATTCTCTAAGTAGCTCGTGCCGTTTTGTTGGTACTG	43459	A_95_P271061	EB450067
44822	528	27	723	CAAGTGGAAACCAATTTCATGAAGTTTTTCAAATTTCATAGGAAGGTGTATGGTCTA	43463	A_95_P268556	EB451235
44824	528	29	433	GAGCACAACGGAGCCCCATTATTCTTTACTTAAAGCTGAGTTATCACATATTCACATT	43467	A_95_P143742	EB446946
44826	528	31	540	TGCGGCTATTTGGCAATTCCAAACTTTTTTGATATATTTTGCAATGAGATTGAACAGC	43471	A_95_P205737	TA18354_4097
44833	528	38	207	TGTAAAGTTGAGGAAACGCCGAAAGGGTGGTTTATTACATACATTGATAACGATTCA	43485	A_95_P141962	EB445556
44835	528	40	175	CCGTAGCTCCTTGTAGATGTAGAGTTCTATTTTCAGAATTTCTGTACAATCCTTTTTCT	43489	A_95_P092683	BP531930
44836	528	41	418	TCAACAAATTCAGGATATGAAATCCTGTCCTCATCATTACGAGGAAACAAAGCAAAA	43491	A_95_P100668	BP535479
44837	528	42	703	GTGTTCATAGTTTGTTTGCGATCTTTGTGAAATGAATTTCCGTTCGGAAAGTAAAGTT	43493	A_95_P221487	TA21829_4097
44839	528	44	185	TGGGTTTACTCCAAATCTCCTTGCATCTGGAGCTGATGAAGGTGAAATCAATCACTA	43497	A_95_P154662	EG649695
44842	528	47	1576	GAACGAGCTTTGTTATTGAGAATCGGATAATATGGATTAGTAGCATCTGATTTACTG	43503	A_95_P026186	TA15524_4097
44845	528	50	768	GAGTTGCAAATCGCTTTATTTTCGACAGGGACATTGCAATATCAGCAAGGGGACCAA	43509	A_95_P145422	EB449176
44847	528	52	237	TTTAGCTGTAGCAGTTTTTCACATGTCACATCCTGATTAATTCATGGTGTTCCTTCAGC	43513	A_95_P114897	CV021809
44853	528	58	700	TGTAAACAGTAGTTTCATATCATATGTGCAAATCATGCATCACTGCTCTTTGAGCGAG	43524	A_95_P220332	EB445616
44855	528	60	613	CATTTGGTGTTACTGATGTTAGGCTATATGCCCAATTCTACAGAAAGACTATTTTCAG	43528	A_95_P177657	TA12037_4097
44857	528	62	356	TGTAAATTTGTAGCCTTAGTGTTTGGCAAGTACTTTAAAACTGTTTCTTCGCACTCCA	43532	A_95_P090403	BP530937
44858	528	63	476	CGTTCATCTTTGGGTACTGTTAAACATGTCTGGAAATCCGTTACTTTATATGACTATCT	43534	A_95_P021871	TA15047_4097
44866	528	71	855	CTCCCCTCTGTTTTTCTGTGGCGCATAGGTTGTACATTGTAAAAATTTCCCAATACCAA	43550	A_95_P116902	DV159682
44868	528	73	1717	GTAATAGTAGGCATATGAGGGGAGGGATTTTACACATATTTATATATGACAAGAGCT	43554	A_95_P259246	AY366400
44891	529	11	222	TGCTTTGTTTGTAAAGGAAGAGCTTGATTGTTGGCCAGAACAGAACCGCCGGAAAA	43563	A_95_P090778	BP531089
44892	529	12	1371	ACCTATTGACAAGCTCATAAAGGTGGGCATTTGCTAATATATGGTGTTTCAGGTAAA	43565	A_95_P237714	U81312
44895	529	15	458	CACATTGTTGACATTCAGTAACCTCACCTTAACAGGAGATACAAGTTTACATGTTACA	43571	A_95_P023646	DW002686
44896	529	16	730	GGATTTGGTTTTGTTGTGTACGTGGTTTGAACATTTCTGGTTAAGTAATTGTAATTGG	43573	A_95_P236574	DV160976
44900	529	20	562	GAGAGGTTTGAAGAAAATTTTGGGAAAACGTCAACGACTCCTAGCTTATTTGTCAAA	43581	A_95_P020901	TA21374_4097
44901	529	21	89	CTCTTCAGCATTTGATCTGTCAAATTGAATCGGCCTCCCTCTCCTAATTTTGGGACCCT	43583	A_95_P042581	BP130396
44902	529	22	551	ATAAATGTACTCCTTCGATTTTAGTTGTTGTTGTATCCTAGTCTACGACTAAATCTGTC	43585	A_95_P139882	EB443800
44903	529	23	485	CGAACATTGAATTCTATGGCATTGTCACTTGCAGTTTGGTATACATGTGAATGTTTTG	43587	A_95_P096443	BP533628
44910	529	30	1775	GCGAGTGTTAGTATTGGGTACTTCTTTGTCATTTTTATACATGTCGTCAAAGTATTGT	43601	A_95_P195317	TA16089_4097
44912	529	32	875	AAGAGCAAAATGAGTTCAGGTCTGTACCTCGTGATTTTGGTAGGGCATGGAAGGAG	43605	A_95_P215192	TA20431_4097
44913	529	33	866	ACCTCATGGATCTTCCTTGGTAGAACAACATTTTCCAAATGAACAACCAAAGCGTTTG	43607	A_95_P245687	DV162199
44914	529	34	543	GGGCAATGCGGAAGGAAGTCTGAGATATGGACATTTTCTTTGAATTTCAAGAAGTCT	43609	A_95_P026816	BP133938
44918	529	38	523	ATTAGATCGAAGATTCAGTGCCCTAGTTGAGGTACAAGTGTGTGGATCAATGGTGA	43617	A_95_P208872	EB681754
44919	529	39	848	CCTTTCCTGAGGAAGAACTTCGTAGTTTAATATCTGAACAGTGGAAAGAAATGGGCT	43619	A_95_P297263	EB682547

44920	529	40	1054	AATAGGTAAGAAGTGCTCAGCAAAGAACCTGCCTAAGTCTTGTGCAATTTCTTCTTTT	43621	A_95_P108132	TA12400_4097
44926	529	46	1778	TTTTATGGACTTGATGGCGGTTTTCCTTTGTGATATTGTTAGACAACCCGTATGTCTAT	43633	A_95_P238424	AF137288
44930	529	50	443	TGGATGCTAAAATTTTGTGCTTCATGACACTTTTCATTTGCACAAGTGTGACAACATG	43641	A_95_P058486	FG172441
44937	529	57	261	ACTTTGAACAATATCACAGAGATACGAACGGATGCACTTAAATTGCTTGCCATGTTA	43655	A_95_P075795	EB678149
44938	529	58	351	TTTGACCTTTACGATCAAGACCATAACGGCTTGATTACTGCTGCGGAGCTCCAACAA	43657	A_95_P111637	CV020289
44942	529	62	343	GTCTGATTGTTTTGTTGTCTAGTACCTACAGCAAAATGGTGTTTAGATTTCATGGAAA	43665	A_95_P094583	BP532783
44951	529	71	1065	CCTTTGAAAGCCATTACTTAAAACAACCTCAGTCCATCTGATCTACAATTGGATCATA	43682	A_95_P181927	TA13095_4097
44954	529	74	116	CATGGATTGCTGAAGACGATCGGTATGTTACAGTTGTTGAATGATTTTATACTGGTTT	43688	A_95_P106177	CV017785
44955	529	75	148	GACGTTGATGATGATCTAGTTTATCTATATTTACGTCGCCGTATTTGGACTTAGTATT	43690	A_95_P106497	CV017921
44975	530	10	1392	GGGCAGATGCTTCCTGTATTCAGTTTTCCGTTTTGATATCTTTTCACAATCCACAAAA	43562	A_95_P239724	AY619953
44983	530	18	683	GTTACTGGTTTTGTTGGGTCATATTTACTTGCTAGACAGATGTGTTTGCTTTAAGTAA	43578	A_95_P121657	DW001777
44984	530	19	656	ATGATCTTTTGTATCCAAATTATTTGAAGCTCTCTTCTGTCGGTCCTATGAGACCGAAT	43580	A_95_P023331	FG163977
44986	530	21	728	TTTGGGTAATGACACTACTGCAAGCTAGCGCTTTATCATTCTTGACTTCGACTTCAGG	43584	A_95_P288708	FG194389
44988	530	23	526	CAGAGAAAATGTCTTGGTAAATATGGTCTGGTGGAGAAATTGGGAAACCTGAGTTC	43588	A_95_P086425	BP529534
44989	530	24	798	ATCCACGATGACTGGTCGTAGACCCTGAAACACCAGCATTTATCAAAGCATGTTTGCT	43590	A_95_P235039	FG143827
44993	530	28	923	ATTTACTAAGGAGATTTAACAGTTGTTCAAGTCGTGCTTGTAGCTTCTCTTCTACTGAT	43598	A_95_P181387	DV999233
44997	530	32	148	TCTTCTTCGTCATGTTACCTCGCCGGAAACTTCTAAAGCTCTAGATCGGGTCAAAACA	43606	A_95_P106312	CV017860
44999	530	34	1137	GTATGATGTGGATCTTAGATTTTGGACCTATAGATTTCCTGTAACTGTCTTATTCGAA	43610	A_95_P191157	TA15168_4097
45002	530	37	646	CTCTATAGCATGTCAATTTGCATTGCTGTCAACACCTCTCTTTCTCCCACACTGAAAAA	43616	A_95_P064480	BP136066
45003	530	38	901	ATTTGAATTCCTTGGGGATCTCATTAGCATTATCTGCTATTCCTTGTCGATTTTAGTTT	43618	A_95_P000386	DV157743
45004	530	39	430	GCACTGTGTTTTGGCAGAAGTGATGAGTTTGTCGAGTTCAAGACTTCCTCCTCCTACA	43620	A_95_P020986	BP533513
45007	530	42	455	CCGCATACAGTATATTTGATATGTTTCATCATTGCGTCAAGTAAAATGACAGACACAT	43626	A_95_P073315	BP526186
45010	530	45	453	TTTCCGGTCCAAGCCAGTGCATATAGGAAAGCATGCCTTAGAACAGTTGTCTTTCTTA	43632	A_95_P049116	BP132086
45015	530	50	835	TTATAGGGACAAGATTAAGAGTCTTGGAAGATGTTTAGTGATTGGATTTGGAGGTG	43642	A_95_P125797	EB424893
45016	530	51	691	GTAGGATAACCATTTTTGTACCATATTCTTTTTAGTAGGGAAAGGCCCTGAATGACCA	43644	A_95_P152927	EB683252
45017	530	52	1086	TGTAGGAACGCTTGCAAAGATTGATCATAAAGTTGGACACTTGTTCTGTTTTCTGCCT	43646	A_95_P204267	TA18029_4097
45019	530	54	683	CTACATTGGATCCTGACAACATAGTGAAAATTGTACAAACATTTGTCATCTGATAGAC	43650	A_95_P196042	TA16253_4097
45026	530	61	759	CAAGAGATTCGACTCAGGTATATTAAGGCTATCCCTTCTTTCTTTTCGTCATGATCTAT	43664	A_95_P135497	EB438990
45032	530	67	790	TGATGGCAAGCTGGTTGGGATTATCACAAGGGGCAATGTTGTTAGAGCTGCTCTACA	43676	A_95_P146217	EB441030
45035	530	70	291	GGCTTTGTCTTAGTAAGAATTATTGCTCAGAATTTTGCAGTACTAATTGGTTTTCACC	43681	A_95_P002166	TA12144_4097
45062	531	12	947	CCCTTTCCCATTGATAGATCAATTTCAGAAGCAGATAAAATTTAACCACCTTGTTGCTT	43693	A_95_P201937	TA17527_4097
45064	531	14	738	ACTGACTTGTTGGAACAGCATGACCAATTTGTTGGCTTATGCAATCTCGTTTGGCAAA	43697	A_95_P299713	FG194432
45065	531	15	788	CAGTGGGAGTTTGTCAAGGTAAGTTGCATTGTGGAATAAACTGATCTCCAGTTGCTG	43699	A_95_P159207	EH617171
45078	531	28	391	TACTGATTGGAAGCTGTCCCCACTCATGACAATTATTGCACCAGCTTCCTGAATTTAA	43725	A_95_P204742	TA18129_4097

45082	531	32	786	ACAGCGCGAACACCAGCAGTCAAGTAGAGCAATGCCCACAATGTCATCTAAGATTTT	43733	A_95_P136242	EB439893
45083	531	33	488	GCTTAGGCCGAGGGGATCTAAGTATAGTGGATCAACTTGCTTGAGAAACATGTGATT	43735	A_95_P055606	BP133743
45087	531	37	366	CAAAACCACCATGGATGTTGTTTCTAATGCTAGCTGTACTACCAATTGCCTTGCTCCC	43743	A_95_P127337	EH665096
45088	531	38	362	CAAGTAGATGTGGCATCTAAACTACAAGCGGAGGCCGTCTGCCTCAATGAAAAGAA	43745	A_95_P277558	AM789373
45089	531	39	46	AAAGAGAAGTCTATTCCCCAAGAGTATAAACTGGGGCAACTCTTAGAAAGGTTCAA	43747	A_95_P131997	EB432437
45093	531	43	1330	GGAGTTCTCCCATCGAAATGACTTCAACACTTTGTAACTATTTATTCCGTTACATTATG	43755	A_95_P021861	AB433897
45097	531	47	360	CTGAGACTTGACTTGTTCTTCAGTTTTTTAGATACAGGGAGTAGTATACTACTAATGA	43763	A_95_P094523	BP532761
45099	531	49	421	AATGTGAAGGAAATGGCAGATTTCTCCTCGAAACTATTATCGTGGCTTGATGACATG	43767	A_95_P080325	BP527977
45101	531	51	840	GAAAACCGCTTACAACAGTTCAAGCTACCAGAACCGGTACTTTGCATTGGTGGATAT	43770	A_95_P291703	EB424646
45103	531	53	254	ATCGGAGTCTTGTAATTGCCTTCGTATTAACTCCCGGGTTTTGATATGATCAGTTTTT	43774	A_95_P052916	BP133046
45104	531	54	747	GGGCTATTGATAGACTGTTGAAAGTGATTAAGATGCCACATCCAGTACCAGAAGTG	43776	A_95_P148397	EB677705
45106	531	56	468	ACACGTGACTCTCCGAATTCCTGGGCTTCCAAAATCCAATAGCTCAAAGAAGGCTAA	43780	A_95_P039416	BP129542
45108	531	58	1488	GACGGTATAAAGCATAAATGATCTTATGTTCTATTGAAGGGTTTGTATTTGTACTGG	43784	A_95_P196927	TA16450_4097
45109	531	59	532	ACATGTTAGTTCTTGGAAAAGGTGCCCCTGAGAAAAACTTCTTTTCTCAAAATAATCA	43786	A_95_P069045	DW001751
45111	531	61	689	AACACAGCAACAACCCATAGTACATGTCCAAGTCCAACCTTTACTTAAACTAGATTAA	43790	A_95_P001981	FG645246
45112	531	62	945	CTGGTTTCTATTTAAGGCTACTCATTGTTCATTGAAACTGGTACTCAATGTGCAAAGA	43792	A_95_P200712	TA17265_4097
45113	531	63	1371	AGGATTAGGAATGAAACTGATAATCCGCTGCAGTATGTAGATCAGTTAGATGTTCGA	43794	A_95_P217567	TA20962_4097
45114	531	64	481	ATTGCGTGATGACACTGGAACGGATTATTGTGGCTATGTTGTAATAGATGTCAAATT	43796	A_95_P221092	EH614536
45116	531	66	550	AATGGTGAAAGAGCTGAATGTGTATGTATCTTCAACATCAAAATTGATTGGAACCTC	43800	A_95_P218857	TA21267_4097
45121	531	71	307	ACCTCCAGTTTCCAAAGGGGCTAAATTTCAGTCTCAGAATAAGACTGCAGTTCCTGC	43810	A_95_P070415	BP192630
45123	531	73	621	TTTTCACGCTGAGGGGAAGGTATATTGTGTTGAAGGTTCCATTCCCTTTTTCTCTGTA	43814	A_95_P069725	BP137467
45147	532	12	905	GTTGGTTATGTATGAGCAGTGAAATGTCAAGTCTTTCATTAACTATGCTTGTTTTCTC	43694	A_95_P193257	TA15632_4097
45151	532	16	451	TTGGGGAATAAGGCTACAAATAATCAGATCATACTCAGTGTAGCCATTGTCTTATTG	43702	A_95_P077755	BP135562
45152	532	17	673	TTATTTGATCACTCGAAAGCAAGAAGCTTGGATCACTTATGGTTGCCTTGTTCCTGTT	43704	A_95_P316263	TC50772
45156	532	21	795	GAAATGGCTCTGTAATACTACAGTTTGGAAAATATGCAATGATGTTTGTCTAGGTTC	43712	A_95_P009446	TA12124_4097
45158	532	23	1215	GAAATGATGATCGCAAAAACAGCCTCTGGGTCATTTATCTCATAAACATCTGACGTG	43716	A_95_P209167	TA19131_4097
45162	532	27	316	ATCTAAGCAATGCCGGAAGCCACAAAGAGGCCAACTTGCTGCGTTTTGGTAACAAA	43724	A_95_P114507	CV021641
45163	532	28	909	AAGTGCAGAGGACAATGCTCGAACTTCTGAATCAGCTTGATGGATTTGAGGCATCA	43726	A_95_P215522	TA20505_4097
45166	532	31	554	GCAGATCGTCCTATTATCCCTTTCCCATAGTGTGTACAAGTAGATTTTTTGCAGAAAG	43732	A_95_P123517	DW003368
45167	532	32	723	AAAGTGAAAACAGAAACGGATGCCAAACCTGGGAAAGATGAAACTCCGTCTACTGC	43734	A_95_P242882	EB445623
45169	532	34	713	TCTGATGACACTGCTCCATATGACTCCTAAAGACATGGTGGTGTGTGTTCTCGCTTTC	43738	A_95_P256469	EB447983
45173	532	38	232	GAGTAGTGTTTTTGTCCTAAGGGCACTGAATTGAGATTCTGATATCCGTATTTTTGTT	43746	A_95_P184022	TA13594_4097
45174	532	39	786	ATCTCATAACTGATTGAGGTGGTACAGGAGGACTGGATGGCAGGTGAAGCTTTTCA	43748	A_95_P235919	DV158264
45182	532	47	822	TTTTGGCACGACCATGAACATTCTCTACGGTGATAGTGTTTGTGGTCAAGGTGGTGT	43764	A_95_P229795	EB438532

45191	532	56	407	TCAATCCACTAGCTCCCTAGGAAGTTTTGTCGCTTATTATGTACTGGGACTAGCAGCA	43781	A_95_P096578	BP533685
45193	532	58	117	TCCATTGAAGCAACTTGGATGTCTTCAGTCTTTTTTGCCTCTGCATAGCGCAGTAGCA	43785	A_95_P208732	FG633958
45200	532	65	219	ACAGCGTTTACCGTAAGTGAAGTTCAGGCATTATTTGAGATGTTCAAGACTATTAGC	43799	A_95_P101813	EB681917
45201	532	66	821	TAGTCAATCAAATATAAGATGGGTCACTGTCTCAGCAGCAGCGCTAGAAGCAGAGA	43801	A_95_P304403	FG158815
45207	532	72	734	AGAGGAAGGACTTGCCATGATTGATGATGGTCACATAGATGGAAGACGTCGATACT	43813	A_95_P224857	EB451913

Description	PT24	Det Call - WAB
gb|KL4B.113B11F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.113B11, mR	28.61	1
Unknown	82.66	1
tc|Rep: Chromosome undetermined scaffold_30, whole genome shotgun sequence	29.26	1
gb|29G06 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5',	513.64	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	92.35	1
gb|KN6B.105E07F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105E07,	25.93	1
gb|KT7C.109D22F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109D22, mR	97.58	1
tc|Rep: Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vi	18.75	1
gb|KF8C.103A06F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103A06, mR	507.33	1
gb|KT7C.112E04F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112E04, mR	49.29	1
gb|AM817961 COL, cold overnight library Nicotiana tabacum cDNA clone nt006115	22.75	1
gb|KL4B.104M22F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104M22,	106.45	1
tc|Rep: Chromosome chr18 scaffold_24, whole genome shotgun sequence - Vitis vi	643.54	1
Unknown	18.9	1
tc|Rep: Hydroxy-methylglutaryl-coenzyme A reductase - Nicotiana tabacum (Com	5245.78	1
gb|KF8C.104I01F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104I01, mRN	67.71	1
tc|Rep: Fructose-bisphosphate aldolase - Solanum tuberosum (Potato), partial (65	384.65	1
gb|AM798722 seedling library, SL Nicotiana tabacum cDNA clone nt002106047, m	26.3	1
Unknown	99.38	1
Unknown	54.75	1
tc|Rep: Blue-light photoreceptor PHR2 - Arabidopsis thaliana (Mouse-ear cress), pa	27.1	1
tc|Rep: Polypeptide with a gag-like domain - Petunia hybrida (Petunia), partial (9%)	190.91	1
gb|AM807618 seedling library, SL Nicotiana tabacum cDNA clone nt002189039, m	57.28	1
Unknown	20617.25	1
tc|Rep: Transformer-SR ribonucleoprotein - Nicotiana tabacum (Common tobacco)	512.76	1
gb|CHO_SL024xm08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	42.25	1
tc|Rep: Chromosome chr1 scaffold_84, whole genome shotgun sequence - Vitis vin	185.4	1
Unknown	31.08	1
Unknown	22.86	1
Unknown	406.13	1
tc|Rep: TGB12K interacting protein 3 - Nicotiana tabacum (Common tobacco), com	85.99	1
gb|KR3B.111G01F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111G01,	19.99	1
Unknown	1115.99	1

<table>
<tr><td>gb|CHO_SL028xe24f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6</td><td>174.43</td><td>1</td></tr>
<tr><td>gb|KL4B.105N10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105N10, m</td><td>23.79</td><td>1</td></tr>
<tr><td>tc|Rep: BZIP transcription factor bZIP122 - Glycine max (Soybean), partial (26%) [TC</td><td>73.56</td><td>1</td></tr>
<tr><td>Unknown</td><td>33.26</td><td>1</td></tr>
<tr><td>Unknown</td><td>53.52</td><td>1</td></tr>
<tr><td>gb|KF8C.102C07F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102C07, mR</td><td>90.47</td><td>1</td></tr>
<tr><td>tc|Rep: Formate dehydrogenase, mitochondrial precursor - Solanum tuberosum (P</td><td>28.01</td><td>1</td></tr>
<tr><td>tc|Rep: Glycolate oxidase - Solanum lycopersicum (Tomato) (Lycopersicon esculent</td><td>51.45</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi</td><td>150.37</td><td>1</td></tr>
<tr><td>gb|TT-07_J04 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sequ</td><td>30.88</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin</td><td>201.46</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin</td><td>233.86</td><td>1</td></tr>
<tr><td>Unknown</td><td>30.86</td><td>1</td></tr>
<tr><td>gb|AGN_RNC129xo20r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequen</td><td>22.68</td><td>1</td></tr>
<tr><td>gb|TT-07_O10 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se</td><td>29.94</td><td>1</td></tr>
<tr><td>gb|CHO_SL022xb18f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6</td><td>66.21</td><td>1</td></tr>
<tr><td>gb|KF8C.110D11F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110D11, mR</td><td>191.67</td><td>1</td></tr>
<tr><td>gb|FS407121 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA</td><td>1183.39</td><td>1</td></tr>
<tr><td>tc|Rep: Triosephosphate isomerase, chloroplast precursor - Spinacia oleracea (Spin</td><td>418.38</td><td>1</td></tr>
<tr><td>gb|KR3B.105E15F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.105E15, m</td><td>51.81</td><td>1</td></tr>
<tr><td>gb|AGN_RNC114xj01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc</td><td>133.75</td><td>1</td></tr>
<tr><td>Unknown</td><td>138.38</td><td>1</td></tr>
<tr><td>gb|KP1B.110G19F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110G19, m</td><td>61.46</td><td>1</td></tr>
<tr><td>Unknown</td><td>33.56</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi</td><td>1668.96</td><td>1</td></tr>
<tr><td>Unknown</td><td>49.37</td><td>1</td></tr>
<tr><td>Unknown</td><td>46035.85</td><td>1</td></tr>
<tr><td>Unknown</td><td>22.37</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr10 scaffold_312, whole genome shotgun sequence - Vitis</td><td>2826.88</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif</td><td>44.54</td><td>1</td></tr>
<tr><td>tc|Rep: Proteasome subunit beta type-1 - Petunia hybrida (Petunia), complete [TC6</td><td>72.22</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi</td><td>24.48</td><td>1</td></tr>
<tr><td>Unknown</td><td>69.56</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif</td><td>87.19</td><td>1</td></tr>
</table>

gb|CHO_SL015xd16f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	2783.71	1
Unknown	3211.75	1
tc|Rep: Chromosome chr14 scaffold_211, whole genome shotgun sequence - Vitis	116.52	1
tc|Rep: Uracil phosphoribosyltransferase - Nicotiana tabacum (Common tobacco),	26.23	1
tc|Rep: Expansin-2 - Petunia hybrida (Petunia), partial (52%) [TC59451]	231.24	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	34.77	1
tc|Rep: At4g04200 - Arabidopsis thaliana (Mouse-ear cress), partial (84%) [TC5587	536.93	1
tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin	24.81	1
tc|Rep: Chromosome chr11 scaffold_14, whole genome shotgun sequence - Vitis vi	39.08	1
tc|Rep: Protein BCCIP homolog - Arabidopsis thaliana (Mouse-ear cress), partial (42	31.2	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	2770.57	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	104.99	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	25.87	1
gb|Nicotiana tabacum S-adenosylmethionine decarboxylase mRNA, complete cds [	13112.45	1
Unknown	98.35	1
tc|Rep: Thioredoxin - Limonium bicolor, partial (64%) [TC42824]	48.84	1
tc|Rep: Voltage-dependent anion channel - Nicotiana tabacum (Common tobacco),	241.45	1
gb|AGN_RPC019xj22f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	42.07	1
gb|AGN_RNC021xd11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	126.99	1
Unknown	2121.79	1
tc|Rep: 3-hydroxy-3-methylglutaryl-coenzyme A reductase - Nicotiana sylvestris (W	11592.65	1
Unknown	19.16	1
Unknown	35.14	1
gb|TT-31_K08 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	190.91	1
gb|KN6B.009M14F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009M14,	14483.65	1
Unknown	31.61	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	29.55	1
gb|AM791244 DL, diurnal library Nicotiana tabacum cDNA clone nt005034008, mR	26.07	1
Unknown	1476.92	1
tc|Rep: Pyruvate kinase - Vitis vinifera (Grape), partial (34%) [TC50143]	153.37	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	15143.15	1
gb|N.tabacum mRNA for c subunit of V-type ATPase (980 bp) [X95752]	2861.12	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	59.33	1
tc|Rep: ATP-dependent RNA helicase-like protein DB10 - Nicotiana sylvestris (Woo	42.35	1

gb|KN6B.115P14F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.115P14, m	51.47	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	695.46	1
tc|Rep: Chromosome undetermined scaffold_100, whole genome shotgun sequenc	29.17	1
Unknown	28.14	1
gb|AGN_ELP024xn11f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	72.26	1
tc|Rep: Chromosome chr12 scaffold_57, whole genome shotgun sequence - Vitis vi	879.19	1
Unknown	36.15	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	633.58	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	30.69	1
Unknown	51.88	1
gb|Nicotiana tabacum MADS box protein (Mads1;11) mRNA, complete cds [AY1837	10095.53	1
gb|KF8C.103P09F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103P09, mRN	129.61	1
tc|Rep: Alpha-tubulin 4 - Populus tremuloides (Quaking aspen), complete [TC44871	10251.15	1
Unknown	34.85	1
gb|TT-05_A21 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	195.16	1
tc|Rep: Thaliana 60S ribosomal protein L7 - Solanum tuberosum (Potato), partial (9	51.27	1
tc|Rep: Thioredoxin h-like protein - Nicotiana tabacum (Common tobacco), comple	533.86	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	355.38	1
tc|Rep: Actin-97 - Solanum tuberosum (Potato), partial (57%) [TC46429]	54331.4	1
gb|KF8C.104N24F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104N24, mR	293.45	1
tc|Rep: Tonoplast intrinsic protein bobTIP26-1 - Brassica oleracea var. botrytis (Cau	169.57	1
tc|Rep: Translationally controlled tumor protein like protein - Nicotiana tabacum (	456.6	1
tc|Rep: Ferredoxin--NADP reductase, root-type isozyme, chloroplast precursor - Nic	61.35	1
Unknown	22.28	1
gb|AGN_RNC018xn18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	18.49	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT43-4-330, cultivar Bright Yellow 2	178.98	1
gb|KR3B.104B03F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.104B03, m	247.87	1
tc|Rep: Chromosome chr11 scaffold_14, whole genome shotgun sequence - Vitis vi	583.42	1
Unknown	1113.21	1
Unknown	92.53	1
tc|Rep: Uncharacterized protein At1g06515.2 - Arabidopsis thaliana (Mouse-ear cre	269.96	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	374.67	1
tc|Rep: Cytochrome c, monohaem - Medicago truncatula (Barrel medic), partial (54	1012.86	1
tc|Rep: Chromosome chr14 scaffold_26, whole genome shotgun sequence - Vitis vi	1129.31	1

gb|AM840768 seedling library, SL Nicotiana tabacum cDNA clone nt002017057, m	40.04	1
gb|KL4B.104L10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104L10, mR	27.93	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	59.76	1
gb|AGN_PNL214br1_h11.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRN	74.77	1
gb|KR3B.110M18F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110M18, r	450.96	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	25.79	1
gb|AGN_RNC124xk20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	23.83	1
gb|AGN_ELP004xg14f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	69.09	1
Unknown	17.8	1
gb|TT-05_O02 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	88.29	1
Unknown	1788	1
gb|KP1B.109P07F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109P07, m	20.63	1
gb|KN6B.103J11F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103J11, m	24.43	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	57.74	1
tc|Rep: Chromosome undetermined scaffold_133, whole genome shotgun sequenc	22.47	1
gb|24B08 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', r	48.96	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	144.33	1
gb|KR3B.105P09F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.105P09, m	45.86	1
Unknown	24.12	1
tc|Rep: NADH dehydrogenase subunit II - Dicyema misakiense, partial (9%) [TC6863	27.57	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	20.19	1
gb|KG9B.106A24F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106A24, m	59.58	1
Unknown	200.81	1
tc|Rep: 6-4 photolyase - Arabidopsis thaliana (Mouse-ear cress), partial (38%) [TC5	56.3	1
gb|FS424443 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	24.09	1
gb|TT-10_E15 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	149.49	1
gb|KR2B.002B04F.051019T7 KR2B Nicotiana tabacum cDNA clone KR2B.002B04, m	32.2	1
Unknown	18.26	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	240.13	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	4291.13	1
gb|KP1B.037A10F.050623T7 KP1B Nicotiana tabacum cDNA clone KP1B.037A10, m	108.57	1
tc|Rep: Chromosome chr11 scaffold_14, whole genome shotgun sequence - Vitis vi	1139.7	1
gb|Nicotiana tabacum squalene synthase mRNA, complete cds [U60057]	10499.3	1
tc|Rep: Ribosomal protein L1 - Oryza sativa subsp. japonica (Rice), partial (72%) [TC	19.56	1

gb|AGN_RNC029xf13f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	145.84	1
tc|Rep: Chromosome undetermined scaffold_60, whole genome shotgun sequence	189.21	1
gb|Nicotiana tabacum mRNA for putative cytosolic cysteine synthase 7 (oas7 gene)	5439.63	1
tc|Rep: UDP-apiose/xylose synthase - Solanum tuberosum (Potato), partial (41%) [T	17216.9	1
Unknown	728.22	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	44.48	1
Unknown	55.77	1
Unknown	1038.32	1
tc|Rep: Polyubiquitin - Populus tremula x Populus tremuloides, complete [TC54238	25.88	1
Unknown	72.16	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	628.18	1
Unknown	41.2	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	56.67	1
Unknown	18.65	1
gb|18.2B08 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5'	60.68	1
gb|AGN_RNC019xl15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	64.03	1
Unknown	23.26	1
Unknown	912.18	1
gb|KG9B.003G22F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003G22, n	99.16	1
Unknown	911.25	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	373.71	1
gb|AGN_RPC019xe13f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	835.73	1
tc|Rep: S-adenosylmethionine synthetase - Solanum tuberosum (Potato), partial (9	189.67	1
tc|Rep: Chromosome undetermined scaffold_91, whole genome shotgun sequence	140.05	1
tc|Rep: Chromosome chr1 scaffold_166, whole genome shotgun sequence - Vitis vi	55.24	1
gb|AGN_RNC012xg17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	191.93	1
Unknown	222.6	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	1736.25	1
tc|Rep: Actin-depolymerizing factor 2 - Petunia hybrida (Petunia), partial (96%) [TC	597.31	1
Unknown	75.72	1
gb|BP534995 MAT005 Nicotiana tabacum cDNA clone BY34204, mRNA sequence [	73.96	1
tc|Rep: Fatty acid desaturase; Peptidase M, neutral zinc metallopeptidases, zinc-bir	23234.9	1
Unknown	2679.18	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	132.94	1

gb|KF8B.100M03F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100M03, m	998.42	1
gb|Nicotiana tabacum hairy root 4 (HR4) mRNA, complete cds [AF043554]	48568.55	1
gb|AGN_RNC121xm10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	21.23	1
gb|Nicotiana tabacum mRNA for microtubule bundling polypeptide TMBP200, com	1151.85	1
gb|TT-04_B13 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	24.99	1
tc|Rep: AT4g05320/C17L7_240 - Arabidopsis thaliana (Mouse-ear cress), complete	375.29	1
Unknown	780.57	1
Unknown	58.24	1
gb|KR2B.110H02F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110H02, m	32.13	1
gb|KR3B.109D09F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109D09, m	38.07	1
Unknown	17506.4	1
gb|EST_CSP005xl20f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	41.49	1
Unknown	102.11	1
gb|KR2B.001E12F.050815T7 KR2B Nicotiana tabacum cDNA clone KR2B.001E12, m	644.71	1
gb|AGN_RNC007xn07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	26.79	1
gb|TT-29_K19 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	82.14	1
gb|KL4B.108H11F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108H11, m	85.2	1
tc|Rep: Translationally-controlled tumor protein homolog - Solanum tuberosum (P	6282.1	1
tc|Rep: Photosystem II 44 kDa reaction center protein - Nicotiana tabacum (Comm	20.61	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (12%) [TC6	23.24	1
tc|Rep: At1g20110/T20H2_10 - Arabidopsis thaliana (Mouse-ear cress), partial (25	190.42	1
tc|Rep: Glycoprotease family protein - Synechococcus sp. (strain CC9311), partial (	557.3	1
gb|AGN_RNC125xk01r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequen	209.51	1
tc|Rep: Chromosome chr1 scaffold_136, whole genome shotgun sequence - Vitis vi	729.52	1
tc|Rep: Chromosome chr14 scaffold_26, whole genome shotgun sequence - Vitis vi	37.58	1
Unknown	17.78	1
Unknown	76.46	1
gb|Nicotiana tabacum diphenol oxidase mRNA, partial cds [U45243]	38.41	1
Unknown	1092.14	1
gb|KP1B.111K06F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.111K06, m	132.46	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	21.99	1
gb|KL4B.111P09F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111P09, mR	271.98	1
Unknown	133.6	1
gb|AGN_RPC024xg07f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	31.42	1

gb|TT-10_I08 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	111.8	1
tc|Rep: Chromosome undetermined scaffold_226, whole genome shotgun sequenc	704.96	1
gb|KF8B.201A17F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201A17, mR	85.67	1
Unknown	24.3	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	89.15	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	80.53	1
Unknown	183.77	1
gb|Nicotiana tabacum NTS1 protein mRNA, complete cds [AF248538]	17512.75	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	59.18	1
gb|AGN_PNL222cf1_e9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	174.22	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	1556.71	1
gb|BP136210 MAT001 Nicotiana tabacum cDNA clone BY8791, mRNA sequence [B	431.62	1
gb|BP535041 MAT005 Nicotiana tabacum cDNA clone BY34252, mRNA sequence [	100.25	1
Unknown	49.91	1
tc|Rep: 26S proteasome subunit 7-like protein - Lactuca sativa (Garden lettuce), pa	76.97	1
Unknown	129.38	1
gb|KN6B.009N02F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009N02, r	21.47	1
gb|AGN_PNL205bf1_d1.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	89.18	1
gb|FS390767 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	687.97	1
gb|KR2B.002K11F.051019T7 KR2B Nicotiana tabacum cDNA clone KR2B.002K11, m	79.81	1
gb|AGN_RNC105xd19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	17.53	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	423.1	1
gb|KG9B.003C06F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003C06, m	90.13	1
tc|Rep: Homolog of defender against apoptotic death 1 homolog - Nicotiana suave	153.61	1
gb|Nicotiana tabacum NtWRKY-6 mRNA for WRKY DNA-binding protein, complete	74	1
tc|Rep: UDP-apiose/xylose synthase - Solanum tuberosum (Potato), partial (96%) [T	14053.65	1
Unknown	52.28	1
tc|Rep: Ubiquitin-like protein SMT3 - Oryza sativa subsp. japonica (Rice), partial (86	143.23	1
tc|Rep: Beta-carotene hydroxylase 2 - Capsicum annuum (Bell pepper), partial (75%	215.92	1
gb|TT-49_H17 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	23.63	1
Unknown	25.3	1
gb|KF8B.201E11F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201E11, mRN	22752.4	1
Unknown	527.14	1
gb|TT-08_F14 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	50	1

tc|Rep: Chromosome chr8 scaffold_68, whole genome shotgun sequence - Vitis vin	333.04	1
Unknown	35.47	1
Unknown	103.15	1
gb|KL5B.118M13F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.118M13, m	104.71	1
gb|FS383363 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	39	1
gb|KG9B.005L07F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005L07, m	203.95	1
gb|KF8C.102G18F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102G18, mR	53349	1
gb|BL12.103G21F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.103G21, m	3079.23	1
Unknown	1072.91	1
gb|KF8C.106N11F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106N11, mR	411.39	1
gb|TT-41_J12 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	33.04	1
Unknown	24.79	1
tc|Rep: SINA1 - Medicago truncatula (Barrel medic), partial (86%) [TC40495]	988.07	1
tc|Rep: AT3g47831/T23J7 - Arabidopsis thaliana (Mouse-ear cress), partial (89%) [T	197.06	1
gb|KP1B.102B01F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102B01, m	183.96	1
tc|Rep: Ribosomal protein L33 - Castanea sativa (Sweet chestnut), complete [TC60	186.94	1
tc|Rep: Ribosomal protein L7/L12 C-terminal domain containing protein - Solanum	29.63	1
Unknown	91.77	1
Unknown	767.78	1
gb|AGN_RNC022xp24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	748.04	1
tc|Rep: Constitutive plastid-lipid associated protein - Solanum lycopersicum (Toma	57.53	1
tc|Rep: UDP-galactose transporter homolog 1, related - Medicago truncatula (Barr	2327.12	1
Unknown	47.26	1
gb|AGN_RNC005xn15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	50.18	1
Unknown	41.72	1
gb|KP1B.104G11F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104G11, m	995.65	1
gb|KL4B.105P04F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105P04, mR	70.14	1
tc|Rep: Chromosome undetermined scaffold_928, whole genome shotgun sequenc	42.28	1
gb|BP131950 MAT001 Nicotiana tabacum cDNA clone BY4065, mRNA sequence [B	33.51	1
gb|CHO_SL024xm14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	35.66	1
tc|Rep: RS2 protein - Beta vulgaris subsp. vulgaris, partial (25%) [TC48506]	40.5	1
tc|Rep: Isoform 2 of Q9XI05 - Arabidopsis thaliana (Mouse-ear cress), complete [T	130.39	1
gb|KL4B.111G14F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111G14, m	20.02	1
gb|CHO_SL002xo04f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	64.26	1

Unknown	161.92	1
Unknown	22.6	1
gb|KR3B.111K10F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111K10, m	92.18	1
tc|Rep: Eukaryotic translation initiation factor 5A-4 - Solanum lycopersicum (Tomat	212.71	1
tc|Rep: Chromosome undetermined scaffold_51, whole genome shotgun sequence	454.81	1
gb|KL4B.107K19F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107K19, mR	27.28	1
tc|Rep: Fructose-bisphosphate aldolase - Vitis vinifera (Grape), partial (96%) [TC44	6280.91	1
gb|KT7B.103H01F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.103H01, mR	71.67	1
tc|Rep: Ribosomal protein L30e - Pisum sativum (Garden pea), complete [TC57011]	45.39	1
gb|AGN_RPC022xm11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	103.65	1
Unknown	420.22	1
tc|Rep: 3-ketoacyl-CoA reductase 1 - Gossypium hirsutum (Upland cotton) (Gossypi	30.15	1
gb|KT7C.110I10F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110I10, mRN	32.15	1
gb|BL12.103H16F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.103H16, m	41.17	1
gb|Nicotiana tabacum mRNA for cytosolic glucose-6-phosphate dehydrogenase TC	94.98	1
Unknown	81.31	1
gb|TT-01_E01 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	78.83	1
gb|KN6B.102A15F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102A15,	672.78	1
gb|Nicotiana tabacum mRNA for TBZ17, complete cds [D63951]	1008.01	1
Unknown	47.92	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	134.43	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	25.45	1
gb|KF8C.101L11F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101L11, mRN	130.13	1
tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	3697.3	1
gb|KG9B.004E04F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004E04, m	81.94	1
gb|AGN_RNC023xb17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	41.99	1
Unknown	88.49	1
gb|KN6B.109P08F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.109P08,	504.87	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	286.65	1
gb|CHO_SL008xa12f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	4054.92	1
gb|KT7C.112H03F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112H03, mR	118.21	1
gb|KT7C.110O14F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110O14, mR	1304.79	1
gb|AM807541 seedling library, SL Nicotiana tabacum cDNA clone nt002034037, m	1473.37	1
Unknown	322.84	1

Unknown	37.73	1
Unknown	63.73	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	2441.93	1
Unknown	26.18	1
tc|Rep: Pathogenesis-related thaumatin family protein - Brassica campestris (Field	374.85	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	549.8	1
gb|Nicotiana tabacum mRNA for cysteine proteinase precursor [Z99173]	21.35	1
Unknown	504.49	1
gb|KT7B.103J24F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.103J24, mRN	65.05	1
gb|N.tabacum mRNA for glycine rich protein [X83731]	518.17	1
Unknown	80.63	1
gb|Nicotiana tabacum mRNA for cullin 1B (cul1B gene) [AJ344534]	121.78	1
tc|Rep: Chromosome chr5 scaffold_98, whole genome shotgun sequence - Vitis vin	72.46	1
tc|Rep: Chromosome chr12 scaffold_238, whole genome shotgun sequence - Vitis	49.31	1
Unknown	89.38	1
Unknown	568.73	1
gb|KF8C.101J06F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101J06, mRN	223.68	1
gb|KT7C.105O15F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105O15, mR	77.61	1
gb|KP1B.108O07F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108O07, m	81.51	1
tc|Rep: Formate--tetrahydrofolate ligase - Spinacia oleracea (Spinach), partial (41%	144.09	1
Unknown	966.73	1
tc|Rep: Insulin degrading enzyme - Solanum lycopersicum (Tomato) (Lycopersicon	125.46	1
tc|Rep: Zinc finger A20 and AN1 domain-containing stress-associated protein 8 - Or	203.81	1
gb|BL12.103G13F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.103G13, m	1187.59	1
tc|Rep: Vicilin-like storage protein - Picea glauca (White spruce), partial (22%) [TC4	163.02	1
tc|Rep: Chromosome chr15 scaffold_82, whole genome shotgun sequence - Vitis vi	20547.6	1
tc|Rep: S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC) [C	5443.64	1
gb|Nicotiana tabacum internal-motor kinesin mRNA, partial cds [DQ156499]	40.46	1
tc|Rep: Cyc07 - Nicotiana tabacum (Common tobacco), partial (72%) [TC72415]	116.89	1
tc|Rep: Chromosome chr12 scaffold_38, whole genome shotgun sequence - Vitis vi	29.09	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	494.18	1
Unknown	50.99	1
gb|AGN_RNC014xe20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	2559.76	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	520.12	1

gb|TOBESTR034C08 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	4674.07	1
gb|KP1B.110G24F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110G24, m	90.28	1
tc|Rep: 60S ribosomal protein L13 - Solanum tuberosum (Potato), complete [TC416	18.4	1
Unknown	31544.75	1
tc|Rep: Glutamate synthase (Ferredoxin) (Clone C(35)) - Nicotiana tabacum (Comm	58.42	1
gb|KF8C.101H07F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101H07, mR	491.2	1
Unknown	256.19	1
Unknown	29.55	1
gb|KG9B.103O14F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103O14,	48.51	1
Unknown	48.26	1
gb|KG9B.005I19F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005I19, m	30.22	1
gb|CHO_SL026xg23f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1463.89	1
Unknown	185.33	1
gb|KT7B.107P18F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107P18, mR	29.01	1
tc|Rep: Os01g0332900 protein - Oryza sativa subsp. japonica (Rice), partial (45%) [T	24.49	1
Unknown	20	1
Unknown	86.91	1
tc|Rep: Chromosome chr1 scaffold_166, whole genome shotgun sequence - Vitis vi	43.05	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	58.19	1
Unknown	63.38	1
Unknown	145.34	1
gb|AGN_RNC024xj04f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	30.59	1
gb|KF8C.104N06F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104N06, mR	3330.51	1
gb|AGN_RPC019xd19f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	23.65	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	557.46	1
gb|KF8C.104K08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104K08, mR	101.03	1
Unknown	189.06	1
Unknown	1624.33	1
gb|AGN_RNC010xp20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	527.45	1
tc|Rep: Chromosome chr18 scaffold_121, whole genome shotgun sequence - Vitis	26.08	1
gb|KL4B.102D03F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102D03, m	1588.11	1
gb|AGN_RPC015xe06f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	442.48	1
gb|N.tabacum mRNA for phosphoglyceromutase [X70651]	1141.13	1
gb|KP1B.001L22F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001L22, m	762.48	1

gb|AGN_RNC026xp07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	26.7	1
gb|BP531034 MAT005 Nicotiana tabacum cDNA clone BY23306, mRNA sequence [	26.76	1
Unknown	371.85	1
tc|Rep: Serine/threonine protein phosphatase - Vitis vinifera (Grape), partial (9%) [	420.11	1
gb|BP530134 MAT005 Nicotiana tabacum cDNA clone BY21119, mRNA sequence [	170.63	1
Unknown	32.46	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (96%) [TC4	79.5	1
tc|Rep: Calcium binding protein - Sesbania rostrata, partial (41%) [TC45153]	305.87	1
gb|KL5B.117D22F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.117D22, m	107.23	1
tc|Rep: Alpha-amylase - Plantago major (Common plantain), partial (53%) [TC4459	103.3	1
gb|KP1B.104A02F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104A02, m	123.36	1
Unknown	17.64	1
gb|Nicotiana tabacum partial mRNA for glutamyl tRNA Reductase (hemA gene) [A	105.09	1
gb|Nicotiana tabacum NtGPDL mRNA for putative glycerophosphoryl diester phosp	686.07	1
gb|KF8C.105B14F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105B14, mR	224.41	1
gb|KT7C.113G06F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.113G06, mR	3545.7	1
Unknown	68.39	1
tc|Rep: cyclin K - Gallus gallus, partial (3%) [TC50933]	40.79	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	45.35	1
tc|Rep: Small GTP-binding protein - Solanum lycopersicum (Tomato) (Lycopersicon	64.8	1
Unknown	28.94	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	28.12	1
gb|KT7C.112B04F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112B04, mR	30.22	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	100.24	1
tc|Rep: Brain protein 44-like - Zea mays (Maize), partial (89%) [TC53445]	511.52	1
gb|KL4B.112P14F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112P14, mR	1078.47	1
gb|TOBESTR006A09 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	185.18	1
gb|KR3B.110C05F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110C05, m	30.68	1
Unknown	220.61	1
Unknown	478.2	1
tc|Rep: AT4g32020/F10N7_170 - Arabidopsis thaliana (Mouse-ear cress), partial (1	351.69	1
Unknown	66.79	1
gb|Nicotiana tabacum callus-expressing factor (CEF1) mRNA, complete cds [AY286	51.41	1
Unknown	21.01	1

tc|Rep: Chromosome chr11 scaffold_56, whole genome shotgun sequence - Vitis vi	152.26	1
gb|AGN_RNC025xi12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	32.23	1
gb|KL4B.105E10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105E10, mR	84.43	1
gb|BP529465 MAT001 Nicotiana tabacum cDNA clone BY14363, mRNA sequence [	81.49	1
tc|Rep: GAGA-motif binding transcriptional activator - Populus trichocarpa (Wester	18.79	1
gb|KT7C.112M21F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112M21, m	60.93	1
tc|Rep: LIM-domain SF3 protein - Nicotiana tabacum (Common tobacco), complete	234.49	1
gb|KG9B.005L24F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005L24, m	140.21	1
Unknown	27.87	1
gb|KG9B.103M11F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103M11,	107.84	1
tc|Rep: Membrane-anchored ubiquitin-fold protein 2 - Arabidopsis thaliana (Mous	42.11	1
gb|KG9B.002G17F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002G17,	23.23	1
Unknown	2646.04	1
tc|Rep: Glutathione-regulated potassium-efflux system protein - Azoarcus sp. (strai	28.6	1
gb|AM812698 COL, cold overnight library Nicotiana tabacum cDNA clone nt006139	23.76	1
gb|KN6B.100E22F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100E22, m	21.07	1
tc|Rep: FtsH-like protein - Solanum lycopersicum (Tomato) (Lycopersicon esculentu	21.31	1
tc|Rep: Chloroplast methionine sulfoxide reductase B1 precursor - Nicotiana tabacu	54.86	1
gb|TT-27_F19 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	139.75	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	189.37	1
gb|KL5B.103N16F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.103N16, m	97.42	1
tc|Rep: Chromosome undetermined scaffold_129, whole genome shotgun sequenc	2675.92	1
Unknown	35.43	1
gb|KT7C.102B06F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102B06, mR	500.61	1
Unknown	690.03	1
gb|FS417555 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	511.04	1
Unknown	17.32	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	13433.65	1
tc|Rep: Alpha tubulin - Plantago major (Common plantain), partial (86%) [TC42970]	102.78	1
tc|Rep: Chromosome chr14 scaffold_26, whole genome shotgun sequence - Vitis vi	358	1
gb|KF8C.103M11F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103M11, m	16987.05	1
gb|AGN_ELP011xg12f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	18.43	1
gb|KN6B.108G03F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.108G03,	1569.56	1
gb|KR3B.110P19F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110P19, m	26	1

gb|BP132833 MAT001 Nicotiana tabacum cDNA clone BY5038, mRNA sequence [B	106.45	1
gb|TT-38_N21 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	44.75	1
Unknown	10314.25	1
gb|KL4B.101L06F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101L06, mR	2695.45	1
tc|Rep: Chromosome chr13 scaffold_74, whole genome shotgun sequence - Vitis vi	83.91	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	100.86	1
gb|KR3B.111P23F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111P23, m	134.07	1
tc|Rep: CTR1-like protein kinase - Solanum lycopersicum (Tomato) (Lycopersicon es	52.44	1
gb|Nicotiana tabacum WERBP-1 mRNA, complete cds [AB017693]	819.62	1
gb|KL4B.111L18F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111L18, mR	131.26	1
tc|Rep: S-adenosylmethionine synthetase - Nicotiana suaveolens, complete [TC435	15261.4	1
gb|CHO_SL004xg01f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	225.02	1
gb|KL4B.106F03F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106F03, mR	20.38	1
gb|KP1B.001P21F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001P21, m	1172.01	1
tc|Rep: Photosystem I assembly protein ycf3 - Nicotiana sylvestris (Wood tobacco),	1179.6	1
gb|KF8C.103A10F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103A10, mR	264.99	1
gb|KN6B.106G04F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.106G04,	103.69	1
gb|KF8C.105J07F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105J07, mRN	494.1	1
Unknown	2048.97	1
gb|KL5B.111F20F.060117T7 KL5B Nicotiana tabacum cDNA clone KL5B.111F20, mR	65.37	1
gb|AGN_RNC116xg09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	301.78	1
tc|Rep: ARG1 protein - Arabidopsis thaliana (Mouse-ear cress), partial (31%) [TC54	920.81	1
Unknown	47.79	1
gb|FS432984 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	191.35	1
gb|TT-04_O15 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	89.86	1
gb|BP128961 MAT001 Nicotiana tabacum cDNA clone BY777, mRNA sequence [BP	20.21	1
gb|TT-02_O18 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	139.19	1
gb|FS391062 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	53.28	1
gb|Nicotiana tabacum adc mRNA for arginine decarboxylase, complete cds [AB110	3347	1
tc|Rep: Chromosome undetermined scaffold_79, whole genome shotgun sequence	278.23	1
gb|KL4B.111E15F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111E15, mR	32.98	1
tc|Rep: Vacuolar membrane ATPase subunit c'' - Citrus limon (Lemon), partial (97%	135.29	1
gb|AM799542 seedling library, SL Nicotiana tabacum cDNA clone nt002063056, m	149	1
gb|KR2B.110B10F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110B10, m	144.91	1

Unknown	47.03	1
gb|KR2B.108P18F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.108P18, m	101.25	1
gb|KR3B.106M07F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106M07,	179.07	1
Unknown	7150.41	1
tc|Rep: Ribosomal protein L30e - Pisum sativum (Garden pea), complete [TC54597]	165.76	1
tc|Rep: Ferredoxin III - Musa acuminata (Banana), partial (90%) [TC51824]	34.04	1
Unknown	989.08	1
Unknown	73.66	1
gb|KF8C.104I01F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104I01, mRN	147.03	1
tc|Rep: Chromosome undetermined scaffold_129, whole genome shotgun sequenc	3169.82	1
gb|AGN_RPC024xh14f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	86.43	1
Unknown	34.68	1
gb|KL4B.102L05F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102L05, mR	116	1
tc|Rep: Cysteine-rich protein - Nicotiana tabacum (Common tobacco), complete [T	47428.45	1
Unknown	72.84	1
Unknown	125.92	1
tc|Rep: Isocitrate lyase - Solanum lycopersicum (Tomato) (Lycopersicon esculentu	32.16	1
Unknown	255.67	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	132.04	1
gb|KP1B.102L12F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102L12, mR	8969.11	1
tc|Rep: Nascent polypeptide-associated complex subunit alpha-like protein 2 - Ara	65.49	1
Unknown	37.23	1
Unknown	310.24	1
Unknown	159.41	1
gb|TL13.109O07F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.109O07, mR	35.85	1
Unknown	30.16	1
gb|AGN_RNC030xf11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	20.07	1
tc|Rep: Chromosome chr4 scaffold_208, whole genome shotgun sequence - Vitis vi	51.09	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	178.2	1
Unknown	117.05	1
tc|Rep: ATP-dependent Clp protease ATP-binding subunit clpA homolog CD4B, chlo	480.76	1
Unknown	28.7	1
gb|AGN_ELP026xi20f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	92.61	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	25.52	1

tc|Rep: PHD5 - Glycine max (Soybean), partial (96%) [TC57518]	169.98	1
tc|Rep: Chromosome undetermined scaffold_296, whole genome shotgun sequenc	23.87	1
tc|Rep: Chromosome chr10 scaffold_312, whole genome shotgun sequence - Vitis	9306.46	1
tc|Rep: Chromosome undetermined scaffold_91, whole genome shotgun sequence	40.17	1
Unknown	100.26	1
gb|Nicotiana tabacum NtH1 mRNA for histone H1, complete cds [AB029614]	89.04	1
Unknown	4320.92	1
gb|Nicotiana tabacum mRNA for protoporphyrin IX oxidase, ppxI gene [Y13465]	220.83	1
gb|KP1B.102C18F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102C18, m	1009.71	1
tc|Rep: Os01g0279200 protein - Oryza sativa subsp. japonica (Rice), partial (95%) [T	30.71	1
tc|Rep: Chromosome chr2 scaffold_112, whole genome shotgun sequence - Vitis vi	4017.32	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	72.12	1
gb|KL4B.108P15F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108P15, mR	19.85	1
Unknown	427.6	1
gb|AM789132 DL, diurnal library Nicotiana tabacum cDNA clone nt005072014, mR	121.52	1
tc|Rep: Chromosome chr13 scaffold_45, whole genome shotgun sequence - Vitis vi	186.52	1
tc|Rep: RNA helicase - Arabidopsis thaliana (Mouse-ear cress), partial (6%) [TC6825	57.91	1
tc|Rep: Chromosome chr16 scaffold_94, whole genome shotgun sequence - Vitis vi	1033.7	1
tc|Rep: BZIP transcriptional activator RSG - Nicotiana tabacum (Common tobacco),	26.03	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	632.78	1
tc|Rep: Chromosome undetermined scaffold_123, whole genome shotgun sequenc	60.16	1
tc|Rep: Glutathione peroxidase - Vitis vinifera (Grape), partial (82%) [TC55722]	28.25	1
tc|Rep: Chromosome chr13 scaffold_210, whole genome shotgun sequence - Vitis	40.16	1
Unknown	29.51	1
Unknown	50.8	1
Unknown	192.49	1
gb|CHO_SL027xg05f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	512.72	1
Unknown	29.19	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	143.2	1
gb|KT7C.101L06F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.101L06, mR	593.72	1
tc|Rep: Transformer-SR ribonucleoprotein - Nicotiana tabacum (Common tobacco)	25.29	1
Unknown	31.32	1
tc|Rep: 40S ribosomal protein S4 - Solanum tuberosum (Potato), complete [TC4036	373.88	1
tc|Rep: Heme-binding-like protein At3g10130, chloroplast precursor - Arabidopsis t	79.83	1

gb|AGN_RPC015xk16f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	844.73	1
gb|KR2B.108C01F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.108C01, m	285.61	1
gb|CHO_SL002xo10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	2654.9	1
tc|Rep: Os01g0706500 protein - Oryza sativa subsp. japonica (Rice), complete [TC7	384.26	1
Unknown	106.2	1
tc|Rep: CONSTANS interacting protein 2b - Solanum lycopersicum (Tomato) (Lycope	66.14	1
gb|TT-05_A21 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	190.53	1
gb|TT-47_L06 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	57.09	1
gb|BP530879 MAT005 Nicotiana tabacum cDNA clone BY23143, mRNA sequence [E	45.98	1
Unknown	23.04	1
gb|Nicotiana tabacum NtADH mRNA for allyl alcohol dehydrogenase, complete cds	1073.46	1
Unknown	58.52	1
gb|KF8C.101C03F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101C03, mRN	5406.92	1
gb|TOBESTR023F04 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	1201.05	1
gb|TOBESTR046E09 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	71.83	1
gb|BP134550 MAT001 Nicotiana tabacum cDNA clone BY6958, mRNA sequence [BF	49.74	1
tc|Rep: Ran binding protein - Nicotiana benthamiana, complete [TC44128]	26.92	1
Unknown	236.52	1
gb|KF8C.101G03F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101G03, mR	1123.5	1
tc|Rep: OJ000223_09.9 protein - Oryza sativa subsp. japonica (Rice), partial (93%) [	37.43	1
tc|Rep: protein kinase family protein - Arabidopsis thaliana, partial (48%) [TC51224	25.13	1
gb|KT7C.101P04F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.101P04, mRN	2396.45	1
tc|Rep: Acyltransferase family protein - Cytophaga hutchinsonii (strain ATCC 33406	1001.71	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	111.71	1
gb|KT7C.101L17F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.101L17, mRN	170.3	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	97.68	1
gb|TT-03_E01 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	28.7	1
tc|Rep: Chromosome chr8 scaffold_115, whole genome shotgun sequence - Vitis vi	43.32	1
Unknown	19.55	1
gb|AM803627 seedling library, SL Nicotiana tabacum cDNA clone nt002334084, mR	1159.87	1
Unknown	2681.85	1
gb|BP530854 MAT005 Nicotiana tabacum cDNA clone BY23117, mRNA sequence [E	28.63	1
gb|N.tabacum mRNA for zinc finger protein, BBF2aO [X97945]	32.21	1
gb|TT-15_K03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	18.91	1

gb|N.tabacum mRNA for phosphoenolpyruvate carboxylase [X59016]	2720.79	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	779.1	1
Unknown	46.2	1
tc|Rep: Chromosome undetermined scaffold_108, whole genome shotgun sequenc	57.09	1
gb|AGN_RNC126xg10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	152.18	1
Unknown	95.25	1
gb|CHO_SL005xe14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	40.56	1
tc|Rep: Protein TOC75, chloroplast precursor - Pisum sativum (Garden pea), partial	79.66	1
gb|KF8C.101M04F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101M04, m	42.83	1
gb|CHO_SL020xm13f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	44.57	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	234.27	1
tc|Rep: Cytoplasmic ribosomal protein S13-like - Solanum tuberosum (Potato), com	237.13	1
gb|TT-09_A07 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	130.95	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	71.55	1
tc|Rep: Cytochrome c oxidase family protein-like - Solanum tuberosum (Potato), co	515.07	1
gb|KN6B.105L09F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105L09, m	17.55	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	498.6	1
tc|Rep: Phototropin-1 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum	217.03	1
Unknown	43.51	1
Unknown	228.46	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	233.47	1
tc|Rep: Phage integrase - Frankia sp. (strain CcI3), partial (9%) [TC73383]	93.13	1
gb|KT7C.106O18F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106O18, mR	1063.27	1
tc|Rep: Chlorophyll a-b binding protein, chloroplast precursor - Petunia hybrida (Pe	27.17	1
gb|FS418967 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	44.84	1
Unknown	65.53	1
gb|KT7C.105N12F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105N12, mR	1012.42	1
Unknown	640.95	1
gb|Nicotiana tabacum mRNA for aspartate aminotransferase, partial cds [AB12625	100.33	1
gb|BP530798 MAT005 Nicotiana tabacum cDNA clone BY23059, mRNA sequence [	402.89	1
tc|Rep: Triosephosphate isomerase - Solanum tuberosum (Potato), partial (49%) [T	1952.42	1
Unknown	376.5	1
tc|Rep: Chromosome undetermined scaffold_30, whole genome shotgun sequence	32.16	1
Unknown	253.3	1

gb|TT-23_P04 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	579.95	1
Unknown	216.29	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	525.42	1
Unknown	4611.31	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	104.59	1
tc|Rep: 14-3-3 protein - Nicotiana tabacum (Common tobacco), partial (98%) [TC44	25.57	1
tc|Rep: Hin19 - Nicotiana tabacum (Common tobacco), complete [TC51319]	1369.84	1
Unknown	59.73	1
gb|AGN_RNC007xf06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	196.74	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	188.15	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	26.1	1
tc|Rep: Ribosomal protein L23 family protein - Solanum tuberosum (Potato), partia	53.33	1
gb|Nicotiana tabacum mRNA for cyclin B1 (cycB1 gene) [Z37978]	32.07	1
Unknown	40.94	1
Unknown	23.16	1
gb|KP1B.103O13F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103O13, m	171.64	1
gb|KG9B.003M18F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003M18,	49.75	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC21-4-280, cultivar Bright Yellow 2	45.33	1
gb|AM834279 seedling library, SL Nicotiana tabacum cDNA clone nt002087062, m	19.68	1
gb|AGN_RNC019xc19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	434.05	1
Unknown	515.77	1
Unknown	362.98	1
gb|TT-13_C05 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	750.86	1
gb|KP1B.001P15F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001P15, m	25.81	1
tc|Rep: Cell division cycle protein 48 homolog - Capsicum annuum (Bell pepper), pa	1373.7	1
gb|KR3B.110I14F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110I14, mR	1455.13	1
Unknown	97.51	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	19.76	1
Unknown	25.09	1
tc|Rep: Chromosome undetermined scaffold_279, whole genome shotgun sequenc	49.26	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	134.09	1
gb|KP1B.112H03F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.112H03, m	256.61	1
gb|KF8C.101H24F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101H24, mR	527.63	1
gb|KF8C.105N05F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105N05, mR	50154.1	1

gb|AGN_RNC014xm12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	80.26	1
Unknown	520.46	1
gb|AGN_RNC105xg07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	117.69	1
Unknown	32.25	1
gb|KR3B.101J02F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101J02, mR	367.36	1
gb|KL5B.109A12F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.109A12, m	3235.21	1
gb|Nicotiana tabacum WD-repeat protein mRNA, complete cds [GQ260131]	60.93	1
tc|Rep: Pm27 protein - Prunus mume (Japanese flowering apricot), partial (58%) [T	978.02	1
Unknown	22.89	1
Unknown	526.93	1
Unknown	526.95	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	125.12	1
gb|FS414230 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	160.39	1
Unknown	149.5	1
gb|KP1B.102I17F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102I17, mR	19.59	1
gb|CHO_SL016xl10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	118.04	1
Unknown	83.63	1
tc|Rep: Predicted protein - Coccidioides immitis, partial (12%) [TC55624]	40.65	1
gb|KG9B.101F22F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101F22, m	153.91	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	50.6	1
gb|AGN_PNL233cf1_d7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	773.28	1
gb|KF8C.105O04F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105O04, mR	70.49	1
gb|KF8C.106P02F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106P02, mR	144.27	1
Unknown	1766.57	1
gb|TT-27_L08 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	178.05	1
gb|EST T1P015 Tobacco Leaves Express Library Nicotiana tabacum cDNA clone t1p3	40.63	1
tc|Rep: Eukaryotic translation initiation factor 2 beta subunit-like - Solanum tubero	513.91	1
gb|AM838454 seedling library, SL Nicotiana tabacum cDNA clone nt002321027, m	48.06	1
tc|Rep: Histone H4 [Contains: Osteogenic growth peptide (OGP)]. - Rattus norvegic	1120.1	1
tc|Rep: P40-like protein - Solanum tuberosum (Potato), partial (93%) [TC43627]	54.64	1
gb|TT-12_P07 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	3187.88	1
tc|Rep: Cytosolic ascorbate peroxidase - Capsicum annuum (Bell pepper), partial (7	3100.81	1
gb|KF8C.106J18F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106J18, mRN	461.08	1
tc|Rep: NmrA-like family protein - Solanum demissum (Wild potato), partial (21%) [	300.96	1

tc|Rep: AML1 - Solanum tuberosum (Potato), partial (26%) [TC47870]	19.61	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	106.64	1
gb|KG9B.004B18F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004B18, m	87.87	1
gb|AGN_RNC211xn23f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	212.09	1
tc|Rep: Chromosome chr10 scaffold_179, whole genome shotgun sequence - Vitis	512.76	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	56.69	1
gb|KL5B.104B08F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.104B08, mR	117.88	1
tc|Rep: KH domain-containing protein-like - Oryza sativa subsp. japonica (Rice), par	100.38	1
Unknown	24.33	1
Unknown	545.67	1
Unknown	250.89	1
Unknown	18.81	1
tc|Rep: Chromosome undetermined scaffold_30, whole genome shotgun sequence	168.78	1
tc|Rep: Glutathione S-transferase - Solanum commersonii (Commerson's wild potat	103.59	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	258.25	1
tc|Rep: SGT1 - Nicotiana benthamiana, partial (49%) [TC48609]	27.06	1
Unknown	194.86	1
gb|KP1B.112P05F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.112P05, m	183.48	1
gb|KG9B.005C19F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005C19, m	192.55	1
Unknown	36.87	1
Unknown	74.79	1
gb|KP1B.102H10F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102H10, m	262.58	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	41.99	1
gb|KG9B.103J22F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103J22, m	107.11	1
gb|KN6B.115G01F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.115G01, r	19.97	1
gb|KT7C.104N04F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104N04, mR	21.59	1
gb|KP1B.101E12F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101E12, m	416.24	1
gb|CHO_SL006xj24f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	91.81	1
Unknown	48.41	1
tc|Rep: Chromosome undetermined scaffold_247, whole genome shotgun sequenc	29.37	1
gb|TT-36_B15 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	56.77	1
gb|KL4B.104C21F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104C21, mR	631.68	1
gb|KF8B.200M19F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200M19, m	91.09	1
gb|Nicotiana tabacum BYtuba mRNA for alpha tubulin, complete cds [AB052822]	44634.85	1

gb|EST_FLW001xi17f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [EH	172.03	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	581.43	1
Unknown	349.18	1
gb|Nicotiana tabacum rubisco activase precursor (Rca) mRNA, complete cds [U351	17.16	1
Unknown	445.8	1
gb|AGN_ELP009xa18f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	27.25	1
gb|KP1B.108I18F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108I18, mR	68.22	1
gb|Nicotiana tabacum calcium-dependent protein kinase (CPK5) mRNA, complete c	211.92	1
gb|KL4B.106D17F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106D17, mR	40.4	1
gb|KL4B.104G07F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104G07, mR	788.55	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	134.51	1
Unknown	565.88	1
gb|N.tabacum PKTL7 mRNA for protein kinase [X71057]	1525.61	1
gb|KT7C.105L12F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105L12, mRN	75.5	1
gb|TT-20_O05 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	58.46	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	1572.7	1
Unknown	18.9	1
gb|D58-AD7 Ethylene Induced Tobacco Leaf cDNA Library Nicotiana tabacum cDNA	229.49	1
Unknown	43.53	1
Unknown	62.61	1
Unknown	193.99	1
Unknown	962.57	1
Unknown	80.74	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (93%) [TC5	999.1	1
Unknown	992.26	1
Unknown	123.38	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	929.95	1
Unknown	36.33	1
tc|Rep: Cholinephosphate cytidylyltransferase - Pisum sativum (Garden pea), partia	3150.42	1
tc|Rep: Glutamate dehydrogenase A - Nicotiana plumbaginifolia (Leadwort-leaved	91.17	1
Unknown	17.65	1
Unknown	86.51	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	413.7	1
Unknown	467.73	1

Unknown	27.83	1
gb|KP1B.103L09F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103L09, mR	3985.69	1
Unknown	81.57	1
tc|Rep: Lipoxygenase - Nicotiana attenuata, partial (32%) [TC51546]	71.54	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	131.59	1
gb|KG9B.002B09F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002B09, m	23.59	1
tc|Rep: RRM-containing RNA-binding protein-like protein - Solanum tuberosum (Po	48.51	1
gb|Nicotiana tabacum SR1 6,7-dimethyl-8-ribityllumazine synthase precursor mRN	43.68	1
gb|TT-36_A02 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	107.92	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	48.44	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	140.24	1
Unknown	23.03	1
gb|Nicotiana tabacum mRNA for ferredoxin-NADP oxidoreductase, complete cds [	103.37	1
tc|Rep: Genomic DNA, chromosome 3, TAC clone:K24M9 - Arabidopsis thaliana (M	267.33	1
gb|TOBESTR133B11 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	65.98	1
gb|BP530353 MAT005 Nicotiana tabacum cDNA clone BY21369, mRNA sequence [	23.67	1
Unknown	18.03	1
gb|KP1B.001M05F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001M05, r	42.58	1
gb|KP1B.101G19F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101G19, m	177.86	1
gb|KN6B.101N11F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101N11, r	649.2	1
gb|TL13.109B21F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.109B21, mR	64.12	1
Unknown	1439.9	1
gb|AGN_ELP010xn14f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	31.51	1
gb|BL12.100O18F.060308T7 BL12 Nicotiana tabacum cDNA clone BL12.100O18, m	85.35	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	75.98	1
gb|KF8C.103P09F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103P09, mR	144.81	1
Unknown	213.84	1
Unknown	247.09	1
gb|TT-38_E01 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	24.08	1
tc|Rep: Chromosome chr11 scaffold_14, whole genome shotgun sequence - Vitis vi	349.11	1
tc|Rep: Chromosome undetermined scaffold_225, whole genome shotgun sequenc	235.16	1
gb|TOBESTR055D06 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	581.21	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	37.48	1
tc|Rep: Mini zinc finger protein - Solanum lycopersicum (Tomato) (Lycopersicon esc	22.96	1

Unknown	4651.56	1
Unknown	100.63	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	240.4	1
gb|TT-36_L19 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sequ	30.22	1
Unknown	420.08	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	58.36	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT21-1-270, cultivar Bright Yellow 2	21.96	1
gb|AM783661 seedling library, SL Nicotiana tabacum cDNA clone nt002328038, mR	107.15	1
Unknown	512.12	1
tc|Rep: Histone H2A - Vitis vinifera (Grape), partial (97%) [TC42842]	1017.21	1
Unknown	54.49	1
tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin	190.01	1
Unknown	324.72	1
tc|Rep: Chromosome undetermined scaffold_161, whole genome shotgun sequenc	376.01	1
tc|Rep: Mitochondrial carnitine/acylcarnitine carrier-like protein - Arabidopsis thali	179.73	1
Unknown	48.65	1
Unknown	134.5	1
Unknown	392.27	1
gb|TT-30_F12 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	19.02	1
gb|KN6B.009J12F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009J12, m	152.72	1
tc|Rep: Hydroxyphenylpyruvate reductase - Solenostemon scutellarioides (Coleus)	217.2	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	1641.16	1
Unknown	25.77	1
gb|KN6B.114A23F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.114A23, m	84.14	1
gb|Nicotiana tabacum EIG-I24 mRNA, complete cds [AB041514]	1391.73	1
gb|KP1B.108O07F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108O07, m	163.99	1
Unknown	54.66	1
tc|Rep: NAD-dependent epimerase/dehydratase family protein-like protein - Solanu	11694.3	1
tc|Rep: 26S protease regulatory subunit 6B homolog - Solanum tuberosum (Potato)	468.59	1
Unknown	169.65	1
gb|CHO_SL012xa06f1.ab1 CHO_SL Nicotiana tabacum cDNA 5', mRNA sequence [FG	1140.16	1
gb|KL4B.112G15F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112G15, mR	62.85	1
tc|Rep: Cytochrome b-c1 complex subunit 8 - Solanum tuberosum (Potato), comple	1796.08	1
gb|KF8C.109O24F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109O24, mR	86.07	1

Unknown	276.15	1
gb|KP1B.107I12F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107I12, mR	104.29	1
Unknown	171.22	1
tc|Rep: Poly(A)-binding protein - Nicotiana tabacum (Common tobacco), complete	856.4	1
Unknown	45.99	1
gb|Nicotiana tabacum mRNA for ras-related protein RAB8-5, complete cds [AB079	17079.9	1
gb|Nicotiana tabacum NTH23 mRNA, complete cds [AB004797]	231.16	1
Unknown	35.55	1
tc|Rep: Chromosome undetermined scaffold_123, whole genome shotgun sequenc	56.14	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	25.52	1
tc|Rep: Heat shock protein 70-3 - Nicotiana tabacum (Common tobacco), partial (3	610.65	1
gb|KT7C.104N15F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104N15, mR	218.22	1
Unknown	266.77	1
gb|TT-40_D01 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	11051.1	1
gb|AGN_PNL221bf1_d2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	31.94	1
gb|TT-16_K24 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	137.33	1
gb|CHO_SL019xb08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	439.45	1
Unknown	251.59	1
gb|Nicotiana tabacum extracellular Ca2+ sensing receptor (cas) mRNA, complete c	35.29	1
tc|Rep: Rab1-like small GTP-binding protein - Petunia hybrida (Petunia), complete [	254.16	1
Unknown	22.95	1
gb|CHO_SL010xl21f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	30.79	1
gb|KG9B.002F12F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002F12, m	104.43	1
gb|TT-10_C03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	48.79	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	1167.5	1
tc|Rep: Late embryogenis abundant protein 5 - Nicotiana tabacum (Common tobac	498.39	1
gb|CHO_SL006xl08f1.ab1 CHO_SL Nicotiana tabacum cDNA 5', mRNA sequence [FG	135.18	1
gb|TT-21_K02 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	407.1	1
tc|Rep: Chromosome undetermined scaffold_52, whole genome shotgun sequence	182.91	1
Unknown	80.57	1
Unknown	763.5	1
gb|AGN_RNC120xl16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	23.01	1
gb|BP133167 MAT001 Nicotiana tabacum cDNA clone BY5404, mRNA sequence [B	185.06	1
tc|Rep: Lysine decarboxylase-like protein At5g11950 - Arabidopsis thaliana (Mouse	80.6	1

Unknown	18.74	1
tc|Rep: VAP27 - Nicotiana plumbaginifolia (Leadwort-leaved tobacco), partial (49%)	509.22	1
gb|N.tabacum mRNA for NAD-dependent isocitrate dehydrogenase [X96727]	3267.07	1
tc|AAD43171.1 - Arabidopsis thaliana (Mouse-ear cress), partial (79%) [TC47386]	554.67	1
tc|Rep: LRR protein - Solanum lycopersicum (Tomato) (Lycopersicon esculentum),	536.59	1
Unknown	76.72	1
Unknown	19.03	1
tc|Rep: Calmodulin-related protein - Petunia hybrida (Petunia), partial (83%) [TC70	79.85	1
tc|Rep: Avr9/Cf-9 rapidly elicited protein 65 - Nicotiana tabacum (Common tobacc	85.33	1
tc|Rep: Cellulose synthase - Populus tremula x Populus tremuloides, partial (33%) [	30.09	1
tc|Rep: DNA-directed RNA polymerase IIb - Nicotiana tabacum (Common tobacco),	139.74	1
tc|Rep: Chromosome chr4 scaffold_162, whole genome shotgun sequence - Vitis vi	24.27	1
Unknown	414.88	1
gb|AGN_RNC110xf12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	182.49	1
tc|Rep: Allyl alcohol dehydrogenase - Nicotiana tabacum (Common tobacco), comp	359.4	1
Unknown	36.98	1
Unknown	289.48	1
gb|Nicotiana tabacum SR1 Nt-rab11a mRNA, complete cds [L29271]	534.09	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	70.32	1
tc|Rep: Heat shock cognate 70 kDa protein - Petunia hybrida (Petunia), partial (43%	170.34	1
Unknown	63.44	1
gb|AGN_RNC127xg06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	258.56	1
gb|KR2B.110A15F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110A15, m	1653.78	1
gb|KR3B.112M13F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112M13,	760.58	1
gb|AGN_PNL219cf1_d4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	767.49	1
gb|TT-20_M23 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	4132.55	1
tc|Rep: Proteasome subunit beta type - Vitis vinifera (Grape), complete [TC54925]	27.65	1
gb|TT-05_C12 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	112.46	1
tc|Rep: Os01g0861000 protein - Oryza sativa subsp. japonica (Rice), partial (20%) [T	25.51	1
gb|AGN_RNC127xe18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	103.09	1
Unknown	59.62	1
gb|AGN_ELP008xp13f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	48.86	1
Unknown	19.33	1
gb|KL4B.111N06F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111N06, m	26.91	1

gb|AM804984 seedling library, SL Nicotiana tabacum cDNA clone nt002163074, m	514.56	1
gb|AGN_RNC117xc19r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	69.21	1
gb|KF8C.101G12F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101G12, mR	48.35	1
tc|Rep: Prephenate dehydratase - Ipomoea trifida (Morning glory), partial (51%) [T	24.93	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	395.01	1
Unknown	702.78	1
tc|Rep: Aspartic proteinase - Theobroma cacao (Cacao) (Cocoa), partial (95%) [TC4	7597.34	1
tc|Rep: Chromosome chr11 scaffold_170, whole genome shotgun sequence - Vitis	10363.5	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	67.49	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	187.28	1
Unknown	28.36	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	53.84	1
gb|CHO_SL018xn22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	2821.21	1
Unknown	62.54	1
gb|Nicotiana tabacum cDNA-AFLP fragment H-N_BT1M21-375 sequence [DQ46017	33.07	1
Unknown	57.34	1
gb|TT-06_G20 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	1097.98	1
tc|Rep: SSU ribosomal protein S1P - Pediococcus pentosaceus (strain ATCC 25745 /	18.52	1
gb|Nicotiana tabacum pollen specific LIM domain protein 1b mRNA, complete cds [	10220.2	1
gb|TT-11_G22 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	146.06	1
Unknown	25.79	1
tc|Rep: Eukaryotic translation initiation factor 5A-1 - Nicotiana plumbaginifolia (Le	224.43	1
tc|Rep: T23J18.17 - Arabidopsis thaliana (Mouse-ear cress), partial (12%) [TC48947	46.09	1
tc|Rep: Proton pump interactor - Arabidopsis thaliana (Mouse-ear cress), partial (1	673.07	1
gb|TT-39_G05 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	623.15	1
Unknown	87.23	1
gb|CHO_SL011xo17f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	567.59	1
gb|CHO_SL008xe01f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	113.35	1
gb|TT-29_E04 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	143.54	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	211.63	1
gb|Nicotiana tabacum partial mRNA for cullin 1D (cul1D gene) [AJ344536]	40.56	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	63.28	1
Unknown	279.3	1
tc|Rep: Chromosome chr18 scaffold_59, whole genome shotgun sequence - Vitis vi	982.63	1

tc|Rep: 60s acidic ribosomal protein - Prunus dulcis (Almond) (Prunus amygdalus), p	38.16	1
Unknown	207.17	1
Unknown	31.6	1
Unknown	209.37	1
gb|KR2B.102B10F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.102B10, m	1393.97	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	70.58	1
Unknown	101.32	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	41.35	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	34.89	1
gb|KG9B.001M14F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001M14,	264.53	1
gb|KF8B.201A15F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201A15, mRN	22.86	1
Unknown	516.51	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	20.8	1
gb|KG9B.005B04F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005B04, m	276.61	1
tc|Rep: Chromosome chr10 scaffold_50, whole genome shotgun sequence - Vitis vi	1094.74	1
gb|KP1B.001G12F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001G12, m	712.53	1
tc|Rep: Chromosome chr3 scaffold_199, whole genome shotgun sequence - Vitis vi	4393.18	1
gb|TT-02_E03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	1326.88	1
tc|Rep: Autophagy protein beclin1 - Nicotiana benthamiana, partial (47%) [TC5064	51.02	1
gb|AGN_RNC007xj09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	34.64	1
Unknown	72.26	1
Unknown	20.75	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	191.26	1
gb|AM791353 seedling library, SL Nicotiana tabacum cDNA clone nt002082049, mR	18.81	1
gb|KR3B.110P02F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110P02, m	22.65	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	25.82	1
gb|AGN_ELP026xc22f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	21.95	1
gb|TT-14_L16 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	802.08	1
gb|KR3B.102P19F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.102P19, m	45.91	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	108.13	1
Unknown	34.31	1
tc|Rep: Ubiquitin carrier protein - Capsicum annuum (Bell pepper), complete [TC5	572.89	1
gb|AGN_RNC112xa13f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	22.89	1
Unknown	1035.67	1

tc|Rep: Chromosome chr11 scaffold_56, whole genome shotgun sequence - Vitis vi	228.73	1
Unknown	22.22	1
gb|KR3B.114I24F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.114I24, mR	25.72	1
Unknown	11096.9	1
tc|Rep: Chromosome undetermined scaffold_155, whole genome shotgun sequenc	5331.15	1
Unknown	27.34	1
Unknown	237.86	1
gb|Nicotiana tabacum MADS-box protein MADS5 (NtMADS5) mRNA, complete cds	93.36	1
Unknown	95.65	1
gb|AM833244 DL, diurnal library Nicotiana tabacum cDNA clone nt005091082, mR	20.17	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	36.2	1
tc|Rep: Ubiquitin-fusion degradation protein-like - Arabidopsis thaliana (Mouse-ear	85	1
gb|KF8C.109O22F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109O22, mR	38.21	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	555.67	1
gb|KT7C.104A06F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104A06, mR	253.73	1
Unknown	20.98	1
tc|Rep: 2-isopropylmalate synthase B - Solanum pennellii (Tomato) (Lycopersicon p	21.59	1
gb|TT-09_H15 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	94.06	1
gb|AGN_RNC014xn22f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	204.61	1
tc|Rep: Betaine aldehyde dehydrogenase - Amaranthus hypochondriacus (Prince-of	44.98	1
Unknown	17.68	1
gb|FS416721 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	146.53	1
gb|TT-03_G14 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	379.55	1
tc|Rep: Chromosome chr2 scaffold_176, whole genome shotgun sequence - Vitis vi	30.67	1
gb|TL13.103C23F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.103C23, mR	40.19	1
gb|KF8B.202F11F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202F11, mRN	49327.65	1
tc|Rep: Syntaxin - Glycine max (Soybean), partial (87%) [TC44874]	85.3	1
gb|KF8C.106A11F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106A11, mRN	52.98	1
gb|TT-16_C09 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	29.63	1
tc|CPY18934 Solanum nigrum chloroplast tRNA-Ala, tRNA-Ile, 16S rRNA, tRNA-Val,	88.73	1
gb|KL4B.101K21F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101K21, mR	54.89	1
gb|KL4B.102J10F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102J10, mRN	28.41	1
gb|Nicotiana tabacum geranylgeranylated protein NTGP3 mRNA, complete cds [U6	90.66	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	1066.97	1

Unknown	35.75	1
gb|N.tabacum mRNA for protein phosphatase 2A, 65kD regulatory subunit [X97913	953.5	1
Unknown	197.5	1
tc|Rep: WD40-like beta propeller repeat protein - Synechococcus sp. (strain JA-2-3	108.02	1
gb|BP132634 MAT001 Nicotiana tabacum cDNA clone BY4821, mRNA sequence [B	96.31	1
gb|CHO_SL026xo06f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	33.16	1
gb|KN6B.110N02F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.110N02,	58.98	1
gb|KP1B.037H23F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.037H23, m	129.19	1
gb|EST_FLW005xi04f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	32710.8	1
gb|KF8C.106C22F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106C22, mR	1786.31	1
Unknown	38.5	1
Unknown	265.6	1
Unknown	478.8	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	207.12	1
tc|Rep: Actin depolymerizing factor - Nicotiana benthamiana, partial (22%) [TC686	132.23	1
gb|KL4B.103E17F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103E17, mR	637.25	1
gb|TT-12_N13 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	91.89	1
gb|TT-03_L11 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	1304.71	1
Unknown	147.3	1
tc|Rep: ABC oligo-dipeptide/nickel transporter, permease subunit precursor - Yersi	773.41	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	127.93	1
gb|Nicotiana tabacum Avr9 [AY220483]	1375.79	1
Unknown	258.76	1
gb|Nicotiana tabacum phospholipase C2 mRNA, complete cds [AF223573]	21.34	1
Unknown	343.13	1
tc|Rep: Chloroplast 30S ribosomal protein S16 - Nicotiana sylvestris (Wood tobacc	782.91	1
gb|KN6B.105H12F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105H12,	1510.33	1
Unknown	598.78	1
tc|Rep: Chromosome chr19 scaffold_111, whole genome shotgun sequence - Vitis	25.06	1
Unknown	24.8	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	79.09	1
gb|BP534246 MAT005 Nicotiana tabacum cDNA clone BY32203, mRNA sequence [	18.86	1
gb|Nicotiana tabacum mRNA for myo-inositol 1-phosphate synthase, complete cds	673.11	1
Unknown	178.91	1

tc|Rep: Heat shock protein 90 - Nicotiana tabacum (Common tobacco), complete [T	24.94	1
Unknown	124.88	1
gb|AGN_RPC009xh11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	795.03	1
tc|Rep: Ribosomal protein L39 - Triticum aestivum (Wheat), complete [TC62239]	51.16	1
tc|Rep: UDP-glucuronate 4-epimerase 2 - Arabidopsis thaliana (Mouse-ear cress), p	3011.9	1
tc|Rep: MYC transcription factor - Solanum tuberosum (Potato), partial (29%) [TC4	209.46	1
gb|TT-48_M13 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	34.27	1
tc|Rep: Chromosome chr1 scaffold_166, whole genome shotgun sequence - Vitis vi	1470.22	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	43.14	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	556.01	1
tc|Rep: 40S ribosomal protein S4 - Solanum tuberosum (Potato), complete [TC4036	41.87	1
Unknown	73.65	1
Unknown	20.7	1
Unknown	89.67	1
Unknown	246.25	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	50.06	1
gb|KR3B.112E20F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112E20, m	79.47	1
Unknown	268.17	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	18.48	1
gb|KF8C.105B07F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105B07, mR	182.58	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	42.47	1
gb|KG9B.001N12F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001N12,	72.89	1
gb|KP1B.102C05F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102C05, m	551.44	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	21472.25	1
gb|KL5B.105P16F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.105P16, mR	22.81	1
gb|Nicotiana tabacum Avr9 [AY220480]	1160.34	1
Unknown	247.83	1
gb|KF8B.200C05F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200C05, mR	34.86	1
gb|KG9B.002I22F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002I22, m	131.42	1
gb|TT-48_K20 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	35.18	1
Unknown	38.09	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	115.07	1
Unknown	36.3	1
gb|CHO_SL016xl02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	564.84	1

Unknown	22.54	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	32.3	1
gb|KF8B.201C21F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201C21, mRN	2837.54	1
gb|KG9B.001K05F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001K05, m	104.59	1
tc|Rep: Chromosome chr11 scaffold_14, whole genome shotgun sequence - Vitis vi	479.25	1
tc|Rep: Chromosome chr3 scaffold_95, whole genome shotgun sequence - Vitis vin	133.99	1
Unknown	37.07	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	365.7	1
gb|TT-15_B05 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	105.51	1
gb|KL4B.108C04F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108C04, mR	27.64	1
gb|KG9B.002B17F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002B17, m	139.22	1
tc|Rep: DNA-binding protein - Nicotiana tomentosiformis (Tobacco), partial (84%) [	92.89	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	1626.86	1
tc|Rep: Striated muscle activator-like protein - Oryza sativa subsp. japonica (Rice), p	1195.8	1
tc|Rep: Profilin - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), comp	99.13	1
gb|BP131006 MAT001 Nicotiana tabacum cDNA clone BY3027, mRNA sequence [B	107.5	1
gb|KF8C.101G19F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101G19, mR	36.75	1
Unknown	2713.34	1
Unknown	147.18	1
gb|KN6B.102M01F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102M01,	34893.35	1
tc|Rep: Genomic DNA, chromosome 3, P1 clone: MXO21 - Arabidopsis thaliana (Mo	19.35	1
gb|KF8C.108E23F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108E23, mRN	11246.45	1
gb|AGN_PNL216cf1_d9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	110.14	1
gb|KF8C.101K12F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101K12, mRN	18375.5	1
tc|Rep: Erwinia induced protein 2 - Solanum tuberosum (Potato), complete [TC532	100.96	1
gb|BP535201 MAT005 Nicotiana tabacum cDNA clone BY35035, mRNA sequence [E	450.95	1
gb|KT7C.110I19F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110I19, mRN	206.11	1
gb|KT7C.108G08F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108G08, mR	1809.09	1
Unknown	37.16	1
gb|AGN_RNC126xb13r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	125.57	1
tc|Rep: Ribosomal protein L3A - Nicotiana tabacum (Common tobacco), complete [	72.02	1
Unknown	3322.88	1
Unknown	14685.65	1
tc|Rep: Chromosome undetermined scaffold_267, whole genome shotgun sequenc	168.94	1

Unknown	24.89	1
Unknown	17.64	1
tc|Rep: Chromosome undetermined scaffold_69, whole genome shotgun sequence	10606.75	1
tc|Rep: Single-stranded nucleic acid binding R3H - Medicago truncatula (Barrel med	4373.44	1
Unknown	122.64	1
Unknown	19.6	1
Unknown	93.16	1
Unknown	62.97	1
Unknown	1662.08	1
tc|Rep: Polyubiquitin - Pinus sylvestris (Scots pine), partial (60%) [TC51659]	687.97	1
Unknown	56.49	1
gb|CHO_SL015xp08f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	70.06	1
Unknown	143.26	1
Unknown	474.84	1
Unknown	1193.32	1
tc|Rep: Adenylyl-sulfate reductase precursor - Solanum lycopersicum (Tomato) (Ly	1180.19	1
tc|Rep: Chromosome chr5 scaffold_156, whole genome shotgun sequence - Vitis vi	509.16	1
Unknown	263.72	1
gb|KL4B.105E12F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105E12, mR	32.85	1
tc|Rep: Polypepetide with reverse transcriptase and RNaseH domains - Petunia hyb	138.79	1
tc|Rep: En/Spm-like transposon protein - Arabidopsis thaliana (Mouse-ear cress), p	203.17	1
tc|GB|AB053091.1|BAB40702.1 kinesin-like polypeptides 3 [Nicotiana tabacum] [N	41.24	1
tc|Rep: Chromosome chr16 scaffold_189, whole genome shotgun sequence - Vitis	188.62	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	125.59	1
gb|AGN_PNL203ar1_g7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	32.25	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	600.91	1
tc|Rep: Chromosome undetermined scaffold_838, whole genome shotgun sequenc	95.48	1
tc|Rep: Oxidoreductase - Setaria italica (Foxtail millet), partial (84%) [TC57787]	57.99	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	26.26	1
Unknown	2432.89	1
tc|Rep: Fiber protein Fb15 - Gossypium barbadense (Sea-island cotton) (Egyptian c	2901.13	1
tc|Rep: Ubiquitin carrier protein - Solanum tuberosum (Potato), complete [TC4631	193.29	1
gb|AGN_RNC116xe09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	796.23	1
Unknown	2143.92	1

gb|KR3B.112O22F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112O22, m	1069.24	1
tc|Rep: Ribosomal protein L3A - Nicotiana tabacum (Common tobacco), partial (52	71.8	1
gb|TT-31_F22 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	23.89	1
gb|KL5B.001A13F.050901T7 KL5B Nicotiana tabacum cDNA clone KL5B.001A13, m	765.47	1
Unknown	22.04	1
tc|Rep: Chromosome chr3 scaffold_157, whole genome shotgun sequence - Vitis vi	49.64	1
tc|Rep: Chromosome chr4 scaffold_208, whole genome shotgun sequence - Vitis vi	56.68	1
gb|KG9B.103M20F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103M20,	517.66	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	101.75	1
gb|KF8C.105M06F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105M06, m	939.33	1
gb|AM784351 seedling library, SL Nicotiana tabacum cDNA clone nt002295065, m	59.24	1
gb|KR2B.112K16F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.112K16, m	18.64	1
Unknown	68.17	1
Unknown	29	1
tc|Rep: Protein transport protein SEC61 subunit gamma - Oryza sativa subsp. japon	1885.39	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	438.6	1
gb|KF8B.200O10F.060128T7 KF8 Nicotiana tabacum cDNA clone KF8B.200O10, mR	120.95	1
Unknown	969.86	1
Unknown	630.52	1
gb|AGN_RPC023xp04f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	31.87	1
Unknown	311.48	1
gb|KN6B.100L06F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100L06, m	231.77	1
Unknown	41.49	1
gb|AGN_PNL212cf1_d9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	40.89	1
gb|KF8C.110P24F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110P24, mR	1269.91	1
Unknown	1018.46	1
gb|KL4B.108K12F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108K12, mR	274.6	1
Unknown	38.49	1
tc|Rep: Small GTP-binding protein - Capsicum annuum (Bell pepper), complete [TC	10847.75	1
gb|BP130610 MAT001 Nicotiana tabacum cDNA clone BY2594, mRNA sequence [B	18.97	1
tc|Rep: Adenylyl-sulfate reductase precursor - Solanum lycopersicum (Tomato) (Ly	5751.9	1
Unknown	16.61	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	2779.83	1
gb|Nicotiana tabacum obtusifoliol-14-demethylase (CYP51) mRNA, complete cds [	61.29	1

tc|Rep: Ribulose bisphosphate carboxylase large chain precursor - Nicotiana sylvest	594.4	1
Unknown	52.54	1
gb|KF8C.106M16F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106M16, mF	36.33	1
gb|AGN_PNL229br1_f3.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	25.63	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	462.53	1
Unknown	62.07	1
Unknown	29.15	1
gb|AGN_RNC024xa10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	57.05	1
gb|KR2B.110N10F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110N10, m	9294.71	1
gb|Nicotiana tabacum Wisconsin 38 vitronectin-like adhesion protein mRNA, comp	1089.42	1
tc|Rep: Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vi	331.94	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	31.78	1
Unknown	22.28	1
gb|FS403828 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	2858.53	1
gb|KT7B.107N02F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107N02, mR	32.03	1
gb|KR3B.106M07F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106M07, r	194.24	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	565.58	1
tc|Rep: Serine/threonine protein phosphatase - Vitis vinifera (Grape), partial (47%)	792.22	1
Unknown	88.67	1
gb|TT-27_K03 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	111.24	1
gb|KP1B.102J11F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102J11, mR	79.02	1
Unknown	389.97	1
Unknown	377.8	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	2366.56	1
gb|10G12 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', r	181.21	1
Unknown	24.85	1
Unknown	55.16	1
tc|Rep: Similarity to EH domain containing proteins - Arabidopsis thaliana (Mouse-e	556.02	1
gb|KR2B.101K12F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.101K12, m	228.9	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC11-1-240, cultivar Bright Yellow 2	29.22	1
tc|Rep: Chromosome undetermined scaffold_55, whole genome shotgun sequence	905.9	1
gb|KN6B.102K01F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102K01, m	299.07	1
tc|Rep: Chromosome chr1 scaffold_136, whole genome shotgun sequence - Vitis vi	21.26	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	175.81	1

Unknown	98.65	1
gb|TL13.110O19F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.110O19, mR	504.73	1
Unknown	129.44	1
Unknown	1032.57	1
Unknown	887.95	1
tc|Rep: Chromosome chr10 scaffold_50, whole genome shotgun sequence - Vitis vi	84.65	1
gb|KL5B.106L07F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.106L07, mR	56.41	1
Unknown	3017.19	1
gb|TT-49_J11 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sequ	468.8	1
Unknown	36.26	1
gb|KL4B.105A02F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105A02, mR	36.02	1
tc|Rep: Constitutive plastid-lipid associated protein - Solanum lycopersicum (Tomat	68.37	1
Unknown	124.68	1
tc|Rep: Chromosome chr5 scaffold_58, whole genome shotgun sequence - Vitis vin	243	1
Unknown	1009.08	1
gb|TT-12_I21 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	171.82	1
gb|AGN_RNC018xi14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	139.99	1
Unknown	76.29	1
gb|TT-07_G04 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	17.45	1
gb|KG9B.107C11F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107C11, m	751.64	1
gb|FS401498 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	93.12	1
gb|Nicotiana tabacum mRNA for protoporphyrin IX oxidase, ppxII gene [Y13466]	80.95	1
Unknown	88.34	1
Unknown	39.01	1
tc|Rep: Chromosome chr2 scaffold_112, whole genome shotgun sequence - Vitis vi	4740.5	1
tc|Rep: Mu opioid receptor mMOR-1R1 - Mus musculus (Mouse), partial (6%) [TC65	30.46	1
Unknown	40.17	1
Unknown	94.34	1
gb|AGN_ELP005xf15f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	56.73	1
gb|KL4B.103I05F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103I05, mRN	57.21	1
tc|Rep: Thaliana 60S ribosomal protein L7 - Solanum tuberosum (Potato), complete	28.28	1
Unknown	99.36	1
gb|TT-27_O16 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	76.86	1
Unknown	994.9	1

tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	138.73	1
Unknown	29.12	1
tc|Rep: Mitochondrial processing peptidase-like - Solanum tuberosum (Potato), par	100.75	1
tc|Rep: Autophagy-related protein 3 - Vitis vinifera (Grape), complete [TC47245]	53.4	1
gb|AGN_RNC121xf18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	390.71	1
gb|KG9B.106J17F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106J17, m	5741.26	1
Unknown	26.69	1
tc|Rep: Pyridoxine biosynthesis protein - Glycine max (Soybean), partial (98%) [TC4	1502.31	1
Unknown	120.73	1
gb|TT-21_B07 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	411.93	1
gb|Nicotiana tabacum chaperone GrpE type 1 (GrpE1) mRNA, nuclear gene encodi	84.41	1
tc|Rep: Heat shock protein 90 - Nicotiana tabacum (Common tobacco), partial (29%	533.66	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	18.96	1
Unknown	190.36	1
Unknown	59.82	1
tc|Rep: Avr9/Cf-9 rapidly elicited protein 31 - Nicotiana tabacum (Common tobacc	22	1
tc|Rep: Endosomal protein-like - Arabidopsis thaliana (Mouse-ear cress), partial (33	849.58	1
tc|Rep: Chromosome undetermined scaffold_87, whole genome shotgun sequence	539.16	1
tc|Rep: Protein kinase - Medicago truncatula (Barrel medic), partial (37%) [TC5805	2204.86	1
gb|KR2B.104A09F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.104A09, m	51.79	1
tc|Rep: Chromosome chr18 scaffold_59, whole genome shotgun sequence - Vitis vi	26.44	1
Unknown	1118.08	1
tc|Rep: Chromosome chr18 scaffold_59, whole genome shotgun sequence - Vitis vi	83.04	1
tc|Rep: Ribosomal protein L3A - Nicotiana tabacum (Common tobacco), complete [	40.05	1
gb|KN6B.101D07F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101D07,	33.77	1
gb|TT-20_G03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	942.5	1
tc|Rep: Chromosome chr10 scaffold_204, whole genome shotgun sequence - Vitis	36.49	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	92.2	1
gb|BP129613 MAT001 Nicotiana tabacum cDNA clone BY1485, mRNA sequence [B	23.18	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	895.83	1
gb|BP134806 MAT001 Nicotiana tabacum cDNA clone BY7249, mRNA sequence [B	23.02	1
gb|FS416927 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	514.33	1
Unknown	90.26	1
gb|TT-23_E16 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	844.58	1

tc|Rep: NB-ARC domain containing protein - Solanum tuberosum (Potato), partial (	80.3	1
gb|KT7B.100O10F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100O10, mR	960.62	1
tc|Rep: Chromosome undetermined scaffold_60, whole genome shotgun sequence	471.53	1
gb|TT-47_A04 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	41.84	1
gb|KT7C.102L01F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102L01, mR	63.67	1
gb|AGN_RNC014xf18r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	18.36	1
Unknown	17175.1	1
tc|Rep: Chromosome undetermined scaffold_611, whole genome shotgun sequenc	35.63	1
gb|KF8C.101E06F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101E06, mR	32138	1
Unknown	244.93	1
gb|Nicotiana tabacum basic helix-loop-helix protein mRNA, complete cds [EU88027	3142.46	1
gb|AGN_RNC022xp13f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	55.78	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	800.28	1
Unknown	20.64	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	627.4	1
gb|KP1B.105P02F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105P02, m	184.31	1
Unknown	43.66	1
gb|Nicotiana tabacum partial mRNA for chloroplast FtsZ-like protein (ftsZ gene), cl	244.75	1
gb|BP135430 MAT001 Nicotiana tabacum cDNA clone BY7940, mRNA sequence [B	19.89	1
Unknown	48.21	1
gb|AGN_RPC015xe14f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	65.78	1
gb|KN6B.102C03F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102C03,	235.42	1
tc|Rep: Branched-chain amino acid ABC transporter, ATP-binding protein - Roseova	754.59	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT32-4-220, cultivar Bright Yellow 2	35.58	1
gb|KP1B.105H02F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105H02, m	685.24	1
Unknown	177.51	1
gb|KG9B.101D07F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101D07,	72.67	1
Unknown	19.44	1
gb|KG9B.002I22F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002I22, m	31.28	1
gb|KG9B.005G05F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005G05,	24.59	1
Unknown	2039.51	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	755.78	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	755.46	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	63.85	1

gb|AGN_RPC012xh11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	62.63	1
gb|KR2B.108O20F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.108O20, m	348.62	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	19.49	1
Unknown	522.21	1
gb|KP1B.105O03F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105O03, m	95.89	1
Unknown	43.5	1
gb|KN6B.009I22F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009I22, m	19015.1	1
gb|TT-04_E07 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	202.19	1
gb|KP1B.037L23F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.037L23, m	579.06	1
tc|Rep: S-adenosylmethionine synthetase 3 - Solanum lycopersicum (Tomato) (Lyc	20232.85	1
gb|KN6B.101L09F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101L09, m	168.36	1
gb|tbt_002261 Normalized Nicotiana tabacum cDNA library Nicotiana tabacum cD	644.37	1
gb|KG9B.102P01F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102P01, m	187.51	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	209.31	1
Unknown	22.06	1
Unknown	482.75	1
gb|KF8B.202F14F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202F14, mR	49925.7	1
Unknown	26.3	1
gb|HAP5-7 Cultured tobacco cells Nicotiana tabacum cDNA 3' similar to Virus resist	23.72	1
Unknown	28.02	1
gb|KT7B.107A21F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107A21, mR	68.38	1
tc|Rep: Ubiquitin carrier protein - Solanum tuberosum (Potato), complete [TC4404	263.05	1
Unknown	175.38	1
gb|N.tabacum mRNA for caffeoyl-CoA O-methyltransferase [Z56282]	493.04	1
gb|KT7C.110P04F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110P04, mR	58.47	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	182.82	1
gb|KL4B.104J20F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104J20, mR	92.15	1
tc|Rep: Chromosome undetermined scaffold_163, whole genome shotgun sequenc	56.95	1
gb|KF8C.101K08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101K08, mR	210.52	1
gb|AGN_ELP026xk21f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	382.84	1
Unknown	86.67	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	108.98	1
tc|Rep: NtEIG-E80 protein - Nicotiana tabacum (Common tobacco), partial (62%) [T	306.15	1
Unknown	360.19	1

gb|KL4B.106D01F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106D01, mF	183.82	1
Unknown	2171.2	1
Unknown	1253.25	1
gb|Nicotiana tabacum arcA mRNA for G protein beta subunit-like protein, complete	32.65	1
tc|Rep: Chromosome undetermined scaffold_77, whole genome shotgun sequence	97.94	1
tc|Rep: Ubiquitin carrier protein - Nicotiana tabacum (Common tobacco), complete	152.34	1
Unknown	550.9	1
tc|Rep: Vacuolar protein sorting-associated protein 26-like protein - Solanum tuber	267.61	1
Unknown	624.25	1
gb|TT-11_F16 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	2318.11	1
Unknown	22.4	1
gb|AGN_ELP008xf19f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	31.92	1
Unknown	31.81	1
gb|KP1B.107H16F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107H16, m	1573.11	1
gb|KN6B.105P08F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105P08, m	1531.17	1
gb|KR3B.110I21F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110I21, mR	18.56	1
tc|Rep: Cullin 1-like protein C - Petunia integrifolia subsp. inflata, partial (18%) [TC5	108.53	1
tc|Rep: Plastid glucose-6-phosphate/phosphate translocator - Helianthus annuus (C	40.94	1
gb|TT-29_G11 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	530.66	1
tc|Rep: Chromosome chr18 scaffold_59, whole genome shotgun sequence - Vitis vi	32.58	1
Unknown	983.01	1
gb|TT-06_M10 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	542.11	1
gb|KL4B.104H17F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104H17, mF	486.24	1
gb|KP1B.001N14F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001N14, m	244.64	1
gb|AGN_RNC121xg06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	18.86	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	603.27	1
Unknown	11128.85	1
Unknown	107.85	1
Unknown	31.28	1
gb|CHO_SL003xc11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	23.9	1
Unknown	42.57	1
gb|AGN_PNL218cf1_g10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	24.1	1
Unknown	22.18	1
Unknown	30.3	1

Unknown	481.73	1
Unknown	70.83	1
tc|Rep: Chromosome undetermined scaffold_80, whole genome shotgun sequence	245.4	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	505.07	1
gb|KP1B.104D17F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104D17, m	600.44	1
gb|CHO_SL001xm09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	135.03	1
gb|TT-38_O14 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	211.29	1
gb|AGN_RPC019xj22f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	62.87	1
tc|Rep: NtSar1 protein - Nicotiana tabacum (Common tobacco), complete [TC4108	2558.27	1
gb|KL4B.102P15F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102P15, mR	31.86	1
gb|KR2B.104G24F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.104G24, m	412.26	1
tc|Rep: Transformer-SR ribonucleoprotein - Nicotiana tabacum (Common tobacco),	1014.39	1
Unknown	36.65	1
Unknown	256.83	1
gb|Nicotiana tabacum mRNA for phragmoplastin, dynamin-like protein [AJ244024]	2178.99	1
gb|AGN_RNC127xa14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	28.89	1
gb|KG9B.005P12F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005P12, m	134.88	1
tc|Rep: Tubulin folding cofactor A - Hordeum vulgare var. distichum (Two-rowed ba	51.99	1
tc|Rep: Chromosome undetermined scaffold_245, whole genome shotgun sequenc	33.95	1
gb|KF8C.102B17F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102B17, mRN	33.58	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	28.72	1
Unknown	23.37	1
gb|KL4B.104I18F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104I18, mRN	28.28	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	66.21	1
Unknown	32.88	1
Unknown	361.63	1
gb|KP1B.109O17F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109O17, m	48.37	1
Unknown	106.22	1
gb|KP1B.107M24F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107M24, m	57.89	1
gb|KN6B.110B21F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.110B21, m	16.98	1
tc|Rep: EIL1 - Petunia hybrida (Petunia), partial (5%) [TC63787]	238.67	1
tc|Rep: Chromosome undetermined scaffold_133, whole genome shotgun sequenc	179.51	1
Unknown	11508.45	1
Unknown	16.93	1

Unknown	45.52	1
Unknown	245.08	1
tc|Rep: ATP synthase subunit a - Nicotiana tabacum (Common tobacco), complete [	204.08	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	41.56	1
Unknown	19.82	1
gb|AGN_PNL224df1_b4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	57.58	1
Unknown	24.69	1
gb|TT-28_F14 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	36.64	1
tc|Rep: NADH dehoydrogenase - Arabidopsis thaliana (Mouse-ear cress), partial (75	400	1
tc|Rep: Ubiquitin carrier protein - Capsicum annuum (Bell pepper), complete [TC47	342.83	1
Unknown	41.77	1
gb|TT-20_H01 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	1176.99	1
Unknown	6746.11	1
tc|Rep: Dem protein - Solanum lycopersicum (Tomato) (Lycopersicon esculentum),	39.89	1
tc|Rep: AT5g64840/MXK3_6 - Arabidopsis thaliana (Mouse-ear cress), partial (73%)	63.49	1
gb|TT-21_K17 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	607.1	1
tc|Rep: Chromosome chr8 scaffold_99, whole genome shotgun sequence - Vitis vin	926.38	1
gb|15C04 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5',	24.79	1
tc|Rep: Hydroproline-rich glycoprotein like protein - Nicotiana tabacum (Common	97.19	1
gb|KN6B.107O10F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.107O10,	113.85	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	98.68	1
gb|AGN_RNC108xf20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	46.07	1
gb|tbt_007895 Normalized Nicotiana tabacum cDNA library Nicotiana tabacum cD	949.36	1
Unknown	46.95	1
tc|Rep: Dehydroascorbate reductase - Solanum tuberosum (Potato), partial (60%)	94.64	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	1584.18	1
Unknown	68.6	1
Unknown	852.6	1
tc|Rep: Ribosomal protein S6-like protein - Solanum tuberosum (Potato), complete	21.47	1
tc|Rep: Chromosome undetermined scaffold_891, whole genome shotgun sequenc	458.66	1
Unknown	50.44	1
gb|KF8C.108E23F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108E23, mR	9399.86	1
gb|KN6B.102G20F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102G20,	539.64	1
tc|Rep: Chromosome chr11 scaffold_56, whole genome shotgun sequence - Vitis vi	933.79	1

Unknown	33.63	1
tc|Rep: Mitochondrial processing peptidase-like - Solanum tuberosum (Potato), par	264.04	1
gb|TT-14_C13 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	104.79	1
Unknown	192.33	1
Unknown	35.45	1
tc|Rep: ALG2-interacting protein X - Nicotiana tabacum (Common tobacco), partial	23.92	1
gb|TT-13_G17 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	98.88	1
gb|KL5B.115B07F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.115B07, mR	42.81	1
gb|KL5B.001P11F.050901T7 KL5B Nicotiana tabacum cDNA clone KL5B.001P11, mR	405.16	1
tc|Rep: EIL1 - Nicotiana tabacum (Common tobacco), complete [TC41476]	97.85	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	328.34	1
gb|TT-20_M23 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	9264.01	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	223.01	1
gb|KN6B.115P21F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.115P21, m	42.92	1
gb|KR3B.106G05F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106G05, m	227.13	1
Unknown	1565.76	1
gb|KF8C.102B08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102B08, mRN	27.05	1
Unknown	23.1	1
gb|KR3B.109F02F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109F02, mR	18500.5	1
Unknown	44.49	1
gb|KF8B.201N07F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201N07, mR	27.26	1
tc|Rep: At2g43020/MFL8.12 - Arabidopsis thaliana (Mouse-ear cress), partial (94%)	585.44	1
tc|Rep: ER lumen protein retaining receptor - Vitis vinifera (Grape), complete [TC56	1142.27	1
tc|Rep: 40S ribosomal protein S4 - Solanum tuberosum (Potato), partial (68%) [TC6	34.4	1
gb|KT7C.104K05F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104K05, mRN	762.61	1
Unknown	57.62	1
gb|KL5B.111A10F.060117T7 KL5B Nicotiana tabacum cDNA clone KL5B.111A10, mR	3288.15	1
Unknown	34.74	1
tc|Rep: 4-hydroxyphenylpyruvate dioxygenase - Daucus carota (Carrot), partial (47	53.83	1
tc|Rep: Chromosome chr19 scaffold_111, whole genome shotgun sequence - Vitis v	97.94	1
tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin	9450.72	1
Unknown	577.77	1
Unknown	29.14	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	96.29	1

tc|Rep: Chlorophyll a/b binding protein CP29 - Phaseolus aureus (Mung bean) (Vign	255.88	1
gb|N.tabacum mRNA for ornithine decarboxylase [Y10472]	639.21	1
Unknown	41.57	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	73.12	1
gb|KF8C.105O11F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105O11, mR	212.21	1
gb|AGN_PNL221df1_g3.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	541.44	1
gb|KG9B.002I22F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002I22, m	48.57	1
gb|KT7B.100K06F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100K06, mR	3475.54	1
Unknown	112.74	1
tc|Rep: SNF1-related kinase complex anchoring protein SIP1 - Solanum lycopersicu	144.48	1
gb|KP1B.109H22F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109H22, m	66.75	1
Unknown	105.62	1
tc|Rep: Na+/H+ antiporter precursor - Populus euphratica (Euphrates poplar), parti	169.21	1
tc|Rep: MYB transcription factor - Catharanthus roseus (Rosy periwinkle) (Madagas	24.01	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	295.54	1
gb|Nicotiana tabacum mRNA for SET-domain-containing protein (set1 gene) [AJ294	260.31	1
gb|KL4B.101A01F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101A01, m	21.24	1
gb|AGN_PNL225bf1_h12.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	7877.44	1
gb|TT-22_M21 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA se	25.71	1
gb|Nicotiana tabacum mRNA for putative cytosolic cysteine synthase 7 (oas7 gene)	1160.99	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	185.29	1
Unknown	21.02	1
tc|Rep: Glycine-rich protein-like - Oryza sativa subsp. japonica (Rice), partial (35%)	178.7	1
gb|AGN_RNC116xg18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	171.88	1
Unknown	87.11	1
tc|Rep: Complex: S. cerevisiae L29 is part of the 60S subunit of the ribosome - Aspe	18.22	1
Unknown	81.01	1
Unknown	269.07	1
gb|AGN_RPC013xb23f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	30.06	1
Unknown	400.69	1
tc|Rep: Malonyl-CoA:ACP transacylase - Perilla frutescens (Beefsteak plant) (Chines	270.03	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	1921.35	1
gb|KP1B.037B08F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.037B08, m	30.43	1
gb|KN6B.110M01F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.110M01,	69.38	1

Unknown	9070.69	1
tc|Rep: Chromosome chr1 scaffold_84, whole genome shotgun sequence - Vitis vin	42.45	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	86.11	1
tc|Rep: Voltage-dependent anion channel - Nicotiana tabacum (Common tobacco),	128.34	1
Unknown	50.46	1
tc|Rep: AG-motif binding protein-2 - Nicotiana tabacum (Common tobacco), compl	96.87	1
Unknown	258.7	1
gb|KT7B.103E12F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.103E12, mRN	93.62	1
Unknown	26.01	1
gb|CHO_SL023xa21f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	3439.66	1
gb|KT7C.113L02F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.113L02, mRN	21.71	1
Unknown	205.82	1
gb|KL5B.112K19F.060210T7 KL5B Nicotiana tabacum cDNA clone KL5B.112K19, mR	1581.61	1
Unknown	253.14	1
Unknown	84.31	1
Unknown	967.03	1
gb|AGN_PNL227cf1_f6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	22.38	1
gb|KR2B.001O08F.050815T7 KR2B Nicotiana tabacum cDNA clone KR2B.001O08, m	19.81	1
Unknown	32.55	1
Unknown	34.84	1
Unknown	41.47	1
gb|KL4B.106E21F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106E21, mR	35.85	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	46.27	1
tc|Rep: 40S ribosomal protein S7 - Avicennia marina (Grey mangrove), complete [T	1012.11	1
tc|Rep: ChaC-like family protein-like - Solanum tuberosum (Potato), partial (94%) [T	3180.31	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	32.37	1
tc|Rep: Zinc finger, RING-type; Thioredoxin-related - Medicago truncatula (Barrel m	86.29	1
Unknown	226.61	1
gb|FS436570 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	76.97	1
gb|KP1B.103D12F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103D12, m	142	1
tc|Rep: Soluble inorganic pyrophosphatase - Solanum tuberosum (Potato), partial (	981.01	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	191.03	1
Unknown	62.29	1
gb|KR3B.109H16F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109H16, m	27.74	1

tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	1121.68	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	94.96	1
Unknown	35.19	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	584.56	1
gb|KG9B.103F10F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103F10, m	30.18	1
gb|KG9B.102C17F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102C17, r	327.31	1
Unknown	827.92	1
gb|KL4B.109B08F.051108T7 KL4B Nicotiana tabacum cDNA clone KL4B.109B08, mR	191.54	1
gb|AGN_RNC123xf10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	210.67	1
Unknown	18.9	1
tc|Rep: Ly200 protein - Capsicum annuum (Bell pepper), complete [TC55451]	41.35	1
gb|FS399667 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	1829.68	1
tc|Rep: Phosphoenolpyruvate carboxylase - Solanum tuberosum (Potato), partial (8	109.33	1
tc|Rep: Glutathione S-transferase, class-phi - Solanum commersonii (Commerson's	128.04	1
gb|TT-38_N08 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	169.68	1
gb|AGN_RNC013xl12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	67.13	1
gb|TT-16_K24 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	71.61	1
gb|KL4B.105H09F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105H09, mF	165.99	1
Unknown	4319.57	1
Unknown	20.73	1
gb|KG9B.104B10F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104B10, r	152.38	1
tc|Rep: 3'-5' exonuclease domain-containing protein-like - Solanum tuberosum (Pot	9897.3	1
tc|Rep: PttA - Petunia hybrida (Petunia), partial (39%) [TC49360]	1292.13	1
tc|Rep: Predicted protein - Chlamydomonas reinhardtii, partial (4%) [TC73662]	1913.55	1
Unknown	25.98	1
gb|AGN_RNC117xl01r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	24.7	1
gb|CHO_SL011xo14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	34.28	1
gb|AGN_ELP002xl14f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	183.05	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	717.98	1
gb|Nicotiana tabacum mRNA for calmodulin NtCaM1, complete cds [AB050837]	1098.29	1
Unknown	1601.16	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	2928.6	1
gb|KG9B.102A05F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102A05, r	107.34	1
gb|KR3B.111G24F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111G24, m	3556.91	1

tc|Rep: F2P3.9 protein - Arabidopsis thaliana (Mouse-ear cress), partial (24%) [TC6	27.29	1
Unknown	22.1	1
gb|KN6B.108L12F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.108L12, m	84.83	1
gb|CHO_SL012xm16f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	563.07	1
Unknown	73.09	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	167.77	1
gb|AGN_PNL226bf1_h4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	23.72	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	65.25	1
gb|KP1B.103J03F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103J03, mR	23.29	1
gb|FS405146 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	28.22	1
gb|KR3B.110C13F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110C13, m	8065.7	1
tc|Rep: Cellulose synthase - Solanum tuberosum (Potato), partial (40%) [TC50352]	26.51	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	28.43	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	1067.4	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	9518.3	1
tc|Rep: Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vi	549.89	1
tc|Rep: NtEIG-E80 protein - Nicotiana tabacum (Common tobacco), partial (87%) [T	34416.15	1
Unknown	223.55	1
gb|AGN_RPC023xd13f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	135.06	1
gb|KT7C.112O19F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112O19, mR	319.33	1
gb|Nicotiana tabacum sucrose-phosphate synthase isoform B (SPSB) mRNA, compl	481.08	1
tc|Rep: Ovule receptor-like kinase 28 precursor - Solanum chacoense (Chaco potat	29.75	1
Unknown	177.7	1
tc|Rep: Calcium-dependent protein kinase CDPK1 - Solanum lycopersicum (Tomato	24.79	1
Unknown	31.45	1
gb|Nicotiana tabacum urate oxidase mRNA, complete cds [DQ365933]	19.06	1
gb|KR3B.106G20F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106G20, m	783.24	1
Unknown	525.15	1
gb|TT-07_D22 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	19.11	1
gb|KN6B.103M10F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103M10,	24.75	1
Unknown	2778.77	1
gb|Nicotiana tabacum arginine decarboxylase mRNA, complete cds [AF321137]	9815.62	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	159.41	1
gb|TOBESTR059A07 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	273.11	1

tc|Rep: Chromosome chr1 scaffold_180, whole genome shotgun sequence - Vitis vi	93.77	1
gb|KN6B.101A12F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101A12, m	43.48	1
gb|KL4B.113D21F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.113D21, mR	18.86	1
gb|CHO_SL018xj10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	1599.46	1
tc|Rep: Chromosome chr8 scaffold_115, whole genome shotgun sequence - Vitis vi	208.23	1
Unknown	29.38	1
gb|KF8C.102A10F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102A10, mRN	209.42	1
Unknown	58.15	1
tc|Rep: Ubiquitin-conjugating enzyme family protein-like protein - Solanum tuberos	106.53	1
gb|TT-47_G16 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	133.09	1
gb|KF8C.102E08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102E08, mRN	95.05	1
gb|TT-15_M17 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	29.78	1
Unknown	161.01	1
gb|KF8B.201P01F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201P01, mRN	139.66	1
Unknown	24.93	1
gb|Nicotiana tabacum cytosolic aconitase (ACO) mRNA, complete cds [AF194945]	38.18	1
gb|CHO_SL023xn20f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	2293.59	1
gb|KT7C.108D17F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108D17, mR	186.87	1
gb|KF8B.200A11F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200A11, mRN	474.95	1
tc|Rep: Chromosome chr8 scaffold_68, whole genome shotgun sequence - Vitis vin	201.05	1
gb|TT-23_C05 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	122.56	1
Unknown	20.42	1
gb|BP534517 MAT005 Nicotiana tabacum cDNA clone BY33097, mRNA sequence [E	167.73	1
gb|KF8C.101E16F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101E16, mRN	214.85	1
tc|Rep: Chromosome undetermined scaffold_203, whole genome shotgun sequenc	11066.15	1
Unknown	169.9	1
tc|Rep: Chromosome chr9 scaffold_65, whole genome shotgun sequence - Vitis vin	102.64	1
gb|AGN_RPC002xi02f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	49.57	1
Unknown	31.01	1
Unknown	17.58	1
gb|KP1B.107H01F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107H01, m	150.79	1
Unknown	53.51	1
gb|TT-30_J08 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sequ	319.45	1
Unknown	476.38	1

gb|KL4B.106M13F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106M13, m	106.77	1
tc|Rep: Chromosome undetermined scaffold_1484, whole genome shotgun sequen	2429.48	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	410.71	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	263.08	1
tc|CPY18934 Solanum nigrum chloroplast tRNA-Ala, tRNA-Ile, 16S rRNA, tRNA-Val,	1254.49	1
gb|BP533691 MAT005 Nicotiana tabacum cDNA clone BY31006, mRNA sequence [E	37.27	1
Unknown	1673.72	1
gb|KL4B.110E10F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110E10, mR	60.18	1
Unknown	21.88	1
gb|KG9B.101O01F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101O01, r	140.1	1
Unknown	507.74	1
gb|AGN_RNC127xf14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	26.83	1
gb|AM824642 seedling library, SL Nicotiana tabacum cDNA clone nt002330037, mR	31	1
tc|Rep: Pyruvate dehydrogenase E1 beta subunit isoform 2 - Zea mays (Maize), part	190.34	1
Unknown	41.27	1
gb|KL4B.113I12F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.113I12, mRN	198.01	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	150.83	1
gb|AGN_RNC109xi21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	46.41	1
gb|TT-09_B10 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	27.13	1
Unknown	1299.28	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	42.08	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT2-32-460, cultivar Bright Yellow 2	252.72	1
gb|Nicotiana tabacum adenyl cyclase (Axi 141) mRNA, complete cds [AF026389]	17.43	1
gb|KL4B.111C19F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111C19, mR	30.76	1
Unknown	603.42	1
Unknown	831.53	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	379.32	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	18.16	1
gb|FS406426 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	107.07	1
gb|CHO_SL008xm11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	134.64	1
tc|Rep: Chromosome chr19 scaffold_126, whole genome shotgun sequence - Vitis v	1085.61	1
gb|AGN_RPC022xm24f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	33.26	1
tc|Rep: Glycoprotein-like protein - Solanum tuberosum (Potato), partial (97%) [TC5	27.82	1
Unknown	18.75	1

gb|Nicotiana tabacum receptor-like protein kinase (PRK2) mRNA, partial cds [AF246	2839.53	1
Unknown	24.12	1
Unknown	29.54	1
Unknown	2036.14	1
gb|KL4B.103L05F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103L05, mR	1378.94	1
tc|Rep: Os01g0170400 protein - Oryza sativa subsp. japonica (Rice), partial (7%) [TC	501.29	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	267.13	1
gb|KG9B.001A11F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001A11, m	744.04	1
Unknown	987.33	1
gb|TT-12_L01 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	6419.59	1
gb|AGN_RNC022xa22f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	134.57	1
gb|AGN_RNC017xc08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	27.73	1
Unknown	31.59	1
Unknown	37.21	1
Unknown	127.35	1
Unknown	405.43	1
gb|KN6B.103P10F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103P10, m	36.06	1
Unknown	233.28	1
gb|KL5B.114H13F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.114H13, m	36.42	1
Unknown	943.03	1
tc|Rep: Glycolate oxidase - Solanum lycopersicum (Tomato) (Lycopersicon esculent	65.58	1
gb|KR2B.110H02F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110H02, m	17.46	1
gb|AGN_PNL202df1_a7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	76.31	1
gb|TT-07_L12 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	34.91	1
Unknown	150.16	1
gb|AGN_ELP006xd10f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	57.45	1
Unknown	19.67	1
gb|KR2B.108I01F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.108I01, mR	93.69	1
tc|Rep: Eukaryotic initiation factor 4A-9 - Nicotiana tabacum (Common tobacco), c	1148.53	1
Unknown	248.9	1
Unknown	189.08	1
gb|KG9B.001K05F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001K05, m	57.93	1
gb|KG9B.004E10F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004E10, m	156.65	1
Unknown	26.12	1

Unknown	19.82	1
gb|KG9B.005P12F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005P12, m	73.77	1
gb|Nicotiana tabacum JD1 (JD1) mRNA, complete cds [AF316320]	577.34	1
Unknown	32.09	1
gb|KL4B.101N15F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101N15, m	544.45	1
Unknown	21.45	1
gb|FS419329 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	1786.63	1
tc|Rep: Tyrosyl-tRNA synthetase - Nicotiana tabacum (Common tobacco), partial (1	18.26	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	1329.52	1
tc|Rep: Farnesyl pyrophosphate synthase - Solanum lycopersicum (Tomato) (Lycop	236.63	1
Unknown	27.41	1
gb|FS417684 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	466.84	1
Unknown	125.61	1
tc|Rep: CXE carboxylesterase - Malus pumila, partial (59%) [TC55745]	28.18	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	43.16	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	59.53	1
Unknown	48.82	1
Unknown	51.09	1
gb|CHO_SL019xe14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	613.12	1
gb|AGN_RNC124xh08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	23.28	1
tc|Rep: Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha - Lactob	429.36	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	185.44	1
gb|AGN_RNC029xh18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	18.71	1
tc|Rep: Uncharacterized protein At2g18460.2 - Arabidopsis thaliana (Mouse-ear cr	25.1	1
Unknown	87.03	1
tc|Rep: 14-3-3 protein isoform g - Nicotiana tabacum (Common tobacco), complet	90.58	1
Unknown	92.19	1
Unknown	20.68	1
tc|Rep: Chromosome chr17 scaffold_101, whole genome shotgun sequence - Vitis	519.45	1
gb|N.tabacum mRNA for pyruvate kinase (plastid isozyme) [Z28374]	1887.86	1
Unknown	103.82	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	913.14	1
gb|Nicotiana tabacum mRNA for vacuolar invertase (vi gene) [AJ305044]	59.15	1
Unknown	492.37	1

tc|Rep: UDP-glucose glucosyltransferase - Catharanthus roseus (Rosy periwinkle) (N	241.21	1
tc|Rep: Signal peptidase 22 kDa subunit - Medicago truncatula (Barrel medic), parti	1558.95	1
tc|Rep: Chromosome chr19 scaffold_35, whole genome shotgun sequence - Vitis vi	86.42	1
gb|AGN_RPC005xc12f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	56.71	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	76.95	1
Unknown	25.8	1
tc|CAB63010.1 - Arabidopsis thaliana (Mouse-ear cress), partial (35%) [TC72930]	1667.59	1
tc|Rep: Chromosome chr9 scaffold_33, whole genome shotgun sequence - Vitis vin	10484.35	1
Unknown	195.13	1
gb|BL12.104I03F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.104I03, mRN	584.01	1
tc|Rep: Chromosome undetermined scaffold_484, whole genome shotgun sequenc	594.59	1
gb|FS416927 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	614.16	1
Unknown	103.03	1
gb|TOBESTR007A07 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	69.87	1
tc|Rep: Transcription factor - Nicotiana tabacum (Common tobacco), partial (33%)	57.25	1
tc|Rep: Chromosome chr1 scaffold_180, whole genome shotgun sequence - Vitis vi	671.7	1
Unknown	80.16	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	198.71	1
gb|KN6B.101H18F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101H18, n	453.63	1
Unknown	22.1	1
Unknown	54.45	1
tc|Rep: Chromosome chr4 scaffold_443, whole genome shotgun sequence - Vitis vi	75.09	1
gb|ntsm10 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [E	211.1	1
gb|KF8C.101D18F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101D18, mRI	97.86	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	1308.3	1
gb|AGN_PNL227df1_e5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	27.61	1
Unknown	25.41	1
gb|KL4B.106C07F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106C07, mR	30.34	1
tc|Rep: Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplast precursor - S	8574.15	1
Unknown	39.6	1
Unknown	436.49	1
gb|KR3B.105J07F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.105J07, mR	37.21	1
gb|TT-07_L07 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	110.58	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	21.2	1

Unknown	61.25	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	41.38	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	257.61	1
gb|Nicotiana tabacum hexokinase 1a (Hxk1a) mRNA, complete cds [AY553214]	1629.83	1
gb|Nicotiana tabacum mRNA for chloroplast ribosomal protein L4, complete cds [A	2739.71	1
gb|KT7B.114K15F.060127T7 KT7 Nicotiana tabacum cDNA clone KT7B.114K15, mRN	29.21	1
gb|KP1B.102O17F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102O17, m	761.73	1
tc|Rep: Probable pectate lyase P59 precursor - Solanum lycopersicum (Tomato) (Ly	45576.1	1
gb|KP1B.101O17F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101O17, m	22.82	1
gb|EST_CSP001xo12f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	36.51	1
Unknown	120.53	1
tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	511.96	1
gb|AGN_RNC010xm14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	199.26	1
gb|AGN_RNC116xo18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	23.87	1
Unknown	58.63	1
gb|Nicotiana tabacum UDP-glucuronate decarboxylase 1 mRNA, complete cds [AY6	685.54	1
gb|KT7C.104B05F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104B05, mRN	80.78	1
tc|Rep: Diacylglycerol kinase-like protein - Arabidopsis thaliana (Mouse-ear cress),	80.49	1
Unknown	24.68	1
Unknown	4398.04	1
Unknown	42.25	1
Unknown	1833.69	1
tc|Rep: Chromosome undetermined scaffold_608, whole genome shotgun sequenc	57.88	1
Unknown	49.37	1
Unknown	101.19	1
tc|Rep: Chromosome chr16 scaffold_94, whole genome shotgun sequence - Vitis vi	170.08	1
tc|Rep: Os09g0505800 protein - Oryza sativa subsp. japonica (Rice), partial (86%) [T	40.28	1
gb|TT-23_B20 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	745.65	1
gb|TT-10_G24 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	9379.51	1
Unknown	95.68	1
gb|AM818948 seedling library, SL Nicotiana tabacum cDNA clone nt002252015, mR	514.2	1
gb|KP1B.111H16F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.111H16, m	57.99	1
Unknown	152.91	1
gb|KL4B.100M14F.050922T7 KL4B Nicotiana tabacum cDNA clone KL4B.100M14, m	72.45	1

gb|KR2B.103H05F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.103H05, m	47.99	1
tc|Rep: 60S ribosomal protein L38 - Solanum lycopersicum (Tomato) (Lycopersicon	287.91	1
Unknown	286.21	1
gb|CHO_SL027xb23f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1600.38	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	31.41	1
gb|KN6B.103I10F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103I10, m	431.63	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	52.56	1
Unknown	19.6	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (93%) [TC5	48.55	1
Unknown	31.61	1
gb|KR3B.101E16F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101E16, m	388.77	1
Unknown	134.43	1
gb|AGN_RNC014xf08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	29.31	1
gb|AGN_PNL213cf1_g3.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	51.86	1
gb|KL4B.104H17F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104H17, m	200.59	1
gb|CHO_SL004xd15f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	31.66	1
gb|KG9B.001M19F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001M19,	35.39	1
Unknown	30	1
Unknown	79.95	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	561.16	1
Unknown	18.86	1
tc|Rep: Chromosome undetermined scaffold_69, whole genome shotgun sequence	896.24	1
Unknown	20.69	1
gb|CHO_SL001xa19f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	37.91	1
gb|EST T1P015 Tobacco Leaves Express Library Nicotiana tabacum cDNA clone t1p	25.25	1
Unknown	934.07	1
gb|KL4B.103G13F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103G13, m	1148.75	1
tc|Rep: Metal transporter - Solanum lycopersicum (Tomato) (Lycopersicon esculent	66.8	1
tc|Rep: Chromosome chr10 scaffold_179, whole genome shotgun sequence - Vitis	16.72	1
Unknown	95.7	1
Unknown	20.23	1
gb|KT7B.114H13F.060127T7 KT7 Nicotiana tabacum cDNA clone KT7B.114H13, mR	709.89	1
gb|KG9B.001J02F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001J02, m	18.71	1
gb|TT-17_O12 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	111.59	1

tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	91.8	1
Unknown	283.17	1
gb|AGN_RNC018xe23f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	28.11	1
gb|AGN_RNC007xd13r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	35.96	1
Unknown	69.51	1
Unknown	25.46	1
Unknown	1353.1	1
gb|KT7C.104K01F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104K01, mRN	8096.84	1
tc|Rep: Methionine synthase - Nicotiana suaveolens, partial (48%) [TC42734]	11569	1
tc|Rep: Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	104.13	1
gb|FS393498 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	57.54	1
tc|Rep: Ripening regulated protein-like - Solanum tuberosum (Potato), partial (56%	98.51	1
gb|Nicotiana tabacum sucrose transporter-like protein (SUT3) mRNA, complete cds	207.99	1
Unknown	175.95	1
tc|Rep: Ribosomal protein L24E - Medicago truncatula (Barrel medic), complete [TC	1144.73	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	275.05	1
Unknown	400.51	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	28.28	1
gb|Nicotiana tabacum NtTOM3 mRNA for tobamovirus multiplication 3, complete	2904.04	1
Unknown	32.11	1
tc|Rep: Salt tolerance protein 5-like protein - Solanum tuberosum (Potato), partial	121.41	1
gb|Nicotiana tabacum GA2ox2 mRNA for gibberellin 2-oxidase 2, complete cds [AB	22.2	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	4248.78	1
tc|Rep: Chromosome chr13 scaffold_210, whole genome shotgun sequence - Vitis	1594.83	1
Unknown	196.1	1
gb|KF8C.109L18F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109L18, mRN	53.84	1
Unknown	29.21	1
tc|Rep: Chromosome chr1 scaffold_84, whole genome shotgun sequence - Vitis vin	77.73	1
gb|AGN_RNC020xo16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	57.63	1
tc|Rep: 26S protease regulatory subunit 7 - Prunus persica (Peach), partial (34%) [T	115.8	1
gb|KL4B.106D12F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106D12, m	528.84	1
tc|Rep: Chromosome chr5 scaffold_72, whole genome shotgun sequence - Vitis vin	42.21	1
Unknown	1190.58	1
Unknown	25.88	1

Unknown	24.18	1
gb|KG9B.004H15F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004H15, n	64.68	1
gb|TT-05_D19 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	825.02	1
gb|N.tabacum NeIF-4A14 mRNA [X79141]	3475.99	1
gb|KR3B.103F10F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.103F10, m	7836.53	1
tc|Rep: S25-PR6 - Nicotiana tabacum (Common tobacco), partial (98%) [TC47521]	37.62	1
tc|Rep: Avr9 elicitor response protein - Nicotiana tabacum (Common tobacco), part	30.83	1
tc|Rep: T8F5.5 protein - Arabidopsis thaliana (Mouse-ear cress), partial (43%) [TC5	201.42	1
tc|Rep: Chromosome undetermined scaffold_623, whole genome shotgun sequenc	456.85	1
gb|TT-09_J11 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	18.43	1
Unknown	21.08	1
Unknown	2368.7	1
tc|Rep: Probable pectate lyase P59 precursor - Solanum lycopersicum (Tomato) (Ly	21446.2	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	22.35	1
Unknown	57.9	1
gb|KP1B.101N23F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101N23, m	44.71	1
tc|Rep: CDPK - Ipomoea nil (Japanese morning glory) (Pharbitis nil), partial (93%) [T	127.66	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	1115.05	1
gb|TT-20_O05 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	292.32	1
tc|GB|AY532658.1|AAS92257.1 putative pyridoxine biosynthesis protein [Nicotian	79.33	1
gb|TL13.105B12F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.105B12, mR	16968.15	1
gb|Nicotiana tabacum NtVPE-1b mRNA for vacuolar processing enzyme-1b complet	31.67	1
gb|AGN_RNC022xo24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	183.48	1
gb|KP1B.109P14F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109P14, m	43.71	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	43.91	1
gb|Nicotiana tabacum Nt-5beta-POR-B mRNA for progesterone 5beta reductase-B,	525.2	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	3212.4	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	88.96	1
Unknown	24.45	1
tc|Rep: Chromosome chr9 scaffold_104, whole genome shotgun sequence - Vitis vi	73.12	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	25.96	1
gb|EST_FLW004xb16f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	129.48	1
Unknown	184.54	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	2899.64	1

tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	533.24	1
tc|Rep: LEA1-like protein - Capsicum annuum (Bell pepper), partial (97%) [TC51846	21.48	1
tc|Rep: BRCT domain protein - Neosartorya fischeri (strain ATCC 1020 / DSM 3700	66.32	1
Unknown	113.41	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	1876.24	1
tc|Rep: Isoform 2 of Q5FBB7 - Homo sapiens (Human), partial (5%) [TC56658]	58.33	1
gb|KP1B.101J08F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101J08, mR	186.5	1
gb|CHO_SL028xk23f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	462.88	1
gb|Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds [D8672	595.94	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	103.41	1
gb|KT7C.102F22F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102F22, mR	138.3	1
Unknown	26.52	1
tc|Rep: AT3g42050/F4M19_10 - Arabidopsis thaliana (Mouse-ear cress), complete	486.11	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	134.55	1
gb|AGN_RNC018xd16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	22.46	1
gb|KP1B.110L05F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110L05, m	16.98	1
Unknown	445.83	1
tc|Rep: ATP synthase subunit beta - Nicotiana sylvestris (Wood tobacco), partial (2	388.92	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT32-1-320, cultivar Bright Yellow 2	47.58	1
gb|KP1B.037D07F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.037D07, m	273.64	1
gb|Nicotiana tabacum ankyrin-repeat protein HBP1 mRNA, complete cds [AF35279	229.07	1
gb|TT-28_H14 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	501.79	1
Unknown	704.65	1
gb|KL5B.111N24F.060117T7 KL5B Nicotiana tabacum cDNA clone KL5B.111N24, m	10227.9	1
Unknown	22.74	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	25.89	1
gb|AGN_RPC021xh10f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	4807.83	1
tc|Rep: Chloride channel protein CLC-d - Arabidopsis thaliana (Mouse-ear cress), pa	150.54	1
Unknown	49.18	1
gb|AGN_PNL208ar1_e6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	17.36	1
tc|Rep: 6-phosphogluconate dehydrogenase, decarboxylating - Vitis vinifera (Grape	146.85	1
tc|Rep: Glutaredoxin related protein - Oryza sativa subsp. indica (Rice), partial (32	104.4	1
tc|Rep: 40S ribosomal protein S15-like - Solanum tuberosum (Potato), complete [T	87.01	1
Unknown	209.69	1

tc|Rep: Protein kinase SRK - Nicotiana tabacum (Common tobacco), partial (23%) [T	547.2	1
tc|Rep: Zinc finger, RING-type; Thioredoxin-related - Medicago truncatula (Barrel m	63.62	1
gb|KR3B.112E20F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112E20, m	190.5	1
Unknown	47.94	1
gb|KT7C.105D04F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105D04, mR	987.58	1
Unknown	27.47	1
Unknown	58.71	1
tc|Rep: Chromosome chr10 scaffold_81, whole genome shotgun sequence - Vitis vi	517.9	1
tc|Rep: Chromosome chr11 scaffold_177, whole genome shotgun sequence - Vitis v	84.08	1
gb|KL4B.112G15F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112G15, m	57.1	1
gb|AGN_PNL228df1_c8.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	779.93	1
gb|EST_FLW004xn20f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	30.91	1
gb|FS436591 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	103.89	1
gb|CHO_SL013xc21f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	32.68	1
tc|Rep: Chromosome chr5 scaffold_72, whole genome shotgun sequence - Vitis vin	47.03	1
Unknown	93.91	1
tc|Rep: CBL-interacting protein kinase 25 - Populus trichocarpa (Western balsam p	910.11	1
tc|Rep: Chromosome undetermined scaffold_763, whole genome shotgun sequenc	193.18	1
gb|TT-14_C11 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	80.16	1
gb|KL4B.111G19F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111G19, m	112.64	1
Unknown	475.5	1
tc|Rep: Salt tolerance protein 5-like protein - Solanum tuberosum (Potato), partial	756.02	1
Unknown	31.87	1
Unknown	2580.39	1
Unknown	28.86	1
gb|KG9B.105I05F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105I05, m	43.02	1
gb|Nicotiana tabacum ankyrin-repeat protein HBP1 mRNA, complete cds [AF35279	377.42	1
gb|AGN_PNL215dr1_h5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	22.41	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	194.41	1
gb|Nicotiana tabacum A15 mRNA for hypothetical protein, complete cds [AB03253	246.28	1
gb|KT7C.102K16F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102K16, mR	61.68	1
gb|KL4B.105B08F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105B08, mR	1218.9	1
Unknown	18.87	1
Unknown	3295.61	1

tc|Rep: Genomic DNA, chromosome 3, P1 clone: MUO10 - Arabidopsis thaliana (M	59.11	1
gb|Nicotiana tabacum mRNA for FtsZ-like chloroplast protein [AJ133453]	81.59	1
Unknown	39.86	1
gb|KT7C.105J02F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105J02, mRN	29.94	1
gb|KL4B.104C03F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104C03, mR	171.52	1
gb|KR3B.110C13F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110C13, m	1599.77	1
gb|TT-10_I04 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	17.33	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	62.3	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	21.55	1
gb|KN6B.104I06F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104I06, m	26.99	1
gb|KG9B.102C13F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102C13, m	4190.3	1
tc|Rep: Ribosomal protein L15 - Vitis vinifera (Grape), partial (60%) [TC52772]	456.63	1
tc|Rep: NADH:ubiquinone oxidoreductase-like - Solanum tuberosum (Potato), com	803.56	1
Unknown	500.17	1
gb|KG9B.001F13F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001F13, m	389.01	1
gb|AGN_ELP024xn09f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	85.89	1
Unknown	29.18	1
gb|KR3B.112F15F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112F15, m	142.66	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	378.68	1
Unknown	288.73	1
gb|KN6B.105M14F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105M14,	431.11	1
Unknown	1505.89	1
Unknown	72.77	1
gb|KF8C.108I23F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108I23, mRN	7148.89	1
gb|KR2B.108F04F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.108F04, m	940.28	1
Unknown	1028.97	1
gb|AM808565 seedling library, SL Nicotiana tabacum cDNA clone nt002221007, m	47.68	1
Unknown	114.73	1
gb|FS412600 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	1635.69	1
gb|AGN_ELP012xf07f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	498.76	1
Unknown	14660.95	1
Unknown	44.84	1
tc|Rep: Mitogen-activated protein kinase - Solanum lycopersicum (Tomato) (Lycop	22.83	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	106.78	1

gb|TT-48_A24 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	103.75	1
Unknown	2916.71	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	183.25	1
Unknown	193.48	1
tc|Rep: Vacuolar proton pump subunit F - Corchorus olitorius, complete [TC50244]	10813.15	1
gb|AGN_RNC021xa02f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	137.94	1
Unknown	1048.11	1
Unknown	10870.2	1
gb|KP1B.110N05F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110N05, m	687.17	1
tc|Rep: Heat shock protein 83 - Ipomoea nil (Japanese morning glory) (Pharbitis nil)	120.21	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	731.37	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	291.9	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	120	1
tc|Rep: Malate dehydrogenase - Solanum tuberosum (Potato), partial (46%) [TC430	511.43	1
Unknown	154.46	1
tc|Rep: Chloroplast small heat shock protein class I - Capsicum frutescens (Cayenne	747.85	1
gb|AM791968 DL, diurnal library Nicotiana tabacum cDNA clone nt005134088, mR	24.42	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	55.07	1
gb|Nicotiana tabacum chloroplast carbonic anhydrase gene, complete cds [M9413	8190.35	1
gb|KG9B.004J17F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004J17, m	50.26	1
tc|Rep: Chromosome chr9 scaffold_104, whole genome shotgun sequence - Vitis vi	183.46	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	32.43	1
Unknown	807.38	1
Unknown	25.43	1
Unknown	179.81	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	277.57	1
gb|KR2B.110K09F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110K09, m	29.15	1
gb|KF8B.200I19F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200I19, mRN	219.89	1
gb|KP1B.104N15F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104N15, m	562.1	1
gb|KL4B.105A02F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105A02, m	82.92	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	56.76	1
gb|KR3B.105A04F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.105A04, m	509.3	1
tc|Rep: Chromosome chr13 scaffold_210, whole genome shotgun sequence - Vitis	227.72	1
Unknown	71.08	1

tc|Rep: Expressed protein - Oryza sativa subsp. japonica (Rice), partial (7%) [TC673	250.97	1
Unknown	111.96	1
gb|AGN_ELP025xj05f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	8161.18	1
gb|Nicotiana tabacum clone PR51 mRNA sequence [AF154660]	2783.87	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	20.95	1
tc|Rep: Microsomal omega-6-desaturase - Nicotiana tabacum (Common tobacco),	20650.35	1
gb|TT-03_J06 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sequ	27.5	1
tc|Rep: Short-chain dehydrogenase Tic32 - Pisum sativum (Garden pea), partial (23	41.69	1
gb|KN6B.009J12F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009J12, m	19.12	1
Unknown	950.9	1
tc|Rep: Small subunit ribosomal protein - Berberis thunbergii (Japanese barberry),	926.53	1
gb|KP1B.001B10F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001B10, m	1183.53	1
gb|KR3B.109G03F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109G03, m	132.83	1
tc|Rep: Small GTP-binding protein Sar1BNt - Nicotiana tabacum (Common tobacco)	3908.71	1
Unknown	18.02	1
Unknown	1040.58	1
gb|KG9B.103C09F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103C09,	72.79	1
tc|Rep: Chromosome undetermined scaffold_134, whole genome shotgun sequenc	46.05	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	3344.87	1
gb|AGN_RNC020xk07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	17.5	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	77.63	1
tc|Rep: Calnexin-like protein - Solanum lycopersicum (Tomato) (Lycopersicon escul	697.07	1
gb|KL4B.105D03F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105D03, m	9508.01	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	17.89	1
gb|KL4B.111P09F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111P09, mR	76.32	1
gb|EST_FLW002xd24f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	394.42	1
tc|Rep: Chromosome chr10 scaffold_81, whole genome shotgun sequence - Vitis vi	2848.14	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	176.58	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	187.24	1
Unknown	26759.2	1
tc|Rep: S-adenosylmethionine synthetase 2 - Solanum lycopersicum (Tomato) (Lyc	228.01	1
Unknown	120.5	1
gb|AGN_RNC127xj12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	38.66	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	3599.62	1

Unknown	90.44	1
gb|KG9B.104C04F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104C04, m	980.48	1
tc|Rep: 3-hydroxy-3-methylglutaryl coenzyme A synthase - Solanum lycopersicum (	1774.46	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	1179.26	1
Unknown	84.74	1
gb|AGN_RNC128xg02f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	72.24	1
tc|Rep: Chromosome chr16 scaffold_189, whole genome shotgun sequence - Vitis	48.19	1
gb|Nicotiana tabacum phosphoinositide-specific phospholipase C mRNA, complete	19.11	1
Unknown	750.89	1
gb|KL4B.102I08F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102I08, mR	64.25	1
gb|TT-03_H09 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	130.56	1
gb|KN6B.109A10F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.109A10, m	385.37	1
Unknown	157.07	1
gb|N.tabacum mRNA for pyruvate kinase [Z29492]	157.98	1
gb|KP1B.107M10F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107M10, r	39.39	1
gb|KP1B.105I23F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105I23, mR	319.3	1
tc|Rep: Vacuolar ATP synthase 16 kDa proteolipid subunit - Nicotiana tabacum (Cor	11127.05	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	181.61	1
tc|Rep: Pollen specific actin-depolymerizing factor 2 - Nicotiana tabacum (Common	38105.3	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	380.76	1
tc|Rep: Lon protease homolog - Vitis vinifera (Grape), partial (48%) [TC45253]	47.05	1
tc|Rep: ADP-ribosylation factor - Daucus carota (Carrot), complete [TC50475]	247.68	1
tc|Rep: Cytochrome b-c1 complex subunit 7 - Solanum tuberosum (Potato), comple	5208.68	1
gb|N.tabacum mRNA for inorganic pyrophosphatase (TVP9 clone) [X83730]	209.15	1
Unknown	273.61	1
gb|KL5B.104D12F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.104D12, m	51.94	1
tc|Rep: Chromosome chr8 scaffold_115, whole genome shotgun sequence - Vitis vi	191.81	1
Unknown	192.49	1
Unknown	399.98	1
Unknown	1145.38	1
gb|FS383836 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	1054.45	1
gb|TT-37_H10 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	121.29	1
Unknown	77.24	1
Unknown	542.72	1

tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	193.58	1
Unknown	126.61	1
tc|Rep: CCR4 associated factor 1-related protein - Capsicum annuum (Bell pepper),	102.84	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	6083.03	1
gb|AGN_ELP022xf13f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	24.18	1
gb|KP1B.101G15F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101G15, m	36.22	1
gb|AGN_ELP019xd01f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	883.7	1
gb|KP1B.101E24F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101E24, mR	62.84	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	26.05	1
Unknown	20.06	1
Unknown	264	1
Unknown	7869.44	1
Unknown	43.21	1
gb|Nicotiana tabacum hexokinase 1a (Hxk1a) mRNA, complete cds [AY553214]	3068.37	1
tc|GB|AB053091.1|BAB40702.1 kinesin-like polypeptides 3 [Nicotiana tabacum] [N	44.03	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	61.97	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	90.33	1
gb|KF8B.201P07F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201P07, mRN	255.51	1
gb|KN6B.102M01F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102M01,	36295.25	1
gb|KG9B.002K10F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002K10, m	26.47	1
Unknown	29	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	17.43	1
gb|FS379071 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	71.02	1
gb|TL13.106A20F.060315T7 TL13 Nicotiana tabacum cDNA clone TL13.106A20, mR	34.84	1
tc|Rep: Methionine synthase - Nicotiana suaveolens, partial (36%) [TC40848]	18920.85	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	67.57	1
tc|Rep: 60S ribosomal protein L24 - Cicer arietinum (Chickpea) (Garbanzo), complet	56.7	1
gb|AGN_ELP012xi11f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	38.81	1
gb|KR3B.113A02F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.113A02, m	2898.29	1
gb|BP532939 MAT005 Nicotiana tabacum cDNA clone BY28373, mRNA sequence [B	73.09	1
gb|TT-25_O04 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	254.36	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	2443.18	1
Unknown	31.67	1
gb|AGN_RNC020xe06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	53.44	1

gb|KL4B.108H20F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108H20, mF	107.04	1
tc|Rep: Cytosolic ascorbate peroxidase - Nicotiana tabacum (Common tobacco), pa	1102.44	1
gb|AGN_RPC009xg19f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	29.69	1
gb|TT-11_J07 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA sec	24.82	1
Unknown	246.76	1
gb|KF8B.100H08F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100H08, mRI	32.57	1
gb|TT-22_K08 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	3722.18	1
tc|Rep: Chromosome chr10 scaffold_81, whole genome shotgun sequence - Vitis vi	573.64	1
gb|TT-04_G22 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	532.96	1
Unknown	265.75	1
gb|KG9B.103D21F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103D21, n	53.76	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC1-32-280, cultivar Bright Yellow 2	3317.27	1
gb|TT-06_L13 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	196.64	1
Unknown	49.22	1
tc|Rep: Chromosome chr2 scaffold_187, whole genome shotgun sequence - Vitis vi	143.63	1
gb|N.tabacum mRNA for TAF-3 [Z48603]	28.83	1
gb|KG9B.102L23F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102L23, m	523.65	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	503.47	1
tc|Rep: 14-3-3 protein - Nicotiana tabacum (Common tobacco), complete [TC40281	362.04	1
tc|Rep: Reversibly glycosylated protein - Phaseolus vulgaris (Kidney bean) (French b	5475.97	1
Unknown	32.38	1
Unknown	67.76	1
Unknown	548.83	1
Unknown	35.89	1
gb|TT-24_K09 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	2058.26	1
Unknown	158.96	1
gb|KR2B.002L05F.051019T7 KR2B Nicotiana tabacum cDNA clone KR2B.002L05, mF	421.81	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	90.88	1
tc|Rep: Calcium homeostasis regulator CHoR1 - Solanum tuberosum (Potato), parti	164.5	1
Unknown	22.76	1
Unknown	221.97	1
Unknown	310.95	1
gb|KP1B.103D12F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103D12, m	239.92	1
gb|AM803681 DL, diurnal library Nicotiana tabacum cDNA clone nt005177068, mRI	75429.7	1

tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	515.8	1
Unknown	24.01	1
tc|Rep: Ribosomal protein L11-like - Nicotiana tabacum (Common tobacco), comple	189.83	1
tc|Rep: 40S ribosomal protein S4 - Solanum tuberosum (Potato), complete [TC4076	32.07	1
gb|KL4B.110M08F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110M08, m	798.82	1
Unknown	7073	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	192.66	1
gb|KT7C.110B17F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110B17, mRN	166.65	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	1590.65	1
tc|Rep: Dihydrolipoyllysine-residue acetyltransferase component 3 of pyruvate deh	2741.87	1
tc|Rep: 14-3-3 protein - Nicotiana tabacum (Common tobacco), partial (77%) [TC43	525.93	1
tc|Rep: double-stranded DNA-binding family protein - Arabidopsis thaliana, partial	479.5	1
tc|Rep: Mal d 1-associated protein - Malus domestica (Apple) (Malus sylvestris), par	37.7	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	31.9	1
Unknown	27.71	1
gb|AGN_RNC016xa18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	26.18	1
Unknown	272.83	1
gb|KG9B.002A13F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002A13, m	81.86	1
gb|KN6B.109M18F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.109M18,	115.8	1
Unknown	19.11	1
gb|KT7C.102J04F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102J04, mRN	40.66	1
gb|AGN_PNL228cf1_e8.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	30.13	1
Unknown	81.79	1
gb|KR3B.103F10F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.103F10, mR	3772.02	1
tc|Rep: Cytochrome c oxidase polypeptide Vc-2 - Arabidopsis thaliana (Mouse-ear c	1017.91	1
gb|KG9B.005H19F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005H19, n	910.87	1
tc|Rep: Serine hydroxymethyltransferase - Populus tremuloides (Quaking aspen), pa	4358.03	1
Unknown	26.72	1
tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin	135.09	1
Unknown	188.85	1
gb|AGN_RNC005xe02f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	46.24	1
Unknown	22.43	1
Unknown	5868.24	1
Unknown	38.56	1

Unknown	25.11	1
Unknown	53640.45	1
tc|Rep: Dihydrolipoamide dehydrogenase precursor - Solanum tuberosum (Potato)	1574.1	1
gb|AGN_RNC105xi18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	36.52	1
tc|Rep: Sugar transport protein 10 - Arabidopsis thaliana (Mouse-ear cress), partial	54020.75	1
tc|Rep: At5g22480 - Arabidopsis thaliana (Mouse-ear cress), partial (35%) [TC5011	41.3	1
gb|KF8C.106A01F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106A01, mR	272.3	1
Unknown	508.48	1
Unknown	90.8	1
Unknown	19321.95	1
gb|CHO_SL014xg24f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	28.4	1
gb|KP1B.107J12F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107J12, mR	104.02	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	347.32	1
gb|AGN_RPC014xd06f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	25.89	1
gb|KP1B.102P18F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102P18, m	355.66	1
Unknown	22.22	1
Unknown	26.5	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	53.45	1
gb|KG9B.106K08F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106K08, m	91.33	1
tc|Rep: Chromosome undetermined scaffold_127, whole genome shotgun sequenc	44.8	1
gb|KF8B.200B01F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200B01, mR	61.89	1
Unknown	53.62	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	10512.85	1
Unknown	237.08	1
Unknown	178.37	1
gb|KL4B.101H15F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101H15, m	49.57	1
tc|Rep: CONSTANS interacting protein 6 - Solanum lycopersicum (Tomato) (Lycope	20.82	1
tc|Rep: Serine/threonine-protein phosphatase PP2A catalytic subunit - Nicotiana ta	438.34	1
Unknown	8227.04	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	78.76	1
gb|KP1B.107L17F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107L17, m	22.78	1
gb|BP530524 MAT005 Nicotiana tabacum cDNA clone BY22160, mRNA sequence [	32.02	1
Unknown	999.98	1
gb|CHO_SL011xl02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	930.15	1

Unknown	20.93	1
tc|Rep: Chromosome chr14 scaffold_211, whole genome shotgun sequence - Vitis	140.18	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	20.04	1
gb|KL4B.102A16F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102A16, m	10615.15	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	48.17	1
tc|Rep: PilT protein domain protein - Mycobacterium sp. (strain KMS), partial (9%)	41.2	1
Unknown	250.22	1
Unknown	20.8	1
Unknown	56.15	1
gb|KN6B.102E13F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102E13, m	132.48	1
Unknown	87.18	1
Unknown	230.57	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	197.1	1
gb|AGN_RPC022xe13f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	10620.75	1
gb|TT-22_M06 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	437.2	1
tc|Rep: Histone H4 [Contains: Osteogenic growth peptide (OGP)]. - Rattus norvegic	484.67	1
gb|KL4B.103C02F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103C02, mR	917.96	1
Unknown	516.67	1
gb|AGN_RNC002xo09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	31.5	1
gb|KL5B.115M12F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.115M12, m	29.35	1
gb|Nicotiana tabacum cig2 mRNA, complete cds [AB031321]	105.04	1
gb|KN6B.113E10F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.113E10, m	67.25	1
gb|KL4B.105M02F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105M02, m	84.89	1
Unknown	2663.06	1
Unknown	22.4	1
Unknown	385.5	1
gb|AGN_RNC015xd21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1067.86	1
Unknown	60.98	1
tc|Rep: Calmodulin cam-210 - Daucus carota (Carrot), complete [TC44872]	130.25	1
tc|Rep: Voltage-dependent anion channel - Nicotiana tabacum (Common tobacco),	173.13	1
gb|KR3B.110I10F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110I10, mR	50.18	1
gb|KN6B.103B01F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103B01, m	133.89	1
Unknown	40.86	1
gb|KL4B.102M23F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102M23, m	619.63	1

Unknown	19.16	1
gb|Nicotiana tabacum SAICAR synthetase (purC) mRNA, complete cds [AY429423]	18.24	1
tc|Rep: Pseudouridine synthase - Shewanella loihica (strain BAA-1088 / PV-4), parti	482.22	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	515.03	1
tc|Rep: 40S ribosomal protein S4 - Solanum tuberosum (Potato), complete [TC4041	411.67	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	23.78	1
Unknown	79.74	1
gb|Nicotiana tabacum NtbZIP60 mRNA for basic region leucine zipper protein, com	2528.48	1
Unknown	19.26	1
Unknown	152.81	1
gb|KP1B.105O22F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105O22, m	96.92	1
gb|TT-17_L22 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	27.83	1
gb|CHO_SL011xo14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	34.61	1
tc|Rep: Chromosome chr11 scaffold_14, whole genome shotgun sequence - Vitis vi	465.66	1
tc|Rep: Ribosomal protein S8 - Vitis vinifera (Grape), partial (94%) [TC64936]	119.33	1
gb|KN6B.101P10F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101P10, m	22.52	1
gb|KT7C.108L15F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108L15, mRN	122	1
gb|AGN_RNC114xj01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	254.04	1
gb|CHO_SL028xe19f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	32.25	1
gb|FS407121 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	943.28	1
gb|AGN_ELP012xc18f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	189.08	1
gb|AGN_ELP023xm08f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequenc	48.49	1
tc|Rep: Glutaredoxin - Solanum lycopersicum (Tomato) (Lycopersicon esculentum),	45.22	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	151.18	1
gb|KN6B.102L11F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102L11, m	1083.47	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	387.18	1
gb|CHO_SL026xg23f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1131.2	1
gb|TT-41_L16 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	39.89	1
gb|AGN_RNC127xl10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	20.84	1
gb|KG9B.101D11F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101D11, m	574.51	1
gb|TT-06_K13 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	133.78	1
gb|Nicotiana tabacum arm repeat-containing protein mRNA, complete cds [AY2192	99.17	1
tc|Rep: Metacaspase type II - Nicotiana benthamiana, partial (66%) [TC43115]	19.91	1
Unknown	33.75	1

gb|Nicotiana tabacum mRNA for 14-3-3 c-2 protein, complete cds [AB119470]	2112.84	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	1393.35	1
gb|AGN_RNC022xm16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	90.92	1
gb|TT-18_I13 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sequ	25.01	1
tc|Rep: Fiber protein Fb15 - Gossypium barbadense (Sea-island cotton) (Egyptian c	2711.54	1
gb|TOBESTR039E03 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA sequ	35.39	1
gb|AGN_RNC022xc19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	21.17	1
Unknown	30.81	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	390.41	1
Unknown	147.43	1
Unknown	41.64	1
gb|FS390471 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	476.01	1
tc|Rep: RNA Binding Protein 45 - Nicotiana plumbaginifolia (Leadwort-leaved tobac	228.15	1
tc|Rep: Ripening regulated protein DDTFR10-like - Solanum tuberosum (Potato), co	2580.07	1
gb|AM841116 seedling library, SL Nicotiana tabacum cDNA clone nt002150071, mR	694.76	1
Unknown	18.7	1
tc|Rep: Transcription factor IIA, beta-barrel - Medicago truncatula (Barrel medic), p	3274.07	1
gb|KL4B.104P21F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104P21, mR	470.05	1
tc|Rep: Chromosome undetermined scaffold_203, whole genome shotgun sequenc	15965.9	1
Unknown	63.35	1
Unknown	30.26	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	340.07	1
tc|Rep: Acetolactate synthase 1, chloroplast precursor - Nicotiana tabacum (Comm	120.78	1
gb|KL4B.103L20F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103L20, mR	444.96	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	152.01	1
Unknown	129.31	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	946.83	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	28.3	1
gb|TT-40_L10 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	3684.89	1
Unknown	20.93	1
gb|KG9B.102P02F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102P02, m	478.76	1
gb|CHO_SL027xl15f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	23.03	1
tc|Rep: Fas-associated factor 1-like protein - Capsicum annuum (Bell pepper), partia	218.76	1
gb|TOBESTR046G03 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	60.27	1

gb|Nicotiana tabacum Avr9 [AY220484]	209.09	1
tc|Rep: ATP-dependent Clp protease proteolytic subunit - Vitis vinifera (Grape), par	25.9	1
tc|Rep: Cyprosin - Cynara cardunculus (Cardoon), partial (5%) [TC74489]	21.83	1
gb|KL5B.115B21F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.115B21, mR	50.72	1
gb|AGN_RNC014xf09r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	18.57	1
Unknown	128.67	1
Unknown	127.37	1
gb|KT7C.110E06F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110E06, mR	28.46	1
gb|EST_FLW001xa21f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	20.86	1
tc|Rep: CCCH-type Zn-finger protein - Ostreococcus tauri, partial (8%) [TC76477]	18.66	1
Unknown	98.98	1
gb|KG9B.003P21F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003P21, m	24.05	1
gb|Nicotiana tabacum Rac-like GTPase 1 mRNA, complete cds [AY029330]	1041.41	1
Unknown	401.63	1
gb|KP1B.104E09F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104E09, m	93.99	1
gb|Nicotiana tabacum 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase, co	694.49	1
gb|KG9B.102G14F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102G14,	533.46	1
tc|Rep: Histone H2A - Vitis vinifera (Grape), partial (97%) [TC42842]	1836.58	1
Unknown	35561.15	1
gb|AM833705 seedling library, SL Nicotiana tabacum cDNA clone nt002132050, m	183.5	1
gb|FS406206 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	85.31	1
Unknown	24.12	1
tc|Rep: Small basic intrinsic protein 1 - Vitis vinifera (Grape), partial (81%) [TC4630	47.32	1
tc|Rep: Splicing factor-like protein - Vitis riparia (Frost grape) (Vitis vulpina), partial	187.74	1
gb|Nicotiana tabacum S-adenosyl-methionine-sterol-C-methyltransferase mRNA, c	18071.5	1
tc|Rep: Chromosome chr10 scaffold_50, whole genome shotgun sequence - Vitis vi	178.83	1
gb|KF8B.100O16F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100O16, mR	180.47	1
tc|Rep: Chromosome chr8 scaffold_99, whole genome shotgun sequence - Vitis vin	268.26	1
tc|Rep: 60s acidic ribosomal protein-like protein - Solanum tuberosum (Potato), co	1173.73	1
tc|Rep: SJCHGC06320 protein - Schistosoma japonicum (Blood fluke), partial (7%) [	87.13	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (96%) [TC5	90.01	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	38.26	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	1178.94	1
Unknown	91.45	1

tc|Rep: Alpha-glucan water dikinase, chloroplast precursor - Solanum tuberosum (P	26.05	1
gb|AGN_RNC005xf07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	45.04	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	849.13	1
gb|KR3B.114O13F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.114O13, m	60.75	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	54.52	1
Unknown	270.6	1
gb|AGN_RPC023xf04f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	183.64	1
Unknown	30.33	1
gb|KN6B.103N23F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103N23, r	141.71	1
Unknown	20.69	1
gb|AM807618 seedling library, SL Nicotiana tabacum cDNA clone nt002189039, mR	277	1
gb|N.tabacum mRNA for aldehyde dehydrogenase [Y09876]	1970.67	1
tc|Rep: GrpE protein - Arabidopsis thaliana (Mouse-ear cress), partial (52%) [TC450	56.35	1
gb|KG9B.005L07F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005L07, m	625.6	1
Unknown	977.07	1
tc|Rep: Ribosomal protein L41 - Candida maltosa (Yeast), complete [TC54676]	56.95	1
gb|KP1B.101C01F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101C01, m	152.74	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	7623.95	1
gb|AGN_RNC127xk14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	31.2	1
Unknown	110.85	1
gb|KG9B.005N18F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005N18, r	673.31	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	94.59	1
gb|AGN_RNC123xe03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	50.08	1
tc|Rep: Chromosome chr3 scaffold_117, whole genome shotgun sequence - Vitis vi	19.82	1
gb|KN6B.103G24F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103G24, r	202.87	1
gb|AGN_RNC023xh11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	120.72	1
tc|Rep: Protein tyrosine phosphatase - Fagus sylvatica (Beechnut), partial (43%) [TC	202.43	1
gb|Nicotiana tabacum elongation factor 1-alpha mRNA, complete cds [AF120093]	2311.89	1
tc|Rep: Beta-galactosidase - Vitis vinifera (Grape), partial (26%) [TC46252]	36.06	1
Unknown	51.51	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	27.19	1
tc|Rep: Chromosome chr3 scaffold_199, whole genome shotgun sequence - Vitis vi	51.48	1
tc|Rep: Chromosome chr17 scaffold_101, whole genome shotgun sequence - Vitis v	24.85	1
gb|TT-16_F21 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	50.11	1

gb|AGN_RNC026xj22f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	167.21	1
Unknown	19.93	1
gb|KL4B.108F02F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108F02, mR	856.64	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	445.85	1
tc|Rep: RAB5B - Lotus japonicus, partial (90%) [TC42073]	1178.22	1
gb|CHO_SL012xf08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	10961.7	1
tc|Rep: Small GTP-binding protein - Nicotiana plumbaginifolia (Leadwort-leaved to	4327.31	1
gb|KR3B.001M09F.050815T7 KR3B Nicotiana tabacum cDNA clone KR3B.001M09,	142.09	1
gb|KL4B.101M14F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101M14, m	34.93	1
Unknown	2922.69	1
tc|GB|X03481.1|CAA27200.1 putative ribosomal protein S12 [Nicotiana tabacum] |	1673.24	1
gb|KT7C.112C08F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112C08, mR	642.18	1
Unknown	59.33	1
gb|BL12.103G21F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.103G21, m	2839.83	1
gb|KF8C.103G19F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103G19, mR	1600.35	1
gb|BP525578 MAT001 Nicotiana tabacum cDNA clone BY10260, mRNA sequence [	46.17	1
gb|AM843516 seedling library, SL Nicotiana tabacum cDNA clone nt002111072, m	321.51	1
gb|AGN_PNL206cf1_f5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	29.54	1
Unknown	30.17	1
tc|Rep: Catalase isozyme 3 - Nicotiana plumbaginifolia (Leadwort-leaved tobacco),	3707.46	1
Unknown	44.48	1
gb|KF8C.102I02F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102I02, mRN	59.08	1
gb|KT7C.108N19F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108N19, mR	233.47	1
gb|KP1B.113H24F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.113H24, m	125.24	1
Unknown	67.91	1
tc|Rep: Chromosome chr14 scaffold_26, whole genome shotgun sequence - Vitis vi	153.98	1
gb|KG9B.102F13F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102F13, m	60.59	1
Unknown	49.93	1
tc|Rep: UDP-glucuronic acid decarboxylase 1 - Populus tomentosa (Chinese white p	2625.08	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	330.19	1
Unknown	131.17	1
gb|KG9B.103N07F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103N07,	237.32	1
Unknown	33.16	1
gb|KF8C.101E15F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101E15, mR	462.96	1

gb|AM822487 COL, cold overnight library Nicotiana tabacum cDNA clone nt006178	34.11	1
Unknown	31.39	1
tc|Rep: 40S ribosomal protein S19-like - Solanum tuberosum (Potato), complete [T	79.69	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	40.39	1
gb|KL5B.103B17F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.103B17, mR	500.41	1
gb|Nicotiana tabacum mRNA, transcriptionally up-regulated region associated with	3921.61	1
gb|KP1B.101D13F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101D13, m	607.1	1
gb|KP1B.105G24F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105G24, m	1253.08	1
tc|Rep: Chromosome chr10 scaffold_433, whole genome shotgun sequence - Vitis	31053.85	1
gb|KF8B.100D10F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100D10, mR	3451.52	1
tc|Rep: Transcriptional coactivator multiprotein bridging factor - Solanum lycopersi	63.93	1
gb|KF8C.109H20F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109H20, mR	5276.74	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	20.76	1
gb|Nicotiana tabacum mRNA for cytosolic ascorbate peroxidase, complete cds [D8	1081.93	1
gb|Nicotiana tabacum cultivar Burley 21 arginine decarboxylase 1 (ADC1) mRNA, c	8930.92	1
tc|Rep: Chromosome chr12 scaffold_38, whole genome shotgun sequence - Vitis vi	219.44	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	107.7	1
gb|KG9B.102K02F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102K02,	519.07	1
gb|KG9B.105M08F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105M08,	864.73	1
Unknown	33.26	1
gb|TT-48_L05 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	44.79	1
tc|Rep: Clp-like energy-dependent protease precursor - Solanum lycopersicum (To	38.36	1
tc|Rep: Chromosome undetermined scaffold_533, whole genome shotgun sequenc	1155.94	1
gb|KG9B.106G12F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106G12,	145.38	1
gb|AGN_RNC030xa01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	24.19	1
gb|TT-47_P04 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	253.15	1
Unknown	30.75	1
gb|KF8B.201I20F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201I20, mRN	29.1	1
gb|AGN_RPC019xl08f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	64.39	1
gb|AGN_ELP008xk06f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	20.7	1
gb|BP534288 MAT005 Nicotiana tabacum cDNA clone BY32245, mRNA sequence [	40.14	1
gb|KL4B.107L11F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107L11, mR	28.97	1
Unknown	107.87	1
Unknown	19.4	1

tc|Rep: DNA polymerase - Brassica napus (Rape), partial (18%) [TC65518]	26.63	1
gb|AGN_RNC016xi07r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	23.46	1
tc|Rep: Beta-1,3-glucanase, acidic - Coffea arabica (Coffee), partial (73%) [TC46708	24649.95	1
gb|30F11 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', n	393.09	1
gb|EST_CSP005xi13f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	146.49	1
Unknown	28.77	1
tc|Rep: Ethylene-responsive small GTP-binding protein - Solanum lycopersicum (To	4108.67	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	17483.15	1
gb|CHO_SL025xn08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1021.5	1
gb|TT-21_K22 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	28.56	1
gb|Nicotiana tabacum blp4 mRNA for luminal binding protein (BiP) [X60057]	4775.39	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	31.57	1
gb|N.tabacum NeIF-4A15 mRNA [X79138]	231.76	1
gb|AGN_RNC025xm15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	53.33	1
tc|Rep: Proteasome subunit alpha type - Solanum tuberosum (Potato), complete [T	30.64	1
gb|AGN_PNL225df1_f1.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	161.79	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	116.53	1
Unknown	272.49	1
Unknown	377.5	1
tc|Rep: 2,3-bisphosphoglycerate-independent phosphoglycerate mutase - Nicotian	10713.95	1
Unknown	21	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	205.68	1
gb|CHO_SL021xp22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	76.69	1
Unknown	34.5	1
gb|AGN_RPC022xl07f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	18.72	1
gb|AGN_PNL210cr1_c4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	21.57	1
tc|Rep: Chromosome undetermined scaffold_91, whole genome shotgun sequence	92.7	1
tc|Rep: Chromosome undetermined scaffold_203, whole genome shotgun sequenc	108.85	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	46.78	1
tc|Rep: Chromosome chr4 scaffold_83, whole genome shotgun sequence - Vitis vin	112.34	1
gb|TT-04_J02 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	24.37	1
gb|TT-34_I06 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	148.04	1
Unknown	86.27	1
tc|GB|X06310.1|CAA29629.1 unnamed protein product [Nicotiana tabacum] [NP9	541.47	1

Unknown	49.7	1
Unknown	3170.97	1
gb|KT7C.102N07F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102N07, mR	135.41	1
Unknown	50.77	1
Unknown	22.96	1
tc|Rep: Pyruvate kinase - Oryza sativa subsp. japonica (Rice), partial (71%) [TC4448	270.2	1
gb|KN6B.108A05F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.108A05, n	71.34	1
Unknown	185.12	1
tc|Rep: ER lumen protein retaining receptor - Petunia hybrida (Petunia), partial (27	1278.29	1
tc|Rep: Nitrate reductase [NADH] 2 - Nicotiana tabacum (Common tobacco), partia	293.39	1
gb|AGN_RNC020xg03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	29.98	1
Unknown	201.29	1
gb|KP1B.001B15F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001B15, m	336.32	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	26.21	1
gb|KP1B.101P01F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101P01, m	4327.31	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	200.72	1
gb|TT-09_B08 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	686.09	1
tc|Rep: Ribosomal protein L37 - Glycine max (Soybean), partial (97%) [TC58707]	57.96	1
Unknown	468.2	1
gb|TT-06_C03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	3130.07	1
gb|TT-39_E01 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	410.44	1
Unknown	548.57	1
tc|Rep: Glutathione synthetase, chloroplast precursor - Solanum lycopersicum (To	23.48	1
Unknown	35.62	1
gb|KF8B.201M04F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201M04, m	1715.36	1
gb|KT7C.108H18F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108H18, mR	152.85	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	50.17	1
Unknown	78.19	1
tc|Rep: Chromosome chr11 scaffold_56, whole genome shotgun sequence - Vitis vi	366.66	1
gb|N.tabacum mRNA for protein phosphatase 2A, 65kD regulatory subunit [X97913	488.74	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	531.85	1
tc|Rep: Actin-101 - Solanum tuberosum (Potato), partial (19%) [TC62782]	10862.75	1
gb|Nicotiana tabacum mRNA for ethylene responsive element binding factor, comp	4683.18	1
tc|Rep: Alpha chain of nascent polypeptide associated complex - Nicotiana bentha	373.91	1

tc|Rep: Pyruvate kinase - Arabidopsis thaliana (Mouse-ear cress), partial (84%) [TC5	49.6	1
tc|Rep: Dehydrin-like protein - Solanum sogarandinum, partial (86%) [TC57177]	5019.95	1
tc|Rep: Chromosome chr8 scaffold_68, whole genome shotgun sequence - Vitis vin	22.69	1
tc|Rep: DnaJ homolog - Salix gilgiana (Willow), partial (41%) [TC58289]	277.95	1
gb|KF8B.100B11F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100B11, mRN	26.49	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	199.19	1
gb|KF8C.103J18F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103J18, mRN	1326.74	1
Unknown	1578.17	1
gb|Nicotiana tabacum NtTOM1 mRNA for tobamovirus multiplication 1, complete	93.65	1
gb|KP1B.108E01F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108E01, m	495.74	1
gb|CHO_SL006xm14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	649.04	1
tc|Rep: Elongation factor 1-alpha - Nicotiana paniculata, partial (53%) [TC48055]	92.04	1
gb|KG9B.104P17F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104P17, m	101	1
gb|KL4B.104I05F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104I05, mRN	183.44	1
Unknown	22.86	1
tc|Rep: Integrase core domain containing protein - Solanum demissum (Wild potat	61.19	1
tc|Rep: GTP-binding nuclear protein Ran-A1 - Nicotiana tabacum (Common tobacc	2862.21	1
gb|AM830968 COL, cold overnight library Nicotiana tabacum cDNA clone nt006147	112.76	1
Unknown	3303.57	1
tc|Rep: Chromosome undetermined scaffold_223, whole genome shotgun sequenc	1326.98	1
gb|AGN_RNC017xd12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	942.25	1
Unknown	53.52	1
tc|Rep: Gamma hydroxybutyrate dehydrogenase - Arabidopsis thaliana (Mouse-ear	789.8	1
tc|Rep: Glycosyltransferase - Pseudomonas stutzeri (strain A1501), partial (5%) [TC	18.69	1
gb|Nicotiana tabacum cDNA-AFLP fragment N_BC2M23-2 sequence [DQ460091]	37.78	1
gb|KL4B.103D07F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103D07, m	25.66	1
gb|AM783785 DL, diurnal library Nicotiana tabacum cDNA clone nt005196078, mR	49.96	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	888.14	1
Unknown	764.55	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	1591.41	1
gb|AGN_RNC021xp16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	107.52	1
gb|TOBESTR009E12 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	361.48	1
gb|AGN_RNC026xn20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	362.51	1
gb|TT-40_L02 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	27.42	1

gb|KR2B.111F22F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.111F22, m	1400.23	1
gb|AM799744 seedling library, SL Nicotiana tabacum cDNA clone nt002285028, m	91.4	1
tc|Rep: Chromosome chr8 scaffold_68, whole genome shotgun sequence - Vitis vin	580.33	1
Unknown	569.8	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	41.59	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	37.16	1
gb|FS412189 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	42.52	1
Unknown	164.43	1
gb|KL4B.111E15F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111E15, mR	41.27	1
tc|Rep: Proteasome subunit alpha type - Nicotiana tabacum (Common tobacco), co	137.22	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	215.99	1
tc|Rep: Superoxide dismutase [Mn], mitochondrial precursor - Capsicum annuum (	114.68	1
gb|KP1B.102C18F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102C18, m	334.4	1
tc|Rep: NADH ubiquinone oxidoreductase PSST subunit - Lupinus luteus (European	16619.1	1
gb|KT7C.113K05F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.113K05, mR	59.83	1
gb|KG9B.004J08F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004J08, m	27.56	1
gb|KP1B.104L24F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104L24, m	80.82	1
Unknown	185.71	1
gb|AGN_RNC016xd11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	29.55	1
tc|Rep: RNA Binding Protein 45 - Nicotiana plumbaginifolia (Leadwort-leaved tobac	479.57	1
tc|Rep: AT5g64840/MXK3_6 - Arabidopsis thaliana (Mouse-ear cress), partial (73%)	54.74	1
tc|Rep: Chromosome chr8 scaffold_99, whole genome shotgun sequence - Vitis vin	1383.71	1
Unknown	168.18	1
gb|AGN_RNC018xl18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	800.26	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	467.63	1
Unknown	38.27	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	974.67	1
gb|AM835908 DL, diurnal library Nicotiana tabacum cDNA clone nt005254053, mR	776.56	1
Unknown	79.94	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	137.18	1
tc|Rep: Methionine aminopeptidase - Vitis vinifera (Grape), partial (55%) [TC55832	23.15	1
Unknown	47.86	1
gb|KG9B.107A16F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107A16,	66.73	1
tc|Rep: Os07g0192300 protein - Oryza sativa subsp. japonica (Rice), partial (68%) [	183.42	1

gb|KR2B.110B08F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110B08, m	109.63	1
gb|AGN_RNC014xg12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	263.18	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT22-430, cultivar Bright Yellow 2 [A	654.43	1
tc|Rep: Aminomethyltransferase, mitochondrial precursor - Solanum tuberosum (P	140.35	1
Unknown	31.54	1
gb|TT-22_D24 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	244.59	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	42.69	1
gb|AGN_RNC014xg05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	22.35	1
gb|Nicotiana tabacum cystathionine gamma-synthase precursor (metB) mRNA, con	1285.3	1
tc|Rep: Alpha-1,6-xylosyltransferase - Gossypium raimondii (New World cotton), pa	10291.65	1
Unknown	95.51	1
gb|Nicotiana tabacum mRNA for 21D7, complete cds [AB001422]	35.77	1
gb|AGN_RNC003xc14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	53.2	1
tc|Rep: Alpha-soluble NSF attachment protein - Solanum tuberosum (Potato), parti	788.69	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	256.41	1
gb|KP1B.109J17F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109J17, mR	79.58	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	130.63	1
gb|Nicotiana tabacum mRNA for putative cytosolic cysteine synthase 7 (oas7 gene)	10374.1	1
Unknown	335.52	1
tc|Rep: Os05g0119300 protein - Oryza sativa subsp. japonica (Rice), partial (64%) [T	2188.3	1
gb|KF8B.100K21F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100K21, mRN	3402.71	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	89.25	1
gb|AGN_RNC128xg24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	98.08	1
tc|Rep: Auxin conjugate hydrolase - Medicago truncatula (Barrel medic), partial (56	56.63	1
gb|KG9B.003N01F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003N01, m	259.76	1
tc|Rep: Adenylate kinase family-like protein - Solanum tuberosum (Potato), partial	1574.29	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	515.71	1
Unknown	105.32	1
gb|EST_FLW002xn13f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	536.87	1
gb|KG9B.104N08F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104N08, m	164.25	1
gb|KF8B.202O24F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202O24, mR	359.2	1
Unknown	138.16	1
tc|Rep: Expressed protein - Arabidopsis thaliana (Mouse-ear cress), partial (83%) [T	33.41	1
Unknown	21.67	1

Unknown	27.59	1
Unknown	642	1
gb|KL4B.112G06F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112G06, m	3081.18	1
gb|KG9B.103J21F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103J21, m	185.92	1
gb|KG9B.002J23F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002J23, m	5446.56	1
gb|KL4B.110B23F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110B23, mR	1282.86	1
gb|AGN_RNC007xa17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	66.02	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	64.63	1
gb|KG9B.102F20F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102F20, m	20.68	1
gb|Nicotiana tabacum dehydroascorbate reductase (DHAR) mRNA, complete cds [	372.9	1
Unknown	524.18	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	20902.75	1
gb|Nicotiana tabacum mRNA for nucleosome assembly protein 1 - like protein 4 [A	219.81	1
tc|Rep: Developmentally regulated GTP binding protein 1 - Pisum sativum (Garden	93.47	1
tc|Rep: UMP/CMP kinase like protein - Arabidopsis thaliana (Mouse-ear cress), part	23.13	1
gb|CHO_SL026xi01f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	30.43	1
tc|Rep: Callus-expressing factor - Nicotiana tabacum (Common tobacco), partial (7	52.76	1
Unknown	60.12	1
Unknown	242.87	1
gb|Nicotiana tabacum mRNA for N-ethylmaleimide sensitive fusion protein, compl	510.54	1
Unknown	28.53	1
gb|AGN_ELP006xc12f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	21.55	1
Unknown	517.98	1
Unknown	30.5	1
gb|AGN_RPC020xb05f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	87.68	1
Unknown	27.61	1
gb|KN6B.110B11F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.110B11, m	61.75	1
tc|Rep: Chromosome chr17 scaffold_101, whole genome shotgun sequence - Vitis	20.84	1
tc|Rep: Chromosome chr9 scaffold_90, whole genome shotgun sequence - Vitis vin	29.26	1
gb|KR3B.101J01F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101J01, mR	157.57	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	160.86	1
Unknown	1592.17	1
gb|Nicotiana tabacum calreticulin mRNA, complete cds [EU984501]	325.48	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	522.47	1

tc|Rep: Cytosolic aconitase - Nicotiana tabacum (Common tobacco), partial (17%) [	529.36	1
gb|KP1B.102B23F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102B23, m	1054.5	1
tc|Rep: Eukaryotic translation initiation factor 4E - Nicotiana benthamiana, comple	187.4	1
gb|KL4B.104H02F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104H02, m	25.38	1
gb|AGN_PNL230bf1_e7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	53579.45	1
tc|Rep: Beta-soluble nsf attachment protein - Plasmodium yoelii yoelii, partial (7%)	24.24	1
Unknown	937.47	1
Unknown	39.45	1
Unknown	7930.07	1
gb|AM788929 seedling library, SL Nicotiana tabacum cDNA clone nt002233046, m	199.56	1
tc|Rep: Rop subfamily GTPase - Nicotiana tabacum (Common tobacco), partial (98	4826.18	1
Unknown	84.18	1
gb|AGN_RNC126xn17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	20.8	1
Unknown	8729.25	1
Unknown	17.01	1
gb|AGN_RNC029xc14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	25.89	1
Unknown	22.81	1
tc|Rep: TA4 protein - Oryza sativa subsp. japonica (Rice), partial (38%) [TC51802]	28.43	1
tc|Rep: Aerobic azoreductase - Pigmentiphaga kullae, partial (8%) [TC73062]	832.2	1
gb|CHO_SL015xd24f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	351.37	1
Unknown	37.18	1
gb|KF8C.103I13F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103I13, mRN	8545.26	1
tc|Rep: Chromosome chr9 scaffold_90, whole genome shotgun sequence - Vitis vin	78.19	1
gb|Nicotiana tabacum NtFAD3 mRNA for microsomal omega-3 acid desaturase, co	4840.46	1
gb|BL12.104N17F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.104N17, m	202.37	1
Unknown	186.04	1
gb|AGN_PNL203dr1_c8.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	20.53	1
gb|KL4B.107L17F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107L17, mR	517.37	1
tc|Rep: Senescence-associated protein-like - Oryza sativa subsp. japonica (Rice), pa	539.36	1
Unknown	66.79	1
Unknown	108.53	1
gb|AM783542 seedling library, SL Nicotiana tabacum cDNA clone nt002007045, m	141.41	1
Unknown	23.97	1
gb|CHO_SL025xj15f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	940.27	1

gb|Nicotiana tabacum 3-dehydroquinate dehydratase [AY578143]	57.55	1
tc|Rep: Tic20-like protein - Solanum tuberosum (Potato), partial (69%) [TC70352]	113	1
gb|Nicotiana tabacum S-adenosyl-L-methionine synthetase (SAMS) mRNA, complet	7368.1	1
gb|KL4B.101M16F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101M16, m	99.36	1
tc|Rep: Chromosome undetermined scaffold_11, whole genome shotgun sequence	1007.02	1
tc|Rep: Chromosome chr5 scaffold_124, whole genome shotgun sequence - Vitis vi	403.85	1
Unknown	235.82	1
gb|KG9B.005I19F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005I19, mR	167.4	1
gb|CHO_SL009xe06f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	187.61	1
gb|TT-29_F01 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	26.13	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	1353.52	1
gb|KG9B.003O07F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003O07, r	184.96	1
gb|AGN_RNC017xf14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	36.91	1
gb|TT-22_F21 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	153.67	1
Unknown	510.09	1
Unknown	37.66	1
Unknown	24.34	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	138.94	1
Unknown	37.41	1
gb|Nicotiana tabacum NtMPO2 mRNA for N-methylputrescine oxidase, complete c	251.64	1
gb|KR3B.108H08F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.108H08, m	341.51	1
gb|AGN_RNC109xl22r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	28.24	1
tc|Rep: Chromosome chr4 scaffold_205, whole genome shotgun sequence - Vitis vi	16.91	1
gb|AGN_PNL228bf1_d12.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	176.26	1
gb|AGN_ELP018xm14f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	50.54	1
gb|KT7C.110K22F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110K22, mRN	55.51	1
tc|Rep: Chromosome chr1 scaffold_180, whole genome shotgun sequence - Vitis vi	112.2	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	1374.56	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	1138.7	1
gb|N.tabacum mRNA for ribonucleotide reductase R2 protein [X92443]	246.26	1
gb|Nicotiana tabacum ankyrin-repeat protein HBP1 mRNA, complete cds [AF35279	476.5	1
Unknown	124.45	1
gb|KG9B.003N18F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003N18, r	386.23	1
gb|TT-08_E01 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	57.82	1

tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	1059.07	1
gb|KG9B.105B23F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105B23, m	28.76	1
gb|KR2B.101F09F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.101F09, mR	12153.3	1
Unknown	24.36	1
gb|CHO_SL016xd21f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	528.24	1
tc|Rep: Uncharacterized protein At5g47430.2 - Arabidopsis thaliana (Mouse-ear cre	81.98	1
Unknown	52.87	1
Unknown	1360.13	1
tc|Rep: Chromosome chr8 scaffold_99, whole genome shotgun sequence - Vitis vin	2937.28	1
tc|Rep: S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC) [C	21915.05	1
gb|Nicotiana tabacum vacuolar H+-ATPase B subunit mRNA, complete cds [AF2206	427.57	1
tc|Rep: Polygalacturonase inhibitor protein precursor - Solanum lycopersicum (Tom	19.04	1
tc|Rep: MYST-type acetyltransferase - Solanum chacoense (Chaco potato), partial (	115.16	1
gb|TT-40_D14 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	884.54	1
Unknown	21.57	1
gb|KF8C.103B05F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103B05, mRN	2362.9	1
Unknown	37.08	1
gb|KF8B.202F17F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202F17, mRN	51.2	1
gb|AGN_RPC016xj21f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	101.24	1
gb|KG9B.106A17F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106A17, m	901.45	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	176.49	1
gb|KR2B.109J14F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.109J14, mR	501.16	1
gb|KR2B.101B04F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.101B04, m	9689.17	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	1113.7	1
gb|KP1B.103L09F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103L09, mR	1120.87	1
gb|KP1B.102M02F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102M02, r	902.23	1
gb|AGN_ELP025xb18f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	104.13	1
gb|AGN_PNL221af1_b5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	18608.15	1
gb|TT-30_J08 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sequ	248.6	1
gb|KR2B.001N16F.050815T7 KR2B Nicotiana tabacum cDNA clone KR2B.001N16, m	5513.15	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	1522.73	1
Unknown	475.87	1
Unknown	137.46	1
gb|KF8C.106A19F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106A19, mRN	45.19	1

gb|KP1B.102A05F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102A05, m	99.36	1
tc|Rep: T-complex protein 1, alpha subunit - Bruguiera sexangula, partial (11%) [TC	55.1	1
Unknown	58.51	1
gb|KR3B.107H04F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.107H04, m	650.69	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	112.81	1
tc|Rep: Chromosome chr19 scaffold_126, whole genome shotgun sequence - Vitis	2786.73	1
gb|KG9B.102H09F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102H09, n	18.18	1
gb|KT7C.110E22F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110E22, mRN	37.76	1
Unknown	583.9	1
gb|KN6B.102E21F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102E21, m	223.11	1
gb|TOBESTR046E09 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	47.68	1
gb|Nicotiana tabacum microsomal omega-6-desaturase (FAD2) mRNA, complete cc	35668.25	1
gb|AGN_RNC014xp12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	70.79	1
tc|Rep: DEAD-box ATP-dependent RNA helicase 56 - Oryza sativa subsp. japonica (R	205.62	1
tc|Rep: 60s acidic ribosomal protein-like protein - Solanum tuberosum (Potato), par	4797.74	1
gb|Nicotiana tabacum cDNA-AFLP fragment H-N_BC1M33-1 sequence [DQ460062]	38.94	1
gb|KL4B.101O02F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101O02, m	43.96	1
gb|CHO_SL028xm03f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	53.92	1
gb|TT-41_D05 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	178.62	1
gb|KT7C.106J08F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106J08, mRN	27.26	1
tc|Rep: 60s acidic ribosomal protein-like protein - Solanum tuberosum (Potato), cor	2507.36	1
Unknown	464.71	1
gb|KG9B.103H20F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103H20, n	24.66	1
Unknown	34.75	1
gb|CHO_SL008xk07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	185.41	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	86.05	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	73.33	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	367.16	1
gb|TOBESTR086A03 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	71.52	1
tc|Rep: Chromosome chr10 scaffold_138, whole genome shotgun sequence - Vitis	144.56	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT12-4-420, cultivar Bright Yellow 2	51.1	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	70.46	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	185.76	1
gb|KT7C.101B19F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.101B19, mR	31.53	1

tc|Rep: Chromosome undetermined scaffold_87, whole genome shotgun sequence	127.81	1
Unknown	138.22	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	1473.73	1
tc|Rep: Chromosome undetermined scaffold_296, whole genome shotgun sequenc	27.29	1
gb|KL4B.112C24F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112C24, mR	354.88	1
Unknown	29.17	1
gb|KF8B.100B17F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100B17, mR	51504.25	1
gb|AGN_PNL223dr1_g6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	34.06	1
Unknown	75.95	1
Unknown	230.31	1
Unknown	27.11	1
Unknown	83.24	1
tc|Rep: DNA-binding protein - Solanum lycopersicum (Tomato) (Lycopersicon escul	55.29	1
Unknown	99.28	1
gb|KT7C.113A06F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.113A06, mR	25.66	1
Unknown	16.37	1
gb|KF8C.105O02F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105O02, mR	100.67	1
Unknown	2278.43	1
tc|Rep: Chromosome undetermined scaffold_248, whole genome shotgun sequenc	821.14	1
Unknown	43.18	1
gb|KL4B.105L10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105L10, mR	3702.77	1
gb|TT-15_L06 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	32.5	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	10505.1	1
tc|Rep: Genomic DNA, chromosome 5, BAC clone:F6N7 - Arabidopsis thaliana (Mo	170.65	1
tc|Rep: 60S ribosomal protein L31 - Nicotiana glutinosa (Tobacco), complete [TC59	25.53	1
gb|Nicotiana tabacum nuclease mRNA, partial cds [AY029749]	55.27	1
Unknown	26.89	1
gb|FS387202 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	2833.51	1
gb|KL4B.105B08F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105B08, mR	1107.53	1
Unknown	33.41	1
Unknown	43.65	1
Unknown	18.94	1
gb|Nicotiana tabacum dehydroascorbate reductase (DHAR) mRNA, complete cds [	181.59	1
gb|KR3B.109I23F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109I23, mR	101.37	1

gb|FS405424 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	450.13	1
gb|KG9B.106M17F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106M17,	180.69	1
gb|AGN_RNC007xi24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1097.1	1
gb|TT-07_C08 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	35.27	1
Unknown	1073.45	1
gb|TT-36_L19 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	25.23	1
Unknown	1180.8	1
gb|KR3B.101E04F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101E04, m	130.15	1
tc|Rep: Chromosome chr1 scaffold_22, whole genome shotgun sequence - Vitis vin	40.58	1
gb|AGN_PNL208dr1_a3.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	28.64	1
Unknown	19.72	1
gb|KT7B.100G10F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100G10, mR	4422.62	1
gb|Nicotiana tabacum S-adenosyl-L-homocysteine hydrolase (SAHH3) mRNA, parti	9401.12	1
tc|Rep: Bypass1 - Nicotiana benthamiana, partial (68%) [TC45349]	1467.83	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	986.22	1
gb|AGN_PNL226af1_a6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	122.87	1
gb|KN6B.108P09F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.108P09, m	265.7	1
gb|KN6B.104I03F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104I03, m	28.05	1
gb|KN6B.009M09F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009M09,	22.72	1
Unknown	57.01	1
Unknown	20.25	1
tc|Rep: At5g44450 - Arabidopsis thaliana (Mouse-ear cress), partial (79%) [TC5462	83.83	1
Unknown	26.49	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	29.15	1
gb|KG9B.106J18F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106J18, m	71.4	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	1178.45	1
gb|TT-41_F01 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	45.01	1
Unknown	549.41	1
tc|Rep: Serine/threonine protein phosphatase - Vitis vinifera (Grape), complete [TC	116.83	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	21.06	1
gb|AGN_RPC020xk06f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	82.12	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	94.53	1
gb|KP1B.101L14F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101L14, mR	92.33	1
tc|Rep: Chromosome undetermined scaffold_324, whole genome shotgun sequenc	18.19	1

Unknown	2165.79	1
tc|Rep: Chromosome chr2 scaffold_112, whole genome shotgun sequence - Vitis vi	312.98	1
gb|AGN_RNC004xo16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	46.22	1
gb|FS433138 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	150.83	1
gb|N.tabacum 5-enolpyruvylshikimate-3-phosphate synthase mRNA, complete cds	97	1
tc|Rep: Silicatein - Halichondria okadai (Marine sponge), partial (15%) [TC67373]	70.89	1
gb|KL4B.100B12F.050922T7 KL4B Nicotiana tabacum cDNA clone KL4B.100B12, mR	515.25	1
gb|KL4B.103C20F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103C20, mR	31.72	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	85.04	1
gb|AGN_PNL225df1_f4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	265.62	1
tc|Rep: MYB transcription factor MYB173 - Glycine max (Soybean), partial (55%) [T	2926.33	1
gb|KP1B.001H14F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001H14, m	161.2	1
Unknown	41.52	1
gb|TT-07_O15 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	683.27	1
gb|CHO_SL003xc11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	129.51	1
Unknown	35.17	1
gb|KR2B.103E15F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.103E15, m	671.53	1
gb|Nicotiana tabacum nack1 mRNA for kinesin-like protein NACK1, complete cds [A	82.02	1
tc|Rep: Ribosomal protein L3A - Nicotiana tabacum (Common tobacco), partial (59	69	1
gb|KN6B.102D04F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102D04,	294.95	1
Unknown	60.68	1
Unknown	683.99	1
tc|Rep: Chromosome chr3 scaffold_117, whole genome shotgun sequence - Vitis vi	127.09	1
tc|Rep: Chromosome undetermined scaffold_334, whole genome shotgun sequenc	376.13	1
tc|Rep: Chromosome chr7 scaffold_270, whole genome shotgun sequence - Vitis vi	690.98	1
tc|Rep: Ubiquinol-cytochrome c reductase complex 6.7 kDa protein - Solanum tube	107.32	1
tc|Rep: 60S ribosomal protein L24 - Cicer arietinum (Chickpea) (Garbanzo), complet	51.49	1
gb|AB032546 Nicotiana tabacum immature pollen grains Nicotiana tabacum cDNA	86.21	1
tc|Rep: Chromosome undetermined scaffold_52, whole genome shotgun sequence	27.61	1
gb|KR3B.111A19F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111A19, m	36.64	1
Unknown	58.45	1
tc|Rep: Calcium homeostasis regulator CHoR1 - Solanum tuberosum (Potato), parti	357.63	1
tc|Rep: Pollen coat-like protein - Camellia sinensis (Tea), complete [TC76886]	1204.66	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	97.44	1

tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	207.59	1
Unknown	206.99	1
Unknown	204.3	1
gb|KG9B.003P21F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003P21, m	38.95	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	59.38	1
tc|Rep: Alpha-amylase - Plantago major (Common plantain), partial (53%) [TC4459	170.84	1
gb|KP1B.101F02F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101F02, m	102.39	1
gb|KF8C.103B03F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103B03, mR	484	1
gb|KG9B.103K21F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103K21, m	40.95	1
tc|Rep: At2g43020/MFL8.12 - Arabidopsis thaliana (Mouse-ear cress), partial (38%)	677.97	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	2233	1
gb|KF8C.103P24F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103P24, mR	500.22	1
gb|CHO_SL027xb23f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1670.19	1
gb|AGN_PNL229bf1_a3.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	27.4	1
gb|AGN_RPC017xc15f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	1557.97	1
gb|KG9B.103M11F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103M11,	92.21	1
Unknown	252.12	1
Unknown	55.92	1
Unknown	513.22	1
tc|Rep: At2g39050/T7F6.22 - Arabidopsis thaliana (Mouse-ear cress), partial (43%)	1029.41	1
tc|Rep: Eukaryotic translation initiation factor 3 subunit B - Nicotiana tabacum (Co	21.19	1
tc|Rep: CBL-interacting protein kinase 7 - Populus trichocarpa (Western balsam po	7991.15	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	37.43	1
Unknown	21.56	1
gb|KG9B.001H02F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001H02, n	1092.16	1
Unknown	562.09	1
gb|KG9B.102D18F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102D18, n	465.51	1
gb|AGN_RNC112xp19r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	24.52	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	48.85	1
gb|AGN_RNC111xd18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	47.93	1
gb|AGN_RNC110xk10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	38.45	1
gb|KR2B.107D18F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.107D18, m	253.77	1
tc|Rep: Glutathione S-transferase, class-phi - Solanum commersonii (Commerson's	102.59	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	91.11	1

tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	2702.44	1
gb|TT-34_B01 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	135.15	1
gb|KT7C.102B03F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102B03, mR	19.97	1
gb|KR3B.107D14F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.107D14, m	829.81	1
gb|KP1B.101M16F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101M16,	1003.66	1
gb|TT-38_G05 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	38.74	1
tc|Rep: Mitochondrial phosphate transporter - Glycine max (Soybean), partial (44%	5132.18	1
gb|KG9B.107K13F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107K13,	1930.67	1
gb|KR3B.113D07F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.113D07, m	173.27	1
gb|KT7C.102O08F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102O08, mR	31.89	1
gb|AGN_RNC109xb08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	200.69	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	92.16	1
gb|KF8B.200N06F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200N06, mR	1403.18	1
Unknown	3546.7	1
tc|Rep: S-adenosylmethionine synthetase - Solanum tuberosum (Potato), partial (9	87.57	1
gb|KL4B.111N08F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111N08, m	68.75	1
gb|AGN_PNL231bf1_h8.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	11263.65	1
gb|Nicotiana tabacum mRNA for nucleosome assembly protein 1 - like protein 2 [A	888.66	1
gb|AGN_RPC009xn03f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	98.4	1
tc|Rep: Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Pro	20.84	1
tc|Rep: Chromosome undetermined scaffold_80, whole genome shotgun sequence	188.95	1
gb|KF8C.109L20F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109L20, mRN	520.02	1
Unknown	260.9	1
Unknown	19.97	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	94.75	1
gb|KP1B.105D21F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105D21, m	430.65	1
tc|Rep: Proteasome subunit alpha type-6 - Nicotiana tabacum (Common tobacco),	216.06	1
tc|Rep: Tryptophan synthase beta subunit - Persicaria tinctoria, partial (83%) [TC49	530.13	1
gb|KG9B.102A13F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102A13,	59.17	1
tc|Rep: Chromosome undetermined scaffold_91, whole genome shotgun sequence	105.43	1
gb|KG9B.102D21F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102D21,	107.8	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	466.8	1
Unknown	916.41	1
Unknown	202.45	1

tc|Rep: Induced stolon tip protein - Capsicum annuum (Bell pepper), partial (66%) [	1541.12	1
tc|Rep: Chromosome undetermined scaffold_200, whole genome shotgun sequenc	134.11	1
Unknown	47.38	1
gb|KT7C.104B12F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104B12, mR	824.95	1
gb|KL4B.104P21F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104P21, mR	146.08	1
Unknown	450.11	1
gb|AGN_RNC020xa24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	26.09	1
gb|TT-01_E10 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	2436.48	1
gb|TT-31_K08 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	105.77	1
tc|Rep: Shikimate kinase, chloroplast precursor - Solanum lycopersicum (Tomato) (	505.08	1
gb|KF8C.101D04F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101D04, mR	5205.75	1
Unknown	22.44	1
gb|CHO_SL028xj15f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	144.82	1
tc|Rep: Chromosome chr9 scaffold_104, whole genome shotgun sequence - Vitis vi	1539.95	1
Unknown	23.95	1
gb|KP1B.101E23F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101E23, m	34.54	1
Unknown	94.3	1
gb|BL12.102O24F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.102O24, m	80.15	1
gb|KL4B.112I23F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112I23, mR	66.1	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	4194.42	1
gb|KL4B.103O05F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103O05, m	22.95	1
gb|AGN_RPC017xo19f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	238.06	1
Unknown	73.62	1
tc|Rep: Quinolinate phosphoribosyltransferase - Nicotiana tabacum (Common toba	33.46	1
gb|AM843409 seedling library, SL Nicotiana tabacum cDNA clone nt002193022, m	23.15	1
gb|KR3B.104N14F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.104N14, m	35.28	1
Unknown	2885.87	1
tc|Rep: Bypass2 - Nicotiana benthamiana, partial (57%) [TC58115]	58.76	1
tc|Rep: Joka2 - Nicotiana plumbaginifolia (Leadwort-leaved tobacco), partial (50%)	120.75	1
Unknown	443.7	1
Unknown	139.89	1
tc|Rep: Eukaryotic translation initiation factor 3 subunit A - Nicotiana tabacum (Co	152.38	1
tc|Rep: Voltage-dependent anion channel - Nicotiana tabacum (Common tobacco),	251.03	1
gb|KG9B.103F14F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103F14, m	1038.11	1

gb|TT-28_H09 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	52.55	1
gb|KG9B.105F03F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105F03, m	552.41	1
tc|Rep: 50S ribosomal protein L4 - Arabidopsis thaliana (Mouse-ear cress), partial (	44.06	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	249.9	1
Unknown	48.94	1
tc|Rep: Molecular chaperone Hsp90-2 - Nicotiana benthamiana, partial (25%) [TC4	2878.78	1
tc|Rep: Cellulose synthase - Populus tremula x Populus tremuloides, partial (86%) [	280.63	1
Unknown	45.12	1
Unknown	49.53	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	182.84	1
tc|Rep: Chromosome chr9 scaffold_104, whole genome shotgun sequence - Vitis vi	244.01	1
gb|KF8C.106J03F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106J03, mRN	132.4	1
tc|Rep: Gamma hydroxybutyrate dehydrogenase - Arabidopsis thaliana (Mouse-ear	462.32	1
tc|Rep: Joka2 - Nicotiana plumbaginifolia (Leadwort-leaved tobacco), partial (40%)	226.22	1
Unknown	18.72	1
tc|GB|AJ937852.1|CAI78906.1 putative glutathione S-transferase [NP8635400]	197.67	1
gb|KP1B.113B11F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.113B11, m	55	1
tc|Rep: Temperature-induced lipocalin - Solanum lycopersicum (Tomato) (Lycopers	139.59	1
tc|Rep: Chromosome chr2 scaffold_187, whole genome shotgun sequence - Vitis vi	23.91	1
gb|KN6B.102M07F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102M07,	517.52	1
gb|KL4B.104B16F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104B16, m	30.4	1
gb|KR3B.101F04F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101F04, m	30.65	1
Unknown	41.56	1
gb|BP528807 MAT001 Nicotiana tabacum cDNA clone BY13673, mRNA sequence [	26.69	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	64.19	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	180.95	1
Unknown	223.57	1
gb|KF8C.106M20F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106M20, m	66.76	1
tc|Rep: Uncharacterized protein At4g38130.2 - Arabidopsis thaliana (Mouse-ear cr	27.26	1
gb|KP1B.101K20F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101K20, m	103.23	1
Unknown	11705.25	1
gb|AGN_RNC129xp14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	182.41	1
gb|FS409302 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	5984.76	1
gb|Nicotiana tabacum mRNA for hypothetical protein (T407 gene) [AM851016]	950.05	1

gb|AGN_RNC116xi22f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	23.43	1
gb|EST_FLW001xi04f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	32.42	1
Unknown	485.96	1
gb|KL4B.101O02F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101O02, m	49.46	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	1964.38	1
gb|TL13.105E03F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.105E03, mR	44.59	1
gb|KF8C.101C08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101C08, mR	85.71	1
gb|KT7B.107C22F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107C22, mR	21.13	1
tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	148.41	1
gb|CHO_SL027xj10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	144.26	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	238.84	1
Unknown	19.62	1
gb|KG9B.003B08F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003B08, m	21.38	1
gb|KP1B.102P18F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102P18, m	909.69	1
gb|CHO_SL008xn09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	25.02	1
Unknown	35594.25	1
Unknown	177.77	1
tc|Rep: Nucleosome assembly protein 1-like protein 4 - Nicotiana tabacum (Comm	400.51	1
gb|Nicotiana tabacum WREBP-2 mRNA, complete cds [AB017694]	152.22	1
tc|Rep: Chromosome chr10 scaffold_179, whole genome shotgun sequence - Vitis	725.78	1
gb|KL4B.104J05F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104J05, mR	82.85	1
tc|Rep: Chromosome chr1 scaffold_136, whole genome shotgun sequence - Vitis vi	4402.81	1
tc|Rep: Heat-shock protein - Arabidopsis thaliana (Mouse-ear cress), partial (52%) [	64.25	1
Unknown	19.07	1
Unknown	63.63	1
gb|Nicotiana tabacum partial mRNA for cullin 1C (cul1C gene) [AJ344535]	91.94	1
tc|Rep: Chloroplast threonine deaminase 1 - Solanum lycopersicum (Tomato) (Lyco	2273.61	1
tc|Rep: Xylose isomerase - Vitis vinifera (Grape), partial (43%) [TC71501]	254.12	1
tc|Rep: Chaperone GrpE type 1 - Nicotiana tabacum (Common tobacco), partial (97	72.44	1
gb|TT-35_P15 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	25.43	1
Unknown	126.37	1
gb|KL5B.118N24F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.118N24, m	90.07	1
tc|Rep: Sucrose-phosphate synthase isoform B - Nicotiana tabacum (Common toba	2919.81	1
gb|CHO_SL003xk23f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	48.52	1

tc|Rep: Multiprotein bridging factor 1c - Solanum lycopersicum (Tomato) (Lycopers	1645.17	1
gb|TT-17_O12 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	144.75	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	134.82	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	179.55	1
tc|Rep: Chromosome undetermined scaffold_248, whole genome shotgun sequenc	105.5	1
gb|KP1B.109I14F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109I14, mR	19.04	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	135.17	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	42.57	1
gb|TT-38_J23 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	1277.45	1
Unknown	24.29	1
tc|Rep: Chromosome chr16 scaffold_94, whole genome shotgun sequence - Vitis vi	1867.19	1
gb|KT7C.112K05F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112K05, mR	97.77	1
tc|Rep: Hsp20.1 protein - Solanum peruvianum (Peruvian tomato) (Lycopersicon pe	134.79	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	511.22	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT12-4-420, cultivar Bright Yellow 2	65.75	1
gb|FS436012 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	56.39	1
tc|Rep: Glutathione S-transferase - Euphorbia esula (Leafy spurge), partial (87%) [T	4373.96	1
tc|Rep: Chromosome chr13 scaffold_120, whole genome shotgun sequence - Vitis	109.49	1
Unknown	82.45	1
tc|Rep: Chromosome undetermined scaffold_116, whole genome shotgun sequenc	1593.52	1
gb|EST_FLW001xn16f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	1683.3	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	549.08	1
gb|KR2B.105N22F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.105N22, m	50.85	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	316.98	1
gb|KL4B.111O19F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111O19, m	1340.44	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT2-32-210, cultivar Bright Yellow 2	35.84	1
gb|TT-36_C17 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	552.77	1
gb|TOBESTR089A07 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	75.6	1
tc|Rep: Ubiquitin - Hevea brasiliensis (Para rubber tree), partial (67%) [TC48522]	1757.97	1
tc|Rep: Myosin XI - Nicotiana tabacum (Common tobacco), partial (3%) [TC55717]	65.71	1
Unknown	392.5	1
tc|Rep: Triosephosphate isomerase - Solanum tuberosum (Potato), partial (49%) [T	496.09	1
gb|Nicotiana tabacum mRNA for nucleic acid binding protein (nbp1 gene) [AJ34453	91.33	1
Unknown	782.26	1

gb|EST_FLW005xb18f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	178.07	1
tc|Rep: Glyceraldehyde-3-phosphate dehydrogenase - Capsicum annuum (Bell pep	136.7	1
Unknown	57.13	1
tc|Rep: Lysophospholipase-like protein - Arabidopsis thaliana (Mouse-ear cress), pa	968.24	1
gb|KR3B.001L06F.050815T7 KR3B Nicotiana tabacum cDNA clone KR3B.001L06, m	24.88	1
gb|KR3B.109P05F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109P05, m	184.48	1
tc|Rep: Magnesium dependent soluble inorganic pyrophosphatase - Solanum tuber	4511.76	1
gb|KT7C.109C01F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109C01, mR	258.25	1
gb|TOBESTR043F12 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	43.01	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	183.01	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	158.43	1
gb|KF8C.102O07F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102O07, mR	13365.8	1
gb|TT-09_F04 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	599.19	1
tc|Rep: Chromosome chr9 scaffold_33, whole genome shotgun sequence - Vitis vin	14305.55	1
Unknown	56.35	1
gb|Nicotiana tabacum A31 mRNA for chromomethylase-like protein, complete cds	302.5	1
Unknown	21.08	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	24.36	1
Unknown	30.33	1
Unknown	37.43	1
gb|KN6B.102E03F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102E03, m	142.63	1
Unknown	43.81	1
tc|Rep: Na+/H+ antiporter - Mesembryanthemum crystallinum (Common ice plant)	88.93	1
Unknown	24.35	1
gb|Nicotiana tabacum mRNA for gibberellin 3beta-hydroxylase, complete cds [AB0	67.33	1
Unknown	30.15	1
gb|FS416927 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	1218.11	1
Unknown	10048.38	1
Unknown	37.49	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	1094.87	1
gb|TT-12_L04 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	26.12	1
gb|TL13.109B21F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.109B21, mR	517.41	1
gb|KP1B.104B24F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104B24, m	1084.98	1
gb|KL4B.109M15F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.109M15, m	29.86	1

tc|Rep: Fructose-bisphosphate aldolase - Solanum tuberosum (Potato), partial (55%	4218.34	1
gb|CHO_SL015xi10f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	56.28	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	24.3	1
gb|CHO_SL013xb17f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	2436.19	1
gb|KP1B.107I12F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107I12, mR	274.56	1
gb|KN6B.105C09F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105C09, m	96.4	1
Unknown	235.68	1
Unknown	183.85	1
Unknown	22.41	1
Unknown	19.32	1
tc|Rep: Chromosome chr1 scaffold_180, whole genome shotgun sequence - Vitis vi	47.81	1
Unknown	51.3	1
Unknown	20.01	1
gb|BP530129 MAT005 Nicotiana tabacum cDNA clone BY21114, mRNA sequence [	651.87	1
gb|KF8B.100G13F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100G13, mR	33379.55	1
tc|Rep: Chromosome chr13 scaffold_74, whole genome shotgun sequence - Vitis vi	22.88	1
Unknown	649.89	1
tc|Rep: Chromosome chr2 scaffold_113, whole genome shotgun sequence - Vitis vi	294.8	1
gb|Nicotiana tabacum NtCHI1 mRNA for chalcone isomerase, complete cds [AB213	19.9	1
Unknown	62.91	1
Unknown	639.21	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	138.75	1
gb|KF8C.110B13F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110B13, mRN	2942.77	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	1678.6	1
gb|TOBESTR098B05 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	67414.15	1
gb|BP128854 MAT001 Nicotiana tabacum cDNA clone BY661, mRNA sequence [BP	100.79	1
gb|TT-47_F05 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	463.63	1
Unknown	208.88	1
gb|BP129934 MAT001 Nicotiana tabacum cDNA clone BY1843, mRNA sequence [B	471.29	1
tc|Rep: Polyprotein - Solanum melongena (Eggplant) (Aubergine), partial (58%) [TC	21.74	1
tc|Rep: Chromosome chr12 scaffold_78, whole genome shotgun sequence - Vitis vi	500.1	1
gb|Nicotiana tabacum calcium-dependent protein kinase-like mRNA, partial seque	110.06	1
tc|Rep: SLT1 protein - Nicotiana tabacum (Common tobacco), partial (37%) [TC529	31.81	1
gb|KF8C.108E01F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108E01, mRN	58.27	1

Unknown	1284.86	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	1052.12	1
Unknown	19.58	1
tc|Rep: ATP synthase subunit d, mitochondrial - Arabidopsis thaliana (Mouse-ear cr	603.22	1
tc|Rep: Protein yippee-like - Solanum tuberosum (Potato), complete [TC46422]	20.72	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis v	80.99	1
tc|Rep: Chromosome undetermined scaffold_133, whole genome shotgun sequenc	268.31	1
tc|Rep: Os07g0192300 protein - Oryza sativa subsp. japonica (Rice), partial (68%) [T	103.99	1
Unknown	24.08	1
gb|KG9B.005B15F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005B15, m	41.56	1
tc|Rep: Chromosome chr3 scaffold_157, whole genome shotgun sequence - Vitis vi	58.39	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	928.02	1
gb|TT-03_C06 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	213.11	1
gb|KF8C.108M07F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108M07, mF	31.21	1
gb|AGN_PNL226df1_e5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	124.44	1
Unknown	48.71	1
gb|KF8C.105O05F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105O05, mRI	175.95	1
Unknown	582.85	1
tc|Rep: NTGP5 - Nicotiana tabacum (Common tobacco), complete [TC75301]	102.38	1
gb|KP1B.111O06F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.111O06, m	51.3	1
Unknown	50.35	1
Unknown	183.62	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	262.21	1
gb|TT-10_J17 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sequ	24.84	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	115.9	1
tc|Rep: Ubiquitin carrier protein - Vitis vinifera (Grape), complete [TC44653]	514.29	1
tc|Rep: Uncharacterized protein At4g17310.2 - Arabidopsis thaliana (Mouse-ear cre	25.38	1
Unknown	386.31	1
gb|KR2B.115K02F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115K02, ml	227.87	1
Unknown	33.81	1
gb|KP1B.001N14F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001N14, m	214.28	1
Unknown	872.57	1
gb|KP1B.107P21F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107P21, ml	133.51	1
gb|AGN_ELP005xb01f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	36.07	1

tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	525.46	1
Unknown	357.67	1
gb|TT-12_E09 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	64.45	1
Unknown	35.4	1
gb|KP1B.110C13F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110C13, mI	488.47	1
gb|KL5B.104O21F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.104O21, mI	1057.94	1
gb|KF8C.101M24F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101M24, mF	18224.15	1
gb|KL4B.110O19F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110O19, mI	38	1
Unknown	989.92	1
tc|Rep: Chromosome chr3 scaffold_95, whole genome shotgun sequence - Vitis vin	29.16	1
Unknown	522.61	1
tc|Rep: Chromosome chr13 scaffold_210, whole genome shotgun sequence - Vitis v	766.57	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	27.1	1
Unknown	443.26	1
gb|AGN_RPC005xi07f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	280.49	1
gb|CHO_SL023xo07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	262.53	1
tc|Rep: Chromosome undetermined scaffold_168, whole genome shotgun sequenc	24.12	1
tc|Rep: Chromosome chr9 scaffold_104, whole genome shotgun sequence - Vitis vi	244.29	1
Unknown	35.37	1
Unknown	123.64	1
gb|KG9B.106L14F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106L14, m	28.69	1
Unknown	40.3	1
tc|Rep: Chromosome chr1 scaffold_136, whole genome shotgun sequence - Vitis vi	409.56	1
Unknown	19.49	1
gb|AGN_RNC006xp17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	21.72	1
gb|KP1B.111I22F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.111I22, mRI	80.34	1
gb|AM783100 seedling library, SL Nicotiana tabacum cDNA clone nt002102024, mF	61.25	1
Unknown	20.6	1
Unknown	280.24	1
gb|KL4B.102I22F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102I22, mRN	273.68	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	655.36	1
tc|Rep: Membrane cofactor protein precursor - Callithrix jacchus (Common marmo	21.16	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT3-42-370, cultivar Bright Yellow 2	181.97	1
Unknown	169.33	1

Unknown	6521.98	1
Unknown	27.25	1
Unknown	905.15	1
gb|Nicotiana tabacum microsomal omega-6-desaturase (FAD2) mRNA, complete cc	19132.75	1
Unknown	24.37	1
gb|KL4B.109F14F.051108T7 KL4B Nicotiana tabacum cDNA clone KL4B.109F14, mR	128.19	1
Unknown	1360.66	1
gb|KF8B.201D21F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201D21, mR	649.52	1
tc|Rep: 14-3-3 protein - Nicotiana tabacum (Common tobacco), complete [TC4021	18626.3	1
Unknown	18.3	1
Unknown	73.64	1
gb|AGN_RNC022xp13f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	25.9	1
gb|TT-23_N18 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	1685.78	1
Unknown	35.63	1
Unknown	23.01	1
Unknown	762.18	1
Unknown	327.19	1
gb|KL4B.101A09F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101A09, mR	19.4	1
gb|FS377087 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	53.79	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	26.34	1
Unknown	93.8	1
Unknown	576.93	1
gb|KP1B.109K06F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109K06, m	51.13	1
gb|TT-08_E04 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	210	1
gb|KR3B.113P03F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.113P03, m	1850.37	1
tc|Rep: RING E3 ligase protein - Arabidopsis thaliana (Mouse-ear cress), partial (15	101.67	1
gb|KL4B.107P19F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107P19, mR	30.33	1
gb|KF8C.104N08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104N08, mR	33137.7	1
tc|Rep: Pyruvate dehydrogenase E1 beta subunit isoform 1 - Zea mays (Maize), part	293.48	1
gb|TT-11_H14 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	517.91	1
gb|KL4B.109L22F.051108T7 KL4B Nicotiana tabacum cDNA clone KL4B.109L22, mR	28.35	1
Unknown	43.61	1
tc|Rep: ARF-like small GTPase-like protein - Solanum tuberosum (Potato), complete	9134.44	1
gb|TT-38_F18 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence |	18.84	1

gb|KN6B.104J07F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104J07, mI	18.9	1
tc|Rep: Chromosome undetermined scaffold_203, whole genome shotgun sequenc	19.31	1
Unknown	184.91	1
gb|FS417360 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	838.15	1
tc|Rep: Chromosome undetermined scaffold_203, whole genome shotgun sequenc	21.01	1
gb|KF8C.106K08F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106K08, mRN	87.81	1
tc|Rep: Chromosome chr8 scaffold_68, whole genome shotgun sequence - Vitis vin	186	1
gb|Nicotiana tabacum mRNA for NAD-dependent isocitrate dehydrogenase, clone	673.82	1
gb|KT7C.106G23F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106G23, mR	502.8	1
tc|Rep: Chromosome chr18 scaffold_121, whole genome shotgun sequence - Vitis	264.23	1
Unknown	48.77	1
Unknown	236.02	1
Unknown	515.59	1
gb|KL5B.117A02F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.117A02, mR	26.25	1
Unknown	2998.83	1
gb|TT-09_E09 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	19.64	1
gb|TT-01_B04 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	136.96	1
gb|AGN_PNL228cf1_a10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	2764.14	1
tc|Rep: Chromosome undetermined scaffold_3075, whole genome shotgun sequen	37.2	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	65.14	1
gb|KT7B.103C07F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.103C07, mRI	1281.67	1
tc|Rep: Inorganic pyrophosphatase - Nicotiana tabacum (Common tobacco), compl	47.66	1
gb|KL4B.104A02F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104A02, mR	4297.26	1
gb|KL5B.114F14F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.114F14, mR	30.65	1
Unknown	109.9	1
Unknown	22.99	1
gb|KG9B.002C07F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002C07, m	131.29	1
gb|AM816107 seedling library, SL Nicotiana tabacum cDNA clone nt002273078, mR	255.12	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	327.77	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	31.43	1
Unknown	526.24	1
gb|TT-22_B20 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	140.06	1
tc|Rep: Adenine phosphoribosyltransferase-like - Solanum tuberosum (Potato), cor	532.61	1
tc|Rep: Squalene monooxygenase - Datura innoxia (Downy thornapple) (Datura me	11233.7	1

gb|TT-08_G17 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	11692.55	1
Unknown	28.65	1
gb|KR3B.104B22F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.104B22, m	114.58	1
gb|AGN_RNC012xp24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	530.28	1
tc|Rep: Tocopherol cyclase - Solanum tuberosum (Potato), partial (50%) [TC52369]	23.34	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	500.92	1
Unknown	116.55	1
Unknown	31.63	1
gb|TT-06_C12 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	2069.43	1
gb|CHO_SL024xf08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	147.84	1
gb|KN6B.104O01F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104O01, r	1293.13	1
tc|Rep: Citrate synthase - Nicotiana tabacum (Common tobacco), partial (50%) [TC4	122.17	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	863.21	1
gb|KT7C.104M15F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104M15, m	21.37	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	109.41	1
Unknown	62.56	1
gb|KL4B.103F10F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103F10, mR	4853.76	1
gb|CHO_SL026xf21f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	741.36	1
Unknown	26.71	1
gb|KP1B.109K02F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109K02, m	18.73	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	551.24	1
gb|KR3B.113P20F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.113P20, m	24.93	1
Unknown	91.14	1
gb|AGN_RNC019xi20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	127.17	1
gb|TT-30_H11 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	183.19	1
gb|BP526356 MAT001 Nicotiana tabacum cDNA clone BY11073, mRNA sequence [E	17.92	1
gb|KL4B.111O01F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111O01, m	1168.62	1
gb|Nicotiana tabacum NtmybA2 mRNA for Myb, complete cds [AB056123]	61.77	1
tc|Rep: Chromosome chr3 scaffold_157, whole genome shotgun sequence - Vitis vi	338.83	1
gb|TT-24_J23 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	172.62	1
Unknown	457.82	1
tc|Rep: Chromosome undetermined scaffold_127, whole genome shotgun sequenc	20.66	1
gb|KG9B.001G18F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001G18, n	2709.73	1
gb|EST_FLW005xl21f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [EH	294.2	1

Unknown	27.44	1
tc|Rep: 40S ribosomal protein S12 - Vitis vinifera (Grape), complete [TC53841]	19.03	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	454.27	1
gb|Nicotiana tabacum mRNA for nucleosome assembly protein 1 - like protein 3 [A	578.6	1
tc|Rep: AN11 - Petunia hybrida (Petunia), partial (50%) [TC52222]	147.61	1
gb|Nicotiana tabacum S25-PR6 mRNA, complete cds [U44760]	24.94	1
gb|KL5B.115A14F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.115A14, mF	168.79	1
Unknown	93.43	1
tc|Rep: Uncharacterized protein At1g53880.1 - Arabidopsis thaliana (Mouse-ear cre	45.92	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	27.29	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	142.89	1
Unknown	189.65	1
gb|AGN_RNC007xo06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	226.41	1
Unknown	58.33	1
Unknown	22.09	1
gb|KG9B.105C22F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105C22, m	181.22	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	42.42	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	27.85	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	80.87	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	1630.59	1
gb|AGN_PNL226df1_d2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	9459.27	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	236.29	1
gb|AGN_RNC116xh11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	89.04	1
gb|KR3B.001C12F.050815T7 KR3B Nicotiana tabacum cDNA clone KR3B.001C12, m	836.49	1
tc|Rep: Ubiquitin conjugating enzyme 2 - Solanum lycopersicum (Tomato) (Lycoper	154.16	1
Unknown	976.19	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	22.45	1
tc|Rep: Chromosome undetermined scaffold_267, whole genome shotgun sequenc	468.34	1
tc|Rep: Chromosome chr5 scaffold_72, whole genome shotgun sequence - Vitis vin	25.18	1
Unknown	55.43	1
gb|AGN_RPC005xi08f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	37.6	1
gb|AGN_RNC125xp24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	551.57	1
gb|KR3B.114M20F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.114M20, r	1716.86	1
gb|TT-31_N23 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	633.09	1

Unknown	1705.42	1
gb|KT7C.112P22F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112P22, mR	57.46	1
gb|KF8C.105J14F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105J14, mRN	1805.38	1
gb|KL4B.104K06F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104K06, mR	10861.5	1
tc|Rep: Pathogenesis-related homeodomain protein - Petroselinum crispum (Parsl	71.03	1
tc|Rep: Arginine/serine-rich-splicing factor RSP31 - Arabidopsis thaliana (Mouse-ea	229.4	1
gb|KF8C.102O07F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102O07, mR	7703.98	1
tc|Rep: Fructose-bisphosphate aldolase - Vitis vinifera (Grape), complete [TC54270	64.11	1
gb|Nicotiana tabacum ferritin 2 (Fer2) mRNA, complete cds [AY141105]	80.61	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	1275.3	1
gb|KL4B.101B07F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101B07, mR	809.81	1
gb|TT-35_J09 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	911.5	1
tc|Rep: Mitochondrial small heat shock protein - Solanum lycopersicum (Tomato) (	176.03	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	172.7	1
gb|TT-35_I12 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	23.12	1
gb|AGN_RNC211xl11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	226.16	1
Unknown	155.51	1
gb|AGN_RNC026xp05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	93.16	1
gb|KR2B.107M04F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.107M04,	27.42	1
Unknown	40.06	1
Unknown	115.36	1
tc|Rep: Mannose-6-phosphate isomerase - Vitis vinifera (Grape), partial (88%) [TC7	510.91	1
tc|Rep: Chromosome chr2 scaffold_140, whole genome shotgun sequence - Vitis vi	7492.8	1
tc|Rep: Metallothionein-like protein - Nicotiana tabacum (Common tobacco), com	35785.3	1
tc|Rep: Cycloartenol synthase - Dioscorea zingiberensis, partial (24%) [TC52278]	75.41	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	555.87	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	121.48	1
Unknown	10537.65	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	27.72	1
gb|CHO_SL016xb06f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	517.84	1
gb|AGN_PNL230bf1_e6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	2792.52	1
Unknown	1073.68	1
gb|CHO_SL015xh02f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	146.32	1
gb|TT-47_D17 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	39.58	1

tc|Rep: Chromosome chr5 scaffold_72, whole genome shotgun sequence - Vitis vin	41.28	1
gb|KN6B.101B06F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101B06, m	267.17	1
gb|CHO_SL013xn02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	959.76	1
Unknown	414.29	1
gb|CHO_SL027xj07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	24.93	1
gb|AGN_PNL212df1_f1.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	43517.95	1
gb|10F11 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', n	42.13	1
gb|KG9B.105G06F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105G06, n	52.53	1
Unknown	72.05	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	79.71	1
Unknown	54.72	1
Unknown	107.45	1
Unknown	43.47	1
gb|TT-41_E09 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	105.44	1
tc|Rep: AML1 - Medicago truncatula (Barrel medic), partial (23%) [TC52177]	32.44	1
gb|AGN_RNC004xk06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	45.63	1
tc|Rep: Glycoprotein endopeptidase-like protein - Solanum tuberosum (Potato), co	56.03	1
gb|CHO_SL007xl02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	423.08	1
Unknown	182.1	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	320.13	1
Unknown	475.39	1
tc|Rep: Luminal-binding protein 5 precursor - Nicotiana tabacum (Common tobacc	8207.34	1
Unknown	22.25	1
gb|KF8C.103B09F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103B09, mRN	1398.96	1
Unknown	26.46	1
tc|Rep: Glutathione S-transferase GST 23 - Glycine max (Soybean), partial (89%) [TC	1087.39	1
Unknown	24.31	1
gb|BP530590 MAT005 Nicotiana tabacum cDNA clone BY22227, mRNA sequence [	34.76	1
tc|Rep: N.plumbaginifolia H+-translocating ATPase mRNA - Nicotiana plumbaginifol	254.92	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	163.89	1
gb|N.tabacum mRNA for phosphoglycerate kinase (chloroplast isoenzyme) [Z48977	102.79	1
Unknown	31.96	1
tc|Rep: LEA1-like protein - Capsicum annuum (Bell pepper), partial (97%) [TC51846	174.21	1
tc|Rep: UDP-glucuronate decarboxylase 1 - Nicotiana tabacum (Common tobacco),	16284.1	1

gb|KL5B.106G19F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.106G19, mF	130.5	1
gb|CHO_SL024xj20f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	27.56	1
gb|KL4B.111K19F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111K19, mR	103.91	1
Unknown	35.97	1
tc|Rep: Mitochondrial import receptor subunit TOM20 - Solanum tuberosum (Pota	161.54	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	21.07	1
gb|CHO_SL018xk07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	2834.81	1
gb|KN6B.009J12F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009J12, m	498.08	1
Unknown	144.55	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	888.05	1
tc|Rep: Chromosome undetermined scaffold_87, whole genome shotgun sequence	49.59	1
tc|Rep: Rar1 - Nicotiana tabacum (Common tobacco), complete [TC56002]	17.8	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	62.01	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	34.78	1
gb|KL4B.107D11F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107D11, mF	763.12	1
gb|AGN_ELP011xp03f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	67.29	1
Unknown	1167.27	1
Unknown	186.91	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	203.21	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	56.98	1
gb|KR3B.102P15F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.102P15, m	21.04	1
tc|Rep: Sigma factor - Nicotiana tabacum (Common tobacco), complete [TC74868]	81.28	1
gb|FS437774 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	49.51	1
gb|KR2B.111C20F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.111C20, m	56.47	1
gb|TT-25_L17 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	31.76	1
gb|KG9B.102J05F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102J05, mF	1680.74	1
gb|KR3B.101P22F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101P22, m	1142.54	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	213.51	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	460.27	1
gb|AGN_RNC014xn24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	144.67	1
gb|Nicotiana tabacum mRNA for S-adenosyl-L-homocysteine hydrolase, complete c	2060.56	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	477.67	1
gb|KT7C.109J05F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109J05, mRN	876.35	1
gb|KP1B.104O18F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104O18, m	27.73	1

gb|Nicotiana tabacum PAP mRNA for purple acid phosphatase, complete cds, isolat	18.92	1
gb|CHO_SL005xb10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	197.7	1
gb|KG9B.103K10F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103K10, m	979.55	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	3948.44	1
gb|KP1B.001P06F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001P06, m	4200.96	1
Unknown	60.48	1
gb|KF8C.105D01F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105D01, mR	222.27	1
Unknown	165.35	1
Unknown	874.55	1
gb|BP526377 MAT001 Nicotiana tabacum cDNA clone BY11094, mRNA sequence [	31.32	1
Unknown	4666.11	1
gb|KR3B.109H16F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109H16, m	136.42	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	88.29	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	1524.98	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	27.61	1
gb|KR3B.111D19F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111D19, m	58.24	1
tc|Rep: Predicted protein - Ostreococcus lucimarinus (strain CCE9901), partial (5%)	4574.94	1
tc|Rep: BTF3 - Nicotiana benthamiana, complete [TC61707]	45.15	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	2405.12	1
gb|KL4B.105A09F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105A09, m	249.64	1
Unknown	30.7	1
tc|Rep: Clp protease 2 proteolytic subunit precursor - Solanum lycopersicum (Tom	55.62	1
Unknown	65.09	1
gb|TT-36_C22 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	17.13	1
gb|KL4B.113D18F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.113D18, m	63.87	1
gb|KG9B.102P17F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102P17, m	252.77	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	10181.39	1
gb|KT7C.104I04F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104I04, mRN	1026.47	1
Unknown	26.36	1
gb|Nicotiana tabacum 3-dehydroquinate dehydratase [AY578144]	250.21	1
Unknown	50.34	1
gb|KG9B.001H23F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001H23, m	54.21	1
Unknown	93.82	1
tc|Rep: Chromosome undetermined scaffold_254, whole genome shotgun sequenc	4739.07	1

gb|Nicotiana tabacum blp2 mRNA for luminal binding protein (BiP), partial [X60059	8250.76	1
tc|Rep: Peptide methionine sulfoxide reductase (Protein- methionine-S-oxide redu	27.53	1
tc|Rep: Aspartate aminotransferase - Vitis vinifera (Grape), partial (53%) [TC40773]	79.88	1
gb|Nicotiana tabacum TBK11 mRNA for kinesin-like polypeptides 11, partial cds [A	79.63	1
tc|Rep: ALY protein - Nicotiana benthamiana, partial (37%) [TC59866]	449.81	1
tc|Rep: S-adenosylmethionine synthetase - Nicotiana suaveolens, partial (24%) [TC	1007.98	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	25.58	1
Unknown	61.38	1
gb|AGN_RNC024xl08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	44.69	1
gb|KG9B.102L21F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102L21, m	79.03	1
Unknown	28.78	1
Unknown	112.07	1
Unknown	32.07	1
Unknown	263.94	1
Unknown	18150.3	1
Unknown	747.96	1
tc|Rep: Carotenoid cleavage dioxygenase 1B - Solanum lycopersicum (Tomato) (Lyc	121.18	1
Unknown	32.04	1
gb|AGN_RNC012xh02f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	71.47	1
gb|KN6B.104F22F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104F22, m	32.29	1
gb|Nicotiana tabacum mRNA for ras-related protein RAB8-4, complete cds [AB079	3290.49	1
gb|ntsm9 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [EB	86.63	1
Unknown	252.2	1
tc|Rep: Protein kinase CK2 alpha subunit - Nicotiana tabacum (Common tobacco), c	190.69	1
gb|KP1B.037P02F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.037P02, m	184.74	1
Unknown	22.96	1
Unknown	87.92	1
tc|Rep: Malonyl-CoA:ACP transacylase - Perilla frutescens (Beefsteak plant) (Chines	141.75	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	411.07	1
tc|Rep: Chromosome chr14 scaffold_54, whole genome shotgun sequence - Vitis vi	797.16	1
Unknown	66.29	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	528.28	1
Unknown	46.15	1
tc|Rep: Ubiquitin carrier protein - Nicotiana benthamiana, complete [TC50166]	130.55	1

gb|Nicotiana tabacum calcium [AF435452]	71.04	1
gb|KF8B.202G14F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202G14, mR	44.22	1
gb|KG9B.105N12F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105N12,	70.98	1
tc|Rep: Aldehyde dehydrogenase family 7 member A1 - Euphorbia characias (Spurg	106.7	1
Unknown	24.51	1
tc|Rep: Chromosome undetermined scaffold_107, whole genome shotgun sequenc	40.11	1
gb|CHO_SL014xo09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	17.3	1
Unknown	23.9	1
tc|Rep: Syntaxin-like protein - Solanum tuberosum (Potato), partial (44%) [TC4662	1077.73	1
gb|KG9B.003C10F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003C10,	43.45	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	502.6	1
tc|Rep: Avr9/Cf-9 rapidly elicited protein 31 - Nicotiana tabacum (Common tobacc	74.96	1
tc|Rep: RNA-binding gricine-rich protein-1 - Nicotiana sylvestris (Wood tobacco), c	17174.15	1
Unknown	26.22	1
Unknown	42.86	1
Unknown	466.72	1
gb|KT7C.102N05F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102N05, mR	32.16	1
Unknown	173.61	1
gb|TOBESTR011H07 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	14454.35	1
gb|TT-20_O05 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	188.91	1
gb|Nicotiana tabacum partial mRNA for putative rac protein (rac3 gene) [AJ496227	22.22	1
gb|CHO_SL012xf09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	21.86	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT22-430, cultivar Bright Yellow 2 [	1642.58	1
Unknown	266.83	1
gb|KF8C.105N24F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105N24, mR	278.56	1
tc|Rep: Chromosome chr13 scaffold_210, whole genome shotgun sequence - Vitis	373.76	1
Unknown	1121.38	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	30.91	1
Unknown	28.14	1
gb|CHO_SL013xf01f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	259.77	1
Unknown	845.5	1
tc|Rep: Chromosome chr8 scaffold_99, whole genome shotgun sequence - Vitis vin	320.59	1
gb|AGN_RPC015xi06f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	37.06	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	63.16	1

gb|KN6B.101C02F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101C02,	468.8	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	151.6	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	34.97	1
gb|TT-16_E09 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	764.17	1
Unknown	6663.42	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	23.99	1
Unknown	19.34	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	149.07	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	185.65	1
gb|TT-19_E12 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	210.34	1
Unknown	170.88	1
gb|KG9B.102F14F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102F14, m	129.29	1
gb|KP1B.109D18F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109D18, m	2862.21	1
tc|Rep: Pantothenate kinase 2 - Arabidopsis thaliana (Mouse-ear cress), partial (56	49.18	1
Unknown	22.87	1
Unknown	18.57	1
gb|KT7C.108O12F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108O12, mR	33.11	1
gb|AGN_PNL224bf1_a9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	9412.87	1
Unknown	85.78	1
Unknown	21.38	1
tc|Rep: Ribosomal protein L11-like - Nicotiana tabacum (Common tobacco), compl	24.29	1
Unknown	39.01	1
Unknown	100.52	1
gb|EST_FLW001xi04f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	101.27	1
Unknown	162.45	1
gb|Nicotiana tabacum mRNA for chloroplast FtsZ-like protein (ftsZ gene), clone Fts	86.21	1
gb|AGN_RNC019xc18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	50.22	1
gb|KT7C.104N24F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104N24, mR	97.15	1
gb|CHO_SL014xb10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1243.11	1
gb|AGN_PNL221cr1_g7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	139.51	1
Unknown	953.02	1
tc|Rep: Probable pectate lyase P59 precursor - Solanum lycopersicum (Tomato) (L	11548.7	1
tc|Rep: MYB transcription factor MYB123 - Glycine max (Soybean), partial (29%) [T	25.88	1
tc|Rep: Protein kinase MK5 - Mesembryanthemum crystallinum (Common ice plant	272.63	1

tc|Rep: Chromosome undetermined scaffold_130, whole genome shotgun sequenc	30.16	1
gb|FS407656 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	2617.54	1
gb|TT-03_J18 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA sec	182.69	1
Unknown	54.96	1
gb|KT7C.109P07F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109P07, mR	113.91	1
gb|KT7C.106N03F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106N03, mR	17.63	1
Unknown	213.96	1
tc|Rep: Ultraviolet hypersensitive 1 - Arabidopsis thaliana (Mouse-ear cress), partia	41.06	1
gb|TT-12_L23 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	903.33	1
gb|AGN_RNC024xc18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	2212.81	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	24.66	1
Unknown	124.9	1
Unknown	104.16	1
tc|Rep: Potyviral helper component protease-interacting protein 2 - Solanum tuber	298.71	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	117.87	1
Unknown	4076.58	1
tc|Rep: Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vi	147.43	1
gb|AGN_RNC129xf15r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	21.09	1
tc|Rep: RPN9 - Nicotiana benthamiana, complete [TC56014]	43.38	1
Unknown	20.71	1
tc|Rep: Chromosome undetermined scaffold_186, whole genome shotgun sequenc	39.18	1
Unknown	104.24	1
gb|KT7C.110C06F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110C06, mR	26.76	1
tc|Rep: Callus-expressing factor - Nicotiana tabacum (Common tobacco), partial (5	179.93	1
gb|TT-34_J22 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	271.87	1
Unknown	3060.29	1
gb|KR2B.115K02F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115K02, m	109.89	1
tc|Rep: Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vi	21.59	1
gb|AGN_ELP007xo11f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	19.83	1
tc|Rep: RBX1-like protein - Petunia integrifolia subsp. inflata, complete [TC53068]	389.68	1
gb|CHO_SL005xb10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	106.62	1
gb|KP1B.109I14F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109I14, mR	17.24	1
gb|AM828261 DL, diurnal library Nicotiana tabacum cDNA clone nt005224018, mR	586.36	1
gb|EST_YP002xo15f1.ab1 EST_YP Nicotiana tabacum cDNA, mRNA sequence [EH61	35.52	1

gb|KN6B.115L21F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.115L21, m	414.31	1
Unknown	80.37	1
gb|KT7C.112F11F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112F11, mRN	1431.94	1
Unknown	41.94	1
gb|KP1B.102F06F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102F06, mF	1360.97	1
gb|Nicotiana tabacum osmotic stress-activated protein kinase (OSAK) mRNA, comp	112.34	1
tc|Rep: Regulator of gene silencing - Nicotiana tabacum (Common tobacco), partial	27.91	1
Unknown	163.15	1
gb|AGN_RPC015xn07f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	25.11	1
gb|KT7C.106N04F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106N04, mR	135.02	1
gb|AM838831 seedling library, SL Nicotiana tabacum cDNA clone nt002239060, mF	29.73	1
tc|Rep: Cytochrome b-c1 complex subunit Rieske-5, mitochondrial precursor - Nico	8162.59	1
gb|FS416760 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	112.52	1
gb|AGN_PNL221af1_e9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	879.45	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis v	69.5	1
tc|Rep: Small GTPase Rab2 - Nicotiana tabacum (Common tobacco), complete [TC5	349.89	1
tc|Rep: Ammonium transporter 1 member 1 - Solanum lycopersicum (Tomato) (Lyc	7860.53	1
Unknown	32.6	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	122.82	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	242.47	1
gb|AM799615 seedling library, SL Nicotiana tabacum cDNA clone nt002172018, mF	28.32	1
gb|KL4B.104L10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104L10, mRI	37.88	1
gb|BP534904 MAT005 Nicotiana tabacum cDNA clone BY34113, mRNA sequence [E	418.49	1
gb|KT7C.105B20F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105B20, mRI	69.92	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC31-2-190, cultivar Bright Yellow 2	51.34	1
gb|KG9B.103M20F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103M20,	801.21	1
gb|KT7C.112I04F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112I04, mRN	59.83	1
gb|AGN_RPC002xi06f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	181.42	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	44.22	1
tc|Rep: Thioredoxin peroxidase - Nicotiana tabacum (Common tobacco), complete	39.47	1
gb|TT-08_O21 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	58.84	1
tc|Rep: Actin - Nicotiana tabacum (Common tobacco), complete [TC53994]	5988.99	1
gb|AGN_RNC118xp08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	88.3	1
tc|Rep: 1-aminocyclopropane-1-carboxylate oxidase 3 - Petunia hybrida (Petunia),	28.75	1

gb|KL4B.107H24F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107H24, mR	21.96	1
gb|AM842133 COL, cold overnight library Nicotiana tabacum cDNA clone nt006001	31.02	1
Unknown	44.98	1
Unknown	180.28	1
gb|AM818734 COL, cold overnight library Nicotiana tabacum cDNA clone nt006087	98.89	1
gb|KG9B.104B06F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104B06, m	101.74	1
tc|Rep: Chromosome chr10 scaffold_179, whole genome shotgun sequence - Vitis v	131.35	1
Unknown	23.24	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	2343.99	1
tc|Rep: Sulfate adenylyltransferase - Solanum tuberosum (Potato), partial (37%) [TC	4138.03	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	379.33	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	101.11	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	60.85	1
gb|AGN_RNC021xj04f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	22.34	1
gb|KL4B.104G11F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104G11, mR	452.7	1
tc|Rep: Glutamyl-tRNA reductase 1, chloroplast precursor - Cucumis sativus (Cucum	144.16	1
tc|Rep: tetra-peptide repeat homeobox-like (TPRXL) on chromosome 3 - Homo sapi	47029.1	1
Unknown	504.63	1
tc|Rep: Chromosome chr2 scaffold_140, whole genome shotgun sequence - Vitis vi	133.88	1
tc|Rep: Expressed protein - Arabidopsis thaliana (Mouse-ear cress), partial (48%) [T	35.85	1
gb|KR3B.105P17F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.105P17, m	509.75	1
Unknown	18.84	1
gb|KN6B.101G11F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101G11, r	108.37	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	178.21	1
gb|KT7C.108D21F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108D21, mR	421.12	1
Unknown	21.34	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	1052.57	1
Unknown	63.83	1
Unknown	27.64	1
Unknown	24.67	1
gb|KR2B.107D18F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.107D18, m	107.05	1
gb|BP129711 MAT001 Nicotiana tabacum cDNA clone BY1592, mRNA sequence [BP	331.67	1
Unknown	379.49	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	300.88	1

tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	234.29	1
gb|KT7C.104G04F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104G04, mR	133.24	1
tc|Rep: Polyprotein - Glycine max (Soybean), partial (5%) [TC55953]	60.32	1
tc|Rep: Chromosome undetermined scaffold_87, whole genome shotgun sequence	22.57	1
Unknown	1170.75	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	188.8	1
gb|CHO_SL028xc16f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	81.27	1
gb|AGN_RNC108xa04f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	129.65	1
gb|TT-01_C07 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	271.34	1
gb|KF8C.104L11F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104L11, mRN	133.39	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	31.63	1
gb|CHO_SL014xo02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	134.88	1
gb|TT-38_P23 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	1124.61	1
tc|Rep: Cp protein - Celosia cristata, complete [TC69499]	26.51	1
gb|AGN_RNC007xa08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	56.64	1
Unknown	33.03	1
gb|Nicotiana tabacum Bax inhibitor 1 (BI-1) mRNA, complete cds [AF390556]	15529.75	1
gb|AM824341 seedling library, SL Nicotiana tabacum cDNA clone nt002316042, mR	3237.09	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	20.87	1
gb|AM806952 DL, diurnal library Nicotiana tabacum cDNA clone nt005191060, mR	29.59	1
gb|CHO_SL015xl08f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	1004.12	1
gb|KG9B.002G09F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002G09, n	635.65	1
Unknown	31.34	1
tc|Rep: Chromosome chr10 scaffold_179, whole genome shotgun sequence - Vitis v	186	1
gb|TT-10_O03 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	475.41	1
tc|Rep: Cellulose synthase catalytic subunit - Nicotiana alata (Winged tobacco) (Per	61.55	1
tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	32.32	1
tc|Rep: PH-regulated protein 1 - Candida dubliniensis (Yeast), partial (3%) [TC48134	47.28	1
gb|KN6B.103B01F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103B01, m	114.84	1
gb|KR3B.112G03F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112G03, m	59.49	1
Unknown	61.71	1
gb|KL4B.111O01F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111O01, mI	984.28	1
tc|Rep: Chorismate synthase 1, chloroplast precursor - Solanum lycopersicum (Tom	846.43	1
Unknown	27	1

gb|AGN_RPC005xm05f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	33.92	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	4176.64	1
gb|KF8B.200P07F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200P07, mRN	1590.67	1
Unknown	95.1	1
tc|Rep: Polyubiquitin - Thlaspi caerulescens (Alpine penny-cress) (Thlaspi calaminar	9677.81	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	9490.25	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	34.12	1
Unknown	197.47	1
tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin	458.24	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	178.65	1
gb|tbt_010277 Normalized Nicotiana tabacum cDNA library Nicotiana tabacum cDN	27.78	1
gb|Nicotiana tabacum ADP-glucose pyrophosphorylase small subunit (AGP) mRNA,	36.39	1
gb|KP1B.103L09F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103L09, mR	1102.53	1
Unknown	713.42	1
gb|KR3B.102L11F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.102L11, mR	111.26	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	1433.71	1
gb|KF8C.101E06F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101E06, mRN	38248.15	1
gb|KF8C.102F16F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102F16, mRN	710.03	1
gb|KF8C.102C04F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102C04, mRN	512.66	1
gb|KP1B.101G01F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101G01, m	4544.43	1
Unknown	530.55	1
gb|TT-41_F16 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA sec	1675.97	1
gb|KG9B.104B13F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104B13, m	1548.4	1
tc|Rep: Chromosome chr13 scaffold_45, whole genome shotgun sequence - Vitis vi	28.77	1
gb|TT-10_M22 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	85.23	1
Unknown	599.1	1
gb|AGN_RNC108xp19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	28.23	1
tc|Rep: Multisubunit Na+/H+ antiporter, MnhF subunit - Rickettsia bellii (strain RMI	120.9	1
gb|KR3B.102F03F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.102F03, mR	44.77	1
Unknown	55.41	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	200.41	1
gb|KR3B.111F02F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111F02, mR	18.5	1
Unknown	78.61	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	18382.85	1

tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	112.71	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	79.67	1
gb|AGN_RNC007xm13f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	85.11	1
tc|Rep: Chromosome undetermined scaffold_975, whole genome shotgun sequenc	22.1	1
Unknown	7162.46	1
Unknown	122.67	1
gb|KL5B.104M05F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.104M05,	54.2	1
tc|Rep: Protein transport protein SEC61 subunit gamma - Oryza sativa subsp. japon	2428.71	1
gb|CHO_SL008xp13f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	696.47	1
gb|TT-03_G14 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	247.85	1
tc|Rep: Class II ethylene responsive element binding factor-like protein - Nicotiana	826.3	1
tc|Rep: DNA-binding protein - Solanum lycopersicum (Tomato) (Lycopersicon escul	35.52	1
Unknown	1382.99	1
gb|TL13.101D12F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.101D12, mR	515.44	1
Unknown	5080.34	1
Unknown	201.27	1
gb|KF8C.103O22F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103O22, mR	23.72	1
gb|KR3B.106F03F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106F03, m	1293.43	1
Unknown	187.75	1
gb|TT-05_K06 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	17.34	1
tc|Rep: GRP-like protein 2 - Gossypium hirsutum (Upland cotton) (Gossypium mexi	1432.65	1
Unknown	818.54	1
gb|AGN_PNL223df1_d6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	648.7	1
gb|FS416181 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	64.96	1
gb|KR2B.001F05F.050815T7 KR2B Nicotiana tabacum cDNA clone KR2B.001F05, m	189.92	1
gb|AGN_RNC008xp03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1302.15	1
Unknown	24.79	1
Unknown	463.37	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	505.82	1
tc|Rep: Calmodulin cam-210 - Daucus carota (Carrot), complete [TC42995]	4445.4	1
tc|Rep: Pre-mRNA splicing factor-like protein - Solanum tuberosum (Potato), partia	321.08	1
gb|KR3B.110K20F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110K20, m	153.34	1
gb|KG9B.105D18F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105D18,	80.96	1
gb|AGN_RNC018xc01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	74.46	1

Unknown	429.08	1
gb|BL12.103A13F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.103A13, mR	129.84	1
gb|KL4B.100K05F.050922T7 KL4B Nicotiana tabacum cDNA clone KL4B.100K05, mR	30.2	1
Unknown	22.95	1
tc|Rep: ARF_AJECA ADP-RIBOSYLATION FACTOR - Emericella nidulans (Aspergillus r	26.96	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	185.95	1
gb|AGN_RNC211xf07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	8633.3	1
gb|KF8C.101J06F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101J06, mRN	975.16	1
Unknown	102.73	1
tc|Rep: Chromosome chr12 scaffold_103, whole genome shotgun sequence - Vitis	786.08	1
tc|Rep: S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC) [C	2981.58	1
tc|Rep: AT5g44790/K23L20_14 - Arabidopsis thaliana (Mouse-ear cress), partial (18	56.22	1
gb|ntsm26 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [E	454.79	1
gb|CHO_SL027xo13f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	24.34	1
gb|AGN_RNC023xc06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	476.08	1
tc|Rep: Calcineurin B-like protein 2 - Arabidopsis thaliana (Mouse-ear cress), partial	502.64	1
Unknown	18.57	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	63.94	1
Unknown	138.46	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	23	1
Unknown	1401.55	1
Unknown	58624.35	1
Unknown	47.97	1
tc|Rep: Transcription factor - Nicotiana tabacum (Common tobacco), partial (33%)	147.31	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	257.46	1
gb|KN6B.101I22F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101I22, mR	923.78	1
gb|TT-47_I07 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	27.85	1
gb|FS421124 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	635.81	1
Unknown	93.94	1
tc|Rep: Succinyl-CoA ligase alpha 2 subunit - Solanum lycopersicum (Tomato) (Lyco	504.97	1
tc|Rep: Chromosome chr1 scaffold_135, whole genome shotgun sequence - Vitis vi	10392.3	1
tc|Rep: MybSt1 - Solanum tuberosum (Potato), partial (96%) [TC51706]	415.67	1
gb|KP1B.105L07F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105L07, mR	465.31	1
Unknown	91.45	1

gb|AGN_ELP022xi18f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	119.01	1
Unknown	140.9	1
Unknown	210.75	1
tc|Rep: Cp protein - Celosia cristata, complete [TC45097]	47.9	1
gb|TT-13_P17 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	49394.65	1
gb|KT7C.109B04F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109B04, mR	94.77	1
gb|KP1B.001I21F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001I21, mR	29.23	1
gb|AGN_RPC014xn11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	108.41	1
Unknown	37102.7	1
Unknown	9473.72	1
gb|AGN_RNC023xp10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	63.79	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	57.54	1
Unknown	126.86	1
tc|Rep: Heat shock protein 90 - Nicotiana tabacum (Common tobacco), partial (29	270.7	1
Unknown	34.3	1
gb|KG9B.001J02F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001J02, m	26.98	1
tc|Rep: Gamma hydroxybutyrate dehydrogenase - Arabidopsis thaliana (Mouse-ear	218.72	1
gb|KF8C.101J01F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101J01, mRN	957.4	1
gb|KL4B.107P08F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107P08, mR	51.05	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	104.16	1
gb|KG9B.005E09F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005E09, m	390.63	1
gb|KF8C.103B23F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103B23, mR	375.43	1
gb|AM848538 DL, diurnal library Nicotiana tabacum cDNA clone nt005047013, mR	151.12	1
Unknown	27.07	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	61.78	1
gb|KP1B.107H01F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107H01, m	117.93	1
gb|CHO_SL008xf07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	787.62	1
gb|KL4B.107A04F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107A04, m	711.46	1
Unknown	23.3	1
gb|N.tabacum mRNA for delta proteasome subunit [Y09505]	103.03	1
gb|KF8C.103O13F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103O13, mR	20223.9	1
gb|KG9B.106J08F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106J08, m	151.62	1
gb|AGN_ELP017xo20f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	19.25	1
gb|KT7B.107I23F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107I23, mRN	88.28	1

gb|Tabacco Cab40 mRNA for major chlorophyll a [X52744]	26.99	1
tc|Rep: Histone H4 [Contains: Osteogenic growth peptide (OGP)]. - Rattus norvegicu	1522.46	1
gb|KG9B.101P01F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101P01, m	489.23	1
gb|KP1B.103O07F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103O07, m	141.24	1
tc|Rep: Chromosome undetermined scaffold_80, whole genome shotgun sequence	32.22	1
Unknown	23.01	1
gb|KG9B.001D20F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001D20, n	1442.74	1
tc|Rep: Ubiquitin carrier protein - Capsicum annuum (Bell pepper), complete [TC47	275.89	1
gb|KG9B.105D04F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105D04, n	1008.54	1
gb|KN6B.106O06F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.106O06, r	8017.56	1
tc|Rep: Chromosome chr9 scaffold_33, whole genome shotgun sequence - Vitis vin	3334.78	1
Unknown	2594.11	1
gb|KG9B.103N06F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103N06, r	68.61	1
gb|Nicotiana tabacum NtMFP mRNA for multifunctional protein, complete cds [AB	528.34	1
Unknown	18.46	1
Unknown	21.27	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	35.69	1
gb|KF8C.103C05F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103C05, mR	32.71	1
gb|N.tabacum mRNA for protein disulfide-isomerase precursor [Y11209]	3944.4	1
gb|KF8C.106M22F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106M22, m	71.72	1
Unknown	230.53	1
gb|AM822174 DL, diurnal library Nicotiana tabacum cDNA clone nt005006055, mR	56.9	1
gb|KP1B.108L23F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108L23, m	23.54	1
gb|KT7C.101I10F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.101I10, mRN	221.99	1
gb|KP1B.104H11F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104H11, m	65.53	1
tc|Rep: 60S ribosomal protein L6 - Mesembryanthemum crystallinum (Common ice	269.41	1
Unknown	150.83	1
gb|TOBESTR047H11 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	19162.2	1
tc|Rep: Light harvesting chlorophyll a/b-binding protein precursor - Nicotiana sylve	57.01	1
gb|KG9B.001E04F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001E04, m	1894.32	1
Unknown	71.58	1
Unknown	247.29	1
Unknown	4405.64	1
Unknown	413.85	1

gb|KR3B.102D10F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.102D10, m	404.61	1
gb|KR2B.001F05F.050815T7 KR2B Nicotiana tabacum cDNA clone KR2B.001F05, mR	219.17	1
Unknown	56.4	1
gb|KT7C.102C14F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102C14, mRN	26.07	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	32.26	1
gb|KN6B.113A16F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.113A16, n	481.04	1
Unknown	115.27	1
gb|BP129638 MAT001 Nicotiana tabacum cDNA clone BY1514, mRNA sequence [BP	78.8	1
gb|KP1B.104B06F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104B06, m	35.83	1
tc|Rep: Chromosome chr11 scaffold_56, whole genome shotgun sequence - Vitis vi	30.87	1
tc|Rep: Class II small heat shock protein Le-HSP17.6 - Solanum lycopersicum (Toma	64.91	1
tc|Rep: Ribosomal protein S8 - Vitis vinifera (Grape), partial (25%) [TC71744]	93.5	1
Unknown	40.74	1
gb|KG9B.001G19F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001G19, n	66.01	1
gb|KL4B.110O19F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110O19, m	48.79	1
gb|AGN_PNL212ar1_c9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	36.46	1
Unknown	19.19	1
gb|N.tabacum mRNA for c subunit of V-type ATPase (980 bp) [X95752]	2987.9	1
Unknown	88.71	1
gb|KL4B.103C18F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103C18, mR	184.89	1
gb|KG9B.004I10F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004I10, mR	142.13	1
tc|Rep: Chromosome chr14 scaffold_128, whole genome shotgun sequence - Vitis v	26.41	1
Unknown	653.96	1
gb|KP1B.109C10F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109C10, m	92.23	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	2542.39	1
gb|AGN_RPC025xn11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	152.49	1
gb|KF8C.103N19F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103N19, mR	56365.15	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	303.84	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	993.73	1
Unknown	1564.76	1
tc|Rep: Chromosome undetermined scaffold_142, whole genome shotgun sequenc	39.18	1
gb|KL5B.103C20F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.103C20, mR	21.17	1
tc|Rep: Histidinol dehydrogenase - Vitis vinifera (Grape), partial (54%) [TC43398]	139.29	1
gb|Nicotiana tabacum adenosine kinase isoform 2S mRNA, complete cds [AY69505	18212.3	1

gb|KR3B.109A07F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109A07, m	1648.72	1
Unknown	160.03	1
gb|AGN_RNC021xl08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1633.89	1
gb|TT-49_L17 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	730.64	1
gb|KG9B.003L23F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003L23, m	249.58	1
gb|KP1B.101N01F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101N01, m	153.28	1
tc|Rep: Uncharacterized protein At1g77540 - Arabidopsis thaliana (Mouse-ear cres	112.02	1
tc|Rep: S-adenosylmethionine synthetase - Nicotiana suaveolens, complete [TC435	15213.15	1
gb|Nicotiana tabacum NtHSF2 mRNA for heat shock factor, complete cds [AB01448	402.99	1
gb|KP1B.107C03F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107C03, m	248.55	1
gb|KP1B.113B24F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.113B24, m	128.44	1
gb|KF8C.108E12F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108E12, mR	23.83	1
Unknown	558.45	1
gb|BP129154 MAT001 Nicotiana tabacum cDNA clone BY986, mRNA sequence [BP	472.53	1
tc|Rep: 3'-5'-exoribonuclease/RNA binding-like protein - Solanum tuberosum (Pota	82.22	1
tc|Rep: Actin - Phalaenopsis hybrid cultivar, partial (39%) [TC69811]	19236.85	1
gb|TT-21_I16 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	26.07	1
Unknown	61.19	1
tc|Rep: Calcium-dependent protein kinase CPK1 adapter protein 2-like - Oryza sativ	259	1
gb|KN6B.102E19F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102E19, m	1031.88	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	59.66	1
gb|Nicotiana tabacum NtMKP1 mRNA for MAP kinase phosphatase, complete cds [	1992.54	1
tc|Rep: Chromosome undetermined scaffold_838, whole genome shotgun sequenc	241.6	1
tc|Rep: Plastidic ATP/ADP-transporter - Solanum tuberosum (Potato), partial (20%)	543.58	1
gb|Nicotiana tabacum ACS4 mRNA, partial cds [EU123523]	46.74	1
Unknown	25.18	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC4-12-390, cultivar Bright Yellow 2	37.39	1
gb|KP1B.101H09F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101H09, m	56.83	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	94.84	1
tc|Rep: ETAG-A3 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), par	43.78	1
gb|CHO_SL010xk15f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	9800.72	1
gb|KF8C.101K12F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101K12, mR	15771.5	1
tc|Rep: Mitochondrial phosphate transporter - Glycine max (Soybean), partial (44%	1407.04	1
gb|CHO_SL026xc11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	533.97	1

gb|KF8C.104J14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104J14, mRN	415.75	1
Unknown	8936.17	1
gb|TT-33_C07 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	40.78	1
gb|CHO_SL008xb09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	161.44	1
Unknown	29.57	1
gb|AGN_RNC020xd19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	64.92	1
tc|Rep: Chromosome chr9 scaffold_33, whole genome shotgun sequence - Vitis vin	9857.42	1
Unknown	29.97	1
tc|Rep: Chromosome undetermined scaffold_644, whole genome shotgun sequenc	1023.57	1
gb|KN6B.109N22F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.109N22, r	26.85	1
gb|FS429988 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	2848.11	1
gb|Nicotiana tabacum cytosolic acetoacetyl-coenzyme A thiolase (AACT1) mRNA, c	1533.76	1
gb|KN6B.105M19F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105M19,	773.99	1
gb|KL4B.101O19F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101O19, mI	826.36	1
gb|Nicotiana tabacum internal-motor kinesin mRNA, partial cds [DQ156499]	564.97	1
gb|KR2B.111N18F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.111N18, m	94.99	1
gb|TT-11_G14 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	63.3	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	75.79	1
gb|KF8C.104F18F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104F18, mRN	3458.81	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	86.59	1
gb|FS407121 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	2607.96	1
Unknown	61.58	1
Unknown	67.17	1
Unknown	375.82	1
Unknown	187.81	1
tc|Rep: Probable signal peptidase complex subunit 1 - Arabidopsis thaliana (Mouse-	3133.03	1
Unknown	24.16	1
Unknown	168.08	1
Unknown	25.01	1
tc|Rep: Delta-12 fatty acid desaturase - Borago officinalis (Bourrache) (Borage), con	71594.8	1
Unknown	79.37	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	945.2	1
Unknown	694.58	1
gb|FS389605 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	36.62	1

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<tr><td>gb|KP1B.102L07F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102L07, mR</td><td>552.61</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin</td><td>491.6</td><td>1</td></tr>
<tr><td>Unknown</td><td>199.15</td><td>1</td></tr>
<tr><td>Unknown</td><td>954.76</td><td>1</td></tr>
<tr><td>gb|KT7C.104B18F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104B18, mR</td><td>30.81</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi</td><td>31.48</td><td>1</td></tr>
<tr><td>gb|EST_CSP008xl12f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH</td><td>632.36</td><td>1</td></tr>
<tr><td>Unknown</td><td>1082.3</td><td>1</td></tr>
<tr><td>Unknown</td><td>32.42</td><td>1</td></tr>
<tr><td>gb|TT-32_N03 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F</td><td>101.34</td><td>1</td></tr>
<tr><td>gb|KF8C.104P10F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104P10, mR</td><td>560.2</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi</td><td>643.26</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin</td><td>914.88</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin</td><td>153.14</td><td>1</td></tr>
<tr><td>gb|AGN_PNL207dr1_h7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA</td><td>32.72</td><td>1</td></tr>
<tr><td>gb|CHO_SL024xo11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6</td><td>2066.93</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin</td><td>1563</td><td>1</td></tr>
<tr><td>gb|KG9B.004P01F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004P01, m</td><td>923.83</td><td>1</td></tr>
<tr><td>tc|Rep: Dihydrolipoyl dehydrogenase - Solanum lycopersicum (Tomato) (Lycopersic</td><td>2798.52</td><td>1</td></tr>
<tr><td>gb|AGN_ELP022xh17f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence</td><td>167.84</td><td>1</td></tr>
<tr><td>gb|KF8B.200N06F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200N06, mR</td><td>1170.66</td><td>1</td></tr>
<tr><td>Unknown</td><td>163.61</td><td>1</td></tr>
<tr><td>gb|KT7C.106I01F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106I01, mRN</td><td>20.72</td><td>1</td></tr>
<tr><td>tc|Rep: Thioredoxin - Limonium bicolor, partial (64%) [TC42824]</td><td>30.77</td><td>1</td></tr>
<tr><td>gb|TT-47_E16 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence</td><td>202.28</td><td>1</td></tr>
<tr><td>gb|AGN_RPC014xb03f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc</td><td>108.79</td><td>1</td></tr>
<tr><td>Unknown</td><td>212.6</td><td>1</td></tr>
<tr><td>Unknown</td><td>526.42</td><td>1</td></tr>
<tr><td>tc|Rep: Probable phospholipid hydroperoxide glutathione peroxidase - Nicotiana sy</td><td>4095.56</td><td>1</td></tr>
<tr><td>Unknown</td><td>382.11</td><td>1</td></tr>
<tr><td>Unknown</td><td>27.25</td><td>1</td></tr>
<tr><td>Unknown</td><td>2887.62</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin</td><td>21650.75</td><td>1</td></tr>
</table>

tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	31.03	1
tc|Rep: ORMDL family protein-like - Oryza sativa subsp. japonica (Rice), partial (97	69.52	1
tc|Rep: Thioredoxin h-like protein - Nicotiana tabacum (Common tobacco), comple	623.67	1
tc|Rep: 14-3-3-like protein C - Nicotiana tabacum (Common tobacco), complete [T	20127.4	1
Unknown	382.98	1
gb|FS393322 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	842.41	1
tc|Rep: Arginase 2 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), c	124.24	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	98.14	1
tc|Rep: Chromosome chr4 scaffold_205, whole genome shotgun sequence - Vitis vi	28.62	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	138.39	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	81.78	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	80.47	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	142.43	1
gb|KF8C.101G03F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101G03, mR	661.21	1
tc|Rep: Chromosome chr10 scaffold_43, whole genome shotgun sequence - Vitis vi	30.46	1
Unknown	452.23	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	217.56	1
gb|TT-07_L06 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	23.04	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	124.47	1
tc|Rep: Ubiquitin-conjugating enzyme E2-17 kDa - Solanum lycopersicum (Tomato)	4312.65	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	107.09	1
gb|AM848505 seedling library, SL Nicotiana tabacum cDNA clone nt002165079, m	87.26	1
Unknown	11095.2	1
gb|AGN_ELP008xd10f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	506.76	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	512.12	1
Unknown	1185.07	1
gb|AGN_ELP023xe14f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	58.82	1
gb|KG9B.106K09F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106K09, m	857.53	1
gb|KL5B.114N09F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.114N09, m	215.59	1
Unknown	137.82	1
gb|AGN_RPC004xc02f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	28.23	1
Unknown	117.9	1
tc|Rep: Expressed protein - Arabidopsis thaliana (Mouse-ear cress), partial (59%) [T	50.85	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	264.75	1

Unknown	25.81	1
gb|KL4B.105B13F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105B13, mR	26.99	1
gb|KP1B.104N22F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104N22, m	564.3	1
Unknown	77.11	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	60.17	1
gb|KF8B.200H02F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200H02, mR	24418.2	1
Unknown	26.26	1
tc|Rep: Calcium-dependent protein kinase 1 - Datura metel (Devil's trumpet) (Datu	17.81	1
Unknown	26.53	1
Unknown	37.95	1
tc|Rep: Actin-7 - Arabidopsis thaliana (Mouse-ear cress), complete [TC40665]	50.63	1
Unknown	96.64	1
Unknown	184.32	1
tc|Rep: Ubiquitin - Medicago truncatula (Barrel medic), partial (79%) [TC50721]	10684.05	1
Unknown	21.72	1
gb|FS409048 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	25.54	1
tc|LERYGTOM5 L.esculentum (rY mutant) GTOM5 mRNA for mutant phytoene synt	21.92	1
Unknown	180.6	1
gb|BP131358 MAT001 Nicotiana tabacum cDNA clone BY3395, mRNA sequence [B	31.09	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	158.64	1
gb|EST_FLW001xo10f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	586.59	1
gb|AGN_RNC014xk22f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	39.34	1
tc|Rep: Predicted protein - Emericella nidulans (Aspergillus nidulans), partial (5%) [	86.74	1
Unknown	229.65	1
gb|KP1B.101F06F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101F06, m	67.03	1
tc|Rep: Chromosome chr1 scaffold_135, whole genome shotgun sequence - Vitis vi	35.57	1
gb|KF8C.104F18F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104F18, mRN	3236.85	1
tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin	3332.82	1
Unknown	34.32	1
gb|KL4B.101J21F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101J21, mR	32.08	1
gb|KG9B.003H04F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003H04,	28.87	1
tc|Rep: Chalcone--flavonone isomerase - Ipomoea purpurea (Common morning glo	102.97	1
tc|Rep: Thylakoid-bound ascorbate peroxidase - Nicotiana tabacum (Common toba	19.13	1
tc|Rep: Maturase K - Nicotiana glutinosa (Tobacco), partial (64%) [TC75865]	30.51	1

gb|CHO_SL014xb10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	998.79	1
Unknown	125.71	1
Unknown	21.37	1
Unknown	513.02	1
gb|CHO_SL026xc04f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	819.88	1
gb|AGN_RPC022xo13f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	36.81	1
Unknown	738.09	1
gb|KN6B.104I12F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104I12, m	398.45	1
gb|KL5B.104G13F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.104G13, m	266.21	1
gb|AGN_RPC018xd15f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	27.74	1
gb|FS429988 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	1818.06	1
Unknown	367.77	1
tc|Rep: Uncharacterized protein At1g04960.2 - Arabidopsis thaliana (Mouse-ear cr	44.31	1
Unknown	37.35	1
Unknown	22.12	1
Unknown	34.83	1
gb|AM817974 seedling library, SL Nicotiana tabacum cDNA clone nt002102049, m	203.02	1
gb|AGN_RPC002xf04f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	37.09	1
gb|TT-03_L03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	26.72	1
gb|Nicotiana tabacum poly(A)-binding protein (PABP) mRNA, complete cds [AF190	11612.2	1
Unknown	39.95	1
tc|Rep: Cyc07 - Nicotiana tabacum (Common tobacco), partial (48%) [TC73875]	255.34	1
gb|KL4B.107J08F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107J08, mR	40.37	1
tc|Rep: Chromosome chr11 scaffold_170, whole genome shotgun sequence - Vitis	987.66	1
Unknown	104.67	1
gb|CHO_SL022xd02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	201.79	1
gb|KR3B.107D17F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.107D17, m	54.02	1
gb|TT-33_J14 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	3202.52	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	284.64	1
gb|KG9B.001A06F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001A06,	24.23	1
Unknown	24.8	1
gb|KF8C.110H03F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110H03, mR	19784.4	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	134.31	1
tc|Rep: BcDNA.GH02712 - Drosophila melanogaster (Fruit fly), partial (7%) [TC5214	48.15	1

tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	32.54	1
Unknown	61.1	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT4-11-350, cultivar Bright Yellow 2	30.39	1
Unknown	18.65	1
Unknown	23.49	1
gb|TT-07_L06 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	81.95	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, complete [TC4768	45.41	1
gb|FS381087 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	2922.27	1
gb|AM796827 DL, diurnal library Nicotiana tabacum cDNA clone nt005216065, mR	21.15	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	126.62	1
Unknown	26.52	1
gb|KG9B.106I24F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106I24, m	191.45	1
tc|Rep: Chromosome chr16 scaffold_94, whole genome shotgun sequence - Vitis vi	18.37	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (48%) [TC6	18500.15	1
Unknown	2750.77	1
gb|BP526533 MAT001 Nicotiana tabacum cDNA clone BY11263, mRNA sequence [	556.26	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	198.6	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	29.93	1
Unknown	93.02	1
tc|Rep: Chromosome chr13 scaffold_152, whole genome shotgun sequence - Vitis	723.46	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	187.8	1
gb|KN6B.105A24F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105A24, n	277.13	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	449.37	1
gb|AGN_PNL205cr1_e5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	100.44	1
Unknown	88.08	1
Unknown	104.21	1
gb|AGN_PNL228bf1_d5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	9919.17	1
Unknown	42.45	1
tc|Rep: Chromosome chr1 scaffold_136, whole genome shotgun sequence - Vitis vi	2545.85	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	18.18	1
tc|Rep: NAD-dependent malic enzyme 62 kDa isoform, mitochondrial precursor - S	36.5	1
tc|Rep: Glucose-6-phosphate/phosphate translocator 1, chloroplast precursor - Ara	215.47	1
gb|AGN_RPC018xh17f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	194.57	1
tc|Rep: ATPase - Camellia sinensis (Tea), complete [TC71603]	1525.01	1

Unknown	72.67	1
Unknown	41.27	1
Unknown	22.32	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	201.81	1
gb|CHO_SL014xb22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	3288.78	1
tc|Rep: Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vi	47.84	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	794.67	1
gb|Nicotiana tabacum cultivar Havana SR1 cytosine-5-methyltransferase (MET1) m	21.03	1
gb|KP1B.037G07F.050623T7 KP1B Nicotiana tabacum cDNA clone KP1B.037G07, m	21.81	1
tc|Rep: Enoyl-CoA hydratase/isomerase - Medicago truncatula (Barrel medic), parti	1064.82	1
gb|AGN_ELP025xp16f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	238.82	1
gb|KT7C.112H06F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112H06, mR	1903.76	1
Unknown	28.86	1
gb|KN6B.106O01F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.106O01,	23.19	1
tc|Rep: Predicted protein - Chlamydomonas reinhardtii, partial (9%) [TC58990]	31.24	1
tc|Rep: F17F8.6 - Arabidopsis thaliana (Mouse-ear cress), partial (68%) [TC47498]	95.26	1
gb|N.tabacum mRNA ap24 [X65700]	18.07	1
gb|AGN_ELP007xh11f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	20.94	1
tc|Rep: Oligopeptidase A - Medicago truncatula (Barrel medic), partial (98%) [TC46	22.75	1
tc|Rep: Histone H3 - Nematostella vectensis (Starlet sea anemone), partial (97%) [T	28.02	1
tc|Rep: Chromosome chr16 scaffold_189, whole genome shotgun sequence - Vitis	433.72	1
Unknown	390.84	1
gb|KL4B.112G20F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112G20, m	38.36	1
tc|Rep: Chromosome undetermined scaffold_87, whole genome shotgun sequence	274.56	1
gb|KG9B.003D22F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003D22, n	532.79	1
gb|KL4B.104C12F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104C12, mR	511.6	1
gb|AGN_RNC024xc06r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	28.83	1
gb|AGN_RNC110xf13f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	28.07	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (6%) [TC65	28.94	1
gb|TT-28_H09 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	222.09	1
gb|KL4B.109E12F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.109E12, mR	20.58	1
gb|CHO_SL015xe18f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	25.96	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	207.88	1
Unknown	4360.61	1

tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	151.36	1
tc|Rep: 60S ribosomal protein L34 - Nicotiana tabacum (Common tobacco), comple	118.03	1
Unknown	80.72	1
tc|Rep: Transcription factor bZIP63 - Glycine max (Soybean), partial (41%) [TC7400	133.84	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	412.84	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	88.34	1
Unknown	761.26	1
Unknown	6306.85	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	244.16	1
gb|KL4B.105I22F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105I22, mRN	62.2	1
tc|Rep: Chromosome undetermined scaffold_174, whole genome shotgun sequenc	520.11	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	1057.45	1
gb|N.tabacum mRNA for phosphoglycerate kinase (chloroplast isoenzyme) [Z48977	43.69	1
gb|EST_FLW001xi17f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [EH	404.01	1
Unknown	222.13	1
Unknown	206.98	1
gb|AGN_RPC023xa05f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	225.12	1
tc|Rep: Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vi	228.33	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	185.45	1
gb|KL4B.104M07F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104M07, m	21.51	1
Unknown	22.53	1
gb|KF8B.200A23F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200A23, mR	57.2	1
gb|KG9B.102G04F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102G04, m	62.17	1
gb|AGN_ELP024xk02f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	58.54	1
gb|KT7C.113I24F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.113I24, mRN	165.39	1
Unknown	20.24	1
Unknown	31.15	1
gb|N.tabacum mRNA for inorganic pyrophosphatase (TVP5clone) [X77915]	253.38	1
Unknown	43.63	1
gb|KL4B.107E16F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107E16, mR	9523.83	1
tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	258.03	1
gb|KN6B.101P09F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101P09, m	1030.87	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	950.71	1
gb|CHO_SL005xm05f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	1414.11	1

gb|AGN_RPC018xe15f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	42.78	1
tc|Rep: Small GTPase Rab2 - Capsicum annuum (Bell pepper), complete [TC41836]	2855.41	1
gb|AGN_ELP014xc05f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	30.77	1
Unknown	23.05	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	85.8	1
gb|BP528616 MAT001 Nicotiana tabacum cDNA clone BY13472, mRNA sequence [	29.66	1
gb|KF8B.100M23F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100M23, m	84.33	1
tc|Rep: Ankyrin repeat-rich protein - Solanum tuberosum (Potato), partial (34%) [T	22.94	1
tc|Rep: Chromosome chr5 scaffold_58, whole genome shotgun sequence - Vitis vin	352.34	1
Unknown	712.38	1
gb|AGN_RPC025xl04f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	24.69	1
tc|Rep: Chromosome chr10 scaffold_81, whole genome shotgun sequence - Vitis vi	409.63	1
Unknown	19.12	1
tc|Rep: Chromosome undetermined scaffold_525, whole genome shotgun sequenc	122.37	1
gb|AGN_RPC020xb19f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	732.18	1
Unknown	18.26	1
gb|N.tabacum mRNA for LIM-domain protein [Y11002]	501.86	1
Unknown	252.51	1
Unknown	583.58	1
gb|KT7C.108F18F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108F18, mR	871.91	1
tc|Rep: 40S ribosomal protein S15-like - Solanum tuberosum (Potato), complete [T	570.48	1
gb|TOBESTR050A01 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	839.5	1
Unknown	1190.43	1
tc|Rep: Os07g0680900 protein - Oryza sativa subsp. japonica (Rice), partial (67%) [T	53.72	1
gb|TT-49_J01 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	622.36	1
Unknown	63.38	1
gb|KG9B.003G13F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003G13,	26.28	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	141.48	1
gb|KR3B.110O13F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110O13,	89.91	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT41-4-210, cultivar Bright Yellow 2	40.4	1
gb|KG9B.106M11F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106M11,	211.38	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	29.2	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	687.89	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	71.95	1

gb|N.tabacum repeat region (Eco4) [X68590]	39.11	1
tc|Rep: Ly200 protein - Capsicum annuum (Bell pepper), complete [TC54024]	22.91	1
tc|Rep: Chromosome chr11 scaffold_177, whole genome shotgun sequence - Vitis	63.13	1
gb|KN6B.105M11F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105M11,	2909.02	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	478.85	1
Unknown	26.64	1
tc|Rep: helicase domain-containing protein - Arabidopsis thaliana, partial (7%) [TC6	28.31	1
Unknown	92.69	1
Unknown	184.16	1
gb|KF8B.100C21F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100C21, mR	1347.5	1
gb|KG9B.005C17F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005C17, m	151.47	1
tc|Rep: NADH:cytochrome b5 reductase - Vernicia fordii (Tung) (Aleurites fordii), c	106.16	1
Unknown	142.83	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	84.21	1
tc|Rep: Chromosome undetermined scaffold_171, whole genome shotgun sequenc	165.24	1
gb|KT7C.106N04F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106N04, mR	35.7	1
gb|KL4B.106I18F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106I18, mR	23.86	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	17.94	1
gb|TT-20_G03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	2592.46	1
Unknown	17.79	1
gb|AGN_RPC021xo04f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	3330.38	1
gb|KR2B.002K11F.051019T7 KR2B Nicotiana tabacum cDNA clone KR2B.002K11, m	118.52	1
gb|KF8C.103D11F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103D11, mR	648.15	1
gb|Nicotiana tabacum GUT15 mRNA, complete cds [U84972]	3200.72	1
gb|CHO_SL015xf03f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	438	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	48.77	1
gb|TT-50_E13 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	36.27	1
tc|Rep: Chromosome chr3 scaffold_95, whole genome shotgun sequence - Vitis vin	2639.48	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	1445.07	1
gb|AGN_PNL201af1_d3.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	34472.8	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	2722.59	1
Unknown	103.25	1
gb|KL4B.111C19F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111C19, mR	20.5	1
Unknown	28.52	1

tc|Rep: Ribosomal protein S27 - Vitis vinifera (Grape), complete [TC56463]	52.21	1
gb|CHO_SL028xe08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	25.36	1
tc|Rep: 60S ribosomal protein L34 - Nicotiana tabacum (Common tobacco), partial	155.37	1
gb|N.tabacum NeIF-4A9 mRNA [X79135]	57.9	1
Unknown	128.32	1
tc|Rep: Ferrochelatase - Vitis vinifera (Grape), partial (42%) [TC54815]	30.89	1
tc|Rep: AT3g06540/F5E6_13 - Arabidopsis thaliana (Mouse-ear cress), partial (37%)	466.92	1
Unknown	411.58	1
Unknown	30.2	1
Unknown	21.33	1
tc|Rep: Chromosome undetermined scaffold_1268, whole genome shotgun sequen	138.59	1
Unknown	9444.84	1
gb|TT-29_M10 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA se	22.25	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	10199.75	1
Unknown	30.26	1
gb|KF8C.110M11F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110M11, m	101.86	1
gb|KT7C.109E03F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109E03, mR	937.6	1
gb|KG9B.003H12F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003H12,	142.29	1
gb|Nicotiana tabacum mRNA for carbamoyl phosphate synthase small subunit [AJ3	434.26	1
Unknown	20.87	1
gb|KL5B.118E14F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.118E14, mR	456.45	1
gb|Nicotiana tabacum calcium-dependent protein kinase CPK4 mRNA, complete cd	1328.68	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	54.19	1
gb|AGN_ELP009xm05f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequenc	56.05	1
gb|AGN_ELP012xm10f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequenc	95.37	1
gb|KL4B.105P04F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105P04, mR	107.87	1
gb|KP1B.102C22F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102C22, m	62.37	1
Unknown	17.19	1
Unknown	184.83	1
gb|KG9B.105K12F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105K12, m	250.1	1
gb|AM801363 seedling library, SL Nicotiana tabacum cDNA clone nt002027020, m	256.34	1
Unknown	50.01	1
tc|Rep: Ethylene-responsive transcription factor 3 - Nicotiana tabacum (Common t	7308.04	1
gb|KL4B.105E10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105E10, mR	60.15	1

Unknown	51.66	1
tc|Rep: Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A (PNGase A)	37.27	1
Unknown	29.33	1
gb|EST_FLW005xi04f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [EH	9806.58	1
tc|Rep: Aldose 1-epimerase-like protein - Arabidopsis thaliana (Mouse-ear cress), p	20.6	1
Unknown	1683.85	1
tc|Rep: Eukaryotic translation initiation factor 5A-3 - Solanum tuberosum (Potato),	7317.95	1
Unknown	71.46	1
Unknown	25.34	1
Unknown	188.47	1
gb|AM791671 DL, diurnal library Nicotiana tabacum cDNA clone nt005009046, mR	23.75	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	3503.91	1
gb|AGN_RNC211xp11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	34.14	1
tc|Rep: U1snRNP-specific protein, U1A - Solanum tuberosum (Potato), partial (98%	89.48	1
Unknown	10027.7	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	344.94	1
Unknown	4676.01	1
tc|Rep: Pyruvate kinase - Oryza sativa subsp. japonica (Rice), partial (28%) [TC7447	254.42	1
Unknown	31.85	1
tc|Rep: Prolyl 4-hydroxylase - Dianthus caryophyllus (Carnation) (Clove pink), partia	93.94	1
Unknown	184.49	1
gb|AGN_RNC125xp24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	535.25	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	47.51	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	181.27	1
gb|KL4B.105O01F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105O01, m	589.53	1
Unknown	87.27	1
tc|Rep: Vacuolar ATP synthase catalytic subunit A - Daucus carota (Carrot), partial (	1407.6	1
gb|AM793907 seedling library, SL Nicotiana tabacum cDNA clone nt002270041, m	43.35	1
Unknown	26.87	1
Unknown	229.06	1
gb|CHO_SL024xi23f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1127.7	1
tc|Rep: 40S ribosomal protein S23 - Fragaria ananassa (Strawberry), complete [TC4	60.39	1
gb|KG9B.106A07F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106A07,	57.54	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	258.47	1

tc|Rep: Malate dehydrogenase - Solanum tuberosum (Potato), partial (62%) [TC454	143.82	1
gb|KL4B.101K11F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101K11, mR	573.94	1
gb|KT7C.108A21F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108A21, mR	134.9	1
Unknown	39.61	1
gb|TT-05_D19 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	3050.42	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	135.24	1
gb|AM789234 seedling library, SL Nicotiana tabacum cDNA clone nt002190071, m	5756.97	1
tc|Rep: Expressed protein - Arabidopsis thaliana (Mouse-ear cress), partial (5%) [TC	759.19	1
gb|BP129233 MAT001 Nicotiana tabacum cDNA clone BY1074, mRNA sequence [B	2097.46	1
gb|Nicotiana tabacum A26 mRNA for NtEPc-like protein, complete cds [AB032528]	21.39	1
gb|KN6B.102G19F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102G19, r	520.48	1
tc|Rep: Cystathionine gamma-synthase isoform 2 - Solanum tuberosum (Potato), p	7966.72	1
tc|Rep: Ketol-acid reductoisomerase, chloroplast precursor - Spinacia oleracea (Spi	337.91	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	494.84	1
gb|KL4B.107L17F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107L17, mR	570	1
Unknown	78.99	1
gb|KF8B.100E05F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100E05, mR	22.98	1
gb|KF8C.109I04F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109I04, mRN	31.05	1
gb|KP1B.102O01F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102O01, m	90.96	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	684.87	1
gb|Nicotiana tabacum partial mRNA for hypothetical protein, clone PBF80non [AJ3	47.7	1
tc|Rep: Chromosome undetermined scaffold_171, whole genome shotgun sequenc	21.03	1
gb|TOBESTR033H07 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	51.16	1
Unknown	19.48	1
gb|TT-09_I07 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	21.06	1
gb|Nicotiana tabacum mRNA for protein phosphatase 2A catalytic subunit [AJ0074	721.88	1
gb|KL4B.103B21F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103B21, mR	1040.12	1
gb|KN6B.105F14F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105F14, m	53.52	1
gb|KP1B.101G01F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101G01, m	7202.28	1
gb|AGN_RNC029xc12r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	22.14	1
gb|Nicotiana tabacum NtFAD3 mRNA for microsomal omega-3 acid desaturase, co	41833.85	1
gb|AGN_RNC024xc10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	77.83	1
Unknown	70.83	1
Unknown	35.37	1

Unknown	230.4	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	114.25	1
Unknown	375.43	1
gb|KF8B.100O01F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100O01, mR	519.19	1
gb|CHO_SL023xh08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	84.55	1
gb|KF8C.105P14F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105P14, mR	41.4	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	41.01	1
Unknown	251.9	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	107.99	1
gb|AM829948 seedling library, SL Nicotiana tabacum cDNA clone nt002139094, m	174.58	1
tc|Rep: Chromosome chr10 scaffold_179, whole genome shotgun sequence - Vitis	19.85	1
tc|Rep: 60S ribosomal protein L7A-like protein - Solanum tuberosum (Potato), com	30.23	1
gb|KN6B.101A21F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101A21,	35.23	1
gb|KG9B.103N02F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103N02,	673.11	1
tc|Rep: Ribosomal protein PETRP - Capsicum annuum (Bell pepper), complete [TC4	132.81	1
Unknown	84.19	1
gb|TT-17_E04 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	2907.79	1
gb|BP129575 MAT001 Nicotiana tabacum cDNA clone BY1446, mRNA sequence [B	23.32	1
Unknown	96.75	1
gb|AGN_RNC013xb13f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	31.92	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	115.76	1
tc|Rep: 40S ribosomal protein S4 - Solanum tuberosum (Potato), complete [TC4076	129.89	1
gb|TT-47_D22 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	23.53	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	254.63	1
tc|Rep: Chromosome undetermined scaffold_448, whole genome shotgun sequenc	84.96	1
gb|AGN_RPC014xk09f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	33.01	1
Unknown	270.7	1
tc|Rep: PSI-H precursor - Nicotiana sylvestris (Wood tobacco), partial (50%) [TC555	29.75	1
gb|KF8B.202H20F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202H20, mR	45.2	1
tc|Rep: Expressed protein - Arabidopsis thaliana (Mouse-ear cress), partial (17%) [T	36.95	1
gb|TT-23_F13 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	1420.32	1
gb|TT-03_G14 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	263.65	1
Unknown	32.44	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	99.24	1

tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	46.57	1
Unknown	101.53	1
gb|KG9B.002F23F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002F23, m	104.54	1
Unknown	38.18	1
Unknown	31.26	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	186.96	1
gb|KR2B.109N16F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.109N16, m	260.23	1
gb|TT-06_D09 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	18.7	1
gb|KL4B.108E19F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108E19, mR	30.27	1
tc|Rep: Chromosome undetermined scaffold_91, whole genome shotgun sequence	36.26	1
gb|KT7C.109M19F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109M19, m	1315.22	1
Unknown	85.6	1
gb|AGN_RNC008xp03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1199.03	1
gb|BP533801 MAT005 Nicotiana tabacum cDNA clone BY31121, mRNA sequence [E	254.2	1
gb|AGN_RPC010xa17f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	253.09	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	18.68	1
gb|KG9B.001L02F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001L02, m	194.96	1
gb|AM827696 seedling library, SL Nicotiana tabacum cDNA clone nt002053082, mR	67.88	1
gb|CHO_SL008xi09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	350.39	1
tc|Rep: Urate oxidase - Nicotiana tabacum (Common tobacco), complete [TC40906	28.16	1
gb|AGN_RNC003xe02f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	31.96	1
Unknown	23.79	1
Unknown	19.52	1
tc|Rep: Small subunit ribosomal protein - Berberis thunbergii (Japanese barberry),	520.04	1
tc|Rep: Sulfate adenylyltransferase - Solanum tuberosum (Potato), partial (37%) [T	5268.74	1
gb|AGN_RNC012xg16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	111.45	1
Unknown	103.93	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	3314.99	1
gb|AGN_RPC006xp21f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	26.21	1
gb|CHO_SL006xd12f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	18055.15	1
Unknown	94.41	1
gb|Nicotiana tabacum peptidyl-prolyl cis [EF051139]	36.62	1
gb|KG9B.104B16F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104B16, m	51.07	1
Unknown	21.2	1

gb|AGN_RNC029xc03r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	17.77	1
gb|BP133207 MAT001 Nicotiana tabacum cDNA clone BY5446, mRNA sequence [B	112.93	1
gb|KT7B.100K11F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100K11, mR	511.52	1
tc|Rep: Chromosome chr4 scaffold_83, whole genome shotgun sequence - Vitis vin	62.49	1
gb|AM783661 seedling library, SL Nicotiana tabacum cDNA clone nt002328038, m	147.62	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	27.41	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	1364.1	1
Unknown	746.77	1
Unknown	25.41	1
tc|Rep: 60S ribosomal protein L19 - Capsicum annuum (Bell pepper), partial (80%) [	155.2	1
Unknown	39.21	1
Unknown	845.67	1
gb|KP1B.103P19F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103P19, m	24.15	1
Unknown	57559.3	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	28.08	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	34.65	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT22-1-195, cultivar Bright Yellow 2	156.73	1
gb|KT7C.110P12F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110P12, mR	2784.58	1
Unknown	22.31	1
Unknown	516.04	1
tc|Rep: Thylakoid lumenal 15.0 kDa protein 2, chloroplast precursor - Arabidopsis t	80.09	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	63.43	1
gb|AGN_PNL205cf1_b2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	18.42	1
gb|AGN_RPC015xi11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	25.08	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	1585.68	1
Unknown	60.25	1
Unknown	1466.48	1
Unknown	24.9	1
Unknown	49.38	1
gb|ntsm8 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [EB	108.14	1
gb|KG9B.101P14F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101P14, m	19.54	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	28.82	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	40.87	1
gb|AGN_PNL215dr1_f7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	61	1

gb|AM835641 COL, cold overnight library Nicotiana tabacum cDNA clone nt006016	29.4	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	107.42	1
Unknown	33.45	1
Unknown	14869.2	1
gb|AM845282 seedling library, SL Nicotiana tabacum cDNA clone nt002332051, mR	935.96	1
gb|AGN_RPC020xa07f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	182.18	1
Unknown	22.52	1
gb|KR3B.113P03F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.113P03, m	1211.86	1
Unknown	134.1	1
gb|AGN_RNC007xl24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	295.29	1
gb|KT7C.110O11F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110O11, mR	5186.49	1
gb|CHO_SL016xh03f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	3849	1
gb|TT-36_P10 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	30.64	1
tc|Rep: 14-3-3 protein - Nicotiana tabacum (Common tobacco), partial (98%) [TC44	52.53	1
tc|Rep: Chromosome chr14 scaffold_26, whole genome shotgun sequence - Vitis vi	21.81	1
Unknown	1056.09	1
gb|TT-38_K22 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	485.73	1
gb|KT7C.112M02F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112M02, m	796.72	1
gb|TT-30_F03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	165.16	1
gb|Nicotiana tabacum plastid phosphate [U66402]	199.61	1
tc|Rep: Like-Sm ribonucleoprotein-related, core - Medicago truncatula (Barrel med	30.07	1
gb|KT7C.102F13F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102F13, mRN	262.69	1
Unknown	107.96	1
gb|KG9B.104O21F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104O21,	24.7	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	5394.17	1
tc|Rep: DnaJ-like protein isoform - Solanum phureja, partial (75%) [TC43875]	395.95	1
gb|KN6B.105G06F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105G06,	211.11	1
tc|Rep: 1-acyl-sn-glycerol-3-phosphate acyltransferase - Prunus dulcis (Almond) (Pr	3995.65	1
gb|TL13.106B21F.060315T7 TL13 Nicotiana tabacum cDNA clone TL13.106B21, mR	159.4	1
tc|Rep: Peroxidase - Nicotiana tabacum (Common tobacco), partial (65%) [TC69233	44.66	1
gb|FS425927 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	16986.4	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	134.74	1
tc|AAD27719.1 - Arabidopsis thaliana (Mouse-ear cress), partial (46%) [TC55496]	87.97	1
gb|KG9B.005F14F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005F14, m	29.3	1

gb|KF8B.200P08F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200P08, mRN	28199.55	1
Unknown	514.49	1
gb|CHO_SL022xi08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	194.49	1
Unknown	57.53	1
gb|KP1B.103B19F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103B19, mR	103.82	1
tc|Rep: Chromosome chr18 scaffold_24, whole genome shotgun sequence - Vitis vi	60.37	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	35.96	1
gb|KF8C.102P14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102P14, mRN	24.35	1
gb|TT-06_E05 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	47.97	1
gb|CHO_SL022xi08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	224.94	1
gb|KG9B.103I21F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103I21, mR	39.51	1
gb|AGN_RPC018xk07f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	18.94	1
gb|CHO_SL007xo02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	972.24	1
Unknown	122.94	1
tc|Rep: Chromosome undetermined scaffold_69, whole genome shotgun sequence	10669.2	1
gb|CHO_SL002xf06f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	24.71	1
gb|Nicotiana tabacum mRNA for peroxidase, complete cds, clone:NTPXC8.1 [AB044	30.14	1
tc|Rep: Chromosome undetermined scaffold_1179, whole genome shotgun sequen	9455.55	1
gb|TT-48_C09 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	358.4	1
tc|Rep: BZIP transcription factor bZIP124 - Glycine max (Soybean), partial (54%) [TC	572.48	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	22.82	1
Unknown	17.98	1
Unknown	81.63	1
Unknown	332.8	1
Unknown	107.21	1
Unknown	34.7	1
gb|Nicotiana tabacum mRNA for shaggy-like kinase 59 [AJ002315]	948.88	1
tc|Rep: Chromosome undetermined scaffold_91, whole genome shotgun sequence	157.53	1
tc|Rep: Chromosome chr1 scaffold_84, whole genome shotgun sequence - Vitis vin	76.74	1
tc|Rep: Ethylene-responsive element binding protein 6 - Nicotiana tabacum (Comm	531.54	1
gb|KR3B.108M05F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.108M05,	21958.8	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	20.32	1
gb|KP1B.110I21F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110I21, mR	174.23	1
tc|Rep: Chromosome chr14 scaffold_63, whole genome shotgun sequence - Vitis vi	512.01	1

tc|Rep: ATP synthase subunit delta', mitochondrial precursor - Ipomoea batatas (Sv	681.01	1
Unknown	486.58	1
tc|Rep: G/HBF-1 - Glycine max (Soybean), complete [TC48109]	653.44	1
Unknown	377.37	1
tc|Rep: Serine acetyltransferase 1 - Nicotiana tabacum (Common tobacco), partial (	263.17	1
Unknown	25.14	1
Unknown	379.12	1
Unknown	22.09	1
tc|Rep: T1K7.26 protein - Arabidopsis thaliana (Mouse-ear cress), partial (17%) [TC4	1157.25	1
gb|AM819928 seedling library, SL Nicotiana tabacum cDNA clone nt002008041, mR	19.62	1
tc|Rep: Cystathionine gamma-synthase isoform 2 - Solanum tuberosum (Potato), pa	1061.9	1
Unknown	86.97	1
tc|Rep: RAD23-like - Solanum tuberosum (Potato), complete [TC48167]	59.1	1
gb|KT7C.112H03F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112H03, mR	184.15	1
tc|Rep: Eukaryotic initiation factor iso4E - Nicotiana tabacum (Common tobacco), p	1299.05	1
Unknown	209.56	1
gb|KP1B.108L06F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108L06, mR	29.4	1
gb|AGN_RNC029xp09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	40.13	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	48.97	1
Unknown	21.52	1
Unknown	20.19	1
gb|KP1B.111C19F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.111C19, ml	22.68	1
tc|Rep: Chromosome undetermined scaffold_984, whole genome shotgun sequenc	2624.35	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	153.67	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	86.75	1
gb|TT-29_J20 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	131.51	1
tc|Rep: Chromosome undetermined scaffold_71, whole genome shotgun sequence	618.39	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	19.23	1
gb|Nicotiana tabacum NtNRAMP1 mRNA for metal transporter, complete cds [AB5	30.39	1
tc|Rep: Chromosome undetermined scaffold_296, whole genome shotgun sequenc	33.01	1
gb|Nicotiana tabacum NtNRAMP1 mRNA for metal transporter, complete cds [AB5	34.26	1
Unknown	58.57	1
gb|AGN_RPC022xi19f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	556.4	1
tc|Rep: CBL-interacting protein kinase 25 - Populus trichocarpa (Western balsam pc	1137.94	1

gb|CHO_SL018xb09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	108.28	1
Unknown	30.78	1
Unknown	51301.6	1
Unknown	250.26	1
gb|KL4B.101K06F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101K06, mR	519.26	1
gb|Nicotiana tabacum adc mRNA for arginine decarboxylase, complete cds [AB110	3527.65	1
tc|Rep: H+-transporting two-sector ATPase, C (AC39) subunit - Medicago truncatul	3297.93	1
tc|Rep: Serine hydroxymethyltransferase - Populus tremuloides (Quaking aspen), p	14924.95	1
Unknown	23.11	1
tc|Rep: 26S protease regulatory subunit 6A homolog (TAT-binding protein homolog	614.91	1
gb|AGN_RNC024xp05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	18830.75	1
Unknown	89.69	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	74.72	1
tc|Rep: Ribosomal protein L23 family protein - Solanum tuberosum (Potato), partia	86.9	1
gb|Tobacco mRNA fragment for nitrate reductase [X06134]	25.77	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (96%) [TC6	41.61	1
gb|KG9B.003J03F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003J03, m	5073.25	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	1505.79	1
Unknown	222.27	1
gb|AGN_RPC003xo05f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	21.04	1
tc|Rep: Formate--tetrahydrofolate ligase - Spinacia oleracea (Spinach), partial (25%	487.65	1
gb|AM784687 seedling library, SL Nicotiana tabacum cDNA clone nt002217060, m	86.67	1
gb|tbt_009695 Normalized Nicotiana tabacum cDNA library Nicotiana tabacum cD	136.01	1
Unknown	22.3	1
gb|AM830119 seedling library, SL Nicotiana tabacum cDNA clone nt002310054, m	1044.97	1
gb|KG9B.105M12F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105M12,	25.33	1
Unknown	24.2	1
gb|TT-21_M06 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA se	429.86	1
tc|Rep: Transcription factor bZIP63 - Glycine max (Soybean), partial (41%) [TC7400	891.88	1
gb|N.tabacum mRNA for pectate lyase [X67159]	50341	1
gb|Nicotiana tabacum mRNA for putative putative beta-(1,2)-xylosyltransferase (xy	28.92	1
gb|KP1B.101G10F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101G10, m	43.82	1
Unknown	28.41	1
Unknown	48.94	1

tc|Rep: Calcium-binding protein CAST - Solanum tuberosum (Potato), partial (87%)	359.14	1
tc|Rep: Heat shock 70 kDa protein, mitochondrial precursor - Pisum sativum (Garde	80.93	1
gb|KF8C.103M04F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103M04, m	54.06	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (96%) [TC6	129.74	1
tc|Rep: Splicing factor-like protein - Vitis riparia (Frost grape) (Vitis vulpina), partial	70.63	1
gb|EST_YP003xg02f1.ab1 EST_YP Nicotiana tabacum cDNA, mRNA sequence [EH61	82.49	1
Unknown	165.84	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	142.81	1
gb|AM824464 DL, diurnal library Nicotiana tabacum cDNA clone nt005080040, mR	59.77	1
tc|Rep: Chromosome chr11 scaffold_56, whole genome shotgun sequence - Vitis vi	75.54	1
tc|Rep: Chloride channel Stclc1 - Solanum tuberosum (Potato), partial (27%) [TC551	607.99	1
gb|KG9B.107M14F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107M14,	594.23	1
gb|TT-03_F12 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	426.13	1
gb|Nicotiana tabacum mRNA for putative 16kDa membrane protein [AJ272037]	47.95	1
gb|KR2B.109P14F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.109P14, m	1087.5	1
gb|TT-03_B09 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	459.59	1
gb|AM803568 COL, cold overnight library Nicotiana tabacum cDNA clone nt006165	27.2	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	32.05	1
Unknown	76.03	1
gb|TT-21_K15 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	530.21	1
Unknown	786.35	1
Unknown	2816.52	1
Unknown	179.64	1
gb|KP1B.001I07F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001I07, mR	249.53	1
Unknown	151.59	1
tc|Rep: Chromosome undetermined scaffold_310, whole genome shotgun sequenc	24.02	1
Unknown	502.48	1
Unknown	51.06	1
tc|Rep: Histone H3 - Vitis vinifera (Grape), complete [TC47009]	869.11	1
Unknown	37.4	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	23.71	1
gb|KG9B.105H20F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105H20, n	283.09	1
gb|AGN_RNC211xl21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	4424.67	1
tc|Rep: Chromosome chr13 scaffold_210, whole genome shotgun sequence - Vitis	564.36	1

Unknown	123.24	1
gb|AGN_PNL206af1_g11.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	25.97	1
gb|KL4B.102B08F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102B08, mR	31.38	1
tc|Rep: Nucleic acid binding protein - Nicotiana tabacum (Common tobacco), partia	1642.32	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	141.5	1
tc|Rep: S-adenosylmethionine synthetase 3 - Solanum lycopersicum (Tomato) (Lyco	50106.4	1
gb|AGN_RNC012xc03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	185.77	1
gb|KN6B.103G02F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103G02, r	8329.68	1
Unknown	181.32	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	73.18	1
tc|Rep: Transport protein particle component Bet3-like protein - Oryza sativa subsp	61.13	1
gb|KG9B.106E05F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106E05, m	208.28	1
gb|KR3B.105K07F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.105K07, m	296.98	1
tc|Rep: ACS2 - Ricinus communis (Castor bean), partial (22%) [TC54234]	91.61	1
tc|Rep: Ubiquitin carrier protein - Nicotiana benthamiana, complete [TC69183]	17.14	1
tc|Rep: Serine acetyltransferase 4 - Nicotiana tabacum (Common tobacco), comple	490.96	1
Unknown	107.24	1
Unknown	99.72	1
tc|Rep: Chromosome chr1 scaffold_84, whole genome shotgun sequence - Vitis vin	72.5	1
Unknown	146.96	1
gb|AGN_RNC017xp19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	90.08	1
gb|Nicotiana tabacum hydroxy-methyl-glutaryl-coenzyme A reductase (HMGR2) m	48369.85	1
gb|Nicotiana tabacum cyclin-dependent kinase B1-2 (CdkB1-2) mRNA, complete cd	29.19	1
gb|TL13.109B21F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.109B21, mR	379.86	1
tc|Rep: Chromosome chr5 scaffold_58, whole genome shotgun sequence - Vitis vin	7922.05	1
gb|Nicotiana tabacum Avr9 [AY220479]	224.37	1
tc|Rep: 40S ribosomal protein S15-like - Solanum tuberosum (Potato), complete [T	234.35	1
gb|Tobacco (N.tabacum) GapC mRNA encoding cytosolic glyceraldehyde-3-phosph	1174.17	1
gb|N.tabacum mRNA for aquaporin 1 [Y08161]	1018.07	1
Unknown	88.98	1
Unknown	28.18	1
tc|Rep: U1 snRNP-interacting 70 kDa protein - Triticum aestivum (Wheat), partial (2	251.89	1
Unknown	3680.16	1
tc|Rep: RNA-binding protein RZ-1 - Nicotiana sylvestris (Wood tobacco), complete [	635.21	1

Unknown	26.68	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	17.43	1
Unknown	727.35	1
Unknown	61.32	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	27.63	1
gb|KR2B.105G16F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.105G16, m	63.15	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	2569.59	1
tc|Rep: Sulfite oxidase-like - Solanum tuberosum (Potato), partial (71%) [TC47831]	2864.09	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	106.85	1
gb|KT7B.114M24F.060127T7 KT7 Nicotiana tabacum cDNA clone KT7B.114M24, m	40	1
gb|TT-36_P15 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	10214.55	1
gb|KR3B.107K07F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.107K07, m	66.88	1
tc|Rep: Impa2 - Nicotiana benthamiana, partial (98%) [TC72049]	3056.52	1
Unknown	22.06	1
tc|Rep: Chromosome chr5 scaffold_72, whole genome shotgun sequence - Vitis vin	168.33	1
gb|AM845812 seedling library, SL Nicotiana tabacum cDNA clone nt002002037, m	120.24	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	59.02	1
Unknown	28.47	1
Unknown	78.81	1
Unknown	93.68	1
gb|AGN_ELP023xo22f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	77.19	1
gb|AGN_ELP018xj16f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	2209.87	1
gb|CHO_SL002xn01f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	6493.57	1
Unknown	421.09	1
Unknown	177.95	1
gb|TT-01_F11 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	39.08	1
gb|tbt_010968 Normalized Nicotiana tabacum cDNA library Nicotiana tabacum cD	15870.95	1
gb|KL5B.115L21F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.115L21, mR	386.53	1
gb|KL5B.106E03F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.106E03, mR	1075.21	1
gb|KL4B.103K02F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103K02, mR	842.21	1
Unknown	20.02	1
tc|Rep: Digalactosyldiacylglycerol synthase 2, chloroplast - Glycine max (Soybean),	10202.06	1
gb|CHO_SL017xp04f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	57.07	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	131.62	1

gb|N.tabacum cDNA for glutamine synthetase (3' region) [X68604]	1473.21	1
Unknown	85.65	1
gb|KP1B.001B19F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001B19, m	26.5	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	1491.75	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	259.65	1
Unknown	276.54	1
Unknown	269.08	1
tc|Rep: Chromosome undetermined scaffold_69, whole genome shotgun sequence	352.5	1
gb|KN6B.101B19F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101B19, m	25.57	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	601.01	1
Unknown	1121.29	1
tc|Rep: Endo-1,4-beta-glucanase - Solanum lycopersicum (Tomato) (Lycopersicon e	93.17	1
gb|KG9B.001H19F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001H19, n	925.36	1
gb|KL4B.100C13F.050922T7 KL4B Nicotiana tabacum cDNA clone KL4B.100C13, mR	143.07	1
gb|TOBESTR060C10 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	70.6	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	155.82	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	165.48	1
gb|KR2B.104F07F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.104F07, m	80.67	1
tc|Rep: Peptidyl-prolyl cis-trans isomerase - Solanum lycopersicum (Tomato) (Lyco	296.69	1
tc|Rep: RNA binding protein - Nicotiana sylvestris (Wood tobacco), complete [TC44	54.18	1
Unknown	255.04	1
gb|KP1B.101J23F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101J23, mR	255.64	1
tc|Rep: Os05g0227700 protein - Oryza sativa subsp. japonica (Rice), partial (32%) [T	207.03	1
Unknown	151.93	1
gb|FS388031 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	521.18	1
Unknown	64.76	1
gb|KG9B.106A17F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106A17, n	525.5	1
tc|Rep: Inorganic pyrophosphatase - Nicotiana tabacum (Common tobacco), compl	265.65	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	130.44	1
tc|Rep: Brain protein 44-like - Zea mays (Maize), partial (89%) [TC53445]	1918.09	1
tc|Rep: Regulatory protein, TetR:Tetracyclin repressor, C-terminal - Enterococcus fa	77.5	1
gb|TT-09_B21 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	88.12	1
tc|Rep: Chromosome chr2 scaffold_187, whole genome shotgun sequence - Vitis vi	49.41	1
gb|AGN_RPC010xl18f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	71.6	1

gb|TT-02_K13 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	27.14	1
tc|Rep: Chloroplast photosystem I reaction center V - Camellia sinensis (Tea), parti	18.96	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	380.83	1
tc|Rep: Elongation factor 1-alpha - Nicotiana paniculata, partial (23%) [TC64911]	3603.4	1
Unknown	71.29	1
tc|CHEVIARRN E.virginiana plastid ribosomal RNA operon, trnI and trnA pseudogen	231.53	1
gb|Nicotiana tabacum mRNA for putative alpha7 proteasome subunit (a7 gene) [AJ	23.01	1
Unknown	21.88	1
gb|AGN_RPC007xp13f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	19.49	1
Unknown	19.65	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	11122.25	1
tc|Rep: Hypersensitive-induced reaction protein - Capsicum annuum (Bell pepper),	833.23	1
Unknown	116.64	1
gb|KP1B.108N20F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108N20, m	36.04	1
gb|Nicotiana tabacum mRNA for hsr203J, complete cds [AB091430]	43.14	1
tc|Rep: Methionine aminopeptidase - Vitis vinifera (Grape), partial (92%) [TC51281	34.58	1
Unknown	140.21	1
gb|AGN_RNC025xo07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	74.59	1
gb|AGN_RNC017xo13f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	50.4	1
Unknown	54.98	1
gb|Nicotiana tabacum mRNA for malate dehydrogenase (md1 gene) [AJ299256]	111.79	1
tc|Rep: Late embryogenis abundant protein 5 - Nicotiana tabacum (Common tobac	18585.7	1
Unknown	36.95	1
gb|KG9B.102C13F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102C13, m	8894.49	1
Unknown	2004.87	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	1078.14	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	86.07	1
Unknown	55.03	1
gb|KG9B.105O22F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105O22, r	3280.16	1
gb|CHO_SL018xo19f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	395.28	1
gb|KP1B.103C08F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103C08, m	72.44	1
gb|KG9B.105L09F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105L09, m	429.21	1
gb|CHO_SL025xf23f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	31.48	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	508.39	1

gb|CHO_SL024xm08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	137.64	1
gb|KL4B.105L07F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105L07, mR	21.57	1
tc|Rep: AT3g06540/F5E6_13 - Arabidopsis thaliana (Mouse-ear cress), partial (8%) |	1211.89	1
gb|KL4B.113H18F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.113H18, mR	51.63	1
gb|TT-47_P04 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	1317.3	1
tc|Rep: Avr9/Cf-9 rapidly elicited protein 284 - Nicotiana tabacum (Common tobacc	1298.45	1
gb|AGN_RPC024xa10f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	23.78	1
gb|KL4B.103G04F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103G04, mR	89.93	1
gb|KG9B.001E12F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001E12, m	23.28	1
Unknown	20.9	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	48.8	1
gb|KL5B.001F15F.050901T7 KL5B Nicotiana tabacum cDNA clone KL5B.001F15, mR	2962.4	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	22.63	1
gb|TT-29_K04 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	150.3	1
Unknown	20.89	1
tc|Rep: Ubiquitin carboxyl-terminal hydrolase - Vitis vinifera (Grape), partial (31%) |	63.52	1
gb|KG9B.104F17F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104F17, m	1013	1
tc|Rep: RSH2 - Nicotiana tabacum (Common tobacco), partial (35%) [TC57269]	2856.5	1
gb|CHO_SL019xk08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	441.97	1
tc|Rep: Endonuclease/Exonuclease/phosphatase family protein, expressed - Oryza s	58.4	1
Unknown	35.1	1
tc|Rep: Chromosome chr1 scaffold_166, whole genome shotgun sequence - Vitis vi	111.94	1
tc|Rep: ATP synthase subunit a - Nicotiana tabacum (Common tobacco), complete |	142.55	1
tc|Rep: Heat shock protein 90 - Nicotiana tabacum (Common tobacco), partial (29%	69.51	1
gb|KG9B.102L14F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102L14, m	85.84	1
tc|Rep: Lipoprotein signal peptidase - Bradyrhizobium japonicum, partial (9%) [TC6	147.29	1
Unknown	119.17	1
tc|Rep: Chromosome undetermined scaffold_235, whole genome shotgun sequenc	24.16	1
tc|Rep: Chromosome chr4 scaffold_83, whole genome shotgun sequence - Vitis vin	558.09	1
gb|KR2B.103A09F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.103A09, m	567.6	1
Unknown	123.18	1
tc|Rep: Glycine dehydrogenase [decarboxylating], mitochondrial precursor - Solanu	2949.05	1
Unknown	77.01	1
gb|KF8C.102D20F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102D20, mR	644.18	1

Unknown	355.32	1
Unknown	172.26	1
tc|Rep: Chromosome undetermined scaffold_203, whole genome shotgun sequenc	10258.25	1
gb|Nicotiana tabacum cultivar Havana SR1 cytosine-5-methyltransferase (MET1) m	32.47	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	84.84	1
Unknown	82.58	1
Unknown	29.94	1
tc|Rep: G/HBF-1 - Glycine max (Soybean), partial (68%) [TC41471]	495.22	1
Unknown	106.4	1
Unknown	632.37	1
tc|Rep: ASC1-like protein - Solanum lycopersicum (Tomato) (Lycopersicon esculent	436.42	1
gb|AGN_RPC008xi04f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	38.39	1
tc|Rep: F18O14.8 - Arabidopsis thaliana (Mouse-ear cress), partial (90%) [TC46547]	528.15	1
gb|KG9B.004E04F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004E04, m	57.95	1
Unknown	157.14	1
Unknown	575.95	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	72.03	1
gb|AGN_RNC003xh03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	38	1
gb|KL4B.106F05F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106F05, mR	750.99	1
Unknown	5697	1
gb|KR3B.108M02F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.108M02, r	28.88	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	134.62	1
tc|Rep: Chromosome chr9 scaffold_49, whole genome shotgun sequence - Vitis vin	985.76	1
Unknown	108.81	1
gb|KP1B.104M15F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104M15, r	551.68	1
Unknown	520.62	1
Unknown	1360.88	1
tc|Rep: Enhanced disease susceptibility 5 - Arabidopsis thaliana (Mouse-ear cress),	37.21	1
gb|TL13.108B10F.060315T7 TL13 Nicotiana tabacum cDNA clone TL13.108B10, mR	179.95	1
gb|KR3B.110K10F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110K10, m	102.2	1
Unknown	40.17	1
gb|KT7C.105E05F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105E05, mRN	35.13	1
gb|AGN_RNC003xe06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	57.47	1
gb|KF8C.102P17F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102P17, mRN	9897.97	1

gb|TT-23_E11 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	51.69	1
gb|BP134667 MAT001 Nicotiana tabacum cDNA clone BY7087, mRNA sequence [B	80.03	1
gb|KG9B.001K19F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001K19,	262.96	1
Unknown	115.09	1
tc|Rep: 1-acyl-sn-glycerol-3-phosphate acyltransferase - Prunus dulcis (Almond) (Pr	3256.92	1
tc|Rep: Sodium/hydrogen exchanger - Solanum lycopersicum (Tomato) (Lycopersic	432.73	1
gb|AGN_RNC127xb08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	51.04	1
Unknown	816.29	1
gb|TT-11_H14 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	1185.07	1
Unknown	3551.59	1
gb|TT-28_J08 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	20.73	1
gb|KF8C.102M21F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102M21, m	19094.7	1
Unknown	257.93	1
Unknown	104.48	1
Unknown	144.32	1
gb|AGN_RNC023xe14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	84.02	1
gb|TT-07_I07 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	1053.72	1
Unknown	533.94	1
tc|Rep: Photosystem II P680 chlorophyll A apoprotein - Solanum lycopersicum (Ton	67.13	1
Unknown	31.62	1
gb|KG9B.002E04F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002E04, m	518.73	1
gb|Nicotiana tabacum pectin methylesterase (PPME1) mRNA, complete cds [AY772	89600.8	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	1495.9	1
gb|Nicotiana tabacum D31 mRNA for 14-3-3 protein, complete cds [AB071967]	39100.1	1
gb|FS416927 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	1225	1
Unknown	50.84	1
gb|N.tabacum mRNA for ribonucleotide reductase, clone R1-2 [Y10862]	19.24	1
tc|Rep: Chromosome chr13 scaffold_210, whole genome shotgun sequence - Vitis	442.66	1
tc|Rep: Chromosome undetermined scaffold_147, whole genome shotgun sequenc	107.47	1
gb|AGN_PNL230df1_g11.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	351.82	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	811.66	1
tc|Rep: Ubiquitin conjugating enzyme 2 - Solanum lycopersicum (Tomato) (Lycoper	626.78	1
tc|Rep: 60S ribosomal protein L19-like protein - Solanum tuberosum (Potato), parti	219.4	1
tc|Rep: Calmodulin binding heat shock protein - Gossypium hirsutum (Upland cotto	24.36	1

tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	89.83	1
gb|KG9B.001E17F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001E17, m	1867.47	1
gb|KL4B.110F15F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110F15, mR	93.84	1
Unknown	4898.63	1
gb|KF8C.106A11F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106A11, mRN	1344.4	1
gb|Nicotiana tabacum cig3 mRNA, complete cds [AB041352]	2778.45	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	104.99	1
tc|Rep: Chromosome undetermined scaffold_80, whole genome shotgun sequence	270.31	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	218.14	1
gb|AGN_RPC024xk11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	135.31	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	19.66	1
gb|KL4B.103K19F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103K19, mR	81.11	1
tc|Rep: High mobility group protein 2 HMG2 - Ipomoea nil (Japanese morning glory	7725.68	1
gb|TT-04_H17 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	109.09	1
gb|AGN_PNL201br1_c10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRN	109.24	1
Unknown	29.37	1
tc|Rep: Urease accessory protein G - Solanum tuberosum (Potato), partial (94%) [T	61.42	1
gb|KL4B.103J08F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103J08, mRN	115.08	1
gb|KP1B.104L22F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104L22, mR	651.28	1
gb|KP1B.107M11F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107M11, r	212.8	1
Unknown	67.92	1
gb|KN6B.100P17F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100P17, m	166.28	1
tc|Rep: Ras-related GTP-binding protein - Nicotiana tabacum (Common tobacco), c	8183.04	1
Unknown	416.77	1
tc|Rep: Genomic DNA, chromosome 5, TAC clone:K17O22 - Arabidopsis thaliana (M	391.85	1
gb|AM819186 DL, diurnal library Nicotiana tabacum cDNA clone nt005051041, mR	55.79	1
gb|KR3B.103O03F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.103O03, m	37.79	1
gb|AGN_PNL219dr1_e8.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	29.76	1
gb|KP1B.107H01F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107H01, m	110.13	1
Unknown	486.37	1
Unknown	147.54	1
tc|Rep: Dehydroquinate dehydratase/shikimate dehydrogenase precursor - Nicotia	683.21	1
gb|CHO_SL009xa08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	271.1	1
tc|Rep: Oxysterol-binding protein - Solanum tuberosum (Potato), partial (47%) [TC5	172.89	1

tc|Rep: Chromosome chr17 scaffold_101, whole genome shotgun sequence - Vitis v	42.29	1
Unknown	18.96	1
tc|Rep: DNA-binding protein phosphatase 2C - Nicotiana tabacum (Common tobacc	38.83	1
tc|Rep: 60S ribosomal protein L41 - Homo sapiens (Human), complete [TC69557]	224.68	1
Unknown	515.66	1
gb|KR2B.102N04F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.102N04, m	20.78	1
gb|AM840689 seedling library, SL Nicotiana tabacum cDNA clone nt002001079, mR	31.18	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	3005.38	1
Unknown	67.15	1
Unknown	948.98	1
tc|Rep: Chromosome chr17 scaffold_101, whole genome shotgun sequence - Vitis v	29.25	1
Unknown	143.77	1
tc|Rep: Chromosome undetermined SCAF8942, whole genome shotgun sequence -	436.75	1
Unknown	70.92	1
Unknown	63.45	1
gb|KR3B.101H09F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101H09, m	25.87	1
gb|KG9B.106D20F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106D20, n	26.15	1
gb|KN6B.115K16F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.115K16, m	2697.26	1
tc|Rep: Probable transcriptional regulator - Pseudomonas aeruginosa (strain PA7),	84.77	1
Unknown	51.37	1
gb|TT-07_I07 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	1236.43	1
tc|Rep: NtEIG-E80 protein - Nicotiana tabacum (Common tobacco), complete [TC6	57366.1	1
tc|Rep: Induced stolon tip protein - Capsicum annuum (Bell pepper), partial (66%) [	7542.56	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	225.05	1
tc|Rep: Os01g0945800 protein - Oryza sativa subsp. japonica (Rice), partial (75%) [T	324.19	1
gb|KP1B.107L14F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107L14, mR	22.23	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	124.03	1
tc|Rep: Chromosome chr13 scaffold_45, whole genome shotgun sequence - Vitis vi	35.56	1
tc|Rep: DnaJ-like protein - Solanum lycopersicum (Tomato) (Lycopersicon esculent	4715.85	1
gb|Nicotiana tabacum NIM1-like protein 1 (NML1) mRNA, complete cds [AY640382	162.34	1
gb|AGN_RPC022xl10f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	50.16	1
tc|Rep: GDA2 protein - Pisum sativum (Garden pea), partial (70%) [TC48476]	29.89	1
gb|AGN_RNC105xi20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	34.69	1
tc|Rep: Induced stolon tip protein - Capsicum annuum (Bell pepper), partial (66%) [	3173.16	1

Unknown	2669.84	1
tc|Rep: B-type cyclin - Nicotiana tabacum (Common tobacco), partial (24%) [TC660	46.64	1
gb|KG9B.002H24F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002H24,	18.03	1
gb|AGN_RNC105xe02f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	2804.73	1
gb|KP1B.110A01F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110A01, m	47.03	1
Unknown	31.98	1
gb|KN6B.105G10F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105G10,	76.75	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT31-540, cultivar Bright Yellow 2 [	71.22	1
Unknown	19.15	1
Unknown	92.81	1
Unknown	182.28	1
tc|Rep: SGT1-2 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), parti	97.15	1
gb|Nicotiana tabacum ankyrin-repeat protein HBP1 mRNA, complete cds [AF35279	540.04	1
gb|EST_FLW004xb16f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	118.06	1
Unknown	27.74	1
gb|AGN_RPC012xj12f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	26.11	1
gb|Nicotiana tabacum mRNA for putative esterase (T36 gene) [AM851012]	22.94	1
gb|KP1B.001L15F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001L15, m	253.72	1
gb|TT-30_P14 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	99.72	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	489.41	1
gb|AM839155 COL, cold overnight library Nicotiana tabacum cDNA clone nt006221	78.58	1
gb|KF8C.101M05F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101M05, m	517.51	1
tc|Rep: Chromosome chr3 scaffold_199, whole genome shotgun sequence - Vitis vi	247.54	1
Unknown	180.21	1
gb|CHO_SL002xi14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	821.82	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	29.62	1
tc|Rep: Protein ABIL1 - Arabidopsis thaliana (Mouse-ear cress), partial (12%) [TC72	219.95	1
gb|KF8C.102P04F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102P04, mR	27.37	1
gb|AGN_ELP014xd23f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	514.5	1
gb|KG9B.105J18F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105J18, m	408.82	1
Unknown	240.36	1
gb|TT-50_M03 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA se	848.26	1
tc|Rep: Nitrate reductase [NADH] 1 - Nicotiana tabacum (Common tobacco), compl	85.97	1
gb|KP1B.110M19F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110M19,	192.52	1

tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	55.32	1
gb|KL4B.102J09F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102J09, mRN	3814.1	1
tc|Rep: Chromosome chr17 scaffold_101, whole genome shotgun sequence - Vitis	169.81	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC2-23-220, cultivar Bright Yellow 2	46.42	1
Unknown	36.45	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	746.25	1
tc|Rep: Ly200 protein - Capsicum annuum (Bell pepper), complete [TC52727]	86.09	1
tc|Rep: Chromosome chr13 scaffold_210, whole genome shotgun sequence - Vitis	3960.46	1
Unknown	40.48	1
tc|Rep: Pre-mRNA-splicing factor SLU7 - Oryza sativa subsp. indica (Rice), partial (7	680.42	1
Unknown	478.59	1
Unknown	53.57	1
Unknown	24.36	1
Unknown	81.06	1
Unknown	102.89	1
Unknown	326.46	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	38.85	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	53.15	1
tc|Rep: F5D14.18 protein - Arabidopsis thaliana (Mouse-ear cress), partial (11%) [T	798.17	1
tc|Rep: SNF2-related; Zinc finger, RING-type; ATP-requiring DNA helicase RecQ - M	28.89	1
gb|KG9B.002O05F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002O05, r	107.03	1
tc|Rep: NADH:ubiquinone oxidoreductase-like - Solanum tuberosum (Potato), com	1031.07	1
Unknown	21.52	1
Unknown	682.09	1
gb|TT-47_N21 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	113.6	1
gb|TOBESTR020D12 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	194.89	1
Unknown	40.18	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	36.37	1
gb|KG9B.103M10F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103M10,	2980.14	1
Unknown	23.21	1
Unknown	35.77	1
Unknown	31.34	1
Unknown	50.68	1
tc|Rep: Actin - Phalaenopsis hybrid cultivar, partial (39%) [TC69811]	33203.05	1

gb|Nicotiana tabacum partial mRNA for putative chloroplast cysteine synthase 1 pr	90.95	1
Unknown	251.3	1
gb|KN6B.102M01F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102M01,	39811.6	1
tc|Rep: ATP synthase delta chain - Buchnera aphidicola subsp. Schizaphis graminu	38.41	1
tc|Rep: Serine/threonine-protein phosphatase PP1 - Brassica napus (Rape), partial (	2762.99	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	22.22	1
gb|BP133763 MAT001 Nicotiana tabacum cDNA clone BY6059, mRNA sequence [B	64.35	1
gb|Nicotiana tabacum NtYSL1 mRNA for putative yellow stripe-like protein, comple	142.55	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	130.36	1
Unknown	336.65	1
gb|KG9B.005J14F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005J14, m	1548.76	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT12-4-420, cultivar Bright Yellow 2	67.03	1
tc|Rep: Pyrroline-5-carboxylate reductase - Actinidia chinensis (Kiwi) (Yangtao), par	96.12	1
tc|Rep: Salt-induced AAA-Type ATPase - Mesembryanthemum crystallinum (Comm	139.07	1
gb|TL13.111K09F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.111K09, mR	223.38	1
Unknown	57.65	1
gb|KL4B.112I10F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112I10, mRN	1019.17	1
gb|TT-17_K11 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	72.47	1
gb|Nicotiana tabacum proline oxidase [AY639145]	4073.13	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	56.9	1
gb|KR2B.109P14F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.109P14, m	834.78	1
Unknown	42.25	1
Unknown	352.41	1
Unknown	230.47	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	151.31	1
tc|Rep: Eukaryotic translation initiation factor 3 subunit A - Nicotiana tabacum (Co	103.99	1
gb|KL4B.105A10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105A10, m	2654.06	1
gb|KP1B.108C10F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108C10, m	951.63	1
gb|KL4B.103E09F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103E09, mR	1589.8	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	166.44	1
Unknown	26.79	1
Unknown	19040.9	1
tc|Rep: StubSNF1 protein - Solanum tuberosum (Potato), partial (45%) [TC41271]	5123.64	1
tc|Rep: Chromosome undetermined scaffold_608, whole genome shotgun sequenc	31.59	1

Unknown	107.59	1
tc|Rep: Pollen coat-like protein - Arabidopsis thaliana (Mouse-ear cress), partial (58	26.76	1
Unknown	21.08	1
gb|CHO_SL023xn07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	43.54	1
tc|Rep: Ribosome recycling factor, chloroplast precursor - Daucus carota (Carrot), p	38.51	1
tc|Rep: Serine/threonine protein kinase SAPK8-like protein - Solanum tuberosum (P	35.93	1
gb|KG9B.001M19F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001M19,	59.62	1
Unknown	590.49	1
gb|AGN_RNC030xm24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	55.64	1
tc|Rep: UDP-glucose:protein transglucosylase-like protein SlUPTG1 - Solanum lycop	681.95	1
gb|Nicotiana tabacum osmotic stress-activated protein kinase (OSAK) mRNA, comp	93.39	1
tc|Rep: BZIP transcription factor BZI-4 - Nicotiana tabacum (Common tobacco), con	4692.86	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	140.7	1
Unknown	24.26	1
Unknown	18.94	1
Unknown	151.25	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	3204.68	1
gb|TT-19_N02 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	560.4	1
gb|BP534468 MAT005 Nicotiana tabacum cDNA clone BY33047, mRNA sequence [E	747.47	1
gb|AGN_RPC027xi20f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	1528.13	1
tc|Rep: E1 alpha subunit of pyruvate dehydrogenase - Petunia hybrida (Petunia), pa	5937.15	1
tc|Rep: F9L1.14 protein - Arabidopsis thaliana (Mouse-ear cress), partial (28%) [TC7	25.57	1
Unknown	978.6	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	36.31	1
tc|Rep: Prephenate dehydratase family protein - Solanum demissum (Wild potato),	51.64	1
Unknown	115.61	1
gb|TT-18_O05 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	16432.95	1
Unknown	23.62	1
Unknown	31.07	1
Unknown	151.31	1
gb|EST_FLW002xc16f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	206.79	1
Unknown	20.7	1
gb|AGN_RPC020xk05f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	31.5	1
tc|Rep: Predicted protein - Botryotinia fuckeliana (strain B05.10) (Noble rot fungus)	21.27	1

Unknown	79.25	1
gb|KP1B.110D03F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110D03, m	250.92	1
tc|Rep: Chromosome chr9 scaffold_104, whole genome shotgun sequence - Vitis vi	42.33	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	2868.94	1
Unknown	87.98	1
gb|Nicotiana tabacum NtWRKY-6 mRNA for WRKY DNA-binding protein, complete	112.94	1
tc|Rep: Chromosome undetermined scaffold_339, whole genome shotgun sequenc	54	1
Unknown	80.78	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	213.28	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	1164.69	1
gb|Nicotiana tabacum nack2 mRNA for kinesin-like protein NACK2, complete cds [	38.18	1
tc|Rep: Cysteine synthase - Solanum tuberosum (Potato), partial (97%) [TC46420]	20.37	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	273.46	1
Unknown	189.38	1
tc|Rep: Ubiquinol-cytochrome c reductase complex 6.7 kDa protein - Solanum tube	9775.27	1
Unknown	44.97	1
Unknown	1289.97	1
tc|Rep: NADH-ubiquinone oxidoreductase chain 1 - Stomoxys calcitrans (Stable fly),	1766.54	1
gb|KR2B.113M10F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.113M10,	118.54	1
gb|KL4B.106C07F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106C07, mR	73.04	1
gb|TT-09_J12 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	525.15	1
Unknown	55.62	1
gb|KN6B.115A02F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.115A02, n	103.84	1
tc|Rep: Chromosome chr3 scaffold_199, whole genome shotgun sequence - Vitis vi	2588.18	1
tc|Rep: Chromosome undetermined scaffold_144, whole genome shotgun sequenc	2856.84	1
gb|KL4B.101A05F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101A05, m	249.73	1
Unknown	17.71	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	229.34	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (69%) [TC5	522.44	1
gb|XXXP141 Nicotiana tabacum Pollen PCR-based subtractive library Nicotiana taba	36.52	1
gb|FS391062 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	79.32	1
tc|Rep: Histone H4 [Contains: Osteogenic growth peptide (OGP)]. - Rattus norvegic	1259.24	1
gb|KT7C.106J08F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106J08, mRN	23.61	1
gb|KT7C.102B06F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102B06, mR	201.29	1

tc|Rep: SAT5 - Pisum sativum (Garden pea), partial (70%) [TC41109]	521.39	1
Unknown	114.62	1
gb|KN6B.105B12F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105B12, m	14449.7	1
gb|KL4B.105H12F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105H12, mR	161.09	1
tc|Rep: MRNA, complete cds, clone: RAFL25-18-P16 - Arabidopsis thaliana (Mouse-	52.15	1
tc|Rep: Sulfate adenylyltransferase - Solanum tuberosum (Potato), partial (95%) [T	1538.66	1
tc|Rep: Mitochondrial phosphate transporter - Lotus japonicus, partial (88%) [TC44	31.35	1
Unknown	539.59	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	150.16	1
tc|Rep: Chromosome chr17 scaffold_101, whole genome shotgun sequence - Vitis	220.47	1
gb|TT-19_G14 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	85.33	1
tc|Rep: Chromosome chr11 scaffold_170, whole genome shotgun sequence - Vitis	383.5	1
Unknown	2234.77	1
Unknown	105.27	1
tc|Rep: Proteasome subunit beta type-6 precursor - Nicotiana tabacum (Common t	110.26	1
Unknown	259.87	1
gb|KL4B.104H17F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104H17, mR	721.86	1
Unknown	790.42	1
gb|KG9B.102A13F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102A13, m	152.64	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	1620.97	1
gb|10D01 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', r	237.93	1
gb|KG9B.106L19F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106L19, m	92.75	1
Unknown	309.3	1
gb|KR2B.105A21F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.105A21, m	1143.52	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT44-3-240, cultivar Bright Yellow 2	48.24	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	570.93	1
gb|AGN_RNC025xc17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	18.2	1
Unknown	61.82	1
gb|KG9B.002E04F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002E04, m	643.84	1
gb|Nicotiana tabacum S-adenosyl-L-homocysteine hydrolase (SAHH4) mRNA, comp	1601.49	1
Unknown	2374.83	1
gb|Nicotiana tabacum mRNA for proteasome A-type subunit [Y16644]	125.13	1
gb|KT7C.112B13F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112B13, mR	5019.44	1
gb|AGN_RNC029xd05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	21.48	1

tc|Rep: 2-polyprenyl-3-methyl-5-hydroxy-6-metoxy-1, 4-benzoquinol methylase - T	100.21	1
Unknown	26.64	1
tc|Rep: Ethylene-responsive small GTP-binding protein - Solanum lycopersicum (To	9590.44	1
gb|AGN_PNL222af1_c12.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	2702.05	1
gb|FS423299 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	62.33	1
tc|Rep: 50S ribosomal protein L17 - Syntrophomonas wolfei subsp. wolfei (strain G	1379.59	1
gb|KN6B.109M18F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.109M18,	165.44	1
Unknown	119.86	1
gb|KR3B.104I03F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.104I03, mR	57.2	1
gb|AGN_ELP012xj01f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	54.61	1
gb|CHO_SL017xj24f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	37.4	1
gb|KL4B.101N15F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101N15, m	1489.04	1
gb|KR2B.002L12F.051019T7 KR2B Nicotiana tabacum cDNA clone KR2B.002L12, m	100.71	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	268.26	1
tc|Rep: Chromosome chr1 scaffold_84, whole genome shotgun sequence - Vitis vin	854.26	1
Unknown	877.05	1
gb|Nicotiana tabacum mRNA for putative 16kDa membrane protein [AJ272037]	61.63	1
gb|Nicotiana tabacum microsomal omega-6-desaturase (FAD2) mRNA, complete c	45283.55	1
tc|Rep: Chromosome chr4 scaffold_162, whole genome shotgun sequence - Vitis vi	287.32	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	433.58	1
gb|KF8B.202N08F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202N08, mR	42.51	1
tc|Rep: Ribosomal protein L37 - Glycine max (Soybean), complete [TC54477]	326.91	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	28.41	1
gb|KL5B.114K06F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.114K06, mR	43.05	1
Unknown	18.98	1
gb|KL5B.112H09F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.112H09, m	47.76	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (9%) [TC68	33.87	1
tc|Rep: NADPH-cytochrome P450 oxidoreductase - Nicotiana tabacum (Common t	38.94	1
tc|Rep: Progesterone 5-beta-reductase - Digitalis minor var. minor, partial (40%) [T	2181.64	1
gb|AGN_PNL213cr1_d6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	21.81	1
tc|Rep: 40S ribosomal protein S15-like - Solanum tuberosum (Potato), complete [T	70.28	1
Unknown	273.19	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	699.91	1
tc|Rep: Chromosome chr8 scaffold_68, whole genome shotgun sequence - Vitis vin	27.24	1

Unknown	692.58	1
tc|Rep: Voltage-dependent anion channel - Nicotiana tabacum (Common tobacco),	375.48	1
Unknown	92.19	1
gb|AGN_ELP016xe16f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	96.8	1
Unknown	34.49	1
Unknown	87.05	1
tc|Rep: 14-3-3-like protein B - Nicotiana tabacum (Common tobacco), partial (50%)	49.46	1
Unknown	62.74	1
tc|Rep: Metallothionein-like protein - Nicotiana tabacum (Common tobacco), com	42437.55	1
Unknown	36.09	1
Unknown	39546.6	1
gb|TL13.110G08F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.110G08, m	152.73	1
gb|KT7C.102G19F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102G19, m	199.69	1
gb|CHO_SL004xm10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	135.63	1
gb|KR3B.103F05F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.103F05, m	33.28	1
gb|BP530311 MAT005 Nicotiana tabacum cDNA clone BY21319, mRNA sequence [	89.95	1
gb|N.tabacum mRNA for glutamine synthetase, gln1-3 [X95933]	244.59	1
gb|Nicotiana tabacum mRNA for proteasome A-type subunit [Y16644]	242	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	713.77	1
Unknown	157.11	1
Unknown	140.58	1
tc|Rep: CPR1-like cysteine proteinase - Nicotiana tabacum (Common tobacco), com	61.8	1
Unknown	200.99	1
Unknown	65.93	1
gb|KP1B.110N09F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110N09, m	973.82	1
Unknown	475.61	1
tc|Rep: Proteasome subunit alpha type - Vitis vinifera (Grape), partial (74%) [TC584	25.47	1
Unknown	57.31	1
gb|AGN_RNC129xd21r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	40.26	1
gb|KL5B.117K21F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.117K21, m	2511.41	1
gb|basic chitinase [Nicotiana tabacum=tobacco, cv Samsun nn, floral bud day 7 exp	133.79	1
gb|Nicotiana tabacum clone PR20 mRNA sequence [AF154644]	21.44	1
tc|Rep: Histone H3 - Vitis vinifera (Grape), complete [TC47009]	159.68	1
Unknown	59.2	1

gb|AGN_PNL222dr1_c8.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	573.27	1
Unknown	1373.47	1
gb|AGN_PNL210df1_h6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	38.6	1
tc|Rep: H+-transporting two-sector ATPase, C (AC39) subunit - Medicago truncatula	9378.59	1
gb|KT7C.105K23F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105K23, mRN	24.66	1
gb|KF8B.200P08F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200P08, mRN	23446.8	1
gb|KP1B.001F10F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001F10, mF	406.92	1
tc|Rep: Ly200 protein - Capsicum annuum (Bell pepper), complete [TC65471]	21.66	1
Unknown	61.48	1
Unknown	123.05	1
Unknown	2724.7	1
Unknown	923.77	1
gb|Nicotiana tabacum obtusifoliol-14-demethylase (CYP51) mRNA, complete cds [A	72.45	1
Unknown	792.76	1
tc|Rep: Two-component response regulator-like PRR37 - Oryza sativa subsp. indica	46.44	1
gb|N.tabacum mRNA for phosphoglycerate kinase (cytosolic isoenzyme) [Z48976]	1914.08	1
tc|Rep: Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vi	66.78	1
Unknown	41.83	1
gb|TT-47_I23 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	810.12	1
Unknown	43.11	1
tc|Rep: Chromosome undetermined scaffold_91, whole genome shotgun sequence	221.52	1
tc|Rep: Fas-associated factor 1-like protein - Capsicum annuum (Bell pepper), partia	472.54	1
gb|AGN_ELP019xp05f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	19.18	1
gb|KP1B.107F12F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107F12, mF	21.15	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	2244.71	1
tc|Rep: Acireductone dioxygenase - Solanum tuberosum (Potato), complete [TC405	1019.7	1
Unknown	229.64	1
gb|KG9B.005L07F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005L07, m	840.87	1
Unknown	30.92	1
Unknown	241.2	1
gb|KG9B.004M18F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004M18,	64.96	1
Unknown	26.02	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	28.25	1
tc|Rep: Cell division cycle protein 48 homolog - Capsicum annuum (Bell pepper), pa	4801.17	1

gb|KP1B.112G11F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.112G11, m	248.92	1
Unknown	65.56	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	495.91	1
tc|Rep: Vacuolar proton pump subunit F - Corchorus olitorius, complete [TC69780]	1270.49	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	35.83	1
tc|Rep: Nudix hydrolase 17, mitochondrial precursor - Arabidopsis thaliana (Mouse	119.15	1
Unknown	93.77	1
gb|KP1B.107P09F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107P09, mR	9960.34	1
tc|Rep: Chromosome chr4 scaffold_83, whole genome shotgun sequence - Vitis vin	58.31	1
gb|Nicotiana tabacum blp1 mRNA for luminal binding protein (BiP), partial [X60060	16599	1
gb|Nicotiana tabacum mRNA for protein kinase Ck2 regulatory subunit 2 (ck2beta2	484.63	1
tc|Rep: Chromosome chr19 scaffold_111, whole genome shotgun sequence - Vitis v	157.52	1
Unknown	29.29	1
gb|Nicotiana tabacum diacylglycerol acylCoA acyltransferase (DAGAT) mRNA, comp	593.06	1
Unknown	22.37	1
tc|Rep: ORF45 protein - Spinacia oleracea (Spinach), partial (60%) [TC76983]	24.07	1
Unknown	100.92	1
tc|Rep: GPI-anchored protein - Vigna radiata, partial (24%) [TC66563]	910	1
tc|Rep: Ubiquitin carrier protein - Arachis hypogaea (Peanut), complete [TC49627]	419.62	1
gb|CHO_SL006xm14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	969.9	1
Unknown	27.69	1
gb|AGN_RNC023xo09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	123.79	1
gb|KP1B.001O22F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001O22, m	649.21	1
gb|TT-25_O16 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	778.64	1
gb|CHO_SL025xf17f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	540.94	1
Unknown	18.7	1
gb|KR2B.115C11F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115C11, m	172.04	1
gb|ntsm10 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [E	224.65	1
gb|KT7C.105A16F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105A16, mR	174.84	1
gb|KG9B.106P22F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106P22, m	2393.36	1
gb|TT-40_F13 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	278.5	1
Unknown	33.1	1
gb|BP132909 MAT001 Nicotiana tabacum cDNA clone BY5120, mRNA sequence [B	18.5	1
gb|CHO_SL008xb22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	23.27	1

Unknown	43.53	1
Unknown	626.81	1
gb|KN6B.109C02F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.109C02, m	26.19	1
Unknown	4256.2	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	4552.52	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	24.65	1
gb|CHO_SL006xc12f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1058.21	1
gb|AM802729 COL, cold overnight library Nicotiana tabacum cDNA clone nt006217	87.26	1
gb|KP1B.104K12F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104K12, m	11083.95	1
tc|Rep: Granule-bound starch synthase 1, chloroplast precursor - Solanum tuberosu	45.66	1
gb|KG9B.001I09F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001I09, mR	964.55	1
gb|Nicotiana tabacum mitogen-activated protein kinase Ntf4-1 mRNA, complete c	1392.31	1
Unknown	60.27	1
gb|AGN_PNL216cf1_b9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	1111.34	1
tc|Rep: lipase class 3 family protein - Arabidopsis thaliana, partial (65%) [TC44539]	387.26	1
tc|Rep: Microtubule-associated protein 1 light chain 3 - Gossypium hirsutum (Uplar	1543.86	1
gb|KG9B.103C11F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103C11, m	45.49	1
Unknown	187.85	1
gb|KR3B.001P23F.050815T7 KR3B Nicotiana tabacum cDNA clone KR3B.001P23, m	653.04	1
tc|Rep: Possible DNA polymerase III delta prime subunit - Bifidobacterium adolesce	72.95	1
tc|Rep: Transcription factor - Enterocytozoon bieneusi H348, partial (11%) [TC7714	588.85	1
Unknown	25.57	1
tc|Rep: Peptide methionine sulfoxide reductase (Protein- methionine-S-oxide redu	74.66	1
gb|CHO_SL017xb13f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	190.73	1
tc|Rep: Superoxide dismutase [Mn], mitochondrial precursor - Capsicum annuum (	89.43	1
Unknown	73.03	1
gb|KL4B.101M16F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101M16, m	98.1	1
gb|KG9B.003L23F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003L23, m	136.65	1
Unknown	42.77	1
gb|AGN_RPC025xj09f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	23.41	1
tc|Rep: Histone H4 [Contains: Osteogenic growth peptide (OGP)]. - Rattus norvegicu	1039.44	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	45882	1
Unknown	21.22	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	107.19	1

gb|KF8B.100D07F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100D07, mR	1183.42	1
gb|KF8C.103M14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103M14, m	35.49	1
Unknown	441.56	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	580.75	1
Unknown	31.63	1
tc|Rep: Chromosome chr10 scaffold_138, whole genome shotgun sequence - Vitis	970.62	1
gb|KN6B.102A05F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102A05,	52.38	1
gb|KF8C.108G03F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108G03, mR	65.33	1
gb|AGN_RPC017xn01f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	61.32	1
gb|KT7C.110M19F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110M19, m	793.68	1
Unknown	240.71	1
Unknown	2774.6	1
Unknown	80.31	1
Unknown	22.81	1
gb|TT-30_H15 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	28.78	1
Unknown	62.3	1
tc|Rep: Ubiquitin carrier protein - Vitis vinifera (Grape), complete [TC56781]	627.28	1
Unknown	211.97	1
gb|KP1B.107J22F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107J22, mR	273.14	1
gb|BP135342 MAT001 Nicotiana tabacum cDNA clone BY7842, mRNA sequence [B	14037.65	1
tc|Rep: Chromosome chr8 scaffold_41, whole genome shotgun sequence - Vitis vin	24.95	1
tc|Rep: 40S ribosomal protein S24 - Vitis vinifera (Grape), partial (96%) [TC48753]	33.59	1
Unknown	38.55	1
tc|Rep: DNA-binding protein - Nicotiana tabacum (Common tobacco), partial (63%)	2702.32	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	453.99	1
Unknown	388.5	1
gb|Nicotiana tabacum mRNA for phage-type RNA polymerase (rpoT1-tom gene) [A	82.66	1
gb|KF8B.202M24F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202M24, m	39.55	1
gb|AGN_PNL205df1_a12.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	207.12	1
Unknown	29.74	1
gb|TT-13_P17 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	9440.15	1
tc|Rep: Eukaryotic translation initiation factor 3 subunit K - Oryza sativa subsp. jap	84.9	1
gb|CHO_SL007xl24f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	69.11	1
tc|Rep: Protein ULTRAPETALA 1 - Arabidopsis thaliana (Mouse-ear cress), partial (5	1689.25	1

gb|KG9B.106M19F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106M19,	27.68	1
gb|KL4B.112K18F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112K18, mR	473.52	1
Unknown	41.72	1
tc|Rep: Plastid glucose-6-phosphate/phosphate translocator - Helianthus annuus (C	721.77	1
gb|AGN_RNC017xg05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1161.1	1
gb|KG9B.103F04F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103F04, m	30.2	1
Unknown	379.39	1
tc|Rep: Ribosomal protein S27 - Vitis vinifera (Grape), complete [TC58062]	64.23	1
Unknown	685.19	1
tc|Rep: Succinyl CoA ligase beta subunit - Solanum lycopersicum (Tomato) (Lycoper	506.42	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	1178.66	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	243.96	1
gb|Nicotiana tabacum clone PR19 mRNA sequence [AF154643]	18.87	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, complete [TC5815	46.61	1
Unknown	94.24	1
gb|KL5B.001F22F.050901T7 KL5B Nicotiana tabacum cDNA clone KL5B.001F22, mR	23.04	1
gb|KL4B.109O09F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.109O09, m	523.87	1
tc|Rep: Chromosome chr4 scaffold_83, whole genome shotgun sequence - Vitis vin	99.67	1
Unknown	42.79	1
gb|TT-09_J12 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	150.33	1
Unknown	22.81	1
Unknown	21.37	1
Unknown	35.65	1
gb|KL4B.108M21F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108M21, m	114.63	1
tc|Rep: Chromosome chr9 scaffold_33, whole genome shotgun sequence - Vitis vin	52682.3	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	244.88	1
gb|KL4B.102L15F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102L15, mR	1591.03	1
tc|Rep: Chromosome undetermined scaffold_383, whole genome shotgun sequenc	116.45	1
Unknown	47.61	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	538.93	1
Unknown	21.87	1
gb|AGN_RNC107xj15r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	21.06	1
Unknown	21.68	1
Unknown	43.66	1

tc|Rep: Salt-induced AAA-Type ATPase - Mesembryanthemum crystallinum (Comm	80.65	1
tc|Rep: 26S protease regulatory subunit 6A homolog (TAT-binding protein homolog	442.75	1
Unknown	690.32	1
gb|KF8B.200B10F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200B10, mRN	54.9	1
tc|Rep: 40S ribosomal protein S23 - Fragaria ananassa (Strawberry), complete [TC5	206.18	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	807.56	1
Unknown	33.82	1
tc|Rep: Ubiquitin carboxyl-terminal hydrolase - Vitis vinifera (Grape), partial (7%) [T	59.86	1
Unknown	53.91	1
tc|Rep: Ubiquitin extension protein - Solanum tuberosum (Potato), complete [TC51	98.62	1
Unknown	2722.76	1
gb|TT-12_H24 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	173.75	1
tc|Rep: N-(5'-phosphoribosyl)anthranilate isomerase - Vitis vinifera (Grape), partial	521.5	1
Unknown	75.83	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	29.81	1
gb|KR3B.104M16F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.104M16, r	291.48	1
Unknown	65.36	1
gb|BP534280 MAT005 Nicotiana tabacum cDNA clone BY32237, mRNA sequence [E	57.48	1
gb|KT7C.113E07F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.113E07, mRN	272.6	1
gb|KG9B.103O07F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103O07, r	539.67	1
gb|AGN_PNL229bf1_a1.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	79	1
gb|KL4B.103K19F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103K19, mR	51.24	1
Unknown	37.94	1
Unknown	30.23	1
tc|Rep: Ribosomal protein L24E - Medicago truncatula (Barrel medic), complete [TC	151.53	1
gb|KF8C.106B04F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106B04, mRN	86.13	1
Unknown	1122.1	1
tc|Rep: EMB1579 (EMBRYO DEFECTIVE 1579); binding - Arabidopsis thaliana, partia	133.8	1
Unknown	613.11	1
Unknown	19.17	1
Unknown	28.4	1
gb|CHO_SL011xi16f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	1732.8	1
gb|KF8C.101K11F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101K11, mRN	43.96	1
gb|TT-23_O11 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	1547.81	1

tc|Rep: Glutathione S-transferase - Euphorbia esula (Leafy spurge), partial (87%) [T	4321.05	1
gb|BP534488 MAT005 Nicotiana tabacum cDNA clone BY33067, mRNA sequence [	246.76	1
Unknown	20.82	1
gb|KG9B.105G09F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105G09,	151.38	1
gb|AGN_RNC007xf16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	74.96	1
tc|Rep: At1g04290/F19P19_27 - Arabidopsis thaliana (Mouse-ear cress), partial (80	125.96	1
gb|KN6B.103G24F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103G24,	227.14	1
gb|KP1B.101E18F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101E18, m	694.8	1
gb|AM796086 seedling library, SL Nicotiana tabacum cDNA clone nt002064010, m	333.98	1
Unknown	65.74	1
tc|Rep: Os05g0119300 protein - Oryza sativa subsp. japonica (Rice), partial (63%) [T	9994.08	1
Unknown	79.56	1
gb|KF8C.103N03F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103N03, mR	3007.89	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	175.69	1
tc|Rep: Luminal-binding protein 3 - Nicotiana tabacum (Common tobacco), partial (	11114.4	1
gb|KN6B.105L17F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105L17, m	100.49	1
gb|TT-09_J21 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	324.4	1
gb|TT-16_J10 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	34.46	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	57.57	1
tc|Rep: 40S ribosomal protein S5 - Capsicum annuum (Bell pepper), partial (96%) [T	71.3	1
gb|Nicotiana tabacum GNOM-like 1 protein mRNA, complete cds [EF520731]	3287.13	1
Unknown	51.79	1
tc|Rep: Ribonuclease E - Lyngbya sp. PCC 8106, partial (3%) [TC65320]	32.44	1
tc|Rep: ADP ribosylation factor 002 - Daucus carota (Carrot), partial (93%) [TC5148	13479.5	1
gb|KL4B.105C19F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105C19, mR	423.77	1
Unknown	123.43	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	129.52	1
Unknown	66.57	1
tc|Rep: Regulator of ribonuclease-like protein 3 - Arabidopsis thaliana (Mouse-ear	23.8	1
tc|Rep: Chromosome chr5 scaffold_58, whole genome shotgun sequence - Vitis vin	513.02	1
tc|Rep: Ribosomal protein S10, eukaryotic and archaeal form - Medicago truncatul	200.49	1
tc|Rep: Inositol-3-phosphate synthase - Nicotiana tabacum (Common tobacco), par	468.14	1
gb|AGN_RPC005xd06f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	100.62	1
gb|TT-22_D24 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	239.81	1

gb|KF8C.101E14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101E14, mRN	22488.65	1
gb|KR3B.106M07F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106M07, r	277.48	1
Unknown	19.57	1
tc|Rep: Eukaryotic peptide chain release factor subunit 1-3 - Oryza sativa subsp. jap	59.07	1
Unknown	25.83	1
gb|KN6B.105B09F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105B09, m	101.55	1
tc|Rep: Triosephosphate isomerase - Solanum tuberosum (Potato), complete [TC40	5840.61	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	153.2	1
gb|Nicotiana tabacum mRNA for NtSar1 protein, complete cds [D87821]	19715.4	1
gb|TT-30_F06 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	22.96	1
gb|KN6B.009O23F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009O23, r	2388.72	1
tc|Rep: Predicted protein - Chlamydomonas reinhardtii, partial (3%) [TC45915]	375.89	1
gb|AGN_RPC005xd04f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	365.35	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	511.32	1
tc|Rep: Chromosome undetermined scaffold_257, whole genome shotgun sequenc	148.98	1
gb|Nicotiana tabacum ribosomal protein L3A (RPL3A) mRNA, complete cds [AY395	34.75	1
gb|KL5B.011G19F.051129T7 KL5B Nicotiana tabacum cDNA clone KL5B.011G19, m	179.58	1
Unknown	102.78	1
gb|Nicotiana tabacum NtJAZ2 mRNA for jasmonate ZIM-domain protein 2, complet	531.82	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	124.39	1
Unknown	41.47	1
Unknown	105.9	1
tc|Rep: POM30-like protein - Solanum tuberosum (Potato), partial (36%) [TC64626]	523.28	1
Unknown	1680.26	1
Unknown	535.51	1
tc|Rep: Hypersensitive-induced response protein - Oryza sativa (Rice), partial (96%)	73.67	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	42.02	1
tc|Rep: Acyl-CoA binding protein - Digitalis lanata (Foxglove), partial (97%) [TC6334	7678.46	1
tc|Rep: 60S ribosomal protein L21-like protein - Solanum tuberosum (Potato), com	130.75	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	1790.8	1
Unknown	17371.85	1
tc|Rep: 50S ribosomal protein L33 - Vitis vinifera (Grape), partial (86%) [TC62776]	37.61	1
Unknown	2127	1
gb|KR2B.107E11F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.107E11, m	21.13	1

gb|AGN_RPC007xn02f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	29.08	1
Unknown	1179.18	1
Unknown	22.96	1
tc|Rep: 40S ribosomal protein S15a-1 - Arabidopsis thaliana (Mouse-ear cress), com	67.26	1
gb|Nicotiana tabacum mRNA for protoporphyrin IX oxidase, ppxII gene [Y13466]	82.88	1
gb|AM847113 DL, diurnal library Nicotiana tabacum cDNA clone nt005140079, mR	25.11	1
gb|TOBESTR123H09 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	513.19	1
tc|Rep: Delta-1-pyrroline-5-carboxylate synthetase (P5CS) [Includes: Glutamate 5-k	42.17	1
tc|Rep: Chromosome undetermined scaffold_171, whole genome shotgun sequenc	264.18	1
gb|KG9B.103J17F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103J17, m	1297.36	1
gb|KP1B.037J03F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.037J03, mR	38.22	1
tc|Rep: Chromosome undetermined scaffold_298, whole genome shotgun sequenc	380.34	1
gb|TT-27_O15 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	18.34	1
gb|Nicotiana tabacum apyrase-like protein (APY1) mRNA, complete cds [EF051589]	5180.85	1
gb|KP1B.113I05F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.113I05, mR	698.76	1
gb|KF8B.200E12F.060128T7 KF8 Nicotiana tabacum cDNA clone KF8B.200E12, mR	1950.3	1
gb|BP129934 MAT001 Nicotiana tabacum cDNA clone BY1843, mRNA sequence [B	92.93	1
gb|FS437228 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	3342.41	1
tc|Rep: Glutamate/malate translocator - Nicotiana tabacum (Common tobacco), co	88.6	1
tc|Rep: Chromosome chr5 scaffold_156, whole genome shotgun sequence - Vitis vi	152.55	1
tc|Rep: Guanine nucleotide-binding protein subunit beta - Nicotiana tabacum (Com	110.47	1
Unknown	178.6	1
tc|Rep: Chromosome undetermined scaffold_346, whole genome shotgun sequenc	40.09	1
gb|AGN_PNL229bf1_b6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	45.64	1
tc|Rep: Expressed protein - Oryza sativa subsp. japonica (Rice), partial (57%) [TC70	13019.9	1
Unknown	106.31	1
gb|KG9B.105N09F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105N09,	136.3	1
tc|Rep: Chromosome undetermined scaffold_123, whole genome shotgun sequenc	257.29	1
gb|AGN_RNC129xp14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	128.54	1
gb|TT-11_C11 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	8569.66	1
Unknown	6679.68	1
gb|AGN_RPC021xc19f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	60.05	1
gb|KG9B.101P02F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101P02, m	950.14	1
gb|TT-10_L06 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	25.15	1

gb|Nicotiana tabacum B38 mRNA for DnaJ homolog, complete cds [AB032545]	974.3	1
Unknown	11150.1	1
gb|CHO_SL010xi12f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	3224.87	1
gb|KF8B.100F20F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100F20, mRN	2803.87	1
tc|Rep: Chromosome chr12 scaffold_38, whole genome shotgun sequence - Vitis vi	152.36	1
gb|KR3B.113N05F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.113N05, m	514.72	1
tc|Rep: Chromosome chr11 scaffold_56, whole genome shotgun sequence - Vitis vi	22.31	1
gb|CHO_SL020xp20f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	142.9	1
tc|Rep: 2-oxoglutarate dehydrogenase E2 subunit - Arabidopsis thaliana (Mouse-ea	181.57	1
gb|KL4B.109A09F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.109A09, m	164.7	1
gb|BP531659 MAT005 Nicotiana tabacum cDNA clone BY25183, mRNA sequence [	17.96	1
Unknown	3437.2	1
Unknown	134.55	1
gb|AGN_ELP009xm05f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	78.61	1
tc|Rep: Chromosome chr11 scaffold_56, whole genome shotgun sequence - Vitis vi	119.47	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	19.7	1
gb|Nicotiana tabacum NtYSL1 mRNA for putative yellow stripe-like protein, comple	151.65	1
Unknown	23.69	1
gb|KP1B.102P18F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102P18, m	822.31	1
Unknown	64.95	1
Unknown	507.86	1
tc|Rep: HSR203J - Nicotiana tabacum (Common tobacco), partial (59%) [TC48050]	28.52	1
Unknown	27.77	1
gb|TOBESTR062H06 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	18.93	1
Unknown	428.13	1
Unknown	106.59	1
gb|KP1B.102J04F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102J04, mR	127.78	1
gb|KT7C.108B12F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108B12, mR	1845.75	1
Unknown	27.86	1
gb|KN6B.102L11F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102L11, m	152.12	1
tc|Rep: Gamma response I protein-like - Oryza sativa subsp. japonica (Rice), partial	26.31	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	129.28	1
tc|Rep: CPD photolyase - Spinacia oleracea (Spinach), partial (30%) [TC50636]	496.47	1
gb|TT-35_B02 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	961.82	1

Unknown	28.13	1
gb|KF8C.108H04F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108H04, mR	28.94	1
Unknown	72.21	1
gb|KL5B.111M22F.060117T7 KL5B Nicotiana tabacum cDNA clone KL5B.111M22, m	649.06	1
gb|Nicotiana tabacum mRNA for 14-3-3 f-1 protein, complete cds [AB119476]	18316.3	1
Unknown	105.93	1
Unknown	67.39	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (9%) [TC59	517.9	1
gb|KG9B.102G14F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102G14, m	668.46	1
gb|BP132748 MAT001 Nicotiana tabacum cDNA clone BY4943, mRNA sequence [B	18.26	1
tc|Rep: Molecular chaperone Hsp90-2 - Nicotiana benthamiana, partial (76%) [TC4	871.66	1
tc|Rep: Cyc07 - Nicotiana tabacum (Common tobacco), partial (72%) [TC72415]	524.33	1
gb|KN6B.102A05F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102A05, m	97.22	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	31.42	1
gb|CHO_SL017xj01f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	30.55	1
Unknown	61.36	1
tc|Rep: Similarity - Yarrowia lipolytica (Candida lipolytica), partial (7%) [TC65945]	375.72	1
gb|KL4B.102B04F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102B04, mR	18.85	1
tc|Rep: ribosomal protein L16 - Paramecium aurelia, partial (15%) [TC43985]	45.34	1
Unknown	239.05	1
gb|AGN_RNC116xe20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	19.23	1
tc|Rep: Chromosome undetermined scaffold_70, whole genome shotgun sequence	13968.6	1
gb|AGN_RPC027xk03f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	43.08	1
Unknown	29.88	1
Unknown	525.91	1
Unknown	993.05	1
gb|N.tabacum NeIF-4A14 mRNA [X79141]	8135.52	1
Unknown	46.88	1
gb|KN6B.105K11F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105K11, m	64.58	1
tc|Rep: Nucleobase-ascorbate transporter 6 - Arabidopsis thaliana (Mouse-ear cres	58.92	1
Unknown	61.03	1
gb|AGN_RNC021xj19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	36.27	1
gb|KF8C.101O13F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101O13, mR	191.08	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT33-1-270, cultivar Bright Yellow 2	477.13	1

gb|AM832190 DL, diurnal library Nicotiana tabacum cDNA clone nt005007062, mR	35.43	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	245.8	1
tc|Rep: Enolase - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), parti	485.25	1
gb|TT-22_O05 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	44.31	1
gb|TL13.106C03F.060315T7 TL13 Nicotiana tabacum cDNA clone TL13.106C03, mR	19.91	1
gb|TT-31_F05 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	58.95	1
gb|Nicotiana tabacum sphingolipid delta-8 desaturase (DXDES) mRNA, complete cd	133.9	1
Unknown	22.26	1
gb|KP1B.113H03F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.113H03, m	19.04	1
gb|CHO_SL025xe13f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	155.13	1
tc|Rep: 101 kDa heat shock protein - Nicotiana tabacum (Common tobacco), partial	73.43	1
Unknown	48.27	1
Unknown	54.63	1
tc|Rep: TPSI1 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), partial	56.03	1
Unknown	35.96	1
gb|Tabacco Cab21 mRNA for major chlorophyll a [X52743]	26.54	1
gb|KT7C.102H09F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102H09, mR	1250.83	1
gb|AGN_RNC211xf07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	2726.88	1
Unknown	208.93	1
Unknown	47.59	1
Unknown	46.64	1
gb|Nicotiana tabacum calcium-dependent protein kinase CDPK5 (CDPK5) mRNA, co	57.49	1
gb|AGN_RNC020xa07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	22.5	1
Unknown	36.7	1
Unknown	763.67	1
tc|Rep: Peptidyl-prolyl cis-trans isomerase - Solanum tuberosum (Potato), partial (9	516.59	1
tc|Rep: Enod93 protein - Sonneratia alba, partial (80%) [TC68459]	27.62	1
gb|AGN_ELP024xp15f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	18.97	1
gb|KF8C.103L11F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103L11, mRN	26.49	1
gb|KR3B.108F08F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.108F08, m	87.45	1
tc|Rep: Methylenetetrahydrofolate reductase - Vitis vinifera (Grape), partial (34%)	1233.47	1
tc|Rep: Hydroxyacylglutathione hydrolase cytoplasmic-like - Solanum tuberosum (	25.12	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	25.37	1
gb|KP1B.101C11F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101C11, m	32.07	1

Unknown	21.76	1
tc|Rep: Pyruvate kinase - Arabidopsis thaliana (Mouse-ear cress), partial (84%) [TC	62.95	1
gb|TOBESTR030H01 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	36.16	1
Unknown	19.01	1
Unknown	25.24	1
Unknown	21.67	1
gb|KF8B.100B22F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100B22, mR	21.88	1
gb|AGN_RNC118xn10r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequen	78.44	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	46.46	1
Unknown	11392	1
gb|KR3B.106J18F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106J18, mR	183.16	1
gb|AGN_PNL228ar1_h4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	71.4	1
tc|Rep: Transcription factor JERF1 - Solanum lycopersicum (Tomato) (Lycopersicon	1032.99	1
gb|EST_CSP005xf15f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	87.41	1
Unknown	553.71	1
tc|Rep: 4D11_4 - Brassica rapa subsp. pekinensis (Chinese cabbage), partial (26%) [	39.23	1
tc|Rep: Chloroplast heavy metal P-type ATPase precursor - Arabidopsis thaliana (M	1176.03	1
Unknown	61.67	1
tc|Rep: Ribosomal protein S10, eukaryotic and archaeal form - Medicago truncatul	505.74	1
Unknown	1806.08	1
Unknown	22.31	1
tc|Rep: Chromosome chr2 scaffold_196, whole genome shotgun sequence - Vitis vi	221.15	1
Unknown	246.7	1
Unknown	32.09	1
Unknown	37.07	1
tc|Rep: Ferrochelatase - Vitis vinifera (Grape), partial (16%) [TC55575]	228.42	1
gb|AGN_RNC127xi20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	86.47	1
tc|Rep: ATP synthase subunit d, mitochondrial - Arabidopsis thaliana (Mouse-ear cr	2877.03	1
gb|Nicotiana tabacum NtLCB2 mRNA for serine palmitpoyltransferase subunit2, co	11712.05	1
Unknown	21.26	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	528.37	1
gb|N.tabacum mRNA for glutamate-1-semialdehyde aminotransferase [X65974]	20.32	1
Unknown	2430.15	1
tc|Rep: Ascorbate peroxidase - Capsicum annuum (Bell pepper), complete [TC4715	1167.33	1

gb|KG9B.002B01F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002B01, m	213.33	1
tc|Rep: Superoxide dismutase [Mn], mitochondrial precursor - Capsicum annuum (E	263.03	1
gb|FS416927 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	2913.01	1
Unknown	33.58	1
gb|TT-24_A21 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	607.04	1
tc|Rep: Endoglucanase-like protein - Saccharophagus degradans (strain 2-40 / ATCC	92.49	1
gb|N.tabacum mRNA for GTP-binding protein, SAR1 [X97967]	7095.38	1
tc|Rep: Metallothionein-like protein type 2 - Nicotiana plumbaginifolia (Leadwort-l	48.06	1
gb|KF8B.100M11F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100M11, mR	170.99	1
gb|KR3B.101A06F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101A06, m	43.95	1
tc|Rep: Glycoprotein-like protein - Solanum tuberosum (Potato), partial (55%) [TC6	33.74	1
Unknown	101	1
gb|AGN_ELP024xf21f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	61.1	1
Unknown	74.62	1
tc|Rep: Chromosome undetermined scaffold_69, whole genome shotgun sequence	127.84	1
tc|Rep: Ubiquitin activating enzyme 2 - Nicotiana tabacum (Common tobacco), com	226.5	1
Unknown	265.94	1
tc|Rep: Chromosome undetermined scaffold_222, whole genome shotgun sequenc	31.84	1
gb|AGN_RNC116xi22f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	61.92	1
gb|KR3B.110G23F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110G23, m	1303.8	1
Unknown	640.3	1
Unknown	74.11	1
gb|CHO_SL004xn19f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	86.92	1
gb|KL4B.108P15F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108P15, mR	35.95	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	25.43	1
gb|KT7B.100A12F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100A12, mR	257.91	1
gb|AGN_RNC025xb07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	103.42	1
gb|KG9B.005C06F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005C06, m	26.6	1
gb|KF8C.102B01F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102B01, mRN	96.89	1
gb|KP1B.111O22F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.111O22, m	191.87	1
gb|Nicotiana tabacum S-adenosylmethionine synthase mRNA, complete cds [AF321	18678.15	1
gb|KP1B.101E15F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101E15, mR	66.98	1
gb|KL4B.101I19F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101I19, mRN	20.64	1
Unknown	403.87	1

gb|KG9B.105F07F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105F07, m	41.85	1
gb|KL4B.107F01F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107F01, mR	91.66	1
gb|AGN_RNC026xj02f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	1163.15	1
tc|Rep: Chromosome chr5 scaffold_58, whole genome shotgun sequence - Vitis vin	2521.32	1
gb|KT7C.108F18F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108F18, mRN	594.73	1
tc|Rep: Chromosome undetermined scaffold_257, whole genome shotgun sequenc	115.39	1
Unknown	23.55	1
Unknown	33.32	1
gb|KP1B.110K21F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110K21, ml	25.47	1
tc|Rep: Chromosome undetermined scaffold_53, whole genome shotgun sequence	48.98	1
gb|Nicotiana tabacum peptidyl-prolyl cis [EF051139]	33	1
gb|Nicotiana tabacum calcium [AF435452]	92.66	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	57.37	1
tc|Rep: Ubiquitin carrier protein - Nicotiana benthamiana, complete [TC50166]	127.65	1
Unknown	20.85	1
Unknown	22.76	1
tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	532.1	1
gb|EST_FLW001xa18f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [EI	649.7	1
Unknown	40292.5	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (32%) [TC4	85.2	1
Unknown	260.1	1
Unknown	1536.5	1
Unknown	227.04	1
tc|Rep: Progesterone 5beta-reductase - Isoplexis chalcantha, partial (47%) [TC4716	2549.3	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	1569.92	1
Unknown	99.94	1
gb|AM821017 seedling library, SL Nicotiana tabacum cDNA clone nt002264067, mF	147.26	1
gb|KF8B.200C17F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200C17, mRN	527.88	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	49.35	1
gb|Nicotiana tabacum mRNA for 14-3-3 i-1 protein, complete cds [AB119480]	492.01	1
gb|CHO_SL023xa21f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	498.23	1
Unknown	34.83	1
tc|Rep: Beta-carbonic anhydrase - Nicotiana tabacum (Common tobacco), complet	824.97	1
gb|AGN_ELP006xn23f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	71.98	1

tc|Rep: Fumarate hydratase - Synechococcus sp. WH 5701, partial (4%) [TC45005]	18.24	1
gb|CHO_SL016xb13f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	21.73	1
gb|EST_FLW001xl23f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [EH	760.41	1
gb|BL12.001G14F.060117T7 BL12 Nicotiana tabacum cDNA clone BL12.001G14, mR	552.47	1
Unknown	24.2	1
tc|Rep: Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha	185.72	1
gb|TT-17_K11 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	71.41	1
tc|Rep: Chromosome chr5 scaffold_124, whole genome shotgun sequence - Vitis vi	32.18	1
gb|AGN_RNC017xc21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	32.22	1
Unknown	58.57	1
tc|Rep: DNAJ heat shock protein - Nicotiana tabacum (Common tobacco), partial (9	155.07	1
gb|AM828280 seedling library, SL Nicotiana tabacum cDNA clone nt002181074, mR	98.86	1
gb|AGN_RPC011xi02f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	136.04	1
Unknown	79.83	1
gb|AGN_RNC025xl24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	497.32	1
Unknown	37.07	1
tc|Rep: Thiosulfate sulfurtransferase - Datisca glomerata (Durango root), partial (8	30.99	1
Unknown	29.78	1
gb|N.tabacum mRNA for cyclin A-like protein (clone 30) [X92967]	56.34	1
gb|N.tabacum mRNA for PRT1 protein [Y11996]	136.28	1
Unknown	267.08	1
gb|KR3B.103O02F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.103O02, m	456.17	1
Unknown	35.57	1
gb|Nicotiana tabacum mRNA for glyceraldehyde-3-phosphate dehydrogenase [AJ1	517.03	1
gb|KG9B.005H16F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005H16, m	30.96	1
gb|FS429628 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	10740.45	1
gb|KT7C.110G02F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110G02, mR	119.41	1
tc|Rep: Chromosome undetermined scaffold_221, whole genome shotgun sequenc	324.19	1
gb|Nicotiana tabacum B37 mRNA for MCM protein-like protein, complete cds [AB0	21.12	1
tc|Rep: ATP-dependent Clp protease ATP-binding subunit clpA homolog CD4B, chlo	62.5	1
tc|Rep: Chromosome undetermined scaffold_55, whole genome shotgun sequence	144.41	1
gb|AGN_RNC021xj15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	26.37	1
gb|KG9B.106G24F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106G24, m	80.61	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	812.59	1

tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	27.03	1
tc|Rep: F3O9.16 - Arabidopsis thaliana (Mouse-ear cress), partial (48%) [TC63404]	163.4	1
tc|Rep: Fiber protein Fb12 - Gossypium barbadense (Sea-island cotton) (Egyptian c	1727.93	1
Unknown	995.84	1
tc|Rep: Chromosome chr2 scaffold_112, whole genome shotgun sequence - Vitis vi	46263.35	1
tc|Rep: DNA binding protein homolog - Solanum tuberosum (Potato), partial (13%)	80.46	1
tc|Rep: Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial p	125.73	1
gb|TT-24_M03 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	133.79	1
gb|TT-31_B14 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	134.25	1
gb|TT-18_E11 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	23.25	1
tc|Rep: Protein phosphatase 2C - Solanum lycopersicum (Tomato) (Lycopersicon es	249.88	1
Unknown	26.56	1
gb|Nicotiana tabacum Fas-associated factor-like protein mRNA, partial cds [AY7405	209.36	1
gb|KP1B.001N23F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001N23, m	31983.1	1
tc|Rep: F-ATPase family transporter: protons - Ostreococcus lucimarinus (strain CC	23.42	1
gb|KP1B.109P05F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109P05, m	61.44	1
gb|KL4B.101J19F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101J19, mR	77.57	1
tc|Rep: Cellulose synthase 3 - Eucalyptus grandis (Flooded gum), partial (58%) [TC6	502.04	1
Unknown	124.81	1
Unknown	1926.15	1
gb|KF8C.102H19F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102H19, mR	57.29	1
gb|AM819908 DL, diurnal library Nicotiana tabacum cDNA clone nt005005087, mR	79.97	1
gb|Nicotiana tabacum cinnamyl alcohol dehydrogenase 1 (CAD1-7) mRNA, complet	986.55	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (90%) [TC6	99.17	1
tc|Rep: Chromosome undetermined scaffold_448, whole genome shotgun sequenc	264.85	1
gb|AGN_PNL227af1_d11.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	36.28	1
tc|Rep: 40S ribosomal protein S15-like - Solanum tuberosum (Potato), complete [T	111.03	1
gb|KT7C.104K01F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104K01, mR	2762.76	1
gb|BP130751 MAT001 Nicotiana tabacum cDNA clone BY2751, mRNA sequence [B	41.23	1
tc|Rep: Chromosome undetermined scaffold_235, whole genome shotgun sequenc	55.75	1
gb|CHO_SL009xf05f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	977.39	1
Unknown	236.7	1
Unknown	26.13	1
gb|KF8C.106G12F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106G12, mR	443.54	1

gb|TT-01_A03 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	679.89	1
Unknown	28.12	1
gb|KG9B.103D08F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103D08,	362.26	1
tc|Rep: Phosphosulfolactate synthase-related protein - Solanum lycopersicum (To	309.78	1
gb|N.tabacum mRNA for cyclin A-like protein (clone 19) [X92966]	46.19	1
Unknown	23.66	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	410.59	1
Unknown	256.96	1
gb|CHO_SL014xb10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1054.03	1
Unknown	78.06	1
gb|KG9B.001B21F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001B21,	185.61	1
gb|KG9B.003B22F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003B22,	132.02	1
gb|KF8B.201A07F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201A07, mR	21.4	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	34.82	1
gb|KG9B.103P09F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103P09,	322.27	1
gb|TT-41_F01 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	35.71	1
Unknown	52.92	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	40.23	1
Unknown	32.6	1
Unknown	62.53	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	1032.46	1
Unknown	18.96	1
gb|Nicotiana tabacum clone D222-BH4 CYP71AU1 mRNA, complete cds [DQ350357	92.43	1
gb|KP1B.101O10F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101O10,	513.57	1
Unknown	245.98	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	2865.6	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	32.39	1
tc|Rep: Chromosome undetermined scaffold_298, whole genome shotgun sequenc	45.56	1
tc|Rep: Ribulose-5-phosphate-3-epimerase - Pisum sativum (Garden pea), partial (	192.02	1
tc|Rep: AML1 - Medicago truncatula (Barrel medic), partial (38%) [TC58030]	69.96	1
gb|KR3B.114P19F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.114P19, m	226.36	1
Unknown	20.76	1
gb|AGN_RPC015xi19f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	28.12	1
gb|FS391824 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	32.25	1

Unknown	61.74	1
tc|Rep: Predicted protein - Chlamydomonas reinhardtii, partial (5%) [TC56158]	514.51	1
tc|Rep: MYB-CC type transfactor - Solanum tuberosum (Potato), partial (89%) [TC5	469.89	1
gb|AGN_RPC007xg16f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	48.24	1
Unknown	2986.99	1
tc|LERYGTOM5 L.esculentum (rY mutant) GTOM5 mRNA for mutant phytoene synt	25.72	1
gb|AGN_ELP008xn07f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	79.95	1
gb|KP1B.107P23F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107P23, m	1116.21	1
gb|BP135456 MAT001 Nicotiana tabacum cDNA clone BY7971, mRNA sequence [B	23.18	1
Unknown	19.09	1
gb|Nicotiana tabacum callus associated protein (CAP) mRNA, partial cds [U01961]	45.03	1
gb|KF8C.101E15F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101E15, mR	1206.88	1
Unknown	44.82	1
tc|Rep: Glycine dehydrogenase [decarboxylating], mitochondrial precursor - Solanu	15693.2	1
Unknown	7930.03	1
Unknown	42.28	1
gb|Nicotiana tabacum Avr9 [AF211537]	624.3	1
gb|KP1B.107F16F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107F16, m	1755.19	1
Unknown	41.23	1
gb|AGN_PNL224bf1_d7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	60.95	1
Unknown	18.23	1
tc|Rep: Common plant regulatory factor 7 - Petroselinum crispum (Parsley) (Petros	1044.3	1
gb|TT-04_C17 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	4747.74	1
gb|TL13.102D10F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.102D10, mR	232.38	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	68.94	1
tc|Rep: Ribulose-5-phosphate-3-epimerase - Pisum sativum (Garden pea), partial (	135.3	1
Unknown	28.73	1
tc|Rep: Ran binding protein - Nicotiana benthamiana, partial (89%) [TC70300]	85.05	1
Unknown	43.25	1
tc|Rep: Tubby-like F-box protein 7 - Arabidopsis thaliana (Mouse-ear cress), partial	71.93	1
tc|Rep: 26S proteasome regulatory particle non-ATPase subunit5 - Oryza sativa sub	534.03	1
gb|3H05 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', m	59.33	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	97.55	1
gb|TT-09_F08 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	41.63	1

tc|Rep: Ribosomal protein L11-like - Nicotiana tabacum (Common tobacco), compl	176.92	1
tc|Rep: Adenylate kinase family-like protein - Solanum tuberosum (Potato), partial	615.47	1
tc|Rep: Peptidyl-prolyl cis-trans isomerase - Vitis vinifera (Grape), partial (82%) [TC	505.41	1
Unknown	1617.05	1
tc|Rep: Cyc07 - Nicotiana tabacum (Common tobacco), partial (72%) [TC72415]	756.43	1
gb|KP1B.101J04F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101J04, mR	29.73	1
gb|KG9B.104P06F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104P06, m	226.08	1
gb|AGN_RNC021xm19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	24.64	1
tc|Rep: PRP38 - Medicago truncatula (Barrel medic), partial (90%) [TC60543]	443.5	1
gb|AGN_RNC114xb17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	365.24	1
tc|Rep: Ubiquitin carrier protein - Mesembryanthemum crystallinum (Common ice	8953.59	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	27.11	1
gb|AGN_RNC007xc16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	489.32	1
gb|AM809125 seedling library, SL Nicotiana tabacum cDNA clone nt002125036, m	503.16	1
tc|Rep: YUP8H12R.36 - Arabidopsis thaliana (Mouse-ear cress), partial (9%) [TC502	32.02	1
tc|Rep: Chlorophyll a-b binding protein 7, chloroplast precursor - Solanum lycopers	78.56	1
tc|Rep: Small basic intrinsic protein 1 - Vitis vinifera (Grape), partial (76%) [TC7066	26.15	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	64.68	1
tc|Rep: Per1-like family protein - Solanum tuberosum (Potato), partial (97%) [TC40	32.41	1
gb|KG9B.004H05F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004H05, n	25.23	1
Unknown	44.28	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	180.61	1
gb|N.tabacum npp1 mRNA for protein phosphatase type 1 [Z93768]	2622.26	1
Unknown	34.32	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (40%) [TC4	2870.93	1
gb|AGN_RNC021xp22f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	26.03	1
tc|Rep: P40-like protein - Solanum tuberosum (Potato), partial (93%) [TC43627]	36.77	1
gb|Nicotiana tabacum UDP-glucuronate decarboxylase 1 mRNA, complete cds [AY6	1454.72	1
Unknown	547.58	1
gb|KR3B.106B02F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106B02, m	387.95	1
tc|Rep: Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial precursor	128.9	1
Unknown	2822.87	1
gb|KL4B.108M21F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108M21, m	41.3	1
tc|Rep: Histone deacetylase HDT1 - Solanum chacoense (Chaco potato), partial (88	78.46	1

tc|Rep: Predicted protein - Chlamydomonas reinhardtii, partial (12%) [TC75316]	248.37	1
gb|TL13.101G08F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.101G08, mR	1988.4	1
tc|Rep: Probable U6 snRNA-associated Sm-like protein LSm4 - Nicotiana tabacum (	271.66	1
gb|KP1B.112B14F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.112B14, m	39.46	1
tc|Rep: Actin-related protein 3 - Nicotiana tabacum (Common tobacco), complete [	18.21	1
tc|Rep: GRAS1 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), partia	18.9	1
tc|Rep: NmrA-like family protein - Solanum demissum (Wild potato), complete [TC	198.96	1
gb|AGN_ELP009xo18f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	29.59	1
tc|Rep: 1,4-alpha-glucan-maltohydrolase - Solanum lycopersicum (Tomato) (Lycope	616.02	1
tc|Rep: Chromosome chr5 scaffold_58, whole genome shotgun sequence - Vitis vin	900.07	1
gb|TT-21_J07 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	851.92	1
Unknown	29.92	1
gb|BP136794 MAT001 Nicotiana tabacum cDNA clone BY9418, mRNA sequence [B	512.89	1
gb|KG9B.105H19F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105H19, n	342.39	1
Unknown	99.9	1
tc|Rep: ATP synthase subunit d, mitochondrial - Arabidopsis thaliana (Mouse-ear cr	2944.23	1
Unknown	23.11	1
Unknown	19.72	1
Unknown	346.99	1
gb|KR3B.113F23F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.113F23, m	243.68	1
Unknown	18.61	1
Unknown	278.54	1
Unknown	97.75	1
tc|Rep: Tobamovirus multiplication 1 - Nicotiana tabacum (Common tobacco), part	138.06	1
Unknown	102.91	1
gb|AGN_RNC015xc08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	182.83	1
tc|Rep: Glyceraldehyde-3-phosphate dehydrogenase - Nicotiana tabacum (Commo	336.59	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	174.72	1
tc|Rep: KH domain-containing protein-like - Oryza sativa subsp. japonica (Rice), par	21.56	1
Unknown	88.38	1
tc|Rep: Ribosomal protein S19 - Nicotiana tabacum (Common tobacco), complete [	165.48	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	68.21	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	376.82	1
Unknown	676.25	1

tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	1511.33	1
tc|Rep: Chromosome chr12 scaffold_78, whole genome shotgun sequence - Vitis vi	230.79	1
gb|KG9B.103L11F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103L11, m	66.32	1
tc|Rep: Chromosome chr13 scaffold_74, whole genome shotgun sequence - Vitis vi	80.63	1
tc|Rep: ATP synthase subunit beta, mitochondrial precursor - Nicotiana plumbagini	445.85	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	915.44	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	57.8	1
tc|Rep: DnaJ-like protein - Solanum tuberosum (Potato), partial (41%) [TC52062]	146.38	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	650.55	1
tc|Rep: Chromosome chr2 scaffold_112, whole genome shotgun sequence - Vitis vi	38.74	1
tc|Rep: Plasma membrane ATPase 4 - Nicotiana plumbaginifolia (Leadwort-leaved t	71.02	1
gb|KN6B.106O06F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.106O06, r	7816.97	1
Unknown	30.74	1
gb|KT7B.107M20F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107M20, m	22.95	1
Unknown	29.23	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT24-1-320, cultivar Bright Yellow 2	89.17	1
gb|CHO_SL013xn02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	765.11	1
Unknown	382.56	1
Unknown	148.39	1
gb|AGN_ELP012xk06f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	182.87	1
Unknown	43.08	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	513.17	1
tc|Rep: Ankyrin domain protein - Nicotiana tabacum (Common tobacco), partial (4	174.54	1
gb|N.tabaccum mRNA for ubiquitin activating enzyme E1 [Y10804]	301.52	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	85.98	1
gb|AGN_RNC016xb07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	139.09	1
Unknown	26	1
Unknown	21.96	1
Unknown	27.46	1
gb|Peg19C Early stage of anther development specific suppression subtractive cDN	352.56	1
Unknown	58.03	1
gb|CHO_SL011xi16f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	1676.78	1
gb|AGN_PNL227af1_b12.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	1691.29	1
gb|KG9B.104B08F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104B08, m	916.4	1

gb|KF8C.109L11F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109L11, mRN	11532.4	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	24.54	1
Unknown	457.79	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	247.48	1
gb|KF8B.201F18F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201F18, mRN	136.45	1
Unknown	83.4	1
tc|Rep: Chromosome undetermined scaffold_257, whole genome shotgun sequenc	4651.02	1
gb|KN6B.100I14F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100I14, mF	36.82	1
tc|Rep: Chromosome chr10 scaffold_312, whole genome shotgun sequence - Vitis	16489.9	1
Unknown	34379.6	1
gb|AGN_RNC026xk17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	133.66	1
gb|KT7C.108N19F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108N19, mR	234.59	1
Unknown	20.98	1
tc|Rep: Chromosome chr5 scaffold_72, whole genome shotgun sequence - Vitis vin	134.92	1
tc|Rep: Cell division cycle protein 48 homolog - Capsicum annuum (Bell pepper), pa	1111.55	1
gb|Nicotiana tabacum PK12 protein kinase (PK12) mRNA, complete cds [U73937]	113.83	1
gb|TT-30_N17 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	127.89	1
tc|Rep: Beta-ketoacyl-ACP synthase III - Jatropha curcas, partial (38%) [TC52485]	8641.23	1
gb|AM830473 seedling library, SL Nicotiana tabacum cDNA clone nt002049033, mF	49.84	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	72.73	1
Unknown	46.28	1
gb|TT-10_C12 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	23.71	1
Unknown	49.83	1
tc|Rep: Eukaryotic peptide chain release factor subunit 1-3-like - Solanum tuberosu	24.62	1
gb|KT7C.108J02F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108J02, mRN	1585.58	1
tc|Rep: Plasma membrane ATPase 4 - Nicotiana plumbaginifolia (Leadwort-leaved t	68.78	1
gb|CHO_SL022xm01f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	2905.6	1
tc|Rep: Chromosome undetermined scaffold_129, whole genome shotgun sequenc	370.86	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	249.93	1
gb|AGN_PNL210af1_h12.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	44.38	1
Unknown	564.37	1
Unknown	531.68	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	31.85	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	517.71	1

gb|AGN_ELP009xl12f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	18.28	1
tc|Rep: Alcohol dehydrogenase class III-like protein - Solanum tuberosum (Potato),	176.24	1
gb|KF8B.202P17F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202P17, mRN	56.74	1
tc|Rep: Heat shock factor 2-binding protein. - Gallus gallus, partial (6%) [TC66474]	25.4	1
gb|KG9B.005M08F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005M08,	41.66	1
Unknown	903	1
gb|KF8C.101D17F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101D17, mR	2689.41	1
gb|TT-31_K24 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	55.3	1
gb|Nicotiana tabacum SR1 Nt-rab7b mRNA, complete cds [L29275]	250.39	1
gb|Nicotiana tabacum putative mitotic phosphoprotein N' end family protein-like n	115.31	1
Unknown	42.17	1
tc|Rep: Chromosome undetermined scaffold_2548, whole genome shotgun sequen	25.37	1
Unknown	26.66	1
Unknown	17.86	1
gb|AGN_RPC024xg23f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	79.74	1
gb|TT-23_H10 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	276.21	1
gb|KN6B.100O16F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100O16, r	256.48	1
gb|KT7C.101C21F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.101C21, mR	47.1	1
Unknown	122.44	1
Unknown	421.73	1
Unknown	525.48	1
gb|KN6B.106B02F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.106B02, m	31.14	1
gb|BP534117 MAT005 Nicotiana tabacum cDNA clone BY32072, mRNA sequence [	25.26	1
gb|Nicotiana tabacum vacuolar H+-ATPase B subunit mRNA, complete cds [AF2206	505.83	1
gb|KF8C.105D01F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105D01, mR	978.37	1
tc|Rep: Chromosome undetermined scaffold_345, whole genome shotgun sequenc	65.94	1
gb|BP534541 MAT005 Nicotiana tabacum cDNA clone BY33121, mRNA sequence [	91.63	1
gb|TOBESTR023F04 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	784.64	1
Unknown	18317.6	1
gb|AGN_RPC015xd09f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	24.87	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	144.23	1
gb|KR3B.108H08F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.108H08, m	409.13	1
gb|KR2B.109K19F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.109K19, m	36.95	1
gb|AGN_RPC020xn11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	99.95	1

Unknown	66.04	1
Unknown	21.39	1
gb|AGN_RNC020xm19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	889.57	1
gb|KP1B.001G02F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001G02, m	33.56	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	528.7	1
tc|Rep: AML1 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), partial	11549	1
gb|KT7C.112F11F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112F11, mRN	936.62	1
Unknown	36.38	1
Unknown	26.33	1
tc|Rep: Os08g0518300 protein - Oryza sativa subsp. japonica (Rice), partial (8%) [TC	42.02	1
Unknown	3742.22	1
Unknown	128.34	1
tc|Rep: Impa2 - Nicotiana benthamiana, partial (98%) [TC72049]	4741.67	1
gb|KP1B.101O18F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101O18, m	67.49	1
gb|AGN_RPC021xl03f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	36.66	1
gb|KR2B.107P02F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.107P02, m	2643.33	1
gb|KG9B.001F13F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001F13, m	168.6	1
gb|Nicotiana tabacum putative UDP-glucuronate decarboxylase 4 mRNA, partial cd	2961.5	1
gb|CHO_SL005xm18f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	1757.5	1
tc|Rep: Mitochondrial phosphate transporter - Lotus japonicus, partial (88%) [TC44	18531.65	1
gb|CHO_SL013xg16f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	523.05	1
tc|Rep: Hsp20.1 protein - Solanum peruvianum (Peruvian tomato) (Lycopersicon pe	18.98	1
tc|Rep: Chromosome chr12 scaffold_78, whole genome shotgun sequence - Vitis vi	51.11	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	144.46	1
gb|FS411604 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	24.44	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	1447.96	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	150.92	1
Unknown	23.75	1
Unknown	116.41	1
Unknown	81.36	1
gb|KF8C.102A21F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102A21, mRN	53080.1	1
tc|Rep: Elongation factor 1-alpha - Nicotiana tabacum (Common tobacco), partial (	189.46	1
Unknown	511.39	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	245.59	1

tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	33698.05	1
gb|AGN_RPC019xj05f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	27.37	1
Unknown	92.95	1
gb|KG9B.001K12F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001K12, m	23.04	1
gb|KL5B.116F12F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.116F12, mR	86.32	1
tc|Rep: Centrin - Nicotiana tabacum (Common tobacco), complete [TC41163]	39.67	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	388.22	1
gb|Nicotiana tabacum mRNA for thioredoxin peroxidase [AJ309009]	625.38	1
gb|BP132942 MAT001 Nicotiana tabacum cDNA clone BY5155, mRNA sequence [B	33.82	1
tc|Rep: Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vi	33.41	1
gb|AGN_RNC109xb01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	171.05	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	346.55	1
gb|KL4B.101G02F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101G02, m	48.63	1
Unknown	18.05	1
gb|TOBESTR017C04 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	49.77	1
gb|AGN_RNC019xg12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	116.9	1
Unknown	44.48	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	61.09	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	24.39	1
tc|Rep: Chromosome chr8 scaffold_115, whole genome shotgun sequence - Vitis vi	519.25	1
gb|CHO_SL025xc21f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	2588.02	1
gb|TOBESTR094D04 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	144.36	1
gb|KP1B.101N06F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101N06, m	185.55	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	140.03	1
Unknown	41.23	1
gb|TT-27_J08 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	1714.38	1
gb|TL13.102I09F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.102I09, mRN	58.67	1
tc|Rep: AMP-binding protein - Arabidopsis thaliana (Mouse-ear cress), partial (29%	160.69	1
gb|AGN_RNC010xj15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	17.29	1
tc|Rep: Ras-related protein Rab5 - Nicotiana tabacum (Common tobacco), complet	206.36	1
gb|AGN_PNL221cf1_d10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	23.71	1
gb|Nicotiana tabacum mRNA for transcription factor Ntlim1, complete cds [AB023	28.9	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	105.81	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	89.22	1

tc|Rep: Chromosome chr5 scaffold_124, whole genome shotgun sequence - Vitis vi	123.27	1
gb|TT-27_L12 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	31.55	1
tc|Rep: Chromosome undetermined scaffold_734, whole genome shotgun sequenc	428.99	1
Unknown	44.76	1
gb|KR2B.110C17F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110C17, m	24.71	1
tc|Rep: Nucleoside diphosphate kinase 2, chloroplast precursor - Nicotiana tabacu	343.17	1
gb|KG9B.003K05F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003K05, m	37.07	1
gb|AGN_RNC106xd06r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	47.43	1
Unknown	23.94	1
tc|Rep: SLT1 protein - Nicotiana tabacum (Common tobacco), partial (41%) [TC530	83.63	1
tc|Rep: Common plant regulatory factor 7 - Petroselinum crispum (Parsley) (Petros	1185.69	1
gb|KN6B.107N21F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.107N21, r	60.6	1
Unknown	25.1	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	423.57	1
tc|Rep: RNA-binding protein - Medicago truncatula (Barrel medic), partial (50%) [TC	460.12	1
gb|KF8C.102A06F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102A06, mRN	1022.51	1
Unknown	497.76	1
Unknown	406.8	1
Unknown	141.03	1
gb|TDF16 Tobacco BY-2 ESTs modulated by Rhodococcus fascians Nicotiana tabacu	3124.07	1
Unknown	1301.08	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	263.96	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT33-3-245, cultivar Bright Yellow 2	22.49	1
Unknown	34.15	1
Unknown	1073.85	1
Unknown	43.85	1
tc|Rep: Elicitor-inducible protein EIG-J7 - Capsicum annuum (Bell pepper), partial (	3137.84	1
Unknown	1103.02	1
gb|TT-38_D17 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	424.79	1
gb|KR3B.109F02F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109F02, m	12519.15	1
tc|Rep: Proline oxidase/dehydrogenase 1 - Nicotiana tabacum (Common tobacco),	1348.28	1
tc|Rep: Chromosome chr13 scaffold_152, whole genome shotgun sequence - Vitis	28.75	1
gb|TT-18_H11 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	159.77	1
gb|KL4B.111C04F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111C04, mR	101.44	1

tc|Rep: Chromosome undetermined scaffold_1169, whole genome shotgun sequen	52.62	1
gb|EST_CSP001xg06f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	32.85	1
gb|TT-19_N13 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	642.47	1
tc|Rep: Potassium channel NKT1 - Nicotiana tabacum (Common tobacco), complete	1442.57	1
gb|AGN_RPC007xc24f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	129.85	1
gb|AGN_PNL213ar1_b8.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	94.36	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	22.9	1
gb|TL13.111M15F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.111M15, m	573.91	1
gb|FS412034 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	18.17	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	1046.43	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	721.27	1
tc|Rep: Glutamine synthetase - Nicotiana plumbaginifolia (Leadwort-leaved tobacc	3266.36	1
tc|Rep: Chromosome undetermined scaffold_349, whole genome shotgun sequenc	45.64	1
gb|TT-47_I23 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	444.25	1
tc|Rep: Chromosome undetermined scaffold_143, whole genome shotgun sequenc	19.14	1
Unknown	821.91	1
tc|Rep: Cell division cycle protein 48 homolog - Glycine max (Soybean), partial (42%	510.06	1
tc|Rep: GDP-D-mannose pyrophosphorylase - Nicotiana tabacum (Common tobacc	328.27	1
gb|KR3B.111D18F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111D18, m	171.15	1
tc|Rep: Chromosome chr10 scaffold_43, whole genome shotgun sequence - Vitis vi	763.59	1
gb|EST_YP003xn17f1.ab1 EST_YP Nicotiana tabacum cDNA, mRNA sequence [EH61	19.54	1
Unknown	610.88	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	208	1
Unknown	126.47	1
tc|Rep: Chromosome chr3 scaffold_95, whole genome shotgun sequence - Vitis vin	27.06	1
tc|Rep: 50S ribosomal protein L33 - Vitis vinifera (Grape), partial (86%) [TC61399]	19.74	1
Unknown	40.17	1
gb|TT-29_J20 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	109.98	1
gb|BP530118 MAT005 Nicotiana tabacum cDNA clone BY21102, mRNA sequence [	9479.35	1
gb|KF8C.106A11F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106A11, mRN	667.73	1
tc|Rep: Chromosome chr7 scaffold_275, whole genome shotgun sequence - Vitis vi	734.51	1
Unknown	1166.48	1
gb|AJ632774 Nicotiana tabacum leaf Nicotiana tabacum cDNA clone Nt02-F06, mR	25.69	1
gb|KP1B.105D14F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105D14, m	183.73	1

gb|EST_FLW001xk07f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	679.22	1
tc|Rep: Catalase isozyme 3 - Nicotiana plumbaginifolia (Leadwort-leaved tobacco),	9346.91	1
tc|Rep: Peroxisomal acyl-CoA oxidase 1A - Solanum lycopersicum (Tomato) (Lycop	906.82	1
tc|Rep: PRL1 protein - Arabidopsis thaliana (Mouse-ear cress), partial (83%) [TC587	331.85	1
Unknown	756.19	1
gb|Nicotiana tabacum Mg protoporphyrin chelatase subunit (Chl I) mRNA, complet	26.95	1
gb|AM832067 DL, diurnal library Nicotiana tabacum cDNA clone nt005227057, mR	22.3	1
gb|AGN_PNL225dr1_b12.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRN	120.42	1
gb|KL4B.103L20F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103L20, mR	517.02	1
Unknown	41.25	1
gb|FS392203 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	226.89	1
Unknown	198.69	1
Unknown	75.2	1
gb|KF8B.200B01F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200B01, mR	42.22	1
Unknown	23.92	1
gb|TT-08_N19 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	42.31	1
tc|Rep: Chromosome chr12 scaffold_57, whole genome shotgun sequence - Vitis vi	201.59	1
tc|Rep: Chromosome undetermined scaffold_171, whole genome shotgun sequenc	1034.32	1
Unknown	4729.49	1
tc|Rep: ADP ribosylation factor 002 - Daucus carota (Carrot), partial (93%) [TC5148	13808.05	1
gb|Nicotiana tabacum mRNA for Avr9 elicitor response protein [AJ006228]	52.57	1
tc|Rep: Ycf3 - Ranunculus macranthus (Large buttercup), partial (71%) [TC72285]	41.13	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	144.04	1
gb|AM802310 seedling library, SL Nicotiana tabacum cDNA clone nt002093050, m	157.73	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	234.37	1
Unknown	117.16	1
gb|KR3B.108J11F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.108J11, mR	148.38	1
gb|TT-07_I17 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	151.83	1
Unknown	108.61	1
gb|KL5B.001H06F.050901T7 KL5B Nicotiana tabacum cDNA clone KL5B.001H06, m	938.95	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	723.35	1
Unknown	23.29	1
gb|Nicotiana tabacum GTP-binding protein (Ran-A1) mRNA, complete cds [L16767]	2873.9	1
gb|KP1B.101O07F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101O07, m	33.26	1

gb|KP1B.101G06F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101G06, m	1150.02	1
gb|KL4B.109G08F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.109G08, m	38.1	1
Unknown	101.06	1
gb|KP1B.104L17F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104L17, m	138.13	1
Unknown	113.67	1
gb|CHO_SL008xc16f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	576.98	1
tc|Rep: Chromosome chr2 scaffold_140, whole genome shotgun sequence - Vitis vi	3212.76	1
tc|Rep: inositol or phosphatidylinositol phosphatase/ phosphoric monoester hydro	23.72	1
gb|KL5B.110N11F.060117T7 KL5B Nicotiana tabacum cDNA clone KL5B.110N11, m	184.79	1
gb|KF8C.104K05F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104K05, mR	181.44	1
tc|Rep: Luminal-binding protein 3 - Nicotiana tabacum (Common tobacco), partial (	10914.55	1
Unknown	26.39	1
gb|TT-36_F22 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	158.58	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	163.66	1
tc|Rep: SNF7 family protein, expressed - Oryza sativa subsp. japonica (Rice), partial	1034.11	1
gb|KN6B.103P05F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103P05, m	24.45	1
Unknown	33.14	1
gb|AGN_RNC127xd05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	20.45	1
Unknown	511.97	1
Unknown	35.16	1
Unknown	65.33	1
tc|Rep: Nuclear transport factor 2 - Arabidopsis thaliana (Mouse-ear cress), partial	1200.9	1
gb|N.tabacum PKTL7 mRNA for protein kinase [X71057]	189.65	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	221.24	1
Unknown	25014.75	1
gb|KF8C.102A21F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102A21, mR	53803.5	1
tc|Rep: Ripening regulated protein-like - Solanum tuberosum (Potato), complete [T	97.55	1
gb|TT-17_J16 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	3338.33	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	28.55	1
gb|AGN_RNC018xn19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	32.13	1
Unknown	102.81	1
Unknown	19.44	1
gb|AGN_RNC010xc01r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	55.42	1
gb|Nicotiana tabacum cDNA-AFLP fragment N_BC2M34-310 sequence [DQ460102]	471.29	1

tc|Rep: Acyl-CoA binding protein - Digitalis lanata (Foxglove), partial (97%) [TC6334	510.22	1
Unknown	1138.27	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	2013.15	1
Unknown	20748.85	1
Unknown	106.9	1
Unknown	44.28	1
gb|CHO_SL019xi02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	489.44	1
tc|Rep: Luminal-binding protein 8 - Nicotiana tabacum (Common tobacco), comple	8226.14	1
gb|AGN_PNL224af1_h1.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	51.66	1
gb|AM783324 COL, cold overnight library Nicotiana tabacum cDNA clone nt006021	96.21	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	43.43	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	1576.36	1
Unknown	45.96	1
tc|Rep: Acireductone dioxygenase - Solanum tuberosum (Potato), complete [TC405	7594.06	1
gb|KN6B.105P12F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105P12, m	36.03	1
tc|Rep: Nt-rab7c protein - Nicotiana tabacum (Common tobacco), partial (52%) [TC	18407.6	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT1-31-215, cultivar Bright Yellow 2	32.21	1
gb|TT-34_N02 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	348	1
Unknown	962.33	1
gb|TT-01_B03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	24.73	1
gb|KF8C.102F19F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102F19, mRN	101.3	1
Unknown	84.87	1
tc|Rep: Acyltransferase family protein - Cytophaga hutchinsonii (strain ATCC 33406	210.73	1
gb|BP131040 MAT001 Nicotiana tabacum cDNA clone BY3062, mRNA sequence [BI	147.42	1
gb|CHO_SL018xn22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	2094.89	1
gb|KR3B.108D01F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.108D01, m	22.4	1
gb|KN6B.105P19F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105P19, m	41.09	1
gb|TT-17_I13 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	43.23	1
Unknown	13902.5	1
gb|AGN_RPC019xa16f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	1139.21	1
tc|Rep: Galactinol synthase - Brassica napus (Rape), partial (65%) [TC72414]	27.67	1
gb|AGN_RPC011xd05f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	185.72	1
Unknown	122.98	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	757.99	1

Unknown	21.7	1
gb|TT-47_H20 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	64.43	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	159.35	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	519.15	1
Unknown	8538.06	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	18.26	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	29.55	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	49.68	1
tc|Rep: Glycoprotein-like protein - Solanum tuberosum (Potato), partial (97%) [TC5	53.49	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	839.87	1
Unknown	27.68	1
tc|Rep: Branched-chain amino acid aminotransferase - Solanum tuberosum (Potatc	102.07	1
Unknown	246.75	1
Unknown	41.69	1
gb|KF8B.202A03F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202A03, mRI	10466.9	1
tc|Rep: DnaJ-like protein - Solanum tuberosum (Potato), partial (46%) [TC44527]	8103.07	1
Unknown	3303.59	1
gb|AGN_RNC026xd16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	40.32	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	83.93	1
gb|KP1B.102J04F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102J04, mR	34.81	1
gb|Nicotiana tabacum NtADH mRNA for allyl alcohol dehydrogenase, complete cds	1092.09	1
gb|AGN_RNC005xc17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	224.59	1
gb|BP534488 MAT005 Nicotiana tabacum cDNA clone BY33067, mRNA sequence [E	179.65	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	23.99	1
tc|Rep: MYB-CC type transfactor - Solanum tuberosum (Potato), partial (97%) [TC4	31.12	1
tc|GB|U66264.1|AAC49970.1 ubiquitin [Nicotiana tabacum] [NP917335]	30228.45	1
Unknown	44.15	1
tc|Rep: Tousled-like protein kinase - Nicotiana glutinosa (Tobacco), partial (44%) [T	20.79	1
Unknown	79.07	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	91.15	1
tc|Rep: AT4g05320/C17L7_240 - Arabidopsis thaliana (Mouse-ear cress), partial (98	648.43	1
gb|KR3B.111J10F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111J10, mR	47.73	1
tc|Rep: ATP synthase subunit delta', mitochondrial precursor - Ipomoea batatas (Sv	663.41	1
Unknown	27.66	1

tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (93%) [TC5	42.28	1
Unknown	58.05	1
tc|Rep: Homolog of defender against apoptotic death 1 homolog - Nicotiana suave	886.84	1
tc|Rep: NtK-1-like - Solanum tuberosum (Potato), complete [TC43192]	10458.85	1
gb|AGN_RNC125xn09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	133.29	1
Unknown	2483.77	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC1-12-275, cultivar Bright Yellow 2	2858.45	1
gb|KP1B.111O22F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.111O22, m	189.37	1
gb|KG9B.001M18F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001M18,	44.89	1
Unknown	156.24	1
Unknown	31.76	1
tc|Rep: Chromosome undetermined scaffold_143, whole genome shotgun sequenc	387.3	1
gb|AGN_PNL222br1_d1.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	112.16	1
tc|Rep: 3-isopropylmalate dehydrogenase 2, chloroplast precursor - Arabidopsis th	26.7	1
tc|Rep: Os05g0119300 protein - Oryza sativa subsp. japonica (Rice), partial (63%) [T	474.78	1
gb|KR3B.112J23F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112J23, mR	79.85	1
gb|TT-35_B15 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	298.07	1
gb|TT-34_K15 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	69.41	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	21.47	1
gb|Nicotiana tabacum relA [AY046898]	682.45	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	39.59	1
tc|Rep: RanBP2-type zinc finger protein At1g67325 - Arabidopsis thaliana (Mouse-e	478.97	1
gb|AGN_ELP005xb08f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	73	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	196.99	1
Unknown	22.69	1
Unknown	97.73	1
Unknown	25.71	1
gb|Nicotiana tabacum S25-PR6 mRNA, complete cds [U44760]	31.17	1
tc|Rep: F3L24.22 protein - Arabidopsis thaliana (Mouse-ear cress), partial (78%) [TC	35.12	1
Unknown	265.1	1
Unknown	29.95	1
Unknown	20.74	1
Unknown	68.78	1
gb|KN6B.102J12F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102J12, m	24.84	1

tc|Rep: Diacylglycerol acylCoA acyltransferase - Nicotiana tabacum (Common toba	135.15	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	241.15	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	53.62	1
gb|AM782197 seedling library, SL Nicotiana tabacum cDNA clone nt002176022, m	49.35	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	27.17	1
Unknown	1538.11	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	38.73	1
tc|Rep: Polyubiquitin - Thlaspi caerulescens (Alpine penny-cress) (Thlaspi calaminar	686.87	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	23.31	1
Unknown	27.16	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	2326.56	1
tc|Rep: MYB-CC type transfactor - Solanum tuberosum (Potato), partial (97%) [TC4	21.36	1
Unknown	197.39	1
Unknown	36.06	1
Unknown	377.67	1
gb|KR3B.113N15F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.113N15, m	1451.56	1
gb|AGN_RNC009xg09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	28.5	1
tc|Rep: Chromosome chr19 scaffold_35, whole genome shotgun sequence - Vitis vi	2721.98	1
gb|CHO_SL004xg01f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	145.84	1
gb|TT-30_F22 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	3686.88	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	59.58	1
gb|AGN_ELP022xa22f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	45.25	1
gb|AGN_RPC014xb21f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	38.46	1
tc|Rep: Succinate dehydrogenase subunit 3 - Solanum lycopersicum (Tomato) (Lyco	2808.97	1
gb|KL4B.103H20F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103H20, m	47.89	1
Unknown	220.26	1
Unknown	103.71	1
gb|KG9B.103L12F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103L12, m	197.9	1
gb|KF8C.108A02F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108A02, mR	9828.19	1
tc|Rep: Cytochrome c1-1, heme protein, mitochondrial precursor - Solanum tubero	4078.27	1
tc|Rep: Chromosome undetermined scaffold_2463, whole genome shotgun sequen	486.72	1
gb|Nicotiana tabacum phospholipase C2 mRNA, complete cds [AF223573]	52.66	1
gb|AGN_RNC013xn09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	35.62	1
gb|N.tabacum mRNA for pyruvate kinase [Z29492]	264.41	1

gb|KR2B.107G14F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.107G14, m	57.99	1
gb|AGN_ELP019xk13f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	197.21	1
gb|TT-23_K11 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	201.81	1
Unknown	178.26	1
Unknown	85.46	1
gb|TT-13_H21 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	510.34	1
Unknown	50.4	1
gb|TT-26_M20 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	8304.63	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT2-12-440, cultivar Bright Yellow 2	32.2	1
gb|KR3B.001E07F.050815T7 KR3B Nicotiana tabacum cDNA clone KR3B.001E07, m	136.29	1
tc|Rep: Mature anther-specific protein LAT61 - Solanum lycopersicum (Tomato) (Ly	41.88	1
gb|Nicotiana tabacum blp4 mRNA for luminal binding protein (BiP) [X60057]	5073.58	1
gb|KT7C.104I03F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104I03, mRN	575.8	1
Unknown	23.45	1
Unknown	27.98	1
Unknown	45547.15	1
tc|Rep: Chromosome undetermined scaffold_53, whole genome shotgun sequence	19.27	1
gb|TT-10_J09 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	488.95	1
gb|AGN_RNC022xb02f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	25.67	1
Unknown	62.71	1
tc|Rep: Chromosome chr4 scaffold_373, whole genome shotgun sequence - Vitis vi	194.69	1
Unknown	25.21	1
gb|KL5B.118B19F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.118B19, mR	152.78	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	95.7	1
Unknown	31.21	1
Unknown	4106.82	1
Unknown	67.58	1
tc|Rep: 26S proteasome regulatory particle non-ATPase subunit 12 - Camellia sinen	36.08	1
gb|Nicotiana tabacum mRNA for protein kinase CK2 alpha chain (ck2A2 gene) [AJ43	123.64	1
Unknown	387.26	1
gb|KP1B.037F02F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.037F02, m	54.06	1
tc|Rep: Proteasome subunit beta type-1 - Petunia hybrida (Petunia), complete [TC4	117.77	1
tc|Rep: Guanine nucleotide-binding protein subunit beta-2 - Nicotiana tabacum (Co	86.94	1
Unknown	273.31	1

gb|CHO_SL018xl20f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	86.76	1
tc|Rep: Copper-transporting P-type ATPase - Brassica napus (Rape), partial (37%) [T	346.79	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	122.65	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	635.32	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	121.91	1
tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	291.43	1
tc|Rep: Chromosome chr15 scaffold_82, whole genome shotgun sequence - Vitis vi	39893.4	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	96.31	1
gb|BP128844 MAT001 Nicotiana tabacum cDNA clone BY650, mRNA sequence [BP	31.55	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	595.52	1
Unknown	23.36	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	84.26	1
Unknown	30.43	1
Unknown	747.98	1
gb|KN6B.100O04F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100O04, r	29.61	1
tc|Rep: Glyoxalase/bleomycin resistance protein/dioxygenase - Sphingomonas witt	587.47	1
gb|KL4B.103F22F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103F22, mR	550.33	1
gb|27E04 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', r	170.57	1
Unknown	2704.08	1
Unknown	6109.6	1
tc|Rep: Chloride channel Stclc1 - Solanum tuberosum (Potato), partial (27%) [TC551	988.98	1
Unknown	78.33	1
gb|EST_CSP001xg06f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	22.18	1
gb|KL4B.103C02F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103C02, mR	934.69	1
gb|KR3B.110K15F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110K15, m	1347.54	1
tc|Rep: Chromosome partitioning parB family protein - Clostridium tetani, partial (	24.39	1
tc|Rep: Syntaxin-52 - Arabidopsis thaliana (Mouse-ear cress), partial (86%) [TC4342	1024.75	1
Unknown	21.8	1
Unknown	181.42	1
gb|KL5B.118O02F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.118O02, m	1504.38	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	755.8	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	656.23	1
gb|CHO_SL014xb22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	3647.46	1
tc|Rep: GTP cyclohydrolase I - Solanum lycopersicum (Tomato) (Lycopersicon escul	1035.97	1

gb|CHO_SL011xk16f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1983.07	1
Unknown	933.01	1
gb|KF8C.101J01F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101J01, mRN	422.89	1
tc|Rep: 40S ribosomal protein S24 - Vitis vinifera (Grape), partial (96%) [TC50264]	67.91	1
Unknown	514.4	1
gb|KF8C.102O14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102O14, mR	551.88	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	151.06	1
gb|KF8C.102C14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102C14, mR	107.39	1
gb|KF8B.100A11F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100A11, mR	348.54	1
gb|TOBESTR057A06 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	220.73	1
gb|KG9B.002O02F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002O02, r	52.65	1
Unknown	32.99	1
gb|TT-08_O03 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	31.94	1
gb|KR2B.115F21F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115F21, m	26.14	1
Unknown	32.01	1
Unknown	24.7	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	139.38	1
gb|Nicotiana tabacum mRNA for ras-related protein RAB8-2, complete cds [AB079	1477.54	1
Unknown	443.48	1
gb|KR2B.104E14F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.104E14, m	181.86	1
gb|TT-50_E13 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	4574.07	1
gb|KT7C.102A17F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102A17, mR	397.48	1
gb|TT-09_K18 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	241.32	1
tc|Rep: Chromosome chr2 scaffold_140, whole genome shotgun sequence - Vitis vi	120.36	1
Unknown	260.31	1
Unknown	2883.79	1
tc|Rep: Chromosome undetermined scaffold_131, whole genome shotgun sequenc	160.77	1
tc|Rep: UDP-glucuronic acid 4-epimerase - Zea mays (Maize), partial (84%) [TC5277	11347.2	1
Unknown	28.59	1
gb|TT-05_F02 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	19.12	1
tc|Rep: Chromosome chr9 scaffold_33, whole genome shotgun sequence - Vitis vin	5357.3	1
Unknown	1207.34	1
Unknown	28.71	1
gb|KG9B.002J02F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002J02, m	175.88	1

Unknown	980.96	1
gb|KT7C.105E22F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105E22, mRN	126.86	1
Unknown	106.99	1
Unknown	38.1	1
tc|Rep: Enolase - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), parti	1530.62	1
gb|Nicotiana tabacum mRNA for putative hydrolase (C171 gene) [AM851007]	52.84	1
gb|Nicotiana tabacum Avr9 [AF211537]	53.66	1
gb|TT-08_A23 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	513.91	1
gb|EST_FLW001xl22f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [EH	18.74	1
gb|BP128827 MAT001 Nicotiana tabacum cDNA clone BY631, mRNA sequence [BP	23.4	1
tc|Rep: Acireductone dioxygenase - Solanum tuberosum (Potato), complete [TC443	4615.85	1
gb|KF8B.100D08F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100D08, mR	283.04	1
gb|TT-10_P03 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	103.01	1
gb|KF8B.202A23F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202A23, mRN	9030.24	1
Unknown	32.84	1
Unknown	60.72	1
tc|Rep: Chromosome chr5 scaffold_156, whole genome shotgun sequence - Vitis vi	28410.3	1
gb|EST_FLW004xa24f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	16069.4	1
tc|Rep: Sensor protein - Marinobacter sp. ELB17, partial (4%) [TC42609]	184.53	1
gb|BP533680 MAT005 Nicotiana tabacum cDNA clone BY30378, mRNA sequence [	46.64	1
Unknown	631.67	1
tc|Rep: Chromosome chr2 scaffold_187, whole genome shotgun sequence - Vitis vi	174.57	1
gb|KG9B.102I18F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102I18, m	101.22	1
gb|TT-47_K11 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	325.16	1
tc|Rep: Mitochondrial import receptor subunit TOM6 homolog - Arabidopsis thalia	79.64	1
gb|KF8C.103C17F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103C17, mRN	1264.17	1
gb|AGN_PNL229af1_c8.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	28.55	1
gb|TL13.002I13F.060117T7 TL13 Nicotiana tabacum cDNA clone TL13.002I13, mRN	105.85	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	728.31	1
tc|Rep: Single-stranded nucleic acid binding R3H - Medicago truncatula (Barrel med	8572.56	1
tc|Rep: ATP-dependent Clp protease proteolytic subunit - Vitis vinifera (Grape), par	281.14	1
gb|KP1B.102C06F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102C06, m	32.89	1
gb|EST_YP003xi04f1.ab1 EST_YP Nicotiana tabacum cDNA, mRNA sequence [EH61	447.34	1
gb|TT-15_M17 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	129.29	1

tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	718.83	1
tc|Rep: Chromosome chr1 scaffold_166, whole genome shotgun sequence - Vitis vi	78.44	1
gb|KG9B.001K18F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001K18, m	592.76	1
Unknown	804.65	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	481.63	1
Unknown	465.48	1
gb|Nicotiana tabacum mRNA for cytosolic ascorbate peroxidase, complete cds [D85	1528.76	1
gb|TT-36_I13 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	34.54	1
tc|Rep: 60S ribosomal protein L41 - Homo sapiens (Human), complete [TC71128]	86.12	1
gb|BP530129 MAT005 Nicotiana tabacum cDNA clone BY21114, mRNA sequence [	307.94	1
gb|EST_FLW002xl09f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	1675.47	1
gb|AGN_PNL224dr1_g6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	44.99	1
tc|Rep: Bax inhibitor 1 - Nicotiana tabacum (Common tobacco), complete [TC4129	8974.62	1
Unknown	23.71	1
gb|KP1B.001H22F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001H22, m	44.69	1
tc|Rep: L-galactose dehydrogenase - Nicotiana langsdorffii x Nicotiana sanderae (O	1358.87	1
tc|Rep: Ubiquitin carrier protein - Vitis vinifera (Grape), partial (75%) [TC47081]	144.13	1
Unknown	758.5	1
gb|N.tabacum mRNA for transformer-SR ribonucleoprotein [Y09506]	226.76	1
gb|KN6B.009I02F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009I02, m	244.94	1
gb|CHO_SL003xp03f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	20.17	1
tc|Rep: Joka2 - Nicotiana plumbaginifolia (Leadwort-leaved tobacco), partial (78%)	23.22	1
gb|KG9B.002B01F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002B01, m	66.15	1
Unknown	51.32	1
gb|KP1B.102P18F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102P18, m	19915.05	1
Unknown	248.6	1
gb|AGN_RNC005xc17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	210.68	1
Unknown	33769.9	1
Unknown	4067.36	1
Unknown	25.67	1
gb|KG9B.106M06F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106M06,	45.37	1
gb|EST_YP004xo19f1.ab1 EST_YP Nicotiana tabacum cDNA, mRNA sequence [EH61	519.46	1
tc|Rep: Splicing factor U2AF 65 kDa subunit - Caenorhabditis briggsae, partial (6%) [	765.7	1
tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	41.89	1

gb|BP192620 Nicotiana tabacum BY-2 Nicotiana tabacum cDNA clone n4, mRNA se	24.17	1
gb|KP1B.110N09F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110N09, m	751.74	1
gb|TT-38_G05 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	34.16	1
gb|KN6B.105C10F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105C10, m	21452.25	1
Unknown	354.06	1
gb|KF8C.106A10F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106A10, mRN	78.25	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	544.64	1
gb|Nicotiana tabacum putative chloroplast ribonucleoprotein-like mRNA, partial se	172.77	1
gb|KG9B.003K18F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003K18, m	118.87	1
Unknown	56.2	1
gb|FS411044 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	99.58	1
tc|Rep: Endoplasmin homolog precursor - Catharanthus roseus (Rosy periwinkle) (M	342.97	1
gb|N.tabacum mRNA for pyruvate decarboxylase 2 [X81855]	157.07	1
gb|KF8B.201M04F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201M04, mR	1595.65	1
tc|Rep: Chromosome chr8 scaffold_68, whole genome shotgun sequence - Vitis vin	26.67	1
tc|Rep: Os05g0557700 protein - Oryza sativa subsp. japonica (Rice), partial (23%) [T	27.49	1
gb|KP1B.107F21F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107F21, mR	26.81	1
tc|Rep: 40S ribosomal protein S2-3 - Arabidopsis thaliana (Mouse-ear cress), partial	187.79	1
Unknown	835.99	1
Unknown	238.61	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	27.3	1
tc|Rep: Chromosome undetermined scaffold_77, whole genome shotgun sequence	72.14	1
gb|EST_FLW002xn07f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	30.52	1
Unknown	51.47	1
tc|Rep: Thioredoxin - Limonium bicolor, partial (64%) [TC42824]	63.13	1
gb|N.tabacum mRNA for GTP-binding protein, SAR1 [X97967]	13089.45	1
tc|Rep: UDP-glucose:protein transglucosylase-like - Solanum tuberosum (Potato), c	1317.7	1
Unknown	60.52	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	1031.91	1
Unknown	37.61	1
gb|TT-04_H17 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	37.7	1
Unknown	518.09	1
gb|TT-49_L11 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	568.91	1
gb|BP533240 MAT005 Nicotiana tabacum cDNA clone BY29305, mRNA sequence [E	21.24	1

<table>
<tr><th></th><th></th><th></th></tr>
<tr><td>Unknown</td><td>159.26</td><td>1</td></tr>
<tr><td>Unknown</td><td>52.43</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin</td><td>34.82</td><td>1</td></tr>
<tr><td>tc|Rep: GDP-mannose-3',5'-epimerase - Vitis vinifera (Grape), partial (44%) [TC446</td><td>3205.04</td><td>1</td></tr>
<tr><td>gb|AGN_ELP003xf11f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence</td><td>20.87</td><td>1</td></tr>
<tr><td>tc|Rep: AGAP000318-PA - Anopheles gambiae str. PEST, partial (9%) [TC72511]</td><td>25.04</td><td>1</td></tr>
<tr><td>Unknown</td><td>29.38</td><td>1</td></tr>
<tr><td>gb|KG9B.005B15F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005B15,</td><td>199.52</td><td>1</td></tr>
<tr><td>Unknown</td><td>139.86</td><td>1</td></tr>
<tr><td>gb|KG9B.003K21F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003K21,</td><td>23.04</td><td>1</td></tr>
<tr><td>tc|Rep: RAN GTPase-activating protein 2 - Nicotiana benthamiana, partial (19%) [T</td><td>138</td><td>1</td></tr>
<tr><td>gb|AGN_RNC008xd08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen</td><td>32.53</td><td>1</td></tr>
<tr><td>gb|Tobacco (N.tabacum) endochitinase mRNA, partial cds [M15173]</td><td>56.95</td><td>1</td></tr>
<tr><td>tc|Rep: 3-phosphoshikimate 1-carboxyvinyltransferase 1, chloroplast precursor - Ni</td><td>145.84</td><td>1</td></tr>
<tr><td>gb|KG9B.001N04F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001N04,</td><td>35.36</td><td>1</td></tr>
<tr><td>gb|KN6B.102A09F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102A09,</td><td>123.93</td><td>1</td></tr>
<tr><td>gb|Nicotiana tabacum mRNA for 14-3-3 a-1 protein, complete cds [AB119466]</td><td>7097.38</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif</td><td>46.69</td><td>1</td></tr>
<tr><td>tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (72%) [TC6</td><td>85.74</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin</td><td>71.87</td><td>1</td></tr>
<tr><td>Unknown</td><td>264.25</td><td>1</td></tr>
<tr><td>tc|Rep: TPR repeat - Medicago truncatula (Barrel medic), partial (75%) [TC62088]</td><td>18.87</td><td>1</td></tr>
<tr><td>Unknown</td><td>138.27</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif</td><td>249.1</td><td>1</td></tr>
<tr><td>gb|KP1B.104N18F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104N18, m</td><td>1183.64</td><td>1</td></tr>
<tr><td>gb|KL4B.105F18F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105F18, mR</td><td>13984.7</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi</td><td>152.62</td><td>1</td></tr>
<tr><td>gb|KP1B.101L08F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101L08, m</td><td>2913.68</td><td>1</td></tr>
<tr><td>gb|KN6B.110B11F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.110B11,</td><td>56.87</td><td>1</td></tr>
<tr><td>tc|Rep: EF hand family protein - Solanum demissum (Wild potato), complete [TC58</td><td>105.97</td><td>1</td></tr>
<tr><td>gb|CHO_SL013xb17f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6</td><td>50.12</td><td>1</td></tr>
<tr><td>Unknown</td><td>138.75</td><td>1</td></tr>
<tr><td>tc|Rep: Plasma membrane ATPase 1 - Nicotiana plumbaginifolia (Leadwort-leaved t</td><td>26.32</td><td>1</td></tr>
<tr><td>gb|KG9B.102A23F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102A23,</td><td>2911.92</td><td>1</td></tr>
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Unknown	17.09	1
gb|TT-36_F05 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	2784.75	1
tc|Rep: Chromosome undetermined scaffold_1021, whole genome shotgun sequen	108.75	1
Unknown	107.33	1
tc|Rep: Chromosome chr1 scaffold_136, whole genome shotgun sequence - Vitis vi	81.63	1
gb|Nicotiana tabacum NtINV mRNA for invertase, partial cds [AB055500]	17845	1
gb|CHO_SL020xm13f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	334.47	1
gb|KP1B.103C08F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103C08, m	70.6	1
Unknown	35.08	1
Unknown	1563.39	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	106.87	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	686.54	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	489.26	1
Unknown	118.57	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	227.49	1
Unknown	225	1
tc|Rep: Chromosome chr10 scaffold_138, whole genome shotgun sequence - Vitis	558.34	1
tc|Rep: Histone H3.2 - Encephalartos altensteinii (Altenstein's bread tree) (Cycad),	25.5	1
Unknown	2862.37	1
Unknown	27.48	1
Unknown	20.73	1
gb|Nicotiana tabacum bZIP transcription factor (BZI-1) mRNA, complete cds [AY061	455.51	1
gb|KR3B.113A04F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.113A04, m	102.98	1
gb|Nicotiana tabacum mRNA for hypothetical protein [AJ133502]	465.42	1
tc|Rep: Predicted protein - Chlamydomonas reinhardtii, partial (9%) [TC69281]	267.65	1
tc|Rep: Chromosome chr10 scaffold_312, whole genome shotgun sequence - Vitis	3755.07	1
Unknown	211.71	1
tc|Rep: Eukaryotic translation initiation factor eIF4E - Nicotiana tabacum (Common	268.65	1
gb|BP134733 MAT001 Nicotiana tabacum cDNA clone BY7163, mRNA sequence [B	20.91	1
tc|Rep: H+-transporting two-sector ATPase, C (AC39) subunit - Medicago truncatul	3276.36	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	4040.26	1
Unknown	145.12	1
tc|Rep: Expressed protein - Oryza sativa subsp. japonica (Rice), partial (60%) [TC47	98.69	1
tc|Rep: Glutathione S-transferase - Capsicum annuum (Bell pepper), partial (85%) [	20.41	1

gb|TT-20_A05 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	23.91	1
gb|AGN_PNL223br1_a3.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	80.69	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	3075.27	1
tc|Rep: Ubiquitin carrier protein - Solanum tuberosum (Potato), complete [TC4631	463.84	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	377.14	1
Unknown	24.47	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, complete [TC5338	22.44	1
gb|KN6B.102G12F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102G12, r	3322.54	1
tc|Rep: Ubiquitin carboxyl-terminal hydrolase - Vitis vinifera (Grape), partial (7%) [T	65.27	1
gb|TT-09_M01 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	242.7	1
gb|CHO_SL014xg01f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	397.92	1
gb|Nicotiana tabacum glutamate [AY123847]	138.82	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	2758.1	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	749.99	1
Unknown	88.33	1
gb|TT-39_O03 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	128.45	1
Unknown	1484.6	1
Unknown	118.03	1
tc|Rep: Bypass2 - Nicotiana benthamiana, complete [TC47299]	80.35	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	3358.36	1
Unknown	586.89	1
Unknown	1254.93	1
gb|FS408454 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	258.1	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	42.71	1
Unknown	29.78	1
gb|AGN_ELP006xn06f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	36.74	1
Unknown	40.14	1
gb|Nicotiana tabacum fatty acid hydroperoxide lyase mRNA, complete cds [DQ129	900.67	1
gb|KR2B.115K01F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115K01, m	26.61	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	53.39	1
tc|Rep: Chromosome chr14 scaffold_190, whole genome shotgun sequence - Vitis	30.96	1
Unknown	20.55	1
gb|KR3B.106G05F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106G05, m	810.66	1
gb|KR2B.101B04F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.101B04, m	2625.67	1

gb|AGN_RNC025xl24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	511.38	1
Unknown	90.68	1
gb|KP1B.108O07F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108O07, m	135.01	1
Unknown	76.98	1
gb|KL4B.101I21F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101I21, mRN	151.57	1
Unknown	20.77	1
Unknown	48.31	1
gb|Nicotiana tabacum clone PR26 mRNA sequence [AF154645]	47.97	1
gb|CHO_SL013xk01f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	891.12	1
Unknown	72.79	1
Unknown	1149.79	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	2719.44	1
gb|KL4B.101I23F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101I23, mRN	28.75	1
gb|KR3B.111N12F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111N12, m	685.17	1
gb|KF8C.110J01F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110J01, mRN	15026.65	1
Unknown	453.26	1
gb|KP1B.104N22F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104N22, m	3420.21	1
gb|KG9B.002C21F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002C21, m	22.92	1
gb|KR3B.108M01F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.108M01, r	10834.85	1
gb|KN6B.102L11F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102L11, m	3738.55	1
Unknown	34.73	1
tc|Rep: E-class P450, group I - Medicago truncatula (Barrel medic), partial (17%) [TC	90.39	1
gb|KR3B.112M13F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112M13, r	540.08	1
Unknown	40.08	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	182.67	1
gb|KF8C.101J09F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101J09, mRN	937.13	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	382.19	1
tc|Rep: ADP-ribosylation factor - Hyacinthus orientalis (Common hyacinth), partial (	44701.85	1
gb|CHO_SL027xa24f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	259.13	1
gb|KG9B.106H16F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106H16, n	376.32	1
tc|Rep: Alpha-amylase precursor - Solanum tuberosum (Potato), complete [TC4059	186.09	1
Unknown	31.69	1
gb|AM790664 seedling library, SL Nicotiana tabacum cDNA clone nt002250054, mR	31.98	1
gb|KL4B.102K23F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102K23, mR	29246.25	1

Unknown	21.41	1
gb|N.tabacum mRNA for acidic chitinase PR-P [X51426]	42.32	1
gb|Nicotiana tabacum geranylgeranylated protein NTGP2 mRNA, complete cds [U6	1590.56	1
Unknown	34.86	1
Unknown	81.25	1
gb|KT7C.104P01F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104P01, mR	2990.07	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	557.37	1
tc|Rep: UDP-glucuronic acid 4-epimerase - Zea mays (Maize), partial (53%) [TC4874	6561.96	1
tc|Rep: Chromosome undetermined scaffold_254, whole genome shotgun sequenc	25.57	1
gb|KF8B.200H02F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200H02, mR	34814.55	1
Unknown	229.48	1
Unknown	518.49	1
gb|AGN_RNC026xj12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	53.95	1
gb|CHO_SL016xd16f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	23.95	1
Unknown	22.93	1
gb|KR3B.107E09F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.107E09, m	414.16	1
gb|KL4B.102E02F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102E02, mR	27.62	1
gb|Nicotiana tabacum NtVDAC2 mRNA for voltage-dependent anion channel, comp	237.73	1
Unknown	1153.33	1
gb|AM827545 seedling library, SL Nicotiana tabacum cDNA clone nt002038039, m	26.39	1
gb|N.tabacum mRNA for alcohol dehydrogenase [X81853]	2766.67	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	513.95	1
gb|KG9B.002A07F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002A07,	628.28	1
gb|AGN_PNL212cr1_e11.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRN	37.75	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT12-2-230, cultivar Bright Yellow 2	62.23	1
gb|KP1B.111A19F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.111A19, m	25.08	1
tc|Rep: P18 - Solanum chacoense (Chaco potato), complete [TC54135]	212.19	1
Unknown	60.19	1
Unknown	907.11	1
gb|KF8C.106P09F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106P09, mR	491.19	1
gb|KL4B.103E19F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103E19, mR	25.39	1
gb|KN6B.104N20F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104N20,	135.25	1
gb|AM807444 seedling library, SL Nicotiana tabacum cDNA clone nt002277076, m	25.04	1
tc|Rep: Light harvesting chlorophyll a/b-binding protein precursor - Nicotiana sylve	36.7	1

tc|Rep: WERBP-1 protein - Nicotiana tabacum (Common tobacco), partial (29%) [TC	791.84	1
tc|Rep: ER lumen protein retaining receptor - Vitis vinifera (Grape), partial (54%) [T	1185.74	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	73.08	1
Unknown	984.73	1
gb|CHO_SL023xa21f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	721.76	1
tc|Rep: Chromosome chr16 scaffold_94, whole genome shotgun sequence - Vitis vi	17.88	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	25489.05	1
Unknown	67.3	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	50.16	1
gb|AGN_RNC105xb24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	21.88	1
tc|Rep: SGS3-like protein - Solanum lycopersicum (Tomato) (Lycopersicon esculent	48.09	1
Unknown	169.53	1
Unknown	816.57	1
gb|Nicotiana tabacum NtP4H2.2 mRNA for type 2 proly 4-hydroxylase, complete cd	1768.63	1
tc|Rep: Glycine-rich RNA-binding protein - Ricinus communis (Castor bean), partial	732.68	1
Unknown	67.2	1
gb|KR2B.107K23F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.107K23, m	462.88	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	372.99	1
gb|KL4B.105N07F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105N07, m	71.38	1
tc|Rep: Chromosome chr8 scaffold_41, whole genome shotgun sequence - Vitis vin	54.49	1
Unknown	1447.78	1
tc|Rep: Glucose-6-phosphate isomerase - Solanum lycopersicum (Tomato) (Lycope	498.73	1
gb|KN6B.101J14F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101J14, m	268.94	1
tc|Rep: P40-like protein - Solanum tuberosum (Potato), partial (93%) [TC71777]	72.9	1
tc|Rep: Cysteine proteinase inhibitor - Petunia hybrida (Petunia), partial (86%) [TC4	683.08	1
gb|KF8C.110N09F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110N09, mR	43238.75	1
tc|Rep: UDP-glucuronate 4-epimerase 5 - Arabidopsis thaliana (Mouse-ear cress), p	2440.37	1
Unknown	151.21	1
tc|Rep: DWARF1/DIMINUTO - Solanum lycopersicum (Tomato) (Lycopersicon escul	527.52	1
gb|TT-14_D11 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	56.39	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	1546.57	1
Unknown	20.22	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	580.3	1
tc|Rep: TPK1 - Nicotiana tabacum (Common tobacco), complete [TC64081]	74.63	1

tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	109.09	1
gb|CHO_SL004xp09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	106.87	1
gb|KT7B.107I23F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107I23, mRN	126.44	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	141.35	1
Unknown	270.32	1
tc|Rep: Histone H4 - Tetraodon nigroviridis (Green puffer), partial (45%) [TC59268]	1741.64	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	684.26	1
Unknown	67.6	1
gb|KP1B.107E12F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107E12, m	48.46	1
Unknown	83.5	1
tc|Rep: Citrate synthase - Nicotiana tabacum (Common tobacco), partial (46%) [TC	11130.35	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	110.77	1
tc|Rep: Predicted protein - Emericella nidulans (Aspergillus nidulans), partial (5%) [	102.06	1
gb|TT-20_A05 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	122.38	1
Unknown	1511.92	1
Unknown	466.91	1
Unknown	21.42	1
gb|AGN_RNC026xh22f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	24.33	1
gb|KG9B.003N01F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003N01,	179.09	1
gb|KT7C.106N02F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106N02, mR	249.42	1
gb|TT-41_E06 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	31.7	1
Unknown	20.66	1
gb|KL4B.102M10F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102M10, m	19.13	1
Unknown	27.91	1
Unknown	103.52	1
tc|Rep: Ferredoxin--NADP reductase, root-type isozyme, chloroplast precursor - Nic	30.59	1
gb|AGN_RNC013xm11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	530.57	1
gb|KP1B.001I07F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001I07, mR	246.4	1
gb|20.2D01 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5'	535.95	1
Unknown	442.47	1
tc|Rep: Glycine dehydrogenase [decarboxylating], mitochondrial precursor - Solanu	14322.7	1
tc|Rep: Chromosome chr1 scaffold_166, whole genome shotgun sequence - Vitis vi	144.7	1
gb|AM786200 seedling library, SL Nicotiana tabacum cDNA clone nt002063089, m	1362.71	1
tc|Rep: Decreased apical dominance protein - Petunia hybrida (Petunia), partial (47	51.42	1

Unknown	54.56	1
tc|Rep: 50S ribosomal protein L27, chloroplast precursor - Nicotiana tabacum (Com	33.84	1
tc|Rep: Nuclear-localized RNA binding protein - Capsicum annuum (Bell pepper), pa	35.33	1
Unknown	2376.78	1
gb|KG9B.106L01F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106L01, m	212.35	1
gb|TOBESTR046E09 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA sequ	92.76	1
gb|KG9B.105L07F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105L07, m	181.74	1
Unknown	21.13	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	67.12	1
Unknown	29.24	1
Unknown	211.42	1
tc|Rep: Chromosome chr5 scaffold_72, whole genome shotgun sequence - Vitis vin	104.67	1
gb|KP1B.109K19F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109K19, mI	523.91	1
Unknown	1090.87	1
Unknown	68.28	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	97.65	1
gb|Nicotiana tabacum mRNA for hypothetical protein (c17 gene) [AJ966358]	17.89	1
Unknown	40.31	1
tc|Rep: Chromosome chr13 scaffold_74, whole genome shotgun sequence - Vitis vi	21.66	1
gb|KN6B.103M03F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103M03,	81.6	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	882.85	1
tc|Rep: RWD domain-containing protein - Solanum tuberosum (Potato), partial (93	19.65	1
gb|AGN_RNC114xj01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	146.33	1
gb|TT-25_H03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	72.67	1
Unknown	262.01	1
tc|Rep: Pm27 protein - Prunus mume (Japanese flowering apricot), partial (57%) [T	550.21	1
tc|Rep: Vacuolar ATP synthase 16 kDa proteolipid subunit - Nicotiana tabacum (Cor	2678.67	1
tc|Rep: Polygalacturonase-like protein-like - Solanum tuberosum (Potato), partial (	202.23	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	43.01	1
gb|KF8C.102C22F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102C22, mRN	140413.5	1
gb|KR2B.108M01F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.108M01, r	176.04	1
Unknown	27.24	1
Unknown	175.57	1
tc|Rep: Low temperature and salt responsive protein - Solanum tuberosum (Potato	1231.2	1

tc|Rep: 60S ribosomal protein L6 - Mesembryanthemum crystallinum (Common ice	107.2	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	749.65	1
gb|AGN_RNC003xn20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	24.78	1
gb|AGN_RPC007xp13f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	28.2	1
gb|KL4B.105P21F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105P21, mR	158.35	1
Unknown	42.73	1
tc|Rep: Ethylene-responsive element binding protein 5 - Nicotiana tabacum (Comm	211.29	1
gb|TT-48_J10 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	416.61	1
tc|Rep: Enolase - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), parti	259.22	1
Unknown	45.76	1
gb|TT-30_L15 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	41.13	1
tc|Rep: Glutamine synthetase - Nicotiana plumbaginifolia (Leadwort-leaved tobacc	1679.35	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	135.09	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	882.02	1
tc|Rep: Nucleic acid binding protein - Brassica campestris (Field mustard), partial (7	17.42	1
gb|CHO_SL022xi08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	213.9	1
gb|KF8C.110G08F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110G08, mR	367.2	1
Unknown	88.92	1
Unknown	29.41	1
gb|TT-15_O07 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	98.18	1
Unknown	140.19	1
gb|KL4B.105L10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105L10, mR	17074.6	1
tc|Rep: Chromosome undetermined scaffold_438, whole genome shotgun sequenc	107.5	1
Unknown	23.35	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	95.79	1
Unknown	321.95	1
gb|AGN_RNC025xl24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	502.26	1
gb|TT-19_K15 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	5899.97	1
Unknown	12457	1
Unknown	69.29	1
gb|Nicotiana tabacum adenosine kinase isoform 2T mRNA, complete cds [AY69505	11131.65	1
gb|KT7C.113M12F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.113M12, m	1118.3	1
Unknown	22.7	1
Unknown	19.34	1

gb|KR2B.115B01F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115B01, m	165.92	1
Unknown	18.6	1
gb|AGN_RNC108xf20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	133.73	1
tc|Rep: AT5g19750/T29J13_170 - Arabidopsis thaliana (Mouse-ear cress), partial (3	26.8	1
Unknown	19039.75	1
Unknown	891.54	1
Unknown	70.23	1
Unknown	25.42	1
gb|KT7C.112O16F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112O16, mR	105.66	1
Unknown	48.12	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	69.32	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	137.53	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	652.67	1
gb|BP128651 MAT001 Nicotiana tabacum cDNA clone BY423, mRNA sequence [BP	222.5	1
Unknown	219.53	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	505.05	1
gb|KP1B.109H15F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109H15, m	241.97	1
Unknown	187.53	1
gb|N.tabacum NTP303 pollen specific mRNA [X61146]	61177.85	1
tc|Rep: Chromosome chr1 scaffold_135, whole genome shotgun sequence - Vitis vi	18.85	1
Unknown	20.01	1
Unknown	52.87	1
gb|KL4B.101K21F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101K21, mR	58.68	1
gb|KL4B.102G10F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102G10, m	840.47	1
gb|KR2B.105H17F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.105H17, m	82.02	1
Unknown	9962.55	1
tc|Rep: CDC5-like protein - Solanum lycopersicum (Tomato) (Lycopersicon esculent	190.89	1
tc|Rep: Chromosome chr17 scaffold_101, whole genome shotgun sequence - Vitis	84.93	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	749.6	1
Unknown	22.16	1
gb|KF8C.106O11F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106O11, mR	27.78	1
Unknown	1580.43	1
Unknown	17959.2	1
Unknown	78.06	1

tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	552.64	1
Unknown	177.19	1
tc|Rep: Delta-1-pyrroline-5-carboxylate synthetase (P5CS) [Includes: Glutamate 5-k	2858	1
Unknown	38.95	1
gb|BP530158 MAT005 Nicotiana tabacum cDNA clone BY21148, mRNA sequence [E	633.55	1
gb|KR3B.114C14F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.114C14, m	64.45	1
tc|Rep: Chromosome chr13 scaffold_74, whole genome shotgun sequence - Vitis vi	131.37	1
gb|KN6B.103A01F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103A01, n	641.62	1
gb|ntsm20 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [E	34.3	1
gb|KR3B.102K01F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.102K01, m	234.99	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	436.45	1
Unknown	28.81	1
gb|FS422353 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	1884.47	1
tc|Rep: MYB-CC type transfactor - Solanum tuberosum (Potato), partial (64%) [TC6	208.95	1
gb|KF8B.202D12F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202D12, mR	31.23	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	96.82	1
tc|Rep: Potyviral capsid protein interacting protein 1 - Nicotiana tabacum (Commo	40.79	1
gb|TT-14_N07 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	81.12	1
Unknown	864.04	1
tc|Rep: Chromosome chr12 scaffold_103, whole genome shotgun sequence - Vitis	1837.41	1
gb|CHO_SL012xd11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	9560.95	1
tc|Rep: Fiber protein Fb2 - Gossypium barbadense (Sea-island cotton) (Egyptian cot	262.91	1
gb|KN6B.109N09F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.109N09, r	45.84	1
tc|Rep: Chromosome chr4 scaffold_373, whole genome shotgun sequence - Vitis vi	54.91	1
tc|Rep: DNA-directed RNA polymerase subunit beta'' - Nicotiana tomentosiformis (	131.52	1
tc|Rep: F6A14.10 protein - Arabidopsis thaliana (Mouse-ear cress), partial (78%) [T	20.74	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	152.61	1
tc|Rep: binding - Arabidopsis thaliana, partial (72%) [TC49231]	27.31	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	23.18	1
gb|KF8C.106P01F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106P01, mRN	3365.9	1
tc|Rep: Glucose-6-phosphate isomerase - Solanum tuberosum (Potato), complete [	1217.02	1
tc|Rep: Chromosome chr15 scaffold_82, whole genome shotgun sequence - Vitis vi	28173.2	1
gb|KN6B.104I12F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104I12, mF	60.41	1
gb|TT-20_E11 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	1122.05	1

gb|KL4B.105L08F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105L08, mR	78.17	1
tc|Rep: Molecular chaperone Hsp90-2 - Nicotiana benthamiana, partial (35%) [TC45	1111.44	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	110.98	1
tc|Rep: Ubiquitin carrier protein - Vitis vinifera (Grape), partial (69%) [TC62639]	253.95	1
gb|AM793637 COL, cold overnight library Nicotiana tabacum cDNA clone nt006155	35.76	1
gb|KL4B.102P10F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102P10, mR	19.01	1
tc|Rep: Microtubule-associated protein MAP65-1a - Nicotiana tabacum (Common t	29.43	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	106.41	1
gb|KG9B.104J04F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104J04, m	227.26	1
Unknown	67.35	1
gb|KT7C.106O09F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106O09, mR	32.65	1
gb|TOBESTR130D05 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	539.41	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	86.88	1
gb|Nicotiana tabacum NtbZIP60 mRNA for basic region leucine zipper protein, com	3006.53	1
gb|KF8B.100E16F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100E16, mR	43786.65	1
gb|Nicotiana tabacum mRNA for omega-3 fatty acid desaturase, complete cds [D79	7905.51	1
gb|AGN_ELP025xl06f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	30.33	1
Unknown	267.07	1
tc|Rep: STY-L protein - Antirrhinum majus (Garden snapdragon), partial (40%) [TC53	51.74	1
Unknown	1136.24	1
tc|Rep: Adenylyl cyclase-associated protein - Vitis vinifera (Grape), partial (43%) [TC	28.74	1
gb|KF8C.102B07F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102B07, mR	951.32	1
tc|Rep: Ferrochelatase-2, chloroplast precursor - Hordeum vulgare (Barley), partial	86.24	1
gb|TT-38_H12 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	50.46	1
Unknown	1125.08	1
Unknown	29.51	1
Unknown	37.31	1
Unknown	66.71	1
tc|Rep: RAN - Nicotiana sylvestris (Wood tobacco), complete [TC41527]	93	1
tc|Rep: Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K9D7 - Arabi	111.8	1
Unknown	61.98	1
Unknown	182.84	1
gb|KF8C.103M15F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103M15, m	55486.8	1
gb|KR2B.110D06F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110D06, m	266.82	1

gb|BP529129 MAT001 Nicotiana tabacum cDNA clone BY14015, mRNA sequence [	42.41	1
tc|Rep: 28 kDa small subunit ribosomal protein - Capsicum annuum (Bell pepper), c	17.7	1
gb|Nicotiana tabacum partial mRNA for putative calcium dependent protein kinase	31.14	1
gb|CHO_SL003xl06f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	377.01	1
Unknown	173	1
gb|KN6B.009L20F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009L20, m	29.41	1
tc|Rep: Chitinase 134 - Nicotiana tabacum (Common tobacco), partial (98%) [TC70	36.28	1
gb|KN6B.113H03F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.113H03,	74.4	1
Unknown	97.37	1
Unknown	155.08	1
gb|KL4B.104M03F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104M03,	203.04	1
gb|KG9B.105H03F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105H03,	495.54	1
Unknown	48.53	1
tc|Rep: Serine hydroxymethyltransferase, mitochondrial precursor - Solanum tuber	3809.15	1
tc|Rep: Adenosylhomocysteinase - Nicotiana sylvestris (Wood tobacco), partial (57	21791.1	1
gb|TL13.103C23F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.103C23, mR	60.88	1
gb|FSI_51 flooding-treated Nicotiana tabacum cDNA library Nicotiana tabacum cD	259.08	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	608.92	1
tc|Rep: Phytoene dehydrogenase-like protein - Oryza sativa subsp. japonica (Rice),	128.89	1
gb|KF8C.109F12F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109F12, mRN	46299	1
gb|AGN_RNC023xl07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	39.46	1
Unknown	244.74	1
tc|Rep: 28 kDa small subunit ribosomal protein - Capsicum annuum (Bell pepper), c	169.34	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	29.15	1
Unknown	237.06	1
Unknown	1027.32	1
Unknown	48.63	1
gb|TT-41_K18 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	136.62	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	25.69	1
tc|Rep: Elongation factor 1-gamma 2 - Oryza sativa subsp. japonica (Rice), partial (9	330.77	1
gb|Nicotiana tabacum mRNA for vacuolar invertase (vi gene) [AJ305044]	84.96	1
Unknown	69.17	1
tc|Rep: Chromosome chr5 scaffold_72, whole genome shotgun sequence - Vitis vin	22.46	1
gb|CHO_SL024xb11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	197.77	1

<table>
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<tr><td>gb|KG9B.105I09F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105I09, mF</td><td>981.48</td><td>1</td></tr>
<tr><td>gb|KN6B.104H04F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104H04, n</td><td>65.39</td><td>1</td></tr>
<tr><td>gb|CHO_SL015xh04f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6</td><td>21.05</td><td>1</td></tr>
<tr><td>gb|KG9B.002B01F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002B01, n</td><td>150.1</td><td>1</td></tr>
<tr><td>Unknown</td><td>21.13</td><td>1</td></tr>
<tr><td>gb|AM807789 COL, cold overnight library Nicotiana tabacum cDNA clone nt006056</td><td>57.75</td><td>1</td></tr>
<tr><td>Unknown</td><td>2112.25</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin</td><td>1503.63</td><td>1</td></tr>
<tr><td>gb|AM819791 seedling library, SL Nicotiana tabacum cDNA clone nt002152035, mF</td><td>327.55</td><td>1</td></tr>
<tr><td>gb|KF8C.101H12F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101H12, mRI</td><td>18.19</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr12 scaffold_103, whole genome shotgun sequence - Vitis v</td><td>151.71</td><td>1</td></tr>
<tr><td>gb|KG9B.102B16F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102B16, n</td><td>72.73</td><td>1</td></tr>
<tr><td>gb|FS422353 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA</td><td>2036.35</td><td>1</td></tr>
<tr><td>Unknown</td><td>4341.57</td><td>1</td></tr>
<tr><td>tc|Rep: Profilin - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), comp</td><td>2891.99</td><td>1</td></tr>
<tr><td>gb|KR2B.112B23F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.112B23, m</td><td>30.49</td><td>1</td></tr>
<tr><td>gb|KG9B.102B10F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102B10, n</td><td>222.4</td><td>1</td></tr>
<tr><td>gb|KT7C.110D02F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110D02, mRI</td><td>146.35</td><td>1</td></tr>
<tr><td>gb|Nicotiana tabacum cDNA-AFLP fragment H-N_BC4M31-261 sequence [DQ46016</td><td>22.43</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi</td><td>390.05</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin</td><td>266.59</td><td>1</td></tr>
<tr><td>gb|CHO_SL012xk03f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6</td><td>3282.58</td><td>1</td></tr>
<tr><td>tc|Rep: DEAD-box ATP-dependent RNA helicase 53 - Oryza sativa subsp. japonica (R</td><td>35.5</td><td>1</td></tr>
<tr><td>tc|Rep: Plasma membrane proton ATPase 5 - Nicotiana plumbaginifolia (Leadwort-l</td><td>32038.65</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin</td><td>236.74</td><td>1</td></tr>
<tr><td>gb|KL4B.104J20F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104J20, mRN</td><td>127.81</td><td>1</td></tr>
<tr><td>gb|KR3B.109J15F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109J15, mR</td><td>572.55</td><td>1</td></tr>
<tr><td>gb|KF8C.101I13F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101I13, mRNA</td><td>1471.39</td><td>1</td></tr>
<tr><td>Unknown</td><td>23.75</td><td>1</td></tr>
<tr><td>Unknown</td><td>95.64</td><td>1</td></tr>
<tr><td>Unknown</td><td>259.49</td><td>1</td></tr>
<tr><td>gb|KP1B.108F23F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108F23, mF</td><td>144.06</td><td>1</td></tr>
<tr><td>Unknown</td><td>26.72</td><td>1</td></tr>
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gb|KT7C.108F09F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108F09, mRN	2602.06	1
Unknown	21.84	1
Unknown	10626.9	1
gb|KP1B.111B04F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.111B04, m	600.83	1
gb|KT7B.100M10F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100M10, m	32.75	1
gb|KF8B.100E17F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100E17, mRN	529.76	1
tc|Rep: Chromosome chr16 scaffold_271, whole genome shotgun sequence - Vitis	1159.02	1
Unknown	29.37	1
Unknown	1021.36	1
Unknown	37.06	1
gb|KG9B.001H20F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001H20, m	88.42	1
gb|KP1B.001O05F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001O05, m	104.65	1
gb|KG9B.001G24F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001G24, m	86.01	1
gb|AM838397 seedling library, SL Nicotiana tabacum cDNA clone nt002112049, m	2209.66	1
Unknown	3116.78	1
tc|Rep: Chromosome chr10 scaffold_297, whole genome shotgun sequence - Vitis	221.05	1
gb|KN6B.107N03F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.107N03, r	213.52	1
tc|Rep: CONSTANS interacting protein 2a - Solanum lycopersicum (Tomato) (Lycop	5022.8	1
Unknown	60.96	1
gb|AGN_ELP014xd23f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	2932.4	1
gb|KL5B.111A10F.060117T7 KL5B Nicotiana tabacum cDNA clone KL5B.111A10, m	2602.24	1
gb|KT7C.110C22F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110C22, mRN	924.02	1
Unknown	202.65	1
tc|Rep: Protein kinase Pti1 - Glycine max (Soybean), partial (69%) [TC45973]	3030.78	1
Unknown	16.08	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT22-1-360, cultivar Bright Yellow 2	84.35	1
gb|KN6B.105M18F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105M18,	24.81	1
gb|KR2B.108G23F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.108G23, m	973.01	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	58.25	1
tc|Rep: Mitochondrial import receptor subunit TOM7-1 - Solanum tuberosum (Pot	176.37	1
Unknown	68.19	1
gb|TL13.105M01F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.105M01, m	122.57	1
gb|KG9B.003L11F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003L11, m	39.8	1
gb|TOBESTR071C10 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	270.21	1

Unknown	31.86	1
Unknown	399.37	1
gb|KG9B.105B16F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105B16, m	35.05	1
Unknown	30.75	1
gb|KL4B.107A04F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107A04, m	510.88	1
Unknown	24.9	1
gb|KN6B.104B18F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104B18, m	36.15	1
tc|Rep: 6,7-dimethyl-8-ribityllumazine synthase - Nicotiana tabacum (Common tob	52.76	1
tc|Rep: Uncharacterized protein At2g43190.3 - Arabidopsis thaliana (Mouse-ear cre	269.05	1
gb|CHO_SL015xf10f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	72.89	1
tc|Rep: Chromosome undetermined scaffold_60, whole genome shotgun sequence	48.38	1
Unknown	34.91	1
gb|KL4B.102B08F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102B08, mR	49.31	1
Unknown	2994.36	1
gb|KN6B.108C13F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.108C13, m	45.88	1
gb|KL4B.100G09F.050922T7 KL4B Nicotiana tabacum cDNA clone KL4B.100G09, m	470.92	1
tc|Rep: Cytochrome b561 - Citrullus lanatus (Watermelon) (Citrullus vulgaris), parti	148.59	1
gb|TT-12_I21 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	144.61	1
Unknown	43.33	1
tc|Rep: Signal recognition particle receptor beta subunit-like protein - Arabidopsis t	68.65	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	403.59	1
gb|KN6B.104I22F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104I22, m	674.02	1
gb|AGN_PNL226df1_h12.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	2940.04	1
gb|KL4B.105A02F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105A02, m	50.78	1
gb|AGN_RNC018xi16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	100.78	1
Unknown	145.86	1
gb|KG9B.106H08F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106H08, m	133.77	1
gb|CHO_SL008xh08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	217.74	1
gb|AM836818 seedling library, SL Nicotiana tabacum cDNA clone nt002035064, m	540.93	1
gb|KN6B.102M01F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102M01,	40191.75	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	63.49	1
tc|Rep: Non-intrinsic ABC protein - Nicotiana benthamiana, partial (30%) [TC71223	107.5	1
Unknown	31.07	1
Unknown	23.83	1

tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	1674.32	1
gb|KG9B.103F01F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103F01, m	256.76	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	21.52	1
tc|Rep: Ubiquitin-like protein SMT3 - Oryza sativa subsp. japonica (Rice), partial (87	366.44	1
Unknown	28.19	1
gb|Nicotiana tabacum mRNA for protein kinase 1 (pk1 gene) [AJ608156]	211.79	1
tc|Rep: Endoplasmin homolog precursor - Catharanthus roseus (Rosy periwinkle) (N	19.4	1
tc|Rep: 50S ribosomal protein L3, chloroplast precursor - Nicotiana tabacum (Comn	18.58	1
tc|Rep: Chromosome chr4 scaffold_73, whole genome shotgun sequence - Vitis vin	91.16	1
tc|Rep: DEAD-box ATP-dependent RNA helicase 8 - Arabidopsis thaliana (Mouse-ea	126.12	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	26.34	1
tc|Rep: Peptide deformylase, chloroplast precursor - Solanum lycopersicum (Tomat	25.64	1
gb|Nicotiana tabacum ethylene-responsive element binding protein 5 mRNA, comp	532.45	1
tc|Rep: Allyl alcohol dehydrogenase - Nicotiana tabacum (Common tobacco), partia	89.2	1
Unknown	6550.06	1
Unknown	22.59	1
tc|Rep: Ubiquitin carrier protein - Vitis vinifera (Grape), partial (88%) [TC66484]	103.71	1
Unknown	818.62	1
Unknown	619.26	1
gb|AGN_RPC003xd07f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	58.17	1
tc|Rep: Expressed protein - Arabidopsis thaliana (Mouse-ear cress), partial (5%) [TC	753.43	1
gb|KT7C.105B24F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105B24, mRI	1108.73	1
Unknown	118.66	1
tc|Rep: NRC1 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), partial	35.5	1
gb|KG9B.004A05F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004A05, n	95.25	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	276.32	1
gb|KF8C.106P09F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106P09, mRN	935.35	1
tc|Rep: GDP dissociation inhibitor 1-like - Solanum tuberosum (Potato), partial (41%	285.7	1
tc|Rep: Chromosome undetermined scaffold_252, whole genome shotgun sequenc	159.49	1
tc|Rep: Glutathione peroxidase - Vitis vinifera (Grape), complete [TC72413]	4089.54	1
Unknown	114.34	1
tc|Rep: 60S ribosomal protein L41 - Homo sapiens (Human), complete [TC69610]	219.89	1
gb|TT-15_P19 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	80.37	1
tc|Rep: Chromosome undetermined scaffold_768, whole genome shotgun sequenc	95.01	1

tc|Rep: 40S ribosomal protein S15-like - Solanum tuberosum (Potato), complete [T(	475.03	1
gb|KG9B.105G16F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105G16, n	1185.41	1
Unknown	42.27	1
gb|Nicotiana tabacum inosine-5'-phosphate dehydrogenase (guaB) mRNA, partial c	50.4	1
Unknown	23.04	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	121.91	1
gb|AM809865 DL, diurnal library Nicotiana tabacum cDNA clone nt005093022, mRI	74.06	1
gb|TOBESTR014E12 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA sequ	88.22	1
gb|TT-12_L04 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	67.09	1
gb|KG9B.102L17F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102L17, m	446.89	1
tc|Rep: Phosphate/phosphoenolpyruvate translocator - Nicotiana tabacum (Comm	51.74	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	49809.75	1
tc|Rep: 26S protease regulatory subunit 6B homolog - Solanum tuberosum (Potato)	178.11	1
Unknown	10302.3	1
tc|Rep: Protein translation factor SUI1 homolog - Sporobolus stapfianus (Ressurecti	289.78	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	422.98	1
tc|Rep: Autophagy-related protein 3 - Arabidopsis thaliana (Mouse-ear cress), parti	25.34	1
gb|KF8C.102F16F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102F16, mRN	240.43	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	22.79	1
Unknown	45.48	1
gb|KG9B.105H03F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105H03, n	1023.58	1
gb|Nicotiana tabacum CYI 1a mRNA, complete cds [AF019202]	54.44	1
tc|Rep: 2-oxoacid dehydrogenase family protein - Arabidopsis thaliana, partial (55%	58.06	1
tc|Rep: Chromosome chr16 scaffold_271, whole genome shotgun sequence - Vitis v	1358.59	1
Unknown	71.2	1
Unknown	21.3	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	97.82	1
Unknown	26.49	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	24.26	1
Unknown	105.12	1
Unknown	81.4	1
Unknown	1359.37	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	69.06	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	199.89	1

Unknown	79.29	1
Unknown	2975.16	1
Unknown	2753.94	1
Unknown	116.71	1
tc|Rep: Chromosome undetermined scaffold_69, whole genome shotgun sequence	10638.45	1
tc|Rep: ORF459 - Beta vulgaris subsp. vulgaris, partial (63%) [TC62558]	36.15	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	32.22	1
tc|Rep: Proteasome subunit alpha type - Solanum tuberosum (Potato), partial (98%	66.22	1
gb|KF8C.105J14F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105J14, mRN	2755.88	1
gb|Nicotiana tabacum mRNA for alpha-tubulin (tubA2 gene) [AJ421412]	49053.45	1
gb|N.tabacum mRNA for voltage-dependent chloride channel [X95576]	508.05	1
tc|Rep: Os11g0496400 protein - Oryza sativa subsp. japonica (Rice), partial (45%) [T	5187.91	1
gb|KF8C.109O04F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109O04, mR	6670.05	1
Unknown	1126.79	1
gb|AGN_ELP006xa11f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	63.88	1
gb|Nicotiana tabacum DNA topoisomerase II mRNA, complete cds [AY169238]	55.7	1
tc|Rep: Glutamate/malate translocator - Nicotiana tabacum (Common tobacco), co	92.82	1
Unknown	29.1	1
gb|TOBESTR046E09 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	82.1	1
gb|KF8C.102G18F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102G18, mR	54122	1
gb|TT-21_L02 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	133.83	1
Unknown	63.39	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	471.62	1
gb|KF8C.109G06F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109G06, mR	25.62	1
gb|Nicotiana tabacum cDNA-AFLP fragment H-N_BT3M23-215 sequence [DQ46019	55.43	1
gb|KR3B.001D06F.050815T7 KR3B Nicotiana tabacum cDNA clone KR3B.001D06, m	222.37	1
tc|Rep: Hexose transporter 6 - Vitis vinifera (Grape), partial (50%) [TC56604]	143.11	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	33.25	1
Unknown	8641.39	1
tc|MRARRHA M.racemosus (Zygomycetes) 25S ribosomal RNA gene, partial (9%) [T	661.06	1
tc|Rep: RPN9 - Nicotiana benthamiana, partial (43%) [TC52004]	60.62	1
Unknown	47.19	1
Unknown	563	1
tc|Rep: Coatomer subunit epsilon-1 - Arabidopsis thaliana (Mouse-ear cress), partia	744.61	1

tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	630.38	1
Unknown	529.75	1
Unknown	53.87	1
gb|KR3B.110K20F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110K20, m	30.11	1
gb|KP1B.107I22F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107I22, mR	1404.7	1
gb|TT-40_F21 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	76.87	1
tc|Rep: Chromosome undetermined scaffold_644, whole genome shotgun sequenc	261.56	1
Unknown	67.6	1
tc|Rep: Pyridoxal kinase - Solanum tuberosum (Potato), partial (33%) [TC65370]	196.96	1
gb|KN6B.104P14F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104P14, m	31.31	1
gb|AGN_RNC011xk14r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	40.36	1
gb|KR3B.105E09F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.105E09, m	49.04	1
gb|Nicotiana tabacum mRNA for NtSar1 protein, complete cds [D87821]	11240.65	1
Unknown	30.78	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	135.77	1
gb|AGN_PNL211df1_f11.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	40.7	1
tc|Rep: Peptidyl-prolyl cis-trans isomerase 1 - Malus domestica (Apple) (Malus sylv	24	1
tc|Rep: Ribosomal protein L24E - Medicago truncatula (Barrel medic), complete [TC	384.43	1
gb|AM792691 DL, diurnal library Nicotiana tabacum cDNA clone nt005153020, mR	67.2	1
Unknown	20.43	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	336.82	1
Unknown	207.28	1
gb|KT7B.107O17F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107O17, mR	2789.26	1
tc|Rep: Mitochondrial ribosomal protein S13 - Nicotiana tabacum (Common tobacc	95.96	1
gb|TOBESTR057D10 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	159.73	1
tc|Rep: Chromosome chr4 scaffold_443, whole genome shotgun sequence - Vitis vi	73.78	1
Unknown	46.81	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	104.57	1
tc|Rep: F3O9.16 - Arabidopsis thaliana (Mouse-ear cress), partial (48%) [TC63404]	379.84	1
tc|Rep: Sulfite reductase - Nicotiana tabacum (Common tobacco), partial (16%) [TC	3387.09	1
Unknown	230.26	1
gb|AGN_RPC015xj05f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	31.91	1
gb|TT-05_N04 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	44.55	1
tc|Rep: Alpha-tubulin - Nicotiana tabacum (Common tobacco), complete [TC41070	42134.85	1

tc|Rep: RNA-binding protein RZ-1 - Nicotiana sylvestris (Wood tobacco), complete [	964.07	1
gb|KF8C.101J22F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101J22, mRN	383.11	1
tc|Rep: Ferric-chelate reductase - Solanum lycopersicum (Tomato) (Lycopersicon es	28.15	1
Unknown	18041.45	1
tc|Rep: Ribosomal protein S6-like protein - Solanum tuberosum (Potato), complete	223.13	1
gb|Nicotiana tabacum TORK1 mRNA for potassium channel TORK1, complete cds [	29.86	1
gb|AGN_RNC005xe12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	49.39	1
Unknown	519.93	1
gb|CHO_SL004xl02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	43.75	1
gb|AGN_RNC012xp06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	377.79	1
Unknown	118.78	1
gb|AGN_RNC129xb18r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	25.93	1
Unknown	88.2	1
Unknown	48.75	1
gb|KF8B.202J14F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202J14, mRN	1482.54	1
gb|Nicotiana tabacum mRNA, complete cds, 1290 bp sequence [AB024511]	511.84	1
gb|AGN_ELP022xg17f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	35.45	1
gb|KP1B.102P01F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102P01, m	24.85	1
Unknown	134.39	1
gb|BL12.101D20F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.101D20, m	29.65	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	29.07	1
Unknown	24.35	1
gb|KR3B.107D17F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.107D17, m	32.12	1
tc|Rep: 60S ribosomal protein L7A-like protein - Solanum tuberosum (Potato), com	30.66	1
gb|AGN_RNC024xc18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	6535.26	1
tc|Rep: Vacuolar H(+)-ATPase subunit B - Suaeda salsa (Seepweed) (Chenopodium s	303.81	1
gb|TT-11_H13 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	1132.91	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	195.21	1
gb|N.tabacum Nthsp70 mRNA for heat shock protein 70 [X63106]	33.73	1
gb|AGN_RPC005xl10f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	19.98	1
gb|KL4B.111A04F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111A04, m	35.42	1
Unknown	181.12	1
gb|KG9B.105B20F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105B20, m	1901.48	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	29.57	1

tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	44.26	1
gb|CHO_SL028xk23f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	473.62	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	563.58	1
Unknown	203.74	1
gb|KG9B.001G15F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001G15, n	1844.69	1
Unknown	1921.39	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	179.6	1
Unknown	21.61	1
tc|Rep: Ubiquitin-conjugating enzyme E2-17 kDa - Solanum lycopersicum (Tomato)	1271.08	1
tc|Rep: Chromosome chr8 scaffold_99, whole genome shotgun sequence - Vitis vin	25.82	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	82.24	1
Unknown	2496.86	1
gb|Tobacco (N.tabacum) GapA mRNA encoding A-subunit of chloroplast glyceradeh	21.25	1
Unknown	379.77	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	83.54	1
Unknown	135.62	1
Unknown	32.46	1
gb|TT-36_B15 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	81.35	1
gb|AGN_RPC006xp21f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	155.65	1
gb|Nicotiana tabacum kinesin-like protein (tck1) mRNA, complete cds [U52078]	112.48	1
gb|KL4B.103C22F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103C22, mR	54.39	1
gb|FS382718 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	91.71	1
tc|Rep: Formate--tetrahydrofolate ligase - Spinacia oleracea (Spinach), partial (25%	147.65	1
gb|KG9B.107B23F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107B23, m	87.8	1
gb|TT-04_H10 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	24.86	1
Unknown	56.81	1
gb|BP528671 MAT001 Nicotiana tabacum cDNA clone BY13532, mRNA sequence [	143.46	1
gb|AGN_RNC020xb11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	18.14	1
Unknown	22.84	1
gb|Nicotiana tabacum mRNA for putative reductase (MC118 gene) [AM851011]	44.77	1
tc|Rep: Brain and reproductive organ-expressed protein-like - Arabidopsis thaliana	23.58	1
gb|AGN_RNC107xa04r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	18.71	1
tc|Rep: Thioredoxin peroxidase - Nicotiana tabacum (Common tobacco), partial (85	44.05	1
tc|Rep: 40S ribosomal protein S12 - Vitis vinifera (Grape), partial (96%) [TC67348]	31.34	1

gb|EST_FLW002xp07f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	32.74	1
tc|Rep: Ci21A protein - Solanum tuberosum (Potato), partial (94%) [TC69256]	346.69	1
Unknown	951.46	1
gb|TT-31_J19 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	26.46	1
Unknown	62.62	1
tc|Rep: ATP:citrate lyase - Capsicum annuum (Bell pepper), partial (76%) [TC45257]	31.66	1
tc|Rep: Triosephosphate isomerase, chloroplast precursor - Fragaria ananassa (Stra	3973.99	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	158.18	1
tc|Rep: Chromosome undetermined scaffold_1331, whole genome shotgun sequen	203.78	1
Unknown	159.79	1
Unknown	103.78	1
Unknown	150.51	1
Unknown	897.25	1
gb|TT-05_M07 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA se	143.74	1
gb|FS409145 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	21.19	1
gb|AM840564 seedling library, SL Nicotiana tabacum cDNA clone nt002013085, m	162.77	1
gb|KG9B.105O22F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105O22, r	3338	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	27.74	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	70.83	1
Unknown	545.72	1
Unknown	502.67	1
gb|KR3B.110K16F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110K16, m	37.7	1
gb|TT-27_D09 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	370.55	1
Unknown	53.94	1
gb|KP1B.107G01F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107G01, m	91.48	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	58.89	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	189.36	1
gb|KP1B.108G24F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108G24, m	2623.76	1
tc|Rep: Lactoylglutathione lyase - Solanum lycopersicum (Tomato) (Lycopersicon es	507.08	1
tc|Rep: DNA-directed RNA polymerase IIb - Nicotiana tabacum (Common tobacco),	57.55	1
gb|AGN_RNC116xg16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	18.57	1
Unknown	497.48	1
Unknown	24.93	1
tc|Rep: 40S ribosomal protein S23 - Fragaria ananassa (Strawberry), complete [TC5	113.96	1

Unknown	85.84	1
gb|KR3B.105C01F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.105C01, m	522.39	1
gb|AM780197 seedling library, SL Nicotiana tabacum cDNA clone nt002317013, mR	54.5	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	204.86	1
tc|Rep: Spermidine synthase 1 - Datura stramonium (Jimsonweed) (Common thorn	942.64	1
Unknown	75.78	1
tc|Rep: Class II small heat shock protein Le-HSP17.6 - Solanum lycopersicum (Toma	180.97	1
gb|CHO_SL028xe24f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	35.23	1
gb|KF8C.103J18F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103J18, mRN	2709.88	1
gb|KP1B.108G15F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108G15, m	35.68	1
tc|Rep: Genomic DNA, chromosome 5, TAC clone:K2A18 - Arabidopsis thaliana (Mo	203.85	1
Unknown	59.11	1
gb|AGN_RNC017xd14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	2925.97	1
gb|ntsm10 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [E	177.11	1
Unknown	8875.84	1
tc|Rep: AT3g42050/F4M19_10 - Arabidopsis thaliana (Mouse-ear cress), complete	212.63	1
Unknown	140.73	1
Unknown	247.76	1
gb|KG9B.002E03F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002E03, m	1171.93	1
gb|TT-36_P10 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	109.87	1
Unknown	63.44	1
tc|Rep: Chromosome chr15 scaffold_82, whole genome shotgun sequence - Vitis vi	63.32	1
Unknown	86.33	1
gb|KL4B.112M07F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112M07, m	167.77	1
gb|AGN_PNL226bf1_d6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	33.82	1
Unknown	234.18	1
Unknown	28.54	1
gb|AM794263 COL, cold overnight library Nicotiana tabacum cDNA clone nt006206	97.5	1
Unknown	996.31	1
Unknown	27.65	1
gb|KG9B.102E19F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102E19, m	100.65	1
Unknown	378.03	1
gb|Nicotiana tabacum mRNA for gamma tubulin (gtub gene) [AJ278739]	35.53	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (25%) [TC6	207.17	1

Unknown	183.15	1
tc|Rep: Chromosome chr1 scaffold_84, whole genome shotgun sequence - Vitis vin	167.66	1
Unknown	27.44	1
gb|CHO_SL002xi14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	431.24	1
gb|TT-06_M07 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sec	69.28	1
Unknown	284.49	1
gb|TOBESTR120F08 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA sequ	168.21	1
tc|Rep: Phosphoenolpyruvate carboxylase - Nicotiana sylvestris (Wood tobacco), pa	98.14	1
Unknown	23.04	1
gb|CHO_SL015xj07f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	120.75	1
gb|KR3B.112M13F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112M13, r	250.77	1
gb|TT-06_A07 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	54.98	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	29.94	1
Unknown	40.57	1
tc|Rep: Chromosome undetermined scaffold_114, whole genome shotgun sequenc	50.54	1
Unknown	21.59	1
gb|KF8C.104G19F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104G19, mR	1650.45	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	4138.79	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	232.51	1
gb|AGN_ELP012xa10f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	27.96	1
Unknown	23.76	1
Unknown	49.47	1
gb|Nicotiana tabacum cultivar Samsun respiratory burst oxidase protein mRNA, par	536.31	1
gb|KF8C.110N22F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110N22, mR	75.81	1
Unknown	548.8	1
gb|TT-12_O24 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	640.37	1
Unknown	2539.65	1
tc|Rep: Chromosome chr10 scaffold_43, whole genome shotgun sequence - Vitis vi	1083.94	1
Unknown	136.42	1
tc|Rep: B2-type cyclin dependent kinase - Solanum lycopersicum (Tomato) (Lycoper	100.1	1
gb|KR3B.105H05F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.105H05, m	3969.89	1
tc|Rep: Pyruvate decarboxylase - Solanum tuberosum (Potato), complete [TC48760	22.03	1
gb|AGN_RNC009xg01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	904.6	1
Unknown	5812.16	1

gb|KG9B.101D11F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101D11, n	816.06	1
gb|KT7B.107P18F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107P18, mRI	30.59	1
gb|KR2B.115F20F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115F20, mI	49.13	1
tc|Rep: AT4g05320/C17L7_240 - Arabidopsis thaliana (Mouse-ear cress), partial (98	3951.3	1
gb|AGN_ELP010xd20f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	113.72	1
gb|KR2B.102E02F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.102E02, ml	46.3	1
gb|TT-03_F07 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	184.36	1
Unknown	515.19	1
tc|Rep: Arginine decarboxylase 1 - Nicotiana tabacum (Common tobacco), partial (2	3581.77	1
Unknown	32.95	1
tc|Rep: AGAP000318-PA - Anopheles gambiae str. PEST, partial (9%) [TC72511]	71.02	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	100.25	1
gb|KT7C.104G18F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104G18, mR	1433.18	1
tc|Rep: CDPK-like protein - Solanum tuberosum (Potato), partial (77%) [TC63214]	22.97	1
tc|Rep: 1,4-alpha-glucan-maltohydrolase - Solanum lycopersicum (Tomato) (Lycope	255.07	1
gb|KP1B.108I18F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108I18, mRI	57.28	1
gb|AGN_ELP019xm04f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	79.8	1
Unknown	38.28	1
Unknown	28.7	1
tc|Rep: Xaa-Pro aminopeptidase 2 - Solanum lycopersicum (Tomato) (Lycopersicon	1101.58	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	1896.5	1
Unknown	22.76	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	1024.18	1
gb|N.tabacum mRNA for transformer-SR ribonucleoprotein [Y09506]	396.31	1
Unknown	1048.33	1
Unknown	1504.87	1
tc|Rep: Chromosome chr19 scaffold_35, whole genome shotgun sequence - Vitis vi	138.65	1
gb|AM806329 seedling library, SL Nicotiana tabacum cDNA clone nt002240007, mF	33.72	1
gb|KG9B.101O02F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101O02, r	2852.49	1
gb|AGN_RNC023xe15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	32.37	1
tc|Rep: Ubiquitin carboxyl-terminal hydrolase - Vitis vinifera (Grape), partial (23%) |	202.9	1
gb|AGN_RNC005xf04f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	870.66	1
gb|TT-07_G15 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	65.66	1
Unknown	105.76	1

gb|Nicotiana tabacum putative chloroplast thiazole biosynthetic protein (ThiI) mRN	41.86	1
tc|Rep: Chromosome chr12 scaffold_38, whole genome shotgun sequence - Vitis vi	257.53	1
gb|Nicotiana tabacum heterotrimeric GTP-binding protein subunit beta 1 mRNA, cc	41.4	1
gb|AB257509 MAT001 Nicotiana tabacum cDNA clone BY4861 similar to KED, mRN	181.74	1
gb|Nicotiana tabacum cyclin-dependent kinase B1-2 (CdkB1-2) mRNA, complete cd	18.59	1
gb|KT7B.100M14F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100M14, m	522.19	1
tc|Rep: Chromosome chr2 scaffold_112, whole genome shotgun sequence - Vitis vi	222.25	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	509.47	1
tc|Rep: T23O15.3/T23O15.3 - Arabidopsis thaliana (Mouse-ear cress), partial (33%)	1568.58	1
tc|Rep: Endomembrane protein EMP70 precusor isolog; 68664-64364 - Arabidopsis	4462.03	1
gb|CHO_SL007xb23f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1559.08	1
tc|Rep: Silicatein - Halichondria okadai (Marine sponge), partial (15%) [TC67373]	240.52	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	4995.82	1
tc|Rep: Chromosome undetermined scaffold_147, whole genome shotgun sequenc	478.89	1
Unknown	56.47	1
tc|Rep: Aspartic proteinase precursor - Cucurbita pepo (Vegetable marrow) (Summ	19285.8	1
gb|Nicotiana tabacum anther-specific myb-related protein 2 (mybAS2) mRNA, com	1099.82	1
Unknown	284.28	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	750.32	1
Unknown	19.84	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	1521.83	1
gb|KL4B.103I18F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103I18, mRN	38969.75	1
gb|AGN_RNC008xk13f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	100.4	1
gb|KL4B.100C09F.050922T7 KL4B Nicotiana tabacum cDNA clone KL4B.100C09, mR	21098.3	1
gb|CB_NPSSHcDNA_26 CB_NPSSHcDNA Library Nicotiana tabacum cDNA clone NP	621.57	1
Unknown	19.92	1
tc|Rep: Cytochrome b5 - Nicotiana tabacum (Common tobacco), complete [TC7205	4758.8	1
gb|BP534328 MAT005 Nicotiana tabacum cDNA clone BY32285, mRNA sequence [	34.03	1
Unknown	41.5	1
gb|TT-06_I16 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	58.38	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	3374.37	1
gb|KG9B.004E04F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004E04, m	153.2	1
Unknown	22.21	1
Unknown	291.98	1

Unknown	336.15	1
tc|Rep: Aspartate aminotransferase - Vitis vinifera (Grape), partial (97%) [TC43521]	151.31	1
Unknown	61.05	1
gb|KF8C.104F20F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104F20, mRN	37007.2	1
Unknown	23.97	1
Unknown	2774.29	1
gb|KR3B.109F13F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109F13, mR	59.5	1
tc|Rep: Fumarylacetoacetase - Medicago truncatula (Barrel medic), partial (55%) [T	31	1
gb|KL4B.102A12F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102A12, mR	243.01	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	590.91	1
Unknown	93.94	1
tc|Rep: BTF3 - Nicotiana benthamiana, complete [TC68489]	32.49	1
Unknown	21.59	1
Unknown	25.08	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	20.47	1
Unknown	70.82	1
Unknown	87	1
gb|KT7C.110F03F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110F03, mRN	225.57	1
gb|TT-40_K09 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	291.93	1
gb|KT7B.103H05F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.103H05, mR	38.49	1
gb|BL12.001C03F.060117T7 BL12 Nicotiana tabacum cDNA clone BL12.001C03, mR	82.01	1
tc|Rep: DCK/dGK-like deoxyribonucleoside kinase - Solanum lycopersicum (Tomato	28.72	1
tc|Rep: Chromosome undetermined scaffold_91, whole genome shotgun sequence	136.77	1
Unknown	105.69	1
gb|AGN_RPC015xi03f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	91.99	1
gb|AGN_PNL210af1_f11.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	68.69	1
gb|CHO_SL013xg13f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	184	1
gb|TT-06_N13 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	422.6	1
Unknown	50.64	1
gb|Nicotiana tabacum mRNA for mitochondrial 2-oxoglutarate [AJ299250]	1576.9	1
Unknown	27.35	1
tc|Rep: Ubiquitin carrier protein - Gossypium hirsutum (Upland cotton) (Gossypium	1392.25	1
tc|Rep: Chromosome chr5 scaffold_124, whole genome shotgun sequence - Vitis vi	35.33	1
gb|KG9B.105I20F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105I20, mR	25.84	1

Unknown	31.38	1
gb|CHO_SL022xp22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	95.88	1
gb|KL4B.111M23F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111M23, m	22.2	1
tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin	8258.06	1
Unknown	19.43	1
gb|AGN_RNC211xb13f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	224.94	1
Unknown	62.26	1
gb|KP1B.113A16F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.113A16, m	251.52	1
tc|Rep: Water channel protein - Nicotiana excelsior, complete [TC40274]	26.16	1
tc|Rep: Eukaryotic translation initiation factor 5A-1/2 - Solanum tuberosum (Potat	1883.66	1
Unknown	22.66	1
tc|Rep: Ubiquitin fusion-degradation protein-like - Solanum tuberosum (Potato), pa	24.97	1
Unknown	2950.81	1
Unknown	254.46	1
Unknown	2638.24	1
Unknown	557.39	1
Unknown	490.63	1
tc|Rep: Elongation factor EF-2 - Arabidopsis thaliana (Mouse-ear cress), partial (27%	273.44	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	2632.13	1
tc|Rep: ABC transporter - Populus tremula x Populus tremuloides, partial (42%) [TC	20.5	1
gb|KG9B.104F17F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104F17, m	34.54	1
tc|Rep: Glutaredoxin - Solanum lycopersicum (Tomato) (Lycopersicon esculentum),	289.3	1
tc|Rep: Chromosome chr18 scaffold_24, whole genome shotgun sequence - Vitis vi	43.39	1
gb|Nicotiana tabacum SR1 Nt-rab11a mRNA, complete cds [L29271]	744.16	1
gb|KP1B.103C06F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103C06, m	1570.6	1
gb|KT7C.105D06F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105D06, mR	89.63	1
gb|KG9B.107P08F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107P08, m	145.94	1
tc|Rep: Histone H2B-like protein - Solanum tuberosum (Potato), partial (98%) [TC5	393.87	1
gb|AGN_RNC002xm03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	24.82	1
Unknown	56.45	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	80.7	1
gb|AGN_ELP015xh06f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	19.08	1
tc|Rep: Ras-related protein RAB8-4 - Nicotiana tabacum (Common tobacco), compl	467.35	1
Unknown	20.66	1

Unknown	21.64	1
gb|AGN_PNL231af1_b2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	22535.75	1
Unknown	678.1	1
Unknown	379.91	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	2388.94	1
Unknown	61.97	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	50.33	1
gb|TT-08_O04 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	350.05	1
gb|KR3B.110K10F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110K10, m	85.27	1
gb|KF8C.110H13F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110H13, mR	26.39	1
gb|AM779996 seedling library, SL Nicotiana tabacum cDNA clone nt002097061, m	150.9	1
gb|AGN_RPC017xd20f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	47.74	1
tc|Rep: NRC1 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), partial	26.51	1
Unknown	21.55	1
Unknown	505.27	1
tc|Rep: Chromosome chr10 scaffold_179, whole genome shotgun sequence - Vitis	112.19	1
Unknown	23	1
gb|AM835066 seedling library, SL Nicotiana tabacum cDNA clone nt002084073, m	94.21	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	216.76	1
gb|KR3B.106M07F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106M07,	500.86	1
gb|KG9B.102O14F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102O14,	859.35	1
gb|KG9B.103F12F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103F12, m	165.62	1
gb|KN6B.101L22F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101L22, m	740.92	1
tc|Rep: NADPH-dependent mannose 6-phosphate reductase - Orobanche ramosa (	50.93	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	466.78	1
tc|Rep: Ozone-responsive stress-related protein-like - Oryza sativa subsp. japonica	640.05	1
gb|KL4B.101L06F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101L06, mR	7793.21	1
gb|KL4B.101J12F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101J12, mR	386.13	1
tc|Rep: Chromosome chr4 scaffold_333, whole genome shotgun sequence - Vitis vi	28.09	1
gb|KR3B.101A04F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101A04, m	126.24	1
gb|12.2A02 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5'	4644.71	1
gb|TL13.106E17F.060315T7 TL13 Nicotiana tabacum cDNA clone TL13.106E17, mR	605.72	1
gb|Nicotiana tabacum mRNA for hypothetical protein (mc304 gene) [AJ966361]	1758.98	1
Unknown	43.83	1

Unknown	46.54	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	119.87	1
Unknown	27.14	1
tc|Rep: Ubiquitin carrier protein - Solanum tuberosum (Potato), partial (98%) [TC41	25.57	1
Unknown	95.41	1
gb|AGN_RNC029xh08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	94.09	1
gb|TT-08_I07 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	63.12	1
tc|Rep: Low molecular weight heat-shock protein - Nicotiana tabacum (Common to	27.36	1
Unknown	1124.47	1
tc|Rep: UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase - Brucella suis	84.99	1
gb|KF8C.102A04F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102A04, mR	758.26	1
gb|N.tabacum mRNA for ras-related GTP-binding protein [X72212]	2232.78	1
gb|TL13.101P14F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.101P14, mR	99.38	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	47.77	1
gb|AM840678 seedling library, SL Nicotiana tabacum cDNA clone nt002181068, m	23.09	1
Unknown	151.2	1
gb|AGN_RNC017xd21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	458.29	1
gb|Nicotiana tabacum cytosolic aconitase (ACO) mRNA, complete cds [AF194945]	19.04	1
Unknown	284.9	1
gb|KG9B.106K08F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106K08, m	61	1
tc|Rep: Heat shock protein 70-3 - Nicotiana tabacum (Common tobacco), partial (3	765.14	1
gb|Nicotiana tabacum mRNA for NAD-dependent isocitrate dehydrogenase, clone	491.87	1
gb|30G03 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5',	844.18	1
gb|AGN_RNC116xe09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	260.45	1
gb|CHO_SL025xj11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	512.05	1
Unknown	36.68	1
Unknown	32.38	1
gb|KL4B.103D12F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103D12, m	76.04	1
gb|BP535201 MAT005 Nicotiana tabacum cDNA clone BY35035, mRNA sequence [	793.94	1
tc|Rep: HyPRP2 - Gossypium hirsutum (Upland cotton) (Gossypium mexicanum), pa	18.75	1
gb|TT-07_D03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	134.43	1
Unknown	85.45	1
gb|KF8B.201H23F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201H23, mR	20.78	1
gb|AM818672 DL, diurnal library Nicotiana tabacum cDNA clone nt005209092, mR	49.49	1

tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	40.04	1
gb|3H05 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', m	89.55	1
Unknown	18	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	137.89	1
tc|Rep: Mitochondrial small heat shock protein - Solanum lycopersicum (Tomato) (	833.07	1
tc|Rep: Pyruvate kinase - Vitis vinifera (Grape), partial (19%) [TC70531]	3312.58	1
Unknown	26.42	1
gb|TOBESTR023C01 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	370.45	1
Unknown	87.22	1
Unknown	118.82	1
tc|Rep: TCTR2 protein - Solanum lycopersicum (Tomato) (Lycopersicon esculentum	184.16	1
tc|Rep: 60S ribosomal protein L35 - Euphorbia esula (Leafy spurge), complete [TC5	169.5	1
gb|TT-20_O05 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	522.68	1
Unknown	139.79	1
Unknown	548.9	1
tc|Rep: Chromosome undetermined scaffold_533, whole genome shotgun sequenc	131.01	1
tc|Rep: ZTL - Ipomoea nil (Japanese morning glory) (Pharbitis nil), partial (96%) [TC	270.93	1
gb|TT-11_N02 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	450.79	1
gb|KN6B.100O15F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100O15, r	80.16	1
gb|KL4B.106B16F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106B16, mR	55.78	1
tc|Rep: Chromosome undetermined scaffold_363, whole genome shotgun sequenc	2253.42	1
tc|Rep: Uncharacterized protein At1g73350.2 - Arabidopsis thaliana (Mouse-ear cre	42.38	1
Unknown	44.23	1
gb|AGN_PNL222df1_e5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	3099.98	1
tc|Rep: Chromosome chr5 scaffold_156, whole genome shotgun sequence - Vitis vi	24180.15	1
Unknown	952.84	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	58.2	1
gb|AGN_RNC023xi12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	25.75	1
Unknown	40.27	1
gb|KF8C.108O20F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108O20, mR	93.43	1
Unknown	21.23	1
tc|Rep: Nt-rab7c protein - Nicotiana tabacum (Common tobacco), partial (97%) [TC	160.84	1
tc|Rep: 26S proteasome regulatory particle non-ATPase subunit5 - Oryza sativa sub	743.97	1
tc|Rep: Tuber-specific protein - Capsicum annuum (Bell pepper), partial (37%) [TC4	46.26	1

gb|KG9B.102G16F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102G16,	1888.05	1
gb|TT-07_D06 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	21.85	1
gb|KL4B.104D09F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104D09, m	85.8	1
gb|KG9B.003L13F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003L13, m	22.93	1
Unknown	205.57	1
Unknown	233.14	1
tc|Rep: Ubiquitin carrier protein - Arachis hypogaea (Peanut), partial (11%) [TC668	1233.82	1
gb|KP1B.037J20F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.037J20, mR	20.98	1
Unknown	25.56	1
tc|Rep: Chromosome chr16 scaffold_189, whole genome shotgun sequence - Vitis	79.45	1
tc|Rep: PRL1 protein - Arabidopsis thaliana (Mouse-ear cress), partial (83%) [TC587	86.25	1
Unknown	21.18	1
gb|KT7C.109C11F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109C11, mR	110.32	1
gb|TT-05_F22 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	128.77	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	21.73	1
gb|AGN_RNC003xm07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	38.3	1
Unknown	18.47	1
gb|KP1B.102L17F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102L17, m	27.66	1
gb|AGN_RNC020xf15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	115.24	1
tc|Rep: Eukaryotic initiation factor 4A-3 - Nicotiana plumbaginifolia (Leadwort-leav	1050.38	1
tc|Rep: Spliceosomal protein - Solanum tuberosum (Potato), partial (35%) [TC5154	235.89	1
gb|Nicotiana tabacum WREBP-2 mRNA, complete cds [AB017694]	96.68	1
tc|Rep: Chromosome chr10 scaffold_179, whole genome shotgun sequence - Vitis	563.5	1
gb|KF8C.101N10F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101N10, mR	255.01	1
tc|Rep: CONSTANS interacting protein 2b - Solanum lycopersicum (Tomato) (Lycop	561.24	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	208.78	1
gb|KF8C.106E15F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106E15, mR	671.25	1
Unknown	25.7	1
tc|Rep: Ribosomal protein L33 - Castanea sativa (Sweet chestnut), complete [TC531	353.29	1
gb|AGN_ELP025xg20f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	58.71	1
gb|BL12.103D22F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.103D22, m	524.25	1
gb|TT-36_A04 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	82.91	1
Unknown	237.78	1
gb|KG9B.103F19F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103F19, m	110.75	1

tc|Rep: AN14 - Zea mays (Maize), partial (75%) [TC45728]	708.79	1
gb|KT7B.100M05F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100M05, m	40.07	1
gb|KL4B.108B07F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108B07, mR	216.21	1
Unknown	781.57	1
gb|TT-36_N18 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	178.16	1
Unknown	3523.23	1
gb|TT-48_F18 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	3324.32	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	75.78	1
tc|Rep: Arm repeat containing protein homolog-like - Oryza sativa subsp. japonica (	75.81	1
Unknown	23.59	1
gb|KP1B.107N10F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107N10, m	739.25	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	240.49	1
Unknown	58.03	1
gb|Nicotiana tabacum mRNA for phosphate translocator [X75088]	768.38	1
gb|TT-21_P08 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	18.05	1
Unknown	2479.59	1
Unknown	4151.93	1
Unknown	63.89	1
tc|Rep: Chromosome chr12 scaffold_38, whole genome shotgun sequence - Vitis vi	545.96	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	30.29	1
Unknown	97.26	1
tc|Rep: Chloroplast photosystem I reaction center V - Camellia sinensis (Tea), partia	49	1
tc|Rep: Ribosomal protein L11-like - Nicotiana tabacum (Common tobacco), comple	94.32	1
tc|Rep: Thioredoxin - Limonium bicolor, partial (65%) [TC49822]	23.43	1
gb|KL4B.103H13F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103H13, m	2625.9	1
tc|Rep: Ribosomal protein S10 containing protein - Tetrahymena thermophila SB21	35	1
gb|KR2B.111L06F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.111L06, m	17.96	1
Unknown	158.75	1
Unknown	781.14	1
Unknown	2472.43	1
gb|TT-31_E17 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	21.74	1
tc|Rep: Peptidyl-prolyl cis-trans isomerase - Vitis vinifera (Grape), partial (91%) [TC	14167.6	1
Unknown	55.21	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	52.29	1

tc|Rep: Ripening regulated protein DDTFR19 - Solanum lycopersicum (Tomato) (Lyc	114.52	1
Unknown	103.82	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	22.72	1
gb|AGN_RPC022xe13f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	8525.87	1
Unknown	27.67	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	3078.9	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	813.08	1
gb|TOBESTR043D08 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	37321.95	1
tc|Rep: Chromosome undetermined scaffold_44, whole genome shotgun sequence	23.58	1
gb|AM817228 seedling library, SL Nicotiana tabacum cDNA clone nt002051027, m	25.35	1
gb|KP1B.108B21F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108B21, m	101.35	1
Unknown	52.15	1
gb|KN6B.102G12F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102G12,	3094.8	1
Unknown	100.8	1
Unknown	46.85	1
gb|Nicotiana tabacum Tobacco mosaic virus helicase domain-binding protein mRN	223.7	1
Unknown	961.28	1
Unknown	22.13	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	53993.5	1
tc|Rep: SWIb domain-containing protein - Solanum chacoense (Chaco potato), com	50.32	1
gb|KF8B.200J22F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200J22, mRN	251.68	1
tc|Rep: Nuclear transport factor 2 - Arabidopsis thaliana (Mouse-ear cress), partial	1011.77	1
Unknown	239.9	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	672.43	1
gb|TT-03_L14 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	3955.02	1
gb|AGN_ELP024xd21f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	30.19	1
Unknown	1607.83	1
Unknown	766.22	1
gb|KT7C.106G04F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106G04, mR	19.08	1
gb|KN6B.100C14F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100C14, m	214.46	1
gb|KL4B.112O03F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112O03, m	78.24	1
tc|Rep: Glucose-1-phosphate adenylyltransferase - Nicotiana tabacum (Common t	18.1	1
tc|Rep: Chromosome chr5 scaffold_72, whole genome shotgun sequence - Vitis vin	144.09	1
Unknown	124.67	1

gb|AGN_ELP007xg03f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	47.74	1
Unknown	55.3	1
tc|Rep: Chromosome chr2 scaffold_187, whole genome shotgun sequence - Vitis vi	123.29	1
gb|Nicotiana tabacum pollen specific actin-depolymerizing factor 1 (ADF1) mRNA,	18226.8	1
gb|BP530854 MAT005 Nicotiana tabacum cDNA clone BY23117, mRNA sequence [	48.94	1
tc|Rep: Protein transport protein SEC61 subunit gamma - Oryza sativa subsp. japon	1858.3	1
tc|Rep: Tonoplast intrinsic protein bobTIP26-1 - Brassica oleracea var. botrytis (Cau	138.04	1
Unknown	80.22	1
Unknown	44.42	1
gb|TT-35_B02 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	92.74	1
gb|KT7C.108P21F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108P21, mR	194.7	1
gb|KT7C.105L12F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105L12, mRN	98.24	1
gb|KL4B.100E12F.050922T7 KL4B Nicotiana tabacum cDNA clone KL4B.100E12, mR	29.82	1
Unknown	139.94	1
gb|AGN_RNC004xc19r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	25.67	1
Unknown	373.02	1
Unknown	140.47	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	49.07	1
gb|KN6B.109O12F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.109O12, r	43.24	1
tc|Rep: Chromosome chr10 scaffold_179, whole genome shotgun sequence - Vitis	9546.57	1
tc|Rep: Chromosome undetermined scaffold_134, whole genome shotgun sequenc	20.08	1
gb|KP1B.109O15F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109O15, m	866.44	1
tc|Rep: Beta-amylase 1 - Nicotiana langsdorffii x Nicotiana sanderae (Ornamental t	44.16	1
Unknown	216.7	1
tc|Rep: Genomic DNA, chromosome 3, P1 clone: MUO10 - Arabidopsis thaliana (M	29.86	1
gb|AM818734 COL, cold overnight library Nicotiana tabacum cDNA clone nt006087	114.35	1
gb|KL4B.110N18F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110N18, m	29.43	1
tc|Rep: Septin - Candida albicans (Yeast), partial (3%) [TC45048]	26.57	1
Unknown	659.4	1
Unknown	179	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	569.86	1
Unknown	98.36	1
Unknown	195.06	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	444.54	1

gb|CHO_SL004xm23f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	1655.36	1
gb|KL4B.111A08F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111A08, m	64.97	1
tc|Rep: Chromosome undetermined scaffold_139, whole genome shotgun sequenc	1415.38	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	590.58	1
gb|TT-18_L23 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	49.97	1
tc|Rep: Chromosome chr3 scaffold_199, whole genome shotgun sequence - Vitis vi	145.14	1
gb|KP1B.101E12F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101E12, m	568.51	1
tc|Rep: LEA1-like protein - Capsicum annuum (Bell pepper), partial (97%) [TC51846	35.57	1
Unknown	267.54	1
gb|KT7B.103H05F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.103H05, mR	41.07	1
gb|BP532909 MAT005 Nicotiana tabacum cDNA clone BY28342, mRNA sequence [	95.32	1
Unknown	13769	1
gb|BP132789 MAT001 Nicotiana tabacum cDNA clone BY4987, mRNA sequence [B	67.75	1
gb|KN6B.106I24F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.106I24, m	92.38	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (66%) [TC6	94.9	1
Unknown	236.05	1
gb|AGN_PNL216af1_h10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	784.9	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	549.12	1
Unknown	107.47	1
gb|BL12.001M03F.060117T7 BL12 Nicotiana tabacum cDNA clone BL12.001M03, m	1179.33	1
gb|KG9B.002B01F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002B01, m	645.11	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	38.77	1
gb|KF8B.100L06F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100L06, mRN	86.26	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC4-41-230, cultivar Bright Yellow 2	174.49	1
gb|KP1B.110A22F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110A22, m	137.97	1
gb|CHO_SL005xa16f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	244.03	1
Unknown	319.51	1
Unknown	27.82	1
gb|KT7C.110F08F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110F08, mRN	971.45	1
Unknown	90.01	1
gb|KL5B.116A10F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.116A10, m	61.52	1
Unknown	1617.63	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	19191.05	1
gb|KG9B.002H24F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002H24, m	20.65	1

Unknown	19.23	1
tc|Rep: Thioredoxin peroxidase - Nicotiana tabacum (Common tobacco), partial (85	25.69	1
gb|TT-39_L02 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	38.92	1
gb|Nicotiana tabacum mRNA for carbamoyl phosphate synthase small subunit [AJ3	193.42	1
Unknown	85.36	1
gb|BP530687 MAT005 Nicotiana tabacum cDNA clone BY22326, mRNA sequence [	17.62	1
gb|TT-36_L19 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	48.68	1
Unknown	91.09	1
Unknown	179.23	1
gb|AGN_PNL221df1_g3.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	244.45	1
gb|AGN_RPC008xm20f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	166.83	1
Unknown	22.02	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	109.26	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	659.15	1
tc|Rep: Chromosome chr13 scaffold_210, whole genome shotgun sequence - Vitis	47.4	1
gb|CHO_SL023xa21f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	56.47	1
gb|TT-04_L05 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	538.98	1
Unknown	26.89	1
tc|Rep: Histone H2B-like protein - Solanum tuberosum (Potato), complete [TC5538	39.47	1
gb|TL13.101C08F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.101C08, mR	2829.35	1
gb|AGN_RNC116xc13f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	17622.1	1
Unknown	32593.85	1
gb|KF8C.101A13F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101A13, mR	4664.06	1
Unknown	27.68	1
gb|KL5B.111K19F.060117T7 KL5B Nicotiana tabacum cDNA clone KL5B.111K19, mR	14798.7	1
tc|Rep: Chromosome undetermined scaffold_52, whole genome shotgun sequence	39.06	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	69.55	1
gb|AGN_RPC014xi17f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	68.1	1
tc|Rep: Delta-1-pyrroline-5-carboxylate synthetase (P5CS) [Includes: Glutamate 5-k	2726.93	1
Unknown	56.82	1
tc|Rep: Chromosome undetermined scaffold_89, whole genome shotgun sequence	280.25	1
gb|CHO_SL005xa23f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	580.28	1
Unknown	27.24	1
gb|KL4B.110O11F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110O11, m	25.69	1

gb|KL4B.101H07F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101H07, mF	746.29	1
Unknown	135.38	1
Unknown	429.64	1
Unknown	112.85	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	26.52	1
tc|Rep: Elongation factor 1-alpha - Nicotiana paniculata, partial (34%) [TC52938]	1288.59	1
tc|Rep: Selenocysteine methyltransferase - Camellia sinensis (Tea), partial (43%) [T	80.44	1
tc|Rep: Chromosome chr13 scaffold_149, whole genome shotgun sequence - Vitis v	258.97	1
tc|Rep: Aspartate aminotransferase - Nicotiana tabacum (Common tobacco), comp	995.04	1
gb|TT-20_O19 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	535.3	1
gb|AGN_PNL204dr1_a9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	26.79	1
gb|KF8B.202M15F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202M15, mF	37649.5	1
gb|KP1B.109I09F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109I09, mRI	266.48	1
tc|Rep: Light harvesting chlorophyll a/b-binding protein precursor - Nicotiana sylve	128.53	1
gb|AGN_PNL221df1_b7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	28614.15	1
gb|KF8C.105B21F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105B21, mRN	245.62	1
tc|Rep: Chromosome undetermined scaffold_221, whole genome shotgun sequenc	101.23	1
gb|TT-12_H17 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	32.76	1
gb|KG9B.107A02F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107A02, m	983.76	1
gb|KN6B.110L20F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.110L20, m	47.12	1
gb|KL5B.116C11F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.116C11, mR	32.87	1
Unknown	81.54	1
tc|Rep: LeOPT1 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), parti	396.04	1
gb|KF8C.102A19F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102A19, mRN	7544.71	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	527.29	1
Unknown	1138.96	1
Unknown	556.01	1
gb|TT-07_K11 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	86.33	1
gb|AGN_RNC121xg07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	44.78	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	20.47	1
Unknown	81.87	1
Unknown	32.79	1
Unknown	25.59	1
gb|KP1B.104P16F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104P16, mI	546.02	1

gb|TT-41_B11 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	116.54	1
gb|Nicotiana tabacum chloroplast carbonic anhydrase gene, complete cds [M9413	8349.84	1
gb|KL4B.113A05F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.113A05, m	229.65	1
Unknown	100.47	1
Unknown	426.54	1
Unknown	262.43	1
tc|Rep: Acetyl-CoA synthetase - Solanum tuberosum (Potato), partial (58%) [TC518	2642.49	1
gb|TT-17_K19 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	82.17	1
tc|Rep: Methionine synthase - Nicotiana suaveolens, partial (20%) [TC64608]	22767.9	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	1487.92	1
gb|AGN_RNC005xg15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	43.4	1
gb|KF8C.103M14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103M14, m	113.33	1
gb|Nicotiana tabacum putative ethylene receptor (NTHK2) mRNA, complete cds [A	182.5	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	20.09	1
gb|KR2B.110I09F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110I09, mR	84.57	1
tc|Rep: Acetolactate synthase 2, chloroplast precursor - Nicotiana tabacum (Comm	1034.81	1
gb|KR2B.109J07F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.109J07, mR	144.17	1
Unknown	96.24	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	21.31	1
Unknown	27.96	1
Unknown	21.14	1
tc|Rep: MYB transcription factor MYB143 - Glycine max (Soybean), partial (53%) [T	9458.4	1
Unknown	2817.85	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	233.12	1
Unknown	4956.01	1
tc|Rep: Chromosome undetermined scaffold_133, whole genome shotgun sequenc	43.54	1
tc|Rep: EIN3-binding F-box protein 2 - Solanum lycopersicum (Tomato) (Lycopersic	1601.56	1
tc|Rep: LYTB-like protein-like - Solanum tuberosum (Potato), partial (17%) [TC7404	20.35	1
tc|Rep: Thaliana 60S ribosomal protein L7 - Solanum tuberosum (Potato), complete	25.23	1
gb|CHO_SL025xa09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	360.68	1
tc|Rep: Common plant regulatory factor 7 - Petroselinum crispum (Parsley) (Petros	1570.86	1
Unknown	422.89	1
gb|TL13.110G08F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.110G08, mR	217.39	1
tc|Rep: Chromosome chr8 scaffold_150, whole genome shotgun sequence - Vitis vi	61.5	1

gb|KT7B.100G14F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100G14, mR	111.57	1
gb|AGN_RNC127xf10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	32.07	1
Unknown	141.93	1
tc|Rep: Pleckstrin homology domain-containing protein 1 - Arabidopsis thaliana (M	53.78	1
gb|KG9B.005A19F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005A19, m	121.22	1
gb|TT-29_N16 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	35.7	1
Unknown	521.6	1
Unknown	151.27	1
gb|KR2B.113N20F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.113N20, m	51.81	1
gb|N.tabacum mRNA for chloroplast glucose-6-phosphate dehydrogenase [X99405	518.2	1
gb|Nicotiana tabacum peroxisome biogenesis factor 10 (PEX10) mRNA, complete c	35.86	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (65%) [TC4	23.44	1
Unknown	74.24	1
Unknown	24.99	1
gb|CHO_SL013xk10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	71.46	1
tc|Rep: Delta-tonoplast intrinsic protein - Gossypium hirsutum (Upland cotton) (Go	100.64	1
Unknown	80.72	1
gb|Nicotiana tabacum 14-3-3 isoform f T14-3f mRNA, complete cds [U91727]	2678.16	1
gb|AM808208 seedling library, SL Nicotiana tabacum cDNA clone nt002145096, m	21.37	1
tc|Rep: Nudix hydrolase 17, mitochondrial precursor - Arabidopsis thaliana (Mouse	519.19	1
gb|TT-28_P10 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	72.76	1
tc|Rep: Calcineurin B-like interacting protein kinase - Solanum lycopersicum (Toma	109.64	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	24.36	1
tc|Rep: Pectin methylesterase - Nicotiana tabacum (Common tobacco), partial (34	42.3	1
gb|KL4B.103H13F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103H13, m	2368.57	1
tc|Rep: CBS1 - Hyacinthus orientalis (Common hyacinth), partial (93%) [TC50285]	38.92	1
Unknown	41.25	1
gb|AGN_RNC023xa09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	24.39	1
tc|Rep: Chromosome chr18 scaffold_59, whole genome shotgun sequence - Vitis vi	54.45	1
tc|Rep: Fiber protein Fb2 - Gossypium barbadense (Sea-island cotton) (Egyptian cot	542.14	1
tc|Rep: Ribosomal protein L17 - Branchiostoma belcheri tsingtauense, partial (50%)	21.4	1
Unknown	112.46	1
tc|Rep: Chromosome chr2 scaffold_140, whole genome shotgun sequence - Vitis vi	6111.62	1
tc|Rep: Probable histone-arginine methyltransferase CARM1 - Oryza sativa subsp. i	38.99	1

Unknown	83.83	1
tc|Rep: Glycolate oxidase - Cucurbita cv. Kurokawa Amakuri, partial (44%) [TC4227	51.84	1
gb|AGN_RPC006xo06f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	1585.01	1
gb|TT-48_C07 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	54	1
Unknown	80.82	1
gb|ntsm5 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [EB	121.36	1
tc|Rep: 40S ribosomal protein S19-like - Solanum tuberosum (Potato), complete [T	487.59	1
Unknown	65.04	1
tc|Rep: Proteasome subunit alpha type - Nicotiana tabacum (Common tobacco), co	21.76	1
Unknown	37.95	1
tc|Rep: Histone H4 [Contains: Osteogenic growth peptide (OGP)]. - Rattus norvegic	394.61	1
tc|Rep: Chromosome chr13 scaffold_45, whole genome shotgun sequence - Vitis vi	796.05	1
Unknown	400.44	1
Unknown	63.77	1
gb|KN6B.109M07F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.109M07,	80.11	1
Unknown	33.99	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	24.74	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	92.2	1
tc|Rep: Adenylate kinase family-like protein - Solanum tuberosum (Potato), partial	1850.76	1
gb|TT-08_M12 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	105.86	1
tc|Rep: AG-motif binding protein-2 - Nicotiana tabacum (Common tobacco), compl	980.33	1
gb|TT-23_L07 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	100.49	1
tc|Rep: 40S ribosomal protein S16 - Euphorbia esula (Leafy spurge), partial (97%) [T	1115.35	1
Unknown	245.07	1
tc|GB|DQ536198.1|ABK81124.1 spermidine synthase;tSPDS [NP8635107]	4740.66	1
Unknown	18.05	1
tc|Rep: Homolog of Homo sapiens "Histone 1, H2ai - Takifugu rubripes, partial (30%	173.8	1
Unknown	261.64	1
gb|KG9B.102L17F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102L17, m	293.28	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	22.68	1
Unknown	44.02	1
gb|AGN_RNC017xi07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	23.7	1
tc|Rep: ATP-dependent Clp protease ATP-binding subunit clpA homolog CD4B, chlo	609.31	1
Unknown	57.02	1

Unknown	1277.26	1
tc|Rep: Histone H1 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), p	24.14	1
gb|CHO_SL015xc14f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	784.67	1
tc|Rep: Genomic DNA, chromosome 5, BAC clone:F6N7 - Arabidopsis thaliana (Mou	570.47	1
gb|TT-22_O04 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	922.08	1
gb|KR2B.001N02F.050815T7 KR2B Nicotiana tabacum cDNA clone KR2B.001N02, m	793.96	1
Unknown	27.71	1
Unknown	252.53	1
tc|Rep: DNA-directed RNA polymerase - Glycine max (Soybean), partial (25%) [TC7	25.27	1
tc|Rep: Chromosome chr2 scaffold_187, whole genome shotgun sequence - Vitis vi	593.25	1
gb|KF8C.103A11F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103A11, mR	149.12	1
gb|KT7C.106J06F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106J06, mRN	507.46	1
gb|TT-23_L09 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	67.82	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	29.03	1
tc|Rep: 26S protease regulatory subunit 6B homolog - Solanum tuberosum (Potato	29.8	1
Unknown	249.37	1
gb|KP1B.110N09F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110N09, m	217.06	1
Unknown	8929.38	1
gb|TT-12_E19 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	79.45	1
Unknown	195.2	1
gb|AM808541 seedling library, SL Nicotiana tabacum cDNA clone nt002203031, m	60.08	1
tc|Rep: Os09g0554000 protein - Oryza sativa subsp. japonica (Rice), partial (37%) [T	52.2	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	119.25	1
Unknown	707.23	1
Unknown	73.86	1
Unknown	25.37	1
Unknown	52.49	1
gb|KL4B.104O13F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104O13, m	50.56	1
gb|KR3B.110O13F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110O13, m	185.56	1
gb|KT7C.110J10F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110J10, mRN	129.11	1
Unknown	38.48	1
gb|TT-34_B02 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	30.26	1
Unknown	72.36	1
Unknown	506.09	1

gb|TT-24_N22 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	387.15	1
tc|Rep: Protein phosphatase 2C - Nicotiana benthamiana, partial (69%) [TC54430]	107.92	1
gb|FS413263 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	680.95	1
tc|Rep: 60S ribosomal protein L34 - Nicotiana tabacum (Common tobacco), comple	67.24	1
gb|CHO_SL013xh02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	23.72	1
gb|KT7C.102N01F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102N01, mR	85.54	1
gb|Nicotiana tabacum putative red chlorophyll catabolite reductase mRNA, comple	21.44	1
gb|FS438234 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	78.26	1
gb|KF8C.104F02F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104F02, mRN	2950.84	1
tc|Rep: Cytochrome P450 52 - Aspergillus niger, partial (3%) [TC75821]	376.36	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	159.66	1
gb|Nicotiana tabacum RhoGAP1 mRNA, complete cds [DQ813657]	941.11	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	405.82	1
gb|KL4B.109D12F.051108T7 KL4B Nicotiana tabacum cDNA clone KL4B.109D12, mF	29.25	1
Unknown	28.06	1
gb|CHO_SL010xl06f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	561.35	1
gb|AGN_PNL220bf1_b1.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	152.72	1
Unknown	1571.16	1
tc|Rep: Dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate deh	5490.39	1
gb|KG9B.005I12F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005I12, mF	292.47	1
gb|KP1B.103E06F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103E06, mI	32.41	1
gb|CHO_SL020xm13f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	103.18	1
gb|KN6B.104B07F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104B07, m	1170.23	1
gb|TT-10_M22 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	41.93	1
tc|Rep: Allyl alcohol dehydrogenase - Nicotiana tabacum (Common tobacco), partia	150.21	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	476.18	1
gb|KG9B.105P22F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105P22, m	585.48	1
Unknown	1036.64	1
tc|Rep: Ribosomal protein L24-like protein - Solanum tuberosum (Potato), partial (2	1229.11	1
gb|KT7C.110O15F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110O15, mR	21.33	1
gb|TT-21_K15 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	24.77	1
Unknown	2744.94	1
gb|AGN_RPC007xg20f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	43.07	1
gb|FS403398 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	101.06	1

Unknown	32.8	1
tc|Rep: 26S proteasome subunit 4-like - Solanum tuberosum (Potato), complete [TC	263.37	1
gb|TT-50_I09 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sequ	150.75	1
gb|KF8C.103M14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103M14, mR	150.48	1
gb|CHO_SL027xe15f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	25.69	1
gb|KP1B.107J17F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107J17, mR	136.96	1
gb|TT-04_B13 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	25.88	1
gb|TT-08_C20 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	20.04	1
Unknown	640.92	1
tc|AAC32911.1 - Arabidopsis thaliana (Mouse-ear cress), partial (24%) [TC63379]	69.41	1
Unknown	980.82	1
Unknown	24.13	1
gb|KP1B.107F21F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107F21, mR	23.83	1
tc|Rep: Nucleosome assembly protein 1-like protein 1 - Nicotiana tabacum (Commo	51.53	1
gb|CHO_SL020xa06f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	342.9	1
gb|KF8C.101H24F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101H24, mR	181.45	1
gb|KP1B.108B21F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108B21, m	60.84	1
Unknown	26.61	1
gb|KT7B.107G19F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107G19, mR	575.62	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	18127.2	1
tc|Rep: Endoglucanase-like protein - Saccharophagus degradans (strain 2-40 / ATCC	56.14	1
gb|KL4B.100L09F.050922T7 KL4B Nicotiana tabacum cDNA clone KL4B.100L09, mR	107.8	1
tc|Rep: Vacuolar ATP synthase catalytic subunit A - Daucus carota (Carrot), partial (	1153.91	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	3852.26	1
Unknown	440.38	1
tc|Rep: Inositol-1,4,5-triphosphate-5-phosphatase - Solanum lycopersicum (Tomato	21.8	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	72.85	1
Unknown	7621.34	1
gb|KL4B.104N10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104N10, mR	561.77	1
tc|Rep: SKP1-like protein - Nicotiana clevelandii (Wild tobacco), complete [TC50857	1206.63	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	453.9	1
Unknown	78.25	1
tc|Rep: Cellulose synthase - Solanum tuberosum (Potato), partial (40%) [TC50352]	91.67	1
tc|Rep: Ubiquitin-like protein SMT3 - Oryza sativa subsp. japonica (Rice), partial (85	4055.48	1

Unknown	520.68	1
gb|Nicotiana tabacum EIL5 mRNA, complete cds [AY248907]	55.05	1
Unknown	134.96	1
gb|KN6B.104G15F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104G15, r	1128.02	1
tc|Rep: Targeting protein for Xklp2 containing protein, expressed - Oryza sativa sub	1102.37	1
gb|Nicotiana tabacum EIL2 mRNA, complete cds [AY248904]	65.76	1
gb|KF8C.101C13F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101C13, mRN	22.13	1
gb|KT7C.109A05F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109A05, mRI	188.27	1
gb|AGN_PNL226df1_e5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	255.46	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	25.65	1
gb|KL4B.106A05F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106A05, mF	41.56	1
gb|FS408551 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	9621.67	1
tc|Rep: Fructose-bisphosphate aldolase - Vitis vinifera (Grape), complete [TC54270	85.1	1
gb|2A-2 tobacco suppression subtractive hybridization cDNA library Nicotiana taba	171.47	1
Unknown	2093.86	1
gb|AGN_ELP008xk23f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	21.18	1
gb|TT-41_B09 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	79.8	1
gb|KR3B.110I21F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110I21, mRI	28.69	1
Unknown	14937.05	1
Unknown	426.72	1
Unknown	376.32	1
tc|Rep: Aminoalcoholphosphotransferase - Brassica campestris (Field mustard), par	1606.48	1
Unknown	2675.4	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	1468.38	1
gb|KG9B.002N07F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002N07, r	4915.45	1
Unknown	2445.5	1
Unknown	26.13	1
Unknown	28.51	1
gb|KP1B.101K20F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101K20, mI	370.26	1
gb|AM837768 COL, cold overnight library Nicotiana tabacum cDNA clone nt006109	24.61	1
gb|KN6B.104G15F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104G15, r	1247.01	1
Unknown	75.57	1
Unknown	24.82	1
tc|Rep: Bifunctional dihydrofolate reductase-thymidylate synthase (DHFR-TS) [Inclu	68.46	1

tc|Rep: Signal recognition particle 54 kDa protein 2 - Solanum lycopersicum (Tomat	329.8	1
tc|Rep: Glycosyl hydrolase family-like protein - Salvia miltiorrhiza (Chinese sage), pa	23.45	1
tc|Rep: Chromosome chr1 scaffold_22, whole genome shotgun sequence - Vitis vin	82.88	1
Unknown	36.06	1
gb|TT-25_J09 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	44.31	1
tc|Rep: Fumarase - Solanum tuberosum (Potato), partial (69%) [TC58517]	1031.11	1
gb|TT-09_A07 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	152.73	1
Unknown	40.64	1
tc|Rep: Serpin-like protein - Citrus paradisi (Grapefruit), partial (86%) [TC43466]	21.54	1
gb|AGN_ELP006xa10f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	77.71	1
tc|Rep: BTF3 - Nicotiana benthamiana, complete [TC68489]	34	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	121.54	1
tc|Rep: Possible high light inducible protein - Prochlorococcus marinus (strain MIT	31.13	1
Unknown	658.26	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	23.02	1
gb|KF8C.101M19F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101M19, m	415.21	1
gb|KF8C.101C08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101C08, mRN	895.07	1
gb|Nicotiana tabacum partial mRNA for glutamyl tRNA Reductase (hemA gene) [A	1526.08	1
tc|Rep: Pyruvate kinase - Vitis vinifera (Grape), partial (91%) [TC46839]	25.98	1
gb|KF8B.202C03F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202C03, mRN	4029.88	1
tc|Rep: 60S ribosomal protein l2 - Oryza sativa subsp. indica (Rice), partial (36%) [T	229.55	1
tc|Rep: Chromosome undetermined scaffold_734, whole genome shotgun sequenc	498.55	1
tc|Rep: 2OG-Fe(II) oxygenase - Medicago truncatula (Barrel medic), partial (8%) [TC	60.41	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	789.54	1
gb|KR3B.103H22F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.103H22, m	331.3	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	101.03	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (43%) [TC6	520.48	1
gb|KL4B.105C19F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105C19, mR	85.97	1
gb|AGN_RNC021xc12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	136.37	1
Unknown	795.26	1
gb|KR3B.111A24F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111A24, m	185.44	1
Unknown	2270.29	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	1258.73	1
gb|KG9B.001F17F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001F17, m	31.97	1

tc|Rep: Thioredoxin H-type 1 - Nicotiana tabacum (Common tobacco), partial (71%	42.25	1
gb|AGN_RPC013xb19f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	57.66	1
Unknown	87.99	1
gb|TT-18_F15 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	81.78	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	95.98	1
Unknown	666.95	1
Unknown	438.13	1
gb|KR2B.104L20F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.104L20, m	60.13	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	197.82	1
gb|KT7C.108N21F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108N21, mR	92.33	1
tc|Rep: Bromodomain-containing RNA-binding protein 1 - Nicotiana benthamiana,	2775.92	1
Unknown	53.53	1
tc|Rep: Probable phospholipid hydroperoxide glutathione peroxidase - Nicotiana ta	4668.53	1
tc|Rep: Chromosome chr19 scaffold_35, whole genome shotgun sequence - Vitis vi	515.42	1
tc|Rep: Cytochrome c oxidase family protein-like - Solanum tuberosum (Potato), co	250.55	1
gb|TT-07_O15 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	1049.06	1
Unknown	108.49	1
tc|Rep: Ribulose bisphosphate carboxylase small chain, chloroplast precursor - Nic	261.64	1
gb|KN6B.101E05F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101E05, m	141.75	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	18.23	1
Unknown	202.5	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	261.51	1
Unknown	107.26	1
gb|KL4B.108J06F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108J06, mR	27.06	1
gb|BP131514 MAT001 Nicotiana tabacum cDNA clone BY3567, mRNA sequence [B	21.11	1
gb|KT7C.112M02F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112M02, m	1089.37	1
tc|Rep: Shaggy-like kinase - Ricinus communis (Castor bean), partial (40%) [TC5354	497.57	1
Unknown	205.55	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	22.81	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (43%) [TC6	40.16	1
gb|KN6B.105A01F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105A01, m	18.13	1
Unknown	1066.29	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	104.88	1
gb|KF8C.102E09F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102E09, mR	135.1	1

gb|KL4B.103M04F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103M04, m	756.39	1
gb|KF8B.202M15F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202M15, mR	43215.5	1
tc|Rep: Chromosome chr2 scaffold_140, whole genome shotgun sequence - Vitis vi	26.86	1
gb|KP1B.109K06F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109K06, ml	175.42	1
Unknown	62.05	1
Unknown	46.63	1
gb|TT-30_J08 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sequ	770.62	1
tc|Rep: Phosphate/phosphoenolpyruvate translocator - Nicotiana tabacum (Comm	72.47	1
gb|Nicotiana tabacum cysteine-rich protein mRNA, complete cds [AF213464]	10468.15	1
gb|Nicotiana tabacum NtPOX1 mRNA for peroxidase, complete cds [AB178953]	72.83	1
tc|Rep: 14-3-3-like protein A - Nicotiana tabacum (Common tobacco), partial (59%)	59.93	1
Unknown	86.29	1
gb|KF8C.106N01F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106N01, mRl	47361.9	1
tc|Rep: Chromosome chr10 scaffold_81, whole genome shotgun sequence - Vitis vi	79.08	1
Unknown	29.33	1
gb|ntsm32 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [E	17.85	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	20.98	1
gb|TT-06_G20 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	2502.83	1
gb|KL4B.101J19F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101J19, mRN	137.85	1
Unknown	199.16	1
Unknown	1502.9	1
gb|CHO_SL022xm01f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	3208.79	1
gb|KN6B.114I07F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.114I07, mR	46.71	1
gb|KF8C.101K10F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101K10, mRN	60	1
Unknown	18.83	1
tc|Rep: 40S ribosomal protein S16 - Euphorbia esula (Leafy spurge), complete [TC54	272.5	1
Unknown	73.28	1
gb|TT-09_B08 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	90.8	1
gb|KG9B.106J02F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106J02, mR	518.31	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	23574.6	1
Unknown	19.71	1
gb|KR2B.108F12F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.108F12, mR	64.16	1
tc|Rep: Chromosome chr9 scaffold_65, whole genome shotgun sequence - Vitis vin	21.58	1
gb|KP1B.037O02F.050623T7 KP1B Nicotiana tabacum cDNA clone KP1B.037O02, m	43.46	1

gb|TT-40_P15 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	238.01	1
gb|CHO_SL010xl21f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	31.43	1
Unknown	184.15	1
Unknown	1179.56	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	19.44	1
Unknown	28.92	1
gb|AGN_RNC013xl19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	23.05	1
Unknown	184.54	1
Unknown	305.17	1
gb|KT7B.100E11F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100E11, mR	817.36	1
gb|Nicotiana tabacum mRNA for bromodomain-containing RNA-binding protein 1 (	65.96	1
Unknown	41.89	1
Unknown	33.58	1
gb|Nicotiana tabacum mRNA for BY-2 kinesin-like protein 10, complete cds [AB003	155.73	1
tc|Rep: Chromosome chr6 scaffold_28, whole genome shotgun sequence - Vitis vin	33.28	1
Unknown	77.44	1
gb|KP1B.037C22F.050623T7 KP1B Nicotiana tabacum cDNA clone KP1B.037C22, m	700.19	1
tc|Rep: DnaJ-like protein - Solanum lycopersicum (Tomato) (Lycopersicon esculent	8640.44	1
Unknown	392.21	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	4004.34	1
tc|Rep: Chromosome undetermined scaffold_143, whole genome shotgun sequenc	23.57	1
gb|AGN_PNL233br1_b11.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRN	287.29	1
Unknown	1430.65	1
gb|Nicotiana tabacum SR1 Nt-rab11a mRNA, complete cds [L29271]	525.52	1
tc|Rep: Expressed protein - Arabidopsis thaliana (Mouse-ear cress), partial (50%) [T	71.35	1
gb|KN6B.101A12F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101A12, m	55.08	1
Unknown	27.87	1
gb|TT-37_C13 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	77.41	1
gb|AGN_RPC024xn15f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	174.66	1
Unknown	749.44	1
gb|KG9B.001J01F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001J01, m	242.66	1
gb|AGN_RNC030xg05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	101.25	1
tc|Rep: 60S ribosomal protein L10 - Solanum lycopersicum (Tomato) (Lycopersicon	937.34	1
Unknown	35.67	1

gb|FS396507 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	280.64	1
tc|Rep: 6-phosphogluconate dehydrogenase, decarboxylating - Spinacia oleracea (S	23.69	1
gb|Nicotiana tabacum adenyl cyclase (Axi 141) mRNA, complete cds [AF026389]	108.94	1
gb|AGN_RNC024xj10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	215.35	1
Unknown	105.24	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	298.1	1
Unknown	30.17	1
gb|TT-04_J11 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	3240.78	1
gb|KL4B.101K10F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101K10, mR	103.13	1
tc|Rep: Pyruvate kinase - Vitis vinifera (Grape), partial (58%) [TC41042]	4518.97	1
gb|KL5B.103N15F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.103N15, m	527.1	1
tc|Rep: Os01g0371800 protein - Oryza sativa subsp. japonica (Rice), partial (17%) [T	25.16	1
gb|KF8C.105G12F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105G12, mR	16.83	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	578.17	1
Unknown	28.89	1
Unknown	20.65	1
gb|KT7C.108B19F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108B19, mR	973.11	1
gb|KG9B.102H18F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102H18, n	2884.87	1
Unknown	117.74	1
gb|CHO_SL023xb16f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	46.33	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	34.73	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	39.24	1
gb|KL4B.102O16F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102O16, m	46.87	1
Unknown	160.36	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	231.63	1
Unknown	22.29	1
tc|Rep: Luminal-binding protein 3 - Nicotiana tabacum (Common tobacco), partial (	10537.35	1
gb|TT-04_N05 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	47.62	1
gb|KP1B.101H12F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101H12, m	102.69	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	72.02	1
gb|KF8C.104J24F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104J24, mRN	25.23	1
Unknown	59	1
gb|TT-11_C20 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	133.67	1
gb|KF8B.201P16F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201P16, mR	130.07	1

tc|Rep: Fiber protein Fb15 - Gossypium barbadense (Sea-island cotton) (Egyptian cc	442.7	1
Unknown	170.06	1
Unknown	74.32	1
gb|AGN_RNC007xa15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	27.95	1
gb|Nicotiana tabacum Nict2 mRNA for pollen-specific calcium-binding protein, com	3934.52	1
Unknown	51.34	1
tc|Rep: Arogenate dehydrogenase 2, chloroplast precursor - Arabidopsis thaliana (M	424.22	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	1505.91	1
gb|AM787843 seedling library, SL Nicotiana tabacum cDNA clone nt002165074, mR	3080.01	1
gb|CHO_SL002xh18f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	53263.6	1
tc|Rep: Serine hydroxymethyltransferase, mitochondrial precursor - Solanum tuber	3455.25	1
Unknown	29.27	1
Unknown	21.41	1
Unknown	18722.65	1
gb|KF8C.109C04F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109C04, mRN	49289	1
gb|TL13.109N17F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.109N17, mR	2867.71	1
gb|CHO_SL008xb09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	237.47	1
gb|TT-16_E09 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	510.89	1
tc|Rep: Chromosome chr12 scaffold_93, whole genome shotgun sequence - Vitis vi	439.02	1
gb|Nicotiana tabacum putative UDP-glucose dehydrogenase 1 mRNA, complete cds	2830.55	1
gb|KR3B.112N15F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112N15, m	19.35	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	144.85	1
gb|AGN_RNC105xc17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	119.77	1
gb|TL13.110N07F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.110N07, mR	270.5	1
tc|Rep: Os11g0425600 protein - Oryza sativa subsp. japonica (Rice), partial (69%) [T	1097.24	1
gb|KL4B.102O04F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102O04, mI	53.62	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (63%) [TC5	380.23	1
gb|AGN_RNC012xg17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	20.55	1
gb|KP1B.107J04F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107J04, mR	25.39	1
Unknown	81.82	1
gb|KL4B.108L14F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108L14, mRI	185.35	1
tc|Rep: Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vi	2081.1	1
tc|Rep: Chromosome undetermined scaffold_247, whole genome shotgun sequenc	385.88	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	25.39	1

tc|Rep: PFE18 protein - Ananas comosus (Pineapple), partial (46%) [TC53747]	263.74	1
gb|KF8C.103H15F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103H15, mR	55.79	1
gb|Nicotiana tabacum ntp805 (pntp805) mRNA, complete cds [AY366400]	56713.9	1
gb|TOBESTR027C02 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	53.7	1
tc|Rep: Proteasome subunit alpha type - Solanum tuberosum (Potato), partial (98%	124.1	1
gb|KP1B.109D12F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109D12, m	103.55	1
tc|Rep: N-carbamoylputrescine amidase - Solanum tuberosum (Potato), complete [	660.67	1
Unknown	186.52	1
tc|Rep: Acetyl-CoA carboxylase - Medicago sativa (Alfalfa), partial (5%) [TC49232]	62.86	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	534.32	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	24.9	1
Unknown	184.94	1
gb|KF8B.201I21F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201I21, mRN	66	1
Unknown	20.78	1
gb|TT-05_L05 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	118.24	1
gb|KL4B.105B08F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105B08, mR	663.95	1
Unknown	455.54	1
gb|KF8C.102K09F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102K09, mR	514.23	1
tc|Rep: Chromosome undetermined scaffold_139, whole genome shotgun sequenc	135.04	1
Unknown	18.15	1
tc|Rep: ATP synthase subunit O, mitochondrial precursor - Ipomoea batatas (Sweet	518.05	1
tc|Rep: Type III chlorophyll a/b-binding protein - Nicotiana tabacum (Common toba	20.43	1
gb|AGN_RNC115xl03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	24.67	1
gb|Nicotiana tabacum acetyl-CoA carboxylase (biotin carboxylase subunit) mRNA, c	82.79	1
gb|KL4B.110B13F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110B13, mR	10918.4	1
Unknown	57.73	1
gb|KL4B.105K12F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105K12, mR	51.49	1
tc|Rep: Chromosome chr2 scaffold_176, whole genome shotgun sequence - Vitis vi	57.77	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	761.16	1
Unknown	18.9	1
gb|Nicotiana tabacum S-adenosyl-methionine cycloartenol-C24-methyltransferase	781.4	1
Unknown	37.38	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	752.27	1
gb|KL4B.106N22F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106N22, m	538.64	1

Unknown	54.29	1
tc|Rep: UDP-apiose/xylose synthase - Solanum tuberosum (Potato), partial (42%) [T	2741.79	1
gb|Nicotiana tabacum mRNA for proteasome A-type subunit [Y16644]	97.48	1
gb|Nicotiana tabacum putative chloroplast thiazole biosynthetic protein (ThiI) mRN	36.96	1
gb|TT-03_B09 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	140.41	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	9655.86	1
Unknown	50756.2	1
gb|TT-14_G23 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	2686.33	1
gb|KR2B.115P20F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115P20, m	978.18	1
gb|KN6B.110B04F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.110B04, m	45.94	1
Unknown	246.93	1
gb|KF8C.103O23F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103O23, mR	70.47	1
gb|AGN_RNC025xl24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	481.08	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	60.37	1
Unknown	26.57	1
gb|Nicotiana tabacum putative high mobility group protein 2-like mRNA, partial se	9218.73	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (93%) [TC6	781.2	1
gb|TT-02_I17 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	1734.66	1
tc|Rep: Probable protein VP2 - Torque teno virus (isolate Human/Japan/TRM1/199	49.17	1
gb|KF8B.100B16F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100B16, mR	23.2	1
tc|Rep: Chromosome chr18 scaffold_121, whole genome shotgun sequence - Vitis	94.87	1
gb|TT-02_C03 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	62.01	1
Unknown	79.47	1
Unknown	571.6	1
Unknown	49.18	1
gb|Nicotiana tabacum mRNA for thylakoid-bound ascorbate peroxidase, complete	187.83	1
gb|AGN_ELP004xg14f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	100.18	1
Unknown	208.69	1
gb|TT-02_K24 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	41.39	1
tc|Rep: Expressed protein - Oryza sativa subsp. japonica (Rice), partial (21%) [TC70	21.26	1
gb|Nicotiana tabacum glycine-rich protein (ntGRP15) mRNA, partial cds [U74325]	47.31	1
Unknown	1678.54	1
Unknown	1329.37	1
Unknown	284.04	1

Unknown	25.16	1
gb|TT-18_J08 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	67.87	1
gb|AGN_RNC008xp03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1226.96	1
Unknown	393.62	1
Unknown	25.31	1
tc|Rep: Ataxin-2 related protein - Ipomoea nil (Japanese morning glory) (Pharbitis n	281.5	1
gb|KR3B.106C01F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106C01, m	493.01	1
gb|KL5B.001L18F.050901T7 KL5B Nicotiana tabacum cDNA clone KL5B.001L18, mRI	31.56	1
gb|KL5B.106L07F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.106L07, mRI	188.41	1
gb|FS413762 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	153.1	1
gb|TL13.102J20F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.102J20, mRN	109.08	1
gb|15B09 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', r	134.72	1
Unknown	1473.43	1
Unknown	1155.52	1
tc|Rep: Aromatic amino acid decarboxylase 2 - Solanum lycopersicum (Tomato) (Ly	743.36	1
Unknown	18224.5	1
gb|TT-04_N01 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	78.63	1
tc|Rep: DNA-binding protein - Solanum lycopersicum (Tomato) (Lycopersicon escul	102.85	1
Unknown	40.56	1
Unknown	42.42	1
tc|Rep: Chromosome chr12 scaffold_103, whole genome shotgun sequence - Vitis v	48.09	1
gb|ntsm25 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [E	21.56	1
tc|Rep: 4-coumarate:CoA ligase-like - Nicotiana sylvestris (Wood tobacco), partial (	23.22	1
Unknown	1048.65	1
gb|KT7C.105K09F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105K09, mRN	68.25	1
gb|KL4B.102D11F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102D11, mF	16267.9	1
gb|KN6B.102A21F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102A21, n	70.24	1
gb|Nicotiana tabacum GMPase mRNA for GDP-D-mannose pyrophosphorylase, con	183.19	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	524.28	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	16977.9	1
Unknown	196.29	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	222.63	1
tc|Rep: Ran binding protein-1 - Solanum lycopersicum (Tomato) (Lycopersicon escu	18.47	1
gb|KR2B.001F12F.050815T7 KR2B Nicotiana tabacum cDNA clone KR2B.001F12, mF	250.68	1

Unknown	38.09	1
Unknown	32.45	1
gb|CHO_SL024xd04f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	89.14	1
gb|Tobacco (N.tabacum) endochitinase mRNA, partial cds [M15173]	44.87	1
Unknown	88.26	1
gb|KL4B.102A16F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102A16, mF	13647.35	1
tc|Rep: Probable histone H2AXa - Arabidopsis thaliana (Mouse-ear cress), complete	517.85	1
gb|AGN_RPC023xj11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	30.8	1
gb|TT-15_K03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	20.52	1
gb|Nicotiana tabacum clone 7 poly(A)-binding protein (PABP) mRNA, partial cds [AF	9387.75	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	134.45	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis v	21.22	1
gb|KT7C.101N20F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.101N20, mR	2368.74	1
Unknown	31.72	1
Unknown	40.38	1
gb|KN6B.114I07F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.114I07, mF	31.21	1
Unknown	53.94	1
gb|AM798360 COL, cold overnight library Nicotiana tabacum cDNA clone nt006071	52.59	1
gb|BP131165 MAT001 Nicotiana tabacum cDNA clone BY3193, mRNA sequence [BF	177.26	1
Unknown	27.33	1
Unknown	27.61	1
gb|KT7B.107M01F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107M01, ml	21.49	1
tc|Rep: Chromosome undetermined scaffold_91, whole genome shotgun sequence	129.55	1
gb|N.tabacum mRNA for p45Ntf4 [X83880]	724.94	1
Unknown	31.88	1
Unknown	32.6	1
gb|KL4B.105K07F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105K07, mR	533.59	1
tc|Rep: DnaJ homolog - Salix gilgiana (Willow), partial (41%) [TC58289]	495.66	1
Unknown	27.6	1
Unknown	125.9	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	80.45	1
Unknown	73.12	1
tc|Rep: Histone H2B - Gossypium hirsutum (Upland cotton) (Gossypium mexicanum	2683.96	1
gb|CHO_SL010xl06f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	301.55	1

tc|Rep: Ras-related GTP-binding protein - Nicotiana tabacum (Common tobacco), c	2997.4	1
gb|KG9B.002L13F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002L13, m	27.3	1
gb|TT-05_E03 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	39.48	1
Unknown	7785.69	1
tc|Rep: VAP27 - Nicotiana plumbaginifolia (Leadwort-leaved tobacco), partial (46%	222.88	1
gb|TT-08_A20 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	85.32	1
Unknown	242.49	1
gb|KT7C.105M17F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105M17, m	245.25	1
tc|Rep: Chromosome chr16 scaffold_94, whole genome shotgun sequence - Vitis vi	54.11	1
gb|KF8C.104I02F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104I02, mRN	9070.43	1
gb|KG9B.105C09F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105C09, m	256.02	1
Unknown	21.1	1
Unknown	769.76	1
Unknown	32.83	1
Unknown	57.4	1
Unknown	91.58	1
Unknown	2862.02	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	86.74	1
tc|Rep: Betaine aldehyde dehydrogenase - Panax ginseng (Korean ginseng), partial (	406.57	1
Unknown	65.74	1
tc|Rep: S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC) [C	18544.95	1
gb|AGN_RNC127xb09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	29.47	1
Unknown	694.69	1
tc|Rep: EBP1 - Solanum tuberosum (Potato), complete [TC47559]	22.91	1
Unknown	50.32	1
gb|KT7C.109M07F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109M07, m	500.05	1
tc|Rep: Chromosome undetermined scaffold_142, whole genome shotgun sequenc	148.47	1
tc|Rep: Ubiquitin carrier protein - Solanum tuberosum (Potato), complete [TC4631	454.72	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	552.61	1
gb|KP1B.113N24F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.113N24, m	915.53	1
Unknown	36.48	1
tc|Rep: 3-hydroxy-3-methylglutaryl coenzyme A reductase - Artemisia annua (Swee	1105.79	1
Unknown	686.5	1
tc|Rep: Guanine nucleotide-binding protein subunit beta-like protein - Nicotiana pl	69.23	1

gb|AGN_RNC108xa19r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	83.41	1
gb|KF8B.100G17F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100G17, mR	45140.45	1
tc|Rep: Chromosome undetermined scaffold_339, whole genome shotgun sequenc	23.15	1
Unknown	81.44	1
gb|KP1B.001N14F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001N14, m	79.24	1
gb|KL5B.109B20F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.109B20, mR	1034.11	1
gb|TT-04_L12 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	857.16	1
gb|KF8C.104N01F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104N01, mR	24.24	1
gb|KG9B.001L10F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001L10, m	88.51	1
tc|Rep: Heat shock protein 90 - Nicotiana tabacum (Common tobacco), partial (16%	233.55	1
tc|Rep: H+-transporting two-sector ATPase, B/B' subunit - Pelobacter propionicus (	187.41	1
gb|KL4B.102C04F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102C04, mR	85.07	1
tc|Rep: Pleiotropic drug resistance protein 1 - Nicotiana plumbaginifolia (Leadwort-	235417	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	27.3	1
tc|Rep: Chromosome chr2 scaffold_113, whole genome shotgun sequence - Vitis vi	19.15	1
gb|KF8C.110N19F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110N19, mR	189.62	1
gb|KN6B.100N07F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100N07, r	110.25	1
tc|Rep: Heat shock protein 90 - Nicotiana tabacum (Common tobacco), complete [	314.6	1
gb|KL4B.102I08F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102I08, mRN	37.66	1
tc|Rep: Ubiquitin-conjugating enzyme E2-17 kDa - Solanum lycopersicum (Tomato)	859.73	1
gb|AGN_PNL221bf1_h2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	25.78	1
tc|Rep: NtSar1 protein - Nicotiana tabacum (Common tobacco), complete [TC4081	8454.97	1
Unknown	37.89	1
gb|KF8C.101E13F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101E13, mRN	32.23	1
gb|AGN_ELP022xi24f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	33.65	1
Unknown	920.11	1
gb|KT7C.101D22F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.101D22, mR	23.07	1
gb|AGN_RNC024xj02f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	27.65	1
Unknown	22.26	1
tc|Rep: Branched-chain amino acid ABC transporter, ATP-binding protein - Roseova	3632.49	1
Unknown	33.52	1
gb|EST_FLW001xm03f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [	24.04	1
Unknown	1915.83	1
gb|AGN_RNC022xm16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	136.16	1

gb|KG9B.001G16F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001G16, m	178.56	1
Unknown	236.58	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	170.18	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	23.68	1
gb|Nicotiana tabacum auxin-repressed protein-like protein (Arpl1;1) mRNA, comple	774.15	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	36.04	1
Unknown	168.36	1
gb|KF8C.101F11F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101F11, mRN	78.94	1
gb|TL13.110I15F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.110I15, mRN	804.28	1
Unknown	1044.75	1
tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin	50.11	1
gb|KT7C.110M21F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110M21, m	241.87	1
gb|KF8C.108C05F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108C05, mR	421.42	1
tc|Rep: Delta-aminolevulinic acid dehydratase - Vitis vinifera (Grape), partial (48%)	1008.02	1
gb|KP1B.037G02F.050623T7 KP1B Nicotiana tabacum cDNA clone KP1B.037G02, m	691.37	1
Unknown	24.28	1
Unknown	468.44	1
gb|TT-06_P09 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	26.65	1
tc|Rep: Transaldolase - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	133.38	1
tc|Rep: Chromosome undetermined scaffold_342, whole genome shotgun sequenc	847.75	1
gb|KT7C.108E22F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108E22, mR	43.56	1
tc|Rep: Tobamovirus multiplication 1 homolog - Solanum lycopersicum (Tomato) (L	433.99	1
Unknown	1081.68	1
gb|KR3B.101F21F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101F21, m	21.34	1
Unknown	159.05	1
gb|Nicotiana tabacum A22 mRNA for hypothetical protein, complete cds [AB18604	108.17	1
tc|Rep: ChaC-like family protein-like - Solanum tuberosum (Potato), partial (94%) [T	1203.7	1
Unknown	556.14	1
gb|CHO_SL022xi01f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	258.94	1
gb|KL4B.101J19F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101J19, mR	21.91	1
tc|Rep: Chromosome chr9 scaffold_33, whole genome shotgun sequence - Vitis vin	1841.06	1
gb|KP1B.001H09F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001H09, m	2530.31	1
gb|AGN_ELP026xa20f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	819.1	1
gb|KN6B.009D17F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009D17, m	68.76	1

Unknown	1030.93	1
gb|AGN_ELP026xe19f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	24.86	1
tc|Rep: Allantoate amidohydrolase - Glycine max (Soybean), partial (60%) [TC4093	203.64	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	757.7	1
gb|TT-17_M23 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA s	451.78	1
gb|KP1B.109E18F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109E18, m	575.77	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	110.1	1
tc|Rep: Chromosome undetermined scaffold_69, whole genome shotgun sequence	94.52	1
tc|Rep: Syntaxin-52 - Arabidopsis thaliana (Mouse-ear cress), complete [TC40892]	482.81	1
gb|KL4B.102D07F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102D07, m	243.98	1
Unknown	120.2	1
Unknown	47.35	1
tc|Rep: Avr9/Cf-9 rapidly elicited protein 76 - Nicotiana tabacum (Common tobacc	53.94	1
gb|CHO_SL022xc24f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	501.38	1
Unknown	79.8	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	31.51	1
Unknown	466.63	1
gb|KT7C.110B02F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110B02, mR	21645.6	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	203.83	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	636.28	1
gb|KR3B.109K20F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109K20, m	39.15	1
tc|Rep: ChaC-like family protein-like - Solanum tuberosum (Potato), partial (94%) [	4006.68	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	12596.75	1
tc|Rep: F14D16.17 - Arabidopsis thaliana (Mouse-ear cress), partial (6%) [TC75073]	55.69	1
Unknown	23769.2	1
Unknown	26.69	1
gb|KN6B.103A01F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103A01,	992.74	1
gb|KF8C.101L11F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101L11, mRN	64.65	1
gb|AM790765 seedling library, SL Nicotiana tabacum cDNA clone nt002016048, m	21.83	1
Unknown	99.91	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	132.84	1
gb|AM793576 seedling library, SL Nicotiana tabacum cDNA clone nt002297024, m	151.01	1
gb|AGN_PNL216df1_a7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	27.24	1
Unknown	18.19	1

gb|TT-07_J21 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	2784.45	1
Unknown	102.63	1
gb|AGN_ELP024xh01f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	34.64	1
gb|Nicotiana tabacum fertilization-independent endosperm protein (FIE) mRNA, co	18.17	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	135.66	1
Unknown	230.41	1
gb|FS408169 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	693.74	1
gb|AGN_RPC020xg11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	496.95	1
Unknown	25.2	1
gb|AGN_PNL221bf1_c2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	856.55	1
tc|Rep: CRABS CLAW protein - Quercus glauca, partial (8%) [TC70877]	105.92	1
gb|KR2B.115K01F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115K01, m	52.29	1
gb|Nicotiana tabacum NtMATE1 mRNA for multi antimicrobial extrusion family pro	50.14	1
gb|AGN_RNC123xj03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	268.4	1
gb|AM788420 seedling library, SL Nicotiana tabacum cDNA clone nt002001046, m	31.3	1
gb|KG9B.106G11F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106G11,	177.62	1
gb|AM802537 COL, cold overnight library Nicotiana tabacum cDNA clone nt006166	22.51	1
tc|Rep: Avr9 elicitor response protein - Nicotiana tabacum (Common tobacco), par	547.92	1
Unknown	41.6	1
gb|TT-41_E08 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	268.72	1
tc|Rep: Retrotransposon gag protein - Solanum demissum (Wild potato), partial (4	30.15	1
Unknown	120.63	1
gb|KR2B.113H17F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.113H17, m	563.24	1
gb|Nicotiana tabacum S-adenosyl-L-methionine synthetase (SAMS) mRNA, complet	8388.7	1
gb|KG9B.002A18F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002A18, m	870.39	1
gb|AGN_RNC021xb24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	111.2	1
Unknown	18.97	1
tc|Rep: Os03g0702000 protein - Oryza sativa subsp. japonica (Rice), partial (32%) [T	186.01	1
tc|GB|AJ298071.1|CAC18552.1 cell division cycle protein [Nicotiana tabacum] [NP	23.54	1
gb|KL4B.105N14F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105N14, m	929.25	1
gb|TT-50_M03 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA se	377.89	1
tc|Rep: Chromosome undetermined scaffold_1484, whole genome shotgun sequen	3509.98	1
gb|FS416927 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	1077.29	1
Unknown	42.91	1

Unknown	569.35	1
gb|KF8C.104O18F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104O18, mR	116.11	1
gb|CHO_SL023xf22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1550.26	1
gb|CHO_SL013xm10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	189.41	1
Unknown	101.33	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	237.56	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	1883.38	1
tc|Rep: Tubby-like protein - Cicer arietinum (Chickpea) (Garbanzo), partial (13%) [T	592.41	1
tc|Rep: Microtubule bundling polypeptide TMBP200 - Nicotiana tabacum (Commo	1295.98	1
tc|Rep: Chromosome undetermined scaffold_91, whole genome shotgun sequence	506.92	1
tc|Rep: Chromosome chr3 scaffold_199, whole genome shotgun sequence - Vitis vi	1220.73	1
gb|KG9B.106K09F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106K09, m	3221.98	1
gb|BP133832 MAT001 Nicotiana tabacum cDNA clone BY6138, mRNA sequence [B	178.51	1
gb|AGN_RNC014xn22f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	100.78	1
gb|TT-50_C15 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	37.82	1
gb|TT-19_L02 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	51.68	1
tc|Rep: Adenylate kinase, chloroplast precursor - Solanum tuberosum (Potato), par	1053.13	1
gb|KT7B.107M01F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107M01, m	20.03	1
gb|BP527163 MAT001 Nicotiana tabacum cDNA clone BY11938, mRNA sequence [	23.72	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	77.57	1
gb|KF8C.105G05F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105G05, mR	1118.4	1
Unknown	10210.05	1
gb|FS424594 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	23.03	1
tc|Rep: 60S ribosomal protein L12 - Capsicum annuum (Bell pepper), complete [TC	86.17	1
gb|KL4B.103F10F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103F10, mR	25536.1	1
Unknown	239.45	1
Unknown	128.72	1
gb|CHO_SL013xa08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	251.33	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	980.26	1
Unknown	527.53	1
gb|AGN_ELP012xd15f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	33.08	1
gb|TT-12_E09 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	183.81	1
Unknown	104.11	1
Unknown	511.98	1

gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC1-41-230, cultivar Bright Yellow 2	122.38	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	839.2	1
gb|KF8C.110D01F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110D01, mR	19.08	1
gb|KP1B.101P05F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101P05, m	67.43	1
Unknown	4830.97	1
tc|Rep: Histone H3 - Vitis vinifera (Grape), complete [TC47009]	141.68	1
Unknown	18.96	1
gb|KN6B.110M04F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.110M04,	92.33	1
tc|Rep: Chromosome chr5 scaffold_156, whole genome shotgun sequence - Vitis vi	415.21	1
Unknown	85.87	1
gb|KG9B.002O20F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002O20, r	114.32	1
gb|Nicotiana tabacum mRNA for hypothetical protein (c18 gene) [AJ966359]	167.48	1
Unknown	134.83	1
Unknown	19.65	1
gb|KL4B.104A12F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104A12, m	522.52	1
gb|BP525566 MAT001 Nicotiana tabacum cDNA clone BY10248, mRNA sequence [	28.45	1
gb|KL4B.102C03F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102C03, mR	14130.35	1
tc|Rep: Homolog of Homo sapiens "Histone 1, H2ai - Takifugu rubripes, partial (30	416.34	1
gb|KG9B.101F04F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101F04, m	422.4	1
gb|KR2B.111P22F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.111P22, m	52.67	1
tc|Rep: Chromosome chr16 scaffold_94, whole genome shotgun sequence - Vitis vi	21.49	1
tc|Rep: Polyubiquitin - Thlaspi caerulescens (Alpine penny-cress) (Thlaspi calaminar	316.03	1
Unknown	22.8	1
gb|CHO_SL015xm16f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	2996.93	1
gb|N.tabacum mRNA for inorganic pyrophosphatase (TVP31 clone) [X83729]	412.85	1
gb|TT-29_O01 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	26.02	1
tc|Rep: Chromosome chr1 scaffold_180, whole genome shotgun sequence - Vitis vi	814.23	1
gb|KF8B.100P06F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100P06, mR	184.95	1
Unknown	48.44	1
gb|TT-38_F24 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	48.31	1
gb|TT-36_L21 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	51.65	1
tc|Rep: Ras-related protein Rab11A - Nicotiana tabacum (Common tobacco), compl	410.39	1
tc|Rep: GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM K+/H+ ANTIPORT	52.95	1
Unknown	5667.76	1

gb|AGN_ELP017xm07f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	157.8	1
Unknown	20.75	1
Unknown	947.68	1
tc|Rep: Serine acetyltransferase 1 - Nicotiana tabacum (Common tobacco), partial (	25.9	1
gb|TT-05_H21 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	30.57	1
gb|Nicotiana tabacum mRNA for NAD-malate dehydrogenase [AJ006974]	8958.5	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	2586.71	1
tc|Rep: Chromosome undetermined scaffold_60, whole genome shotgun sequence	142.59	1
tc|Rep: Syntaxin-like protein - Solanum tuberosum (Potato), partial (38%) [TC46504	84.95	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	112.66	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (35%) [TC53	52.01	1
gb|KF8C.106N19F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106N19, mRN	52.69	1
tc|Rep: Plastid quinol oxidase - Solanum lycopersicum (Tomato) (Lycopersicon escu	360.38	1
gb|Nicotiana tabacum chloroplast NADP-malic enzyme precursor, mRNA, complete	997.68	1
tc|Rep: Pyruvate kinase, cytosolic isozyme - Nicotiana tabacum (Common tobacco),	1184.38	1
gb|KL4B.103E18F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103E18, mR	147.15	1
Unknown	29.89	1
gb|KL4B.104A04F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104A04, mR	28.29	1
tc|Rep: Predicted protein - Nematostella vectensis (Starlet sea anemone), partial (1	47.48	1
gb|KG9B.101D19F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101D19, n	20.36	1
gb|Nicotiana tabacum mRNA for mitochondrial 2-oxoglutarate [AJ299250]	756.22	1
tc|Rep: Chromosome undetermined scaffold_91, whole genome shotgun sequence	896.45	1
gb|BP531480 MAT005 Nicotiana tabacum cDNA clone BY24380, mRNA sequence [B	442.66	1
gb|AGN_RNC020xn18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	21.15	1
Unknown	20.04	1
Unknown	32.74	1
gb|KG9B.005D18F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005D18, n	3979.66	1
Unknown	34.66	1
tc|Rep: 60s acidic ribosomal protein-like protein - Solanum tuberosum (Potato), par	4489.49	1
gb|KP1B.107G18F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107G18, m	48.62	1
tc|Rep: Ubiquitin carrier protein - Capsicum annuum (Bell pepper), complete [TC51	3697.16	1
gb|KL4B.102H07F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102H07, mR	223.49	1
gb|AM780931 seedling library, SL Nicotiana tabacum cDNA clone nt002043053, mR	25.36	1
gb|Nicotiana tabacum mRNA for chloroplast FtsZ-like protein (ftsZ gene), clone FtsZ	110.85	1

gb|KF8C.103J17F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103J17, mRN	121.87	1
gb|Nicotiana tabacum mRNA for putative zinc transporter (C477 gene) [AM851010	144.69	1
Unknown	226.87	1
gb|KF8C.102I23F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102I23, mRN	17779.35	1
Unknown	1399.27	1
gb|KL4B.105O20F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105O20, m	130.63	1
Unknown	36.69	1
Unknown	90.97	1
tc|Rep: Chromosome chr5 scaffold_72, whole genome shotgun sequence - Vitis vin	167.24	1
Unknown	35.24	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	744.54	1
gb|Nicotiana tabacum guanylate kinase (GK-1) mRNA, complete cds [AF205130]	1033.24	1
gb|tbt_000462 Normalized Nicotiana tabacum cDNA library Nicotiana tabacum cD	5659.21	1
tc|Rep: VTC2-like protein - Actinidia chinensis (Kiwi) (Yangtao), partial (56%) [TC423	40.78	1
gb|TT-19_K15 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	1175.75	1
gb|KF8C.104F18F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104F18, mRN	1964.63	1
gb|AM789086 COL, cold overnight library Nicotiana tabacum cDNA clone nt006143	20.67	1
gb|TT-01_D04 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	827.33	1
Unknown	371.63	1
Unknown	787.1	1
gb|TT-39_I22 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	261.67	1
tc|Rep: Transcription factor JERF1 - Solanum lycopersicum (Tomato) (Lycopersicon	79.84	1
Unknown	30.98	1
tc|Rep: Chromosome undetermined scaffold_53, whole genome shotgun sequence	735.61	1
gb|AM801892 COL, cold overnight library Nicotiana tabacum cDNA clone nt006056	28.75	1
gb|KP1B.037O12F.050623T7 KP1B Nicotiana tabacum cDNA clone KP1B.037O12, m	79.67	1
tc|Rep: Capsid protein - Olive latent virus 1, partial (5%) [TC57852]	188.64	1
gb|KR3B.113B04F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.113B04, m	975.91	1
Unknown	190.82	1
gb|Nicotiana tabacum peroxisomal acetoacetyl-coenzyme A thiolase (AACT2) mRN	178.61	1
gb|KP1B.110E09F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110E09, m	33.02	1
gb|KG9B.004N13F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004N13,	55.27	1
gb|KT7B.107H09F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107H09, mR	269.8	1
tc|Rep: Ovule receptor-like kinase 28 precursor - Solanum chacoense (Chaco potat	89.25	1

tc|Rep: Chromosome undetermined scaffold_2685, whole genome shotgun sequen	179.24	1
tc|Rep: Mature anther-specific protein LAT61 - Solanum lycopersicum (Tomato) (Ly	22.54	1
gb|KF8C.102B01F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102B01, mR	128.1	1
tc|Rep: Chromosome chr4 scaffold_443, whole genome shotgun sequence - Vitis vi	507.74	1
Unknown	767.9	1
tc|Rep: Uncharacterized protein At5g46250.3 - Arabidopsis thaliana (Mouse-ear cr	578.06	1
gb|AGN_RNC024xj15r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	89.92	1
tc|Rep: Chromosome chr10 scaffold_76, whole genome shotgun sequence - Vitis vi	1823.06	1
gb|N.tabacum npp2 mRNA for protein phosphatase type 1 [Z93769]	1544.15	1
gb|TT-11_F18 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	80.38	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	28.78	1
gb|KL4B.103B21F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103B21, mR	2897.23	1
gb|KG9B.001L18F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001L18, m	114.61	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	24.46	1
gb|Nicotiana tabacum mRNA for hypothetical protein (mc307 gene) [AJ966362]	850.28	1
Unknown	17.97	1
gb|KT7C.106A21F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106A21, mR	31.12	1
gb|KF8C.102D11F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102D11, mR	134.71	1
tc|Rep: Beta-amylase 1 - Nicotiana langsdorffii x Nicotiana sanderae (Ornamental t	73.22	1
Unknown	98.69	1
Unknown	735.81	1
tc|Rep: 14-3-3 protein - Nicotiana tabacum (Common tobacco), complete [TC5144	563.2	1
tc|Rep: GAGA-motif binding transcriptional activator - Populus trichocarpa (Wester	2707.34	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	964.71	1
gb|KG9B.101D07F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101D07,	221.99	1
gb|KF8B.100L14F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100L14, mRN	50.63	1
tc|Rep: RAN GTPase-activating protein 1 - Nicotiana benthamiana, partial (23%) [T	265.06	1
gb|KG9B.103G15F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103G15,	79.04	1
gb|Nicotiana tabacum Tobacco mosaic virus helicase domain-binding protein mRN	145.63	1
tc|Rep: Prohibitin - Nicotiana tabacum (Common tobacco), complete [TC52074]	21.92	1
gb|Nicotiana tabacum guanylate kinase (GK-1) mRNA, complete cds [AF205130]	5445.24	1
Unknown	115.08	1
tc|Rep: Chromosome undetermined scaffold_203, whole genome shotgun sequen	35453.05	1
tc|Rep: ATP synthase subunit beta, mitochondrial precursor - Nicotiana plumbagini	87.3	1

gb|KL4B.104B18F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104B18, mR	24.25	1
tc|Rep: Chromosome chr10 scaffold_81, whole genome shotgun sequence - Vitis vi	61.98	1
gb|KG9B.107G06F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107G06, n	22.74	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	37.54	1
Unknown	2826.36	1
gb|KG9B.107L18F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107L18, m	895.95	1
gb|Nicotiana tabacum calcium [AF435450]	30.34	1
tc|Rep: STYLOSA protein - Antirrhinum majus (Garden snapdragon), partial (29%) [T	120.56	1
gb|KF8C.106P02F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106P02, mR	127.84	1
Unknown	203.28	1
gb|KF8C.104H23F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104H23, mR	2111.04	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	147.18	1
tc|Rep: AN14 - Zea mays (Maize), partial (75%) [TC44451]	519.1	1
Unknown	80.62	1
gb|EST_YP002xa17f1.ab1 EST_YP Nicotiana tabacum cDNA, mRNA sequence [EH61	125.3	1
gb|TT-22_F04 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	22.97	1
tc|Rep: Ribosomal protein L3A - Nicotiana tabacum (Common tobacco), partial (59	44.99	1
tc|Rep: Threonine synthase, chloroplast precursor - Solanum tuberosum (Potato),	16.31	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	127.12	1
gb|AM843365 seedling library, SL Nicotiana tabacum cDNA clone nt002201085, m	59.61	1
Unknown	31.3	1
Unknown	23.2	1
tc|Rep: Fructose-bisphosphate aldolase - Solanum tuberosum (Potato), partial (65	288.23	1
Unknown	514.67	1
gb|BP528348 MAT001 Nicotiana tabacum cDNA clone BY13188, mRNA sequence [	122.39	1
tc|Rep: TPK1 - Nicotiana tabacum (Common tobacco), complete [TC64081]	56.72	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	494.03	1
gb|KF8B.100P16F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100P16, mR	507.97	1
Unknown	749.75	1
Unknown	61.79	1
gb|KP1B.001F04F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001F04, m	329.96	1
Unknown	158.32	1
Unknown	29.68	1
gb|TT-22_N03 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	26.19	1

Unknown	63.64	1
Unknown	491.41	1
Unknown	21.05	1
Unknown	18.69	1
Unknown	25.77	1
gb|AGN_RNC017xg05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	3165.36	1
gb|AGN_RNC014xe03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	70.34	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	136.37	1
Unknown	103.02	1
gb|KL5B.001P11F.050901T7 KL5B Nicotiana tabacum cDNA clone KL5B.001P11, mR	268.15	1
gb|TT-07_H19 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	281.48	1
tc|Rep: Chromosome chr1 scaffold_180, whole genome shotgun sequence - Vitis vi	94.61	1
Unknown	500.83	1
gb|KT7C.112H24F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112H24, mR	1992.27	1
gb|FS407656 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	1775.58	1
tc|Rep: Os06g0186900 protein - Oryza sativa subsp. japonica (Rice), partial (41%) [T	42.61	1
tc|Rep: Betaine aldehyde dehydrogenase - Panax ginseng (Korean ginseng), partial (	737.4	1
Unknown	36273.1	1
tc|Rep: Neutral leucine aminopeptidase preprotein precursor - Solanum lycopersicu	564.55	1
gb|KR3B.001D06F.050815T7 KR3B Nicotiana tabacum cDNA clone KR3B.001D06, m	134.49	1
gb|KP1B.108B16F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108B16, m	271.21	1
tc|Rep: Transcription Factor IIF, Rap30/Rap74, interaction - Medicago truncatula (B	214.36	1
Unknown	28.88	1
Unknown	848.32	1
gb|AGN_RNC211xk21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	2673.21	1
gb|TT-18_N15 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	86.08	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	130.81	1
Unknown	65.86	1
gb|AJ632923 Nicotiana tabacum leaf Nicotiana tabacum cDNA clone Nt05-B07, mR	26.73	1
gb|AGN_RNC007xf18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	47.2	1
gb|Nicotiana tabacum partial mRNA for villin 2 (vln2 gene) [AJ577853]	4157.97	1
tc|Rep: Polyubiquitin - Fragaria ananassa (Strawberry), partial (48%) [TC46813]	18125.3	1
tc|Rep: Chromosome undetermined scaffold_310, whole genome shotgun sequenc	757.32	1
gb|CHO_SL005xh14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	66.45	1

tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	1023.16	1
tc|Rep: Splicing factor-like - Oryza sativa subsp. japonica (Rice), partial (12%) [TC68	249.09	1
gb|KN6B.106I23F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.106I23, m	458.14	1
Unknown	865.51	1
Unknown	31.8	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	37.42	1
tc|Rep: 60S ribosomal protein L34 - Nicotiana tabacum (Common tobacco), comple	66.95	1
gb|TT-07_C15 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	2673.14	1
Unknown	92.17	1
tc|Rep: Chromosome chr3 scaffold_199, whole genome shotgun sequence - Vitis vi	103.69	1
tc|Rep: Mitochondrial processing peptidase - Solanum tuberosum (Potato), partial	93.99	1
tc|Rep: Chromosome undetermined scaffold_332, whole genome shotgun sequenc	68.72	1
Unknown	65.67	1
tc|Rep: Serine hydroxymethyltransferase - Vitis vinifera (Grape), partial (55%) [TC5	19.8	1
gb|KN6B.009A01F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009A01, m	40.17	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	64.02	1
gb|KR3B.109O22F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109O22, m	56.31	1
Unknown	96.28	1
Unknown	4579.52	1
Unknown	104.16	1
gb|KT7B.107A11F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107A11, mR	20.93	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	35.66	1
tc|Rep: Farnesyl pyrophosphate synthase - Solanum lycopersicum (Tomato) (Lycop	133.64	1
Unknown	208.58	1
gb|TT-16_H13 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	32.97	1
Unknown	35.93	1
tc|Rep: Asparagine synthetase - Helianthus annuus (Common sunflower), partial (2	68.82	1
gb|KL4B.103P04F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103P04, mR	6937.11	1
tc|Rep: ATP:citrate lyase - Capsicum annuum (Bell pepper), partial (24%) [TC62642]	471.89	1
gb|KT7C.108M22F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108M22, m	65.53	1
gb|KF8B.200I11F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200I11, mRN	43573.3	1
gb|KL4B.101K21F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101K21, mR	85.48	1
tc|Rep: Dihydrolipoyllysine-residue acetyltransferase component 3 of pyruvate deh	1556.96	1
gb|TT-08_D07 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	130.68	1

tc|Rep: Chromosome undetermined scaffold_3075, whole genome shotgun sequen	81.57	1
Unknown	11135.25	1
Unknown	186.5	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	111.49	1
Unknown	152.47	1
gb|AGN_PNL208bf1_c6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	218.6	1
tc|Rep: Chromosome undetermined scaffold_161, whole genome shotgun sequenc	31.74	1
Unknown	119.91	1
gb|AGN_PNL227cf1_g8.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	16999.55	1
gb|Nicotiana tabacum MADS-box protein MADS5 (NtMADS5) mRNA, complete cds	87.02	1
Unknown	158.36	1
Unknown	88.8	1
tc|Rep: Phosphoglycerate kinase, chloroplast precursor - Nicotiana tabacum (Comn	19.32	1
Unknown	26.37	1
Unknown	935.42	1
tc|Rep: Phosphatidic acid phosphatase alpha - Vigna unguiculata (Cowpea), partial (	84.36	1
gb|AM816248 DL, diurnal library Nicotiana tabacum cDNA clone nt005094030, mRI	9804.92	1
tc|Rep: Chromosome undetermined scaffold_3017, whole genome shotgun sequen	272.44	1
Unknown	822.82	1
Unknown	50112.6	1
Unknown	559.26	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	67.62	1
tc|Rep: Superoxide dismutase [Cu-Zn] - Nicotiana plumbaginifolia (Leadwort-leavec	1016.59	1
Unknown	566.4	1
gb|KF8B.201D11F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201D11, mRI	370.82	1
tc|Rep: Cryptic phage CTXphi transcriptional repressor rstR - Vibrio cholerae, partia	406	1
gb|AM785983 seedling library, SL Nicotiana tabacum cDNA clone nt002287087, mF	18.71	1
gb|KF8C.103C08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103C08, mRN	473.53	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	1816.18	1
tc|Rep: Os09g0505800 protein - Oryza sativa subsp. japonica (Rice), partial (86%) [T	16.95	1
tc|Rep: Sterol desaturase family protein - Solanum demissum (Wild potato), partial	344.33	1
gb|TT-29_O23 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	521.62	1
gb|TOBESTR053C09 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	30.67	1
gb|AGN_RNC004xn01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	630.59	1

gb|KG9B.106H08F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106H08, n	35.45	1
tc|Rep: Cytochrome c1-1, heme protein, mitochondrial precursor - Solanum tubero	229.7	1
tc|Rep: Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplast precursor - S	906.82	1
gb|KT7B.100K11F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100K11, mRN	897.34	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	159.24	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	113.36	1
tc|Rep: Chromosome chr1 scaffold_136, whole genome shotgun sequence - Vitis vi	498.53	1
gb|CHO_SL002xi14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	249.77	1
Unknown	24.77	1
Unknown	2715.54	1
gb|KG9B.004N23F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004N23, n	27.72	1
gb|KL4B.103N16F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103N16, mR	267.66	1
Unknown	129.97	1
Unknown	33.92	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	31.72	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	4702.13	1
gb|AGN_PNL221df1_h2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	77.63	1
gb|AGN_ELP026xh16f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	3011.04	1
gb|AGN_RPC007xi20f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	9894.43	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	139.56	1
gb|AGN_RPC024xe08f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	71.89	1
Unknown	93.66	1
gb|KG9B.106C11F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106C11, m	142.51	1
gb|KF8C.106J12F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106J12, mRN	97.18	1
gb|KP1B.105L15F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105L15, mR	79.42	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	174.57	1
gb|AGN_RPC011xp08f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	529.88	1
gb|KL4B.108H04F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108H04, mR	95.6	1
gb|AGN_RNC014xf15r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequence	101.34	1
tc|Rep: Uncharacterized protein At2g33847.2 - Arabidopsis thaliana (Mouse-ear cre	55.46	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	28.81	1
gb|KT7C.109K13F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109K13, mRN	1530.87	1
gb|EST_FLW001xe19f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	43.83	1
Unknown	22.76	1

tc|Rep: Oligouridylate binding protein - Nicotiana plumbaginifolia (Leadwort-leavec	5641.94	1
Unknown	310.61	1
tc|Rep: Chromosome undetermined scaffold_332, whole genome shotgun sequenc	22.43	1
tc|Rep: Anther ethylene-upregulated protein ER1 - Nicotiana tabacum (Common to	71.5	1
gb|EST_CSP005xb11f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	47.73	1
Unknown	766.65	1
Unknown	172.43	1
tc|Rep: Histidinol dehydrogenase - Vitis vinifera (Grape), partial (94%) [TC73650]	53.22	1
tc|Rep: 3-dehydroquinate dehydratase / shikimate dehydrogenase isoform 2 - Nico	23.86	1
tc|Rep: Chromosome undetermined scaffold_489, whole genome shotgun sequenc	539.23	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	268.34	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	154.05	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	1591.96	1
tc|Rep: PHD5 - Glycine max (Soybean), partial (96%) [TC57518]	20.76	1
tc|Rep: Spliceosomal protein - Solanum tuberosum (Potato), partial (35%) [TC5154	215.11	1
Unknown	179.51	1
gb|KR3B.109O08F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109O08, m	2163.94	1
gb|KF8C.103F16F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103F16, mRN	35.74	1
gb|KL4B.101H07F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101H07, mF	46.51	1
gb|KP1B.105A01F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105A01, m	189.69	1
gb|KG9B.106F01F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106F01, m	267.74	1
gb|KP1B.037L14F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.037L14, mF	515.96	1
tc|Rep: Pol polyprotein - Citrus paradisi (Grapefruit), partial (12%) [TC60940]	86.19	1
gb|Nicotiana tabacum fertilization-independent endosperm protein (FIE) mRNA, co	29.37	1
gb|KF8C.106P03F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106P03, mRN	49329.35	1
gb|TT-28_F07 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence		36.61	1
gb|TT-03_F17 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	456.42	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	351.83	1
gb|AGN_ELP026xp07f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	3633.99	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	850.75	1
gb|Nicotiana tabacum NtWRKY-9 mRNA for WRKY DNA-binding protein, complete	1121.97	1
Unknown	472.76	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	143.92	1
tc|Rep: Ubiquitin carrier protein - Vitis vinifera (Grape), complete [TC56781]	2995.08	1

gb|KP1B.107M05F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107M05, r	185.72	1
tc|Rep: NT3 - Nicotiana tabacum (Common tobacco), partial (22%) [TC56605]	486.12	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	457.77	1
tc|Rep: Polygalacturonase inhibitor protein precursor - Solanum lycopersicum (Tom	498.45	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC3-33-350, cultivar Bright Yellow 2	243.53	1
gb|KG9B.103E14F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103E14, m	515.57	1
Unknown	34.76	1
tc|Rep: Chromosome chr8 scaffold_68, whole genome shotgun sequence - Vitis vin	187.42	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	25.03	1
tc|Rep: Embryonic flower 2 - Solanum lycopersicum (Tomato) (Lycopersicon escule	417.95	1
gb|AM789368 seedling library, SL Nicotiana tabacum cDNA clone nt002018082, mR	522.29	1
gb|N.tabacum mRNA for phosphoglycerate kinase (chloroplast isoenzyme) [Z48977	37.41	1
tc|Rep: Chromosome chr11 scaffold_56, whole genome shotgun sequence - Vitis vi	105.31	1
tc|Rep: Chromosome chr9 scaffold_90, whole genome shotgun sequence - Vitis vin	1024.61	1
tc|Rep: Chromosome chr16 scaffold_271, whole genome shotgun sequence - Vitis	1124.27	1
gb|AM812458 DL, diurnal library Nicotiana tabacum cDNA clone nt005112026, mR	25.03	1
Unknown	31.27	1
gb|KP1B.037E06F.050623T7 KP1B Nicotiana tabacum cDNA clone KP1B.037E06, m	32.23	1
Unknown	479.16	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	984.59	1
gb|AGN_PNL216bf1_g6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	62.46	1
gb|KL5B.112O22F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.112O22, m	59.14	1
Unknown	1552.87	1
tc|Rep: Calcineurin B-like protein 2-1 - Populus euphratica (Euphrates poplar), parti	2147.19	1
gb|CHO_SL022xd02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	465.12	1
gb|FS406815 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	58.19	1
tc|Rep: Phosphomevalonate kinase - Hevea brasiliensis (Para rubber tree), partial (	19.61	1
tc|Rep: Chromosome chr5 scaffold_72, whole genome shotgun sequence - Vitis vin	45.13	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	983.81	1
gb|BP133500 MAT001 Nicotiana tabacum cDNA clone BY5775, mRNA sequence [B	43284.85	1
Unknown	14698.55	1
gb|KR3B.114I17F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.114I17, mR	59.87	1
Unknown	77.81	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	84.74	1

tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	241.33	1
gb|TT-38_H14 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	46.19	1
Unknown	563.08	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	29.42	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT21-1-550, cultivar Bright Yellow 2	77.61	1
gb|AGN_ELP012xb20f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	21.82	1
Unknown	1526.21	1
Unknown	47.58	1
gb|CHO_SL006xj24f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	2744.78	1
gb|CHO_SL022xm10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	45.13	1
Unknown	20.84	1
Unknown	43.12	1
Unknown	105.31	1
gb|TT-29_D19 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	969.12	1
tc|Rep: Phosphoserine aminotransferase - Arabidopsis thaliana (Mouse-ear cress),	1783.47	1
gb|AGN_RNC020xm19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	28.64	1
gb|EST_CSP005xn06f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	80.32	1
Unknown	37.63	1
gb|KT7B.100B11F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100B11, mR	61.32	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	505.6	1
gb|KP1B.001G12F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001G12, m	1177.87	1
Unknown	252.31	1
Unknown	57.35	1
tc|Rep: Chromosome undetermined scaffold_100, whole genome shotgun sequenc	92.06	1
Unknown	171.14	1
gb|KN6B.105E09F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105E09, m	140.59	1
tc|Rep: Chromosome chr4 scaffold_162, whole genome shotgun sequence - Vitis vi	1085.23	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	457.72	1
gb|KG9B.102D18F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102D18, n	67.56	1
Unknown	119.79	1
gb|FS409302 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	4166.64	1
Unknown	133.55	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	569.87	1
gb|Nicotiana tabacum tetratricoredoxin mRNA, complete cds [AY064253]	26.49	1

gb|KF8C.105F01F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105F01, mRN	2166.43	1
Unknown	531.74	1
gb|KP1B.101L11F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101L11, mR	752.04	1
Unknown	1512.81	1
tc|Rep: PttA' - Petunia hybrida (Petunia), partial (16%) [TC73454]	286.14	1
Unknown	157.22	1
Unknown	1003.67	1
Unknown	57.9	1
Unknown	31.89	1
Unknown	45.67	1
tc|Rep: Gll2364 protein - Gloeobacter violaceus, partial (11%) [TC64550]	35.24	1
gb|TT-36_L21 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	30.51	1
gb|N.tabacum dhdps mRNA [X79675]	207.47	1
gb|Nicotiana tabacum NtEIG-E80 mRNA, complete cds [AB041515]	9613.23	1
Unknown	205.03	1
gb|ntsm55 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [E	218.85	1
gb|N.tabacum npp2 mRNA for protein phosphatase type 1 [Z93769]	1331.83	1
tc|Rep: CA-responsive protein - Brassica oleracea (Wild cabbage), partial (7%) [TC5	28.21	1
Unknown	44.03	1
Unknown	141.98	1
gb|KL4B.103J09F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103J09, mR	19.6	1
gb|AGN_PNL226bf1_d1.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	1104.04	1
Unknown	1561.33	1
gb|KN6B.114I07F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.114I07, m	92.42	1
gb|KR3B.101B02F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101B02, m	1592.57	1
tc|Rep: RNA Binding Protein 45 - Nicotiana plumbaginifolia (Leadwort-leaved tobac	70.37	1
gb|TT-14_C13 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	82.4	1
tc|Rep: STY-L protein - Antirrhinum majus (Garden snapdragon), partial (52%) [TC5	29.87	1
gb|KF8C.102A12F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102A12, mR	76.84	1
gb|AGN_RNC025xm15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	93.02	1
gb|AM789132 DL, diurnal library Nicotiana tabacum cDNA clone nt005072014, mR	105.84	1
Unknown	478.84	1
gb|TOBESTR043G10 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	1009.86	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	871.96	1

tc|Rep: Mitochondrial import receptor subunit TOM7-1 - Solanum tuberosum (Pota	190.39	1
gb|CHO_SL026xf21f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	870.07	1
Unknown	20.08	1
Unknown	72.93	1
gb|Nicotiana tabacum basic helix-loop-helix protein mRNA, complete cds [EU8802	4387.37	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	62.36	1
tc|Rep: Chromosome chr10 scaffold_43, whole genome shotgun sequence - Vitis vi	848.58	1
tc|Rep: Chromosome chr18 scaffold_24, whole genome shotgun sequence - Vitis vi	10185.17	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	398.83	1
gb|TT-04_N05 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	159.96	1
Unknown	115.01	1
gb|AGN_PNL227af1_b10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	134.84	1
gb|KF8C.102O14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102O14, mR	1020.64	1
tc|Rep: Eukaryotic translation initiation factor 5A-1 - Nicotiana plumbaginifolia (Lea	142.4	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	29.22	1
gb|KN6B.105G06F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105G06, r	629.7	1
gb|CHO_SL004xl02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	46.86	1
gb|AGN_RPC021xi20f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	103.43	1
gb|TT-11_H23 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	134.44	1
tc|Rep: Aluminum-induced protein - Codonopsis lanceolata, partial (97%) [TC40256	67.44	1
gb|Nicotiana tabacum putative chloroplast ribonucleoprotein-like mRNA, partial se	80.62	1
Unknown	117.35	1
gb|KF8C.103I13F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103I13, mRN	1802.63	1
tc|Rep: Ammonium transporter 1 member 1 - Solanum lycopersicum (Tomato) (Lyc	243.73	1
gb|KR3B.001B04F.050815T7 KR3B Nicotiana tabacum cDNA clone KR3B.001B04, m	787.49	1
tc|Rep: Hydrolase, alpha/beta hydrolase fold family precursor - Shewanella amazo	107.6	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	664.85	1
gb|TT-38_O13 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	261.78	1
gb|AGN_PNL211df1_d4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	127.69	1
gb|AGN_RPC014xi23f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	99.26	1
gb|KL4B.101O20F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101O20, m	21.36	1
gb|KT7B.100G14F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100G14, mR	92.18	1
gb|KF8C.105H23F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105H23, mR	2722.13	1
Unknown	31.2	1

gb|CHO_SL010xe03f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	545.53	1
gb|TT-39_B05 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	124.5	1
tc|Rep: COG0245: 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase - Pasteuri	559.42	1
tc|Rep: 60S ribosomal protein L31 - Nicotiana glutinosa (Tobacco), partial (98%) [T	59.97	1
gb|AGN_PNL223df1_e10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	859.28	1
Unknown	190.39	1
tc|Rep: Metal transporter - Solanum lycopersicum (Tomato) (Lycopersicon esculent	35.27	1
tc|Rep: Phytochelatin synthetase-like protein - Phaseolus vulgaris (Kidney bean) (Fr	26.95	1
Unknown	108.49	1
gb|KG9B.105D04F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105D04, n	458.71	1
Unknown	182.73	1
gb|TT-40_P15 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	137.13	1
tc|Rep: 60S ribosomal protein L37a - Capsicum chinense (Scotch bonnet) (Bonnet p	200.51	1
gb|KL4B.109I20F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.109I20, mR	690.16	1
Unknown	39.12	1
gb|KF8C.105F11F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105F11, mR	395.47	1
Unknown	26.69	1
gb|KL4B.112P08F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112P08, mR	25.88	1
gb|KF8B.200B21F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200B21, mR	41.91	1
gb|KL4B.106A13F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106A13, m	169.97	1
tc|Rep: Chromosome undetermined scaffold_168, whole genome shotgun sequenc	536.31	1
gb|KN6B.105M02F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105M02,	25.52	1
gb|Tobacco (N.tabacum) GapC mRNA encoding cytosolic glyceraldehyde-3-phosph	1308.17	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	20.92	1
gb|KF8C.110B02F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110B02, mR	4583.45	1
tc|Rep: 60S ribosomal protein L10a-1 - Arabidopsis thaliana (Mouse-ear cress), part	129.02	1
tc|Rep: NAD-dependent malic enzyme 59 kDa isoform, mitochondrial precursor - S	864.88	1
Unknown	17.62	1
gb|AM790347 DL, diurnal library Nicotiana tabacum cDNA clone nt005227037, mR	1147.49	1
Unknown	22.68	1
tc|Rep: Orotate phosphoribosyltransferase - Sulfolobus solfataricus, partial (8%) [T	67.22	1
Unknown	219.04	1
Unknown	209.03	1
Unknown	22.78	1

gb|FS381087 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	4649.33	1
gb|AGN_ELP006xd03f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	38.53	1
gb|TOBESTR120F08 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA sequ	698.89	1
Unknown	62.75	1
gb|KG9B.102G13F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102G13, n	58.98	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	2819.37	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	50.31	1
tc|Rep: Dicarboxylate/tricarboxylate carrier - Nicotiana tabacum (Common tobacco	234.93	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	227.55	1
gb|AGN_RNC019xk19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	25.61	1
Unknown	249.63	1
gb|KL4B.103D04F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103D04, mR	1292.19	1
gb|N.tabacum mRNA for ornithine decarboxylase [Y10472]	10546.4	1
Unknown	3894.83	1
gb|KT7C.109N01F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109N01, mR	100.8	1
gb|KG9B.106F06F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106F06, m	24.99	1
gb|AGN_RNC002xm03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	39.38	1
Unknown	43.52	1
tc|Rep: SGT1 - Nicotiana benthamiana, partial (49%) [TC48609]	186.89	1
Unknown	78.26	1
Unknown	32.72	1
tc|Rep: Ribosomal protein L33 - Castanea sativa (Sweet chestnut), complete [TC492	72.55	1
Unknown	238.27	1
gb|6.2B09 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5',	209.44	1
tc|Rep: Chromosome chr12 scaffold_38, whole genome shotgun sequence - Vitis vi	51	1
Unknown	4041.04	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	47.88	1
Unknown	21.98	1
Unknown	1960.98	1
gb|KG9B.003O07F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003O07, r	94.99	1
Unknown	17.95	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	46	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	26.67	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	81.61	1

tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	189.07	1
gb|KT7C.105P01F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105P01, mR	103.81	1
gb|TT-15_O08 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	367.9	1
Unknown	223.4	1
Unknown	104.83	1
gb|KT7C.110O01F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110O01, mR	522.31	1
gb|KT7B.100O20F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100O20, mR	302.21	1
Unknown	50.24	1
gb|KG9B.105A19F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105A19,	8182.38	1
gb|BP134817 MAT001 Nicotiana tabacum cDNA clone BY7260, mRNA sequence [B	80.9	1
gb|Nicotiana tabacum mitogen-activated protein kinase Ntf4-1 mRNA, complete c	1199.56	1
gb|AGN_RNC127xp13f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	50.62	1
Unknown	24.33	1
Unknown	25.25	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	3227.76	1
gb|AM833831 DL, diurnal library Nicotiana tabacum cDNA clone nt005173074, mR	217.92	1
gb|Nicotiana tabacum mRNA for phosphate translocator [X75088]	413.9	1
tc|Rep: Chromosome chr2 scaffold_112, whole genome shotgun sequence - Vitis vi	33.43	1
tc|Rep: Phosphatidic acid phosphatase alpha - Vigna unguiculata (Cowpea), partial	181.59	1
gb|TT-04_O15 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	283.77	1
gb|KT7C.106B13F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106B13, mR	16738.6	1
Unknown	26	1
gb|BP136509 MAT001 Nicotiana tabacum cDNA clone BY9112, mRNA sequence [B	25.37	1
gb|KP1B.101N21F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101N21, m	66.59	1
gb|KP1B.105B05F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105B05, m	120.53	1
gb|KF8C.101N16F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101N16, mR	151.4	1
tc|Rep: Os05g0113500 protein - Oryza sativa subsp. japonica (Rice), partial (15%) [	3325.48	1
gb|TT-41_E09 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	90.04	1
Unknown	32.16	1
gb|TT-04_G09 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	41.35	1
gb|KN6B.102H23F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102H23,	36.05	1
tc|Rep: Inorganic pyrophosphatase - Nicotiana tabacum (Common tobacco), compl	104.12	1
Unknown	182.01	1
gb|KP1B.104D05F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104D05, m	77.49	1

gb|CHO_SL014xp06f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	263.02	1
Unknown	193.4	1
gb|KG9B.106G16F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106G16, m	3042.99	1
gb|AGN_ELP022xa22f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	41.31	1
tc|Rep: 40S ribosomal protein S4 - Solanum tuberosum (Potato), complete [TC4036	40.42	1
Unknown	2425.02	1
Unknown	43	1
Unknown	147.36	1
tc|Rep: Chromosome chr2 scaffold_140, whole genome shotgun sequence - Vitis vi	235.94	1
gb|KL4B.107I09F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107I09, mRN	101.42	1
gb|CHO_SL015xf03f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	400.49	1
gb|KG9B.002J23F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002J23, mR	5128.09	1
gb|AGN_RPC010xj11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	84.32	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	1860.27	1
gb|AGN_RNC211xl23f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	1104.26	1
gb|AM782821 seedling library, SL Nicotiana tabacum cDNA clone nt002335061, mR	392.3	1
gb|KL4B.104J12F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104J12, mRN	224.2	1
Unknown	25.97	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	55.6	1
tc|Rep: Malate dehydrogenase - Nicotiana tabacum (Common tobacco), partial (58	111.32	1
Unknown	33.8	1
Unknown	667.59	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	515.47	1
gb|KN6B.101B18F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101B18, m	2719.92	1
Unknown	10285.9	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	77.58	1
gb|FS406206 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	127.71	1
Unknown	28494.34	1
gb|KG9B.102J17F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102J17, mR	17.88	1
tc|Rep: Os04g0644200 protein - Oryza sativa subsp. japonica (Rice), partial (3%) [TC	1059.96	1
Unknown	152.18	1
Unknown	71.38	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	96.95	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	1060.34	1

Unknown	253.69	1
Unknown	1613.56	1
gb|BP530068 MAT005 Nicotiana tabacum cDNA clone BY21050, mRNA sequence [E	22.06	1
Unknown	1827.79	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	31.93	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	598.68	1
Unknown	163	1
tc|Rep: Protein kinase - Nicotiana tabacum (Common tobacco), partial (43%) [TC74	3485.68	1
gb|AGN_ELP022xo07f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	17.55	1
Unknown	178.38	1
gb|TT-11_H13 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	182.52	1
gb|TL13.002J10F.060117T7 TL13 Nicotiana tabacum cDNA clone TL13.002J10, mRN	256.33	1
tc|CAB62118.1 - Arabidopsis thaliana (Mouse-ear cress), partial (9%) [TC67043]	35.31	1
gb|Nicotiana tabacum NtRb1 mRNA, complete cds [AB015221]	955	1
gb|FS377589 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	2549.83	1
gb|TT-50_B23 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	206.32	1
gb|AGN_PNL227ar1_a9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	264.14	1
Unknown	2670.62	1
gb|KG9B.003P01F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003P01, m	829.35	1
Unknown	46.57	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	231.25	1
gb|KG9B.102H04F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102H04, m	8264.01	1
gb|TT-10_O09 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	522.02	1
gb|BP533083 MAT005 Nicotiana tabacum cDNA clone BY29136, mRNA sequence [E	470.53	1
gb|TT-41_B11 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	377.71	1
tc|Rep: Chromosome chr10 scaffold_179, whole genome shotgun sequence - Vitis v	267.85	1
gb|EST_FLW001xk07f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [El	483.25	1
tc|Rep: Chromosome undetermined scaffold_100, whole genome shotgun sequenc	65	1
gb|KG9B.101A23F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101A23, m	261.6	1
Unknown	93.59	1
Unknown	191.74	1
Unknown	625.75	1
gb|KF8B.100J14F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100J14, mRN	22.86	1
tc|Rep: Chromosome undetermined scaffold_139, whole genome shotgun sequenc	21.5	1

gb|KL4B.106J20F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106J20, mR	20.53	1
tc|Rep: GRF zinc finger family protein - Oryza sativa subsp. japonica (Rice), partial (	464.99	1
tc|Rep: Chromosome chr18 scaffold_59, whole genome shotgun sequence - Vitis vi	1583.65	1
gb|AGN_PNL229df1_e6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	237.54	1
Unknown	22.18	1
Unknown	143.45	1
Unknown	26.58	1
Unknown	184.09	1
gb|KG9B.105B06F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105B06, m	19.48	1
gb|TT-19_K15 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	5369.43	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	86.64	1
Unknown	77.28	1
tc|Rep: Chromosome undetermined scaffold_235, whole genome shotgun sequenc	49.33	1
gb|KR3B.102N16F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.102N16, m	4092.58	1
gb|KR3B.107H04F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.107H04, m	1825.9	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	104.85	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	759.09	1
gb|BP525990 MAT001 Nicotiana tabacum cDNA clone BY10688, mRNA sequence [	25.8	1
gb|KR3B.108D14F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.108D14, m	752.06	1
Unknown	100	1
Unknown	236.1	1
gb|KP1B.001L22F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001L22, mR	104.08	1
Unknown	148.96	1
tc|Rep: Glucose-6-phosphate/phosphate translocator 1, chloroplast precursor - Ara	232.99	1
gb|AGN_RNC124xo11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	24.52	1
gb|AGN_RNC009xb01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	182.63	1
gb|EST_CSP005xh22f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	142.07	1
gb|Nicotiana tabacum mRNA for WIPK, complete cds [D61377]	191.21	1
gb|KP1B.001B10F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001B10, m	1128.47	1
gb|ntsm55 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [E	257.15	1
tc|Rep: Chromosome chr4 scaffold_162, whole genome shotgun sequence - Vitis vi	124.86	1
tc|Rep: At1g26740/T24P13_11 - Arabidopsis thaliana (Mouse-ear cress), partial (37	231.13	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	22.17	1
gb|KN6B.104B07F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104B07, m	1219.21	1

tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	157.07	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	40.93	1
gb|KF8C.101M10F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101M10, mF	43.12	1
Unknown	21.28	1
gb|KP1B.112I24F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.112I24, mRI	1383.42	1
tc|Rep: Salicylic acid-activated MAP kinase - Nicotiana tabacum (Common tobacco)	184.9	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	464.16	1
Unknown	41.21	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	587.5	1
Unknown	24.63	1
gb|N.tabacum mRNA for ribonucleotide reductase, clone R1-1 [Y10861]	50.45	1
tc|Rep: Chromosome chr12 scaffold_57, whole genome shotgun sequence - Vitis vi	503.93	1
gb|AGN_RNC021xf21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	418.45	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	1779.75	1
Unknown	28.42	1
gb|KL4B.103J22F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103J22, mRN	427.77	1
gb|KT7B.103B20F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.103B20, mRI	20.15	1
gb|TT-48_F19 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	26.67	1
tc|Rep: Chromosome chr14 scaffold_26, whole genome shotgun sequence - Vitis vi	9414.19	1
gb|CHO_SL007xk13f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	31.74	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	44.55	1
gb|TT-31_B14 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	57.42	1
gb|KT7B.103G18F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.103G18, mR	32.39	1
gb|KN6B.115H07F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.115H07, n	60.09	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	25.42	1
gb|ntsm1 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [EB	101.57	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	1592.78	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	566.64	1
gb|KT7C.102J01F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102J01, mRN	70.52	1
gb|KN6B.100O15F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100O15, r	40.59	1
Unknown	151.67	1
tc|Rep: ATP synthase subunit d, mitochondrial - Arabidopsis thaliana (Mouse-ear cr	462.03	1
Unknown	17084.85	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	169.84	1

gb|TT-32_M09 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA se	223.15	1
gb|AGN_RNC023xk18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	23	1
tc|Rep: Ribosomal protein L11-like - Nicotiana tabacum (Common tobacco), compl	402.58	1
tc|Rep: Plastoglobulin-1, chloroplast precursor - Pisum sativum (Garden pea), parti	145.98	1
Unknown	9461.27	1
gb|KG9B.005P17F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005P17, m	1819.8	1
Unknown	57.59	1
tc|Rep: COME operon protein 1 - Streptococcus pyogenes serotype M4 (strain MG	460.32	1
gb|KR2B.112K16F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.112K16, m	140.38	1
tc|Rep: Oxysterol-binding protein, expressed - Oryza sativa subsp. japonica (Rice), p	24.24	1
Unknown	116.09	1
gb|TT-11_D05 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	26.66	1
gb|KN6B.102M01F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102M01,	38362.5	1
tc|Rep: NADH dehoydrogenase - Arabidopsis thaliana (Mouse-ear cress), partial (74	331.15	1
gb|KL4B.101G23F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101G23, m	61.94	1
gb|KP1B.110N11F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110N11, m	8033.46	1
tc|Rep: Chromosome undetermined scaffold_129, whole genome shotgun sequenc	189.92	1
gb|KN6B.102D06F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102D06, n	83.2	1
Unknown	22.5	1
Unknown	108.7	1
gb|TT-07_E11 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	79.55	1
gb|TT-36_E22 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	151.8	1
gb|TT-29_L17 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	22.39	1
tc|Rep: DnaJ-like protein - Glycine max (Soybean), partial (55%) [TC64413]	799.19	1
tc|Rep: Ly200 protein - Capsicum annuum (Bell pepper), complete [TC52727]	58.31	1
gb|KR3B.111A19F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111A19, m	32.76	1
Unknown	211.73	1
tc|Rep: Chromosome undetermined scaffold_235, whole genome shotgun sequenc	25.42	1
gb|KL5B.105P01F.060224T7 KL5B Nicotiana tabacum cDNA clone KL5B.105P01, mR	146.43	1
gb|N.tabacum mRNA for 14-3-3-like protein (A) [Y11212]	1237.08	1
gb|AGN_PNL219af1_f4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	1599.38	1
tc|Rep: Vesicle transport v-SNARE 11-like - Solanum tuberosum (Potato), complete	766.28	1
tc|Rep: Chromosome chr10 scaffold_76, whole genome shotgun sequence - Vitis vi	4428.33	1
gb|KR3B.107K23F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.107K23, m	36.18	1

Unknown	20.97	1
tc|Rep: Zinc finger A20 and AN1 domain-containing stress-associated protein 8 - Or	3572.72	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	248.11	1
Unknown	19.11	1
gb|KP1B.113H03F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.113H03, m	31.85	1
tc|Rep: Bax inhibitor - Solanum lycopersicum (Tomato) (Lycopersicon esculentum),	1147.59	1
Unknown	179.48	1
Unknown	355.61	1
Unknown	42.04	1
gb|KR3B.111G08F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111G08, m	1176.43	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	588.55	1
gb|TT-36_L19 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	27.92	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC3-42-285, cultivar Bright Yellow 2	440.3	1
Unknown	34.79	1
gb|AM803406 seedling library, SL Nicotiana tabacum cDNA clone nt002129011, m	21.84	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	1236.34	1
tc|Rep: Chromosome chr18 scaffold_24, whole genome shotgun sequence - Vitis vi	58.03	1
gb|AGN_ELP025xh21f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	1844.06	1
gb|AGN_RNC030xe05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	58.97	1
gb|TL13.102M08F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.102M08, m	840.89	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	593.41	1
gb|KN6B.103B02F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103B02, m	3371.41	1
Unknown	46.71	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	19.1	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	212.82	1
gb|AGN_ELP021xe05f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	54.03	1
Unknown	6612.04	1
tc|Rep: Adenylate kinase, chloroplast - Zea mays (Maize), partial (91%) [TC42642]	25.83	1
gb|KR3B.105E15F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.105E15, m	107.18	1
gb|AM818174 seedling library, SL Nicotiana tabacum cDNA clone nt002012037, m	50.09	1
Unknown	219.72	1
gb|AGN_RNC022xi06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	63.19	1
gb|FS423755 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	2686.27	1
tc|Rep: Fumarylacetoacetase - Medicago truncatula (Barrel medic), partial (73%) [T	84.27	1

Unknown	481.87	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	137.96	1
tc|Rep: Diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase - Lupinus angustifolius (	380.45	1
tc|Rep: Papain-like cysteine peptidase XBCP3 - Arabidopsis thaliana (Mouse-ear cre	7651.71	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	29.77	1
gb|KN6B.104D18F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104D18, m	518.81	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	24.99	1
tc|Rep: Chromosome chr6 scaffold_28, whole genome shotgun sequence - Vitis vin	532.04	1
Unknown	24.44	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	508.88	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	27.49	1
gb|TOBESTR130D05 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	1109.41	1
gb|BP534995 MAT005 Nicotiana tabacum cDNA clone BY34204, mRNA sequence [	133.99	1
Unknown	80.35	1
gb|TT-39_L16 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	127.41	1
gb|AGN_PNL225af1_b9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	26.8	1
gb|KP1B.104N22F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104N22, m	7627.96	1
gb|KG9B.002L06F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002L06, m	1604.2	1
Unknown	625.82	1
tc|Rep: Transcription factor APFI-like - Solanum tuberosum (Potato), partial (97%) [	412.67	1
Unknown	7606.1	1
gb|TT-18_O23 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	33.41	1
tc|Rep: Mitogen-activated protein kinase - Solanum lycopersicum (Tomato) (Lycope	743.36	1
Unknown	29.59	1
gb|KP1B.102C20F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102C20, m	366.11	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	1521.51	1
tc|Rep: Chromosome chr19 scaffold_126, whole genome shotgun sequence - Vitis	30.99	1
tc|Rep: 60S ribosomal protein L19 - Capsicum annuum (Bell pepper), partial (32%) [	117.15	1
tc|Rep: Extensin - Nicotiana tabacum (Common tobacco), partial (98%) [TC76880]	176.91	1
gb|TT-09_B16 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	222.1	1
gb|AGN_PNL229af1_a9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	133.67	1
gb|TT-08_L08 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sequ	102.21	1
Unknown	63.83	1
tc|Rep: Calcium-dependent protein kinase 8 - Nicotiana plumbaginifolia (Leadwort-	3284.45	1

Unknown	970.39	1
tc|Rep: Chromosome undetermined scaffold_123, whole genome shotgun sequenc	19.17	1
Unknown	80.48	1
gb|AGN_ELP018xl03f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	18.01	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (43%) [TC5	153.02	1
gb|KR3B.111M22F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111M22,	622.56	1
gb|AGN_RPC017xk02f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	67.81	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT2-14-500, cultivar Bright Yellow 2	33.92	1
gb|TT-22_G14 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	216.27	1
gb|AGN_RNC108xf20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	58.83	1
tc|Rep: Chromosome chr13 scaffold_210, whole genome shotgun sequence - Vitis	48.9	1
Unknown	24.93	1
Unknown	18.27	1
Unknown	41	1
gb|FTP P15 Tobacco stigma cDNA Nicotiana tabacum cDNA similar to PIP1 aquapor	134.99	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	491.73	1
Unknown	3086.38	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	91.71	1
gb|KF8C.103F17F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103F17, mRN	92.58	1
gb|KF8C.105J06F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105J06, mRN	2922.38	1
gb|KR2B.101F09F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.101F09, m	14946.2	1
tc|Rep: CXE carboxylesterase - Actinidia deliciosa (Kiwi), partial (57%) [TC50334]	55.64	1
Unknown	28.56	1
gb|KP1B.104H11F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104H11, m	73.91	1
gb|AM826041 seedling library, SL Nicotiana tabacum cDNA clone nt002236018, m	34.05	1
tc|Rep: 40S ribosomal protein S4 - Solanum tuberosum (Potato), complete [TC4292	27.61	1
gb|AGN_RPC020xp05f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	198.82	1
tc|Rep: Chromosome chr9 scaffold_49, whole genome shotgun sequence - Vitis vin	338.2	1
tc|Rep: FACT complex subunit SPT16 - Zea mays (Maize), partial (46%) [TC57557]	437.44	1
tc|Rep: Alpha chain of nascent polypeptide associated complex - Nicotiana benthar	107.08	1
gb|KR3B.114C14F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.114C14, m	51.55	1
tc|Rep: Hexokinase 6 - Nicotiana tabacum (Common tobacco), complete [TC53358]	25.11	1
tc|Rep: Cullin 1A - Nicotiana tabacum (Common tobacco), partial (17%) [TC43631]	1255.82	1
tc|Rep: Acyl-[acyl-carrier-protein] desaturase, chloroplast precursor - Solanum tub	739.62	1

tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	42.88	1
gb|KL5B.117D22F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.117D22, mF	43.7	1
Unknown	32.66	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	25.35	1
tc|Rep: MGC84401 protein - Xenopus laevis (African clawed frog), partial (5%) [TC7.	23.98	1
tc|Rep: STYLOSA protein - Antirrhinum majus (Garden snapdragon), partial (45%) [T	185.6	1
gb|KT7C.110F01F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110F01, mRN	932.43	1
gb|KL4B.104F08F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104F08, mR	182.24	1
tc|Rep: Chromosome undetermined scaffold_69, whole genome shotgun sequence	262.78	1
gb|AM844046 seedling library, SL Nicotiana tabacum cDNA clone nt002335074, mF	300.62	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT12-4-420, cultivar Bright Yellow 2	64.49	1
Unknown	27.5	1
tc|Rep: Phosphosulfolactate synthase-related protein - Solanum lycopersicum (Tom	312.54	1
gb|KL4B.112M18F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112M18, m	49.25	1
gb|KG9B.001M04F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001M04,	26.76	1
Unknown	31.35	1
gb|KR3B.105E21F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.105E21, ml	69.79	1
gb|AGN_PNL232ar1_h2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	34.76	1
gb|KP1B.108H05F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108H05, m	108.23	1
gb|KP1B.037C20F.050623T7 KP1B Nicotiana tabacum cDNA clone KP1B.037C20, ml	80.13	1
gb|KR2B.115P20F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115P20, m	2000.42	1
gb|KF8B.100G01F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100G01, mR	185.11	1
gb|Nicotiana tabacum mRNA for NAD-dependent isocitrate dehydrogenase, clone p	266.61	1
tc|Rep: Jasmonic acid-amino acid-conjugating enzyme - Nicotiana attenuata, compl	24.75	1
tc|Rep: Chromosome undetermined scaffold_143, whole genome shotgun sequenc	87.22	1
gb|AGN_RPC015xi11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	51.1	1
gb|KF8C.102M10F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102M10, mF	43	1
gb|KR2B.001C18F.050815T7 KR2B Nicotiana tabacum cDNA clone KR2B.001C18, m	106.26	1
gb|BP133968 MAT001 Nicotiana tabacum cDNA clone BY6288, mRNA sequence [BF	21.23	1
Unknown	23.89	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	105.79	1
gb|KN6B.103H03F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103H03, n	189.99	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	149.47	1
tc|Rep: Calcium-dependent protein kinase 4 - Capsicum annuum (Bell pepper), part	22.48	1

Unknown	111.18	1
gb|TT-25_O16 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	2972.62	1
Unknown	232	1
gb|KG9B.003L14F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003L14, m	85.35	1
tc|Rep: GTP cyclohydrolase I - Solanum lycopersicum (Tomato) (Lycopersicon escul	961.4	1
Unknown	1566.41	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	11168.3	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	2827.95	1
tc|Rep: Chromosome chr3 scaffold_117, whole genome shotgun sequence - Vitis vi	59.71	1
gb|Nicotiana tabacum Rac-like GTPase 1 mRNA, complete cds [AY029330]	1793.21	1
tc|GB|AJ291736.1|CAC43321.1 putative beta proteasome subunit [Nicotiana tabac	29.33	1
tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin	25.62	1
gb|KN6B.104G15F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104G15,	867.78	1
gb|KF8B.202A04F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202A04, mR	42020.05	1
Unknown	74.57	1
gb|KG9B.002E23F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002E23, m	135.86	1
Unknown	349.55	1
Unknown	22.45	1
Unknown	514.57	1
tc|Rep: Endoplasmin homolog precursor - Catharanthus roseus (Rosy periwinkle) (	559.17	1
gb|AGN_RNC030xn21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	24.58	1
gb|Nicotiana tabacum peroxisomal targeting signal 1 receptor (PEX5) mRNA, comp	91.42	1
gb|AGN_PNL212af1_e7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	1565.09	1
gb|KP1B.108B20F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108B20, m	739.37	1
Unknown	9069.23	1
tc|Rep: Ubiquitin carrier protein - Vitis vinifera (Grape), complete [TC44653]	567.74	1
gb|AM799834 COL, cold overnight library Nicotiana tabacum cDNA clone nt006142	26.23	1
Unknown	272.85	1
gb|KP1B.037G05F.050623T7 KP1B Nicotiana tabacum cDNA clone KP1B.037G05, m	101.74	1
gb|FS412805 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	141.21	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	2761.69	1
gb|AM784309 DL, diurnal library Nicotiana tabacum cDNA clone nt005204030, mR	33.6	1
tc|Rep: Chromosome undetermined scaffold_129, whole genome shotgun sequenc	213.77	1
tc|Rep: Glyceraldehyde-3-phosphate dehydrogenase - Capsicum annuum (Bell pep	48.64	1

gb|KG9B.104N24F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104N24, n	66.58	1
gb|EST_FLW002xj10f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [EH	24.12	1
gb|KL4B.108H18F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108H18, mF	94.73	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	32.93	1
Unknown	40.19	1
gb|KG9B.103D08F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103D08, n	49.8	1
gb|KL4B.101G02F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101G02, mF	36.53	1
tc|Rep: Mitochondrial F1-ATPase gamma subunit - Ipomoea nil (Japanese morning	408.29	1
Unknown	65.56	1
gb|FS435586 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	23.83	1
gb|KR3B.101F03F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101F03, mF	79.65	1
Unknown	45.48	1
gb|Nicotiana tabacum S-adenosyl-L-methionine synthetase (SAMS) mRNA, complet	3262.46	1
gb|KP1B.102J04F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102J04, mR	28.65	1
gb|KL5B.118K17F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.118K17, mR	81.89	1
gb|AGN_RNC014xk11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	21.5	1
gb|TT-40_E03 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	35.09	1
Unknown	21.12	1
gb|KT7C.110M10F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110M10, ml	1136.67	1
gb|KT7C.109M07F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109M07, ml	209.48	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	917.61	1
Unknown	38.77	1
Unknown	62.12	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	18.17	1
gb|AGN_RNC007xc16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	184.67	1
gb|TT-38_N12 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	476.88	1
Unknown	31.69	1
Unknown	91.4	1
Unknown	15785.45	1
gb|AGN_ELP005xo16f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	29	1
Unknown	134.72	1
Unknown	27.82	1
gb|KF8C.103I12F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103I12, mRN	43.45	1
tc|Rep: Heat shock cognate 70 kDa protein - Petunia hybrida (Petunia), partial (14%	45.23	1

Unknown	19.66	1
Unknown	23.73	1
Unknown	33.73	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	120.61	1
gb|KG9B.004G03F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004G03, n	399.17	1
Unknown	22.83	1
tc|Rep: Calmodulin-related protein - Arabidopsis thaliana (Mouse-ear cress), partia	579.44	1
tc|Rep: 40S ribosomal protein S9 - Catharanthus roseus (Rosy periwinkle) (Madagas	99.93	1
gb|Nicotiana tabacum calcium-dependent protein kinase-like mRNA, partial sequer	26.83	1
gb|KG9B.104F18F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104F18, m	77.78	1
gb|EST_FLW001xc13f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [EI	1161.86	1
gb|TT-29_J20 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	121.19	1
Unknown	507.15	1
tc|Rep: Rac-like GTP-binding protein RHO1 precursor - Pisum sativum (Garden pea)	1012.65	1
gb|KL4B.105A08F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105A08, mF	623.19	1
tc|Rep: 40S ribosomal protein S9 - Catharanthus roseus (Rosy periwinkle) (Madagas	38.55	1
gb|AGN_RNC008xp03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1178.39	1
gb|Nicotiana tabacum NtCK2a2 mRNA for casein kinase 2 catalytic subunit, comple	87.31	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	28313.6	1
Unknown	416.11	1
tc|Rep: YA4 - Antirrhinum majus (Garden snapdragon), partial (50%) [TC77063]	80.32	1
tc|Rep: Eukaryotic translation initiation factor 4E - Solanum lycopersicum (Tomato)	59.14	1
Unknown	19.11	1
gb|KF8C.101B06F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101B06, mRN	244.3	1
Unknown	93.74	1
gb|TT-25_N08 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	27.28	1
gb|Nicotiana tabacum mRNA for protein kinase 2 (pk2 gene) [AJ608157]	2875.61	1
gb|CHO_SL023xf22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	1074.76	1
Unknown	27.19	1
Unknown	153.85	1
gb|CHO_SL007xc15f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	26.14	1
gb|KL5B.112P02F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.112P02, mR	717.6	1
gb|KT7C.110I19F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110I19, mRN	195.55	1
Unknown	43.64	1

gb|Nicotiana tabacum SAICAR synthetase (purC) mRNA, complete cds [AY429423]	29.1	1
Unknown	649.83	1
Unknown	2745.85	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	30.52	1
tc|Rep: NtK-1-like - Solanum tuberosum (Potato), partial (41%) [TC67891]	5759.12	1
gb|AGN_PNL224af1_a4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	118.48	1
Unknown	3220.19	1
gb|KL5B.105J24F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.105J24, mRN	44.75	1
Unknown	563.59	1
tc|Rep: L-aspartate oxidase-like protein - Arabidopsis thaliana (Mouse-ear cress), pa	62.88	1
tc|Rep: Cytochrome b-c1 complex subunit Rieske-2, mitochondrial precursor - Nico	15945.75	1
Unknown	60.13	1
gb|BP534468 MAT005 Nicotiana tabacum cDNA clone BY33047, mRNA sequence [	1282.8	1
Unknown	21.39	1
gb|basic chitinase [Nicotiana tabacum=tobacco, cv Samsun nn, floral bud day 7 exp	218.48	1
Unknown	54.43	1
Unknown	31.68	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	55.73	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	22.16	1
tc|Rep: 4-coumarate--CoA ligase 1 - Nicotiana tabacum (Common tobacco), partial	16.34	1
gb|Nicotiana tabacum geranylgeranylated protein NTGP2 mRNA, complete cds [U6	3136.48	1
Unknown	17.15	1
Unknown	21.61	1
gb|N.tabacum mRNA for pyruvate kinase [Z29492]	580.34	1
Unknown	25.08	1
gb|KT7B.100B14F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100B14, mRN	3252.93	1
tc|Rep: Protein phosphatase inhibitor - Medicago truncatula (Barrel medic), partial	27.72	1
tc|Rep: DEM2 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), partial	46.89	1
gb|KF8B.202A23F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202A23, mRN	5422.48	1
gb|KF8C.104O14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104O14, mR	269.06	1
gb|KR3B.103D10F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.103D10, m	141.78	1
gb|KL4B.104G07F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104G07, mR	500.54	1
gb|TOBESTR018E07 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	30.46	1
Unknown	64.44	1

gb|KP1B.107C03F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107C03, m	140.89	1
gb|TL13.110I04F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.110I04, mRN	275.36	1
gb|AGN_RNC116xm16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	37.56	1
Unknown	39.52	1
tc|Rep: SUI1 protein - Coffea arabica (Coffee), complete [TC50228]	1030.49	1
tc|Rep: Os03g0719500 protein - Oryza sativa subsp. japonica (Rice), partial (52%) [T	27.03	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	222.19	1
gb|KF8C.106O13F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106O13, mR	90.8	1
Unknown	3897.14	1
Unknown	420.18	1
Unknown	50.49	1
Unknown	25.35	1
Unknown	127.81	1
tc|Rep: Deacetylase-like protein - Solanum tuberosum (Potato), partial (68%) [TC44	530.37	1
gb|KF8C.101E14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101E14, mRN	27125.95	1
Unknown	48353.8	1
gb|KP1B.104P01F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104P01, m	29.09	1
Unknown	25.73	1
tc|Rep: MRNA, , clone: RAFL25-03-N20 - Arabidopsis thaliana (Mouse-ear cress), pa	258.52	1
tc|Rep: Polyubiquitin - Fragaria ananassa (Strawberry), partial (60%) [TC50969]	3087.15	1
tc|Rep: Granule-bound starch synthase 1, chloroplast precursor - Solanum tuberos	137.08	1
gb|N.tabacum mRNA for caffeoyl-CoA O-methyltransferase [Z56282]	255.44	1
Unknown	71.98	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT4-24-270, cultivar Bright Yellow 2	1876.28	1
gb|20.2H05 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5'	68.43	1
Unknown	5600.42	1
Unknown	86.6	1
Unknown	530.68	1
gb|KF8C.104K05F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104K05, mRN	27.35	1
gb|KL4B.101E04F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101E04, mR	88.05	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	85.67	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	247.26	1
tc|Rep: Glycylpeptide N-tetradecanoyltransferase - Vitis vinifera (Grape), partial (9	1095.69	1
Unknown	174.36	1

gb|CHO_SL023xf22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	882.74	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (86%) [TC6	100.69	1
tc|Rep: Translationally-controlled tumor protein homolog - Nicotiana tabacum (Co	19469.9	1
tc|Rep: Lecithine cholesterol acyltransferase-like protein - Medicago truncatula (Ba	7433.61	1
tc|Rep: Heat shock protein 82 - Nicotiana tabacum (Common tobacco), partial (19	346.3	1
Unknown	3760.65	1
gb|Nicotiana tabacum cDNA-AFLP fragment H-N_BT3M14-319 sequence [DQ4601	21.56	1
Unknown	27.13	1
gb|KP1B.001O09F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001O09, m	27.47	1
gb|AGN_RNC004xe11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	220.6	1
tc|Rep: Ubiquitin carboxyl-terminal hydrolase - Vitis vinifera (Grape), partial (18%)	293.69	1
gb|TT-22_M06 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequen	451.09	1
tc|Rep: Chromosome chr1 scaffold_135, whole genome shotgun sequence - Vitis vi	89.56	1
gb|AGN_PNL223df1_b2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	107.03	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	110.09	1
gb|KN6B.105G11F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105G11,	239.97	1
gb|KN6B.009B01F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009B01,	459.9	1
Unknown	97.29	1
gb|KL4B.103I17F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103I17, mR	2757.01	1
gb|CHO_SL014xn09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	49.21	1
gb|KG9B.105I02F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105I02, m	193.21	1
gb|KG9B.102M10F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102M10,	1152.34	1
gb|KL4B.103B21F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103B21, m	951.23	1
gb|Nicotiana tabacum mRNA for peroxidase, complete cds, clone:NTPXC7.5 [AB04	24.63	1
tc|Rep: NADH-ubiquinone oxidoreductase chain 1 - Naegleria gruberi, partial (6%)	61.81	1
gb|BP533599 MAT005 Nicotiana tabacum cDNA clone BY30291, mRNA sequence	19.45	1
tc|Rep: Inositol-3-phosphate synthase - Nicotiana tabacum (Common tobacco), par	3264.47	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	257.44	1
gb|TT-19_O08 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	202.99	1
tc|Rep: Elicitor-inducible cytochrome P450 - Nicotiana tabacum (Common tobacco	32.53	1
gb|KG9B.104B19F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104B19,	17.23	1
tc|Rep: Ribosomal protein L9 - Bigelowiella natans (Pedinomonas minutissima) (Chl	52.11	1
Unknown	31.52	1
tc|Rep: Sensor protein - Ralstonia eutropha (strain ATCC 17699 / H16 / DSM 428 /	176.32	1

tc|Rep: Chromosome undetermined scaffold_252, whole genome shotgun sequenc	19090.5	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (82%) [TC4	237	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT21-1-268, cultivar Bright Yellow 2	192.66	1
Unknown	54.68	1
Unknown	2065.87	1
gb|KG9B.002N08F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002N08,	136.51	1
tc|Rep: Cytochrome c - Oryza sativa subsp. indica (Rice), complete [TC58147]	60.93	1
Unknown	661.64	1
Unknown	26.47	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	86.47	1
gb|KN6B.009K14F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009K14,	2291.34	1
gb|AGN_RPC014xi23f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	100.09	1
Unknown	377.32	1
tc|Rep: Chromosome undetermined scaffold_466, whole genome shotgun sequenc	517.12	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	479	1
gb|N.tabacum SUT1a mRNA for sucrose transporter [X82276]	41.5	1
Unknown	104.77	1
gb|FS415057 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	248.32	1
gb|KT7C.102F03F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102F03, mR	93.19	1
tc|Rep: Heat stress transcription factor B-2a - Arabidopsis thaliana (Mouse-ear cres	124.38	1
Unknown	144.35	1
tc|Rep: Os05g0119300 protein - Oryza sativa subsp. japonica (Rice), partial (61%) [T	4649.29	1
tc|Rep: Erwinia induced protein 2 - Solanum tuberosum (Potato), complete [TC565	1534.08	1
gb|KG9B.103K24F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103K24,	508.28	1
tc|Rep: Salt-induced AAA-Type ATPase - Mesembryanthemum crystallinum (Comm	249.75	1
gb|KL4B.106B16F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106B16, m	94.28	1
Unknown	23.08	1
gb|KL5B.116A22F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.116A22, m	32.51	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	185.37	1
tc|Rep: At4g27040 - Arabidopsis thaliana (Mouse-ear cress), complete [TC56578]	90.77	1
Unknown	117.15	1
gb|AGN_RPC004xo04f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	91.29	1
tc|Rep: 6-phosphogluconolactonase - Oryza brachyantha, partial (82%) [TC41006]	35.34	1
gb|KL4B.102P19F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102P19, m	21.2	1

Unknown	29.64	1
tc|Rep: Ribosomal protein L41 - Candida maltosa (Yeast), complete [TC60925]	38.69	1
tc|Rep: Carbonic anhydrase, chloroplast precursor - Nicotiana tabacum (Common t	428.45	1
gb|TL13.105J04F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.105J04, mRN	187.9	1
Unknown	8301.91	1
Unknown	3979.22	1
gb|KL4B.100B12F.050922T7 KL4B Nicotiana tabacum cDNA clone KL4B.100B12, mR	756.17	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	2121.46	1
gb|KL5B.115I05F.060302T7 KL5B Nicotiana tabacum cDNA clone KL5B.115I05, mRN	7631.19	1
gb|KT7C.104L17F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104L17, mRN	722.26	1
gb|Nicotiana tabacum small ras-related protein (Ran-B1) mRNA, complete cds [L16	822.88	1
Unknown	25.06	1
gb|AGN_RNC001xf09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	220.39	1
gb|CHO_SL013xd09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	84.09	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	19.69	1
gb|BP131286 MAT001 Nicotiana tabacum cDNA clone BY3322, mRNA sequence [B	472.56	1
gb|AGN_RNC111xc18r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	22.3	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	195.64	1
gb|AGN_ELP014xc17f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	49.56	1
Unknown	32.59	1
Unknown	99.96	1
Unknown	1053.08	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	93.22	1
gb|Nicotiana tabacum mRNA for calmodulin NtCaM7, complete cds [AB050843]	1694.48	1
Unknown	266.76	1
tc|Rep: Eukaryotic translation initiation factor 5A-1/2 - Solanum tuberosum (Potat	1139.55	1
gb|KL4B.104K08F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104K08, mR	1128.47	1
tc|Rep: Potyvirus VPg interacting protein - Nicotiana benthamiana, partial (43%) [T	724.39	1
tc|Rep: Proteasome subunit beta type-6 precursor - Nicotiana tabacum (Common t	516.33	1
gb|Nicotiana tabacum SR1 Nt-rab7c mRNA, complete cds [L29276]	113.99	1
gb|AGN_PNL222ar1_c5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	94.82	1
tc|Rep: Chemokine receptor 4 - Hydromantes italicus (Italian cave salamander), par	165.68	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	136.56	1
tc|Rep: SPFH domain / Band 7 family protein - Solanum demissum (Wild potato), pa	3940.94	1

gb|CHO_SL007xk19f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	741.51	1
gb|KN6B.101I21F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101I21, mR	40.72	1
Unknown	20.43	1
tc|Rep: 40S ribosomal protein S9 - Catharanthus roseus (Rosy periwinkle) (Madagas	127.52	1
Unknown	23.29	1
gb|CHO_SL024xb11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	39.16	1
Unknown	24.33	1
Unknown	2170.52	1
gb|KP1B.111F04F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.111F04, mR	453.43	1
gb|BP534671 MAT005 Nicotiana tabacum cDNA clone BY33256, mRNA sequence [E	8873.03	1
Unknown	49.05	1
gb|KG9B.102G11F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102G11, m	104.81	1
Unknown	111.9	1
gb|KG9B.106L19F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106L19, m	144.4	1
Unknown	152.83	1
Unknown	25.91	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	730.19	1
tc|Rep: Nuclear transport factor 2 - Arabidopsis thaliana (Mouse-ear cress), partial	693.5	1
gb|TL13.101P16F.060313T7 TL13 Nicotiana tabacum cDNA clone TL13.101P16, mR	51.41	1
tc|Rep: Arabinogalactan-protein precursor - Nicotiana alata (Winged tobacco) (Pers	32.71	1
gb|AGN_RNC104xf12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	58.06	1
tc|Rep: Non-cell-autonomous heat shock cognate protein 70 - Cucurbita maxima (P	7860.26	1
gb|Nicotiana tabacum NT3 mRNA, complete cds [AF124369]	305.87	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	25.25	1
gb|KP1B.104I19F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104I19, mR	212.76	1
Unknown	52.53	1
gb|Nicotiana tabacum CaMB-channel protein mRNA, complete cds [U65390]	137.64	1
gb|KG9B.106E06F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106E06, m	13354.8	1
gb|KL4B.102L09F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102L09, mR	1193.53	1
Unknown	32.09	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	19.08	1
gb|Nicotiana tabacum phospholipase C2 mRNA, complete cds [AF223573]	64.58	1
Unknown	213.48	1
Unknown	183.29	1

gb|KG9B.001G16F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001G16, n	508.73	1
gb|TT-03_E05 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	7691.17	1
tc|Rep: Chromosome chr1 scaffold_136, whole genome shotgun sequence - Vitis vi	310.92	1
tc|Rep: RAD23-like - Solanum tuberosum (Potato), complete [TC48167]	44.83	1
gb|Nicotiana tabacum mRNA for sulfite reductase, complete cds [D83583]	3216.16	1
gb|AGN_RNC015xl13f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	93.71	1
gb|AM820007 seedling library, SL Nicotiana tabacum cDNA clone nt002065007, mR	95.53	1
gb|N.tabacum mRNA ap24 [X65700]	29.5	1
Unknown	199.08	1
tc|Rep: Chromosome undetermined scaffold_129, whole genome shotgun sequenc	1662.44	1
gb|AM786095 DL, diurnal library Nicotiana tabacum cDNA clone nt005209016, mR	50.46	1
gb|AGN_PNL221dr1_a10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRN	38.02	1
Unknown	72.77	1
tc|Rep: Chromosome chr4 scaffold_83, whole genome shotgun sequence - Vitis vin	51.99	1
tc|Rep: Proteasome subunit beta type-1 - Petunia hybrida (Petunia), complete [TC4	52.56	1
gb|TT-21_C04 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	25.72	1
gb|KL4B.104P10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104P10, mR	55.18	1
tc|Rep: Ubiquitin carboxyl-terminal hydrolase - Vitis vinifera (Grape), partial (6%) [T	113.14	1
gb|KT7C.108N20F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108N20, mR	522.97	1
gb|KL4B.104J01F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104J01, mR	189.41	1
gb|CHO_SL008xj22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1174.55	1
gb|AGN_ELP008xl06f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	104.1	1
Unknown	63.56	1
Unknown	61.57	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	272.22	1
gb|KG9B.102M06F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102M06,	37.2	1
Unknown	36.87	1
gb|KP1B.105L07F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105L07, mR	509.6	1
Unknown	96.28	1
gb|AM827414 DL, diurnal library Nicotiana tabacum cDNA clone nt005243064, mR	31.54	1
gb|TT-49_O20 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	5970.83	1
gb|KT7B.107O10F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107O10, mR	275.12	1
gb|KT7C.109D22F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109D22, mR	87.74	1
tc|Rep: S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC) [C	10290.05	1

tc|Rep: Adenylate kinase A - Oryza sativa subsp. japonica (Rice), complete [TC4219	56.83	1
gb|AGN_RNC026xj22f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	187.97	1
tc|Rep: Malate dehydrogenase - Solanum tuberosum (Potato), partial (62%) [TC454	744.69	1
gb|BP526819 MAT001 Nicotiana tabacum cDNA clone BY11566, mRNA sequence [	18.26	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	2919.91	1
tc|Rep: Chromosome undetermined scaffold_30, whole genome shotgun sequence	470.69	1
tc|Rep: Os01g0332900 protein - Oryza sativa subsp. japonica (Rice), partial (45%) [T	54.16	1
tc|Rep: Chromosome chr1 scaffold_84, whole genome shotgun sequence - Vitis vin	495.99	1
Unknown	231.28	1
gb|Nicotiana tabacum JEI1 mRNA for hypothetical protein, complete cds [AB30077	55.17	1
tc|Rep: RNA-binding protein precursor - Nicotiana tabacum (Common tobacco), co	22.09	1
Unknown	65.26	1
tc|Rep: C-type cytochrome biogenesis protein - Glycine max (Soybean), partial (75	23.3	1
gb|BP132437 MAT001 Nicotiana tabacum cDNA clone BY4605, mRNA sequence [B	92.75	1
tc|Rep: Chromosome chr18 scaffold_59, whole genome shotgun sequence - Vitis vi	1114.22	1
gb|KR3B.110D19F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110D19, m	32.6	1
Unknown	1173.03	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	58.44	1
tc|Rep: 3-hydroxy-3-methylglutaryl coenzyme A synthase - Solanum lycopersicum (	979.8	1
Unknown	95.87	1
gb|Nicotiana tabacum mRNA for bromodomain-containing RNA-binding protein 1 (	1275.09	1
tc|Rep: Uncharacterized 12.4 kDa protein in 33 kDa protein region - Human adenov	41.19	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	435.17	1
tc|Rep: HrpN-interacting protein from Malus - Malus domestica (Apple) (Malus syl	17.28	1
tc|Rep: ER6 protein - Solanum lycopersicum (Tomato) (Lycopersicon esculentum),	192.39	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	401.29	1
Unknown	988.72	1
gb|AGN_RNC012xc03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	59.46	1
Unknown	22.42	1
gb|KG9B.005A12F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005A12,	212.08	1
gb|BP526949 MAT001 Nicotiana tabacum cDNA clone BY11708, mRNA sequence [	44.76	1
tc|Rep: Granule-bound starch synthase 1, chloroplast precursor - Solanum tuberos	384.45	1
tc|Rep: ATP-dependent Clp protease proteolytic subunit - Fritillaria agrestis (Stinkb	84.65	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	91.51	1

tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	983.35	1
gb|18.2A08 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5'	29.44	1
tc|Rep: 40S ribosomal protein S25 - Solanum lycopersicum (Tomato) (Lycopersicon	184.55	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	406.61	1
tc|Rep: Phosphoglucomutase, cytoplasmic - Solanum tuberosum (Potato), partial (4	104.71	1
Unknown	107.81	1
Unknown	697.16	1
tc|Rep: Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K10D20 - Ar	82.56	1
gb|KN6B.103M17F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103M17,	18.12	1
gb|AM789623 seedling library, SL Nicotiana tabacum cDNA clone nt002159082, mR	523	1
tc|Rep: Mitochondrial processing peptidase - Solanum tuberosum (Potato), partial (	1102.38	1
Unknown	58.28	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	24.33	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	131.5	1
gb|BP525818 MAT001 Nicotiana tabacum cDNA clone BY10512, mRNA sequence [B	104.13	1
Unknown	123.83	1
gb|Nicotiana tabacum DnaJ-like protein mRNA, complete cds [AF191497]	236.42	1
gb|AGN_ELP011xp07f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	538.06	1
gb|KL5B.106L07F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.106L07, mRN	59.4	1
Unknown	23.4	1
gb|AGN_RPC005xg20f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	145.65	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	156.98	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	151.72	1
Unknown	532.88	1
gb|Nicotiana tabacum arm repeat-containing protein mRNA, complete cds [AY2192	115.35	1
gb|Nicotiana tabacum cinnamyl alcohol dehydrogenase 1 (CAD1-1) mRNA, complet	17.44	1
tc|Rep: Drm3-like protein - Solanum tuberosum (Potato), partial (88%) [TC52491]	42.93	1
gb|KG9B.005F09F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005F09, m	754.71	1
gb|KP1B.105G14F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105G14, m	86.38	1
gb|TT-29_E24 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	370.8	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	562.3	1
gb|KN6B.100K06F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100K06, m	28.75	1
gb|TT-10_L06 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	19.71	1
gb|KF8C.106B20F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106B20, mRN	19.56	1

gb|KP1B.105P05F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105P05, mI	726.09	1
gb|CHO_SL005xe14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	17.65	1
Unknown	240.24	1
tc|Rep: Chromosome chr11 scaffold_56, whole genome shotgun sequence - Vitis vi	803.43	1
tc|Rep: Rar1 - Nicotiana tabacum (Common tobacco), complete [TC40955]	25.14	1
gb|KL4B.104P21F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104P21, mR	251.57	1
Unknown	610.01	1
gb|KG9B.004F01F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004F01, m	25.72	1
tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin	4181.15	1
tc|Rep: Fasciclin-like arabinogalactan protein 3 - Gossypium hirsutum (Upland cotto	52.34	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	107.03	1
tc|Rep: NADH glutamate synthase precursor - Phaseolus vulgaris (Kidney bean) (Fre	30.3	1
Unknown	22.64	1
gb|AGN_PNL214ar1_d9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	108.81	1
gb|CHO_SL009xh09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	59.58	1
gb|Nicotiana tabacum partial mRNA for serine acetyltransferase 4 (sat4 gene) [AJ4	210.54	1
Unknown	1743.2	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	1869.62	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	536.45	1
Unknown	25.94	1
gb|KR3B.103A01F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.103A01, m	89.25	1
gb|KG9B.002C03F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002C03, m	467.63	1
gb|TT-49_L09 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	32.69	1
tc|Rep: Chromosome undetermined scaffold_91, whole genome shotgun sequence	481.74	1
gb|KG9B.003N16F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003N16, n	105.8	1
gb|AGN_PNL230bf1_e6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	4532.15	1
tc|Rep: Protein kinase - Carica papaya (Papaya), partial (11%) [TC66002]	100.25	1
tc|Rep: Nucleic acid binding protein - Nicotiana tabacum (Common tobacco), partia	1814.82	1
gb|AM808565 seedling library, SL Nicotiana tabacum cDNA clone nt002221007, mF	60.52	1
gb|AGN_RNC025xm06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	27.26	1
tc|Rep: 40S ribosomal protein S24 - Vitis vinifera (Grape), partial (96%) [TC54072]	70.25	1
Unknown	242.66	1
tc|Rep: Cytochrome c oxidase subunit Vb - Pisum sativum (Garden pea), partial (68	18.86	1
Unknown	356.31	1

gb|KF8C.109P17F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109P17, mRN	30.34	1
Unknown	60.62	1
gb|KL5B.113A20F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.113A20, m	32.93	1
tc|Rep: Transcription factor APFI-like - Solanum tuberosum (Potato), partial (94%) [	621.54	1
Unknown	536.37	1
Unknown	11855.55	1
gb|AGN_RNC007xe20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	2843.31	1
gb|TT-03_M04 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	56.49	1
Unknown	49567.25	1
gb|TT-25_O04 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	309.09	1
tc|Rep: Chromosome chr13 scaffold_120, whole genome shotgun sequence - Vitis	58.81	1
tc|Rep: Carotenoid cleavage dioxygenase 1 - Petunia hybrida (Petunia), partial (33%	59.84	1
Unknown	517.23	1
gb|AM809585 seedling library, SL Nicotiana tabacum cDNA clone nt002013044, m	158.22	1
gb|KP1B.110K05F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110K05, m	41.16	1
tc|Rep: N-carbamoylputrescine amidase - Solanum tuberosum (Potato), partial (89	138.18	1
gb|TT-40_P15 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	152	1
tc|Rep: ASH1 protein - Cupiennius salei (Wandering spider), partial (7%) [TC72324]	241.02	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	5976.4	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	32.73	1
gb|TT-05_I02 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	835.86	1
gb|TL13.107M09F.060315T7 TL13 Nicotiana tabacum cDNA clone TL13.107M09, m	68.48	1
gb|Nicotiana tabacum ORF mRNA, complete cds [U66266]	1171.06	1
gb|AGN_RNC021xo20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	18.58	1
gb|AM839551 COL, cold overnight library Nicotiana tabacum cDNA clone nt006145	25.47	1
gb|KR3B.111I14F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111I14, mR	336.73	1
gb|Nicotiana tabacum mRNA for 14-3-3 e-2 protein, complete cds [AB119475]	85.77	1
tc|Rep: 50S ribosomal protein L4 - Arabidopsis thaliana (Mouse-ear cress), partial (	40.97	1
Unknown	438.6	1
tc|Rep: Proteasome regulatory subunit-like - Arabidopsis thaliana (Mouse-ear cress	85.79	1
tc|Rep: S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC) [C	38865.1	1
Unknown	75.73	1
gb|Nicotiana tabacum beta tubulin-like mRNA, partial sequence [EF051136]	55927.45	1
Unknown	433.71	1

gb|KF8C.109C04F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109C04, mRN	33341.6	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	1116.63	1
gb|Nicotiana tabacum DSK2 mRNA, complete cds [DQ672264]	29.74	1
Unknown	109.11	1
gb|KR3B.001N20F.050815T7 KR3B Nicotiana tabacum cDNA clone KR3B.001N20, m	50.03	1
gb|KP1B.104P12F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104P12, m	100.13	1
gb|KN6B.100O04F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100O04,	135.2	1
gb|KT7C.106D03F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106D03, mR	276.32	1
tc|Rep: Fumarylacetoacetase - Medicago truncatula (Barrel medic), partial (55%) [T	26.29	1
gb|TOBESTR057A11 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	2803.6	1
gb|KT7B.103H13F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.103H13, mR	1025.49	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	384.29	1
gb|KF8C.101G14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101G14, mR	50663.2	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	208.28	1
gb|KR2B.112D12F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.112D12, m	1518.95	1
gb|KR3B.109A07F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109A07, m	2171.19	1
gb|KP1B.101D14F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101D14, m	2215.02	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	35.46	1
gb|AGN_RNC024xi05r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	21.72	1
Unknown	18709.35	1
gb|TOBESTR063G03 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	462.62	1
gb|KG9B.005F19F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005F19, m	203.46	1
tc|Rep: Chromosome undetermined scaffold_247, whole genome shotgun sequenc	29.4	1
tc|Rep: Chromosome chr1 scaffold_180, whole genome shotgun sequence - Vitis vi	116.18	1
Unknown	98.2	1
gb|Nicotiana tabacum extracellular Ca2+ sensing receptor (cas) mRNA, complete c	96.92	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	81.59	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	129.24	1
gb|KN6B.104B13F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104B13,	42.97	1
gb|KP1B.105A13F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105A13, m	134.45	1
gb|KF8B.201G17F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201G17, mR	22.57	1
tc|Rep: Nuclear RNA binding protein - Nicotiana tabacum (Common tobacco), parti	73.85	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	269.07	1
Unknown	213.23	1

Unknown	18.92	1
gb|Nicotiana tabacum mRNA for protein kinase 2 beta chain (ck2B1 gene) [AJ4382	444.13	1
tc|Rep: Cellulose synthase - Solanum tuberosum (Potato), partial (9%) [TC56534]	57.93	1
gb|TT-04_E09 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	38.67	1
tc|Rep: 14-3-3 i-2 protein - Nicotiana tabacum (Common tobacco), partial (39%) [T	187.89	1
tc|Rep: Granule-bound starch synthase 1, chloroplast precursor - Solanum tuberosu	237.56	1
gb|KL4B.107M19F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107M19, m	49	1
gb|BP526621 MAT001 Nicotiana tabacum cDNA clone BY11358, mRNA sequence [	22.66	1
gb|TT-35_A18 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	178.66	1
gb|AGN_RNC123xj03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	134.51	1
tc|Rep: Chromosome chr1 scaffold_84, whole genome shotgun sequence - Vitis vin	26.22	1
gb|AGN_RNC024xg22f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	644.74	1
Unknown	30.82	1
Unknown	19.87	1
tc|Rep: Ubiquitin carrier protein - Vitis vinifera (Grape), complete [TC48976]	1131.53	1
gb|AGN_RNC006xi21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	32.48	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	391.02	1
tc|Rep: ADP-ribosylation factor - Daucus carota (Carrot), partial (96%) [TC46343]	184.79	1
tc|Rep: Chromosome undetermined scaffold_53, whole genome shotgun sequence	1192.08	1
Unknown	66.63	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	9458.26	1
tc|Rep: Peroxiredoxin - Ipomoea batatas (Sweet potato) (Batate), complete [TC462	45.76	1
Unknown	521.01	1
tc|Rep: Chromosome chr5 scaffold_72, whole genome shotgun sequence - Vitis vin	331.57	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	1421.91	1
gb|KT7C.109G08F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109G08, mR	251.52	1
Unknown	79.89	1
gb|Nicotina tabacum mRNA for caffeoyl-CoA O-methyltransferase 5, CCoAOMT-5 g	73.58	1
tc|Rep: Polypepetide with reverse transcriptase and RNaseH domains - Petunia hyb	26.56	1
tc|Rep: Cytochrome b6 - Nicotiana sylvestris (Wood tobacco), partial (48%) [TC741	27.07	1
Unknown	79.73	1
tc|Rep: Ubiquitin carboxyl-terminal hydrolase - Vitis vinifera (Grape), partial (58%)	92.07	1
gb|EST_CSP003xo16f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	35.05	1
Unknown	1363.76	1

tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	103.25	1
Unknown	31.48	1
gb|KP1B.112H03F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.112H03, m	413.84	1
gb|KL4B.104D22F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104D22, mF	106.58	1
gb|CHO_SL026xb05f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	192.86	1
gb|KF8C.106B04F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106B04, mRN	87.15	1
Unknown	545.47	1
tc|Rep: Biotin carboxylase carrier protein - Solanum lycopersicum (Tomato) (Lycope	54.93	1
Unknown	11867.95	1
tc|Rep: Voltage-dependent anion channel - Nicotiana tabacum (Common tobacco),	221.25	1
tc|Rep: FOG: CBS domain protein - Vibrio sp. MED222, partial (4%) [TC50283]	34.7	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	982.8	1
gb|KL4B.102A03F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102A03, mF	26.59	1
gb|TT-13_H21 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	546.61	1
Unknown	180.49	1
gb|KR3B.109F14F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109F14, mF	103.01	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	31.03	1
Unknown	516.81	1
tc|Rep: CXE carboxylesterase - Actinidia eriantha, partial (45%) [TC41276]	79.45	1
gb|KF8C.101H16F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101H16, mRI	47.89	1
gb|Nicotiana tabacum potyviral capsid protein interacting protein 1 (CPIP1) mRNA,	19.11	1
gb|KR3B.103K10F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.103K10, m	18.82	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	29.07	1
gb|KN6B.102N01F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102N01, r	20.56	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	558.97	1
gb|AGN_RPC011xo17f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	49.14	1
Unknown	11149.6	1
gb|TT-21_L03 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	258.32	1
gb|KF8B.100N14F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100N14, mRI	44.37	1
Unknown	26.33	1
tc|Rep: Chromosome undetermined scaffold_296, whole genome shotgun sequenc	48.02	1
Unknown	13457.95	1
Unknown	16508.35	1
tc|Rep: Ribosomal protein L3A - Nicotiana tabacum (Common tobacco), partial (59	31.91	1

gb|AGN_ELP026xk21f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	294.22	1
gb|AGN_RNC116xo18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	20.31	1
Unknown	21.38	1
gb|KG9B.103A12F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103A12, m	80.56	1
tc|Rep: Alpha chain of nascent polypeptide associated complex - Nicotiana benthar	29.8	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	79.78	1
gb|AGN_RNC112xn05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	68.04	1
Unknown	1537.65	1
gb|Nicotiana tabacum mRNA for putative zinc transporter (C477 gene) [AM851010	515.86	1
tc|Rep: Chromosome chr8 scaffold_99, whole genome shotgun sequence - Vitis vin	2301.12	1
Unknown	31.06	1
gb|BP128741 MAT001 Nicotiana tabacum cDNA clone BY522, mRNA sequence [BP	27.83	1
Unknown	25.47	1
Unknown	169.42	1
gb|KN6B.110O02F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.110O02, r	99.35	1
gb|KP1B.113M20F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.113M20, r	170.88	1
gb|AGN_PNL210bf1_h1.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	44.64	1
gb|TT-03_A08 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	1123.73	1
tc|Rep: Auxin conjugate hydrolase - Medicago truncatula (Barrel medic), partial (56	23.62	1
gb|Nicotiana tabacum mRNA for protein kinase (NPK2), complete cds [D31964]	74.86	1
gb|TT-24_I03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	25.09	1
Unknown	57.87	1
tc|Rep: Enolase - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), parti	72.4	1
Unknown	1561.83	1
gb|TT-24_N21 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FC	31.31	1
Unknown	136.85	1
Unknown	38.16	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT4-23-480, cultivar Bright Yellow 2	101.19	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	21.24	1
gb|KG9B.103K15F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103K15, m	38.43	1
tc|Rep: NAD-dependent epimerase/dehydratase family protein-like protein - Solanu	8914.59	1
Unknown	28.21	1
tc|Rep: Chromosome chr11 scaffold_14, whole genome shotgun sequence - Vitis vi	41.19	1
gb|N.tabacum mRNA for NAD-dependent isocitrate dehydrogenase [X96727]	1565.63	1

gb|Nicotiana tabacum NtTPC1B mRNA for two-pore calcium channel, complete cds	51.79	1
gb|TOBESTR029D10 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	1217.02	1
gb|KN6B.100G11F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100G11, r	3233.17	1
tc|Rep: Signal recognition particle 54 kDa protein 1 - Solanum lycopersicum (Tomat	1489.89	1
Unknown	604.2	1
gb|KG9B.003P13F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003P13, m	238.62	1
Unknown	390.27	1
tc|Rep: ATP-dependent RNA helicase-like protein DB10 - Nicotiana sylvestris (Wooc	524.59	1
gb|KP1B.110I19F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110I19, mRI	219.48	1
gb|TT-29_E24 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	162.7	1
gb|KN6B.103K11F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103K11, m	59.34	1
gb|CHO_SL028xg02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	2913.95	1
tc|Rep: 60s acidic ribosomal protein-like protein - Solanum tuberosum (Potato), pa	5775.65	1
tc|Rep: Genomic DNA, chromosome 5, TAC clone: K19P17 - Arabidopsis thaliana (M	143.18	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	93.01	1
gb|TT-02_F09 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence |	95.8	1
tc|Rep: zinc finger (C3HC4-type RING finger) family protein - Arabidopsis thaliana, p	120.96	1
Unknown	17.24	1
gb|KF8C.109K05F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109K05, mRN	38.07	1
Unknown	26.72	1
gb|AGN_PNL210br1_g4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	139.94	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	72.56	1
gb|KP1B.001P21F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001P21, mI	985.12	1
tc|Rep: MRNA, complete cds, clone: RAFL25-18-P16 - Arabidopsis thaliana (Mouse-	28.59	1
gb|KP1B.037G02F.050623T7 KP1B Nicotiana tabacum cDNA clone KP1B.037G02, m	905.21	1
gb|TOBESTR068F07 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA sequ	915.31	1
gb|AGN_ELP006xa10f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	28.76	1
gb|AGN_ELP006xa11f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	100.56	1
tc|Rep: Hexokinase 6 - Nicotiana tabacum (Common tobacco), complete [TC53358]	25.31	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	109.81	1
Unknown	58.07	1
gb|KT7C.101N20F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.101N20, mR	5197.05	1
Unknown	32.21	1
tc|Rep: PttA' - Petunia hybrida (Petunia), partial (24%) [TC70893]	118.34	1

gb|KP1B.102L23F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102L23, mR	8538.08	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	92.71	1
Unknown	592.51	1
gb|Nicotiana tabacum NtUGPase mRNA for UDP-glucose pyrophosphorylase, partia	222.57	1
Unknown	20.53	1
gb|AGN_RNC105xg14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	42.52	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	46.2	1
Unknown	3169.71	1
Unknown	142.36	1
tc|Rep: Uncharacterized protein At5g64816 precursor - Arabidopsis thaliana (Mous	54.19	1
gb|KN6B.101J07F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101J07, m	256.57	1
gb|KR2B.101M21F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.101M21, r	42.63	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	23.17	1
gb|KG9B.004D22F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004D22, n	88.43	1
tc|Rep: Genomic DNA, chromosome 3, P1 clone: MJK13 - Arabidopsis thaliana (Mo	22.16	1
Unknown	995.99	1
Unknown	81.03	1
tc|Rep: Protein kinase CK2 alpha chain - Nicotiana tabacum (Common tobacco), co	27.56	1
gb|EST_CSP001xb13f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	525.75	1
tc|Rep: Chromosome undetermined scaffold_1169, whole genome shotgun sequen	66.32	1
Unknown	111.13	1
Unknown	517.87	1
gb|CHO_SL028xg02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	2700.04	1
gb|TT-38_F10 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	36.89	1
tc|Rep: Os09g0505800 protein - Oryza sativa subsp. japonica (Rice), partial (86%) [T	50.89	1
gb|KT7C.108C02F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108C02, mR	24.78	1
Unknown	825.19	1
gb|KL4B.105M19F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105M19, m	94.91	1
Unknown	76.65	1
Unknown	4093.72	1
gb|KL4B.102K07F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102K07, mR	449.73	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	243.91	1
tc|Rep: AT4g32020/F10N7_170 - Arabidopsis thaliana (Mouse-ear cress), partial (1	675.25	1
tc|Rep: Expressed protein - Oryza sativa subsp. japonica (Rice), partial (91%) [TC511	36.15	1

gb|AGN_ELP017xe10f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	27.7	1
gb|TT-49_B08 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	362.44	1
tc|Rep: Chromosome chr14 scaffold_26, whole genome shotgun sequence - Vitis vi	710.43	1
Unknown	31.26	1
Unknown	116.3	1
Unknown	70.79	1
gb|KT7B.114G03F.060127T7 KT7 Nicotiana tabacum cDNA clone KT7B.114G03, mR	71.28	1
gb|TT-06_E16 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	34.94	1
Unknown	20465.15	1
Unknown	25.95	1
tc|Rep: Hsc70 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), partial	49.8	1
Unknown	26.6	1
Unknown	31.82	1
tc|Rep: Arginine decarboxylase 2 - Nicotiana tabacum (Common tobacco), complet	11260.8	1
Unknown	984.59	1
tc|Rep: F22G5.1 - Arabidopsis thaliana (Mouse-ear cress), partial (51%) [TC62580]	29.88	1
gb|KL4B.107L17F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107L17, mR	178.65	1
gb|KF8C.110C04F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110C04, mR	854.75	1
gb|KL4B.100H13F.050922T7 KL4B Nicotiana tabacum cDNA clone KL4B.100H13, m	58.36	1
gb|KL4B.105G10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105G10, m	88.84	1
gb|Nicotiana tabacum hexokinase 3 (Hxk3) mRNA, complete cds [AY553216]	2583.37	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	159.15	1
gb|KG9B.002C22F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002C22, m	215.17	1
gb|Nicotiana tabacum anther ethylene-upregulated protein ER1 (ER1) mRNA, parti	45.8	1
Unknown	76.94	1
Unknown	20.93	1
gb|KL4B.102L15F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102L15, mR	637.1	1
tc|Rep: Flagellin - Escherichia coli, partial (5%) [TC72631]	28	1
Unknown	444.3	1
gb|KT7C.105D19F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105D19, mR	128.81	1
gb|BP526356 MAT001 Nicotiana tabacum cDNA clone BY11073, mRNA sequence [	57.84	1
Unknown	242.19	1
gb|AGN_RNC023xf11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	24.56	1
gb|KG9B.103I01F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103I01, m	111.46	1

gb|AGN_RNC106xf10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	9321.23	1
tc|Rep: Diacylglycerol kinase variant A - Solanum lycopersicum (Tomato) (Lycopersi	2730.44	1
gb|TOBESTR061H08 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	29.09	1
Unknown	1410.41	1
tc|Rep: Chromosome chr2 scaffold_176, whole genome shotgun sequence - Vitis vi	335.75	1
gb|AGN_ELP017xm11f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	94.42	1
gb|Nicotiana tabacum phospholipase C1 mRNA, complete cds [AF223351]	9654.21	1
gb|KR3B.107O20F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.107O20, m	139.9	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	146.58	1
gb|Nicotiana tabacum NtRDR6 mRNA for RNA-dependent RNA polymerase 6, comp	22.6	1
tc|Rep: Chromosome undetermined scaffold_1099, whole genome shotgun sequen	1833.94	1
tc|Rep: Chromosome undetermined scaffold_125, whole genome shotgun sequenc	2417.96	1
tc|Rep: Dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate deh	525.55	1
tc|GB|AJ311779.1|CAC84548.1 dicarboxylate/tricarboxylate carrier [Nicotiana tab	27.64	1
tc|Rep: M19 protein - Murine cytomegalovirus (strain K181), partial (11%) [TC5787	107.19	1
Unknown	866.38	1
gb|Nicotiana tabacum plastid phosphate [U66402]	177.05	1
gb|KP1B.110H07F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110H07, m	54.1	1
gb|KT7C.106B03F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106B03, mR	11308.9	1
gb|TT-24_E16 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	25.69	1
gb|KL4B.101K17F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101K17, mR	70.6	1
gb|TT-05_A21 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	267.4	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	128.89	1
gb|AGN_ELP024xn17f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	448.3	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	651.7	1
tc|Rep: Chromosome undetermined scaffold_147, whole genome shotgun sequenc	22.96	1
gb|BP528728 MAT001 Nicotiana tabacum cDNA clone BY13589, mRNA sequence [	84.62	1
gb|AGN_RNC127xb20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	841.38	1
tc|Rep: Chromosome undetermined scaffold_1268, whole genome shotgun sequen	153.16	1
tc|Rep: Acyltransferase homolog - Petunia hybrida (Petunia), partial (65%) [TC5160	32.59	1
gb|AGN_PNL222af1_e7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	56.45	1
Unknown	17.06	1
Unknown	35.4	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	192.46	1

gb|Nicotiana tabacum nuclease mRNA, partial cds [AY029749]	57.38	1
Unknown	755.86	1
Unknown	27.95	1
gb|AGN_ELP017xg15f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	92.19	1
tc|Rep: Chromosome chr2 scaffold_176, whole genome shotgun sequence - Vitis vi	141.14	1
gb|KF8C.103N20F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103N20, mR	27.35	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT21-1-220, cultivar Bright Yellow 2	48.75	1
gb|TT-48_C09 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	507.57	1
gb|KR3B.104D11F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.104D11, m	1717.12	1
gb|TT-05_J09 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	252.55	1
Unknown	51.56	1
gb|TT-23_H09 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	64.06	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	35.28	1
Unknown	26.14	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	21.56	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	70.38	1
tc|Rep: Ribosomal protein L39 - Triticum aestivum (Wheat), complete [TC62239]	52.12	1
Unknown	42.49	1
gb|TT-36_B15 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	95.86	1
tc|Rep: Growth-on protein GRO11 - Euphorbia esula (Leafy spurge), partial (21%) [T	30.96	1
Unknown	72.83	1
gb|KL4B.111C19F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111C19, mR	43.64	1
gb|Nicotiana tabacum PCNA mRNA for proliferating cell nuclear antigen, complete	19.09	1
gb|KR2B.115B01F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115B01, m	124.02	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	64.4	1
gb|AGN_PNL210df1_g3.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	377.93	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	242.23	1
gb|KP1B.105G14F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105G14, m	94.89	1
Unknown	1889.92	1
Unknown	24.45	1
Unknown	40.63	1
Unknown	2904.33	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	22.06	1
gb|TT-29_O01 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	122.82	1

gb|KG9B.001D20F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001D20, n	339.39	1
Unknown	79.04	1
tc|Rep: JAB - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), partial (8	107.48	1
gb|KL4B.103L20F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103L20, mRI	391.53	1
Unknown	859.06	1
gb|KG9B.003O19F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003O19, r	22.4	1
gb|TT-21_B07 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	411.21	1
Unknown	219.34	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	512.45	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	101.55	1
gb|KF8C.101C05F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101C05, mRN	499.38	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC3-41-290, cultivar Bright Yellow 2	3369.91	1
gb|KF8C.101G18F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101G18, mRI	199.08	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	24.64	1
gb|KR3B.113P03F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.113P03, mI	1114.71	1
gb|KN6B.108G03F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.108G03, r	1855.2	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	273.02	1
tc|Rep: Cathepsin B-like cysteine proteinase - Nicotiana rustica (Aztec tobacco), par	4070.85	1
tc|Rep: Pto-like serine/threonine kinase - Capsicum chinense (Scotch bonnet) (Bonr	66.45	1
gb|KL4B.106M24F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106M24, m	512.33	1
tc|Rep: Endoplasmin homolog precursor - Catharanthus roseus (Rosy periwinkle) (N	517.63	1
tc|Rep: SKP1-like protein - Nicotiana clevelandii (Wild tobacco), complete [TC50857	3566.56	1
Unknown	723.38	1
gb|N.tabacum npp4 mRNA for protein phosphatase type 2A [Z93771]	550.2	1
tc|Rep: Chromosome chr2 scaffold_176, whole genome shotgun sequence - Vitis vi	753.22	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	65.28	1
gb|AGN_ELP005xm21f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	19.04	1
Unknown	187.5	1
gb|KP1B.109B14F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109B14, mI	85.68	1
Unknown	160.72	1
Unknown	79.82	1
tc|Rep: Copper-transporting P-type ATPase - Brassica napus (Rape), partial (37%) [T	265.18	1
gb|KP1B.108P09F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108P09, mI	4140.98	1
gb|AGN_ELP005xp12f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	26.56	1

tc|Rep: Ubiquitin carrier protein - Glycine max (Soybean), complete [TC51935]	38.1	1
Unknown	18.8	1
Unknown	35.64	1
gb|KR3B.110I10F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110I10, mR	83.92	1
Unknown	20.94	1
Unknown	100.49	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	1494.73	1
tc|Rep: Chromosome chr8 scaffold_68, whole genome shotgun sequence - Vitis vin	1174.84	1
gb|TT-50_M03 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA se	542.37	1
tc|Rep: Chromosome chr13 scaffold_210, whole genome shotgun sequence - Vitis	551.36	1
gb|CHO_SL002xg07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	233.33	1
Unknown	593.42	1
Unknown	541.88	1
gb|KN6B.115A22F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.115A22,	250.98	1
gb|KN6B.102F13F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102F13, m	947.51	1
gb|KP1B.109C17F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109C17, m	252.31	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	42.13	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	12122.2	1
Unknown	26.85	1
gb|CHO_SL022xd02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	742.07	1
Unknown	80.88	1
gb|AGN_RNC003xl16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	24.58	1
gb|Nicotiana tabacum NtSIP1 mRNA for 6b-interacting protein 1, complete cds [AB	103.04	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	26.82	1
gb|KF8C.110N22F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110N22, mR	18.31	1
tc|Rep: Chromosome chr10 scaffold_76, whole genome shotgun sequence - Vitis vi	25.87	1
tc|Rep: Nt-rab6 protein - Nicotiana tabacum (Common tobacco), complete [TC564	467.28	1
gb|KF8C.106P01F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106P01, mR	2705.3	1
gb|KP1B.102P06F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102P06, m	2923.28	1
Unknown	118.08	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	56.47	1
Unknown	6494.96	1
gb|KP1B.110A06F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110A06, m	27.1	1
Unknown	1401.56	1

Unknown	251.47	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	407.96	1
gb|AGN_PNL215bf1_f10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	37.62	1
Unknown	730.65	1
gb|KF8C.106C09F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106C09, mRN	30.17	1
tc|Rep: Proline-rich protein family-like - Oryza sativa subsp. japonica (Rice), partial (	30.94	1
gb|KF8B.100E05F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100E05, mRN	58.54	1
Unknown	238.16	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, complete [TC5517	107.12	1
tc|Rep: Poly(A)-binding protein II-like - Brassica campestris (Field mustard), partial (	744.03	1
Unknown	48.69	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	528.78	1
gb|KL4B.101K21F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101K21, mR	80.83	1
tc|Rep: Calnexin-like protein - Solanum lycopersicum (Tomato) (Lycopersicon escule	1088.24	1
Unknown	149.49	1
tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin	30.23	1
tc|Rep: Sucrose-6-phosphate phosphatase - Nicotiana tabacum (Common tobacco)	116.02	1
Unknown	75.47	1
tc|Rep: GDP-mannose pyrophosphorylase - Solanum tuberosum (Potato), partial (8	217.14	1
Unknown	253	1
gb|KF8C.104I02F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104I02, mRNA	11565.85	1
Unknown	52.11	1
gb|EST_FLW005xi04f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [EH	6592.05	1
tc|Rep: Carotenoid cleavage dioxygenase 1 - Lactuca sativa (Garden lettuce), partia	23.88	1
Unknown	330.23	1
Unknown	22.58	1
tc|Rep: Striated muscle activator-like protein - Oryza sativa subsp. japonica (Rice), p	12232.7	1
Unknown	2848.74	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	563.54	1
Unknown	758.1	1
Unknown	97.64	1
Unknown	138.78	1
gb|Nicotiana tabacum NtROS1 mRNA for repressor of silencing 1, complete cds [AB	149.35	1
gb|KL4B.106D03F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106D03, mR	1564.64	1

Unknown	263.27	1
tc|Rep: Chromosome undetermined scaffold_257, whole genome shotgun sequenc	4735.15	1
Unknown	4550.37	1
Unknown	560.84	1
gb|CHO_SL003xc11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	17.56	1
gb|KL4B.109C14F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.109C14, mR	104.4	1
gb|TT-04_P08 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	44.37	1
gb|KP1B.112E21F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.112E21, m	1700.43	1
Unknown	2650.83	1
Unknown	560.57	1
gb|AGN_RNC014xh16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	189.14	1
tc|Rep: NADH glutamate synthase precursor - Phaseolus vulgaris (Kidney bean) (Fre	80.6	1
Unknown	686.83	1
Unknown	42.29	1
gb|KT7C.110A10F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110A10, mR	33.42	1
Unknown	37292.75	1
gb|AGN_RPC005xi10f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	183.2	1
tc|Rep: Lecithine cholesterol acyltransferase-like protein - Solanum lycopersicum (T	255.02	1
gb|KR2B.107H19F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.107H19, m	54.61	1
gb|KP1B.108A18F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108A18, m	121.33	1
tc|Rep: DnaJ - Viola baoshanensis, partial (95%) [TC46205]	1117.3	1
gb|BP530317 MAT005 Nicotiana tabacum cDNA clone BY21327, mRNA sequence [E	2362.36	1
tc|Rep: Chromosome chr8 scaffold_68, whole genome shotgun sequence - Vitis vin	34.7	1
tc|Rep: Chromosome chr13 scaffold_286, whole genome shotgun sequence - Vitis v	844.54	1
gb|KT7C.102F22F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102F22, mRN	86.38	1
tc|Rep: SRC2-like protein - Nicotiana benthamiana, partial (73%) [TC75258]	70.58	1
gb|CHO_SL010xe03f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	638.75	1
tc|Rep: NAD-dependent isocitrate dehydrogenase precursor - Nicotiana tabacum (C	1578.98	1
Unknown	71.6	1
Unknown	23824.25	1
tc|Rep: 40S ribosomal protein S19-like - Solanum tuberosum (Potato), complete [TC	82.09	1
gb|KT7C.105I02F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105I02, mRN	128.33	1
Unknown	264.78	1
Unknown	27.8	1

gb|KF8C.105G15F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105G15, mR	248.9	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	113.04	1
Unknown	48.04	1
tc|Rep: Ribosomal protein PETRP - Capsicum annuum (Bell pepper), complete [TC43	29.7	1
gb|KT7C.110O15F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110O15, mR	34.13	1
Unknown	16.35	1
Unknown	90.55	1
tc|Rep: Cysteine synthase - Solanum tuberosum (Potato), partial (83%) [TC40893]	37.75	1
Unknown	97.12	1
gb|AGN_RNC009xn17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	17.45	1
Unknown	615.83	1
gb|KL4B.105H09F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105H09, m	190.9	1
Unknown	152.83	1
gb|KP1B.108B17F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108B17, m	63.27	1
tc|Rep: Nodulin-like protein - Poncirus trifoliata (Hardy orange), partial (4%) [TC734	44.59	1
Unknown	954.34	1
Unknown	114.49	1
tc|Rep: Nam-like protein 6 - Petunia hybrida (Petunia), partial (86%) [TC66061]	78.91	1
tc|Rep: 14-3-3 i-2 protein - Nicotiana tabacum (Common tobacco), partial (39%) [TC	61.52	1
Unknown	1096.64	1
Unknown	107.15	1
tc|Rep: Adenylate kinase family-like protein - Solanum tuberosum (Potato), partial	3207.46	1
gb|EST T1P020 Tobacco Leaves Express Library Nicotiana tabacum cDNA clone JS11	490.67	1
gb|KP1B.102G19F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102G19, m	215.97	1
gb|TT-20_L14 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	44.49	1
tc|Rep: Chromosome chr1 scaffold_135, whole genome shotgun sequence - Vitis vi	20.82	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	19.53	1
gb|Nicotiana tabacum alpha-expansin precursor (Nt-EXPA6) mRNA, partial cds [AFC	22.51	1
Unknown	28.79	1
gb|KL4B.105D03F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105D03, m	9751.74	1
Unknown	50.47	1
tc|Rep: At2g37480 - Arabidopsis thaliana (Mouse-ear cress), partial (24%) [TC50022	1382.16	1
tc|Rep: Ribosomal protein L41 - Candida maltosa (Yeast), complete [TC51829]	134.36	1
Unknown	140.12	1

tc|Rep: Inositol-3-phosphate synthase - Nicotiana tabacum (Common tobacco), par	114.12	1
tc|Rep: ATP synthase subunit gamma, mitochondrial precursor - Ipomoea batatas (	226.86	1
tc|Rep: Ribosomal protein L37 - Glycine max (Soybean), complete [TC56573]	106.91	1
Unknown	190.27	1
tc|Rep: Succinyl CoA ligase beta subunit - Solanum lycopersicum (Tomato) (Lycoper	486.25	1
gb|KL5B.111G02F.060117T7 KL5B Nicotiana tabacum cDNA clone KL5B.111G02, m	51.76	1
gb|KP1B.109D12F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109D12, m	79.55	1
gb|KL4B.105D03F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105D03, m	10628.75	1
gb|AM811238 seedling library, SL Nicotiana tabacum cDNA clone nt002230064, m	17.83	1
gb|KF8C.103D08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103D08, mR	11955.3	1
Unknown	112.1	1
Unknown	111.25	1
gb|KG9B.105K03F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105K03, m	41.18	1
Unknown	510.35	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	141.35	1
gb|Nicotiana tabacum clone PR33 mRNA sequence [AF154648]	116.63	1
tc|Rep: Chromosome chr14 scaffold_128, whole genome shotgun sequence - Vitis	2723.61	1
tc|Rep: ADP ribosylation factor 002 - Daucus carota (Carrot), complete [TC49072]	9518.09	1
gb|AGN_PNL201cf1_e10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	385.87	1
Unknown	3267.79	1
Unknown	70.28	1
gb|KT7C.105B14F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105B14, mR	86.74	1
gb|KL4B.110F24F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110F24, mR	23.49	1
tc|Rep: T6D22.12 - Arabidopsis thaliana (Mouse-ear cress), partial (54%) [TC51666]	592.44	1
gb|KT7C.104L12F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104L12, mRN	980.74	1
gb|KG9B.106O05F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106O05,	1016.01	1
Unknown	135.08	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	251.29	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	21.01	1
gb|AGN_RPC018xg11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	2808.34	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	231.31	1
Unknown	63.69	1
gb|Nicotiana tabacum pectin methylesterase (PPME1) mRNA, complete cds [AY772	45665.5	1
Unknown	62.06	1

gb|KT7C.106G08F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106G08, mR	605.12	1
Unknown	1134.73	1
tc|Rep: 60S ribosomal protein L6 - Mesembryanthemum crystallinum (Common ice	132.1	1
Unknown	38.24	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	730.48	1
Unknown	30.55	1
gb|AGN_PNL221ar1_e10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRN	402.21	1
gb|KP1B.001F10F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001F10, m	461.83	1
gb|AGN_PNL232bf1_b2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	114.81	1
gb|AGN_RNC008xp03f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1398.09	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	164.08	1
tc|Rep: ALG2-interacting protein X - Nicotiana tabacum (Common tobacco), partial	135.24	1
Unknown	514.55	1
Unknown	626.82	1
Unknown	43.49	1
gb|KG9B.005L24F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005L24, m	754.3	1
gb|KG9B.102D21F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102D21,	147.69	1
gb|TT-34_A21 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	34.96	1
gb|AM787875 COL, cold overnight library Nicotiana tabacum cDNA clone nt006146	23.63	1
Unknown	47.05	1
Unknown	99.83	1
gb|TT-06_C12 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	11366	1
tc|Rep: ATP synthase subunit beta - Nicotiana sylvestris (Wood tobacco), partial (2	821.45	1
gb|KT7C.105E05F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105E05, mR	19.81	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	945.92	1
gb|KT7C.106K21F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106K21, mR	2399.58	1
tc|Rep: Chromosome chr7 scaffold_192, whole genome shotgun sequence - Vitis vi	127.03	1
tc|Rep: Cystathionine gamma-synthase isoform 2 - Solanum tuberosum (Potato), p	2588.6	1
Unknown	158.07	1
gb|KR3B.106L15F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106L15, m	79.48	1
tc|Rep: Chromosome chr8 scaffold_115, whole genome shotgun sequence - Vitis vi	178.35	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	558.21	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	342.79	1
gb|AGN_PNL226cf1_c12.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	120.8	1

gb|KN6B.101N24F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101N24, r	691.72	1
Unknown	30.84	1
Unknown	50.79	1
Unknown	2902.1	1
gb|KF8B.200N17F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200N17, mR	26.21	1
tc|Rep: WSSV375 - White spot syndrome virus (WSSV), partial (25%) [TC76905]	34.58	1
gb|TT-47_B22 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	18.9	1
gb|AM803975 seedling library, SL Nicotiana tabacum cDNA clone nt002191015, mF	21.93	1
gb|AGN_PNL225br1_g2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	236.64	1
Unknown	31.89	1
gb|EST_FLW002xp11f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	1590.09	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	122.84	1
gb|KP1B.108H13F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108H13, m	134.87	1
gb|KP1B.001C10F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001C10, m	64.2	1
gb|AGN_RNC127xb20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1572.93	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	1815.85	1
Unknown	59.62	1
gb|AGN_ELP008xp13f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	61.48	1
gb|KP1B.101A13F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101A13, m	104.26	1
gb|CHO_SL025xj11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	2808.66	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	274.9	1
tc|Rep: Chloroplast threonine deaminase 1 - Solanum lycopersicum (Tomato) (Lyco	530.82	1
Unknown	18.69	1
gb|FS417555 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	523.39	1
gb|KL4B.108H18F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108H18, mF	59.99	1
gb|AGN_RPC014xo22f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	781.04	1
tc|Rep: VAP27 - Nicotiana plumbaginifolia (Leadwort-leaved tobacco), partial (96%)	375.45	1
tc|Rep: Cellulose synthase catalytic subunit - Nicotiana alata (Winged tobacco) (Per	53.86	1
gb|KP1B.110I21F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110I21, mR	220.14	1
gb|KF8B.200D19F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200D19, mR	752.88	1
tc|Rep: Pyridoxal kinase - Solanum tuberosum (Potato), partial (33%) [TC65370]	684.25	1
Unknown	103.96	1
Unknown	377.76	1
tc|Rep: Aquaporin 1 - Nicotiana tabacum (Common tobacco), complete [TC63014]	628.1	1

Unknown	433.62	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	525.54	1
Unknown	229.52	1
Unknown	508.96	1
gb|KN6B.100E12F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100E12, m	24.96	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	95.32	1
tc|Rep: Chromosome undetermined scaffold_226, whole genome shotgun sequenc	1347.1	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	571.47	1
Unknown	176.28	1
gb|KP1B.107M11F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107M11, r	207.21	1
Unknown	53.98	1
gb|AGN_RNC021xo20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	48.35	1
gb|KT7C.113A13F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.113A13, mR	212.04	1
tc|Rep: Thaliana 60S ribosomal protein L7 - Solanum tuberosum (Potato), complete	29.3	1
Unknown	67.89	1
gb|Nicotiana tabacum NtFAD3 mRNA for microsomal omega-3 acid desaturase, co	17212.35	1
gb|KG9B.001P18F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001P18, m	20.47	1
gb|CHO_SL025xj11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	2262.74	1
gb|AGN_ELP006xj06f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	28.77	1
tc|Rep: Chromosome chr3 scaffold_117, whole genome shotgun sequence - Vitis vi	349.37	1
tc|Rep: Homolog of defender against apoptotic death 1 homolog - Nicotiana suave	256.64	1
tc|Rep: GDP-D-mannose pyrophosphorylase - Viola baoshanensis, partial (48%) [TC	183.35	1
gb|Nicotiana tabacum putative high mobility group protein 2-like mRNA, partial se	3238.75	1
tc|Rep: Salt-induced AAA-Type ATPase - Mesembryanthemum crystallinum (Comm	1010.8	1
gb|BP532403 MAT005 Nicotiana tabacum cDNA clone BY27199, mRNA sequence [	232.42	1
tc|Rep: Chromosome undetermined scaffold_69, whole genome shotgun sequence	4547.28	1
gb|KT7B.107P03F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107P03, mR	50.97	1
Unknown	117.14	1
Unknown	27.21	1
gb|Nicotiana tabacum EF-1-alpha-related GTP-binding protein (SUP1) mRNA, comp	23.64	1
Unknown	105.13	1
Unknown	175.28	1
Unknown	207.09	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	2865.07	1

Unknown	3088.26	1
gb|TT-06_B02 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	445.49	1
tc|Rep: Cytosine-specific methyltransferase - Vitis vinifera (Grape), partial (20%) [T	32.95	1
Unknown	66.61	1
Unknown	37.74	1
tc|Rep: Tryptophan synthase beta subunit - Persicaria tinctoria, partial (83%) [TC49	2419.52	1
gb|KF8C.104F15F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104F15, mRN	24.86	1
gb|KR3B.114O14F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.114O14, m	127.81	1
Unknown	255.26	1
gb|TT-29_C09 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	76.65	1
gb|KP1B.101B11F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101B11, m	777.23	1
gb|KT7B.107J11F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107J11, mRN	524.47	1
gb|KT7C.112F07F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112F07, mR	1851.95	1
gb|AGN_RNC017xb07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	43.67	1
Unknown	65.29	1
tc|Rep: ALY protein - Nicotiana benthamiana, partial (20%) [TC72720]	2315.46	1
gb|KG9B.001A24F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001A24, m	145.22	1
Unknown	227.14	1
gb|KG9B.106J11F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106J11, m	107.11	1
tc|Rep: CBL-interacting protein kinase 25 - Populus trichocarpa (Western balsam po	534.58	1
tc|Rep: Chromosome chr10 scaffold_179, whole genome shotgun sequence - Vitis	212.47	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	4586.26	1
Unknown	31.26	1
tc|Rep: Succinate dehydrogenase subunit 3 - Solanum lycopersicum (Tomato) (Lyco	2655.38	1
Unknown	1141	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT24-2-320, cultivar Bright Yellow 2	175.43	1
gb|KF8C.108F01F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108F01, mRN	21.48	1
gb|KF8C.101N16F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101N16, mR	23.37	1
gb|TT-24_N22 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	240.44	1
Unknown	731.15	1
gb|KR2B.002O22F.051019T7 KR2B Nicotiana tabacum cDNA clone KR2B.002O22, m	8412.54	1
tc|Rep: Predicted protein - Aspergillus terreus (strain NIH 2624), partial (10%) [TC5	29.32	1
tc|Rep: Os06g0661900 protein - Oryza sativa subsp. japonica (Rice), partial (26%) [T	1287.34	1
tc|Rep: Chromosome undetermined scaffold_438, whole genome shotgun sequenc	44.5	1

gb|TT-17_E04 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	4194.22	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	25.46	1
tc|Rep: Ribosomal protein L15 - Vitis vinifera (Grape), partial (60%) [TC52772]	169.88	1
tc|Rep: Chromosome undetermined scaffold_133, whole genome shotgun sequenc	1123.09	1
tc|Rep: Glycoprotein-like protein - Solanum tuberosum (Potato), partial (55%) [TC6	39.87	1
gb|KP1B.037G15F.050623T7 KP1B Nicotiana tabacum cDNA clone KP1B.037G15, m	80.51	1
Unknown	18.62	1
tc|Rep: DNA-binding protein - Nicotiana tabacum (Common tobacco), complete [T	243.13	1
tc|Rep: Chromosome chr13 scaffold_74, whole genome shotgun sequence - Vitis vi	1537.18	1
gb|AGN_RNC011xb17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	509.01	1
tc|Rep: Chromosome chr9 scaffold_90, whole genome shotgun sequence - Vitis vin	708.25	1
tc|Rep: Pectate lyase precursor - Nicotiana tabacum (Common tobacco), complete	73262.2	1
tc|Rep: Histone H4 [Contains: Osteogenic growth peptide (OGP)]. - Rattus norvegicu	204.29	1
tc|Rep: Chromosome undetermined scaffold_142, whole genome shotgun sequenc	33.31	1
tc|Rep: Water channel protein - Nicotiana excelsior, complete [TC40230]	27.13	1
gb|KP1B.110K12F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110K12, m	58.23	1
gb|AGN_RNC020xh17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	64.14	1
Unknown	345.98	1
gb|Nicotiana tabacum NtGPDL mRNA for putative glycerophosphoryl diester phosp	1061.26	1
Unknown	102.62	1
Unknown	405.73	1
gb|AGN_RNC023xg21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	22.75	1
Unknown	256.81	1
gb|KL4B.102J02F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102J02, mR	1104.05	1
Unknown	36.03	1
gb|KP1B.104L05F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104L05, m	253.43	1
tc|Rep: Chromosome chr12 scaffold_38, whole genome shotgun sequence - Vitis vi	184.76	1
Unknown	828.82	1
tc|Rep: 60S ribosomal protein L41 - Homo sapiens (Human), complete [TC65131]	7587.38	1
Unknown	351.72	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	235.48	1
gb|BP534288 MAT005 Nicotiana tabacum cDNA clone BY32245, mRNA sequence [	185.17	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	1003.64	1
tc|Rep: Zinc finger, RING-type; Thioredoxin-related - Medicago truncatula (Barrel m	18.22	1

Unknown	20689.8	1
tc|Rep: Proline-rich protein - Solanum tuberosum (Potato), partial (66%) [TC64223]	51.54	1
gb|AGN_PNL229cf1_a7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	386.37	1
tc|Rep: Phosphoenolpyruvate carboxykinase - Solanum lycopersicum (Tomato) (Lyc	32.91	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	73.59	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	454.09	1
gb|TT-35_B11 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	136.85	1
Unknown	135.42	1
Unknown	34.25	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	31.16	1
gb|KL4B.101F22F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101F22, mR	113.2	1
gb|KN6B.105M14F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105M14,	246.77	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	449.94	1
Unknown	25.31	1
Unknown	85.76	1
Unknown	18.6	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	438.91	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	264.46	1
tc|Rep: Ubiquitin-conjugating enzyme family protein-like protein - Solanum tuberos	492.51	1
Unknown	778.99	1
tc|Rep: Chromosome undetermined scaffold_77, whole genome shotgun sequence	48.94	1
Unknown	2678.79	1
gb|KL4B.102A16F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102A16, mF	10972.75	1
gb|BP134254 MAT001 Nicotiana tabacum cDNA clone BY6612, mRNA sequence [BF	56.36	1
tc|Rep: Os01g0950800 protein - Oryza sativa subsp. japonica (Rice), partial (30%) [T	516.69	1
gb|KN6B.105P14F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105P14, m	325.68	1
gb|KG9B.105A19F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105A19, m	1742.17	1
Unknown	26.22	1
gb|KG9B.107B04F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107B04, m	23.41	1
Unknown	545.58	1
tc|Rep: Chromosome undetermined scaffold_79, whole genome shotgun sequence	41.9	1
tc|Rep: Chromosome chr19 scaffold_111, whole genome shotgun sequence - Vitis v	51.2	1
gb|BP128766 MAT001 Nicotiana tabacum cDNA clone BY549, mRNA sequence [BP1	70.68	1
gb|KP1B.103B19F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103B19, ml	65	1

gb|TT-23_L09 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	39.23	1
gb|KG9B.105A02F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105A02,	263.74	1
gb|3C05 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', m	3372.33	1
gb|KR3B.101B15F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101B15, m	94.12	1
tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	98.42	1
tc|Rep: Chromosome chr4 scaffold_333, whole genome shotgun sequence - Vitis vi	25.72	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	135.5	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	49.75	1
Unknown	34.72	1
Unknown	154.52	1
tc|Rep: ATPase - Camellia sinensis (Tea), complete [TC71603]	700.71	1
Unknown	513.79	1
Unknown	31.59	1
gb|AGN_RPC012xf15f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	121.53	1
tc|Rep: 60S ribosomal protein L15 - Petunia hybrida (Petunia), complete [TC41795]	145.28	1
gb|AM794030 COL, cold overnight library Nicotiana tabacum cDNA clone nt006077	22.88	1
gb|KP1B.105G14F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105G14, m	72.34	1
gb|BP132658 MAT001 Nicotiana tabacum cDNA clone BY4846, mRNA sequence [B	58.6	1
Unknown	33.24	1
tc|Rep: Malate dehydrogenase, glyoxysomal precursor - Citrullus lanatus (Waterme	250.25	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	34.91	1
Unknown	148.73	1
gb|Nicotiana tabacum mRNA for proteasome A-type subunit [Y16644]	184.61	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (63%) [TC5	26.57	1
Unknown	572.42	1
Unknown	30.41	1
Unknown	86.91	1
Unknown	18396.7	1
tc|Rep: Sucrose synthase - Solanum lycopersicum (Tomato) (Lycopersicon esculent	375.79	1
Unknown	256.59	1
Unknown	57.82	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	124.72	1
gb|KN6B.110L17F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.110L17, m	19217.6	1
gb|KP1B.109O08F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109O08, m	110.44	1

Unknown	28.66	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	122.84	1
gb|KL5B.104B08F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.104B08, mR	143.43	1
Unknown	26.56	1
Unknown	444.93	1
tc|Rep: Predicted protein - Chlamydomonas reinhardtii, partial (9%) [TC69281]	367.15	1
tc|Rep: Anionic peroxidase swpb1 - Ipomoea batatas (Sweet potato) (Batate), parti	272.65	1
Unknown	29.59	1
gb|KF8C.104H20F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104H20, mR	19.01	1
gb|TT-50_L03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	24.51	1
Unknown	434.74	1
tc|Rep: Flavin reductase domain protein, FMN-binding - Arthrobacter sp. (strain FB	31.31	1
gb|KL4B.107K22F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107K22, mR	23.28	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	458.83	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	223.98	1
Unknown	90.92	1
gb|FS435766 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	21.66	1
Unknown	125.34	1
Unknown	86.22	1
gb|TT-20_D22 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	1203.52	1
Unknown	24.76	1
Unknown	477.54	1
Unknown	224.28	1
gb|KL4B.103E08F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103E08, mR	83.1	1
tc|Rep: Os03g0254900 protein - Oryza sativa subsp. japonica (Rice), partial (62%) [T	7544.73	1
tc|Rep: WD domain protein-like - Arabidopsis thaliana (Mouse-ear cress), partial (3	192.2	1
Unknown	19.6	1
tc|Rep: Chromosome undetermined scaffold_3112, whole genome shotgun sequen	27.61	1
Unknown	167.28	1
tc|Rep: Bypass1 - Nicotiana benthamiana, partial (61%) [TC44015]	1562.92	1
gb|CHO_SL023xo07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	231.1	1
tc|Rep: 60S ribosomal protein L34 - Nicotiana tabacum (Common tobacco), comple	236.99	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	249.78	1
gb|TT-03_B19 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	477.26	1

gb|KN6B.009J12F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009J12, m	633.01	1
Unknown	94.14	1
tc|Rep: ATP citrate lyase alpha subunit - Glycyrrhiza uralensis, partial (38%) [TC414	20.25	1
tc|Rep: K+ potassium transporter - Limnobacter sp. MED105, partial (3%) [TC60498	129	1
gb|TT-19_B02 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	67.54	1
gb|Nicotiana tabacum chloroplast pigment-binding protein CP29 (Lhcb4) mRNA, co	291.08	1
Unknown	23.01	1
gb|TT-12_A08 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	513.92	1
gb|KP1B.105M23F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105M23,	476.87	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	27.38	1
gb|KF8C.104H02F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104H02, mR	68.75	1
gb|AGN_RPC009xd19f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	63.85	1
tc|Rep: Proton/glutamate symporter - Salinibacter ruber (strain DSM 13855), partia	71.12	1
gb|KT7B.100K02F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100K02, mR	323.52	1
Unknown	577.61	1
Unknown	52.24	1
gb|KP1B.108C22F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108C22, m	345.8	1
tc|Rep: Ferritin-1, chloroplast precursor - Nicotiana tabacum (Common tobacco), c	571.57	1
Unknown	85.84	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	34.39	1
Unknown	441.25	1
tc|Rep: Predicted protein - Monosiga brevicollis MX1, partial (5%) [TC67653]	474.26	1
Unknown	1143.24	1
gb|KG9B.101K13F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101K13, m	274.95	1
gb|EST_YP003xp04f1.ab1 EST_YP Nicotiana tabacum cDNA, mRNA sequence [EH61	176.02	1
gb|AGN_RNC021xf17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	71.21	1
tc|Rep: Uncharacterized protein At5g09230.6 - Arabidopsis thaliana (Mouse-ear cre	115.51	1
Unknown	235.83	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	29.28	1
gb|KF8C.103F17F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103F17, mRN	137.14	1
Unknown	630.25	1
gb|KG9B.001E11F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001E11, m	563.14	1
gb|KP1B.101L10F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101L10, m	1176.76	1
gb|CHO_SL003xa08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	7628.77	1

gb|BP532057 MAT005 Nicotiana tabacum cDNA clone BY26222, mRNA sequence [	26.97	1
tc|Rep: Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K9D7 - Arabi	280.1	1
tc|Rep: Chromosome chr16 scaffold_94, whole genome shotgun sequence - Vitis vi	939.09	1
Unknown	69.7	1
Unknown	447.22	1
Unknown	863.23	1
Unknown	86.41	1
tc|Rep: Protein transport protein SEC61 subunit gamma - Oryza sativa subsp. japon	1181.35	1
tc|Rep: Chromosome chr3 scaffold_95, whole genome shotgun sequence - Vitis vin	482.6	1
Unknown	220.2	1
gb|AM812473 seedling library, SL Nicotiana tabacum cDNA clone nt002287006, m	144.3	1
gb|Nicotiana tabacum NtWAF mRNA for hypothetical protein, complete cds [AB08	32.37	1
gb|TT-36_O24 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	19.15	1
tc|Rep: Nudix hydrolase 17, mitochondrial precursor - Arabidopsis thaliana (Mouse	923.17	1
tc|Rep: Integral membrane protein - Leifsonia xyli subsp. xyli, partial (7%) [TC57723	238.32	1
gb|CHO_SL007xf08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	3317.35	1
tc|Rep: Eukaryotic initiation factor 4A-6 - Nicotiana tabacum (Common tobacco), p	815.72	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	195.18	1
tc|Rep: Mitochondrial carrier-like protein - Solanum tuberosum (Potato), partial (5	59.84	1
Unknown	48.17	1
Unknown	18.93	1
gb|KT7B.103C07F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.103C07, mR	2463.56	1
tc|Rep: Mitochondrial F1-ATPase gamma subunit - Ipomoea nil (Japanese morning	1392.6	1
gb|KP1B.101L08F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101L08, m	3240.41	1
gb|KG9B.105O10F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105O10, r	1113.12	1
gb|KT7C.109M16F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109M16, m	515.51	1
Unknown	189.44	1
Unknown	92.51	1
Unknown	24.49	1
gb|AGN_RNC007xg14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	223.95	1
gb|N.tabacum NeIF-4A11 mRNA [X79136]	219.87	1
gb|TT-07_E11 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	132.46	1
tc|Rep: Chromosome 15 contig 1, DNA sequence - Ostreococcus tauri, partial (30%)	101.63	1
Unknown	18.56	1

tc|Rep: Chromosome chr4 scaffold_73, whole genome shotgun sequence - Vitis vin	256.95	1
gb|KF8C.101J21F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101J21, mRN	2445.1	1
gb|AGN_RNC116xi23f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	30.08	1
Unknown	32.76	1
tc|Rep: Chromosome chr5 scaffold_58, whole genome shotgun sequence - Vitis vin	35.39	1
Unknown	61.53	1
Unknown	228.21	1
gb|KP1B.104D09F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104D09, m	574.4	1
Unknown	21.09	1
gb|KT7C.108A08F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108A08, mR	155.02	1
gb|TDF16 Tobacco BY-2 ESTs modulated by Rhodococcus fascians Nicotiana tabacu	2403.66	1
gb|KP1B.109H20F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109H20, m	34.14	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	261.61	1
gb|AGN_RNC013xc01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	928.14	1
gb|TT-23_K17 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	133.35	1
gb|Nicotiana tabacum mRNA for nucleosome assembly protein 1 - like protein 1 [A	43.62	1
tc|Rep: Cyc07 - Nicotiana tabacum (Common tobacco), complete [TC44577]	408.18	1
tc|Rep: Alanine aminotransferase - Capsicum annuum (Bell pepper), partial (41%) [	267.64	1
gb|AGN_RPC016xd16f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	21.08	1
gb|Nicotiana tabacum mRNA for microtubule-associated protein MAP65-1c (map6	17.19	1
Unknown	29.84	1
Unknown	100.61	1
gb|Nicotiana tabacum L-galactose-1-phosphate phosphatase mRNA, complete cds	820.29	1
tc|Rep: Predicted protein - Populus tremula x Populus alba, partial (80%) [TC43847]	58.48	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT31-4-590, cultivar Bright Yellow 2	388.06	1
gb|KP1B.104D09F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104D09, m	517.94	1
tc|Rep: Chromosome chr18 scaffold_24, whole genome shotgun sequence - Vitis vi	65.93	1
gb|AGN_RNC116xe01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	44.6	1
Unknown	170.56	1
tc|Rep: S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC) [C	2771.79	1
tc|Rep: Heme-binding-like protein At3g10130, chloroplast precursor - Arabidopsis t	135.88	1
Unknown	648.29	1
gb|KG9B.104D21F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104D21,	20.9	1
Unknown	52.06	1

tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	21.26	1
gb|AGN_PNL223df1_d4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	6142.46	1
tc|Rep: Betaine aldehyde dehydrogenase - Panax ginseng (Korean ginseng), partial	64.7	1
tc|Rep: Chromosome undetermined scaffold_763, whole genome shotgun sequenc	194.67	1
gb|KF8C.101F22F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101F22, mRN	334.47	1
gb|KR3B.101E16F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101E16, m	519.2	1
Unknown	42.09	1
gb|BL12.101J09F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.101J09, mR	585.89	1
Unknown	137.87	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	224.74	1
gb|TT-22_A22 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	66.99	1
Unknown	33.28	1
gb|CHO_SL014xk02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	181.3	1
Unknown	18.69	1
tc|Rep: Ribosomal protein S27 - Vitis vinifera (Grape), complete [TC56735]	73.88	1
Unknown	49.65	1
gb|KR3B.113P03F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.113P03, m	1585.64	1
gb|AGN_RPC008xj24f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	65.76	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	219.95	1
tc|Rep: Pectin methylesterase precursor - Nicotiana plumbaginifolia (Leadwort-lea	923.63	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	104.97	1
gb|KL4B.105D03F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105D03, m	9991.6	1
gb|AGN_RNC020xh06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	497.02	1
tc|Rep: U2 snRNP auxiliary factor, large subunit - Nicotiana plumbaginifolia (Leadw	79.35	1
gb|AM802231 seedling library, SL Nicotiana tabacum cDNA clone nt002188047, m	829.83	1
tc|Rep: Chromosome chr9 scaffold_33, whole genome shotgun sequence - Vitis vin	516.36	1
gb|Nicotiana tabacum calcium-dependent protein kinase (CPK5) mRNA, complete	7911.7	1
tc|Rep: Plastid-lipid-Associated Protein - Nicotiana tabacum (Common tobacco), pa	142.82	1
gb|TT-34_M06 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	8456.05	1
Unknown	46.46	1
gb|KL4B.101E24F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101E24, mR	167.28	1
gb|CHO_SL003xl06f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	152.35	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	628.3	1
gb|AGN_RNC024xf04f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	75.38	1

gb|KR3B.112G03F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112G03, m	122.05	1
gb|TT-06_D16 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	79.67	1
tc|Rep: Chromosome chr4 scaffold_83, whole genome shotgun sequence - Vitis vin	55.09	1
Unknown	26.08	1
gb|BP134553 MAT001 Nicotiana tabacum cDNA clone BY6961, mRNA sequence [B	511.05	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	194	1
Unknown	8512.7	1
tc|Rep: Aconitase - Solanum pennellii (Tomato) (Lycopersicon pennellii), partial (40	934.3	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, complete [TC5815	27	1
gb|KT7C.105D13F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105D13, mR	20.01	1
gb|KL4B.105G06F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105G06, m	51.36	1
tc|Rep: Beta tubulin - Setaria viridis, partial (76%) [TC46386]	4313.96	1
gb|CHO_SL005xm18f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	44346.85	1
Unknown	674.3	1
gb|KG9B.104O21F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104O21, r	2686.04	1
Unknown	739.92	1
Unknown	85.68	1
gb|CHO_SL010xk15f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	20164.5	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	70.3	1
gb|CHO_SL028xe07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	267.77	1
gb|KL4B.112E14F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112E14, mR	53.37	1
gb|CHO_SL014xb10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	17.2	1
gb|AGN_RPC025xh13f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	28.33	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	37.85	1
Unknown	57.3	1
gb|KL4B.101F01F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101F01, mR	48.09	1
gb|KG9B.103D07F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103D07, n	768.82	1
tc|Rep: Uncharacterized protein At1g03900 - Arabidopsis thaliana (Mouse-ear cres	171.39	1
gb|BP525788 MAT001 Nicotiana tabacum cDNA clone BY10478, mRNA sequence [	272.28	1
Unknown	37.68	1
gb|KP1B.109O02F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109O02, m	92.53	1
tc|Rep: Nthsp18p - Nicotiana tabacum (Common tobacco), complete [TC72115]	18.42	1
gb|KF8C.105B01F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105B01, mR	1574.82	1
gb|KL5B.116F12F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.116F12, mR	75.49	1

tc|GB|AF053076.1|AAC06242.1 late embryogenis abundant protein 5 [Nicotiana ta	1544.34	1
Unknown	117.42	1
tc|Rep: Photosystem I psaH protein precursor - Nicotiana sylvestris (Wood tobacco	26.72	1
Unknown	204.6	1
Unknown	10860.85	1
gb|AM793808 seedling library, SL Nicotiana tabacum cDNA clone nt002044052, mR	21.14	1
gb|TT-36_I01 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	95.07	1
tc|Rep: Chromosome chr17 scaffold_101, whole genome shotgun sequence - Vitis v	56.27	1
Unknown	92.31	1
gb|AGN_PNL231br1_e4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	160.88	1
Unknown	984.43	1
gb|AGN_PNL231br1_b4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	17.23	1
gb|KP1B.001H09F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001H09, m	928.45	1
Unknown	148.23	1
tc|Rep: Predicted protein - Nematostella vectensis (Starlet sea anemone), partial (3	56665.3	1
gb|KG9B.103I01F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103I01, mR	152.13	1
Unknown	2759.75	1
gb|KR3B.112C03F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112C03, m	25.23	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	162.27	1
gb|KF8C.101A08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101A08, mRN	87.65	1
Unknown	99.77	1
gb|TT-39_B06 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	256.13	1
tc|Rep: Syntaxin-like protein - Solanum tuberosum (Potato), partial (50%) [TC66570	2927.75	1
tc|Rep: eukaryotic translation initiation factor 2 family protein / eIF-2 family protein	259.54	1
gb|KT7C.106J01F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106J01, mRN	23.65	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	283.58	1
Unknown	254.56	1
gb|KG9B.004C13F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004C13, m	506.41	1
tc|Rep: Chromosome chr11 scaffold_14, whole genome shotgun sequence - Vitis vi	15925.65	1
gb|KT7C.105L01F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105L01, mRN	171.53	1
gb|FS433680 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	114.84	1
tc|Rep: Inositol polyphosphate kinase - Solanum tuberosum (Potato), partial (36%)	134.76	1
gb|KT7C.106P02F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106P02, mRN	61.44	1
tc|Rep: Chromosome undetermined scaffold_30, whole genome shotgun sequence	912.86	1

gb|KN6B.104A12F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104A12, m	419.23	1
Unknown	36.23	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	145.06	1
gb|N.tabacum npp3 mRNA for protein phosphatase type 1 [Z93770]	57.09	1
Unknown	262.22	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	20.82	1
tc|Rep: SGT1-2 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), partia	57.8	1
gb|EST_CSP008xd16f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	64.61	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	449.36	1
gb|KG9B.103C13F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103C13, m	49.23	1
gb|AGN_ELP022xk22f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	120.34	1
gb|KP1B.105F01F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105F01, mR	529.95	1
tc|Rep: Ribosomal protein L24-like protein - Solanum tuberosum (Potato), partial (2	89.09	1
gb|AGN_PNL230br1_b2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	145.68	1
tc|Rep: Chromosome chr12 scaffold_38, whole genome shotgun sequence - Vitis vi	1171.65	1
gb|Nicotiana tabacum AGP4 mRNA for AG-motif binding protein-4, complete cds [A	1115.7	1
gb|Nicotiana tabacum NtTOM3 mRNA for tobamovirus multiplication 3, complete c	10380.05	1
gb|AGN_RNC021xh10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	21.08	1
gb|BP137050 MAT001 Nicotiana tabacum cDNA clone BY9702, mRNA sequence [B	181.23	1
tc|Rep: ATP synthase delta chain - Buchnera aphidicola subsp. Schizaphis graminum	92	1
gb|KF8C.103I08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103I08, mRNA	468.31	1
gb|AGN_RNC026xn20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	621.5	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	107.61	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	29.34	1
gb|KR3B.104F16F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.104F16, mR	52.74	1
gb|FS435443 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	220.24	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	113.53	1
Unknown	174.54	1
gb|KF8C.102H18F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102H18, mR	2682.92	1
Unknown	737.92	1
Unknown	40.18	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	17567.2	1
gb|TT-40_M13 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	313.07	1
gb|Nicotiana tabacum mRNA for 14-3-3 a-1 protein, complete cds [AB119466]	3720.45	1

gb|Nicotiana tabacum NtMFP mRNA for multifunctional protein, complete cds [AB4	47.74	1
tc|Rep: DNA mismatch repair protein - Solanum lycopersicum (Tomato) (Lycopersic	22.91	1
tc|Rep: Chromosome undetermined scaffold_77, whole genome shotgun sequence	139.25	1
tc|Rep: 40S ribosomal protein S25 - Solanum lycopersicum (Tomato) (Lycopersicon	178.84	1
gb|KL4B.105A10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105A10, mR	2655.93	1
gb|Nicotiana tabacum DNA-directed RNA polymerase IIb (NT193) mRNA, complete	94.63	1
gb|KP1B.102E02F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102E02, mR	55.31	1
tc|Rep: Chromosome undetermined scaffold_142, whole genome shotgun sequenc	112.85	1
gb|AGN_ELP010xg05f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	56.38	1
tc|Rep: Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vi	320.76	1
tc|Rep: Chromosome chr12 scaffold_38, whole genome shotgun sequence - Vitis vi	1076.56	1
gb|KR2B.110H02F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110H02, m	31.47	1
gb|Nicotiana tabacum plastid phosphate [U66401]	274.83	1
tc|Rep: Ribosomal protein L33 - Castanea sativa (Sweet chestnut), complete [TC492	146.81	1
Unknown	25.34	1
Unknown	44.48	1
gb|AM831732 seedling library, SL Nicotiana tabacum cDNA clone nt002273057, mR	18.92	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	109.33	1
gb|TT-49_H10 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	256.83	1
Unknown	1595.32	1
Unknown	92.53	1
Unknown	684.95	1
gb|KT7C.112H06F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112H06, mR	2426.7	1
Unknown	4218.18	1
Unknown	177.37	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	562.99	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	151.77	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	525.03	1
gb|KN6B.105M12F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105M12,	464.76	1
gb|KN6B.100E17F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100E17, m	993.75	1
gb|AM835801 seedling library, SL Nicotiana tabacum cDNA clone nt002090022, mR	31.81	1
Unknown	41.6	1
gb|TT-14_N05 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	42.45	1
Unknown	408.44	1

gb|KP1B.109O08F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109O08, m	152.44	1
tc|Rep: Dehydroquinate synthase - Solanum lycopersicum (Tomato) (Lycopersicon	508.91	1
Unknown	2857.19	1
gb|KT7C.101K21F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.101K21, mR	2989.93	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	32.48	1
gb|KG9B.106E24F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106E24, m	89.36	1
gb|TT-36_P22 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	602.5	1
gb|Nicotiana tabacum phospholipase C2 mRNA, complete cds [AF223573]	27.1	1
tc|Rep: Beta tubulin - Setaria viridis, partial (47%) [TC42115]	9592	1
gb|KF8C.106C20F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106C20, mR	564.47	1
gb|KL5B.011M16F.051129T7 KL5B Nicotiana tabacum cDNA clone KL5B.011M16,	573.03	1
gb|KR3B.103C13F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.103C13, m	5263.62	1
Unknown	29.52	1
Unknown	54.58	1
gb|KF8B.201C11F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201C11, mR	27.88	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	49.87	1
Unknown	58.98	1
gb|KG9B.106D04F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106D04,	146.2	1
gb|KG9B.005J14F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005J14, m	564.23	1
tc|Rep: Isocitrate dehydrogenase [NADP] (Oxalosuccinate decarboxylase) (IDH) (N	55.72	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	80.51	1
Unknown	139	1
gb|TT-41_F01 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	51.83	1
gb|KF8B.202P11F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202P11, mR	20854.95	1
Unknown	29.91	1
Unknown	1031.78	1
Unknown	86.33	1
gb|KL4B.102D19F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102D19, m	258.27	1
tc|Rep: Expressed protein - Arabidopsis thaliana (Mouse-ear cress), partial (20%) [T	138.94	1
gb|KT7B.100B15F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100B15, mR	51830.9	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	33.52	1
gb|KF8C.103D10F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103D10, mR	82.05	1
tc|Rep: Carotenoid cleavage dioxygenase 1B - Solanum lycopersicum (Tomato) (Lyc	108.68	1
Unknown	10836.45	1

tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	95.99	1
tc|Rep: UP-9A - Nicotiana tabacum (Common tobacco), complete [TC51728]	44.66	1
gb|AGN_RNC127xf06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	55.54	1
Unknown	122.34	1
Unknown	259.76	1
gb|AGN_RNC111xf20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	20.91	1
tc|Rep: Chromosome chr8 scaffold_68, whole genome shotgun sequence - Vitis vin	43.34	1
gb|KL4B.108D06F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108D06, m	20.76	1
gb|KL4B.101M04F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101M04, m	524.76	1
tc|Rep: Ripening regulated protein DDTFR10-like - Solanum tuberosum (Potato), pa	593.23	1
Unknown	62.45	1
tc|Rep: Chromosome chr10 scaffold_138, whole genome shotgun sequence - Vitis	121.35	1
gb|KG9B.102L19F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102L19, m	57.63	1
tc|Rep: High mobility group protein 2 HMG2 - Ipomoea nil (Japanese morning glory	5535.92	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	92.52	1
gb|AM802407 DL, diurnal library Nicotiana tabacum cDNA clone nt005088022, mR	64.81	1
gb|Nicotiana tabacum partial mRNA for villin 1 (vln1 gene) [AJ577852]	4563.2	1
tc|Rep: Thiosulfate sulfurtransferase - Datisca glomerata (Durango root), partial (5	31.2	1
Unknown	214.35	1
tc|Rep: Extracellular solute-binding protein, family 1 precursor - Roseiflexus sp. (str	31.59	1
gb|KG9B.101N18F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101N18,	199.03	1
tc|Rep: Chromosome chr8 scaffold_150, whole genome shotgun sequence - Vitis vi	578.94	1
tc|Rep: Vacuolar protein sorting-associated protein 26-like protein - Solanum tuber	150.3	1
tc|Rep: Chromosome chr4 scaffold_83, whole genome shotgun sequence - Vitis vin	105.8	1
gb|KG9B.001A15F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001A15,	133.04	1
Unknown	312.21	1
Unknown	43.3	1
gb|KL4B.111N06F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111N06, m	27.25	1
tc|Rep: 14-3-3 e-1 protein - Nicotiana tabacum (Common tobacco), complete [TC4	34.62	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	379.64	1
Unknown	435.67	1
Unknown	30.16	1
gb|KF8C.104D06F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104D06, mR	152.01	1
tc|Rep: Eukaryotic initiation factor 4A-3 - Nicotiana plumbaginifolia (Leadwort-leav	948.4	1

gb|CHO_SL018xn22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	35.97	1
tc|Rep: At4g40042 - Arabidopsis thaliana (Mouse-ear cress), partial (88%) [TC65781	721.01	1
Unknown	100.94	1
Unknown	26.39	1
gb|BP128992 MAT001 Nicotiana tabacum cDNA clone BY816, mRNA sequence [BP1	103.13	1
gb|KP1B.104H11F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104H11, m	60.01	1
Unknown	126.07	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (7%) [TC74	218.29	1
tc|Rep: Alanine aminotransferase - Capsicum annuum (Bell pepper), partial (41%) [	99.89	1
Unknown	109.4	1
Unknown	56.24	1
Unknown	472.16	1
tc|Rep: Chromosome undetermined scaffold_334, whole genome shotgun sequenc	107.27	1
gb|UFRST92 tobacco root and stem SSH cDNA Library Nicotiana tabacum cDNA, m	120.12	1
Unknown	101.81	1
Unknown	745.75	1
Unknown	3317.22	1
gb|KF8C.101G01F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101G01, mR	536.73	1
tc|Rep: EIN2 - Petunia hybrida (Petunia), partial (19%) [TC50365]	18.97	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	967.99	1
Unknown	980.85	1
tc|Rep: Mevalonate kinase - Hevea brasiliensis (Para rubber tree), partial (91%) [TC	144.12	1
gb|KG9B.004C13F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004C13, m	62.68	1
tc|Rep: Proteasome subunit alpha type - Vitis vinifera (Grape), partial (74%) [TC440	198.87	1
tc|Rep: Isoform 2 of Q8L828 - Arabidopsis thaliana (Mouse-ear cress), partial (13%	654.48	1
tc|Rep: OrfB protein - Nicotiana tabacum (Common tobacco), complete [TC46100]	289.47	1
Unknown	219.56	1
tc|Rep: Glyceraldehyde-3-phosphate dehydrogenase - Nicotiana tabacum (Commo	91.69	1
Unknown	56.4	1
gb|KL4B.101L06F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101L06, mR	1329.98	1
gb|BP534527 MAT005 Nicotiana tabacum cDNA clone BY33107, mRNA sequence [	219.37	1
tc|Rep: ADP-ribosylation factor - Hyacinthus orientalis (Common hyacinth), partial	10597.6	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (87%) [TC6	194.14	1
Unknown	18.06	1

<table>
<tr><td>gb|KL5B.109O08F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.109O08, m</td><td>2410.7</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin</td><td>248.53</td><td>1</td></tr>
<tr><td>Unknown</td><td>128.84</td><td>1</td></tr>
<tr><td>gb|KL5B.103D14F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.103D14, m</td><td>163.56</td><td>1</td></tr>
<tr><td>gb|AGN_RNC012xp10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc</td><td>70.12</td><td>1</td></tr>
<tr><td>Unknown</td><td>1526.26</td><td>1</td></tr>
<tr><td>gb|TT-03_J18 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se</td><td>82.42</td><td>1</td></tr>
<tr><td>tc|Rep: Histone H2A - Euphorbia esula (Leafy spurge), partial (95%) [TC53700]</td><td>404.78</td><td>1</td></tr>
<tr><td>Unknown</td><td>35.24</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin</td><td>143.75</td><td>1</td></tr>
<tr><td>gb|TT-07_C15 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se</td><td>496.83</td><td>1</td></tr>
<tr><td>gb|KF8C.105A17F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105A17, mR</td><td>55.44</td><td>1</td></tr>
<tr><td>gb|KL4B.103P04F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103P04, mR</td><td>11728.35</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi</td><td>437.11</td><td>1</td></tr>
<tr><td>gb|KP1B.108C05F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108C05, m</td><td>164.38</td><td>1</td></tr>
<tr><td>gb|TT-29_G12 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq</td><td>116.53</td><td>1</td></tr>
<tr><td>Unknown</td><td>8754.4</td><td>1</td></tr>
<tr><td>gb|Nicotiana tabacum calcium-dependent protein kinase CDPK5 (CDPK5) mRNA, co</td><td>21.25</td><td>1</td></tr>
<tr><td>gb|KN6B.101I24F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101I24, m</td><td>53.13</td><td>1</td></tr>
<tr><td>gb|TT-09_K02 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence</td><td>1529.43</td><td>1</td></tr>
<tr><td>gb|KG9B.002P06F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002P06, m</td><td>155.29</td><td>1</td></tr>
<tr><td>Unknown</td><td>201.23</td><td>1</td></tr>
<tr><td>gb|KR2B.107K23F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.107K23, m</td><td>922.76</td><td>1</td></tr>
<tr><td>Unknown</td><td>159.9</td><td>1</td></tr>
<tr><td>Unknown</td><td>228.86</td><td>1</td></tr>
<tr><td>gb|AGN_RNC124xe12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc</td><td>49.81</td><td>1</td></tr>
<tr><td>tc|Rep: Ferredoxin - Impatiens balsamina (Balsam), partial (79%) [TC48877]</td><td>919.11</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi</td><td>250.73</td><td>1</td></tr>
<tr><td>Unknown</td><td>2135.8</td><td>1</td></tr>
<tr><td>Unknown</td><td>27.32</td><td>1</td></tr>
<tr><td>tc|Rep: Galactose-1-phosphate uridylyltransferase - Vitis vinifera (Grape), partial (9</td><td>1863.77</td><td>1</td></tr>
<tr><td>gb|KT7C.101J05F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.101J05, mRN</td><td>116.11</td><td>1</td></tr>
<tr><td>gb|TT-27_F19 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence</td><td>252.87</td><td>1</td></tr>
<tr><td>gb|KT7B.107L23F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107L23, mRN</td><td>91.26</td><td>1</td></tr>
</table>

gb|ntsm41 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [E	80.91	1
Unknown	37.89	1
gb|TT-08_H01 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	149.71	1
gb|BP128500 MAT001 Nicotiana tabacum cDNA clone BY252, mRNA sequence [BP	30.43	1
gb|Nicotiana tabacum ferritin mRNA, complete cds [AY083924]	919.85	1
gb|KF8C.103H08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103H08, mR	989.28	1
tc|Rep: Extensin - Nicotiana tabacum (Common tobacco), partial (98%) [TC76880]	150.43	1
gb|KF8C.106O02F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106O02, mR	56.72	1
gb|KR2B.109M17F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.109M17,	181.68	1
gb|KT7C.110P16F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110P16, mR	31.72	1
Unknown	56.53	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	613.99	1
Unknown	45.93	1
Unknown	39.27	1
Unknown	62.99	1
Unknown	104.18	1
tc|Rep: ADP,ATP carrier protein 1, mitochondrial precursor - Gossypium hirsutum (	18698.5	1
Unknown	513.02	1
tc|Rep: BH1020 protein - Bacillus halodurans, partial (6%) [TC76180]	208.54	1
Unknown	218.45	1
gb|CHO_SL005xf23f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	97.78	1
tc|Rep: At2g36630/F1O11.26 - Arabidopsis thaliana (Mouse-ear cress), partial (21%	864.61	1
gb|KR3B.108K21F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.108K21, m	32.65	1
gb|TT-41_B17 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	72.35	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	29.53	1
gb|AM831626 DL, diurnal library Nicotiana tabacum cDNA clone nt005230023, mR	24.82	1
Unknown	2902.32	1
tc|Rep: Chromosome undetermined scaffold_528, whole genome shotgun sequenc	438.01	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	1592.25	1
tc|Rep: Bromodomain-containing RNA-binding protein 2 - Nicotiana tabacum (Com	2408.03	1
tc|Rep: Chromosome chr11 scaffold_14, whole genome shotgun sequence - Vitis vi	491.11	1
Unknown	146.87	1
gb|KF8C.101D01F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101D01, mR	28321.3	1
Unknown	2712.93	1

Unknown	63.59	1
Unknown	81.21	1
Unknown	2656.63	1
gb|AGN_RNC106xk10r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	17.58	1
tc|Rep: SUMO protein - Solanum lycopersicum (Tomato) (Lycopersicon esculentum	788.84	1
gb|FS436463 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	52.76	1
gb|KN6B.102G06F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102G06, r	4891.31	1
Unknown	189.28	1
tc|Rep: T-complex protein 1, alpha subunit - Bruguiera sexangula, partial (38%) [TC	90	1
tc|Rep: 60S ribosomal protein l2 - Oryza sativa subsp. indica (Rice), partial (36%) [T	90.87	1
Unknown	101.85	1
tc|Rep: Chromosome chr12 scaffold_103, whole genome shotgun sequence - Vitis v	1131.7	1
gb|KG9B.103K07F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103K07, m	706.84	1
tc|Rep: CDK/cyclin inhibitor - Nicotiana sylvestris (Wood tobacco), complete [TC61	589.07	1
gb|KR3B.104G23F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.104G23, m	84.32	1
gb|KG9B.002G08F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002G08, n	226.06	1
Unknown	862.15	1
tc|Rep: AT3g20300/MQC12_5 - Arabidopsis thaliana (Mouse-ear cress), partial (18	79.17	1
Unknown	22.62	1
gb|KP1B.102J06F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102J06, mR	650.47	1
Unknown	253.74	1
Unknown	937.04	1
gb|KG9B.005H08F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005H08, n	250.84	1
gb|AGN_ELP014xc17f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	60.05	1
Unknown	1529.81	1
Unknown	5817.67	1
gb|N.tabacum mRNA for L-Glutamate:tRNA-Glu ligase [X83524]	268.18	1
tc|Rep: CAX-interacting protein 4 - Arabidopsis thaliana (Mouse-ear cress), partial (	271.62	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	2946.68	1
tc|Rep: 60S ribosomal protein L21-like protein - Solanum tuberosum (Potato), comp	967.55	1
gb|KN6B.104C22F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104C22, m	23.2	1
Unknown	710.89	1
gb|AGN_PNL215df1_e5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	42.53	1
Unknown	90.96	1

tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	20.86	1
tc|Rep: Mitochondrial-processing peptidase subunit alpha, mitochondrial precurso	1508.11	1
tc|Rep: Chromosome chr2 scaffold_112, whole genome shotgun sequence - Vitis vi	182.86	1
gb|KP1B.101E03F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101E03, m	215	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	496.47	1
tc|Rep: Molecular chaperone Hsp90-2 - Nicotiana benthamiana, partial (25%) [TC4	365.6	1
gb|Peg94C Early stage of anther development specific suppression subtractive cDN	56.13	1
Unknown	26.91	1
gb|KT7C.112J04F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112J04, mRN	469.31	1
Unknown	26.32	1
Unknown	18.96	1
tc|Rep: Uncharacterized aarF domain-containing protein kinase At5g05200, chloro	25.62	1
gb|KF8B.201B11F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201B11, mR	44.88	1
gb|KG9B.001M18F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001M18,	32.36	1
tc|Rep: Chloroplast methionine sulfoxide reductase B1 precursor - Nicotiana tabac	397.08	1
gb|KF8B.100P17F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100P17, mR	151.44	1
Unknown	58.05	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	11226.8	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	23.9	1
tc|Rep: Chromosome chr10 scaffold_76, whole genome shotgun sequence - Vitis vi	172.54	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	90.91	1
gb|CHO_SL010xe03f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1194.86	1
tc|GB|AJ291736.1|CAC43321.1 putative beta proteasome subunit [Nicotiana taba	27.69	1
tc|Rep: Serine/threonine protein phosphatase - Vitis vinifera (Grape), partial (24%)	254.74	1
gb|KP1B.001J22F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001J22, mR	112.44	1
tc|Rep: Multidrug Resistance associated Protein 1 - Catharanthus roseus (Rosy peri	101.24	1
gb|AB032546 Nicotiana tabacum immature pollen grains Nicotiana tabacum cDNA	32223.15	1
gb|KR2B.001N12F.050815T7 KR2B Nicotiana tabacum cDNA clone KR2B.001N12, m	107.53	1
tc|Rep: Superoxide dismutase [Cu-Zn] - Populus tremula x Populus tremuloides, par	19.42	1
gb|KG9B.002K23F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002K23, m	490.24	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	1566.38	1
gb|AGN_PNL219ar1_c5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	88.15	1
Unknown	26.2	1
gb|KL4B.104F10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104F10, mR	100.68	1

tc|Rep: Chromosome undetermined scaffold_100, whole genome shotgun sequenc	27.04	1
gb|KF8C.105K17F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105K17, mRN	24.87	1
gb|CHO_SL023xn20f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1115.57	1
gb|KP1B.105G14F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105G14, m	23.42	1
Unknown	18721.4	1
gb|KL4B.106I23F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106I23, mRN	29.77	1
gb|KR2B.001F01F.050815T7 KR2B Nicotiana tabacum cDNA clone KR2B.001F01, mR	192.81	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	112.1	1
Unknown	139.42	1
tc|Rep: UDP-glucose glucosyltransferase - Catharanthus roseus (Rosy periwinkle) (M	55.53	1
gb|KP1B.103J10F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103J10, mR	520.63	1
Unknown	32.29	1
gb|KF8C.106J19F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106J19, mRN	227.93	1
Unknown	17.78	1
tc|Rep: Alpha-soluble NSF attachment protein - Solanum tuberosum (Potato), parti	1237.3	1
tc|Rep: S-adenosylmethionine decarboxylase - Prunus persica (Peach), partial (52%)	243.61	1
gb|KL4B.113C20F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.113C20, mR	100.26	1
gb|BL12.101F22F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.101F22, mR	60.76	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	60.84	1
Unknown	797.22	1
gb|KL4B.102E08F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102E08, mR	186.45	1
tc|Rep: AT5g51450/MFG13_16 - Arabidopsis thaliana (Mouse-ear cress), partial (21	355.47	1
Unknown	23.35	1
gb|FS433102 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	32.15	1
gb|KR2B.002I08F.051019T7 KR2B Nicotiana tabacum cDNA clone KR2B.002I08, mR	112.6	1
gb|KT7C.104J03F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104J03, mRN	804.24	1
gb|KL4B.113D22F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.113D22, mR	285.37	1
gb|KF8B.200N01F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200N01, mR	18.26	1
tc|Rep: 40S ribosomal protein S15a-1 - Arabidopsis thaliana (Mouse-ear cress), com	122.62	1
gb|KR2B.001D18F.050815T7 KR2B Nicotiana tabacum cDNA clone KR2B.001D18, m	60.75	1
Unknown	25.03	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	393.86	1
Unknown	24.56	1
tc|Rep: EF hand family protein - Solanum demissum (Wild potato), partial (92%) [T	1495.95	1

tc|Rep: Hypoxia-responsive family protein - Citrus sinensis (Sweet orange), partial (	1525.26	1
gb|KG9B.005C11F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005C11, m	32.55	1
gb|KP1B.101D02F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101D02, m	142.76	1
gb|KT7B.107E21F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107E21, mRN	3233.74	1
tc|Rep: GAMYB-like2 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum),	1521.43	1
gb|EST_CSP004xc12f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	144.53	1
tc|Rep: Microsomal omega-6-desaturase - Nicotiana tabacum (Common tobacco),	19400.15	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	121.41	1
gb|KF8B.201A19F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201A19, mRN	25.61	1
gb|AGN_PNL229af1_c1.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	22.82	1
tc|Rep: Alcohol dehydrogenase class III-like protein - Solanum tuberosum (Potato),	147.01	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	233.32	1
tc|Rep: Chromosome chr17 scaffold_101, whole genome shotgun sequence - Vitis v	524.46	1
tc|Rep: Chromosome chr11 scaffold_170, whole genome shotgun sequence - Vitis v	330.09	1
gb|TT-11_O20 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	80.04	1
tc|Rep: Hsp20.1 protein - Solanum peruvianum (Peruvian tomato) (Lycopersicon pe	136.28	1
gb|KR3B.104I14F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.104I14, mR	29.88	1
Unknown	63.77	1
gb|KT7C.108D17F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108D17, mR	370.39	1
Unknown	36.56	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	1746.62	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	25.67	1
gb|CHO_SL015xd16f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	254.85	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	1581.05	1
gb|N.tabacum mRNA for acidic chitinase PR-P [X51426]	58.22	1
Unknown	57.82	1
Unknown	128.62	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	239.07	1
gb|TT-36_L21 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	22.76	1
tc|Rep: Ubiquitin carrier protein - Arachis hypogaea (Peanut), complete [TC48462]	141.68	1
gb|KF8C.105M11F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105M11, m	10276.9	1
tc|Rep: Chromosome chr5 scaffold_98, whole genome shotgun sequence - Vitis vin	99.97	1
gb|Nicotiana tabacum mRNA for ras-related protein RAB8-4, complete cds [AB079	4421.82	1
gb|Nicotiana tabacum dehydroascorbate reductase (DHAR) mRNA, complete cds [A	84.34	1

<table>
<tr><td>tc|Rep: Protein kinase SRK - Nicotiana tabacum (Common tobacco), partial (44%) [T</td><td>26.81</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin</td><td>184.3</td><td>1</td></tr>
<tr><td>tc|Rep: F5D14.18 protein - Arabidopsis thaliana (Mouse-ear cress), partial (15%) [T</td><td>73.57</td><td>1</td></tr>
<tr><td>Unknown</td><td>60.89</td><td>1</td></tr>
<tr><td>tc|Rep: Dynein light chain - Lupinus albus (White lupin), partial (71%) [TC70067]</td><td>77.66</td><td>1</td></tr>
<tr><td>Unknown</td><td>37.17</td><td>1</td></tr>
<tr><td>Unknown</td><td>180.22</td><td>1</td></tr>
<tr><td>tc|Rep: Osr40g2 protein - Oryza sativa (Rice), partial (27%) [TC56940]</td><td>1927.93</td><td>1</td></tr>
<tr><td>Unknown</td><td>106.96</td><td>1</td></tr>
<tr><td>Unknown</td><td>81.82</td><td>1</td></tr>
<tr><td>tc|Rep: MRNA, , clone: RAFL25-03-N20 - Arabidopsis thaliana (Mouse-ear cress), pa</td><td>235.49</td><td>1</td></tr>
<tr><td>tc|Rep: ALY protein - Nicotiana benthamiana, complete [TC50221]</td><td>204.28</td><td>1</td></tr>
<tr><td>gb|KP1B.110G13F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110G13, m</td><td>31.44</td><td>1</td></tr>
<tr><td>gb|AGN_PNL222af1_c12.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN</td><td>2897.67</td><td>1</td></tr>
<tr><td>Unknown</td><td>263.69</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi</td><td>1693.03</td><td>1</td></tr>
<tr><td>gb|FS417555 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA</td><td>1007.85</td><td>1</td></tr>
<tr><td>gb|KP1B.001I21F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001I21, mR</td><td>30.14</td><td>1</td></tr>
<tr><td>gb|TT-13_M02 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA se</td><td>53.8</td><td>1</td></tr>
<tr><td>gb|EST_FLW001xk08f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E</td><td>37.99</td><td>1</td></tr>
<tr><td>gb|Nicotiana tabacum NtSIP2 mRNA for 6b-interacting protein 2, complete cds [AB</td><td>49.89</td><td>1</td></tr>
<tr><td>Unknown</td><td>2315.39</td><td>1</td></tr>
<tr><td>tc|Rep: At2g37790 - Arabidopsis thaliana (Mouse-ear cress), partial (50%) [TC4543</td><td>72.91</td><td>1</td></tr>
<tr><td>Unknown</td><td>95.36</td><td>1</td></tr>
<tr><td>Unknown</td><td>37.04</td><td>1</td></tr>
<tr><td>gb|TT-04_H19 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F</td><td>135.36</td><td>1</td></tr>
<tr><td>gb|Nicotiana tabacum BYtuba mRNA for alpha tubulin, complete cds [AB052822]</td><td>45013.8</td><td>1</td></tr>
<tr><td>Unknown</td><td>596.31</td><td>1</td></tr>
<tr><td>Unknown</td><td>36.49</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin</td><td>43.21</td><td>1</td></tr>
<tr><td>gb|AGN_RNC019xl15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc</td><td>31.19</td><td>1</td></tr>
<tr><td>tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin</td><td>3250.42</td><td>1</td></tr>
<tr><td>gb|KG9B.001O11F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001O11,</td><td>25.16</td><td>1</td></tr>
<tr><td>tc|Rep: Predicted protein - Chaetomium globosum (Soil fungus), partial (10%) [TC6</td><td>110.69</td><td>1</td></tr>
</table>

Unknown	87.55	1
gb|CHO_SL015xd16f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	3250.31	1
gb|Nicotiana tabacum ferritin 2 (Fer2) mRNA, complete cds [AY141105]	66.66	1
Unknown	153.66	1
gb|KL4B.110M02F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110M02, m	118.1	1
tc|Rep: 1,4-alpha-glucan branching enzyme - Solanum tuberosum (Potato), partial (	27.85	1
Unknown	42.81	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	227.01	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	154.41	1
Unknown	114.1	1
gb|KG9B.102A05F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102A05, m	68.39	1
gb|KF8C.106G13F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106G13, mR	296.41	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	7331.72	1
tc|Rep: Programmed cell death protein 6 (Probable calcium-binding protein ALG- 2	39.06	1
gb|TT-09_H15 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	172.64	1
gb|AGN_ELP012xa20f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	40.92	1
tc|Rep: Protein tyrosine phosphatase - Phaseolus vulgaris (Kidney bean) (French be	23.38	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	62.37	1
Unknown	142.34	1
gb|AM818654 COL, cold overnight library Nicotiana tabacum cDNA clone nt006195	8090.53	1
Unknown	48.24	1
Unknown	32.29	1
gb|Nicotiana tabacum proline oxidase [AY639146]	1421.62	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	35667.85	1
gb|TOBESTR029D10 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	861.47	1
Unknown	743.11	1
tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	1512.29	1
gb|AGN_RNC102xe07f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	27.64	1
gb|KF8C.105M04F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105M04, m	60.19	1
gb|BP136083 MAT001 Nicotiana tabacum cDNA clone BY8654, mRNA sequence [B	27.51	1
gb|KG9B.103K10F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103K10, m	273.56	1
Unknown	883.96	1
tc|Rep: Chromosome chr10 scaffold_179, whole genome shotgun sequence - Vitis	588.21	1
gb|TT-35_J14 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	23.47	1

tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	1455.18	1
gb|AM817228 seedling library, SL Nicotiana tabacum cDNA clone nt002051027, mR	43	1
gb|KR3B.110P06F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110P06, m	82.33	1
tc|Rep: WERBP-1 protein - Nicotiana tabacum (Common tobacco), partial (41%) [TC	300.09	1
Unknown	21.3	1
gb|KT7C.104G04F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104G04, mR	64.02	1
gb|CHO_SL022xd02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	538.11	1
Unknown	65.88	1
Unknown	4056.6	1
Unknown	128.88	1
gb|CHO_SL010xj06f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	610.13	1
gb|TT-24_E16 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	86.19	1
tc|Rep: Chromosome undetermined scaffold_77, whole genome shotgun sequence	527.18	1
gb|FS418200 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	179.97	1
gb|KL4B.104J05F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104J05, mR	97.09	1
tc|Rep: RNA Binding Protein 45 - Nicotiana plumbaginifolia (Leadwort-leaved tobac	215.72	1
Unknown	32.28	1
Unknown	1449.64	1
gb|KT7B.107B02F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107B02, mR	56.64	1
gb|KR3B.102G14F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.102G14, m	174.41	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	21.95	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	3230.48	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	124.11	1
gb|KL5B.103C20F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.103C20, mR	51.66	1
gb|TT-38_G14 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	39.67	1
tc|Rep: Chromosome chr9 scaffold_104, whole genome shotgun sequence - Vitis vi	22.59	1
gb|KR2B.112G07F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.112G07, m	941.8	1
tc|Rep: Chromosome chr14 scaffold_54, whole genome shotgun sequence - Vitis vi	280.71	1
Unknown	155.4	1
gb|KG9B.105A06F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105A06, m	45.3	1
gb|KP1B.109H16F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109H16, m	662.92	1
gb|Nicotiana tabacum Ntmy170 mRNA for myosin XI, complete cds [AB180675]	32.52	1
gb|AGN_RNC025xc19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	178.14	1
gb|Nicotiana tabacum mRNA for FtsZ-like chloroplast protein [AJ133453]	74.51	1

Unknown	46.13	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	52.46	1
gb|KG9B.003K23F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003K23, m	22.2	1
tc|Rep: HrcQ - Pseudomonas cichorii, partial (5%) [TC42590]	25.7	1
Unknown	21.05	1
tc|Rep: Cell growth defect factor-like - Solanum tuberosum (Potato), partial (59%) [	268.25	1
Unknown	506.32	1
Unknown	133.84	1
Unknown	39.61	1
gb|BP530047 MAT005 Nicotiana tabacum cDNA clone BY21025, mRNA sequence [	101.46	1
tc|Rep: Elongation factor 1-alpha - Nicotiana paniculata, partial (23%) [TC64911]	642.78	1
tc|Rep: Chromosome chr2 scaffold_112, whole genome shotgun sequence - Vitis vi	32.73	1
gb|AGN_RNC012xl06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	34.12	1
Unknown	613.06	1
tc|Rep: Acetolactate synthase 2, chloroplast precursor - Nicotiana tabacum (Comm	56.01	1
tc|Rep: Chromosome chr14 scaffold_211, whole genome shotgun sequence - Vitis v	66.13	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	22.45	1
gb|KG9B.001B09F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001B09, m	137.08	1
Unknown	732.68	1
tc|Rep: MYBR6 - Malus domestica (Apple) (Malus sylvestris), partial (22%) [TC60692	41.32	1
gb|AGN_ELP014xl20f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	100.81	1
gb|TT-05_H10 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	21.5	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	2265.77	1
gb|AGN_RNC211xf15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	220.98	1
Unknown	38.81	1
gb|18.2F04 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5',	35.19	1
tc|Rep: Chromosome chr11 scaffold_170, whole genome shotgun sequence - Vitis v	103.7	1
gb|TT-05_B15 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	70.51	1
tc|Rep: Arabinosidase ARA-1 - Solanum lycopersicum (Tomato) (Lycopersicon escul	2342.78	1
tc|Rep: Histone H3 - Vitis vinifera (Grape), complete [TC47864]	205.94	1
gb|KN6B.102G17F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102G17, r	75.59	1
tc|Rep: Dihydrolipoamide dehydrogenase precursor - Solanum tuberosum (Potato)	2184.06	1
gb|N.tabacum mRNA for subunit of NADH:ubiquinone oxidoreductase complex I [Y	617.81	1
tc|Rep: Chromosome undetermined scaffold_127, whole genome shotgun sequenc	46.93	1

tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	20.79	1
Unknown	63.24	1
tc|Rep: 40S ribosomal protein S2-3 - Arabidopsis thaliana (Mouse-ear cress), partial	570.84	1
gb|KG9B.107L18F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107L18, m	711.14	1
tc|Rep: Ribosome recycling factor, chloroplast precursor - Daucus carota (Carrot), p	27.51	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	103.13	1
Unknown	103.31	1
gb|BP526432 MAT001 Nicotiana tabacum cDNA clone BY11154, mRNA sequence [B	54.71	1
Unknown	985.56	1
Unknown	25.89	1
gb|D58-BG10 Ethylene Induced Tobacco Leaf cDNA Library Nicotiana tabacum cDN	22.84	1
gb|KR2B.115M23F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115M23, r	95.04	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	26.6	1
Unknown	11236.9	1
gb|KR3B.112G18F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112G18, m	48.21	1
gb|TT-49_L17 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	517.19	1
gb|Nicotiana tabacum geranylgeranylated protein NTGP3 mRNA, complete cds [U6	79.1	1
tc|Rep: BTF3 - Nicotiana benthamiana, partial (75%) [TC52337]	133.31	1
Unknown	11169.6	1
gb|BP135456 MAT001 Nicotiana tabacum cDNA clone BY7971, mRNA sequence [B	17.71	1
gb|KP1B.001O09F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001O09, m	104.22	1
gb|AGN_RNC119xm14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	3007.76	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	45.01	1
Unknown	35.54	1
gb|KR3B.101G24F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101G24, m	118.42	1
tc|Rep: Cytochrome c1-1, heme protein, mitochondrial precursor - Solanum tubero	3125.59	1
gb|TOBESTR027A02 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	97.31	1
tc|Rep: Chromosome undetermined scaffold_342, whole genome shotgun sequenc	433.96	1
tc|Rep: VAP27 - Nicotiana plumbaginifolia (Leadwort-leaved tobacco), partial (46%)	219.72	1
Unknown	102.45	1
Unknown	20.27	1
tc|Rep: Pollen coat-like protein - Camellia sinensis (Tea), complete [TC60885]	53.76	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	250.39	1
Unknown	2558.73	1

gb|AGN_RNC127xg02f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	8515.05	1
gb|TT-08_G07 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	137.6	1
Unknown	127.35	1
gb|AM791244 DL, diurnal library Nicotiana tabacum cDNA clone nt005034008, mR	61.36	1
Unknown	926.76	1
gb|Nicotiana tabacum ethylene receptor ETR1 homolog mRNA, complete cds [AF0	155.95	1
gb|Tobacco mRNA fragment for nitrate reductase [X06134]	51.64	1
gb|BP134784 MAT001 Nicotiana tabacum cDNA clone BY7223, mRNA sequence [B	29.88	1
tc|Rep: Translationally-controlled tumor protein homolog - Nicotiana tabacum (Co	1592.24	1
tc|Rep: GAGA-motif binding transcriptional activator - Populus trichocarpa (Wester	22.42	1
tc|Rep: Probable N(2),N(2)-dimethylguanosine tRNA methyltransferase (tRNA(gua	32.52	1
tc|Rep: Chromosome chr10 scaffold_43, whole genome shotgun sequence - Vitis vi	480.4	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	1111.53	1
gb|Nicotiana tabacum NtRSH1 mRNA for RelA-SpoT like protein RSH1, complete cd	152.68	1
gb|KT7C.106E15F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106E15, mR	2198.65	1
tc|Rep: Chromosome chr4 scaffold_83, whole genome shotgun sequence - Vitis vin	210.01	1
Unknown	67.49	1
gb|Nicotiana tabacum NtNRT1.2-t mRNA for nitrate transporter, complete cds [AB	39.97	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	138.79	1
Unknown	32.43	1
gb|Nicotiana tabacum mRNA for putative putative beta-(1,2)-xylosyltransferase (xy	35.33	1
tc|Rep: Chromosome chr8 scaffold_115, whole genome shotgun sequence - Vitis vi	24.81	1
tc|Rep: Eukaryotic peptide chain release factor subunit 1-3-like - Solanum tuberosu	43.73	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	153.7	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	697.48	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	949.81	1
gb|Nicotiana tabacum inosine-5'-phosphate dehydrogenase (guaB) mRNA, partial c	27.68	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	444.11	1
gb|TT-19_E12 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	122.87	1
gb|BL12.103G21F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.103G21, m	1574.71	1
Unknown	2403.4	1
Unknown	547.32	1
tc|Rep: Signal recognition particle 54 kDa protein 1 - Solanum lycopersicum (Tomat	3086.07	1
Unknown	64.26	1

gb|AGN_PNL210bf1_h6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	40.39	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	37344.75	1
Unknown	357.87	1
gb|KF8C.104K10F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104K10, mRN	18.22	1
tc|Rep: Ornithine decarboxylase - Nicotiana tabacum (Common tobacco), complete	8147.9	1
Unknown	238.78	1
gb|KF8B.201I20F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201I20, mRN	37.49	1
tc|Rep: Chromosome undetermined scaffold_310, whole genome shotgun sequenc	1758.99	1
gb|AGN_RNC013xe15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	805.97	1
tc|Rep: 5-phosphoribosyl-1-pyrophosphate amidotransferase - Nicotiana tabacum	3106.04	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	94.63	1
tc|Rep: Alcohol dehydrogenase - Nicotiana tabacum (Common tobacco), partial (69	2923.73	1
gb|AGN_RPC014xb03f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	837.96	1
Unknown	1037.89	1
tc|Rep: Actin-97 - Solanum tuberosum (Potato), partial (57%) [TC46429]	52085.95	1
tc|Rep: Fiber protein Fb2 - Gossypium barbadense (Sea-island cotton) (Egyptian cot	4588.84	1
gb|KT7C.104B19F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104B19, mR	2623.76	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	425.54	1
tc|Rep: RelA-SpoT like protein RSH1 - Nicotiana tabacum (Common tobacco), partia	35.97	1
Unknown	127.91	1
Unknown	22.98	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	524.61	1
Unknown	21.01	1
gb|KN6B.103D20F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103D20,	69.03	1
gb|KL4B.103N16F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103N16, m	178.26	1
gb|KN6B.104L12F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104L12, m	74.13	1
gb|KF8B.100B18F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100B18, mR	261.38	1
gb|BP530524 MAT005 Nicotiana tabacum cDNA clone BY22160, mRNA sequence [	43.06	1
tc|Rep: Uncharacterized protein At5g64816 precursor - Arabidopsis thaliana (Mous	57.29	1
Unknown	18.99	1
gb|KN6B.101O14F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101O14,	228.72	1
gb|AGN_RNC010xl14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	50.25	1
Unknown	52.15	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	274.4	1

Unknown	269.6	1
Unknown	49.61	1
gb|KL4B.104E10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104E10, mR	24.42	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	1751.31	1
Unknown	22.28	1
tc|Rep: CXE carboxylesterase - Actinidia eriantha, partial (45%) [TC41276]	72.36	1
tc|Rep: Chromosome chr17 scaffold_263, whole genome shotgun sequence - Vitis v	101.08	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	34.28	1
tc|Rep: Glycolipid transfer protein-like - Oryza sativa subsp. japonica (Rice), comple	22.46	1
gb|KT7C.106G23F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106G23, mR	1531.46	1
gb|KT7C.106D22F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106D22, mR	42.08	1
gb|KG9B.004D19F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004D19, n	35.21	1
Unknown	29.77	1
tc|Rep: Alpha chain of nascent polypeptide associated complex - Nicotiana benthar	221.25	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	505.94	1
Unknown	42.34	1
Unknown	147.46	1
Unknown	350.87	1
tc|Rep: Chromosome chr19 scaffold_126, whole genome shotgun sequence - Vitis v	22.69	1
gb|KN6B.103F12F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103F12, m	3982.48	1
gb|AM819871 COL, cold overnight library Nicotiana tabacum cDNA clone nt006113	739.78	1
Unknown	52.18	1
Unknown	104.26	1
gb|Nicotiana tabacum mRNA for putative rac protein (rac gene) [AJ250174]	4727.28	1
Unknown	131.88	1
gb|AGN_ELP019xb01f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	31.26	1
Unknown	133.78	1
gb|AM799412 DL, diurnal library Nicotiana tabacum cDNA clone nt005141043, mR	244.03	1
gb|TT-25_E01 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	42.74	1
Unknown	219.25	1
tc|Rep: Mutator-like transposase - Arabidopsis thaliana (Mouse-ear cress), partial (	46.67	1
gb|KG9B.001P01F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001P01, m	519.54	1
gb|CHO_SL015xj07f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	98.37	1
gb|KP1B.102O16F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102O16, m	51.81	1

tc|Rep: Fiber protein Fb2 - Gossypium barbadense (Sea-island cotton) (Egyptian cot	7543.15	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	2732.06	1
Unknown	675.07	1
Unknown	64.24	1
Unknown	142.52	1
gb|KG9B.105G09F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105G09, n	67.83	1
gb|KP1B.101G22F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101G22, m	180.4	1
Unknown	27.81	1
gb|AGN_RNC009xp18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	535.98	1
gb|TT-07_N14 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	639.88	1
gb|TT-47_D12 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	31.88	1
gb|KG9B.004D22F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004D22, n	87.17	1
Unknown	169.13	1
Unknown	71.6	1
gb|KP1B.101D12F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101D12, m	87.1	1
Unknown	418.51	1
tc|Rep: Protein kinase Ck2 regulatory subunit 2 - Nicotiana tabacum (Common toba	1577.51	1
Unknown	231.18	1
Unknown	290.69	1
Unknown	26.88	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	2828.68	1
Unknown	852.76	1
gb|KT7C.110K14F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110K14, mRI	642.46	1
Unknown	79.44	1
Unknown	673.9	1
tc|Rep: Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vi	28.83	1
gb|TT-36_B15 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	188.01	1
gb|TT-07_I07 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	103.45	1
Unknown	5765.34	1
Unknown	18.67	1
gb|CHO_SL009xa08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	829.83	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	61.69	1
tc|Rep: Chromosome chr2 scaffold_187, whole genome shotgun sequence - Vitis vi	1988.29	1
Unknown	609.44	1

Unknown	22.62	1
gb|KL4B.108P19F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108P19, mR	9701.21	1
tc|AAD10662.1 - Arabidopsis thaliana (Mouse-ear cress), partial (58%) [TC67894]	238.19	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	858.77	1
gb|TT-09_G07 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	26.69	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	168.3	1
gb|KP1B.103M16F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103M16, r	52.36	1
gb|TT-06_H17 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	26.96	1
gb|AGN_PNL226cf1_g4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	80.56	1
gb|Nicotiana tabacum cig2 mRNA, complete cds [AB031321]	81.52	1
gb|KL4B.105B03F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105B03, mR	147.87	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	324.64	1
Unknown	88.02	1
Unknown	84.47	1
gb|AGN_RNC001xi15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	17.09	1
Unknown	21.83	1
gb|KF8C.105P02F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105P02, mRN	143.22	1
Unknown	35.46	1
gb|AGN_RPC004xg02f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	18.59	1
tc|Rep: GAL83 - Nicotiana attenuata, partial (77%) [TC57681]	79.52	1
Unknown	23.15	1
gb|AGN_PNL209cr1_a3.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	18.82	1
tc|Rep: Vicilin-like storage protein - Picea glauca (White spruce), partial (22%) [TC4	114.94	1
tc|Rep: 30S ribosomal protein S6 alpha, chloroplast precursor [Contains: 30S riboso	100.72	1
Unknown	30.58	1
gb|KG9B.106J08F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106J08, m	85.09	1
Unknown	914.99	1
Unknown	222.66	1
gb|BP529347 MAT001 Nicotiana tabacum cDNA clone BY14241, mRNA sequence [	392.9	1
Unknown	151.39	1
gb|Nicotiana tabacum sterol-C5(6)-desaturase mRNA, complete cds [AF081794]	152.85	1
tc|Rep: Chromosome chr5 scaffold_156, whole genome shotgun sequence - Vitis vi	20.25	1
gb|BL12.104M18F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.104M18, m	210.29	1
gb|AGN_RNC009xh05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	47.8	1

Unknown	1117.07	1
Unknown	41.92	1
gb|AM840784 COL, cold overnight library Nicotiana tabacum cDNA clone nt006214	224.21	1
Unknown	275.79	1
gb|AM830869 seedling library, SL Nicotiana tabacum cDNA clone nt002031015, mF	70.53	1
gb|CHO_SL017xb07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	742.85	1
Unknown	217.12	1
gb|TT-06_C03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	196.15	1
gb|KG9B.106G11F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106G11, n	103.04	1
tc|Rep: Glucose-6-phosphate 1-dehydrogenase, chloroplast precursor - Nicotiana ta	2848.87	1
Unknown	226.54	1
Unknown	48.12	1
tc|Rep: Chromosome undetermined scaffold_147, whole genome shotgun sequenc	155.22	1
gb|EST_CSP014xa03f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	30.84	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	1519.76	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	395.94	1
Unknown	477.35	1
gb|Nicotiana tabacum NtVPE-3 mRNA for vacuolar processing enzyme-3 complete	1073.03	1
Unknown	18.4	1
Unknown	376.99	1
tc|Rep: Chromosome chr9 scaffold_49, whole genome shotgun sequence - Vitis vin	186.62	1
Unknown	41.48	1
gb|KT7C.104L09F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104L09, mRN	1073.01	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	331.79	1
gb|AGN_ELP009xo12f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	101.88	1
tc|Rep: Fructokinase-2 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum	12623.95	1
gb|KG9B.102D19F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102D19, n	43.42	1
tc|Rep: NADPH-cytochrome P450 oxidoreductase - Nicotiana tabacum (Common tc	37.82	1
Unknown	84.31	1
gb|TT-08_P05 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	40.84	1
tc|Rep: Transcription initiation factor - Plantago major (Common plantain), partial (	403.76	1
gb|TOBESTR094D04 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	105.73	1
gb|KG9B.106K11F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106K11, m	24.49	1
Unknown	71.12	1

gb|KF8C.110O24F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110O24, mR	194.46	1
gb|KP1B.113O10F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.113O10, m	95.38	1
tc|Rep: Chromosome chr10 scaffold_81, whole genome shotgun sequence - Vitis vi	45.96	1
Unknown	30.98	1
gb|KF8C.110C21F.051216T7 KF8 Nicotiana tabacum cDNA clone KF8C.110C21, mR	24.62	1
gb|KG9B.102P18F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102P18, m	163.36	1
Unknown	183.57	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	68.38	1
tc|Rep: Phosphoglucomutase, cytoplasmic - Solanum tuberosum (Potato), partial (	5510.12	1
Unknown	20.46	1
gb|KP1B.101J07F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101J07, mR	1358.72	1
tc|Rep: Dihydrolipoyl dehydrogenase - Capsicum annuum (Bell pepper), partial (39	1164.43	1
Unknown	385.17	1
gb|TT-50_B23 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	264.45	1
gb|FS383363 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	32.54	1
gb|KP1B.107G18F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107G18, m	22	1
tc|Rep: Glyoxalase/bleomycin resistance protein/dioxygenase - Sphingomonas witt	41.31	1
Unknown	77.09	1
tc|Rep: 60S acidic ribosomal protein P0 - Solanum tuberosum (Potato), partial (83	252.4	1
Unknown	43.67	1
tc|Rep: Glycosyl hydrolase family-like protein - Salvia miltiorrhiza (Chinese sage), p	25.95	1
gb|AGN_RNC116xj11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	49.12	1
Unknown	122.88	1
Unknown	237.53	1
Unknown	663.85	1
gb|AGN_PNL210af1_d2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	1130.55	1
tc|Rep: Chromosome undetermined scaffold_133, whole genome shotgun sequenc	116.02	1
Unknown	377.8	1
Unknown	121.75	1
Unknown	196.48	1
gb|TT-07_N20 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	820.06	1
Unknown	25.01	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	138.56	1
gb|BL12.001I10F.060117T7 BL12 Nicotiana tabacum cDNA clone BL12.001I10, mR	34.98	1

gb|AGN_PNL212ar1_b4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	135.99	1
gb|KG9B.101J02F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101J02, m	22.56	1
Unknown	103.48	1
gb|TOBESTR015D12 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	1496.42	1
Unknown	45.01	1
gb|FS405773 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	3288.07	1
tc|Rep: Plastid enolase - Helianthus annuus (Common sunflower), partial (41%) [TC	273.04	1
Unknown	72.57	1
gb|BP533488 MAT005 Nicotiana tabacum cDNA clone BY30178, mRNA sequence [	346.38	1
Unknown	9396.39	1
Unknown	49.71	1
gb|CHO_SL018xn22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	3266.59	1
gb|KR2B.002D13F.051019T7 KR2B Nicotiana tabacum cDNA clone KR2B.002D13, m	2945.69	1
tc|Rep: Profilin - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), comp	689.55	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	3332.86	1
tc|Rep: Ribosomal protein S14-like - Solanum tuberosum (Potato), partial (96%) [TC	120.27	1
tc|Rep: Citrate synthase, glyoxysomal precursor - Cucurbita maxima (Pumpkin) (Wi	265.36	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	45.44	1
tc|Rep: Histone H2A - Vitis vinifera (Grape), partial (88%) [TC71367]	24.42	1
gb|BP530801 MAT005 Nicotiana tabacum cDNA clone BY23062, mRNA sequence [	103.38	1
Unknown	50.7	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT4-43-390, cultivar Bright Yellow 2	22.54	1
Unknown	50.28	1
tc|Rep: AT3g06820/F3E22_4 - Arabidopsis thaliana (Mouse-ear cress), partial (46%)	72.24	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	1421.76	1
gb|Nicotiana tabacum sucrose-6-phosphate phosphatase (SPP2) mRNA, complete c	261.52	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	10493.5	1
gb|Nicotiana tabacum Avr9 [AY220479]	186.85	1
Unknown	298.84	1
gb|N.tabacum mRNA pNLA-35 [X79794]	176.49	1
gb|KG9B.105O13F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105O13, r	179.83	1
gb|KP1B.037P02F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.037P02, m	43.33	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	242.01	1
Unknown	28.38	1

gb|BP531361 MAT005 Nicotiana tabacum cDNA clone BY24256, mRNA sequence [E	46.21	1
Unknown	316.47	1
Unknown	508.23	1
Unknown	19.73	1
Unknown	85.94	1
gb|KP1B.109A05F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109A05, m	221.48	1
gb|KR2B.112B19F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.112B19, m	414.51	1
gb|KR3B.106M07F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106M07, r	151.28	1
tc|Rep: AT3g47831/T23J7 - Arabidopsis thaliana (Mouse-ear cress), partial (89%) [T	225.24	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis v	267.14	1
gb|KR3B.103O01F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.103O01, m	1483.22	1
gb|TT-28_H11 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	44.53	1
Unknown	248.32	1
gb|AGN_RNC013xn01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	81.16	1
tc|Rep: Chromosome undetermined scaffold_143, whole genome shotgun sequenc	382.62	1
gb|Nicotiana tabacum VTC2-like protein mRNA, complete cds [EU700061]	9032.92	1
gb|KF8C.101E17F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101E17, mRN	1529.51	1
gb|AM811421 seedling library, SL Nicotiana tabacum cDNA clone nt002215062, mR	19.9	1
Unknown	21.89	1
gb|TOBESTR046E09 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA sequ	78.46	1
gb|KN6B.105P08F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105P08, m	1112.82	1
tc|Rep: Protein kinase-like protein - Vitis aestivalis (Grape), partial (51%) [TC57156]	712.46	1
gb|AGN_PNL222cr1_c3.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	235.35	1
gb|Nicotiana tabacum partial mRNA for chloroplast FtsZ-like protein (ftsZ gene), clo	383.07	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	1732.37	1
Unknown	18.44	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	505.08	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	1869.84	1
gb|TT-13_A18 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	95.66	1
gb|KT7C.106O18F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106O18, mR	49.5	1
gb|KG9B.101O13F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101O13, r	35.69	1
tc|Rep: Os03g0742400 protein - Oryza sativa subsp. japonica (Rice), partial (71%) [T	2848.06	1
tc|Rep: SUI1 protein - Coffea arabica (Coffee), complete [TC71048]	55.9	1
tc|Rep: 40S ribosomal protein S15-like - Solanum tuberosum (Potato), complete [T	311.4	1

gb|TT-11_G22 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FC	268.86	1
tc|Rep: Growth regulator like protein - Arabidopsis thaliana (Mouse-ear cress), part	114.22	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	20.94	1
Unknown	824.73	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	280.51	1
tc|Rep: ATP-dependent Clp protease proteolytic subunit - Nicotiana sylvestris (Woc	1835.53	1
tc|Rep: Hydroxyproline-rich glycoprotein - Chlamydomonas reinhardtii, partial (6%)	2599.53	1
Unknown	4696.44	1
Unknown	1993.96	1
gb|AGN_RNC127xh11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	34.9	1
Unknown	266.27	1
Unknown	30.86	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT1-21-250, cultivar Bright Yellow 2	148.46	1
gb|KN6B.104D21F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104D21, n	23.42	1
tc|Rep: Chromosome chr10 scaffold_50, whole genome shotgun sequence - Vitis vi	25.44	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	121.93	1
gb|KR2B.115D09F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115D09, m	92.41	1
gb|N.tabacum npp1 mRNA for protein phosphatase type 1 [Z93768]	2002.47	1
tc|Rep: Cytochrome b-c1 complex subunit 7 - Solanum tuberosum (Potato), comple	2875.36	1
gb|AM820707 COL, cold overnight library Nicotiana tabacum cDNA clone nt006042	126.62	1
Unknown	89.24	1
gb|AGN_PNL231df1_g2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	1565.58	1
tc|Rep: Chromosome chr9 scaffold_65, whole genome shotgun sequence - Vitis vin	55.07	1
gb|CHO_SL012xd11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	4251.44	1
gb|KG9B.107L23F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107L23, m	943.65	1
gb|29A04 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', r	283.43	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	10892.55	1
Unknown	6299.97	1
gb|KR3B.107C16F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.107C16, m	269.34	1
tc|Rep: Chromosome chr19 scaffold_35, whole genome shotgun sequence - Vitis vi	9131.95	1
tc|Rep: Probable ubiquitin-fold modifier 1 precursor - Oryza sativa subsp. japonica (	2730.12	1
Unknown	175.61	1
gb|TT-26_M08 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sec	987.61	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	59.44	1

gb|KR2B.112G14F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.112G14, m	517.21	1
Unknown	914.34	1
gb|AGN_ELP024xf11f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	68.57	1
gb|KT7C.104A20F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104A20, mR	39.06	1
gb|KG9B.005N08F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005N08,	467.45	1
tc|Rep: Calcium/calmodulin-dependent protein kinase CaMK3 - Nicotiana tabacum	28.5	1
gb|KF8C.103J07F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103J07, mRN	64.46	1
gb|KG9B.001N04F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001N04,	26.07	1
gb|KG9B.103D09F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103D09,	60.51	1
Unknown	531.98	1
Unknown	101.19	1
gb|AGN_RNC007xl06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	43.15	1
gb|KF8C.102F19F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102F19, mRN	188.46	1
gb|KP1B.104C19F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104C19, m	17334.7	1
gb|KT7B.100P11F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100P11, mR	85.57	1
Unknown	112.77	1
Unknown	1140.72	1
Unknown	17783.5	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	2128.55	1
gb|N.tabacum mRNA for phosphoglycerate kinase (chloroplast isoenzyme) [Z48977	28.94	1
gb|KF8C.103C02F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103C02, mR	1165.75	1
Unknown	33.55	1
gb|KT7C.106H18F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106H18, mR	169.41	1
tc|Rep: Xylose isomerase - Vitis vinifera (Grape), partial (50%) [TC40722]	269.86	1
Unknown	382.68	1
tc|Rep: NmrA-like family protein - Solanum demissum (Wild potato), partial (21%) [	294.29	1
tc|Rep: UDP-glucose dehydrogenase - Cinnamomum osmophloeum, partial (93%) [	3295.87	1
gb|KR3B.112H24F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112H24, m	1024	1
Unknown	71.26	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	22.77	1
tc|Rep: NADH dehydrogenase subunit 2 - Apalacris nigrogeniculata, partial (7%) [TC	226.66	1
Unknown	851.5	1
Unknown	28.97	1
gb|AGN_RPC016xe03f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	425.61	1

gb|KN6B.105J11F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105J11, mI	370.23	1
tc|Rep: 26S proteasome subunit 7-like protein - Lactuca sativa (Garden lettuce), cor	206.3	1
tc|Rep: Gibberellic acid receptor - Gossypium hirsutum (Upland cotton) (Gossypium	28.57	1
Unknown	45.54	1
gb|N.tabacum mRNA for L-Glutamate:tRNA-Glu ligase [X83524]	190.41	1
Unknown	392.67	1
gb|Nicotiana tabacum partial sat1 gene for serine acetyltransferase 1, genomic RNA	21.88	1
gb|Nicotiana tabacum trehalose-phosphate phosphatase mRNA, complete cds [AY5	2706.36	1
Unknown	81.59	1
tc|Rep: Chromosome undetermined scaffold_1205, whole genome shotgun sequen	544.15	1
tc|Rep: Chromosome chr5 scaffold_72, whole genome shotgun sequence - Vitis vin	177.15	1
Unknown	68.64	1
tc|Rep: Asparagine synthetase - Striga hermonthica (Purple witchweed), partial (34	995.63	1
gb|Nicotiana tabacum Avr9 [AF211536]	459.98	1
Unknown	278.84	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	151.15	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (3%) [TC474	101.69	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	16600.7	1
gb|TT-06_N13 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	177.53	1
gb|KR3B.110P06F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110P06, mI	179.66	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	3934.77	1
gb|KG9B.106H12F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106H12, n	304.64	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	46.57	1
gb|BP129674 MAT001 Nicotiana tabacum cDNA clone BY1554, mRNA sequence [BI	451.02	1
tc|Rep: NTMTP1A - Nicotiana tabacum (Common tobacco), complete [TC40171]	763	1
Unknown	20.95	1
gb|KL5B.109A12F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.109A12, mR	2421.64	1
gb|KL4B.109C03F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.109C03, mR	408.46	1
gb|TT-10_O13 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	68.95	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	645.47	1
gb|KL4B.105L08F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105L08, mRI	61.75	1
gb|ntsm8 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [EB	114.11	1
gb|AM793040 seedling library, SL Nicotiana tabacum cDNA clone nt002063082, mR	31.15	1
gb|KR2B.104A23F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.104A23, m	71.92	1

gb|KT7C.102E05F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102E05, mRN	192.42	1
gb|CHO_SL002xh18f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	34720.65	1
Unknown	1924.72	1
Unknown	500.48	1
gb|KL4B.101N08F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101N08, mR	354.73	1
gb|TT-21_K22 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	27.16	1
Unknown	194.89	1
gb|Nicotiana tabacum mRNA cytosolic glucose-6-phosphate dehydrogenase TCG6 [	93.2	1
gb|KR3B.109F16F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109F16, mR	26.06	1
gb|AGN_RNC003xf15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	58.13	1
tc|Rep: Tonoplast intrinsic protein bobTIP26-1 - Brassica oleracea var. botrytis (Cau	261.37	1
gb|AM829948 seedling library, SL Nicotiana tabacum cDNA clone nt002139094, mR	197.8	1
Unknown	52.63	1
gb|18.2F11 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5',	1001.41	1
gb|KG9B.103H16F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103H16, n	2129.36	1
Unknown	127.51	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	98.88	1
gb|BP528938 MAT001 Nicotiana tabacum cDNA clone BY13812, mRNA sequence [B	136.55	1
gb|AM793251 seedling library, SL Nicotiana tabacum cDNA clone nt002213012, mR	142.68	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	472.98	1
gb|KN6B.104G23F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104G23, r	17243.75	1
Unknown	26.63	1
tc|Rep: Chromosome undetermined scaffold_437, whole genome shotgun sequenc	31.38	1
Unknown	45.73	1
Unknown	207.11	1
gb|BP129537 MAT001 Nicotiana tabacum cDNA clone BY1408, mRNA sequence [BP	28.45	1
tc|AAD10662.1 - Arabidopsis thaliana (Mouse-ear cress), partial (58%) [TC67894]	63.24	1
tc|Rep: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor	132.7	1
tc|Rep: Chromosome chr17 scaffold_101, whole genome shotgun sequence - Vitis v	1526.33	1
tc|Rep: Protein phosphatase 2C - Fagus sylvatica (Beechnut), partial (54%) [TC4462	1169.63	1
Unknown	148.15	1
gb|KG9B.107N18F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107N18, r	136.83	1
gb|KP1B.109O15F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109O15, m	633.96	1
Unknown	1505.44	1

tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	904.73	1
Unknown	24.67	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	4960.6	1
tc|Rep: Pyruvate kinase - Medicago truncatula (Barrel medic), partial (48%) [TC451	909.38	1
tc|Rep: NADH-ubiquinone oxidoreductase chain 1 - Arion anthracius, partial (10%)	42.67	1
tc|Rep: Syntaxin-52 - Arabidopsis thaliana (Mouse-ear cress), complete [TC76446]	376.34	1
gb|KF8C.103O14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103O14, mR	99.17	1
gb|KG9B.107G19F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107G19,	1919.07	1
tc|Rep: Histone H4 [Contains: Osteogenic growth peptide (OGP)]. - Rattus norvegic	812.74	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	67.09	1
Unknown	89.29	1
tc|Rep: Uncharacterized protein At5g64130.3 - Arabidopsis thaliana (Mouse-ear cr	1147.53	1
Unknown	191.92	1
Unknown	23	1
gb|KP1B.109G14F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109G14, m	85.51	1
gb|BL12.104B18F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.104B18, mR	126.4	1
tc|Rep: MADF; Homeodomain-like - Medicago truncatula (Barrel medic), partial (20	575.71	1
Unknown	64.66	1
Unknown	47.47	1
tc|Rep: Peptide methionine sulfoxide reductase (Protein- methionine-S-oxide redu	120.05	1
gb|KG9B.104N03F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104N03,	53.04	1
gb|KP1B.103B13F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103B13, m	40.9	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	413.52	1
tc|Rep: Tic20-like protein - Solanum tuberosum (Potato), partial (77%) [TC49054]	568.5	1
tc|Rep: Homolog of Homo sapiens "Megakaryocyte stimulating factor - Takifugu ru	58.48	1
Unknown	33.13	1
Unknown	226.92	1
Unknown	26.81	1
Unknown	1763.65	1
Unknown	31.04	1
Unknown	42.86	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	26.75	1
gb|N.tabacum mRNA for subunit of NADH:ubiquinone oxidoreductase complex I [Y	218.4	1
tc|Rep: Calcium-dependent protein kinases 5 - Solanum tuberosum (Potato), partia	1037.94	1

gb|Nicotiana tabacum NtPITSLRE alpha mRNA for homolog of mammalian PITSLRE	52.44	1
gb|BP131286 MAT001 Nicotiana tabacum cDNA clone BY3322, mRNA sequence [B	3120.26	1
gb|Nicotiana tabacum cyclin B-like protein mRNA, complete cds [AY776171]	71.53	1
Unknown	219.1	1
gb|AGN_RNC211xh01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	4060.51	1
Unknown	870.08	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	260.46	1
Unknown	107.36	1
gb|KG9B.103C12F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103C12, m	162.38	1
tc|Rep: Chromosome chr10 scaffold_43, whole genome shotgun sequence - Vitis vi	268.73	1
tc|Rep: Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vi	189.56	1
gb|TT-05_A08 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	113.42	1
gb|KL4B.103G09F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103G09, m	597.38	1
tc|Rep: RNA-binding protein-like - Oryza sativa subsp. japonica (Rice), partial (10%)	44.01	1
gb|ntsm10 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [E	110.56	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	513.36	1
gb|AM800056 seedling library, SL Nicotiana tabacum cDNA clone nt002096042, m	76.25	1
Unknown	436.34	1
tc|Rep: Zinc finger protein - Zea mays (Maize), partial (68%) [TC43008]	3174.3	1
tc|Rep: Protein kinase Ck2 regulatory subunit 2 - Nicotiana tabacum (Common tob	197.8	1
gb|KR3B.111I05F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111I05, mR	27.58	1
gb|TT-10_H14 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	46.48	1
Unknown	44.17	1
gb|KL4B.106N10F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106N10, m	2900.3	1
gb|KF8C.106L14F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106L14, mRN	490.26	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	670.09	1
gb|KP1B.001E04F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001E04, m	754.02	1
tc|Rep: Ribosomal protein S8 - Vitis vinifera (Grape), partial (96%) [TC40909]	105.6	1
Unknown	103.37	1
tc|Rep: Chromosome chr4 scaffold_83, whole genome shotgun sequence - Vitis vin	222.52	1
tc|Rep: DWARF1/DIMINUTO - Solanum lycopersicum (Tomato) (Lycopersicon escul	101.57	1
tc|Rep: Chromosome undetermined scaffold_226, whole genome shotgun sequenc	591.18	1
gb|EST_CSP004xa06f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	86.08	1
tc|Rep: Chromosome undetermined scaffold_383, whole genome shotgun sequenc	359.34	1

tc|Rep: MYB transcription factor MYB123 - Glycine max (Soybean), partial (29%) [T	35.02	1
tc|Rep: Hypersensitive-induced reaction protein - Capsicum annuum (Bell pepper),	708.45	1
tc|Rep: Cytochrome b561 family protein - marine gamma proteobacterium HTCC21	33.28	1
Unknown	26.98	1
gb|BL12.101H02F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.101H02, m	9758.84	1
Unknown	1119	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	178.41	1
tc|Rep: Chromosome chr1 scaffold_136, whole genome shotgun sequence - Vitis vi	693.97	1
gb|AGN_RNC014xe20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	176.77	1
tc|Rep: Chromosome undetermined scaffold_296, whole genome shotgun sequenc	434	1
gb|TT-18_O10 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	1684.93	1
gb|AGN_RNC022xb20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	74.12	1
gb|Nicotiana tabacum DNA-binding protein phosphatase 2C (DBP1) mRNA, complet	111.52	1
tc|BAA90353.1 - Arabidopsis thaliana (Mouse-ear cress), partial (78%) [TC41734]	159.41	1
gb|KP1B.001J22F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001J22, mR	63.99	1
Unknown	139.35	1
gb|N.tabacum RL2 mRNA for 60S ribosomal protein L2 [X62500]	20.73	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	410.19	1
tc|Rep: Chromosome chr12 scaffold_78, whole genome shotgun sequence - Vitis vi	21.2	1
gb|AGN_ELP009xd12f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	24.25	1
gb|CHO_SL022xi08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	162.27	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	879.3	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	258.67	1
tc|Rep: Histone H2A - Vitis vinifera (Grape), partial (96%) [TC55406]	165.53	1
gb|KG9B.103J21F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103J21, m	34.07	1
gb|Nicotiana tabacum sucrose-phosphate synthase isoform B (SPSB) mRNA, compl	245.27	1
Unknown	57.04	1
tc|Rep: Os01g0610400 protein - Oryza sativa subsp. japonica (Rice), partial (84%) [T	37.81	1
Unknown	46.62	1
gb|CHO_SL006xj24f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	1635.98	1
gb|AGN_ELP022xm08f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	85.01	1
gb|KN6B.009M21F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009M21,	390.99	1
Unknown	23.6	1
gb|Nicotiana tabacum protein kinase SRK mRNA, complete cds [DQ340760]	448.57	1

Unknown	87.83	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	31	1
Unknown	26.31	1
gb|CHO_SL013xn19f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	92.12	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	142.29	1
Unknown	81.38	1
tc|Rep: Thioredoxin peroxidase - Capsicum annuum (Bell pepper), complete [TC448	162.57	1
Unknown	156.72	1
tc|Rep: Phosphoenolpyruvate carboxylase - Ricinus communis (Castor bean), partia	134.94	1
tc|Rep: Isocitrate dehydrogenase (NAD+) precursor - Nicotiana tabacum (Common	967.7	1
tc|Rep: Peptidyl-prolyl cis-trans isomerase - Solanum lycopersicum (Tomato) (Lyco	47.48	1
tc|Rep: 60S ribosomal protein l2 - Oryza sativa subsp. indica (Rice), partial (36%) [T	164.84	1
Unknown	28.75	1
tc|Rep: Phosphate translocator precursor - Nicotiana tabacum (Common tobacco),	134.97	1
tc|Rep: Cytochrome b-c1 complex subunit Rieske-2, mitochondrial precursor - Nico	18351.35	1
gb|KG9B.103M12F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103M12,	607.95	1
gb|KN6B.101A12F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101A12,	31.91	1
gb|KR2B.113B15F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.113B15, m	2334.34	1
Unknown	87.02	1
tc|Rep: ATP synthase A chain - Psychroflexus torquis ATCC 700755, partial (6%) [TC	250.82	1
Unknown	25.16	1
gb|Nicotiana tabacum clone PR15 mRNA sequence [AF154640]	52383.1	1
Unknown	139.47	1
gb|KG9B.102A15F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102A15,	34.12	1
Unknown	35.94	1
tc|Rep: Metallothionein-like protein type 2 - Nicotiana glutinosa (Tobacco), partial	458.9	1
Unknown	18.53	1
Unknown	1002.53	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	26.02	1
tc|Rep: UDP-glucose:protein transglucosylase-like - Solanum tuberosum (Potato), p	1100.78	1
gb|FTP P2 Tobacco anther cDNA Nicotiana tabacum cDNA similar to NIP aquaporin,	11210.55	1
tc|Rep: Lecithine cholesterol acyltransferase-like protein - Solanum lycopersicum (T	96.42	1
gb|TT-24_K09 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	4091.35	1
tc|Rep: CBL-interacting protein kinase 9 - Populus trichocarpa (Western balsam po	53.08	1

gb|CHO_SL023xl17f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	220.78	1
gb|TT-29_F23 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	80.85	1
Unknown	25.45	1
gb|KL4B.103H23F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103H23, mR	239.4	1
tc|Rep: Chemotaxis protein CheW - Methanosarcina mazei (Methanosarcina frisia),	828.88	1
Unknown	768.79	1
gb|KT7B.100G05F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100G05, mR	906.95	1
gb|KL4B.101J13F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101J13, mRN	938.01	1
gb|KR3B.001M04F.050815T7 KR3B Nicotiana tabacum cDNA clone KR3B.001M04,	22.77	1
tc|Rep: Chromosome chr9 scaffold_104, whole genome shotgun sequence - Vitis vi	47.53	1
gb|KG9B.102E11F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102E11, m	42.49	1
gb|TT-07_A10 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FG	213.03	1
gb|KN6B.103O22F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103O22,	483.84	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	47.97	1
Unknown	31.27	1
Unknown	254.72	1
Unknown	51.83	1
tc|Rep: Chromosome chr8 scaffold_99, whole genome shotgun sequence - Vitis vin	2467.72	1
Unknown	60.17	1
tc|Rep: Alpha chain of nascent polypeptide associated complex - Nicotiana benthar	86.49	1
tc|Rep: ADP ribosylation factor 002 - Daucus carota (Carrot), complete [TC77221]	23.52	1
Unknown	158.04	1
gb|AGN_PNL220br1_g11.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRN	72.89	1
Unknown	29.78	1
Unknown	2682.74	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	20.62	1
tc|Rep: Serine-glyoxylate aminotransferase - Spirodela polyrrhiza (Giant duckweed)	23.87	1
gb|CHO_SL028xd07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	155.41	1
gb|AGN_PNL215br1_b10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRN	22.13	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	182.26	1
gb|KT7C.113I03F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.113I03, mRN	38.86	1
Unknown	18.06	1
gb|FS382929 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	21.83	1
gb|KF8B.100B16F.151010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100B16, mRN	24.39	1

gb|CHO_SL008xl05f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	24.54	1
gb|AGN_PNL228af1_h10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	16582.8	1
Unknown	35.22	1
gb|AGN_RNC101xc24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	73.93	1
tc|Rep: DSBA oxidoreductase precursor - Ochrobactrum anthropi (strain ATCC 4918	18.59	1
Unknown	104.57	1
gb|KG9B.005I19F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005I19, mR	41.24	1
gb|KG9B.102D13F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102D13, n	116.62	1
Unknown	19.25	1
gb|KL4B.108D20F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108D20, mR	32.73	1
gb|KP1B.001O22F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001O22, m	399.65	1
gb|KG9B.104B16F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104B16, m	56.41	1
gb|KG9B.104L10F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104L10, m	32.82	1
Unknown	198.59	1
Unknown	20.77	1
gb|KP1B.102E02F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102E02, mR	26.84	1
tc|Rep: TA4 protein - Oryza sativa subsp. japonica (Rice), partial (38%) [TC47117]	1546.34	1
gb|TT-16_G20 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	71.78	1
gb|KN6B.110P12F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.110P12, m	216.1	1
tc|Rep: Chromosome undetermined scaffold_127, whole genome shotgun sequenc	28.39	1
tc|Rep: Chromosome chr12 scaffold_38, whole genome shotgun sequence - Vitis vi	151.59	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	31.8	1
Unknown	27.79	1
gb|KP1B.102P22F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102P22, mR	102.32	1
gb|BL12.001I10F.060117T7 BL12 Nicotiana tabacum cDNA clone BL12.001I10, mRN	101.24	1
Unknown	87.51	1
Unknown	4388.22	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	759.89	1
Unknown	30.36	1
Unknown	36.08	1
gb|KL4B.113C19F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.113C19, mR	511.89	1
tc|RICRGSBHA Rice gene encoding three ribosomal RNA's: the 17S, 3' end; 5.8S, cor	137464	1
Unknown	31.55	1
Unknown	61.45	1

gb|CHO_SL024xg05f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	178.39	1
gb|KP1B.102D24F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102D24, m	61.22	1
gb|KR3B.104B12F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.104B12, m	2719.1	1
gb|KL5B.114E19F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.114E19, mR	1107.92	1
gb|KG9B.005B18F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005B18, m	96.32	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	114.61	1
tc|Rep: Chromosome chr3 scaffold_117, whole genome shotgun sequence - Vitis vi	119.72	1
Unknown	55.34	1
tc|GB|AY596684.1|AAT69047.1 F1-ATPase alpha subunit [NP8634928]	7953.46	1
Unknown	621.93	1
tc|Rep: Chromosome undetermined scaffold_3328, whole genome shotgun sequen	18.17	1
Unknown	17.95	1
Unknown	53.94	1
gb|KN6B.114I07F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.114I07, mF	79.84	1
Unknown	30.11	1
gb|CHO_SL008xe15f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	173.41	1
Unknown	22.36	1
tc|Rep: Uncharacterized protein At5g64130.3 - Arabidopsis thaliana (Mouse-ear cre	413.86	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	41.95	1
Unknown	903.72	1
gb|Nicotiana tabacum pollen specific LIM domain protein 1a mRNA, complete cds [	48146.25	1
Unknown	500.44	1
gb|AGN_RNC116xe22f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	375.12	1
gb|KR3B.112E08F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112E08, ml	95.53	1
Unknown	3518.24	1
Unknown	57.09	1
gb|AGN_RNC121xb17f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	145.85	1
gb|KL4B.101C10F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101C10, mR	190.96	1
gb|TT-22_H05 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [FC	648.03	1
gb|FS429988 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	823.35	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	5144.98	1
gb|KG9B.107O05F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107O05, r	41.24	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	34.04	1
Unknown	235.81	1

tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	51.64	1
gb|tbt_000462 Normalized Nicotiana tabacum cDNA library Nicotiana tabacum cDN	1111.2	1
Unknown	106.74	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	186.57	1
tc|Rep: Poly(A)-binding protein II-like - Brassica campestris (Field mustard), partial (	375.55	1
Unknown	124.34	1
gb|KG9B.105P06F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105P06, m	162	1
gb|AGN_RNC008xi01f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	41.3	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	78.42	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	73.31	1
Unknown	521.6	1
Unknown	207.84	1
gb|KR2B.109F05F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.109F05, mR	560.63	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	187.01	1
tc|Rep: Mitochondrial carrier-like protein - Solanum tuberosum (Potato), partial (8	254.7	1
gb|KG9B.002J02F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002J02, mR	191.88	1
gb|AGN_ELP017xg05f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	284.55	1
gb|KF8C.101E14F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101E14, mRN	19630.4	1
gb|BL12.103A12F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.103A12, mR	387.2	1
Unknown	21.64	1
gb|KG9B.001J08F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001J08, mR	2024.53	1
gb|KR3B.106I07F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106I07, mR	129.44	1
gb|N.tabacum mRNA for cyclin A-like protein (clone 30) [X92967]	37.57	1
gb|AM783645 DL, diurnal library Nicotiana tabacum cDNA clone nt005005046, mR	166.83	1
Unknown	96.11	1
gb|FS406615 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	1519.42	1
gb|KP1B.102E11F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102E11, mR	27.22	1
tc|Rep: ATP synthase subunit beta, mitochondrial precursor - Nicotiana plumbagini	1020.47	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	188.02	1
gb|TT-07_D01 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	203.61	1
gb|KL5B.109B20F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.109B20, mR	1190.57	1
gb|KL4B.110M21F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110M21, m	781.6	1
gb|KL4B.103L01F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103L01, mR	20.67	1
tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin	21.96	1

Unknown	20.77	1
gb|AGN_PNL221df1_h10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	473.94	1
gb|Nicotiana tabacum mitochondrial Rieske Fe-S protein mRNA, complete cds [M7	17794.35	1
Unknown	255.6	1
tc|Rep: 60S ribosomal protein L13a-like protein - Solanum tuberosum (Potato), co	132.48	1
tc|Rep: Bypass2 - Nicotiana benthamiana, complete [TC47299]	26.56	1
Unknown	2984.72	1
gb|KP1B.109E07F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.109E07, m	108.11	1
Unknown	70	1
gb|KP1B.101K12F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101K12, m	83.63	1
Unknown	174.17	1
tc|Rep: GDA2 protein - Pisum sativum (Garden pea), partial (77%) [TC41998]	24.09	1
gb|KR2B.102L10F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.102L10, m	231.72	1
Unknown	23.8	1
gb|TT-05_M08 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	51.27	1
Unknown	25.8	1
Unknown	29.77	1
Unknown	72.35	1
Unknown	86.04	1
tc|Rep: Vacuolar proton-ATPase subunit-like protein - Lotus japonicus, partial (58%	2166.34	1
gb|KL5B.118O02F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.118O02, m	536.87	1
Unknown	21.83	1
Unknown	20.99	1
Unknown	229.24	1
Unknown	954.43	1
gb|CHO_SL008xh22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	34.64	1
tc|Rep: Chromosome chr1 scaffold_22, whole genome shotgun sequence - Vitis vin	33.13	1
tc|Rep: MADS-box protein 15 - Petunia hybrida (Petunia), partial (82%) [TC43610]	398.79	1
tc|Rep: Calreticulin precursor - Nicotiana plumbaginifolia (Leadwort-leaved tobacc	397.17	1
tc|Rep: Chromosome undetermined scaffold_771, whole genome shotgun sequenc	20.86	1
gb|KN6B.103B02F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103B02, m	3153.83	1
gb|KF8B.100H01F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100H01, mR	4597.93	1
gb|KP1B.108B08F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108B08, m	53.4	1
tc|Rep: Small GTP-binding protein domain containing protein, expressed - Oryza sa	1461.63	1

gb|TT-49_O20 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	4484.25	1
tc|Rep: Hsc70 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), partial	172.91	1
tc|Rep: Glycine rich protein-interacting protein - Nicotiana tabacum (Common toba	183.7	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	568.7	1
tc|Rep: Chromosome chr2 scaffold_140, whole genome shotgun sequence - Vitis vi	11635.1	1
tc|Rep: Chromosome undetermined scaffold_142, whole genome shotgun sequenc	36.48	1
tc|Rep: Chromosome undetermined scaffold_734, whole genome shotgun sequenc	32.48	1
tc|Rep: ATP synthase subunit gamma, mitochondrial precursor - Ipomoea batatas (	973.9	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	144.53	1
Unknown	394.93	1
gb|Nicotiana tabacum NtGPDL mRNA for putative glycerophosphoryl diester phosp	67.61	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	183.51	1
tc|Rep: Genomic DNA, chromosome 5, BAC clone:F6N7 - Arabidopsis thaliana (Mou	173.31	1
Unknown	2742.88	1
Unknown	1001.14	1
gb|XXXP159 Nicotiana tabacum Pollen PCR-based subtractive library Nicotiana taba	151.48	1
Unknown	67.08	1
Unknown	18.74	1
gb|ntsm20 embryogenic microspores Nicotiana tabacum cDNA, mRNA sequence [E	25.87	1
gb|KG9B.106M11F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106M11,	183.76	1
gb|KL4B.102H18F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102H18, m	30.29	1
gb|KG9B.005J05F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005J05, m	13177	1
gb|KF8B.201M14F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201M14, m	45.53	1
gb|KT7C.105J18F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105J18, mRN	26.76	1
tc|Rep: Chromosome chr1 scaffold_84, whole genome shotgun sequence - Vitis vin	102.21	1
gb|KL4B.107B08F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107B08, mR	969.24	1
Unknown	110.09	1
tc|Rep: 60S ribosomal protein L10 - Solanum lycopersicum (Tomato) (Lycopersicon	171.92	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	162.86	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	131.53	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT12-4-420, cultivar Bright Yellow 2	47.93	1
gb|KG9B.106B12F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106B12, m	1525.8	1
Unknown	805.53	1
Unknown	80.03	1

gb|AGN_RPC004xo04f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	40.98	1
gb|KG9B.103K10F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103K10, m	512.1	1
gb|KG9B.102E04F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102E04, m	85.89	1
Unknown	33.98	1
tc|Rep: Adenosine kinase isoform 2S - Nicotiana tabacum (Common tobacco), com	526.77	1
gb|KF8C.108A06F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108A06, mRN	28.66	1
tc|Rep: At4g08320 - Arabidopsis thaliana (Mouse-ear cress), partial (27%) [TC6968	42.9	1
Unknown	538.93	1
gb|Nicotiana tabacum centrin (CEN1) mRNA, complete cds [AF072519]	29.17	1
gb|CHO_SL017xn06f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	186.55	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	85.11	1
gb|BP534049 MAT005 Nicotiana tabacum cDNA clone BY32003, mRNA sequence [	42.27	1
tc|Rep: RRM-containing RNA-binding protein-like protein - Solanum tuberosum (Po	25.52	1
Unknown	27	1
tc|Rep: NTGP3 - Nicotiana tabacum (Common tobacco), complete [TC53712]	81.9	1
gb|AM827537 DL, diurnal library Nicotiana tabacum cDNA clone nt005089091, mR	105.95	1
gb|AGN_ELP011xe21f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	129.54	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	152.39	1
Unknown	31.48	1
Unknown	66.99	1
gb|AM811486 DL, diurnal library Nicotiana tabacum cDNA clone nt005190038, mR	52.78	1
gb|KR2B.001I12F.050815T7 KR2B Nicotiana tabacum cDNA clone KR2B.001I12, mR	29.37	1
Unknown	182.94	1
Unknown	43.46	1
gb|AGN_PNL226bf1_c11.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	70.77	1
gb|KG9B.002C07F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002C07, m	119.23	1
Unknown	18.06	1
gb|AGN_RPC015xe14f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	43.31	1
Unknown	19.1	1
Unknown	434.23	1
gb|KF8C.102H18F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102H18, mR	2592.84	1
gb|TT-11_B01 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	32.69	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	46.96	1
tc|Rep: ATPase - Camellia sinensis (Tea), complete [TC71603]	635.8	1

gb|KP1B.107F20F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107F20, mF	41.22	1
gb|KL4B.101G14F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101G14, mF	912.09	1
Unknown	878.54	1
Unknown	24.46	1
gb|KL5B.103D14F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.103D14, mF	180.18	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	101.67	1
Unknown	549.77	1
gb|AGN_RPC020xo11f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	81.15	1
Unknown	493.7	1
gb|EST_FLW001xk08f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [EI	19.65	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	27.57	1
gb|TT-12_G09 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	20.69	1
tc|Rep: Non-specific lipid-transfer protein - Zinnia elegans (Zinnia), partial (25%) [TC	31.96	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	40.59	1
gb|Nicotiana tabacum putative calmodulin binding protein-like mRNA, partial sequ	71.62	1
tc|Rep: Heat shock factor binding protein 2 - Zea mays (Maize), partial (72%) [TC53	609.97	1
gb|KL4B.106P14F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106P14, mR	50.07	1
gb|KG9B.001E24F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001E24, m	40.31	1
tc|Rep: 40S ribosomal protein S15-like - Solanum tuberosum (Potato), complete [TC	88.53	1
gb|AM822222 seedling library, SL Nicotiana tabacum cDNA clone nt002195045, mF	45.08	1
tc|Rep: Chromosome chr9 scaffold_90, whole genome shotgun sequence - Vitis vin	267.18	1
gb|KT7C.105A10F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105A10, mRI	28.22	1
Unknown	38.38	1
Unknown	178.82	1
gb|AGN_RNC030xg21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	131.05	1
tc|Rep: Extensin-like protein - Solanum lycopersicum (Tomato) (Lycopersicon escul	8249.71	1
Unknown	513.33	1
tc|Rep: Cinnamyl alcohol dehydrogenase 1 - Nicotiana tabacum (Common tobacco)	119.48	1
gb|TT-36_M19 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sec	94.48	1
Unknown	20.87	1
gb|KP1B.103O09F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103O09, m	22.55	1
gb|AGN_RNC118xk11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	148.51	1
gb|TT-40_H23 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	667.11	1
gb|KG9B.004H10F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004H10, n	195.89	1

gb|TOBESTR050A01 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	1283.16	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	159.46	1
gb|Nicotiana tabacum NtbZIP60 mRNA for basic region leucine zipper protein, com	6907.68	1
gb|AGN_RPC025xk21f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	17118.75	1
Unknown	157.37	1
gb|KP1B.107G01F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107G01, m	129.78	1
gb|KG9B.005A19F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.005A19, m	747.39	1
gb|AGN_ELP012xk14f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	19.78	1
gb|Nicotiana tabacum putative spindle disassembly related protein CDC48 mRNA, c	56.53	1
gb|N.tabacum npp3 mRNA for protein phosphatase type 1 [Z93770]	29.45	1
Unknown	91.66	1
gb|Nicotiana tabacum peroxisomal acetoacetyl-coenzyme A thiolase (AACT2) mRN	97.92	1
gb|AGN_RNC007xg14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	173.7	1
Unknown	28.8	1
gb|AGN_RNC015xp08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	185.5	1
Unknown	40.9	1
Unknown	1176.26	1
gb|KT7B.103J24F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.103J24, mRN	124.76	1
Unknown	846.33	1
gb|AGN_RNC023xf11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	84.64	1
gb|TOBESTR046E09 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	65.58	1
tc|Rep: Phosphatidylinositol synthase - Solanum tuberosum (Potato), complete [TC	638.98	1
gb|AGN_RNC014xf06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	494.7	1
tc|Rep: 60S ribosomal protein L34 - Nicotiana tabacum (Common tobacco), partial	41.37	1
gb|AGN_RPC015xk16f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	594.01	1
gb|AGN_RPC003xb12f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	20.1	1
tc|Rep: Chromosome chr14 scaffold_164, whole genome shotgun sequence - Vitis v	250.56	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	168.04	1
Unknown	21.26	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	253.48	1
gb|CHO_SL005xj24f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	45.45	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	54.29	1
gb|KG9B.102N08F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102N08, r	802.62	1
Unknown	330.17	1

gb|KF8C.109L20F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.109L20, mRN	119.03	1
gb|AM833236 DL, diurnal library Nicotiana tabacum cDNA clone nt005124044, mR	47.96	1
Unknown	148.68	1
gb|KF8B.100E17F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100E17, mR	2113.54	1
gb|BP130642 MAT001 Nicotiana tabacum cDNA clone BY2632, mRNA sequence [B	85.83	1
Unknown	82.17	1
Unknown	22.49	1
Unknown	258.5	1
tc|Rep: Kinase-associated protein phosphatase 1 - Solanum peruvianum (Peruvian	99.12	1
Unknown	144.72	1
Unknown	53.52	1
gb|AGN_RPC018xb10f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	57.57	1
tc|Rep: Uncharacterized protein At3g49720 - Arabidopsis thaliana (Mouse-ear cres	850.22	1
tc|Rep: Chromosome chr10 scaffold_50, whole genome shotgun sequence - Vitis vi	1159.68	1
Unknown	32.67	1
gb|KL4B.111O15F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111O15, m	203.21	1
Unknown	24.79	1
Unknown	528.61	1
Unknown	42.04	1
Unknown	184.03	1
Unknown	405.73	1
tc|Rep: At3g12480-like protein - Boechera drummondii (Rock-cress) (Arabis drumm	370.2	1
Unknown	363.17	1
gb|AM830869 seedling library, SL Nicotiana tabacum cDNA clone nt002031015, m	103.92	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (81%) [TC4	82.43	1
tc|Rep: L-lysine permease - Bifidobacterium adolescentis (strain ATCC 15703 / DSM	24.26	1
Unknown	517.95	1
Unknown	45.13	1
gb|KL4B.103M12F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103M12, m	31.23	1
gb|KG9B.001O11F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001O11, r	47.85	1
Unknown	132.5	1
gb|Nicotiana tabacum NtVDAC3 mRNA for voltage-dependent anion channel, com	509.98	1
gb|KP1B.108A10F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108A10, m	78.03	1
tc|Rep: COV1-like protein - Solanum chacoense (Chaco potato), complete [TC7707	23.58	1

tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	235.13	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	53.18	1
gb|KT7C.106J14F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106J14, mRN	17.47	1
gb|AM800292 seedling library, SL Nicotiana tabacum cDNA clone nt002002017, mR	100.88	1
gb|KR3B.104K14F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.104K14, m	24.19	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	31.44	1
gb|KL4B.102K12F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102K12, mR	27.14	1
Unknown	83.43	1
tc|Rep: ChaC-like family protein-like - Solanum tuberosum (Potato), partial (94%) [T	2335.65	1
tc|Rep: Chromosome undetermined scaffold_466, whole genome shotgun sequenc	248.81	1
gb|KL4B.107E16F.051126T7 KL4B Nicotiana tabacum cDNA clone KL4B.107E16, mR	1853.17	1
gb|BP133134 MAT001 Nicotiana tabacum cDNA clone BY5366, mRNA sequence [B	62.03	1
Unknown	76.31	1
tc|Rep: Gip1-like protein - Petunia hybrida (Petunia), partial (93%) [TC55977]	21.8	1
gb|AGN_RNC211xg09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	52.23	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	17.83	1
Unknown	8738.97	1
gb|AGN_RNC025xm06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	33.09	1
tc|Rep: Chromosome chr18 scaffold_61, whole genome shotgun sequence - Vitis vi	115.69	1
gb|KF8C.106A10F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106A10, mRN	31.98	1
Unknown	470.66	1
Unknown	40.69	1
tc|Rep: Zinc finger, ZZ-type; Zinc finger, C2H2-type - Medicago truncatula (Barrel m	81.6	1
tc|Rep: Unconventional myosin - Helianthus annuus (Common sunflower), partial (2	23.9	1
Unknown	19.18	1
tc|AAD20127.1 - Arabidopsis thaliana (Mouse-ear cress), partial (24%) [TC67580]	591.34	1
gb|CHO_SL025xh14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	44.97	1
Unknown	133.77	1
gb|AGN_PNL210bf1_f1.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	134.5	1
tc|Rep: Chromosome chr10 scaffold_50, whole genome shotgun sequence - Vitis vi	1084.99	1
gb|CHO_SL007xb02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	184.87	1
gb|KT7C.110F08F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110F08, mRN	2223.6	1
gb|AGN_RNC004xe11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	128.01	1
Unknown	121.98	1

Unknown	86.28	1
tc|Rep: Chromosome undetermined scaffold_252, whole genome shotgun sequenc	124.26	1
Unknown	247.49	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	274.05	1
tc|Rep: SufE-like protein, chloroplast precursor - Arabidopsis thaliana (Mouse-ear c	233.94	1
gb|AGN_RNC108xh11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	34.41	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	383.9	1
gb|TT-36_F05 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	589.37	1
gb|KL4B.111F18F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111F18, mR	76.35	1
gb|KP1B.001E04F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001E04, m	59.34	1
gb|TT-05_K04 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	591.76	1
Unknown	21.57	1
Unknown	20.58	1
tc|Rep: Plastid quinol oxidase - Solanum lycopersicum (Tomato) (Lycopersicon escu	787.11	1
Unknown	1228.57	1
tc|Rep: lipase-related - Arabidopsis thaliana, partial (26%) [TC64373]	103.36	1
tc|Rep: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor	460.28	1
gb|Nicotiana tabacum DnaJ-like protein mRNA, complete cds [AF191497]	177.76	1
tc|Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vi	469.46	1
gb|BP131939 MAT001 Nicotiana tabacum cDNA clone BY4053, mRNA sequence [B	49.7	1
tc|Rep: Probable phospholipid hydroperoxide glutathione peroxidase - Nicotiana ta	4832.24	1
gb|KN6B.109B22F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.109B22, m	199.24	1
gb|Nicotiana tabacum mRNA for ras-related protein RAB8-1, complete cds [AB079	2732.19	1
tc|Rep: Dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate deh	4205.63	1
Unknown	191.7	1
gb|KP1B.107E17F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107E17, m	174.03	1
Unknown	862.94	1
Unknown	19.69	1
tc|Rep: SGS3-like protein - Solanum lycopersicum (Tomato) (Lycopersicon esculent	24.73	1
gb|CHO_SL028xd22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	34.22	1
gb|KG9B.004B19F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004B19, m	975.67	1
tc|Rep: Ubiquitin fusion protein - Arachis hypogaea (Peanut), complete [TC53803]	79.07	1
Unknown	145.36	1
gb|D35-AC12 Ethylene Induced Tobacco Leaf cDNA Library Nicotiana tabacum cDN	407.1	1

Unknown	28.38	1
tc|Rep: Ubiquitin carrier protein - Vitis vinifera (Grape), complete [TC56781]	745.9	1
Unknown	8223.87	1
gb|TT-29_D08 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	548.44	1
gb|26.2D12 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5'	510.28	1
Unknown	189.38	1
tc|Rep: AT5g66850/MUD21_11 - Arabidopsis thaliana (Mouse-ear cress), partial (1	3039.62	1
Unknown	110.01	1
gb|KP1B.107H13F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107H13, m	177.28	1
gb|KF8C.104H23F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104H23, mR	4010.1	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	4316.87	1
tc|Rep: Succinyl CoA ligase beta subunit - Solanum lycopersicum (Tomato) (Lycoper	41.62	1
Unknown	46.68	1
gb|AGN_RNC211xj15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	65.88	1
tc|Rep: Chromosome chr12 scaffold_78, whole genome shotgun sequence - Vitis vi	1019.65	1
gb|AGN_ELP025xd18f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	140.62	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	190.13	1
gb|Nicotiana tabacum mRNA for histone H3, complete cds [AB015760]	1593.56	1
tc|Rep: Shaggy-like kinase 59 - Nicotiana tabacum (Common tobacco), complete [T	381.81	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTT2-23-370, cultivar Bright Yellow 2	43.57	1
tc|Rep: Tubby-like F-box protein 7 - Arabidopsis thaliana (Mouse-ear cress), partial	91.42	1
gb|AGN_PNL231af1_b2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	12783.4	1
Unknown	33.08	1
tc|Rep: Chromosome chr10 scaffold_433, whole genome shotgun sequence - Vitis	18272.65	1
gb|AGN_PNL229af1_c1.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	27.68	1
Unknown	267.12	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	23.58	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	978.51	1
gb|AGN_ELP015xb20f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	41.47	1
Unknown	186.12	1
gb|KP1B.104E07F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104E07, m	2723.56	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	144.78	1
Unknown	1572.96	1
gb|BP534904 MAT005 Nicotiana tabacum cDNA clone BY34113, mRNA sequence [	2195.88	1

Unknown	140.68	1
Unknown	2716.11	1
Unknown	18.98	1
Unknown	24.52	1
gb|AGN_RNC211xc05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	2828.75	1
tc|Rep: Chromosome undetermined scaffold_259, whole genome shotgun sequenc	93.71	1
gb|KL4B.102J02F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102J02, mRN	1188.06	1
gb|FS411833 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	9407.13	1
Unknown	85.48	1
tc|Rep: Chromosome chr17 scaffold_101, whole genome shotgun sequence - Vitis v	18.57	1
Unknown	1054.94	1
gb|TT-12_E09 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	31.72	1
gb|KL4B.105G15F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105G15, mR	226.05	1
gb|AGN_RNC020xj24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	136.97	1
gb|CHO_SL023xn07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	24.26	1
gb|Nicotiana tabacum mRNA for alpha-tubulin (tubA3 gene) [AJ421413]	10741.4	1
tc|Rep: Mini-chromosome maintenance protein - Medicago sativa (Alfalfa), partial (	70.17	1
gb|KP1B.112P14F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.112P14, m	543.67	1
tc|Rep: Ribosomal Pr 117 - Triticum aestivum (Wheat), partial (95%) [TC71894]	58	1
tc|Rep: Similarity to kinesin heavy chain - Arabidopsis thaliana (Mouse-ear cress), p	79.72	1
Unknown	22.69	1
Unknown	24.84	1
Unknown	80.11	1
gb|Nicotiana tabacum mRNA for putative DNAJ protein [AJ299254]	264.7	1
Unknown	512.09	1
gb|Nicotiana tabacum Bax inhibitor 1 (BI-1) mRNA, complete cds [AF390556]	140.05	1
gb|KF8C.104D13F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104D13, mRN	161.47	1
Unknown	28.87	1
gb|KT7C.110O09F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110O09, mR	29.85	1
Unknown	34.75	1
gb|KG9B.102F13F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102F13, m	36.59	1
Unknown	35.19	1
gb|TT-50_A15 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	39.05	1
gb|AGN_PNL210cf1_h6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	68.01	1

tc|Rep: Chromosome undetermined scaffold_184, whole genome shotgun sequenc	4659.34	1
tc|Rep: PII protein - Nicotiana tabacum (Common tobacco), partial (65%) [TC72036	102.39	1
gb|KG9B.105B07F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105B07,	4513.12	1
Unknown	5508.4	1
gb|KT7C.108O06F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108O06, mR	78.87	1
Unknown	810.38	1
gb|EST_YP003xb07f1.ab1 EST_YP Nicotiana tabacum cDNA, mRNA sequence [EH61	119.66	1
gb|Nicotiana tabacum mRNA for shaggy-like kinase 111 [AJ002314]	1300.41	1
gb|TT-04_O04 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	68.12	1
gb|KN6B.115D14F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.115D14,	68.71	1
gb|TT-36_F01 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	441.31	1
gb|KP1B.102H10F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102H10, m	129.8	1
gb|TT-05_M07 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA se	130.36	1
gb|FS433138 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	179.25	1
gb|AGN_RNC018xm19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	608.24	1
tc|Rep: Dihydroneopterin aldolase - Solanum lycopersicum (Tomato) (Lycopersicon	30.37	1
tc|Rep: Os01g0706500 protein - Oryza sativa subsp. japonica (Rice), complete [TC5	61.96	1
gb|KP1B.113I05F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.113I05, mR	106.31	1
gb|TT-24_G19 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	380.98	1
Unknown	412.66	1
Unknown	31.6	1
Unknown	29.7	1
Unknown	2703.83	1
gb|AGN_RNC123xg10r1.ab1 AGN_RNC Nicotiana tabacum cDNA 3', mRNA sequenc	20.36	1
gb|KL4B.102H16F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102H16, m	1193.33	1
tc|Rep: Plastidial delta-12 oleate desaturase - Olea europaea (Common olive), parti	28.68	1
tc|Rep: 26S proteasome subunit 11 - Platanus acerifolia (London plane tree), partia	185.46	1
tc|Rep: Chromosome undetermined scaffold_1132, whole genome shotgun sequen	32.07	1
gb|TT-36_L05 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sequ	141.25	1
Unknown	33.56	1
Unknown	529.79	1
gb|KT7C.106O17F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106O17, mR	84.72	1
gb|KT7C.110A05F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110A05, mR	313.59	1
Unknown	63.5	1

gb|AGN_RPC022xd24f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	18.81	1
gb|KL4B.104D04F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104D04, mR	32.14	1
Unknown	626.71	1
Unknown	32.89	1
Unknown	18357.15	1
tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	526.14	1
tc|Rep: Calcineurin B-like interacting protein kinase - Solanum lycopersicum (Tomat	189.97	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	155.92	1
gb|CHO_SL013xm13f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	578	1
Unknown	18.86	1
gb|TT-22_G18 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	2889.2	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	90.69	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	71.79	1
Unknown	117.02	1
gb|KL5B.111A15F.060117T7 KL5B Nicotiana tabacum cDNA clone KL5B.111A15, mR	38.53	1
Unknown	103.8	1
tc|Rep: Heat stress transcription factor B-2a - Arabidopsis thaliana (Mouse-ear cres	122.71	1
gb|CHO_SL008xc16f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	472.09	1
gb|Nicotiana tabacum ipi2 mRNA for isopentenyl diphosphate isomerase 2, comple	189.87	1
tc|Rep: Chromosome undetermined scaffold_734, whole genome shotgun sequenc	47.35	1
gb|KL4B.103F18F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.103F18, mR	110.03	1
Unknown	130.63	1
tc|Rep: Importin alpha 1 - Capsicum annuum (Bell pepper), partial (35%) [TC54948]	1090.78	1
gb|AM792648 seedling library, SL Nicotiana tabacum cDNA clone nt002178014, mR	109.51	1
Unknown	29.86	1
Unknown	29.11	1
gb|AGN_ELP022xm08f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	18.85	1
Unknown	55.4	1
tc|Rep: Ethylene-responsive transcription factor 3 - Nicotiana tabacum (Common to	2369.05	1
Unknown	98.51	1
gb|Nicotiana tabacum ankyrin-repeat protein HBP1 mRNA, complete cds [AF35279	413.09	1
tc|Rep: Chromosome chr6 scaffold_28, whole genome shotgun sequence - Vitis vin	21.15	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	20.9	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC3-42-285, cultivar Bright Yellow 2	573.04	1

gb|Nicotiana tabacum NtNRAMP1 mRNA for metal transporter, complete cds [AB5	23.87	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	65.89	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	21.66	1
gb|KG9B.002C16F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002C16,	168.84	1
tc|Rep: Serine/threonine-protein phosphatase PP2A-5 catalytic subunit - Nicotiana	718.48	1
tc|Rep: Casein kinase - Beta vulgaris (Sugar beet), partial (72%) [TC73343]	61.12	1
gb|TT-47_H24 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	443.88	1
Unknown	269.96	1
Unknown	801.53	1
Unknown	29.81	1
tc|Rep: ATP synthase subunit O, mitochondrial precursor - Ipomoea batatas (Sweet	23.61	1
Unknown	38.5	1
gb|KN6B.115E04F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.115E04,	108.39	1
Unknown	235.23	1
gb|KG9B.004L12F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004L12, m	214.71	1
gb|KG9B.106J08F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106J08, m	104.92	1
gb|KG9B.002M07F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002M07,	411.78	1
Unknown	145.02	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	2714.28	1
Unknown	105.85	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	177.36	1
Unknown	18.36	1
Unknown	26.66	1
tc|Rep: Eukaryotic translation initiation factor 2 beta subunit-like - Solanum tubero	650.36	1
gb|Nicotiana tabacum DNA-binding protein 2 (WRKY2) mRNA, complete cds [AF09	86.12	1
tc|Rep: Pectin methylesterase precursor - Nicotiana plumbaginifolia (Leadwort-lea	1600.05	1
Unknown	260.19	1
Unknown	95.49	1
tc|Rep: Chromosome chr5 scaffold_156, whole genome shotgun sequence - Vitis vi	9894.16	1
gb|Nicotiana tabacum partial mRNA for cullin 1C (cul1C gene) [AJ344535]	36.47	1
gb|TT-05_M18 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	39.3	1
Unknown	572.7	1
Unknown	42.82	1
gb|KG9B.105D01F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105D01,	62.57	1

tc|Rep: Chromosome undetermined scaffold_409, whole genome shotgun sequenc	49.22	1
gb|AGN_ELP003xl18f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	657.53	1
tc|Rep: Chromosome undetermined scaffold_51, whole genome shotgun sequence	37.57	1
Unknown	133.35	1
tc|Rep: Aspartic proteinase precursor - Cucurbita pepo (Vegetable marrow) (Summ	25.72	1
gb|KG9B.003D18F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003D18, n	25.78	1
tc|Rep: NADH:ubiquinone oxidoreductase-like - Solanum tuberosum (Potato), com	633.7	1
gb|TL13.110O19F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.110O19, mR	300.16	1
Unknown	294.12	1
gb|CHO_SL017xh04f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	3232.82	1
gb|Nicotiana tabacum MAPK mRNA for MAP kinase homolog, partial cds [AB19547	23.04	1
gb|FS407121 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	2702.87	1
tc|Rep: Os01g0706500 protein - Oryza sativa subsp. japonica (Rice), complete [TC7	88.13	1
tc|Rep: Chromosome undetermined scaffold_147, whole genome shotgun sequenc	333.13	1
gb|KF8C.102G07F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102G07, mR	142.54	1
gb|KP1B.037D10F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.037D10, m	56.08	1
gb|KP1B.001N14F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001N14, m	59.56	1
Unknown	76.07	1
gb|KR2B.002L21F.051019T7 KR2B Nicotiana tabacum cDNA clone KR2B.002L21, m	45.9	1
Unknown	19.49	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	85.77	1
gb|KL4B.110E24F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110E24, mR	29.15	1
gb|TT-07_D01 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	177.24	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	29.24	1
Unknown	1803.5	1
Unknown	139.6	1
gb|AGN_RPC023xo08f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	24.45	1
Unknown	30.44	1
tc|Rep: Protein kinase MK5 - Mesembryanthemum crystallinum (Common ice plan	274.45	1
tc|Rep: Embryo-specific 3 - Medicago truncatula (Barrel medic), partial (63%) [TC52	232.94	1
Unknown	50.78	1
Unknown	46.21	1
Unknown	158.25	1
Unknown	37.97	1

Unknown	168.2	1
Unknown	343.68	1
tc|Rep: 60S ribosomal protein L19 - Capsicum annuum (Bell pepper), partial (32%) [	168.96	1
Unknown	152.08	1
tc|Rep: 3-isopropylmalate dehydrogenase 2, chloroplast precursor - Arabidopsis th	30.62	1
tc|Rep: Chromosome undetermined scaffold_183, whole genome shotgun sequenc	63.97	1
Unknown	50.73	1
gb|KT7B.107C11F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107C11, mRI	271.1	1
tc|Rep: Shaggy-related protein kinase NtK-1 - Nicotiana tabacum (Common tobacc	881.28	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	581.5	1
Unknown	18310.8	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	224.23	1
Unknown	138.82	1
tc|Rep: Chromosome undetermined scaffold_226, whole genome shotgun sequenc	125.54	1
Unknown	71.93	1
gb|Nicotiana tabacum centrin (CEN1) mRNA, complete cds [AF072519]	24.86	1
gb|CHO_SL015xk10f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	139.59	1
gb|TT-15_A22 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	330.38	1
gb|CHO_SL008xa12f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	5236.92	1
Unknown	360.11	1
tc|Rep: Small GTP-binding protein domain containing protein, expressed - Oryza sa	8156.25	1
gb|Nicotiana tabacum clone PR18 mRNA sequence [AF154642]	63.6	1
gb|KP1B.108G24F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108G24, m	2050.48	1
tc|Rep: Peptidyl-prolyl cis-trans isomerase - Solanum tuberosum (Potato), partial (	1521.22	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	927.91	1
gb|TT-01_F03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	106.27	1
Unknown	84.96	1
Unknown	513.15	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	2691.53	1
tc|Rep: ADP-ribosylation factor 1 - Arabidopsis thaliana (Mouse-ear cress), partial (	2287.16	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	79.3	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	210.82	1
Unknown	26.12	1
gb|KP1B.001J17F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001J17, mR	146.92	1

gb|FS429988 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	744.05	1
Unknown	20.56	1
gb|KT7C.105C02F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105C02, mR	134.01	1
gb|AGN_RNC007xi21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	21.91	1
gb|BL12.103D11F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.103D11, m	4468.21	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	45.93	1
Unknown	22.77	1
tc|Rep: Chromosome chr19 scaffold_126, whole genome shotgun sequence - Vitis	124.43	1
tc|Rep: Chromosome undetermined scaffold_89, whole genome shotgun sequence	200.5	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	90.69	1
Unknown	23.31	1
gb|KR2B.102J17F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.102J17, mR	47.04	1
Unknown	31.41	1
tc|Rep: Chromosome undetermined scaffold_69, whole genome shotgun sequence	521.56	1
tc|Rep: Hydrogenase-4 component E - Campylobacter concisus (strain 13826), parti	41.25	1
gb|Nicotiana tabacum DNA-binding protein 2 (WRKY2) mRNA, complete cds [AF09	100.61	1
gb|KP1B.102G07F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102G07, m	119.14	1
tc|Rep: Glyceraldehyde-3-phosphate dehydrogenase - Capsicum annuum (Bell pep	176.75	1
gb|AGN_PNL221br1_c2.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	28.86	1
gb|KP1B.101K05F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101K05, m	80.84	1
gb|BP131465 MAT001 Nicotiana tabacum cDNA clone BY3516, mRNA sequence [B	126.18	1
Unknown	38.94	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	22.41	1
gb|KR2B.115G13F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115G13, m	104.83	1
tc|Rep: Chromosome chr11 scaffold_56, whole genome shotgun sequence - Vitis vi	38.14	1
gb|KL4B.104H15F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104H15, m	46.6	1
Unknown	433.81	1
Unknown	85.36	1
gb|KN6B.009K14F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009K14, m	440.81	1
Unknown	302.36	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	2262.12	1
gb|KL4B.106F14F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106F14, mR	287.29	1
gb|Nicotiana tabacum multicopy suppressor of IRA1 (MSI1) mRNA, complete cds [E	181.67	1
Unknown	21.87	1

Unknown	625	1
tc|Rep: SLL1 protein - Primula vulgaris, partial (73%) [TC56544]	3082.96	1
gb|TT-20_P09 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	98.48	1
Unknown	19.12	1
Unknown	144.75	1
Unknown	136.41	1
Unknown	36.71	1
tc|Rep: 26S proteasome regulatory subunit S2 - Arabidopsis thaliana (Mouse-ear cr	38.98	1
tc|Rep: Maturase K - Bryanthus gmelini (Heath), partial (7%) [TC74232]	72.11	1
tc|Rep: ATP synthetase, delta chain - Leifsonia xyli subsp. xyli, partial (5%) [TC53587	207.09	1
Unknown	357.36	1
gb|KG9B.103P03F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103P03, m	32.47	1
gb|AGN_PNL219af1_g9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	365.19	1
gb|Nicotiana tabacum geranylgeranylated protein NTGP5 mRNA, complete cds [U6	59.61	1
gb|CHO_SL001xo03f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	47.01	1
tc|Rep: WD domain protein-like - Arabidopsis thaliana (Mouse-ear cress), partial (6	717.87	1
tc|Rep: F2401.12 - Arabidopsis thaliana (Mouse-ear cress), partial (24%) [TC53009]	25.63	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	1324.4	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	992.38	1
gb|KR3B.109I13F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109I13, mR	535.71	1
Unknown	467.11	1
gb|KP1B.101M19F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101M19, r	22.77	1
tc|Rep: Protein TOC75, chloroplast precursor - Pisum sativum (Garden pea), partial	24.71	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	21.96	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	60.58	1
tc|Rep: Omega-3 fatty acid desaturase - Nicotiana tabacum (Common tobacco), cor	850.74	1
tc|Rep: F1N21.10 - Arabidopsis thaliana (Mouse-ear cress), partial (25%) [TC67342]	50.27	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	92.17	1
gb|AGN_ELP006xp09f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	160.82	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	26.14	1
gb|Nicotiana tabacum aspartic protease mRNA, complete cds [DQ648018]	81.93	1
Unknown	180.74	1
Unknown	80.46	1
gb|KN6B.100O05F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100O05, r	1151.15	1

gb|TT-29_M09 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	26.91	1
Unknown	1439.66	1
gb|AGN_ELP012xl03f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	58.93	1
gb|KP1B.001A12F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001A12, m	29.15	1
gb|AGN_ELP024xg01f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	60.58	1
tc|Rep: Glutamate dehydrogenase A - Nicotiana plumbaginifolia (Leadwort-leaved	154.83	1
gb|AM842139 COL, cold overnight library Nicotiana tabacum cDNA clone nt006046	98.23	1
Unknown	102.18	1
Unknown	1193.23	1
tc|Rep: 60S ribosomal protein L21-like protein - Solanum tuberosum (Potato), com	85.63	1
gb|BP535041 MAT005 Nicotiana tabacum cDNA clone BY34252, mRNA sequence [	26.85	1
tc|Rep: 50S ribosomal protein L29, chloroplast precursor - Zea mays (Maize), partia	56.45	1
gb|KT7B.100G14F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100G14, mR	115.19	1
gb|KP1B.001D12F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001D12, m	22.05	1
gb|KL4B.101D05F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101D05, m	514.45	1
gb|AGN_RNC025xe05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1855.41	1
gb|AGN_RNC129xp14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	106.76	1
gb|KL4B.100K21F.050922T7 KL4B Nicotiana tabacum cDNA clone KL4B.100K21, mR	18.16	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	643.54	1
Unknown	79.95	1
tc|Rep: Signal recognition particle 14 kDa protein - Arabidopsis thaliana (Mouse-ea	231.63	1
Unknown	59.79	1
gb|Nicotiana tabacum Fas-associated factor-like protein mRNA, partial cds [AY740	554.32	1
gb|FS406426 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	55.96	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	19822.75	1
gb|KL4B.111B13F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111B13, mR	23.9	1
Unknown	263.94	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	28.69	1
tc|Rep: UDP-D-apiose/UDP-D-xylose synthase - Nicotiana benthamiana, partial (41	4337.35	1
gb|KR2B.110D07F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110D07, m	62.46	1
tc|Rep: Water stress induced protein - Brassica oleracea (Wild cabbage), partial (91	4023.57	1
tc|Rep: Chromosome chr14 scaffold_54, whole genome shotgun sequence - Vitis vi	397.3	1
Unknown	737.12	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	186.83	1

gb|KL4B.102L05F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.102L05, mRI	1301.36	1
gb|KR3B.104E14F.051108T7 KR3B Nicotiana tabacum cDNA clone KR3B.104E14, ml	201.99	1
Unknown	22.46	1
tc|Rep: UDP-glucuronate decarboxylase 1 - Nicotiana tabacum (Common tobacco),	12634.05	1
Unknown	179.33	1
Unknown	126.61	1
tc|Rep: Chromosome undetermined scaffold_533, whole genome shotgun sequenc	113.97	1
tc|Rep: RNA export 1 - Nicotiana benthamiana, complete [TC48695]	153.99	1
gb|KF8B.200H02F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200H02, mRI	19301.85	1
gb|KP1B.102N18F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102N18, m	123.76	1
tc|Rep: NAD(P)H:quinone oxidoreductase (NAD(P)H:QR) - Solanum tuberosum (Pot	35.27	1
tc|Rep: COG3307: Lipid A core - O-antigen ligase and related enzymes - Yersinia inte	376.36	1
gb|KG9B.001B09F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001B09, m	182.42	1
tc|Rep: Chromosome chr13 scaffold_210, whole genome shotgun sequence - Vitis v	100.31	1
tc|Rep: Methionine synthase - Nicotiana suaveolens, partial (11%) [TC72168]	13959.95	1
Unknown	141.53	1
gb|TT-32_H01 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	206.27	1
gb|KL4B.104P10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104P10, mR	28.27	1
gb|Nicotiana tabacum squalene synthase mRNA, complete cds [U60057]	9692.98	1
gb|FS433957 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	61.52	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	5050.04	1
tc|Rep: Os01g0279200 protein - Oryza sativa subsp. japonica (Rice), partial (95%) [T	63.67	1
gb|KL4B.101H16F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101H16, mF	107.33	1
Unknown	101.95	1
tc|Rep: Chromosome undetermined scaffold_147, whole genome shotgun sequenc	476.61	1
Unknown	23.1	1
gb|KR3B.110I10F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110I10, mRI	26.43	1
gb|AGN_RNC013xe15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	332.81	1
gb|AM828280 seedling library, SL Nicotiana tabacum cDNA clone nt002181074, mF	31.52	1
gb|KF8C.102D02F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102D02, mRI	144.52	1
Unknown	119.01	1
gb|KG9B.103G12F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103G12, n	152.26	1
Unknown	184.63	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	86.8	1

tc|Rep: Succinyl-CoA ligase alpha 1 subunit-like - Solanum tuberosum (Potato), part	65.82	1
gb|KF8C.101G15F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101G15, mRI	523.48	1
tc|Rep: Glutamyl-tRNA reductase - Nicotiana tabacum (Common tobacco), complet	1303.68	1
gb|KG9B.003N07F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003N07, r	915.64	1
gb|KR3B.102E17F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.102E17, ml	507.06	1
gb|CHO_SL024xp10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	143.53	1
gb|KL4B.113M01F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.113M01, r	146.47	1
gb|AM793740 seedling library, SL Nicotiana tabacum cDNA clone nt002088018, mF	73.69	1
gb|KG9B.003E07F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003E07, m	224.13	1
Unknown	434.32	1
tc|Rep: T23E18.20 - Arabidopsis thaliana (Mouse-ear cress), partial (29%) [TC64017	186.93	1
gb|KN6B.104I04F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104I04, mF	183.82	1
gb|TT-20_O04 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	1025.33	1
tc|Rep: UDP-apiose/xylose synthase - Solanum tuberosum (Potato), partial (90%) [T	9783.69	1
Unknown	1126.96	1
tc|Rep: Enoyl-CoA hydratase/isomerase - Bordetella bronchiseptica (Alcaligenes bro	23.18	1
tc|Rep: ASH1 protein - Cupiennius salei (Wandering spider), partial (7%) [TC72324]	471.29	1
gb|CHO_SL021xn16f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	18.64	1
gb|N.tabacum mRNA for phosphoglyceromutase [X70651]	4449.54	1
tc|Rep: Chromosome chr11 scaffold_56, whole genome shotgun sequence - Vitis vi	27.2	1
tc|Rep: Pre-mRNA splicing factor - Solanum tuberosum (Potato), partial (26%) [TC7	102.34	1
Unknown	20.82	1
Unknown	50.71	1
Unknown	163.75	1
Unknown	1112.55	1
gb|TT-09_A07 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	177.34	1
gb|KP1B.101J08F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101J08, mR	509.04	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	273.61	1
gb|KF8B.201F08F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201F08, mRN	10516.4	1
Unknown	107.02	1
gb|TT-34_N23 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	22	1
Unknown	25.49	1
Unknown	95.19	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	16.88	1

gb|AGN_ELP012xj21f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	354.64	1
tc|Rep: Expressed protein - Oryza sativa subsp. japonica (Rice), partial (19%) [TC60	53.92	1
Unknown	130.04	1
tc|Rep: Chromosome chr1 scaffold_136, whole genome shotgun sequence - Vitis vi	16852.7	1
Unknown	447.36	1
Unknown	1121.65	1
gb|KR2B.104F24F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.104F24, m	48.56	1
Unknown	19.26	1
tc|Rep: Glucose-6-phosphate isomerase - Solanum tuberosum (Potato), complete [	49.13	1
Unknown	46.19	1
gb|Nicotiana tabacum cDNA-AFLP fragment H-N_BC4M23-283 sequence [DQ4601	52.67	1
gb|TOBESTR024A06 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	188.28	1
gb|TT-20_F08 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	34.36	1
Unknown	509.54	1
gb|KR3B.001M18F.050815T7 KR3B Nicotiana tabacum cDNA clone KR3B.001M18,	124.63	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	1549.67	1
Unknown	40.78	1
gb|FS419162 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	34.86	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	276.58	1
tc|Rep: Protein transport SEC13-like protein - Solanum tuberosum (Potato), partial	1104.04	1
Unknown	86.09	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	24.99	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	40.57	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	386.65	1
Unknown	1575.25	1
gb|AGN_RPC018xc10f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	247.3	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	27.88	1
Unknown	880.2	1
Unknown	25.05	1
tc|Rep: Alpha chain of nascent polypeptide associated complex - Nicotiana bentha	122.07	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	104.07	1
tc|Rep: Chromosome chr10 scaffold_297, whole genome shotgun sequence - Vitis	47.37	1
Unknown	1582.96	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	91.58	1

gb|CHO_SL024xo11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	1107.24	1
tc|Rep: D-ribose ABC transporter, substrate-binding protein precursor - Clostridium	107.12	1
gb|AGN_RPC014xl21f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	63.69	1
gb|KG9B.106N15F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106N15,	215.34	1
Unknown	266.75	1
gb|KP1B.102P22F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102P22, m	72.3	1
gb|AGN_RPC004xc15f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	18.97	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	554.44	1
tc|Rep: Expressed protein - Oryza sativa subsp. japonica (Rice), partial (7%) [TC685	1284.26	1
tc|Rep: Serine/threonine protein phosphatase 5 - Solanum lycopersicum (Tomato)	53.93	1
gb|CHO_SL015xj19f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	173.07	1
Unknown	691.81	1
gb|N.tabacum npp2 mRNA for protein phosphatase type 1 [Z93769]	5579.87	1
gb|KP1B.111E13F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.111E13, m	106.46	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC4-41-220, cultivar Bright Yellow 2	151.75	1
tc|Rep: ADP ribosylation factor 002 - Daucus carota (Carrot), complete [TC64847]	10606.75	1
Unknown	20.88	1
Unknown	19.1	1
tc|Rep: Lipoxygenase - Nicotiana attenuata, partial (32%) [TC51546]	42	1
gb|AGN_PNL222bf1_a11.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	24.81	1
Unknown	26.59	1
tc|Rep: Chromosome chr11 scaffold_118, whole genome shotgun sequence - Vitis	533.52	1
gb|KN6B.103N06F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103N06,	25.6	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	134.67	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	4105.18	1
Unknown	81.6	1
tc|Rep: Avr9/Cf-9 rapidly elicited protein 216 - Nicotiana tabacum (Common tobac	255.99	1
Unknown	517.65	1
gb|KG9B.102H18F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102H18,	1039.46	1
gb|KL5B.115K01F.060302T7 KL5B Nicotiana tabacum cDNA clone KL5B.115K01, mR	42.52	1
gb|AGN_RNC007xf09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	62.71	1
Unknown	766.86	1
tc|Rep: Chromosome chr9 scaffold_33, whole genome shotgun sequence - Vitis vin	1583.57	1
gb|AGN_RNC010xj24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	49.12	1

Unknown	33.18	1
Unknown	777.29	1
gb|TT-34_B02 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	26.97	1
gb|KL4B.106F12F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106F12, mR	20.62	1
gb|KG9B.105I17F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105I17, m	271.87	1
gb|AGN_RNC116xf14f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	63.68	1
Unknown	19.37	1
Unknown	2599.69	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	159.03	1
gb|KP1B.110I21F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110I21, mR	105.52	1
gb|TT-06_P10 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	31.46	1
Unknown	21.16	1
gb|KR2B.111C20F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.111C20, m	29.82	1
Unknown	99.64	1
Unknown	54.86	1
gb|CHO_SL002xh18f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	52362.2	1
tc|Rep: Glucose-6-phosphate/phosphate translocator 1, chloroplast precursor - Ara	158.36	1
gb|TT-04_N01 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	139.38	1
tc|Rep: PSP, proline-rich - Medicago truncatula (Barrel medic), partial (21%) [TC659	239.04	1
gb|AGN_RPC003xm05f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	16.67	1
gb|KN6B.110I24F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.110I24, m	146.96	1
Unknown	21.83	1
gb|TOBESTR050A12 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	1068.86	1
gb|KL4B.111M01F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111M01, m	134.76	1
tc|Rep: 40S ribosomal protein S23 - Fragaria ananassa (Strawberry), complete [TC5	100.21	1
Unknown	224.47	1
tc|Rep: Chromosome chr8 scaffold_88, whole genome shotgun sequence - Vitis vin	147.73	1
Unknown	287.8	1
gb|KG9B.004D12F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004D12,	56.12	1
gb|TT-12_P21 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	1140.63	1
tc|Rep: Pyruvate kinase - Medicago truncatula (Barrel medic), complete [TC49477]	471.4	1
tc|Rep: Signal recognition particle receptor beta subunit-like protein - Arabidopsis t	65.28	1
Unknown	23.48	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	88.13	1

tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	129.72	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	16.28	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	906.05	1
gb|KT7C.104C07F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104C07, mR	776.47	1
Unknown	1309.63	1
gb|AGN_PNL225df1_c5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	734.09	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	829.2	1
tc|NTU82638 Nicotiana tabacum small subunit ribosomal RNA gene, mitochondrial	55187.35	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	34.42	1
gb|KR3B.112B20F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.112B20, m	378.86	1
gb|TOBESTR034B01 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	1339.02	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	710.08	1
gb|TT-04_I24 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	59.55	1
gb|KR2B.107D18F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.107D18, m	107.14	1
Unknown	256.99	1
gb|AM833236 DL, diurnal library Nicotiana tabacum cDNA clone nt005124044, mR	21.08	1
gb|KT7C.109M22F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109M22, m	24.94	1
Unknown	51.47	1
Unknown	469.17	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	122.21	1
tc|Rep: Dehydroquinate synthase - Solanum lycopersicum (Tomato) (Lycopersicon	191.19	1
Unknown	74.4	1
gb|TT-20_H08 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	65.3	1
Unknown	230.47	1
gb|AGN_ELP019xm04f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequenc	62.14	1
tc|Rep: Nod factor-like protein - Plantago major (Common plantain), partial (16%) [	39.87	1
gb|KF8B.200P05F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200P05, mR	87.43	1
gb|AGN_RNC014xo18f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1544.99	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	244.17	1
gb|Nicotiana tabacum JEI1 mRNA for hypothetical protein, complete cds [AB30077	632.98	1
tc|Rep: Chromosome undetermined scaffold_125, whole genome shotgun sequenc	979.16	1
gb|CHO_SL013xh20f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	58.69	1
Unknown	96.27	1
Unknown	184.46	1

tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	25.87	1
gb|Nicotiana tabacum vacuole-associated annexin VCaB42 (Anx3) mRNA, complete	130.07	1
gb|KP1B.107P12F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107P12, mI	135.05	1
tc|Rep: Predicted protein - Chlamydomonas reinhardtii, partial (12%) [TC75316]	170.78	1
gb|KF8B.200P07F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200P07, mRN	464.87	1
tc|Rep: Chromosome chr8 scaffold_68, whole genome shotgun sequence - Vitis vin	1158.01	1
Unknown	27.3	1
gb|CHO_SL011xg05f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	518.95	1
Unknown	23.14	1
gb|CHO_SL022xi08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH61	172.73	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	27.83	1
gb|KF8B.201A20F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201A20, mRI	80.37	1
gb|Nicotiana tabacum topoisomerase I (TOP I) mRNA, complete cds [AF115482]	1165.77	1
Unknown	18.88	1
tc|Rep: Cyclin-like F-box - Medicago truncatula (Barrel medic), partial (64%) [TC549	255.5	1
gb|AGN_RNC017xd12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1599.73	1
gb|KT7C.104H17F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104H17, mR	328.81	1
tc|Rep: Chromosome undetermined scaffold_147, whole genome shotgun sequenc	88.79	1
tc|Rep: Protein kinase-like protein - Vitis aestivalis (Grape), partial (82%) [TC48691]	941.13	1
gb|KL4B.109B14F.051108T7 KL4B Nicotiana tabacum cDNA clone KL4B.109B14, mR	23.12	1
gb|AGN_PNL214dr1_b6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	33.32	1
Unknown	49.97	1
gb|Nicotiana tabacum A20 mRNA for hypothetical protein, complete cds [AB03253	27.1	1
Unknown	88.01	1
Unknown	106.38	1
Unknown	145.06	1
tc|Rep: Chromosome chr1 scaffold_136, whole genome shotgun sequence - Vitis vi	30.01	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	38.15	1
Unknown	23.62	1
Unknown	238.73	1
Unknown	21.17	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	152.47	1
gb|N.tabacum NtK-1 mRNA [X77763]	296.24	1
tc|Rep: Ubiquitin fusion protein - Arachis hypogaea (Peanut), complete [TC54478]	236.05	1

tc|Rep: Chromosome chr4 scaffold_333, whole genome shotgun sequence - Vitis vi	30.35	1
gb|TT-06_O22 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	2679.4	1
Unknown	48.48	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (19%) [TC5	66.53	1
gb|BP129575 MAT001 Nicotiana tabacum cDNA clone BY1446, mRNA sequence [B	32.65	1
Unknown	3144.59	1
Unknown	171.96	1
gb|AGN_ELP007xh11f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	20.45	1
tc|Rep: Chromosome chr5 scaffold_67, whole genome shotgun sequence - Vitis vin	132.63	1
gb|KF8B.202O12F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202O12, mR	152.83	1
gb|KT7C.113C13F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.113C13, mR	81.11	1
gb|N.tabacum mRNA for pyruvate kinase (plastid isozyme) [Z28373]	45.5	1
gb|AGN_RNC015xg11f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	98.16	1
tc|Rep: Chromosome undetermined scaffold_168, whole genome shotgun sequenc	27.7	1
gb|KN6B.113A23F.060127T7 KN6B Nicotiana tabacum cDNA clone KN6B.113A23,	28.12	1
gb|TT-24_M01 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	66.11	1
gb|CHO_SL007xl24f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	983.13	1
Unknown	1102.53	1
Unknown	41.24	1
Unknown	80.53	1
gb|AGN_PNL226ar1_d7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	137.64	1
Unknown	18.74	1
gb|KF8C.101J07F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101J07, mRN	49.93	1
Unknown	1765.7	1
tc|Rep: Ubiquitin - Hevea brasiliensis (Para rubber tree), partial (67%) [TC48522]	2501.15	1
gb|KR3B.107H08F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.107H08, m	415.56	1
gb|KP1B.101P10F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101P10, m	399.02	1
gb|KR2B.101F09F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.101F09, m	7701.34	1
gb|KG9B.107G17F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.107G17,	997.02	1
Unknown	8865.1	1
tc|Rep: Carbonic anhydrase - Solanum lycopersicum (Tomato) (Lycopersicon escule	20.9	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	43.03	1
gb|EST_CSP004xo20f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	35.92	1
tc|Rep: NADPH--cytochrome P450 reductase - Phaseolus aureus (Mung bean) (Vign	144.29	1

gb|AGN_RPC012xb10f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	21.21	1
Unknown	2722.47	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	31.32	1
tc|Rep: Isopentenyl diphosphate isomerase 2 - Nicotiana tabacum (Common tobac	139.65	1
Unknown	130.72	1
Unknown	64.36	1
Unknown	32.98	1
tc|Rep: UTP--glucose-1-phosphate uridylyltransferase - Solanum tuberosum (Potat	57.79	1
Unknown	92.35	1
tc|Rep: Autophagy-related protein 3 - Vitis vinifera (Grape), complete [TC47245]	42.14	1
Unknown	19.04	1
gb|EST_CSP004xe10f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	118.38	1
tc|Rep: Chromosome chr8 scaffold_68, whole genome shotgun sequence - Vitis vin	195.45	1
gb|Nicotiana tabacum clone 7 poly(A)-binding protein (PABP) mRNA, partial cds [A	87.61	1
tc|Rep: Chromosome chr10 scaffold_433, whole genome shotgun sequence - Vitis	468.76	1
Unknown	67.63	1
gb|AGN_RNC012xc16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	31.24	1
Unknown	44.7	1
tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	76.24	1
Unknown	1129.05	1
gb|KR3B.102K16F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.102K16, m	90.35	1
gb|AGN_RNC110xf12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	96.7	1
gb|Nicotiana tabacum mRNA for protein kinase NPK5, complete cds [D26602]	546.65	1
gb|KT7C.104P02F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104P02, mR	106.9	1
tc|Rep: Actin - Phalaenopsis hybrid cultivar, partial (39%) [TC69811]	22878.35	1
Unknown	18.88	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	137.66	1
gb|TT-38_D16 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	83.86	1
tc|Rep: RNA-binding protein AKIP1-like - Solanum tuberosum (Potato), partial (29%	185.76	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	59.86	1
Unknown	110.21	1
gb|Nicotiana tabacum partial mRNA for hypothetical protein, clone PBF80non [AJ3	41.97	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	79.45	1
Unknown	23.64	1

tc|Rep: 40S ribosomal protein S5 - Capsicum annuum (Bell pepper), complete [TC4	131.5	1
gb|KL4B.111H15F.060128T7 KL4B Nicotiana tabacum cDNA clone KL4B.111H15, m	57.62	1
gb|KG9B.103D21F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103D21, n	52.32	1
tc|Rep: Prohibitin - Nicotiana tabacum (Common tobacco), complete [TC52074]	20.97	1
gb|AM789925 COL, cold overnight library Nicotiana tabacum cDNA clone nt006213	32	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	84.41	1
Unknown	23.87	1
gb|AGN_ELP024xi02f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	18.95	1
gb|CHO_SL023xa21f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	7444.3	1
gb|AGN_RNC007xk10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	51.45	1
tc|Rep: Predicted protein - Chlamydomonas reinhardtii, partial (3%) [TC56068]	1037.75	1
gb|AGN_RNC022xe16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	20.94	1
gb|TT-47_L19 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	44.51	1
gb|KN6B.100K15F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100K15, m	124.24	1
gb|KL4B.104H18F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104H18, m	342.42	1
tc|Rep: Chromosome undetermined scaffold_11, whole genome shotgun sequence	126.84	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	24.14	1
gb|KG9B.003E17F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003E17, m	20.63	1
gb|2A03 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', m	265.9	1
Unknown	45.25	1
tc|Rep: Chromosome chr7 scaffold_20, whole genome shotgun sequence - Vitis vin	81.87	1
gb|TOBESTR030H01 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	19.27	1
Unknown	1551.86	1
gb|Nicotiana tabacum heat shock protein 90 (OINtHsp90) mRNA, complete cds [AY	257.73	1
gb|TT-36_J10 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	56.45	1
gb|KR3B.101I10F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101I10, mR	472.76	1
gb|KG9B.103H05F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103H05, n	19.9	1
gb|KF8C.103J19F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103J19, mRN	185.7	1
gb|KG9B.002K06F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002K06, m	84.51	1
Unknown	373.11	1
Unknown	116.97	1
gb|AGN_RPC009xp03f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	288.11	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	1092.34	1
Unknown	237.86	1

tc|Rep: Proline oxidase/dehydrogenase 2 - Nicotiana tabacum (Common tobacco),	264.64	1
gb|Nicotiana tabacum chaperone GrpE type 2 (GrpE2) mRNA, nuclear gene encodir	36.74	1
Unknown	99.72	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	251.3	1
tc|Rep: Chromosome chr2 scaffold_105, whole genome shotgun sequence - Vitis vi	87.78	1
tc|Rep: Small GTP-binding protein - Carica papaya (Papaya), complete [TC59352]	44.4	1
Unknown	49.17	1
gb|AM782816 DL, diurnal library Nicotiana tabacum cDNA clone nt005252007, mRI	51.53	1
gb|KF8C.106H14F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.106H14, mRI	27.77	1
Unknown	631.51	1
Unknown	436.52	1
Unknown	22.07	1
gb|KP1B.102K14F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102K14, mI	180.04	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	50.06	1
gb|KG9B.105G17F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105G17, n	483.17	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	121.57	1
Unknown	37.28	1
Unknown	135.65	1
Unknown	87	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	120.6	1
gb|KF8C.105E21F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105E21, mRN	1563.06	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	77.81	1
gb|KL5B.117N23F.060217T7 KL5B Nicotiana tabacum cDNA clone KL5B.117N23, mF	272.51	1
gb|EST_CSP008xf21f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	64.65	1
gb|KL4B.100P18F.050922T7 KL4B Nicotiana tabacum cDNA clone KL4B.100P18, mR	1477.32	1
gb|Nicotiana tabacum NtRSH1 mRNA for RelA-SpoT like protein RSH1, complete cd	95.1	1
tc|Rep: Actin-7 - Arabidopsis thaliana (Mouse-ear cress), complete [TC40665]	38.88	1
Unknown	32.83	1
Unknown	1009.25	1
gb|AGN_PNL228cf1_h4.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	197.27	1
tc|Rep: Chromosome chr18 scaffold_137, whole genome shotgun sequence - Vitis	112.01	1
tc|Rep: Chromosome chr14 scaffold_54, whole genome shotgun sequence - Vitis vi	216.12	1
tc|Rep: F-box/Kelch-repeat protein At1g16250 - Arabidopsis thaliana (Mouse-ear cr	30.36	1
gb|KF8C.105P23F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105P23, mRN	683.84	1

gb|AGN_PNL221df1_a10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	4083.58	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	102.87	1
Unknown	87.91	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	264.79	1
gb|KN6B.106I24F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.106I24, m	43.34	1
tc|Rep: Heat shock protein 90 - Nicotiana tabacum (Common tobacco), partial (16	690.03	1
gb|Nicotiana tabacum mRNA for proliferating cell nuclear antigen [AJ012662]	35.43	1
Unknown	111.92	1
tc|Rep: Beta 1,3-glycosyltransferase-like protein I - Solanum lycopersicum (Tomato	66.43	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	531.93	1
tc|Rep: Tetratricoredoxin - Nicotiana tabacum (Common tobacco), complete [TC65	30.99	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	116.1	1
gb|N.tabacum mRNA for heat shock protein 82 [X63195]	732.74	1
gb|KL4B.106C04F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106C04, mR	41.84	1
Unknown	21.68	1
gb|KG9B.002K18F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002K18, m	32.67	1
tc|Rep: AT4g37280/C7A10_80 - Arabidopsis thaliana (Mouse-ear cress), partial (84	108.26	1
gb|AGN_RPC014xh01f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	946.95	1
gb|BP532651 MAT005 Nicotiana tabacum cDNA clone BY28076, mRNA sequence [	26.84	1
tc|Rep: Alkaline alpha-galactosidase seed imbibition protein - Solanum lycopersicu	1292.07	1
Unknown	351.76	1
Unknown	369.25	1
tc|Rep: NADH dehydrogenase - Solanum tuberosum (Potato), partial (58%) [TC616	134.79	1
gb|KP1B.110A01F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110A01, m	16.88	1
tc|Rep: At4g27040 - Arabidopsis thaliana (Mouse-ear cress), complete [TC56578]	100.98	1
gb|KN6B.104G12F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.104G12, r	184.84	1
tc|Rep: Glycolate oxidase - Mesembryanthemum crystallinum (Common ice plant),	53.18	1
gb|TT-05_L10 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	97.12	1
gb|KR3B.114K17F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.114K17, m	18.35	1
Unknown	3802.08	1
Unknown	387.24	1
gb|KT7C.102L13F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102L13, mRN	27.91	1
tc|Rep: COP1 homolog - Solanum lycopersicum (Tomato) (Lycopersicon esculentu	40.94	1
tc|Rep: Alpha-soluble NSF attachment protein - Solanum tuberosum (Potato), parti	1683.31	1

Unknown	29.07	1
gb|N.tabacum mRNA for citrate synthase [X84226]	7860.2	1
gb|KP1B.102O09F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102O09, m	470.02	1
Unknown	28.81	1
gb|KG9B.106L14F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106L14, m	47.65	1
gb|Nicotiana tabacum adenosine kinase isoform 2S mRNA, complete cds [AY69505	8804.38	1
gb|TT-29_I03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	190.01	1
gb|CHO_SL006xm14f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	609.15	1
Unknown	1254.77	1
tc|Rep: Cytochrome P450 - Nicotiana tabacum (Common tobacco), complete [TC45	26.57	1
gb|16E01 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5',	582.46	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	51.82	1
gb|KF8C.103L11F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103L11, mRN	27.72	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	26.67	1
Unknown	267.74	1
gb|TT-01_C06 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	55.53	1
tc|Rep: Phosphate translocator precursor - Nicotiana tabacum (Common tobacco),	38.94	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	3652.05	1
tc|Rep: Protein translation factor SUI1 homolog - Sporobolus stapfianus (Ressurecti	3014.66	1
gb|TT-38_F10 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	24.41	1
gb|AGN_ELP008xj24f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	21.83	1
Unknown	452.24	1
gb|CHO_SL008xp13f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	512.33	1
gb|KR3B.106J18F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106J18, mR	159.09	1
tc|Rep: Chromosome chr7 scaffold_192, whole genome shotgun sequence - Vitis vi	116.43	1
tc|Rep: NAD-malate dehydrogenase precursor - Nicotiana tabacum (Common toba	5771.32	1
tc|Rep: Chromosome chr2 scaffold_187, whole genome shotgun sequence - Vitis vi	28.34	1
gb|TOBESTR055B09 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	24.34	1
gb|KL4B.104O03F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104O03, m	31.71	1
gb|TT-18_N11 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	60.37	1
tc|Rep: EIN3-binding F-box protein 2 - Solanum lycopersicum (Tomato) (Lycopersic	965.41	1
gb|FS411114 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	24.13	1
tc|Rep: Secretory carrier-associated membrane protein 3 - Arabidopsis thaliana (M	374.55	1
Unknown	135.28	1

gb|Nicotiana tabacum GDP dissociation inhibitor (GDI) mRNA, complete cds [AF012	5334.27	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	409.8	1
tc|Rep: At1g19680 - Arabidopsis thaliana (Mouse-ear cress), partial (17%) [TC60167	959.09	1
Unknown	1118.33	1
Unknown	3383.81	1
gb|AGN_RNC010xh16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	18.3	1
Unknown	626.43	1
gb|TT-09_E17 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	100.09	1
gb|KG9B.002N07F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002N07, r	3785.57	1
Unknown	40.11	1
tc|Rep: Chromosome chr5 scaffold_64, whole genome shotgun sequence - Vitis vin	32.64	1
gb|AGN_RNC023xk20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	18.95	1
tc|Rep: SM10 - Nicotiana tabacum (Common tobacco), complete [TC40181]	78.31	1
gb|AGN_PNL210ar1_b6.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 3', mRNA	23.56	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	104.47	1
gb|TT-23_E13 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	1134.02	1
gb|KT7B.107O10F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.107O10, mR	60.25	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	1489.5	1
gb|KF8C.101C08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101C08, mRN	399.51	1
tc|Rep: Mitochondrial prohibitin 1 - Petunia hybrida (Petunia), complete [TC47520]	20.95	1
gb|TT-10_E12 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	35.39	1
Unknown	783.97	1
Unknown	60.85	1
gb|KN6B.107P11F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.107P11, m	24.96	1
tc|Rep: Transcription factor MYB48 - Arabidopsis thaliana (Mouse-ear cress), partia	26.04	1
Unknown	51.52	1
tc|Rep: Chromosome chr10 scaffold_81, whole genome shotgun sequence - Vitis vi	433.47	1
gb|TT-06_J15 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	189.7	1
gb|N.tabacum mRNA for citrate synthase [X84226]	1210.75	1
gb|TL13.109H18F.060320T7 TL13 Nicotiana tabacum cDNA clone TL13.109H18, mR	7224.52	1
gb|KF8C.104B19F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104B19, mRN	29.37	1
gb|TT-14_P19 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	497.8	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	50.87	1
tc|Rep: Ribulose-5-phosphate-3-epimerase - Pisum sativum (Garden pea), partial (9	26.53	1

gb|TT-50_B23 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	57.2	1
gb|AM839082 seedling library, SL Nicotiana tabacum cDNA clone nt002152044, m	89.77	1
Unknown	1130.66	1
gb|Nicotiana tabacum osmotic stress-activated protein kinase (OSAK) mRNA, comp	27.69	1
tc|Rep: Chromosome chr17 scaffold_101, whole genome shotgun sequence - Vitis	18.48	1
tc|Rep: Brassinosteroid insensitive 1 - Nicotiana tabacum (Common tobacco), parti	44.25	1
gb|TT-05_D07 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	240.78	1
tc|Rep: RanBP2-type zinc finger protein At1g67325 - Arabidopsis thaliana (Mouse-e	261.37	1
tc|Rep: Eukaryotic translation initiation factor 5A-4 - Solanum lycopersicum (Tomat	2403.76	1
Unknown	401.03	1
gb|TT-36_M06 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequenc	33.69	1
gb|EST_FLW002xd23f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	110.03	1
gb|AM824464 DL, diurnal library Nicotiana tabacum cDNA clone nt005080040, mR	91.51	1
gb|AGN_ELP011xe21f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	107.57	1
gb|AGN_PNL220af1_b11.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	19.68	1
gb|AGN_RNC211xf09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	466.3	1
tc|Rep: Vacuolar proton pump subunit F - Corchorus olitorius, complete [TC69780]	1436.56	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	25.92	1
Unknown	32.25	1
Unknown	31.65	1
Unknown	130.55	1
tc|Rep: AT3g47831/T23J7 - Arabidopsis thaliana (Mouse-ear cress), partial (89%) [T	72.87	1
gb|KL4B.113C19F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.113C19, mR	516.57	1
Unknown	19.36	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	7505.29	1
tc|Rep: Ribosomal protein S27 - Vitis vinifera (Grape), complete [TC58062]	34.16	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	3463.14	1
Unknown	1109.51	1
gb|KT7C.108N18F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108N18, mR	34.07	1
tc|Rep: SKP1 - Nicotiana tabacum (Common tobacco), complete [TC48833]	5242.52	1
Unknown	1055.58	1
Unknown	75.3	1
gb|AGN_RNC018xk12f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	43.48	1
Unknown	4417.18	1

Unknown	243.71	1
gb|AGN_ELP005xk12f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	23.58	1
Unknown	58.44	1
gb|TOBESTR089A07 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	20.97	1
gb|TT-18_N12 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	519.68	1
gb|AM789543 seedling library, SL Nicotiana tabacum cDNA clone nt002101067, m	18.07	1
tc|Rep: Metallothionein-like protein type 2 - Nicotiana plumbaginifolia (Leadwort-l	1526.79	1
tc|Rep: H+-transporting two-sector ATPase, C (AC39) subunit - Medicago truncatul	4573.07	1
gb|N.tabacum eIF-4A8 mRNA [X79004]	516.29	1
tc|Rep: Pm27 protein - Prunus mume (Japanese flowering apricot), partial (57%) [T	1251.21	1
Unknown	25.78	1
tc|Rep: Molecular chaperone Hsp90-2 - Nicotiana benthamiana, partial (28%) [TC4	2663.5	1
gb|KT7B.100E11F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100E11, mR	1043.92	1
gb|KF8C.102F08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102F08, mRN	445.6	1
gb|BL12.103K16F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.103K16, mR	372.62	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	87.17	1
tc|Rep: Peptidyl-prolyl cis-trans isomerase - Solanum lycopersicum (Tomato) (Lyco	539.38	1
tc|Rep: Malate dehydrogenase, glyoxysomal precursor - Citrullus lanatus (Waterm	314.47	1
tc|Rep: STYLOSA protein - Antirrhinum majus (Garden snapdragon), partial (29%) [T	42.42	1
Unknown	111.78	1
tc|Rep: RRM-containing RNA-binding protein-like protein - Solanum tuberosum (Po	68.08	1
tc|Rep: Chromosome chr10 scaffold_433, whole genome shotgun sequence - Vitis	28.28	1
Unknown	85.03	1
gb|1H08 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5', m	81.66	1
Unknown	798.61	1
Unknown	2802.64	1
Unknown	957.35	1
gb|KL4B.113L02F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.113L02, mR	25.71	1
gb|KF8C.102B08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102B08, mR	26.61	1
gb|KR2B.112E09F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.112E09, m	32.19	1
tc|Rep: Chromosome undetermined scaffold_52, whole genome shotgun sequence	23.84	1
gb|AM834148 seedling library, SL Nicotiana tabacum cDNA clone nt002270045, m	41.93	1
Unknown	220.03	1
gb|AGN_ELP002xf10f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	27.18	1

Unknown	273.06	1
tc|Rep: Chromosome chr4 scaffold_443, whole genome shotgun sequence - Vitis vi	389.75	1
Unknown	141.6	1
Unknown	121.43	1
gb|TT-07_H09 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG63	61.11	1
gb|CHO_SL025xf17f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	389.63	1
gb|KG9B.104E17F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104E17, m	53.52	1
Unknown	29.71	1
tc|Rep: OJ000223_09.9 protein - Oryza sativa subsp. japonica (Rice), partial (93%) [T	114.55	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	940.78	1
gb|KF8C.103M05F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103M05, mR	517.04	1
Unknown	77.3	1
Unknown	83.62	1
Unknown	85.89	1
Unknown	18.09	1
gb|Nicotiana tabacum DNA-directed RNA polymerase IIb (NT193) mRNA, complete	19.09	1
gb|KT7C.104N15F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104N15, mR	32.1	1
gb|CHO_SL012xd21f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	24.41	1
gb|TT-19_O16 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	108.54	1
gb|KP1B.112G11F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.112G11, m	40.37	1
Unknown	196.99	1
Unknown	20.29	1
gb|KP1B.108I18F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108I18, mRI	44.51	1
gb|AGN_ELP008xp13f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	29.31	1
Unknown	22.14	1
gb|KG9B.104O15F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104O15, r	1080.45	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	63.21	1
gb|BL12.103H14F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.103H14, mR	25.88	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	28.75	1
gb|CHO_SL023xf22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	591.22	1
tc|Rep: Syntaxin-52 - Arabidopsis thaliana (Mouse-ear cress), complete [TC40892]	112.1	1
tc|Rep: RAN GTPase-activating protein 2 - Nicotiana benthamiana, complete [TC49	80.29	1
gb|KG9B.004M17F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004M17,	132.34	1
gb|Nicotiana tabacum elongation factor 1-alpha mRNA, complete cds [AF120093]	1521.12	1

Unknown	210.48	1
tc|Rep: Serine hydroxymethyltransferase, mitochondrial precursor - Solanum tuber	3167.09	1
Unknown	40.7	1
Unknown	151.73	1
tc|Rep: Chromosome undetermined scaffold_143, whole genome shotgun sequenc	72.32	1
tc|Rep: Heat shock protein HslU - Chlorobium phaeobacteroides BS1, partial (4%) [T	60.46	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	663.18	1
gb|KP1B.108I18F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108I18, mRI	48.23	1
tc|Rep: Transmembrane protein C1orf215 - Homo sapiens (Human), partial (5%) [T	52.41	1
Unknown	30.47	1
gb|Nicotiana tabacum cDNA-AFLP-fragment BSTC1-32-250, cultivar Bright Yellow 2	25.91	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	42.98	1
gb|AGN_ELP024xn09f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	67.15	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	981.44	1
tc|Rep: Histone H2B - Nicotiana tabacum (Common tobacco), complete [TC55592]	32.59	1
gb|KP1B.107H16F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107H16, m	856.42	1
tc|Rep: Chromosome chr4 scaffold_39, whole genome shotgun sequence - Vitis vin	2854.23	1
Unknown	44.2	1
tc|Rep: DELLA protein GAI1 - Vitis vinifera (Grape), partial (78%) [TC48661]	94.1	1
gb|FS413389 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	128.67	1
gb|TT-18_I12 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	33.04	1
Unknown	474.22	1
gb|KG9B.104C04F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104C04, m	966.2	1
tc|Rep: SAT5 - Pisum sativum (Garden pea), partial (70%) [TC41109]	191.95	1
Unknown	1190.74	1
tc|Rep: Chromosome chr10 scaffold_76, whole genome shotgun sequence - Vitis vi	10743.35	1
Unknown	260.11	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	560.41	1
gb|KR3B.110J03F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.110J03, mR	21.1	1
tc|Rep: Chromosome chr2 scaffold_112, whole genome shotgun sequence - Vitis vi	17.87	1
gb|KN6B.105F14F.060104T7 KN6B Nicotiana tabacum cDNA clone KN6B.105F14, m	80.19	1
tc|Rep: SEU1 protein - Antirrhinum majus (Garden snapdragon), partial (13%) [TC62	277.16	1
Unknown	24.39	1
gb|CHO_SL013xk10f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	377.25	1

Unknown	2296.51	1
tc|Rep: Chromosome undetermined scaffold_114, whole genome shotgun sequenc	32.18	1
Unknown	621.65	1
gb|KR3B.107I24F.051110T7 KR3B Nicotiana tabacum cDNA clone KR3B.107I24, mR	133.84	1
tc|Rep: Chromosome chr9 scaffold_49, whole genome shotgun sequence - Vitis vin	101.05	1
tc|Rep: Chromosome undetermined scaffold_155, whole genome shotgun sequenc	80.57	1
gb|KF8B.100B17F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100B17, mR	39955.75	1
gb|KL5B.106A09F.060215T7 KL5B Nicotiana tabacum cDNA clone KL5B.106A09, m	28.87	1
Unknown	89.42	1
gb|AGN_PNL210df1_b3.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	1179.71	1
Unknown	25.82	1
Unknown	26.21	1
Unknown	1654.23	1
Unknown	66.65	1
gb|AGN_ELP017xe10f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	21.93	1
tc|Rep: Proteasome subunit alpha type - Solanum tuberosum (Potato), complete [T	31.54	1
gb|KT7C.102N18F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102N18, mR	6532.99	1
gb|KG9B.002J07F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002J07, m	182.33	1
tc|Rep: Phosphoglycerate kinase, chloroplast precursor - Nicotiana tabacum (Comn	217.59	1
gb|KG9B.103I06F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103I06, m	518.74	1
tc|Rep: Chromosome chr18 scaffold_59, whole genome shotgun sequence - Vitis vi	57.85	1
Unknown	25.31	1
gb|KR2B.111K11F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.111K11, m	27.71	1
tc|Rep: Chromosome undetermined scaffold_1573, whole genome shotgun sequen	644.67	1
tc|Rep: Os05g0119300 protein - Oryza sativa subsp. japonica (Rice), partial (41%) [T	101.05	1
Unknown	3004.18	1
gb|KP1B.001I20F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001I20, mR	22.88	1
Unknown	931.65	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	48.88	1
gb|KP1B.001J23F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001J23, mR	641.58	1
gb|KF8B.100P17F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100P17, mR	511.35	1
tc|Rep: Chromosome chr14 scaffold_211, whole genome shotgun sequence - Vitis	182.43	1
tc|Rep: Protein arginine N-methyltransferase 5 - Oryza sativa subsp. indica (Rice), p	23.66	1
tc|Rep: Expressed protein - Arabidopsis thaliana (Mouse-ear cress), partial (48%) [T	43.1	1

Unknown	421.51	1
tc|Rep: S-adenosylmethionine decarboxylase - Prunus persica (Peach), partial (45%	7605.18	1
Unknown	78.62	1
gb|AGN_RNC117xl06f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	98.72	1
Unknown	520.11	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	1575.75	1
tc|Rep: Methylenetetrahydrofolate reductase - Vitis vinifera (Grape), partial (61%)	206.72	1
tc|Rep: Phosphatidylinositol transfer-like protein III - Lotus japonicus, partial (59%)	182.59	1
Unknown	2213.34	1
gb|KR2B.115M23F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.115M23,	59.93	1
Unknown	19.86	1
gb|KF8C.103O13F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103O13, mR	9146.88	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	62.31	1
gb|KF8C.105N02F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.105N02, mR	47.7	1
gb|Nicotiana tabacum salicylic acid-activated MAP kinase (NtSIPK) mRNA, complet	1609.6	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	299.94	1
Unknown	41.45	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	249.91	1
tc|Rep: 14-3-3 i-2 protein - Nicotiana tabacum (Common tobacco), partial (39%) [T	88.84	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	9671.26	1
gb|KL4B.101G15F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101G15, m	99.47	1
Unknown	29.55	1
gb|KT7C.104J03F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104J03, mRN	124.24	1
gb|KP1B.101J07F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101J07, mR	547.69	1
Unknown	28.38	1
tc|Rep: F-box protein At1g47340 - Arabidopsis thaliana (Mouse-ear cress), partial (	46.62	1
Unknown	138.53	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	564.28	1
Unknown	253.43	1
tc|Rep: PII-like protein - Solanum lycopersicum (Tomato) (Lycopersicon esculentu	26.98	1
tc|Rep: Chromosome chr8 scaffold_106, whole genome shotgun sequence - Vitis vi	106.7	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	92.31	1
Unknown	37.41	1
Unknown	85.99	1

tc|Rep: Plastidic ATP/ADP-transporter - Solanum tuberosum (Potato), partial (56%)	26.29	1
Unknown	152.41	1
tc|Rep: Protein 108 precursor - Solanum lycopersicum (Tomato) (Lycopersicon escu	19.29	1
gb|KR3B.106G17F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106G17, m	297.36	1
gb|KP1B.101B02F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101B02, m	250.26	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	197.18	1
Unknown	127.76	1
tc|Rep: ATP synthase subunit beta - Nicotiana sylvestris (Wood tobacco), partial (2	193.54	1
gb|Nicotiana tabacum callus-expressing factor (CEF1) mRNA, complete cds [AY286	21.7	1
tc|Rep: Chromosome undetermined scaffold_53, whole genome shotgun sequence	179.35	1
tc|Rep: Ribosomal protein L41 - Candida maltosa (Yeast), complete [TC51829]	34.05	1
Unknown	52.9	1
tc|Rep: Chromosome chr4 scaffold_32, whole genome shotgun sequence - Vitis vin	136.72	1
Unknown	43.34	1
tc|Rep: NADH-ubiquinone oxidoreductase subunit-like - Solanum tuberosum (Potat	1388.75	1
gb|CHO_SL005xe09f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	24.26	1
Unknown	134.25	1
gb|AGN_RNC001xf09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	544.4	1
tc|Rep: DNA damage-binding protein 1 - Solanum cheesmanii (Galapagos island ton	65.83	1
Unknown	2467.72	1
gb|TT-11_E13 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	127.42	1
Unknown	284	1
gb|CHO_SL008xj22f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	1264.82	1
Unknown	1192.73	1
tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	516.67	1
gb|FS412805 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	172.93	1
tc|Rep: Chorismate synthase 1, chloroplast precursor - Solanum lycopersicum (Tom	291.04	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	48.87	1
tc|Rep: 40S ribosomal protein S16 - Euphorbia esula (Leafy spurge), partial (97%) [T	24.93	1
gb|TOBESTR026D08 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA seq	687.54	1
tc|Rep: Histone deacetylase HDT1 - Solanum chacoense (Chaco potato), partial (85	161.81	1
Unknown	25.72	1
Unknown	20.83	1
tc|Rep: Protein kinase Ck2 regulatory subunit 2 - Nicotiana tabacum (Common toba	171.55	1

Unknown	20.39	1
Unknown	82.47	1
gb|AM839972 seedling library, SL Nicotiana tabacum cDNA clone nt002240050, m	50.13	1
tc|Rep: Probable pectate lyase P59 precursor - Solanum lycopersicum (Tomato) (Ly	53747	1
gb|AGN_RNC025xl24f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	249.63	1
tc|Rep: Chromosome undetermined scaffold_141, whole genome shotgun sequenc	62.89	1
gb|AGN_ELP019xb18f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	169	1
Unknown	2144.69	1
Unknown	52.16	1
gb|KL4B.105B13F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105B13, mR	72.85	1
tc|Rep: Cytochrome c oxidase family protein-like - Solanum tuberosum (Potato), co	183.81	1
tc|Rep: Chromosome chr7 scaffold_44, whole genome shotgun sequence - Vitis vin	114.03	1
tc|Rep: K+-dependent Na+/Ca+ exchanger related-protein - Desulfovibrio desulfuri	28.56	1
gb|KP1B.110K12F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110K12, m	38.37	1
gb|KL5B.104O21F.060207T7 KL5B Nicotiana tabacum cDNA clone KL5B.104O21, m	61.44	1
gb|KL5B.001F15F.050901T7 KL5B Nicotiana tabacum cDNA clone KL5B.001F15, mR	2682.6	1
tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	501.84	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	61.58	1
Unknown	2406.12	1
gb|KF8C.102A13F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102A13, mR	74.83	1
Unknown	50.39	1
gb|Nicotiana tabacum NKT1 mRNA for potassium channel NKT1, complete cds [AB	75.61	1
gb|KG9B.101P02F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.101P02, m	968.25	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	82.44	1
gb|KP1B.001L22F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.001L22, m	502.08	1
Unknown	27.29	1
tc|Rep: Chromosome chr1 scaffold_180, whole genome shotgun sequence - Vitis vi	158.45	1
tc|Rep: Ubiquitin-conjugating enzyme family protein-like protein - Solanum tuberos	24.63	1
Unknown	160.22	1
tc|Rep: Cytochrome c assembly protein - Nocardioides sp. (strain BAA-499 / JS614),	24.8	1
gb|KG9B.102N02F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102N02, m	795.76	1
Unknown	43.91	1
Unknown	832.03	1
gb|KG9B.103M10F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103M10,	3356.56	1

tc|Rep: Chromosome chr18 scaffold_24, whole genome shotgun sequence - Vitis vi	31.78	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	57.26	1
Unknown	205.04	1
Unknown	32.37	1
Unknown	624.96	1
gb|KG9B.105O08F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105O08, r	234.01	1
gb|KR2B.113A02F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.113A02, m	5342.67	1
gb|Nicotiana tabacum TPK1 mRNA, complete cds [EU161633]	256.6	1
tc|Rep: Expressed protein - Arabidopsis thaliana (Mouse-ear cress), partial (44%) [T	509.72	1
gb|KR3B.109L19F.051111T7 KR3B Nicotiana tabacum cDNA clone KR3B.109L19, mR	43.89	1
tc|Rep: Ubiquitin carrier protein - Solanum tuberosum (Potato), partial (98%) [TC44	1296.24	1
tc|Rep: T25K16.8 - Arabidopsis thaliana (Mouse-ear cress), partial (22%) [TC46417]	479.29	1
Unknown	26.5	1
tc|Rep: Mitochondrial phosphate transporter - Zea mays (Maize), partial (64%) [TC4	802.93	1
tc|Rep: Chromosome chr10 scaffold_81, whole genome shotgun sequence - Vitis vi	139.46	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	86.66	1
tc|Rep: Chromosome chr16 scaffold_189, whole genome shotgun sequence - Vitis v	107.47	1
Unknown	7921.24	1
gb|CHO_SL028xj15f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH62	90.03	1
Unknown	32.07	1
gb|KR2B.109H17F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.109H17, m	854.37	1
gb|AM788334 DL, diurnal library Nicotiana tabacum cDNA clone nt005251061, mR	60.27	1
tc|Rep: Mitochondrial processing peptidase - Solanum tuberosum (Potato), partial (	169.4	1
tc|Rep: Cyc07 - Nicotiana tabacum (Common tobacco), partial (72%) [TC72415]	171.19	1
gb|KG9B.105B11F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105B11, m	72.31	1
gb|KF8C.103N20F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103N20, mR	30.65	1
gb|CHO_SL007xc07f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	424.35	1
tc|Rep: Aspartate aminotransferase - Vitis vinifera (Grape), partial (47%) [TC45425]	207.81	1
Unknown	152.49	1
gb|Nicotiana tabacum sigA2 mRNA for sigma factor, complete cds [AB023572]	195.93	1
gb|AM799412 DL, diurnal library Nicotiana tabacum cDNA clone nt005141043, mR	527.12	1
gb|TT-02_K02 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	886.11	1
gb|AM786721 seedling library, SL Nicotiana tabacum cDNA clone nt002088073, mR	21.38	1
tc|Rep: Metacaspase type II - Nicotiana benthamiana, partial (74%) [TC42092]	40.93	1

gb|AGN_PNL205cf1_f7.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	57.41	1
tc|Rep: ATP synthase subunit delta', mitochondrial precursor - Ipomoea batatas (Sv	143.28	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	82.35	1
tc|Rep: Chromosome chr12 scaffold_18, whole genome shotgun sequence - Vitis vi	1104.56	1
gb|TT-17_J16 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA sequ	517.56	1
tc|Rep: Chromosome undetermined scaffold_142, whole genome shotgun sequenc	189.88	1
gb|KR3B.101B05F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101B05, m	51.98	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	275.04	1
gb|Nicotiana tabacum unknown mRNA [EF051135]	27.23	1
gb|AGN_PNL203bf1_a10.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	34.95	1
gb|KF8C.102P04F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102P04, mR	91.77	1
Unknown	258.19	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	464.58	1
Unknown	26.97	1
Unknown	18.57	1
gb|KG9B.106K16F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106K16, m	25.1	1
tc|Rep: Chromosome undetermined scaffold_404, whole genome shotgun sequenc	230.52	1
Unknown	125.7	1
tc|Rep: Chromosome chr10 scaffold_138, whole genome shotgun sequence - Vitis	464.67	1
tc|AF036494 Eucryphia lucida large subunit 26S ribosomal RNA gene, partial seque	36.05	1
Unknown	68.93	1
tc|Rep: Chromosome undetermined scaffold_1009, whole genome shotgun sequen	58.94	1
Unknown	66.94	1
tc|Rep: Intracellular chloride channel - Medicago truncatula (Barrel medic), comple	19.28	1
gb|KR2B.105H17F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.105H17, m	69.04	1
tc|Rep: Elongation factor 1-alpha - Nicotiana paniculata, partial (53%) [TC48055]	40.46	1
Unknown	535.38	1
Unknown	251.28	1
Unknown	189.25	1
tc|Rep: ATP/GTP/Ca++ binding protein - Cucumis melo (Muskmelon), partial (80%)	29.93	1
tc|Rep: Bromodomain-containing RNA-binding protein 1 - Nicotiana benthamiana,	1742.47	1
gb|BP534468 MAT005 Nicotiana tabacum cDNA clone BY33047, mRNA sequence [	706.63	1
gb|KT7C.106D10F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106D10, mR	264.5	1
gb|KF8B.100M16F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100M16, m	688.45	1

gb|Nicotiana tabacum S-adenosyl-L-homocysteine hydrolase (SAHH2) mRNA, comp	816.88	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	4468.38	1
tc|Rep: 6-phosphogluconate dehydrogenase, decarboxylating - Spinacia oleracea (S	172.91	1
tc|Rep: 3-phosphoinositide-dependent protein kinase-1 - Solanum lycopersicum (T	2052.32	1
gb|AM816159 DL, diurnal library Nicotiana tabacum cDNA clone nt005033080, mR	132.32	1
Unknown	183.7	1
gb|KT7C.101C19F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.101C19, mR	83.38	1
Unknown	85.31	1
gb|FS411112 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	512.48	1
gb|KT7C.108N05F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108N05, mR	17.24	1
gb|KL4B.101J19F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101J19, mR	49.91	1
gb|KF8C.108M17F.051215T7 KF8 Nicotiana tabacum cDNA clone KF8C.108M17, m	2417.46	1
Unknown	324.89	1
Unknown	22.43	1
gb|KP1B.104M15F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104M15,	146.63	1
gb|KT7C.102D07F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102D07, mR	59.39	1
tc|Rep: eukaryotic translation initiation factor 2 family protein / eIF-2 family protei	145.56	1
tc|Rep: Heat shock 70 kDa protein, mitochondrial precursor - Phaseolus vulgaris (Ki	29.06	1
gb|AGN_RNC030xh20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	136.34	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	476.67	1
Unknown	19.01	1
tc|Rep: Chromosome undetermined scaffold_174, whole genome shotgun sequenc	185.72	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	4268.6	1
gb|KL4B.112B04F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112B04, mR	91.11	1
gb|TT-40_K13 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	272.19	1
Unknown	115.74	1
gb|KG9B.001P11F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001P11,	54.31	1
Unknown	73.03	1
tc|Rep: AT3g42050/F4M19_10 - Arabidopsis thaliana (Mouse-ear cress), partial (35	160.66	1
gb|AGN_RPC019xa03f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	535.63	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	9377.25	1
gb|KP1B.105L12F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105L12, mR	39.95	1
Unknown	249.17	1
tc|Rep: Mutator-like transposase - Arabidopsis thaliana (Mouse-ear cress), partial (	24.15	1

gb|KP1B.102J14F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.102J14, mR	830.92	1
Unknown	54.82	1
gb|Nicotiana tabacum PAP mRNA for purple acid phosphatase, complete cds, isolat	99.02	1
gb|KN6B.109A22F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.109A22,	44.96	1
Unknown	278.15	1
gb|CHO_SL028xe07f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	183.2	1
Unknown	35.5	1
gb|KN6B.109B22F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.109B22,	104.63	1
gb|KT7C.112N01F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112N01, mR	112.73	1
Unknown	247.23	1
gb|TT-47_E02 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	18.93	1
tc|Rep: Bet1-like SNARE 1-2 - Arabidopsis thaliana (Mouse-ear cress), partial (44%)	19.04	1
tc|Rep: 6-phosphogluconate dehydrogenase, decarboxylating - Spinacia oleracea (S	95.15	1
Unknown	171.71	1
tc|Rep: Cap-binding protein CBP20 - Oryza sativa subsp. japonica (Rice), partial (76	124.54	1
gb|KG9B.003K24F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003K24,	48.68	1
tc|Rep: Peroxidase 21 precursor - Arabidopsis thaliana (Mouse-ear cress), partial (2	94.89	1
tc|Rep: Chromosome chr8 scaffold_41, whole genome shotgun sequence - Vitis vin	32.4	1
gb|KP1B.107J12F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107J12, mR	97.62	1
tc|Rep: Serine/threonine protein phosphatase - Oryza sativa subsp. japonica (Rice),	789.66	1
gb|KG9B.001N14F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001N14,	110.83	1
Unknown	22.89	1
gb|KG9B.104J04F.060120T7 KG9B Nicotiana tabacum cDNA clone KG9B.104J04, m	77.8	1
gb|TT-35_A06 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	2022.48	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	130.19	1
gb|KN6B.100I11F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100I11, m	213.8	1
gb|KR3B.111G24F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.111G24, m	1158.43	1
gb|CHO_SL013xo13f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	781.89	1
tc|Rep: Methionine synthase - Nicotiana suaveolens, partial (40%) [TC45556]	18887.3	1
tc|Rep: Calcium-dependent protein kinases 5 - Solanum tuberosum (Potato), partia	1385.79	1
gb|AGN_RNC110xf05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	22.29	1
gb|Nicotiana tabacum cig3 mRNA, complete cds [AB041352]	938.54	1
gb|KT7C.109A11F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109A11, mR	89.73	1
gb|BP129744 MAT001 Nicotiana tabacum cDNA clone BY1631, mRNA sequence [B	71.81	1

Unknown	208.56	1
gb|KL4B.105D03F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105D03, mF	8068.72	1
Unknown	27.5	1
Unknown	4496.06	1
gb|AGN_RNC007xo05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	189.08	1
tc|Rep: SRp25 nuclear protein isoform 4 - Takifugu rubripes, partial (11%) [TC6115€	56.46	1
tc|Rep: Chromosome chr2 scaffold_11, whole genome shotgun sequence - Vitis vin	91.84	1
Unknown	476.75	1
tc|Rep: 40S ribosomal protein S12 - Vitis vinifera (Grape), partial (91%) [TC56412]	67.91	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	244.72	1
gb|KN6B.109B20F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.109B20, m	26.48	1
Unknown	153.36	1
Unknown	928.86	1
tc|Rep: Chromosome chr19 scaffold_66, whole genome shotgun sequence - Vitis vi	172.56	1
tc|Rep: Chromosome chr12 scaffold_78, whole genome shotgun sequence - Vitis vi	95.15	1
tc|Rep: Galactinol synthase - Brassica napus (Rape), partial (65%) [TC72414]	16.78	1
tc|Rep: Predicted protein - Physcomitrella patens subsp. patens, partial (46%) [TC4:	2080.37	1
gb|BP534683 MAT005 Nicotiana tabacum cDNA clone BY33268, mRNA sequence [E	88.83	1
Unknown	63.63	1
gb|KP1B.105A05F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105A05, m	103.28	1
gb|KR2B.110A15F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110A15, m	969.35	1
gb|KF8C.101E10F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101E10, mRN	86.14	1
gb|Nicotiana tabacum mRNA for cullin 1B (cul1B gene) [AJ344534]	124.74	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	109.13	1
tc|Rep: Chromosome undetermined scaffold_125, whole genome shotgun sequenc	185.65	1
gb|KR2B.110N10F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110N10, m	6208.21	1
Unknown	87.76	1
Unknown	964.6	1
Unknown	89.26	1
gb|TT-36_H09 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	57.27	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	85.31	1
Unknown	40.63	1
gb|KN6B.100N07F.051019T7 KN6B Nicotiana tabacum cDNA clone KN6B.100N07, r	21.42	1
gb|AM801773 seedling library, SL Nicotiana tabacum cDNA clone nt002125039, mF	20.78	1

gb|KF8B.200P08F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200P08, mRN	21012.9	1
gb|N.tabacum mRNA for profilin [X82120]	9631.51	1
gb|KL4B.104N10F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.104N10, m	570.32	1
Unknown	19.49	1
Unknown	186	1
gb|Nicotiana tabacum mRNA for malate dehydrogenase (md1 gene) [AJ299256]	75.58	1
gb|Nicotiana tabacum mRNA for 14-3-3 g-1 protein, complete cds [AB119477]	254.92	1
Unknown	57.41	1
gb|TT-36_P21 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	224.17	1
tc|Rep: Chaperone GrpE type 2 - Nicotiana tabacum (Common tobacco), complete	20.91	1
gb|KT7C.102C17F.051216T7 KT7 Nicotiana tabacum cDNA clone KT7C.102C17, mRN	119.74	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	52.04	1
gb|TT-37_M04 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	65.84	1
gb|Nicotiana tabacum kinesin-like protein (tck1) mRNA, complete cds [U52078]	68.53	1
gb|KR3B.102G03F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.102G03, m	83.21	1
tc|Rep: Chromosome chr17 scaffold_16, whole genome shotgun sequence - Vitis vi	501.56	1
gb|Nicotiana tabacum NtVDAC3 mRNA for voltage-dependent anion channel, comp	513.85	1
tc|Rep: Polyubiquitin - Fragaria ananassa (Strawberry), partial (60%) [TC50969]	1739.68	1
tc|Rep: Chromosome chr2 scaffold_176, whole genome shotgun sequence - Vitis vi	559.5	1
tc|Rep: Mitochondrial carrier-like protein - Solanum tuberosum (Potato), partial (9	54.52	1
tc|Rep: Chromosome chr2 scaffold_132, whole genome shotgun sequence - Vitis vi	482.5	1
Unknown	132.97	1
Unknown	89.87	1
tc|Rep: TGF-beta receptor-interacting protein 1 - Phaseolus vulgaris (Kidney bean) (	645.74	1
Unknown	51.14	1
Unknown	46.79	1
tc|Rep: Pseudouridylate synthase - Vitis vinifera (Grape), partial (29%) [TC42500]	28.34	1
gb|KF8C.102A24F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102A24, mRN	942	1
tc|Rep: Expressed protein - Oryza sativa subsp. japonica (Rice), partial (94%) [TC561	262.23	1
tc|Rep: Chromosome chr14 scaffold_9, whole genome shotgun sequence - Vitis vin	70.42	1
tc|Rep: Os05g0119300 protein - Oryza sativa subsp. japonica (Rice), partial (64%) [T	1373.5	1
gb|KT7C.110I08F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.110I08, mRN	120.3	1
gb|KP1B.037H17F.050628T7 KP1B Nicotiana tabacum cDNA clone KP1B.037H17, m	59.64	1
gb|KG9B.002J18F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002J18, m	248.14	1

Unknown	20.57	1
tc|Rep: Chromosome chr16 scaffold_86, whole genome shotgun sequence - Vitis vi	80.34	1
Unknown	73.54	1
gb|TT-03_K11 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	39.05	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	80.41	1
tc|Rep: Cell growth defect factor-like - Solanum tuberosum (Potato), complete [TC	206.35	1
Unknown	36.08	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	93.85	1
tc|Rep: Chromosome chr12 scaffold_36, whole genome shotgun sequence - Vitis vi	7591.49	1
gb|EST_CSP008xj14f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	253.2	1
gb|KP1B.112K24F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.112K24, m	180.01	1
tc|Rep: Ribosomal protein L11-like - Nicotiana tabacum (Common tobacco), comple	158.36	1
Unknown	67.9	1
Unknown	25.16	1
gb|KP1B.103K05F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103K05, m	23.28	1
gb|AGN_RNC009xn21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	69.48	1
gb|Nicotiana tabacum NtFAD3 mRNA for microsomal omega-3 acid desaturase, co	38861.75	1
tc|Rep: Carbonic anhydrase, chloroplast precursor - Nicotiana tabacum (Common t	767.14	1
Unknown	515.53	1
gb|TT-08_A10 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	29.17	1
gb|CHO_SL027xm02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	27.9	1
gb|KT7C.105B24F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105B24, mR	4361.11	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	43.13	1
Unknown	34.94	1
Unknown	45.1	1
tc|Rep: Small GTP-binding protein Sar1BNt - Nicotiana tabacum (Common tobacco)	10029.17	1
gb|KF8B.200B21F.060120T7 KF8 Nicotiana tabacum cDNA clone KF8B.200B21, mR	42.52	1
gb|KL4B.113H19F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.113H19, m	84.98	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	198.71	1
gb|KG9B.103C12F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103C12, m	76.39	1
Unknown	218.22	1
gb|KG9B.102A23F.051126T7 KG9B Nicotiana tabacum cDNA clone KG9B.102A23, m	1732.6	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	39.91	1
gb|KL4B.108L11F.051105T7 KL4B Nicotiana tabacum cDNA clone KL4B.108L11, mR	231.54	1

gb|KN6B.103M01F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103M01,	28.35	1
gb|AGN_PNL223af1_d5.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	466.72	1
Unknown	111.05	1
Unknown	133.28	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	19.05	1
gb|KG9B.001M06F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001M06,	997.64	1
Unknown	153.01	1
Unknown	96.22	1
gb|KP1B.113N02F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.113N02, m	84.46	1
Unknown	61.91	1
tc|Rep: BAC19.10 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum), pa	26	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	526.74	1
tc|Rep: Klra21 protein - Mus musculus (Mouse), partial (7%) [TC71239]	47.95	1
Unknown	380.66	1
Unknown	89.38	1
Unknown	66.94	1
gb|AGN_ELP022xg17f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	81.62	1
gb|AGN_RNC211xc19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	86.33	1
gb|KL4B.101P03F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101P03, mR	168.22	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	25.56	1
tc|Rep: Chromosome undetermined scaffold_80, whole genome shotgun sequence	85.8	1
gb|KP1B.037A22F.050623T7 KP1B Nicotiana tabacum cDNA clone KP1B.037A22, m	238.54	1
Unknown	668.33	1
gb|EST_CSP008xb10f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	187.23	1
tc|Rep: Polyprotein - Glycine max (Soybean), partial (3%) [TC62321]	27.6	1
gb|EST_CSP008xp15f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	294	1
Unknown	84.25	1
tc|Rep: ATP synthase subunit gamma, mitochondrial precursor - Ipomoea batatas (	483.8	1
Unknown	40.55	1
Unknown	1673.93	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	549.83	1
gb|TT-40_N12 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	373.66	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	543.49	1
Unknown	193.37	1

Unknown	1127.75	1
tc|Rep: Chromosome undetermined scaffold_80, whole genome shotgun sequence	79.26	1
Unknown	80.19	1
Unknown	21.46	1
tc|Rep: Chromosome chr13 scaffold_74, whole genome shotgun sequence - Vitis vi	30.83	1
gb|AGN_RNC020xm09f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequen	53.49	1
tc|Rep: ATP-dependent Clp protease proteolytic subunit - Vitis vinifera (Grape), par	31.66	1
tc|Rep: Chromosome chr6 scaffold_25, whole genome shotgun sequence - Vitis vin	254.41	1
gb|KR2B.104N05F.051227T7 KR2B Nicotiana tabacum cDNA clone KR2B.104N05, m	16898.35	1
Unknown	254.61	1
Unknown	161.93	1
gb|KN6B.009F03F.050901T7 KN6B Nicotiana tabacum cDNA clone KN6B.009F03, m	21.9	1
gb|AGN_ELP025xj05f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	4442.94	1
Unknown	184.57	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	149.68	1
Unknown	46.47	1
Unknown	34.54	1
tc|MIOBRN26 Oenothera berteriana mitochondrial gene for 26S ribosomal RNA, pa	47914.85	1
gb|KF8C.102F17F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102F17, mRN	11073.05	1
Unknown	106.58	1
gb|KT7C.104K12F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.104K12, mRN	20.92	1
Unknown	118.92	1
gb|BL12.104I03F.060309T7 BL12 Nicotiana tabacum cDNA clone BL12.104I03, mRN	264.29	1
gb|KF8B.100E05F.051010T7 KF8 Nicotiana tabacum cDNA clone KF8B.100E05, mRN	39.39	1
gb|AGN_RNC014xn22f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	125.15	1
gb|Nicotiana tabacum asparagine synthetase (din6) mRNA, partial cds [AY061820]	279.85	1
gb|TOBESTR124F07 TOBEST cDNA library 1 Nicotiana tabacum cDNA 5', mRNA sequ	1377.03	1
gb|AGN_RNC106xf10f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequence	796.59	1
gb|Nicotiana tabacum receptor-like protein kinase (PRK4) mRNA, partial cds [AF252	694.64	1
tc|Rep: RNA-binding protein-like - Oryza sativa subsp. japonica (Rice), partial (9%) [T	25.49	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	211.52	1
gb|KT7B.100K19F.051010T7 KT7 Nicotiana tabacum cDNA clone KT7B.100K19, mRN	271.66	1
gb|KR2B.111D04F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.111D04, m	1262.99	1
tc|Rep: Brain protein 44-like - Zea mays (Maize), partial (89%) [TC53445]	1624.29	1

tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	1016.62	1
gb|KN6B.103B18F.060103T7 KN6B Nicotiana tabacum cDNA clone KN6B.103B18, m	29.38	1
Unknown	2903.76	1
gb|Nicotiana tabacum squalene synthase mRNA, complete cds [U60057]	11311.55	1
gb|KG9B.001M17F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001M17,	21.67	1
tc|Rep: SRp25 nuclear protein isoform 4 - Takifugu rubripes, partial (11%) [TC6115	59.6	1
gb|CHO_SL028xh11f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	140.66	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	35.27	1
Unknown	31.4	1
Unknown	22.27	1
tc|Rep: Chromosome undetermined scaffold_147, whole genome shotgun sequenc	97.55	1
gb|AGN_PNL217af1_f3.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	23.66	1
Unknown	1502.21	1
tc|Rep: Chloroplast pigment-binding protein CP29 - Nicotiana tabacum (Common t	133.28	1
gb|TT-02_P09 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	65.55	1
gb|KP1B.104H11F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104H11, m	64.16	1
Unknown	727.68	1
gb|KG9B.105L24F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105L24, m	6482.08	1
gb|AM840522 seedling library, SL Nicotiana tabacum cDNA clone nt002322095, m	177.67	1
gb|KF8C.102M09F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102M09, m	2824.86	1
tc|Rep: Peroxisomal acyl-CoA oxidase 1A - Solanum lycopersicum (Tomato) (Lycope	493.48	1
gb|KG9B.103N16F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103N16,	31.03	1
tc|Rep: Chromosome chr5 scaffold_98, whole genome shotgun sequence - Vitis vin	1601.77	1
Unknown	80.12	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	153.49	1
gb|KG9B.103J02F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103J02, m	224.21	1
tc|Rep: Ribosomal protein S6-like protein - Solanum tuberosum (Potato), complete	220.65	1
Unknown	29.91	1
tc|Rep: Ketol-acid reductoisomerase, chloroplast precursor - Arabidopsis thaliana (	220.27	1
tc|Rep: Chromosome undetermined scaffold_141, whole genome shotgun sequenc	92.6	1
gb|KF8B.201O22F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.201O22, mR	48.8	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	664.32	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	235.1	1
tc|Rep: Phosphoglycerate mutase 1 - Lodderomyces elongisporus (Yeast) (Saccharo	20.9	1

gb|KF8C.104D03F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104D03, mR	264.6	1
tc|Rep: Chromosome undetermined scaffold_484, whole genome shotgun sequenc	22.67	1
Unknown	399.8	1
gb|KR3B.106K12F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.106K12, m	111.28	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	423.23	1
Unknown	2817.87	1
Unknown	31.94	1
gb|KN6B.102A05F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102A05,	30.32	1
gb|AGN_RPC024xe18f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequenc	23.11	1
gb|KG9B.003J03F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003J03, m	1355.86	1
Unknown	21.46	1
tc|Rep: 26S proteasome subunit 4-like - Solanum tuberosum (Potato), complete [T	186.61	1
Unknown	28.41	1
Unknown	64.83	1
gb|CHO_SL015xa22f2.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	216.04	1
Unknown	118.54	1
gb|TT-39_G18 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	45.95	1
gb|EST_FLW004xn16f1.ab1 EST_FLW Nicotiana tabacum cDNA, mRNA sequence [E	3283.78	1
gb|KR2B.113C15F.060128T7 KR2B Nicotiana tabacum cDNA clone KR2B.113C15, m	85.28	1
Unknown	7613.28	1
tc|Rep: Chromosome chr2 scaffold_187, whole genome shotgun sequence - Vitis vi	586.42	1
tc|Rep: Ly200-like protein - Solanum tuberosum (Potato), complete [TC54910]	152.86	1
gb|KP1B.105P17F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105P17, m	58.54	1
gb|CHO_SL016xl02f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	96.95	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	149.2	1
Unknown	8470.53	1
gb|FS411872 normalized full-length tobacco cDNA library Nicotiana tabacum cDNA	118.94	1
gb|AM792645 DL, diurnal library Nicotiana tabacum cDNA clone nt005008015, mR	165.29	1
tc|Rep: Chromosome chr7 scaffold_31, whole genome shotgun sequence - Vitis vin	24.21	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	87.05	1
tc|Rep: Chromosome chr9 scaffold_7, whole genome shotgun sequence - Vitis vinif	35.73	1
tc|Rep: Ubiquitin carrier protein - Mesembryanthemum crystallinum (Common ice	4072.76	1
gb|KN6B.102H06F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102H06,	973.12	1
gb|AGN_RNC003xo15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	531.77	1

tc|Rep: Chromosome chr13 scaffold_210, whole genome shotgun sequence - Vitis	39.51	1
Unknown	86.04	1
gb|TT-22_E07 Burley21 trichome library Nicotiana tabacum cDNA, mRNA sequence	41.83	1
gb|KF8C.103J17F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103J17, mRN	72.8	1
gb|TT-16_O13 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence	1176.37	1
gb|KP1B.107N12F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107N12, m	54.66	1
gb|KT7C.105A10F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105A10, mR	61.03	1
tc|Rep: Cytochrome b-c1 complex subunit Rieske-2, mitochondrial precursor - Nico	11475.35	1
Unknown	46.68	1
gb|KT7C.106M08F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106M08, m	226.03	1
Unknown	509.44	1
tc|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vi	74.87	1
Unknown	2193.69	1
Unknown	2421.75	1
gb|KF8C.101D20F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101D20, mR	61.94	1
gb|KL4B.110N16F.051106T7 KL4B Nicotiana tabacum cDNA clone KL4B.110N16, m	50.71	1
tc|Rep: 6-phosphogluconate dehydrogenase, decarboxylating - Spinacia oleracea (S	19.85	1
gb|CHO_SL004xk19f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	260.13	1
tc|Rep: AGO4-2 - Nicotiana benthamiana, partial (24%) [TC49762]	198.87	1
gb|AGN_ELP005xb08f1.ab1 AGN_ELP Nicotiana tabacum cDNA 5', mRNA sequence	64.27	1
tc|Rep: Chromosome chr1 scaffold_22, whole genome shotgun sequence - Vitis vin	69.29	1
tc|Rep: Fiber protein Fb15 - Gossypium barbadense (Sea-island cotton) (Egyptian c	984.62	1
Unknown	38.78	1
Unknown	70.77	1
Unknown	32.17	1
gb|KG9B.004L06F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004L06, m	270.19	1
gb|Nicotiana tabacum callus associated protein (CAP) mRNA, partial cds [U01961]	59.82	1
Unknown	36.07	1
gb|KT7C.106O01F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106O01, mR	73.65	1
gb|AGN_RNC014xg05f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	88.57	1
tc|Rep: 14-3-3-like protein C - Nicotiana tabacum (Common tobacco), complete [T	1511.75	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	942.51	1
Unknown	75.19	1
gb|KN6B.110B13F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.110B13, m	176.33	1

tc|Rep: Cysteine synthase - Nicotiana plumbaginifolia (Leadwort-leaved tobacco), c	7815.95	1
Unknown	46.95	1
gb|KR2B.110P09F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110P09, m	23.97	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	151.25	1
Unknown	951.24	1
gb|KG9B.004I08F.050721T7 KG9B Nicotiana tabacum cDNA clone KG9B.004I08, m	37.18	1
gb|TT-01_E10 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	1476.11	1
Unknown	29.36	1
gb|KF8B.202G14F.060124T7 KF8 Nicotiana tabacum cDNA clone KF8B.202G14, mR	82.39	1
gb|Nicotiana tabacum mRNA for NtWRKY1, complete cds [AB022693]	17.9	1
Unknown	193.25	1
tc|Rep: Chromosome chr15 scaffold_82, whole genome shotgun sequence - Vitis vi	17923.3	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	31.07	1
Unknown	3242.43	1
gb|KF8C.102H18F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102H18, mR	2979.47	1
tc|Rep: Chromosome chr14 scaffold_21, whole genome shotgun sequence - Vitis vi	41.88	1
tc|Rep: Chromosome undetermined scaffold_163, whole genome shotgun sequenc	2844.86	1
Unknown	1568.51	1
gb|KL4B.112F04F.060131T7 KL4B Nicotiana tabacum cDNA clone KL4B.112F04, mR	144.39	1
tc|Rep: Chromosome chr19 scaffold_35, whole genome shotgun sequence - Vitis vi	524.47	1
tc|Rep: Histone H2A - Vitis vinifera (Grape), partial (96%) [TC64662]	250.26	1
gb|Nicotiana tabacum NtVDAC1 mRNA for voltage-dependent anion channel, comp	167.96	1
Unknown	1432.1	1
gb|Nicotiana tabacum clone pHSM4 cytosolic class I small heat shock protein 6 mR	104.32	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	211.63	1
tc|Rep: Chromosome chr6 scaffold_3, whole genome shotgun sequence - Vitis vinif	126.58	1
gb|AGN_PNL208df1_e9.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	171.48	1
Unknown	66.47	1
gb|Nicotiana tabacum pectin methylesterase (PPME1) mRNA, complete cds [AY772	27019.15	1
gb|KT7C.106P02F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.106P02, mR	39.8	1
Unknown	59.72	1
gb|AGN_RNC015xe23f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	99.08	1
tc|Rep: DNA cross-link repair protein SNM1 - Arabidopsis thaliana (Mouse-ear cres	67.18	1
tc|Rep: 40S ribosomal protein S12 - Vitis vinifera (Grape), partial (91%) [TC53842]	80.76	1

Unknown	544.38	1
gb|KL4B.106D12F.051125T7 KL4B Nicotiana tabacum cDNA clone KL4B.106D12, mR	401.49	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	32.21	1
Unknown	255.25	1
gb|KL4B.105D02F.051104T7 KL4B Nicotiana tabacum cDNA clone KL4B.105D02, mR	211.35	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	29.26	1
Unknown	1559.93	1
gb|KP1B.107J01F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.107J01, mR	525.76	1
gb|EST_CSP005xn18f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	28.51	1
tc|Rep: Chromosome undetermined scaffold_334, whole genome shotgun sequenc	3498.71	1
Unknown	114.21	1
tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vin	10716	1
tc|Rep: At5g12240 - Arabidopsis thaliana (Mouse-ear cress), partial (67%) [TC61967	465.85	1
tc|Rep: Proline-rich protein family-like - Oryza sativa subsp. japonica (Rice), partial (	474.59	1
gb|Nicotiana tabacum mRNA for cullin 1A (cul1A gene) [AJ344533]	1782.92	1
tc|Rep: Chromosome chr13 scaffold_17, whole genome shotgun sequence - Vitis vi	1283.88	1
gb|Nicotiana tabacum calcium-dependent protein kinase CPK4 mRNA, complete cd	532.23	1
gb|KL4B.100M24F.050922T7 KL4B Nicotiana tabacum cDNA clone KL4B.100M24, m	70.11	1
Unknown	32.38	1
gb|Nicotiana tabacum mRNA for alpha-tubulin (tubA2 gene) [AJ421412]	18301.7	1
gb|KN6B.102A21F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.102A21, m	27.24	1
Unknown	461.87	1
Unknown	154.03	1
gb|Nicotiana tabacum PCNA mRNA for proliferating cell nuclear antigen, complete	32.42	1
Unknown	154.97	1
tc|Rep: Chromosome chr8 scaffold_29, whole genome shotgun sequence - Vitis vin	69.18	1
Unknown	79.49	1
Unknown	412.04	1
gb|KR3B.114A02F.060119T7 KR3B Nicotiana tabacum cDNA clone KR3B.114A02, m	298.38	1
Unknown	17.25	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	183.71	1
gb|KG9B.002F15F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.002F15, m	24.67	1
gb|KG9B.106A24F.051129T7 KG9B Nicotiana tabacum cDNA clone KG9B.106A24, m	39.6	1
gb|KR3B.102G14F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.102G14, m	49.89	1

Unknown	48.8	1
gb|KF8C.102A03F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102A03, mR	35.35	1
gb|CHO_SL012xm12f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH	33.81	1
tc|Rep: Chromosome chr11 scaffold_14, whole genome shotgun sequence - Vitis vi	50.28	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	432.01	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	52.67	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	33.45	1
gb|TT-06_K08 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	239.79	1
tc|Rep: Chromosome chr10 scaffold_50, whole genome shotgun sequence - Vitis vi	3115.85	1
gb|Nicotiana tabacum hexose transporter (pGlcT) mRNA, partial cds; nuclear gene	42.15	1
Unknown	84.34	1
Unknown	79.74	1
gb|KP1B.110B02F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110B02, m	3513.35	1
Unknown	136.01	1
Unknown	162.88	1
gb|10F11 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5',	44.9	1
gb|KF8C.104L08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104L08, mRN	720.97	1
Unknown	61.76	1
Unknown	25.98	1
gb|TT-48_D03 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	18.64	1
gb|KP1B.103G20F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.103G20, m	31.85	1
gb|TT-07_C15 K326 early senescent leaf library Nicotiana tabacum cDNA, mRNA se	379.61	1
gb|AGN_RNC014xe20f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	1996.17	1
Unknown	31.85	1
gb|TT-29_D08 K326 trichome library Nicotiana tabacum cDNA, mRNA sequence [F	395.46	1
gb|Nicotiana tabacum inosine-5'-phosphate dehydrogenase (guaB) mRNA, partial c	31.22	1
gb|KP1B.101G06F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101G06, m	1016.53	1
gb|KG9B.001K18F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001K18, m	92.34	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	37.55	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	722.12	1
Unknown	977.12	1
gb|KG9B.001P10F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001P10, m	19.98	1
gb|Nicotiana tabacum mRNA for BY-2 kinesin-like protein 5, complete cds [AB0030	464.17	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	253.16	1

tc|Rep: Chromosome chr3 scaffold_8, whole genome shotgun sequence - Vitis vinif	137.62	1
Unknown	1014.36	1
tc|Rep: Anthocyanidin 3-O-glucosyltransferase - Petunia hybrida (Petunia), partial (	21.91	1
gb|KR2B.110E10F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.110E10, m	55.88	1
tc|Rep: Chromosome chr8 scaffold_115, whole genome shotgun sequence - Vitis vi	49.16	1
gb|AGN_RNC108xi21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	392.98	1
Unknown	955.71	1
Unknown	29.76	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	23.7	1
gb|KP1B.108I06F.050726T7 KP1B Nicotiana tabacum cDNA clone KP1B.108I06, mR	521.14	1
Unknown	41.67	1
gb|Nicotiana tabacum EIL5 mRNA, complete cds [AY248907]	26.58	1
tc|Rep: Chromosome chr12 scaffold_47, whole genome shotgun sequence - Vitis vi	762.89	1
gb|CHO_SL013xa08f1.ab1 CHO_SL Nicotiana tabacum cDNA, mRNA sequence [EH6	661.32	1
Unknown	18.78	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	123.55	1
tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vin	18446.8	1
gb|KF8C.102K09F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.102K09, mR	389.23	1
gb|KF8C.104O06F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104O06, mR	34.83	1
gb|KG9B.105N17F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.105N17,	24.47	1
Unknown	17.25	1
gb|KR2B.112I06F.051230T7 KR2B Nicotiana tabacum cDNA clone KR2B.112I06, mR	729.89	1
tc|Rep: Protein phosphatase 2C - Mesembryanthemum crystallinum (Common ice	4317.2	1
gb|TT-19_K24 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	44.33	1
Unknown	22.2	1
gb|KF8C.101M24F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101M24, m	4445.65	1
gb|TT-14_E22 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	61.42	1
tc|Rep: Chromosome chr1 scaffold_75, whole genome shotgun sequence - Vitis vin	547.94	1
Unknown	1523.52	1
gb|TT-26_I03 Samsun trichome library Nicotiana tabacum cDNA, mRNA sequence [	30.14	1
gb|AGN_RPC005xl10f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	20.05	1
gb|KR3B.105A06F.051109T7 KR3B Nicotiana tabacum cDNA clone KR3B.105A06, m	383.8	1
gb|N.tabacum mRNA for c subunit of V-type ATPase (980 bp) [X95752]	777.17	1
gb|KF8C.104K08F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.104K08, mR	186.68	1

gb|KF8C.103D11F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.103D11, mR	929.35	1
tc|Rep: Ribosomal protein PETRP - Capsicum annuum (Bell pepper), complete [TC4	27.99	1
gb|KT7C.105K19F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.105K19, mR	101.82	1
gb|KT7C.109P20F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109P20, mR	166.23	1
tc|Rep: Chromosome undetermined scaffold_470, whole genome shotgun sequenc	24.15	1
tc|Rep: Chromosome chr13 scaffold_48, whole genome shotgun sequence - Vitis vi	101.16	1
Unknown	50.46	1
Unknown	351.28	1
tc|Rep: Chromosome chr5 scaffold_2, whole genome shotgun sequence - Vitis vinif	80.27	1
tc|Rep: Chromosome chr10 scaffold_43, whole genome shotgun sequence - Vitis vi	47.23	1
Unknown	47.69	1
tc|Rep: Oligopeptidase A - Medicago truncatula (Barrel medic), partial (98%) [TC46	26.51	1
tc|Rep: Mitochondrial processing peptidase - Solanum tuberosum (Potato), partial	1143.05	1
Unknown	637.6	1
gb|KR2B.108M13F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.108M13,	39.56	1
tc|Rep: Thioredoxin H-type 1 - Nicotiana tabacum (Common tobacco), partial (96%	139.55	1
Unknown	94.18	1
tc|Rep: Chromosome chr11 scaffold_13, whole genome shotgun sequence - Vitis vi	28.89	1
gb|KP1B.101B18F.050722T7 KP1B Nicotiana tabacum cDNA clone KP1B.101B18, m	172.53	1
gb|Nicotiana tabacum ntp805 (pntp805) mRNA, complete cds [AY366400]	52979.2	1
Unknown	2397.11	1
gb|Nicotiana tabacum S-adenosyl-methionine-sterol-C-methyltransferase mRNA, c	14979.95	1
tc|Rep: Chromosome chr8 scaffold_23, whole genome shotgun sequence - Vitis vin	46.61	1
gb|KP1B.104L22F.050725T7 KP1B Nicotiana tabacum cDNA clone KP1B.104L22, mR	946.97	1
tc|Rep: Chloroplast 30S ribosomal protein S15 - Nicotiana sylvestris (Wood tobacco	23.38	1
Unknown	24.66	1
tc|Rep: Calmodulin-related protein - Petunia hybrida (Petunia), partial (83%) [TC70	82.43	1
Unknown	380.38	1
tc|Rep: Chromosome undetermined scaffold_235, whole genome shotgun sequenc	85.71	1
tc|Rep: Chromosome chr6 scaffold_15, whole genome shotgun sequence - Vitis vin	175.57	1
gb|KP1B.110G12F.050727T7 KP1B Nicotiana tabacum cDNA clone KP1B.110G12, m	88.03	1
Unknown	180.03	1
gb|KP1B.105H02F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105H02, m	4498.45	1
gb|KP1B.112P05F.060117T7 KP1B Nicotiana tabacum cDNA clone KP1B.112P05, m	139.81	1

tc|Rep: Aluminum-induced protein - Codonopsis lanceolata, partial (78%) [TC42573	36	1
gb|Nicotiana tabacum putative translation initiation factor 2B beta subunit (NIFb) n	35.72	1
gb|AGN_RNC128xh08f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	195.21	1
gb|KG9B.103L12F.051128T7 KG9B Nicotiana tabacum cDNA clone KG9B.103L12, m	223.08	1
Unknown	4637.61	1
tc|Rep: Pyruvate dehydrogenase E1 beta subunit - Arabidopsis thaliana (Mouse-ear	50.79	1
tc|Rep: Thioredoxin peroxidase - Nicotiana tabacum (Common tobacco), complete	32.15	1
Unknown	542.12	1
Unknown	67.77	1
gb|Nicotiana tabacum putative UDP-glucuronate decarboxylase 4 mRNA, partial cd	1578.87	1
gb|KR3B.101B08F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101B08, m	65.14	1
gb|AGN_RNC013xe15f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	527.29	1
gb|AGN_PNL221df1_d12.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRN	428.19	1
tc|Rep: TPK1 - Nicotiana tabacum (Common tobacco), complete [TC64081]	254.9	1
gb|AGN_RPC017xc15f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA sequence	1372.17	1
gb|KL4B.101H01F.051103T7 KL4B Nicotiana tabacum cDNA clone KL4B.101H01, mF	29.64	1
Unknown	22.91	1
Unknown	1542.29	1
Unknown	21.29	1
gb|KG9B.001L18F.050628T7 KG9B Nicotiana tabacum cDNA clone KG9B.001L18, m	86.14	1
tc|Rep: Formate--tetrahydrofolate ligase - Spinacia oleracea (Spinach), partial (25%	57.82	1
Unknown	27.76	1
tc|Rep: Chromosome chr1 scaffold_46, whole genome shotgun sequence - Vitis vin	57.35	1
Unknown	745.43	1
tc|Rep: Plant viral-response family protein - Solanum bulbocastanum (Wild potato)	223.06	1
tc|Rep: Chromosome chr10 scaffold_43, whole genome shotgun sequence - Vitis vi	70.67	1
tc|Rep: Chromosome chr16 scaffold_10, whole genome shotgun sequence - Vitis vi	31.65	1
Unknown	21.05	1
gb|KN6B.108A05F.060106T7 KN6B Nicotiana tabacum cDNA clone KN6B.108A05, n	130.14	1
tc|Rep: Ribosomal Pr 117 - Triticum aestivum (Wheat), partial (95%) [TC48773]	172.53	1
Unknown	41.77	1
gb|AGN_PNL221df1_g8.trimmed.seq AGN_PNL Nicotiana tabacum cDNA 5', mRNA	23.3	1
tc|Rep: Chromosome chr7 scaffold_42, whole genome shotgun sequence - Vitis vin	117.78	1
Unknown	2785.34	1

tc|Rep: Chromosome chr8 scaffold_34, whole genome shotgun sequence - Vitis vin	1688.91	1
Unknown	21.68	1
gb|18.2A08 Transformed tobacco Lambda Zap II library Nicotiana tabacum cDNA 5'	87.55	1
gb|AM789373 seedling library, SL Nicotiana tabacum cDNA clone nt002266080, mF	21.02	1
Unknown	31.66	1
gb|Nicotiana tabacum NtJAZ2 mRNA for jasmonate ZIM-domain protein 2, complet	649.27	1
tc|Rep: Chromosome chr4 scaffold_373, whole genome shotgun sequence - Vitis vi	79.85	1
tc|Rep: Zinc finger, ZZ-type; Zinc finger, C2H2-type - Medicago truncatula (Barrel m	23.76	1
gb|KF8C.101B23F.051214T7 KF8 Nicotiana tabacum cDNA clone KF8C.101B23, mRN	64.18	1
Unknown	107.73	1
Unknown	50.7	1
tc|Rep: V226 - Cowpox virus (CPV), partial (5%) [TC71551]	38.45	1
Unknown	619.4	1
gb|KR3B.101A06F.051107T7 KR3B Nicotiana tabacum cDNA clone KR3B.101A06, m	420.48	1
gb|TT-47_C04 K326 late senescent leaf library Nicotiana tabacum cDNA, mRNA seq	911.92	1
tc|Rep: Chromosome chr1 scaffold_5, whole genome shotgun sequence - Vitis vinif	37.77	1
tc|Rep: Chromosome chr17 scaffold_12, whole genome shotgun sequence - Vitis vi	150.6	1
gb|EST_CSP001xe20f1.ab1 EST_CSP Nicotiana tabacum cDNA, mRNA sequence [EH	4356.9	1
Unknown	21.75	1
Unknown	40.76	1
Unknown	20.41	1
tc|Rep: 60S ribosomal protein L7A-like protein - Solanum tuberosum (Potato), com	185.69	1
gb|BP135562 MAT001 Nicotiana tabacum cDNA clone BY8090, mRNA sequence [BF	184.11	1
tc|Rep: Phosphate/phosphoenolpyruvate translocator-like protein - Arabidopsis tha	13725.25	1
tc|Rep: Chromosome chr14 scaffold_27, whole genome shotgun sequence - Vitis vi	16656.85	1
tc|Rep: Chromosome chr2 scaffold_113, whole genome shotgun sequence - Vitis vi	1205.81	1
Unknown	20.91	1
tc|Rep: Chromosome chr4 scaffold_6, whole genome shotgun sequence - Vitis vinif	103.48	1
Unknown	692.76	1
gb|KR2B.108M21F.051229T7 KR2B Nicotiana tabacum cDNA clone KR2B.108M21, r	72.13	1
gb|KT7B.103K21F.060124T7 KT7 Nicotiana tabacum cDNA clone KT7B.103K21, mRN	19.67	1
Unknown	109.08	1
gb|KG9B.003C19F.050720T7 KG9B Nicotiana tabacum cDNA clone KG9B.003C19, m	36.25	1
gb|KN6B.101A17F.051230T7 KN6B Nicotiana tabacum cDNA clone KN6B.101A17, n	197.57	1

Unknown	173.59	1
gb|TT-07_G15 tobacco leaf library Nicotiana tabacum cDNA, mRNA sequence [FG6	55.2	1
gb|KP1B.105P05F.060116T7 KP1B Nicotiana tabacum cDNA clone KP1B.105P05, m	439.21	1
gb|AGN_RNC023xn19f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA sequenc	80.07	1
gb|KT7C.112O13F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.112O13, mR	80.2	1

						Detection call	
Arabidopsis SIV enriched	Closest tobacco	Description	MPG	PT4	PT24	MPG	PT4
AT3G12940	BP134405	Unknown	86.48275	108.26305	82.66	1	1
AT1G78070	EB447894	tc|Rep: Chromosome chr18 sca	85.835	109.2045	347.32	1	1
AT5G23090	EB425683	gb|KF8C.103P24F.051214T7 KF	620.859	362.908	500.22	1	1
AT5G41150	EB681945	tc|Rep: Ultraviolet hypersensiti	4.97	1.8	41.06	0	0
AT5G61640	DV160066	gb|KP1B.102C22F.050722T7 KP	203.917	153.4315	62.37	1	1
AT2G17900	EB446556	Unknown	86.48275	108.26305	82.66	1	1
AT1G07160	EB683563	Unknown	86.48275	108.26305	82.66	1	1
AT2G40650	DW002772	gb|KR3B.103O02F.051108T7 KR	478.4005	459.129	456.17	1	1
AT1G08680	DW003203	gb|KR3B.105C01F.051109T7 KR	445.294	336.26	522.39	1	1
AT2G41070	EB427718	gb|KF8C.110N19F.051216T7 KF	146.24	113.2575	189.62	1	1
AT1G03950	FG642430	gb|TT-17_M23 K326 early senes	329.925	425.637	451.78	1	1
AT3G19510	DV162276	gb|KP1B.110K05F.050727T7 KP	14.703335	19.24275	41.16	0	0
AT5G40440	D31964	gb|Nicotiana tabacum mRNA fo	813.125	299.9965	74.86	1	1
AT1G09810	EB427609	Unknown	86.48275	108.26305	82.66	1	1
AT1G76270	DV160855	gb|KP1B.104G11F.050725T7 KP	161.4811	308.5635	995.65	1	1
AT3G45740	DV161891	gb|KP1B.109H22F.050727T7 KP	62.53875	70.9167	66.75	1	1
AT5G17370	DV160207	gb|KP1B.102J11F.050722T7 KP1	21.79	22.5662	79.02	0	0

SIV-enriched Arabidopsis genes (Qin et al., 2009) with the closest identified Nicotiana tabacum homologs.

Supplementary Table S2.
SIV-enriched Arabidopsis genes8 with the closest identified *Nicotiana tabacum* homologs.

PT24
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