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347	intercellular adhesion molecule 1	0.0054
348	interferon induced transmembrane protein 2 (1-8D)	0.0225
349	IQ motif containing GTPase activating protein 3 (predicted)	0.0338
350	junction plakoglobin	0.0153
351	Karyopherin (importin) beta 1	0.0105
352	karyopherin (importin) beta 3 (predicted)	0.0009
353	K-Cl cotransporter KCC4	0.0018
354	KDEL (Lys-Asp-Glu-Leu) containing 1 (predicted)	0.0188
355	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (predicted)	0.0000
356	keratin 20	0.0083
357	keratin complex 2, basic, gene 7 (predicted)	0.0001
358	kidney predominant protein NCU-G1	0.0090
359	kinesin family member 22 (predicted)	0.0003
360	Kinesin family member 3a	0.0002
361	kinesin family member 3B (predicted)	0.0045
362	kinesin family member 5B	0.0353
363	kinesin family member C1	0.0062
364	Kinesin heavy chain member 2	0.0097
365	Kit ligand	0.0004
366	Kit ligand	0.0217
367	Kruppel-like factor 4 (gut)	0.0022
368	Kruppel-like factor 7 (ubiquitous) (predicted)	0.0278
369	I(3)mbt-like 2 (Drosophila) (predicted)	0.0279
370	lamin A	0.0161
371	Lamin B receptor	0.0033
372	Laminin receptor 1 (67kD, ribosomal protein SA)	0.0267
373	laminin receptor 1 (67kD, ribosomal protein SA)	0.0009
374	laminin, beta 2	0.0019
375	Laminin, gamma 1	0.0019
376	latent transforming growth factor beta binding protein 1	0.0034
377	lectin, galactose binding, soluble 1	0.0301
378	lectin, galactoside-binding, soluble 2	0.0073
379	lectin, galactoside-binding, soluble, 4 (galectin 4)	0.0143
380	legumain	0.0090
381	leprecan 1	0.0061
382	leptin receptor overlapping transcript	0.0002
383	leucine zipper protein 1	0.0348
384	leucine zipper transcription factor-like 1 (predicted)	0.0031
385	leucine-zipper-like transcriptional regulator, 1 (predicted)	0.0286

386	leucyl-tRNA synthetase (predicted)	0.0139
387	ligase I, DNA, ATP-dependent	0.0019
388	ligase I, DNA, ATP-dependent	0.0414
389	LIM domain only protein 7	0.0325
390	LIM homeobox protein 3	0.0044
391	lipocalin 7	0.0144
392	LOC361485 (predicted)	0.0041
393	LOC362113 (predicted)	0.0027
394	LOC362113 (predicted)	0.0152
395	Low Mr GTP-binding protein	0.0128
396	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	0.0014
397	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	0.0133
398	lysosomal-associated protein transmembrane 4B (predicted)	0.0018
399	lysyl oxidase	0.0446
400	MAD homolog 2 (Drosophila)	0.0089
401	MAD homolog 4 (Drosophila)	0.0071
402	mago-nashi homolog, proliferation-associated (Drosophila) (predicted)	0.0066
403	major vault protein	0.0134
404	maternal embryonic leucine zipper kinase (predicted)	0.0129
405	matrix metalloproteinase 2	0.0266
406	matrix metalloproteinase 11	0.0002
407	melanoma associated antigen (mutated) 1 (predicted)	0.0337
408	melanoma cell adhesion molecule	0.0039
409	membrane-spanning 4-domains, subfamily A, member 8B (predicted)	0.0105
410	mesoderm development candidate 2 (predicted)	0.0136
411	Metastatic lymph node 51	0.0085
412	methyl-CpG binding domain protein 1 (predicted)	0.0145
413	methyltransferase-like 3 (predicted)	0.0297
414	microtubule-associated protein 1 light chain 3 alpha	0.0054
415	microtubule-associated protein 1b	0.0005
416	microtubule-associated protein 1b	0.0297
417	microtubule-associated protein 2	0.0036
418	Microtubule-associated protein 4	0.0111
419	microtubule-associated protein 6	0.0076
420	Microtubule-associated protein, RP/EB family, member 1	0.0010
421	midasin homolog (yeast) (predicted)	0.0249
422	Mitogen activated protein kinase 1	0.0267
423	mitogen activated protein kinase 8 interacting protein	0.0136

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424	Mitogen activated protein kinase kinase kinase 1	0.0104
425	mitogen-activated protein kinase 12	0.0023
426	mitogen-activated protein kinase 7	0.0094
427	mitogen-activated protein kinase kinase kinase kinase 4 (predicted)	0.0018
428	MOB1, Mps One Binder kinase activator-like 2B (yeast) (predicted)	0.0322
429	monocarboxylate transporter	0.0027
430	monocyte to macrophage differentiation-associated	0.0059
431	mucin and cadherin like	0.0455
432	myc induced nuclear antigen	0.0271
433	myelin basic protein expression factor 2, repressor (predicted)	0.0003
434	Myelin oligodendrocyte glycoprotein	0.0106
435	myelocytomatosis viral oncogene homolog (avian)	0.0113
436	myeloid cell leukemia sequence 1	0.0022
437	myeloid-associated differentiation marker	0.0023
438	myosin 5B	0.0252
439	Myosin binding protein H	0.0076
440	myosin heavy chain 10, non-muscle	0.0014
441	myosin VC (predicted)	0.0301
442	myosin, heavy polypeptide 9	0.0165
443	Myotrophin	0.0222
444	myotrophin	0.0141
445	N-acetylglucosamine kinase (predicted)	0.0007
446	N-acetylneuraminic acid synthase (sialic acid synthase) (predicted)	0.0055
447	N-acylsphingosine amidohydrolase 1	0.0023
448	nadrin	0.0218
449	nasal embryonic LHRH factor	0.0283
450	necdin (predicted)	0.0189
451	Nephroblastoma overexpressed gene	0.0309
452	nephronophthisis 1 (juvenile) (predicted)	0.0003
453	nerve growth factor receptor (TNFRSF16) associated protein 1	0.0064
454	nerve growth factor, beta	0.0024
455	nestin	0.0006
456	Neural cell adhesion molecule 2	0.0246
457	neural precursor cell expressed, developmentally down-regulated gene 4A	0.0083
458	neural visinin-like Ca ²⁺ -binding protein type 3	0.0017
459	neuregulin 1	0.0337
460	neurochondrin	0.0089
461	neurofilament, light polypeptide	0.0139
462	neuromedin B (predicted)	0.0201

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463	neuronal pentraxin receptor	0.0141
464	neuropilin (NRP) and tolloid (TLL)-like 2 (predicted)	0.0246
465	Ngfi-A binding protein 2 (predicted)	0.0084
466	NIMA (never in mitosis gene a)-related expressed kinase 6	0.0034
467	nischarin (predicted)	0.0037
468	non-metastatic cells 7, protein expressed in	0.0138
469	NTF2-related export protein 1 (predicted)	0.0090
470	nuclear factor, erythroid derived 2, like 2	0.0493
471	nuclear fragile X mental retardation protein interacting protein 1	0.0075
472	nuclear pore membrane glycoprotein 210	0.0331
473	nuclear protein 1	0.0119
474	nucleolar and coiled-body phosphoprotein 1	0.0137
475	nucleolar protein family A, member 2 (predicted)	0.0063
476	nucleoporin 107	0.0032
477	nucleoporin 133 (predicted)	0.0041
478	nucleoporin 188 (predicted)	0.0139
479	nucleoporin 88	0.0280
480	nucleoporin 93 (predicted)	0.0097
481	Nucleoporin like 1	0.0070
482	nucleoporin like 1	0.0059
483	Nucleosome assembly protein 1-like 1	0.0029
484	nucleosome assembly protein 1-like 1	0.0072
485	nudE nuclear distribution gene E homolog like 1 (<i>A. nidulans</i>)	0.0058
486	nudix-type motif 5	0.0031
487	O-6-methylguanine-DNA methyltransferase	0.0021
488	O-linked mannose beta1,2-N-acetylglucosaminyltransferase	0.0067
489	open reading frame 19 (predicted)	0.0031
490	origin recognition complex, subunit 3-like (<i>S. cerevisiae</i>) (predicted)	0.0369
491	origin recognition complex, subunit 6-like (<i>S. cerevisiae</i>) (predicted)	0.0045
492	ornithine decarboxylase 1	0.0123
493	P34 protein	0.0159
494	P34 protein	0.0380
495	par-3 (partitioning defective 3) homolog (<i>C. elegans</i>)	0.0188
496	paxillin (predicted)	0.0056
497	PC4 and SFRS1 interacting protein 1	0.0150
498	PCTAIRE-motif protein kinase 1	0.0197
499	PDZ and LIM domain 1 (elfin)	0.0013
500	PDZ and LIM domain 2	0.0072
501	PDZ and LIM domain 7	0.0013

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502	pelota homolog	0.0228
503	peptidylglycine alpha-amidating monooxygenase	0.0031
504	peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor	0.0037
505	peptidylprolyl isomerase (cyclophilin)-like 1 (predicted)	0.0108
506	peptidylprolyl isomerase C	0.0058
507	pericentrin 1 (predicted)	0.0097
508	peripheral myelin protein 22	0.0086
509	peripheral myelin protein 22	0.0220
510	peroxiredoxin 2	0.0009
511	peroxisome proliferative activated receptor, gamma, coactivator-related 1 (predicted)	0.0429
512	phosducin-like 3 (predicted)	0.0071
513	phosducin-like 3 (predicted)	0.0099
514	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	0.0442
515	phosphatidylinositol glycan, class Q	0.0045
516	phosphatidylinositol glycan, class T (predicted)	0.0086
517	Phosphatidylinositol-4-phosphate 5-kinase, type I, gamma (predicted)	0.0152
518	phosphoenolpyruvate carboxykinase 2 (mitochondrial) (predicted)	0.0025
519	phosphofructokinase, muscle	0.0028
520	phosphofructokinase, muscle	0.0228
521	phosphofructokinase, platelet	0.0011
522	phospholipase C, delta 1	0.0388
523	phospholipase C, gamma 1	0.0049
524	phospholipase D2	0.0072
525	phospholipase D3 (predicted)	0.0151
526	phospholipid scramblase 3 (predicted)	0.0120
527	phosphoprotein enriched in astrocytes 15 (predicted)	0.0002
528	phosphoribosyl transferase domain containing 1 (predicted)	0.0031
529	pirin	0.0118
530	plakophilin 2 (predicted)	0.0013
531	plasminogen activator, tissue	0.0002
532	plasminogen activator, urokinase receptor	0.0002
533	Platelet derived growth factor, alpha	0.0003
534	platelet-derived growth factor, D polypeptide	0.0145
535	pleckstrin 2 (predicted)	0.0144
536	pleckstrin homology, Sec7 and coiled/coil domains 2	0.0093
537	pleckstrin homology-like domain, family A, member 2 (predicted)	0.0076
538	plectin 1	0.0300
539	Plexin A3	0.0054

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540	Plexin B1 (predicted)	0.0100
541	PLRR-4 polymorphic leucine-rich repeat protein	0.0072
542	poliovirus receptor-related 2 (herpesvirus entry mediator B) (predicted)	0.0021
543	polo-like kinase 1 (Drosophila)	0.0149
544	polo-like kinase 4 (Drosophila) (predicted)	0.0015
545	poly A binding protein, cytoplasmic 4 (predicted)	0.0037
546	poly(A) binding protein, nuclear 1	0.0132
547	poly(rC) binding protein 3 (predicted)	0.0062
548	polyhomeotic-like 1 (Drosophila) (predicted)	0.0214
549	Polymerase (DNA directed), alpha 1	0.0050
550	polymerase (DNA directed), beta	0.0068
551	polymerase (DNA directed), delta 2, regulatory subunit (predicted)	0.0016
552	polymerase (RNA) II (DNA directed) polypeptide G	0.0007
553	polymerase (RNA) II (DNA directed) polypeptide H (predicted) /// similar to polymerase (RNA) II (DNA directed) polypeptide H	0.0029
554	polymerase (RNA) III (DNA directed) polypeptide D (predicted)	0.0381
555	polynucleotide kinase 3'-phosphatase	0.0280
556	polypyrimidine tract binding protein 1	0.0050
557	potassium channel regulator 1	0.0168
558	potassium channel tetramerisation domain containing 13	0.0175
559	potassium channel tetramerisation domain containing 3 (predicted)	0.0013
560	potassium channel tetramerization domain containing 10	0.0032
561	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	0.0002
562	pre-B-cell leukemia transcription factor interacting protein 1 (predicted)	0.0134
563	prepro-Neuropeptide W polypeptide	0.0210
564	procollagen C-proteinase enhancer protein	0.0013
565	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	0.0205
566	procollagen, type IV, alpha 1 (predicted)	0.0013
567	procollagen, type IV, alpha 1 (predicted)	0.0037
568	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	0.0004
569	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	0.0178
570	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide (predicted)	0.0097
571	profilin 1	0.0101
572	profilin 2	0.0003
573	programmed cell death protein 11 (predicted)	0.0067
574	proliferating cell nuclear antigen	0.0014
575	proline-rich protein PRP2	0.0408

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576	prostaglandin F2 receptor negative regulator	0.0031
577	protease, serine, 22 (predicted)	0.0072
578	protease, serine, 23	0.0067
579	protein inhibitor of activated STAT 3	0.0058
580	Protein kinase C, alpha	0.0431
581	protein kinase C, delta	0.0019
582	Protein kinase inhibitor, alpha	0.0009
583	Protein kinase, cAMP dependent regulatory, type I, alpha	0.0146
584	protein kinase, cAMP dependent regulatory, type II beta	0.0210
585	Protein kinase, lysine deficient 1	0.0431
586	protein phosphatase 3, regulatory subunit B, alpha isoform,type 1	0.0017
587	protein phosphatase 1, catalytic subunit, alpha isoform	0.0023
588	protein phosphatase 1, regulatory (inhibitor) subunit 7 (predicted)	0.0162
589	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	0.0068
590	protein phosphatase 2, regulatory subunit B (B56), beta isoform	0.0263
591	protein phosphatase 2a, catalytic subunit, beta isoform	0.0045
592	protein phosphatase 4, regulatory subunit 1	0.0141
593	protein tyrosine kinase 9 (predicted)	0.0040
594	Protein tyrosine phosphatase, non-receptor type 13	0.0011
595	protein tyrosine phosphatase, non-receptor type 23	0.0113
596	protein tyrosine phosphatase, non-receptor type substrate 1	0.0176
597	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein, alpha 1 (predicted)	0.0042
598	protein tyrosine phosphatase, receptor type, N	0.0056
599	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	0.0012
600	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	0.0092
601	pumilio 2 (Drosophila) (predicted)	0.0068
602	putative phosphate-phosphoenolpyruvate translocator	0.0027
603	pyrroline-5-carboxylate reductase family, member 2 (predicted)	0.0028
604	pyruvate dehydrogenase kinase, isoenzyme 3	0.0002
605	quiescin Q6	0.0158
606	quiescin Q6	0.0054
607	RAB26, member RAS oncogene family	0.0048
608	RAB34, member of RAS oncogene family (predicted)	0.0097
609	RAB4B, member RAS oncogene family	0.0122
610	Rab6 interacting protein 1 (predicted)	0.0162
611	Rad and gem related GTP binding protein 2	0.0062
612	ral guanine nucleotide dissociation stimulator	0.0112
613	RAN GTPase activating protein 1 (predicted)	0.0175

614	RAN, member RAS oncogene family	0.0073
615	RAP1, GTPase activating protein 1 (predicted)	0.0033
616	Ras and Rab interactor 1	0.0155
617	Ras association domain family 1	0.0021
618	ras homolog gene family, member Q	0.0028
619	ras homolog gene family, member Q	0.0028
620	RAS protein activator like 2 (predicted)	0.0385
621	receptor-interacting serine-threonine kinase 3	0.0010
622	regulator of G-protein signaling 19 interacting protein 1	0.0154
623	replication protein A2	0.0117
624	reticulon 1	0.0019
625	reticulon 4	0.0020
626	retinitis pigmentosa 1 (autosomal dominant) (predicted) /// similar to cylindromatosis (turban tumor syndrome)	0.0245
627	Rho family GTPase 1 (predicted)	0.0016
628	Rho GTPase activating protein 1 (predicted)	0.0144
629	Rho-associated coiled-coil forming kinase 2	0.0158
630	Rho-associated coiled-coil forming kinase 2	0.0144
631	ribonuclease T2 (predicted)	0.0041
632	ribonucleic acid binding protein S1 (predicted)	0.0056
633	ribosomal protein L10A	0.0032
634	ribosomal protein L12 (predicted)	0.0021
635	ribosomal protein L13A	0.0101
636	ribosomal protein L19	0.0004
637	ribosomal protein L26 (predicted)	0.0023
638	ribosomal protein L28	0.0003
639	ribosomal protein L29	0.0034
640	ribosomal protein L31	0.0019
641	ribosomal protein L34 (predicted)	0.0009
642	ribosomal protein L39	0.0066
643	ribosomal protein S11	0.0012
644	ribosomal protein S12	0.0023
645	ribosomal protein S17	0.0136
646	ribosomal protein S2	0.0026
647	ribosomal protein S6	0.0152
648	ribosomal protein S8	0.0004
649	ribosomal protein S9	0.0153
650	ring finger protein 166	0.0123
651	ring finger protein 20 (predicted)	0.0010
652	ring finger protein 34	0.0260

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653	ring finger protein 41 (predicted)	0.0074
654	RNA terminal phosphate cyclase domain 1	0.0162
655	Rous sarcoma oncogene	0.0134
656	RT1 class I, CE12	0.0168
657	RUN and TBC1 domain containing 3	0.0095
658	S100 calcium binding protein A11 (calizzarin)	0.0009
659	S100 calcium binding protein A13 (predicted)	0.0095
660	S100 calcium binding protein A6 (calcyclin)	0.0000
661	S100 protein, beta polypeptide	0.0056
662	scavenger receptor class F, member 2 (predicted)	0.0019
663	schwannomin interacting protein 1 (predicted)	0.0013
664	SEC24 related gene family, member B (<i>S. cerevisiae</i>) (predicted)	0.0070
665	SECIS binding protein 2	0.0012
666	secretin receptor	0.0008
667	secretory carrier membrane protein 4	0.0126
668	secretory granule neuroendocrine protein 1	0.0246
669	selenoprotein W, muscle 1	0.0045
670	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A (predicted)	0.0023
671	septin 5	0.0028
672	Ser/Thr-like protein kinase lyk4	0.0055
673	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	0.0171
674	serine/threonine kinase	0.0056
675	Serine/threonine kinase 17b (apoptosis-inducing)	0.0036
676	Serine/threonine kinase 2	0.0161
677	serine/threonine kinase 3	0.0007
678	SERTA domain containing 1	0.0278
679	seryl-aminoacyl-tRNA synthetase 1	0.0176
680	sestrin 3 (predicted)	0.0002
681	SET and MYND domain containing 2	0.0054
682	shank-interacting protein	0.0154
683	Shwachman-Bodian-Diamond syndrome (predicted)	0.0076
684	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase)	0.0019
685	signal transducer and activator of transcription 3	0.0246
686	signal transducer and activator of transcription 6 (predicted)	0.0242
687	signal-induced proliferation-associated 1 like 2 (predicted)	0.0089
688	similar to 0910001A06Rik protein (predicted)	0.0016
689	similar to 1700019E19Rik protein (predicted)	0.0021
690	similar to 2010321M09Rik protein	0.0019

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691	similar to 2610027C15Rik protein (predicted)	0.0087
692	similar to 2810407K09Rik protein (predicted)	0.0210
693	similar to 3000004C01Rik protein (predicted)	0.0066
694	similar to 4631422O05Rik protein	0.0017
695	similar to 6030466N05Rik protein	0.0115
696	similar to A230072I16Rik protein (predicted)	0.0159
697	similar to AF1q (predicted)	0.0016
698	similar to Aig1 protein	0.0090
699	similar to ALEX3 protein	0.0026
700	similar to amyloid beta (A4) precursor protein-binding, family B, member 2	0.0345
701	similar to autoantigen	0.0042
702	similar to Autoantigen NGP-1 (predicted)	0.0283
703	similar to Avian reticuloendotheliosis viral (v-rel) oncogene related B	0.0101
704	similar to B99 protein	0.0011
705	similar to BAF53a (predicted)	0.0128
706	similar to BB128963 protein (predicted)	0.0134
707	similar to BC282485_1 (predicted)	0.0083
708	similar to BRIX (predicted)	0.0473
709	similar to C11orf17 protein (predicted)	0.0105
710	similar to C21orf70 protein (predicted)	0.0369
711	similar to calmodulin regulated spectrin-associated protein 1	0.0145
712	similar to CDC45L	0.0134
713	similar to cDNA sequence BC016188 (predicted)	0.0473
714	similar to cDNA sequence BC023151 (predicted)	0.0009
715	similar to CG11030-PA (predicted)	0.0417
716	similar to CG13901-PA (predicted)	0.0127
717	similar to CG14903-PA	0.0271
718	similar to CG8841-PA (predicted)	0.0040
719	similar to CG9117-PA (predicted)	0.0269
720	similar to CGI-09 protein (predicted)	0.0402
721	similar to CGI-130 protein (predicted)	0.0199
722	similar to CGI-96 protein; gastric cancer antigen Zg14 (predicted)	0.0159
723	similar to chromatin assembly factor-I p150 subunit	0.0006
724	similar to chromosome 6 open reading frame 83; similar to RIKEN cDNA 5630401J11	0.0027
725	similar to cyclin-dependent kinase 2-interacting protein	0.0023
726	similar to cytokine receptor related protein 4	0.0068
727	similar to D8Ert812e protein (predicted)	0.0032
728	similar to Dendritic cell protein GA17	0.0071

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729	similar to dJ310O13.3 (novel protein) (predicted)	0.0164
730	similar to DNA segment, Chr 10, Wayne State University 102, expressed	0.0087
731	similar to DNA segment, Chr 13, Wayne State University 50, expressed (predicted)	0.0030
732	similar to DNA segment, Chr 4, Brigham & Womens Genetics 0951 expressed (predicted)	0.0075
733	similar to DXImx40e protein	0.0295
734	similar to Dynein 2 light intermediate chain (predicted)	0.0002
735	similar to Erbb2 interacting protein isoform 2	0.0175
736	similar to eukaryotic translation initiation factor 4E member 3	0.0067
737	similar to EXCretory canal abnormal EXC-7, ELAV type RNA binding protein (48.7 kD) (exc-7)	0.0379
738	similar to EXCretory canal abnormal EXC-7, ELAV type RNA binding protein (48.7 kD) (exc-7)	0.0338
739	similar to Ext1	0.0043
740	similar to FLJ00128 protein (predicted)	0.0168
741	similar to Formin homology 2 domain containing 1	0.0162
742	Similar to glutamine:fructose-6-phosphate amidotransferase	0.0095
743	similar to Glycolipid transfer protein	0.0105
744	similar to Hepatocellular carcinoma-associated antigen 58 homolog (predicted)	0.0485
745	similar to HT014 (predicted)	0.0052
746	Similar to hypothetical protein	0.0074
747	similar to hypothetical protein	0.0086
748	similar to hypothetical protein (predicted)	0.0141
749	similar to hypothetical protein 6720484B16 (predicted)	0.0031
750	similar to hypothetical protein D11Ert497e (predicted)	0.0010
751	similar to hypothetical protein D11Ert497e (predicted)	0.0212
752	similar to hypothetical protein DKFZp434A1319 (predicted)	0.0077
753	similar to hypothetical protein DKFZp434H2010 (predicted)	0.0013
754	similar to hypothetical protein FLJ10233 (predicted)	0.0056
755	similar to hypothetical protein FLJ10300 (predicted)	0.0124
756	similar to hypothetical protein FLJ10652 (predicted)	0.0265
757	similar to hypothetical protein FLJ11752	0.0009
758	similar to hypothetical protein FLJ12442 (predicted)	0.0026
759	similar to hypothetical protein FLJ12484 (predicted)	0.0034
760	similar to hypothetical protein FLJ14681 (predicted)	0.0019
761	similar to hypothetical protein FLJ20514	0.0146
762	similar to hypothetical protein FLJ20522 (predicted)	0.0033
763	similar to hypothetical protein FLJ23451 (predicted)	0.0282

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764	similar to hypothetical protein FLJ30973	0.0027
765	similar to hypothetical protein FLJ31606	0.0077
766	similar to hypothetical protein FLJ90652	0.0117
767	similar to Hypothetical protein KIAA0586 (predicted)	0.0097
768	similar to hypothetical protein MGC13251 (predicted)	0.0097
769	similar to hypothetical protein MGC16491 (predicted)	0.0191
770	similar to hypothetical protein MGC16491 (predicted)	0.0292
771	similar to hypothetical protein MGC2574	0.0306
772	similar to hypothetical protein MGC2574	0.0243
773	similar to Hypothetical protein MGC48332	0.0463
774	similar to KIAA0456 protein	0.0028
775	similar to KIAA0546 protein (predicted)	0.0264
776	similar to KIAA0853 protein (predicted)	0.0357
777	similar to KIAA0892 protein (predicted)	0.0031
778	similar to KIAA0913 protein (predicted)	0.0289
779	similar to KIAA0947 protein (predicted)	0.0066
780	similar to KIAA1052 protein	0.0032
781	similar to KIAA1055 protein (predicted)	0.0025
782	Similar to KIAA1401 protein (predicted)	0.0288
783	similar to KIAA1862 protein (predicted)	0.0194
784	similar to LYST-interacting protein LIP8 (predicted)	0.0212
785	similar to mannose-6-phosphate receptor binding protein 1	0.0459
786	similar to Metal-response element-binding transcription factor 2 (Metal-response element DNA-binding protein M96) (predicted)	0.0044
787	similar to mitsugumin 23	0.0086
788	similar to mKIAA0023 protein (predicted)	0.0324
789	similar to Myoferlin (Fer-1 like protein 3)	0.0003
790	similar to myo-inositol 1-phosphate synthase A1	0.0033
791	similar to nuclear factor kappa B subunit p100 (predicted)	0.0036
792	similar to NYD-SP28 protein	0.0101
793	similar to PDZ domain actin binding protein Shroom (predicted)	0.0069
794	similar to phospholipid scramblase 2	0.0048
795	similar to pinin	0.0362
796	similar to pleckstrin homology-like domain, family B, member 3	0.0008
797	similar to poly (ADP-ribose) polymerase family, member 8	0.0011
798	similar to programmed cell death 10	0.0093
799	similar to Protein C21orf63 homolog precursor (predicted)	0.0010
800	similar to Protein HSPC163	0.0010
801	similar to put. type 5 nonmuscle actin	0.0110
802	similar to putative protein, with at least 9 transmembrane domains, of	0.0242

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	eukaryotic origin (43.9 kD) (2G415) (predicted)	
803	similar to Ran-interacting protein MOG1	0.0152
804	similar to Rap1-interacting factor 1	0.0267
805	similar to Rho guanine nucleotide exchange factor (GEF) 10	0.0004
806	similar to Ribonuclease III (RNase III) (p241) (predicted)	0.0124
807	similar to RIKEN cDNA 0610037L13	0.0282
808	similar to RIKEN cDNA 0610037P05 (predicted)	0.0097
809	similar to RIKEN cDNA 0610040B21 (predicted)	0.0021
810	similar to RIKEN cDNA 1110007C09 (predicted)	0.0083
811	similar to RIKEN cDNA 1110028N05 (predicted)	0.0383
812	similar to RIKEN cDNA 1200004M23 (predicted)	0.0074
813	similar to RIKEN cDNA 1200015A22	0.0004
814	similar to RIKEN cDNA 1210002B07	0.0099
815	similar to RIKEN cDNA 1500009M05	0.0205
816	similar to RIKEN cDNA 1500016L11 (predicted)	0.0007
817	Similar to RIKEN cDNA 1700023M09 (predicted)	0.0013
818	similar to RIKEN cDNA 1700088E04; DNA segment, Human EST J0827E04; Mus EST J0827E04; DNA segment, EST J0827E04	0.0274
819	similar to RIKEN cDNA 1810042K04 (predicted)	0.0168
820	similar to RIKEN cDNA 1810048J11 (predicted)	0.0035
821	similar to RIKEN cDNA 1810048J11 (predicted)	0.0098
822	similar to RIKEN cDNA 2210010N04 gene (predicted)	0.0059
823	similar to RIKEN cDNA 2210016L21 gene (predicted)	0.0059
824	similar to RIKEN cDNA 2210402C18 (predicted)	0.0090
825	similar to RIKEN cDNA 2210415M20 (predicted)	0.0254
826	similar to RIKEN cDNA 2310016C16 (predicted)	0.0114
827	similar to RIKEN cDNA 2310057H16 (predicted)	0.0028
828	similar to RIKEN cDNA 2410005K17 (predicted)	0.0117
829	similar to RIKEN cDNA 2410022L05	0.0083
830	similar to RIKEN cDNA 2410025L10	0.0129
831	similar to RIKEN cDNA 2600001J17 (predicted)	0.0287
832	similar to RIKEN cDNA 2600001P13	0.0131
833	similar to RIKEN cDNA 2600005C20 (predicted)	0.0141
834	similar to RIKEN cDNA 2610017G09 (predicted)	0.0085
835	similar to RIKEN cDNA 2610029G23	0.0084
836	similar to RIKEN cDNA 2610029K21 (predicted)	0.0343
837	similar to RIKEN cDNA 2610301B20; EST AI428449	0.0034
838	similar to RIKEN cDNA 2700067D09 (predicted)	0.0145
839	similar to RIKEN cDNA 2700085E05 (predicted)	0.0073
840	similar to RIKEN cDNA 2810021O14 (predicted)	0.0029

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841	similar to RIKEN cDNA 2810037C14 (predicted)	0.0015
842	similar to RIKEN cDNA 2810453K03 (predicted)	0.0370
843	similar to RIKEN cDNA 3110052N05 (predicted)	0.0468
844	similar to RIKEN cDNA 4121402D02	0.0473
845	similar to RIKEN cDNA 4631403P03 (predicted)	0.0095
846	similar to RIKEN cDNA 4922503N01 (predicted)	0.0179
847	similar to RIKEN cDNA 4930553M18 (predicted)	0.0173
848	similar to RIKEN cDNA 5230400G24 (predicted)	0.0002
849	similar to RIKEN cDNA 5730453I16 (predicted)	0.0474
850	similar to RIKEN cDNA 5730454B08 (predicted)	0.0181
851	similar to RIKEN cDNA 5730470L24 (predicted)	0.0047
852	similar to RIKEN cDNA 5730509K17 gene (predicted)	0.0348
853	similar to RIKEN cDNA 5830446M03 (predicted)	0.0051
854	similar to RIKEN cDNA 6530411B15	0.0027
855	similar to RIKEN cDNA 6720467C03 (predicted)	0.0319
856	similar to RIKEN cDNA 9430023L20	0.0040
857	similar to RIKEN cDNA 9530020D24 (predicted)	0.0164
858	similar to RIKEN cDNA A930008A22 (predicted)	0.0012
859	Similar to RIKEN cDNA C030006K11	0.0426
860	similar to RIKEN cDNA D330050P16 gene	0.0029
861	similar to RIKEN cDNA E030034P13 (predicted)	0.0226
862	similar to ring finger and WD repeat domain 1 isoform 1	0.0136
863	similar to schlafen 8	0.0006
864	similar to scotin (predicted)	0.0462
865	similar to SETA binding protein 1; SB1 (predicted)	0.0228
866	similar to Solute carrier family 23, member 2 (Sodium-dependent vitamin C transporter 2) (mSVCT2) (Na ⁺)/L-ascorbic acid transporter 2) (Yolk sac permease-like molecule 2)	0.0383
867	similar to spermine synthase	0.0042
868	similar to SPI6	0.0014
869	similar to SR rich protein (predicted)	0.0140
870	similar to TR4 orphan receptor associated protein TRA16	0.0045
871	similar to transmembrane protein induced by tumor necrosis factor alpha (predicted)	0.0042
872	similar to Ubiquitin ligase protein DZIP3 (DAZ-interacting protein 3 homolog)	0.0046
873	similar to ubiquitin carboxyl-terminal hydrolase I3	0.0082
874	similar to UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	0.0024
875	similar to WW domain containing transcription regulator 1	0.0067

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876	similar to XAP-5 protein	0.0013
877	similar to zinc finger protein 422, related sequence 1	0.0271
878	SKB1 homolog (S. pombe) (predicted)	0.0011
879	small fragment nuclease (predicted)	0.0029
880	small nuclear ribonucleoprotein E (predicted)	0.0025
881	SMC4 structural maintenance of chromosomes 4-like 1 (yeast) (predicted)	0.0047
882	SMC5 structural maintenance of chromosomes 5-like 1 (yeast) (predicted)	0.0193
883	smooth muscle alpha-actin	0.0245
884	smoothelin (predicted)	0.0294
885	SMT3 suppressor of mif two 3 homolog 2 (yeast)	0.0018
886	sodium channel associated protein 2	0.0007
887	sodium channel, voltage-gated, type III, beta	0.0487
888	sodium channel, voltage-gated, type V, alpha polypeptide	0.0251
889	sodium-dependent neutral amino acid transporter ASCT2	0.0052
890	solute carrier family 12, member 4	0.0032
891	solute carrier family 2 (facilitated glucose transporter), member 1	0.0009
892	solute carrier family 20 (phosphate transporter), member 1	0.0151
893	solute carrier family 22 (organic cation transporter), member 5	0.0298
894	solute carrier family 25 (mitochondrial adenine nucleotide translocator) member 4	0.0026
895	solute carrier family 39 (metal ion transporter), member 6 (predicted)	0.0041
896	solute carrier family 4, sodium bicarbonate transporter-like, member 11 (predicted)	0.0036
897	solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 1	0.0003
898	Solute carrier organic anion transporter family, member 3a1	0.0014
899	Sortilin 1	0.0057
900	sorting nexin 1	0.0101
901	sorting nexin 17 (predicted)	0.0111
902	SP110 nuclear body protein (predicted)	0.0083
903	Spastic paraplegia 7 homolog (human)	0.0095
904	Spermatogenesis associated, serine-rich 1	0.0266
905	spermidine/spermine N1-acetyl transferase	0.0033
906	splicing factor, arginine/serine rich 9 (predicted)	0.0082
907	splicing factor, arginine/serine-rich 3 (SRp20) (predicted)	0.0270
908	sprouty homolog 2 (Drosophila) (predicted)	0.0036
909	squalene epoxidase	0.0191
910	src associated in mitosis, 68 kDa	0.0041

911	SRY-box containing gene 11	0.0258
912	SRY-box containing gene 4 (predicted)	0.0028
913	Sterol O-acyltransferase 1	0.0054
914	striatin, calmodulin binding protein 3	0.0090
915	structure specific recognition protein 1	0.0117
916	SUMO/sentrin specific protease 3 (predicted)	0.0027
917	suppressor of cytokine signaling 6 (predicted)	0.0156
918	survival of motor neuron 1, telomeric	0.0018
919	sushi, nidogen and EGF-like domains 1	0.0119
920	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	0.0357
921	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	0.0191
922	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	0.0188
923	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1 (predicted)	0.0054
924	syndecan 1	0.0165
925	synovial sarcoma translocation, Chromosome 18 (predicted)	0.0023
926	syntaxin 6	0.0021
927	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0.0171
928	TAR DNA binding protein (predicted)	0.0372
929	Taste receptor, type 1, member 2	0.0184
930	Taste receptor, type 1, member 2	0.0467
931	TATA box binding protein-like 1 (predicted)	0.0098
932	Tax1 (human T-cell leukemia virus type I) binding protein 3 (predicted)	0.0004
933	TCF3 (E2A) fusion partner	0.0034
934	tektin 1	0.0002
935	tenascin XA	0.0458
936	tetraspan 2	0.0017
937	tetratricopeptide repeat domain 12	0.0134
938	TG interacting factor (predicted)	0.0027
939	thimet oligopeptidase 1	0.0459
940	thiopurine methyltransferase	0.0016
941	THO complex 1 (predicted)	0.0126
942	thrombomodulin	0.0282
943	Thrombospondin 2 (predicted)	0.0002
944	Thrombospondin 2 (predicted)	0.0021
945	thrombospondin, type I domain containing 6 (predicted)	0.0014

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946	thymic stromal-derived lymphopoietin, receptor	0.0312
947	thymidylate synthase	0.0092
948	thymine-DNA glycosylase	0.0042
949	thymocyte protein thy28	0.0076
950	Thymopoietin	0.0007
951	thymosin beta-like protein	0.0002
952	thymosin, beta 10	0.0001
953	thyroid hormone receptor interactor 10	0.0012
954	Tight junction protein 1 (predicted)	0.0036
955	tight junction protein 2	0.0016
956	tight junction protein 4 (peripheral) (predicted)	0.0443
957	tissue factor pathway inhibitor	0.0327
958	Tissue inhibitor of metalloproteinase 2	0.0013
959	tissue inhibitor of metalloproteinase 2	0.0011
960	tissue inhibitor of metalloproteinase 2	0.0133
961	TNFAIP3 interacting protein 2 (predicted)	0.0036
962	topoisomerase (DNA) 2 alpha	0.0037
963	topoisomerase (DNA) 2 alpha	0.0082
964	TPR domain, ankyrin-repeat and coiled-coil-containing	0.0144
965	TRAF2 binding protein	0.0002
966	trafficking protein particle complex 4	0.0029
967	transcription factor 2	0.0045
968	transcription factor-like 1 (predicted)	0.0153
969	transformation related protein 53 binding protein 1 (predicted)	0.0242
970	transformed mouse 3T3 cell double minute 2 (predicted)	0.0056
971	transforming acidic coiled coil 3	0.0267
972	transforming growth factor, beta 1	0.0118
973	Transforming growth factor, beta 2	0.0007
974	transgelin	0.0030
975	transient receptor potential cation channel, subfamily C, member 1	0.0033
976	transient receptor potential cation channel, subfamily M, member 4	0.0084
977	Translocase of inner mitochondrial membrane 8 homolog b (yeast)	0.0017
978	transmembrane 4 superfamily member 3	0.0010
979	transmembrane 7 superfamily member 1 (predicted)	0.0089
980	transmembrane protein 14A (predicted)	0.0048
981	transmembrane protein 9 (predicted)	0.0028
982	tripartite motif protein 28	0.0029
983	tripartite motif protein 3	0.0301
984	tripartite motif protein 37 (predicted)	0.0202

985	tripartite motif protein 47 (predicted)	0.0167
986	tripartite motif protein 8 (predicted)	0.0127
987	tropomodulin 3 (predicted)	0.0054
988	Tropomyosin 1, alpha	0.0019
989	tropomyosin 1, alpha	0.0028
990	Tropomyosin 1, alpha	0.0047
991	troponin T2, cardiac	0.0233
992	tryptophan rich basic protein	0.0054
993	tryptophan rich basic protein	0.0422
994	Ttk protein kinase (predicted)	0.0309
995	tubulin, alpha 1 /// tubulin, alpha 6 (predicted)	0.0032
996	tumor necrosis factor receptor superfamily, member 12a	0.0009
997	tumor protein p53	0.0301
998	TYRO3 protein tyrosine kinase 3	0.0337
999	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	0.0022
1000	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	0.0019
1001	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	0.0009
1002	tyrosine kinase, non-receptor, 2 (predicted)	0.0145
1003	U1 small nuclear ribonucleoprotein polypeptide A (predicted)	0.0143
1004	ubiquitin specific protease 43 (predicted)	0.0093
1005	ubiquitin-activating enzyme E1-domain containing 1 (predicted)	0.0341
1006	ubiquitin-associated protein 2 (predicted)	0.0062
1007	ubiquitin-conjugating enzyme E2C (predicted)	0.0299
1008	ubiquitin-like 1 (sentrin) activating enzyme E1A (predicted)	0.0098
1009	ubiquitin-like 1 (sentrin) activating enzyme E1B (predicted)	0.0137
1010	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	0.0010
1011	UDP-glucose ceramide glucosyltransferase	0.0034
1012	UDP-glucuronate decarboxylase 1	0.0010
1013	UDP-glucuronate decarboxylase 1	0.0067
1014	Unc-5 homolog B (C. elegans)	0.0112
1015	Unc-84 homolog A	0.0022
1016	Unknown (protein for MGC:72598)	0.0029
1017	Unknown (protein for MGC:72974)	0.0143
1018	Unknown (protein for MGC:73003)	0.0061
1019	UPF3 regulator of nonsense transcripts homolog A (yeast) (predicted)	0.0101
1020	uridine phosphorylase 1 (predicted)	0.0310
1021	vacuolar protein sorting 35	0.0001

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1022	vacuolar protein sorting 39 (yeast) (predicted)	0.0082
1023	vacuole Membrane Protein 1	0.0036
1024	vasodilator-stimulated phosphoprotein (predicted)	0.0042
1025	V-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	0.0056
1026	villin (predicted)	0.0046
1027	vimentin	0.0008
1028	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	0.0158
1029	von Hippel-Lindau syndrome homolog	0.0048
1030	v-ral simian leukemia viral oncogene homolog B	0.0036
1031	WD repeat domain 12	0.0206
1032	WD repeat domain 34	0.0188
1033	WD repeat domain 6 (predicted)	0.0293
1034	wingless-related MMTV integration site 7A	0.0032
1035	WNT1 inducible signaling pathway protein 2	0.0232
1036	X-ray repair cross complementing protein 4	0.0356
1037	zinc finger protein 219	0.0032
1038	zinc finger protein 265	0.0164
1039	zinc finger protein 367 (predicted)	0.0002
1040	zinc finger protein 462 (predicted)	0.0332
1041	zinc finger protein 499 (predicted)	0.0050
1042	zinc finger protein 622 (predicted)	0.0308
1043	zinc finger, CCHC domain containing 10 (predicted)	0.0220
1044	zinc finger, DHHC domain containing 7	0.0062
1045	ZW10 interactor	0.0168

[外国人研究者招へい等事業]
(萌芽的先端医療技術推進研究推進事業)

1. 研究実績報告書
2. 外国人研究者によるレポート