

Supplemental material for Bates et al. , Microarray-Based Gene Expression Profiling Identifies Novel Genes and Functional Relationships in the Adult Mouse Gastrointestinal Tract

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571 cDNAs with 2x or greater expression relative to whole postnatal day 1 mouse in any adult gastrointestinal tissue, using Incyte Mouse GEM1 cDNA microarrays

For each cDNA and tissue, values given are the average log2 of the relative expression ratio for two measurements

S, stomach; D, duodenum; J, jejunum; I, ileum; Ce, cecum; PC, proximal colon; DC, distal colon

Incyte no.	S	D	J	I	Ce	PC	DC	Genbank	Incyte description	Our identification	Rank in Fig. 1A-B	K-means class (Fig. 2)	Rank in Fig. 3	Functional class (Fig. 5)
313529		3.63	2.74	1.42				W10596	ESTs	Prolylcarboxypeptidase (angiotensinase C)	172	E	166	P
313588					1.36	1.35	1.23	W10174	ESTs	EGF receptor-like tyrosine kinase	514	Y	498	C
313859		2.61	2.72	2.28				A1605638	diacylglycerol acyltransferase	Diacylglycerol acyltransferase (same as S2)	159	M	172	M
314078	6.09	6.27						W09829	trefoil factor 2 (spasmodic protein 1)	Trefoil factor 2	534	B	45	C
315676						1.33		W09957	ESTs, Moderately similar to unnamed protein product [H.sapiens]	?	502	Z	543	U
316237			1.50	2.91		1.35	1.38	W08886	dipeptidase 1 (renal)	Dipeptidase 1	393	Q	392	P
316288		4.54	4.59	1.64				A1325330	cytochrome P450, 2b10, phenobarbital inducible, type b	Cytochrome P450, 2b10, phenobarbital inducible, type b	169	I	160	M
316805		2.23	2.00	2.00	2.05		1.24	W11325	ESTs, Weakly similar to unnamed protein product [H.sapiens]	? (related to 134?)	5	G	135	U
317466				1.20				W34061	ESTs	?	353	R	477	U
317806		1.87	2.44	1.04				W13053	microsomal triglyceride transfer protein	Microsomal triglyceride transfer protein	161	I	199	T
317894				1.63	1.71	1.64	1.95	W12956	ESTs, Highly similar to AF161509_1 HSPC160 [H.sapiens]	?	513	Y	437	U
318810					1.68			W34357	ESTs, Highly similar to UDP-GLUCOSE 4-EPIMERASE [Rattus norvegicus]	UDP-glucose 4-epimerase (same as 29)	515	Y	523	M
318922			1.29		1.70			W34507	developmentally regulated repeat element-containing transcript 3	?	362	W	417	U
329563	5.71							W42223	ESTs, Weakly similar to LY6E_MOUSE LYMPHOCYTE ANTIGEN LY-6E PRECURSOR [M.musculus]	Lymphocyte antigen LY-6E	539	A	54	U
329728		1.34						W13320	ESTs, Highly similar to 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR [Homo sapiens]	2-Oxoglutarate dehydrogenase	226	N	359	M
329866		3.92	4.52	3.22				W14138	kallikrein 3, plasma	Kallikrein 3 (same as 162)	247	I	164	I
330336				2.49	2.31	1.94	1.96	W14540	histocompatibility 2, K region	H-2, K region	354	R	434	I
330995				1.25				A1323999	ESTs, Moderately similar to CYTOCHROME P450 IVF3 [Homo sapiens]	Cytochrome P450 IVF3	68	S	475	M
331327		2.20	1.68			2.03	2.16	A1390877	ESTs, Weakly similar to RING finger protein HAC1 [M.musculus]	?	566	C	254	U
331681	1.14							W14332	ESTs, Highly similar to PTERIN-4-ALPHA-CARBONOLAMINE DEHYDRATASE [Homo sapiens; Rattus norvegicus; Mus musculus]	Dimerization cofactor of HNF-1alpha/pterin-4-alpha-carbinolamine dehydratase	556	D	90	U
331968				1.31				A1390902	cathepsin B	? (same as 532)	294	H	470	U
332091			1.32					W08172	sphingosine phosphate lyase 1	Sphingosine phosphate lyase 1	389	K	421	C
332285					3.85	3.36	4.66	W08694	carbonic anhydrase 4	Carbonic anhydrase 4	481	D	486	T
332388	1.69	1.12	1.63					W07943	ESTs, Weakly similar to Ltrpc5 protein [M.musculus]	?	9	S	211	U
332556	1.31						1.30	W08348	phenylalkylamine Ca2+ antagonist (emopamil) binding protein	Sterol isomerase	564	R	331	M
333102						1.05	1.16	W15720	synaptogyrin 2	Synaptogyrin 2/cellugyrin	491	Y	542	P
333274		1.35	1.08		2.20	1.69		W33809.1	Public domain EST (IMAGE:333274)	Public domain EST (IMAGE:333274)	437	W	246	M
333669		1.73	1.51	1.16				W17420	ESTs, Weakly similar to A49366 choline-phosphate cytidylyltransferase [M.musculus]	?	160	M	208	U
334268				1.29	1.43			W36984	ESTs	?	358	R	443	U
334273	1.56							AA052391.1	Public domain EST (IMAGE:334273)	?	553	A	69	U
335112		1.37	1.57	1.82	1.66	1.84	2.12	A1390104	Sid23p	Dextrin/cofilin	322	Y	128	S
336053		5.39	4.14	2.81				W17866	uterine-specific proline-rich acidic protein	Uterine-specific proline-rich acidic protein	145	E	157	U
336296	2.49	2.85	2.23	2.28	3.98	2.91	2.46	W36584	ESTs, Weakly similar to scaffold protein Pbp1 homolog [M.musculus]	?	475	W	7	U
336334		3.70	3.37	3.66	3.27	2.69	2.50	W18457	ESTs, Weakly similar to S14666 keratin 10, type I, cytoskeletal [H.sapiens]	?	3	S	100	U
336509		2.04	1.95	2.53	3.82	2.92	2.84	W18397.1	Public domain EST (IMAGE:336509)	Reg IV	320	V	115	U
336536		3.99	2.29	2.53				A1390951	3'-phosphoadenosine 5'-phosphosulfate synthase 2	3'-phosphoadenosine 5'-phosphosulfate synthase 2 (same as S)	299	E	249	M
336593	1.52							W20659	ESTs, Weakly similar to S113_MOUSE S100 CALCIUM-BINDING PROTEIN A13 [M.musculus]	Calcium binding protein	499	A'	70	U
336727							1.09	A1893900	fructose bisphosphatase 2	Fructose bisphosphatase 2	492	Y	567	M
337219	2.93							W20888	somatostatin	Somatostatin	544	D	56	C
337667			1.09	1.05				W18735	ESTs, Moderately similar to dJ153G14.2 [H.sapiens]	?	74	S	415	U
347906	1.36							W29916	ESTs	? (same as 84)	525	Z	80	U
348245	2.06							W18841	ESTs	?	552	A	63	U
351090		2.59	3.66	4.14	2.49			W41083	ESTs, Weakly similar to AF127035_1 calcium-activated chloride channel protein 2 [H.sapiens]	Chloride channel	34	P	140	T
351123		1.93	1.75	1.20				A1450527	molybdenum cofactor synthesis 2	Molybdenum cofactor synthesis 2	174	N	196	M
352541		1.71	1.36	1.25				W33902	ESTs	?	289	N	210	U
353094		1.59						W34856	ESTs, Highly similar to AF157028_1 protein phosphatase methyltransferase-1 [H.sapiens]	?	109	F	342	U
353215				1.25			1.52	W41682	glutamine fructose-6-phosphate transaminase 1	Glutamine fructose-6-phosphate transaminase 1	400	Y	446	M
353317		1.54	1.43					W41878	pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)	Delta 1-pyrroline-5-carboxylate synthase	162	M	302	M
353521		1.45	1.45	1.82	1.63		1.29	W40904	ESTs	?	348	R	137	U
354215	2.90							W44037.1	Public domain EST (IMAGE:354215)	Protein disulfide isomerase (same as 55)	548	D	57	P
354801							1.06	W44283	casein beta	Casein beta	442	Y	571	U
355755		1.40						W47785	ribosomal protein S6 kinase polypeptide 1	Ribosomal S6 kinase 1	208	H	352	C
355935		1.22	1.38	1.37				W48119	gene rich cluster, C3f gene	? (same as 236)	47	S	239	U
356196		2.27	3.06					W50759	heat shock protein, 84 kDa 1	Apollipoprotein C-III	178	I	270	T
367627	5.07	4.56	2.50					W54349	glutathione S-transferase, alpha 4	Glutathione S-transferase alpha 4	535	C	40	M
368189		2.33	1.51					W53913	ESTs	GATA-4 (same as 41)	122	F	269	D
372468		1.41						W61552	ESTs, Moderately similar to ladinin [H.sapiens]	Ladinin	207	H	351	S
373793	3.12			1.45	1.76	1.82	2.68	W64636	calponin 1	Calponin 1	497	Z	27	S

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374487		1.78	1.69		1.13		1.41	W65246	lactate dehydrogenase 1, A chain	Lactate dehydrogenase 1, A chain	18	G	248	M
374501				1.03				W64075	proline rich protein expressed in brain	?	395	R	482	U
374725					2.18			A1430465	ESTs, Highly similar to CARBONIC ANHYDRASE VI [Ovis aries]	Carbonic anhydrase VI	472	U	517	T
374877					1.49			W62765	histone deacetylase 1	Histone deacetylase 1 (same as 529)	457	V	530	D
385084					2.66	1.55		W64798	epithelial membrane protein 1	Tumor associated membrane protein	467	U	502	S
385341	1.06			1.02	1.05			W74865	ESTs, Highly similar to AF150733_1 AD-014 protein [H.sapiens]	Mitochondrial translocase	297	H	51	P
385729				1.52				W62231	sepin 5	Septin 5	385	Q	459	D
387459		3.00	2.17					W65788.1	Public domain EST (IMAGE:387459)	Adenosine deaminase	220	E	257	M
388288		1.67	1.48		1.95	1.21		W66635	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 10	Mitochondrial dicarboxylate carrier	303	W	247	M
390150		2.19	1.77	1.80				W70677.1	Public domain EST (IMAGE:390150)	?	43	M	187	U
400035	1.17	1.32	1.20	1.77	1.47	1.39	1.41	W77113	FK506 binding protein 4 (59 kDa)	FK506 binding protein 4 (59 kDa)	404	R	18	D
401327	2.26							W98341	keratin complex 2, basic, gene 4	Keratin complex 2, basic, gene 4	558	A	59	S
401809		1.76	1.42	1.39				W78456	ESTs	?	136	M	207	U
401906		2.50	2.76					W82161	ESTs	?	94	I	263	U
402345					1.14			W78591	protein tyrosine kinase 9	Protein tyrosine kinase 9	333	W	539	C
402667					1.70		1.59	A1425791	ESTs	?	517	V	512	U
403034				1.44				W81908	ESTs	?	204	S	464	U
403084		1.23	1.13	1.43	1.06		1.31	W81999	ESTs, Moderately similar to ZINC FINGER PROTEIN GLO3 [Saccharomyces cerevisiae]	ARF GAP family	391	R	139	P
403660					1.29	1.26	1.25	W82194	hypothetical protein, clone:2-31	Mitochondrial ATPK ATP synthase F chain	427	Y	499	M
403728	1.84	2.33	1.50					W82212	lupus nephritis-associated peptide 1	Peroxisomal phytyl-CoA alpha-hydroxylase	119	F	42	M
404339	1.39							W82690	ESTs	Carboxypeptidase D	531	Z	77	P
404499							1.32	W83104	NADH ubiquinone oxidoreductase subunit MWFE	NADH ubiquinone oxidoreductase subunit MWFE	571	Y	557	M
404550	7.05	3.28						W83072	trefoil factor 1	Trefoil factor 1	536	A	44	C
405888					1.41			W83214	ESTs	?	316	V	533	U
406218							1.73	W84060	sialyltransferase 10 (alpha-2,3-sialyltransferase VI)	Sialyltransferase 10 (alpha-2,3-sialyltransferase VI)	569	D'	550	M
408599	2.40	1.19			2.36	1.62	1.97	W85217	RNA polymerase II 3	RNA polymerase II subunit 3	433	A'	32	D
418861			1.36					W89337.1	Public domain EST (IMAGE:418861)	?	95	K	420	U
419711				2.01				W89541	ESTs, Weakly similar to SULFITE OXIDASE PRECURSOR [Rattus norvegicus]	Sulfite oxidase	419	Q	452	M
419895							1.29	W89566	ESTs, Moderately similar to unknown [H.sapiens]	?	506	Z	559	U
420085		1.52	1.20					W89796.1	Public domain EST (IMAGE:420085)	Molybdopterin cofactor sulfurase (putative)	142	N	305	M
420204		1.53	1.90					W89845	ESTs	New member of the peptidase aspartate beta hydroxylase protein family	90	I	303	P
420429				1.35				W89518	annexin A2	Annexin A2	394	R	468	U
420484	1.42							W90822	hypothetical protein 1-82	?	503	Z	74	U
420853			1.16	1.32				W90961	gene rich cluster, C3f gene	?	79	S	412	U
420975	1.28	2.17	2.04	2.01			1.21	W91135	expressed in high-metastatic cells	Expressed in high-metastatic cells	193	N	33	S
421002	1.38	1.94	1.40	1.63				A1893988	protein kinase C, delta	Protein kinase C delta (same as 24 & 26)	284	H	39	P
421150	1.27							W98974	CD24a antigen	CD24a antigen	504	Z	86	I
421714							1.47	W98963	CD9 antigen	CD9 antigen	495	X	554	C
421833		1.27			1.62	1.61	1.48	W91402	glutathione synthetase	Glutathione synthetase	440	Y	325	M
423574				1.09				W98791	ESTs, Moderately similar to T17302 hypothetical protein DKFZp564D177.1 - human [H.sapiens]	?	59	S	481	U
423605		1.43	1.51	2.08				W98919	ESTs, Highly similar to ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL X PRECURSOR (Homo sapiens)	Aldehyde dehydrogenase	58	S	227	M
425297	2.20	2.55	2.03	1.66	2.40		2.73	W99850	transmembrane protease, serine 2	Transmembrane serine protease 2	570	Y	23	P
426059		1.27						AA002845	ESTs	?	198	N	367	U
426510							1.22	AA002379	proteolipid protein (myelin)	proteolipid protein (myelin)	518	Y	563	S
427339		1.32		1.22				AA003303	tight junction protein 2	Tight junction protein 2	273	H	321	S
436935		1.24	1.64	1.25				AA002625	ESTs, Weakly similar to BACR7C10.a [D.melanogaster]	?	49	K	237	U
437209		1.17						AA003451	Mus musculus brain cDNA, clone MNC3-1429, similar to Mus musculus peroxiredoxin V (PxxV) gene	Peroxiredoxin V	118	H	382	M
437290		1.10	1.35	1.93				AA003740	membrane protein, palmitoylated (55 kDa)	?	60	P	243	U
437602			1.38	1.60				AA003725.1	Public domain EST (IMAGE:437602)	Centaurin-alpha (IP3 receptor)	61	S	408	C
438286				1.50				AA008419	ESTs, Moderately similar to pyridoxine 5'-phosphate oxidase [R.norvegicus]	Pyridoxine 5'-phosphate oxidase	471	V	528	M
438506			1.62	1.35				A1466582	DAL1P	Type II brain Protein 4.1	40	K	405	S
438749							1.06	A1466601	solute carrier family 35 (UDP-galactose transporter), member 2	solute carrier family 35 (UDP-galactose transporter), member 2	486	Y	569	T
439033		2.92	2.53					AA008240	bisphosphate 3'-nucleotidase 1	Bisphosphate 3'-nucleotidase 1	214	L	258	M
439213				1.17				A1466630.1	Public domain EST (IMAGE:439213)	?	57	S	479	U
439282				1.22				AA003979	Trk-fused gene	Trk-fused gene	251	K	428	D
439439		1.61	1.55					AA004146.1	Public domain EST (IMAGE:439439)	?	53	N	298	U
439622		1.63	1.65					AA008687	ESTs, Highly similar to THYMIDINE PHOSPHORYLASE [Homo sapiens]	Platelet-derived endothelial cell growth factor	186	L	297	C
439763		1.45	1.38	2.15	1.71			AA008579	ATP-binding cassette, sub-family G (WHITE), member 2	ATP-binding cassette, sub-family G (WHITE), member 2	6	R	151	T
439941		1.23						AA008573	ESTs	?	310	H	375	U
440038		1.13						AA009086	golgi autoantigen, golgin subfamily a, 4	Golgin-245	240	H	383	P
440344	1.41							AA011759	glutamine synthetase	Glutamine synthetase	500	A'	75	M
440879							1.24	A1552464	apyrase 1, homolog (C. lectularius)	?	403	Y	561	U
441695		1.62	1.68	2.55	2.19	2.09	1.87	AA013960	claudin 3	Claudin-3	339	R	124	S
442135		1.32	1.73	1.75				AA013528	ESTs, Highly similar to SODIUM-DEPENDENT CHOLINE TRANSPORTER [Rattus norvegicus]	Sodium-dependent choline transporter	75	K	235	T
442403		2.12	1.67	1.49				AA015351.1	Public domain EST (IMAGE:442403)	?	165	M	189	U
442856				1.45				A1894049	ESTs, Highly similar to PROTEIN KINASE C, ZETA TYPE [Mus musculus]	Protein kinase C zeta	374	Q	463	P
443798		1.56						AA014980	ESTs, Weakly similar to CYTC_MOUSE CYSTATIN C PRECURSOR [M.musculus]	?	291	N	345	U
443870	1.37							AA014127	DNA segment, Chr 15, Wayne State University 77, expressed	Keratin? (same as 50)	529	Z	79	S
444844				1.74	1.13		1.60	AA016731	basic transcription element binding protein 2	Kruppel-like factor 5 (Intestinal kruppel like factor)	396	C'	441	D
445061	1.36			1.03				A1892149	DNA segment, Chr 15, Wayne State University 77, expressed	Keratin? (same as 79)	522	Z	50	S
445088				1.35				A1892150.1	Public domain EST (IMAGE:445088)	Frizzled 5	376	Q	467	C
456716		1.54	2.21	2.44				AA023491	ESTs, Moderately similar to AMILORIDE-SENSITIVE AMINE OXIDASE [Rattus norvegicus]	Amine oxidase	246	P	218	M
457038		2.63	2.10	2.45	2.29		1.50	AA023463	semaF cytoplasmic domain associated protein 2	SemF	366	S	133	U
457253				1.33				AA023595.1	Public domain EST (IMAGE:457253)	?	375	Q	469	U

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457955		1.22	2.07	1.79				AA030193	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	Cationic amino acid transporter 7	80	J	238	T
458944		1.57						AA024255	solute carrier family 22 (organic cation transporter), member 5	Organic cation/carnitine transporter OCTN2	140	N	343	T
458948					1.51			AA024256	ESTs	?	461	V	527	U
459410		2.01	1.67					AA027420	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	ATP-binding cassette transport protein C2	179	L	280	T
459511	5.58	2.13						AA027452	ESTs	Member of an uncharacterized new protein family having casein kinase 2 phosphorylation sites and a myristoylation site	538	A	46	U
463002	1.97	2.30	1.68					AA030573	ESTs	GATA-4 (same as 269)	121	F	41	D
463200				1.42	2.44	1.81	1.59	AA030361	ESTs, Moderately similar to AF220050_1 uncharacterized hematopoietic stem/progenitor cells protein MDS030 [H.sapiens]	?	466	V	439	U
463322		1.33	1.19	1.36				A1324835	ESTs	?	44	S	233	U
463337		1.78	2.33					AA028697.1	Public domain EST (IMAGE:463337)	?	180	K	291	U
463566					2.50	1.78		AA028760	hydroxysteroid dehydrogenase-1, delta<5>-3-beta	Delta 5,3 beta hydroxysteroid dehydrogenase (same as 522)	469	U	503	M
464060	3.07	1.67	1.50	2.71	3.07	2.67	3.25	AA028346	keratin complex 1, acidic, gene 19	Keratin complex 1, acidic, gene 19	490	Y	4	S
464209				1.41				AA028406	ESTs, Weakly similar to AF148145_1 putative thymic stromal co-transporter TSCOT [M.musculus]	?	84	P	466	U
464317					1.19			AA032853.1	Public domain EST (IMAGE:464317)	?	364	R	538	U
464392					2.44	1.88		AA030116	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	439	U	504	M
464575		1.39						AA030534.1	Public domain EST (IMAGE:464575)	?	123	F	355	U
465403		1.06						AA032691	breast cancer anti-estrogen resistance 3	AND-34	69	S	389	I
466280		4.12	4.07	3.62	2.19	2.11	1.82	AA033362.1	Public domain EST (IMAGE:466280)	Claudin-15	28	M	97	S
466428		1.19	1.04					AA032386	ESTs, Weakly similar to AF121862_1 sorting nexin 13 [H.sapiens]	?	192	N	315	U
467134		1.40						AA034829	ESTs	?	104	G	353	U
468859		1.20						AA036170	transducer of ErbB-2.1	Transducer of ErbB-2.1	105	H	377	C
469019		1.23		1.56				AA036034.1	Public domain EST (IMAGE:469019)	?	269	S	322	U
472942		1.66	1.76					AA038039.1	Public domain EST (IMAGE:472942)	?	156	L	295	U
475397		1.51	1.30	1.76				A1323015	phospholipase C, beta 3	Phospholipase C beta 3	67	S	222	C
475505	1.69	2.01	1.88	1.34	1.63	1.54	1.24	AA044475	nuclear, factor, erythroid derived 2, like 2	nuclear, factor, erythroid derived 2, like 2	117	H	14	D
476205		1.90	2.04	2.26	1.83		1.58	AA050695	ESTs, Weakly similar to ASC [H.sapiens]	?	8	S	136	U
476703		1.79	1.13					A1509998	meiotic cohesin REC8	Cohesin Rec8	224	F	290	P
477158		1.81	1.26					A1510020	ESTs	Secretory carrier membrane protein 5	113	F	289	P
477559		1.86	1.82					AA048262	ESTs	?	141	K	287	U
477796		1.23						A1510031	ESTs	?	130	N	374	U
477881		1.28						AA049408	ESTs	?	138	N	365	U
477905		1.16	1.09					AA049221	DNA segment, Chr 14, University of California at Los Angeles 2	NADPH-dependent retinol dehydrogenase/reductase	177	N	316	M
477962							1.06	AA049416	histone H1	Histone H1	484	X	570	D
478710					1.53			A1385784	pleckstrin 2	Pleckstrin 2	474	W	525	S
479126		2.34	2.21	1.79	1.61			A1892115	ESTs, Moderately similar to CYTOCHROME B5, OUTER MITOCHONDRIAL MEMBRANE [Rattus norvegicus]	Cytochrome B5 outer mitochondrial membrane isoform (same as 144)	29	G	141	M
479476	1.78							AA048952	solute carrier family 4 (anion exchanger), member 2	Solute carrier family 4 (anion exchanger), member 2	524	Z	66	T
479758				2.14				AA051675	fibroblast growth factor 15	Fibroblast growth factor 15	420	O	449	C
479846		1.19						AA051480	ESTs	?	190	N	378	U
479913				1.25				AA051561	ESTs	?	85	S	476	U
480901		4.65	4.57	3.51				A1385452	solute carrier family 5, member alpha 1	Solute carrier family 5, member alpha 1	65	L	159	T
480989	1.32							AA059561	ESTs, Weakly similar to skin-specific protein [H.sapiens]	?	555	A	83	U
481204	1.40							AA064326.1	Public domain EST (IMAGE:481204)	?	541	Z	76	U
481341	7.41							A1385475	ESTs, Moderately similar to COLIPASE PRECURSOR [Rattus norvegicus]	Colipase	543	A	53	M
481507		2.16	1.86	1.94				AA060314	ESTs, Weakly similar to AF155354_1 ankyrin repeat-containing protein Asb-3 [M.musculus]	?	380	S	188	U
481641		1.20	1.52	1.38			1.23	AA060226	Max protein	Max protein (same as 242)	22	S	240	D
481956		1.90	1.57	1.91	1.14			AA059636	ESTs, Moderately similar to KIAA1319 protein [H.sapiens]	?	63	S	147	U
482136		2.26	1.95	1.95				AA059642	ESTs, Weakly similar to EP8, HUMAN EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EP8 [H.sapiens]	EGF receptor kinase substrate	258	N	184	C
482138		1.53	1.25	2.05				AA059643	ESTs, Weakly similar to T08675 hypothetical protein DKFz564F0522.1 - human [H.sapiens]	?	55	S	219	U
482328				1.31				AA060898	ESTs, Highly similar to AF151842_1 CGI-84 protein [H.sapiens]	?	399	R	471	U
483493		3.12	3.91					AA061550	retinol binding protein 2, cellular	Retinol binding protein 2	209	I	256	T
483701		2.27	2.14					A1427669	retinol dehydrogenase 7	?	170	L	271	U
483756		3.74	3.71	3.48	2.61	2.10	1.08	A1427990	ESTs	?	27	K	99	U
483777		1.67	2.21	2.03				A1552497	diacylglycerol acyltransferase	Diacylglycerol acyltransferase (same as 172)	254	J	212	M
484134		1.97						AA079969.1	Public domain EST (IMAGE:484134)	Protein phosphatase methyltransferase-1	286	F	338	P
484261	2.38							AA080232	keratin complex 1, acidic, gene 13	Keratin complex 1, acidic, gene 13	551	A	58	S
484485				1.80				AA073913	ESTs	Amnionless	245	P	454	C
492407			1.82					AA097387	ESTs, Weakly similar to T04A11.2 [C.elegans]	?	412	K	418	U
492937		2.11	3.29					AA097421	apolipoprotein A-IV	Apolipoprotein A-IV	92	I	276	T
493182		1.56	1.60					AA097486	solute carrier family 27 (fatty acid transporter), member 4	Fatty acid transport protein	201	N	300	T
493488		1.52	1.47	1.45			1.46	AA087098	ATPase, Na+/K+ transporting, beta 1 polypeptide	Na+/K+ ATPase beta 1	21	R	220	T
493555		5.01	3.63	2.14				AA087125	ESTs	Intestinal alkaline phosphatase	146	E	158	M
493604					1.27		1.18	AA087137	ESTs, Highly similar to UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.2 KD PROTEIN [Bos taurus]	Ubiquinol-cytochrome C reductase complex 7.2 kD protein	428	Y	515	P
493675			1.79	1.11				AA098356	actinin alpha 3	Alpha-actinin 3	411	E	399	S
521951		2.29	1.66	1.97				AA106263	Mus musculus putative hepatic transcription factor (Wbscr14) mRNA, complete cds	Wbscr14	260	M	181	D
522713	1.91	1.35		1.47				AA087673	Mouse (strain 129 G-Ix+) endogenous murine leukemia virus mRNA, clone E1	gag-gene like	414	H	43	U
522891	2.11							AA065888	ESTs, Moderately similar to PROACTIVATOR POLYPEPTIDE PRECURSOR [Homo sapiens]	?	550	A	62	U
523018	2.27	1.65	1.27	2.44	2.29	2.01	2.11	A1892302.1	Public domain EST (IMAGE:523018)	Tetraspanin group	521	Y	9	C
523572		2.48	1.70	1.53				A1614625.1	Public domain EST (IMAGE:523572)	?	150	M	175	U
524086		1.37	1.01	1.62	1.66	1.53	1.53	AA066250	ESTs, Weakly similar to BC-2 protein [H.sapiens]	? (same as 384)	342	R	127	U
524540		1.53	1.14					AA068440	ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Rattus norvegicus]	NADH-cytochrome b5 reductase	218	N	304	M
525119					1.98			A1892342	ESTs, Highly similar to CYSTATHIONINE GAMMA-LYASE [Homo sapiens]	Cystathionine gamma-lyase (same as 329)	332	W	520	M
532186	1.49							AA068375	diaphorase 4 (NADH/NADPH)	Diaphorase 4 (NADH/NADPH)	537	H	71	M
533117							1.32	AA068901	histidine triad nucleotide-binding protein	Histidine triad nucleotide-binding protein	482	Y	558	C
535340		1.40	1.64	1.94				AA087796	Mus musculus PDZK1 mRNA, complete cds	PDZK1	255	P	229	C
550766		2.79	2.40	2.54	2.63	2.62	2.14	A1326615	caspase 1	Caspase 1	338	R	104	P

Incyte no.	S	D	J	I	Ce	PC	DC	Genbank	Incyte description	Our identification	Rank in Fig. 1A-B	K-means class (Fig. 2)	Rank in Fig. 3	Functional class (Fig. 5)
551003				1.58				AA098196	Mus musculus anti-HIV-1 reverse transcriptase single-chain variable fragment mRNA, complete cds	?	390	Q	458	U
551016		2.53	2.68					AA080332	ESTs, Highly similar to TRANS-1,2-DIHYDROBENZENE-1,2-DIOL DEHYDROGENASE [Homo sapiens]	Estradiol 17-beta-dehydrogenase	176	I	261	M
570675		1.27						AA108640	glycerol phosphate dehydrogenase 1, cytoplasmic adult	Glycerol 3 phosphate dehydrogenase	148	L	369	M
570997		2.89	2.48	1.98				AA108438.1	Public domain EST (IMAGE:570997)	Putative N-acetyltransferase Camello 4	149	M	170	C
571334			2.32				2.09	AA108741	ESTs, Weakly similar to GLUTATHIONE S-TRANSFERASE, MITOCHONDRIAL [Rattus norvegicus]	Glutathione S-transferase	408	G	416	M
571633		1.15			1.19			AA108822	ESTs, Highly similar to TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR [Rattus norvegicus]	Mitochondrial citrate transporter	311	H	330	M
571803		2.56	2.35	2.11	2.03	1.69	1.94	A1326958	ESTs, Moderately similar to LAMBDA-CRYSTALLIN [Oryctolagus cuniculus]	Lambda-crystallin	17	G	108	U
571954		1.29	1.50	1.40				AA108340	gene rich cluster, C3f gene	? (same as 239)	50	K	236	U
572002	1.52	1.99	1.87	1.24	2.26	2.06	1.73	AA108370	glutathione S-transferase, pi 2	Glutathione S-transferase, pi 2	306	Y	16	M
572149		1.20						AA110042	RAB1, member RAS oncogene family	RAB1 GTP-binding protein	124	H	376	P
572422							2.36	AA105830	ESTs, Weakly similar to WDNM_MOUSE WDNM1 PROTEIN PRECURSOR [M.musculus]	Major epididymis-specific protein E4	429	D	547	P
572463		1.42	1.35	1.54	1.60		1.50	AA110679	ESTs	?	10	R	138	U
572510				1.17				A1893697	ESTs, Highly similar to HYPOTHETICAL_13.5_KD_PROTEIN_C45G9.7_IN_CHROMOSOME_III [Caenorhabditis elegans]	Tax interaction protein 1	397	R	478	C
572513		1.98	1.57	1.69				AA109944.1	Public domain EST (IMAGE:572513)	Myosin VIIa	64	S	192	S
572542		2.20	2.48	2.22	1.50			AA109951	beta-2 microglobulin	Beta-2 microglobulin	37	K	143	I
572613	1.65			2.87				AA109917.1	Public domain EST (IMAGE:572613)	Sulfite oxidase	418	O	49	M
572614			1.40	1.71				AA109914	aldehyde dehydrogenase 9A	Aldehyde dehydrogenase 9A	78	P	407	M
573063		2.21						AA118422	ESTs	UDP-Glucuronosyltransferase 2B12	222	E	336	M
573526				1.11			1.17	AA110654	ESTs	? (same as 318)	401	Y	447	U
573582				1.04	1.12			AA119372	ESTs, Moderately similar to KIAA0956 protein [H.sapiens]	?	337	R	444	U
574119		1.27						AA119086	ESTs	?	106	N	368	U
574245					1.47		1.14	AA111234	ESTs	?	356	Y	516	U
574395			1.20	1.59				AA119577	ESTs	?	388	R	411	U
574792	3.03	2.48	2.38	2.04	3.34	2.96	2.99	AA120639	ESTs, Moderately similar to GST3_HUMAN MICROSMAL GLUTATHIONE S-TRANSFERASE 3 [H.sapiens]	Glutathione S-transferase 3	431	Y	5	M
574894		1.92	1.70	1.26	2.24	1.70	1.41	AA120757	ectonucleoside triphosphate diphosphohydrolase 5	Ectonucleoside triphosphate diphosphohydrolase 5	328	W	117	M
575397		1.25	1.30	2.86		2.89	3.17	AA119293	small inducible cytokine A6	C10/small inducible cytokine A6	392	C	156	C
575773			2.88	5.03		1.28		AA123026	rat generating islet-derived, mouse homolog 3 gamma	Pancreatitis-associated protein 3	242	O	394	C
575776		1.33						AA120429.1	Public domain EST (IMAGE:575776)	?	191	N	362	U
576076		1.33	1.55	1.78				AA124593	solute carrier family 31, member 1	Solute carrier family 31, member 1 (same as 225)	73	S	232	T
576157		1.63						AA119804	ESTs	?	301	B	341	U
576931							1.95	AA116528	ESTs, Moderately similar to syncollin [R.norvegicus]	Syncollin	509	X	548	P
577021	5.83	5.01	4.18	1.45	1.66	3.26	1.83	AA124355	ESTs, Weakly similar to RoBo-1 [R.norvegicus]	?	533	C	2	U
577109		1.18						AA124476	ESTs, Highly similar to AF163314_1 putative N-acetyltransferase Camello 1 [M.musculus]	N-acetyltransferase Camello 1 (putative)	230	H	381	M
577555					2.11	1.48		AA138025	Mus musculus brain cDNA, clone MNCb-3763, similar to AC004410 fos39554_1 [Homo sapiens]	? (same as 521)	477	V	507	U
577567	1.25							AA139179.1	Public domain EST (IMAGE:577567)	?	417	H	87	U
577698		2.06	1.93	2.39	2.11	1.95		AA140530	ESTs, Weakly similar to Mdes protein [M.musculus]	? (same as 118)	359	R	131	U
577837							1.18	AA122846	ESTs	CTL1 protein	446	Y	564	T
578436		1.46			1.38			A1893710	ESTs, Highly similar to 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING [Sus scrofa]	Phosphogluconate dehydrogenase	308	H	328	M
579339		2.49	1.97	2.00	2.53	1.68	1.56	AA122896	solute carrier family 22 (organic cation transporter), member 1-like	ITM	363	B	110	T
579349		1.89	1.99					AA124202	epoxide hydrolase 2, cytoplasmic	Epoxide hydrolase 2 (same as 265)	211	I	285	M
579391	3.39	1.64			3.63	2.81	3.20	AA122925	carbonic anhydrase 2	Carbonic anhydrase 2	432	A	31	M
579523			1.13	1.84				AA124612	ESTs, Highly similar to HYPOTHETICAL_PROTEIN_C2257.01C_IN_CHROMOSOME_1 [Schizosaccharomyces pombe]	Aminopeptidase P	257	P	414	P
579570					1.58		1.78	AA122975	aldehyde dehydrogenase 2, mitochondrial	Aldehyde dehydrogenase 2	441	X	513	M
579608		1.01						AA116661	ESTs	?	199	H	390	U
579970		1.10						AA137517	syntaxin binding protein 2	Syntaxin binding protein 2	241	H	387	P
580000					1.36	1.21	1.29	AA122471	ESTs, Weakly similar to IAP3_MOUSE INHIBITOR OF APOPTOSIS PROTEIN 3 [M.musculus]	?	445	Y	497	U
580166	1.34							AA138018	ESTs, Moderately similar to HSPC007 [H.sapiens]	?	561	Z	81	U
580381		1.57						AA137688	ESTs	?	14	S	344	U
580505					1.73	1.17		AA137748	Sid470p	Sid470p/p22	454	V	509	C
580715							1.58	AA145865	lymphocyte antigen 6 complex	Lymphocyte antigen 6 complex	483	X	552	C
581126		1.38	1.35					AA140078	solute carrier family 22, member 1	Organic cation transporter	309	H	310	T
582668		1.72	1.38	1.31				A1645355	lysophosphatidic acid phosphatase	Lysophosphatidic acid phosphatase (same as 223)	133	N	209	M
583571		4.03	3.54	3.33				AA144047.1	Public domain EST (IMAGE:583571)	?	135	M	163	U
583638					1.21			AA144013	aminolevulinatase synthase H	Aminolevulinatase synthase H	307	W	537	M
583684		2.37	2.13	1.28	1.80	1.45		AA144098	ESTs, Weakly similar to ORF_YKR092c [S.cerevisiae]	?	304	G	130	U
583759	2.13							A1326760	proprotein convertase subtilisin/kexin type 3	Proprotein convertase subtilisin/kexin type 3	540	D	61	P
595881		2.52						A1586232	RFG	Nuclear receptor coactivator	114	E	333	C
596027	1.59							AA137485	ESTs	?	559	D	68	U
596230		1.62	1.38	1.51				AA122440	ESTs, Weakly similar to TNF-inducible protein CG12-1 [H.sapiens]	?	134	N	216	U
596277		1.30						AA122720	zinc finger protein 103	?	288	H	364	U
596348		1.74	1.71					AA122814	aldehyde dehydrogenase family 1, subfamily A4	Aldehyde dehydrogenase	231	N	293	M
596404					1.84			AA138546	Mus musculus brain cDNA, clone MNCb-3763, similar to AC004410 fos39554_1 [Homo sapiens]	? (same as 507)	479	W	521	U
596447		2.49	2.74	2.42	2.22	1.81	1.43	AA122791	histocompatibility 2, Q region locus 7	H-2, Q region locus 7 (same as 109)	33	S	111	I
596604		4.93	4.25	4.77	3.44	2.93	2.87	AA146478	IG ALPHA CHAIN C REGION	IgA (same as 92 & 93)	24	M	95	I
596893		1.31	1.17					AA145237	ESTs, Moderately similar to unnamed protein product [H.sapiens]	?	188	N	311	U
597031		2.43	2.13	2.42				AA145466	ESTs	?	86	S	176	U
598299			1.29					AA162662.1	Public domain EST (IMAGE:598299)	?	212	I	424	U
598411		2.50	1.33					AA155071	ESTs	?	120	E	264	U
599069		1.42						AA168967	ESTs	?	197	N	348	U
607469		2.65	2.85		1.43			AA172867	purine-nucleoside phosphorylase	Purine-nucleoside phosphorylase	88	K	252	M
617316		2.27	1.90	1.93				AA174320	ESTs, Weakly similar to TNF-inducible protein CG12-1 [H.sapiens]	?	200	N	182	U
617360		1.52	1.23					AA174512	ESTs	?	277	H	307	U
618201		1.13						AA175313	ESTs, Weakly similar to BC-2 protein [H.sapiens]	? (same as 127)	278	H	384	U
618271		2.34	2.11	2.63				AA175329	histocompatibility 2, class II antigen A, beta 1	H-2, class II antigen A, beta 1	203	S	179	I

Incyte no.	S	D	J	I	Ce	PC	DC	Genbank	Incyte description	Our identification	Rank in Fig. 1A-B	K-means class (Fig. 2)	Rank in Fig. 3	Functional class (Fig. 5)
618272				1.65				AA175651	caspase 11	Caspase 11	398	Q	457	P
619141		2.01	2.42	2.48		1.54	2.72	AA175618	ESTs, Weakly similar to GARG-16 [M.musculus]	Interferon-induced protein w/tetratricopeptide repeats	565	C'	154	U
619728	1.51	2.73	2.08	1.85	2.98	1.57	1.74	AA175984	ESTs	New member of the adenosyl homocysteine protein family	365	B'	17	M
619746	1.29							AA172768	ESTs	? (same as 80)	526	Z	84	U
619836				1.14				AA177872	ESTs	Glutathione reductase	416	H	480	M
619845		2.32	1.51	1.49				AA172943	ESTs	Down regulatory protein of interleukin-2 receptor (same as 413)	139	M	180	D
619922		1.27						AA177731	ESTs	?	234	N	370	U
619926		1.10						AI604148	expressed sequence tag mouse EST 25	?	275	H	386	U
620027		1.57	1.39	1.90	2.26	1.84	2.06	AA178121	cathepsin S	Cathepsin S	340	W	125	P
620195					3.21		2.58	AA177949	solute carrier family 20, member 1	Phosphate transporter	448	T	510	T
620655		6.51	6.03	6.37	6.13	5.65	5.54	AA177218	IG ALPHA CHAIN C REGION	IgA (same as 93 & 95)	1	S	92	I
620716			1.25					AI604253	ESTs, Moderately similar to A56391 lamina associated polypeptide 1C long splice form - rat [R.norvegicus]	?	54	S	425	U
621464		1.17	1.11	1.18				AA178585	ESTs	?	202	H	241	U
621483		1.24						AA178745	SEC61, gamma subunit (S. cerevisiae)	SEC61, gamma subunit	126	H	373	T
621715		1.08						AA177791	DNA segment, Chr 2, Wayne State University 58, expressed	?	223	N	388	U
621742				1.29				AA177584.1	Public domain EST (IMAGE:621742)	?	372	R	472	U
622181			1.13	1.25				AA183432	regulatory protein, T lymphocyte 1	Down regulatory protein of interleukin-2 receptor (same as 180)	253	K	413	D
622334		1.33						AA183628	ESTs	?	125	F	361	U
622702					1.35			AA177549	toll-like receptor 1	Toll-like receptor 1	463	V	535	C
633635				1.41	1.72	1.59	1.82	AA184566	caudal type homeo box 1	Cdx1	318	Y	440	D
634469		1.42						AA184958	DNA segment, Chr 14, University of California at Los Angeles 1	?	282	H	350	U
636781		1.88						AA183327	granzyme B	Granzyme B	228	L	286	I
637290		1.89	1.62	1.48				AA185869	UDP-N-acetyl-alpha-D-glucosamine (N-acetylneuraminyl) galactosylglucosyltransferase	UDP-N-acetyl-alpha-D-glucosamine (N-acetylneuraminyl) galactosylglucosyltransferase	143	N	198	M
637849		2.50	2.74	2.53	2.32	1.94	1.76	AA186012	histocompatibility 2, Q region locus 7	H-2, Q region locus 7 (same as 111)	32	S	109	I
638243	1.46							AA200339	secretory leukocyte protease inhibitor	Secretory leukocyte protease inhibitor	554	D	73	P
639502		1.84	1.54	2.08	2.27	1.57	1.37	AA200827	ESTs, Moderately similar to I53908 major vault protein - rat [R.norvegicus]	Major vault protein	349	R	119	U
639994		1.81	1.66	1.68				AA197601	ESTs	?	194	N	203	U
639998		1.28						AA197603	solute carrier family 12, member 7	Cation/chloride cotransporter KCC4 (putative)	285	H	366	T
640762		2.18	1.96	1.48	1.23			AA203975	ESTs, Moderately similar to CYTOCHROME B5, OUTER MITOCHONDRIAL MEMBRANE [Rattus norvegicus]	Cytochrome B5 outer mitochondrial membrane isoform (same as 141)	30	G	144	M
641523		1.16		1.22				AA200282	zinc finger protein 36	Tristetraprolin (RNA binding/destabilization)	262	H	323	D
641906		1.33						AA210213	ESTs, Weakly similar to CG8009 gene product [D.melanogaster]	?	221	N	360	U
642145		2.23	1.75					AA212164	ESTs, Weakly similar to similar to the protein phosphates 2c family [C.elegans]	?	100	L	274	U
642201	1.57	3.86	3.44	2.59	2.84	2.18	2.39	AA212241	ESTs, Highly similar to hypothetical protein [H.sapiens]	?	99	G	15	U
643784		1.78	1.50	1.30	1.30	1.04		AA203922	tropomodulin 3	Tropomodulin 3	87	G	132	S
644887			1.14					AA210606.1	Public domain EST (IMAGE:644887)	?	196	K	431	U
644941		2.25	2.21	1.64				AA210377	ESTs	New member of the glutathione S-transferase protein family	185	M	185	M
653161		3.30	3.10	3.51		2.32	1.77	AI390695.1	Public domain EST (IMAGE:653161)	?	20	S	153	U
658839	1.75							AA217892	hyaluronic acid-binding protein 2	Hyaluronic acid-binding protein 2	415	D	67	P
658905		1.20	1.10					AA217908	ESTs, Highly similar to ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM [Homo sapiens]	Alpha-actinin 1	175	G	313	S
660287							1.45	AA220284	glutathione S-transferase 7 (alpha-N-acetylneuraminyl 2,3-bisectinyl-1,3-N-acetylglucosaminide alpha 2,6-sialyltransferase) D	glutathione S-transferase 7 (alpha-N-acetylneuraminyl 2,3-bisectinyl-1,3-N-acetylglucosaminide alpha 2,6-sialyltransferase) D	485	X	556	M
670050		3.17	1.87		1.27			AA230588	beta-transducin repeat containing protein	?	107	E	253	U
670375		2.03						AA212146	ESTs, Highly similar to PROBABLE 3-OXOADIPATE COA-TRANSFERASE SUBUNIT B [Bacillus subtilis]	?	115	F	337	U
670658	1.12							AA230896	ESTs, Highly similar to PROBABLE 3-OXOADIPATE COA-TRANSFERASE SUBUNIT B [Bacillus subtilis]	?	532	Z	91	U
671133		2.65	2.57	1.89				AA222404	guanidinoacetate methyltransferase	Guanidinoacetate methyltransferase	163	M	171	M
671940		2.24	1.36					AA242702	transmembrane protease, serine 2	?	279	F	272	U
672659		1.12						AA231462.1	Public domain EST (IMAGE:672659)	?	129	H	385	U
676125		2.22	2.04	1.19				AA209096	nitrogen fixation gene 1 (S. cerevisiae)	NifS-like protein	171	N	186	P
676410		2.27	2.60	1.59				AA209065	ESTs, Highly similar to APOLIPOPROTEIN B-100 PRECURSOR [Homo sapiens]	Apolipoprotein B-100 (same as 178)	153	L	183	C
676523		1.56	1.20					AA209594	ESTs	?	290	N	301	U
676579		2.12	1.50					AA209061	thioredoxin reductase 1	Thioredoxin reductase 1	102	G	275	M
676900		3.90	4.58	3.49				AA212964	ESTs	Cytochrome P450	250	I	165	M
676967		2.11	2.41					AA213299	ESTs, Weakly similar to R33590_1 [H.sapiens]	?	154	I	277	U
677180		1.57	1.49	1.41	1.62			AA212899	deiodinase, iodothyronine, type I	Iodothyronine deiodinase	361	R	149	M
677592		3.07	3.17	2.32				AA212893	ESTs	?	248	L	169	U
677605		1.74	1.21					AA213017	flavin containing monooxygenase 3	Flavin containing monooxygenase 3	103	G	294	M
678740		1.44	1.44	1.04				AA237366	thymoma viral proto-oncogene	Thymoma viral proto-oncogene	157	N	226	C
678863		2.30	2.19		2.22	1.74		AA249900	ESTs, Highly similar to ES22, MOUSE LIVER CARBOXYLESTERASE 22 PRECURSOR [M.musculus]	Carboxylesterase 2	302	B'	245	M
678991		4.07	4.83	3.97				AA245959	kallikrein 3, plasma	Kallikrein 3 (same as 164)	249	J	162	I
679007		1.49	1.21	1.61				AA244622	growth factor receptor bound protein 7	Growth factor receptor bound protein 7	378	S	224	C
679163						1.32		AA245698	regulator of G-protein signaling 5	Regulator of G-protein signaling 5	487	Y	544	C
679235		1.39			1.95			AA245993	ESTs, Highly similar to CYSTATHIONINE GAMMA-LYASE [Homo sapiens]	Cystathionine gamma-lyase (same as 520)	330	W	329	M
679244	1.74	4.55	3.17		4.17	2.65	1.49	AA244536	3'-phosphoadenosine 5'-phosphosulfate synthase 2	3'-phosphoadenosine 5'-phosphosulfate synthase 2 (same as 249)	298	B'	21	M
679341		2.61	2.55	2.02				AA245672	ESTs, Weakly similar to similar to aldose 1-epimerases [C.elegans]	?	183	K	173	U
679356		1.40	1.57					AA244770.1	Public domain EST (IMAGE:679356)	?	155	K	309	U
679641							1.45	AA242192	N-terminal Asn amidase	N-terminal Asn amidase (same as 549)	511	Y	555	M
679661		3.13	3.79	4.27	2.08	1.45		AA245078	fatty acid binding protein 2, intestinal	Intestinal fatty acid binding protein 2	38	P	129	P
679895		1.80	1.88	1.54				AA238193	cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	Cell death-inducing DNA frag. factor, alpha subunit-like effector B (same as 193)	46	K	204	C
679896		2.00	2.90	3.28				AA237541	dipeptidylpeptidase 4	Dipeptidylpeptidase 4	77	P	190	P
679920		2.51	2.00					AA237592.1	Public domain EST (IMAGE:679920)	Multidrug resistance associated protein 2 (Mrp2)/canalicular multispecific organic anion transporter	147	L	262	T
680198		1.58	1.33	1.33				AA237916	ATP-binding cassette, sub-family G (WHITE), member 5	ATP-binding cassette, sub-family G (WHITE), member 5	166	N	217	T
680448		2.66	2.90	2.70	2.26	1.81	1.79	AA237173	ESTs, Highly similar to LIVER 60 KD CARBOXYLESTERASE 2 [Oryctolagus cuniculus]	Carboxylesterase	26	S	107	M
680453			1.06					AA237178	flavin containing monooxygenase 5	Flavin containing monooxygenase 5	52	S	432	M
680497		1.68						AI451845	ESTs, Moderately similar to UDSF, MOUSE LIVER G-CELLULAR G-TRANSFERASE 260 PRECURSOR [M.musculus]	?	112	H	340	U
680806	1.74	2.00	2.54	3.04	2.93	2.55	2.44	AA242626	ATPase, class I, type 8B, member 1	ATPase, class I, type 8B, member 1	334	R	12	T

Incyte no.	S	D	J	I	Ce	PC	DC	Genbank	Incyte description	Our identification	Rank in Fig. 1A-B	K-means class (Fig. 2)	Rank in Fig. 3	Functional class (Fig. 5)
680815		1.10		1.34				AA250039	lectin, galactose binding, soluble 9	Galectin-9	238	H	324	S
680958			1.35	1.19				AA241899	ESTs, Highly similar to AOFB_RAT AMINE OXIDASE [R.norvegicus]	Monoamine oxidase B	265	K	409	M
681152					1.08			AA242567	ESTs	Steroid receptor co-activator SRA	438	Y	540	D
681634				2.12				AA237829	angiogenin	Angiogenin	405	Q	450	C
681802			1.71	2.35				AA244590	glutamyl aminopeptidase	Glutamyl aminopeptidase	243	P	401	P
692325				1.27				AA260603	ESTs	?	56	S	473	U
692546	1.27							AA250615	ESTs, Weakly similar to ACYL_MOUSE ACYL-CoA DEHYDROGENASE, SHORT CHAIN SPECIFIC PRECURSOR [M.musculus]	Acyl-CoA dehydrogenase, short chain specific	560	D	85	M
692699		1.86	1.49	1.39				AA239666	ESTs, Moderately similar to PTD015 [H.sapiens]	?	31	G	200	U
692850		1.46	1.88					AA238492	cytochrome P450, 2j5	Cytochrome P450, 2j5	232	K	308	M
693045	1.04	1.52	2.47	3.14	1.87	1.69	1.73	AA397114	annexin A4	Annexin A4	387	Q	20	U
693166		1.48	1.71	1.80			1.02	AA250186	solute carrier family 31, member 1	Solute carrier family 31, member 1 (same as 232)	72	S	225	T
693234					1.42			AA397070	cathepsin B	? (same as 470)	462	V	532	U
693560		2.47						AA239254	ESTs	New member of the long chain fatty acid synthetase protein family	110	F	334	M
693565		1.20	1.28					AA239277	ESTs, Highly similar to PEROXISOMAL CARNITINE OCTANOYLTRANSFERASE [Rattus norvegicus]	Carnitine octanoyltransferase	158	K	314	M
693719		1.50	1.36	1.43				AA265095	lysophosphatidic acid phosphatase	Lysophosphatidic acid phosphatase (same as 209)	25	S	223	M
693774				1.41				AA238911.1	Public domain EST (IMAGE:693774)	?	384	R	465	U
694108		1.82	1.79	1.38				AA238875	alcohol dehydrogenase family 3, subfamily A2	Alcohol dehydrogenase family 3, subfamily A2	227	N	202	M
694133		2.13	2.65	2.87				AA239009	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	Na/H exchanger regulatory protein	41	S	145	C
694651		1.97	2.17	2.03	1.59	1.20	1.27	AA221044	histocompatibility 2, L region	H-2, L region (same as 113)	36	S	116	I
695105		2.35	2.24				2.99	AA221141	alcohol dehydrogenase 1, complex	Alcohol dehydrogenase 1	568	D'	255	M
697010				1.45				AA220699	transcobalamin 2	Transcobalamin 2	256	P	462	T
697092		2.14	2.03	2.50	1.40	1.36	1.35	AA220316	phosphatidic acid phosphatase type 2c	Phosphatidic acid phosphatase type 2c	377	S	112	M
697383							1.67	AA244806	RAB25, member RAS oncogene family	?	519	Y	551	U
697416	1.72	5.21	4.75	3.56	3.45	2.89	3.30	AA245029	DNA segment, Chr 5, Wayne State University 111, expressed	Onzin	97	L	13	U
697481					4.85	3.58	4.06	AA253908	ESTs, Weakly similar to (S)-2-HYDROXY-ACID OXIDASE, PEROXISOMAL [Spinacia oleracea]	(S)-2-hydroxy-acid oxidase (same as 487)	458	T	484	M
697537		1.86	2.33	3.50				AA250652	ESTs	?	407	V	395	U
697569	1.67			1.31	1.55	1.58	1.97	AA230924	myosin light chain, alkali, nonmuscle	Myosin light chain, alkali, nonmuscle	493	Y	28	S
697864							1.24	AA238752	peptidoglycan recognition protein	Peptidoglycan recognition protein	402	C'	560	I
697874				1.77	2.02			AA238566	caudal type homeo box 2	Cdx2	335	W	442	D
697893	1.66	1.39	2.34	1.65	1.39	1.38		AA238765	EST AA238765	?	352	R	123	U
697949			1.23					AA238899	aconitase 1	Aconitase 1	266	K	427	T
697981	3.90	3.13	2.22	2.16	1.92	2.70	1.12	AA239015	ESTs, Weakly similar to TAL6_HUMAN TUMOR-ASSOCIATED ANTIGEN L6 [H.sapiens]	?	16	G	98	U
698100								AA239437	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived)	?	325	Y	566	U
698297				1.25				AA239282	T-cell death associated gene	T-cell death associated gene	421	Q	474	C
699280					1.76	1.38	1.27	AA245545.1	Public domain EST (IMAGE:699280)	Public domain EST (IMAGE:699280)	443	V	494	U
699340	2.40							AA245373	ESTs	Proton-coupled metal-ion transport protein	108	E	335	T
699460				2.12				AA245525	Indian hedgehog homolog, (Drosophila)	Indian hedgehog	357	W	518	C
699461				1.84	2.90	2.16	2.13	AA245546	CEA-related cell adhesion molecule 1	Biliary glycoprotein 1 (same as 391)	317	V	436	S
716523	2.40			1.69				AA265488	ESTs, Highly similar to CALCIUM TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 1 [Rattus norvegicus]	Calcium ATPase	312	B'	326	T
716815	1.36	2.70	2.26	1.49				AA266387	ESTs	?	225	N	38	U
717005		1.24	1.01	1.46			1.47	AA266531	EST AA930106	?	324	Y	317	U
717095		1.59	1.37					AA266087	malate dehydrogenase, mitochondrial	?	219	L	299	U
717121		2.27	2.15	2.16	2.18		1.37	AA266040.1	Public domain EST (IMAGE:717121)	? (related to 135?)	4	S	134	U
717132		1.81			1.68			AA266229.1	Public domain EST (IMAGE:717132)	?	300	B'	327	U
717135		2.08	2.14	2.82	2.06	1.50	1.81	AA266234	claudin 7	Claudin-7	7	S	114	S
717161					1.42		1.27	AA266579	Mus musculus flavo-binding protein mRNA, complete cds	?	444	V	514	U
717208		2.78	2.99	3.47	3.70	3.61	3.94	AA404174	lectin, galactose binding, soluble 6	Galectin-6	321	Y	105	S
717457					1.99			AA403432	fibroblast growth factor binding protein 1	Fibroblast growth factor binding protein 1	473	V	519	C
717819		1.25		1.22			1.21	AA250522	ESTs	? (same as 447)	296	H	318	U
718110	1.41	1.90	1.20	1.68		1.65	1.97	AA266400	ESTs	Calcium transporter 2	567	C'	22	T
718148		1.42						AA266342	zinc finger protein 147	Estrogen-responsive zinc finger protein 147	293	H	349	D
718351		1.37						AA267699	ESTs	?	259	N	356	U
719965	2.29	2.40	2.29	2.46	1.75	1.52	1.50	AA255150	ESTs	Desmocollin-2	272	H	8	S
720380					1.45			AA261577	ESTs	?	336	W	531	U
720640		1.68		1.56				AA261454	ESTs	?	206	N	319	U
721118			1.29					AA267195	ESTs	?	189	L	423	U
721906	2.09				1.09	1.34	2.19	AA267952	calcium binding protein A6 (calcyclin)	Calcyclin/S-100 A6	498	Z	34	U
722782	3.33							AA254546	ESTs, Weakly similar to PDI_MOUSE PROTEIN DISULFIDE ISOMERASE PRECURSOR [M.musculus]	Protein disulfide isomerase (same as 57)	546	A	55	P
723038		2.34	2.08	1.31				AA254389	ESTs, Highly similar to APOLIPOPROTEIN B-100 PRECURSOR [Homo sapiens]	Apolipoprotein B-100 (same as 183)	164	L	178	C
733346		1.55	1.50	1.69	1.35			AA261327	ESTs, Moderately similar to KINESIN LIGHT CHAIN [Rattus norvegicus]	Kinesin?	42	S	150	U
733456							3.36	AA259661	gamma-glutamyl hydrolase	Gamma-glutamyl hydrolase	507	D'	545	M
734101				1.02				AA268592	transforming growth factor, beta induced, 68 kDa	Transforming growth factor, beta induced, 68 kDa	270	P	483	C
734791		2.59	2.71					AA259340	ESTs, Weakly similar to retinal short-chain dehydrogenase/reductase [M.musculus]	?	216	I	260	U
734939		1.70	1.58	1.82	1.50			AA261222	ESTs	?	360	S	148	U
736562		1.98	1.90	2.15				AA270471	sialyltransferase 4c	Sialyltransferase 4c	70	K	191	M
736992		1.75	2.21					AA271959	apolipoprotein CII	Apolipoprotein C-II	93	I	292	T
737084		2.24	2.46	1.74	1.36			AA272501	ESTs, Highly similar to ALANINE AMINOTRANSFERASE [Rattus norvegicus]	Alanine aminotransferase	132	K	142	M
737364		6.30	6.08	5.34	5.87	5.54	5.79	AA277571	polymeric immunoglobulin receptor	Polymeric Ig receptor	15	G	94	T
737669		1.79	1.71	1.87				AA277646.1	Public domain EST (IMAGE:737669)	?	379	S	205	U
737745		1.96	1.65					AA277700	ESTs	Dihydropyrimidine dehydrogenase	137	M	283	M
737803		1.99	1.56	2.57	1.49			AA277329	butyrophilin-like 2	H-2, class II antigen E beta (same as 106)	382	S	146	I
737944							1.07	AA271505	pantophysin	Pantophysin	488	X	568	U
737998	2.20	3.90	3.88	3.32	2.41	1.74	1.57	AA271522	ESTs, Weakly similar to ESTM_MOUSE LIVER CARBOXYLESTERASE PRECURSOR [M.musculus]	Carboxylesterase	131	K	10	M
738140		1.62	1.34		1.87	1.33	1.19	AA271043	ESTs	?	329	W	244	U

Incyte no.	S	D	J	I	Ce	PC	DC	Genbank	Incyte description	Our identification	Rank in Fig. 1A-B	K-means class (Fig. 2)	Rank in Fig. 3	Functional class (Fig. 5)
738239					2.24	1.50		AA271106	ESTs	?	468	U	506	U
747207		1.64	2.12	1.39				AA260409	retinol dehydrogenase type 6	Retinol dehydrogenase type 6	51	K	215	M
747350	1.83	2.01	1.26	1.55	1.96	2.36	1.92	AA268133	ESTs	?	512	Y	11	U
747378		2.84	2.75	3.63	3.38	2.76	2.94	AA272807	histocompatibility 2, class II antigen A, alpha	H-2, class II antigen A, alpha	345	R	102	I
747381				1.48				AA272812	ESTs, Weakly similar to HYPOTHETICAL 91.2 KD PROTEIN IN RP27A-SCH9 INTERGENIC REGION [Saccharomyces cerevisiae]	?	373	R	460	U
747401					3.09	1.44	2.44	AA272836	aquaporin 8	Aquaporin 8 (same as 485)	447	T	488	T
747543		1.83	2.52					AA268977	ESTs, Moderately similar to 45 kDa secretory protein [R.norvegicus]	?	181	I	288	U
747763		1.99	1.49					AA274840	ESTs	?	292	F	282	U
747875				1.71		1.59		AA261313	nuclear receptor subfamily 1, group H, member 4	RXR-interacting protein (same as 461)	343	R	445	D
748112	1.19	2.08						AA260521	uncoupling protein 2, mitochondrial	Mitochondrial uncoupling protein 2	116	F	47	M
748125		2.83	2.48	2.26	3.68	3.13	2.31	AA275042	amine N-sulfotransferase	Amine N-sulfotransferase	326	W	103	M
748132			1.70	1.21				AA260227	fatty acid amide hydrolase	Fatty acid amide hydrolase	268	K	402	M
748318		3.46	3.70	1.78				AA268120	cytochrome P450, steroid inducible 3a11	Cytochrome P450, steroid inducible 3a11	152	I	167	M
748366			1.21					AA267934	ESTs	?	76	S	429	U
748374							1.15	AA274667	ribosomal protein L21	Ribosomal protein L21	496	Y	565	D
748435	1.39							AA272859	ESTs	?	547	D	78	U
748517					1.36			AA272821	ESTs, Highly similar to PUTATIVE ADENOSINE KINASE [Saccharomyces cerevisiae]	Adenosine kinase	489	V	534	M
748569		2.37	2.32					AA269533	cytochrome P450, 2b9, phenobarbital inducible, type a	Testosterone 16-alpha-hydroxylase	215	L	268	M
748587		2.73	2.61	3.60	2.94	2.32	2.45	AA269724	histocompatibility 2, class II antigen E beta	H-2, class II antigen E beta (same as 146)	346	Q	106	I
748622				1.46				AA270183	nuclear receptor subfamily 1, group H, member 4	RXR-interacting protein (same as 445)	344	Q	461	D
748654			1.72					AA270292	leucine zipper-EF-hand containing transmembrane protein 1	EF-hand calcium binding protein (putative)	281	H	339	C
749282							1.82	AA290448	N-terminal Asn amidase	N-terminal Asn amidase (same as 555)	510	C'	549	M
749451	1.64	1.77						AA289657	ESTs, Weakly similar to S45359 polyubiquitin 10 - rat [R.norvegicus]	?	274	H	48	U
749660		6.37	5.80	6.08	5.55	4.78	4.56	AA388939	IG ALPHA CHAIN C REGION	IgA (same as 92 & 95)	2	S	93	I
751399	1.33							AA395963	ESTs	?	527	A'	82	U
760871		1.36						AA386802	ESTs, Weakly similar to T04A11.2 [C.elegans]	?	187	N	357	U
760889	1.49			1.74	2.40	2.07	2.06	AA386807	ESTs, Highly similar to UDP-GLUCOSE 4-EPIMERASE [Rattus norvegicus]	UDP-glucose 4-epimerase (same as 523)	464	Y	29	M
761062		3.25	2.87	1.43				AA387586.1	Public domain EST (IMAGE:761062)	Dopa decarboxylase (same as 174)	98	L	168	M
761578		1.38	1.29	1.93				AA272321	ESTs	?	383	R	230	U
761718					2.35	1.77	1.25	AA272023	ESTs, Weakly similar to RoBo-1 [R.norvegicus]	?	476	V	491	U
762191		1.42	2.65	4.60			2.37	AA277314	ESTs, Moderately similar to ANG3, MOUSE ANGIOGENIN-3 PRECURSOR [M.musculus]	Angiogenin-3	369	O	228	C
762210		1.31	1.46	1.52	1.21			AA277332	mitogen activated protein kinase 13	Mitogen activated protein kinase 13	381	R	152	P
762299			2.43	3.55	4.64	3.76	3.92	AA277736	CEA-related cell adhesion molecule 1	Biliary glycoprotein 1 (same as 436)	319	V	391	S
762313		1.49	1.45	2.21	2.28	1.54	1.71	AA273765	phosphodiesterase 9A	cGMP phosphodiesterase	341	R	126	C
762404		1.73	1.77	2.43	1.96	1.95	2.53	AA273366	trefoil factor 3, intestinal	Trefoil factor 3	323	C'	121	C
762483		1.55						AA274160	ESTs	?	280	H	346	U
762785	1.47							AI595057	ESTs	?	501	A'	72	U
763352	2.00							AA272458.1	Public domain EST (IMAGE:763352)	?	557	D	64	U
763424					1.38	1.40	1.98	AA272260	cysteine-rich protein 2	Cysteine-rich protein 2-smooth muscle lim protein transcription factor	494	X	496	D
763553		1.19						AA285513	ESTs, Weakly similar to CG8195 gene product [D.melanogaster]	NADH dehydrogenase subunit 2	367	R	379	M
764473			1.20	1.64				AA274099	ESTs, Weakly similar to ZIP-kinase [M.musculus]	?	371	R	410	U
764542		2.47	2.45					AA274030	epoxide hydrolase 2, cytoplasmic	Epoxide hydrolase 2 (same as 285)	210	I	265	M
765107		2.02	1.61					AI510251.1	Public domain EST (IMAGE:765107)	Inositol triphosphate receptor	213	L	279	C
765660	1.19							AA275228	ESTs, Highly similar to TRAM PROTEIN [Canis familiaris]	Tram protein	542	H	88	P
766102					1.52			AA275581	ESTs, Weakly similar to steroidogenic acute regulatory protein [R.norvegicus]	?	490	U	526	U
766441			1.18					AA278024	ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II [Caenorhabditis elegans]	Solute carrier family 25	98	K	430	T
766467		1.52	1.68					AA275673	ESTs, Highly similar to ASPARTOACYLASE [Homo sapiens]	?	182	K	306	U
766582			1.24					AA274682	glutathione S-transferase, alpha 3	Glutathione S-transferase, alpha 3	413	F	426	M
766704			1.45	1.16				AA275564	glycerol kinase	Glycerol kinase (same as 400)	271	J	406	M
774877			1.49					AA386758	ESTs	?	264	J	419	U
776007	2.20							AA285921	major urinary protein 2	Major urinary protein 2	549	D	60	U
776058			1.97	1.84				AA276085	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	81	J	398	T
776133	1.63	1.83	1.45	1.79	1.47		1.85	AA276110	cadherin 1	Cadherin 1	295	H	25	S
776543		2.41	2.21					AA275871	solute carrier family 2 (facilitated glucose transporter), member 2	Glucose transporter	89	L	267	T
776770			1.66	2.12				AA273497	solute carrier family 3, member 1	Neutral and basic amino acid transporter (NBAT)	83	P	403	T
777018			2.23	2.10				AA276440	selenoprotein P, plasma, 1	Selenoprotein P, plasma, 1	82	J	397	U
777059					1.71			AA276254	hydroxysteroid dehydrogenase-4, delta⁵-3-beta	Delta 5,3 beta hydroxysteroid dehydrogenase (same as 503)	470	U	522	M
777306		2.35	2.00	2.44				AA276959	Mouse germline Ig-lambda chain gene, J3-C3-J1-C1 cluster, J3 region	IgG	11	S	177	I
777349		1.83	1.99		1.76			AA276928	ESTs	?	305	G	250	U
777379			3.28	3.75		3.20		AA277040	ESTs	?	409	P	393	U
777393		1.40						AA276697	interferon regulatory factor 1	Interferon regulatory factor 1	283	H	354	D
777583	1.43	2.05	1.69	1.90	1.43	1.34		AA276844	protein kinase C, delta	Protein kinase C delta (same as 26 & 39)	235	H	24	P
779373					2.75	2.35	1.45	AA414831	hypoxia induced gene 1	Hypoxia induced gene 1 transcription factor	434	U	490	D
779711				2.37				AA414632	cyclin-dependent kinase-like 2 (CDC2-related kinase)	Cyclin-dependent kinase-like 2 (CDC2-related kinase)	422	O	448	C
780111					2.13	1.51	1.58	AA414751	ESTs, Highly similar to brain acyl-CoA synthase II [R.norvegicus]	Acyl-CoA synthase II	460	V	492	M
790532		1.96	2.12	1.83				AA290390	cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	Cell death-inducing DNA frag. factor, alpha subunit-like effector B (same as 204)	45	K	193	C
790721		1.32						AA388435	peroxisomal sarcosine oxidase	Peroxisomal sarcosine oxidase	151	N	363	M
793537		1.15	1.32	1.26				AA415602	Max protein	Max protein (same as 240)	23	S	242	D
803510					3.80	2.18	2.74	AA473153	ESTs, Weakly similar to (S)-2-HYDROXY-ACID OXIDASE, PEROXISOMAL [Spinacia oleracea]	(S)-2-hydroxy-acid oxidase (same as 484)	459	T	487	M
803600				1.66				AA422752.1	Public domain EST (IMAGE:803600)	?	370	P	456	U
804722		2.55	2.05	1.28				AA474389	dopa decarboxylase	Dopa decarboxylase (same as 168)	217	N	174	M
805250		2.43	1.28					AA473306	xanthine dehydrogenase	Xanthine oxidoreductase (same as 259)	168	E	266	M
807018	1.28			1.33	1.77	1.58	2.02	AA404083	ESTs, Weakly similar to HC1 ORF [M.musculus]	?	516	Y	30	U
807543			1.30					AA413050	ESTs	?	233	K	422	U

Incyte no.	S	D	J	I	Ce	PC	DC	Genbank	Incyte description	Our identification	Rank in Fig. 1A-B	K-means class (Fig. 2)	Rank in Fig. 3	Functional class (Fig. 5)	
808315	1.17							AA433039	ESTs	?	530	Z	89	U	
818313		1.36						AA435123	ESTs, Weakly similar to ZK1058.5 [C.elegans]	?	314	F	358	U	
818508		1.42		1.25				AA434955	catenin alpha 1	Alpha-catenin 1	239	H	320	S	
820155		1.25						AA423143	sialyltransferase 8 (alpha-2, 8-sialyltransferase) A	Alpha-2, 8-sialyltransferase	128	G	372	M	
820157		4.31	3.85	2.41				AA423144	arginase type II	Arginase type II	173	L	161	M	
831744		1.44						AI549713	ESTs, Highly similar to GLYCOPROTEIN 25L PRECURSOR [Canis familiaris]	?	229	N	347	U	
833469		2.00	1.36					AA432689	uteroglobin	?	276	H	281	U	
834291		2.24	1.43					AA413296	ESTs	Esterase/phospholipase	111	F	273	M	
834900		1.35	1.37					AA467249	ESTs	?	252	K	231	U	
837565				1.86	1.42	1.46	1.57	AA432818	ESTs	?	355	R	435	U	
846064					1.57	1.09	1.28	AA416246	peripheral myelin protein, 22 kDa	Peripheral myelin 22 kDa protein Gas-3	465	Y	495	S	
846560		1.83	1.90	1.95				AA433576	ESTs	?	195	S	201	U	
846965		1.18						AA433727	ESTs, Weakly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Glycine max]	?	12	G	380	U	
850164		3.18	3.26	3.79	2.00	2.88	2.88	AA451385	ESTs, Moderately similar to ACTIN-LIKE PROTEIN 14D [Drosophila melanogaster]	Actin-like protein 2	19	S	101	S	
850178	1.04	1.77	1.47	1.89	1.19		1.28	AA451403.1	Public domain EST (IMAGE:850178)	Protein kinase C delta (same as 24 & 39)	236	H	26	P	
850354					1.50			AA451208	histone deacetylase 1	Histone deacetylase 1 (same as 530)	456	V	529	D	
850418		1.32	1.46	1.68				AA451269	guanine nucleotide binding protein, alpha 11	Guanine nucleotide binding protein, alpha 11	39	S	234	C	
850717	3.67	4.11	3.76	2.75	4.39	4.80	4.98	AA451058	ESTs, Highly similar to OIT1_MOUSE ONCOPROTEIN INDUCED PROTEIN 1 [M.musculus]	?	423	X	3	U	
850931		1.25						AA462270	ESTs	?	287	H	371	U	
851593							1.22	AA500704	ESTs	?	520	Y	562	U	
864414		1.90	2.90	2.07				AA458171.1	Public domain EST (IMAGE:864414)	?	48	J	197	U	
871020					1.23	1.37	1.69	AA462323	ESTs, Highly similar to NADH:UBIQUINONE OXIDOREDUCTASE B14 SUBUNIT [Bos taurus]	NADH-ubiquinone oxidoreductase B14 subunit	424	Y	501	M	
871565			3.52	2.77				AA462202	BP-3 alloantigen	ADP-ribosyl cyclase 2	263	J	396	M	
872869							1.54	AA466432	S100 calcium binding protein A1	S100 calcium binding protein A1	430	X	553	U	
872986		1.94	1.80	1.71				AA466235	ESTs	?	205	N	195	U	
873502		1.63	4.70	6.60		3.86		AA473899	pancreatitis-associated protein	Pancreatitis-associated protein 1	368	O	155	U	
873690		1.95	1.60	1.47				AA475121	pyruvate kinase liver and red blood cell	Pyruvate kinase	184	N	194	M	
873849					2.08			AA471960	DNA segment, Chr 2, Wayne State University 88, expressed	Cubilin	244	P	451	C	
873928		2.73	1.63					AA472074	xanthine dehydrogenase	Xanthine oxidoreductase (same as 266)	167	E	259	M	
873973	1.99							AA472164	tissue inhibitor of metalloproteinase 3	tissue inhibitor of metalloproteinase 3	545	D	65	P	
874356		1.65	1.83					AA474934	ESTs	?	91	L	296	U	
875684					1.92		1.33	AA475387	ESTs, Weakly similar to unnamed protein product [H.sapiens]	?	450	W	511	U	
876446				1.79				AA475902	ESTs, Weakly similar to unknown [S.cerevisiae]	?	386	S	455	U	
888512	5.89	4.95	4.38	4.47	4.82	4.02	5.17	AA497620	small proline-rich protein 2A	Small proline-rich protein 2A	528	Z	1	S	
888602				1.98				AA498630	suppressor of initiator codon mutations, related sequence 1 (S. cerevisiae)	Claudin 2	406	Q	453	S	
888687		2.10	1.53					AA498757	ESTs	?	101	G	278	U	
888707	1.08	3.76	2.92	1.78	5.07	4.10	3.94	AA498773	crp-ductin	Crp-ductin	436	U	19	U	
888820					3.95	1.65	3.44	AA498131	aquaporin 8	Aquaporin 8 (same as 488)	449	T	485	T	
889295					3.02	2.67	1.53	AA498281	lamin B1	Lamin B1	453	U	489	S	
889440				3.66	5.02	4.63	4.62	AA498457	guanylate cyclase activator 2 (guanylin 2, intestinal, heatstable)	Guanylin	315	V	433	C	
889659					1.55			AA498312	ESTs, Highly similar to S-ADENOSYLMETHIONINE SYNTHETASE GAMMA FORM [Rattus norvegicus]	Methionine adenosyltransferase 2A	455	U	524	M	
889753			1.64	2.35				AA498410	phosphodiesterase 9A	Phosphodiesterase 9A	410	Q	404	M	
890429					1.91	1.30		AA509566	esterase 1	Carboxylesterase	478	U	508	M	
890444	1.74	1.31	1.58				1.51	AA509565	T-cell specific GTPase	T-cell specific GTPase	562	H	36	P	
890915					2.26	1.58		AA511029	peroxisome proliferator activated receptor gamma	Peroxisome proliferator activated receptor gamma	435	U	505	C	
891261					1.28			AA510877	aldo-keto reductase	?	327	W	536	U	
902264		1.52	1.38	1.40				AA516913	ESTs, Weakly similar to CG1534 gene product [D.melanogaster]	?	144	N	221	U	
903822	2.32	2.33	2.21	2.69				AA521545	ESTs, Moderately similar to GALECTIN-2 [Homo sapiens]	Galectin family member	237	N	37	S	
904618	2.95	4.20	3.20	4.44	2.42	2.51	4.34	AA518112	chloride channel calcium activated 3	Calcium-activated chloride channel 3	563	C'	6	T	
904685	1.18				1.39	1.59	1.62	AA521593	ESTs, Highly similar to Y274_HUMAN HYPOTHETICAL PROTEIN KIAA0274 [H.sapiens]	?	425	Y	35	U	
904900	3.28				3.11			AA519027	myelin and lymphocyte protein; T-cell differentiation protein	Myelin and lymphocyte protein/T-cell differentiation protein	523	A'	52	P	
905403							2.67	AA529046	insulin-like 5	Insulin-like 5	508	D'	546	C	
917776							1.92	AA497742.1	Public domain EST (IMAGE:917776)	?	505	Z	541	U	
917949		1.65	1.37	1.63				AA499756.1	Public domain EST (IMAGE:917949)	?	261	M	214	U	
920211		2.79						AA500296	solute carrier family 39 (iron-regulated transporter), member 1	Iron-regulated transport protein 1	313	E	332	T	
920215		1.42	1.30		1.64			AA500298	mitochondrial carrier homolog 2	Mitochondrial carrier homolog 2	311	W	251	M	
920425		2.10	2.34	2.17	1.87	1.48	1.49	AA538511	histocompatibility 2, L region	H-2, L region (same as 116)	35	S	113	I	
920516					1.29	1.33	1.57	AA541842	interferon gamma receptor	Interferon gamma receptor	426	Y	500	C	
920524		1.86	2.04	2.38	2.14	1.73	1.71	AA541888	ESTs, Weakly similar to Mdes protein [M.musculus]	?	347	R	118	U	
922088					1.47	4.29	3.49	2.72	AA512372	carbonic anhydrase 1	Carbonic anhydrase 1	451	U	438	M
922096		1.78	1.60	2.85	2.04	1.83	1.74	AA512376	serine protease inhibitor, Kazal type 4	Serine protease inhibitor, Kazal type 4	351	Q	120	P	
922126		1.66	1.69	1.85				AA512402	ESTs, Highly similar to CYTOCHROME P450 IVF3 [Homo sapiens]	Cytochrome P450 IVF3	71	S	213	M	
934500		1.77	2.00	1.83				AA536624	ESTs, Highly similar to ERB3_RAT ERBB-3 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR [R.norvegicus]	ErbB-3 receptor protein tyrosine kinase	66	S	206	C	
935463			1.76	1.23				AA543155	glycerol kinase	Glycerol kinase (same as 406)	267	K	400	M	
935570		1.66	1.62	2.27	2.04	1.84	1.55	AA543573	f-box and WD-40 domain protein 4	Fbw4/dactylin	350	R	112	P	
948567		1.22	1.17					AA544713	synaptonemal complex protein 3	?	127	F	322	U	
948845		1.94	2.23					AA544859.1	Public domain EST (IMAGE:948845)	?	13	G	284	U	
949241					2.03	1.72	1.15	AA544904	ESTs	New member of the Ras association domain protein family	452	V	493	C	
949710		4.14	3.95	3.71	2.31	1.70	2.72	AA537426	ESTs, Weakly similar to HuEMAP [H.sapiens]	?	62	M	96	U	