

SNP RS ID	Normal Tissue Major Allele Count	Normal Tissue Minor Allele Count	Tumor Tissue Major Allele Count	Tumor Tissue Minor Allele Count	Normal Tissue Major Allele	Normal Tissue Minor Allele	Tumor Tissue Major Allele	Tumor Tissue Minor Allele	P Value	Amino Acid Change	Definition
1124	37	19	19	1	g	a	g	a	0.00779175	S->N	surfactant protein-C
2660	14	14	30	8	a	g	g	a	0.01076851	R->G	gb AAA39858.1 2--5- oligoadenylate synthetase
2791	78	2	54	6	c	t	c	t	0.00020622	R->H	heat shock protein 75 [Homo sapiens]
3271	154	20	60	0	t	g	t		0.00562385	K->R	unnamed protein product [Homo sapiens]
3273	175	1	50	2	g	c	g	c	0.0016873	R->R	sp Q9Z204 ROC_MOUSE Heter
4574	83	63	16	12	t	c	t	c	0	V->A	proteasome (prosome, macropain) subunit, beta type, 7 [Homo sapiens]
4591	126	58	57	9	c	t	c	t	0.00202668	R->K	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein);
4652	72	46	14	10	c	a	a	c	0.04001459	P->H	mitogaligin [Homo sapiens]
4731	144	9	22	2	a	g	a	g	0	K->R	squalene synthase [Mus musculus]
4864	30	3	23	9	g	c	g	c	0.0379944	V->L	unknown [Homo sapiens]
4893	71	1	31	5	a	g	a	g	0.01418482	I->V	gb AAC51730.1 hematopoietic neural membrane protein
6979	24	16	17	3	a	g	a	g	0.03504075	V->A	Similar to hypothetical protein 24432 [Homo sapiens]
7089	33	25	22	10	c	t	t	c	0.01184025	S->L	unknown [Homo sapiens]
7251	39	15	28	20	g	c	g	c	0.03530654	E->D	Unknown (protein for MGC:15293) [Homo sapiens]
7323	62	20	45	5	g	c	g	c	0.01978454	V->L	gb AAA21873.1 transcription factor IIIA
7338	101	19	39	15	a	g	a	g	0.01750799	H->R	HSPC254 [Homo sapiens]
7391	112	14	205	13	c	g	c	g	0.016094	A->G	unnamed protein product [Homo sapiens]
7462	56	28	51	9	c	t	c	t	0.003002	P->L	Similar to hypothetical protein FLJ20643 [Homo sapiens]
7501	18	8	14	0	g	t	g		0.02031443	R->L	homeotic protein pG2 - human
7567	21	11	37	7	g	t	g	t	0.01155307	C->F	Unknown (protein for IMAGE:3922955) [Homo sapiens]
7824	28	8	18	0	c	t	c		0.02908346	A->V	sp P50238 CRP1_HUMAN Cysteine-rich protein 1 (Cysteine-rich intestinal protein) (CRIP)
7915	25	5	22	16	a	c	a	c	0.01688577	Q->P	MPFYVE [Homo sapiens]
7917	29	15	30	2	g	a	g	a	0.00298339	T->I	gb AAH07654.1 AAH07654 Similar to NIF3 (Ngg1 interacting factor 3, S.pombe homolog)-like 1
7975	49	21	6	0	g	a	a		0.001354	E->K	gb AAB96392.1 glutathione transferase Zeta 1
8388	38	26	37	7	c	t	c	t	0.00105044	V->I	gb AAH32631.1 DC13 protein [Homo sapiens]
8424	177	1	126	4	g	t	g	t	0.00012622	G->V	similar to ribosomal protein L38, cytosolic [validated]
8623	46	6	47	1	c	t	c	t	0.04280441	P->L	unnamed protein product [Homo sapiens]

8875	61	17	27	15	g	c	g	c	0.03190049	V->L	sp O95298 N4BM_HUMAN NADH-ubiquinone oxidoreductase subunit B14.5b (Complex I-B14.5b)
9014	50	6	38	0	c	g	c		0.03987689	P->A	ER-localized type I transmembrane adaptor precursor
9078	12	10	30	9	c	a	c	a	0.04614203	P->Q	TBC1 domain family, member 3; Rab GTPase-activating protein PRC17; prostate cancer gene 17 [Homo sapiens]
9260	29	17	27	5	g	a	g	a	0.02486536	V->M	Homo sapiens major histocompatibility complex, class II, DQ alpha 1 (HLA-DQA1), mRNA
9276	71	13	86	6	g	a	g	a	0.01862335	R->Q	gb AAA63221.1 light chain
9419	75	75	11	3	c	a	a	c	0.02820037	A->E	Unknown (protein for MGC:27221) [Homo sapiens]
9888	123	1	51	3	c	t	c	t	9.76E-05	S->F	Homo sapiens ATP synthase
10618	37	25	11	5	g	a	a	g	0.0297166	R->H	Chain A, Human 3alpha-Hsd Type 3 In Ternary Complex With Nadp And Testosterone
10684	107	5	65	12	g	a	g	a	2.44E-06	R->K	Similar to fusion, derived from t(12;16) malignant liposarcoma [Mus musculus]
10827	278	1	156	4	c	t	c	t	5.88E-06	L->F	gb AAH01032.1 AAH01032 ribosomal prot
10954	219	22	127	2	c	g	c	g	0.00293151	P->P	60S RIBOSOMAL PROTEIN L7
11474	70	26	9	7	a	t	t	a	0.01784279	Q->L	Chain A, Human 3alpha-Hsd Type 3 In Ternary Complex With Nadp And Testosterone
11695	27	5	10	8	c	t	c	t	0.02483176	R->C	gb AAK38615.1 AF293076_1 putative magnesium transporter [Homo sapiens]
11959	121	1	47	3	c	g	c	g	4.97E-05	P->A	gb AAH04441.1 AAH04441 Similar to po
12064	233	1	140	3	a	t	a	t	0.00221356	K->K	similar to 60S RIBOSOMAL PROTEIN L17 (L23) (AMINO ACID STARVATION-INDUCED PROTEIN)
12702	39	5	27	11	a	g	a	g	0.03130994	S->P	gb AAH19262.2 Unknown (protein for MGC:2632)
12841	100	4	50	12	c	g	c	g	2.33E-10	P->R	unnamed protein product [Homo sapiens]
13003	266	37	133	32	c	t	c	t	0.0050521	A->T	gb AAA69923.1 60S ribosomal protein
13021	62	4	31	15	a	g	a	g	5.15E-14	S->G	gb AAB48304.1 pinin [Homo sapiens]
13105	78	2	65	7	t	a	t	a	8.99E-05	V->D	Homo sapiens karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
13269	61	3	38	6	c	t	c	t	0.00522807	S->L	unknown [Homo sapiens]
13294	20	14	24	10	a	g	g	a	0.01021057	S->G	gb AAB88082.1 extracellular matrix protein 1
13441	52	6	27	12	g	a	g	a	0.00942524	V->I	hypothetical protein [Homo sapiens]
13571	59	22	42	6	g	c	g	c	0.02504702	C->S	ribosomal protein L2 [Homo sapiens]
13807	217	1	121	3	c	t	c	t	0.0012455	T->I	ubiquitin-like protein fubi and ribosomal protein S30 precursor; FBR-MuSV-associated ubiquitously expressed gene; ubiquitin-like-S30 fusion protein;
13963	24	10	6	2	a	g	g	a	0.02205029	S->G	The C-Type Lectin Carbohydrate Recognition Domain Of Human Tetranectin

14009	295	3	183	9	c	a	c	a	3.30E-07	P->Q	sp P47914 RL29_HUMAN 60S riboso
14292	198	1	82	2	t	c	t	c	0.01503636	L->R	gb AAK95214.1 AF402840_1 40S ribosomal protein S29 [Ictalurus punctatus]
14408	86	72	52	16	c	t	c	t	0.0003252	T->M	sp Q01629 IFM2_HUMAN Interferon-induced transmembrane protein 2 (Interferon-inducible protein 1-8D)
14602	195	1	138	4	a	g	a	g	0.00011558	K->E	similar to ribosomal protein L38, cytosolic [validated]
17570	22	20	8	0	c	t	c		0.01090177	L->F	Homo sapiens peptidase D [synthetic construct]
17587	21	17	16	0	g	a	g		0.00061037	R->H	proteasome endopeptidase complex (EC 3.4.25.1) - human
25679	32	4	12	10	c	a	c	a	0.00375539	Q->K	Homo sapiens CD68 antigen (CD68), mRNA
180828	18	12	21	13	a	g	g	a	0.04516615	M->V	similar to 5133400C09Rik protein [Homo sapiens]
218741	231	14	198	5	g	a	g	t	0.0005492	N->K	unnamed protein product [Homo sapiens]
323835	160	48	89	43	g	a	g	a	0.010265	A->T	unnamed protein product [Homo sapiens]
343320	39	1	37	4	c	t	c	t	0.0030322	H->Y	(Ca(2+)-dependent phospholipid scramblase 1) (Erythrocyte phospholipid scramblase) (MmTRA1b)
404970	20	4	6	2	g	a	a	g	0.00461196	V->I	sp P02538 K2CA_HUMAN Keratin, type II cytoskeletal 6A (Cytokeratin 6A) (CK 6A) (K6A keratin)
409447	25	15	16	8	g	c	c	a	7.22E-06	E->Q	gb AAH07488.1 AAH07488 Unknown (protein for MGC:15057) [Homo sapiens]
449000	46	18	10	10	g	t	t	g	0.04352415	S->I	gb AAH07488.1 AAH07488 Unknown (protein for MGC:15057) [Homo sapiens]
452623	74	12	8	6	c	t	c	t	0.01497384	P->L	hypothetical protein DKFZp434K1323.1 - human (fragment)
470428	30	6	22	0	t	c	t		0.04812291	T->A	gb AAA35412.1 haptoglobin
482967	227	91	141	79	c	t	c	t	0.01768314	R->Q	unnamed protein product [Homo sapiens]
562047	71	5	14	6	c	g	c	g	0.00811993	D->E	Chain A, Heat-Shock 70kd Protein 42kd Atpase N-Terminal Domain similar to dJ612B15.1 (novel protein similar to 60S ribosomal protein L17 (RPL17)) [Homo sapiens]
566334	220	2	122	8	c	t	c	t	2.38E-10	E->K	
621679	17	17	6	0	a	g	g		0.02629938	T->A	gb AAA59534.1
644706	30	4	36	2	a	g	a	t	0.0505794	S->G	similar to Keratin, type I cytoskeletal 14 (Cytokeratin 14) (K14) (CK 14) [Homo sapiens]
699597	251	1	119	2	c	g	c	g	0.02814168	A->A	similar to ribosomal protein L14; 60S ribosomal protein L14 [Homo sapiens]
701564	38	6	30	12	g	a	g	a	0.00525697	R->H	MHC class II HLA-DQ-beta-1
701829	83	20	81	8	g	a	g	a	0.01382636	V->M	MHC class II antigen HLA-DR-beta 1 [Homo sapiens]
704839	24	4	60	24	a	g	a	g	0.00019939	E->G	unnamed protein product [Mus musculus]
707908	98	62	81	55	g	c	c	g	7.53E-07	E->Q	MHC class I [Pongo pygmaeus]

707910	130	19	32	0	g	a	g		0	R->K	The nucleotide sequence of A*0215N is the same as that of A*0207 except for a single nucleotide substitution which resulted in a stop codon in
707955	55	5	14	8	t	c	t	c	0.00391482	Y->H	gb AAA59693.1 MHC class II DR-beta-1
707957	31	26	16	6	a	c	a	t	0.00028515	Y->S	major histocompatibility class II antigen [Homo sapiens]
708637	64	32	19	1	t	g	t	g	0.00599797	I->S	similar to CG13176-PA [Homo sapiens]
708638	63	6	47	11	g	c	g	c	0.00584627	E->D	unknown [Homo sapiens]
709932	60	12	15	9	g	a	g	a	0.0256751	R->H	alpha-1-antitrypsin
713031	126	39	31	6	g	t	g	t	0	A->S	MHC class I Patr-B*06
713032	83	56	27	11	a	t	a	t	0	Y->F	gb AAA52665.1 transplantation antigen
829867	23	11	12	6	a	g	g	a	0.01505119	K->E	unnamed protein product [Homo sapiens]
856093	13	1	2	0	c	t	t		0.025	A->V	pot. ORF VI [Homo sapiens]
857663	61	23	19	19	c	t	t	c	0.0090904	P->L	similar to HC6 [Homo sapiens]
859208	68	2	6	2	g	c	g	c	0.04740523	Q->H	TPA: aflatoxin B1-aldehyde reductase; AFAR [Homo sapiens]
1042117	46	18	26	2	t	a	t	a	0.01630623	F->Y	sp P04440 HB2P_HUMAN HLA class II histocompatibility antigen, DP(W4) beta chain precursor pir
1042133	58	6	20	8	g	c	g	c	0.01849535	E->D	sp P04440 HB2P_HUMAN HLA class II histocompatibility antigen, DP(W4) beta chain precursor pir
1042136	55	3	14	4	a	c	a	c	0.04318901	I->L	sp P04440 HB2P_HUMAN HLA class II histocompatibility antigen, DP(W4) beta chain precursor pir
1042140	29	27	16	4	a	g	a	g	0.01866591	K->E	sp P04440 HB2P_HUMAN HLA class II histocompatibility antigen, DP(W4) beta chain precursor pir
1042335	34	34	51	21	t	c	c	t	0.00050685	I->T	sp P04440 HB2P_HUMAN HLA class II histocompatibility antigen, DP(W4) beta chain precursor pir
1042434	56	28	62	18	c	g	c	g	0.04372402	A->A	antigen HLA DAalpha
1042917	34	14	10	6	g	a	a	g	0.01540968	R->H	collagen alpha 2(VI) chain precursor, long splice form
1043446	54	10	14	10	a	c	a	c	0.00966383	I->L	NADP-dependent retinol dehydrogenase short isoform
1043478	36	9	23	9	g	t	g	a	0.01798218	G->E	AG02 [Homo sapiens]
1043758	41	3	20	6	t	g	t	g	0.04688606	Y->D	AG1 [Homo sapiens]
1043886	44	6	34	14	a	c	a	c	0.00027905	Q->P	hypothetical protein FLJ12118 [Homo sapiens]
1044184	46	2	2	2	c	a	c	a	0.02499954	H->N	Homo sapiens quinolinate phosphoribosyltransferase
1044641	60	2	37	7	a	c	a	c	2.05E-06	T->P	glyceronephosphate O-acyltransferase [Homo sapiens]
1044921	31	21	25	7	t	c	c	t	0.00056116	W->R	Williams Beuren syndrome chromosome region 20C isoform 1 [Homo sapiens]
1044928	26	24	24	4	g	a	a	g	0.00072366	V->M	Williams Beuren syndrome chromosome region 20C isoform 1 [Homo sapiens]

1044929	30	28	18	6	c	t	t	c	0.01684539	R->C	gb AAH07488.1 AAH07488 Unknown (protein for MGC:15057) [Homo sapiens]
1045141	51	5	44	0	c	a	c		0.03990486	H->Q	gb AAH28904.1 chromosome 12 open reading frame 10 [Homo sapiens]
1045320	41	23	7	3	c	t	t	c	0.03753045	R->W	similar to hypothetical protein [Homo sapiens]
1045321	32	30	10	2	t	c	t	c	0.03325891	W->R	Unknown (protein for MGC:15165) [Homo sapiens]
1045323	32	30	10	2	g	a	g	a	0.03325891	W->*	Unknown (protein for MGC:15165) [Homo sapiens]
1045576	51	12	47	5	c	t	c	g	0.00099863	L->L	hypothetical protein [Homo sapiens]
1045587	61	11	48	16	c	t	c	t	0.03266068	A->V	Unknown (protein for MGC:52000) [Homo sapiens]
1045656	67	1	32	4	g	a	g	a	0.04355622	E->K	LYST-interacting protein LIP4 [Homo sapiens]
1045944	89	1	49	5	g	a	g	a	1.16E-08	E->K	gb AAH09866.1 AAH09866 Unknown (protein for MGC:16393) [Homo sapiens]
1046097	27	17	14	8	a	g	g	a	0.03425831	M->V	gb AAH09670.1 AAH09670 tubulin, gamma 2 [Homo sa
1047291	27	7	30	0	a	c	a		0.00865981	Y->S	light chain of factor I [Homo sapiens]
1048030	346	18	137	13	g	t	g	t	0.03631074	C->F	laminin receptor homolog [Homo sapiens]
1048889	58	2	29	5	c	t	c	t	0.0481164	P->L	gb AAL85336.1 AF478457_1 ATP-dependent RNA helicase [Homo sapiens]
1049100	22	10	24	2	g	a	g	a	0.02351043	V->I	Chain B, Crystal Structure Of A Human Insulin Peptide-Hla-Dq8 Complex
1049330	87	21	23	13	c	g	c	g	0.02401379	R->G	similar to RIKEN cDNA 1810060K07 [Mus musculus]
1049336	357	26	295	11	t	g	t	g	0.0268688	L->W	ferritin, heavy polypeptide 1 [Homo sapiens] emb CAA25086.1 apoferritin H chain [Homo sapiens]
1049431	103	21	36	20	c	g	c	g	0.00020145	A->G	sp Q15388 OM20_HUMAN Mitochondrial import receptor subunit TOM20 homolog (Mitochondrial 20 kDa outer membrane protein)
1049453	103	17	40	18	t	c	t	c	0.00025435	V->A	Chain A, Solution Nmr Structure Of The Mitochondrial Protein Import Receptor Tom20 From Rat In A Complex With A Presequence Peptide Derived From Rat Aldehyde Dehydrogenase (Aldh)
1049475	106	18	43	18	c	t	c	t	0.00097298	P->L	Similar to RIKEN cDNA 1810060K07 gene [Xenopus laevis]
1049825	36	4	12	10	t	c	c	t	0.0002162	I->T	Chain A, Role Of Ethe Mobile Loop In The Mehanism Of Human Salivary Amylase
1049874	40	36	24	6	g	a	g	a	0.00573682	V->I	sp Q13510 ASAH_HUMAN Acid ceramidase precursor
1050043	175	5	79	7	g	a	g	a	0.00255238	R->K	Homo sapiens CD63 antigen (melanoma 1 antigen) [synthetic construct]
1050118	99	38	94	52	g	a	g	a	0.03561508	V->M	gb AAA59847.1 exons 2-8
1050147	100	5	112	12	c	t	c	t	0.0104475	A->V	MHC class I antigen [Homo sapiens]
1050180	190	40	214	26	g	a	g	a	0.00768133	V->M	gb AAA59847.1 exons 2-8
1050241	139	25	139	11	g	a	g	a	0.00739801	V->M	gb AAA70051.1 histocompatibility antigen
1050329	96	2	70	4	c	t	c	t	0.04140365	S->F	gb AAA36396.1 ORF

1050379	83	71	24	14	c	t	c	t	0	H->Y	HLA-B*40 [Homo sapiens]
1050408	128	2	68	4	c	t	c	t	0.00573141	P->L	short heat shock protein 60 Hsp60s2 [Homo sapiens]
1050450	121	51	57	43	c	t	c	t	0.00384339	P->L	glutathione peroxidase [Homo sapiens]
1050654	135	87	41	33	c	a	a	c	0.00493145	R->S	HLA class I histocompatibility antigen, B-35 B*3504 alpha chain precursor
1051147	232	8	142	16	a	c	a	c	2.04E-06	H->P	PNAS-101 [Homo sapiens]
1051334	25	13	35	8	t	g	t	g	0.03542484	S->A	Similar to transmembrane 4 superfamily member 3
1051474	13	7	15	1	t	c	t	c	0.0409883	H->R	gb AAG43365.1 AF153415_1 chromosome 9 open reading frame 5 [Homo sapiens]
1051648	30	20	28	6	c	t	c	t	0.0181296	R->C	gb AAF36166.1 AF151080_1 HSPC246 [Homo sapiens]
1052056	45	7	19	11	c	t	c	t	0.01248956	L->F	Putative alpha-mannosidase C20orf31 precursor
1052643	36	6	19	11	c	t	c	t	0.02113361	S->F	hypothetical protein DKFZp434N0810.1 - human (fragment)
1053490	71	5	53	11	c	g	c	g	0.00065611	R->G	Homo sapiens glycoprotein, synaptic 2
1053534	20	2	11	7	t	c	c	t	0.00061092	V->A	Unknown (protein for MGC:57796) [Homo sapiens]
1053683	129	3	51	7	c	t	c	t	5.84E-07	S->F	gb AAD21026.1 divalent cation tolerant protein CUTA [Homo sapiens] emb CAB63779.1
1054392	58	2	4	4	g	a	a	g	0.00113199	E->K	sp Q14807 KF22_HUMAN Kinesin-like protein KIF22 (Kinesin-like DNA-binding protein) (Kinesin-like protein 4)
1056120	15	11	15	7	c	g	g	c	0.04811461	L->V	Nuclear envelope pore membrane protein POM 121 (Pore membrane protein of 121 kDa) (P145)
1056814	53	15	21	1	t	c	t	c	0.04546644	I->V	gb AAK15585.1 AF228708_1 DiGeorge syndrome critical region 6-like protein [Homo sapiens]
1056818	52	20	20	0	c	g	c		0.00373748	L->V	gb AAK15585.1 AF228708_1 DiGeorge syndrome critical region 6-like protein [Homo sapiens]
1058060	419	5	326	8	a	c	a	c	0.03980429	K->N	Similar to tumor protein, translationally-controlled 1 [Homo sapiens]
1058143	47	29	34	8	c	t	c	t	0.01277052	T->M	hypothetical protein XP_211052 [Homo sapiens]
1058718	19	1	2	0	g	a	a		0.01298701	E->K	gb AAA60208.1 pregnancy-specific beta-1-glycoprotein 4
1058953	369	16	153	17	c	g	c	g	0.00013886	R->G	60S ribosomal protein L13A
1059135	85	53	61	56	t	c	t	c	0.03870555	I->T	LOC339047 protein [Homo sapiens]
1059228	280	11	149	19	c	g	c	g	3.23E-07	L->V	similar to ribosomal protein L18a, cytosolic [validated]
1059454	87	3	190	2	a	c	a	t	0.01067519	T->P	C-terminal propeptide domain [Homo sapiens]
1059558	60	2	23	10	g	a	g	a	0.00032023	G->S	similar to Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-alpha) (RAG cohort protein 1)
1059569	37	13	12	0	t	a	t		0.04271166	F->Y	MHC class II antigen [Homo sapiens]
1059632	155	19	95	49	g	t	g	t	1.11E-16	A->S	MHC class I antigen [Pan troglodytes]

1059688	188	25	62	2	g	t	g	t	0.03411588	V->L	gb AAA30421.1 calpactin I
1059699	80	10	141	32	g	c	g	c	0.00208385	V->L	MHC class II HLA-DR2 [Homo sapiens]
1059828	35	9	6	4	g	a	a	g	0.01720242	S->L	cell division cycle 2-like 1 (PITSLRE proteins) isoform 9; cell division cycle 2-like 1; PITSLRE protein kinase alpha; [Homo sapiens]
1059834	254	3	144	12	a	g	a	g	3.36E-14	E->G	gb AAA61182.1 prothymosin alpha1
1060126	29	9	8	8	t	g	t	g	0.04449227	F->V	HDCMA39P [Homo sapiens]
1060556	227	15	102	16	a	c	a	c	0.00095102	T->P	similar to ribosomal protein L10a [Mus musculus]
1061520	75	29	8	4	a	g	g	a	0.00843388	K->E	Similar to succinate dehydrogenase complex, subunit A, flavoprotein (Fp) [Homo sapiens]
1061543	245	1	118	2	c	t	c	t	0.03022626	L->F	similar to ribosomal protein L30 [Bos taurus]
1062368	274	9	132	18	a	c	a	c	7.81E-10	T->P	ribosomal protein L10a [Homo sapiens]
1062390	250	8	125	12	g	a	g	a	0.00013707	E->K	alpha-tubulin (partial)
1062403	172	4	113	13	a	c	a	c	1.43E-09	T->P	gb AAA84382.1 elongation factor 1 delta
1062413	27	17	10	2	a	g	g	a	0.00613402	M->V	similar to Protein pM5 precursor [Homo sapiens]
1062422	278	12	135	11	c	t	c	t	0.04014005	S->F	gb AAA69923.1 60S ribosomal protein
1062425	196	4	104	12	t	a	t	a	1.42E-10	L->Q	similar to ribosomal protein L37a, cytosolic [validated]
1062438	297	27	165	27	c	t	c	t	0.0042147	S->F	gb AAA69923.1 60S ribosomal protein
1062482	62	2	55	7	g	c	g	c	0.00022929	S->T	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2; thermostable phenol sulfotransferase; phenolic-metabolizing (P) form of PST
1062713	117	7	80	18	a	g	a	g	5.18E-08	K->R	Homo sapiens jumping translocation breakpoint
1063087	40	4	12	6	c	a	c	a	0.02343849	D->E	unknown protein [Homo sapiens]
1063108	240	7	128	9	g	a	g	a	0.00859497	E->K	60S RIBOSOMAL PROTEIN L7
1063323	22	12	14	8	g	a	a	g	0.02638209	A->T	Chain B, Crystal Structure Of A Human Insulin Peptide-Hla-Dq8 Complex
1063607	135	1	94	6	a	c	a	c	7.36E-10	T->P	cytokeratin 18 (232 AA) [Homo sapiens]
1063730	231	2	73	3	c	t	c	t	0.00356374	P->L	similar to basic transcription factor 3
1064682	63	1	52	4	a	c	a	c	0.00078106	T->P	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3; thermolabile phenol sulfotransferase;
1064728	222	13	92	26	c	g	c	g	4.88E-15	L->V	sp P02433 RL32_HUMAN 60S ribosomal protein L32
1064792	283	7	183	11	a	c	a	c	0.00318039	V->G	Very hypothetical protein
1064823	201	74	92	54	t	a	t	a	0.0065125	S->T	tubulin, alpha 4; tubulin alpha 4 [Mus musculus] ref NP_005991.1 tubulin, alpha 1
1065037	289	4	183	9	c	t	c	t	7.40E-05	R->*	sp P47914 RL29_HUMAN 60S riboso
1065059	4	4	10	2	t	g	t	c	0.02287582	W->R	H.sapiens (HC15-1) DNA for immunoglobulin heavy chain variable region.

1065411	33	11	16	10	c	g	g	c	0.00223727	N->K	Chain A, Ligand-Free Human Glutathione S-Transferase M1a-1a
1065718	277	64	173	67	a	g	a	g	0.00030111	I->V	alpha-tubulin (partial)
1071645	36	32	22	8	a	g	a	g	0.03016978	M->V	PHP; putative heart protein [Homo sapiens]
1071649	158	28	27	15	c	a	c	a	0.00020512	L->I	gb AAA59847.1 exons 2-8
1071650	116	49	28	6	t	g	t	g	0	Y->D	HLA-Cw*0801 [Homo sapiens]
1071739	60	59	11	4	c	t	t	a	0.00074456	S->F	HLA-Cw*0801 [Homo sapiens]
1071743	83	39	28	6	a	c	a	g	7.72E-05	I->L	unnamed protein product [Homo sapiens]
1071759	112	5	184	0	g	a	g		0.0042564	R->K	MHC class II HLA-DR2 [Homo sapiens]
1126557	72	4	46	6	a	g	a	g	0.04428472	D->G	Similar to succinate dehydrogenase complex, subunit A, flavoprotein (Fp) [Homo sapiens]
1126599	87	8	57	12	t	c	t	c	0.00768518	Y->H	Similar to succinate dehydrogenase complex, subunit A, flavoprotein (Fp) [Homo sapiens]
1126605	37	9	24	0	g	a	g		0.01694074	E->K	gb AAH35220.1 similar to complement component
1126687	110	4	66	6	g	a	g	a	0.02680079	G->S	succinate dehydrogenase flavoprotein subunit [Macaca fascicularis]
1126821	39	9	20	12	t	a	t	a	0.03748958	L->M	gamma-catenin [Homo sapiens]
1127233	8	2	14	8	a	c	c	a	0.02393964	R->S	gb AAK56861.1 AF286113_1 transmembrane mucin MUC13 [Homo sapiens]
1127618	123	5	25	9	g	t	g	t	0.00025149	W->L	sp O14957 UCRY_HUMAN Ubiquinol-cytochrome C reductase complex 6.4 kDa protein (Complex III subunit XI)
1127787	46	10	20	0	g	a	g		0.03730336	G->R	mitochondrial ribosomal protein S35; MDS023 protein; mitochondrial ribosomal protein S28 [Homo sapiens]
1128362	55	7	6	4	c	t	c	t	0.03417189	H->Y	Rab9 effector p40 [Homo sapiens] emb CAB09808.1 p40 [Homo sapiens]
1128625	258	16	153	20	c	g	c	g	0.00137447	R->G	Unknown (protein for MGC:20328) [Homo sapiens]
1128814	127	7	35	3	c	a	c	a	0	Q->K	gb AAH32717.1 MUM2 protein [Homo sapiens]
1129923	41	7	26	0	g	a	g		0.04091461	G->S	hypothetical protein FLJ20442 [Homo sapiens]
1129957	27	24	34	12	g	c	g	c	0.00541635	E->Q	MHC class II HLA-DQ-alpha chain
1129963	40	18	33	29	g	a	g	a	0.00836295	A->T	MHC class II HLA-DQ-alpha chain
1130409	54	42	12	4	t	g	g	t	0.01529244	D->E	The Crystal Structure Of The Human Dna Repair Endonuclease Hap1 Suggests The Recognition Of Extra-Helical Deoxyribose At Dna Abasic Sites
1130426	63	45	11	3	c	t	t	c	0.0079681	T->M	sp P38117 ETFB_HUMAN Electron transfer flavoprotein beta-subunit (Beta-ETF)
1130653	108	1	66	12	c	t	c	t	0	S->F	glycyl tRNA synthetase [Homo sapiens]
1130729	78	16	18	10	a	g	a	g	0.02439119	N->S	carboxyl terminal LIM domain protein [Homo sapiens]
1130732	28	6	40	2	c	t	c	t	0.03107253	S->F	unnamed protein product [Homo sapiens]

1130760	11	5	22	2	g	a	a	g	0.00010019	G->S	T cell secreted protein
1130863	130	63	158	33	c	g	c	g	6.68E-06	S->C	gb AAA59847.1 exons 2-8
1130993	184	4	166	10	a	c	a	c	0.00110577	H->P	apolipoprotein J precursor
1130995	93	16	91	25	g	a	g	a	0.03818013	E->K	MHC class I antigen Mamu B*06
1131000	108	22	116	12	a	c	a	c	0.02394553	R->S	MHC class I antigen Mamu B*06
1131119	110	33	23	13	c	t	c	t	0	T->I	gb AAA59847.1 exons 2-8
1131165	100	34	14	14	c	g	c	g	0.00745082	L->V	gb AAA19928.1 HLA-B71 variant
1131525	302	2	200	6	t	c	t	c	6.33E-05	M->T	gb AAC52278.1 non-muscle myosin light chain 3
1131665	32	10	21	15	a	g	a	g	0.04797272	Q->R	gb AAB80686.1 interferon regulatory factor 7A [Homo sapiens]
1132128	36	2	12	4	a	g	a	g	0.04953931	E->G	hypothetical protein [Homo sapiens]
1132182	42	2	18	10	c	g	c	g	0.00080806	R->G	sp Q9NPD3 RR41_HUMAN Exosome complex exonuclease RRP41 (Ribosomal RNA processing protein 41) (p12A)
1136480	81	42	51	51	t	c	t	c	0.0008341	V->A	Unknown protein product CIT987SK-A-589H1_1 splice form 1 [Homo sapiens]
1136581	131	5	34	2	c	g	c	g	0	R->G	proteasome activator 28-beta; MCP activator, 31-kD subunit; 11S regulator complex beta subunit;
1136633	71	25	135	19	c	t	c	t	0.00011746	T->M	class II histocompatibility antigen HLA-DR beta-1 chain precursor (clone LS1.1.1) - human
1136692	89	35	30	0	c	a	c		0.00016461	A->D	unnamed protein product [Homo sapiens]
1136695	98	54	21	16	g	a	g	a	0	M->I	unnamed protein product [Homo sapiens]
1136791	62	14	46	8	a	g	a	c	0.00142903	K->E	MHC class II antigen [Bos taurus]
1136795	28	18	19	11	t	g	g	t	0.02292948	S->A	Chain B, Crystal Structure Of Staphylococcal Enterotoxin H In Complex With Human Mhc Class Ii
1136903	103	67	115	37	c	t	c	t	0.00016353	P->L	unnamed protein product [Homo sapiens]
1136949	178	35	172	13	a	g	a	g	0.00059052	I->V	MHC class I antigen [Homo sapiens]
1137127	157	19	126	32	g	a	g	a	0.00013494	R->K	MHC class I antigen [Homo sapiens]
1137160	135	34	130	13	g	c	g	c	0.00108031	K->N	MHC class I antigen [Homo sapiens]
1138693	22	12	16	2	c	t	c	t	0.04742779	P->L	Similar to RIKEN cDNA 0610039C21 gene [Homo sapiens]
1139496	67	1	43	5	g	a	g	a	2.74E-07	S->N	interferon, alpha-inducible protein (clone IFI-15K);
1139915	147	1	64	4	t	g	t	g	1.64E-07	M->R	gb AAB50544.1 spermidine/spermine N-acetyltransferase
1139971	25	3	14	0	g	a	a		1.29E-08	V->I	gb AAH01821.1 Kangai 1 [Homo sapiens]
1140343	20	8	30	28	c	a	c	a	0.00103457	H->Q	human leukocyte antigen-DQ beta chain [Homo sapiens]
1200709	21	9	14	4	a	c	c	a	0.00141418	N->K	unnamed protein product [Homo sapiens]
1260794	24	4	8	4	c	t	t	c	0.0018141	R->S	hypothetical protein (L1H 3- region) - human

1264457	65	37	12	8	t	c	c	t	0.02937716	R->G	major histocompatibility complex, class I, E precursor; HLA class I histocompatibility antigen, E alpha chain
1286275	32	2	6	4	g	a	g	a	0.01668921	P->L	similar to putative p150 [Homo sapiens]
1701296	133	105	84	52	c	a	a	c	4.01E-05	T->M	Similar to nitrogen fixation gene 1 (S. cerevisiae, homolog)
1785323	57	15	35	3	c	t	c	t	0.04887397	P->L	similar to HC6 [Homo sapiens]
1794256	32	20	62	12	g	a	g	a	0.00010112	P->T	similar to nuclear pore complex interacting protein
1801046	29	11	13	11	c	t	t	c	0.02302258	S->L	gb AAA51851.1 human complement C1r
1804905	38	6	14	10	c	g	c	g	0.00942086	T->R	ZP3 [Homo sapiens]
1823684	324	1	201	3	g	t	g	t	0.00272478	G->S	similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens]
2067051	28	11	10	2	g	a	a	g	0.00096648	V->I	unnamed protein product [Homo sapiens]
2073495	24	8	47	6	c	g	c	g	0.02374438	D->E	neutrophil lactoferrin
2152281	393	1	200	2	g	a	g	a	0.0376778	P->L	similar to ribosomal protein L13a; 60S ribosomal protein L13a; 23 kD highly basic protein [Homo sapiens]
2157680	103	25	78	8	c	g	c	g	0.01794169	N->K	MHC class I antigen [Homo sapiens]
2227351	25	17	20	10	g	a	a	g	0.01777093	R->C	similar to hypothetical protein FLJ20958 [Homo sapiens]
2229498	48	10	30	0	a	g	a		0.01156033	Q->R	sp P10124 PGSG_HUMAN Secretory granule proteoglycan core protein precursor (Platelet proteoglycan core protein)
2229780	47	15	10	10	c	t	t	c	0.02273476	T->M	GP50 [Cricetulus griseus]
2229781	47	15	10	8	c	t	t	c	0.01120432	T->M	put. serine protease inhibitor
2229782	45	15	10	8	c	t	t	c	0.01362951	T->M	put. serine protease inhibitor
2230061	32	8	12	10	c	t	c	t	0.02689449	R->W	cathepsin S [Homo sapiens]
2230231	23	9	43	2	c	a	c	a	0.00048787	A->D	sp P59665 DEF1_HUMAN Neutrophil defensin 1 precursor (HNP-1) (HP-1) (HP1) (Defensin, alpha 1)
2235587	61	25	18	2	t	c	t	c	0.04968602	H->R	Similar to proteasome (prosome, macropain) inhibitor subunit 1 (PI31) [Homo sapiens]
2255607	14	12	7	1	c	t	t	c	0.04162875	G->S	KIAA1279 protein [Homo sapiens]
2275848	38	14	12	0	t	g	t		0.03696459	D->A	gb AAP35828.1 ninjurin 1 [Homo sapiens]
2289247	22	20	20	6	c	t	c	t	0.0270264	V->M	E2IG3 [Homo sapiens]
2290766	41	5	3	1	g	c	c	g	0.01021277	G->R	gb AAL85336.1 AF478457_1 ATP-dependent RNA helicase
2293079	36	6	28	0	c	t	c		0.04000874	P->L	unnamed protein product [Homo sapiens]
2295322	34	34	14	0	a	g	g		0.00021937	R->G	CDA04 [Homo sapiens]
2419108	39	7	8	6	c	t	t	c	0.00302166	V->I	sp Q14692 BMS1_HUMAN Ribosome biogenesis protein BMS1 homolog
2430028	127	1	51	3	g	t	g	t	6.91E-05	P->T	similar to ribosomal protein S26 [Mus musculus]
2507990	60	30	18	7	a	t	t	a	0.00050083	E->V	MHC class I protein HLA-C heavy chain

2523956	155	19	95	49	c	a	c	a	1.11E-16	A->S	MHC class I antigen [Pan troglodytes]
2598303	23	15	28	4	t	c	t	c	0.00876356	D->G	similar to retinitis pigmentosa 9 homolog; Pim-1 associated protein [Homo sapiens]
2732417	71	1	6	2	c	t	c	t	0.02453749	P->L	similar to putative methyltransferase [Homo sapiens]
2767468	30	26	8	2	a	g	g	a	0.04268392	W->R	gb AAH09938.1 AAH09938 Unknown (protein for MGC:12647) [Homo sapiens]
2767471	31	18	4	0	c	a	a		0.02498079	A->S	gb AAH09938.1 AAH09938 Unknown (protein for MGC:12647) [Homo sapiens]
2848157	14	6	38	3	g	a	g	c	6.80E-05	G->D	gb AAA58993.1 immunoglobulin kappa chain
2986576	36	17	4	0	c	t	t		0.01515152	A->T	similar to KIAA1273 protein [Homo sapiens]
3087615	69	3	37	5	c	a	c	a	0.01260584	E->D	Unknown (protein for MGC:20582) [Homo sapiens]
3087989	399	5	355	9	c	a	c	a	0.03331404	V->F	gb AAM82753.1 BJ-HCC-24 tumor antigen [Homo sapiens]
3168891	48	2	2	2	c	a	c	a	0.02324103	S->R	unnamed protein product [Homo sapiens]
3176950	31	24	23	9	a	g	g	a	0.00698811	K->R	gb AAA36312.1 SB-beta chain
3177751	59	47	11	5	c	t	t	c	0.04216303	T->M	sp P38117 ETFB_HUMAN Electron transfer flavoprotein beta-subunit (Beta-ETF)
3177809	63	1	4	2	c	t	c	t	0.01753745	A->V	sp P46695 EX1_HUMAN Radiation-inducible
3179039	12	2	2	0	t	c	c		0.05	I->T	pregnancy-specific glycoprotein beta-1 precursor - human
3179218	25	15	8	0	t	a	t		0.03679394	F->Y	MHC class II antigen HLA DR52 [Homo sapiens]
3179771	67	13	87	5	g	a	g	a	0.00527909	R->Q	lymphocyte antigen
3180263	183	2	41	3	t	c	t	c	0.0002398	F->S	similar to heterogeneous nuclear ribonucleoprotein C (C1/C2) [Homo sapiens]
3180956	55	3	28	8	c	t	c	t	0.01352378	S->F	Probable ribosome biogenesis protein NEP1 (C2f protein)
3180961	264	51	214	18	t	g	t	g	0.00051614	F->L	acidic ribosomal phosphoprotein PO [Bos taurus]
3188792	281	5	108	6	c	g	c	g	0.00426836	R->G	similar to 60S ribosomal protein L15 [Mus musculus]
3189320	29	1	2	2	c	t	t	c	0.03008021	A->V	gb AAB31966.1 antiquitin [Homo sapiens]
3191517	109	2	42	6	a	c	a	c	2.65E-08	T->P	gb AAB94642.1 deoxyuridine triphosphate nucleotidohydrolase precursor [Homo sapiens]
3193130	237	2	143	5	g	a	g	a	0.00069717	E->K	similar to ribosomal protein S12 [Bos taurus]
3194286	32	8	58	6	g	a	g	a	0.03619921	S->N	keratin K5
3199701	47	17	16	0	t	c	t		0.01359122	V->A	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) [Homo sapiens]
3199753	379	7	143	13	g	c	g	c	1.08E-09	A->P	60S ribosomal protein L13A
3200107	151	5	16	0	c	a	c		0	R->S	gb AAA59612.1 HLA-A30.3 precursor
3200126	275	2	203	7	a	c	a	c	7.94E-06	H->P	sp P02433 RL32_HUMAN 60S ribosomal protein L32 pir R5HU32 ribosomal prot

3200132	84	70	18	16	a	g	g	a	0	Q->R	HLA-A74 [Homo sapiens]
3200522	263	1	181	9	a	c	a	c	0	H->P	sp P02433 RL32_HUMAN 60S ribosomal protein L32 pir R5HU32 ribosomal prot
3201368	215	7	116	16	c	t	c	t	3.90E-09	S->F	ribosomal protein L35 [Mus musculus]
3201397	226	6	138	8	g	a	g	a	0.02807998	E->K	Similar to tubulin, beta 5 [Mus musculus]
3202446	240	4	145	6	a	c	a	c	0.02420268	H->P	ribosomal protein L17 [Mus musculus]
3205367	234	2	114	4	a	g	a	g	0.00262204	E->G	ribosomal protein, large P2 [Mus musculus]
3205529	232	4	51	3	c	t	c	t	0.0285276	L->F	gb AAP36043.1 ribosomal protein L8 [Homo sapiens]
3205759	290	4	136	9	a	g	a	g	4.83E-07	K->R	sp P47914 RL29_HUMAN 60S riboso
3205903	13	1	2	0	c	t	t		0.025	T->M	gb AAA52590.1 pregnancy-specific beta-1-glycoprotein
3207506	59	7	47	11	c	a	c	a	0.04075509	N->K	gb AAH39951.1 8430423A01Rik protein [Mus musculus]
3207803	195	3	50	8	c	t	c	t	2.05E-14	P->L	Unknown (protein for IMAGE:3349601) [Homo sapiens]
3208406	32	6	24	0	a	g	a		0.04490773	Y->H	gb AAD34097.1 AF151860_1 CGI-102 protein
3209329	105	1	52	6	a	c	a	c	1.36E-13	H->P	Homo sapiens ubiquitin-like 5 [synthetic construct]
3209388	236	8	178	0	a	g	a		0.01429411	E->G	similar to ribosomal protein S6 [Mus musculus]
3209921	82	4	6	4	c	t	c	t	0.00336307	L->F	Lamins C and C2 dbj BAA08570.1 lamin C [Mus musculus domesticus]
3210169	96	2	50	4	c	g	c	g	0.00543329	T->R	thyroid hormone binding protein precursor
3210196	222	19	226	2	a	c	a	c	8.99E-05	T->P	Homo sapiens ferritin, light polypeptide
3210235	310	9	221	3	a	t	a	g	0.01148775	I->F	similar to 40S ribosomal protein S2 [Rattus norvegicus]
3210432	58	6	6	4	t	g	t	g	0.02191601	L->R	similar to hypothetical protein FLJ10661 [Homo sapiens]
3210532	68	4	8	4	g	t	g	t	0.01168137	V->F	Chain C, Ligand Binding Alters The Structure And Dynamics Of Nucleosomal Dna
3210688	71	13	62	4	c	t	c	t	0.03666189	A->V	Unknown (protein for MGC:52000) [Homo sapiens]
3210910	28	2	27	9	g	a	g	a	0.03812772	R->H	Unknown (protein for IMAGE:3140944) [Homo sapiens]
3210961	164	2	6	6	g	c	c	g	0	Q->H	epsilon-COP [Homo sapiens]
3211002	299	7	154	10	c	t	c	t	0.00112302	S->F	gb AAA75449.1 L10 ribosomal protein
3211239	164	2	146	8	a	g	a	g	5.78E-06	D->G	gb AAH00533.1 AAH00533 Similar to eukaryotic translation initiation factor 3
3211570	267	3	167	7	g	c	g	c	0.00025171	A->P	similar to ribosomal protein L13, cytosolic [validated]