Table S1: Signature of 998 differentially expressed genes between various

PrimSeqName	AccessNum	GeneID	SeqCode	change (mean)
ABCA1	NM_005502	19	A_24_P235429	-6,60
ABCB1	NM_000927	5243	A_23_P82523	11,31
ABCG1	NM_207627	9619	A_23_P166297	12,39
ABHD1	NM_032604	84696	A_23_P17242	2,32
ABLIM2	NM_032432	84448	A_23_P255672	5,36
ABLIM3	NM_014945	22885	A_24_P123408	2,92
ABR	NM_021962	29	A_23_P503182	2,08
ACADS	NM_000017	35	A_23_P65022	-4,73
ACBD4	NM_024722	79777	A_23_P107166	-3,77
ACCN3	NM_020322	9311	A_23_P93658	3,61
ACOT2	NM_006821	10965	A_24_P301195	-3,05
ACP5	NM_001611	54	A_23_P142075	-5,18
ACPP	NM_001099	55	A_24_P46130	6,21
ACR	NM_001097	49	A_23_P40734	3,91
ACSF2	NM_025149	80221	A_23_P4190	2,34
ADAM22	AL133090; NM_02	53616	A_24_P355006	5,56
ADAMTS1	NM_006988	9510	A_23_P211039	8,50
ADAMTS14	NM_139155	140766	A_24_P275073	-3,92
ADAMTS15	NM_139055	170689	A_23_P52749	2,40
ADAMTS18	NM_199355	170692	A_32_P34844	6,12
ADAMTS5	NM_007038	11096	A_23_P40415	9,32
ADAMTSL4	NM_019032	54507	A_23_P115011	-2,87
ADCK1	NM_020421	57143	A_23_P25945	-3,27
ADH4	NM_000670	127	A_23_P30098	3,39
ADRB2	NM_000024	154	A_23_P145024	-4,32
AGBL5	NM_021831	60509	A_24_P45767	2,05
AGK	BX640861	55750	A_32_P24059	3,68
AHNAK	NM_024060	79026	A_23_P21363	-1,61
AHR	NM_001621	196	A_23_P215566	6,83
AK123483	AK123483	100506211	A_24_P886966	-2,86
AK7	NM_152327	122481	A_23_P105963	3,74
AKAP12	NM_005100; NM_1	9590	A_32_P152437	-4,60
AKT2	NM_001626	208	A_23_P373475	-2,77
ALCAM	NM_001627	214	A_23_P41227	-3,99
ALK	NM_004304	238	A_23_P324304	-7,27
ALS2CR4	NM_001044385	65062	A_24_P941831	4,05
ALX1	NM_006982	8092	A_23_P83798	8,06
AMN	NM_030943	81693	A_23_P48455	-2,91
AMOT	NM_133265	154796	A_24_P344961	7,30
AMY1C	NM_001008219	278	A_23_P23611	8,35
ANGEL2	NM_144567	90806	A_24_P28622	2,73
ANGPTL2	NM_012098	23452	A_23_P20864	-10,77
ANKRD18A	BC131497	253650	A_24_P172293	2,71
ANKRD5	NM_022096	63926	A_23_P256047	6,98
ANKRD50	NM_020337	57182	A_23_P81017	3,75
ANKRD9	NM_152326	122416	A_23_P307525	-2,76
ANKS6	NM_173551	203286	A_23_P362183	3,69
ANO1	NM_018043	55107	A_24_P87036	4,04
ANO2	NM_020373	57101	A_32_P141238	2,09
ANO4	NM_178826	121601	A_23_P409093	-1,17
ANTXR1	NM_032208	84168	A_24_P131522	6,70

ANXA1	NM_000700	301	A_23_P94501	6,74
ANXA2	NM_001002857	302	A_23_P146644	-2,05
AOC3	NM_003734	8639	A_23_P426305	2,89
APAF1	NM_181861	317	A_23_P36611	-2,07
APC2	NM_005883	10297	A_23_P101905	5,02
ARAP2	NM_015230	116984	A_32_P83784	-6,07
AREG	NM_001657	374	A_23_P259071	4,93
ARHGAP10	NM_024605	79658	A_23_P21548	-2,77
ARHGDIG	NM_001176	398	A_24_P215882	-3,77
ARHGEF6	NM_004840	9459	A_23_P85024	6,43
ARID5B	NM_032199	84159	A_23_P97871	-2,59
ARRB1	NM_004041	408	A_24_P386622	-4,20
ARRDC4	NM_183376	91947	A_23_P339818	2,20
ARSG	NM_014960	22901	A_24_P339416	2,18
ASMTL	NM_004192	8623	A_23_P159539	-3,33
ASPHD1	NM_181718	253982	A_23_P170667	2,71
ATP8A1	NM_006095	10396	A_23_P30075	-3,79
ATP8B1	NM_005603	5205	A_23_P107597	-2,39
ATXN1	NM_000332	6310	A_24_P294842	-4,95
AUTS2	NM_001127232; N	26053	A_32_P809435	10,44
AVIL	NM_006576	10677	A_23_P390157	6,76
B3GALT4	NM_003782	8705	A_23_P111171	-9,77
B4GALT4	NM_212543	8702	A_32_P103945	-4,64
BAG2	NM_004282	9532	A_23_P356554	-3,07
BAI2	NM_001703	576	A_23_P149019	2,52
BC004962	BC004962	100506451	A_32_P144018	3,28
BCAN	BC005081	63827	A_32_P2730	2,88
BCO2	NM_031938	83875	A_23_P116187	4,51
BEAN	NM_001136106	146227	A_32_P153195	5,26
BET1	NM_005868	10282	A_23_P59700	3,01
BHLHE41	NM_030762	79365	A_23_P139500	9,72
BIRC3	NM_001165	330	A_23_P98350	26,85
BLZF1	CR591083	8548	A_23_P23266	4,21
BMI1	NM_005180	648	A_23_P314115	3,11
BMP7	NM_001719	655	A_23_P68487	3,38
BMS1P1	NR_026566	728053	A_32_P142128	6,01
BRCA2	NM_000059	675	A_23_P99452	-6,38
BRIP1	NM_032043	83990	A_23_P15844	-4,14
BX114764	BX114764	100505576	A_32_P226678	3,90
C10orf107	NM_173554	219621	A_32_P8156	8,24
C10orf110	NR_027709	55853	A_23_P24275	3,39
C10orf79	NM_025145	80217	A_23_P333038	15,27
C11orf52	NM_080659	91894	A_23_P1722	-2,88
C11orf61	NM_024631	79684	A_23_P52885	2,80
C11orf66	NM_145017	220004	A_23_P98571	3,77
C11orf9	NM_013279	745	A_23_P75790	2,37
C12orf47	NR_015404	51275	A_24_P256539	2,06
C14orf145	NM_152446	145508	A_23_P320829	-2,49
C14orf21	NM_174913	161424	A_23_P326844	-3,12
C16orf48	NM_032140	84080	A_23_P14975	2,15
C16orf93	NM_001014979	90835	A_24_P842002	2,58
C18orf23	AK091537	147341	A_23_P371276	2,42
C19orf18	NM_152474	147685	A_23_P303803	3,91
C19ORF25	BF436529	148223	A_24_P878992	-2,81
C1orf118	XR_041258	374987	A_24_P110780	5,77
C1orf156	NM_033418	92342	A_23_P85726	3,49

C1orf192	NM_001013625	257177	A_32_P331139	9,26
C1orf194	NM_001122961	127003	A_32_P15512	15,64
C1orf88	NM_181643	128344	A_32_P215700	6,32
C1orf97	NR_026761	84791	A_23_P1014	4,70
C1QL1	NM_006688	10882	A_23_P77993	-9,66
C21orf56	NM_032261	84221	A_23_P371765	-3,28
C21orf88	NR_026543	114041	A_32_P34826	3,85
C21orf90	NR_026547	114043	A_24_P339858	2,18
C22orf23	NM_032561	84645	A_23_P132308	2,29
C2CD2L	NM_014807	9854	A_23_P353056	2,15
C2orf27A	NM_013310	29798	A_24_P8888	2,06
C2orf55	NM_207362	343990	A_24_P272313	7,86
C2orf88	NM_001042519	84281	A_23_P17130	-12,29
C3AR1	NM_004054	719	A_23_P2431	-2,79
C4orf12	NR_015359	404201	A_32_P116271	3,18
C5	NM_001735	727	A_23_P71855	6,78
C5orf37	NM_152408	134359	A_23_P413803	3,38
C5orf53	NM_001007189	492311	A_24_P110558	5,15
C5orf54	NM_022090	63920	A_23_P259103	5,96
C5orf56	AK025221	441108	A_24_P829156	2,30
C5orf62	NM_032947	85027	A_23_P414273	8,00
C6orf132	NM_001164446	647024	A_32_P218355	-8,65
C6orf150	NM_138441	115004	A_32_P1173	-3,86
C6orf165	AK098840; NM_00	154313	A_23_P385980	3,27
C6orf182	NM_173830	285753	A_24_P189112	-2,64
C6orf204	BC045657	387119	A_32_P90709	-3,93
C6orf223	NM_153246	221416	A_23_P348183	-7,12
C6orf35	NM_018452	729515	A_24_P144620	-2,52
C6orf97	NM_025059	80129	A_23_P93514	3,97
C7orf38	NM_145111	221786	A_23_P168810	3,06
C7orf53	NM_182597	286006	A_24_P380679	4,83
C7orf57	NM_001100159	136288	A_32_P3955	15,64
C8orf4	NM_020130	56892	A_23_P253350	-1,80
C9orf117	NM_001012502	286207	A_24_P229638	13,10
C9orf150	NM_203403	286343	A_23_P83007	5,06
C9orf66	NM_152569	157983	A_32_P115220	-6,33
CACNA1H	NM_021098	8912	A_23_P3483	3,30
CACNG6	NM_145814	59285	A_23_P501933	5,88
CADM3	NM_021189	57863	A_23_P201156	-2,61
CALCA	NM_001033953	796	A_24_P198178	5,04
CALCRL	NM_005795	10203	A_23_P39898	-17,44
CALD1	NM_033138	800	A_23_P42575	-3,98
CAMK1D	NM_020397	57118	A_23_P124252	11,11
CAMK2N1	NM_018584	55450	A_23_P11800	6,67
CAMP	NM_004345	820	A_23_P253791	7,55
CAMSAP1L1	NM_203459	23271	A_23_P406702	3,61
CAPG	NM_001747	822	A_23_P165636	-2,66
CARD16	NM_001017534	114769	A_23_P64173	7,92
CASC5	NM_170589	57082	A_24_P378331	-4,63
CAV1	NM_001753	857	A_24_P12626	2,95
CAV3	NM_001234	859	A_24_P251599	2,84
CBX7	NM_175709	23492	A_23_P250735	2,74
CCDC132	NM_017667; NM_	55610	A_24_P409219	5,23
CCDC135	NM_032269	84229	A_23_P129367	9,16
CCDC148	NM_138803	130940	A_23_P411825	4,41
CCDC19	NM_012337	25790	A_23_P62642	4,32

CCDC30	NM_001080850	728621	A_24_P349196	7,13
CCDC42B	NM_001144872	387885	A_24_P84099	3,42
CCNA2	NM_001237	890	A_23_P58321	-5,12
CCNB3	NM_033031	85417	A_23_P171107	3,13
CCNL2	NM_001039577	81669	A_24_P376339	2,49
CCPG1	AF011794; NM_02	9236	A_23_P48897	4,76
CCRK	NM_001039803	23552	A_23_P20752	2,40
CCT6P1	AK092180	643253	A_24_P491087	3,38
CD109	NM_133493	135228	A_23_P331928	-6,52
CD2AP	NM_012120	23607	A_24_P329152	-2,78
CD36	NM_001001547	948	A_23_P111583	5,99
CD44	NM_000610	960	A_23_P24870	-5,98
CD55	NM_000574	1604	A_23_P374862	3,25
CD70	NM_001252	970	A_23_P119202	6,81
CDC5L	NM_001253	988	A_23_P156471	-2,59
CDGAP	NA	57514	A_32_P226620	-14,39
CDH16	NM_004062	1014	A_23_P100240	16,85
CDH23	NM_022124	64072	A_23_P364437	6,97
CDKAL1	CR623381; NM_01	54901	A_23_P44781	-2,41
CDKL2	NM_003948	8999	A_23_P259270	4,16
CEACAM1	NM_001024912; N	634	A_23_P434118	-3,18
CELA3B	NM_007352	23436	A_23_P200579	-11,19
CEP120	NM_153223	153241	A_24_P137602	3,64
CES2	NM_003869; NM_1	8824	A_24_P13790	3,76
CFI	NM_000204	3426	A_23_P7212	16,36
CGNL1	NM_032866	84952	A_23_P163306	-4,37
CGREF1	NM_006569	10669	A_23_P403445	2,76
CHORDC1	NM_012124	26973	A_23_P138805	-2,86
CHRNE	NM_000080	1145	A_23_P304279	-2,82
CITED4	NM_133467	163732	A_23_P306804	-3,75
CKAP2	NM_018204	26586	A_24_P99090	-2,27
CKAP2L	NM_152515	150468	A_23_P388812	-2,89
CLDN12	NM_012129	9069	A_23_P412515	2,63
CLDN3	NM_001306	1365	A_23_P71017	2,08
CLEC3B	NM_003278	7123	A_23_P69497	2,99
CLGN	NM_004362	1047	A_23_P18684	7,30
CLK4	NM_020666	57396	A_24_P123521	4,06
CLPB	NM_030813	81570	A_23_P75978	-3,21
CLSPN	NM_022111	63967	A_23_P126212	-3,28
CMKLR1	NM_001142343	1240	A_24_P766716	10,80
CMTM1	NM_052999	113540	A_23_P106663	2,59
CNTFR	NM_147164	1271	A_23_P9402	-2,68
CNTNAP3	NM_033655	79937	A_23_P9135	8,14
COL12A1	NM_004370	1303	A_23_P214168	-6,52
COL17A1	NM_000494	1308	A_23_P52323	-2,41
COL18A1	NM_030582	80781	A_23_P211212	-2,30
COL20A1	NM_020882	57642	A_32_P185637	4,32
COL24A1	NM_152890	255631	A_23_P74701	11,58
COL25A1	BC036669	84570	A_32_P405010	-6,44
COL5A1	NM_000093	1289	A_23_P158593	6,30
COQ3	NM_017421	51805	A_23_P111228	-2,85
COX6B2	NM_144613	125965	A_24_P267523	-3,47
CR624517	CR624517	100505938	A_32_P162709	5,61
CREB3L4	NM_130898	148327	A_23_P63232	2,10
CRIP1	NM_001311	1396	A_23_P44674	2,75
CRLF1	NM_004750	9244	A_23_P56197	4,81

CROT	NM_021151	54677	A_23_P168669	4,46
CRYM	NM_001888	1428	A_23_P77731	2,03
CSF1R	NM_005211	1436	A_23_P110791	-3,14
CSH1	NM_022640	1442	A_23_P381347	-2,62
CST6	NM_001323	1474	A_23_P146946	-3,85
CSTA	NM_005213	1475	A_23_P170233	-5,17
CTAG1A	NM_139250	246100	A_23_P148541	4,65
CUZD1	NM_022034	50624	A_23_P47058	3,69
CXCL14	NM_004887	9547	A_23_P213745	-4,26
CXCL2	NM_002089	2920	A_23_P315364	23,24
CXCL3	NM_002090	2921	A_24_P183150	2,14
CXCR4	NM_001008540	7852	A_23_P102000	-19,09
CYHR1	NM_032687	50626	A_23_P123555	2,57
CYP4F2	NM_001082	8529	A_24_P168494	-2,86
DBF4	NM_006716	10926	A_24_P943358	4,77
DBNDD2	NM_001048226	55861	A_23_P28772	2,98
DCAKD	NM_024819	79877	A_24_P58331	-3,12
DCDC2	NM_016356	51473	A_23_P134162	-5,24
DCLK1	NM_004734	9201	A_23_P369994	-4,85
DCX	NM_000555	1641	A_23_P500328	3,64
DDC	NM_000790	1644	A_23_P145644	3,09
DDX60	NM_017631	55601	A_23_P41470	6,24
DDX60L	NM_001012967	91351	A_23_P30069	5,91
DEAF1	NM_021008	10522	A_32_P35375	-2,85
DEFB1	NM_005218	1672	A_23_P71480	-3,43
DENND5B	NM_144973	160518	A_23_P379746	-2,66
DEPDC1	NM_017779	55635	A_23_P200310	-3,43
DES	NM_001927	1674	A_23_P90710	-3,23
DGKG	NM_001346	1608	A_23_P40926	-6,98
DHRS1	NM_138452	115817	A_23_P48747	-4,01
DHX29	NM_019030	54505	A_23_P81463	3,51
DIAPH2	Y15909	1730	A_32_P50834	-4,23
DKFZP434I0714	XM_001715987	54553	A_23_P413303	4,69
DKFZP586I1420	NR_002186	222161	A_23_P403398	6,17
DLC1	NM_182643	10395	A_23_P252721	-8,34
DLG2	NM_001364	1740	A_23_P124514	-6,13
DLG4	NM_001365	1742	A_23_P411102	2,53
DLGAP5	NM_014750	9787	A_23_P88331	-3,60
DLL1	NM_005618	28514	A_23_P167920	3,24
DLX3	NM_005220	1747	A_24_P296587	4,55
DMRT3	NM_021240	58524	A_23_P157895	-6,86
DMTF1	NM_021145	9988	A_23_P8664	3,81
DNAH7	NM_018897	56171	A_24_P410776	4,57
DNAJC15	NM_013238	29103	A_23_P117190	-3,40
DNAJC6	NM_014787	9829	A_23_P95359	-5,22
DNALI1	NM_003462	7802	A_23_P160377	3,66
DNM3	NM_015569	26052	A_23_P371266	3,69
DOCK2	NM_004946	1794	A_24_P408704	-4,33
DOCK8	NM_203447	81704	A_32_P181077	-11,06
DPPA2	NM_138815	151871	A_23_P405885	-7,37
DPY19L2	NM_173812	283417	A_23_P374250	8,31
DPY19L2P2	NR_003561	349152	A_24_P186608	4,37
DPY19L2P4	AK098759	442523	A_24_P409483	5,08
DSE	NM_013352	29940	A_23_P19226	5,32
DUSP10	NM_007207	11221	A_23_P51856	2,95
DUSP13	NM_001007271	51207	A_23_P104471	-6,05

DUSP23	NM_017823	54935	A_23_P103232	3,28
E2F8	NM_024680	79733	A_23_P35871	-3,09
EFCAB7	NM_032437	84455	A_32_P137266	3,58
EGF	NM_001963	1950	A_23_P155979	4,05
EID3	NM_001008394	493861	A_23_P65068	3,86
EIF2S2	CR595813	8894	A_32_P11723	3,27
ELK4	AL117645	2005	A_24_P902091	4,13
ENST0000036739	AJ277914	56956	A_24_P910952	-3,61
ENST0000037121	NA	221391	A_23_P58934	1,91
EPB41L2	NM_001431	2037	A_23_P134109	-4,33
EPB41L4B	NM_019114	54566	A_23_P387656	6,27
EPHA8	NM_001006943	2046	A_24_P419239	-6,69
EPHX4	NM_173567	253152	A_23_P43898	-4,26
EPM2AIP1	NM_014805	9852	A_24_P627984	4,38
EPS8	NM_004447	2059	A_23_P136347	-6,61
ERAP2	NM_022350	64167	A_23_P30243	3,50
ERC1	NM_178040	23085	A_24_P162293	-2,45
ERCC6L	NM_017669	54821	A_23_P96325	-4,61
ERN2	NM_033266	10595	A_23_P49310	-3,06
ERP27	NM_152321	121506	A_23_P139687	8,33
ERP44	NM_015051	23071	A_23_P373927	4,55
EVL	NM_016337	51466	A_23_P129038	-2,95
EXD3	NM_017820	54932	A_24_P49183	5,25
EXPH5	NM_015065	23086	A_24_P937691	3,74
EY892390	EY892390	147372	A_32_P171043	2,91
F2RL2	NM_004101	2151	A_32_P60065	8,24
F5	NM_000130	2153	A_23_P148768	35,02
FADS2	NM_004265	9415	A_24_P150160	-3,49
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LETM2	NM_144652	137994	A_23_P348264	-5,36
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RFX2	NM_000635	5990	A_23_P502350	2,74
RGNEF	NM_001080479	64283	A_24_P177932	-2,64
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TEF	NM_003216	7008	A_24_P151582	2,46
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THNSL2	NM_018271	55258	A_23_P259207	2,96
THRA	NM_003250	7067	A_23_P207742	2,59
THSD7A	NM_015204	221981	A_24_P400324	-14,89
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TNFRSF6B	NM_032945	8771	A_23_P218646	7,23
TNNC2	NM_003279	7125	A_23_P131825	3,08
TOX3	NM_001146188	27324	A_23_P54681	4,89
TP53I11	AF010315	9537	A_23_P368028	-3,22
TPD52L1	NM_001003395	7164	A_23_P31143	-7,30
TPM1	NM_001018004	7168	A_23_P391586	2,62
TPO	NM_000547	7173	A_24_P257224	6,86
TPPP3	NM_016140	51673	A_23_P26386	7,93
TRAF3IP2	NM_147686	10758	A_23_P110879	-2,32
TRAM1L1	NM_152402	133022	A_23_P18518	3,92
TRIM2	NM_015271	23321	A_23_P213141	-6,40
TRIM22	NM_006074	10346	A_24_P172481	-1,55
TRIM23	NM_033228	373	A_23_P167384	4,73
TRIM34	NM_130390	53840	A_23_P124190	6,62
TRIM6	NM_001003818	117854	A_23_P33673	-28,67
TRPC2	NR_002720	7221	A_23_P169873	-3,21
TSHZ1	NM_005786	10194	A_23_P27381	3,81
TSPAN10	NM_031945	83882	A_24_P213643	-2,68
TSPAN19	NM_001100917	144448	A_23_P2322	9,62
TSPAN33	NM_178562	340348	A_24_P365901	2,24
TSPAN5	AK055659	10098	A_23_P61886	2,98
TST	NM_003312	7263	A_23_P29248	2,05
TTC18	NM_145170	118491	A_23_P326931	5,69
TTC25	NM_031421	83538	A_23_P73150	6,90
TTN	NM_133378	7273	A_23_P85269	2,46
TTR	NM_000371	7276	A_23_P130333	6,67
TUBA8	NM_018943	51807	A_24_P160104	2,10
TUBAL3	NM_024803	79861	A_23_P95851	-3,84
TUG1	NR_002323	55000	A_23_P68868	3,75
TXNDC5	NM_030810	81567	A_23_P168229	-2,09
TXNDC6	NM_178130	347736	A_23_P212672	2,23
TXNIP	NM_006472	10628	A_23_P97700	3,75
UACA	NM_001008224	55075	A_23_P360340	5,58
UBE2I	BC064492	7329	A_24_P227993	2,40
UBE2J1	NM_016021	51465	A_23_P214185	-2,06
UBXN10	NM_152376	127733	A_23_P85664	8,74
UHMK1	AK026668	127933	A_32_P84389	3,80
UHRF1	NM_013282	29128	A_23_P208880	-2,25
UNC13A	NM_001080421	23025	A_23_P365494	2,84
UNQ3028	AY358789	100131826	A_24_P934008	-3,71
UPK1B	NM_006952	7348	A_24_P200219	-11,30
USP20	NM_001008563	10868	A_23_P217028	2,25
USP36	AB040886	57602	A_23_P352957	2,65

VCAN	NM_004385	1462	A_23_P144959	4,24
VDR	NM_001017535	7421	A_23_P162589	-7,46
VMO1	NM_182566	284013	A_23_P55356	2,17
VPS26B	NM_052875	112936	A_23_P52903	-3,12
VSIG10	NM_019086	54621	A_23_P72059	2,02
VTA1	NM_016485	51534	A_23_P42368	-2,16
VTCN1	NM_024626	79679	A_23_P518	2,65
VWA5B2	NM_138345	90113	A_24_P152881	-2,89
WBSCR28	NM_182504	135886	A_23_P418274	6,22
WDR31	NM_001012361	114987	A_24_P6674	4,62
WDR52	NM_001164496	55779	A_23_P110090	5,37
WDR5B	NM_019069	54554	A_23_P92184	2,68
WDR69	NM_178821	164781	A_23_P28466	-6,32
WIBG	BC009627	84305	A_24_P917612	2,04
WNT2B	NM_004185	7482	A_23_P138352	-2,24
WNT6	NM_006522	7475	A_23_P119916	7,78
WNT7A	NM_004625	7476	A_23_P258410	-6,42
WSCD1	NM_015253	23302	A_24_P942493	-17,56
XPOT	NM_007235	11260	A_23_P340722	2,83
XRCC4	NM_022550	7518	A_23_P122174	3,79
ZADH2	NM_175907	284273	A_23_P375476	3,23
ZBTB24	NM_014797	9841	A_23_P134147	-2,39
ZC3H6	NM_198581	376940	A_24_P826348	4,83
ZCCHC14	NM_015144	23174	A_24_P176484	2,60
ZCWPW1	NM_017984	55063	A_23_P70897	2,72
ZDBF2	NM_020923	57683	A_32_P68504	7,20
ZDHHC14	NM_153746	79683	A_23_P250619	-6,72
ZFPM2	NM_012082	23414	A_24_P273857	-3,35
ZMIZ2	NM_031449	83637	A_24_P29686	3,00
ZMYND10	NM_015896	51364	A_23_P29663	3,22
ZNF100	BC035579	163227	A_32_P48244	-5,42
ZNF175	NM_007147	7728	A_23_P332374	4,53
ZNF207	AK026215	7756	A_24_P116766	6,56
ZNF226	NM_001032374	7769	A_23_P218434	3,20
ZNF23	AF024709	7571	A_24_P935125	4,06
ZNF280D	NM_017661	54816	A_23_P14708	4,19
ZNF295	NM_020727	49854	A_24_P339869	3,24
ZNF35	NM_003420	7584	A_23_P211785	7,36
ZNF350	NM_021632	59348	A_23_P78458	-5,03
ZNF433	NM_001080411	163059	A_23_P27649	-3,67
ZNF486	NM_052852	90649	A_24_P100016	-2,56
ZNF577	NM_032679	84765	A_23_P309207	-5,23
ZNF613	NM_024840	79898	A_24_P173234	-4,07
ZNF649	NM_023074	65251	A_23_P208208	-5,87
ZNF655	NM_001083956	79027	A_23_P345081	3,59
ZNF681	NM_138286	148213	A_32_P167904	-4,90
ZNF682	NM_033196	91120	A_24_P944588	3,35
ZNF704	NM_001033723	619279	A_24_P230074	4,61
ZNF789	AK131429	285989	A_32_P542928	4,13
ZNRF2	NM_147128	223082	A_23_P325017	4,66
ZSWIM5	NM_020883	57643	A_23_P383118	3,08

Table S2: Clinical data of patients recruted for TMA

#	TMA Order	Dis ID	DOB	Benign0/ Cancer1	FKBP7	Months to Recurrence	FOLLOW UP AFTER SURGERY(NONRECURRENT0- RECURRENT 1)	DIAGNOSIS DATE	DATE OF SURGERY/RADIATION	LAST FOLLOW UP/DATE OF PSA RECURRENCE	FOLLOW UP AFTER SURGERY(NONRECURRENT0- RECURRENT 1)	PSA AT DX	BIOPSY TOTAL GLEASON SCORE	RPRTOTAL GLEASON SCORE	EXTRACAPSULAR INVASION (0 &1)	SEMINAL VESICLES (0 &1)	POSITIVE MARGINS?	Positive cores/total cores	Main Treatment; no Tr (0) NHT (1) NHT/TAX2	No Metastasis (0) LN Metastasis (1) distant Metatstasis (2)	PATHOLOGICAL STAGING (1-7)
1	1	3722	18/05/1940	0	1	120,00	0	17/12/2003	20/01/2004	20/01/2014	0	4,7	7	6	0	0	1	0,3	0	0	4
2	2	3722	18/05/1940	0	1	120,00	0	17/12/2003	20/01/2004	20/01/2014	0	4,7	7	6	0	0	1	0,3	0	0	4
3	3	3666	25/02/1952	0	1	49,97	0	17/10/2003	20/01/2004	19/03/2008	0	7,8	6	6	0	0	0	0,3	0	0	4
4	4	3666	25/02/1952	0	1	49,97	0	17/10/2003	20/01/2004	19/03/2008	0	7,8	6	6	0	0	0	0,3	0	0	4
5	5	3641	29/05/1938	0	1	80,47	0	30/09/2003	22/01/2004	06/10/2010	0	7,43	7	6	0		0	0,3	0	0	4
6	6	3641	29/05/1938	1	1	80,47	0	30/09/2003	22/01/2004	06/10/2010	0	7,43	7	6	0		0	0,3	0	0	4
7	7	3748	21/06/1934	0	0	61,17	0	29/05/2003	27/01/2004	02/03/2009	0	8	6	6	0	0	1	0,4	0	0	4
8	8	3748	21/06/1934	1	0	61,17	0	29/05/2003	27/01/2004	02/03/2009	0	8	6	6	0	0	1	0,4	0	0	4
9	9	3669	01/04/1933	1	0	98,43	0	21/10/2003	29/01/2004	12/04/2012	0	6,1	7	6	0	0	0	0,6	0	0	4
10	10	3669	01/04/1933	0	0	98,43	0	21/10/2003	29/01/2004	12/04/2012	0	6,1	7	6	0	0	0	0,6	0	0	4
11	11	3651	25/06/1937	1	1	89,47	0	08/10/2003	30/01/2004	14/07/2011	0	6	7	7	0	0	0	0,4	0	0	2
12	12	3651	25/06/1937	1	1	89,47	0	08/10/2003	30/01/2004	14/07/2011	0	6	7	7	0	0	0	0,4	0	0	2
13	13	3699	08/02/1950	1	1		0	20/11/2003	04/03/2004	04/03/2004	0	8,15	6	7	0	0	0	0,9	0	0	4
14	14	3699	08/02/1950	1	1		0	20/11/2003	04/03/2004	04/03/2004	0	8,15	6	7	0	0	0	0,9	0	0	4
15	15	3699	08/02/1950	0	0		0	20/11/2003	04/03/2004	04/03/2004	0	8,15	6	7	0	0	0	0,9	0	0	4
16	16	3699	08/02/1950	0	0		0	20/11/2003	04/03/2004	04/03/2004	0	8,15	6	7	0	0	0	0,9	0	0	4
17	17	3846	16/02/1939	1	1	30,40	1	16/03/2004	06/05/2004	18/11/2006	1	24,1	7	9	1	1	1	0,5	0	0	5
18	18	3846	16/02/1939	1	1	30,40	1	16/03/2004	06/05/2004	18/11/2006	1	24,1	7	9	1	1	1	0,5	0	0	5
19	19	3846	16/02/1939	1	1	30,40	1	16/03/2004	06/05/2004	18/11/2006	1	24,1	7	9	1	1	1	0,5	0	0	5
20	20	3846	16/02/1939	1	1	30,40	1	16/03/2004	06/05/2004	18/11/2006	1	24,1	7	9	1	1	1	0,5	0	0	5
21	21	3788	30/11/1948	1	0	90,37	0	03/03/2004	25/05/2004	06/12/2011	0	6,9	7	7	0	0	1	0,5	0	0	4
22	22	3788	30/11/1948	1	0	90,37	0	03/03/2004	25/05/2004	06/12/2011	0	6,9	7	7	0	0	1	0,5	0	0	4
23	23	3836	18/11/1961	1	2	120,87	0	22/04/2004	27/05/2004	23/06/2014	0	9	7	7	0	0	0	0,4	0	0	4
24	24	3836	18/11/1961	1	2	120,87	0	22/04/2004	27/05/2004	23/06/2014	0	9	7	7	0	0	0	0,4	0	0	4
25	25	3822	26/05/1935	0	0	113,00	1	07/04/2004	01/06/2004	31/10/2013	1	16	8	9	1	1	1	0,7	0	0	6
26	26	3822	26/05/1935	1	0	113,00	1	07/04/2004	01/06/2004	31/10/2013	1	16	8	9	1	1	1	0,7	0	0	6
27	27	3775	06/10/1952	1	3		0	19/02/2004	27/07/2004		0	6,5	6	6	0	0	1	0,4	0	0	4
28	28	3775	06/10/1952	1	3		0	19/02/2004	27/07/2004		0	6,5	6	6	0	0	1	0,4	0	0	4
29	29	3835	14/12/1941	1	0	85,07	0	22/04/2004	11/08/2004	13/09/2011	0	5,2	7	6	0	0	0	0,3	0	0	4
30	30	3835	14/12/1941	1	1	85,07	0	22/04/2004	11/08/2004	13/09/2011	0	5,2	7	6	0	0	0	0,3	0	0	4
31	31	3866	02/02/1934	1	1	97,60	0	27/05/2004	11/08/2004	29/09/2012	0	1,7	6	6	0	0	0	0,5	0	0	4
32	32	3866	02/02/1934	1	3	97,60	0	27/05/2004	11/08/2004	29/09/2012	0	1,7	6	6	0	0	0	0,5	0	0	4
33	33	3964	09/01/1947	1	2		0		23/09/2004	23/09/2004	0			7	1	0	1		0	0	5
34	34	3964	09/01/1947	1	2		0		23/09/2004	23/09/2004	0			7	1	0	1		0	0	5
35	35	3964	09/01/1947	0	0		0		23/09/2004	23/09/2004	0			7	1	0	1		0	0	5
36	36	3964	09/01/1947	0	0		0		23/09/2004	23/09/2004	0			7	1	0	1		0	0	5
37	37	3862	07/09/1954	1	1	85,33	0	23/06/2004	05/10/2004	15/11/2011	0	5,3	7	6	0	0	0	0,3	0	0	4
38	38	3862	07/09/1954	0	2	85,33	0	23/06/2004	05/10/2004	15/11/2011	0	5,3	7	6	0	0	0	0,3	0	0	4
39	39	3862	07/09/1954	0	1	85,33	0	23/06/2004	05/10/2004	15/11/2011	0	5,3	7	6	0	0	0	0,3	0	0	4
40	40	3862	07/09/1954	0	1	85,33	0	23/06/2004	05/10/2004	15/11/2011	0	5,3	7	6	0	0	0	0,3	0	0	4
41	41	3849	31/07/1938	0	0	121,17	0	12/05/2004	12/10/2004	17/11/2014	0	6,5	7	7	0	0	0	0,3	0	0	4
42	42	3849	31/07/1938	0	0	121,17	0	12/05/2004	12/10/2004	17/11/2014	0	6,5	7	7	0	0	0	0,3	0	0	4
43	43	3678	29/01/1940	1	2	12,80	1	01/10/2003	14/10/2004	08/11/2005	1	6,3	6	8	1	1	1	0,3	0	0	6
44	44	3678	29/01/1940	1	2	12,80	1	01/10/2003	14/10/2004	08/11/2005	1	6,3	6	8	1	1	1	0,3	0	0	6
45	45	3861	15/05/1934	1	0	79,70	0	20/05/2004	19/10/2004	10/06/2011	0	5,1	6	6	1		1	0,1	0	0	5
46	46	3861	15/05/1934	1	0	79,70	0	20/05/2004	19/10/2004	10/06/2011	0	5,1	6	6	1		1	0,1	0	0	5
47	47	3891	04/01/1948	1	1	98,73	1	18/06/2004	09/11/2004	01/02/2013	1		7	7	0	0	0	0,5	0	0	2
48	48	3891	04/01/1948	1	2	98,73	1	18/06/2004	09/11/2004	01/02/2013	1		7	7	0	0	0	0,5	0	0	2
49	49	3750	18/12/1936	1	3	60,97	0	29/01/2004	13/04/2004	12/05/2009	0	15,6	7	9	1	1	0	0,4	0	0	5
50	50	3750	18/12/1936	1	3	60,97	0	29/01/2004	13/04/2004	12/05/2009	0	15,6	7	9	1	1	0	0,4	0	0	5
51	51	3641	29/05/1938	0	0	80,47	0	30/09/2003	22/01/2004	06/10/2010	0	7,43	7	6	0		0	0,3	0	0	4
52	52	3641	29/05/1938	0	0	80,47	0	30/09/2003	22/01/2004	06/10/2010	0	7,43	7	6	0		0	0,3	0	0	4
53	53	3886	31/05/1949	1	0	79,60	0	17/06/2004	23/09/2004	11/05/2011	0	8,2	7	7	0	0	0	0,1	0	0	4
54	54	3886	31/05/1949	1	1	79,60	0	17/06/2004	23/09/2004	11/05/2011	0	8,2	7	7	0	0	0	0,1	0	0	4
55	55	4029	13/01/1938	0	2	52,20	1	31/03/2004	02/12/2004	08/04/2009	1	6	6	6	0	0	0	0,5	0	0	4

56	56	4029	13/01/1938	0	0	52,20	1	31/03/2004	02/12/2004	08/04/2009	1	6	6	6	0	0	0	0,5	0	0	4
57	57	4043	20/11/1933	1	0		1	14/12/2004	19/04/2005		1	7,02	7	7	0	0	1	0,1	0	0	4
58	58	4043	20/11/1933	1	0		1	14/12/2004	19/04/2005		1	7,02	7	7	0	0	1	0,1	0	0	4
59	59	4162	16/10/1939	1	2	85,13	0	26/04/2005	05/07/2005	09/08/2012	0	8,1	8	7	0	0	0	1,0	0	0	4
60	60	4162	16/10/1939	1	2	85,13	0	26/04/2005	05/07/2005	09/08/2012	0	8,1	8	7	0	0	0	1,0	0	0	4
61	61	4235	11/06/1942	1	3	105,80	0	25/04/2005	12/07/2005	06/05/2014	0	7,6	7	7	0	0	1	0,5	0	0	4
62	62	4235	11/06/1942	1	3	105,80	0	25/04/2005	12/07/2005	06/05/2014	0	7,6	7	7	0	0	1	0,5	0	0	4
63	63	4211	24/09/1949	1	2	78,07	1	14/06/2005	30/08/2005	02/03/2012	1	14	7	7	0	0	1	0,5	0	0	4
64	64	4211	24/09/1949	1	1	78,07	1	14/06/2005	30/08/2005	02/03/2012	1	14	7	7	0	0	1	0,5	0	0	4
65	65	4237	17/08/1946	1	1	41,80	0	14/07/2005	06/10/2005	30/03/2009	0	8,3	7	7	0	0	0	0,4	0	0	4
66	66	4237	17/08/1946	0	x	41,80	0	14/07/2005	06/10/2005	30/03/2009	0	8,3	7	7	0	0	0	0,4	0	0	4
67	67	4171	11/02/1948	1	3		0	05/05/2005	11/10/2005		0		7	7	1	0	0	0,5	0	0	5
68	68	4171	11/02/1948	1	3		0	05/05/2005	11/10/2005		0		7	7	1	0	0	0,5	0	0	5
69	69	4257	21/12/1948	1	2	100,67	0	09/08/2005	24/11/2005	14/04/2014	0	6,5	6	7	0	0	0	0,5	0	0	4
70	70	4257	21/12/1948	1	2	100,67	0	09/08/2005	24/11/2005	14/04/2014	0	6,5	6	7	0	0	0	0,5	0	0	4
71	71	3936	17/10/1938	1	2	123,13	0	31/08/2004	06/01/2005	10/04/2015	0	6,06	7	7	1	0	0	0,3	0	0	5
72	72	3936	17/10/1938	1	2	123,13	0	31/08/2004	06/01/2005	10/04/2015	0	6,06	7	7	1	0	0	0,3	0	0	5
73	73	4040	29/05/1942	1	2	39,97	0	13/12/2004	24/03/2005	23/07/2008	0	26	7	7	1	0	1	0,4	0	0	5
74	74	4040	29/05/1942	1	2	39,97	0	13/12/2004	24/03/2005	23/07/2008	0	26	7	7	1	0	1	0,4	0	0	5
75	75	4186	20/09/1939	1	3	116,87	1	18/05/2005	08/09/2005	04/06/2015	1	6,8	7	7	1	0	1	0,5	1	2	5
76	76	4186	20/09/1939	1	x	116,87	1	18/05/2005	08/09/2005	04/06/2015	1	6,8	7	7	1	0	1	0,5	1	2	5
77	77	4384	12/01/1938	1	1	93,77	0	20/12/2005	28/02/2006	23/12/2013	0	12,6	6	7	0	0	1	0,5	0	0	2
78	78	4384	12/01/1938	1	1	93,77	0	20/12/2005	28/02/2006	23/12/2013	0	12,6	6	7	0	0	1	0,5	0	0	2
79	79	4340	19/12/1939	1	1		0	08/11/2005	28/02/2006		0		6	7	0	0	0	0,9	0	0	4
80	80	4340	19/12/1939	1	2		0	08/11/2005	28/02/2006		0		6	7	0	0	0	0,9	0	0	4
81	81	4511	25/05/1934	1	0	81,37	1	11/01/2006	24/03/2006	05/01/2013	1	13	7	7	0	0	1	0,5	0	0	4
82	82	4511	25/05/1934	1	1	81,37	1	11/01/2006	24/03/2006	05/01/2013	1	13	7	7	0	0	1	0,5	0	0	4
83	83	4471	02/12/1942	1	3	98,83	0	21/02/2006	20/04/2006	15/07/2014	0	8,95	8	8	0	0	0	0,3	0	0	4
84	84	4471	02/12/1942	0	3	98,83	0	21/02/2006	20/04/2006	15/07/2014	0	8,95	8	8	0	0	0	0,3	0	0	4
85	85	4594	08/09/1942	1	1	95,77	0	14/06/2006	04/07/2006	27/06/2014	0	26	7	7	1	0	1		0	0	5
86	86	4594	08/09/1942	1	3	95,77	0	14/06/2006	04/07/2006	27/06/2014	0	26	7	7	1	0	1		0	0	5
87	87	4572	06/05/1933	1	x	50,50	1	25/05/2006	13/07/2006	28/09/2010	1	8,9	9	9	1	1	0	0,3	1	0	6
88	88	4572	06/05/1933	1	2	50,50	1	25/05/2006	13/07/2006	28/09/2010	1	8,9	9	9	1	1	0	0,3	1	0	6
89	89	4530	16/09/1958	1	2	28,63	0	12/04/2006	26/07/2006	15/12/2008	0	8,8	7	7	0	0	1	0,3	0	0	3
90	90	4530	16/09/1958	1	2	28,63	0	12/04/2006	26/07/2006	15/12/2008	0	8,8	7	7	0	0	1	0,3	0	0	3
91	91	3596	07/08/1941	1	0		0		13/08/2003	13/08/2003	0	2,85		7	0	0	0		0	0	4
92	92	3596	07/08/1941	1	1		0		13/08/2003	13/08/2003	0	2,85		7	0	0	0		0	0	4
93	93	3596	07/08/1941	1	0		0		13/08/2003	13/08/2003	0	2,85		7	0	0	0		0	0	4
94	94	3596	07/08/1941	1	1		0		13/08/2003	13/08/2003	0	2,85		7	0	0	0		0	0	4
95	95	4624	12/08/1939	1	3		0	19/07/2006	04/10/2006		0	7,1	7	7	0	0	1	0,6	0	0	4
96	96	4624	12/08/1939	1	x		0	19/07/2006	04/10/2006		0	7,1	7	7	0	0	1	0,6	0	0	4
97	97	4533	25/07/1945	0	1	72,23	0	19/04/2006	13/06/2006	20/06/2012	0	4,3	6	7	0	0	0	0,3	0	0	4
98	98	4533	25/07/1945	0	1	72,23	0	19/04/2006	13/06/2006	20/06/2012	0	4,3	6	7	0	0	0	0,3	0	0	4
99	99	4123	15/02/1941	0	2	92,30	0	25/02/2005	15/06/2006	24/02/2014	0	9	8	7	0	0	1		0	0	4
100	100	4123	15/02/1941	0	2	92,30	0	25/02/2005	15/06/2006	24/02/2014	0	9	8	7	0	0	1		0	0	4
101	101	4617	18/06/1954	1	2		0	13/07/2006	04/10/2005		0	6,5	6	6	0	0	1	0,4	0	0	4
102	102	4617	18/06/1954	1	1		0	13/07/2006	04/10/2005		0	6,5	6	6	0	0	1	0,4	0	0	4
103	103	4544	25/10/1933	0	1	45,93	0	02/05/2006	15/06/2006	13/04/2010	0	4,05	7	7	1	1	1	0,6	0	0	5
104	104	4544	25/10/1933	0	2	45,93	0	02/05/2006	15/06/2006	13/04/2010	0	4,05	7	7	1	1	1	0,6	0	0	5
105	105	4700	10/11/1940	1	3	35,50	0	26/10/2006	02/01/2007	17/12/2009	0	7,7	9	9	1	0	0	0,5	0	0	5
106	106	4700	10/11/1940	1	3	35,50	0	26/10/2006	02/01/2007	17/12/2009	0	7,7	9	9	1	0	0	0,5	0	0	5
107	107	4700	10/11/1940	1	3	35,50	0	26/10/2006	02/01/2007	17/12/2009	0	7,7	9	9	1	0	0	0,5	0	0	5
108	108	4700	10/11/1940	1	3	35,50	0	26/10/2006	02/01/2007	17/12/2009	0	7,7	9	9	1	0	0	0,5	0	0	5
109	109	4783	07/10/1947	1	3	36,73	0	11/10/2006	09/01/2007	01/02/2010	0	5,7	7	7	0	0	0	0,4	0	0	4
110	110	4783	07/10/1947	1	2	36,73	0	11/10/2006	09/01/2007	01/02/2010	0	5,7	7	7	0	0	0	0,4	0	0	4
111	111	4812	23/07/1942	1	0		0	31/01/2007	01/02/2007	01/02/2007	0		6	7	0	0	1		0	0	2
112	112	4812	23/07/1942	1	1		0	31/01/2007	01/02/2007	01/02/2007	0		6	7	0	0	1		0	0	2
113	113	4817	30/05/1947	1	3	97,10	0	01/12/2006	06/02/2007	09/03/2015	0	4,07	7	7	0	0	1	0,4	0	0	4
114	114	4817	30/05/1947	1	0	97,10	0	01/12/2006	06/02/2007	09/03/2015	0	4,07	7	7	0	0	1	0,4	0	0	4

115	115	4833	22/07/1942	1	2		0		15/02/2007	15/02/2007	0	13	6	6	0	0	0	0,1	0	0	4
116	116	4833	22/07/1942	1	1		0		15/02/2007	15/02/2007	0	13	6	6	0	0	0	0,1	0	0	4
117	117	4879	10/09/1940	0	x	11,87	0	09/05/2006	23/03/2007	19/03/2008	0	6,8	6		0	0	0	0,1	0	0	1
118	118	4879	10/09/1940	0	1	11,87	0	09/05/2006	23/03/2007	19/03/2008	0	6,8	6		0	0	0	0,1	0	0	1
119	119	4640	13/09/1939	1	3	19,57	0	17/08/2006	23/03/2007	10/11/2008	0	6,6	6	7	1	0	1	0,3	0	0	5
120	120	4640	13/09/1939	1	2	19,57	0	17/08/2006	23/03/2007	10/11/2008	0	6,6	6	7	1	0	1	0,3	0	0	5
121	121	4910	25/08/1936	1	3	36,53	0	21/12/2006	18/04/2007	04/05/2010	0	11	7	8	0	0	1	0,1	0	0	4
122	122	4910	25/08/1936	1	3	36,53	0	21/12/2006	18/04/2007	04/05/2010	0	11	7	8	0	0	1	0,1	0	0	4
123	123	4871	22/05/1947	1	1	33,27	1	16/03/2007	24/04/2007	02/02/2010	1	10,6	8	8	1	0	0	0,4	0	0	5
124	124	4871	22/05/1947	1	1	33,27	1	16/03/2007	24/04/2007	02/02/2010	1	10,6	8	8	1	0	0	0,4	0	0	5
125	125	4871	22/05/1947	1	1	33,27	1	16/03/2007	24/04/2007	02/02/2010	1	10,6	8	8	1	0	0	0,4	0	0	5
126	126	4871	22/05/1947	1	0	33,27	1	16/03/2007	24/04/2007	02/02/2010	1	10,6	8	8	1	0	0	0,4	0	0	5
127	127	4859	14/10/1949	0	0	90,90	0	07/03/2007	22/05/2007	19/12/2014	0	8,02	7	7	0	0	1	0,7	0	0	4
128	128	4859	14/10/1949	1	1	90,90	0	07/03/2007	22/05/2007	19/12/2014	0	8,02	7	7	0	0	1	0,7	0	0	4
129	129	4940	25/06/1939	0	0	84,20	0	29/03/2007	23/05/2007	29/05/2014	0	7,1	9	7	0	0	1	0,5	0	0	4
130	130	4940	25/06/1939	0	0	84,20	0	29/03/2007	23/05/2007	29/05/2014	0	7,1	9	7	0	0	1	0,5	0	0	4
131	131	4852	25/05/1942	0	2	78,63	0	28/02/2007	29/05/2007	18/12/2013	0	5,3	6	7	0	0	1	0,3	0	0	4
132	132	4852	25/05/1942	0	2	78,63	0	28/02/2007	29/05/2007	18/12/2013	0	5,3	6	7	0	0	1	0,3	0	0	4
133	133	4822	10/09/1951	1	1	84,37	0	08/02/2007	29/05/2007	10/06/2014	0	4,3	7	7	1	0	0	0,3	0	0	5
134	134	4822	10/09/1951	1	1	84,37	0	08/02/2007	29/05/2007	10/06/2014	0	4,3	7	7	1	0	0	0,3	0	0	5
135	135	4856	03/01/1951	1	1	7,77	0	01/03/2007	05/06/2007	28/01/2008	0	5,77	6	7	0	0	0	0,5	0	0	4
136	136	4856	03/01/1951	1	1	7,77	0	01/03/2007	05/06/2007	28/01/2008	0	5,77	6	7	0	0	0	0,5	0	0	4
137	137	4846	07/03/1948	1	1	77,23	0	27/02/2007	14/06/2007	21/11/2013	0		8	7	0	0	1	0,4	0	0	4
138	138	4846	07/03/1948	1	1	77,23	0	27/02/2007	14/06/2007	21/11/2013	0		8	7	0	0	1	0,4	0	0	4
139	139	4794	09/09/1937	0	0	92,50	0	19/01/2007	11/09/2007	26/05/2015	0	2,2	7	7	1	0	1	0,5	0	0	5
140	140	4794	09/09/1937	0	0	92,50	0	19/01/2007	11/09/2007	26/05/2015	0	2,2	7	7	1	0	1	0,5	0	0	5
141	141	4970	02/02/1950	1	3	71,13	1	26/07/2007	18/09/2007	22/08/2013	1	7,84	8	8	1	0	1	0,5	0	0	5
142	142	4970	02/02/1950	1	2	71,13	1	26/07/2007	18/09/2007	22/08/2013	1	7,84	8	8	1	0	1	0,5	0	0	5
143	143	4989	30/08/1942	1	x	66,73	0	28/08/2007	20/09/2007	12/04/2013	0	8,11	7	7	0	0	0	0,5	0	0	4
144	144	4989	30/08/1942	1	0	66,73	0	28/08/2007	20/09/2007	12/04/2013	0	8,11	7	7	0	0	0	0,5	0	0	4
145	145	5013	09/09/1942	1	1	64,60	1	21/12/2006	16/10/2007	04/03/2013	1	5,3	6	8	0	0	0	0,4	0	2	4
146	146	5013	09/09/1942	1	1	64,60	1	21/12/2006	16/10/2007	04/03/2013	1	5,3	6	8	0	0	0	0,4	0	2	4
147	147	4977	13/05/1960	1	2	6,13	0	13/08/2007	19/10/2007	23/04/2008	0	6,4	7	7	0	0	0	0,5	0	0	4
148	148	4977	13/05/1960	1	2	6,13	0	13/08/2007	19/10/2007	23/04/2008	0	6,4	7	7	0	0	0	0,5	0	0	4
149	149	5023	26/09/1938	1	2	23,87	0	01/11/2006	06/11/2007	02/11/2009	0	6	7	7	0	0	0	0,3	0	0	4
150	150	5023	26/09/1938	1	3	23,87	0	01/11/2006	06/11/2007	02/11/2009	0	6	7	7	0	0	0	0,3	0	0	4
151	151	5010	15/12/1955	1	1	87,23	0	04/10/2007	27/11/2007	04/03/2015	0	11,8	7	7	0	0	1	0,1	0	0	4
152	152	5010	15/12/1955	1	1	87,23	0	04/10/2007	27/11/2007	04/03/2015	0	11,8	7	7	0	0	1	0,1	0	0	4
153	153	5032	09/04/1947	0	2		0		04/12/2007	04/12/2007	0			9	0	0	1		0	0	4
154	154	5032	09/04/1947	1	0		0		04/12/2007	04/12/2007	0			9	0	0	1		0	0	4
155	155	5017	27/12/1956	1	2	57,77	1	29/10/2007	08/01/2008	31/10/2012	1	3,5	7	7	1		1	0,8	1	1	5
156	156	5017	27/12/1956	1	2	57,77	1	29/10/2007	08/01/2008	31/10/2012	1	3,5	7	7	1		1	0,8	1	1	5
157	157	5017	27/12/1956	0	2	57,77	1	29/10/2007	08/01/2008	31/10/2012	1	3,5	7	7	1		1	0,8	2	1	5
158	158	5017	27/12/1956	1	2	57,77	1	29/10/2007	08/01/2008	31/10/2012	1	3,5	7	7	1		1	0,8	1	1	5
159	159	5029	09/03/1956	1	3	82,67	0	26/11/2007	21/01/2008	11/12/2014	0	2,4	7	6	0	0	1	0,3	0	0	4
160	160	5029	09/03/1956	1	3	82,67	0	26/11/2007	21/01/2008	11/12/2014	0	2,4	7	6	0	0	1	0,3	0	0	4
161	161	4988	19/11/1947	0	1	51,00	1	28/08/2007	09/10/2007	09/01/2012	1	10,2	6	7	1	1	1	0,5	0	1	6
162	162	4988	19/11/1947	0	2	51,00	1	28/08/2007	09/10/2007	09/01/2012	1	10,2	6	7	1	1	1	0,5	0	1	6
163	163	5015	18/02/1947	1	0	0,43	0	22/10/2007	12/02/2008	25/02/2008	0	6,19	7	7	1	1	0	1,0	0	0	5
164	164	5015	18/02/1947	1	0	0,43	0	22/10/2007	12/02/2008	25/02/2008	0	6,19	7	7	1	1	0	1,0	0	0	5
165	165	4981	19/09/1935	0	3	29,33	0	16/08/2007	10/04/2008	20/09/2010	0	10,7	7	7	1	1	1	0,3	0	0	6
166	166	4981	19/09/1935	1	3	29,33	0	16/08/2007	10/04/2008	20/09/2010	0	10,7	7	7	1	1	1	0,3	0	0	6
167	167	5062	17/12/1946	1	3	5,70	1	02/05/2007	18/04/2008	09/10/2008	1	19,1	6	7	0	0	0	0,1	0	0	4
168	168	5062	17/12/1946	1	2	5,70	1	02/05/2007	18/04/2008	09/10/2008	1	19,1	6	7	0	0	0	0,1	0	0	4
169	169	5059	17/09/1945	1	2	83,67	0	11/02/2008	08/05/2008	28/04/2015	0	5,3	7	7	1	0	1	0,8	0	0	5
170	170	5059	17/09/1945	1	2	83,67	0	11/02/2008	08/05/2008	28/04/2015	0	5,3	7	7	1	0	1	0,8	0	0	5
171	171	5059	17/09/1945	1	2	83,67	0	11/02/2008	08/05/2008	28/04/2015	0	5,3	7	7	1	0	1	0,8	0	0	5
172	172	5059	17/09/1945	1	2	83,67	0	11/02/2008	08/05/2008	28/04/2015	0	5,3	7	7	1	0	1	0,8	0	0	5
173	173	5053	09/01/1940	1	1	20,67	1	24/01/2008	03/06/2008	23/02/2010	1	4,32	7	7	0	0	0	0,2	0	0	4
174	174	5053	09/01/1940	1	1	20,67	1	24/01/2008	03/06/2008	23/02/2010	1	4,32	7	7	0	0	0	0,2	0	0	4
175	175	5082	09/09/1939	1	2	22,83	0	01/04/2008	17/06/2008	12/05/2010	0	5,8	7	7	1	0	0	0,3	0	0	5

176	176	5082	09/09/1939	1	1	22,83	0	01/04/2008	17/06/2008	12/05/2010	0	5,8	7	7	1	0	0	0,3	0	0	5
178	1	3328	30/04/1941	1	2	141,90	0	01/11/2002	27/01/2003	24/11/2014	0	3,1	6	6	0	0	1	0,3	0	0	4
179	2	3328	30/04/1941	1	x	141,90	0	01/11/2002	27/01/2003	24/11/2014	0	3,1	6	6	0	0	1	0,3	0	0	4
180	3	3329	21/08/1949	1	1	53,37	0	01/11/2002	04/02/2003	15/07/2007	0	39	6	7	1	1	1	0,1	0	0	5
181	4	3329	21/08/1949	1	0	53,37	0	01/11/2002	04/02/2003	15/07/2007	0	39	6	7	1	1	1	0,1	0	0	5
182	5	3277	24/01/1932	1	0	60,30	1	18/09/2002	13/02/2003	22/02/2008	1	13	7	7	0	0	0	0,5	0	0	4
183	6	3277	24/01/1932	1	0	60,30	1	18/09/2002	13/02/2003	22/02/2008	1	13	7	7	0	0	0	0,5	0	0	4
184	7	3448	29/11/1957	1	0		0	15/01/2003	18/02/2003		0	7,5	7	7	0	0	1	0,5	0	0	4
185	8	3448	29/11/1957	1	1		0	15/01/2003	18/02/2003		0	7,5	7	7	0	0	1	0,5	0	0	4
186	9	3304	25/02/1934	1	1		0	09/10/2002	03/03/2003		0	9	6		0	0	1	0,3	0	0	4
187	10	3304	25/02/1934	1	0		0	09/10/2002	03/03/2003		0	9	6		0	0	1	0,3	0	0	4
188	11	3514	16/01/1950	1	2	18,03	0	08/04/2003	20/05/2003	21/11/2004	0	7,7	8	8	1	1	1	0,5	0	0	6
189	12	3514	16/01/1950	1	1	18,03	0	08/04/2003	20/05/2003	21/11/2004	0	7,7	8	8	1	1	1	0,5	0	0	6
190	13	3480	23/10/1933	1	0	62,27	0	23/09/2002	20/05/2003	28/07/2008	0	8,3	6	7	0	0	0	0,1	0	0	2
191	14	3480	23/10/1933	1	0	62,27	0	23/09/2002	20/05/2003	28/07/2008	0	8,3	6	7	0	0	0	0,1	0	0	2
192	15	3483	21/05/1955	1	1		0	04/04/2003	13/08/2003		0	3,4	7	7	0	0	1	0,3	0	0	4
193	16	3483	21/05/1955	1	1		0	04/04/2003	13/08/2003		0	3,4	7	7	0	0	1	0,3	0	0	4
194	17	3464	06/09/1939	1	1		0	05/03/2003	15/07/2003		0	16	6	7	0	0	0	0,6	0	0	4
195	18	3464	06/09/1939	1	1		0	05/03/2003	15/07/2003		0	16	6	7	0	0	0	0,6	0	0	4
196	19	3513	12/06/1949	1	2	86,00	0	20/05/2003	04/09/2003	04/11/2010	0	6,25	7	7	0	0	0	0,3	0	0	2
197	20	3513	12/06/1949	1	3	86,00	0	20/05/2003	04/09/2003	04/11/2010	0	6,25	7	7	0	0	0	0,3	0	0	2
198	21	3644	14/01/1939	1	1		0		30/09/2003		0	6,8	7	7	0	0	1		0	0	4
199	22	3644	14/01/1939	1	1		0		30/09/2003		0	6,8	7	7	0	0	1		0	0	4
200	23	4143	01/02/1937	1	2	109,70	0	22/03/2005	05/05/2005	26/06/2014	0	9,8	7	7	0	1	0	0,3	0	0	6
201	24	4143	01/02/1937	1	2	109,70	0	22/03/2005	05/05/2005	26/06/2014	0	9,8	7	7	0	1	0	0,3	0	0	6
202	25	3551	19/12/1936	1	0		0	19/06/2003	02/10/2003		0	6,1	7	7	0	0	1	0,6	0	0	4
203	26	3551	19/12/1936	1	0		0	19/06/2003	02/10/2003		0	6,1	7	7	0	0	1	0,6	0	0	4
204	27	3664	18/09/1936	1	0		0	16/05/2003	16/10/2003		0	3,2	6	7	1	0	0	0,8	0	0	5
205	28	3664	18/09/1936	1	1		0	16/05/2003	16/10/2003		0	3,2	6	7	1	0	0	0,8	0	0	5
206	29	3711	11/11/1941	1	2	24,50	1	11/08/2003	04/12/2003	19/12/2005	1	5,7	6	7	0	0	0	0,2	0	0	4
207	30	3711	11/11/1941	1	0	24,50	1	11/08/2003	04/12/2003	19/12/2005	1	5,7	6	7	0	0	0	0,2	0	0	4
208	31	4322	26/05/1942	1	2	42,13	1	26/10/2005	03/01/2006	07/07/2009	1	20	6	7	1	1	0	0,6	0	0	6
209	32	4322	26/05/1942	1	2	42,13	1	26/10/2005	03/01/2006	07/07/2009	1	20	6	7	1	1	0	0,6	0	0	6
210	33	3000	19/03/1943	1	1	85,50	0	02/10/2001	18/04/2002	03/06/2009	0	6,46	6		0	0	0	0,5	1	0	4
211	34	3000	19/03/1943	1	1	85,50	0	02/10/2001	18/04/2002	03/06/2009	0	6,46	6		0	0	0	0,5	1	0	4
212	35	2950	08/09/1931	1	x	125,47	1	01/08/2001	25/04/2002	09/10/2012	1	2,2	7	7	0	0	1	0,5	1	0	4
213	36	2950	08/09/1931	1	x	125,47	1	01/08/2001	25/04/2002	09/10/2012	1	2,2	7	7	0	0	1	0,5	1	0	4
214	37	2732	22/01/1941	1	2	74,80	0	23/11/2000	22/02/2001	16/05/2007	0	9,4	8	7	0	0	1	0,3	1	0	4
215	38	2732	22/01/1941	1	2	74,80	0	23/11/2000	22/02/2001	16/05/2007	0	9,4	8	7	0	0	1	0,3	1	0	4
216	39	3082	13/06/1946	1	3	90,47	1	18/01/2002	30/05/2002	14/12/2009	1	8,35	7		1	0	0	1,0	1	0	5
217	40	3082	13/06/1946	1	1	90,47	1	18/01/2002	30/05/2002	14/12/2009	1	8,35	7		1	0	0	1,0	1	0	5
218	41	3451	20/06/1941	1	x	66,83	0	20/02/2003	15/07/2003	10/02/2009	0	15,1	6	6	0	0	0	0,1	1	0	2
219	42	3451	20/06/1941	1	x	66,83	0	20/02/2003	15/07/2003	10/02/2009	0	15,1	6	6	0	0	0	0,1	1	0	2
220	43	3542	10/04/1940	1	1	29,33	1	10/06/2003	04/09/2003	14/02/2006	1	15,6	8	7	1	0	0	0,1	1	0	5
221	44	3542	10/04/1940	1	1	29,33	1	10/06/2003	04/09/2003	14/02/2006	1	15,6	8	7	1	0	0	0,1	1	0	5
222	45	3434	12/07/1935	1	1	48,07	1	06/02/2003	29/07/2003	01/08/2007	1	13,7	9	9	0	1	1	1,0	1	2	6
223	46	3434	12/07/1935	1	1	48,07	1	06/02/2003	29/07/2003	01/08/2007	1	13,7	9	9	0	1	1	1,0	1	2	6
224	47	3337	28/04/1931	1	0	28,20	1	06/11/2002	11/02/2003	17/06/2005	1	9	7	9	1	1	1	0,8	1	2	6
225	48	3337	28/04/1931	1	x	28,20	1	06/11/2002	11/02/2003	17/06/2005	1	9	7	9	1	1	1	0,8	1	2	6
226	49	3470	08/02/1940	1	1	59,97	0	18/03/2003	29/04/2003	28/04/2008	0	4,61	8	7	0	0	1	0,5	1	0	2
227	50	3470	08/02/1940	1	2	59,97	0	18/03/2003	29/04/2003	28/04/2008	0	4,61	8	7	0	0	1	0,5	1	0	2
228	51	3211	20/11/1936	1	x		0	26/06/2002	29/10/2002		0	5,1	7	6	1	0	0	0,3	1	0	5
229	52	3211	20/11/1936	1	1		0	26/06/2002	29/10/2002		0	5,1	7	6	1	0	0	0,3	1	0	5
230	53	3375	18/05/1934	1	1	60,20	0	09/12/2002	06/05/2003	12/05/2008	0	6,1	7		0	0	0	0,5	1	0	4
231	54	3375	18/05/1934	1	1	60,20	0	09/12/2002	06/05/2003	12/05/2008	0	6,1	7		0	0	0	0,5	1	0	4
232	55	3188	14/05/1943	1	1		0	24/05/2002	01/10/2002		0	8,1	6	7	0	0	1	0,5	0	0	4
233	56	3188	14/05/1943	1	1		0	24/05/2002	01/10/2002		0	8,1	6	7	0	0	1	0,5	0	0	4
234	57	3759	10/04/1940	1	2	78,90	0	01/01/2004	21/10/2004	18/05/2011	0	24	7	7	0	0	0	0,6	1	0	4
235	58	3759	10/04/1940	1	1	78,90	0	01/01/2004	21/10/2004	18/05/2011	0	24	7	7	0	0	0	0,6	1	0	4
236	59	3887	18/11/1955	1	0	76,60	0	17/06/2004	31/03/2005	18/08/2011	0	17,5	7	7	0	0	0	1,0	1	0	4
237	60	3887	18/11/1955	1	1	76,60	0	17/06/2004	31/03/2005	18/08/2011	0	17,5	7	7	0	0	0	1,0	1	0	4

238	61	4312	10/02/1941	1	2	35,13	0	18/10/2005	08/06/2006	12/05/2009	0	5,8	9		0	0	0	0,4	1	0	2
239	62	4312	10/02/1941	1	1	35,13	0	18/10/2005	08/06/2006	12/05/2009	0	5,8	9		0	0	0	0,4	1	0	2
240	63	2732	22/01/1941	1	2	74,80	0	23/11/2000	22/02/2001	16/05/2007	0	9,4	8	7	0	0	1	0,3	1	0	4
241	64	2732	22/01/1941	1	2	74,80	0	23/11/2000	22/02/2001	16/05/2007	0	9,4	8	7	0	0	1	0,3	1	0	4
242	65	3010	21/07/1928	1	1		1	11/10/2001	19/03/2002		1	12,2	9		0	0	0	0,4	2	0	2
243	66	3010	21/07/1928	1	1		1	11/10/2001	19/03/2002		1	12,2	9		0	0	0	0,4	2	0	2
244	67	3290	21/09/1938	1	x	80,33	0	22/09/2002	04/02/2003	14/10/2009	0	9,27	7		0	0	1	0,3	1	0	4
245	68	3290	21/09/1938	1	0	80,33	0	22/09/2002	04/02/2003	14/10/2009	0	9,27	7		0	0	1	0,3	1	0	4
246	69	3116	05/05/1936	1	1	123,27	0	01/08/2001	21/02/2002	29/05/2012	0	6,3	7		0	0	0	0,8	1	0	4
247	70	3116	05/05/1936	1	1	123,27	0	01/08/2001	21/02/2002	29/05/2012	0	6,3	7		0	0	0	0,8	1	0	4
248	71	4062	19/04/1951	1	x	23,90	0	07/01/2005	02/05/2006	29/04/2008	0	5,7	7	7	0	0	0	0,5	1	0	4
249	72	4062	19/04/1951	1	x	23,90	0	07/01/2005	02/05/2006	29/04/2008	0	5,7	7	7	0	0	0	0,5	1	0	4
250	73	4070	27/04/1934	1	0	53,10	1	13/01/2005	04/08/2005	07/01/2010	1	13	9	7	0	0	0	0,9	1	0	4
251	74	4070	27/04/1934	1	1	53,10	1	13/01/2005	04/08/2005	07/01/2010	1	13	9	7	0	0	0	0,9	1	0	4
252	75	3561	23/04/1942	1	1	38,00	1	19/06/2003	06/05/2004	06/07/2007	1	8,4	9		1	1	1	0,5	1	0	6
253	76	3561	23/04/1942	1	1	38,00	1	19/06/2003	06/05/2004	06/07/2007	1	8,4	9		1	1	1	0,5	1	0	6
254	77	2972	10/11/1929	1	2	99,13	0	04/09/2001	06/08/2002	10/11/2010	0	16,1	6	6	0	0	0	0,2	1	0	4
255	78	2972	10/11/1929	1	2	99,13	0	04/09/2001	06/08/2002	10/11/2010	0	16,1	6	6	0	0	0	0,2	1	0	4
256	79	2934	14/12/1935	1	x	144,17	0	12/07/2001	23/04/2002	28/04/2014	0	5,5	7		0	0	0	0,7	1	0	4
257	80	2934	14/12/1935	1	1	144,17	0	12/07/2001	23/04/2002	28/04/2014	0	5,5	7		0	0	0	0,7	1	0	4
258	81	3498	30/08/1943	1	1	7,97	1		01/05/2003	30/12/2003	1	18	6	7	1	0	1		1	0	5
259	82	3498	30/08/1943	1	2	7,97	1		01/05/2003	30/12/2003	1	18	6	7	1	0	1		1	0	5
260	83	3355	05/07/1940	1	x	60,67	0	21/11/2002	10/06/2003	30/06/2008	0	8,8	5	6	0	0	0	0,1	1	0	4
261	84	3355	05/07/1940	1	x	60,67	0	21/11/2002	10/06/2003	30/06/2008	0	8,8	5	6	0	0	0	0,1	1	0	4
262	85	3570	14/05/1941	1	2	58,90	1	15/07/2003	29/04/2004	26/03/2009	1	12,3	7	7	1	1	1	1,0	1	0	6
263	86	3570	14/05/1941	1	1	58,90	1	15/07/2003	29/04/2004	26/03/2009	1	12,3	7	7	1	1	1	1,0	1	0	6
264	87	3954	15/07/1955	1	1	24,83	1	14/09/2004	19/05/2005	14/06/2007	1	40	9		1	0	0	0,5	1	0	5
265	88	3954	15/07/1955	1	2	24,83	1	14/09/2004	19/05/2005	14/06/2007	1	40	9		1	0	0	0,5	1	0	5
266	89	2334	17/09/1936	1	2	110,17	1	27/04/1999	14/02/2002	19/04/2011	1	11,7	6		0	0	1	0,5	1	0	4
267	90	2334	17/09/1936	1	1	110,17	1	27/04/1999	14/02/2002	19/04/2011	1	11,7	6		0	0	1	0,5	1	0	4
268	91	2912	04/02/1934	1	2		0	14/06/2001	07/03/2002		0	13	6		1	0	0	0,3	1	0	5
269	92	2912	04/02/1934	1	2		0	14/06/2001	07/03/2002		0	13	6		1	0	0	0,3	1	0	5
270	93	2854	03/07/1945	1	1	15,27	1	30/03/2001	18/04/2002	26/07/2003	1	25	6	6	1	0	1	0,3	1	0	5
271	94	2854	03/07/1945	1	1	15,27	1	30/03/2001	18/04/2002	26/07/2003	1	25	6	6	1	0	1	0,3	1	0	5
272	95	2976	07/01/1953	1	2	46,23	1	07/09/2001	16/05/2002	23/03/2006	1	10,8	7	7	0	0	0	0,5	1	0	4
273	96	2976	07/01/1953	1	2	46,23	1	07/09/2001	16/05/2002	23/03/2006	1	10,8	7	7	0	0	0	0,5	1	0	4
274	97	2967	04/05/1948	1	1	25,03	1	30/08/2001	04/06/2002	05/07/2004	1	14,7	7		1	1	0	0,8	1	2	5
275	98	2967	04/05/1948	1	1	25,03	1	30/08/2001	04/06/2002	05/07/2004	1	14,7	7		1	1	0	0,8	1	2	5
276	99	2956	30/03/1949	1	2	41,30	1	16/08/2001	06/06/2002	15/11/2005	1	6,2	7	7	1	1	0	0,4	1	0	6
277	100	2956	30/03/1949	1	2	41,30	1	16/08/2001	06/06/2002	15/11/2005	1	6,2	7	7	1	1	0	0,4	1	0	6
278	101	3496	17/01/1936	1	1	135,00	1	30/04/2003	02/12/2003	02/03/2015	1	39,2	7		0	0	0	0,5	1	0	4
279	102	3496	17/01/1936	1	1	135,00	1	30/04/2003	02/12/2003	02/03/2015	1	39,2	7		0	0	0	0,5	1	0	4
280	103	4085	14/03/1936	1	2	25,67	0	26/01/2005	01/12/2005	21/01/2008	0	15,6	7	7	0	0	0	0,3	1	0	4
281	104	4085	14/03/1936	1	2	25,67	0	26/01/2005	01/12/2005	21/01/2008	0	15,6	7	7	0	0	0	0,3	1	0	4
282	105	3731	03/06/1943	1	x	83,27	0	30/12/2003	16/11/2004	24/10/2011	0		7	7	0	0	0	0,9	1	0	4
283	106	3731	03/06/1943	1	x	83,27	0	30/12/2003	16/11/2004	24/10/2011	0		7	7	0	0	0	0,9	1	0	4
284	107	3885	16/01/1937	1	3	122,67	0	17/06/2004	01/03/2005	21/05/2015	0	4,3	9	9	1	1	1	1,0	1	0	6
285	108	3885	16/01/1937	1	3	122,67	0	17/06/2004	01/03/2005	21/05/2015	0	4,3	9	9	1	1	1	1,0	1	0	6
286	109	2910	18/06/1944	1	1	43,40	1	14/06/2001	28/02/2002	12/10/2005	1	10,4	8		1	1	0	0,6	1	0	6
287	110	2910	18/06/1944	1	x	43,40	1	14/06/2001	28/02/2002	12/10/2005	1	10,4	8		1	1	0	0,6	1	0	6
288	111	3744	11/04/1953	1	1	13,00	1	19/01/2004	14/10/2004	14/11/2005	1	32,5	9		1	1	1	1,0	1	2	7
289	112	3744	11/04/1953	1	0	13,00	1	19/01/2004	14/10/2004	14/11/2005	1	32,5	9		1	1	1	1,0	1	2	7
290	113	3609	22/02/1946	1	0		0		26/08/2003		0	8		7	0	0	0		0	0	4
291	114	3609	22/02/1946	1	0		0		26/08/2003		0	8		7	0	0	0		0	0	4
292	115	4060	07/01/1934	1	1	25,20	1	06/01/2005	15/09/2005	21/10/2007	1	14	9		1	1	0	0,9	1	0	6
293	116	4060	07/01/1934	1	x	25,20	1	06/01/2005	15/09/2005	21/10/2007	1	14	9		1	1	0	0,9	1	0	6
294	117	3210	23/02/1950	1	2	12,80	0		20/06/2002	14/07/2003	0	2,3	6	6	0	0	0		1	0	4
295	118	3210	23/02/1950	1	2	12,80	0		20/06/2002	14/07/2003	0	2,3	6	6	0	0	0		1	0	4
296	119	2890	11/04/1941	1	1	21,67	1	11/05/2001	05/02/2002	25/11/2003	1	30	6	6	0	1	0	1,0	1	0	6
297	120	2890	11/04/1941	1	2	21,67	1	11/05/2001	05/02/2002	25/11/2003	1	30	6	6	0	1	0	1,0	1	0	6
298	121	3662	05/05/1936	1	1	10,53	1	16/10/2003	24/09/2004	10/08/2005	1	35	7	7	0	1	0	0,7	1	0	6
299	122	3662	05/05/1936	1	1	10,53	1	16/10/2003	24/09/2004	10/08/2005	1	35	7	7	0	1	0	0,7	1	0	6
300	123	4051	29/12/1939	1	0		0	21/12/2004	05/05/2005		0	4,6	7	8	1	1	1	0,8	0	0	6
301	124	4051	29/12/1939	1	0		0	21/12/2004	05/05/2005		0	4,6	7	8	1	1	1	0,8	0	0	6
302	125	3190	12/06/1934	1	x	112,67	0	29/05/2002	11/03/2003	01/08/2012	0	8,2	7		0	0	0	0,6	1	0	4
303	126	3190	12/06/1934	1	1	112,67	0	29/05/2002	11/03/2003	01/08/2012	0	8,2	7		0	0	0	0,6	1	0	4
304	127	3166	28/10/1936	1	x	28,93	1	25/04/2002	03/04/2003	31/08/2005	1	8,9	7		1	0	0	0,8	1	0	5
305	128	3166	28/10/1936	1	x	28,93	1	25/04/2002	03/04/2003	31/08/2005	1	8,9	7		1	0	0	0,8	1	0	5

306	129	3660	10/01/1934	1	1		0	15/11/2002	14/10/2003		0	8,8	9		0	0	0	0,1	0	0	2
307	130	3660	10/01/1934	1	1		0	15/11/2002	14/10/2003		0	8,8	9		0	0	0	0,1	0	0	2
308	131	3333	03/08/1941	1	1	56,97	1	05/11/2002	18/09/2003	17/06/2008	1	9,8	9	9	1	1	1	0,4	1	0	6
309	132	3333	03/08/1941	1	1	56,97	1	05/11/2002	18/09/2003	17/06/2008	1	9,8	9	9	1	1	1	0,4	1	0	6
310	133	3159	07/05/1949	1	1	7,83	1	18/04/2002	12/06/2003	07/02/2004	1		7		0			0,7	0	0	4
311	134	3159	07/05/1949	1	1	7,83	1	18/04/2002	12/06/2003	07/02/2004	1		7		0			0,7	0	0	4
312	135	3039	13/09/1942	1	2	19,47	1	19/11/2001	12/12/2002	26/07/2004	1	42,9	8		1	1	1	1,0	1	0	6
313	136	3039	13/09/1942	1	0	19,47	1	19/11/2001	12/12/2002	26/07/2004	1	42,9	8		1	1	1	1,0	1	0	6
314	137	3057	15/10/1941	1	1	112,13	1	15/12/2001	28/11/2002	02/04/2012	1	8,53	9		0	1	0		1	2	6
315	138	3057	15/10/1941	1	1	112,13	1	15/12/2001	28/11/2002	02/04/2012	1	8,53	9		0	1	0		1	2	6
316	139	3819	26/06/1939	1	1	87,87	0	01/03/2004	22/12/2004	18/04/2012	0	13	7		0	0	0	0,5	1	0	4
317	140	3819	26/06/1939	1	0	87,87	0	01/03/2004	22/12/2004	18/04/2012	0	13	7		0	0	0	0,5	1	0	4
318	141	3031	05/02/1946	1	0	16,13	1	07/11/2001	13/06/2002	17/10/2003	1	7	6		1	1	1	0,5	1	0	5
319	142	3031	05/02/1946	1	1	16,13	1	07/11/2001	13/06/2002	17/10/2003	1	7	6		1	1	1	0,5	1	0	5
320	143	2643	04/12/1942	1	x	13,73	1	28/06/2000	22/03/2001	14/05/2002	1	16,2	7		1	1	0	0,5	1	0	6
321	144	2643	04/12/1942	1	x	13,73	1	28/06/2000	22/03/2001	14/05/2002	1	16,2	7		1	1	0	0,5	1	0	6
322	145	2566	12/08/1947	1	x	8,23	1	31/03/2000	11/01/2001	18/09/2001	1	22,9	9		1	0	0	0,1	1	2	5
323	146	2566	12/08/1947	1	1	8,23	1	31/03/2000	11/01/2001	18/09/2001	1	22,9	9		1	0	0	0,1	1	2	5
324	147	2740	28/02/1940	1	2	13,30	1	30/11/2000	22/11/2001	01/01/2003	1	35,1	7		1	1	0	0,6	1	1	6
325	148	2740	28/02/1940	1	2	13,30	1	30/11/2000	22/11/2001	01/01/2003	1	35,1	7		1	1	0	0,6	1	1	6
326	149	3246	10/11/1936	1	1	48,63	1	19/08/2002	12/11/2002	01/12/2006	1	17	8	9	1	1	1	0,4	0	2	5
327	150	3246	10/11/1936	1	2	48,63	1	19/08/2002	12/11/2002	01/12/2006	1	17	8	9	1	1	1	0,4	0	2	5
328	151	4556	03/03/1938	1	1	256,13	1		01/01/1990	05/05/2011	1			8	1	1	1		1	1	7
329	152	4556	03/03/1938	1	2	256,13	1		01/01/1990	05/05/2011	1			8	1	1	1		1	1	7
330	153	3392	08/05/1912	1	2		1				1				0				0	0	
331	154	3392	08/05/1912	1	1		1				1				0				0	0	
332	155	3341	09/09/1946	1	1	102,43	1	08/11/2002	25/02/2003	08/09/2011	1	6,59	7	7	1	1	0	0,3	0	1	6
333	156	3341	09/09/1946	1	2	102,43	1	08/11/2002	25/02/2003	08/09/2011	1	6,59	7	7	1	1	0	0,3	0	1	6
334	157	1175	31/03/1927	1	x		0	23/03/1994			0	7,4	5		0			1,0	1	0	5
335	158	1175	31/03/1927	1	1		0	23/03/1994			0	7,4	5		0			1,0	1	0	5
336	159	3522	01/07/1948	1	1	13,50	1	23/05/2003	22/01/2004	07/03/2005	1	3,4	9	9	1	1	1	0,5	1	2	6
337	160	3522	01/07/1948	1	1	13,50	1	23/05/2003	22/01/2004	07/03/2005	1	3,4	9	9	1	1	1	0,5	1	2	6
338	161	4248	05/12/1949	1	x	49,17	0	27/07/2005	03/02/2006	08/03/2010	0	7,8	7		0	0	0	0,5	1	0	4
339	162	4248	05/12/1949	1	1	49,17	0	27/07/2005	03/02/2006	08/03/2010	0	7,8	7		0	0	0	0,5	1	0	4
340	163	4122	19/05/1932	1	2		0				0				0				0	0	
341	164	4122	19/05/1932	1	3		0				0				0				0	0	
342	165	4077	08/09/1946	1	2		0				0				0				0	0	
343	166	4077	08/09/1946	1	3		0				0				0				0	0	
344	167	2776	11/07/1923	1	1		0				0				0				0	0	
345	168	2776	11/07/1923	1	x		0				0				0				0	0	
346	169	2774	10/10/1928	1	2		1			10/07/2001	1		8		0				0	0	5
347	170	2774	10/10/1928	1	2		1			10/07/2001	1		8		0				0	0	5
348	171	2487	15/07/1924	1	1		1	11/07/1994		09/07/2001	1	20,2	5		0			0,0	1	0	2
349	172	2487	15/07/1924	1	3		1	11/07/1994		09/07/2001	1	20,2	5		0			0,0	1	0	2
350	173	3844	02/02/1947	1	1	11,33	1	06/05/2004	05/01/2006	15/12/2006	1	7,4	7	8	0	1	1	0,8	1	1	6
351	174	3844	02/02/1947	1	2	11,33	1	06/05/2004	05/01/2006	15/12/2006	1	7,4	7	8	0	1	1	0,8	1	1	6
352	175	3340	25/04/1940	1	0	27,77	1	08/11/2002	26/08/2003	19/12/2005	1	6,71	7	8	1	0	0	0,8	1	0	5
353	176	3340	25/04/1940	1	x	27,77	1	08/11/2002	26/08/2003	19/12/2005	1	6,71	7	8	1	0	0	0,8	1	0	5
355	1	5666	12/05/1965	0	1	25,60	0	17/07/2009	04/11/2009	22/12/2011	0	5,4	6	7	1	0	0	0,1	0	0	5
356	2	5666	12/05/1965	1	2	25,60	0	17/07/2009	04/11/2009	22/12/2011	0	5,4	6	7	1	0	0	0,1	0	0	5
357	3	5666	12/05/1965	1	2	25,60	0	17/07/2009	04/11/2009	22/12/2011	0	5,4	6	7	1	0	0	0,1	0	0	5
358	4	5657	21/05/1952	0	0	48,47	0	18/06/2009	15/10/2009	29/10/2013	0	6,1	7	7	1	0	0	0,2	0	0	5
359	5	5657	21/05/1952	1	0	48,47	0	18/06/2009	15/10/2009	29/10/2013	0	6,1	7	7	1	0	0	0,2	0	0	5
360	6	5657	21/05/1952	1	2	48,47	0	18/06/2009	15/10/2009	29/10/2013	0	6,1	7	7	1	0	0	0,2	0	0	5
361	7	6922	08/11/1953	0	0	21,43	0	09/09/2011	18/10/2011	31/07/2013	0	27	9	8	0	0	0	0,3	0	0	2
362	8	6922	08/11/1953	1	1	21,43	0	09/09/2011	18/10/2011	31/07/2013	0	27	9	8	0	0	0	0,3	0	0	2
363	9	6922	08/11/1953	1	0	21,43	0	09/09/2011	18/10/2011	31/07/2013	0	27	9	8	0	0	0	0,3	0	0	2
364	10	5567	09/03/1956	0	0	33,80	0	21/01/2009	08/04/2009	02/02/2012	0	8,9	7	7	0	0	0	0,5	0	0	4
365	11	5567	09/03/1956	1	1	33,80	0	21/01/2009	08/04/2009	02/02/2012	0	8,9	7	7	0	0	0	0,5	0	0	4
366	12	5567	09/03/1956	0	1	33,80	0	21/01/2009	08/04/2009	02/02/2012	0	8,9	7	7	0	0	0	0,5	0	0	4
367	13	5564	15/03/1942	1	0	65,60	0	23/10/2008	10/03/2009	28/08/2014	0	5,9	6	6	0	0	0	0,3	0	0	4
368	14	5564	15/03/1942	1	2	65,60	0	23/10/2008	10/03/2009	28/08/2014	0	5,9	6	6	0	0	0	0,3	0	0	4
369	15	5564	15/03/1942	1	2	65,60	0	23/10/2008	10/03/2009	28/08/2014	0	5,9	6	6	0	0	0	0,3	0	0	4
370	16	5669	25/08/1951	1	2	59,93	0	30/04/2009	05/11/2009	03/11/2014	0	5,7	7	7	0	0	0	0,3	0	0	4
371	17	5669	25/08/1951	1	1	59,93	0	30/04/2009	05/11/2009	03/11/2014	0	5,7	7	7	0	0	0	0,3	0	0	4
372	18	5669	25/08/1951	1	2	59,93	0	30/04/2009	05/11/2009	03/11/2014	0	5,7	7	7	0	0	0	0,3	0	0	4
373	19	6823	12/12/1932	1	2	13,13	1	29/03/2011	06/09/2011	10/10/2012	1	8	9		1	1	1	0,2	1	0	6
374	20	6823	12/12/1932	1	0	13,13	1	29/03/2011	06/09/2011	10/10/2012	1	8	9		1	1	1	0,2	1	0	6

375	21	6823	12/12/1932	0	1	13,13	1	29/03/2011	06/09/2011	10/10/2012	1	8	9		1	1	1	0,2	2	0	6
376	22	6850	06/03/1966	1	1	32,23	0	17/06/2011	03/10/2011	10/06/2014	0	4,13	6	7	0	0	0	0,1	0	0	4
377	23	6850	06/03/1966	1	2	32,23	0	17/06/2011	03/10/2011	10/06/2014	0	4,13	6	7	0	0	0	0,1	0	0	4
378	24	6850	06/03/1966	1	2	32,23	0	17/06/2011	03/10/2011	10/06/2014	0	4,13	6	7	0	0	0	0,1	0	0	4
379	25	6808	29/08/1962	1	1	40,77	0	04/07/2011	22/08/2011	15/01/2015	0	26	8	7	1	0	1	0,2	0	0	5
380	26	6808	29/08/1962	1	3	40,77	0	04/07/2011	22/08/2011	15/01/2015	0	26	8	7	1	0	1	0,2	0	0	5
381	27	6808	29/08/1962	1	1	40,77	0	04/07/2011	22/08/2011	15/01/2015	0	26	8	7	1	0	1	0,2	0	0	5
382	28	5638	04/05/1944	0	0	24,70	0	20/05/2009	13/10/2011	04/11/2013	0	4,3	6		0	0	0	0,1	0	0	2
383	29	5638	04/05/1944	1	0	24,70	0	20/05/2009	13/10/2011	04/11/2013	0	4,3	6		0	0	0	0,1	0	0	2
384	30	5638	04/05/1944	1	0	24,70	0	20/05/2009	13/10/2011	04/11/2013	0	4,3	6		0	0	0	0,1	0	0	2
385	31	5674	23/04/1949	0	2	25,77	0	24/06/2009	10/11/2009	03/01/2012	0	5,2	6	6	0	0	0	0,6	0	0	4
386	32	5674	23/04/1949	0	1	25,77	0	24/06/2009	10/11/2009	03/01/2012	0	5,2	6	6	0	0	0	0,6	0	0	4
387	33	5674	23/04/1949	1	2	25,77	0	24/06/2009	10/11/2009	03/01/2012	0	5,2	6	6	0	0	0	0,6	0	0	4
388	34	5660	23/11/1948	1	0	9,50	0	22/07/2009	27/10/2009	12/08/2010	0	5,8	7	9	0	0	1	0,1	0	0	4
389	35	5660	23/11/1948	1	0	9,50	0	22/07/2009	27/10/2009	12/08/2010	0	5,8	7	9	0	0	1	0,1	0	0	4
390	36	5660	23/11/1948	1	0	9,50	0	22/07/2009	27/10/2009	12/08/2010	0	5,8	7	9	0	0	1	0,1	0	0	4
391	37	5636	27/02/1957	0	1	0,43	0	17/04/2009	17/09/2009	30/09/2009	0	5,5	7	7	1	0	1	0,4	0	0	5
392	38	5636	27/02/1957	1	2	0,43	0	17/04/2009	17/09/2009	30/09/2009	0	5,5	7	7	1	0	1	0,4	0	0	5
393	39	5636	27/02/1957	1	1	0,43	0	17/04/2009	17/09/2009	30/09/2009	0	5,5	7	7	1	0	1	0,4	0	0	5
394	40	6771	30/04/1956	0	0	24,00	0	05/05/2011	02/08/2011	02/08/2013	0	2,2	6	7	0	0	0	0,1	0	0	4
395	41	6771	30/04/1956	0	1	24,00	0	05/05/2011	02/08/2011	02/08/2013	0	2,2	6	7	0	0	0	0,1	0	0	4
396	42	6771	30/04/1956	0	1	24,00	0	05/05/2011	02/08/2011	02/08/2013	0	2,2	6	7	0	0	0	0,1	0	0	4
397	43	6836	25/09/1941	0	2	11,90	0	23/06/2011	19/10/2011	16/10/2012	0	5,5	8	7	0	0	0	0,1	0	0	4
398	44	6836	25/09/1941	0	1	11,90	0	23/06/2011	19/10/2011	16/10/2012	0	5,5	8	7	0	0	0	0,1	0	0	4
399	45	6836	25/09/1941	0	1	11,90	0	23/06/2011	19/10/2011	16/10/2012	0	5,5	8	7	0	0	0	0,1	0	0	4
400	46	6810	17/08/1948	0	0	38,33	0	13/07/2011	24/08/2011	04/11/2014	0	6,9	8	7	0	1	0	0,1	0	0	6
401	47	6810	17/08/1948	1	1	38,33	0	13/07/2011	24/08/2011	04/11/2014	0	6,9	8	7	0	1	0	0,1	0	0	6
402	48	6810	17/08/1948	1	2	38,33	0	13/07/2011	24/08/2011	04/11/2014	0	6,9	8	7	0	1	0	0,1	0	0	6
403	49	7025	09/01/1953	0	1	38,03	0	22/09/2011	15/12/2011	16/02/2015	0	5,7	8	7	1	0	1	0,4	0	0	5
404	50	7025	09/01/1953	1	3	38,03	0	22/09/2011	15/12/2011	16/02/2015	0	5,7	8	7	1	0	1	0,4	0	0	5
405	51	7025	09/01/1953	1	3	38,03	0	22/09/2011	15/12/2011	16/02/2015	0	5,7	8	7	1	0	1	0,4	0	0	5
406	52	6891	20/03/1949	0	2	1,03	0	11/07/2011	02/09/2011	03/10/2011	0	5,4	8	7	1	1	0	0,6	0	0	5
407	53	6891	20/03/1949	1	2	1,03	0	11/07/2011	02/09/2011	03/10/2011	0	5,4	8	7	1	1	0	0,6	0	0	5
408	54	6891	20/03/1949	1	1	1,03	0	11/07/2011	02/09/2011	03/10/2011	0	5,4	8	7	1	1	0	0,6	0	0	5
409	55	5562	01/01/1949	0	0	69,33	0	30/10/2007	10/02/2009	20/11/2014	0	0,53	7	7	0	0	1	0,5	0	0	4
410	56	5562	01/01/1949	1	2	69,33	0	30/10/2007	10/02/2009	20/11/2014	0	0,53	7	7	0	0	1	0,5	0	0	4
411	57	5562	01/01/1949	1	1	69,33	0	30/10/2007	10/02/2009	20/11/2014	0	0,53	7	7	0	0	1	0,5	0	0	4
412	58	6983	19/03/1943	0	0	4,57	0	20/07/2011	28/10/2011	15/03/2012	0	7,75	7	7	1	1	0	0,3	0	0	5
413	59	6983	19/03/1943	1	2	4,57	0	20/07/2011	28/10/2011	15/03/2012	0	7,75	7	7	1	1	0	0,3	0	0	5
414	60	6983	19/03/1943	1	2	4,57	0	20/07/2011	28/10/2011	15/03/2012	0	7,75	7	7	1	1	0	0,3	0	0	5
415	61	6851	25/05/1955	1	3	41,90	1	14/07/2011	24/10/2011	21/04/2015	1	7,9	9	9	1	0	0	1,0	0	0	5
416	62	6851	25/05/1955	1	2	41,90	1	14/07/2011	24/10/2011	21/04/2015	1	7,9	9	9	1	0	0	1,0	0	0	5
417	63	6851	25/05/1955	1	2	41,90	1	14/07/2011	24/10/2011	21/04/2015	1	7,9	9	9	1	0	0	1,0	0	0	5
418	64	6655	23/07/1939	0	1	22,27	0	16/03/2011	30/08/2011	08/07/2013	0	19	7	7	1	0	0	0,6	0	0	5
419	65	6655	23/07/1939	1	2	22,27	0	16/03/2011	30/08/2011	08/07/2013	0	19	7	7	1	0	0	0,6	0	0	5
420	66	6655	23/07/1939	1	2	22,27	0	16/03/2011	30/08/2011	08/07/2013	0	19	7	7	1	0	0	0,6	0	0	5
421	67	7061	14/03/1944	0	1	37,60	1	20/10/2011	14/12/2011	02/02/2015	1	7,1	9	9	1	1	1	0,4	0	0	5
422	68	7061	14/03/1944	1	x	37,60	1	20/10/2011	14/12/2011	02/02/2015	1	7,1	9	9	1	1	1	0,4	0	0	5
423	69	7061	14/03/1944	1	x	37,60	1	20/10/2011	14/12/2011	02/02/2015	1	7,1	9	9	1	1	1	0,4	0	0	5
424	70	6863	27/05/1946	0	0	3,90	0	10/05/2011	29/09/2011	26/01/2012	0	8,8	8	6	0	0	0	0,1	0	0	4
425	71	6863	27/05/1946	0	0	3,90	0	10/05/2011	29/09/2011	26/01/2012	0	8,8	8	6	0	0	0	0,1	0	0	4
426	72	6863	27/05/1946	0	1	3,90	0	10/05/2011	29/09/2011	26/01/2012	0	8,8	8	6	0	0	0	0,1	0	0	4
427	73	6920	18/12/1948	1	1	23,27	1	14/04/2011	18/10/2011	26/09/2013	1	162	8		1	1	1	0,3	1	0	6
428	74	6920	18/12/1948	1	1	23,27	1	14/04/2011	18/10/2011	26/09/2013	1	162	8		1	1	1	0,3	1	0	6
429	75	6942	15/09/1940	1	1	2,67	1	10/01/2011	27/10/2011	17/01/2012	1	10,79	8		1	1	1	0,1	1	1	6
430	76	6942	15/09/1940	1	1	2,67	1	10/01/2011	27/10/2011	17/01/2012	1	10,79	8		1	1	1	0,1	1	1	6
431	77	6822	19/10/1939	1	2	34,70	0	06/05/2011	08/09/2011	29/07/2014	0	8,2	7	7	0	0	0	0,4	1	0	4
432	78	6822	19/10/1939	1	3	34,70	0	06/05/2011	08/09/2011	29/07/2014	0	8,2	7	7	0	0	0	0,4	1	0	4
433	79	6655	23/07/1939	1	1	22,27	0	16/03/2011	30/08/2011	08/07/2013	0	19	7	7	1	0	0	0,6	0	0	5

434	80	6655	23/07/1939	1	2	22,27	0	16/03/2011	30/08/2011	08/07/2013	0	19	7	7	1	0	0	0,6	0	0	5
435	81	3783	12/02/1934	1	1	6,47	1	26/02/2004	17/05/2004	01/12/2004	1	0,6	8	9	1	1	0		0	1	6
436	82	3783	12/02/1934	1	1	6,47	1	26/02/2004	17/05/2004	01/12/2004	1	0,6	8	9	1	1	0		0	1	6
437	83	4229	23/07/1948	1	1	69,23	1	06/07/2005	25/08/2005	02/06/2011	1	5,03	7	8	1	0	1	0,1	0	0	5
438	84	4229	23/07/1948	1	0	69,23	1	06/07/2005	25/08/2005	02/06/2011	1	5,03	7	8	1	0	1	0,1	0	0	5
439	85	4537	02/11/1948	1	3	54,87	1	21/04/2006	05/06/2006	31/12/2010	1	4,16	7	8	1	1	1	0,5	0	1	6
440	86	4537	02/11/1948	1	3	54,87	1	21/04/2006	05/06/2006	31/12/2010	1	4,16	7	8	1	1	1	0,5	0	1	6
441	87	4656	26/04/1946	1	1	5,13	1	11/09/2006	09/03/2007	13/08/2007	1	6,53	9	9	1	1	1		1	1	6
442	88	4656	26/04/1946	1	1	5,13	1	11/09/2006	09/03/2007	13/08/2007	1	6,53	9	9	1	1	1		1	1	6
443	89	4776	16/09/1950	1	2	23,50	1	05/01/2007	05/06/2007	20/05/2009	1	19,34	7	9	1	1	1	0,9	1	2	6
444	90	4776	16/09/1950	1	1	23,50	1	05/01/2007	05/06/2007	20/05/2009	1	19,34	7	9	1	1	1	0,9	1	2	6
445	91	5017	27/12/1956	1	2	57,77	1	29/10/2007	08/01/2008	31/10/2012	1	3,5	7	7	1		1	0,8	1	1	5
446	92	5017	27/12/1956	1	3	57,77	1	29/10/2007	08/01/2008	31/10/2012	1	3,5	7	7	1		1	0,8	1	1	5
447	93	4979	20/09/1941	1	x	41,20	1	14/08/2007	04/03/2008	10/08/2011	1	33,4	10		1	0	0	1,0	1	0	5
448	94	4979	20/09/1941	1	x	41,20	1	14/08/2007	04/03/2008	10/08/2011	1	33,4	10		1	0	0	1,0	1	0	5
449	95	5081	17/10/1932	1	x	73,20	1	01/04/2008	21/05/2008	27/06/2014	1	19	9	9	1	0	1	0,5	0	1	5
450	96	5081	17/10/1932	1	2	73,20	1	01/04/2008	21/05/2008	27/06/2014	1	19	9	9	1	0	1	0,5	0	1	5
451	97	5098	19/04/1954	1	0	77,43	1	25/04/2008	29/07/2008	12/01/2015	1	18	7	9	1	1	0	0,5	1	1	6
452	98	5098	19/04/1954	1	1	77,43	1	25/04/2008	29/07/2008	12/01/2015	1	18	7	9	1	1	0	0,5	1	1	6
453	99	5046	10/08/1951	1	x	31,37	1	01/12/2007	05/09/2008	16/04/2011	1	42	9		1	1	1	0,9	1	0	6
454	100	5046	10/08/1951	1	x	31,37	1	01/12/2007	05/09/2008	16/04/2011	1	42	9		1	1	1	0,9	1	0	6
455	101	5517	07/01/1940	1	2	60,70	1	03/08/2007	13/03/2008	04/04/2013	1	6,74	6	9	0	0	0	0,1	1	0	4
456	102	5517	07/01/1940	1	2	60,70	1	03/08/2007	13/03/2008	04/04/2013	1	6,74	6	9	0	0	0	0,1	1	0	4
457	103	5245	25/12/1945	1	2	84,20	1	21/01/2008	25/03/2008	01/04/2015	1	4,96	7	7	1	1	1	0,7	1	2	6
458	104	5245	25/12/1945	1	2	84,20	1	21/01/2008	25/03/2008	01/04/2015	1	4,96	7	7	1	1	1	0,7	1	2	6
459	105	5103	23/01/1939	1	x	27,60	1	17/07/2007	09/05/2008	27/08/2010	1	7,1	9	9	1	1	1	0,5	1	2	6
460	106	5103	23/01/1939	1	1	27,60	1	17/07/2007	09/05/2008	27/08/2010	1	7,1	9	9	1	1	1	0,5	1	2	6
461	107	5139	23/04/1937	1	1	79,20	1	01/11/1997	01/07/1998	07/02/2005	1	12,3	9		0				1	2	5
462	108	5139	23/04/1937	1	1	79,20	1	01/11/1997	01/07/1998	07/02/2005	1	12,3	9		0				1	2	5
463	109	5271	08/05/1936	1	x	9,93	1	13/11/2008	24/12/2008	22/10/2009	1	40,8	9	9	1	0	1	0,5	0	1	5
464	110	5271	08/05/1936	1	x	9,93	1	13/11/2008	24/12/2008	22/10/2009	1	40,8	9	9	1	0	1	0,5	0	1	5
465	111	5527	03/09/1939	1	1	42,33	1	30/04/2009	23/06/2009	03/01/2013	1	15,07	7	7	1	1	0	1,0	0	1	6
466	112	5527	03/09/1939	1	0	42,33	1	30/04/2009	23/06/2009	03/01/2013	1	15,07	7	7	1	1	0	1,0	0	1	6
467	113	1700	31/07/1908	1	2		0	23/10/1996		18/08/1998	0		8		0				0	0	1
468	114	1700	31/07/1908	1	x		0	23/10/1996		18/08/1998	0		8		0				0	0	1
469	115	1701	07/10/1907	1	0		0	20/09/1996		19/07/2000	0		9		0				0	0	
470	116	1701	07/10/1907	1	0		0	20/09/1996		19/07/2000	0		9		0				0	0	
471	117	2776	11/07/1923	1	0		0				0				0				0	0	
472	118	2776	11/07/1923	1	1		0				0				0				0	0	
473	119	2269	02/08/1929	1	x		1	02/12/1999		05/11/2009	1		10		0				1	2	1
474	120	2269	02/08/1929	1	2		1	02/12/1999		05/11/2009	1		10		0				1	2	1
475	121	5538	10/03/1952	1	x	14,07	1	24/11/2008	07/07/2009	09/09/2010	1	6,2	9	9	1	1	1	0,8	1	1	7
476	122	5538	10/03/1952	1	x	14,07	1	24/11/2008	07/07/2009	09/09/2010	1	6,2	9	9	1	1	1	0,8	1	1	7
477	123	6343	01/12/1952	0	2	5,70	1	18/06/2009	25/08/2009	16/02/2010	1	6	6	7	1	0	1	1,0	0	1	5
478	124	6343	01/12/1952	0	2	5,70	1	18/06/2009	25/08/2009	16/02/2010	1	6	6	7	1	0	1	1,0	0	1	5
479	125	5685	17/11/1939	0	3	66,50	1	16/07/2009	27/10/2009	12/05/2015	1	4,7	9	9	1	1	1	0,4	0	2	6
480	126	5685	17/11/1939	0	3	66,50	1	16/07/2009	27/10/2009	12/05/2015	1	4,7	9	9	1	1	1	0,4	0	2	6
481	127	6824	10/05/1947	1	2	20,50	1	12/07/2011	08/09/2011	23/05/2013	1	4,7	7	7	1	1	1	0,5	0	1	6
482	128	6824	10/05/1947	1	2	20,50	1	12/07/2011	08/09/2011	23/05/2013	1	4,7	7	7	1	1	1	0,5	0	1	6
483	129	2764	18/10/1948	1	x	218,77	1	17/01/1996	19/02/1997	12/05/2015	1	50	7		0			1,0	1	2	5
484	130	2764	18/10/1948	1	x	218,77	1	17/01/1996	19/02/1997	12/05/2015	1	50	7		0			1,0	1	2	5
485	131	1175	31/03/1927	1	0		0	23/03/1994			0	7,4	5		0			1,0	1	0	5
486	132	1175	31/03/1927	1	0		0	23/03/1994			0	7,4	5		0			1,0	1	0	5
487	133	3160	20/06/1949	1	0	11,00	1	18/04/2002	08/10/2002	08/09/2003	1	10,4	9	8	1	1	1	1,0	1	0	6
488	134	3160	20/06/1949	1	0	11,00	1	18/04/2002	08/10/2002	08/09/2003	1	10,4	9	8	1	1	1	1,0	1	0	6
489	135	6842	08/01/1933	1	x		1	26/05/2004		10/07/2013	1	27	7		0			0,9	1	0	2
490	136	6842	08/01/1933	1	x		1	26/05/2004		10/07/2013	1	27	7		0			0,9	1	0	2
491	137	1175	31/03/1927	1	1		0	23/03/1994			0	7,4	5		0			1,0	1	0	5
492	138	1175	31/03/1927	1	x		0	23/03/1994			0	7,4	5		0			1,0	1	0	5
493	139	6679	26/03/1933	1	0		0	24/06/1996			0	25,4	8		0			1,0	2	0	5
494	140	6679	26/03/1933	1	1		0	24/06/1996			0	25,4	8		0			1,0	2	0	5
495	141	5016	24/08/1940	1	3	61,33	0	26/10/2007	11/01/2008	21/02/2013	0	12,5	6	7	0	1	0	0,3	0	0	6
496	142	5016	24/08/1940	1	2	61,33	0	26/10/2007	11/01/2008	21/02/2013	0	12,5	6	7	0	1	0	0,3	0	0	6
497	143	5057	31/01/1934	1	1		1				1				0				0	0	
498	144	5057	31/01/1934	1	x		1				1				0				0	0	
499	145	4334	21/10/1936	1	1		1	02/12/1994			1		7		0			0,5	0	0	
500	146	4334	21/10/1936	1	0		1	02/12/1994			1		7		0			0,5	0	0	
501	147	4122	19/05/1932	1	1		0				0				0				0	0	
502	148	4122	19/05/1932	1	2		0				0				0				0	0	
503	149	2773	18/03/1944	1	1		1	01/01/1993		03/08/2003	1	82			0				1	2	
504	150	2773	18/03/1944	1	0		1	01/01/1993		03/08/2003	1	82			0				1	2	
505	151	2776	11/07/1923	1	x		0				0				0				0	0	

506	152	2776	11/07/1923	1	x		0				0				0				0	0	
507	153	5142	07/10/1930	1	3	196,57	1	01/08/1994	02/03/1995	19/07/2011	1		7		0	0	0		1	1	1
508	154	5142	07/10/1930	1	2	196,57	1	01/08/1994	02/03/1995	19/07/2011	1		7		0	0	0		1	1	1
509	155	5274	24/02/1913	1	1		0	17/10/2002		02/02/2015	0	47,4	6		0			1,0	1	0	
510	156	5274	24/02/1913	1	x		0	17/10/2002		02/02/2015	0	47,4	6		0			1,0	1	0	
511	157	4153	17/11/1930	1	1	11,03	1	01/04/2005	22/12/2008	23/11/2009	1		9	9	1	1	1	1,0	0	2	7
512	158	4153	17/11/1930	1	1	11,03	1	01/04/2005	22/12/2008	23/11/2009	1		9	9	1	1	1	1,0	0	2	7
513	159	6342	11/06/1966	1	3		1				1				0				0	0	
514	160	6342	11/06/1966	1	3		1				1				0				0	0	
515	161	5421	10/10/1941	1	1	53,90	1	23/01/2009	31/03/2009	27/09/2013	1	5,48	9	9	1	1	1	0,9	0	0	5
516	162	5421	10/10/1941	1	1	53,90	1	23/01/2009	31/03/2009	27/09/2013	1	5,48	9	9	1	1	1	0,9	0	0	5
517	163	3688	26/07/1940	1	2	3,90	1	10/11/2003	21/04/2009	18/08/2009	1	14,6	8		0	0	1	0,1	1	0	4
518	164	3688	26/07/1940	1	1	3,90	1	10/11/2003	21/04/2009	18/08/2009	1	14,6	8		0	0	1	0,1	1	0	4
519	165	5772	04/09/1940	1	x	22,20	1	01/12/2008	19/05/2009	25/03/2011	1	14	7	7	1	0	1	0,3	0	0	5
520	166	5772	04/09/1940	1	x	22,20	1	01/12/2008	19/05/2009	25/03/2011	1	14	7	7	1	0	1	0,3	0	0	5
521	167	6194	05/06/1920	1	1		1	02/03/2010		25/10/2011	1	78	9		0				2	0	3
522	168	6194	05/06/1920	1	1		1	02/03/2010		25/10/2011	1	78	9		0				2	0	3
523	169	5359	15/09/1936	1	2	14,30	1	16/02/2005	29/11/2010	08/02/2012	1	5,2	6	9	1	0	1	0,1	0	0	5
524	170	5359	15/09/1936	1	2	14,30	1	16/02/2005	29/11/2010	08/02/2012	1	5,2	6	9	1	0	1	0,1	0	0	5
525	171	6834	06/09/1946	1	2	19,30	0	17/12/2010	14/02/2012	23/09/2013	0		8		0				1	0	2
526	172	6834	06/09/1946	1	0	19,30	0	17/12/2010	14/02/2012	23/09/2013	0		8		0				1	0	2
527	173	6627	22/06/1947	1	x	41,90	1	23/08/2000	01/01/2001	28/06/2004	1	7,8	9		0			0,4	1	2	3
528	174	6627	22/06/1947	1	0	41,90	1	23/08/2000	01/01/2001	28/06/2004	1	7,8	9		0			0,4	1	2	3
529	175	6843	31/07/1927	1	3		1	15/05/2011		08/09/2011	1		10		0				1	0	1
530	176	6843	31/07/1927	1	3		1	15/05/2011		08/09/2011	1		10		0				1	0	1
532	1	5703	18/11/1946	0	1	1,30	0	21/05/2009	10/12/2009	19/01/2010	0	11,44	6	7	1	0	1	0,1	0	0	5
533	2	5703	18/11/1946	1	2	1,30	0	21/05/2009	10/12/2009	19/01/2010	0	11,44	6	7	1	0	1	0,1	0	0	5
534	3	5703	18/11/1946	1	1	1,30	0	21/05/2009	10/12/2009	19/01/2010	0	11,44	6	7	1	0	1	0,1	0	0	5
535	4	6876	09/10/1947	0	2	35,77	0	28/03/2011	29/09/2011	22/09/2014	0		7	7	0	0	0	0,6	0	0	4
536	5	6876	09/10/1947	1	0	35,77	0	28/03/2011	29/09/2011	22/09/2014	0		7	7	0	0	0	0,6	0	0	4
537	6	6876	09/10/1947	1	0	35,77	0	28/03/2011	29/09/2011	22/09/2014	0		7	7	0	0	0	0,6	0	0	4
538	7	6905	27/02/1954	0	1	12,53	0	15/06/2011	13/10/2011	29/10/2012	0	3,7	7	7	0	0	0	0,4	0	0	4
539	8	6905	27/02/1954	1	0	12,53	0	15/06/2011	13/10/2011	29/10/2012	0	3,7	7	7	0	0	0	0,4	0	0	4
540	9	6905	27/02/1954	1	1	12,53	0	15/06/2011	13/10/2011	29/10/2012	0	3,7	7	7	0	0	0	0,4	0	0	4
541	10	6878	12/03/1941	0	2	10,03	1	07/06/2011	30/09/2011	01/08/2012	1	5,6	7	6	0	0	0	0,1	0	0	4
542	11	6878	12/03/1941	1	2	10,03	1	07/06/2011	30/09/2011	01/08/2012	1	5,6	7	6	0	0	0	0,1	0	0	4
543	12	6878	12/03/1941	1	2	10,03	1	07/06/2011	30/09/2011	01/08/2012	1	5,6	7	6	0	0	0	0,1	0	0	4
544	13	6784	22/12/1963	0	0	8,03	0	01/02/2011	09/08/2011	10/04/2012	0	4,5	6	6	0	0	0	0,3	0	0	4
545	14	6784	22/12/1963	1	2	8,03	0	01/02/2011	09/08/2011	10/04/2012	0	4,5	6	6	0	0	0	0,3	0	0	4
546	15	6784	22/12/1963	1	2	8,03	0	01/02/2011	09/08/2011	10/04/2012	0	4,5	6	6	0	0	0	0,3	0	0	4
547	16	6858	29/04/1950	0	1	13,23	0	31/05/2011	22/09/2011	29/10/2012	0	4,65	7	6	0	0	0	0,2	0	0	4
548	17	6858	29/04/1950	0	x	13,23	0	31/05/2011	22/09/2011	29/10/2012	0	4,65	7	6	0	0	0	0,2	0	0	4
549	18	6858	29/04/1950	0	1	13,23	0	31/05/2011	22/09/2011	29/10/2012	0	4,65	7	6	0	0	0	0,2	0	0	4
550	19	5693	13/02/1950	0	0	58,40	0	07/02/2009	26/11/2009	08/10/2014	0	9,27	7	7	1	1	1	0,2	0	0	5
551	20	5693	13/02/1950	1	3	58,40	0	07/02/2009	26/11/2009	08/10/2014	0	9,27	7	7	1	1	1	0,2	0	0	5
552	21	5693	13/02/1950	1	1	58,40	0	07/02/2009	26/11/2009	08/10/2014	0	9,27	7	7	1	1	1	0,2	0	0	5
553	22	6879	18/07/1945	1	2	20,67	0	12/07/2011	30/09/2011	20/06/2013	0	7,31	7	7	0	0	0	1,0	0	0	4
554	23	6879	18/07/1945	1	1	20,67	0	12/07/2011	30/09/2011	20/06/2013	0	7,31	7	7	0	0	0	1,0	0	0	4
555	24	6879	18/07/1945	1	2	20,67	0	12/07/2011	30/09/2011	20/06/2013	0	7,31	7	7	0	0	0	1,0	0	0	4
556	25	6825	16/10/1956	0	0	37,40	0	02/08/2011	08/09/2011	20/10/2014	0	6,3	7	7	0	0	0	0,3	0	0	4
557	26	6825	16/10/1956	0	1	37,40	0	02/08/2011	08/09/2011	20/10/2014	0	6,3	7	7	0	0	0	0,3	0	0	4
558	27	6825	16/10/1956	0	3	37,40	0	02/08/2011	08/09/2011	20/10/2014	0	6,3	7	7	0	0	0	0,3	0	0	4
559	28	6757	15/12/1953	0	2	36,67	0	20/04/2011	21/07/2011	11/08/2014	0	8	7	7	0	0	0	0,1	0	0	4
560	29	6757	15/12/1953	1	3	36,67	0	20/04/2011	21/07/2011	11/08/2014	0	8	7	7	0	0	0	0,1	0	0	4
561	30	6757	15/12/1953	1	3	36,67	0	20/04/2011	21/07/2011	11/08/2014	0	8	7	7	0	0	0	0,1	0	0	4
562	31	5680	25/02/1948	0	2	7,67	0	01/09/2009	17/11/2009	07/07/2010	0	5,75	8	8	0		1	0,1	0	0	4
563	32	5680	25/02/1948	1	3	7,67	0	01/09/2009	17/11/2009	07/07/2010	0	5,75	8	8	0		1	0,1	0	0	4
564	33	5680	25/02/1948	1	2	7,67	0	01/09/2009	17/11/2009	07/07/2010	0	5,75	8	8	0		1	0,1	0	0	4
565	34	5681	18/02/1946	0	0	39,50	0	10/03/2009	19/11/2009	04/03/2013	0	3	6	7	0	0	0	0,1	0	0	4
566	35	5681	18/02/1946	0	0	39,50	0	10/03/2009	19/11/2009	04/03/2013	0	3	6	7	0	0	0	0,1	0	0	4
567	36	5681	18/02/1946	1	2	39,50	0	10/03/2009	19/11/2009	04/03/2013	0	3	6	7	0	0	0	0,1	0	0	4
568	37	6982	29/09/1953	0	0		0	06/07/2011	28/10/2011	28/10/2011	0	7,5	6	7	1	0	1	0,6	0	0	5
569	38	6982	29/09/1953	1	0		0	06/07/2011	28/10/2011	28/10/2011	0	7,5	6	7	1	0	1	0,6	0	0	5

570	39	6982	29/09/1953	1	0		0	06/07/2011	28/10/2011	28/10/2011	0	7,5	6	7	1	0	1	0,6	0	0	5
571	40	6874	01/10/1943	0	2	36,37	0	11/08/2011	27/09/2011	08/10/2014	0	3,2	7	7	0	0	0	0,6	0	0	4
572	41	6874	01/10/1943	1	0	36,37	0	11/08/2011	27/09/2011	08/10/2014	0	3,2	7	7	0	0	0	0,6	0	0	4
573	42	6874	01/10/1943	1	0	36,37	0	11/08/2011	27/09/2011	08/10/2014	0	3,2	7	7	0	0	0	0,6	0	0	4
574	43	5309	02/05/1943	0	1	3,20	0	18/09/2007	22/01/2008	28/04/2008	0	6,06	6	6	0	0	0	0,5	0	0	4
575	44	5309	02/05/1943	1	1	3,20	0	18/09/2007	22/01/2008	28/04/2008	0	6,06	6	6	0	0	0	0,5	0	0	4
576	45	5309	02/05/1943	1	0	3,20	0	18/09/2007	22/01/2008	28/04/2008	0	6,06	6	6	0	0	0	0,5	0	0	4
577	46	6983	19/03/1943	0	0	4,57	0	20/07/2011	28/10/2011	15/03/2012	0	7,75	7	7	1	1	0	0,3	0	0	5
578	47	6983	19/03/1943	1	2	4,57	0	20/07/2011	28/10/2011	15/03/2012	0	7,75	7	7	1	1	0	0,3	0	0	5
579	48	6983	19/03/1943	1	3	4,57	0	20/07/2011	28/10/2011	15/03/2012	0	7,75	7	7	1	1	0	0,3	0	0	5
580	49	6958	08/04/1942	0	1	39,53	0	23/06/2011	29/09/2011	15/01/2015	0	5,97	7	7	0	0	0	0,3	0	0	4
581	50	6958	08/04/1942	0	1	39,53	0	23/06/2011	29/09/2011	15/01/2015	0	5,97	7	7	0	0	0	0,3	0	0	4
582	51	6958	08/04/1942	0	1	39,53	0	23/06/2011	29/09/2011	15/01/2015	0	5,97	7	7	0	0	0	0,3	0	0	4
583	52	6893	25/05/1951	0	0	25,63	0	02/06/2011	06/10/2011	25/11/2013	0	5,7	7	7	0	0	0	0,3	0	0	4
584	53	6893	25/05/1951	0	0	25,63	0	02/06/2011	06/10/2011	25/11/2013	0	5,7	7	7	0	0	0	0,3	0	0	4
585	54	6893	25/05/1951	1	2	25,63	0	02/06/2011	06/10/2011	25/11/2013	0	5,7	7	7	0	0	0	0,3	0	0	4
586	55	6774	07/11/1948	0	3	30,67	0	21/02/2011	04/08/2011	24/02/2014	0	9,8	7	7	0	0	0	0,3	0	0	4
587	56	6774	07/11/1948	1	3	30,67	0	21/02/2011	04/08/2011	24/02/2014	0	9,8	7	7	0	0	0	0,3	0	0	4
588	57	6774	07/11/1948	1	3	30,67	0	21/02/2011	04/08/2011	24/02/2014	0	9,8	7	7	0	0	0	0,3	0	0	4
589	58	5308	29/08/1940	0	0	75,60	0	10/04/2007	10/01/2008	28/04/2014	0	14	7	7	0	0	1	0,1	0	0	4
590	59	5308	29/08/1940	1	2	75,60	0	10/04/2007	10/01/2008	28/04/2014	0	14	7	7	0	0	1	0,1	0	0	4
591	60	5308	29/08/1940	1	2	75,60	0	10/04/2007	10/01/2008	28/04/2014	0	14	7	7	0	0	1	0,1	0	0	4
592	61	5689	29/05/1947	1	0	9,43	0	15/06/2009	24/11/2009	07/09/2010	0	7,47	7	7	0	0	1	0,1	0	0	4
593	62	5689	29/05/1947	1	3	9,43	0	15/06/2009	24/11/2009	07/09/2010	0	7,47	7	7	0	0	1	0,1	0	0	4
594	63	5689	29/05/1947	1	2	9,43	0	15/06/2009	24/11/2009	07/09/2010	0	7,47	7	7	0	0	1	0,1	0	0	4
595	64	6749	27/02/1953	0	1	24,50	0	30/03/2011	03/11/2011	18/11/2013	0	4,1	6	7	0	0	0	0,6	0	0	4
596	65	6749	27/02/1953	0	1	24,50	0	30/03/2011	03/11/2011	18/11/2013	0	4,1	6	7	0	0	0	0,6	0	0	4
597	66	6749	27/02/1953	0	1	24,50	0	30/03/2011	03/11/2011	18/11/2013	0	4,1	6	7	0	0	0	0,6	0	0	4
598	67	5683	27/08/1960	0	1	18,13	0	06/10/2009	10/11/2009	14/05/2011	0	6,8	7	7	0	0	0	0,5	0	0	4
599	68	5683	27/08/1960	1	3	18,13	0	06/10/2009	10/11/2009	14/05/2011	0	6,8	7	7	0	0	0	0,5	0	0	4
600	69	5683	27/08/1960	1	3	18,13	0	06/10/2009	10/11/2009	14/05/2011	0	6,8	7	7	0	0	0	0,5	0	0	4
601	70	6626	01/08/1949	0	2	27,07	0	07/04/2011	04/08/2011	06/11/2013	0	8,55	7	7	1	0	1	0,1	0	0	5
602	71	6626	01/08/1949	1	3	27,07	0	07/04/2011	04/08/2011	06/11/2013	0	8,55	7	7	1	0	1	0,1	0	0	5
603	72	6626	01/08/1949	1	2	27,07	0	07/04/2011	04/08/2011	06/11/2013	0	8,55	7	7	1	0	1	0,1	0	0	5
604	73	5295	02/01/1941	0	1	86,10	0	04/10/2007	03/01/2008	06/03/2015	0	2	7	7	0	0	0	0,3	0	0	4
605	74	5295	02/01/1941	1	1	86,10	0	04/10/2007	03/01/2008	06/03/2015	0	2	7	7	0	0	0	0,3	0	0	4
606	75	5295	02/01/1941	1	1	86,10	0	04/10/2007	03/01/2008	06/03/2015	0	2	7	7	0	0	0	0,3	0	0	4
607	76	6808	29/08/1962	0	1	40,77	0	04/07/2011	22/08/2011	15/01/2015	0	26	8	7	1	0	1	0,2	0	0	5
608	77	6808	29/08/1962	1	2	40,77	0	04/07/2011	22/08/2011	15/01/2015	0	26	8	7	1	0	1	0,2	0	0	5
609	78	6808	29/08/1962	1	2	40,77	0	04/07/2011	22/08/2011	15/01/2015	0	26	8	7	1	0	1	0,2	0	0	5
610	79	5535	02/07/1947	1	0	29,30	0		08/01/2009	17/06/2011	0	7,5	7	7	0	0	0	0,1	0	0	2
611	80	5535	02/07/1947	1	2	29,30	0		08/01/2009	17/06/2011	0	7,5	7	7	0	0	0	0,1	0	0	2
612	81	5535	02/07/1947	1	2	29,30	0		08/01/2009	17/06/2011	0	7,5	7	7	0	0	0	0,1	0	0	2
613	82	6958	08/04/1942	0	1	39,53	0	23/06/2011	29/09/2011	15/01/2015	0	5,97	7	7	0	0	0	0,3	0	0	4
614	83	6874	01/10/1943	1	1	36,37	0	11/08/2011	27/09/2011	08/10/2014	0	3,2	7	7	0	0	0	0,6	0	0	4
615	84	6893	25/05/1951	0	1	25,63	0	02/06/2011	06/10/2011	25/11/2013	0	5,7	7	7	0	0	0	0,3	0	0	4
616	85	5309	02/05/1943	1	1	3,20	0	18/09/2007	22/01/2008	28/04/2008	0	6,06	6	6	0	0	0	0,5	0	0	4
617	86	6876	09/10/1947	0	1	35,77	0	28/03/2011	29/09/2011	22/09/2014	0		7	7	0	0	0	0,6	0	0	4
618	87	6770	10/02/1946	1	2	43,33	0	22/06/2011	02/08/2011	12/03/2015	0	8,1	8	9	1	1	1	0,3	1	0	6
619	88	6770	10/02/1946	1	1	43,33	0	22/06/2011	02/08/2011	12/03/2015	0	8,1	8	9	1	1	1	0,3	1	0	6
620	89	5877	01/06/1951	1	1	11,13	1	26/08/2009	31/05/2010	04/05/2011	1	32,25	9		0	1	1	1,0	1	0	6
621	90	5877	01/06/1951	1	1	11,13	1	26/08/2009	31/05/2010	04/05/2011	1	32,25	9		0	1	1	1,0	1	0	6
622	91	6112	16/10/1940	1	2	54,73	0	16/04/2010	26/07/2010	18/02/2015	0	8,1	9		1	0	0	0,5	1	0	5
623	92	6112	16/10/1940	1	1	54,73	0	16/04/2010	26/07/2010	18/02/2015	0	8,1	9		1	0	0	0,5	1	0	5
624	93	5120	11/03/1944	0	1	11,47	1	07/07/2008	21/10/2008	05/10/2009	1	6,2	8		0	0	0	0,4	2	1	4
625	94	5120	11/03/1944	0	2	11,47	1	07/07/2008	21/10/2008	05/10/2009	1	6,2	8		0	0	0	0,4	2	1	4

626	95	6755	20/01/1954	1	2	38,17	0	02/02/2011	19/07/2011	24/09/2014	0	6,9	7		0	0	0	0,6	1	0	4
627	96	6755	20/01/1954	1	2	38,17	0	02/02/2011	19/07/2011	24/09/2014	0	6,9	7		0	0	0	0,6	1	0	4
628	97	5779	01/02/1953	1	2	59,60	1	26/08/2009	03/11/2009	21/10/2014	1	6,3	7	7	1	1	0	0,8	0	1	6
629	98	5779	01/02/1953	1	1	59,60	1	26/08/2009	03/11/2009	21/10/2014	1	6,3	7	7	1	1	0	0,8	0	1	6
630	99	5735	13/05/1948	1	2	18,77	1	07/10/2009	10/03/2010	03/10/2011	1	34	9	9	1	1	0	0,6	1	1	6
631	100	5735	13/05/1948	1	0	18,77	1	07/10/2009	10/03/2010	03/10/2011	1	34	9	9	1	1	0	0,6	1	1	6
632	101	6106	16/10/1941	1	0	58,43	1	10/02/2010	14/07/2010	27/05/2015	1	24,48	7	7	1	1	1	0,8	1	1	6
633	102	6106	16/10/1941	1	0	58,43	1	10/02/2010	14/07/2010	27/05/2015	1	24,48	7	7	1	1	1	0,8	1	1	6
634	103	6765	27/01/1942	1	2		1	13/04/2010	14/07/2010	14/07/2010	1	32	8	9	0	1	1	0,6	0	1	6
635	104	6765	27/01/1942	1	1		1	13/04/2010	14/07/2010	14/07/2010	1	32	8	9	0	1	1	0,6	0	1	6
636	105	6364	15/03/1946	1	1	24,03	1	18/11/2008	23/09/2010	24/09/2012	1	11,7	9		1	1	1	0,3	1	1	5
637	106	6364	15/03/1946	1	1	24,03	1	18/11/2008	23/09/2010	24/09/2012	1	11,7	9		1	1	1	0,3	1	1	5
638	107	6274	16/06/1951	1	1		0	06/08/2010	02/11/2010	02/11/2010	0	27,5	7	9	1	0	1	0,7	0	0	5
639	108	6274	16/06/1951	1	2		0	06/08/2010	02/11/2010	02/11/2010	0	27,5	7	9	1	0	1	0,7	0	0	5
640	109	6956	11/10/1946	1	2	33,83	1	04/11/2010	21/12/2010	16/10/2013	1	11,95	8	9	1	1	1	0,2	0	1	6
641	110	6956	11/10/1946	1	2	33,83	1	04/11/2010	21/12/2010	16/10/2013	1	11,95	8	9	1	1	1	0,2	0	1	6
642	111	6387	26/07/1941	1	0	43,50	1	28/10/2010	26/01/2011	11/09/2014	1	9,2	7	9	1	1	1	0,2	0	1	6
643	112	6387	26/07/1941	1	1	43,50	1	28/10/2010	26/01/2011	11/09/2014	1	9,2	7	9	1	1	1	0,2	0	1	6
644	113	640	04/07/1929	1	2		1				1				0				0	0	
645	114	640	04/07/1929	1	1		1				1				0				0	0	
646	115	6436	12/03/1940	1	1	22,40	1	06/12/2010	01/02/2011	13/12/2012	1	6,7	7	7	1	1	1	1,0	0	1	6
647	116	6436	12/03/1940	1	1	22,40	1	06/12/2010	01/02/2011	13/12/2012	1	6,7	7	7	1	1	1	1,0	0	1	6
648	117	6525	10/05/1962	1	2	11,80	1	21/01/2011	07/03/2011	01/03/2012	1	15	7	9	1	1	1	0,8	0	1	6
649	118	6525	10/05/1962	1	2	11,80	1	21/01/2011	07/03/2011	01/03/2012	1	15	7	9	1	1	1	0,8	0	1	6
650	119	6535	28/10/1942	1	2	21,77	1	30/06/2010	17/03/2011	10/01/2013	1	79,9	9		1	1	1	0,8	1	1	6
651	120	6535	28/10/1942	1	2	21,77	1	30/06/2010	17/03/2011	10/01/2013	1	79,9	9		1	1	1	0,8	1	1	6
652	121	6564	02/03/1947	1	2	10,27	1	02/02/2011	08/04/2011	16/02/2012	1	5,4	9	9	1	0	0	0,3	0	1	5
653	122	6564	02/03/1947	1	2	10,27	1	02/02/2011	08/04/2011	16/02/2012	1	5,4	9	9	1	0	0	0,3	0	1	5
654	123	6574	05/01/1943	1	1	10,53	1	08/02/2011	11/04/2011	27/02/2012	1	13	10	9	1	1	0	0,7	0	1	7
655	124	6574	05/01/1943	1	1	10,53	1	08/02/2011	11/04/2011	27/02/2012	1	13	10	9	1	1	0	0,7	0	1	7
656	125	6616	11/11/1949	1	0	18,50	1	12/04/2011	19/05/2011	04/12/2012	1	9,61	8	9	0	0	1	0,3	0	1	4
657	126	6616	11/11/1949	1	0	18,50	1	12/04/2011	19/05/2011	04/12/2012	1	9,61	8	9	0	0	1	0,3	0	1	4
658	127	6697	11/05/1939	1	1	8,73	1	05/04/2011	06/06/2011	28/02/2012	1	5,8	9	9	1	0	1	0,3	0	0	5
659	128	6697	11/05/1939	1	1	8,73	1	05/04/2011	06/06/2011	28/02/2012	1	5,8	9	9	1	0	1	0,3	0	0	5
660	129	1387	14/09/1919	1	2		0	29/03/1995			0		9		0			0,2	0	0	
661	130	1387	14/09/1919	1	1		0	29/03/1995			0		9		0			0,2	0	0	
662	131	1517	15/10/1930	1	0		1	20/10/1995	29/12/1995		1		5	4	0	0	1		0	0	4
663	132	1517	15/10/1930	1	0		1	20/10/1995	29/12/1995		1		5	4	0	0	1		0	0	4
664	133	1626	30/05/1930	1	0	73,77	0	12/06/1996	10/10/1996	03/12/2002	0	40	8	7	0	0	0		1	0	2
665	134	1626	30/05/1930	1	1	73,77	0	12/06/1996	10/10/1996	03/12/2002	0	40	8	7	0	0	0		1	0	2
666	135	1701	07/10/1907	1	2		0	20/09/1996		19/07/2000	0		9		0				0	0	
667	136	1701	07/10/1907	1	1		0	20/09/1996		19/07/2000	0		9		0				0	0	
668	137	5094	21/07/1950	1	1	28,97	1	07/04/2008	17/07/2008	16/12/2010	1	31,26	7	9	1	0	1	0,9	0	0	5
669	138	5094	21/07/1950	1	1	28,97	1	07/04/2008	17/07/2008	16/12/2010	1	31,26	7	9	1	0	1	0,9	0	0	5
670	139	4999	02/09/1945	1	x	10,37	1	11/09/2007	29/07/2008	10/06/2009	1	3,3	7	8	1	0	1	0,2	1	0	5
671	140	4999	02/09/1945	1	3	10,37	1	11/09/2007	29/07/2008	10/06/2009	1	3,3	7	8	1	0	1	0,2	1	0	5
672	141	5053	09/01/1940	1	x	20,67	1	24/01/2008	03/06/2008	23/02/2010	1	4,32	7	7	0	0	0	0,2	0	0	4
673	142	5053	09/01/1940	1	2	20,67	1	24/01/2008	03/06/2008	23/02/2010	1	4,32	7	7	0	0	0	0,2	0	0	4
674	143	5121	01/03/1935	1	1		1	09/07/2008	30/01/2009		1		10		0				1	0	2
675	144	5121	01/03/1935	1	x		1	09/07/2008	30/01/2009		1		10		0				1	0	2
676	145	2504	10/03/1938	1	2	99,03	0	15/12/1999	12/10/2000	13/01/2009	0	41	7		0	0	0	0,4	1	0	4
677	146	2504	10/03/1938	1	0	99,03	0	15/12/1999	12/10/2000	13/01/2009	0	41	7		0	0	0	0,4	1	0	4
678	147	2269	02/08/1929	1	1		1	02/12/1999		05/11/2009	1		10		0				1	2	1
679	148	2269	02/08/1929	1	1		1	02/12/1999		05/11/2009	1		10		0				1	2	1
680	149	2776	11/07/1923	1	1		0				0				0				0	0	
681	150	2776	11/07/1923	1	1		0				0				0				0	0	
682	151	2774	10/10/1928	1	1		1			10/07/2001	1		8		0				1	0	5
683	152	2774	10/10/1928	1	2		1			10/07/2001	1		8		0				1	0	5
684	153	5628	22/11/1944	1	2	28,33	1	29/05/2009	01/09/2009	11/01/2012	1	3,17	9	9	1	1	1	0,8	1	2	6
685	154	5628	22/11/1944	1	2	28,33	1	29/05/2009	01/09/2009	11/01/2012	1	3,17	9	9	1	1	1	0,8	1	2	6
686	155	1280	31/07/1936	1	x	22,87	1	23/08/1994	11/10/1994	07/09/1996	1	32	7	6	1	0	1	0,2	0	0	5
687	156	1280	31/07/1936	1	1	22,87	1	23/08/1994	11/10/1994	07/09/1996	1	32	7	6	1	0	1	0,2	0	0	5
688	157	4153	17/11/1930	1	1	11,03	1	01/04/2005	22/12/2008	23/11/2009	1		9	9	1	1	1	1,0	0	2	7
689	158	4153	17/11/1930	1	0	11,03	1	01/04/2005	22/12/2008	23/11/2009	1		9	9	1	1	1	1,0	0	2	7
690	159	5695	22/04/1944	1	2	62,87	0	17/08/2009	23/10/2009	19/01/2015	0	4,6	8	9	1	0	0	0,8	0	0	5
691	160	5695	22/04/1944	1	1	62,87	0	17/08/2009	23/10/2009	19/01/2015	0	4,6	8	9	1	0	0	0,8	0	0	5
692	161	1175	31/03/1927	1	2		0	23/03/1994			0	7,4	5		0			1,0	1	0	5
693	162	1175	31/03/1927	1	2		0	23/03/1994			0	7,4	5		0			1,0	1	0	5
694	163	1518	21/06/1921	1	2		0				0				0				0	0	
695	164	1518	21/06/1921	1	1		0				0				0				0	0	
696	165	5258	25/01/1929	1	2		1	30/11/1995			1	10,1			0				0	0	
697	166	5258	25/01/1929	1	1		1	30/11/1995			1	10,1			0				0	0	
698	167	2764	18/10/1948	1	2	218,77	1	17/01/1996	19/02/1997	12/05/2015	1	50	7		0			1,0	1	2	5
699	168	2764	18/10/1948	1	x	218,77	1	17/01/1996	19/02/1997	12/05/2015	1	50	7		0			1,0	1	2	5

700	169	6270	09/05/1931	1	2		1	01/01/2007		03/03/2010	1	250			0				1	1	
701	170	6270	09/05/1931	1	2		1	01/01/2007		03/03/2010	1	250			0				1	1	
702	171	3603	25/10/1930	1	1	34,87	1	21/08/2003	31/05/2004	26/04/2007	1	6,7	10		0			0,8	1	2	4
703	172	3603	25/10/1930	1	1	34,87	1	21/08/2003	31/05/2004	26/04/2007	1	6,7	10		0			0,8	1	2	4
704	173	5105	09/08/1932	1	1	1,13	1	13/05/2008	12/05/2008	16/06/2008	1	15	9		0			1,0	0	1	4
705	174	5105	09/08/1932	1	1	1,13	1	13/05/2008	13/05/2008	17/06/2008	1	15	9		0			1,0	0	1	4
706	175	6951	12/08/1947	1	1		1	26/09/2010		10/05/2012	1	71	8		0				1	2	5
707	176	6951	12/08/1947	1	3		1	26/09/2010		10/05/2012	1	71	8		0				1	2	5
709	1	5528	14/05/1952	1	1	69,27	0	06/11/2008	23/06/2009	01/04/2015	0	36,43	7	7	1	0	0	0,2	2	0	5
710	2	5528	14/05/1952	1	1	69,27	0	06/11/2008	23/06/2009	01/04/2015	0	36,43	7	7	1	0	0	0,2	2	0	5
711	3	5575	04/06/1940	1	x	56,97	1	21/10/2008	16/07/2009	15/04/2014	1	11,8	8		1	0	0	0,5	2	0	5
712	4	5575	04/06/1940	1	1	56,97	1	21/10/2008	16/07/2009	15/04/2014	1	11,8	8		1	0	0	0,5	2	0	5
713	5	5538	10/03/1952	1	x	14,07	1	24/11/2008	07/07/2009	09/09/2010	1	6,2	9	9	1	1	1	0,8	2	1	7
714	6	5538	10/03/1952	1	x	14,07	1	24/11/2008	07/07/2009	09/09/2010	1	6,2	9	9	1	1	1	0,8	2	1	7
715	7	5917	05/06/1942	1	x	65,60	0	09/04/2009	13/10/2009	31/03/2015	0	11	9	9	0	0	0	0,4	2	0	2
716	8	5917	05/06/1942	1	1	65,60	0	09/04/2009	13/10/2009	31/03/2015	0	11	9	9	0	0	0	0,4	2	0	2
717	9	5826	21/05/1954	1	2	58,67	0	21/07/2009	12/01/2010	02/12/2014	0	17,48	8	9	1	0	0	0,6	2	0	5
718	10	5826	21/05/1954	1	2	58,67	0	21/07/2009	12/01/2010	02/12/2014	0	17,48	8	9	1	0	0	0,6	2	0	5
719	11	5877	01/06/1951	1	1	11,13	1	26/08/2009	31/05/2010	04/05/2011	1	32,25	9		0	1	1	1,0	2	0	6
720	12	5877	01/06/1951	1	1	11,13	1	26/08/2009	31/05/2010	04/05/2011	1	32,25	9		0	1	1	1,0	2	0	6
721	13	5740	04/07/1948	1	x	59,80	0	14/05/2009	10/05/2010	04/05/2015	0	5,6	8		0	0	0	0,3	2	0	2
722	14	5740	04/07/1948	1	x	59,80	0	14/05/2009	10/05/2010	04/05/2015	0	5,6	8		0	0	0	0,3	2	0	2
723	15	6124	25/02/1948	1	1	43,93	0	18/12/2009	05/08/2010	03/04/2014	0	22,14	9		0	0	0	0,5	2	0	4
724	16	6124	25/02/1948	1	1	43,93	0	18/12/2009	05/08/2010	03/04/2014	0	22,14	9		0	0	0	0,5	2	0	4
725	17	5908	15/07/1947	1	1	52,87	0	21/12/2009	27/04/2010	23/09/2014	0	16,74	8	8	0	0	0	0,2	2	0	2
726	18	5908	15/07/1947	1	2	52,87	0	21/12/2009	27/04/2010	23/09/2014	0	16,74	8	8	0	0	0	0,2	2	0	2
727	19	6164	28/03/1936	1	2	27,27	1	13/01/2010	26/08/2010	04/12/2012	1	6,3	8	9	1	1	0	0,5	2	0	5
728	20	6164	28/03/1936	1	2	27,27	1	13/01/2010	26/08/2010	04/12/2012	1	6,3	8	9	1	1	0	0,5	2	0	5
729	21	6252	25/05/1946	1	x	51,43	0	18/03/2010	29/10/2010	12/02/2015	0	10,9	8		0	0	0	0,4	2	0	4
730	22	6252	25/05/1946	1	0	51,43	0	18/03/2010	29/10/2010	12/02/2015	0	10,9	8		0	0	0	0,4	2	0	4
731	23	6129	15/07/1945	1	1	50,23	1	22/04/2010	16/11/2010	23/01/2015	1	5,99	9		0	0	1	0,6	2	0	4
732	24	6129	15/07/1945	1	1	50,23	1	22/04/2010	16/11/2010	23/01/2015	1	5,99	9		0	0	1	0,6	2	0	4
733	25	6474	09/08/1947	1	0	50,23	0	24/06/2010	14/02/2011	21/04/2015	0	6,2	9	7	1	0	0	0,3	2	0	5
734	26	6474	09/08/1947	1	0	50,23	0	24/06/2010	14/02/2011	21/04/2015	0	6,2	9	7	1	0	0	0,3	2	0	5
735	27	6334	14/05/1960	1	1	11,97	1	12/10/2010	02/05/2011	01/05/2012	1	9,9	9	7	0	0	0	0,4	2	0	2
736	28	6334	14/05/1960	1	1	11,97	1	12/10/2010	02/05/2011	01/05/2012	1	9,9	9	7	0	0	0	0,4	2	0	2
737	29	6501	06/09/1961	1	2	13,43	1	14/12/2010	22/07/2011	05/09/2012	1	44,38	8		1	1	1	1,0	2	1	6
738	30	6501	06/09/1961	1	2	13,43	1	14/12/2010	22/07/2011	05/09/2012	1	44,38	8		1	1	1	1,0	2	1	6
739	31	6764	25/02/1936	1	1	44,20	0	11/01/2011	25/07/2011	01/04/2015	0	13	9		1	0	1	0,4	2	0	5
740	32	6764	25/02/1936	1	1	44,20	0	11/01/2011	25/07/2011	01/04/2015	0	13	9		1	0	1	0,4	2	0	5
741	33	6979	11/09/1929	1	1	22,10	1	20/12/2007	15/11/2012	18/09/2014	1	2,6	9		0			1,0	2	2	4
742	34	6979	11/09/1929	1	1	22,10	1	20/12/2007	15/11/2012	18/09/2014	1	2,6	9		0			1,0	2	2	4
743	35	7069	22/03/1962	1	0	41,27	0	20/05/2011	19/12/2011	27/05/2015	0	26,2	9		1	1	0	0,7	2	0	6
744	36	7069	22/03/1962	1	0	41,27	0	20/05/2011	19/12/2011	27/05/2015	0	26,2	9		1	1	0	0,7	2	0	6
745	37	7202	29/10/1948	1	0	21,40	1	30/06/2011	21/02/2012	03/12/2013	1	6,95	9	9	1	1	0	0,8	2	1	6
746	38	7202	29/10/1948	1	1	21,40	1	30/06/2011	21/02/2012	03/12/2013	1	6,95	9	9	1	1	0	0,8	2	1	6
747	39	7002	26/06/1951	1	0	31,27	0	13/10/2011	24/04/2012	02/12/2014	0	17,1	9		1	1	0	0,5	2	0	5
748	40	7002	26/06/1951	1	0	31,27	0	13/10/2011	24/04/2012	02/12/2014	0	17,1	9		1	1	0	0,5	2	0	5
749	41	7311	05/10/1954	1	2	24,70	1	06/01/2012	10/07/2012	31/07/2014	1	11	9		0	0	0	0,3	2	0	4
750	42	7311	05/10/1954	1	3	24,70	1	06/01/2012	10/07/2012	31/07/2014	1	11	9		0	0	0	0,3	2	0	4
751	43	7448	23/04/1949	1	1	28,70	1	13/12/2011	28/08/2012	19/01/2015	1	13	8		0	0	0	0,4	2	1	4
752	44	7448	23/04/1949	1	1	28,70	1	13/12/2011	28/08/2012	19/01/2015	1	13	8		0	0	0	0,4	2	1	4
753	45	5479	17/04/1947	1	2	57,10	0	13/08/2008	04/11/2008	07/08/2013	0	6	9	7	1	0	0	0,9	1	0	5
754	46	5479	17/04/1947	1	2	57,10	0	13/08/2008	04/11/2008	07/08/2013	0	6	9	7	1	0	0	0,9	1	0	5
755	47	5346	19/08/1947	1	3	69,53	0	28/11/2008	03/03/2009	19/12/2014	0	5,7	9	9	1	1	0	0,8	0	0	6
756	48	5346	19/08/1947	1	3	69,53	0	28/11/2008	03/03/2009	19/12/2014	0	5,7	9	9	1	1	0	0,8	0	0	6
757	49	5421	10/10/1941	1	3	53,90	1	23/01/2009	31/03/2009	27/09/2013	1	5,48	9	9	1	1	1	0,9	0	0	5
758	50	5421	10/10/1941	1	2	53,90	1	23/01/2009	31/03/2009	27/09/2013	1	5,48	9	9	1	1	1	0,9	0	0	5
759	51	5478	12/10/1956	1	3	52,50	0	03/02/2009	14/04/2009	29/08/2013	0	26,06	9	7	0	0	1	0,8	0	0	4
760	52	5478	12/10/1956	1	2	52,50	0	03/02/2009	14/04/2009	29/08/2013	0	26,06	9	7	0	0	1	0,8	0	0	4
761	53	5427	21/12/1945	1	2	49,17	0	04/12/2007	23/04/2009	28/05/2013	0	5,2	7	9	1	0	0	0,6	0	0	5
762	54	5427	21/12/1945	1	2	49,17	0	04/12/2007	23/04/2009	28/05/2013	0	5,2	7	9	1	0	0	0,6	0	0	5
763	55	5530	05/10/1963	1	2	2,93	1	21/05/2009	23/06/2009	21/09/2009	1	6,3	10	10	1	1	1	0,8	1	1	6
764	56	5530	05/10/1963	1	2	2,93	1	21/05/2009	23/06/2009	21/09/2009	1	6,3	10	10	1	1	1	0,8	1	1	6
765	57	5628	22/11/1944	1	2	28,33	1	29/05/2009	01/09/2009	11/01/2012	1	3,17	9	9	1	1	1	0,8	1	2	6
766	58	5628	22/11/1944	1	2	28,33	1	29/05/2009	01/09/2009	11/01/2012	1	3,17	9	9	1	1	1	0,8	1	2	6
767	59	5695	22/04/1944	1	2	62,87	0	17/08/2009	23/10/2009	19/01/2015	0	4,6	8	9	1	0	0	0,8	0	0	5

768	60	5695	22/04/1944	1	2	62,87	0	17/08/2009	23/10/2009	19/01/2015	0	4,6	8	9	1	0	0	0,8	0	0	5
769	61	5755	22/06/1956	1	2	55,17	1	09/12/2009	11/02/2010	16/09/2014	1	9,5	7	7	1	0	1	0,9	0	0	7
770	62	5755	22/06/1956	1	2	55,17	1	09/12/2009	11/02/2010	16/09/2014	1	9,5	7	7	1	0	1	0,9	0	0	7
771	63	5784	14/03/1957	1	2	58,60	0	15/12/2009	10/03/2010	28/01/2015	0	25	6	7	0	0	0	0,9	0	0	4
772	64	5784	14/03/1957	1	2	58,60	0	15/12/2009	10/03/2010	28/01/2015	0	25	6	7	0	0	0	0,9	0	0	4
773	65	6084	26/01/1960	1	2	49,17	0	19/04/2010	23/07/2010	28/08/2014	0	8,7	7	9	1	0	0	0,7	0	0	5
774	66	6084	26/01/1960	1	2	49,17	0	19/04/2010	23/07/2010	28/08/2014	0	8,7	7	9	1	0	0	0,7	0	0	5
775	67	6113	13/11/1940	1	1	55,27	0	28/05/2010	26/07/2010	04/03/2015	0	12,5	9	7	1	1	0	0,8	0	0	5
776	68	6113	13/11/1940	1	3	55,27	0	28/05/2010	26/07/2010	04/03/2015	0	12,5	9	7	1	1	0	0,8	0	0	5
777	69	6152	12/03/1949	1	1	43,43	1	26/05/2010	19/08/2010	02/04/2014	1	13,3	7	7	1	0	0	0,4	0	0	4
778	70	6152	12/03/1949	1	1	43,43	1	26/05/2010	19/08/2010	02/04/2014	1	13,3	7	7	1	0	0	0,4	0	0	4
779	71	6196	13/07/1957	1	2	52,83	1	30/06/2010	07/09/2010	02/02/2015	1	9,9	10	10	1	1	1	1,0	0	1	6
780	72	6196	13/07/1957	1	2	52,83	1	30/06/2010	07/09/2010	02/02/2015	1	9,9	10	10	1	1	1	1,0	0	1	6
781	73	6564	02/03/1947	1	3	10,27	1	02/02/2011	08/04/2011	16/02/2012	1	5,4	9	9	1	0	0	0,3	0	1	5
782	74	6196	13/07/1957	1	3	52,83	1	30/06/2010	07/09/2010	02/02/2015	1	9,9	10	10	1	1	1	1,0	0	1	6
783	75	6723	17/08/1947	1	1	44,20	1	08/03/2011	28/06/2011	04/03/2015	1	8,9	9		1	1	1	0,4	1	1	5
784	76	6723	17/08/1947	1	1	44,20	1	08/03/2011	28/06/2011	04/03/2015	1	8,9	9		1	1	1	0,4	1	1	5
785	77	6807	28/10/1954	1	x	37,83	0	05/07/2011	22/08/2011	17/10/2014	0	5	9	9	1	1	0	0,3	0	0	5
786	78	6807	28/10/1954	1	2	37,83	0	05/07/2011	22/08/2011	17/10/2014	0	5	9	9	1	1	0	0,3	0	0	5
787	79	6803	07/06/1952	1	2	15,43	1	12/07/2011	17/08/2011	30/11/2012	1	5,53	9	9	1	1	1	0,7	0	0	6
788	80	6803	07/06/1952	1	3	15,43	1	12/07/2011	17/08/2011	30/11/2012	1	5,53	9	9	1	1	1	0,7	0	0	6
789	81	7025	09/01/1953	1	3	38,03	0	22/09/2011	15/12/2011	16/02/2015	0	5,7	8	7	1	0	1	0,4	0	0	5
790	82	7025	09/01/1953	1	3	38,03	0	22/09/2011	15/12/2011	16/02/2015	0	5,7	8	7	1	0	1	0,4	0	0	5
791	83	7050	27/11/1954	1	1	40,37	0	21/09/2011	19/12/2011	30/04/2015	0	2,5	7	8	0	0	1	0,5	0	0	4
792	84	7050	27/11/1954	1	1	40,37	0	21/09/2011	19/12/2011	30/04/2015	0	2,5	7	8	0	0	1	0,5	0	0	4
793	85	7438	27/07/1966	1	1	36,20	1	05/03/2012	14/05/2012	20/05/2015	1	6,5	9	9	0	0	1	0,7	0	1	4
794	86	7438	27/07/1966	1	1	36,20	1	05/03/2012	14/05/2012	20/05/2015	1	6,5	9	9	0	0	1	0,7	0	1	4
796	1	3170	25/11/1942	1	3	80,23	0	29/04/2002	07/11/2002	14/07/2009	0	6,5	6	6	0	0	0	0,1	0	0	4
797	2	3170	25/11/1942	1	3	80,23	0	29/04/2002	07/11/2002	14/07/2009	0	6,5	6	6	0	0	0	0,1	0	0	4
798	3	3219	25/05/1936	1	3	17,70	0	11/07/2002	08/10/2002	29/03/2004	0	9,8	6	6	0	0	0	0,1	0	0	2
799	4	3219	25/05/1936	1	x	17,70	0	11/07/2002	08/10/2002	29/03/2004	0	9,8	6	6	0	0	0	0,1	0	0	2
800	5	3308	23/04/1933	1	x		0		18/10/2002		0			7	0	0	0		0	0	3
801	6	3308	23/04/1933	1	x		0		18/10/2002		0			7	0	0	0		0	0	3
802	7	3264	18/07/1956	1	x	145,87	0	20/06/2002	10/09/2002	06/11/2014	0	3,5	6	7	0	0	0	0,3	0	0	4
803	8	3264	18/07/1956	1	x	145,87	0	20/06/2002	10/09/2002	06/11/2014	0	3,5	6	7	0	0	0	0,3	0	0	4
804	9	3289	02/04/1944	1	x		0	19/08/2002	25/09/2002		0	7,3	9	9	0	0	0	0,1	0	0	4
805	10	3289	02/04/1944	1	2		0	19/08/2002	25/09/2002		0	7,3	9	9	0	0	0	0,1	0	0	4
806	11	3157	08/05/1938	1	x	85,77	0	16/04/2002	10/09/2002	03/11/2009	0	6,9	7	6	0	0	0	0,1	0	0	4
807	12	3157	08/05/1938	1	0	85,77	0	16/04/2002	10/09/2002	03/11/2009	0	6,9	7	6	0	0	0	0,1	0	0	4
808	13	3269	14/09/1938	1	3	60,90	0	16/09/2002	29/10/2002	26/11/2007	0	4,3	7	7	1	0	1	0,9	0	0	5
809	14	3269	14/09/1938	1	3	60,90	0	16/09/2002	29/10/2002	26/11/2007	0	4,3	7	7	1	0	1	0,9	0	0	5
810	15	3272	26/05/1931	1	0	49,10	0	06/06/2002	10/09/2002	13/10/2006	0	7,1	7	7	0	0	0	0,3	0	0	4
811	16	3272	26/05/1931	1	0	49,10	0	06/06/2002	10/09/2002	13/10/2006	0	7,1	7	7	0	0	0	0,3	0	0	4
812	17	3270	16/05/1944	1	x		0	01/05/2002	09/09/2002		0	7,6	6	6	0	0	1	0,4	0	0	2
813	18	3270	16/05/1944	1	x		0	01/05/2002	09/09/2002		0	7,6	6	6	0	0	1	0,4	0	0	2
814	19	2664	11/09/1932	1	0	115,87	0	02/08/2000	15/12/2000	11/08/2010	0	8,3	7	6	0	0	1	1,0	0	0	4
815	20	2664	11/09/1932	1	0	115,87	0	02/08/2000	15/12/2000	11/08/2010	0	8,3	7	6	0	0	1	1,0	0	0	4
816	21	2386	08/12/1937	1	3	19,60	1	16/11/1999	16/11/1999	04/07/2001	1			8	0	1	1		0	0	6
817	22	2386	08/12/1937	1	3	19,60	1	16/11/1999	16/11/1999	04/07/2001	1			8	0	1	1		0	0	6
818	23	2695	20/05/1931	1	1	163,00	0	05/10/2000	06/03/2001	06/10/2014	0	4	7	7	0	0	0	0,5	0	0	4
819	24	2695	20/05/1931	1	2	163,00	0	05/10/2000	06/03/2001	06/10/2014	0	4	7	7	0	0	0	0,5	0	0	4
820	25	2824	04/06/1933	1	x	21,37	0		15/02/2001	26/11/2002	0	1,8	6	6	0	0	0		0	0	2
821	26	2824	04/06/1933	1	x	21,37	0		15/02/2001	26/11/2002	0	1,8	6	6	0	0	0		0	0	2
822	27	3335	20/04/1934	1	2		0		31/10/2002	31/10/2002	0	8	6	6	0	0	0		0	0	4
823	28	3335	20/04/1934	1	2		0		31/10/2002	31/10/2002	0	8	6	6	0	0	0		0	0	4
824	29	2853	14/06/1947	1	2	61,17	1	29/03/2001	29/11/2001	04/01/2007	1	4,4	7	7	0	0	1	0,3	1	0	2
825	30	3335	20/04/1934	1	2		0		31/10/2002	31/10/2002	0	8	6	6	0	0	0		0	0	4
826	31	2081	21/12/1934	1	2	105,00	0	04/03/1998	15/09/1998	15/06/2007	0		5	6	0	0	0	0,5	1	0	4
827	32	2081	21/12/1934	1	2	105,00	0	04/03/1998	15/09/1998	15/06/2007	0		5	6	0	0	0	0,5	1	0	4
828	33	2451	09/03/1937	1	0	24,37	0	04/06/1999	09/11/1999	20/11/2001	0	96,8	9		1	1	1	0,7	1	0	6
829	34	2451	09/03/1937	1	0	24,37	0	04/06/1999	09/11/1999	20/11/2001	0	96,8	9		1	1	1	0,7	1	0	6

830	35	2539	19/02/1933	1	2	63,03	0	17/02/2000	21/09/2000	22/12/2005	0	9,6	7	9	1	1	1	0,5	0	0	6
831	36	2539	19/02/1933	1	2	63,03	0	17/02/2000	21/09/2000	22/12/2005	0	9,6	7	9	1	1	1	0,5	0	0	6
832	37	2967	04/05/1948	1	2	25,03	1	30/08/2001	04/06/2002	05/07/2004	1	14,7	7		1	1	0	0,8	1	2	5
833	38	2967	04/05/1948	1	x	25,03	1	30/08/2001	04/06/2002	05/07/2004	1	14,7	7		1	1	0	0,8	1	2	5
834	39	2778	28/05/1941	1	x	36,57	0	04/01/2001	09/08/2001	26/08/2004	0	4	7	7	0	0	0	0,1	0	0	4
835	40	2778	28/05/1941	1	x	36,57	0	04/01/2001	09/08/2001	26/08/2004	0	4	7	7	0	0	0	0,1	0	0	4
836	41	2796	10/10/1941	1	0		0	04/01/2001	18/01/2001	18/01/2001	0	4	7		0	0	1	0,1	1	0	4
837	42	2796	10/10/1941	1	0		0	04/01/2001	18/01/2001	18/01/2001	0	4	7		0	0	1	0,1	1	0	4
838	43	2839	14/09/1950	1	1	99,27	0	07/03/2001	14/09/2001	22/12/2009	0	13,1	6		0	0	0	0,5	1	0	4
839	44	2839	14/09/1950	1	1	99,27	0	07/03/2001	14/09/2001	22/12/2009	0	13,1	6		0	0	0	0,5	1	0	4
840	45	2869	21/07/1947	1	1	4,33	0	30/12/2001	28/02/2002	10/07/2002	0	1,9	6		0	0	0	0,4	1	0	2
841	46	2869	21/07/1947	1	x	4,33	0	30/12/2001	28/02/2002	10/07/2002	0	1,9	6		0	0	0	0,4	1	0	2
842	47	3002	03/10/1945	1	x	102,37	0	03/10/2001	28/05/2002	09/12/2010	0	7,6	8		1	0	0	1,0	1	0	5
843	48	3002	03/10/1945	1	x	102,37	0	03/10/2001	28/05/2002	09/12/2010	0	7,6	8		1	0	0	1,0	1	0	5
844	49	2906	01/10/1935	1	2	7,20	1	08/06/2001	09/05/2002	15/12/2002	1	15,4	6		0	0	1	0,5	1	0	3
845	50	2906	01/10/1935	1	2	7,20	1	08/06/2001	09/05/2002	15/12/2002	1	15,4	6		0	0	1	0,5	1	0	3
846	51	2901	23/07/1945	1	1	7,10	0	28/05/2001	10/01/2002	13/08/2002	0	7,3	8	7	1	0	1	0,5	1	0	5
847	52	2901	23/07/1945	1	1	7,10	0	28/05/2001	10/01/2002	13/08/2002	0	7,3	8	7	1	0	1	0,5	1	0	5
848	53	2656	14/12/1942	1	x	45,20	1	13/07/2000	16/11/2001	22/08/2005	1	15,1	9		1	1	0	0,9	1	1	5
849	54	2656	14/12/1942	1	1	45,20	1	13/07/2000	16/11/2001	22/08/2005	1	15,1	9		1	1	0	0,9	1	1	5
850	55	2822	10/05/1937	1	1	93,83	0	20/02/2001	04/12/2001	29/09/2009	0	18,1	6		0	0	0	0,3	1	0	4
851	56	2822	10/05/1937	1	1	93,83	0	20/02/2001	04/12/2001	29/09/2009	0	18,1	6		0	0	0	0,3	1	0	4
852	57	2910	18/06/1944	1	2	43,40	1	14/06/2001	28/02/2002	12/10/2005	1	10,4	8		1	1	0	0,6	1	0	6
853	58	2910	18/06/1944	1	2	43,40	1	14/06/2001	28/02/2002	12/10/2005	1	10,4	8		1	1	0	0,6	1	0	6
854	59	2854	03/07/1945	1	2	15,27	1	30/03/2001	18/04/2002	26/07/2003	1	25	6	6	1	0	1	0,3	1	0	5
855	60	2854	03/07/1945	1	2	15,27	1	30/03/2001	18/04/2002	26/07/2003	1	25	6	6	1	0	1	0,3	1	0	5
856	61	1684	04/02/1934	1	1	80,53	1	24/09/1996	19/06/1997	05/03/2004	1	6,3	9		0	0	0	0,5	1	0	2
857	62	1684	04/02/1934	1	1	80,53	1	24/09/1996	19/06/1997	05/03/2004	1	6,3	9		0	0	0	0,5	1	0	2
858	63	3182	14/10/1933	1	1	10,57	1	20/03/2001	14/05/2002	01/04/2003	1	5,7	8	9	1	1	1	1,0	1	1	7
859	64	3182	14/10/1933	1	2	10,57	1	20/03/2001	14/05/2002	01/04/2003	1	5,7	8	9	1	1	1	1,0	1	1	7
860	65	2999	19/11/1940	1	2	41,27	1	25/10/2001	25/07/2002	03/01/2006	1	11,8	8	7	0	0	1	0,7	1	2	4
861	66	2999	19/11/1940	1	2	41,27	1	25/10/2001	25/07/2002	03/01/2006	1	11,8	8	7	0	0	1	0,7	1	2	4
862	67	2747	01/01/1943	1	3	78,27	1	05/12/2000	18/09/2001	26/03/2008	1	8,2	7	7	1	0	1	0,5	1	2	5
863	68	2747	01/01/1943	1	1	78,27	1	05/12/2000	18/09/2001	26/03/2008	1	8,2	7	7	1	0	1	0,5	1	2	5
864	69	1466	08/10/1941	1	3	88,23	0		05/10/1995	12/02/2003	0			5	0	0	0		1	0	2
865	70	1466	08/10/1941	1	2	88,23	0		05/10/1995	12/02/2003	0			5	0	0	0		1	0	2
866	71	2873	11/07/1943	1	2	124,30	0	19/04/2001	15/01/2002	24/05/2012	0	9	7		0	0	0	0,2	2	0	4
867	72	2873	11/07/1943	1	x	124,30	0	19/04/2001	15/01/2002	24/05/2012	0	9	7		0	0	0	0,2	2	0	4
868	73	2993	25/03/1939	1	3	28,93	1	26/09/2001	30/04/2002	28/09/2004	1	6,2	9	9	1	1	1	0,5	2	2	6
869	74	2993	25/03/1939	1	3	28,93	1	26/09/2001	30/04/2002	28/09/2004	1	6,2	9	9	1	1	1	0,5	2	2	6
870	75	2993	25/03/1939	1	3	28,93	1	26/09/2001	30/04/2002	28/09/2004	1	6,2	9	9	1	1	1	0,5	2	2	6
871	76	2993	25/03/1939	1	3	28,93	1	26/09/2001	30/04/2002	28/09/2004	1	6,2	9	9	1	1	1	0,5	2	2	6
872	77	3109	20/06/1936	1	x	53,83	0	14/02/2002	17/09/2002	12/03/2007	0	7,1	9		0	0	0	0,4	2	0	2
873	78	3109	20/06/1936	1	x	53,83	0	14/02/2002	17/09/2002	12/03/2007	0	7,1	9		0	0	0	0,4	2	0	2
874	79	3160	20/06/1949	1	1	11,00	1	18/04/2002	08/10/2002	08/09/2003	1	10,4	9	8	1	1	1	1,0	2	0	6
875	80	3160	20/06/1949	1	1	11,00	1	18/04/2002	08/10/2002	08/09/2003	1	10,4	9	8	1	1	1	1,0	2	0	6
876	81	2882	06/12/1940	1	x	75,60	1	07/11/2000	21/12/2001	09/04/2008	1	4,8	9		1	0	0	0,5	2	0	5
877	82	2882	06/12/1940	1	x	75,60	1	07/11/2000	21/12/2001	09/04/2008	1	4,8	9		1	0	0	0,5	2	0	5
878	83	3148	02/02/1942	1	x	144,77	0	09/04/2002	19/12/2002	12/01/2015	0	4,3	9		0	0	0	0,3	2	0	2
879	84	3148	02/02/1942	1	x	144,77	0	09/04/2002	19/12/2002	12/01/2015	0	4,3	9		0	0	0	0,3	2	0	2
880	85	3096	28/01/1948	1	1	69,03	1	17/01/2002	08/10/2002	09/07/2008	1	19,5	7	8	0	0	0	0,5	2	0	2
881	86	3096	28/01/1948	1	1	69,03	1	17/01/2002	08/10/2002	09/07/2008	1	19,5	7	8	0	0	0	0,5	2	0	2
882	87	3175	09/10/1941	1	0	148,40	0	08/05/2002	30/12/2002	12/05/2015	0	26,1	7		1	1	1	0,8	2	0	5
883	88	3175	09/10/1941	1	0	148,40	0	08/05/2002	30/12/2002	12/05/2015	0	26,1	7		1	1	1	0,8	2	0	5
884	89	3110	21/07/1943	1	1	60,93	0	15/02/2002	17/09/2002	15/10/2007	0	8	7		0	0	0	0,5	2	0	4
885	90	3110	21/07/1943	1	1	60,93	0	15/02/2002	17/09/2002	15/10/2007	0	8	7		0	0	0	0,5	2	0	4
886	91	5393	01/09/1937	1	1	117,30	0	23/01/2003	02/09/2003	11/06/2013	0	21	8		0	0	1	0,5	2	0	2
887	92	5393	01/09/1937	1	1	117,30	0	23/01/2003	02/09/2003	11/06/2013	0	21	8		0	0	1	0,5	2	0	2
888	93	5393	01/09/1937	1	x	117,30	0	23/01/2003	02/09/2003	11/06/2013	0	21	8		0	0	1	0,5	2	0	2
889	94	5393	01/09/1937	1	x	117,30	0	23/01/2003	02/09/2003	11/06/2013	0	21	8		0	0	1	0,5	2	0	2
890	95	5393	01/09/1937	1	x	117,30	0	23/01/2003	02/09/2003	11/06/2013	0	21	8		0	0	1	0,5	2	0	2
891	96	5393	01/09/1937	1	x	117,30	0	23/01/2003	02/09/2003	11/06/2013	0	21	8		0	0	1	0,5	2	0	2
892	97	5393	01/09/1937	1	x	117,30	0	23/01/2003	02/09/2003	11/06/2013	0	21	8		0	0	1	0,5	2	0	2
893	98	5393	01/09/1937	1	x	117,30	0	23/01/2003	02/09/2003	11/06/2013	0	21	8		0	0	1	0,5	2	0	2
894	99	3002	03/10/1945	1	1	102,37	0	03/10/2001	28/05/2002	09/12/2010	0	7,6	8		1	0	0	1,0	2	0	5

895	100	3002	03/10/1945	1	1	102,37	0	03/10/2001	28/05/2002	09/12/2010	0	7,6	8		1	0	0	1,0	2	0	5
896	101	3002	03/10/1945	1	1	102,37	0	03/10/2001	28/05/2002	09/12/2010	0	7,6	8		1	0	0	1,0	2	0	5
897	102	3002	03/10/1945	1	0	102,37	0	03/10/2001	28/05/2002	09/12/2010	0	7,6	8		1	0	0	1,0	2	0	5
898	103	3002	03/10/1945	1	x	102,37	0	03/10/2001	28/05/2002	09/12/2010	0	7,6	8		1	0	0	1,0	2	0	5
899	104	3002	03/10/1945	1	0	102,37	0	03/10/2001	28/05/2002	09/12/2010	0	7,6	8		1	0	0	1,0	2	0	5
900	105	3002	03/10/1945	1	1	102,37	0	03/10/2001	28/05/2002	09/12/2010	0	7,6	8		1	0	0	1,0	2	0	5
901	106	3002	03/10/1945	1	x	102,37	0	03/10/2001	28/05/2002	09/12/2010	0	7,6	8		1	0	0	1,0	2	0	5
902	107	3002	03/10/1945	1	0	102,37	0	03/10/2001	28/05/2002	09/12/2010	0	7,6	8		1	0	0	1,0	2	0	5
903	108	3002	03/10/1945	1	0	102,37	0	03/10/2001	28/05/2002	09/12/2010	0	7,6	8		1	0	0	1,0	2	0	5
904	109	3253	04/06/1937	1	2		1	06/05/2002	22/08/2002		1	8	6	7	1	0	1	0,1	2	0	5
905	110	3253	04/06/1937	1	2		1	06/05/2002	22/08/2002		1	8	6	7	1	0	1	0,1	2	0	5
906	111	3253	04/06/1937	1	1		1	06/05/2002	22/08/2002		1	8	6	7	1	0	1	0,1	2	0	5
907	112	3253	04/06/1937	1	1		1	06/05/2002	22/08/2002		1	8	6	7	1	0	1	0,1	2	0	5
908	113	3034	31/05/1940	1	2	40,00	1	13/11/2001	13/06/2002	13/10/2005	1	6,1	9		1	1	0	0,6	2	2	6
909	114	3034	31/05/1940	1	1	40,00	1	13/11/2001	13/06/2002	13/10/2005	1	6,1	9		1	1	0	0,6	2	2	6
910	115	3034	31/05/1940	1	0	40,00	1	13/11/2001	13/06/2002	13/10/2005	1	6,1	9		1	1	0	0,6	2	2	6
911	116	3034	31/05/1940	1	0	40,00	1	13/11/2001	13/06/2002	13/10/2005	1	6,1	9		1	1	0	0,6	2	2	6
912	117	3034	31/05/1940	1	1	40,00	1	13/11/2001	13/06/2002	13/10/2005	1	6,1	9		1	1	0	0,6	2	2	6
913	118	3034	31/05/1940	1	x	40,00	1	13/11/2001	13/06/2002	13/10/2005	1	6,1	9		1	1	0	0,6	2	2	6
914	119	3034	31/05/1940	1	2	40,00	1	13/11/2001	13/06/2002	13/10/2005	1	6,1	9		1	1	0	0,6	2	2	6
915	120	3034	31/05/1940	1	2	40,00	1	13/11/2001	13/06/2002	13/10/2005	1	6,1	9		1	1	0	0,6	2	2	6
916	121	3034	31/05/1940	1	2	40,00	1	13/11/2001	13/06/2002	13/10/2005	1	6,1	9		1	1	0	0,6	2	2	6
917	122	3034	31/05/1940	1	2	40,00	1	13/11/2001	13/06/2002	13/10/2005	1	6,1	9		1	1	0	0,6	2	2	6
918	123	3034	31/05/1940	1	x	40,00	1	13/11/2001	13/06/2002	13/10/2005	1	6,1	9		1	1	0	0,6	2	2	6
919	124	3034	31/05/1940	1	x	40,00	1	13/11/2001	13/06/2002	13/10/2005	1	6,1	9		1	1	0	0,6	2	2	6
920	125	3253	04/06/1937	1	1		1	06/05/2002	22/08/2002		1	8	6	7	1	0	1	0,1	2	0	5
921	126	3253	04/06/1937	1	1		1	06/05/2002	22/08/2002		1	8	6	7	1	0	1	0,1	2	0	5

Table S3:

A. Specific partners of FKBP7 in RPE-1 cells

ID	Gene symbol	Full Name
Q2M2I8	AAK1	AP2 associated kinase 1
Q9BTE6	AARSD1	alanyl-tRNA synthetase domain containing 1
Q8NE71	ABCF1	ATP-binding cassette, sub-family F (GCN20), member 1
Q9UG63	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2
Q8IZP0	ABI1	abl-interactor 1
Q9NYB9	ABI2	abl-interactor 2
P60709	ACTB	actin, beta
P68032	ACTC1	actin, alpha, cardiac muscle 1
Q5TGY3	AHDC1	AT hook, DNA binding motif, containing 1
Q09666	AHNAK	AHNAK nucleoprotein
Q6P6C2	ALKBH5	alkB homolog 5, RNA demethylase
Q86V81	ALYREF	Aly/REF export factor
Q9NQW6	ANLN	anillin actin binding protein
O14617	AP3D1	adaptor-related protein complex 3, delta 1 subunit
Q9Y2T2	AP3M1	adaptor-related protein complex 3, mu 1 subunit
Q92572	AP3S1	adaptor-related protein complex 3, sigma 1 subunit
Q7Z5H3	ARHGAP22	Rho GTPase activating protein 22
Q92974	ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2
Q66PJ3	ARL6IP4	ADP-ribosylation factor-like 6 interacting protein 4
Q12797	ASPH	aspartate beta-hydroxylase
Q99700	ATXN2	ataxin 2
Q8WWM7	ATXN2L	ataxin 2-like
P11274	BCR	breakpoint cluster region
P20290	BTF3	basic transcription factor 3
P27708	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
P62158	CALM1	calmodulin 1 (Phosphorylase Kinase, Delta)
O43852	CALU	calumenin
Q13557	CAMK2D	calcium/calmodulin-dependent protein kinase II delta
Q08AD1	CAMSAP2	calmodulin regulated spectrin-associated protein family, member 2
Q14444	CAPRIN1	cell cycle associated protein 1
Q96CT7	CCDC124	coiled-coil domain containing 124
P78371	CCT2	chaperonin containing TCP1, subunit 2 (beta)
P40227	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)
Q12834	CDC20	cell division cycle 20
Q9UPN4	CEP131	centrosomal protein 131kDa
Q5SW79	CEP170	centrosomal protein 170kDa
Q14011	CIRBP	cold inducible RNA binding protein
O14578	CIT	citron rho-interacting serine/threonine kinase
Q14008	CKAP5	cytoskeleton associated protein 5
O75122	CLASP2	cytoplasmic linker associated protein 2
A5YKK6	CNOT1	CCR4-NOT transcription complex, subunit 1
Q8NBJ5	COLGALT1	collagen beta(1-O)galactosyltransferase 1
P53621	COPA	coatomer protein complex, subunit alpha
P35606	COPB2	coatomer protein complex, subunit beta 2 (beta prime)
Q9Y678	COPG1	coatomer protein complex, subunit gamma 1
O75534	CSDE1	cold shock domain containing E1, RNA-binding
P48729	CSNK1A1	casein kinase 1, alpha 1
P21291	CSRP1	cysteine and glycine-rich protein 1
P35221	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa
O60716	CTNND1	catenin (cadherin-associated protein), delta 1
Q14247	CTTN	cortactin
Q53TN4	CYBRD1	cytochrome b reductase 1
Q92499	DDX1	DEAD (Asp-Glu-Ala-Asp) box helicase 1
Q92841	DDX17	DEAD (Asp-Glu-Ala-Asp) box helicase 17
Q9UHI6	DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20
O00571	DDX3X	DEAD (Asp-Glu-Ala-Asp) box helicase 3, X-linked
Q9H0S4	DDX47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47
P17844	DDX5	DEAD (Asp-Glu-Ala-Asp) box helicase 5
Q8TDD1	DDX54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54
Q9NSV4	DIAPH3	diaphanous-related formin 3
Q96N67	DOCK7	dedicator of cytokinesis 7
Q14126	DSG2	desmoglein 2
P68104	EEF1A1	eukaryotic translation elongation factor 1 alpha 1
Q9NZN4	EHD2	EH-domain containing 2
Q9H223	EHD4	EH-domain containing 4

P19525	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2
P20042	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa
Q9Y262	EIF3L	eukaryotic translation initiation factor 3, subunit L
P60842	EIF4A1	eukaryotic translation initiation factor 4A1
P23588	EIF4B	eukaryotic translation initiation factor 4B
Q04637	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1
P78344	EIF4G2	eukaryotic translation initiation factor 4 gamma, 2
O60841	EIF5B	eukaryotic translation initiation factor 5B
Q8IUD2	ERC1	ELKS/RAB6-interacting/CAST family member 1
P19447	ERCC3	excision repair cross-complementation group 3
Q03468	ERCC6	excision repair cross-complementation group 6
O00471	EXOC5	exocyst complex component 5
Q9Y2D4	EXOC6B	exocyst complex component 6B
Q9NZB2	FAM120A	family with sequence similarity 120A
Q9BUT9	FAM195A	family with sequence similarity 195, member A
Q9H4H8	FAM83D	family with sequence similarity 83, member D
Q9Y3D0	FAM96B	family with sequence similarity 96, member B
P62861	FAU	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed
Q5T1M5	FKBP15	FK506 binding protein 15, 133kDa
Q00688	FKBP3	FK506 binding protein 3, 25kDa
Q13045	FLII	flightless I actin binding protein
Q14315	FLNC	filamin C, gamma
Q06787	FMR1	fragile X mental retardation 1
Q9P2Q2	FRMD4A	FERM domain containing 4A
Q13283	G3BP1	GTPase activating protein (SH3 domain) binding protein 1
P22102	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
P48507	GCLM	glutamate-cysteine ligase, modifier subunit
Q9NWZ8	GEMIN8	gem (nuclear organelle) associated protein 8
Q6Y7W6	GIGYF2	GRB10 interacting GYF protein 2
Q9Y2X7	GIT1	G protein-coupled receptor kinase interacting ArfGAP 1
Q14161	GIT2	G protein-coupled receptor kinase interacting ArfGAP 2
P15104	GLUL	glutamate-ammonia ligase
P35269	GTF2F1	general transcription factor IIF, polypeptide 1, 74kDa
Q9BZE4	GTPBP4	GTP binding protein 4
Q7Z4H7	HAUS6	HAUS augmin-like complex, subunit 6
Q7Z4V5	HDGFRP2	hepatoma-derived growth factor-related protein 2
Q9ULT8	HECTD1	HECT domain containing E3 ubiquitin protein ligase 1
Q9BW71	HIRIP3	HIRA interacting protein 3
P16401	HIST1H1B	histone cluster 1, H1b
P16402	HIST1H1D	histone cluster 1, H1d
O60814	HIST1H2BK	histone cluster 1, H2bk
P23527	HIST1H2BO	histone cluster 1, H2bo
Q14527	HLTF	helicase-like transcription factor
Q13151	HNRNPA0	heterogeneous nuclear ribonucleoprotein A0
P09651	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1
P22626	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1
P51991	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3
P52272	HNRNPM	heterogeneous nuclear ribonucleoprotein M
Q00839	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
P11021	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
P04792	HSPB1	heat shock 27kDa protein 1
P10809	HSPD1	heat shock 60kDa protein 1 (chaperonin)
Q13418	ILK	integrin-linked kinase
Q9P206	KIAA1522	KIAA1522
P52732	KIF11	kinesin family member 11
Q02241	KIF23	kinesin family member 23
O95239	KIF4A	kinesin family member 4A
P05783	KRT18	keratin 18, type I
P05787	KRT8	keratin 8, type II
P35527	KRT9	keratin 9, type I
Q6PKG0	LARP1	La ribonucleoprotein domain family, member 1
Q14847	LASP1	LIM and SH3 protein 1
Q9UPQ0	LIMCH1	LIM and calponin homology domains 1
Q9UGP4	LIMD1	LIM domains containing 1
P02545	LMNA	lamin A/C
Q8WWI1	LMO7	LIM domain 7
Q14693	LPIN1	lipin 1
Q93052	LPP	LIM domain containing preferred translocation partner in lipoma
Q9Y2L9	LRCH1	leucine-rich repeats and calponin homology (CH) domain containing 1
Q96AG4	LRRC59	leucine rich repeat containing 59

Q86V48	LUZP1	leucine zipper protein 1
P46821	MAP1B	microtubule-associated protein 1B
O43318	MAP3K7	mitogen-activated protein kinase kinase kinase 7
P27816	MAP4	microtubule-associated protein 4
Q3KQU3	MAP7D1	MAP7 domain containing 1
Q8IWC1	MAP7D3	MAP7 domain containing 3
P33991	MCM4	minichromosome maintenance complex component 4
P33993	MCM7	minichromosome maintenance complex component 7
P46013	MKI67	marker of proliferation Ki-67
Q6WCQ1	MPRIP	myosin phosphatase Rho interacting protein
P49959	MRE11A	MRE11 homolog A, double strand break repair nuclease
Q6P1L8	MRPL14	mitochondrial ribosomal protein L14
P52701	MSH6	mutS homolog 6
Q9Y4B5	MTCL1	microtubule crosslinking factor 1
Q86UE4	MTDH	metadherin
Q14764	MVP	major vault protein
Q9P2K5	MYEF2	myelin expression factor 2
P35580	MYH10	myosin, heavy chain 10, non-muscle
P35579	MYH9	myosin, heavy chain 9, non-muscle
P19105	MYL12A	myosin, light chain 12A, regulatory, non-sarcomeric
Q92614	MYO18A	myosin XVIIIA
O00159	MYO1C	myosin IC
Q12965	MYO1E	myosin IE
Q6NZ67	MZT2B	mitotic spindle organizing protein 2B
P55209	NAP1L1	nucleosome assembly protein 1-like 1
Q8NEY1	NAV1	neuron navigator 1
O60934	NBN	nibrin
Q15021	NCAPD2	non-SMC condensin I complex, subunit D2
Q9BPX3	NCAPG	non-SMC condensin I complex, subunit G
Q15003	NCAPH	non-SMC condensin I complex, subunit H
Q9Y618	NCOR2	nuclear receptor corepressor 2
Q9NXR1	NDE1	nudE neurodevelopment protein 1
Q8NHV4	NEDD1	neural precursor cell expressed, developmentally down-regulated 1
Q96PU5	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase
O00712	NFIB	nuclear factor I/B
P08651	NFIC	nuclear factor I/C (CCAAT-binding transcription factor)
Q9BPW8	NIPSNAP1	nipsnap homolog 1 (C. elegans)
P30419	NMT1	N-myristoyltransferase 1
Q9ULX3	NOB1	NIN1/RPN12 binding protein 1 homolog
Q15233	NONO	non-POU domain containing, octamer-binding
P06748	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)
O14786	NRP1	neuropilin 1
Q7Z417	NUFIP2	nuclear fragile X mental retardation protein interacting protein 2
Q14980	NUMA1	nuclear mitotic apparatus protein 1
Q9UQ80	PA2G4	proliferation-associated 2G4, 38kDa
P11940	PABPC1	poly(A) binding protein, cytoplasmic 1
O96013	PAK4	p21 protein (Cdc42/Rac)-activated kinase 4
Q8WX93	PALLD	palladin, cytoskeletal associated protein
O43252	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1
O95340	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2
P09874	PARP1	poly (ADP-ribose) polymerase 1
Q96IZ0	PAWR	PRKC, apoptosis, WT1, regulator
Q15154	PCM1	pericentriolar material 1
O00151	PDLIM1	PDZ and LIM domain 1
Q96HC4	PDLIM5	PDZ and LIM domain 5
Q9NR12	PDLIM7	PDZ and LIM domain 7 (enigma)
Q9UHV9	PFDN2	prefoldin subunit 2
Q01813	PFKP	phosphofructokinase, platelet
Q86UU1	PHLDB1	pleckstrin homology-like domain, family B, member 1
Q86SQ0	PHLDB2	pleckstrin homology-like domain, family B, member 2
Q9NWS0	PIH1D1	PIH1 domain containing 1
Q15149	PLEC	plectin
Q8TCS8	PNPT1	polyribonucleotide nucleotidyltransferase 1
P24928	POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa
Q99575	POP1	POP1 homolog, ribonuclease P/MRP subunit
Q86W92	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)
O14974	PPP1R12A	protein phosphatase 1, regulatory subunit 12A
Q9BZL4	PPP1R12C	protein phosphatase 1, regulatory subunit 12C
O60828	PQBP1	polyglutamine binding protein 1
P78527	PRKDC	protein kinase, DNA-activated, catalytic polypeptide

P48634	PRRC2A	proline-rich coiled-coil 2A
Q5JSZ5	PRRC2B	proline-rich coiled-coil 2B
Q9Y520	PRRC2C	proline-rich coiled-coil 2C
Q9H3S7	PTPN23	protein tyrosine phosphatase, non-receptor type 23
Q6NZI2	PTRF	polymerase I and transcript release factor
Q96QR8	PURB	purine-rich element binding protein B
Q9BRP8	PYM1	PYM homolog 1, exon junction complex associated factor
Q9BXF6	RAB11FIP5	RAB11 family interacting protein 5 (class I)
Q9H0H5	RACGAP1	Rac GTPase activating protein 1
Q9P0K7	RAI14	retinoic acid induced 14
Q9UJF2	RASAL2	RAS protein activator like 2
Q96PK6	RBM14	RNA binding motif protein 14
Q9P2N5	RBM27	RNA binding motif protein 27
Q96EV2	RBM33	RNA binding motif protein 33
Q9Y580	RBM7	RNA binding motif protein 7
P35250	RFC2	replication factor C (activator 1) 2, 40kDa
Q6R327	RICTOR	RPTOR independent companion of MTOR, complex 2
Q9Y508	RNF114	ring finger protein 114
P27635	RPL10	ribosomal protein L10
P62906	RPL10A	ribosomal protein L10a
P62913	RPL11	ribosomal protein L11
P30050	RPL12	ribosomal protein L12
P26373	RPL13	ribosomal protein L13
P40429	RPL13A	ribosomal protein L13a
P50914	RPL14	ribosomal protein L14
P18621	RPL17	ribosomal protein L17
Q07020	RPL18	ribosomal protein L18
Q02543	RPL18A	ribosomal protein L18a
P84098	RPL19	ribosomal protein L19
P46778	RPL21	ribosomal protein L21
P62829	RPL23	ribosomal protein L23
P62750	RPL23A	ribosomal protein L23a
P83731	RPL24	ribosomal protein L24
P61254	RPL26	ribosomal protein L26
Q9UNX3	RPL26L1	ribosomal protein L26-like 1
P46776	RPL27A	ribosomal protein L27a
P46779	RPL28	ribosomal protein L28
P47914	RPL29	ribosomal protein L29
P39023	RPL3	ribosomal protein L3
P62888	RPL30	ribosomal protein L30
P62899	RPL31	ribosomal protein L31
P62910	RPL32	ribosomal protein L32
P49207	RPL34	ribosomal protein L34
P42766	RPL35	ribosomal protein L35
P18077	RPL35A	ribosomal protein L35a
Q9Y3U8	RPL36	ribosomal protein L36
P61927	RPL37	ribosomal protein L37
P61513	RPL37A	ribosomal protein L37a
P63173	RPL38	ribosomal protein L38
P36578	RPL4	ribosomal protein L4
P46777	RPL5	ribosomal protein L5
Q02878	RPL6	ribosomal protein L6
P18124	RPL7	ribosomal protein L7
P62424	RPL7A	ribosomal protein L7a
P62917	RPL8	ribosomal protein L8
P32969	RPL9	ribosomal protein L9
P05388	RPLP0	ribosomal protein, large, P0
P05386	RPLP1	ribosomal protein, large, P1
P46783	RPS10	ribosomal protein S10
P62280	RPS11	ribosomal protein S11
P62277	RPS13	ribosomal protein S13
P62263	RPS14	ribosomal protein S14
P62841	RPS15	ribosomal protein S15
P62244	RPS15A	ribosomal protein S15a
P62249	RPS16	ribosomal protein S16
P0CW22	RPS17	ribosomal protein S17
P62269	RPS18	ribosomal protein S18
P39019	RPS19	ribosomal protein S19
P15880	RPS2	ribosomal protein S2
P60866	RPS20	ribosomal protein S20
P63220	RPS21	ribosomal protein S21

P62266	RPS23	ribosomal protein S23
P62851	RPS25	ribosomal protein S25
P62857	RPS28	ribosomal protein S28
P23396	RPS3	ribosomal protein S3
P61247	RPS3A	ribosomal protein S3A
P46782	RPS5	ribosomal protein S5
P62753	RPS6	ribosomal protein S6
P62081	RPS7	ribosomal protein S7
P62241	RPS8	ribosomal protein S8
P46781	RPS9	ribosomal protein S9
P08865	RPSA	ribosomal protein SA
Q9P2E9	RRBP1	ribosome binding protein 1
Q9Y3I0	RTCB	RNA 2',3'-cyclic phosphate and 5'-OH ligase
Q9Y265	RUVBL1	RuvB-like AAA ATPase 1
Q9BY12	SCAPER	S-phase cyclin A-associated protein in the ER
Q9NVU7	SDAD1	SDA1 domain containing 1
Q15019	SEPT2	septin 2
Q16181	SEPT7	septin 7
Q9UHD8	SEPT9	septin 9
Q8NC51	SERBP1	SERPINE1 mRNA binding protein 1
P50454	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)
P23246	SFPQ	splicing factor proline/glutamine-rich
P34897	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)
Q8TF72	SHROOM3	shroom family member 3
Q9P270	SLAIN2	SLAIN motif family, member 2
Q9UQE7	SMC3	structural maintenance of chromosomes 3
Q16637	SMN1	survival Of Motor Neuron 1, Telomeric
Q7KZF4	SND1	staphylococcal nuclease and tudor domain containing 1
Q13573	SNW1	SNW domain containing 1
O94964	SOGA1	suppressor of glucose, autophagy associated 1
Q69YQ0	SPECC1L	sperm antigen with calponin homology and coiled-coil domains 1-like
Q9Y6N5	SQRDL	sulfide quinone reductase-like (yeast)
Q7Z6B7	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1
O75044	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2
Q9UHB9	SRP68	signal recognition particle 68kDa
Q08945	SSRP1	structure specific recognition protein 1
O15056	SYNJ2	synaptojanin 2
Q9C0D5	TANC1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1
Q13148	TARDBP	TAR DNA binding protein
Q9BYX2	TBC1D2	TBC1 domain family, member 2
O60343	TBC1D4	TBC1 domain family, member 4
Q9UGI8	TES	testin LIM domain protein
Q07157	TJP1	tight junction protein 1
Q9UDY2	TJP2	tight junction protein 2
P29401	TKT	transketolase
Q9C0C2	TNKS1BP1	tankyrase 1 binding protein 1, 182kDa
Q68CZ2	TNS3	tensin 3
O14545	TRAFD1	TRAF-type zinc finger domain containing 1
Q13263	TRIM28	tripartite motif containing 28
O75962	TRIO	trio Rho guanine nucleotide exchange factor
Q9H2D6	TRIOBP	TRIO and F-actin binding protein
Q15650	TRIP4	thyroid hormone receptor interactor 4
Q15654	TRIP6	thyroid hormone receptor interactor 6
P68363	TUBA1B	tubulin, alpha 1b
Q9BQE3	TUBA1C	tubulin, alpha 1c
P07437	TUBB	tubulin, beta class I
Q13885	TUBB2A	tubulin, beta 2A class IIa
Q13509	TUBB3	tubulin, beta 3 class III
P68371	TUBB4B	tubulin, beta 4B class IVb
Q9BUF5	TUBB6	tubulin, beta 6 class V
P49411	TUFM	Tu translation elongation factor, mitochondrial
Q9BZF9	UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats
Q14157	UBAP2L	ubiquitin associated protein 2-like
Q96PU4	UHRF2	ubiquitin-like with PHD and ring finger domains 2, E3 ubiquitin protein ligase
Q92900	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)
Q9HAU5	UPF2	UPF2 regulator of nonsense transcripts homolog (yeast)
Q14694	USP10	ubiquitin specific peptidase 10
P50552	VASP	vasodilator-stimulated phosphoprotein
P08670	VIM	vimentin
Q9ULE0	WWC3	WWC family member 3

O00308	WWP2	WW domain containing E3 ubiquitin protein ligase 2
Q9H0D6	XRN2	5'-3' exoribonuclease 2
P67809	YBX1	Y box binding protein 1
Q9UPT8	ZC3H4	zinc finger CCCH-type containing 4
Q8IWR0	ZC3H7A	zinc finger CCCH-type containing 7A
Q7Z2W4	ZC3HAV1	zinc finger CCCH-type, antiviral 1
Q15942	ZYX	zyxin

B. Specific partners of FKBP7 in IGR-CaP1-Dtx-R cells

ID	Gene symbol	Full Name
P49588	AARS	alanyl-tRNA synthetase
Q5JTZ9	AARS2	alanyl-tRNA synthetase 2, mitochondrial
P08183	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1
P61221	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1
Q8NE71	ABCF1	ATP-binding cassette, sub-family F (GCN20), member 1
Q9UG63	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2
Q9NUQ8	ABCF3	ATP-binding cassette, sub-family F (GCN20), member 3
Q8IZP0	ABI1	abl-interactor 1
P42684	ABL2	ABL proto-oncogene 2, non-receptor tyrosine kinase
Q13085	ACACA	acetyl-CoA carboxylase alpha
P53396	ACLY	ATP citrate lyase
Q9Y305	ACOT9	acyl-CoA thioesterase 9
O95573	ACSL3	acyl-CoA synthetase long-chain family member 3
P60709	ACTB	actin, beta
Q562R1	ACTBL2	actin, beta-like 2
P68032	ACTC1	actin, alpha, cardiac muscle 1
P12814	ACTN1	actinin, alpha 1
O43707	ACTN4	actinin, alpha 4
P61160	ACTR2	ARP2 actin-related protein 2 homolog (yeast)
P61158	ACTR3	ARP3 actin-related protein 3 homolog (yeast)
Q9P2N4	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif, 9
Q9H2P0	ADNP	activity-dependent neuroprotector homeobox
Q09666	AHNAK	AHNAK nucleoprotein
Q9BQI0	AIF1L	allograft inflammatory factor 1-like
Q12904	AIMP1	aminoacyl tRNA synthetase complex-interacting multifunctional protein 1
Q13155	AIMP2	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2
Q9Y3D8	AK6	adenylate kinase 6
Q12802	AKAP13	A kinase (PRKA) anchor protein 13
Q99996	AKAP9	A kinase (PRKA) anchor protein 9
P54886	ALDH18A1	aldehyde dehydrogenase 18 family, member A1
Q86V81	ALYREF	Aly/REF export factor
Q9Y303	AMDHD2	amidohydrolase domain containing 2
Q01433	AMPD2	adenosine monophosphate deaminase 2
P16157	ANK1	ankyrin 1, erythrocytic
Q01484	ANK2	ankyrin 2, neuronal
Q12955	ANK3	ankyrin 3, node of Ranvier (ankyrin G)
Q9P2R3	ANKFY1	ankyrin repeat and FYVE domain containing 1
Q8IWZ3	ANKHD1/ANKHD1-EIF4EBP3	ankyrin repeat and KH domain containing 1
Q9H8Y5	ANKZF1	ankyrin repeat and zinc finger domain containing 1
Q9NQW6	ANLN	anillin actin binding protein
P07355	ANXA2	annexin A2
Q10567	AP1B1	adaptor-related protein complex 1, beta 1 subunit
O43747	AP1G1	adaptor-related protein complex 1, gamma 1 subunit
O95782	AP2A1	adaptor-related protein complex 2, alpha 1 subunit
O94973	AP2A2	adaptor-related protein complex 2, alpha 2 subunit
P63010	AP2B1	adaptor-related protein complex 2, beta 1 subunit
Q96CW1	AP2M1	adaptor-related protein complex 2, mu 1 subunit
O00203	AP3B1	adaptor-related protein complex 3, beta 1 subunit
O14617	AP3D1	adaptor-related protein complex 3, delta 1 subunit
Q9Y2T2	AP3M1	adaptor-related protein complex 3, mu 1 subunit
Q92572	AP3S1	adaptor-related protein complex 3, sigma 1 subunit
Q06481	APLP2	amyloid beta (A4) precursor-like protein 2
Q9HDC9	APMAP	adipocyte plasma membrane associated protein
Q8NEU8	APPL2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2
O60306	AQR	aquarius intron-binding spliceosomal factor
P48444	ARCN1	archain 1
O15013	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10
Q9NZN5	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12
Q96PE2	ARHGEF17	Rho guanine nucleotide exchange factor (GEF) 17

Q92974	ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2
Q8N1W1	ARHGEF28	Rho guanine nucleotide exchange factor (GEF) 28
Q14155	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7
P40616	ARL1	ADP-ribosylation factor-like 1
Q8IUR7	ARMC8	armadillo repeat containing 8
O15143	ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa
O15144	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa
Q9ULH1	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1
Q8N9N2	ASCC1	activating signal cointegrator 1 complex subunit 1
Q9H1I8	ASCC2	activating signal cointegrator 1 complex subunit 2
Q8N3C0	ASCC3	activating signal cointegrator 1 complex subunit 3
P08243	ASNS	asparagine synthetase (glutamine-hydrolyzing)
Q12797	ASPH	aspartate beta-hydroxylase
P16615	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
P25705	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle
P46100	ATRX	alpha thalassemia/mental retardation syndrome X-linked
Q99700	ATXN2	ataxin 2
Q8WWM7	ATXN2L	ataxin 2-like
Q13825	AUH	AU RNA binding protein/enoyl-CoA hydratase
O94766	B3GAT3	beta-1,3-glucuronyltransferase 3
O95816	BAG2	BCL2-associated athanogene 2
O95817	BAG3	BCL2-associated athanogene 3
Q9UHR4	BAIAP2L1	BAI1-associated protein 2-like 1
P11274	BCR	breakpoint cluster region
Q9H694	BICC1	BicC family RNA binding protein 1
Q9NR09	BIRC6	baculoviral IAP repeat containing 6
Q9NSY1	BMP2K	BMP2 inducible kinase
Q6PJG6	BRAT1	BRCA1-associated ATM activator 1
Q10589	BST2	bone marrow stromal cell antigen 2
O14981	BTAF1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa
P20290	BTF3	basic transcription factor 3
Q9Y224	C14orf166	chromosome 14 open reading frame 166
Q9BU76	C1orf35	chromosome 1 open reading frame 35
Q9H6R7	C2orf44	chromosome 2 open reading frame 44
Q8WWC4	C2orf47	chromosome 2 open reading frame 47
Q9BRJ6	C7orf50	chromosome 7 open reading frame 50
Q8WUQ7	CACTIN	cactin, spliceosome C complex subunit
P27708	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
Q05682	CALD1	caldesmon 1
P62158	CALM1	calmodulin 1 (Phosphorylase Kinase, Delta)
O43852	CALU	calumenin
Q13557	CAMK2D	calcium/calmodulin-dependent protein kinase II delta
Q13555	CAMK2G	calcium/calmodulin-dependent protein kinase II gamma
Q14444	CAPRIN1	cell cycle associated protein 1
P52907	CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1
P47756	CAPZB	capping protein (actin filament) muscle Z-line, beta
Q9HA77	CARS2	cysteinyl-tRNA synthetase 2, mitochondrial (putative)
P04040	CAT	catalase
Q6P1N0	CC2D1A	coiled-coil and C2 domain containing 1A
Q96CT7	CCDC124	coiled-coil domain containing 124
Q16204	CCDC6	coiled-coil domain containing 6
Q3V6T2	CCDC88A	coiled-coil domain containing 88A
O43303	CCP110	centriolar coiled coil protein 110kDa
P78371	CCT2	chaperonin containing TCP1, subunit 2 (beta)
P49368	CCT3	chaperonin containing TCP1, subunit 3 (gamma)
P50991	CCT4	chaperonin containing TCP1, subunit 4 (delta)
P48643	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)
P40227	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)
Q99832	CCT7	chaperonin containing TCP1, subunit 7 (eta)
P50990	CCT8	chaperonin containing TCP1, subunit 8 (theta)
Q12834	CDC20	cell division cycle 20
P60953	CDC42	cell division cycle 42
Q5VT25	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)
Q9Y5S2	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)
Q00587	CDC42EP1	CDC42 effector protein (Rho GTPase binding) 1
O14735	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase
P06493	CDK1	cyclin-dependent kinase 1
Q96SN8	CDK5RAP2	CDK5 regulatory subunit associated protein 2
Q9BXW7	CECR5	cat eye syndrome chromosome region, candidate 5

Q9UPN4	CEP131	centrosomal protein 131kDa
Q66GS9	CEP135	centrosomal protein 135kDa
Q5SW79	CEP170	centrosomal protein 170kDa
Q9Y4F5	CEP170B	centrosomal protein 170B
Q5JTW2	CEP78	centrosomal protein 78kDa
Q6P2H3	CEP85	centrosomal protein 85kDa
Q8IW35	CEP97	centrosomal protein 97kDa
P41208	CETN2	centrin, EF-hand protein, 2
Q9NX63	CHCHD3	coiled-coil-helix-coiled-coil-helix domain containing 3
Q12873	CHD3	chromodomain helicase DNA binding protein 3
Q14839	CHD4	chromodomain helicase DNA binding protein 4
Q9NZZ3	CHMP5	charged multivesicular body protein 5
Q99653	CHP1	calcineurin-like EF-hand protein 1
Q9Y3Y2	CHTOP	chromatin target of PRMT1
Q14011	CIRBP	cold inducible RNA binding protein
O14578	CIT	citron rho-interacting serine/threonine kinase
Q07065	CKAP4	cytoskeleton-associated protein 4
Q14008	CKAP5	cytoskeleton associated protein 5
P12532	CKMT1A	creatine Kinase, Mitochondrial 1A
Q7Z460	CLASP1	cytoplasmic linker associated protein 1
O75122	CLASP2	cytoplasmic linker associated protein 2
Q9H078	CLPB	ClpB homolog, mitochondrial AAA ATPase chaperonin
O76031	CLPX	caseinolytic mitochondrial matrix peptidase chaperone subunit
Q00610	CLTC	clathrin, heavy chain (Hc)
Q8N1G2	CMTR1	cap methyltransferase 1
Q9P003	CNIH4	cornichon family AMPA receptor auxiliary protein 4
A5YKK6	CNOT1	CCR4-NOT transcription complex, subunit 1
Q9UKZ1	CNOT11	CCR4-NOT transcription complex, subunit 11
Q9NZN8	CNOT2	CCR4-NOT transcription complex, subunit 2
P09543	CNP	2',3'-cyclic nucleotide 3' phosphodiesterase
Q8NBJ5	COLGALT1	collagen beta(1-O)galactosyltransferase 1
P53621	COPA	coatomer protein complex, subunit alpha
P53618	COPB1	coatomer protein complex, subunit beta 1
P35606	COPB2	coatomer protein complex, subunit beta 2 (beta prime)
O14579	COPE	coatomer protein complex, subunit epsilon
Q9Y678	COPG1	coatomer protein complex, subunit gamma 1
Q9UBF2	COPG2	coatomer protein complex, subunit gamma 2
Q9BR76	CORO1B	coronin, actin binding protein, 1B
Q16630	CPSF6	cleavage and polyadenylation specific factor 6, 68kDa
P50416	CPT1A	carnitine palmitoyltransferase 1A (liver)
P52943	CRIP2	cysteine-rich protein 2
O75534	CSDE1	cold shock domain containing E1, RNA-binding
P55060	CSE1L	CSE1 chromosome segregation 1-like (yeast)
P48729	CSNK1A1	casein kinase 1, alpha 1
P49674	CSNK1E	casein Kinase 1, Epsilon
P68400	CSNK2A1	casein kinase 2, alpha 1 polypeptide
P19784	CSNK2A2	casein kinase 2, alpha prime polypeptide
P67870	CSNK2B	casein kinase 2, beta polypeptide
P21291	CSRP1	cysteine and glycine-rich protein 1
P35221	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa
O60716	CTNND1	catenin (cadherin-associated protein), delta 1
P17812	CTPS1	CTP synthase 1
Q14247	CTTN	cortactin
Q69YN2	CWF19L1	CWF19-like 1, cell cycle control (S. pombe)
Q7L576	CYFIP1	cytoplasmic FMR1 interacting protein 1
Q96F07	CYFIP2	cytoplasmic FMR1 interacting protein 2
P53355	DAPK1	death-associated protein kinase 1
P14868	DARS	aspartyl-tRNA synthetase
Q6PI48	DARS2	aspartyl-tRNA synthetase 2, mitochondrial
Q16643	DBN1	drebrin 1
P11182	DBT	dihydrolipoamide branched chain transacylase E2
Q5VU92	DCAF12L1	DDB1 and CUL4 associated factor 12-like 1
Q13561	DCTN2	dynactin 2 (p50)
Q9UJW0	DCTN4	dynactin 4 (p62)
Q8IWE4	DCUN1D3	DCN1, defective in cullin neddylation 1, domain containing 3
P39656	DDOST	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit (non-catalytic)
Q92499	DDX1	DEAD (Asp-Glu-Ala-Asp) box helicase 1
Q92841	DDX17	DEAD (Asp-Glu-Ala-Asp) box helicase 17
Q9NR30	DDX21	DEAD (Asp-Glu-Ala-Asp) box helicase 21
Q9GZR7	DDX24	DEAD (Asp-Glu-Ala-Asp) box helicase 24

O00571	DDX3X	DEAD (Asp-Glu-Ala-Asp) box helicase 3, X-linked
Q9UJV9	DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41
Q9H0S4	DDX47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47
Q9Y6V7	DDX49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49
P17844	DDX5	DEAD (Asp-Glu-Ala-Asp) box helicase 5
Q9Y2R4	DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
Q8TDD1	DDX54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54
Q8NHQ9	DDX55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55
Q9NY93	DDX56	DEAD (Asp-Glu-Ala-Asp) box helicase 56
P26196	DDX6	DEAD (Asp-Glu-Ala-Asp) box helicase 6
Q16698	DECR1	2,4-dienoyl CoA reductase 1, mitochondrial
Q9H4E7	DEF6	DEF6 guanine nucleotide exchange factor
Q15392	DHCR24	24-dehydrocholesterol reductase
O43143	DHX15	DEAH (Asp-Glu-Ala-His) box helicase 15
O60231	DHX16	DEAH (Asp-Glu-Ala-His) box polypeptide 16
Q7Z478	DHX29	DEAH (Asp-Glu-Ala-His) box polypeptide 29
Q7L2E3	DHX30	DEAH (Asp-Glu-Ala-His) box helicase 30
Q14147	DHX34	DEAH (Asp-Glu-Ala-His) box polypeptide 34
Q9H2U1	DHX36	DEAH (Asp-Glu-Ala-His) box polypeptide 36
Q8IY37	DHX37	DEAH (Asp-Glu-Ala-His) box polypeptide 37
Q92620	DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38
Q8IX18	DHX40	DEAH (Asp-Glu-Ala-His) box polypeptide 40
Q6P158	DHX57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57
Q08211	DHX9	DEAH (Asp-Glu-Ala-His) box helicase 9
Q9Y2L1	DIS3	DIS3 homolog, exosome endoribonuclease and 3'-5' exoribonuclease
P36957	DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)
P31689	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1
O60884	DNAJA2	DnaJ (Hsp40) homolog, subfamily A, member 2
Q96EY1	DNAJA3	DnaJ (Hsp40) homolog, subfamily A, member 3
Q9UBS4	DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11
Q8IXB1	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10
P50570	DNM2	dynamin 2
P26358	DNMT1	DNA (cytosine-5-)-methyltransferase 1
Q14185	DOCK1	dedicator of cytokinesis 1
Q96HP0	DOCK6	dedicator of cytokinesis 6
Q96N67	DOCK7	dedicator of cytokinesis 7
O60762	DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
Q9Y295	DRG1	developmentally regulated GTP binding protein 1
Q14126	DSG2	desmoglein 2
P15924	DSP	desmoplakin
Q14204	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1
Q5JPH6	EARS2	glutamyl-tRNA synthetase 2, mitochondrial
Q14213	EBI3	Epstein-Barr virus induced 3
Q6P2E9	EDC4	enhancer of mRNA decapping 4
P68104	EEF1A1	eukaryotic translation elongation factor 1 alpha 1
P24534	EEF1B2	eukaryotic translation elongation factor 1 beta 2
P29692	EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
O43324	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1
P26641	EEF1G	eukaryotic translation elongation factor 1 gamma
P13639	EEF2	eukaryotic translation elongation factor 2
Q9BUP0	EFHD1	EF-hand domain family, member D1
Q96C19	EFHD2	EF-hand domain family, member D2
Q15029	EFTUD2	elongation factor Tu GTP binding domain containing 2
P00533	EGFR	epidermal growth factor receptor
Q9H223	EHD4	EH-domain containing 4
Q9BY44	EIF2A	eukaryotic translation initiation factor 2A, 65kDa
P19525	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2
Q9P2K8	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4
Q9UI10	EIF2B4	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa
P05198	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
P20042	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa
P41091	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa
Q14152	EIF3A	eukaryotic translation initiation factor 3, subunit A
Q99613	EIF3C	eukaryotic translation initiation factor 3, subunit C
O15371	EIF3D	eukaryotic translation initiation factor 3, subunit D
P60228	EIF3E	eukaryotic translation initiation factor 3, subunit E
O00303	EIF3F	eukaryotic translation initiation factor 3, subunit F
Q13347	EIF3I	eukaryotic translation initiation factor 3, subunit I
Q9Y262	EIF3L	eukaryotic translation initiation factor 3, subunit L
P60842	EIF4A1	eukaryotic translation initiation factor 4A1
P38919	EIF4A3	eukaryotic translation initiation factor 4A3

O60573	EIF4E2	eukaryotic translation initiation factor 4E family member 2
Q04637	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1
P63241	EIF5A	eukaryotic translation initiation factor 5A
O60841	EIF5B	eukaryotic translation initiation factor 5B
Q9H9T3	ELP3	elongator acetyltransferase complex subunit 3
Q8N766	EMC1	ER membrane protein complex subunit 1
Q9P0I2	EMC3	ER membrane protein complex subunit 3
P50402	EMD	emerin
Q92979	EMG1	EMG1 N1-specific pseudouridine methyltransferase
Q8N8S7	ENAH	enabled homolog (Drosophila)
O43491	EPB41L2	erythrocyte membrane protein band 4.1-like 2
P07814	EPRS	glutamyl-prolyl-tRNA synthetase
Q9UBC2	EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1
P04626	ERBB2	erb-b2 receptor tyrosine kinase 2
Q8IUD2	ERC1	ELKS/RAB6-interacting/CAST family member 1
Q8IV48	ERI1	exoribonuclease 1
O75477	ERLIN1	ER lipid raft associated 1
O94905	ERLIN2	ER lipid raft associated 2
Q9H501	ESF1	ESF1 nucleolar pre-rRNA processing protein homolog
A0FGR8	ESYT2	extended synaptotagmin-like protein 2
P62495	ETF1	eukaryotic translation termination factor 1
Q01844	EWSR1	EWS RNA-binding protein 1
Q96A65	EXOC4	exocyst complex component 4
Q13868	EXOSC2	exosome component 2
P15311	EZR	ezrin
Q9NZB2	FAM120A	family with sequence similarity 120A
Q641Q2	FAM21A/FAM21C	family with sequence similarity 21, member C
Q9H4H8	FAM83D	family with sequence similarity 83, member D
Q6ZRV2	FAM83H	family with sequence similarity 83, member H
Q658Y4	FAM91A1	family with sequence similarity 91, member A1
Q9Y3D0	FAM96B	family with sequence similarity 96, member B
Q8NCA5	FAM98A	family with sequence similarity 98, member A
Q52LJ0	FAM98B	family with sequence similarity 98, member B
Q9Y285	FARSA	phenylalanyl-tRNA synthetase, alpha subunit
Q7L8L6	FASTKD5	FAST kinase domains 5
P62861	FAU	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed
P22087	FBL	fibrillarin
P07332	FES	FES proto-oncogene, tyrosine kinase
Q96M96	FGD4	FYVE, RhoGEF and PH domain containing 4
Q13642	FHL1	four and a half LIM domains 1
Q00688	FKBP3	FK506 binding protein 3, 25kDa
Q9Y680	FKBP7	FK506 binding protein 7
Q13045	FLII	flightless I actin binding protein
P21333	FLNA	filamin A, alpha
O75369	FLNB	filamin B, beta
Q14315	FLNC	filamin C, gamma
Q96PY5	FMNL2	formin-like 2
Q5T0N5	FNBP1L	formin binding protein 1-like
Q14331	FRG1	FSHD region gene 1
Q8IY81	FTSJ3	FtsJ homolog 3 (E. coli)
P35637	FUS	FUS RNA binding protein
P51114	FXR1	fragile X mental retardation, autosomal homolog 1
P51116	FXR2	fragile X mental retardation, autosomal homolog 2
Q13283	G3BP1	GTPase activating protein (SH3 domain) binding protein 1
Q9UN86	G3BP2	GTPase activating protein (SH3 domain) binding protein 2
P04406	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
O75323	GBAS	glioblastoma amplified sequence
Q92616	GCN1	GCN1 eIF2 alpha kinase activator homolog
O14893	GEMIN2	gem (nuclear organelle) associated protein 2
P57678	GEMIN4	gem (nuclear organelle) associated protein 4
Q8TEQ6	GEMIN5	gem (nuclear organelle) associated protein 5
Q8WXD5	GEMIN6	gem (nuclear organelle) associated protein 6
Q06210	GFPT1	glutamine--fructose-6-phosphate transaminase 1
Q9NWU2	GID8	GID complex subunit 8
Q6Y7W6	GIGYF2	GRB10 interacting GYF protein 2
O14908	GIPC1	GIPC PDZ domain containing family, member 1
Q9Y2X7	GIT1	G protein-coupled receptor kinase interacting ArfGAP 1
Q14161	GIT2	G protein-coupled receptor kinase interacting ArfGAP 2
Q9H4G4	GLIPR2	GLI pathogenesis-related 2
P00367	GLUD1	glutamate dehydrogenase 1
P63096	GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1

P04899	GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2
P08754	GNAI3	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3
P50148	GNAQ	guanine nucleotide binding protein (G protein), q polypeptide
P63092	GNAS	GNAS complex locus
P62879	GNB2	guanine nucleotide binding protein (G protein), beta polypeptide 2
P63244	GNB2L1	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
Q9Y223	GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase
P50151	GNG10	guanine nucleotide binding protein (G protein), gamma 10
Q9UBI6	GNG12	guanine nucleotide binding protein (G protein), gamma 12
Q13823	GNL2	guanine nucleotide binding protein-like 2 (nucleolar)
P46926	GNPDA1	glucosamine-6-phosphate deaminase 1
Q8TDQ7	GNPDA2	glucosamine-6-phosphate deaminase 2
Q9HD26	GOPC	golgi-associated PDZ and coiled-coil motif containing
P35052	GPC1	glypican 1
O75487	GPC4	glypican 4
Q8NFJ5	GPRC5A	G protein-coupled receptor, class C, group 5, member A
Q14451	GRB7	growth factor receptor-bound protein 7
Q12849	GRSF1	G-rich RNA sequence binding factor 1
P06396	GSN	gelsolin
P09211	GSTP1	glutathione S-transferase pi 1
Q92759	GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa
P78347	GTF2I	general transcription factor IIi
Q9Y5Q9	GTF3C3	general transcription factor IIIC, polypeptide 3, 102kDa
Q9UBP9	GULP1	GULP, engulfment adaptor PTB domain containing 1
P13807	GYS1	glycogen synthase 1 (muscle)
P07305	H1F0	H1 histone family, member 0
P16104	H2AFX	H2A histone family, member X
P40939	HADHA	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit
Q68CZ6	HAUS3	HAUS augmin-like complex, subunit 3
O94927	HAUS5	HAUS augmin-like complex, subunit 5
Q7Z4H7	HAUS6	HAUS augmin-like complex, subunit 6
Q99871	HAUS7	HAUS augmin-like complex, subunit 7
Q9BT25	HAUS8	HAUS augmin-like complex, subunit 8
Q13547	HDAC1	histone deacetylase 1
Q7Z4V5	HDGFRP2	hepatoma-derived growth factor-related protein 2
Q00341	HDLBP	high density lipoprotein binding protein
Q9NRZ9	HELLS	helicase, lymphoid-specific
P42694	HELZ	helicase with zinc finger
O95714	HERC2	HECT and RLD domain containing E3 ubiquitin protein ligase 2
O94992	HEXIM1	hexamethylene bis-acetamide inducible 1
P16401	HIST1H1B	histone cluster 1, H1b
P16402	HIST1H1D	histone cluster 1, H1d
P04908	HIST1H2AB	histone Cluster 1, H2ab
P58876	HIST1H2BD	histone cluster 1, H2bd
P62805	HIST1H4A	histone Cluster 1, H4a
Q16777	HIST2H2AC	histone cluster 2, H2ac
Q8N257	HIST3H2BB	histone cluster 3, H2bb
P19367	HK1	hexokinase 1
Q2TB90	HKDC1	hexokinase domain containing 1
Q14527	HLTF	helicase-like transcription factor
O75330	HMMR	hyaluronan-mediated motility receptor (RHAMM)
Q13151	HNRNPA0	heterogeneous nuclear ribonucleoprotein A0
P09651	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1
P22626	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1
Q99729	HNRNPAB	heterogeneous nuclear ribonucleoprotein A/B
P07910	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)
Q14103	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
P52597	HNRNPF	heterogeneous nuclear ribonucleoprotein F
P31943	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H)
P55795	HNRNPH2	heterogeneous nuclear ribonucleoprotein H2 (H')
P31942	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)
P61978	HNRNPK	heterogeneous nuclear ribonucleoprotein K
P14866	HNRNPL	heterogeneous nuclear ribonucleoprotein L
Q8WVV9	HNRNPLL	heterogeneous nuclear ribonucleoprotein L-like
P52272	HNRNPM	heterogeneous nuclear ribonucleoprotein M
Q00839	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
Q9BUJ2	HNRNPUL1	heterogeneous nuclear ribonucleoprotein U-like 1
Q86VS8	HOOK3	hook microtubule-tethering protein 3
P51659	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4

P07900	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1
P08238	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1
Q58FF6	HSP90AB4P	heat shock protein 90kDa alpha (cytosolic), class B member 4, pseudogene
P14625	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1
P08107	HSPA1A	heat Shock 70kDa Protein 1A
P34932	HSPA4	heat shock 70kDa protein 4
P11021	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
P11142	HSPA8	heat shock 70kDa protein 8
P38646	HSPA9	heat shock 70kDa protein 9 (mortalin)
P04792	HSPB1	heat shock 27kDa protein 1
P10809	HSPD1	heat shock 60kDa protein 1 (chaperonin)
P41252	IARS	isoleucyl-tRNA synthetase
Q9NSE4	IARS2	isoleucyl-tRNA synthetase 2, mitochondrial
Q9HBG6	IFT122	intraflagellar transport 122
Q9NZI8	IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1
Q9Y6M1	IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2
O00425	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3
O95163	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein
Q12906	ILF3	interleukin enhancer binding factor 3, 90kDa
Q13418	ILK	integrin-linked kinase
Q16891	IMMT	inner membrane protein, mitochondrial
P20839	IMPDH1	IMP (inosine 5'-monophosphate) dehydrogenase 1
P12268	IMPDH2	IMP (inosine 5'-monophosphate) dehydrogenase 2
Q14642	INPP5A	inositol polyphosphate-5-phosphatase A
O95373	IPO7	importin 7
Q96P70	IPO9	importin 9
P46940	IQGAP1	IQ motif containing GTPase activating protein 1
Q7Z5L9	IRF2BP2	interferon regulatory factor 2 binding protein 2
Q9NPH2	ISYNA1	inositol-3-phosphate synthase 1
Q14573	ITPR3	inositol 1,4,5-trisphosphate receptor, type 3
P14923	JUP	junction plakoglobin
Q63ZY3	KANK2	KN motif and ankyrin repeat domains 2
O60341	KDM1A	lysine (K)-specific demethylase 1A
Q07666	KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1
Q12768	KIAA0196	KIAA0196
Q2M389	KIAA1033	KIAA1033
Q96Q89	KIF20B	kinesin family member 20B
Q02241	KIF23	kinesin family member 23
O00139	KIF2A	kinesin heavy chain member 2A
Q99661	KIF2C	kinesin family member 2C
O95239	KIF4A	kinesin family member 4A
Q9BW19	KIFC1	kinesin family member C1
Q9BVG8	KIFC3	kinesin family member C3
Q1ED39	KNOP1	lysine-rich nucleolar protein 1
P50748	KNTC1	kinetochore associated 1
P52294	KPNA1	karyopherin alpha 1 (importin alpha 5)
P52292	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
O15131	KPNA5	karyopherin alpha 5 (importin alpha 6)
P04264	KRT1	keratin 1, type II
P13645	KRT10	keratin 10, type I
P02533	KRT14	keratin 14, type I
P08779	KRT16	keratin 16, type I
P35908	KRT2	keratin 2, type II
P13647	KRT5	keratin 5, type II
P02538	KRT6A	keratin 6A, type II
P04259	KRT6B	keratin 6B, type II
Q01546	KRT76	keratin 76, type II
P35527	KRT9	keratin 9, type I
Q86UP2	KTN1	kinectin 1 (kinesin receptor)
O00515	LAD1	ladinin 1
P11047	LAMC1	laminin, gamma 1 (formerly LAMB2)
P28838	LAP3	leucine aminopeptidase 3
Q6PKG0	LARP1	La ribonucleoprotein domain family, member 1
Q71RC2	LARP4	La ribonucleoprotein domain family, member 4
Q92615	LARP4B	La ribonucleoprotein domain family, member 4B
Q4G0J3	LARP7	La ribonucleoprotein domain family, member 7
Q9P2J5	LARS	leucyl-tRNA synthetase
Q15031	LARS2	leucyl-tRNA synthetase 2, mitochondrial
Q14847	LASP1	LIM and SH3 protein 1
P00338	LDHA	lactate dehydrogenase A

P07195	LDHB	lactate dehydrogenase B
P09382	LGALS1	lectin, galactoside-binding, soluble, 1
Q9UPQ0	LIMCH1	LIM and calponin homology domains 1
P48059	LIMS1	LIM and senescent cell antigen-like domains 1
Q9H9Z2	LIN28A	lin-28 homolog A (C. elegans)
Q9BRT6	LLPH	LLP homolog, long-term synaptic facilitation (Aplysia)
P02545	LMNA	lamin A/C
O43272	LOC102724788/PRODH	proline dehydrogenase (oxidase) 1
P36776	LONP1	lon peptidase 1, mitochondrial
Q93052	LPP	LIM domain containing preferred translocation partner in lipoma
Q96II8	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3
O75427	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4
P30533	LRPAP1	low density lipoprotein receptor-related protein associated protein 1
Q8N1G4	LRRC47	leucine rich repeat containing 47
Q96AG4	LRRC59	leucine rich repeat containing 59
Q32MZ4	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1
Q9Y608	LRRFIP2	leucine rich repeat (in FLII) interacting protein 2
Q3MHD2	LSM12	LSM12 homolog
Q9NQ29	LUC7L	LUC7-like
Q9Y383	LUC7L2	LUC7-like 2 pre-mRNA splicing factor
Q86V48	LUZP1	leucine zipper protein 1
Q9NX58	LYAR	Ly1 antibody reactive
P07948	LYN	LYN proto-oncogene, Src family tyrosine kinase
Q7L5Y9	MAEA	macrophage erythroblast attacher
Q9Y5V3	MAGED1	melanoma antigen family D1
Q9UNF1	MAGED2	melanoma antigen family D2
Q9H0U3	MAGT1	magnesium transporter 1
Q66K74	MAP1S	microtubule-associated protein 1S
P27816	MAP4	microtubule-associated protein 4
O95819	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4
Q3KQU3	MAP7D1	MAP7 domain containing 1
Q15555	MAPRE2	microtubule-associated protein, RP/EB family, member 2
Q7KZI7	MARK2	MAP/microtubule affinity-regulating kinase 2
P27448	MARK3	MAP/microtubule affinity-regulating kinase 3
P56192	MARS	methionyl-tRNA synthetase
O60307	MAST3	microtubule associated serine/threonine kinase 3
P31153	MAT2A	methionine adenosyltransferase II, alpha
P43243	MATR3	matrin 3
Q96RQ3	MCCC1	methylcrotonoyl-CoA carboxylase 1 (alpha)
Q9HCC0	MCCC2	methylcrotonoyl-CoA carboxylase 2 (beta)
P25205	MCM3	minichromosome maintenance complex component 3
P33991	MCM4	minichromosome maintenance complex component 4
P33992	MCM5	minichromosome maintenance complex component 5
Q14566	MCM6	minichromosome maintenance complex component 6
P33993	MCM7	minichromosome maintenance complex component 7
Q14680	MELK	maternal embryonic leucine zipper kinase
Q9Y316	MEMO1	mediator of cell motility 1
Q8N6R0	METTL13	methyltransferase like 13
Q7RTP6	MICAL3	microtubule associated monooxygenase, calponin and LIM domain containing 3
Q8IUF8	MINA	MYC induced nuclear antigen
Q8N4C8	MINK1	misshapen-like kinase 1
Q9NXC5	MIOS	missing oocyte, meiosis regulator, homolog (Drosophila)
P55196	MLLT4	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 4
Q13724	MOGS	mannosyl-oligosaccharide glucosidase
Q9Y6X9	MORC2	MORC family CW-type zinc finger 2
Q9HCE1	MOV10	Mov10 RISC complex RNA helicase
Q6UVY6	MOXD1	monooxygenase, DBH-like 1
Q6WCQ1	MPRIP	myosin phosphatase Rho interacting protein
Q9BV20	MRI1	methylthioribose-1-phosphate isomerase 1
Q9Y2R9	MRPS7	mitochondrial ribosomal protein S7
Q9UKD2	MRTO4	MRT4 homolog, ribosome maturation factor
P26038	MSN	moesin
Q9Y4B5	MTCL1	microtubule crosslinking factor 1
Q86UE4	MTDH	metadherin
P11586	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
P13995	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase
Q9NXD2	MTMR10	myotubularin related protein 10
Q14764	MVP	major vault protein
Q9BQG0	MYBBP1A	MYB binding protein (P160) 1a

O75592	MYCBP2	MYC binding protein 2, E3 ubiquitin protein ligase
P35580	MYH10	myosin, heavy chain 10, non-muscle
P35749	MYH11	myosin, heavy chain 11, smooth muscle
Q7Z406	MYH14	myosin, heavy chain 14, non-muscle
P35579	MYH9	myosin, heavy chain 9, non-muscle
P19105	MYL12A	myosin, light chain 12A, regulatory, non-sarcomeric
O14950	MYL12B	myosin, light chain 12B, regulatory
P60660	MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle
P14649	MYL6B	myosin, light chain 6B, alkali, smooth muscle and non-muscle
P24844	MYL9	myosin, light chain 9, regulatory
Q92614	MYO18A	myosin XVIIIA
Q96H55	MYO19	myosin XIX
O00159	MYO1C	myosin IC
Q12965	MYO1E	myosin IE
Q9Y4I1	MYO5A	myosin VA
Q9ULV0	MYO5B	myosin VB
Q9NQX4	MYO5C	myosin VC
Q9UM54	MYO6	myosin VI
Q13459	MYO9B	myosin IXB
Q9NZM1	MYOF	myoferlin
Q6NZ67	MZT2B	mitotic spindle organizing protein 2B
Q13765	NACA	nascent polypeptide-associated complex alpha subunit
P43490	NAMPT	nicotinamide phosphoribosyltransferase
Q99733	NAP1L4	nucleosome assembly protein 1-like 4
O43776	NARS	asparaginyl-tRNA synthetase
Q15021	NCAPD2	non-SMC condensin I complex, subunit D2
P42695	NCAPD3	non-SMC condensin II complex, subunit D3
Q9BPX3	NCAPG	non-SMC condensin I complex, subunit G
Q86XI2	NCAPG2	non-SMC condensin II complex, subunit G2
Q15003	NCAPH	non-SMC condensin I complex, subunit H
Q9Y2A7	NCKAP1	NCK-associated protein 1
P19338	NCL	nucleolin
Q969V3	NCLN	nicalin
O75489	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)
P18615	NELFE	negative elongation factor complex member E
O60524	NEMF	nuclear export mediator factor
P21359	NF1	neurofibromin 1
Q9BYG3	NIFK	nucleolar protein interacting with the FHA domain of MKI67
Q9BPW8	NIPSNAP1	nipsnap homolog 1 (C. elegans)
Q96D46	NMD3	NMD3 ribosome export adaptor
Q9Y5B8	NME7	NME/NM23 family member 7
P30419	NMT1	N-myristoyltransferase 1
Q8NC60	NOA1	nitric oxide associated 1
Q9ULX3	NOB1	NIN1/RPN12 binding protein 1 homolog
Q15233	NONO	non-POU domain containing, octamer-binding
P78316	NOP14	NOP14 nucleolar protein
P46087	NOP2	NOP2 nucleolar protein
O00567	NOP56	NOP56 ribonucleoprotein
Q9Y2X3	NOP58	NOP58 ribonucleoprotein
P06748	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)
Q96P11	NSUN5	NOP2/Sun domain family, member 5
Q7Z417	NUFIP2	nuclear fragile X mental retardation protein interacting protein 2
Q14980	NUMA1	nuclear mitotic apparatus protein 1
Q9Y6R0	NUMBL	numb homolog (Drosophila)-like
P57740	NUP107	nucleoporin 107kDa
Q92621	NUP205	nucleoporin 205kDa
Q9UBU9	NXF1	nuclear RNA export factor 1
O60313	OPA1	optic atrophy 1 (autosomal dominant)
O60890	OPHN1	oligophrenin 1
O43929	ORC4	origin recognition complex, subunit 4
Q9BZF1	OSBPL8	oxysterol binding protein-like 8
O15460	P4HA2	prolyl 4-hydroxylase, alpha polypeptide II
P07237	P4HB	prolyl 4-hydroxylase, beta polypeptide
Q9UQ80	PA2G4	proliferation-associated 2G4, 38kDa
P11940	PABPC1	poly(A) binding protein, cytoplasmic 1
Q13310	PABPC4	poly(A) binding protein, cytoplasmic 4 (inducible form)
Q9UNF0	PACSIN2	protein kinase C and casein kinase substrate in neurons 2
Q9UKS6	PACSIN3	protein kinase C and casein kinase substrate in neurons 3
O96013	PAK4	p21 protein (Cdc42/Rac)-activated kinase 4
Q9NVE7	PANK4	pantothenate kinase 4

O43252	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1
O95340	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2
Q8TEW0	PARD3	par-3 family cell polarity regulator
Q9BYG5	PARD6B	par-6 family cell polarity regulator beta
P09874	PARP1	poly (ADP-ribose) polymerase 1
Q9UGN5	PARP2	poly (ADP-ribose) polymerase 2
Q9UKK3	PARP4	poly (ADP-ribose) polymerase family, member 4
Q7L3T8	PARS2	prolyl-tRNA synthetase 2, mitochondrial (putative)
Q86TB9	PATL1	protein associated with topoisomerase II homolog 1 (yeast)
Q96IZ0	PAWR	PRKC, apoptosis, WT1, regulator
Q96AQ6	PBXIP1	pre-B-cell leukemia homeobox interacting protein 1
Q15365	PCBP1	poly(rC) binding protein 1
Q15366	PCBP2	poly(rC) binding protein 2
Q5JVF3	PCID2	PCI domain containing 2
Q16822	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
Q15154	PCM1	pericentriolar material 1
P12004	PCNA	proliferating cell nuclear antigen
Q13442	PDAP1	PDGFA associated protein 1
Q5VU43	PDE4DIP	phosphodiesterase 4D interacting protein
O00151	PDLIM1	PDZ and LIM domain 1
Q96HC4	PDLIM5	PDZ and LIM domain 5
Q9NUG6	PDRG1	p53 and DNA-damage regulated 1
Q29RF7	PDS5A	PDS5 cohesin associated factor A
Q9NTI5	PDS5B	PDS5 cohesin associated factor B
Q86TG7	PEG10	paternally expressed 10
Q9BRX2	PELO	pelota homolog (Drosophila)
P50542	PEX5	peroxisomal biogenesis factor 5
Q9UHV9	PFDN2	prefoldin subunit 2
P17858	PFKL	phosphofructokinase, liver
P08237	PFKM	phosphofructokinase, muscle
Q01813	PFKP	phosphofructokinase, platelet
Q8IWS0	PHF6	PHD finger protein 6
O43175	PHGDH	phosphoglycerate dehydrogenase
Q86UU1	PHLDB1	pleckstrin homology-like domain, family B, member 1
Q969N2	PIGT	phosphatidylinositol glycan anchor biosynthesis, class T
Q9NWS0	PIH1D1	PIH1 domain containing 1
Q99755	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha
Q9Y446	PKP3	plakophilin 3
Q8IV08	PLD3	phospholipase D family, member 3
Q15149	PLEC	plectin
Q8IVE3	PLEKHH2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2
Q02809	PLOD1	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1
O60568	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
P13797	PLS3	plastin 3
Q9NRX1	PNO1	partner of NOB1 homolog
Q8IY17	PNPLA6	patatin-like phospholipase domain containing 6
Q8TCS8	PNPT1	polyribonucleotide nucleotidyltransferase 1
P28340	POLD1	polymerase (DNA directed), delta 1, catalytic subunit
P24928	POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa
P30876	POLR2B	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa
P36954	POLR2I	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa
Q9GZM3	POLR2J2/POLR2J3	polymerase (RNA) II (DNA directed) polypeptide J3
O14802	POLR3A	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa
Q99575	POP1	POP1 homolog, ribonuclease P/MRP subunit
P0CG38	POTEI	POTE ankyrin domain family, member I
Q9NQ55	PPAN	peter pan homolog (Drosophila)
Q13136	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1
Q86W92	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)
Q8ND30	PPFIBP2	PTPRF interacting protein, binding protein 2 (liprin beta 2)
Q13356	PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2
O60437	PPL	periplakin
P62136	PPP1CA	protein phosphatase 1, catalytic subunit, alpha isozyme
P62140	PPP1CB	protein phosphatase 1, catalytic subunit, beta isozyme
P36873	PPP1CC	protein phosphatase 1, catalytic subunit, gamma isozyme
O14974	PPP1R12A	protein phosphatase 1, regulatory subunit 12A
Q9BZL4	PPP1R12C	protein phosphatase 1, regulatory subunit 12C
Q6NYC8	PPP1R18	protein phosphatase 1, regulatory subunit 18
P62714	PPP2CB	protein phosphatase 2, catalytic subunit, beta isozyme
Q06830	PRDX1	peroxiredoxin 1
Q9Y478	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit

P54619	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit
P13861	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha
Q05655	PRKCD	protein kinase C, delta
Q9BZL6	PRKD2	protein kinase D2
O94806	PRKD3	protein kinase D3
P78527	PRKDC	protein kinase, DNA-activated, catalytic polypeptide
O14744	PRMT5	protein arginine methyltransferase 5
O94906	PRPF6	pre-mRNA processing factor 6
Q6P2Q9	PRPF8	pre-mRNA processing factor 8
P60891	PRPS1	phosphoribosyl pyrophosphate synthetase 1
P11908	PRPS2	phosphoribosyl pyrophosphate synthetase 2
P48634	PRRC2A	proline-rich coiled-coil 2A
P35998	PSMC2	proteasome 26S subunit, ATPase 2
P62195	PSMC5	proteasome 26S subunit, ATPase 5
Q13200	PSMD2	proteasome 26S subunit, non-ATPase 2
Q8WXF1	PSPC1	paraspeckle component 1
P26599	PTBP1	polypyrimidine tract binding protein 1
Q15678	PTPN14	protein tyrosine phosphatase, non-receptor type 14
Q6NZI2	PTRF	polymerase I and transcript release factor
Q15397	PUM3	pumilio RNA-binding family member 3
Q13610	PWP1	PWP1 homolog, endonuclein
P49023	PXN	paxillin
P32322	PYCR1	pyrroline-5-carboxylate reductase 1
Q96C36	PYCR2	pyrroline-5-carboxylate reductase family, member 2
P47897	QARS	glutaminyl-tRNA synthetase
P61026	RAB10	RAB10, member RAS oncogene family
Q9BXF6	RAB11FIP5	RAB11 family interacting protein 5 (class I)
P51153	RAB13	RAB13, member RAS oncogene family
Q15286	RAB35	RAB35, member RAS oncogene family
Q9H0H5	RACGAP1	Rac GTPase activating protein 1
O60216	RAD21	RAD21 cohesin complex component
Q92878	RAD50	RAD50 homolog, double strand break repair protein
P04049	RAF1	Raf-1 proto-oncogene, serine/threonine kinase
Q9P0K7	RAI14	retinoic acid induced 14
P11233	RALA	v-ral simian leukemia viral oncogene homolog A (ras related)
Q15311	RALBP1	ralA binding protein 1
Q6GYQ0	RALGAPA1	Ral GTPase activating protein, alpha subunit 1 (catalytic)
Q2PPJ7	RALGAPA2	Ral GTPase activating protein, alpha subunit 2 (catalytic)
Q86X10	RALGAPB	Ral GTPase activating protein, beta subunit (non-catalytic)
Q9UKM9	RALY	RALY heterogeneous nuclear ribonucleoprotein
P62826	RAN	RAN, member RAS oncogene family
Q6VN20	RANBP10	RAN binding protein 10
P61224	RAP1B	RAP1B, member of RAS oncogene family
P54136	RARS	arginyl-tRNA synthetase
Q96PK6	RBM14	RNA binding motif protein 14
Q9NW64	RBM22	RNA binding motif protein 22
Q9P2N5	RBM27	RNA binding motif protein 27
Q9NW13	RBM28	RNA binding motif protein 28
P98179	RBM3	RNA binding motif (RNP1, RRM) protein 3
Q14498	RBM39	RNA binding motif protein 39
Q9BWF3	RBM4	RNA binding motif protein 4
Q9Y580	RBM7	RNA binding motif protein 7
Q15434	RBMS2	RNA binding motif, single stranded interacting protein 2
P38159	RBMX	RNA binding motif protein, X-linked
Q93062	RBPMS	RNA binding protein with multiple splicing
P18754	RCC1	regulator of chromosome condensation 1
Q9P258	RCC2	regulator of chromosome condensation 2
Q15293	RCN1	reticulocalbin 1, EF-hand calcium binding domain
Q14257	RCN2	reticulocalbin 2, EF-hand calcium binding domain
P35241	RDX	radixin
P46063	RECQL	RecQ helicase-like
Q9BWE0	REPIN1	replication initiator 1
Q96D71	REPS1	RALBP1 associated Eps domain containing 1
P35251	RFC1	replication factor C (activator 1) 1, 145kDa
P35250	RFC2	replication factor C (activator 1) 2, 40kDa
P40938	RFC3	replication factor C (activator 1) 3, 38kDa
P35249	RFC4	replication factor C (activator 1) 4, 37kDa
P40937	RFC5	replication factor C (activator 1) 5, 36.5kDa
Q14699	RFTN1	raftlin, lipid raft linker 1
Q9NPQ8	RIC8A	RIC8 guanine nucleotide exchange factor A
Q06587	RING1	ring finger protein 1

Q9BRS2	RIOK1	RIO kinase 1
Q9BVS4	RIOK2	RIO kinase 2
O43353	RIPK2	receptor-interacting serine-threonine kinase 2
Q9H871	RMND5A	required for meiotic nuclear division 5 homolog A
O15541	RNF113A	ring finger protein 113A
Q5VTR2	RNF20	ring finger protein 20, E3 ubiquitin protein ligase
Q63HN8	RNF213	ring finger protein 213
O75150	RNF40	ring finger protein 40, E3 ubiquitin protein ligase
Q15287	RNPS1	RNA binding protein S1, serine-rich domain
Q13464	ROCK1	Rho-associated, coiled-coil containing protein kinase 1
O75116	ROCK2	Rho-associated, coiled-coil containing protein kinase 2
P27694	RPA1	replication protein A1, 70kDa
Q9H6T3	RPAP3	RNA polymerase II associated protein 3
P27635	RPL10	ribosomal protein L10
P62906	RPL10A	ribosomal protein L10a
P62913	RPL11	ribosomal protein L11
P30050	RPL12	ribosomal protein L12
P26373	RPL13	ribosomal protein L13
P40429	RPL13A	ribosomal protein L13a
P50914	RPL14	ribosomal protein L14
P61313	RPL15	ribosomal protein L15
P18621	RPL17	ribosomal protein L17
Q07020	RPL18	ribosomal protein L18
P84098	RPL19	ribosomal protein L19
P46778	RPL21	ribosomal protein L21
P35268	RPL22	ribosomal protein L22
Q6P5R6	RPL22L1	ribosomal protein L22-like 1
P62829	RPL23	ribosomal protein L23
P62750	RPL23A	ribosomal protein L23a
P83731	RPL24	ribosomal protein L24
P61254	RPL26	ribosomal protein L26
Q9UNX3	RPL26L1	ribosomal protein L26-like 1
P61353	RPL27	ribosomal protein L27
P46776	RPL27A	ribosomal protein L27a
P46779	RPL28	ribosomal protein L28
P47914	RPL29	ribosomal protein L29
P39023	RPL3	ribosomal protein L3
P62888	RPL30	ribosomal protein L30
P62899	RPL31	ribosomal protein L31
P62910	RPL32	ribosomal protein L32
P49207	RPL34	ribosomal protein L34
P42766	RPL35	ribosomal protein L35
P18077	RPL35A	ribosomal protein L35a
Q9Y3U8	RPL36	ribosomal protein L36
P83881	RPL36A	ribosomal protein L36a
Q969Q0	RPL36AL	ribosomal protein L36a-like
P61513	RPL37A	ribosomal protein L37a
P63173	RPL38	ribosomal protein L38
P36578	RPL4	ribosomal protein L4
P46777	RPL5	ribosomal protein L5
Q02878	RPL6	ribosomal protein L6
P18124	RPL7	ribosomal protein L7
P62424	RPL7A	ribosomal protein L7a
Q6DKI1	RPL7L1	ribosomal protein L7-like 1
P62917	RPL8	ribosomal protein L8
P32969	RPL9	ribosomal protein L9
P05388	RPLP0	ribosomal protein, large, P0
P05386	RPLP1	ribosomal protein, large, P1
P05387	RPLP2	ribosomal protein, large, P2
P04843	RPN1	ribophorin I
P04844	RPN2	ribophorin II
P46783	RPS10	ribosomal protein S10
P62280	RPS11	ribosomal protein S11
P62277	RPS13	ribosomal protein S13
P62263	RPS14	ribosomal protein S14
P62841	RPS15	ribosomal protein S15
P62244	RPS15A	ribosomal protein S15a
P62249	RPS16	ribosomal protein S16
P0CW22	RPS17	ribosomal protein S17
P62269	RPS18	ribosomal protein S18
P39019	RPS19	ribosomal protein S19

P15880	RPS2	ribosomal protein S2
P60866	RPS20	ribosomal protein S20
P63220	RPS21	ribosomal protein S21
P62266	RPS23	ribosomal protein S23
P62847	RPS24	ribosomal protein S24
P62851	RPS25	ribosomal protein S25
P62854	RPS26	ribosomal protein S26
P42677	RPS27	ribosomal protein S27
P62979	RPS27A	ribosomal protein S27a
P62857	RPS28	ribosomal protein S28
P62273	RPS29	ribosomal protein S29
P23396	RPS3	ribosomal protein S3
P61247	RPS3A	ribosomal protein S3A
P62701	RPS4X	ribosomal protein S4, X-linked
P46782	RPS5	ribosomal protein S5
P62753	RPS6	ribosomal protein S6
Q15418	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1
P51812	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3
Q9UBS0	RPS6KB2	ribosomal protein S6 kinase, 70kDa, polypeptide 2
P62081	RPS7	ribosomal protein S7
P62241	RPS8	ribosomal protein S8
P46781	RPS9	ribosomal protein S9
P08865	RPSA	ribosomal protein SA
Q92600	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)
P10301	RRAS	related RAS viral (r-ras) oncogene homolog
P62070	RRAS2	related RAS viral (r-ras) oncogene homolog 2
P56182	RRP1	ribosomal RNA processing 1
Q96EU6	RRP36	ribosomal RNA processing 36
O43818	RRP9	ribosomal RNA processing 9, small subunit (SSU) processome component, homolog (yeast)
Q15404	RSU1	Ras suppressor protein 1
Q9Y3I0	RTCB	RNA 2',3'-cyclic phosphate and 5'-OH ligase
Q9BST9	RTKN	rhotekin
Q9Y265	RUVBL1	RuvB-like AAA ATPase 1
Q9Y230	RUVBL2	RuvB-like AAA ATPase 2
P60903	S100A10	S100 calcium binding protein A10
Q9NTJ5	SACM1L	SAC1 suppressor of actin mutations 1-like (yeast)
Q9Y3Z3	SAMHD1	SAM domain and HD domain 1
Q9Y6U3	SCIN	scinderin
P34741	SDC2	syndecan 2
Q9HCN8	SDF2L1	stromal cell-derived factor 2-like 1
Q9BRK5	SDF4	stromal cell derived factor 4
O95810	SDPR	serum deprivation response
O15027	SEC16A	SEC16 homolog A, endoplasmic reticulum export factor
Q9P0V9	SEPT10	septin 10
Q9NVA2	SEPT11	septin 11
Q15019	SEPT2	septin 2
Q16181	SEPT7	septin 7
Q92599	SEPT8	septin 8
Q9UHD8	SEPT9	septin 9
Q8NC51	SERBP1	SERPINE1 mRNA binding protein 1
P50454	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)
O75533	SF3B1	splicing factor 3b, subunit 1, 155kDa
Q13435	SF3B2	splicing factor 3b, subunit 2, 145kDa
Q15427	SF3B4	splicing factor 3b, subunit 4, 49kDa
P23246	SFPQ	splicing factor proline/glutamine-rich
O95470	SGPL1	sphingosine-1-phosphate lyase 1
Q8TBC3	SHKBP1	SH3KBP1 binding protein 1
P34897	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)
Q8TF72	SHROOM3	shroom family member 3
Q96FS4	SIPA1	signal-induced proliferation-associated 1
P42285	SKIV2L2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)
Q00325	SLC25A3	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3
P05141	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
Q5K4L6	SLC27A3	solute carrier family 27 (fatty acid transporter), member 3
Q9ULF5	SLC39A10	solute carrier family 39 (zinc transporter), member 10
Q01650	SLC7A5	solute carrier family 7 (amino acid transporter light chain, L system), member 5
P84022	SMAD3	SMAD family member 3
O60264	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5

Q14683	SMC1A	structural maintenance of chromosomes 1A
O95347	SMC2	structural maintenance of chromosomes 2
Q9UQE7	SMC3	structural maintenance of chromosomes 3
Q9NTJ3	SMC4	structural maintenance of chromosomes 4
Q16637	SMN1	survival Of Motor Neuron 1
Q2TAY7	SMU1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)
O00161	SNAP23	synaptosomal-associated protein, 23kDa
Q7KZF4	SND1	staphylococcal nuclease and tudor domain containing 1
O75643	SNRNP200	small nuclear ribonucleoprotein 200kDa (U5)
P09661	SNRPA1	small nuclear ribonucleoprotein polypeptide A'
P62314	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa
P62306	SNRPF	small nuclear ribonucleoprotein polypeptide F
P55769	SNU13	SNU13 homolog, small nuclear ribonucleoprotein (U4/U6.U5)
Q9Y5X1	SNX9	sorting nexin 9
Q8NB90	SPATA5	spermatogenesis associated 5
Q9BVQ7	SPATA5L1	spermatogenesis associated 5-like 1
Q69YQ0	SPECC1L	sperm antigen with calponin homology and coiled-coil domains 1-like
Q08AE8	SPIRE1	spire-type actin nucleation factor 1
Q13813	SPTAN1	spectrin, alpha, non-erythrocytic 1
Q01082	SPTBN1	spectrin, beta, non-erythrocytic 1
O15020	SPTBN2	spectrin, beta, non-erythrocytic 2
Q13501	SQSTM1	sequestosome 1
P12931	SRC	SRC proto-oncogene, non-receptor tyrosine kinase
Q7Z6B7	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1
O75044	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2
P37108	SRP14	signal recognition particle 14kDa (homologous Alu RNA binding protein)
Q9UHB9	SRP68	signal recognition particle 68kDa
O76094	SRP72	signal recognition particle 72kDa
P49458	SRP9	signal recognition particle 9kDa
Q96SB4	SRPK1	SRSF protein kinase 1
P78362	SRPK2	SRSF protein kinase 2
Q9Y5M8	SRPRB	signal recognition particle receptor, B subunit
Q07955	SRSF1	serine/arginine-rich splicing factor 1
Q01130	SRSF2	serine/arginine-rich splicing factor 2
Q08170	SRSF4	serine/arginine-rich splicing factor 4
Q13243	SRSF5	serine/arginine-rich splicing factor 5
Q16629	SRSF7	serine/arginine-rich splicing factor 7
Q8WYL5	SSH1	slingshot protein phosphatase 1
Q76I76	SSH2	slingshot protein phosphatase 2
Q08945	SSRP1	structure specific recognition protein 1
P42224	STAT1	signal transducer and activator of transcription 1, 91kDa
O95793	STAU1	staufen double-stranded RNA binding protein 1
P31948	STIP1	stress-induced phosphoprotein 1
Q8WXE9	STON2	stonin 2
Q9Y3F4	STRAP	serine/threonine kinase receptor associated protein
O43815	STRN	striatin, calmodulin binding protein
Q13033	STRN3	striatin, calmodulin binding protein 3
Q9NRL3	STRN4	striatin, calmodulin binding protein 4
P53999	SUB1	SUB1 homolog, transcriptional regulator
Q9P2R7	SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit
P53597	SUCLG1	succinate-CoA ligase, alpha subunit
Q9Y5B9	SUPT16H	SPT16 homolog, facilitates chromatin remodeling subunit
Q15022	SUZ12	SUZ12 polycomb repressive complex 2 subunit
O60506	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein
Q96BW9	TAMM41	TAM41 mitochondrial translocator assembly and maintenance homolog
Q9UL54	TAOK2	TAO kinase 2
Q9BW92	TARS2	threonyl-tRNA synthetase 2, mitochondrial (putative)
O60343	TBC1D4	TBC1 domain family, member 4
Q9UHD2	TBK1	TANK-binding kinase 1
Q9Y4P3	TBL2	transducin (beta)-like 2
Q12788	TBL3	transducin (beta)-like 3
Q15369	TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)
Q14241	TCEB3	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)
Q9BQ70	TCF25	transcription factor 25 (basic helix-loop-helix)
Q13428	TCOF1	Treacher Collins-Franceschetti syndrome 1
P17987	TCP1	t-complex 1
Q9NZ01	TECR	trans-2,3-enoyl-CoA reductase
P54274	TERF1	telomeric repeat binding factor (NIMA-interacting) 1
Q9UGI8	TES	testin LIM domain protein
Q9H5Q4	TFB2M	transcription factor B2, mitochondrial
P49746	THBS3	thrombospondin 3

Q9Y2W1	THRAP3	thyroid hormone receptor associated protein 3
O43615	TIMM44	translocase of inner mitochondrial membrane 44 homolog (yeast)
Q07157	TJP1	tight junction protein 1
Q86UE8	TLK2	tousled-like kinase 2
Q9BVC6	TMEM109	transmembrane protein 109
Q9NYL9	TMOD3	tropomodulin 3 (ubiquitous)
P42166	TMPO	thymopoietin
P42167	TMPO	thymopoietin
O95407	TNFRSF6B	tumor necrosis factor receptor superfamily, member 6b, decoy
O95271	TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
Q9C0C2	TNKS1BP1	tankyrase 1 binding protein 1, 182kDa
Q96GM8	TOE1	target of EGR1, member 1 (nuclear)
P11387	TOP1	topoisomerase (DNA) I
P11388	TOP2A	topoisomerase (DNA) II alpha
Q02880	TOP2B	topoisomerase (DNA) II beta
Q5JTV8	TOR1AIP1	torsin A interacting protein 1
P04637	TP53	tumor protein p53
P09493	TPM1	tropomyosin 1 (alpha)
P06753	TPM3	tropomyosin 3
P67936	TPM4	tropomyosin 4
P29144	TPP2	tripeptidyl peptidase II
Q12931	TRAP1	TNF receptor-associated protein 1
Q96Q05	TRAPPC9	trafficking protein particle complex 9
P19474	TRIM21	tripartite motif containing 21
Q14258	TRIM25	tripartite motif containing 25
Q13263	TRIM28	tripartite motif containing 28
Q9BRZ2	TRIM56	tripartite motif containing 56
Q9C026	TRIM9	tripartite motif containing 9
Q9H2D6	TRIOBP	TRIO and F-actin binding protein
Q15650	TRIP4	thyroid hormone receptor interactor 4
Q9UI30	TRMT112	tRNA methyltransferase 11-2 homolog (S. cerevisiae)
Q7Z2T5	TRMT1L	tRNA methyltransferase 1-like
Q92574	TSC1	tuberous sclerosis 1
P49815	TSC2	tuberous sclerosis 2
Q2NL82	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)
Q96AY4	TTC28	tetratricopeptide repeat domain 28
Q71U36	TUBA1A	tubulin, alpha 1a
Q9BQE3	TUBA1C	tubulin, alpha 1c
P68366	TUBA4A	tubulin, alpha 4a
P07437	TUBB	tubulin, beta class I
Q13885	TUBB2A	tubulin, beta 2A class IIa
Q9BVA1	TUBB2B	tubulin, beta 2B class IIb
Q13509	TUBB3	tubulin, beta 3 class III
P04350	TUBB4A	tubulin, beta 4A class IVa
P68371	TUBB4B	tubulin, beta 4B class IVb
Q9BUF5	TUBB6	tubulin, beta 6 class V
P23258	TUBG1	tubulin, gamma 1
Q9BSJ2	TUBGCP2	tubulin, gamma complex associated protein 2
Q96CW5	TUBGCP3	tubulin, gamma complex associated protein 3
Q9UGJ1	TUBGCP4	tubulin, gamma complex associated protein 4
Q96RT8	TUBGCP5	tubulin, gamma complex associated protein 5
Q96RT7	TUBGCP6	tubulin, gamma complex associated protein 6
P49411	TUFM	Tu translation elongation factor, mitochondrial
P40222	TXLNA	taxilin alpha
Q9NUQ3	TXLNG	taxilin gamma
Q01081	U2AF1/U2AF1L5	U2 small nuclear RNA auxiliary factor 1
O15042	U2SURP	U2 snRNP-associated SURP domain containing
Q14157	UBAP2L	ubiquitin associated protein 2-like
P17480	UBTF	upstream binding transcription factor, RNA polymerase I
P22695	UQCRC2	ubiquinol-cytochrome c reductase core protein II
O94763	URI1	URI1, prefoldin-like chaperone
Q14694	USP10	ubiquitin specific peptidase 10
Q86UV5	USP48	ubiquitin specific peptidase 48
P46939	UTRN	utrophin
P50552	VASP	vasodilator-stimulated phosphoprotein
P08670	VIM	vimentin
Q9H269	VPS16	vacuolar protein sorting 16 homolog (S. cerevisiae)
Q9P253	VPS18	vacuolar protein sorting 18 homolog (S. cerevisiae)
Q96AX1	VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)
Q9H267	VPS33B	vacuolar protein sorting 33 homolog B (yeast)
Q9UN37	VPS4A	vacuolar protein sorting 4 homolog A (S. cerevisiae)

Q7Z5K2	WAPL	WAPL cohesin release factor
Q9Y6W5	WASF2	WAS protein family, member 2
C4AMC7	WASH3P	WAS protein family homolog 3 pseudogene
Q9Y2W2	WBP11	WW domain binding protein 11
O43709	WBSCR22	Williams Beuren syndrome chromosome region 22
O75717	WDHD1	WD repeat and HMG-box DNA binding protein 1
Q9BZH6	WDR11	WD repeat domain 11
Q6PJI9	WDR59	WD repeat domain 59
Q9GZS3	WDR61	WD repeat domain 61
O43379	WDR62	WD repeat domain 62
Q14191	WRN	Werner syndrome, RecQ helicase-like
Q8IX03	WWC1	WW and C2 domain containing 1
P13010	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)
P12956	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6
Q8IZH2	XRN1	5'-3' exoribonuclease 1
Q9Y2Z4	YARS2	tyrosyl-tRNA synthetase 2, mitochondrial
P67809	YBX1	Y box binding protein 1
P07947	YES1	YES proto-oncogene 1, Src family tyrosine kinase
P62699	YPEL5	yippee-like 5
Q9H6S0	YTHDC2	YTH domain containing 2
P31946	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta
P61981	YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma
Q04917	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta
P27348	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta
P63104	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta
Q96DT7	ZBTB10	zinc finger and BTB domain containing 10
Q9ULJ3	ZBTB21	zinc finger and BTB domain containing 21
Q96GY0	ZC2HC1A	zinc finger, C2HC-type containing 1A
Q8WU90	ZC3H15	zinc finger CCCH-type containing 15
Q9UPT8	ZC3H4	zinc finger CCCH-type containing 4
Q7Z2W4	ZC3HAV1	zinc finger CCCH-type, antiviral 1
Q9NUD5	ZCCHC3	zinc finger, CCHC domain containing 3
P17029	ZKSCAN1	zinc finger with KRAB and SCAN domains 1
Q9Y2X9	ZNF281	zinc finger protein 281
Q5BKZ1	ZNF326	zinc finger protein 326
Q9Y3S2	ZNF330	zinc finger protein 330
Q86UK7	ZNF598	zinc finger protein 598
Q9P2E3	ZNFX1	zinc finger, NFX1-type containing 1
Q9Y5A6	ZSCAN21	zinc finger and SCAN domain containing 21
O43264	ZW10	zw10 kinetochore protein
Q15942	ZYX	zyxin

Table S4:

A. SILAC on RPE-1 cells.

Full name	Light/Heavy Ratio 1	Light/Heavy Ratio 2	Light/Heavy Ratio 3	Average
1,4-alpha-glucan-branching enzyme OS=Homo sapiens GN=GBE1 PE=1 SV=3 - [GLGB_HUMAN]	0,83	0,67	0,81	0,77
116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1	1,06	0,87	1,25	1,06
14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1 -	1,70	-	-	1,70
14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 - [1433B_HUMAN]	0,93	2,46	1,19	1,53
14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 - [1433E_HUMAN]	1,02	1,04	0,93	1,00
14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 - [1433G_HUMAN]	1,00	1,34	1,30	1,21
14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 - [1433T_HUMAN]	1,09	1,05	0,94	1,03
14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 - [1433Z_HUMAN]	0,73	0,86	0,73	0,77
182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4 -	-	1,30	-	1,30
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3 OS=Homo sapiens GN=PLCB3	1,88	1,31	-	1,59
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase eta-1 OS=Homo sapiens GN=PLCH1	1,21	1,40	-	1,30
26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1 - [PRS4_HUMAN]	0,70	0,68	0,61	0,66
26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3 -	-	-	1,61	1,61
26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 - [PRS7_HUMAN]	1,35	1,94	-	1,65
26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2 -	0,91	1,35	0,91	1,06
26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3 -	-	0,97	-	0,97
26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2 -	4,56	-	-	4,56
26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 -	0,97	1,37	1,00	1,11
26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2 -	1,06	1,41	1,32	1,26
2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3 -	1,25	1,60	0,54	1,13
40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1 - [RS10_HUMAN]	0,70	0,63	0,70	0,67
40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 - [RS11_HUMAN]	0,66	-	0,95	0,80
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 - [RS12_HUMAN]	-	0,27	-	0,27
40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 - [RS14_HUMAN]	1,57	1,65	-	1,61
40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=1 SV=2 - [RS15_HUMAN]	-	1,53	-	1,53
40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2 - [RS15A_HUMAN]	0,84	0,93	1,05	0,94
40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 - [RS16_HUMAN]	0,96	0,91	0,74	0,87
40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=1 SV=1 - [RS17L_HUMAN]	-	-	0,98	0,98
40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]	1,51	0,87	1,33	1,24
40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19_HUMAN]	-	-	1,03	1,03
40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 - [RS2_HUMAN]	1,04	1,04	0,67	0,92
40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20_HUMAN]	1,99	-	-	1,99
40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 - [RS23_HUMAN]	0,75	0,75	0,76	0,76
40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1 - [RS24_HUMAN]	0,61	0,62	1,23	0,82
40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 - [RS25_HUMAN]	-	0,69	-	0,69
40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3 - [RS26_HUMAN]	-	-	1,00	1,00
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	0,72	0,70	0,94	0,79
40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A_HUMAN]	1,29	0,88	1,49	1,22
40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 - [RS4X_HUMAN]	2,11	1,14	0,85	1,37
40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 - [RS5_HUMAN]	0,72	0,69	0,78	0,73
40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	-	1,22	-	1,22
40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 - [RS7_HUMAN]	0,99	1,09	1,06	1,05
40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 - [RS8_HUMAN]	1,11	1,10	1,06	1,09
40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 - [RSSA_HUMAN]	0,87	1,34	1,12	1,11
4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=3 - [4F2_HUMAN]	0,81	0,69	0,90	0,80
4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 - [AL9A1_HUMAN]	1,14	0,99	-	1,07
5'-nucleotidase OS=Homo sapiens GN=NT5E PE=1 SV=1 - [5NTD_HUMAN]	1,02	0,93	0,92	0,96
60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]	0,88	1,01	0,90	0,93
60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 - [RLA0_HUMAN]	0,82	0,71	0,87	0,80
60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 - [RLA1_HUMAN]	2,12	1,27	1,95	1,78
60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1 - [RLA2_HUMAN]	0,64	0,77	0,90	0,77
60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 - [RL10A_HUMAN]	1,19	-	-	1,19
60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]	0,89	0,92	1,11	0,98
60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	0,56	0,57	0,70	0,61
60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2 - [RL13A_HUMAN]	1,16	1,38	1,31	1,28
60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 - [RL14_HUMAN]	1,09	0,81	0,95	0,95
60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2 - [RL15_HUMAN]	-	1,37	1,41	1,39
60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2 - [RL18_HUMAN]	1,14	1,03	0,93	1,04
60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 - [RL18A_HUMAN]	-	-	0,42	0,42
60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 - [RL19_HUMAN]	-	1,41	1,40	1,41
60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2 - [RL21_HUMAN]	-	0,71	-	0,71
60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 - [RL22_HUMAN]	1,41	0,93	0,65	1,00
60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 - [RL23_HUMAN]	1,16	1,44	1,47	1,36
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	0,86	1,02	1,45	1,11
60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 - [RL24_HUMAN]	0,74	0,66	0,59	0,66
60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1 - [RL26_HUMAN]	2,65	1,16	-	1,91
60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2 - [RL27_HUMAN]	0,91	0,89	0,92	0,91
60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 - [RL27A_HUMAN]	1,27	1,28	-	1,28
60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 - [RL28_HUMAN]	1,02	1,21	1,14	1,12
60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2 - [RL29_HUMAN]	1,75	1,84	-	1,80

60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 - [RL3_HUMAN]	0,88	0,90	1,12	0,97
60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	1,08	1,03	0,97	1,03
60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1 - [RL31_HUMAN]	-	1,25	1,69	1,47
60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 - [RL36A_HUMAN]	1,20	-	1,26	1,23
60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2 - [RL37A_HUMAN]	0,76	-	-	0,76
60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 - [RL4_HUMAN]	1,04	0,91	1,07	1,01
60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3 - [RL5_HUMAN]	1,09	1,01	1,04	1,05
60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3 - [RL6_HUMAN]	1,05	1,05	0,90	1,00
60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 - [RL7_HUMAN]	1,08	0,89	0,93	0,97
60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2 - [RL7A_HUMAN]	0,82	0,94	1,00	0,92
60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 - [RL8_HUMAN]	-	0,91	0,93	0,92
60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1 - [RL9_HUMAN]	1,50	1,89	1,42	1,61
6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2 - [K6PP_HUMAN]	0,83	0,88	0,82	0,84
6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 - [K6PL_HUMAN]	-	-	1,51	1,51
6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3 - [6PGD_HUMAN]	0,88	1,08	0,86	0,94
72 kDa type IV collagenase OS=Homo sapiens GN=MMP2 PE=1 SV=2 - [MMP2_HUMAN]	1,13	1,03	0,96	1,04
78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]	0,96	1,04	0,92	0,97
7-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR7 PE=1 SV=1 - [DHCR7_HUMAN]	0,74	0,75	0,89	0,80
Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 - [THIC_HUMAN]	1,34	1,62	1,14	1,37
Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	2,33	-	-	2,33
Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2 - [ACON_HUMAN]	1,63	1,71	2,15	1,83
Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]	1,06	1,11	1,06	1,08
Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	1,49	1,41	1,33	1,41
Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]	-	1,97	-	1,97
Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3 - [ARC1B_HUMAN]	-	0,81	0,82	0,82
Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 - [ARPC2_HUMAN]	-	-	0,91	0,91
Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3 - [ARPC3_HUMAN]	-	0,25	-	0,25
Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3 - [ARPC4_HUMAN]	1,48	1,70	0,98	1,39
Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 - [ARP3_HUMAN]	0,96	0,99	0,81	0,92
Activating signal cointegrator 1 complex subunit 2 OS=Homo sapiens GN=ASCC2 PE=1 SV=3 - [ASCC2_HUMAN]	20,23	-	-	20,23
Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4 - [ACPH_HUMAN]	1,27	1,64	1,00	1,30
Acyl-protein thioesterase 2 OS=Homo sapiens GN=LYPLA2 PE=1 SV=1 - [LYPA2_HUMAN]	0,96	-	-	0,96
Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2 - [APT_HUMAN]	2,36	2,18	-	2,27
Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 - [ADK_HUMAN]	0,69	1,56	1,28	1,18
Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4 - [SAHH_HUMAN]	0,89	0,80	2,54	1,41
Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5 - [CAP1_HUMAN]	0,88	0,91	0,79	0,86
ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	0,70	0,98	1,45	1,04
ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]	0,84	-	2,14	1,49
ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2 - [ARF3_HUMAN]	2,43	1,04	1,39	1,62
ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 - [ARF4_HUMAN]	0,97	0,88	0,71	0,85
A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=4 - [AKA12_HUMAN]	1,09	1,23	1,34	1,22
A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2 PE=1 SV=3 - [AKAP2_HUMAN]	2,68	2,31	1,81	2,27
Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2 - [SYAC_HUMAN]	0,84	0,80	0,84	0,83
Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3 - [ALDR_HUMAN]	0,76	1,46	0,77	1,00
Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1 - [ADAS_HUMAN]	-	1,51	-	1,51
All-trans-retinol 13,14-reductase OS=Homo sapiens GN=RETSAT PE=1 SV=2 - [RETST_HUMAN]	-	6,50	-	6,50
Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 - [ACTN1_HUMAN]	0,97	0,97	0,96	0,97
Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 - [ACTN4_HUMAN]	1,00	1,04	1,06	1,03
Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2 - [ADDA_HUMAN]	0,54	-	0,63	0,58
Alpha-aminoadipic semialdehyde synthase, mitochondrial OS=Homo sapiens GN=AASS PE=1 SV=1 - [AASS_HUMAN]	-	4,23	-	4,23
Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 - [ACTZ_HUMAN]	0,49	0,54	0,95	0,66
Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	0,92	0,96	0,91	0,93
Alpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2 - [MA2A1_HUMAN]	-	-	0,89	0,89
Alpha-parvin OS=Homo sapiens GN=PARVA PE=1 SV=1 - [PARVA_HUMAN]	0,71	-	-	0,71
Amphoterin-induced protein 2 OS=Homo sapiens GN=AMIGO2 PE=1 SV=1 - [AMGO2_HUMAN]	0,76	-	1,77	1,26
Amyloid beta A4 protein OS=Homo sapiens GN=APP PE=1 SV=3 - [A4_HUMAN]	0,98	0,97	0,94	0,96
Amyloid-like protein 2 OS=Homo sapiens GN=APLP2 PE=1 SV=2 - [APLP2_HUMAN]	0,72	0,71	0,78	0,74
Anion exchange protein 2 OS=Homo sapiens GN=SLC4A2 PE=1 SV=4 - [B3A2_HUMAN]	2,30	-	-	2,30
Ankycorbin OS=Homo sapiens GN=RAI14 PE=1 SV=2 - [RAI14_HUMAN]	0,77	1,05	0,79	0,87
Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 - [ANXA1_HUMAN]	0,94	1,00	1,08	1,01
Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1 - [ANX11_HUMAN]	1,83	0,90	1,06	1,26
Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 - [ANXA2_HUMAN]	0,92	0,96	0,95	0,94
Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4 - [ANXA4_HUMAN]	0,57	0,97	0,84	0,79

Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]	0,92	0,91	0,87	0,90
Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	0,95	0,94	0,88	0,92
Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 - [ANXA7_HUMAN]	0,94	2,05	1,05	1,35
AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2 - [AP1B1_HUMAN]	1,00	1,06	1,32	1,12
AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=1 SV=5 - [AP1G1_HUMAN]	0,90	1,54	1,18	1,21
AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3 - [AP2A1_HUMAN]	1,29	1,13	1,06	1,16
AP-2 complex subunit alpha-2 OS=Homo sapiens GN=AP2A2 PE=1 SV=2 - [AP2A2_HUMAN]	1,54	1,19	1,90	1,54
AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1 - [AP2B1_HUMAN]	1,23	1,13	1,06	1,14
AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=1 SV=2 - [AP2M1_HUMAN]	1,49	-	0,99	1,24
AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=1 SV=3 - [AP3B1_HUMAN]	0,98	0,56	0,80	0,78
AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 PE=1 SV=1 - [AP3D1_HUMAN]	1,46	1,35	1,99	1,60
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1 - [APOE_HUMAN]	-	-	3,50	3,50
Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	0,98	-	-	0,98
Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 - [SYRC_HUMAN]	0,64	1,06	0,97	0,89
Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1 - [SYNC_HUMAN]	0,92	1,82	1,28	1,34
Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3 - [AATM_HUMAN]	2,07	1,50	1,11	1,56
Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN]	-	1,22	-	1,22
Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3 - [ASPH_HUMAN]	0,84	1,00	0,91	0,92
Astrocytic phosphoprotein PEA-15 OS=Homo sapiens GN=PEA15 PE=1 SV=2 - [PEA15_HUMAN]	0,83	0,78	0,68	0,76
ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	1,15	1,04	1,18	1,12
ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 - [ATPB_HUMAN]	1,60	1,50	1,22	1,44
ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1 - [ATPG_HUMAN]	-	-	1,17	1,17
ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B PE=1 SV=1 - [ATD3B_HUMAN]	-	-	0,84	0,84
ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1 - [ABCE1_HUMAN]	0,72	-	-	0,72
ATP-binding cassette sub-family F member 1 OS=Homo sapiens GN=ABCF1 PE=1 SV=2 - [ABCF1_HUMAN]	0,78	1,09	1,03	0,97
ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]	1,02	1,04	0,98	1,01
ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	0,85	0,92	0,88	0,88
ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 - [DDX1_HUMAN]	0,85	0,88	0,76	0,83
ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X_HUMAN]	0,86	0,63	0,68	0,73
ATP-dependent RNA helicase DHX29 OS=Homo sapiens GN=DHX29 PE=1 SV=2 - [DHX29_HUMAN]	-	0,56	-	0,56
BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3 - [BAG3_HUMAN]	-	-	0,52	0,52
Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=1 SV=1 - [E41L2_HUMAN]	0,14	-	-	0,14
Basigin OS=Homo sapiens GN=BSG PE=1 SV=2 - [BASI_HUMAN]	0,91	0,83	2,40	1,38
Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2 - [BCLF1_HUMAN]	-	1,00	-	1,00
Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]	0,95	1,01	0,91	0,95
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 OS=Homo sapiens GN=PAPSS2 PE=1 SV=2 - [PAPS2_HUMAN]	1,64	0,42	1,76	1,27
Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 - [SYEP_HUMAN]	0,90	0,96	0,88	0,92
Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PUR9_HUMAN]	1,33	1,26	1,36	1,32
Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2 - [BASP1_HUMAN]	2,82	1,91	2,63	2,45
Brain protein I3 OS=Homo sapiens GN=BRI3 PE=2 SV=1 - [BRI3_HUMAN]	1,81	-	-	1,81
C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	1,22	1,10	1,15	1,15
CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 - [PYR1_HUMAN]	1,03	3,31	0,82	1,72
Calcium-activated potassium channel subunit alpha-1 OS=Homo sapiens GN=KCNMA1 PE=1 SV=2 - [KCMA1_HUMAN]	1,57	-	0,26	0,92
Calcium-binding and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=CALCOCO1 PE=1 SV=2 - [CACO1_HUMAN]	1,59	2,40	1,31	1,76
Calcium-transporting ATPase type 2C member 1 OS=Homo sapiens GN=ATP2C1 PE=1 SV=3 - [AT2C1_HUMAN]	0,60	-	0,48	0,54
Caldesmon OS=Homo sapiens GN=CALD1 PE=1 SV=3 - [CALD1_HUMAN]	1,55	1,22	1,60	1,45
Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2 - [CALM_HUMAN]	1,12	0,96	0,76	0,95
Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 - [CALX_HUMAN]	1,47	1,43	1,23	1,37
Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 - [CPNS1_HUMAN]	2,54	1,06	-	1,80
Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1 - [CAN1_HUMAN]	1,41	1,24	1,38	1,34
Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 - [CAN2_HUMAN]	1,24	1,11	1,20	1,18
Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4 - [ICAL_HUMAN]	1,51	1,77	2,07	1,78
Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 - [CNN2_HUMAN]	6,53	-	-	6,53
Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 - [CNN3_HUMAN]	0,97	0,95	0,83	0,92
Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1 - [CALR_HUMAN]	1,66	1,54	1,34	1,51
Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2 - [CALU_HUMAN]	1,15	1,03	0,90	1,02

cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens GN=PRKAR1A PE=1 SV=1 - [KAP0_HUMAN]	1,73	1,83	1,23	1,59
Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2 - [CAPR1_HUMAN]	0,56	0,84	0,59	0,66
Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3 - [CBR1_HUMAN]	-	-	1,25	1,25
Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2 - [CPT1A_HUMAN]	0,69	0,83	1,36	0,96
Catalase OS=Homo sapiens GN=CAT PE=1 SV=3 - [CATA_HUMAN]	0,45	-	-	0,45
Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1 - [CTNA1_HUMAN]	0,82	0,78	0,72	0,77
Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	1,75	2,19	1,82	1,92
Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1 - [CTND1_HUMAN]	0,89	1,96	1,41	1,42
Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	1,14	0,97	1,02	1,05
Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1 - [MPRD_HUMAN]	0,86	1,51	1,23	1,20
Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3 - [MPRI_HUMAN]	1,05	1,04	1,07	1,05
Caveolin-1 OS=Homo sapiens GN=CAV1 PE=1 SV=4 - [CAV1_HUMAN]	1,29	1,21	1,20	1,23
CD151 antigen OS=Homo sapiens GN=CD151 PE=1 SV=3 - [CD151_HUMAN]	0,71	0,71	0,67	0,70
CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=2 - [CD166_HUMAN]	1,23	1,07	1,00	1,10
CD276 antigen OS=Homo sapiens GN=CD276 PE=1 SV=1 - [CD276_HUMAN]	2,28	-	-	2,28
CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=3 - [CD44_HUMAN]	0,69	0,72	0,69	0,70
CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1 - [CD59_HUMAN]	0,94	0,97	0,97	0,96
CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2 - [CD63_HUMAN]	0,56	1,06	1,42	1,01
CD81 antigen OS=Homo sapiens GN=CD81 PE=1 SV=1 - [CD81_HUMAN]	1,11	1,42	-	1,26
Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2 - [CCAR2_HUMAN]	0,90	1,09	1,11	1,03
Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2 - [CDC42_HUMAN]	-	-	1,19	1,19
Centrosomal protein of 170 kDa OS=Homo sapiens GN=CEP170 PE=1 SV=1 - [CE170_HUMAN]	0,77	-	0,84	0,80
Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 - [CLIC1_HUMAN]	1,13	1,24	1,11	1,16
Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 - [CLIC4_HUMAN]	-	2,23	1,16	1,69
Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2 - [CISY_HUMAN]	-	1,67	0,91	1,29
Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 - [CLH1_HUMAN]	0,92	0,96	0,96	0,95
Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=1 SV=2 - [CPSF6_HUMAN]	0,55	0,74	1,95	1,08
Cleft lip and palate transmembrane protein 1 OS=Homo sapiens GN=CLPTM1 PE=1 SV=1 - [CLPT1_HUMAN]	1,67	1,40	1,51	1,53
Coactosin-like protein OS=Homo sapiens GN=COTL1 PE=1 SV=3 - [COTL1_HUMAN]	1,13	0,91	1,09	1,04
Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2 - [COPA_HUMAN]	0,87	0,97	0,88	0,91
Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3 - [COPB_HUMAN]	1,09	0,89	1,36	1,11
Coatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2 - [COPB2_HUMAN]	0,87	0,98	1,03	0,96
Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1 - [COPD_HUMAN]	-	-	1,13	1,13
Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 - [COPG1_HUMAN]	1,42	1,16	1,20	1,26
Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	0,98	1,37	1,15	1,17
Cold shock domain-containing protein E1 OS=Homo sapiens GN=CSDE1 PE=1 SV=2 - [CSDE1_HUMAN]	0,71	1,13	1,59	1,14
Complement decay-accelerating factor OS=Homo sapiens GN=CD55 PE=1 SV=4 - [DAF_HUMAN]	0,67	-	-	0,67
Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=1 SV=3 - [CND1_HUMAN]	1,14	-	-	1,14
Connective tissue growth factor OS=Homo sapiens GN=CTGF PE=1 SV=2 - [CTGF_HUMAN]	-	0,55	-	0,55
Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 - [F120A_HUMAN]	1,33	1,55	1,05	1,31
Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 - [CPNE1_HUMAN]	1,17	1,41	3,55	2,04
Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1 - [CPNE3_HUMAN]	0,64	1,00	0,96	0,87
Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1 - [COR1B_HUMAN]	1,04	1,43	1,13	1,20
Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 - [COR1C_HUMAN]	0,99	0,98	1,09	1,02
CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=1 SV=2 - [PYRG1_HUMAN]	-	-	2,57	2,57
Cullin-2 OS=Homo sapiens GN=CUL2 PE=1 SV=2 - [CUL2_HUMAN]	0,77	-	-	0,77
Cullin-4B OS=Homo sapiens GN=CUL4B PE=1 SV=4 - [CUL4B_HUMAN]	0,87	0,77	0,88	0,84
Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	0,92	0,87	0,94	0,91
Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2 - [CYTB_HUMAN]	0,85	-	1,05	0,95
Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3 - [CSRP1_HUMAN]	-	0,64	0,69	0,67
Cysteine-rich motor neuron 1 protein OS=Homo sapiens GN=CRIM1 PE=1 SV=1 - [CRIM1_HUMAN]	1,24	0,88	0,98	1,04
Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3 - [QCR2_HUMAN]	-	1,83	1,30	1,57
Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2 - [CYC_HUMAN]	0,91	0,83	0,89	0,88
Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3 - [ACOC_HUMAN]	1,26	1,61	1,50	1,46
Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	1,00	0,97	0,96	0,98
Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3 - [DC1I2_HUMAN]	0,77	0,98	0,91	0,88
Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1 - [CYFP1_HUMAN]	0,96	0,90	0,72	0,86
Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2 - [CKAP4_HUMAN]	0,91	0,91	0,81	0,87

Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3 - [CKAP5_HUMAN]	0,80	0,91	-	0,86
Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 PE=1 SV=3 - [BACH_HUMAN]	0,91	-	-	0,91
Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2 - [CNDP2_HUMAN]	-	-	6,53	6,53
D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 - [SERA_HUMAN]	0,72	0,51	0,43	0,55
Delta and Notch-like epidermal growth factor-related receptor OS=Homo sapiens GN=DNER PE=1 SV=1 - [DNER_HUMAN]	0,79	0,70	0,68	0,72
Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=1 SV=2 - [DHC24_HUMAN]	2,20	1,21	-	1,71
Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	1,29	1,69	1,86	1,61
Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2 - [DSG2_HUMAN]	1,60	0,56	0,49	0,89
Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 - [DEST_HUMAN]	0,73	0,81	0,65	0,73
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=1 SV=4 - [ODO2_HUMAN]	-	0,71	-	0,71
Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 - [DPYL2_HUMAN]	0,89	1,02	0,88	0,93
Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1 - [DPYL3_HUMAN]	0,74	-	-	0,74
Dipeptidyl peptidase 3 OS=Homo sapiens GN=DPP3 PE=1 SV=2 - [DPP3_HUMAN]	1,08	0,99	1,03	1,03
Dipeptidyl peptidase 9 OS=Homo sapiens GN=DPP9 PE=1 SV=3 - [DPP9_HUMAN]	-	0,99	-	0,99
Disabled homolog 2 OS=Homo sapiens GN=DAB2 PE=1 SV=3 - [DAB2_HUMAN]	-	-	0,82	0,82
Discoidin domain-containing receptor 2 OS=Homo sapiens GN=DDR2 PE=1 SV=2 - [DDR2_HUMAN]	0,76	0,61	-	0,68
Discoidin, CUB and LCCL domain-containing protein 2 OS=Homo sapiens GN=DCBLD2 PE=1 SV=1 - [DCBD2_HUMAN]	0,84	0,76	0,73	0,78
Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens GN=ADAM9 PE=1 SV=1 - [ADAM9_HUMAN]	0,95	1,33	1,03	1,10
Disks large homolog 1 OS=Homo sapiens GN=DLG1 PE=1 SV=2 - [DLG1_HUMAN]	1,29	0,81	0,79	0,96
DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 - [DDB1_HUMAN]	0,66	0,76	0,90	0,78
DNA replication licensing factor MCM2 OS=Homo sapiens GN=MCM2 PE=1 SV=4 - [MCM2_HUMAN]	-	-	0,22	0,22
DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 - [TOP1_HUMAN]	1,01	0,72	0,98	0,90
DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	0,88	0,88	0,81	0,86
DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2 - [DNJA1_HUMAN]	0,42	0,34	0,46	0,41
DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1 - [DNJA2_HUMAN]	0,60	0,64	0,57	0,60
DnaJ homolog subfamily C member 10 OS=Homo sapiens GN=DNAJC10 PE=1 SV=2 - [DJC10_HUMAN]	1,42	1,14	-	1,28
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4 - [OST48_HUMAN]	1,56	1,55	1,30	1,47
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 - [RPN1_HUMAN]	1,13	1,17	1,11	1,14
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3 - [RPN2_HUMAN]	1,08	1,24	1,21	1,18
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2 - [STT3A_HUMAN]	1,07	1,10	1,05	1,07
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1 - [STT3B_HUMAN]	-	-	1,77	1,77
Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN]	0,59	-	-	0,59
Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4 - [DREB_HUMAN]	1,17	1,10	1,18	1,15
Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 - [DBNL_HUMAN]	2,84	0,91	0,95	1,57
Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3 - [DCTN1_HUMAN]	0,94	1,16	0,81	0,97
Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4 - [DCTN2_HUMAN]	-	-	1,91	1,91
Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 - [DNM1L_HUMAN]	1,10	0,55	-	0,82
Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 - [DYN2_HUMAN]	2,53	-	0,63	1,58
Dynamin-binding protein OS=Homo sapiens GN=DNMBP PE=1 SV=1 - [DNMBP_HUMAN]	-	-	1,46	1,46
Dysferlin OS=Homo sapiens GN=DYSF PE=1 SV=1 - [DYSF_HUMAN]	1,14	1,19	1,63	1,32
Dystonin OS=Homo sapiens GN=DST PE=1 SV=4 - [DYST_HUMAN]	1,03	-	-	1,03
E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2 - [RBP2_HUMAN]	-	-	1,02	1,02
E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 - [TRI25_HUMAN]	-	1,00	1,29	1,14
E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 - [HUWE1_HUMAN]	2,16	0,61	2,14	1,64
E3 ubiquitin-protein ligase MYLIP OS=Homo sapiens GN=MYLIP PE=1 SV=2 - [MYLIP_HUMAN]	0,63	-	-	0,63
E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1 - [UBR4_HUMAN]	1,72	3,22	-	2,47
Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2 - [EEA1_HUMAN]	1,08	1,08	0,97	1,04
Ectopic P granules protein 5 homolog OS=Homo sapiens GN=EPG5 PE=2 SV=2 - [EPG5_HUMAN]	-	1,63	-	1,63
EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2 - [EHD1_HUMAN]	5,18	-	-	5,18
Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1 - [ETFA_HUMAN]	1,30	-	-	1,30
Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]	1,55	1,35	1,28	1,39
Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 - [EF1B_HUMAN]	2,27	1,44	1,76	1,82
Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5 - [EF1D_HUMAN]	0,69	1,11	0,89	0,90

Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN]	0,97	1,00	0,87	0,95
Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	0,92	1,03	0,97	0,97
Elongation factor Tu GTP-binding domain-containing protein 1 OS=Homo sapiens GN=EFTUD1 PE=1 SV=2 - [ETUD1_HUMAN]	0,23	-	-	0,23
Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2 - [EFTU_HUMAN]	0,83	0,80	-	0,82
Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=ERAP1 PE=1 SV=3 - [ERAP1_HUMAN]	2,48	1,65	1,93	2,02
Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase OS=Homo sapiens GN=MAN1B1 PE=1 SV=2 - [MA1B1_HUMAN]	0,53	1,80	-	1,17
Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [ENPL_HUMAN]	0,92	0,97	0,90	0,93
Endothelin-converting enzyme 1 OS=Homo sapiens GN=ECE1 PE=1 SV=2 - [ECE1_HUMAN]	1,55	0,95	1,03	1,18
Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1 - [EDC4_HUMAN]	1,36	0,30	0,78	0,81
Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 - [ECHM_HUMAN]	-	1,46	1,40	1,43
Ephrin type-A receptor 2 OS=Homo sapiens GN=EPHA2 PE=1 SV=2 - [EPHA2_HUMAN]	1,02	0,87	0,73	0,87
Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2 - [EGFR_HUMAN]	1,05	0,70	0,63	0,79
ER lumen protein retaining receptor 2 OS=Homo sapiens GN=KDELR2 PE=1 SV=1 - [ERD22_HUMAN]	-	0,67	-	0,67
Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1 - [ERLN2_HUMAN]	-	1,26	1,45	1,36
ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2 - [ERO1A_HUMAN]	1,84	1,20	0,96	1,34
Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 - [DHB12_HUMAN]	2,06	-	2,61	2,33
Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 - [IF4A1_HUMAN]	0,77	0,85	0,94	0,85
Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1 PE=1 SV=1 - [ERF3A_HUMAN]	0,56	0,58	0,53	0,56
Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3 - [IF2A_HUMAN]	-	2,27	2,07	2,17
Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3 - [IF2G_HUMAN]	3,20	3,00	1,14	2,45
Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1 - [EIF3A_HUMAN]	0,87	0,85	0,82	0,85
Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3 - [EIF3B_HUMAN]	0,85	0,86	0,50	0,74
Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=1 SV=1 - [EIF3C_HUMAN]	0,90	1,07	0,82	0,93
Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 - [EIF3D_HUMAN]	-	0,25	-	0,25
Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=1 SV=1 - [EIF3F_HUMAN]	-	0,81	1,03	0,92
Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1 - [EIF3L_HUMAN]	1,20	1,11	-	1,16
Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 - [IF4G1_HUMAN]	1,25	0,93	1,11	1,10
Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens GN=EIF4G2 PE=1 SV=1 - [IF4G2_HUMAN]	0,41	0,51	0,32	0,41
Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=1 SV=2 - [IF4B_HUMAN]	0,99	-	-	0,99
Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 - [IF5A1_HUMAN]	0,83	0,70	0,89	0,81
Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4 - [IF2P_HUMAN]	1,08	0,98	1,02	1,03
Exocyst complex component 1 OS=Homo sapiens GN=EXOC1 PE=1 SV=4 - [EXOC1_HUMAN]	1,26	-	-	1,26
Exocyst complex component 2 OS=Homo sapiens GN=EXOC2 PE=1 SV=1 - [EXOC2_HUMAN]	3,24	-	-	3,24
Exocyst complex component 4 OS=Homo sapiens GN=EXOC4 PE=1 SV=1 - [EXOC4_HUMAN]	1,12	-	-	1,12
Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 - [XPO1_HUMAN]	0,62	0,73	0,69	0,68
Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN]	0,82	0,73	0,74	0,76
Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 - [ESYT1_HUMAN]	1,69	1,44	1,75	1,63
Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=1 SV=1 - [ESYT2_HUMAN]	-	0,90	-	0,90
Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	0,86	0,81	0,81	0,83
FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1 - [SP16H_HUMAN]	0,46	0,93	-	0,70
F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3 - [CAZA1_HUMAN]	0,97	1,16	0,76	0,96
F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 - [CAPZB_HUMAN]	5,44	1,61	-	3,53
Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4 - [FUBP2_HUMAN]	1,14	1,08	1,03	1,08
Farnesyl pyrophosphate synthase OS=Homo sapiens GN=FDPS PE=1 SV=4 - [FPPS_HUMAN]	0,93	-	-	0,93
Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3 - [FSCN1_HUMAN]	0,77	0,81	0,77	0,78
Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FAS_HUMAN]	1,00	1,05	1,01	1,02
Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 PE=1 SV=1 - [FERM2_HUMAN]	0,90	0,81	0,95	0,89
Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2 - [FRIH_HUMAN]	1,15	1,26	1,19	1,20
Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]	1,53	0,88	1,68	1,36
Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4 - [FINC_HUMAN]	1,21	1,05	0,98	1,08
Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	1,21	1,22	1,21	1,21
Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2 - [FLNB_HUMAN]	1,04	1,18	1,03	1,08

Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3 - [FLNC_HUMAN]	1,22	1,25	1,22	1,23
Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3 - [FLOT1_HUMAN]	0,79	0,76	0,94	0,83
Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=3 - [FXR1_HUMAN]	-	-	0,63	0,63
Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]	0,96	0,80	0,80	0,85
Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2 - [ALDOC_HUMAN]	1,31	1,23	1,79	1,44
Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN]	0,85	0,88	1,18	0,97
Gamma-interferon-inducible protein 16 OS=Homo sapiens GN=IFI16 PE=1 SV=3 - [IF16_HUMAN]	1,24	-	-	1,24
Gap junction alpha-1 protein OS=Homo sapiens GN=GJA1 PE=1 SV=2 - [CXA1_HUMAN]	-	0,70	-	0,70
Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1 - [GELS_HUMAN]	1,27	1,65	1,03	1,31
General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2 - [USO1_HUMAN]	0,89	0,91	0,93	0,91
Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 - [G6PD_HUMAN]	1,11	1,41	0,96	1,16
Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4 - [G6PI_HUMAN]	0,89	1,02	0,91	0,94
Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2 - [GLU2B_HUMAN]	0,89	0,99	0,82	0,90
Glucosylceramidase OS=Homo sapiens GN=GBA PE=1 SV=3 - [GLCM_HUMAN]	1,38	0,92	-	1,15
Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2 - [DHE3_HUMAN]	0,93	1,55	1,47	1,32
Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS PE=1 SV=1 - [GLSK_HUMAN]	1,17	0,76	0,68	0,87
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	0,54	0,60	1,24	0,79
Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1 - [SYQ_HUMAN]	2,22	1,45	1,53	1,73
Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 - [GSTO1_HUMAN]	0,96	1,24	0,83	1,01
Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	1,14	1,40	1,25	1,26
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	0,92	1,08	0,93	0,98
Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 - [SYG_HUMAN]	0,77	0,76	0,94	0,82
Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	1,24	0,99	1,01	1,08
Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	1,60	1,28	2,60	1,83
Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2 - [GSLG1_HUMAN]	1,03	0,88	0,98	0,96
Golgi reassembly-stacking protein 2 OS=Homo sapiens GN=GORASP2 PE=1 SV=3 - [GORS2_HUMAN]	1,12	-	-	1,12
Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 - [GCP60_HUMAN]	2,00	1,12	0,84	1,32
Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 PE=1 SV=3 - [GOGA2_HUMAN]	0,50	0,45	-	0,47
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens GN=GBF1 PE=1 SV=2 - [GBF1_HUMAN]	1,06	0,96	0,94	0,99
Growth arrest-specific protein 6 OS=Homo sapiens GN=GAS6 PE=1 SV=2 - [GAS6_HUMAN]	1,09	0,89	-	0,99
GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 - [RAN_HUMAN]	1,12	0,78	1,07	0,99
GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 - [SAR1A_HUMAN]	-	-	0,64	0,64
Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 - [GNAI2_HUMAN]	-	1,08	0,57	0,82
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3 - [GBB1_HUMAN]	-	1,31	-	1,31
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 - [GBB2_HUMAN]	0,79	-	0,38	0,58
Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3 - [GBLP_HUMAN]	0,84	0,77	1,07	0,89
Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN]	1,92	0,93	1,61	1,49
Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 - [HSP74_HUMAN]	0,99	1,28	1,04	1,10
Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3 - [HS74L_HUMAN]	6,79	-	-	6,79
Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]	0,72	0,74	0,72	0,73
Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 - [HS105_HUMAN]	0,68	0,72	0,70	0,70
Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 - [HSPB1_HUMAN]	1,57	0,82	1,30	1,23
Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN]	0,91	0,83	0,93	0,89
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]	0,92	0,81	0,90	0,88
Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Homo sapiens GN=HGS PE=1 SV=1 - [HGS_HUMAN]	0,99	1,01	-	1,00
Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens GN=HDGFRP2 PE=1 SV=1 - [HDGR2_HUMAN]	-	-	1,21	1,21
Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1 - [HP1B3_HUMAN]	0,73	-	-	0,73
Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=1 SV=2 - [ROAA_HUMAN]	0,75	0,88	1,09	0,91
Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 - [ROA1_HUMAN]	0,64	0,67	0,80	0,71
Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 - [ROA3_HUMAN]	0,90	1,07	0,97	0,98

Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1 - [HNRPD_HUMAN]	0,57	0,76	0,72	0,68
Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 - [HNRH1_HUMAN]	0,97	1,56	1,52	1,35
Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 - [HNRPK_HUMAN]	0,83	0,88	0,83	0,85
Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 - [HNRPL_HUMAN]	0,72	0,64	0,60	0,65
Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 - [HNRPM_HUMAN]	1,10	1,14	0,86	1,03
Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [HNRPQ_HUMAN]	0,75	0,76	0,70	0,74
Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 - [HNRPU_HUMAN]	0,71	0,83	0,78	0,77
Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=2 - [HNRL1_HUMAN]	-	-	1,36	1,36
Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	0,52	-	0,68	0,60
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]	0,92	0,84	0,88	0,88
Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4 - [HNRPC_HUMAN]	0,70	0,71	0,75	0,72
Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 - [HXK1_HUMAN]	0,82	0,87	0,79	0,83
Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 - [HXK2_HUMAN]	0,52	0,57	1,28	0,79
Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2 - [H12_HUMAN]	0,27	0,88	0,84	0,66
Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3 - [H2A1H_HUMAN]	0,85	0,87	0,86	0,86
Histone H2B type 1-J OS=Homo sapiens GN=HIST1H2BJ PE=1 SV=3 - [H2B1J_HUMAN]	0,90	-	-	0,90
Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	0,65	0,64	0,59	0,63
Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	-	0,69	-	0,69
Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3 - [H32_HUMAN]	0,82	-	0,84	0,83
Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2 - [H33_HUMAN]	0,68	-	-	0,68
Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	0,73	0,79	0,62	0,71
HLA class I histocompatibility antigen, A-2 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 - [1A02_HUMAN]	1,20	1,10	0,98	1,09
Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Homo sapiens GN=HMGCS1 PE=1 SV=2 - [HMCS1_HUMAN]	1,11	-	0,82	0,97
Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 - [HYOU1_HUMAN]	1,07	1,12	1,25	1,15
Importin subunit alpha-3 OS=Homo sapiens GN=KPNA4 PE=1 SV=1 - [IMA3_HUMAN]	0,60	-	-	0,60
Importin subunit alpha-4 OS=Homo sapiens GN=KPNA3 PE=1 SV=2 - [IMA4_HUMAN]	1,58	-	-	1,58
Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]	0,93	0,99	0,87	0,93
Importin-11 OS=Homo sapiens GN=IPO11 PE=1 SV=1 - [IPO11_HUMAN]	0,89	-	-	0,89
Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=2 - [IPO4_HUMAN]	1,70	1,50	1,44	1,54
Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 - [IPO5_HUMAN]	0,91	0,91	0,83	0,88
Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 - [IPO7_HUMAN]	0,69	0,75	0,80	0,75
Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3 - [IPO9_HUMAN]	1,72	1,31	1,43	1,49
Inhibitor of nuclear factor kappa-B kinase subunit beta OS=Homo sapiens GN=IKBKB PE=1 SV=1 - [IKKB_HUMAN]	0,31	-	-	0,31
Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 - [IPYR_HUMAN]	1,01	2,06	1,73	1,60
Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 - [IMDH2_HUMAN]	0,40	-	-	0,40
Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 PE=1 SV=1 - [IBP7_HUMAN]	0,97	-	-	0,97
Integral membrane protein 2B OS=Homo sapiens GN=ITM2B PE=1 SV=1 - [ITM2B_HUMAN]	0,67	-	-	0,67
Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1 - [ITA2_HUMAN]	0,76	1,65	0,92	1,11
Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5 - [ITA3_HUMAN]	1,01	1,18	1,09	1,09
Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2 - [ITA5_HUMAN]	0,99	1,04	1,13	1,06
Integrin alpha-V OS=Homo sapiens GN=ITGAV PE=1 SV=2 - [ITAV_HUMAN]	1,08	0,76	1,05	0,96
Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2 - [ITB1_HUMAN]	0,88	0,88	0,89	0,89
Integrin beta-5 OS=Homo sapiens GN=ITGB5 PE=1 SV=1 - [ITB5_HUMAN]	0,98	1,16	1,01	1,05
Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2 - [ILF2_HUMAN]	-	2,40	-	2,40
Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3 - [ILF3_HUMAN]	0,92	0,97	0,93	0,94
Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 - [INF2_HUMAN]	1,29	1,26	1,77	1,44
Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 - [IDHC_HUMAN]	1,84	1,30	1,45	1,53
Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 - [SYIC_HUMAN]	1,12	1,15	1,05	1,11
Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=1 SV=2 - [SYIM_HUMAN]	2,04	1,32	1,88	1,75
Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN]	1,02	1,21	1,19	1,14
Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2 - [K1C18_HUMAN]	1,02	1,17	1,22	1,14
Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7 - [K2C8_HUMAN]	1,15	1,07	1,19	1,14
KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1 - [KHDR1_HUMAN]	-	-	0,78	0,78
Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1 - [KTN1_HUMAN]	0,77	0,91	0,71	0,80
Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1 - [KINH_HUMAN]	0,85	0,87	0,86	0,86
Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4 - [LGUL_HUMAN]	-	0,83	-	0,83
Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2 - [LMNB1_HUMAN]	0,66	0,64	0,86	0,72
Lamin-B2 OS=Homo sapiens GN=LMNB2 PE=1 SV=3 - [LMNB2_HUMAN]	1,09	-	-	1,09
Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=2 - [LAMB1_HUMAN]	0,96	0,89	1,53	1,13
Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3 - [LAMC1_HUMAN]	1,59	1,06	1,13	1,26
Lanosterol synthase OS=Homo sapiens GN=LSS PE=1 SV=1 - [ERG7_HUMAN]	1,76	1,29	1,14	1,40

La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2 - [LARP1_HUMAN]	0,70	0,60	-	0,65
Large neutral amino acids transporter small subunit 1 OS=Homo sapiens GN=SLC7A5 PE=1 SV=2 - [LAT1_HUMAN]	-	-	1,06	1,06
Large proline-rich protein BAG6 OS=Homo sapiens GN=BAG6 PE=1 SV=2 - [BAG6_HUMAN]	1,57	5,65	2,23	3,15
Leptin receptor gene-related protein OS=Homo sapiens GN=LEPROT PE=2 SV=1 - [OBRG_HUMAN]	0,96	1,05	0,94	0,99
Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3 - [LPPRC_HUMAN]	0,93	1,09	1,12	1,05
Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2 - [LRRF1_HUMAN]	1,20	0,83	0,90	0,98
Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1 - [LRC47_HUMAN]	2,43	-	-	2,43
Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1 - [LRC59_HUMAN]	0,97	-	-	0,97
Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2 - [SYLC_HUMAN]	0,67	0,99	1,01	0,89
Leucyl-cystinyl aminopeptidase OS=Homo sapiens GN=LNPEP PE=1 SV=3 - [LCAP_HUMAN]	0,98	-	-	0,98
Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2 - [LKHA4_HUMAN]	0,94	2,22	1,25	1,47
LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2 - [LASP1_HUMAN]	1,05	1,00	-	1,02
LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1 - [LIMA1_HUMAN]	1,29	1,17	1,33	1,26
LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3 - [LMO7_HUMAN]	0,89	0,88	0,94	0,90
Lipoma-preferred partner OS=Homo sapiens GN=LPP PE=1 SV=1 - [LPP_HUMAN]	2,31	-	1,82	2,06
LisH domain-containing protein ARMC9 OS=Homo sapiens GN=ARMC9 PE=1 SV=2 - [ARMC9_HUMAN]	1,30	1,71	-	1,50
L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 - [LDHA_HUMAN]	0,92	0,95	0,92	0,93
L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	0,93	0,93	0,92	0,93
Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2 - [LONM_HUMAN]	0,85	0,92	1,02	0,93
Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2 - [ACSL4_HUMAN]	0,43	1,36	-	0,89
Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR PE=1 SV=1 - [LDLR_HUMAN]	1,05	0,70	1,33	1,03
Low-density lipoprotein receptor-related protein 10 OS=Homo sapiens GN=LRP10 PE=1 SV=2 - [LRP10_HUMAN]	1,10	1,46	3,61	2,06
Low-density lipoprotein receptor-related protein 12 OS=Homo sapiens GN=LRP12 PE=1 SV=1 - [LRP12_HUMAN]	1,37	1,35	-	1,36
Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 - [LA_HUMAN]	-	1,36	-	1,36
Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]	1,30	1,17	1,18	1,22
Lysophospholipid acyltransferase 7 OS=Homo sapiens GN=MBOAT7 PE=1 SV=2 - [MBOA7_HUMAN]	-	21,98	-	21,98
Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]	2,32	-	-	2,32
Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2 - [SCRB2_HUMAN]	0,92	0,92	1,20	1,02
Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]	1,00	0,94	0,96	0,97
Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2 - [LAMP2_HUMAN]	0,83	0,90	0,86	0,86
Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1 - [LOXL2_HUMAN]	1,62	1,20	1,17	1,33
Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4 - [MIF_HUMAN]	1,02	1,16	1,00	1,06
Macrosialin OS=Homo sapiens GN=CD68 PE=1 SV=2 - [CD68_HUMAN]	-	-	0,73	0,73
Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	1,09	1,13	1,11	1,11
Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4 - [MDHC_HUMAN]	1,14	1,01	1,11	1,09
Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]	1,61	1,81	1,41	1,61
Mannosyl-oligosaccharide glucosidase OS=Homo sapiens GN=MOGS PE=1 SV=5 - [MOGS_HUMAN]	1,34	1,25	1,10	1,23
Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2 - [MATR3_HUMAN]	0,69	0,78	0,82	0,77
Matrix metalloproteinase-14 OS=Homo sapiens GN=MMP14 PE=1 SV=3 - [MMP14_HUMAN]	1,04	2,65	0,69	1,46
Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=1 SV=2 - [MAGD2_HUMAN]	-	3,28	-	3,28
Membrane cofactor protein OS=Homo sapiens GN=CD46 PE=1 SV=3 - [MCP_HUMAN]	4,45	-	-	4,45
Metalloproteinase inhibitor 2 OS=Homo sapiens GN=TIMP2 PE=1 SV=2 - [TIMP2_HUMAN]	-	1,18	-	1,18
Metalloreductase STEAP3 OS=Homo sapiens GN=STEAP3 PE=1 SV=2 - [STEA3_HUMAN]	0,78	-	1,23	1,00
Metallothionein-2 OS=Homo sapiens GN=MT2A PE=1 SV=1 - [MT2_HUMAN]	0,90	1,09	0,84	0,94
Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2 - [SYMC_HUMAN]	0,99	1,48	1,23	1,23
Methylsterol monooxygenase 1 OS=Homo sapiens GN=MSMO1 PE=1 SV=1 - [MSMO1_HUMAN]	1,39	2,67	0,91	1,66
Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1 - [MGST3_HUMAN]	0,81	0,91	-	0,86
Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4 - [MACF1_HUMAN]	1,17	0,84	0,97	0,99
Microtubule-associated protein 1A OS=Homo sapiens GN=MAP1A PE=1 SV=6 - [MAP1A_HUMAN]	1,61	-	1,40	1,51
Microtubule-associated protein 1B OS=Homo sapiens GN=MAP1B PE=1 SV=2 - [MAP1B_HUMAN]	0,68	0,68	0,70	0,69
Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2 - [MAP1S_HUMAN]	-	0,56	-	0,56

Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 - [MAP4_HUMAN]	1,22	1,41	1,10	1,24
Microtubule-associated proteins 1A/1B light chain 3 beta 2 OS=Homo sapiens GN=MAP1LC3B2 PE=2 SV=1 - [MP3B2_HUMAN]	-	-	1,18	1,18
Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1 - [HM13_HUMAN]	-	-	2,33	2,33
Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS PE=1 SV=2 - [MAVS_HUMAN]	2,68	1,59	-	2,13
Mitochondrial import receptor subunit TOM70 OS=Homo sapiens GN=TOMM70A PE=1 SV=1 - [TOM70_HUMAN]	-	0,99	1,39	1,19
Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=1 SV=1 - [IMMT_HUMAN]	0,60	1,04	1,29	0,98
MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2 - [MMS19_HUMAN]	1,08	1,05	0,99	1,04
Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN]	0,82	0,83	0,81	0,82
Monocarboxylate transporter 4 OS=Homo sapiens GN=SLC16A3 PE=1 SV=1 - [MOT4_HUMAN]	0,83	1,00	0,97	0,93
Mucolipin-1 OS=Homo sapiens GN=MCOLN1 PE=1 SV=1 - [MCLN1_HUMAN]	-	-	3,12	3,12
Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 - [PUR6_HUMAN]	0,70	-	1,50	1,10
Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2 - [MBB1A_HUMAN]	1,64	1,28	2,12	1,68
Myeloid-associated differentiation marker OS=Homo sapiens GN=MYADM PE=1 SV=2 - [MYADM_HUMAN]	1,61	1,33	-	1,47
Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1 - [MYOF_HUMAN]	1,12	1,13	1,08	1,11
Myosin light chain kinase, smooth muscle OS=Homo sapiens GN=MYLK PE=1 SV=4 - [MYLK_HUMAN]	-	0,61	1,21	0,91
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 - [MYL6_HUMAN]	0,94	1,11	0,88	0,98
Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 - [ML12A_HUMAN]	1,03	0,96	-	1,00
Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 - [MYH10_HUMAN]	1,19	1,21	0,95	1,12
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	1,03	1,01	1,00	1,01
Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4 - [MARCS_HUMAN]	1,58	2,01	2,08	1,89
Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens GN=SLC9A3R1 PE=1 SV=4 - [NHRF1_HUMAN]	2,30	-	-	2,30
N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3 - [GNS_HUMAN]	1,86	0,82	2,99	1,89
N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=1 SV=2 - [NAT10_HUMAN]	1,25	-	2,12	1,69
NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3 - [NNTM_HUMAN]	1,64	1,17	1,23	1,35
NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1 - [NQO1_HUMAN]	1,70	2,22	1,26	1,73
NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3 - [NB5R3_HUMAN]	1,22	1,02	1,16	1,13
NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	-	0,55	0,60	0,58
N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 - [NAA15_HUMAN]	0,36	0,97	0,97	0,76
Nardilysin OS=Homo sapiens GN=NRD1 PE=1 SV=2 - [NRDC_HUMAN]	-	1,53	0,17	0,85
Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Homo sapiens GN=NACA PE=1 SV=1 - [NACAM_HUMAN]	0,73	0,93	0,87	0,84
Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1 - [NCKP1_HUMAN]	1,05	1,48	0,61	1,05
NEDD4 family-interacting protein 2 OS=Homo sapiens GN=NDFIP2 PE=1 SV=2 - [NFIP2_HUMAN]	-	-	1,41	1,41
Neprilysin OS=Homo sapiens GN=MME PE=1 SV=2 - [NEP_HUMAN]	0,85	0,69	0,88	0,81
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 - [AHNK_HUMAN]	1,08	1,06	1,05	1,06
Neurogenic locus notch homolog protein 2 OS=Homo sapiens GN=NOTCH2 PE=1 SV=3 - [NOTC2_HUMAN]	1,59	1,45	1,57	1,53
Neuropathy target esterase OS=Homo sapiens GN=PNPLA6 PE=1 SV=2 - [PLPL6_HUMAN]	1,41	-	-	1,41
Neuropilin-1 OS=Homo sapiens GN=NRP1 PE=1 SV=3 - [NRP1_HUMAN]	0,58	0,73	0,67	0,66
Neuroplastin OS=Homo sapiens GN=NPTN PE=1 SV=2 - [NPTN_HUMAN]	0,91	1,03	0,96	0,97
Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 - [GANAB_HUMAN]	1,04	1,25	1,14	1,14
Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2 - [AAAT_HUMAN]	1,14	0,72	0,81	0,89
Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1 PE=1 SV=3 - [NCEH1_HUMAN]	-	0,87	0,77	0,82
Nexilin OS=Homo sapiens GN=NEXN PE=1 SV=1 - [NEXN_HUMAN]	0,24	-	-	0,24
Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 - [NIBL1_HUMAN]	0,93	0,99	0,90	0,94
Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2 - [NICA_HUMAN]	0,99	1,11	0,78	0,96
Niemann-Pick C1 protein OS=Homo sapiens GN=NPC1 PE=1 SV=2 - [NPC1_HUMAN]	1,06	2,42	0,92	1,46
Nodal modulator 3 OS=Homo sapiens GN=NOMO3 PE=2 SV=2 - [NOMO3_HUMAN]	0,75	0,64	1,04	0,81
Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 - [NONO_HUMAN]	0,90	0,86	1,36	1,04
Nuclear factor of activated T-cells, cytoplasmic 1 OS=Homo sapiens GN=NFATC1 PE=1 SV=3 - [NFAC1_HUMAN]	-	-	2,43	2,43
Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 - [NUDC_HUMAN]	1,03	0,79	0,37	0,73
Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	3,34	-	-	3,34
Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1 - [NU155_HUMAN]	-	1,59	-	1,59
Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=3 - [NU205_HUMAN]	1,32	-	-	1,32

Nuclear pore complex protein Nup88 OS=Homo sapiens GN=NUP88 PE=1 SV=2 - [NUP88_HUMAN]	1,39	-	-	1,39
Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 - [NUP93_HUMAN]	-	0,83	-	0,83
Nuclear protein localization protein 4 homolog OS=Homo sapiens GN=NPLOC4 PE=1 SV=3 - [NPL4_HUMAN]	1,33	-	-	1,33
Nuclear receptor coactivator 4 OS=Homo sapiens GN=NCOA4 PE=1 SV=1 - [NCOA4_HUMAN]	1,38	-	0,69	1,04
Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3 - [YBOX1_HUMAN]	2,21	1,25	1,85	1,77
Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 - [NOC2L_HUMAN]	1,11	-	-	1,11
Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 - [NOP56_HUMAN]	-	-	0,32	0,32
Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5 - [DDX21_HUMAN]	0,53	0,73	0,36	0,54
Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 - [NUCL_HUMAN]	0,68	0,61	0,67	0,66
Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 - [NPM_HUMAN]	0,92	1,14	1,08	1,04
Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3 - [TPR_HUMAN]	0,71	1,16	0,82	0,90
Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]	-	-	2,32	2,32
Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]	1,51	1,91	-	1,71
Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 - [NP1L1_HUMAN]	1,05	0,95	1,01	1,00
Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1 - [NP1L4_HUMAN]	-	2,64	2,48	2,56
Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 - [OLA1_HUMAN]	0,93	0,96	1,03	0,97
Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1 - [OAT_HUMAN]	1,28	0,60	0,57	0,82
Oxysterol-binding protein 1 OS=Homo sapiens GN=OSBP PE=1 SV=1 - [OSBP1_HUMAN]	2,23	1,98	-	2,10
Palladin OS=Homo sapiens GN=PALLD PE=1 SV=3 - [PALLD_HUMAN]	1,48	2,55	2,11	2,05
Paraspeckle component 1 OS=Homo sapiens GN=PSPC1 PE=1 SV=1 - [PSPC1_HUMAN]	2,82	-	-	2,82
PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5 PE=1 SV=5 - [PDLI5_HUMAN]	1,22	1,18	0,85	1,08
PDZ and LIM domain protein 7 OS=Homo sapiens GN=PDLIM7 PE=1 SV=1 - [PDLI7_HUMAN]	-	0,54	-	0,54
Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]	0,92	0,90	0,83	0,88
Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2 - [PPIB_HUMAN]	1,21	1,07	0,91	1,07
Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Homo sapiens GN=FKBP10 PE=1 SV=1 - [FKB10_HUMAN]	1,79	1,52	1,79	1,70
Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2 - [FKB1A_HUMAN]	0,69	0,53	0,63	0,61
Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	1,34	6,18	-	3,76
Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2 - [PXDN_HUMAN]	0,73	-	-	0,73
Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	0,92	0,87	0,75	0,84
Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]	0,75	0,83	0,96	0,85
Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 - [PRDX6_HUMAN]	1,28	2,70	1,71	1,90
Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3 - [DHB4_HUMAN]	0,75	0,84	0,94	0,84
PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 PE=1 SV=1 - [PERQ2_HUMAN]	1,32	-	0,57	0,94
Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMAN]	1,07	1,12	0,92	1,04
Phosphatidate phosphatase LPIN1 OS=Homo sapiens GN=LPIN1 PE=1 SV=2 - [LPIN1_HUMAN]	1,14	-	-	1,14
Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 - [PEBP1_HUMAN]	-	1,00	-	1,00
Phosphatidylinositol 4-kinase type 2-alpha OS=Homo sapiens GN=PI4K2A PE=1 SV=1 - [P4K2A_HUMAN]	1,49	-	-	1,49
Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens GN=PICALM PE=1 SV=2 - [PICAL_HUMAN]	1,40	1,24	0,92	1,19
Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3 - [PGM1_HUMAN]	-	3,83	-	3,83
Phosphoglucomutase-2 OS=Homo sapiens GN=PGM2 PE=1 SV=4 - [PGM2_HUMAN]	2,60	-	-	2,60
Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]	1,17	1,13	1,22	1,18
Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 - [PGAM1_HUMAN]	1,03	1,15	1,24	1,14
Phospholipase A-2-activating protein OS=Homo sapiens GN=PLAA PE=1 SV=2 - [PLAP_HUMAN]	-	0,47	-	0,47
Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1 - [PLD3_HUMAN]	2,04	2,23	4,97	3,08
Phostensin OS=Homo sapiens GN=PPP1R18 PE=1 SV=1 - [PPR18_HUMAN]	1,32	1,88	-	1,60
Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens GN=ATP2B1 PE=1 SV=3 - [AT2B1_HUMAN]	0,73	-	0,78	0,75
Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4 PE=1 SV=2 - [AT2B4_HUMAN]	0,92	1,28	1,70	1,30
Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]	0,80	0,77	0,85	0,81
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 - [PAIRB_HUMAN]	-	1,05	-	1,05
Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 - [PLST_HUMAN]	1,22	1,62	1,39	1,41
Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - [PLEC_HUMAN]	1,08	1,14	1,03	1,08
Plexin-B2 OS=Homo sapiens GN=PLXNB2 PE=1 SV=3 - [PLXB2_HUMAN]	-	1,07	0,88	0,97
Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN]	0,23	1,03	-	0,63

Poly [ADP-ribose] polymerase 4 OS=Homo sapiens GN=PARP4 PE=1 SV=3 - [PARP4_HUMAN]	0,97	1,30	1,25	1,17
Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	0,77	0,86	0,81	0,81
Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 - [PCBP2_HUMAN]	-	-	1,56	1,56
Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2 - [PABP1_HUMAN]	0,69	0,62	0,73	0,68
Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1 - [PTRF_HUMAN]	-	-	1,20	1,20
Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1 - [GALT2_HUMAN]	0,93	1,14	1,34	1,14
Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 - [PTBP1_HUMAN]	1,09	0,95	1,21	1,08
Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3 - [UBC_HUMAN]	0,93	0,91	1,10	0,98
POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]	1,17	-	1,45	1,31
PRA1 family protein 3 OS=Homo sapiens GN=ARL6IP5 PE=1 SV=1 - [PRAF3_HUMAN]	1,56	1,28	-	1,42
Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Homo sapiens GN=PBXIP1 PE=1 SV=1 - [PBIP1_HUMAN]	-	-	1,43	1,43
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 - [LMNA_HUMAN]	0,86	0,90	0,87	0,88
Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN]	0,80	0,62	-	0,71
Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1 PE=1 SV=3 - [PREP_HUMAN]	1,36	2,18	2,57	2,04
PRKC apoptosis WT1 regulator protein OS=Homo sapiens GN=PAWR PE=1 SV=1 - [PAWR_HUMAN]	0,90	1,41	-	1,15
Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 - [DDX17_HUMAN]	1,91	1,13	1,01	1,35
Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=2 - [DDX46_HUMAN]	2,93	0,67	-	1,80
Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	0,13	0,74	0,49	0,45
Probable ATP-dependent RNA helicase DDX58 OS=Homo sapiens GN=DDX58 PE=1 SV=2 - [DDX58_HUMAN]	-	1,13	-	1,13
Probable ATP-dependent RNA helicase DHX36 OS=Homo sapiens GN=DHX36 PE=1 SV=2 - [DHX36_HUMAN]	1,08	-	-	1,08
Probable cation-transporting ATPase 13A1 OS=Homo sapiens GN=ATP13A1 PE=1 SV=2 - [AT131_HUMAN]	-	0,74	-	0,74
Probable E3 ubiquitin-protein ligase HERC4 OS=Homo sapiens GN=HERC4 PE=1 SV=1 - [HERC4_HUMAN]	0,89	1,94	1,34	1,39
Probable fructose-2,6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 - [TIGAR_HUMAN]	1,49	-	-	1,49
Probable phospholipid-transporting ATPase IC OS=Homo sapiens GN=ATP8B1 PE=1 SV=3 - [AT8B1_HUMAN]	-	1,23	1,45	1,34
Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3 - [USP9X_HUMAN]	0,84	0,89	0,92	0,88
Procollagen galactosyltransferase 1 OS=Homo sapiens GN=COLGALT1 PE=1 SV=1 - [GT251_HUMAN]	-	-	1,15	1,15
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2 - [PLOD1_HUMAN]	1,09	0,93	1,54	1,19
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens GN=PLOD2 PE=1 SV=2 - [PLOD2_HUMAN]	0,68	0,65	0,84	0,72
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1 - [PLOD3_HUMAN]	-	0,54	0,84	0,69
Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2 - [PROF1_HUMAN]	0,83	0,88	0,87	0,86
Profilin-2 OS=Homo sapiens GN=PFN2 PE=1 SV=3 - [PROF2_HUMAN]	1,70	-	-	1,70
Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1 - [PDC6I_HUMAN]	0,67	0,71	0,64	0,67
Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2 - [PHB2_HUMAN]	-	0,42	-	0,42
Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 - [PCNA_HUMAN]	0,52	0,66	0,60	0,59
Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3 - [PA2G4_HUMAN]	0,97	0,89	1,03	0,96
Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2 - [LRP1_HUMAN]	1,07	0,88	0,94	0,96
Prolyl 3-hydroxylase 1 OS=Homo sapiens GN=LEPRE1 PE=1 SV=2 - [P3H1_HUMAN]	0,87	0,81	1,68	1,12
Prolyl 3-hydroxylase 3 OS=Homo sapiens GN=LEPREL2 PE=1 SV=1 - [P3H3_HUMAN]	0,79	1,81	-	1,30
Prosaposin OS=Homo sapiens GN=PSAP PE=1 SV=2 - [SAP_HUMAN]	0,99	1,11	1,10	1,07
Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 - [PSME2_HUMAN]	0,97	1,89	-	1,43
Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2 - [PSA2_HUMAN]	0,68	-	1,21	0,95
Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2 - [PSA3_HUMAN]	-	-	1,69	1,69
Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 - [PSA4_HUMAN]	-	1,72	-	1,72
Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3 - [PSA5_HUMAN]	-	-	1,78	1,78
Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1 - [PSA6_HUMAN]	1,28	-	1,35	1,31
Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1 - [PSB2_HUMAN]	1,69	2,26	1,69	1,88
Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4 - [PSB4_HUMAN]	-	1,47	-	1,47

Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN]	1,59	1,17	0,69	1,15
Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 - [AHNK2_HUMAN]	1,28	1,20	1,26	1,25
Protein CutA OS=Homo sapiens GN=CUTA PE=1 SV=2 - [CUTA_HUMAN]	-	1,88	1,63	1,76
Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1 - [CYR61_HUMAN]	0,80	0,92	0,71	0,81
Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1 - [DEK_HUMAN]	-	0,75	-	0,75
Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 - [DIAP1_HUMAN]	-	1,13	-	1,13
Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 - [PDIA3_HUMAN]	1,00	1,04	0,92	0,99
Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 - [PDIA4_HUMAN]	0,87	1,00	0,87	0,91
Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 - [PDIA6_HUMAN]	1,53	1,42	1,07	1,34
Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3 - [PDIA1_HUMAN]	0,92	0,97	1,04	0,98
Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 - [PARK7_HUMAN]	1,73	-	-	1,73
Protein enabled homolog OS=Homo sapiens GN=ENAH PE=1 SV=2 - [ENAH_HUMAN]	-	-	4,67	4,67
Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2 - [FLII_HUMAN]	1,14	1,24	0,87	1,09
Protein NOXP20 OS=Homo sapiens GN=FAM114A1 PE=1 SV=2 - [NXP20_HUMAN]	0,67	0,69	0,68	0,68
Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens GN=PPP1R12A PE=1 SV=1 - [MYPT1_HUMAN]	0,70	0,62	0,75	0,69
Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 - [S10AB_HUMAN]	1,87	0,58	3,43	1,96
Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]	0,72	0,82	0,84	0,79
Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 - [SET_HUMAN]	-	1,76	0,77	1,27
Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=3 - [SC16A_HUMAN]	-	-	5,35	5,35
Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2 - [SC23A_HUMAN]	0,70	0,96	0,19	0,62
Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2 - [SC23B_HUMAN]	3,09	-	2,59	2,84
Protein transport protein Sec24B OS=Homo sapiens GN=SEC24B PE=1 SV=2 - [SC24B_HUMAN]	0,86	-	-	0,86
Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=3 - [SC24C_HUMAN]	1,62	2,39	1,38	1,79
Protein transport protein Sec31A OS=Homo sapiens GN=SEC31A PE=1 SV=3 - [SC31A_HUMAN]	0,94	0,90	0,84	0,89
Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=1 SV=2 - [S61A1_HUMAN]	2,22	1,51	2,07	1,93
Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1 - [UN45A_HUMAN]	2,05	0,80	-	1,43
Protein VAC14 homolog OS=Homo sapiens GN=VAC14 PE=1 SV=1 - [VAC14_HUMAN]	0,75	1,37	1,38	1,17
Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2 - [TGM2_HUMAN]	1,25	1,20	1,25	1,23
Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2 - [THRB_HUMAN]	3,36	-	-	3,36
Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2 - [PNPH_HUMAN]	0,90	-	-	0,90
Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	0,91	0,97	0,98	0,96
Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=1 SV=1 - [DHX30_HUMAN]	-	1,37	-	1,37
Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens GN=HSP90AB4P PE=5 SV=1 - [H90B4_HUMAN]	0,73	-	0,54	0,63
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2 - [DHX15_HUMAN]	0,52	0,35	0,53	0,47
Putative protein FAM10A4 OS=Homo sapiens GN=ST13P4 PE=5 SV=1 - [ST134_HUMAN]	-	2,16	1,63	1,89
Putative ribosomal RNA methyltransferase NOP2 OS=Homo sapiens GN=NOP2 PE=1 SV=2 - [NOP2_HUMAN]	1,16	-	-	1,16
Pyridoxal kinase OS=Homo sapiens GN=PDXK PE=1 SV=1 - [PDXK_HUMAN]	-	-	5,80	5,80
Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	0,88	0,99	1,02	0,97
Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 - [GDIA_HUMAN]	-	-	1,64	1,64
Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 - [GDIB_HUMAN]	0,84	1,32	1,13	1,10
Rab3 GTPase-activating protein catalytic subunit OS=Homo sapiens GN=RAB3GAP1 PE=1 SV=3 - [RB3GP_HUMAN]	-	1,35	-	1,35
Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1 - [RBGPR_HUMAN]	-	-	1,23	1,23
Radixin OS=Homo sapiens GN=RDX PE=1 SV=1 - [RADI_HUMAN]	-	1,45	2,10	1,77
Raftlin OS=Homo sapiens GN=RFTN1 PE=1 SV=4 - [RFTN1_HUMAN]	-	4,50	-	4,50
Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1 - [RAGP1_HUMAN]	1,82	0,88	0,56	1,09
Rap1 GTPase-GDP dissociation stimulator 1 OS=Homo sapiens GN=RAP1GDS1 PE=1 SV=3 - [GDS1_HUMAN]	-	0,84	0,73	0,78
Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1 - [G3BP1_HUMAN]	1,56	0,94	1,16	1,22
Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	0,91	0,94	0,93	0,92
Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1 - [RAB10_HUMAN]	0,43	0,71	-	0,57
Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A PE=1 SV=3 - [RB11A_HUMAN]	1,15	1,19	0,96	1,10
Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 - [RAB14_HUMAN]	0,53	-	-	0,53
Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	2,23	-	-	2,23
Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2 - [RAB5C_HUMAN]	1,48	0,94	1,15	1,19
Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1 - [RAB7A_HUMAN]	1,10	1,33	0,82	1,09
Ras-related protein Rap-1b-like protein OS=Homo sapiens PE=2 SV=1 - [RP1BL_HUMAN]	1,68	-	1,44	1,56
Ras-related protein R-Ras2 OS=Homo sapiens GN=RRAS2 PE=1 SV=1 - [RRAS2_HUMAN]	1,40	2,73	0,84	1,66
Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2 - [RENT1_HUMAN]	1,39	1,56	1,22	1,39
Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1 - [RCN1_HUMAN]	-	0,82	-	0,82

Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2 - [RTN4_HUMAN]	0,90	0,70	0,70	0,77
Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3 - [GDIR1_HUMAN]	9,46	2,35	1,96	4,59
Rho GTPase-activating protein 18 OS=Homo sapiens GN=ARHGAP18 PE=1 SV=3 - [RHG18_HUMAN]	1,19	1,12	0,85	1,05
Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1 - [RHOC_HUMAN]	-	2,55	-	2,55
Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 - [RINI_HUMAN]	1,02	1,26	1,10	1,13
Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1 - [RIR1_HUMAN]	0,43	1,03	-	0,73
Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2 - [PRPS1_HUMAN]	0,48	-	0,59	0,53
Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RSL1D1 PE=1 SV=3 - [RL1D1_HUMAN]	-	-	0,60	0,60
Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=1 SV=2 - [BOP1_HUMAN]	2,00	3,56	-	2,78
Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4 - [RRBP1_HUMAN]	1,01	1,03	0,93	0,99
RNA binding motif protein, X-linked-like-1 OS=Homo sapiens GN=RBMXL1 PE=1 SV=1 - [RMXL1_HUMAN]	-	0,70	-	0,70
RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2 - [RBM14_HUMAN]	1,44	1,66	1,53	1,54
RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1 - [EWS_HUMAN]	1,20	0,92	1,14	1,09
RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1 - [FUS_HUMAN]	-	1,76	1,53	1,64
RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 - [RRP12_HUMAN]	1,28	1,06	1,16	1,17
RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	-	-	0,76	0,76
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1 - [AT2A2_HUMAN]	0,79	0,86	0,94	0,86
Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB PE=1 SV=4 - [SAFB1_HUMAN]	0,28	0,57	1,38	0,74
Scavenger receptor class B member 1 OS=Homo sapiens GN=SCARB1 PE=1 SV=1 - [SCRB1_HUMAN]	-	0,85	-	0,85
SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=1 SV=1 - [S23IP_HUMAN]	0,87	0,93	0,62	0,81
Secernin-1 OS=Homo sapiens GN=SCRN1 PE=1 SV=2 - [SCRN1_HUMAN]	1,32	-	5,18	3,25
Secreted frizzled-related protein 1 OS=Homo sapiens GN=SFRP1 PE=1 SV=1 - [SFRP1_HUMAN]	-	1,01	-	1,01
Secretory carrier-associated membrane protein 3 OS=Homo sapiens GN=SCAMP3 PE=1 SV=3 - [SCAM3_HUMAN]	1,24	-	-	1,24
Secretory carrier-associated membrane protein 4 OS=Homo sapiens GN=SCAMP4 PE=2 SV=1 - [SCAM4_HUMAN]	-	1,02	0,83	0,92
Semaphorin-3C OS=Homo sapiens GN=SEMA3C PE=1 SV=2 - [SEM3C_HUMAN]	-	0,45	-	0,45
Semaphorin-7A OS=Homo sapiens GN=SEMA7A PE=1 SV=1 - [SEM7A_HUMAN]	4,06	0,72	0,51	1,76
Seprase OS=Homo sapiens GN=FAP PE=1 SV=5 - [SEPR_HUMAN]	-	1,33	1,06	1,20
Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3 - [SEP11_HUMAN]	-	1,80	-	1,80
Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 - [SEPT2_HUMAN]	1,51	-	-	1,51
Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 - [SEPT9_HUMAN]	1,17	1,17	1,20	1,18
Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 - [SQSTM_HUMAN]	0,93	0,99	1,32	1,08
Serglycin OS=Homo sapiens GN=SRGN PE=1 SV=3 - [SRGN_HUMAN]	0,83	0,87	-	0,85
Serine beta-lactamase-like protein LACTB, mitochondrial OS=Homo sapiens GN=LACTB PE=1 SV=2 - [LACTB_HUMAN]	0,51	0,64	0,68	0,61
Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 - [GLYM_HUMAN]	-	0,40	0,38	0,39
Serine incorporator 1 OS=Homo sapiens GN=SERINC1 PE=1 SV=1 - [SERC1_HUMAN]	-	0,82	0,59	0,71
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A PE=1 SV=1 - [2ABA_HUMAN]	0,82	0,61	-	0,71
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 - [2AAA_HUMAN]	1,06	0,96	1,18	1,06
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC PE=1 SV=1 - [PP1G_HUMAN]	-	1,52	-	1,52
Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 - [STRAP_HUMAN]	-	-	1,48	1,48
Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 - [SYSC_HUMAN]	0,88	1,22	0,99	1,03
Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN]	1,20	1,05	1,01	1,09
Serrate RNA effector molecule homolog OS=Homo sapiens GN=SRRT PE=1 SV=1 - [SRRT_HUMAN]	0,83	0,82	-	0,82
S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 - [ESTD_HUMAN]	-	1,68	-	1,68
SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1 - [SH3L3_HUMAN]	-	0,24	-	0,24
Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2 - [SRP14_HUMAN]	1,41	0,82	1,32	1,18
Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72 PE=1 SV=3 - [SRP72_HUMAN]	1,13	1,13	-	1,13
Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2 - [STAT1_HUMAN]	0,70	1,07	1,06	0,94
Signal transducer and activator of transcription 2 OS=Homo sapiens GN=STAT2 PE=1 SV=1 - [STAT2_HUMAN]	-	1,45	-	1,45
Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2 - [STAT3_HUMAN]	1,63	0,54	-	1,09
Signal transducer and activator of transcription 6 OS=Homo sapiens GN=STAT6 PE=1 SV=1 - [STAT6_HUMAN]	1,42	-	-	1,42
Signal-induced proliferation-associated protein 1 OS=Homo sapiens GN=SIPA1 PE=1 SV=1 - [SIPA1_HUMAN]	-	0,88	-	0,88
SLIT-ROBO Rho GTPase-activating protein 1 OS=Homo sapiens GN=SRGAP1 PE=1 SV=1 - [SRGP1_HUMAN]	1,06	1,69	1,75	1,50

Small ubiquitin-related modifier 2 OS=Homo sapiens GN=SUMO2 PE=1 SV=3 - [SUMO2_HUMAN]	0,66	-	0,58	0,62
Sodium bicarbonate cotransporter 3 OS=Homo sapiens GN=SLC4A7 PE=1 SV=2 - [S4A7_HUMAN]	-	1,24	-	1,24
Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1 - [AT1A1_HUMAN]	0,88	0,87	0,88	0,88
Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1 - [AT1B3_HUMAN]	-	1,54	-	1,54
Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens GN=SLC38A2 PE=1 SV=2 - [S38A2_HUMAN]	1,03	0,76	0,94	0,91
Sodium-dependent phosphate transporter 1 OS=Homo sapiens GN=SLC20A1 PE=1 SV=1 - [S20A1_HUMAN]	0,65	0,58	0,69	0,64
Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=2 - [GTR1_HUMAN]	1,30	1,11	1,01	1,14
Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3 - [SORT_HUMAN]	1,14	3,23	1,41	1,93
Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=3 - [SNX1_HUMAN]	0,95	0,50	0,60	0,68
Spartin OS=Homo sapiens GN=SPG20 PE=1 SV=1 - [SPG20_HUMAN]	1,32	0,80	1,24	1,12
Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3 - [SPTN1_HUMAN]	0,83	0,82	0,84	0,83
Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2 - [SPTB2_HUMAN]	0,85	0,81	0,82	0,83
Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=1 SV=1 - [DX39B_HUMAN]	1,80	0,35	1,31	1,15
Splicing factor 1 OS=Homo sapiens GN=SF1 PE=1 SV=4 - [SF01_HUMAN]	-	0,47	-	0,47
Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN]	0,99	0,87	0,89	0,92
Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2 - [SF3B2_HUMAN]	1,23	1,30	-	1,27
Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMAN]	0,61	0,82	0,62	0,69
Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2 - [SFPQ_HUMAN]	1,23	0,92	1,20	1,12
Squalene synthase OS=Homo sapiens GN=FDFT1 PE=1 SV=1 - [FDFT_HUMAN]	-	0,21	-	0,21
Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	0,79	0,86	0,77	0,81
Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1 - [SND1_HUMAN]	1,10	1,03	0,85	0,99
Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3 - [STMN1_HUMAN]	-	0,40	-	0,40
Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 - [GRP75_HUMAN]	0,88	0,91	0,88	0,89
Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 - [STIP1_HUMAN]	0,76	0,95	0,59	0,76
Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2 - [SMC3_HUMAN]	0,44	0,53	-	0,49
Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3 - [QSOX1_HUMAN]	1,00	-	-	1,00
Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2 - [SODM_HUMAN]	1,59	1,32	1,12	1,34
Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 PE=1 SV=3 - [SURF4_HUMAN]	0,77	0,80	0,89	0,82
SURP and G-patch domain-containing protein 2 OS=Homo sapiens GN=SUGP2 PE=1 SV=2 - [SUGP2_HUMAN]	0,72	0,60	-	0,66
Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2 - [VAT1_HUMAN]	1,19	2,49	1,39	1,69
Syndecan-1 OS=Homo sapiens GN=SDC1 PE=1 SV=3 - [SDC1_HUMAN]	0,80	1,07	0,83	0,90
Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 - [TLN1_HUMAN]	0,95	0,95	0,94	0,94
Target of Myb protein 1 OS=Homo sapiens GN=TOM1 PE=1 SV=2 - [TOM1_HUMAN]	1,30	1,54	1,00	1,28
T-box brain protein 1 OS=Homo sapiens GN=TBR1 PE=1 SV=1 - [TBR1_HUMAN]	0,40	-	0,73	0,56
T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 - [TCPA_HUMAN]	1,05	1,18	1,01	1,08
T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 - [TCPB_HUMAN]	0,92	0,78	0,77	0,82
T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 - [TCPD_HUMAN]	0,99	0,85	0,75	0,86
T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 - [TCPE_HUMAN]	0,69	0,69	1,15	0,84
T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 - [TCPH_HUMAN]	1,05	1,26	1,07	1,13
T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 - [TCPG_HUMAN]	1,20	0,91	1,06	1,06
T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 - [TCPQ_HUMAN]	0,93	0,94	1,11	0,99
T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3 - [TCPZ_HUMAN]	1,20	0,96	0,77	0,98
Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 - [TENS3_HUMAN]	0,82	0,96	1,41	1,07
Tetraspanin-3 OS=Homo sapiens GN=TSPAN3 PE=2 SV=1 - [TSN3_HUMAN]	0,56	0,88	1,41	0,95
Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2 - [TXND5_HUMAN]	1,05	1,06	1,09	1,07
Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=3 - [TRXR1_HUMAN]	1,80	1,38	1,57	1,58
Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3 - [SYTC_HUMAN]	0,86	0,91	0,82	0,86
Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2 - [TSP1_HUMAN]	0,81	0,86	0,86	0,84
Thy-1 membrane glycoprotein OS=Homo sapiens GN=THY1 PE=1 SV=2 - [THY1_HUMAN]	1,02	0,76	0,75	0,84
Thyroid adenoma-associated protein OS=Homo sapiens GN=THADA PE=1 SV=1 - [THADA_HUMAN]	-	-	0,52	0,52
Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2 - [TR150_HUMAN]	0,68	1,08	-	0,88
Thyroid receptor-interacting protein 6 OS=Homo sapiens GN=TRIP6 PE=1 SV=3 - [TRIP6_HUMAN]	2,38	-	-	2,38
Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1 - [TF_HUMAN]	1,07	0,89	1,23	1,06

Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	1,00	0,96	0,90	0,95
Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	0,46	0,68	0,39	0,51
Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2 - [TFR1_HUMAN]	0,64	0,68	0,68	0,67
Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4 - [TAGL_HUMAN]	1,29	0,77	0,71	0,92
Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 - [TAGL2_HUMAN]	1,08	1,00	1,31	1,13
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN]	1,19	1,15	1,04	1,12
Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 - [TKT_HUMAN]	1,07	0,99	1,06	1,04
Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6 - [GCN1L_HUMAN]	1,49	1,35	1,41	1,42
Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=1 SV=3 - [SSRA_HUMAN]	-	1,60	-	1,60
Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2 - [TM9S3_HUMAN]	1,52	1,23	1,37	1,37
Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2 - [TMEDA_HUMAN]	0,77	0,88	0,79	0,81
Transmembrane glycoprotein NMB OS=Homo sapiens GN=GPNMB PE=1 SV=2 - [GPNMB_HUMAN]	0,84	0,88	0,81	0,85
Transmembrane protein 106B OS=Homo sapiens GN=TMEM106B PE=1 SV=2 - [T106B_HUMAN]	1,23	1,26	1,11	1,20
Transmembrane protein 165 OS=Homo sapiens GN=TMEM165 PE=1 SV=1 - [TM165_HUMAN]	-	1,12	0,89	1,00
Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2 - [TNPO1_HUMAN]	0,87	0,75	0,88	0,83
Transportin-3 OS=Homo sapiens GN=TNPO3 PE=1 SV=3 - [TNPO3_HUMAN]	1,23	-	-	1,23
Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN]	0,85	1,20	0,95	1,00
Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 - [ECHB_HUMAN]	1,32	0,92	0,81	1,02
Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 - [PUR2_HUMAN]	1,34	1,07	1,43	1,28
Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 - [TPIS_HUMAN]	0,82	1,01	0,97	0,93
Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4 - [TPP2_HUMAN]	0,70	0,57	0,65	0,64
Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 - [TPM4_HUMAN]	1,07	1,17	1,27	1,17
Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 - [SYWC_HUMAN]	-	2,20	-	2,20
Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 - [TBA1A_HUMAN]	0,62	0,64	0,73	0,66
Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 - [TBA1B_HUMAN]	1,06	0,99	1,02	1,02
Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	1,57	1,11	1,08	1,26
Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 - [TBA8_HUMAN]	-	1,69	-	1,69
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]	0,70	0,62	0,63	0,65
Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]	2,27	0,84	-	1,55
Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	0,96	0,44	1,55	0,98
Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]	0,49	-	0,54	0,52
Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]	0,56	0,59	0,57	0,57
Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]	1,21	0,90	1,31	1,14
Tumor necrosis factor receptor superfamily member 10B OS=Homo sapiens GN=TNFRSF10B PE=1 SV=2 - [TR10B_HUMAN]	0,77	-	-	0,77
Tumor necrosis factor receptor superfamily member 10D OS=Homo sapiens GN=TNFRSF10D PE=1 SV=1 - [TR10D_HUMAN]	-	3,03	-	3,03
Tyrosine-protein kinase receptor UFO OS=Homo sapiens GN=AXL PE=1 SV=3 - [UFO_HUMAN]	1,15	0,82	0,84	0,94
Tyrosine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4 - [SYYC_HUMAN]	2,12	-	-	2,12
U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2 - [U520_HUMAN]	0,75	0,92	0,75	0,81
Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=3 - [UBP14_HUMAN]	1,48	1,02	1,61	1,37
Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2 - [UBP5_HUMAN]	1,17	1,30	1,54	1,34
Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2 - [UCHL1_HUMAN]	1,10	0,95	0,89	0,98
Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=1 SV=2 - [UBP2L_HUMAN]	1,29	0,74	-	1,02
Ubiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens GN=UBE2V2 PE=1 SV=4 - [UB2V2_HUMAN]	0,93	1,06	-	0,99
Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 - [UBA1_HUMAN]	1,09	1,10	1,18	1,13
UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 - [UGDH_HUMAN]	0,63	1,33	0,92	0,96
UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3 - [UGGG1_HUMAN]	1,04	1,01	1,05	1,03
UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1 PE=1 SV=3 - [UAP1_HUMAN]	-	0,49	0,33	0,41
Uncharacterized protein KIAA0090 OS=Homo sapiens GN=KIAA0090 PE=1 SV=1 - [K0090_HUMAN]	0,73	1,14	2,13	1,34
Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 - [MYO1C_HUMAN]	1,14	1,28	0,93	1,12
Unconventional myosin-Ie OS=Homo sapiens GN=MYO1E PE=1 SV=2 - [MYO1E_HUMAN]	-	0,46	1,23	0,85
Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=1 SV=4 - [MYO6_HUMAN]	2,04	1,28	1,00	1,44
Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO18A PE=1 SV=3 - [MY18A_HUMAN]	1,93	-	-	1,93
UPF0505 protein C16orf62 OS=Homo sapiens GN=C16orf62 PE=1 SV=2 - [CP062_HUMAN]	0,65	-	-	0,65
UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1 - [RD23B_HUMAN]	1,29	1,71	1,03	1,35

Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C PE=1 SV=1 - [VP13C_HUMAN]	-	3,71	-	3,71
Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	1,14	0,97	0,95	1,02
Vacuolar protein sorting-associated protein 52 homolog OS=Homo sapiens GN=VPS52 PE=1 SV=1 - [VPS52_HUMAN]	5,53	-	-	5,53
Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4 - [SYVC_HUMAN]	1,47	1,67	1,67	1,60
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1 - [ACADV_HUMAN]	1,07	1,81	1,33	1,40
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=1 SV=2 - [HACD3_HUMAN]	-	2,35	0,73	1,54
Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=1 SV=1 - [TECR_HUMAN]	0,75	-	0,67	0,71
Vesicle transport protein GOT1B OS=Homo sapiens GN=GOLT1B PE=1 SV=1 - [GOT1B_HUMAN]	3,18	-	1,80	2,49
Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4 - [SC22B_HUMAN]	1,04	1,01	1,05	1,03
Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2 - [VIGLN_HUMAN]	0,92	0,96	0,77	0,88
Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 - [VIME_HUMAN]	0,84	0,88	0,82	0,85
Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4 - [VINC_HUMAN]	0,81	0,84	0,78	0,81
Vitamin K epoxide reductase complex subunit 1 OS=Homo sapiens GN=VKORC1 PE=1 SV=1 - [VKOR1_HUMAN]	0,75	0,75	-	0,75
Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2 - [VDAC1_HUMAN]	1,01	1,13	1,16	1,10
Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 - [VDAC2_HUMAN]	0,75	1,50	1,01	1,09
V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=2 SV=3 - [VPP1_HUMAN]	-	2,32	-	2,32
V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 - [VATA_HUMAN]	0,76	0,79	0,81	0,79
V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3 - [VATB2_HUMAN]	0,77	0,45	1,92	1,05
WASH complex subunit 7 OS=Homo sapiens GN=KIAA1033 PE=1 SV=2 - [WASH7_HUMAN]	0,58	1,08	-	0,83
WASH complex subunit FAM21C OS=Homo sapiens GN=FAM21C PE=1 SV=3 - [FA21C_HUMAN]	-	0,89	-	0,89
WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 - [WDR1_HUMAN]	1,03	1,03	1,04	1,03
Wolframin OS=Homo sapiens GN=WFS1 PE=1 SV=2 - [WFS1_HUMAN]	2,08	0,55	1,19	1,27
Xaa-Pro aminopeptidase 1 OS=Homo sapiens GN=XPNPEP1 PE=1 SV=3 - [XPP1_HUMAN]	-	0,83	1,40	1,12
X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 - [XRCC5_HUMAN]	0,86	0,83	0,87	0,85
X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2 - [XRCC6_HUMAN]	1,15	1,04	0,95	1,05
YLP motif-containing protein 1 OS=Homo sapiens GN=YLPM1 PE=1 SV=3 - [YLPM1_HUMAN]	1,25	-	-	1,25
Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1 - [ZYX_HUMAN]	1,62	1,54	1,21	1,46

B. SILAC on IGR-CaP1-Dtx-R cells.

Full name	Light/Heavy Ratio 1	Light/Heavy Ratio 2	Light/Heavy Ratio 3	Average
10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2 - [CH10_HUMAN]	1,03	0,96	0,97	0,99
116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1 - [U5S1_HUMAN]	1,00	1,04	1,12	1,05
14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1 - [PHP14_HUMAN]	0,84	0,93	0,92	0,90
14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 - [1433B_HUMAN]	0,92	1,06	1,00	0,99
14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 - [1433E_HUMAN]	0,94	1,04	1,05	1,01
14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	1,15	1,21	1,06	1,14
14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 - [1433G_HUMAN]	1,10	1,11	1,29	1,17
14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	1,16	0,94	1,12	1,08
14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 - [1433T_HUMAN]	1,07	1,43	1,42	1,31
14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 - [1433Z_HUMAN]	0,97	0,93	0,93	0,94
182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4 - [TB182_HUMAN]	1,49	1,08	1,12	1,23
26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 - [PRS10_HUMAN]	0,60	-	0,89	0,75
26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1 - [PRS4_HUMAN]	0,78	0,85	0,91	0,85
26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3 - [PRS6A_HUMAN]	1,54	0,86	0,99	1,13
26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 - [PRS6B_HUMAN]	1,47	1,14	7,67	3,43
26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 - [PRS7_HUMAN]	0,59	0,65	1,37	0,87
26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1 - [PRS8_HUMAN]	-	0,34	-	0,34
26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2 - [PSMD1_HUMAN]	1,12	1,08	1,04	1,08
26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3 - [PSD11_HUMAN]	1,05	-	-	1,05
26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3 - [PSD12_HUMAN]	0,59	-	0,47	0,53

26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1 - [PSDE_HUMAN]	-	2,19	-	2,19
26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 - [PSMD2_HUMAN]	1,00	1,01	0,99	1,00
26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2 - [PSMD3_HUMAN]	0,79	0,92	1,83	1,18
26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 - [PSMD4_HUMAN]	1,18	1,58	-	1,38
26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2 - [PSMD7_HUMAN]	-	0,66	-	0,66
26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2 - [PSMD8_HUMAN]	0,86	-	-	0,86
2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3 - [ODO1_HUMAN]	1,13	-	1,27	1,20
3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 - [HCD2_HUMAN]	1,54	1,13	1,47	1,38
3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	0,41	0,24	-	0,33
40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1 - [RS10_HUMAN]	1,23	0,80	0,75	0,92
40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 - [RS11_HUMAN]	0,83	0,92	0,94	0,90
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 - [RS12_HUMAN]	0,74	0,86	0,84	0,81
40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2 - [RS13_HUMAN]	0,82	0,87	0,88	0,86
40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 - [RS14_HUMAN]	1,08	1,18	1,36	1,20
40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=1 SV=2 - [RS15_HUMAN]	1,40	1,58	1,12	1,36
40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2 - [RS15A_HUMAN]	0,71	0,79	0,69	0,73
40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 - [RS16_HUMAN]	0,72	0,84	0,99	0,85
40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=1 SV=1 - [RS17L_HUMAN]	0,97	0,84	0,87	0,89
40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]	0,87	0,95	0,90	0,91
40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19_HUMAN]	0,86	1,04	0,87	0,92
40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 - [RS2_HUMAN]	0,82	1,02	0,94	0,93
40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20_HUMAN]	0,99	0,90	0,89	0,93
40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 - [RS21_HUMAN]	0,78	0,66	0,70	0,71
40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 - [RS23_HUMAN]	0,74	0,79	0,86	0,80
40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1 - [RS24_HUMAN]	1,15	0,78	0,71	0,88
40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 - [RS25_HUMAN]	0,90	1,17	0,90	0,99
40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3 - [RS26_HUMAN]	1,07	0,92	-	1,00
40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 - [RS27_HUMAN]	0,90	-	1,24	1,07
40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1 - [RS28_HUMAN]	0,96	1,01	0,83	0,93
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	0,83	0,94	0,93	0,90
40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A_HUMAN]	0,90	0,81	0,89	0,87
40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 - [RS4X_HUMAN]	0,72	0,91	0,88	0,84
40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 - [RS5_HUMAN]	0,99	0,93	0,88	0,93
40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	0,79	-	-	0,79
40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 - [RS7_HUMAN]	0,78	0,91	0,88	0,86
40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 - [RS8_HUMAN]	0,90	0,92	0,87	0,90
40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]	-	1,01	1,32	1,16
40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 - [RSSA_HUMAN]	0,90	0,98	1,12	1,00
4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 - [AL9A1_HUMAN]	1,30	1,12	0,83	1,08
5'-3' exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=1 SV=1 - [XRN2_HUMAN]	1,03	1,07	1,18	1,10
60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]	0,95	0,95	0,94	0,95
60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 - [RLA0_HUMAN]	0,89	0,91	0,86	0,89
60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 - [RLA1_HUMAN]	1,28	1,28	1,10	1,22
60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1 - [RLA2_HUMAN]	1,22	0,82	-	1,02
60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 - [RL10_HUMAN]	0,69	0,72	0,93	0,78
60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 - [RL10A_HUMAN]	0,88	0,86	0,93	0,89
60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 - [RL11_HUMAN]	-	0,65	0,67	0,66
60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]	0,84	0,91	0,96	0,90
60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	0,77	0,87	0,65	0,76
60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2 - [RL13A_HUMAN]	0,87	0,83	0,83	0,84
60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 - [RL14_HUMAN]	0,81	0,83	0,79	0,81
60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2 - [RL15_HUMAN]	-	0,41	0,63	0,52
60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 - [RL17_HUMAN]	0,68	0,65	1,00	0,78
60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2 - [RL18_HUMAN]	0,96	0,97	1,03	0,98
60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 - [RL18A_HUMAN]	0,74	0,57	0,71	0,67
60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 - [RL19_HUMAN]	0,99	-	-	0,99
60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2 - [RL21_HUMAN]	0,97	1,14	1,01	1,04
60S ribosomal protein L22-like 1 OS=Homo sapiens GN=RPL22L1 PE=1 SV=2 - [RL22L_HUMAN]	1,01	-	1,23	1,12
60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 - [RL23_HUMAN]	0,85	0,90	1,01	0,92
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	1,87	0,75	1,01	1,21
60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 - [RL24_HUMAN]	0,84	0,94	0,89	0,89
60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1 - [RL26_HUMAN]	0,88	-	0,62	0,75
60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2 - [RL27_HUMAN]	1,13	1,03	0,71	0,96
60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 - [RL27A_HUMAN]	1,08	0,91	0,94	0,98
60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 - [RL28_HUMAN]	0,79	1,05	0,86	0,90
60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2 - [RL29_HUMAN]	1,21	-	-	1,21
60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 - [RL3_HUMAN]	0,84	0,86	0,80	0,83
60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	0,90	0,87	0,79	0,85

60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1 - [RL31_HUMAN]	-	-	0,73	0,73
60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 - [RL32_HUMAN]	0,47	-	-	0,47
60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 - [RL34_HUMAN]	0,60	0,87	0,49	0,65
60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35_HUMAN]	1,35	-	1,81	1,58
60S ribosomal protein L36a-like OS=Homo sapiens GN=RPL36AL PE=1 SV=3 - [RL36L_HUMAN]	1,05	0,94	-	1,00
60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 - [RL4_HUMAN]	0,77	0,78	0,75	0,76
60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3 - [RL5_HUMAN]	0,87	0,94	0,79	0,87
60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3 - [RL6_HUMAN]	0,79	0,82	0,79	0,80
60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 - [RL7_HUMAN]	0,85	0,93	0,79	0,86
60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2 - [RL7A_HUMAN]	0,93	1,71	1,66	1,43
60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 - [RL8_HUMAN]	1,07	0,92	0,80	0,93
60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1 - [RL9_HUMAN]	0,57	0,78	0,86	0,74
6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2 - [K6PP_HUMAN]	-	-	1,05	1,05
6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2 - [K6PF_HUMAN]	1,24	1,15	1,28	1,22
6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3 - [6PGD_HUMAN]	1,13	0,97	1,04	1,05
78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]	1,01	0,94	0,99	0,98
Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2 - [ILVBL_HUMAN]	1,79	-	-	1,79
Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	1,17	-	1,41	1,29
Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1 - [AN32A_HUMAN]	0,91	0,76	0,82	0,83
Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1 - [AN32B_HUMAN]	0,93	0,74	0,83	0,84
Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E PE=1 SV=1 - [AN32E_HUMAN]	0,54	0,82	0,40	0,59
Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2 - [ACON_HUMAN]	1,00	1,15	1,07	1,07
Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]	0,91	1,12	1,15	1,06
Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	1,14	1,04	1,21	1,13
Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2 - [ANLN_HUMAN]	-	0,52	-	0,52
Actin-like protein 6A OS=Homo sapiens GN=ACTL6A PE=1 SV=1 - [ACL6A_HUMAN]	0,90	-	-	0,90
Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]	1,32	1,24	2,34	1,63
Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3 - [ARC1B_HUMAN]	0,62	0,57	0,73	0,64
Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 - [ARPC2_HUMAN]	1,68	1,69	1,35	1,58
Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3 - [ARPC3_HUMAN]	0,63	0,60	0,58	0,60
Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3 - [ARPC4_HUMAN]	1,58	1,53	1,32	1,48
Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 - [ARP3_HUMAN]	0,89	0,99	0,85	0,91
Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHSA1 PE=1 SV=1 - [AHSA1_HUMAN]	0,54	1,76	0,59	0,96
Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4 - [ACPH_HUMAN]	1,00	0,70	0,77	0,82
Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2 - [APT_HUMAN]	1,16	1,00	2,71	1,62
Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4 - [SAHH_HUMAN]	1,07	0,98	1,01	1,02
Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2 PE=1 SV=2 - [KAD2_HUMAN]	0,91	1,20	1,35	1,15
Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3 - [KAD1_HUMAN]	1,42	-	-	1,42
Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 - [PUR8_HUMAN]	0,91	0,91	1,05	0,95
Adenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=1 SV=3 - [PURA2_HUMAN]	0,85	1,08	0,83	0,92
Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5 - [CAP1_HUMAN]	0,98	1,29	1,16	1,14
Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2 - [APMAP_HUMAN]	1,49	-	0,99	1,24
ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	-	0,81	0,79	0,80
ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]	1,11	0,90	0,78	0,93
ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2 - [ARF3_HUMAN]	1,15	2,02	1,14	1,44
ADP-ribosylation factor-like protein 6-interacting protein 1 OS=Homo sapiens GN=ARL6IP1 PE=1 SV=2 - [AR6P1_HUMAN]	0,78	-	-	0,78
Adseverin OS=Homo sapiens GN=SCIN PE=1 SV=4 - [ADSV_HUMAN]	1,21	1,17	1,17	1,18
Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2 - [SYAC_HUMAN]	1,04	1,00	1,00	1,01
Alanine--tRNA ligase, mitochondrial OS=Homo sapiens GN=AARS2 PE=1 SV=1 - [SYAM_HUMAN]	1,67	0,56	0,64	0,96
Alcohol dehydrogenase [NADP(+)] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3 - [AK1A1_HUMAN]	1,68	2,28	-	1,98
Alcohol dehydrogenase class-3 OS=Homo sapiens GN=ADH5 PE=1 SV=4 - [ADHX_HUMAN]	3,73	1,03	1,21	1,99
Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2 - [ALDH2_HUMAN]	0,92	0,69	0,76	0,79

Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1 - [AK1C1_HUMAN]	0,86	0,78	0,84	0,83
Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3 - [ALDR_HUMAN]	1,13	1,10	1,05	1,09
Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 - [ACTN1_HUMAN]	0,87	0,92	0,90	0,90
Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 - [ACTN4_HUMAN]	1,02	0,98	1,00	1,00
Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 - [AL7A1_HUMAN]	0,99	1,45	1,28	1,24
Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	1,12	1,11	1,10	1,11
Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3 - [SNAA_HUMAN]	0,84	-	-	0,84
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2 - [AIMP1_HUMAN]	1,29	-	1,51	1,40
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 - [AIMP2_HUMAN]	1,11	0,92	1,68	1,24
Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2 - [AMPB_HUMAN]	1,58	0,86	1,31	1,25
AMP deaminase 2 OS=Homo sapiens GN=AMPD2 PE=1 SV=2 - [AMPD2_HUMAN]	0,87	1,15	1,07	1,03
Amyloid beta A4 protein OS=Homo sapiens GN=APP PE=1 SV=3 - [A4_HUMAN]	0,60	0,91	0,96	0,82
Amyloid-like protein 2 OS=Homo sapiens GN=APLP2 PE=1 SV=2 - [APLP2_HUMAN]	2,95	2,51	-	2,73
Anion exchange protein 2 OS=Homo sapiens GN=SLC4A2 PE=1 SV=4 - [B3A2_HUMAN]	1,93	2,05	1,77	1,92
Ankyrin repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=ANKFY1 PE=1 SV=2 - [ANFY1_HUMAN]	-	-	4,99	4,99
Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 - [ANXA1_HUMAN]	1,07	1,07	1,04	1,06
Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1 - [ANX11_HUMAN]	0,99	-	-	0,99
Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 - [ANXA2_HUMAN]	0,98	0,99	1,02	1,00
Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	1,02	1,20	1,77	1,33
Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4 - [ANXA4_HUMAN]	0,99	0,98	0,98	0,98
Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]	1,01	1,04	1,04	1,03
Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	1,05	1,08	1,01	1,05
Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 - [ANXA7_HUMAN]	0,76	0,58	0,72	0,69
AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2 - [AP1B1_HUMAN]	1,35	0,95	1,13	1,14
AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=1 SV=5 - [AP1G1_HUMAN]	1,28	1,49	1,56	1,44
AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3 - [AP2A1_HUMAN]	1,27	-	1,11	1,19
AP-2 complex subunit alpha-2 OS=Homo sapiens GN=AP2A2 PE=1 SV=2 - [AP2A2_HUMAN]	1,04	0,97	0,89	0,97
AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1 - [AP2B1_HUMAN]	1,02	1,13	1,03	1,06
AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=1 SV=2 - [AP2M1_HUMAN]	1,09	-	-	1,09
AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=1 SV=3 - [AP3B1_HUMAN]	1,08	0,76	0,95	0,93
AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 PE=1 SV=1 - [AP3D1_HUMAN]	0,63	-	1,16	0,89
Apoptosis inhibitor 5 OS=Homo sapiens GN=API5 PE=1 SV=3 - [API5_HUMAN]	0,35	0,41	0,30	0,35
Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	1,30	-	1,74	1,52
Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=1 SV=2 - [ACINU_HUMAN]	0,94	1,36	0,84	1,05
Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 - [SYRC_HUMAN]	0,88	1,00	1,00	0,96
Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4 - [ASNS_HUMAN]	0,81	0,89	0,81	0,83
Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1 - [SYNC_HUMAN]	0,94	0,95	1,05	0,98
Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=GOT1 PE=1 SV=3 - [AATC_HUMAN]	1,08	0,39	1,08	0,85
Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3 - [AATM_HUMAN]	1,30	1,26	1,24	1,27
Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN]	1,06	1,20	1,03	1,10
Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3 - [ASPH_HUMAN]	1,19	1,13	0,90	1,07
Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=2 - [ATX2_HUMAN]	0,82	-	-	0,82
Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2 - [ATX2L_HUMAN]	1,09	2,91	2,86	2,29
Atlastin-3 OS=Homo sapiens GN=ATL3 PE=1 SV=1 - [ATLA3_HUMAN]	2,63	-	-	2,63
ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2 - [AT5F1_HUMAN]	1,11	0,89	1,11	1,04
ATP synthase subunit a OS=Homo sapiens GN=MT-ATP6 PE=1 SV=1 - [ATP6_HUMAN]	0,89	1,08	-	0,99
ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	1,08	0,98	1,13	1,06
ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 - [ATPB_HUMAN]	1,29	1,25	1,20	1,25
ATP synthase subunit f, mitochondrial OS=Homo sapiens GN=ATP5J2 PE=1 SV=3 - [ATPK_HUMAN]	0,97	1,65	1,10	1,24

ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=1 SV=3 - [ATP5L_HUMAN]	1,16	0,81	0,85	0,94
ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1 - [ATPG_HUMAN]	0,86	0,87	0,93	0,89
ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 - [ATPO_HUMAN]	-	0,63	-	0,63
ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=1 SV=2 - [ASNA_HUMAN]	0,92	-	-	0,92
ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A PE=1 SV=2 - [ATD3A_HUMAN]	1,06	-	0,87	0,97
ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=1 SV=1 - [ABCD3_HUMAN]	3,30	-	-	3,30
ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1 - [ABCE1_HUMAN]	1,51	1,43	1,47	1,47
ATP-binding cassette sub-family F member 1 OS=Homo sapiens GN=ABCF1 PE=1 SV=2 - [ABCF1_HUMAN]	-	0,97	-	0,97
ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=1 SV=2 - [ABCF2_HUMAN]	1,00	-	2,23	1,62
ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]	0,98	0,99	1,00	0,99
ATP-dependent DNA helicase Q1 OS=Homo sapiens GN=RECQL PE=1 SV=3 - [RECQ1_HUMAN]	0,56	0,60	0,66	0,61
ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	0,88	0,93	0,95	0,92
ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 - [DDX1_HUMAN]	1,06	1,01	0,80	0,96
ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=DDX18 PE=1 SV=2 - [DDX18_HUMAN]	0,78	0,64	0,96	0,79
ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1 - [DD19A_HUMAN]	-	-	0,71	0,71
ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 - [DX39A_HUMAN]	2,49	-	2,80	2,64
ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X_HUMAN]	0,76	0,75	0,73	0,74
ATP-dependent RNA helicase DDX42 OS=Homo sapiens GN=DDX42 PE=1 SV=1 - [DDX42_HUMAN]	1,01	1,13	0,50	0,88
ATP-dependent RNA helicase DHX29 OS=Homo sapiens GN=DHX29 PE=1 SV=2 - [DHX29_HUMAN]	0,87	0,61	1,23	0,91
Baculoviral IAP repeat-containing protein 6 OS=Homo sapiens GN=BIRC6 PE=1 SV=2 - [BIRC6_HUMAN]	-	0,40	-	0,40
Band 4.1-like protein 1 OS=Homo sapiens GN=EPB41L1 PE=1 SV=2 - [E41L1_HUMAN]	1,60	1,26	1,23	1,37
Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=1 SV=1 - [E41L2_HUMAN]	0,97	0,51	0,73	0,74
Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2 - [BCAM_HUMAN]	1,35	1,11	1,73	1,40
Basigin OS=Homo sapiens GN=BSG PE=1 SV=2 - [BASI_HUMAN]	0,98	1,03	1,12	1,04
Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2 - [BCLF1_HUMAN]	1,01	1,22	1,12	1,12
Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]	0,83	0,53	0,87	0,74
Beta-centractin OS=Homo sapiens GN=ACTR1B PE=1 SV=1 - [ACTY_HUMAN]	-	1,63	-	1,63
Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=1 SV=2 - [BGAL_HUMAN]	1,28	-	-	1,28
Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3 - [HEXB_HUMAN]	0,63	1,02	0,95	0,87
Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6 OS=Homo sapiens GN=JMJD6 PE=1 SV=1 - [JMJD6_HUMAN]	0,62	-	-	0,62
Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4 - [COASY_HUMAN]	0,86	0,82	0,80	0,82
Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 - [SYEP_HUMAN]	0,90	1,02	0,95	0,96
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial OS=Homo sapiens GN=MTHFD2 PE=1 SV=2 - [MTDC_HUMAN]	-	0,29	0,80	0,55
Bifunctional protein NCOAT OS=Homo sapiens GN=MGEA5 PE=1 SV=2 - [NCOAT_HUMAN]	-	0,80	1,22	1,01
Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PUR9_HUMAN]	1,08	0,78	0,96	0,94
BolA-like protein 2 OS=Homo sapiens GN=BOLA2 PE=1 SV=1 - [BOLA2_HUMAN]	1,44	-	-	1,44
Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1 OS=Homo sapiens GN=BAIAP2L1 PE=1 SV=2 - [BI2L1_HUMAN]	-	0,92	-	0,92
BRCA2 and CDKN1A-interacting protein OS=Homo sapiens GN=BCCIP PE=1 SV=1 - [BCCIP_HUMAN]	1,00	-	-	1,00
Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens GN=ARFGEF1 PE=1 SV=2 - [BIG1_HUMAN]	-	0,19	-	0,19
C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	1,04	1,14	1,12	1,10
CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 - [PYR1_HUMAN]	1,13	1,15	1,05	1,11
Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=1 SV=3 - [CHERP_HUMAN]	1,27	1,06	2,62	1,65
Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Homo sapiens GN=CAMK2D PE=1 SV=3 - [KCC2D_HUMAN]	-	-	0,36	0,36
Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens GN=SLC25A24 PE=1 SV=2 - [SCMC1_HUMAN]	1,14	1,01	0,97	1,04
Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2 - [CYBP_HUMAN]	0,67	0,82	0,79	0,76

Caldesmon OS=Homo sapiens GN=CALD1 PE=1 SV=3 - [CALD1_HUMAN]	1,30	-	1,06	1,18
Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 - [CALX_HUMAN]	1,37	1,29	1,23	1,30
Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 - [CPNS1_HUMAN]	0,88	0,85	0,85	0,86
Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1 - [CAN1_HUMAN]	1,61	1,56	1,18	1,45
Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 - [CAN2_HUMAN]	1,44	1,40	1,39	1,41
Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4 - [ICAL_HUMAN]	1,40	1,27	1,48	1,38
Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 - [CNN2_HUMAN]	0,89	0,99	0,83	0,90
Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 - [CNN3_HUMAN]	3,51	2,57	-	3,04
Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1 - [CALR_HUMAN]	1,52	1,06	1,40	1,33
Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2 - [CALU_HUMAN]	1,10	1,43	1,15	1,23
Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2 - [CAPR1_HUMAN]	0,67	0,65	0,87	0,73
Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	1,16	1,49	1,32	1,32
Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3 - [CBR1_HUMAN]	1,14	1,16	1,15	1,15
Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2 - [CPT1A_HUMAN]	1,46	1,14	1,42	1,34
Casein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=1 SV=1 - [CSK21_HUMAN]	2,50	2,54	1,96	2,33
Catalase OS=Homo sapiens GN=CAT PE=1 SV=3 - [CATA_HUMAN]	3,02	2,06	1,86	2,31
Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1 - [CTNA1_HUMAN]	0,15	0,55	-	0,35
Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1 - [CTND1_HUMAN]	1,00	1,25	1,10	1,11
Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	0,88	0,96	0,88	0,91
Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	-	0,94	0,66	0,80
CCAAT/enhancer-binding protein zeta OS=Homo sapiens GN=CEBPZ PE=1 SV=3 - [CEBPZ_HUMAN]	1,09	-	-	1,09
CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2 - [CNOT1_HUMAN]	0,79	1,50	-	1,15
CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1 - [CD2AP_HUMAN]	0,71	-	-	0,71
Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2 - [CCAR2_HUMAN]	1,22	1,03	1,13	1,13
Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2 - [CDC42_HUMAN]	-	-	1,16	1,16
Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2 - [CDC5L_HUMAN]	3,38	-	0,85	2,11
Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2 - [CCAR1_HUMAN]	0,74	1,28	0,90	0,97
Centrosomal protein of 170 kDa OS=Homo sapiens GN=CEP170 PE=1 SV=1 - [CE170_HUMAN]	0,75	0,67	0,64	0,69
Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 - [CLIC1_HUMAN]	0,98	0,91	1,08	0,99
Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 - [CLIC4_HUMAN]	0,94	1,27	-	1,11
Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 - [CBX3_HUMAN]	1,26	0,68	0,79	0,91
Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=1 SV=2 - [CHD4_HUMAN]	1,37	-	-	1,37
Chromosome-associated kinesin KIF4A OS=Homo sapiens GN=KIF4A PE=1 SV=3 - [KIF4A_HUMAN]	-	-	0,42	0,42
Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2 - [CISY_HUMAN]	1,07	0,98	1,01	1,02
C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 PE=1 SV=4 - [JIP4_HUMAN]	1,55	1,24	1,29	1,36
Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 - [CLH1_HUMAN]	1,00	1,02	0,99	1,00
Clathrin interactor 1 OS=Homo sapiens GN=CLINT1 PE=1 SV=1 - [EPN4_HUMAN]	-	0,64	-	0,64
Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens GN=CPSF1 PE=1 SV=2 - [CPSF1_HUMAN]	0,73	0,96	0,89	0,86
Cleavage and polyadenylation specificity factor subunit 2 OS=Homo sapiens GN=CPSF2 PE=1 SV=2 - [CPSF2_HUMAN]	0,80	-	1,07	0,94
Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens GN=NUDT21 PE=1 SV=1 - [CPSF5_HUMAN]	-	-	1,03	1,03
Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=1 SV=2 - [CPSF6_HUMAN]	-	1,28	0,88	1,08
Cleavage stimulation factor subunit 3 OS=Homo sapiens GN=CSTF3 PE=1 SV=1 - [CSTF3_HUMAN]	0,27	-	-	0,27
Cleft lip and palate transmembrane protein 1 OS=Homo sapiens GN=CLPTM1 PE=1 SV=1 - [CLPT1_HUMAN]	1,06	-	0,69	0,87
CLIP-associating protein 1 OS=Homo sapiens GN=CLASP1 PE=1 SV=1 - [CLAP1_HUMAN]	0,82	-	-	0,82
CLIP-associating protein 2 OS=Homo sapiens GN=CLASP2 PE=1 SV=2 - [CLAP2_HUMAN]	0,92	1,82	0,78	1,17
Coactosin-like protein OS=Homo sapiens GN=COTL1 PE=1 SV=3 - [COTL1_HUMAN]	1,02	0,56	0,80	0,79
Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2 - [COPA_HUMAN]	0,88	0,95	0,90	0,91
Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3 - [COPB_HUMAN]	0,88	0,81	1,14	0,94
Coatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2 - [COPB2_HUMAN]	0,98	1,01	1,02	1,00

Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1 - [COPD_HUMAN]	-	-	0,61	0,61
Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 - [COPG1_HUMAN]	1,10	0,99	0,98	1,02
Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1 - [COPG2_HUMAN]	2,41	-	-	2,41
Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	0,96	0,95	1,03	0,98
Cold shock domain-containing protein E1 OS=Homo sapiens GN=CSDE1 PE=1 SV=2 - [CSDE1_HUMAN]	-	0,94	0,96	0,95
Collagen alpha-1(IV) chain OS=Homo sapiens GN=COL4A1 PE=1 SV=3 - [CO4A1_HUMAN]	-	0,34	0,57	0,46
Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Homo sapiens GN=C1QBP PE=1 SV=1 - [C1QBP_HUMAN]	2,19	1,25	0,77	1,41
Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=1 SV=3 - [CND1_HUMAN]	0,49	0,58	0,43	0,50
Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1 - [CND3_HUMAN]	0,77	0,83	-	0,80
Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 - [F120A_HUMAN]	0,78	0,48	1,00	0,75
COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=4 - [CSN1_HUMAN]	1,10	-	-	1,10
COP9 signalosome complex subunit 3 OS=Homo sapiens GN=COPS3 PE=1 SV=3 - [CSN3_HUMAN]	0,89	-	-	0,89
COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=1 SV=1 - [CSN4_HUMAN]	-	1,14	-	1,14
Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1 - [CPNE3_HUMAN]	0,88	-	-	0,88
Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4 - [H2AY_HUMAN]	0,61	0,89	0,92	0,81
Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1 - [COR1B_HUMAN]	1,03	0,94	0,93	0,97
Coronin-7 OS=Homo sapiens GN=CORO7 PE=1 SV=2 - [CORO7_HUMAN]	2,74	-	-	2,74
CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=1 SV=2 - [PYRG1_HUMAN]	1,31	2,86	0,96	1,71
Cullin-1 OS=Homo sapiens GN=CUL1 PE=1 SV=2 - [CUL1_HUMAN]	0,67	1,21	-	0,94
Cullin-2 OS=Homo sapiens GN=CUL2 PE=1 SV=2 - [CUL2_HUMAN]	0,92	1,07	1,17	1,05
Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	1,01	1,36	1,01	1,13
Cutaneous T-cell lymphoma-associated antigen 5 OS=Homo sapiens GN=CTAGE5 PE=1 SV=4 - [CTGE5_HUMAN]	1,05	-	-	1,05
Cyclic AMP-responsive element-binding protein 1 OS=Homo sapiens GN=CREB1 PE=1 SV=2 - [CREB1_HUMAN]	0,77	-	-	0,77
Cyclin-dependent kinase 11B OS=Homo sapiens GN=CDK11B PE=1 SV=3 - [CD11B_HUMAN]	0,99	0,39	0,57	0,65
Cyclin-G-associated kinase OS=Homo sapiens GN=GAK PE=1 SV=2 - [GAK_HUMAN]	7,14	-	-	7,14
Cystathionine beta-synthase OS=Homo sapiens GN=CBS PE=1 SV=2 - [CBS_HUMAN]	1,09	1,14	1,23	1,15
Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2 - [CYTB_HUMAN]	1,12	1,12	1,12	1,12
Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3 - [CSRP1_HUMAN]	0,98	1,20	-	1,09
Cysteine-rich protein 2 OS=Homo sapiens GN=CRIP2 PE=1 SV=1 - [CRIP2_HUMAN]	-	2,36	-	2,36
Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=CARS PE=1 SV=3 - [SYCC_HUMAN]	1,09	1,06	0,97	1,04
Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 - [QCR1_HUMAN]	1,26	0,91	0,88	1,01
Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3 - [QCR2_HUMAN]	1,30	0,91	1,34	1,18
Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2 - [CYC_HUMAN]	1,19	1,19	1,26	1,21
Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1 - [COX2_HUMAN]	0,76	-	-	0,76
Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3 - [CY1_HUMAN]	0,81	-	-	0,81
Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	0,94	0,93	0,87	0,91
Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3 - [DC1I2_HUMAN]	1,66	1,50	1,40	1,52
Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1 - [CYFP1_HUMAN]	0,88	0,77	0,72	0,79
Cytoplasmic FMR1-interacting protein 2 OS=Homo sapiens GN=CYFIP2 PE=1 SV=2 - [CYFP2_HUMAN]	3,09	-	-	3,09
Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2 - [CKAP4_HUMAN]	0,89	0,97	0,97	0,94
Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3 - [CKAP5_HUMAN]	1,33	1,16	1,18	1,22
Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 - [AMPL_HUMAN]	0,76	1,00	1,08	0,94
Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 PE=1 SV=3 - [BACH_HUMAN]	0,92	0,94	1,18	1,01
D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 - [SERA_HUMAN]	1,17	1,14	0,95	1,09
DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 PE=1 SV=1 - [DAZP1_HUMAN]	2,21	-	1,18	1,70
DBIRD complex subunit ZNF326 OS=Homo sapiens GN=ZNF326 PE=1 SV=2 - [ZN326_HUMAN]	0,55	0,65	0,58	0,59
D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=3 - [DOPD_HUMAN]	1,63	2,12	1,13	1,63

Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2 - [ECH1_HUMAN]	1,15	0,95	1,13	1,08
Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	1,30	1,42	1,11	1,28
Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3 - [DESP_HUMAN]	0,74	0,77	0,59	0,70
Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 - [DEST_HUMAN]	0,87	0,84	0,84	0,85
Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2 - [DLDH_HUMAN]	1,08	0,84	2,58	1,50
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLAT PE=1 SV=3 - [ODP2_HUMAN]	1,06	1,24	1,83	1,38
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=1 SV=4 - [ODO2_HUMAN]	0,43	0,52	1,06	0,67
Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 - [DPYL2_HUMAN]	0,63	0,73	1,31	0,89
Dipeptidyl peptidase 3 OS=Homo sapiens GN=DPP3 PE=1 SV=2 - [DPP3_HUMAN]	-	-	1,23	1,23
Dipeptidyl peptidase 4 OS=Homo sapiens GN=DPP4 PE=1 SV=2 - [DPP4_HUMAN]	0,82	0,89	0,93	0,88
Dipeptidyl peptidase 9 OS=Homo sapiens GN=DPP9 PE=1 SV=3 - [DPP9_HUMAN]	-	1,04	-	1,04
DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1 PE=1 SV=2 - [DNMT1_HUMAN]	0,70	1,18	0,17	0,69
DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 - [DDB1_HUMAN]	0,86	0,79	0,86	0,84
DNA fragmentation factor subunit alpha OS=Homo sapiens GN=DFFA PE=1 SV=1 - [DFFA_HUMAN]	-	-	1,24	1,24
DNA ligase 1 OS=Homo sapiens GN=LIG1 PE=1 SV=1 - [DNLI1_HUMAN]	1,82	-	-	1,82
DNA replication licensing factor MCM2 OS=Homo sapiens GN=MCM2 PE=1 SV=4 - [MCM2_HUMAN]	0,81	0,82	0,87	0,83
DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 - [MCM3_HUMAN]	0,78	0,88	0,85	0,84
DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5 - [MCM4_HUMAN]	0,83	0,78	0,81	0,81
DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5 - [MCM5_HUMAN]	1,05	0,86	0,90	0,94
DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 - [MCM6_HUMAN]	0,83	0,88	0,83	0,84
DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4 - [MCM7_HUMAN]	1,15	1,02	0,96	1,04
DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 - [TOP1_HUMAN]	1,04	1,12	1,34	1,16
DNA topoisomerase 2-beta OS=Homo sapiens GN=TOP2B PE=1 SV=3 - [TOP2B_HUMAN]	0,68	1,03	0,69	0,80
DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens GN=APEX1 PE=1 SV=2 - [APEX1_HUMAN]	1,17	1,46	0,99	1,21
DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	0,88	0,89	0,89	0,89
DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2 - [RPB1_HUMAN]	1,76	1,74	1,41	1,63
DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens GN=POLR2B PE=1 SV=1 - [RPB2_HUMAN]	1,11	1,04	1,39	1,18
DNA-directed RNA polymerase, mitochondrial OS=Homo sapiens GN=POLRMT PE=1 SV=2 - [RPOM_HUMAN]	0,67	1,33	2,20	1,40
DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2 - [DNJA1_HUMAN]	0,91	-	1,05	0,98
DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1 - [DNJA2_HUMAN]	0,77	0,88	0,93	0,86
DnaJ homolog subfamily C member 10 OS=Homo sapiens GN=DNAJC10 PE=1 SV=2 - [DJC10_HUMAN]	0,70	0,51	-	0,61
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4 - [OST48_HUMAN]	0,96	0,68	0,91	0,85
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 - [RPN1_HUMAN]	1,14	0,91	1,04	1,03
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3 - [RPN2_HUMAN]	1,15	0,91	1,03	1,03
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2 - [STT3A_HUMAN]	0,57	0,51	-	0,54
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1 - [STT3B_HUMAN]	1,47	-	1,77	1,62
Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN]	1,15	1,12	1,07	1,11
Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4 - [DREB_HUMAN]	0,88	0,93	0,90	0,90
Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 - [DBNL_HUMAN]	1,15	1,08	1,18	1,13
Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 - [MP2K1_HUMAN]	-	1,01	-	1,01
Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3 - [DCTN1_HUMAN]	1,01	0,96	1,22	1,06
Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 - [DNM1L_HUMAN]	0,99	1,16	0,92	1,02
Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 - [DYN2_HUMAN]	1,26	1,12	1,13	1,17
Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=3 - [OPA1_HUMAN]	-	0,76	-	0,76
Dynein light chain 1, cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1 - [DYL1_HUMAN]	1,12	0,90	1,08	1,03

E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2 - [RBP2_HUMAN]	0,79	1,12	1,21	1,04
E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 - [TRI25_HUMAN]	0,58	0,56	0,32	0,49
E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens GN=RNF20 PE=1 SV=2 - [BRE1A_HUMAN]	-	1,20	2,72	1,96
E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 - [HUWE1_HUMAN]	-	1,11	-	1,11
E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1 - [UBR4_HUMAN]	1,28	0,85	0,68	0,94
Echinoderm microtubule-associated protein-like 4 OS=Homo sapiens GN=EML4 PE=1 SV=3 - [EMAL4_HUMAN]	-	1,14	-	1,14
EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2 - [EHD1_HUMAN]	2,88	3,28	1,60	2,58
ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=1 SV=2 - [ELAV1_HUMAN]	0,84	0,73	0,84	0,80
Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1 - [ETFA_HUMAN]	1,02	1,53	1,32	1,29
Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 - [ETFB_HUMAN]	1,32	1,11	1,24	1,22
ELKS/Rab6-interacting/CAST family member 1 OS=Homo sapiens GN=ERC1 PE=1 SV=1 - [RB6I2_HUMAN]	1,63	-	-	1,63
Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]	1,32	1,12	1,21	1,22
Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 - [EF1A2_HUMAN]	-	-	1,66	1,66
Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 - [EF1B_HUMAN]	0,95	1,17	1,05	1,06
Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5 - [EF1D_HUMAN]	1,29	1,08	1,18	1,18
Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN]	0,88	0,94	1,01	0,94
Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	0,96	0,98	0,97	0,97
Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2 - [EFTU_HUMAN]	1,09	0,95	1,01	1,02
Endophilin-A1 OS=Homo sapiens GN=SH3GL2 PE=1 SV=1 - [SH3G2_HUMAN]	-	-	1,29	1,29
Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4 - [ERP29_HUMAN]	0,83	1,19	0,97	0,99
Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 - [ERP44_HUMAN]	-	3,61	1,36	2,49
Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [ENPL_HUMAN]	0,90	0,90	0,93	0,91
Endothelial differentiation-related factor 1 OS=Homo sapiens GN=EDF1 PE=1 SV=1 - [EDF1_HUMAN]	0,60	-	-	0,60
Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1 - [EDC4_HUMAN]	1,23	1,40	0,91	1,18
Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1 - [ERH_HUMAN]	1,56	-	-	1,56
Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens GN=ECI1 PE=1 SV=1 - [ECI1_HUMAN]	0,91	1,09	1,14	1,05
Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 - [ECHM_HUMAN]	1,43	3,08	1,69	2,07
Ephrin type-A receptor 3 OS=Homo sapiens GN=EPHA3 PE=1 SV=2 - [EPHA3_HUMAN]	-	1,12	1,59	1,36
Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 PE=1 SV=2 - [ES8L2_HUMAN]	1,64	0,56	-	1,10
Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2 - [EGFR_HUMAN]	1,18	0,83	1,37	1,13
Epidermal growth factor receptor substrate 15-like 1 OS=Homo sapiens GN=EPS15L1 PE=1 SV=1 - [EP15R_HUMAN]	-	1,14	0,36	0,75
Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1 SV=1 - [NPC2_HUMAN]	1,70	-	-	1,70
Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 - [EPIPL_HUMAN]	-	-	0,97	0,97
Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1 - [ERLN2_HUMAN]	1,08	1,28	0,92	1,09
ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2 - [ERO1A_HUMAN]	0,73	1,45	-	1,09
Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 - [IF4A1_HUMAN]	0,77	0,78	0,71	0,75
Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4 - [IF4A3_HUMAN]	1,10	1,14	0,84	1,03
Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1 PE=1 SV=1 - [ERF3A_HUMAN]	1,22	1,05	0,89	1,05
Eukaryotic translation elongation factor 1 epsilon-1 OS=Homo sapiens GN=EEF1E1 PE=1 SV=1 - [MCA3_HUMAN]	-	-	1,35	1,35
Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3 - [IF2A_HUMAN]	0,78	1,17	0,75	0,90
Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3 - [IF2G_HUMAN]	-	0,98	1,19	1,09
Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1 - [EIF3A_HUMAN]	0,85	0,85	0,79	0,83
Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3 - [EIF3B_HUMAN]	0,70	0,93	0,86	0,83
Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=1 SV=1 - [EIF3C_HUMAN]	0,92	0,94	0,93	0,93
Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 - [EIF3D_HUMAN]	0,33	0,76	0,68	0,59
Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1 - [EIF3E_HUMAN]	0,77	0,95	0,99	0,90

Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=1 SV=1 - [EIF3F_HUMAN]	0,95	0,66	0,86	0,82
Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2 - [EIF3G_HUMAN]	-	0,61	0,68	0,64
Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1 - [EIF3I_HUMAN]	1,04	1,08	0,88	1,00
Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1 - [EIF3L_HUMAN]	0,54	0,70	0,88	0,71
Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 - [IF4G1_HUMAN]	0,87	0,93	0,92	0,90
Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens GN=EIF4G2 PE=1 SV=1 - [IF4G2_HUMAN]	0,41	0,38	0,53	0,44
Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=1 SV=2 - [IF4B_HUMAN]	1,03	1,21	0,72	0,99
Eukaryotic translation initiation factor 5 OS=Homo sapiens GN=EIF5 PE=1 SV=2 - [IF5_HUMAN]	-	0,50	-	0,50
Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 - [IF5A1_HUMAN]	0,82	0,96	0,89	0,89
Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4 - [IF2P_HUMAN]	1,19	1,02	1,21	1,14
Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 - [IF6_HUMAN]	1,27	1,32	0,93	1,17
Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 PE=1 SV=2 - [RRP44_HUMAN]	1,76	1,43	1,02	1,40
Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 - [XPO1_HUMAN]	0,85	0,89	0,86	0,87
Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN]	0,98	0,99	1,05	1,01
Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1 - [XPO5_HUMAN]	1,12	0,85	0,79	0,92
Exportin-7 OS=Homo sapiens GN=XPO7 PE=1 SV=3 - [XPO7_HUMAN]	1,10	1,23	0,91	1,08
Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2 - [XPOT_HUMAN]	1,19	1,12	1,44	1,25
Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 - [ESYT1_HUMAN]	0,96	1,06	1,00	1,01
Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	0,99	1,02	0,92	0,98
FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1 - [SP16H_HUMAN]	0,99	1,06	0,96	1,00
FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1 - [SSRP1_HUMAN]	0,94	0,89	0,90	0,91
F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3 - [CAZA1_HUMAN]	1,21	0,82	0,95	0,99
F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3 - [CAZA2_HUMAN]	0,81	0,89	1,12	0,94
F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 - [CAPZB_HUMAN]	1,83	1,12	1,14	1,36
Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3 - [FUBP1_HUMAN]	1,05	1,01	0,95	1,01
Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4 - [FUBP2_HUMAN]	1,34	1,14	1,21	1,23
Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2 - [FUBP3_HUMAN]	0,74	-	-	0,74
FAS-associated factor 1 OS=Homo sapiens GN=FAF1 PE=1 SV=2 - [FAF1_HUMAN]	1,24	-	-	1,24
Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3 - [FSCN1_HUMAN]	-	-	0,43	0,43
Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3 - [FABP5_HUMAN]	0,94	0,85	0,89	0,89
Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	0,93	0,96	0,98	0,96
Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2 - [FLNB_HUMAN]	1,04	1,11	1,19	1,11
Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3 - [FLNC_HUMAN]	1,01	0,97	0,95	0,98
FK506-binding protein 15 OS=Homo sapiens GN=FKBP15 PE=1 SV=2 - [FKB15_HUMAN]	1,44	1,16	0,85	1,15
Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1 SV=1 - [FEN1_HUMAN]	1,20	1,50	-	1,35
Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3 - [BLVRB_HUMAN]	0,46	0,93	-	0,70
Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens GN=FXR2 PE=1 SV=2 - [FXR2_HUMAN]	0,74	1,02	0,86	0,87
Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]	1,17	1,12	1,13	1,14
Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2 - [ALDOC_HUMAN]	1,53	1,36	1,34	1,41
Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN]	2,00	1,30	1,18	1,49
FYVE, RhoGEF and PH domain-containing protein 4 OS=Homo sapiens GN=FGD4 PE=1 SV=2 - [FGD4_HUMAN]	4,33	2,79	2,79	3,30
Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN]	0,89	0,89	0,93	0,90
Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 - [LG3BP_HUMAN]	0,98	0,90	0,90	0,93
Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3 - [ENOG_HUMAN]	0,63	1,02	-	0,83
Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1 - [GELS_HUMAN]	1,72	1,66	1,49	1,62
Gem-associated protein 5 OS=Homo sapiens GN=GEMIN5 PE=1 SV=3 - [GEMI5_HUMAN]	0,99	1,09	-	1,04
General transcription factor 3C polypeptide 4 OS=Homo sapiens GN=GTF3C4 PE=1 SV=2 - [TF3C4_HUMAN]	0,68	0,74	-	0,71

General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2 - [GTF2I_HUMAN]	0,93	0,85	1,00	0,92
General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2 - [USO1_HUMAN]	1,04	1,12	1,20	1,12
Glucosamine-6-phosphate isomerase 1 OS=Homo sapiens GN=GNPDA1 PE=1 SV=1 - [GNPI1_HUMAN]	1,14	-	-	1,14
Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 - [G6PD_HUMAN]	1,02	1,02	1,09	1,05
Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4 - [G6PI_HUMAN]	1,16	1,21	1,13	1,17
Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2 - [GLU2B_HUMAN]	1,05	1,00	1,00	1,02
Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2 - [DHE3_HUMAN]	1,08	1,04	1,00	1,04
Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens GN=GCLM PE=1 SV=1 - [GSH0_HUMAN]	-	0,93	-	0,93
Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS PE=1 SV=1 - [GLSK_HUMAN]	1,02	0,94	1,00	0,99
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	0,79	1,08	1,05	0,97
Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1 - [SYQ_HUMAN]	1,00	1,21	1,45	1,22
Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2 - [GSHR_HUMAN]	0,98	1,23	1,45	1,22
Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 PE=1 SV=3 - [GSTK1_HUMAN]	-	1,08	1,70	1,39
Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3 - [GSTM3_HUMAN]	0,94	0,99	1,01	0,98
Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 - [GSTO1_HUMAN]	1,95	1,27	1,26	1,49
Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	1,47	1,54	1,44	1,48
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	1,07	1,11	1,10	1,09
Glycine dehydrogenase (decarboxylating), mitochondrial OS=Homo sapiens GN=GLDC PE=1 SV=2 - [GCSP_HUMAN]	-	1,31	-	1,31
Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 - [SYG_HUMAN]	1,01	0,96	1,17	1,05
Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	1,28	1,07	1,15	1,17
Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	1,04	0,99	1,02	1,02
Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1 - [GLOD4_HUMAN]	0,81	-	0,97	0,89
Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1 - [GRHPR_HUMAN]	-	3,94	-	3,94
Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2 - [GSLG1_HUMAN]	0,45	0,51	0,45	0,47
Golgi reassembly-stacking protein 2 OS=Homo sapiens GN=GORASP2 PE=1 SV=3 - [GORS2_HUMAN]	0,68	1,02	0,97	0,89
Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 - [GCP60_HUMAN]	-	1,64	-	1,64
Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 PE=1 SV=3 - [GOGA2_HUMAN]	0,93	0,93	1,15	1,01
Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2 - [GOGB1_HUMAN]	-	-	0,77	0,77
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens GN=GBF1 PE=1 SV=2 - [GBF1_HUMAN]	0,99	1,97	0,82	1,26
GPI transamidase component PIG-S OS=Homo sapiens GN=PIGS PE=1 SV=3 - [PIGS_HUMAN]	0,60	1,70	0,62	0,98
G-rich sequence factor 1 OS=Homo sapiens GN=GRSF1 PE=1 SV=3 - [GRSF1_HUMAN]	1,19	1,58	1,34	1,37
GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2 - [GAPD1_HUMAN]	1,23	-	1,31	1,27
GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 - [RAN_HUMAN]	0,85	0,94	0,83	0,88
GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 - [SAR1A_HUMAN]	-	-	2,32	2,32
Guanine deaminase OS=Homo sapiens GN=GDA PE=1 SV=1 - [GUAD_HUMAN]	0,89	0,79	1,04	0,91
Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens GN=GNAI1 PE=1 SV=2 - [GNAI1_HUMAN]	1,23	0,81	1,05	1,03
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3 - [GBB1_HUMAN]	1,35	1,11	0,99	1,15
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 - [GBB2_HUMAN]	0,85	0,78	0,93	0,86
Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1 - [GNAS2_HUMAN]	-	0,51	1,46	0,99
Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3 - [GBLP_HUMAN]	0,87	0,84	0,82	0,84
HEAT repeat-containing protein 1 OS=Homo sapiens GN=HEATR1 PE=1 SV=3 - [HEAT1_HUMAN]	1,23	1,04	-	1,14
Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN]	0,99	0,95	0,97	0,97
Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 - [HSP74_HUMAN]	1,08	1,02	1,04	1,05
Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3 - [HS74L_HUMAN]	0,74	0,31	-	0,52

Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]	0,76	0,74	0,75	0,75
Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3 - [TRAP1_HUMAN]	1,07	1,17	0,99	1,08
Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 - [HSPB1_HUMAN]	1,07	1,07	1,11	1,09
Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN]	0,86	0,85	0,92	0,87
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]	1,04	1,03	1,05	1,04
Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Homo sapiens GN=HGS PE=1 SV=1 - [HGS_HUMAN]	1,24	-	1,22	1,23
Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1 - [HDGF_HUMAN]	0,58	-	1,03	0,81
Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens GN=HDGFRP2 PE=1 SV=1 - [HDGR2_HUMAN]	0,97	1,24	1,19	1,13
Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1 - [HP1B3_HUMAN]	1,51	1,65	2,28	1,81
Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=1 SV=2 - [ROAA_HUMAN]	0,65	0,46	0,76	0,62
Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 - [ROA0_HUMAN]	0,87	0,91	0,95	0,91
Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 - [ROA1_HUMAN]	0,94	0,96	0,95	0,95
Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 - [ROA3_HUMAN]	0,83	1,00	0,94	0,92
Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1 - [HNRPD_HUMAN]	0,82	1,08	1,19	1,03
Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3 - [HNRDL_HUMAN]	0,71	0,72	0,71	0,71
Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 - [HNRPF_HUMAN]	0,93	1,00	0,88	0,94
Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 - [HNRH1_HUMAN]	0,69	0,75	0,85	0,76
Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 - [HNRH2_HUMAN]	-	1,30	0,74	1,02
Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2 - [HNRH3_HUMAN]	1,01	0,92	0,83	0,92
Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 - [HNRPK_HUMAN]	1,00	0,95	1,09	1,02
Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 - [HNRPL_HUMAN]	1,22	0,99	0,90	1,04
Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 - [HNRPM_HUMAN]	0,84	0,81	0,80	0,82
Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [HNRPQ_HUMAN]	1,21	0,96	1,56	1,24
Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN]	1,04	1,37	1,10	1,17
Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 - [HNRPU_HUMAN]	0,93	0,92	0,94	0,93
Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=2 - [HNRL1_HUMAN]	1,04	0,99	1,41	1,14
Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	0,79	0,95	0,98	0,91
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]	1,11	1,08	1,00	1,06
Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4 - [HNRPC_HUMAN]	0,97	0,96	1,00	0,98
Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 - [HXK1_HUMAN]	0,76	-	-	0,76
Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 - [HXK2_HUMAN]	1,10	0,88	1,20	1,06
High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3 - [HMGB1_HUMAN]	1,02	0,83	0,90	0,92
High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 - [HMGB2_HUMAN]	0,93	-	0,93	0,93
Histidine triad nucleotide-binding protein 2, mitochondrial OS=Homo sapiens GN=HINT2 PE=1 SV=1 - [HINT2_HUMAN]	1,41	1,40	-	1,41
Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1 - [HDAC1_HUMAN]	1,25	0,93	0,59	0,92
Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3 - [H10_HUMAN]	1,12	1,37	-	1,24
Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2 - [H13_HUMAN]	1,03	1,00	0,80	0,94
Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2 - [H2A1B_HUMAN]	1,37	1,17	1,42	1,32
Histone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3 - [H2A2B_HUMAN]	1,34	-	1,21	1,27
Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4 - [H2A2C_HUMAN]	1,32	1,47	1,46	1,42
Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2 - [H2AZ_HUMAN]	0,99	-	-	0,99
Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3 - [H2B1M_HUMAN]	0,89	0,86	0,85	0,87
Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3 - [H2B3B_HUMAN]	1,06	1,15	1,10	1,10
Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	1,01	1,03	1,02	1,02
Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3 - [H32_HUMAN]	1,06	1,24	0,73	1,01

Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2 - [H33_HUMAN]	1,20	0,97	1,62	1,26
Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	0,89	0,89	0,93	0,90
Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3 - [RBBP4_HUMAN]	0,90	1,10	0,95	0,98
Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1 - [RBBP7_HUMAN]	3,85	-	2,96	3,41
HLA class I histocompatibility antigen, B-8 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 - [1B08_HUMAN]	1,28	0,89	0,97	1,05
Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 - [HCFC1_HUMAN]	1,08	1,35	0,96	1,13
Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2 - [F10A1_HUMAN]	1,08	1,11	1,17	1,12
Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1 - [CDC37_HUMAN]	2,07	1,71	0,83	1,54
Huntingtin-interacting protein 1 OS=Homo sapiens GN=HIP1 PE=1 SV=5 - [HIP1_HUMAN]	1,73	-	-	1,73
Huntingtin-interacting protein 1-related protein OS=Homo sapiens GN=HIP1R PE=1 SV=2 - [HIP1R_HUMAN]	1,26	2,01	-	1,64
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	1,17	-	0,94	1,05
Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 - [HYOU1_HUMAN]	1,07	1,07	0,94	1,02
Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 - [IMA1_HUMAN]	1,18	3,33	1,28	1,93
Importin subunit alpha-7 OS=Homo sapiens GN=KPNA6 PE=1 SV=1 - [IMA7_HUMAN]	0,33	-	-	0,33
Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]	1,10	1,04	1,16	1,10
Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=2 - [IPO4_HUMAN]	1,28	1,06	0,86	1,07
Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 - [IPO5_HUMAN]	0,94	1,02	1,08	1,01
Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 - [IPO7_HUMAN]	1,01	1,01	0,95	0,99
Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3 - [IPO9_HUMAN]	0,81	0,85	0,78	0,82
Inner nuclear membrane protein Man1 OS=Homo sapiens GN=LEMD3 PE=1 SV=2 - [MAN1_HUMAN]	-	-	0,86	0,86
Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 - [IPYR_HUMAN]	1,22	0,76	1,01	1,00
Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 - [IMDH2_HUMAN]	0,82	0,93	0,98	0,91
Inositol 1,4,5-trisphosphate receptor type 3 OS=Homo sapiens GN=ITPR3 PE=1 SV=2 - [ITPR3_HUMAN]	0,99	-	1,15	1,07
Inositol-3-phosphate synthase 1 OS=Homo sapiens GN=ISYNA1 PE=1 SV=1 - [INO1_HUMAN]	1,25	1,24	1,21	1,23
Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4 - [IDE_HUMAN]	0,79	-	1,16	0,97
Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens GN=IGF2BP1 PE=1 SV=2 - [IF2B1_HUMAN]	1,05	1,12	1,17	1,12
Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2 PE=1 SV=2 - [IF2B2_HUMAN]	2,09	-	-	2,09
Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens GN=IGF2BP3 PE=1 SV=2 - [IF2B3_HUMAN]	1,11	1,51	1,04	1,22
Integrator complex subunit 3 OS=Homo sapiens GN=INTS3 PE=1 SV=1 - [INT3_HUMAN]	-	0,95	0,81	0,88
Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2 - [ITB1_HUMAN]	0,38	0,52	0,41	0,44
Integrin-linked kinase-associated serine/threonine phosphatase 2C OS=Homo sapiens GN=ILKAP PE=1 SV=1 - [ILKAP_HUMAN]	0,50	-	-	0,50
Interferon-induced transmembrane protein 1 OS=Homo sapiens GN=IFITM1 PE=1 SV=3 - [IFM1_HUMAN]	1,12	0,98	1,02	1,04
Interferon-induced, double-stranded RNA-activated protein kinase OS=Homo sapiens GN=EIF2AK2 PE=1 SV=2 - [E2AK2_HUMAN]	0,54	-	2,06	1,30
Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2 - [ILF2_HUMAN]	0,82	1,12	0,94	0,96
Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3 - [ILF3_HUMAN]	1,02	1,04	1,01	1,02
Interleukin-18 OS=Homo sapiens GN=IL18 PE=1 SV=1 - [IL18_HUMAN]	-	-	0,82	0,82
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A PE=1 SV=1 - [IDH3A_HUMAN]	2,02	-	-	2,02
Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 - [IDHC_HUMAN]	1,02	1,24	1,12	1,13
Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 - [SYIC_HUMAN]	0,98	1,06	1,01	1,02
Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=1 SV=2 - [SYIM_HUMAN]	0,95	1,09	1,21	1,08
Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	4,38	-	-	4,38
Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	16,84	-	-	16,84
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	-	68,50	16,64	42,57
KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1 - [KHDR1_HUMAN]	1,18	0,88	1,00	1,02
Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1 - [KTN1_HUMAN]	0,96	0,90	0,82	0,89
Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1 - [KINH_HUMAN]	0,89	1,05	1,23	1,06
Kinesin-like protein KIF13A OS=Homo sapiens GN=KIF13A PE=1 SV=2 - [KI13A_HUMAN]	-	-	1,44	1,44
Kinesin-like protein KIF21B OS=Homo sapiens GN=KIF21B PE=1 SV=2 - [KI21B_HUMAN]	-	0,50	-	0,50
Kinesin-like protein KIF2A OS=Homo sapiens GN=KIF2A PE=1 SV=3 - [KIF2A_HUMAN]	0,60	0,94	0,86	0,80

KN motif and ankyrin repeat domain-containing protein 2 OS=Homo sapiens GN=KANK2 PE=1 SV=1 - [KANK2_HUMAN]	-	0,54	0,57	0,55
Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4 - [LGUL_HUMAN]	1,12	0,84	1,06	1,01
Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 - [LAD1_HUMAN]	-	-	1,45	1,45
Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2 - [LAP2B_HUMAN]	0,89	-	-	0,89
Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2 - [LMNB1_HUMAN]	0,88	0,91	0,88	0,89
Lamin-B2 OS=Homo sapiens GN=LMNB2 PE=1 SV=3 - [LMNB2_HUMAN]	0,98	0,94	1,03	0,98
Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8 - [LAMA5_HUMAN]	0,88	-	0,39	0,63
Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=2 - [LAMB1_HUMAN]	0,96	1,00	0,86	0,94
Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3 - [LAMC1_HUMAN]	0,82	0,76	0,82	0,80
La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2 - [LARP1_HUMAN]	1,15	0,89	1,04	1,02
Large proline-rich protein BAG6 OS=Homo sapiens GN=BAG6 PE=1 SV=2 - [BAG6_HUMAN]	0,99	1,66	1,35	1,33
Lethal(2) giant larvae protein homolog 2 OS=Homo sapiens GN=LLGL2 PE=1 SV=2 - [L2GL2_HUMAN]	-	4,80	-	4,80
LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1 - [LETM1_HUMAN]	1,35	0,88	0,91	1,05
Leucine zipper protein 1 OS=Homo sapiens GN=LUZP1 PE=1 SV=2 - [LUZP1_HUMAN]	-	0,66	-	0,66
Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3 - [LPPRC_HUMAN]	0,92	0,93	0,88	0,91
Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2 - [LRRF1_HUMAN]	1,04	1,07	1,01	1,04
Leucine-rich repeat-containing protein 41 OS=Homo sapiens GN=LRRC41 PE=1 SV=3 - [LRC41_HUMAN]	0,75	-	-	0,75
Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1 - [LRC59_HUMAN]	0,89	0,96	0,98	0,94
Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2 - [SYLC_HUMAN]	1,03	0,96	0,94	0,98
Leucyl-cystinyl aminopeptidase OS=Homo sapiens GN=LNPEP PE=1 SV=3 - [LCAP_HUMAN]	1,19	1,22	1,78	1,40
LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2 - [LASP1_HUMAN]	0,99	1,28	1,02	1,10
Liprin-beta-1 OS=Homo sapiens GN=PPFIBP1 PE=1 SV=2 - [LIPB1_HUMAN]	0,58	0,84	1,06	0,83
LisH domain and HEAT repeat-containing protein KIAA1468 OS=Homo sapiens GN=KIAA1468 PE=1 SV=2 - [K1468_HUMAN]	0,75	1,05	0,82	0,87
L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 - [LDHA_HUMAN]	0,99	1,12	1,06	1,06
L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	1,08	1,03	1,12	1,07
Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2 - [LONM_HUMAN]	0,98	1,10	1,00	1,03
Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 - [ACSL3_HUMAN]	-	1,58	-	1,58
Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2 - [ACSL4_HUMAN]	0,24	-	-	0,24
Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 - [LA_HUMAN]	1,15	1,10	1,07	1,11
Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]	0,86	1,00	0,96	0,94
Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2 - [PPGB_HUMAN]	0,90	0,92	0,90	0,91
Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2 - [SCRB2_HUMAN]	-	1,85	1,49	1,67
Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]	0,89	1,11	0,96	0,99
Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2 - [LAMP2_HUMAN]	0,96	1,24	1,05	1,08
Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4 - [MIF_HUMAN]	0,99	0,97	1,00	0,99
Magnesium transporter protein 1 OS=Homo sapiens GN=MAGT1 PE=1 SV=1 - [MAGT1_HUMAN]	-	1,94	-	1,94
Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	1,21	1,14	1,25	1,20
Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4 - [MDHC_HUMAN]	1,07	1,01	1,03	1,03
Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]	1,18	1,16	1,22	1,19
Mannosyl-oligosaccharide glucosidase OS=Homo sapiens GN=MOGS PE=1 SV=5 - [MOGS_HUMAN]	1,09	-	-	1,09
Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2 - [MATR3_HUMAN]	0,96	0,99	1,02	0,99
Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens GN=MDC1 PE=1 SV=3 - [MDC1_HUMAN]	1,34	1,47	-	1,41
Melanoma inhibitory activity protein 3 OS=Homo sapiens GN=MIA3 PE=1 SV=1 - [MIA3_HUMAN]	9,35	-	-	9,35
Metallothionein-2 OS=Homo sapiens GN=MT2A PE=1 SV=1 - [MT2_HUMAN]	1,82	2,79	-	2,31
Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2 - [SYMC_HUMAN]	1,15	1,08	1,21	1,15
Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 - [MCCB_HUMAN]	-	0,35	-	0,35
Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1 - [MGST3_HUMAN]	0,90	0,85	0,86	0,87

Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2 - [MAP1S_HUMAN]	1,29	-	-	1,29
Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 - [MAP4_HUMAN]	1,13	1,14	1,22	1,16
Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3 - [MARE1_HUMAN]	1,27	1,48	-	1,38
Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1 - [HM13_HUMAN]	1,85	1,29	-	1,57
Misshapen-like kinase 1 OS=Homo sapiens GN=MINK1 PE=1 SV=2 - [MINK1_HUMAN]	-	-	1,55	1,55
Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens GN=SLC25A11 PE=1 SV=3 - [M2OM_HUMAN]	-	3,87	-	3,87
Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens GN=TOMM22 PE=1 SV=3 - [TOM22_HUMAN]	1,30	0,95	1,14	1,13
Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40 PE=1 SV=1 - [TOM40_HUMAN]	0,83	0,84	-	0,83
Mitochondrial import receptor subunit TOM70 OS=Homo sapiens GN=TOMM70A PE=1 SV=1 - [TOM70_HUMAN]	1,55	1,03	1,22	1,27
Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=1 SV=1 - [IMMT_HUMAN]	0,86	0,96	1,04	0,96
Mitochondrial-processing peptidase subunit alpha OS=Homo sapiens GN=PMPCA PE=1 SV=2 - [MPPA_HUMAN]	-	-	0,88	0,88
Mitochondrial-processing peptidase subunit beta OS=Homo sapiens GN=PMPCB PE=1 SV=2 - [MPPB_HUMAN]	0,64	-	-	0,64
Mitogen-activated protein kinase 1 OS=Homo sapiens GN=MAPK1 PE=1 SV=3 - [MK01_HUMAN]	1,03	-	-	1,03
Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1 - [BUB3_HUMAN]	1,10	0,90	1,14	1,05
Mitotic spindle assembly checkpoint protein MAD1 OS=Homo sapiens GN=MAD1L1 PE=1 SV=2 - [MD1L1_HUMAN]	-	2,57	-	2,57
MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2 - [MMS19_HUMAN]	1,44	1,65	1,40	1,50
Modulator of apoptosis 1 OS=Homo sapiens GN=MOAP1 PE=1 SV=1 - [MOAP1_HUMAN]	-	-	0,82	0,82
Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN]	1,00	0,82	1,13	0,98
Multidrug resistance protein 1 OS=Homo sapiens GN=ABCB1 PE=1 SV=3 - [MDR1_HUMAN]	0,85	0,75	0,87	0,82
Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 - [PUR6_HUMAN]	0,91	0,96	0,93	0,93
Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2 - [MBB1A_HUMAN]	0,93	1,05	1,11	1,03
Myc box-dependent-interacting protein 1 OS=Homo sapiens GN=BIN1 PE=1 SV=1 - [BIN1_HUMAN]	-	1,22	-	1,22
Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1 - [MYOF_HUMAN]	0,97	1,08	1,04	1,03
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 - [MYL6_HUMAN]	1,04	0,86	0,89	0,93
Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 - [MYH10_HUMAN]	1,12	1,10	1,12	1,11
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	1,07	1,07	1,06	1,07
N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3 - [GNS_HUMAN]	1,77	2,06	2,40	2,08
N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=1 SV=2 - [NAT10_HUMAN]	1,25	2,32	1,11	1,56
NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1 - [NQO1_HUMAN]	1,60	1,41	1,52	1,51
NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens GN=ME2 PE=1 SV=1 - [MAOM_HUMAN]	0,88	1,26	0,89	1,01
NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3 - [NB5R3_HUMAN]	1,67	1,04	1,65	1,46
NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	1,12	1,04	0,96	1,04
N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 - [NAA15_HUMAN]	0,76	2,22	2,14	1,71
Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Homo sapiens GN=NACA PE=1 SV=1 - [NACAM_HUMAN]	0,71	0,93	1,01	0,88
Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1 - [NCKP1_HUMAN]	1,31	0,82	0,78	0,97
NEDD8 OS=Homo sapiens GN=NEDD8 PE=1 SV=1 - [NEDD8_HUMAN]	1,98	1,52	-	1,75
Nesprin-1 OS=Homo sapiens GN=SYNE1 PE=1 SV=4 - [SYNE1_HUMAN]	0,81	-	-	0,81
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 - [AHNK_HUMAN]	1,16	1,05	1,26	1,16
Neurolysin, mitochondrial OS=Homo sapiens GN=NLN PE=1 SV=1 - [NEUL_HUMAN]	1,11	-	-	1,11
Neuropathy target esterase OS=Homo sapiens GN=PNPLA6 PE=1 SV=2 - [PLPL6_HUMAN]	3,05	-	-	3,05
Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 - [GANAB_HUMAN]	1,08	1,07	1,08	1,08
Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2 - [AAAT_HUMAN]	0,89	1,08	1,22	1,07
NHP2-like protein 1 OS=Homo sapiens GN=NHP2L1 PE=1 SV=3 - [NH2L1_HUMAN]	0,66	0,67	0,76	0,69
Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 - [NIBL1_HUMAN]	0,93	0,94	0,79	0,88
Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2 - [NICA_HUMAN]	0,88	-	-	0,88
Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1 - [NAMPT_HUMAN]	0,67	1,63	1,05	1,12
Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3 - [NADC_HUMAN]	0,18	1,58	-	0,88

Nodal modulator 1 OS=Homo sapiens GN=NOMO1 PE=1 SV=5 - [NOMO1_HUMAN]	1,23	0,82	0,95	1,00
Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 - [NONO_HUMAN]	0,98	0,91	1,02	0,97
NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C PE=1 SV=2 - [NSF1C_HUMAN]	1,27	1,55	1,66	1,49
N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=3 - [NTM1A_HUMAN]	0,67	-	-	0,67
Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 - [NASP_HUMAN]	0,89	0,94	0,88	0,90
Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1 - [NCBP1_HUMAN]	0,94	-	0,74	0,84
Nuclear export mediator factor NEMF OS=Homo sapiens GN=NEMF PE=1 SV=4 - [NEMF_HUMAN]	-	0,84	-	0,84
Nuclear factor NF-kappa-B p100 subunit OS=Homo sapiens GN=NFKB2 PE=1 SV=4 - [NFKB2_HUMAN]	1,28	0,96	1,35	1,20
Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens GN=NUFIP2 PE=1 SV=1 - [NUFP2_HUMAN]	-	-	0,25	0,25
Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 - [NUDC_HUMAN]	0,84	0,96	0,93	0,91
Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	0,97	0,95	1,13	1,02
Nuclear pore complex protein Nup107 OS=Homo sapiens GN=NUP107 PE=1 SV=1 - [NU107_HUMAN]	-	1,07	0,75	0,91
Nuclear pore complex protein Nup133 OS=Homo sapiens GN=NUP133 PE=1 SV=2 - [NU133_HUMAN]	1,00	1,22	-	1,11
Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=1 SV=2 - [NU153_HUMAN]	0,93	1,41	0,61	0,98
Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1 - [NU155_HUMAN]	0,90	0,75	0,88	0,84
Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=1 SV=3 - [NU160_HUMAN]	0,95	1,07	1,06	1,03
Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=3 - [NU205_HUMAN]	0,84	0,85	0,98	0,89
Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2 - [NU214_HUMAN]	1,36	1,16	-	1,26
Nuclear pore complex protein Nup85 OS=Homo sapiens GN=NUP85 PE=1 SV=1 - [NUP85_HUMAN]	0,31	-	-	0,31
Nuclear pore complex protein Nup88 OS=Homo sapiens GN=NUP88 PE=1 SV=2 - [NUP88_HUMAN]	0,85	1,14	0,97	0,99
Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 - [NUP93_HUMAN]	1,07	0,79	1,06	0,97
Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4 - [NUP98_HUMAN]	1,23	0,95	0,83	1,01
Nuclear protein localization protein 4 homolog OS=Homo sapiens GN=NPLOC4 PE=1 SV=3 - [NPL4_HUMAN]	1,57	-	-	1,57
Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1 - [NTF2_HUMAN]	1,06	0,96	1,19	1,07
Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3 - [YBOX1_HUMAN]	1,63	1,36	1,34	1,44
Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1 PE=1 SV=2 - [NOLC1_HUMAN]	1,21	1,11	1,08	1,13
Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 - [NOC2L_HUMAN]	0,75	0,42	0,76	0,65
Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 - [NOP56_HUMAN]	0,67	0,56	0,79	0,68
Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 - [NOP58_HUMAN]	1,11	0,99	1,05	1,05
Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5 - [DDX21_HUMAN]	0,95	0,91	0,93	0,93
Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF PE=1 SV=1 - [UBF1_HUMAN]	1,48	1,38	1,39	1,42
Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 - [NUCL_HUMAN]	0,90	0,92	0,93	0,92
Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 - [NPM_HUMAN]	1,00	1,18	1,05	1,07
Nucleoporin NUP188 homolog OS=Homo sapiens GN=NUP188 PE=1 SV=1 - [NU188_HUMAN]	0,49	0,74	-	0,62
Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3 - [TPR_HUMAN]	0,66	0,77	0,80	0,74
Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]	0,98	0,86	0,97	0,94
Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]	1,21	2,11	1,36	1,56
Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 - [NP1L1_HUMAN]	1,44	0,94	1,16	1,18
Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1 - [NP1L4_HUMAN]	1,30	1,03	1,11	1,15
Nucleus accumbens-associated protein 1 OS=Homo sapiens GN=NACC1 PE=1 SV=1 - [NACC1_HUMAN]	0,84	1,12	0,96	0,97
NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 - [NUDC1_HUMAN]	0,99	1,13	1,55	1,22
Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 - [OLA1_HUMAN]	-	1,10	-	1,10
Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=3 - [OGFR_HUMAN]	-	1,31	-	1,31
Osteopontin OS=Homo sapiens GN=SPP1 PE=1 SV=1 - [OSTP_HUMAN]	0,64	1,09	-	0,86
Oxysterol-binding protein 1 OS=Homo sapiens GN=OSBP PE=1 SV=1 - [OSBP1_HUMAN]	1,39	1,70	1,38	1,49

Oxysterol-binding protein-related protein 8 OS=Homo sapiens GN=OSBPL8 PE=1 SV=3 - [OSBL8_HUMAN]	0,78	-	-	0,78
PC4 and SFRS1-interacting protein OS=Homo sapiens GN=PSIP1 PE=1 SV=1 - [PSIP1_HUMAN]	1,08	1,25	0,99	1,10
PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4 - [PDLI1_HUMAN]	2,71	-	1,12	1,91
PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5 PE=1 SV=5 - [PDLI5_HUMAN]	0,87	-	-	0,87
PDZ and LIM domain protein 7 OS=Homo sapiens GN=PDLIM7 PE=1 SV=1 - [PDLI7_HUMAN]	1,16	1,45	1,05	1,22
Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]	1,04	0,95	1,00	0,99
Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2 - [PPIB_HUMAN]	0,56	0,76	0,91	0,75
Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Homo sapiens GN=FKBP10 PE=1 SV=1 - [FKB10_HUMAN]	0,94	0,91	0,55	0,80
Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2 - [FKB1A_HUMAN]	0,79	0,78	0,80	0,79
Peptidyl-prolyl cis-trans isomerase FKBP2 OS=Homo sapiens GN=FKBP2 PE=1 SV=2 - [FKBP2_HUMAN]	1,76	-	-	1,76
Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 - [FKBP4_HUMAN]	1,09	1,15	1,10	1,12
Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens GN=FKBP8 PE=1 SV=2 - [FKBP8_HUMAN]	1,76	1,93	-	1,85
Pericentriolar material 1 protein OS=Homo sapiens GN=PCM1 PE=1 SV=4 - [PCM1_HUMAN]	-	0,95	-	0,95
Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	1,73	1,40	2,23	1,79
Periodic tryptophan protein 2 homolog OS=Homo sapiens GN=PWP2 PE=1 SV=2 - [PWP2_HUMAN]	-	1,16	-	1,16
Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	1,04	1,04	1,28	1,12
Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]	1,24	0,95	1,21	1,14
Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]	1,18	0,83	1,00	1,00
Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4 - [PRDX5_HUMAN]	1,36	0,74	2,14	1,41
Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 - [PRDX6_HUMAN]	1,31	1,35	1,20	1,29
Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3 - [DHB4_HUMAN]	0,94	1,07	1,10	1,03
PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 PE=1 SV=1 - [PERQ2_HUMAN]	0,99	-	0,95	0,97
Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 - [PESC_HUMAN]	0,88	-	-	0,88
PHD finger-like domain-containing protein 5A OS=Homo sapiens GN=PHF5A PE=1 SV=1 - [PHF5A_HUMAN]	0,82	0,82	-	0,82
Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3 - [SYFA_HUMAN]	9,01	-	-	9,01
Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 - [SYFB_HUMAN]	2,30	-	-	2,30
Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMAN]	0,82	0,84	0,97	0,88
Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 - [PEBP1_HUMAN]	0,92	1,50	2,01	1,48
Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=1 SV=2 - [PIPNB_HUMAN]	-	1,50	1,72	1,61
Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2 OS=Homo sapiens GN=INPPL1 PE=1 SV=2 - [SHIP2_HUMAN]	2,55	-	-	2,55
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	1,14	1,13	1,01	1,09
Phosphoglucomutase-like protein 5 OS=Homo sapiens GN=PGM5 PE=1 SV=2 - [PGM5_HUMAN]	0,98	1,73	-	1,36
Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]	1,24	1,18	1,31	1,24
Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 - [PGAM1_HUMAN]	1,49	1,20	1,29	1,33
Phosphoribosylformylglycinamidine synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 - [PUR4_HUMAN]	1,07	1,00	1,10	1,06
Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 - [SERC_HUMAN]	0,98	0,93	0,90	0,94
Pinin OS=Homo sapiens GN=PNN PE=1 SV=4 - [PININ_HUMAN]	0,63	-	-	0,63
Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens GN=ATP2B1 PE=1 SV=3 - [AT2B1_HUMAN]	0,88	-	-	0,88
Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4 PE=1 SV=2 - [AT2B4_HUMAN]	1,03	-	-	1,03
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 - [PAIRB_HUMAN]	0,23	-	-	0,23
Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 - [PLST_HUMAN]	0,92	0,98	1,03	0,98
Platelet-activating factor acetylhydrolase IB subunit alpha OS=Homo sapiens GN=PAFAH1B1 PE=1 SV=2 - [LIS1_HUMAN]	-	1,81	1,13	1,47
Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1 - [PA1B3_HUMAN]	1,12	-	-	1,12
Pleckstrin homology-like domain family B member 1 OS=Homo sapiens GN=PHLDB1 PE=1 SV=1 - [PHLB1_HUMAN]	0,99	-	-	0,99
Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - [PLEC_HUMAN]	0,98	0,89	1,05	0,97
Plexin-B2 OS=Homo sapiens GN=PLXNB2 PE=1 SV=3 - [PLXB2_HUMAN]	0,95	-	-	0,95

Podocalyxin OS=Homo sapiens GN=PODXL PE=1 SV=2 - [PODXL_HUMAN]	0,88	0,91	-	0,89
Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN]	1,08	1,07	1,09	1,08
Poly [ADP-ribose] polymerase 4 OS=Homo sapiens GN=PARP4 PE=1 SV=3 - [PARP4_HUMAN]	0,94	-	-	0,94
Poly(A) polymerase gamma OS=Homo sapiens GN=PAPOLG PE=1 SV=2 - [PAPOG_HUMAN]	0,98	-	-	0,98
Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	0,92	1,22	0,94	1,03
Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 - [PCBP2_HUMAN]	1,11	-	0,84	0,97
Poly(rC)-binding protein 3 OS=Homo sapiens GN=PCBP3 PE=2 SV=2 - [PCBP3_HUMAN]	0,84	-	-	0,84
Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2 - [PABP1_HUMAN]	0,73	0,67	0,72	0,71
Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1 - [PABP4_HUMAN]	0,88	0,59	0,86	0,78
Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 - [PTBP1_HUMAN]	1,11	0,96	1,10	1,06
Prefoldin subunit 3 OS=Homo sapiens GN=VBP1 PE=1 SV=3 - [PFD3_HUMAN]	1,05	-	-	1,05
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 - [LMNA_HUMAN]	0,95	0,95	0,97	0,96
pre-mRNA 3' end processing protein WDR33 OS=Homo sapiens GN=WDR33 PE=1 SV=2 - [WDR33_HUMAN]	0,83	0,66	1,23	0,91
Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1 - [PRP19_HUMAN]	1,22	1,24	0,90	1,12
Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2 - [PR40A_HUMAN]	-	-	0,75	0,75
Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1 - [PRP6_HUMAN]	1,24	1,01	0,96	1,07
Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN]	0,91	1,08	0,96	0,99
pre-rRNA processing protein FTSJ3 OS=Homo sapiens GN=FTSJ3 PE=1 SV=2 - [SPB1_HUMAN]	0,93	1,07	0,87	0,96
Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=1 - [TSR1_HUMAN]	1,16	-	-	1,16
Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1 PE=1 SV=3 - [PREP_HUMAN]	1,38	1,22	-	1,30
PRKC apoptosis WT1 regulator protein OS=Homo sapiens GN=PAWR PE=1 SV=1 - [PAWR_HUMAN]	1,02	-	0,86	0,94
Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 - [DDX17_HUMAN]	1,04	1,11	1,09	1,08
Probable ATP-dependent RNA helicase DDX23 OS=Homo sapiens GN=DDX23 PE=1 SV=3 - [DDX23_HUMAN]	-	0,63	-	0,63
Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=2 - [DDX46_HUMAN]	0,78	-	-	0,78
Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	0,38	0,54	0,52	0,48
Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2 - [DDX6_HUMAN]	1,58	1,37	1,43	1,46
Probable ATP-dependent RNA helicase DHX36 OS=Homo sapiens GN=DHX36 PE=1 SV=2 - [DHX36_HUMAN]	0,68	0,49	0,61	0,59
Probable cation-transporting ATPase 13A1 OS=Homo sapiens GN=ATP13A1 PE=1 SV=2 - [AT131_HUMAN]	-	1,10	-	1,10
Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3 - [USP9X_HUMAN]	0,76	-	0,85	0,81
Probable ubiquitin carboxyl-terminal hydrolase FAF-Y OS=Homo sapiens GN=USP9Y PE=1 SV=2 - [USP9Y_HUMAN]	-	0,73	-	0,73
Procollagen galactosyltransferase 1 OS=Homo sapiens GN=COLGALT1 PE=1 SV=1 - [GT251_HUMAN]	1,19	1,27	1,19	1,22
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2 - [PLOD1_HUMAN]	0,84	0,79	0,76	0,80
Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2 - [PROF1_HUMAN]	1,02	1,00	1,03	1,02
Profilin-2 OS=Homo sapiens GN=PFN2 PE=1 SV=3 - [PROF2_HUMAN]	-	0,84	1,00	0,92
Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1 - [PDC6I_HUMAN]	0,88	1,00	0,91	0,93
Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1 - [PHB_HUMAN]	1,14	1,14	1,03	1,10
Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2 - [PHB2_HUMAN]	0,87	0,93	1,00	0,93
Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 - [PCNA_HUMAN]	0,95	0,88	0,93	0,92
Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3 - [PA2G4_HUMAN]	0,87	0,89	0,87	0,88
Proline dehydrogenase 1, mitochondrial OS=Homo sapiens GN=PRODH PE=1 SV=3 - [PROD_HUMAN]	0,80	0,92	0,79	0,84
Prolyl 3-hydroxylase 1 OS=Homo sapiens GN=LEPRE1 PE=1 SV=2 - [P3H1_HUMAN]	0,78	0,99	-	0,88
Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens GN=P4HA1 PE=1 SV=2 - [P4HA1_HUMAN]	0,77	0,63	0,93	0,78
Prosaposin OS=Homo sapiens GN=PSAP PE=1 SV=2 - [SAP_HUMAN]	1,69	-	-	1,69
Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 - [TEBP_HUMAN]	0,93	0,64	0,73	0,77
Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	-	-	0,79	0,79

Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2 - [ADRM1_HUMAN]	-	0,85	-	0,85
Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1 - [PSME1_HUMAN]	1,04	1,35	0,97	1,12
Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 - [PSME2_HUMAN]	0,91	0,69	0,86	0,82
Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 - [PSA1_HUMAN]	0,84	0,76	0,97	0,86
Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2 - [PSA2_HUMAN]	1,46	1,64	1,77	1,62
Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2 - [PSA3_HUMAN]	1,09	0,99	0,83	0,97
Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 - [PSA4_HUMAN]	1,29	1,39	0,79	1,16
Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3 - [PSA5_HUMAN]	0,96	1,12	0,98	1,02
Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1 - [PSA6_HUMAN]	0,83	0,75	0,83	0,80
Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1 - [PSA7_HUMAN]	0,98	1,16	1,03	1,06
Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2 - [PSB1_HUMAN]	0,98	0,74	0,52	0,75
Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1 - [PSB2_HUMAN]	0,96	1,09	0,96	1,01
Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2 - [PSB3_HUMAN]	-	0,82	0,96	0,89
Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4 - [PSB4_HUMAN]	1,26	1,60	1,47	1,44
Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 - [PSB5_HUMAN]	1,04	0,79	0,83	0,89
Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4 - [PSB6_HUMAN]	1,08	1,18	1,12	1,12
Proteasome subunit beta type-7 OS=Homo sapiens GN=PSMB7 PE=1 SV=1 - [PSB7_HUMAN]	0,77	0,94	0,80	0,83
Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN]	1,02	1,28	1,38	1,23
Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2 - [ANM1_HUMAN]	0,76	-	2,08	1,42
Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4 - [ANM5_HUMAN]	1,38	1,47	-	1,43
Protein canopy homolog 2 OS=Homo sapiens GN=CNPY2 PE=1 SV=1 - [CNPY2_HUMAN]	0,78	0,78	-	0,78
Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1 - [DEK_HUMAN]	1,20	0,72	0,69	0,87
Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 - [DIAP1_HUMAN]	0,95	1,03	1,33	1,10
Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 - [PDIA3_HUMAN]	1,12	1,08	1,14	1,11
Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 - [PDIA4_HUMAN]	0,95	0,98	0,94	0,96
Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 - [PDIA6_HUMAN]	1,09	1,01	1,07	1,06
Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3 - [PDIA1_HUMAN]	0,99	0,97	0,95	0,97
Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 - [PARK7_HUMAN]	0,92	1,01	1,51	1,15
Protein enabled homolog OS=Homo sapiens GN=ENAH PE=1 SV=2 - [ENAH_HUMAN]	0,61	-	-	0,61
Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2 - [FLII_HUMAN]	0,92	1,04	1,48	1,15
Protein HEXIM1 OS=Homo sapiens GN=HEXIM1 PE=1 SV=1 - [HEXI1_HUMAN]	0,71	0,95	-	0,83
Protein Hook homolog 1 OS=Homo sapiens GN=HOOK1 PE=1 SV=2 - [HOOK1_HUMAN]	0,52	-	-	0,52
Protein KIAA0664 OS=Homo sapiens GN=KIAA0664 PE=1 SV=2 - [K0664_HUMAN]	1,13	-	-	1,13
Protein kinase C and casein kinase substrate in neurons protein 2 OS=Homo sapiens GN=PACSIN2 PE=1 SV=2 - [PACN2_HUMAN]	1,67	0,86	1,10	1,21
Protein KRI1 homolog OS=Homo sapiens GN=KRI1 PE=1 SV=3 - [KRI1_HUMAN]	-	0,90	0,79	0,85
Protein LYRIC OS=Homo sapiens GN=MTDH PE=1 SV=2 - [LYRIC_HUMAN]	0,60	0,86	0,83	0,76
Protein MAL2 OS=Homo sapiens GN=MAL2 PE=1 SV=1 - [MAL2_HUMAN]	-	1,93	-	1,93
Protein Niban OS=Homo sapiens GN=FAM129A PE=1 SV=1 - [NIBAN_HUMAN]	0,79	0,90	1,11	0,93
Protein PAT1 homolog 1 OS=Homo sapiens GN=PATL1 PE=1 SV=2 - [PATL1_HUMAN]	-	1,25	1,09	1,17
Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens GN=PPP1R12A PE=1 SV=1 - [MYPT1_HUMAN]	0,81	1,01	0,91	0,91
Protein phosphatase 1G OS=Homo sapiens GN=PPM1G PE=1 SV=1 - [PPM1G_HUMAN]	0,80	1,05	0,86	0,90
Protein PRRC2C OS=Homo sapiens GN=PRRC2C PE=1 SV=4 - [PRC2C_HUMAN]	-	-	1,37	1,37
Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN]	0,71	0,67	0,73	0,70
Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3 - [RRP5_HUMAN]	0,89	0,87	0,96	0,91
Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 - [S10AB_HUMAN]	0,94	0,87	0,88	0,90
Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1 - [S10A4_HUMAN]	1,16	1,06	1,03	1,09
Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]	1,03	-	-	1,03
Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4 - [SCRIB_HUMAN]	1,66	0,65	-	1,15

Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 - [SET_HUMAN]	1,13	1,02	1,09	1,08
Protein TBRG4 OS=Homo sapiens GN=TBRG4 PE=1 SV=1 - [TBRG4_HUMAN]	1,71	-	-	1,71
Protein TFG OS=Homo sapiens GN=TFG PE=1 SV=2 - [TFG_HUMAN]	1,06	0,85	0,94	0,95
Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=3 - [SC16A_HUMAN]	0,74	1,34	1,59	1,22
Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2 - [SC23A_HUMAN]	1,23	-	1,37	1,30
Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2 - [SC23B_HUMAN]	1,20	1,38	1,48	1,35
Protein transport protein Sec24A OS=Homo sapiens GN=SEC24A PE=1 SV=2 - [SC24A_HUMAN]	0,71	-	1,68	1,19
Protein transport protein Sec24B OS=Homo sapiens GN=SEC24B PE=1 SV=2 - [SC24B_HUMAN]	1,51	-	-	1,51
Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=3 - [SC24C_HUMAN]	1,69	1,49	1,62	1,60
Protein transport protein Sec24D OS=Homo sapiens GN=SEC24D PE=1 SV=2 - [SC24D_HUMAN]	0,94	0,85	1,04	0,94
Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=1 SV=2 - [S61A1_HUMAN]	0,43	-	-	0,43
Protein transport protein Sec61 subunit beta OS=Homo sapiens GN=SEC61B PE=1 SV=2 - [SC61B_HUMAN]	0,65	-	0,62	0,64
Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1 - [UN45A_HUMAN]	0,78	0,90	1,03	0,90
Protein YIPF5 OS=Homo sapiens GN=YIPF5 PE=1 SV=1 - [YIPF5_HUMAN]	1,06	-	-	1,06
Prothymosin alpha OS=Homo sapiens GN=PTMA PE=1 SV=2 - [PTMA_HUMAN]	1,32	-	-	1,32
Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2 - [PNPH_HUMAN]	0,87	0,88	-	0,88
Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	1,03	1,09	1,12	1,08
Putative adenosylhomocysteinase 2 OS=Homo sapiens GN=AHCYL1 PE=1 SV=2 - [SAHH2_HUMAN]	-	2,49	1,21	1,85
Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=1 SV=1 - [DHX30_HUMAN]	1,15	1,53	0,89	1,19
Putative coiled-coil-helix-coiled-coil-helix domain-containing protein CHCHD2P9, mitochondrial OS=Homo sapiens GN=CHCHD2P9 PE=5 SV=1 - [CHCH9_HUMAN]	1,31	-	-	1,31
Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens GN=HSP90AB4P PE=5 SV=1 - [H90B4_HUMAN]	0,99	0,99	0,82	0,94
Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1 - [H90B3_HUMAN]	-	1,99	-	1,99
Putative helicase MOV-10 OS=Homo sapiens GN=MOV10 PE=1 SV=2 - [MOV10_HUMAN]	1,35	1,19	1,33	1,29
Putative hexokinase HKDC1 OS=Homo sapiens GN=HKDC1 PE=1 SV=3 - [HKDC1_HUMAN]	0,82	0,78	0,78	0,79
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2 - [DHX15_HUMAN]	0,69	0,85	0,75	0,77
Putative ribosomal RNA methyltransferase NOP2 OS=Homo sapiens GN=NOP2 PE=1 SV=2 - [NOP2_HUMAN]	0,95	1,07	0,95	0,99
Putative RNA-binding protein 15 OS=Homo sapiens GN=RBM15 PE=1 SV=2 - [RBM15_HUMAN]	2,53	-	-	2,53
Pyridoxal kinase OS=Homo sapiens GN=PDXK PE=1 SV=1 - [PDXK_HUMAN]	-	2,00	5,47	3,74
Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=1 SV=2 - [PDXD1_HUMAN]	1,66	-	-	1,66
Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 - [P5CR1_HUMAN]	0,95	0,97	0,84	0,92
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3 - [ODPA_HUMAN]	0,78	0,82	0,56	0,72
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3 - [ODPB_HUMAN]	-	1,20	1,29	1,24
Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 - [PDPR_HUMAN]	1,48	-	-	1,48
Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	1,09	1,10	1,11	1,10
Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1 - [QOR_HUMAN]	1,50	1,31	1,39	1,40
Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 - [GDIA_HUMAN]	1,05	1,27	1,21	1,18
Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 - [GDIB_HUMAN]	1,07	1,13	1,24	1,15
Rab GTPase-activating protein 1 OS=Homo sapiens GN=RABGAP1 PE=1 SV=3 - [RBGP1_HUMAN]	3,44	2,80	1,47	2,57
Rab11 family-interacting protein 1 OS=Homo sapiens GN=RAB11FIP1 PE=1 SV=3 - [RFIP1_HUMAN]	-	0,71	-	0,71
Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1 - [RAGP1_HUMAN]	0,72	-	0,49	0,60
Ran-binding protein 10 OS=Homo sapiens GN=RANBP10 PE=1 SV=1 - [RBP10_HUMAN]	-	-	0,76	0,76
Ran-binding protein 3 OS=Homo sapiens GN=RANBP3 PE=1 SV=1 - [RANB3_HUMAN]	0,97	0,86	1,00	0,94
Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 - [RANG_HUMAN]	0,85	1,02	1,74	1,21
Rap1 GTPase-GDP dissociation stimulator 1 OS=Homo sapiens GN=RAP1GDS1 PE=1 SV=3 - [GDS1_HUMAN]	-	0,40	0,37	0,39
Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1 - [G3BP1_HUMAN]	0,87	0,75	0,54	0,72

Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	0,97	0,98	0,97	0,97
Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1 - [RAC2_HUMAN]	-	0,77	0,91	0,84
Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1 - [RAB10_HUMAN]	0,63	0,47	0,69	0,60
Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4 - [RB11B_HUMAN]	1,14	1,04	1,13	1,10
Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 - [RAB14_HUMAN]	1,25	1,01	0,78	1,01
Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3 - [RAB1A_HUMAN]	-	1,69	1,69	1,69
Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1 - [RAB2A_HUMAN]	-	1,66	0,49	1,07
Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2 - [RAB5C_HUMAN]	1,15	1,23	1,07	1,15
Ras-related protein Rap-1b-like protein OS=Homo sapiens PE=2 SV=1 - [RP1BL_HUMAN]	1,13	0,78	0,82	0,91
Ras-related protein R-Ras2 OS=Homo sapiens GN=RRAS2 PE=1 SV=1 - [RRAS2_HUMAN]	1,05	-	-	1,05
Regulator of chromosome condensation OS=Homo sapiens GN=RCC1 PE=1 SV=1 - [RCC1_HUMAN]	1,16	0,88	0,87	0,97
Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2 - [RENT1_HUMAN]	1,02	0,78	0,85	0,89
Replication factor C subunit 1 OS=Homo sapiens GN=RFC1 PE=1 SV=4 - [RFC1_HUMAN]	0,62	0,74	-	0,68
Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 PE=1 SV=1 - [RFA2_HUMAN]	1,57	-	-	1,57
Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens GN=RPA1 PE=1 SV=2 - [RFA1_HUMAN]	1,35	1,41	0,40	1,05
Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1 - [RCN1_HUMAN]	1,04	1,07	1,05	1,05
Reticulon-3 OS=Homo sapiens GN=RTN3 PE=1 SV=2 - [RTN3_HUMAN]	0,94	-	-	0,94
Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2 - [RTN4_HUMAN]	2,36	0,98	1,47	1,61
Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2 - [AL1A1_HUMAN]	1,10	1,13	1,17	1,13
Retrotransposon-derived protein PEG10 OS=Homo sapiens GN=PEG10 PE=1 SV=2 - [PEG10_HUMAN]	-	0,61	-	0,61
Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3 - [GDIR1_HUMAN]	1,22	-	2,24	1,73
Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1 - [RHG01_HUMAN]	1,11	1,14	1,05	1,10
Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=1 SV=4 - [ARHG2_HUMAN]	0,81	0,98	0,94	0,91
Rho-associated protein kinase 2 OS=Homo sapiens GN=ROCK2 PE=1 SV=4 - [ROCK2_HUMAN]	-	0,52	-	0,52
Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1 - [RHOC_HUMAN]	0,93	0,94	1,05	0,97
Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 - [RINI_HUMAN]	0,91	1,10	1,17	1,06
Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2 - [POP1_HUMAN]	1,18	-	0,86	1,02
Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1 - [RIR1_HUMAN]	1,67	-	0,58	1,13
Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2 PE=1 SV=2 - [PRPS2_HUMAN]	2,92	-	-	2,92
Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RSL1D1 PE=1 SV=3 - [RL1D1_HUMAN]	-	-	0,92	0,92
Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=1 SV=2 - [BOP1_HUMAN]	0,98	-	0,75	0,86
Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4 - [RRBP1_HUMAN]	0,91	0,91	0,95	0,92
RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3 - [RBMX_HUMAN]	0,77	0,71	0,84	0,77
RNA-binding protein 10 OS=Homo sapiens GN=RBM10 PE=1 SV=3 - [RBM10_HUMAN]	0,74	-	-	0,74
RNA-binding protein 12 OS=Homo sapiens GN=RBM12 PE=1 SV=1 - [RBM12_HUMAN]	1,94	1,35	0,98	1,42
RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2 - [RBM14_HUMAN]	1,17	1,17	0,93	1,09
RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3 - [RBM25_HUMAN]	0,85	-	1,22	1,03
RNA-binding protein 26 OS=Homo sapiens GN=RBM26 PE=1 SV=3 - [RBM26_HUMAN]	1,34	-	-	1,34
RNA-binding protein 28 OS=Homo sapiens GN=RBM28 PE=1 SV=3 - [RBM28_HUMAN]	1,31	2,57	-	1,94
RNA-binding protein 8A OS=Homo sapiens GN=RBM8A PE=1 SV=1 - [RBM8A_HUMAN]	0,47	-	-	0,47
RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1 - [EWS_HUMAN]	1,13	1,13	1,15	1,14
RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1 - [FUS_HUMAN]	1,30	1,17	1,34	1,27
RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 SV=1 - [RALY_HUMAN]	1,11	-	-	1,11
rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2 - [FBRL_HUMAN]	1,02	0,87	0,67	0,85
RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 - [RRP12_HUMAN]	1,00	1,46	1,49	1,32
RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	0,79	0,86	0,81	0,82
RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3 - [RUVB2_HUMAN]	-	1,01	0,67	0,84
SAFB-like transcription modulator OS=Homo sapiens GN=SLTM PE=1 SV=2 - [SLTM_HUMAN]	0,58	-	0,86	0,72
SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SARNP PE=1 SV=3 - [SARNP_HUMAN]	1,23	1,33	1,47	1,34

Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1 - [AT2A2_HUMAN]	0,91	0,96	1,00	0,96
Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB PE=1 SV=4 - [SAFB1_HUMAN]	0,71	1,21	0,93	0,95
Secernin-1 OS=Homo sapiens GN=SCRN1 PE=1 SV=2 - [SCRN1_HUMAN]	1,38	1,74	1,29	1,47
Sepiapterin reductase OS=Homo sapiens GN=SPR PE=1 SV=1 - [SPRE_HUMAN]	2,41	-	-	2,41
Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3 - [SEP11_HUMAN]	0,43	-	-	0,43
Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 - [SEPT2_HUMAN]	0,93	0,81	1,39	1,04
Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 - [SEPT7_HUMAN]	0,80	-	0,40	0,60
Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 - [SEPT9_HUMAN]	8,00	-	-	8,00
Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 - [SQSTM_HUMAN]	0,65	0,93	-	0,79
Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 - [GLYM_HUMAN]	0,87	1,17	1,04	1,03
Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 PE=1 SV=1 - [SPTC1_HUMAN]	-	0,72	-	0,72
Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2 - [SRSF1_HUMAN]	0,88	0,83	0,81	0,84
Serine/arginine-rich splicing factor 10 OS=Homo sapiens GN=SRSF10 PE=1 SV=1 - [SRS10_HUMAN]	1,15	0,38	-	0,76
Serine/arginine-rich splicing factor 2 OS=Homo sapiens GN=SRSF2 PE=1 SV=4 - [SRSF2_HUMAN]	1,41	1,01	1,02	1,15
Serine/arginine-rich splicing factor 3 OS=Homo sapiens GN=SRSF3 PE=1 SV=1 - [SRSF3_HUMAN]	0,92	1,45	0,95	1,11
Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2 - [SRSF6_HUMAN]	0,76	0,75	0,85	0,79
Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=1 SV=1 - [SRSF7_HUMAN]	0,94	-	1,04	0,99
Serine/threonine-protein kinase MRCK beta OS=Homo sapiens GN=CDC42BPB PE=1 SV=2 - [MRCKB_HUMAN]	0,88	1,00	-	0,94
Serine/threonine-protein kinase N2 OS=Homo sapiens GN=PKN2 PE=1 SV=1 - [PKN2_HUMAN]	-	0,76	0,50	0,63
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A PE=1 SV=1 - [2ABA_HUMAN]	1,98	1,63	0,73	1,45
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 - [2AAA_HUMAN]	1,02	1,05	1,12	1,06
Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1 - [PP2AB_HUMAN]	1,40	1,49	2,02	1,64
Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens GN=PPP6R3 PE=1 SV=2 - [PP6R3_HUMAN]	0,72	0,81	0,76	0,76
Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 - [PP1B_HUMAN]	-	-	5,06	5,06
Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 - [STRAP_HUMAN]	1,97	1,36	-	1,66
Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 - [SYSC_HUMAN]	1,11	1,00	0,99	1,03
Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN]	1,03	1,07	1,04	1,05
Serrate RNA effector molecule homolog OS=Homo sapiens GN=SRRT PE=1 SV=1 - [SRRT_HUMAN]	0,97	1,19	1,11	1,09
S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 - [ESTD_HUMAN]	-	2,00	1,86	1,93
SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1 - [SH3L3_HUMAN]	0,55	-	-	0,55
Shootin-1 OS=Homo sapiens GN=KIAA1598 PE=1 SV=4 - [SHOT1_HUMAN]	1,21	0,95	1,05	1,07
Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	-	1,62	4,04	2,83
Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2 - [SRP14_HUMAN]	0,85	1,00	0,90	0,92
Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1 - [SRP54_HUMAN]	0,23	-	-	0,23
Signal recognition particle subunit SRP68 OS=Homo sapiens GN=SRP68 PE=1 SV=2 - [SRP68_HUMAN]	0,89	1,00	0,79	0,89
Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72 PE=1 SV=3 - [SRP72_HUMAN]	0,85	1,01	1,07	0,98
Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2 - [STAT1_HUMAN]	0,85	0,79	0,97	0,87
Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2 - [STAT3_HUMAN]	0,64	1,09	1,14	0,96
Signal-induced proliferation-associated protein 1 OS=Homo sapiens GN=SIPA1 PE=1 SV=1 - [SIPA1_HUMAN]	-	0,41	-	0,41
Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1 - [SSBP_HUMAN]	0,71	1,19	0,98	0,96
Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1 - [PDS5A_HUMAN]	0,99	0,91	0,84	0,91
SLIT-ROBO Rho GTPase-activating protein 2 OS=Homo sapiens GN=SRGAP2 PE=1 SV=2 - [SRGP2_HUMAN]	1,04	0,86	0,82	0,91
Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 - [RUXE_HUMAN]	0,97	0,90	1,07	0,98
Small nuclear ribonucleoprotein F OS=Homo sapiens GN=SNRPF PE=1 SV=1 - [RUXF_HUMAN]	1,42	1,18	1,13	1,24

Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1 - [SMD1_HUMAN]	-	3,96	1,46	2,71
Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1 - [SMD2_HUMAN]	0,52	0,68	-	0,60
Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1 - [SMD3_HUMAN]	1,01	0,77	1,05	0,94
Small nuclear ribonucleoprotein-associated proteins B and B' OS=Homo sapiens GN=SNRPB PE=1 SV=2 - [RSMB_HUMAN]	-	-	0,73	0,73
Small ubiquitin-related modifier 1 OS=Homo sapiens GN=SUMO1 PE=1 SV=1 - [SUMO1_HUMAN]	0,64	0,60	0,65	0,63
Small ubiquitin-related modifier 2 OS=Homo sapiens GN=SUMO2 PE=1 SV=3 - [SUMO2_HUMAN]	0,81	0,85	0,84	0,83
S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens GN=MTAP PE=1 SV=2 - [MTAP_HUMAN]	1,34	-	-	1,34
Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1 - [AT1A1_HUMAN]	1,21	1,00	1,14	1,12
Sodium-coupled neutral amino acid transporter 1 OS=Homo sapiens GN=SLC38A1 PE=1 SV=1 - [S38A1_HUMAN]	0,74	1,22	-	0,98
Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens GN=SLC38A2 PE=1 SV=2 - [S38A2_HUMAN]	1,59	-	-	1,59
Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1 - [SORCN_HUMAN]	0,83	0,86	1,04	0,91
Sorting nexin-2 OS=Homo sapiens GN=SNX2 PE=1 SV=2 - [SNX2_HUMAN]	0,89	0,96	1,04	0,96
Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3 - [SPTN1_HUMAN]	1,05	1,08	1,01	1,05
Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2 - [SPTB2_HUMAN]	0,91	0,80	0,96	0,89
Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=1 SV=1 - [DX39B_HUMAN]	0,93	1,08	1,73	1,25
Splicing factor 1 OS=Homo sapiens GN=SF1 PE=1 SV=4 - [SF01_HUMAN]	1,24	-	1,79	1,51
Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1 - [SF3A1_HUMAN]	0,94	0,89	0,90	0,91
Splicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=1 SV=1 - [SF3A3_HUMAN]	-	1,08	1,19	1,13
Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN]	0,89	1,08	1,11	1,03
Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2 - [SF3B2_HUMAN]	1,14	1,06	1,02	1,07
Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMAN]	1,00	0,89	1,07	0,99
Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3 - [U2AF1_HUMAN]	0,83	0,80	0,83	0,82
Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4 - [U2AF2_HUMAN]	1,45	-	1,44	1,44
Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2 - [SFPQ_HUMAN]	1,04	1,11	0,99	1,05
Squamous cell carcinoma antigen recognized by T-cells 3 OS=Homo sapiens GN=SART3 PE=1 SV=1 - [SART3_HUMAN]	1,27	1,39	1,18	1,28
Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	0,91	0,87	0,96	0,91
SRSF protein kinase 3 OS=Homo sapiens GN=SRPK3 PE=1 SV=2 - [SRPK3_HUMAN]	-	-	0,72	0,72
Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1 - [SND1_HUMAN]	1,13	1,02	1,04	1,06
Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3 - [STMN1_HUMAN]	1,15	0,94	1,12	1,07
STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1 - [SLK_HUMAN]	-	0,75	-	0,75
Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 - [STML2_HUMAN]	1,35	1,66	1,36	1,46
Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 - [GRP75_HUMAN]	0,97	0,98	0,92	0,96
Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 - [STIP1_HUMAN]	0,95	0,98	0,96	0,96
Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2 - [SMC1A_HUMAN]	0,80	0,83	0,75	0,80
Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2 - [SMC2_HUMAN]	0,71	1,54	1,35	1,20
Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2 - [SMC3_HUMAN]	2,35	0,99	0,91	1,42
Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 PE=1 SV=2 - [SMC4_HUMAN]	0,61	0,77	0,78	0,72
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2 - [SDHA_HUMAN]	1,11	1,38	1,47	1,32
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLA2 PE=1 SV=3 - [SUCB1_HUMAN]	-	1,43	-	1,43
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2 - [SUCB2_HUMAN]	-	0,53	-	0,53
Sulfatase-modifying factor 2 OS=Homo sapiens GN=SUMF2 PE=1 SV=2 - [SUMF2_HUMAN]	1,04	1,10	1,06	1,07
SUMO-activating enzyme subunit 1 OS=Homo sapiens GN=SAE1 PE=1 SV=1 - [SAE1_HUMAN]	2,50	-	-	2,50
SUMO-activating enzyme subunit 2 OS=Homo sapiens GN=UBA2 PE=1 SV=2 - [SAE2_HUMAN]	-	0,70	0,81	0,76
SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1 - [UBC9_HUMAN]	-	-	1,27	1,27

SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 PE=1 SV=3 - [SUN1_HUMAN]	2,49	1,65	1,17	1,77
Superkiller viralicidic activity 2-like 2 OS=Homo sapiens GN=SKIV2L2 PE=1 SV=3 - [SK2L2_HUMAN]	2,32	0,73	1,01	1,35
Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2 - [SODC_HUMAN]	1,09	0,98	1,16	1,08
Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2 - [SODM_HUMAN]	1,38	1,19	1,42	1,33
Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 PE=1 SV=3 - [SURF4_HUMAN]	0,99	0,98	1,12	1,03
SURP and G-patch domain-containing protein 2 OS=Homo sapiens GN=SUGP2 PE=1 SV=2 - [SUGP2_HUMAN]	0,76	-	-	0,76
SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1 - [SMRC2_HUMAN]	0,71	1,01	-	0,86
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1 - [SMCA5_HUMAN]	0,84	0,75	0,75	0,78
Symplekin OS=Homo sapiens GN=SYMPK PE=1 SV=2 - [SYMPK_HUMAN]	1,26	1,95	0,76	1,33
Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2 - [VAT1_HUMAN]	1,07	1,02	1,35	1,15
Syntaxin-7 OS=Homo sapiens GN=STX7 PE=1 SV=4 - [STX7_HUMAN]	-	-	1,04	1,04
Syntaxin-binding protein 2 OS=Homo sapiens GN=STXBP2 PE=1 SV=2 - [STXB2_HUMAN]	1,02	1,04	-	1,03
Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 - [TLN1_HUMAN]	1,20	1,12	1,19	1,17
Talin-2 OS=Homo sapiens GN=TLN2 PE=1 SV=4 - [TLN2_HUMAN]	0,94	1,61	0,82	1,13
TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 - [TADBP_HUMAN]	1,01	1,07	0,98	1,02
TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15 PE=1 SV=1 - [RBP56_HUMAN]	1,02	0,93	1,03	0,99
T-box brain protein 1 OS=Homo sapiens GN=TBR1 PE=1 SV=1 - [TBR1_HUMAN]	1,00	0,74	0,78	0,84
T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 - [TCPA_HUMAN]	0,99	1,01	0,96	0,99
T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 - [TCPB_HUMAN]	0,88	0,89	0,94	0,90
T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 - [TCPD_HUMAN]	0,97	0,93	0,91	0,93
T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 - [TCPE_HUMAN]	0,89	1,11	1,00	1,00
T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 - [TCPH_HUMAN]	0,99	0,91	1,01	0,97
T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 - [TCPG_HUMAN]	0,94	1,00	0,92	0,95
T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 - [TCPQ_HUMAN]	0,95	0,95	0,90	0,94
T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3 - [TCPZ_HUMAN]	1,02	1,02	0,95	1,00
Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 - [TENS3_HUMAN]	0,70	0,87	1,29	0,95
Testin OS=Homo sapiens GN=TES PE=1 SV=1 - [TES_HUMAN]	1,36	1,50	1,06	1,31
Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 - [TXD17_HUMAN]	-	-	0,88	0,88
Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2 - [TXND5_HUMAN]	1,03	1,03	1,41	1,16
Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 - [THIO_HUMAN]	0,89	0,89	0,97	0,92
Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=3 - [TRXR1_HUMAN]	1,08	1,37	0,99	1,15
Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 - [PRDX3_HUMAN]	1,17	0,91	1,34	1,14
Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3 - [TXNL1_HUMAN]	19,30	-	1,04	10,17
THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=1 SV=3 - [THOC4_HUMAN]	0,67	-	-	0,67
Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3 - [SYTC_HUMAN]	1,15	0,96	0,94	1,01
Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2 - [TR150_HUMAN]	1,00	1,04	1,10	1,05
Tight junction protein ZO-1 OS=Homo sapiens GN=TJP1 PE=1 SV=3 - [ZO1_HUMAN]	-	2,52	1,46	1,99
Torsin-1A-interacting protein 1 OS=Homo sapiens GN=TOR1AIP1 PE=1 SV=2 - [TOIP1_HUMAN]	1,53	1,42	1,39	1,45
Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	0,91	0,96	0,93	0,93
Transcription elongation factor A protein 1 OS=Homo sapiens GN=TCEA1 PE=1 SV=2 - [TCEA1_HUMAN]	0,86	1,01	0,91	0,93
Transcription elongation factor SPT5 OS=Homo sapiens GN=SUPT5H PE=1 SV=1 - [SPT5H_HUMAN]	1,09	0,93	0,86	0,96
Transcription intermediary factor 1-alpha OS=Homo sapiens GN=TRIM24 PE=1 SV=3 - [TIF1A_HUMAN]	0,66	-	-	0,66
Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	0,87	0,82	1,04	0,91
Transcriptional repressor p66-alpha OS=Homo sapiens GN=GATAD2A PE=1 SV=1 - [P66A_HUMAN]	-	1,65	1,58	1,61
Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=1 SV=1 - [TBL2_HUMAN]	1,18	-	0,65	0,92
Transducin beta-like protein 3 OS=Homo sapiens GN=TBL3 PE=1 SV=2 - [TBL3_HUMAN]	0,62	0,72	0,48	0,60
Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2 - [TFR1_HUMAN]	0,82	0,76	0,84	0,81

Transformer-2 protein homolog alpha OS=Homo sapiens GN=TRA2A PE=1 SV=1 - [TRA2A_HUMAN]	-	-	0,56	0,56
Transformer-2 protein homolog beta OS=Homo sapiens GN=TRA2B PE=1 SV=1 - [TRA2B_HUMAN]	0,67	-	-	0,67
Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 - [RHOA_HUMAN]	0,71	0,35	0,86	0,64
Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 - [TAGL2_HUMAN]	1,07	1,02	1,18	1,09
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN]	1,14	1,20	1,10	1,15
Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 - [TKT_HUMAN]	1,16	1,11	1,18	1,15
Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6 - [GCN1L_HUMAN]	1,08	1,12	1,11	1,10
Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1 - [TCTP_HUMAN]	-	0,70	0,69	0,69
Translocator protein OS=Homo sapiens GN=TSPO PE=1 SV=3 - [TSPOA_HUMAN]	1,59	1,49	-	1,54
Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=1 SV=3 - [SSRA_HUMAN]	-	-	1,58	1,58
Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1 - [SSRD_HUMAN]	0,64	1,46	0,47	0,86
Transmembrane 9 superfamily member 4 OS=Homo sapiens GN=TM9SF4 PE=1 SV=2 - [TM9S4_HUMAN]	0,82	-	-	0,82
Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2 - [TMEDA_HUMAN]	0,80	0,94	0,98	0,91
Transmembrane emp24 domain-containing protein 2 OS=Homo sapiens GN=TMED2 PE=1 SV=1 - [TMED2_HUMAN]	0,86	0,85	0,94	0,89
Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=2 - [TMED9_HUMAN]	-	1,86	-	1,86
Transmembrane protein 14C OS=Homo sapiens GN=TMEM14C PE=1 SV=1 - [TM14C_HUMAN]	2,14	-	-	2,14
Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2 - [TNPO1_HUMAN]	0,89	0,85	0,86	0,86
Transportin-3 OS=Homo sapiens GN=TNPO3 PE=1 SV=3 - [TNPO3_HUMAN]	1,18	1,27	1,35	1,27
Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 - [TCOF_HUMAN]	1,25	1,07	1,18	1,16
Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN]	1,21	0,97	1,07	1,08
Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 - [ECHB_HUMAN]	1,43	1,45	1,15	1,34
Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 - [PUR2_HUMAN]	1,00	0,96	0,99	0,98
Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 - [TPIS_HUMAN]	1,02	1,05	1,00	1,02
Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2 - [TPP1_HUMAN]	0,69	1,96	-	1,33
Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4 - [TPP2_HUMAN]	2,16	0,95	2,21	1,77
tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2 - [NSUN2_HUMAN]	0,94	0,73	1,05	0,90
tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1 - [RTCB_HUMAN]	1,02	0,63	-	0,83
Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 - [TPM4_HUMAN]	-	1,02	-	1,02
Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 - [SYWC_HUMAN]	1,27	1,06	1,03	1,12
Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	1,08	1,20	1,19	1,16
Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2 - [TBA3E_HUMAN]	-	-	0,58	0,58
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]	0,84	0,94	0,91	0,89
Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]	1,84	1,43	-	1,63
Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	0,62	0,74	0,89	0,75
Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]	1,13	1,08	0,85	1,02
Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]	0,91	0,87	0,87	0,88
Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]	0,79	0,66	0,71	0,72
Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=1 SV=2 - [TBCD_HUMAN]	1,27	1,44	1,33	1,35
Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE PE=1 SV=1 - [TBCE_HUMAN]	-	-	0,81	0,81
Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTLL12 PE=1 SV=2 - [TTL12_HUMAN]	0,79	1,25	1,02	1,02
Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=1 SV=2 - [TP53B_HUMAN]	-	0,93	1,04	0,98
Twinfilin-1 OS=Homo sapiens GN=TWF1 PE=1 SV=3 - [TWF1_HUMAN]	1,06	-	-	1,06
Twinfilin-2 OS=Homo sapiens GN=TWF2 PE=1 SV=2 - [TWF2_HUMAN]	1,38	-	1,87	1,62
Tyrosine-protein kinase BAZ1B OS=Homo sapiens GN=BAZ1B PE=1 SV=2 - [BAZ1B_HUMAN]	1,15	1,40	0,82	1,12
Tyrosine-protein phosphatase non-receptor type 23 OS=Homo sapiens GN=PTPN23 PE=1 SV=1 - [PTN23_HUMAN]	-	-	0,22	0,22
Tyrosine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4 - [SYYC_HUMAN]	0,98	0,91	0,94	0,95
U1 small nuclear ribonucleoprotein A OS=Homo sapiens GN=SNRPA PE=1 SV=3 - [SNRPA_HUMAN]	0,86	-	-	0,86
U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens GN=U2SURP PE=1 SV=2 - [SR140_HUMAN]	1,54	1,37	-	1,45

U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1 - [SNUT1_HUMAN]	1,55	1,49	1,17	1,40
U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2 - [U520_HUMAN]	0,93	0,94	0,89	0,92
Ubiquilin-2 OS=Homo sapiens GN=UBQLN2 PE=1 SV=2 - [UBQL2_HUMAN]	0,81	-	1,33	1,07
Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2 - [UBP10_HUMAN]	0,97	0,88	-	0,93
Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=3 - [UBP14_HUMAN]	0,73	0,95	1,05	0,91
Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2 - [UBP5_HUMAN]	1,43	1,15	1,28	1,29
Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens GN=USP7 PE=1 SV=2 - [UBP7_HUMAN]	1,01	0,85	1,16	1,00
Ubiquitin conjugation factor E4 A OS=Homo sapiens GN=UBE4A PE=1 SV=2 - [UBE4A_HUMAN]	-	-	1,07	1,07
Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 - [OTUB1_HUMAN]	0,96	1,01	1,07	1,01
Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN]	0,98	0,85	0,97	0,93
Ubiquitin-associated protein 2 OS=Homo sapiens GN=UBAP2 PE=1 SV=1 - [UBAP2_HUMAN]	0,84	0,66	0,63	0,71
Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=1 SV=2 - [UBP2L_HUMAN]	1,07	1,00	0,99	1,02
Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 - [UB2D3_HUMAN]	-	2,72	1,17	1,95
Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3 - [UBE2O_HUMAN]	1,45	1,31	2,18	1,64
Ubiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens GN=UBE2V2 PE=1 SV=4 - [UB2V2_HUMAN]	-	0,82	-	0,82
Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 - [UBA1_HUMAN]	1,22	1,33	1,26	1,27
UDP-glucose 4-epimerase OS=Homo sapiens GN=GALE PE=1 SV=2 - [GALE_HUMAN]	-	3,92	-	3,92
UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 - [UGDH_HUMAN]	1,14	1,27	1,33	1,25
UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3 - [UGGG1_HUMAN]	0,81	0,89	0,86	0,85
UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3 - [KCY_HUMAN]	1,47	-	1,29	1,38
Uncharacterized protein KIAA0090 OS=Homo sapiens GN=KIAA0090 PE=1 SV=1 - [K0090_HUMAN]	0,78	0,95	1,10	0,95
Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 - [MYO1C_HUMAN]	1,04	0,74	0,65	0,81
UPF0160 protein MYG1, mitochondrial OS=Homo sapiens GN=C12orf10 PE=1 SV=2 - [MYG1_HUMAN]	-	-	4,08	4,08
UPF0556 protein C19orf10 OS=Homo sapiens GN=C19orf10 PE=1 SV=1 - [CS010_HUMAN]	0,83	0,77	0,72	0,77
UPF0667 protein C1orf55 OS=Homo sapiens GN=C1orf55 PE=1 SV=1 - [CA055_HUMAN]	0,83	-	-	0,83
Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=2 - [UTRO_HUMAN]	0,70	0,86	0,60	0,72
UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1 - [RD23B_HUMAN]	1,41	1,36	1,21	1,33
Vacuolar protein sorting-associated protein 26A OS=Homo sapiens GN=VPS26A PE=1 SV=2 - [VP26A_HUMAN]	-	1,89	-	1,89
Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	1,17	0,84	0,64	0,88
Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4 - [SYVC_HUMAN]	1,17	1,10	1,15	1,14
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1 - [ACADV_HUMAN]	1,19	1,58	1,06	1,28
Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=1 SV=2 - [HACD3_HUMAN]	2,73	1,28	1,04	1,68
Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=1 SV=1 - [TECR_HUMAN]	1,19	0,96	0,76	0,97
Vesicle transport protein GOT1B OS=Homo sapiens GN=GOLT1B PE=1 SV=1 - [GOT1B_HUMAN]	-	-	2,47	2,47
Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4 - [SC22B_HUMAN]	0,82	-	0,41	0,62
Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2 - [VIGLN_HUMAN]	0,81	1,33	0,85	1,00
Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 - [VIME_HUMAN]	0,85	0,91	0,95	0,90
Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4 - [VINC_HUMAN]	1,01	0,97	1,09	1,02
Vitamin K epoxide reductase complex subunit 1 OS=Homo sapiens GN=VKORC1 PE=1 SV=1 - [VKOR1_HUMAN]	1,07	0,99	0,96	1,01
Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2 - [VDAC1_HUMAN]	1,12	1,06	1,04	1,07
Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 - [VDAC2_HUMAN]	1,02	0,97	1,10	1,03
Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 - [VDAC3_HUMAN]	0,93	0,96	0,94	0,94
V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=2 SV=3 - [VPP1_HUMAN]	1,15	1,22	1,07	1,15
V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 - [VATA_HUMAN]	1,10	1,07	1,41	1,19
V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3 - [VATB2_HUMAN]	0,76	-	-	0,76

WASH complex subunit 7 OS=Homo sapiens GN=KIAA1033 PE=1 SV=2 - [WASH7_HUMAN]	1,10	-	-	1,10
WASH complex subunit strumpellin OS=Homo sapiens GN=KIAA0196 PE=1 SV=1 - [STRUM_HUMAN]	1,41	0,79	2,71	1,64
WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 - [WDR1_HUMAN]	1,41	2,15	-	1,78
WD repeat-containing protein 3 OS=Homo sapiens GN=WDR3 PE=1 SV=1 - [WDR3_HUMAN]	0,93	-	-	0,93
WD repeat-containing protein 36 OS=Homo sapiens GN=WDR36 PE=1 SV=1 - [WDR36_HUMAN]	1,22	1,54	-	1,38
Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens GN=WASF2 PE=1 SV=3 - [WASF2_HUMAN]	-	-	0,19	0,19
Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3 - [PEPD_HUMAN]	1,90	-	-	1,90
X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 - [XRCC5_HUMAN]	0,95	0,97	1,00	0,98
X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2 - [XRCC6_HUMAN]	0,92	1,04	1,03	0,99
YLP motif-containing protein 1 OS=Homo sapiens GN=YLPM1 PE=1 SV=3 - [YLPM1_HUMAN]	0,69	0,65	-	0,67
Zinc finger and BTB domain-containing protein 10 OS=Homo sapiens GN=ZBTB10 PE=1 SV=2 - [ZBT10_HUMAN]	-	0,66	-	0,66
Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens GN=ZC3H11A PE=1 SV=3 - [ZC11A_HUMAN]	0,59	0,59	0,65	0,61
Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 - [ZCCHV_HUMAN]	0,82	0,84	0,91	0,86
Zinc finger FYVE domain-containing protein 26 OS=Homo sapiens GN=ZFYVE26 PE=1 SV=3 - [ZFY26_HUMAN]	-	-	1,20	1,20
Zinc finger RNA-binding protein OS=Homo sapiens GN=ZFR PE=1 SV=2 - [ZFR_HUMAN]	1,21	0,87	0,81	0,96
Zinc phosphodiesterase ELAC protein 2 OS=Homo sapiens GN=ELAC2 PE=1 SV=2 - [RNZ2_HUMAN]	1,17	1,15	1,09	1,14
Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1 - [ZYX_HUMAN]	0,99	1,09	0,86	0,98