Q5H9A7	Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=2 S	85.31	2
F5H265	Polyubiquitin-C (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=	65.77	19
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KR	63.54	1
P00750	Tissue-type plasminogen activator OS=Homo sapiens GN=PLAT PE	60.14	1
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [A	60.00	2
Q16270-2	Isoform 2 of Insulin-like growth factor-binding protein 7 OS=Homo	59.86	2
O00391	Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3 - [	59.71	1
Q08431-2	Isoform 2 of Lactadherin OS=Homo sapiens GN=MFGE8 - [MFGM_	59.29	4
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1	58.39	1
P06702	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1 - [S10	56.14	1
E7ET40	Urokinase-type plasminogen activator chain B OS=Homo sapiens G	54.11	1
P29279	Connective tissue growth factor OS=Homo sapiens GN=CTGF PE=1	53.58	1
Q16610	Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 S	52.96	2
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1	52.73	1
Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1	51.45	1
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1	50.69	1
P07996	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2 - [T	50.51	1
J3KMY5	Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=4	50.00	5
P26022	Pentraxin-related protein PTX3 OS=Homo sapiens GN=PTX3 PE=1	49.08	1
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HU	49.03	1
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 S	48.29	1
O75326	Semaphorin-7A OS=Homo sapiens GN=SEMA7A PE=1 SV=1 - [SEM	46.85	1
Q12841	Follistatin-related protein 1 OS=Homo sapiens GN=FSTL1 PE=1 SV	46.43	1
P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB	45.05	2
H0YN42	Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=2 SV=1 - [	44.92	3
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1	44.28	1
P07602	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2	44.08	5
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HU	43.23	1
Q92820	Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=	43.08	1
Q9BTY2	Plasma alpha-L-fucosidase OS=Homo sapiens GN=FUCA2 PE=1 SV	43.04	1
P08294	Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=	42.92	1
P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=	42.47	2
Q9Y4K0	Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1	41.73	1
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV	41.57	1
P22392-2	Isoform 3 of Nucleoside diphosphate kinase B OS=Homo sapiens G	41.57	4
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=	41.32	1
E9PQX2	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=2 SV=1	40.91	10
P14618-2	Isoform M1 of Pyruvate kinase isozymes M1/M2 OS=Homo sapiens	40.49	1
P61812	Transforming growth factor beta-2 OS=Homo sapiens GN=TGFB2	40.34	2
Q06481	Amyloid-like protein 2 OS=Homo sapiens GN=APLP2 PE=1 SV=2 -	40.10	3
H0YAR1	Lysyl oxidase homolog 2 (Fragment) OS=Homo sapiens GN=LOXL2	40.10	1
P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	39.91	1
B0YJC4	Vimentin OS=Homo sapiens GN=VIM PE=2 SV=1 - [B0YJC4_HUMA	39.91	2
P07686	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE	39.57	1
P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1	38.77	1
P01892	HLA class I histocompatibility antigen, A-2 alpha chain OS=Homo s	38.63	2
P68371	Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	38.43	1
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8	38.24	3
Q99538	Legumain OS=Homo sapiens GN=LGMN PE=1 SV=1 - [LGMN_HUM	37.88	1
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1	37.30	2
P05067-7	Isoform L-APP733 of Amyloid beta A4 protein OS=Homo sapiens G	37.24	5
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HU	36.87	1
O94907	Dickkopf-related protein 1 OS=Homo sapiens GN=DKK1 PE=1 SV=	36.84	1

P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1	35.94	1
E7EUT4;P04406-2	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN	35.84	3
P07093-2	Isoform 2 of Glia-derived nexin OS=Homo sapiens GN=SERPINE2 -	35.77	3
B4E351	Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=	35.44	2
P35625	Metalloproteinase inhibitor 3 OS=Homo sapiens GN=TIMP3 PE=1 S	35.07	1
O94985-2	Isoform 2 of Calsyntenin-1 OS=Homo sapiens GN=CLSTN1 - [CSTN	34.71	1
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [	34.56	1
G3V0E5	Transferrin receptor (P90, CD71), isoform CRA_c OS=Homo sapien	34.46	2
C9IZG4	Protein CutA OS=Homo sapiens GN=CUTA PE=2 SV=1 - [C9IZG4_	34.07	4
Q01459	Di-N-acetylchitobiase OS=Homo sapiens GN=CTBS PE=1 SV=1 - [D	33.77	1
P52823	Stanniocalcin-1 OS=Homo sapiens GN=STC1 PE=1 SV=1 - [STC1_	33.60	1
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 S	32.47	2
Q13740-2	Isoform 2 of CD166 antigen OS=Homo sapiens GN=ALCAM - [CD16	32.28	2
Q8NBP7	Proprotein convertase subtilisin/kexin type 9 OS=Homo sapiens GN	32.23	1
E9PEP6	Protein kinase C-binding protein NELL1 OS=Homo sapiens GN=NRP	31.46	6
P08195-2	Isoform 2 of 4F2 cell-surface antigen heavy chain OS=Homo sapien	31.19	6
Q93063	Exostosin-2 OS=Homo sapiens GN=EXT2 PE=1 SV=1 - [EXT2_HU	31.06	3
F8W1Q3	Biotinidase OS=Homo sapiens GN=BTD PE=2 SV=1 - [F8W1Q3_HU	30.78	4
P48723	Heat shock 70 kDa protein 13 OS=Homo sapiens GN=HSPA13 PE=	29.30	1
P12814	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 - [ACTN	29.15	4
P01130-3	Isoform 3 of Low-density lipoprotein receptor OS=Homo sapiens G	29.15	7
Q14393-2	Isoform 2 of Growth arrest-specific protein 6 OS=Homo sapiens G	29.06	4
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE	29.05	1
P27348	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 -	28.98	1
Q9BZM5	NKG2D ligand 2 OS=Homo sapiens GN=ULBP2 PE=1 SV=1 - [N2DL	28.86	1
P54802	Alpha-N-acetylglucosaminidase OS=Homo sapiens GN=NAGLU PE=	28.80	1
J3KQG4	Glucosylceramidase OS=Homo sapiens GN=GBA PE=4 SV=1 - [J3K	28.73	5
H3BLV0	Complement decay-accelerating factor (Fragment) OS=Homo sapie	28.53	10
P02751-17	Isoform 17 of Fibronectin OS=Homo sapiens GN=FN1 - [FINC_HU	28.11	7
P28799	Granulins OS=Homo sapiens GN=GRN PE=1 SV=2 - [GRN_HUMAN	27.99	1
P16870-2	Isoform 2 of Carboxypeptidase E OS=Homo sapiens GN=CPE - [CB	27.95	2
Q92896	Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2	27.91	3
P35442	Thrombospondin-2 OS=Homo sapiens GN=THBS2 PE=1 SV=2 - [T	27.82	1
D6RHI9	Ribonuclease T2 (Fragment) OS=Homo sapiens GN=RNASET2 PE=	27.56	3
H3BMA1	Mesothelin (Fragment) OS=Homo sapiens GN=MSLN PE=2 SV=2 -	27.54	5
O14792	Heparan sulfate glucosamine 3-O-sulfotransferase 1 OS=Homo sapi	27.36	1
P10586-2	Isoform 2 of Receptor-type tyrosine-protein phosphatase F OS=Ho	27.34	2
P10646	Tissue factor pathway inhibitor OS=Homo sapiens GN=TFPI PE=1	26.97	1
H3BS10	Beta-hexosaminidase OS=Homo sapiens GN=HEXA PE=2 SV=1 - [	26.92	3
Q9UM22	Mammalian ependymin-related protein 1 OS=Homo sapiens GN=EP	26.79	2
Q92626	Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2 - [P	26.77	1
Q9UNN8	Endothelial protein C receptor OS=Homo sapiens GN=PROCR PE=1	26.47	1
P50897	Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1	26.47	3
Q9UKM7	Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannos	26.18	1
O00299	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLI	26.14	1
I3L398	Protein disulfide-isomerase (Fragment) OS=Homo sapiens GN=P4H	26.00	4
O00754	Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=	25.82	2
Q9H3G5	Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CP	25.63	1
P28074-3	Isoform 3 of Proteasome subunit beta type-5 OS=Homo sapiens G	25.62	2
P55287-2	Isoform 2 of Cadherin-11 OS=Homo sapiens GN=CDH11 - [CAD11_	25.54	2
O95150-2	Isoform 2 of Tumor necrosis factor ligand superfamily member 15	25.52	3
B3KTR6	Matrix-remodeling-associated protein 8 OS=Homo sapiens GN=MX	25.40	3
P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 S	25.25	1
B7Z5J4	Carboxypeptidase A4 OS=Homo sapiens GN=CPA4 PE=2 SV=1 - [B	25.24	3

P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_	25.14	1
Q86SR1	Polypeptide N-acetylgalactosaminyltransferase 10 OS=Homo sapien	25.04	1
P24592	Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=	25.00	1
Q8NHP8	Putative phospholipase B-like 2 OS=Homo sapiens GN=PLBD2 PE=	24.96	1
P63104	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=	24.90	2
O00300	Tumor necrosis factor receptor superfamily member 11B OS=Homo	24.69	1
P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1	24.65	1
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV	24.49	2
O43505	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase OS	24.34	1
F5GZK1	Processed exostosin-like 2 OS=Homo sapiens GN=EXTL2 PE=2 SV=	24.29	4
B7Z7A9	Phosphoglycerate kinase OS=Homo sapiens GN=PGK1 PE=2 SV=1	24.16	2
Q8NBJ4-2	Isoform 2 of Golgi membrane protein 1 OS=Homo sapiens GN=GOI	23.79	2
O14773	Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2 -	23.62	1
P31431-2	Isoform 2 of Syndecan-4 OS=Homo sapiens GN=SDC4 - [SDC4_HU	23.53	2
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=	23.40	5
P19883-2	Isoform 2 of Follistatin OS=Homo sapiens GN=FST - [FST_HUMAN]	23.34	2
P04066	Tissue alpha-L-fucosidase OS=Homo sapiens GN=FUCA1 PE=1 SV=	23.18	1
Q13253	Noggin OS=Homo sapiens GN=NOG PE=1 SV=1 - [NOGG_HUMAN]	22.84	1
O00622	Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1 - [CYR61	22.83	1
Q03405	Urokinase plasminogen activator surface receptor OS=Homo sapien	22.69	2
P42785	Lysosomal Pro-X carboxypeptidase OS=Homo sapiens GN=PRCP PE	22.58	1
Q16706	Alpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2	22.38	1
P07225	Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1	22.34	2
Q13308-5	Isoform 5 of Inactive tyrosine-protein kinase 7 OS=Homo sapiens G	22.30	4
O75629	Protein CREG1 OS=Homo sapiens GN=CREG1 PE=1 SV=1 - [CREG	22.27	1
Q9NZ08	Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=E	21.89	2
O00468-6	Isoform 6 of Agrin OS=Homo sapiens GN=AGRN - [AGRIN_HUMAN	21.86	1
P15291-2	Isoform Short of Beta-1,4-galactosyltransferase 1 OS=Homo sapien	21.82	2
P14625	Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [ENPL_	21.67	1
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_	21.66	1
Q9BRK5	45 kDa calcium-binding protein OS=Homo sapiens GN=SDF4 PE=1	21.55	5
P55283-2	Isoform 2 of Cadherin-4 OS=Homo sapiens GN=CDH4 - [CADH4_H	21.14	2
Q14118	Dystroglycan OS=Homo sapiens GN=DAG1 PE=1 SV=2 - [DAG1_HU	20.67	1
Q9NY97-2	Isoform 2 of UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltra	20.61	2
E9PN86	Eukaryotic translation initiation factor 3 subunit M (Fragment) OS=	20.59	3
Q8NES3	Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe OS=Homo	20.58	2
E9PMD7	Serine/threonine-protein phosphatase (Fragment) OS=Homo sapien	20.55	9
Q9GZP0	Platelet-derived growth factor D OS=Homo sapiens GN=PDGFD PE=	20.54	1
C9JRG3	Aspartyl aminopeptidase (Fragment) OS=Homo sapiens GN=DNPE	20.51	9
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2	20.16	1
P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN	20.00	2
O43854-2	Isoform 2 of EGF-like repeat and discoidin I-like domain-containing	20.00	2
B7Z4K6	Deoxyribonuclease-2-alpha OS=Homo sapiens GN=DNASE2 PE=2 S	20.00	2
Q58FF8	Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens GN=	19.95	1
Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1	19.81	2
O75083	WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=	19.80	2
Q6ZRP7	Sulfhydryl oxidase 2 OS=Homo sapiens GN=QSOX2 PE=1 SV=3 - [	19.77	1
Q96B60	5'-nucleotidase OS=Homo sapiens GN=NT5E PE=2 SV=1 - [Q96B6	19.70	3
P15586	N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1	19.57	5
P15151-3	Isoform Gamma of Poliovirus receptor OS=Homo sapiens GN=PVR	19.51	4
H0Y9C7	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase (Fragment) OS=	19.35	2
P22304	Iduronate 2-sulfatase OS=Homo sapiens GN=IDS PE=1 SV=1 - [ID	19.27	2
E7EMM4	Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=2 SV=1 - [E7E	19.19	5
Q02297-8	Isoform 8 of Pro-neuregulin-1, membrane-bound isoform OS=Hom	19.09	14

F5H6A3	N-sulphoglucosamine sulphohydrolase OS=Homo sapiens GN=SGS	19.06	3
Q99650-2	Isoform 2 of Oncostatin-M-specific receptor subunit beta OS=Homo	19.01	2
P08581	Hepatocyte growth factor receptor OS=Homo sapiens GN=MET PE=	18.99	2
P38571-2	Isoform 2 of Lysosomal acid lipase/cholesteryl ester hydrolase OS=	18.95	3
H0YD13	CD44 antigen OS=Homo sapiens GN=CD44 PE=2 SV=2 - [H0YD13_	18.93	22
P62906	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 S	18.89	1
P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	18.82	1
O43707	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 - [ACTN	18.44	1
P22413	Ectonucleotide pyrophosphatase/phosphodiesterase family member	18.27	1
Q8NCC3	Group XV phospholipase A2 OS=Homo sapiens GN=PLA2G15 PE=1	18.20	3
Q10469	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransf	18.12	1
P23284	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB P	18.06	1
J3KS17	Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE	17.31	2
H3BQN4	Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOA PE=	17.17	4
P10619	Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 S	17.08	1
P19021-4	Isoform 4 of Peptidyl-glycine alpha-amidating monooxygenase OS=	17.02	5
P00751	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2 - [CF	16.75	4
P25786	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE	16.73	3
Q16394	Exostosin-1 OS=Homo sapiens GN=EXT1 PE=1 SV=2 - [EXT1_HU	16.49	1
O75503	Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens GN=CL	16.48	1
Q8N0V5	N-acetyllactosaminide beta-1,6-N-acetylglucosaminyl-transferase, is	16.42	2
O14657	Torsin-1B OS=Homo sapiens GN=TOR1B PE=1 SV=2 - [TOR1B_HU	16.37	2
P01008	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1 - [A	16.16	1
D6RIU4	Vesicular integral-membrane protein VIP36 (Fragment) OS=Homo s	16.15	5
F8VQ14	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=	16.11	4
P49720	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=	16.10	1
Q5W0C6	Torsin-3A (Fragment) OS=Homo sapiens GN=TOR3A PE=2 SV=1 -	16.09	3
F5H018	GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN	16.08	4
B4E2J3	Serine protease 23 OS=Homo sapiens GN=PRSS23 PE=2 SV=1 - [B	15.95	2
Q86SJ2	Amphoterin-induced protein 2 OS=Homo sapiens GN=AMIGO2 PE=	15.90	1
P04083	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 - [ANXA1_H	15.90	2
Q14126	Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2 - [DSG2_H	15.83	1
P10124	Serglycin OS=Homo sapiens GN=SRGN PE=1 SV=3 - [SRGN_HUMA	15.82	1
P40189	Interleukin-6 receptor subunit beta OS=Homo sapiens GN=IL6ST P	15.80	1
Q7Z304-2	Isoform 2 of MAM domain-containing protein 2 OS=Homo sapiens	15.79	2
P55268	Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2	15.68	1
E9PL22	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=	15.58	2
P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=	15.49	1
P43121	Cell surface glycoprotein MUC18 OS=Homo sapiens GN=MCAM PE=	15.33	2
Q9GZX9	Twisted gastrulation protein homolog 1 OS=Homo sapiens GN=TW	15.25	1
Q6UWP8	Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=2 - [SBSN_HUM	15.25	1
P08603	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4 - [C	15.19	1
P08107-2	Isoform 2 of Heat shock 70 kDa protein 1A/1B OS=Homo sapiens	15.02	2
E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase OS=	14.55	3
P00736	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1	14.47	2
Q96QC4	MHC class I polypeptide-related sequence A OS=Homo sapiens GN=	14.46	2
Q32P28	Prolyl 3-hydroxylase 1 OS=Homo sapiens GN=LEPRE1 PE=1 SV=2	14.40	2
H0YA55	Serum albumin (Fragment) OS=Homo sapiens GN=ALB PE=4 SV=1	14.32	2
P09603	Macrophage colony-stimulating factor 1 OS=Homo sapiens GN=CS	14.26	1
Q9GZM7-3	Isoform 3 of Tubulointerstitial nephritis antigen-like OS=Homo sapi	14.22	2
Q8N441	Fibroblast growth factor receptor-like 1 OS=Homo sapiens GN=FG	14.09	1
Q9BQT9	Calsyntenin-3 OS=Homo sapiens GN=CLSTN3 PE=1 SV=1 - [CSTN	13.91	2
Q96JB6	Lysyl oxidase homolog 4 OS=Homo sapiens GN=LOXL4 PE=1 SV=1	13.89	1
P08236	Beta-glucuronidase OS=Homo sapiens GN=GUSB PE=1 SV=2 - [BG	13.82	3

Q5W0A2	BRI2, membrane form OS=Homo sapiens GN=ITM2B PE=2 SV=1 -	13.75	2
Q5HY54	Filamin-A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q5HY54_HU	13.66	3
H0YAF8	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment	13.64	9
P23526-2	Isoform 2 of Adenosylhomocysteinase OS=Homo sapiens GN=AHC	13.61	2
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRD	13.57	1
E9PFT6	Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=2 SV=1	13.48	3
Q92187	CMP-N-acetylneuraminate-poly-alpha-2,8-sialyltransferase OS=Hom	13.37	1
A6NIW5	Peroxiredoxin 2, isoform CRA_a OS=Homo sapiens GN=PRDX2 PE=	13.24	2
P07711	Cathepsin L1 OS=Homo sapiens GN=CTSL1 PE=1 SV=2 - [CATL1_	13.21	2
C9J1D9	Interleukin-1 receptor accessory protein (Fragment) OS=Homo sapi	13.10	5
H7C3T4	Peroxiredoxin-4 (Fragment) OS=Homo sapiens GN=PRDX4 PE=4 S	13.04	2
P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN]	13.00	3
O60687	Sushi repeat-containing protein SRPX2 OS=Homo sapiens GN=SRP	12.90	1
H0Y3Z3	Protein disulfide-isomerase (Fragment) OS=Homo sapiens GN=P4H	12.77	1
Q9NPF2-2	Isoform 2 of Carbohydrate sulfotransferase 11 OS=Homo sapiens	12.68	3
O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapie	12.60	1
P08758	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_H	12.50	1
C9J2Q4	Septin-2 (Fragment) OS=Homo sapiens GN=SEPT2 PE=2 SV=1 - [	12.50	4
E9PD92	Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Homo sapie	12.50	6
P25788-2	Isoform 2 of Proteasome subunit alpha type-3 OS=Homo sapiens	12.50	2
Q9Y2E5	Epididymis-specific alpha-mannosidase OS=Homo sapiens GN=MA	12.39	4
Q9NZV1	Cysteine-rich motor neuron 1 protein OS=Homo sapiens GN=CRIM	12.36	1
E7EPS8	Receptor-type tyrosine-protein phosphatase mu OS=Homo sapiens	12.23	4
Q16769	Glutaminyl-peptide cyclotransferase OS=Homo sapiens GN=QPCT	12.19	3
Q86UD1	Out at first protein homolog OS=Homo sapiens GN=OAF PE=2 SV=	12.09	2
B7Z6M1	Plastin-3 OS=Homo sapiens GN=PLS3 PE=2 SV=1 - [B7Z6M1_HUM	11.97	4
O43556-3	Isoform 2 of Epsilon-sarcoglycan OS=Homo sapiens GN=SGCE - [S	11.94	5
H0YH88	Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapie	11.86	16
P51884	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2 - [LUM_HUMAN]	11.83	1
Q9NPR2-2	Isoform 2 of Semaphorin-4B OS=Homo sapiens GN=SEMA4B - [SE	11.80	4
Q15008	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapie	11.57	4
P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 -	11.42	3
H0YN65	Carbohydrate sulfotransferase 14 OS=Homo sapiens GN=CHST14	11.40	2
E7ETU9	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Homo sapie	11.24	3
P49767	Vascular endothelial growth factor C OS=Homo sapiens GN=VEGF	11.22	1
P12109	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 S	11.09	1
B4E0R6	Importin-5 OS=Homo sapiens GN=IPO5 PE=2 SV=1 - [B4E0R6_HU	11.01	4
P52803	Ephrin-A5 OS=Homo sapiens GN=EFNA5 PE=1 SV=1 - [EFNA5_HU	10.96	1
P30530-2	Isoform Short of Tyrosine-protein kinase receptor UFO OS=Homo s	10.85	2
B4DUR8	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3	10.80	3
P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	10.75	4
Q99574	Neuroserpin OS=Homo sapiens GN=SERPINI1 PE=1 SV=1 - [NEUS	10.73	1
Q02818	Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4 - [NUCB	10.63	3
P06280	Alpha-galactosidase A OS=Homo sapiens GN=GLA PE=1 SV=1 - [A	10.49	1
H0YNP1	D-glucuronyl C5-epimerase OS=Homo sapiens GN=GLCE PE=2 SV=	10.49	2
P16035	Metalloproteinase inhibitor 2 OS=Homo sapiens GN=TIMP2 PE=1 S	10.45	3
Q9UHI8	A disintegrin and metalloproteinase with thrombospondin motifs 1	10.44	1
Q6EMK4	Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1 - [VASN_HUMAN	10.40	1
Q14703	Membrane-bound transcription factor site-1 protease OS=Homo sa	10.36	1
Q99523	Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3 - [SORT_HUMA	10.11	1
Q8WX77	Insulin-like growth factor-binding protein-like 1 OS=Homo sapiens	10.07	1
Q11201	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltrans	10.00	1
P11047	Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=	9.88	1
Q9Y696	Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLI	9.88	1

P09668	Pro-cathepsin H OS=Homo sapiens GN=CTSH PE=1 SV=4 - [CATH_	9.85	1
P10909-3	Isoform 3 of Clusterin OS=Homo sapiens GN=CLU - [CLUS_HUMAN	9.85	7
Q9Y6N7-6	Isoform 6 of Roundabout homolog 1 OS=Homo sapiens GN=ROBO1	9.80	6
P23352	Anosmin-1 OS=Homo sapiens GN=KAL1 PE=1 SV=3 - [KALM_HUMA	9.71	1
O43155	Leucine-rich repeat transmembrane protein FLRT2 OS=Homo sapien	9.70	1
O75509	Tumor necrosis factor receptor superfamily member 21 OS=Homo s	9.62	1
F5H325	N-acetylgalactosamine-6-sulfatase OS=Homo sapiens GN=GALNS P	9.62	2
P13284	Gamma-interferon-inducible lysosomal thiol reductase OS=Homo sa	9.60	1
D6RAF8	Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo	9.50	3
P05556-2	Isoform Beta-1B of Integrin beta-1 OS=Homo sapiens GN=ITGB1 -	9.38	5
Q68CR9	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DKFZp7	9.23	3
Q6UX71	Plexin domain-containing protein 2 OS=Homo sapiens GN=PLXDC2	9.07	1
P55058-3	Isoform 3 of Phospholipid transfer protein OS=Homo sapiens GN=P	9.05	4
Q15262	Receptor-type tyrosine-protein phosphatase kappa OS=Homo sapien	9.03	7
P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB P	9.02	1
P01137	Transforming growth factor beta-1 OS=Homo sapiens GN=TGFB1 P	8.97	1
J3QSU6	Tenascin OS=Homo sapiens GN=TNC PE=4 SV=1 - [J3QSU6_HUMA	8.96	9
Q99519	Sialidase-1 OS=Homo sapiens GN=NEU1 PE=1 SV=1 - [NEUR1_HU	8.92	2
Q96L58	Beta-1,3-galactosyltransferase 6 OS=Homo sapiens GN=B3GALT6 P	8.81	1
O43286	Beta-1,4-galactosyltransferase 5 OS=Homo sapiens GN=B4GALT5 P	8.76	1
P54803-4	Isoform 4 of Galactocerebrosidase OS=Homo sapiens GN=GALC - [	8.65	5
Q9UMR5	Lysosomal thioesterase PPT2 OS=Homo sapiens GN=PPT2 PE=1 SV	8.61	3
P09529	Inhibin beta B chain OS=Homo sapiens GN=INHBB PE=1 SV=2 - [I	8.60	1
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapien	8.53	2
Q8WZ75-2	Isoform 2 of Roundabout homolog 4 OS=Homo sapiens GN=ROBO4	8.47	4
P02765	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	8.45	1
P52799	Ephrin-B2 OS=Homo sapiens GN=EFNB2 PE=1 SV=1 - [EFNB2_HU	8.41	1
B4DKB2	Endothelin-converting enzyme 1 OS=Homo sapiens GN=ECE1 PE=2	8.40	5
P32004-3	Isoform 3 of Neural cell adhesion molecule L1 OS=Homo sapiens G	8.33	5
F8W1C3	Matrix metalloproteinase-19 OS=Homo sapiens GN=MMP19 PE=2 S	8.25	2
Q9UHL4	Dipeptidyl peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=3 - [	8.13	1
Q5T985	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=	8.02	2
P00533-4	Isoform 4 of Epidermal growth factor receptor OS=Homo sapiens G	7.96	3
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens	7.91	1
O60911	Cathepsin L2 OS=Homo sapiens GN=CTSL2 PE=1 SV=2 - [CATL2_H	7.78	1
P35555	Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=3 - [FBN1_HUMA	7.77	1
B0QY90	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens	7.73	4
Q5SYT8	Protein NAMPTL (Fragment) OS=Homo sapiens GN=NAMPTL PE=2	7.63	2
P26006	Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5 - [ITA3_	7.61	2
Q5STU3	HLA-B associated transcript 1 OS=Homo sapiens GN=DDX39B PE=4	7.53	7
E7EU96	Casein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=	7.53	3
Q9Y6X5	Bis(5'-adenosyl)-triphosphatase ENPP4 OS=Homo sapiens GN=ENP	7.51	1
Q13219	Pappalysin-1 OS=Homo sapiens GN=PAPPA PE=1 SV=3 - [PAPP1_H	7.44	2
Q5T6W1	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=	7.19	6
P61204	ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2	7.18	2
B4E3P0	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=2 SV=1 - [B4	7.11	3
Q08629	Testican-1 OS=Homo sapiens GN=SPOCK1 PE=1 SV=1 - [TICN1_H	7.06	1
B3KTI1	Alpha-amylase 2B OS=Homo sapiens GN=AMY2B PE=2 SV=1 - [B3	7.03	4
P48745	Protein NOV homolog OS=Homo sapiens GN=NOV PE=1 SV=1 - [N	7.00	1
B4DQH4	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=	6.95	4
Q9Y662	Heparan sulfate glucosamine 3-O-sulfotransferase 3B1 OS=Homo sa	6.92	2
B7Z729	Acid sphingomyelinase-like phosphodiesterase 3a OS=Homo sapien	6.83	2
P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=	6.82	1
P11362-13	Isoform 13 of Fibroblast growth factor receptor 1 OS=Homo sapien	6.80	21

Q29980	MHC class I polypeptide-related sequence B OS=Homo sapiens GN=	6.79	1
Q9UNW1	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens G	6.78	1
C9J8D4	Mannosyl-oligosaccharide glucosidase (Fragment) OS=Homo sapier	6.71	3
Q7Z4H8-3	Isoform 3 of KDEL motif-containing protein 2 OS=Homo sapiens GN	6.60	3
F5GZ08	Amyloid-like protein 1 OS=Homo sapiens GN=APLP1 PE=2 SV=1 -	6.55	4
Q8WVQ1	Soluble calcium-activated nucleotidase 1 OS=Homo sapiens GN=CA	6.48	1
Q92743	Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1	6.46	1
P36955	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF	6.46	1
E7EVJ3	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 OS	6.42	2
F8WC54	Disintegrin and metalloproteinase domain-containing protein 9 OS=	6.37	6
Q14563	Semaphorin-3A OS=Homo sapiens GN=SEMA3A PE=1 SV=1 - [SEM	6.36	1
Q00610-2	Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC -	6.35	2
D6RA82	Annexin OS=Homo sapiens GN=ANXA3 PE=2 SV=1 - [D6RA82_HU	6.34	2
J3KNQ3	26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapie	6.30	2
P05543	Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1	6.27	1
Q7LGC8	Carbohydrate sulfotransferase 3 OS=Homo sapiens GN=CHST3 PE=	6.26	1
B7Z9L0	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=	6.21	3
Q86VR8	Four-jointed box protein 1 OS=Homo sapiens GN=FJX1 PE=2 SV=1	6.18	1
Q96PX8	SLIT and NTRK-like protein 1 OS=Homo sapiens GN=SLITRK1 PE=	6.18	1
O00231	26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapie	6.16	2
Q15758	Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5	6.10	1
Q92692-2	Isoform Alpha of Poliovirus receptor-related protein 2 OS=Homo sa	6.05	3
B4DYD8	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 P	6.03	5
E9PCS3	26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapien	6.01	3
Q13332-6	Isoform 2 of Receptor-type tyrosine-protein phosphatase S OS=Hor	5.92	9
F5H780	Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNR	5.88	16
Q6PCB0	von Willebrand factor A domain-containing protein 1 OS=Homo sap	5.84	1
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=	5.83	1
Q9Y625	Glypican-6 OS=Homo sapiens GN=GPC6 PE=1 SV=1 - [GPC6_HUM	5.77	1
E7EP32	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	5.74	3
Q9H5V8-2	Isoform 2 of CUB domain-containing protein 1 OS=Homo sapiens G	5.70	3
Q7LFX5	Carbohydrate sulfotransferase 15 OS=Homo sapiens GN=CHST15 P	5.70	2
Q12805-2	Isoform 2 of EGF-containing fibulin-like extracellular matrix protein	5.57	5
P11717	Cation-independent mannose-6-phosphate receptor OS=Homo sapi	5.54	1
B4E2S7	Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens	5.51	4
P23470-2	Isoform 2 of Receptor-type tyrosine-protein phosphatase gamma O	5.37	2
E9PFD9	Semaphorin-4D OS=Homo sapiens GN=SEMA4D PE=4 SV=1 - [E9P	5.29	3
Q5T749	Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=	5.18	1
E7EPA6	Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=2 SV=1	5.18	3
D6RF62	Phosphoribosylaminoimidazole carboxylase OS=Homo sapiens GN=	5.11	3
Q24JP5	Transmembrane protein 132A OS=Homo sapiens GN=TMEM132A P	5.08	3
Q9NRB3	Carbohydrate sulfotransferase 12 OS=Homo sapiens GN=CHST12 P	5.07	1
O95497	Pantetheinase OS=Homo sapiens GN=VNN1 PE=1 SV=2 - [VNN1_H	5.07	1
F5H3T8	Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE	5.07	3
P10253	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV	5.04	1
P78539-4	Isoform 4 of Sushi repeat-containing protein SRPX OS=Homo sapie	5.01	5
Q6UXH8	Collagen and calcium-binding EGF domain-containing protein 1 OS=	4.93	1
Q4G148-2	Isoform 2 of Glucoside xylosyltransferase 1 OS=Homo sapiens GN=	4.89	2
O75882-3	Isoform 3 of Attractin OS=Homo sapiens GN=ATRN - [ATRN_HUMA	4.84	3
P10155-3	Isoform 3 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens	4.83	4
P04004	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1 - [VTNC_HUMA	4.81	1
Q9H173	Nucleotide exchange factor SIL1 OS=Homo sapiens GN=SIL1 PE=1	4.77	2
O15230	Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	4.71	1
O00339-3	Isoform 3 of Matrilin-2 OS=Homo sapiens GN=MATN2 - [MATN2_H	4.70	6

F5H335	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapien	4.67	2
Q02742	Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucos	4.67	1
Q09028-4	Isoform 4 of Histone-binding protein RBBP4 OS=Homo sapiens GN	4.62	7
Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	4.57	1
B4DKL4	Lipolysis-stimulated lipoprotein receptor OS=Homo sapiens GN=LS	4.46	5
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [	4.41	1
Q8NFZ8	Cell adhesion molecule 4 OS=Homo sapiens GN=CADM4 PE=1 SV=	4.38	1
P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FA	4.34	1
O94991	SLIT and NTRK-like protein 5 OS=Homo sapiens GN=SLITRK5 PE=	4.28	1
O60462-4	Isoform B0 of Neuropilin-2 OS=Homo sapiens GN=NRP2 - [NRP2_H	4.22	7
C9JP16	Cartilage-associated protein OS=Homo sapiens GN=CRTAP PE=2 S	4.19	2
Q6UXD5-2	Isoform 2 of Seizure 6-like protein 2 OS=Homo sapiens GN=SEZ6L	4.17	5
O95373	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 - [IPO7_HUMA	4.14	1
P35052	Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=2 - [GPC1_HUM	4.12	2
F5H1I8	X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=	3.99	4
H0YGW5	Low-density lipoprotein receptor-related protein 6 (Fragment) OS=	3.99	3
P50895	Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 S	3.98	1
P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE	3.96	1
P27658	Collagen alpha-1(VIII) chain OS=Homo sapiens GN=COL8A1 PE=1	3.90	1
Q9HB63-3	Isoform 3 of Netrin-4 OS=Homo sapiens GN=NTN4 - [NET4_HUMA	3.89	3
B3KVK7	Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS	3.85	2
Q6P9A2	Polypeptide N-acetylgalactosaminyltransferase 18 OS=Homo sapien	3.79	1
O60279	Sushi domain-containing protein 5 OS=Homo sapiens GN=SUSD5 P	3.66	1
Q8WUJ3-2	Isoform 2 of Protein KIAA1199 OS=Homo sapiens GN=KIAA1199 -	3.63	2
P05546	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3 -	3.61	1
C9JIM8	Solute carrier family 2, facilitated glucose transporter member 1 (Fr	3.60	2
P20908	Collagen alpha-1(V) chain OS=Homo sapiens GN=COL5A1 PE=1 S	3.59	1
Q8NBJ5	Procollagen galactosyltransferase 1 OS=Homo sapiens GN=COLGAL	3.54	1
P41250	Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 - [S	3.52	1
P53618	Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	3.46	1
Q12797-10	Isoform 10 of Aspartyl/asparaginyl beta-hydroxylase OS=Homo sap	3.43	2
Q92973-3	Isoform 3 of Transportin-1 OS=Homo sapiens GN=TNPO1 - [TNPO	3.42	3
Q8IXL6	Extracellular serine/threonine protein kinase FAM20C OS=Homo sa	3.42	1
P17301	Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1 - [ITA2_	3.39	2
Q08945	FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1	3.39	1
Q76M96	Coiled-coil domain-containing protein 80 OS=Homo sapiens GN=C	3.37	3
P01024	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2 - [CO3_HU	3.37	1
F8W904;P55060-4	Exportin-2 OS=Homo sapiens GN=CSE1L PE=2 SV=1 - [F8W904_H	3.28	3
Q5TCU6	Talin-1 OS=Homo sapiens GN=TLN1 PE=2 SV=1 - [Q5TCU6_HUMA	3.25	2
P98160	Basement membrane-specific heparan sulfate proteoglycan core pr	3.21	1
F5GXQ1	35 kDa inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapie	3.21	6
P06737-2	Isoform 2 of Glycogen phosphorylase, liver form OS=Homo sapiens	3.20	3
P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4 - [FBLN1_HUM	3.13	2
P08648	Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2 - [ITA5_	3.05	1
Q14680-8	Isoform 8 of Maternal embryonic leucine zipper kinase OS=Homo s	2.99	3
Q13619-2	Isoform 2 of Cullin-4A OS=Homo sapiens GN=CUL4A - [CUL4A_HU	2.88	6
Q7Z3V4-3	Isoform 3 of Ubiquitin-protein ligase E3B OS=Homo sapiens GN=U	2.87	5
Q8N2Q7-2	Isoform 2 of Neuroligin-1 OS=Homo sapiens GN=NLGN1 - [NLGN1_	2.79	4
Q08345-2	Isoform 2 of Epithelial discoidin domain-containing receptor 1 OS=	2.74	4
E9PG71	Ephrin type-A receptor 4 OS=Homo sapiens GN=EPHA4 PE=2 SV=	2.74	2
P34932	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 S	2.74	1
Q9Y5G3-2	Isoform 2 of Protocadherin gamma-B1 OS=Homo sapiens GN=PCD	2.72	2
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMA	2.70	1
P13010	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=	2.60	1

Q9UBG0	C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=	2.57	1
Q9H1B5	Xylosyltransferase 2 OS=Homo sapiens GN=XYLT2 PE=2 SV=2 - [X	2.54	1
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1	2.44	1
Q02487-2	Isoform 2B of Desmocollin-2 OS=Homo sapiens GN=DSC2 - [DSC2_	2.36	2
Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SY	2.35	2
Q01813-2	Isoform 2 of 6-phosphofructokinase type C OS=Homo sapiens GN=	2.32	2
O75197	Low-density lipoprotein receptor-related protein 5 OS=Homo sapie	2.17	1
Q70JA7	Chondroitin sulfate synthase 3 OS=Homo sapiens GN=CHSY3 PE=2	2.15	1
Q86YZ3	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2 - [HORN_HUMA	2.11	1
O14787-2	Isoform 2 of Transportin-2 OS=Homo sapiens GN=TNPO2 - [TNPO	2.03	2
P98155-2	Isoform Short of Very low-density lipoprotein receptor OS=Homo sa	2.01	2
F5H826	Nodal modulator 3 OS=Homo sapiens GN=NOMO3 PE=2 SV=1 - [F	1.91	7
H0Y930	Extracellular matrix protein FRAS1 (Fragment) OS=Homo sapiens G	1.78	3
F8VPD4	CAD protein OS=Homo sapiens GN=CAD PE=2 SV=1 - [F8VPD4_H	1.71	2
P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=	1.69	1
Q7Z7M9	Polypeptide N-acetylgalactosaminyltransferase 5 OS=Homo sapiens	1.60	1
Q15149-7	Isoform 7 of Plectin OS=Homo sapiens GN=PLEC - [PLEC_HUMAN]	1.57	9
Q92859-2	Isoform 2 of Neogenin OS=Homo sapiens GN=NEO1 - [NEO1_HUM	1.56	4
Q14517	Protocadherin Fat 1 OS=Homo sapiens GN=FAT1 PE=1 SV=2 - [FA	1.55	1
E7EN95	Filamin-B OS=Homo sapiens GN=FLNB PE=2 SV=1 - [E7EN95_HU	1.54	8
O95490-3	Isoform 3 of Latrophilin-2 OS=Homo sapiens GN=LPHN2 - [LPHN2_	1.51	10
Q16363-2	Isoform 2 of Laminin subunit alpha-4 OS=Homo sapiens GN=LAMA	1.32	2
J3KR24	Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS P	1.30	2
E7EUA9	Neuron navigator 3 OS=Homo sapiens GN=NAV3 PE=2 SV=2 - [E7	1.28	5
Q5SYB0	FERM and PDZ domain-containing protein 1 OS=Homo sapiens GN=	1.27	1
Q5D862	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1 - [FILA2_HUM	1.25	1
Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sap	0.97	1
Q8TE73	Dynein heavy chain 5, axonemal OS=Homo sapiens GN=DNAH5 PE	0.74	1
Q13813-3	Isoform 3 of Spectrin alpha chain, non-erythrocytic 1 OS=Homo sap	0.69	4
Q99715-4	Isoform 4 of Collagen alpha-1(XII) chain OS=Homo sapiens GN=C	0.57	3
Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1	0.50	1
P20930	Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3 - [FILA_HUMAN]	0.37	1

9	9	292	0.779	0.762	0.825	0.809	0.963
5	5	50	1.368	1.360	1.391	1.404	0.972
31	41	690	**2.496**	**2.052**	**2.457**	**2.259**	0.965
26	26	565	0.822	0.804	0.843	0.848	0.954
18	19	461	1.103	1.126	1.161	1.081	0.946
16	16	471	0.684	**0.637**	0.720	0.738	0.940
46	46	1250	0.988	0.926	1.074	0.998	0.939
17	17	130	1.055	1.025	1.109	1.109	0.918
35	39	686	**2.590**	**2.142**	**2.805**	**2.339**	0.930
4	4	19	0.811	0.793	0.758	0.785	1.086
20	20	372	**0.354**	**0.329**	**0.361**	**0.354**	0.976
19	19	254	0.694	0.686	0.710	0.735	1.021
24	24	307	0.929	0.895	0.932	0.904	0.997
5	22	203	1.174	1.041	1.153	1.093	0.946
27	27	756	0.820	0.793	0.894	0.854	0.931
17	35	391	1.028	0.983	1.002	1.015	0.977
52	56	1193	0.901	0.877	0.930	0.889	0.979
7	7	155	0.778	0.740	0.936	0.867	0.885
16	16	665	1.415	1.312	1.457	1.367	0.941
17	17	597	**0.561**	**0.561**	**0.599**	**0.574**	0.926
32	38	724	**1.859**	**1.650**	**1.945**	**1.720**	0.937
29	29	467	0.878	0.809	0.910	0.844	0.963
13	13	361	0.860	0.891	0.782	0.840	0.980
4	17	190	1.468	1.126	**1.584**	1.400	0.983
10	10	80	0.770	0.825	0.767	0.787	1.052
16	16	294	**0.523**	**0.546**	**0.590**	**0.584**	0.976
20	20	278	**0.666**	0.703	0.693	0.738	0.937
11	11	175	0.695	0.674	0.728	0.734	0.947
16	16	345	0.704	0.725	0.771	0.760	0.943
22	22	337	0.806	0.777	0.882	0.821	0.987
7	7	97	**0.569**	**0.599**	**0.630**	**0.654**	0.989
15	16	155	**1.570**	1.481	1.415	1.465	1.056
25	31	492	0.901	0.841	0.956	0.911	0.938
20	21	388	1.485	1.379	**1.513**	1.446	1.011
6	6	32	1.216	1.156	1.049	1.019	1.063
11	12	129	**1.588**	1.427	1.445	1.386	1.093
2	2	6	1.144	1.411	1.099	1.361	1.041
3	19	37					
17	19	275	1.140	0.970	1.231	1.063	0.929
27	28	918	0.726	0.681	0.703	0.672	0.924
2	8	42					
15	15	180	1.122	1.096	1.154	1.044	1.097
17	18	141	0.890	0.955	0.894	0.966	1.030
20	21	299	0.828	0.792	0.861	0.852	1.055
10	21	231	1.833	1.594	1.488	1.447	1.074
12	12	90	0.980	1.004	0.966	0.974	1.035
2	15	125	1.613	1.899	1.551	1.832	1.040
18	23	200	1.081	1.054	1.104	1.066	0.997
13	13	242	0.557	0.571	0.503	0.565	1.010
17	30	292	1.156	1.132	1.135	1.170	1.013
25	27	1109	0.717	0.664	0.766	0.732	0.966
10	10	92	0.922	0.837	0.947	0.850	0.988
11	11	287	0.985	0.891	1.020	0.919	0.945

8	19	243	1.788	1.674	1.551	1.524	1.072
8	8	71	1.577	1.594	1.355	1.307	1.037
14	14	124	0.960	0.837	0.942	0.867	1.074
5	5	49	0.681	0.624	0.750	0.682	0.952
7	7	59	0.768	0.794	0.721	0.725	1.143
35	36	607	0.846	0.820	0.811	0.793	0.988
17	17	288	0.519	0.511	0.575	0.548	0.950
23	23	193	0.946	0.951	0.901	0.934	1.007
3	3	8	1.417	1.464	1.409	1.436	1.023
11	11	128	0.771	0.780	0.806	0.797	0.964
6	6	66	0.475	0.469	0.475	0.468	1.029
12	12	121	1.168	1.124	1.170	1.124	0.997
19	19	462	0.798	0.728	0.857	0.783	0.938
18	18	257	0.675	0.698	0.660	0.687	0.975
22	22	386	1.110	1.027	1.167	1.084	0.952
17	17	199	1.088	1.072	1.130	1.037	0.981
19	19	156	1.056	1.069	1.013	0.990	1.020
13	13	197	0.918	0.872	0.960	0.907	0.972
12	12	80	0.732	0.793	0.730	0.693	1.030
15	24	272	1.101	1.118	0.983	1.070	1.079
18	19	250	0.980	0.968	1.048	0.991	0.974
18	18	201	0.756	0.752	0.718	0.724	1.038
15	18	112	1.300	1.271	1.160	1.218	1.052
3	6	35	1.386	1.013	1.241	0.901	1.086
7	7	106	0.914	0.853	0.849	0.871	0.984
16	16	90	1.106	1.157	1.063	1.196	1.041
13	13	156	0.599	0.589	0.576	0.590	0.972
12	12	82	1.032	1.028	0.943	1.001	1.034
53	53	469	1.367	1.344	1.267	1.310	1.013
14	14	150	0.725	0.763	0.633	0.678	0.993
10	10	75	0.711	0.709	0.698	0.773	1.028
31	31	238	1.375	1.272	1.292	1.174	1.047
22	26	246	1.031	0.983	1.024	0.975	1.025
7	7	62	0.756	0.806	0.811	0.813	0.978
8	8	84	1.094	1.271	1.065	1.117	1.003
9	9	106	0.561	0.600	0.520	0.578	1.054
38	38	314	1.509	1.421	1.410	1.448	1.018
7	7	70	1.268	1.173	1.177	1.149	1.060
13	14	153	0.801	0.871	0.770	0.815	1.073
6	6	45	0.979	1.023	0.907	0.960	1.081
34	34	334	0.985	0.976	0.995	0.963	0.982
6	6	116	0.958	0.920	1.163	1.050	0.912
8	8	73	0.666	0.627	0.626	0.613	0.962
17	17	173	1.059	1.027	1.116	1.027	1.041
6	6	39	1.312	1.404	1.811	1.667	1.069
3	5	21	1.090	1.630	0.911	1.367	1.197
21	21	269	0.891	0.874	0.913	0.889	0.987
11	11	78	0.752	0.726	0.782	0.809	0.968
3	3	11					
14	14	192	0.874	0.862	0.845	0.867	1.004
5	5	23	0.399	0.387	0.392	0.382	1.018
12	12	99	0.906	1.002	0.889	0.915	1.046
9	21	183	1.782	1.677	1.685	1.644	1.024
6	6	50	1.226	0.946	1.178	1.131	1.063

4	4	15	0.659	1.078	0.616	0.926	1.035
14	14	141	0.644	0.668	0.586	0.617	1.083
6	6	59	0.858	0.893	0.932	0.865	1.011
13	13	74	0.835	0.887	0.809	0.897	0.980
4	7	87	0.961	1.001	1.116	1.059	0.869
11	11	58	1.012	0.930	0.822	0.926	0.964
5	19	196	2.595	2.715	2.387	2.102	1.050
11	11	74	1.163	1.328	1.175	1.163	1.039
8	8	27	0.797	0.772	0.893	0.724	1.002
6	6	54	0.940	1.019	1.050	1.029	0.888
7	7	52	1.560	1.429	1.547	1.580	0.925
8	8	62	1.176	1.100	1.271	1.165	0.971
8	8	115	0.834	0.788	0.836	0.796	0.941
3	3	11	5.624	4.430	5.148	4.072	1.092
8	8	59	1.597	1.422	1.425	1.369	1.030
8	8	66	0.873	0.913	0.906	0.893	0.987
10	10	112	0.674	0.646	0.678	0.661	0.997
5	5	92	0.798	0.778	0.770	0.800	0.992
9	9	106	0.950	0.991	1.062	1.001	1.042
4	4	21	0.469	0.467	0.466	0.466	1.007
11	11	120	0.613	0.620	0.617	0.573	1.006
24	24	196	1.202	1.129	1.214	1.139	1.012
15	15	112	1.039	1.043	1.105	1.115	0.938
15	15	134	0.887	0.848	0.910	0.876	0.990
4	4	34	0.645	0.686	0.642	0.649	1.003
19	19	142	1.282	1.250	1.255	1.195	0.993
37	37	357	2.645	2.348	2.555	2.321	1.012
5	6	37	0.860	0.666	0.914	0.862	0.945
14	16	126	1.480	1.384	1.539	1.440	1.021
9	9	63	1.259	1.198	1.240	1.164	1.027
6	6	28	1.655	1.586	1.612	1.551	1.026
15	15	195	0.911	0.887	0.904	0.873	1.022
15	15	164	0.970	0.911	0.990	0.951	0.999
6	6	37	0.740	0.735	0.696	0.679	1.032
2	2	7	1.550	1.361	1.857	1.574	0.860
7	7	19	0.813	0.755	0.907	0.846	0.895
4	4	23	1.288	1.191	1.259	1.118	1.008
8	9	116	0.978	0.979	0.921	0.977	1.008
2	2	17	1.840	1.298	1.866	1.321	0.986
14	14	53	1.206	1.149	1.103	1.186	1.005
2	2	6	1.155	1.033	1.226	1.216	1.053
9	9	41	0.859	0.818	0.899	0.899	0.955
6	6	78	0.755	0.741	0.772	0.736	1.008
1	8	12					
19	19	111	1.343	1.351	1.356	1.286	1.007
6	6	22	1.143	1.192	1.296	1.197	0.897
13	13	71	1.297	1.148	1.214	1.149	0.996
4	4	25	0.851	0.989	0.785	0.795	1.162
10	10	42	1.342	1.420	1.263	1.371	1.059
7	7	115	1.132	1.032	1.144	1.048	0.986
3	3	41	0.889	0.968	0.803	0.823	0.979
8	8	81	1.238	1.223	1.273	1.307	1.041
8	8	50	1.079	1.134	0.990	0.916	1.055
5	5	26	0.606	0.559	0.743	0.688	0.826

5	5	22	1.041	1.073	1.040	0.998	1.073
5	5	53	1.203	1.203	1.238	1.242	0.940
22	22	200	1.148	1.108	1.177	1.158	1.005
5	5	42	0.825	0.770	0.821	0.770	1.011
4	4	144	1.443	1.286	1.497	1.317	0.939
4	4	17	1.279	1.268	1.187	1.181	1.077
2	4	15	1.076	1.195	1.129	1.257	0.953
6	15	221	1.341	1.324	1.289	1.264	0.999
15	15	86	0.673	0.722	0.700	0.644	1.079
5	6	18	1.000	0.922	0.934	0.864	1.071
7	7	54	0.990	0.937	0.966	0.960	1.025
4	4	28	1.326	1.233	1.240	1.175	1.043
2	2	29	1.200	1.199	1.105	1.108	1.086
5	5	34	1.540	1.546	1.412	1.409	1.085
8	8	120	0.740	0.719	0.748	0.738	1.008
13	13	103	0.852	0.822	0.780	0.782	1.073
11	11	73	0.957	0.974	0.973	0.969	0.956
4	4	26					
11	11	51	1.178	1.051	1.249	1.170	0.955
6	6	48	0.755	0.729	0.766	0.767	0.939
7	7	27	1.045	0.859	0.963	1.115	0.940
4	4	19	0.916	1.040	0.937	1.068	0.966
9	9	153	1.881	1.532	2.188	1.783	0.884
3	3	46	0.766	0.737	0.770	0.700	1.022
4	4	19	1.318	0.978	1.134	0.913	1.147
2	2	4	1.429	1.636	1.319	1.516	1.083
2	2	8					
2	2	7	1.382	1.326	1.607	1.604	0.814
5	5	73	0.530	0.558	0.531	0.567	1.014
9	9	91	0.731	0.658	0.670	0.632	1.021
4	4	16	0.982	1.000	0.978	1.004	1.110
15	15	116	0.921	0.990	0.847	0.887	1.017
3	3	16	11.855	5.169	12.512	5.531	0.952
13	13	56	1.268	1.226	1.405	1.215	0.979
2	2	4					
21	21	104	1.083	1.126	1.036	1.177	0.960
13	13	76	1.130	1.023	1.058	0.999	1.068
2	2	2					
8	8	59	1.053	1.227	1.038	1.050	1.014
3	3	37	0.637	0.623	0.648	0.627	0.991
2	2	18	1.175	1.134	1.171	1.136	0.998
18	18	178	0.901	0.907	0.954	0.940	1.039
5	9	60	1.391	1.334	1.490	1.401	0.965
6	6	17	1.366	1.438	1.369	1.564	0.923
9	9	56	1.041	0.925	0.972	0.897	1.095
4	5	53	0.851	0.870	0.794	0.815	1.033
9	9	60	1.020	0.919	1.040	0.991	0.963
7	7	105	1.692	1.516	1.734	1.551	0.960
8	8	164	0.675	0.611	0.662	0.619	0.990
6	6	63	0.884	0.988	1.034	1.009	1.079
6	6	34	0.753	0.805	0.803	0.809	0.938
12	12	109	1.202	1.164	1.063	1.133	1.015
10	10	34					
9	9	54	0.934	0.858	0.874	0.815	1.027

2	2	4					
25	25	155	1.277	1.286	1.214	1.261	1.019
3	3	12	1.436	1.320	1.306	1.205	1.099
5	5	28	1.175	1.177	1.115	1.121	1.054
2	3	9					
2	2	12	1.520	2.049	1.230	1.664	1.236
4	4	13	0.579	0.536	0.562	0.521	1.031
2	2	6					
4	5	61	0.771	0.896	0.752	0.792	0.991
2	2	5					
1	2	6					
4	9	65	1.164	1.333	0.899	1.001	1.336
4	4	22	1.358	1.238	1.293	1.183	1.050
1	3	3					
4	4	9	0.863	0.929	0.964	0.883	0.954
8	8	55	1.174	1.094	1.112	1.082	0.976
3	3	19	1.057	1.103	1.123	0.994	0.983
2	2	4	1.140	1.227	1.195	1.290	0.954
3	3	6	1.345	1.107	1.373	1.134	0.980
3	3	18					
10	10	77	0.802	0.841	0.791	0.818	1.029
10	10	78	0.949	0.896	0.858	0.808	1.050
14	14	131	0.909	0.921	0.896	0.914	1.006
4	4	28	0.696	0.703	0.727	0.728	0.957
3	3	19	0.902	0.869	0.904	0.846	0.997
6	6	31	1.023	1.030	0.965	0.940	1.027
5	5	36	0.866	0.823	0.874	0.834	1.032
2	2	2	0.480	0.465	0.872	0.848	0.551
3	3	13	0.804	0.809	0.659	0.740	1.108
8	8	46	0.799	0.744	0.808	0.790	0.946
4	4	31	1.234	1.126	1.340	1.223	0.949
4	5	12	1.204	1.207	1.161	1.168	1.037
3	3	9					
7	7	59	0.921	0.931	0.914	0.933	1.017
5	5	40	0.928	0.928	0.960	0.964	1.018
9	9	58	0.843	0.942	0.948	1.024	1.049
9	9	43	1.533	1.476	1.503	1.342	1.028
3	3	12					
8	8	241	1.072	0.996	1.110	1.028	0.950
5	5	12	1.317	1.265	1.312	1.278	1.015
3	8	34					
4	4	64	0.772	0.746	0.724	0.743	1.008
4	4	11	1.043	1.010	0.918	0.893	1.136
5	5	25	0.819	0.735	0.771	0.711	0.987
6	6	27	0.883	1.006	1.036	1.134	0.896
3	3	15					
10	10	81	1.306	1.224	1.325	1.259	0.946
5	5	42	1.051	0.949	1.049	1.025	0.979
7	7	38	0.866	0.880	0.863	0.905	0.940
7	7	41	0.876	0.774	0.742	0.652	1.112
2	2	11	1.029	1.045	1.003	1.022	1.026
3	3	8	1.633	1.649	1.251	1.268	1.305
14	14	64	1.039	0.980	1.070	0.991	0.999
2	2	6					

4	4	24	0.797	0.775	0.769	0.751	1.036
3	3	25	0.779	0.842	0.634	0.831	1.061
11	11	49	0.819	0.883	0.849	0.820	1.085
7	7	29	0.913	1.064	0.759	0.888	1.094
5	5	22	0.923	0.971	0.946	1.057	0.923
6	6	59	0.824	0.874	0.730	0.786	1.048
4	4	57	0.841	0.768	0.855	0.806	0.964
2	2	20	0.992	1.114	0.964	1.079	1.068
2	2	6					
7	7	31					
4	4	10	1.197	1.165	1.042	1.018	1.020
5	5	24					
3	3	12	0.709	0.812	0.661	0.759	1.073
11	11	70	0.692	0.700	0.750	0.778	0.997
6	6	23	1.372	1.262	1.545	1.428	0.888
2	4	8					
14	14	59	1.028	1.055	1.155	1.181	0.954
3	3	10	0.813	0.814	0.928	0.932	0.876
3	3	7					
2	3	12					
5	5	39	0.992	0.914	0.977	0.936	1.033
2	2	19	1.201	1.134	1.230	1.111	0.980
3	3	16	0.933	0.878	0.920	0.856	1.014
5	5	32	0.983	0.990	1.052	0.984	0.980
5	5	20	0.860	0.858	0.853	0.854	1.009
4	4	52	1.114	1.078	1.246	1.195	0.908
2	2	8					
5	5	23	0.948	0.975	0.956	0.986	0.992
9	9	47	0.848	0.708	0.927	0.712	1.035
3	3	15	0.950	0.942	0.963	1.007	1.000
4	4	41	1.236	0.980	1.190	1.006	1.047
10	10	65	1.147	1.076	1.234	1.088	1.001
4	4	41	1.322	1.324	1.437	1.309	1.001
3	3	16	1.580	1.508	1.470	1.373	0.998
2	3	5	0.783	0.835	0.774	0.829	1.049
24	24	160	1.483	1.553	1.673	1.628	0.998
3	3	6	1.408	1.289	1.433	1.317	0.983
3	3	6	1.622	1.597	1.039	1.099	1.458
7	7	51	0.727	0.894	0.652	0.780	1.025
3	3	26	1.380	1.227	1.380	1.318	0.934
2	2	8					
3	3	19	1.411	1.430	1.519	1.542	1.006
8	8	27					
2	2	4	1.386	1.327	1.446	1.390	0.959
2	2	11	1.179	1.084	1.209	1.127	0.988
4	4	24	1.115	1.160	1.163	1.191	1.032
4	4	38	2.091	1.891	2.193	2.023	0.954
2	2	5					
3	3	16	0.725	0.694	0.716	0.688	1.012
3	3	6					
3	3	8					
2	2	8					
2	2	4					
3	3	13					

2	2	5	0.722	0.716	0.786	0.782	0.919
3	3	11	1.057	1.083	0.904	1.096	0.992
2	2	2					
2	2	5	2.655	1.793	2.846	1.929	0.933
2	3	30	1.080	1.121	0.910	0.998	1.110
2	2	3					
3	3	26	0.802	0.852	0.769	0.806	1.043
2	2	6	1.273	1.244	1.259	1.234	1.012
4	5	26	0.982	0.903	0.913	0.895	0.925
3	3	23	0.545	0.528	0.557	0.530	1.000
5	5	31	0.884	0.916	0.888	0.923	0.996
10	10	52	1.511	1.500	1.601	1.625	0.942
2	2	4					
2	2	4					
3	3	31	0.946	1.181	0.959	1.059	1.082
2	2	12	1.230	1.161	1.095	1.038	1.123
2	2	4					
2	2	4	1.378	0.918	1.351	0.882	1.045
5	5	15	0.776	0.848	0.671	0.737	1.156
2	2	4					
2	2	6	0.710	0.689	0.610	0.595	1.163
3	3	6	0.868	0.954	0.779	0.859	1.114
2	2	6	1.255	0.942	1.398	1.160	0.810
3	3	14	1.296	1.303	1.265	1.276	0.941
9	9	36					
2	2	5	1.066	1.056	0.994	0.988	1.073
2	2	4	1.597	1.264	1.357	1.078	1.177
4	4	23	1.564	1.977	1.425	1.424	1.347
2	2	5	1.112	1.036	0.996	0.931	1.117
2	2	3	0.847	0.873	0.735	0.831	1.188
3	3	15	0.756	0.760	0.838	0.832	0.987
3	3	14	0.592	0.621	0.529	0.556	1.119
3	3	6	0.872	0.899	0.795	0.823	1.097
13	13	50	1.035	1.075	1.002	1.019	1.058
2	2	8					
6	6	41	1.013	0.948	1.041	0.929	1.009
2	2	4					
3	3	7	1.093	1.217	1.344	1.501	0.874
4	4	10					
2	2	4					
4	4	11	1.228	1.134	1.408	1.242	0.942
2	2	9	0.952	0.956	1.034	1.042	0.921
2	2	6	0.951	0.934	1.016	0.926	0.936
2	2	4					
4	4	10					
2	2	7	0.880	0.820	0.882	0.825	0.997
2	2	10					
2	2	7					
6	6	15					
2	2	4	1.334	1.202	1.411	1.276	0.945
2	2	44	2.694	2.215	2.572	2.331	0.951
3	3	8	0.960	1.063	1.171	1.153	0.925
15	15	80	1.079	1.104	1.130	1.105	1.003
4	4	12					

6	6	11	1.231	1.108	1.265	1.142	0.973
3	3	8					
2	2	8	1.034	1.199	0.978	1.139	1.057
3	3	30	1.283	1.500	1.459	1.414	0.934
2	2	10	1.292	1.355	1.128	1.198	1.103
7	7	121	1.322	1.227	1.400	1.221	1.002
2	2	2					
8	8	31	1.757	1.513	1.732	1.448	0.999
3	3	16	1.000	0.937	0.983	0.924	1.018
4	4	22	0.888	0.937	0.966	1.023	0.981
2	2	4					
4	4	27	1.152	1.076	1.232	1.156	0.935
3	3	11	1.136	1.010	1.531	1.489	0.770
2	2	4	1.790	2.107	1.301	1.537	1.376
2	2	2	0.337	0.321	0.343	0.328	0.983
4	5	16					
2	2	9					
2	2	2					
2	2	18	1.781	1.576	1.573	1.623	1.132
2	2	10					
2	2	3					
2	2	4	0.817	1.016	0.642	0.802	1.272
2	2	2					
3	3	8					
2	2	14	1.248	1.254	1.236	1.247	1.010
2	2	6					
4	4	45	0.633	0.565	0.683	0.608	0.908
3	3	7	1.260	1.092	1.300	0.992	0.969
2	2	3	0.920	0.901	1.195	1.175	0.770
3	3	5					
2	2	4	1.896	1.514	1.880	1.507	1.009
2	3	18	1.024	0.926	1.017	0.928	1.011
2	2	5					
4	4	18	0.967	0.897	0.923	0.859	1.048
2	2	4					
3	3	10	1.436	1.066	1.213	1.080	1.326
5	5	22	0.934	1.112	0.953	1.010	1.001
3	3	6					
7	7	21	0.961	0.945	0.904	0.920	1.063
11	11	61	1.622	1.721	1.532	1.530	1.025
2	2	23	1.148	0.944	1.127	0.994	0.987
2	2	9	1.116	1.343	1.349	1.628	0.828
2	2	8					
3	3	15					
2	2	2	0.809	0.769	0.873	0.832	0.927
2	2	2	1.581	1.603	1.417	1.442	1.116
1	2	3	0.761	0.680	0.779	0.698	0.977
2	2	5					
2	2	7	0.685	0.673	0.671	0.685	0.986
2	2	27	0.687	0.607	0.729	0.646	0.944
2	2	2	1.073	0.978	0.982	0.898	1.093
2	2	5					
5	5	20	1.361	1.524	1.026	1.152	0.917
2	2	23	0.664	0.662	0.643	0.644	1.032

3	3	14					
2	2	9					
2	2	6					
1	2	2					
2	2	2					
2	2	2					
2	3	3					
2	2	2					
2	2	6	1.166	1.145	1.105	1.090	1.055
1	2	2					
1	2	6					
2	2	5					
3	3	17	1.134	1.245	0.990	1.091	1.146
3	3	5					
2	2	12	1.092	0.994	1.000	0.914	1.092
2	2	2	1.437	1.406	1.119	1.098	1.285
7	7	34	1.418	1.251	1.436	1.271	0.988
2	2	7					
6	6	12	1.123	1.120	1.125	1.126	0.998
2	2	4					
2	2	4					
2	2	6					
2	2	2	1.197	1.088	1.098	1.002	1.090
2	2	2					
2	2	2					
2	2	2					
4	4	14	0.841	0.738	0.940	0.850	0.894
2	2	2					
2	2	4					
2	2	3					
2	2	6	1.677	1.483	1.731	1.536	0.969
2	2	2	1.174	1.165	1.089	1.084	1.079

0.970	0.912	0.972	0.900	0.976	0.967	1.039	0.750
1.018	1.214	1.313	1.305	1.364	0.994	1.000	1.248
0.858	1.182	1.310	1.218	1.350	0.993	1.054	1.376
0.969	1.150	1.213	1.170	1.200	0.984	0.989	0.915
0.935	1.099	1.046	1.016	1.026	0.991	1.027	0.984
0.993	0.808	0.889	0.852	0.945	0.924	1.081	0.826
0.967	0.946	0.997	0.996	1.065	0.954	1.048	1.098
1.002	0.979	1.063	1.000	1.051	1.006	1.034	1.205
0.847	1.190	1.269	1.196	1.347	0.972	1.061	1.287
1.063	1.148	1.257	1.258	1.381	0.918	1.077	
0.974	**0.393**	**0.410**	**0.422**	**0.472**	0.883	1.051	**0.392**
1.012	0.996	1.039	1.033	1.049	0.972	0.994	0.781
0.998	1.010	1.060	1.017	1.049	0.979	1.027	1.024
0.965	1.310	1.337	**1.515**	1.163	1.120	0.711	1.281
0.969	0.809	0.925	0.879	0.996	0.946	1.083	1.010
1.030	0.869	0.940	0.897	0.935	0.981	1.054	1.038
0.981	**1.509**	**1.543**	1.493	**1.572**	0.978	1.040	0.940
0.925	0.795	0.878	0.834	0.944	0.937	1.094	0.718
0.964	1.290	1.376	1.324	1.373	1.022	1.029	1.422
0.941	**0.456**	**0.501**	**0.503**	**0.568**	0.877	1.089	**0.578**
0.898	1.243	1.324	1.246	1.343	0.998	1.040	1.205
0.972	1.036	1.099	1.047	1.091	0.951	1.029	1.118
0.936	1.205	1.302	1.180	1.324	1.000	1.050	1.019
1.004	0.949	0.971	0.876	0.850	1.047	0.971	0.928
1.059	**0.644**	**0.601**	**0.604**	**0.623**	1.054	1.037	0.670
1.048	**0.407**	**0.418**	**0.438**	**0.499**	0.912	1.015	**0.535**
1.017	0.738	0.804	0.814	0.889	0.905	1.094	0.702
1.011	0.741	0.765	0.780	0.809	0.973	1.040	0.882
1.001	0.734	0.809	0.760	0.849	0.958	1.033	0.757
0.977	0.892	0.905	0.942	0.944	0.988	1.036	0.939
1.027	**0.538**	**0.543**	**0.552**	**0.571**	0.976	0.989	**0.653**
1.014	1.238	1.265	1.262	1.307	0.977	0.974	1.352
0.963	0.942	1.029	1.005	1.060	0.945	1.066	0.844
0.970	1.378	1.479	1.440	**1.514**	0.990	1.045	1.226
0.998	0.910	0.944	1.000	1.033	0.915	1.026	1.045
0.924	1.367	1.328	1.388	1.306	1.000	1.011	1.281
1.271							
							1.021
0.937	1.060	1.170	1.112	1.261	0.963	1.040	1.146
0.980	1.094	1.162	1.126	1.191	0.967	1.052	0.863
							1.032
0.945	0.882	0.949	0.888	0.930	0.990	1.037	1.010
1.078	0.832	0.856	0.823	0.899	0.962	1.010	0.827
1.003	0.852	0.911	0.921	0.980	0.964	1.037	1.011
0.940	1.628	1.502	1.459	1.341	1.102	0.981	0.851
1.045	0.864	0.867	0.758	0.807	1.067	1.006	0.845
1.213							1.101
1.029	0.947	0.988	1.014	1.049	1.008	1.012	1.027
1.055	0.733	0.791	0.747	0.779	0.999	1.038	0.701
1.011	1.118	1.086	1.054	0.982	1.096	0.962	1.171
0.983	0.769	0.808	0.768	0.851	0.951	1.067	0.711
1.008	0.745	0.862	0.734	0.825	0.988	1.021	0.834
0.942	1.420	1.650	1.551	1.706	0.952	1.064	1.072

0.958	1.879	1.909	1.832	1.769	0.916	1.000	0.721
1.016	1.101	1.123	1.094	1.112	1.027	0.990	0.971
0.980	0.809	0.854	0.819	0.850	1.048	0.968	0.872
1.015	0.921	0.925	0.910	0.932	1.001	1.014	0.856
1.131	0.822	0.847	0.828	0.878	1.003	0.994	0.721
0.978	0.764	0.839	0.809	0.852	0.953	1.039	0.802
0.957	0.557	0.621	0.632	0.670	0.904	1.020	0.726
1.017	0.904	0.865	0.946	0.864	1.012	0.937	1.074
1.049							
1.010	0.948	0.941	1.006	0.984	0.960	0.939	0.932
0.990	0.501	0.535	0.506	0.528	0.979	1.024	0.586
0.986	1.033	1.139	1.036	1.157	0.980	1.080	1.076
0.938	0.636	0.740	0.731	0.853	0.889	1.093	0.727
0.999	0.699	0.673	0.689	0.741	0.997	1.031	0.773
0.938	0.981	1.046	1.028	1.103	0.949	1.072	1.070
1.002	0.857	0.909	0.885	0.967	0.968	1.050	1.040
1.011	0.987	0.982	0.976	1.044	1.030	0.966	1.129
0.976	0.940	0.919	0.967	0.911	1.007	0.927	0.892
1.090	0.653	0.690	0.713	0.757	0.933	1.009	0.733
1.105	1.248	1.188	1.120	1.121	1.072	0.977	1.167
1.018	1.012	1.049	1.011	1.089	1.000	1.019	0.978
1.029	0.729	0.755	0.706	0.810	0.968	1.019	0.836
1.008	1.198	1.224	1.071	1.129	1.123	0.986	1.297
0.701							
1.061	0.827	0.903	0.883	0.926	0.992	1.023	1.020
1.052	1.165	1.105	1.116	1.009	0.960	0.905	1.186
0.994	0.571	0.623	0.607	0.661	0.947	1.065	0.735
1.080	1.200	1.229	1.180	1.176	1.038	0.992	0.953
1.029	1.885	1.871	1.804	1.831	1.075	0.981	1.552
1.070	0.901	0.928	0.851	0.906	1.025	1.016	0.707
1.026	0.707	0.650	0.635	0.684	1.118	1.022	0.827
0.958	1.312	1.303	1.273	1.205	1.019	0.957	1.003
0.989	1.943	1.864	1.879	1.790	1.016	0.929	1.106
0.982	0.826	0.837	0.812	0.820	0.998	1.031	0.912
1.058	1.020	0.988	0.934	0.955	1.043	1.022	1.107
1.118	0.535	0.479	0.499	0.493	1.095	0.987	0.515
0.997	1.044	1.068	1.050	1.104	1.006	1.007	1.152
0.962	1.057	1.106	1.169	1.042	1.037	0.982	0.880
1.079	0.768	0.769	0.828	0.778	0.980	0.922	0.909
1.022	1.005	0.984	1.079	0.970	1.022	0.949	1.170
1.013	1.067	1.094	1.089	1.079	1.029	0.986	1.093
0.984	0.977	0.924	0.905	0.860	1.032	0.908	0.980
1.015	0.646	0.720	0.714	0.791	0.935	1.092	0.892
0.995	1.139	1.108	1.109	1.065	1.039	0.969	1.144
1.043	1.114	1.142	1.067	1.116	1.010	0.980	1.136
1.541	1.282	1.097	0.989	0.849	1.303	0.842	1.097
0.996	0.919	0.935	0.943	0.955	0.990	0.981	1.009
0.973	0.836	1.061	0.876	0.927	1.105	1.021	0.977
	1.519	1.258	1.248	1.318	1.056	0.927	1.223
1.014	0.753	0.792	0.796	0.822	0.962	1.051	0.934
1.021	0.705	0.696	0.682	0.675	1.053	0.961	0.607
1.056	1.067	1.010	1.028	1.033	1.071	0.963	1.053
0.943	1.482	1.568	1.411	1.512	1.133	1.027	1.205
0.994	1.140	1.204	1.077	1.155	1.072	0.988	1.352

1.163	0.974	0.901	0.901	0.835	1.088	0.909	1.181
1.000	0.658	0.677	0.645	0.668	1.035	1.012	0.704
0.950	1.293	1.313	1.215	1.319	1.021	1.066	0.756
1.022	0.974	0.886	0.931	0.906	0.989	0.973	0.998
1.020	1.390	1.405	1.565	1.587	0.924	0.995	1.103
1.154	0.872	0.852	0.781	0.812	1.059	0.981	0.821
1.019	2.058	1.912	1.809	1.685	1.144	0.914	0.560
1.018	1.104	1.049	1.043	1.086	1.049	0.991	1.026
0.977	0.879	0.933	0.868	0.973	1.013	1.044	1.035
1.006	0.803	0.882	0.862	0.959	1.000	1.136	0.900
0.989	1.214	1.212	1.267	1.217	0.980	0.953	1.383
1.008	1.088	1.125	1.053	1.174	0.984	1.067	1.229
0.989	0.868	0.905	0.824	0.834	1.060	0.983	1.103
0.998							
1.005	1.198	1.091	0.996	0.896	1.080	0.983	1.121
0.980	1.007	1.059	0.953	1.013	1.013	1.035	0.864
0.969	0.869	0.902	0.885	0.944	0.993	1.051	0.937
0.987	0.897	0.974	0.849	0.968	1.043	1.072	0.826
1.000	1.217	1.250	1.224	1.192	1.032	0.992	1.031
1.027							0.700
1.013	0.721	0.747	0.759	0.766	0.976	0.989	0.834
0.990	1.063	1.002	1.044	1.059	0.955	0.900	1.000
1.015	0.971	1.000	0.958	1.024	0.993	1.025	1.082
0.999	0.764	0.825	0.793	0.854	0.959	1.056	0.877
1.038	0.645	0.660	0.658	0.671	1.012	1.001	0.710
0.973	1.254	1.165	1.309	1.137	1.009	0.907	1.220
0.895	1.463	1.509	1.401	1.473	1.051	0.988	1.644
0.954	0.519	0.524	0.773	0.581	0.909	0.837	0.766
1.025	1.288	1.206	1.199	1.152	1.088	0.972	1.610
1.002	1.205	1.369	1.341	1.447	0.912	1.124	1.436
0.988	1.210	1.354	1.141	1.280	1.066	1.101	1.073
1.019	0.806	0.888	0.851	0.919	0.972	1.067	1.121
0.951	0.814	0.831	0.844	0.911	0.944	1.029	0.986
0.983	0.828	0.877	0.886	0.895	0.935	0.991	0.839
0.878							
0.957							0.723
0.992	1.221	1.235	0.994	1.008	0.935	1.019	0.901
1.014	0.923	0.979	0.953	0.977	0.957	1.045	0.841
0.727	0.979	0.894	1.099	1.006	0.896	0.898	0.941
0.971	1.082	1.089	0.951	1.031	1.063	1.006	1.146
1.019							
0.933	0.846	0.870	0.913	0.910	0.961	1.040	0.963
1.024	0.945	1.003	0.984	1.042	0.967	1.051	1.095
0.941	1.384	1.337	1.249	1.305	1.021	0.989	1.315
0.939	1.073	1.119	1.075	1.000	1.128	0.913	1.208
0.982	0.939	0.900	1.026	0.980	0.905	0.945	1.187
1.092	0.835	0.840	0.860	0.859	1.081	0.981	0.819
1.090	1.485	1.348	1.359	1.242	1.091	0.908	1.466
0.920	0.909	0.946	0.956	0.988	0.950	1.039	1.098
1.000	1.138	0.963	0.856	0.956	1.118	1.025	0.924
0.953	1.163	1.248	1.164	1.273	0.978	0.965	1.455
1.036	0.944	0.760	1.122	0.950	0.820	0.973	1.144
0.951	0.985	1.117	1.038	1.153	0.941	1.124	0.718

0.977	1.441	0.996	1.291	0.895	1.123	0.680	0.958
0.996	1.179	1.133	1.221	1.160	0.967	0.952	1.134
0.987	1.058	1.079	1.028	1.047	1.027	1.009	1.108
0.981	0.695	0.818	0.794	0.926	0.899	1.069	0.961
0.927	1.120	1.148	1.172	1.210	0.950	1.052	1.084
1.022							0.942
1.144							
1.067	1.366	1.341	1.352	1.319	1.019	0.970	1.517
0.988	0.683	0.737	0.708	0.780	0.965	1.027	0.732
0.950							0.723
1.044	0.836	0.868	0.905	0.948	0.960	1.014	0.856
0.967	0.930	1.001	1.092	1.178	0.857	1.059	1.315
1.030	1.253	1.411	1.253	1.425	0.999	1.052	1.165
1.025	1.438	1.324	1.326	1.323	1.001	0.957	1.385
1.019	0.874	0.925	0.929	0.999	0.965	1.007	0.864
1.009	0.722	0.832	0.728	0.834	0.989	1.012	0.740
1.016	1.138	1.146	1.029	1.059	1.015	1.096	1.021
	1.295	1.274	1.179	1.197	1.054	0.983	1.191
0.929	1.111	1.031	1.042	0.970	1.041	0.904	1.056
0.944	0.769	0.807	0.776	0.772	1.001	0.981	0.932
1.016	0.850	0.832	0.828	0.869	0.962	0.964	0.978
0.928							0.818
0.826	1.357	1.550	1.423	1.634	0.947	1.104	1.933
0.956	0.650	0.651	0.663	0.699	0.901	1.023	0.588
0.930	1.271	0.940	1.521	1.129	0.840	0.728	1.030
1.180							
							0.986
0.989							
1.032	0.658	0.720	0.679	0.671	0.940	1.069	0.561
0.991	0.775	0.750	0.814	0.811	0.962	0.976	0.760
1.019	0.516	0.524	0.502	0.511	1.034	0.999	
1.067	0.781	0.790	0.739	0.777	1.035	0.975	0.859
0.449							1.564
1.020	1.296	1.234	1.189	1.212	1.016	1.040	1.277
	1.556	1.394	1.515	1.361	1.033	0.882	
1.075	1.314	1.359	1.308	1.246	1.059	0.979	1.102
0.948	1.049	1.077	1.033	1.102	1.069	0.988	1.027
							1.505
1.024	0.766	0.870	0.830	0.921	0.959	1.024	0.883
1.008	0.919	0.968	0.935	0.988	0.988	1.037	0.969
0.996							1.016
1.000	1.544	1.645	1.554	1.524	1.020	1.007	0.953
0.931	0.913	0.889	0.904	0.826	1.016	0.897	1.118
1.151	1.052	1.324	0.993	1.253	1.065	1.238	1.179
0.974	0.938	0.907	0.942	0.908	0.983	0.951	0.937
1.093	0.878	0.796	0.863	0.686	0.988	0.886	0.635
0.977	0.954	1.050	0.975	1.006	1.053	0.973	1.125
0.867	0.907	0.792	0.746	0.855	0.948	1.060	1.669
0.968	0.840	0.858	0.877	0.978	0.946	1.122	0.666
1.068	0.762	0.775	0.731	0.784	0.964	1.040	0.913
1.001	0.803	0.806	0.836	0.786	1.011	0.987	0.689
0.983	1.244	1.162	1.150	1.111	1.075	0.988	1.239
	1.370	1.208	1.184	0.980	1.247	0.882	1.208
0.979	0.921	0.884	0.931	0.958	0.991	1.006	1.004

	0.767	0.783	0.785	0.803	0.984	1.004	
1.047	1.372	1.337	1.313	1.321	1.021	0.952	1.270
0.957							0.982
1.032	1.040	1.145	1.131	1.171	0.998	1.016	1.055
							1.199
1.389							1.425
0.953							0.871
	0.797	0.937	1.188	1.273	0.802	1.023	
1.017	0.954	0.965	0.905	0.874	1.073	0.994	1.111
	1.130	1.090	1.189	1.151	0.956	0.950	
	0.694	0.763	0.928	1.024	0.752	1.083	
1.144	1.062	1.034	1.040	1.031	1.005	0.974	1.159
0.940	1.556	1.633	1.370	1.498	1.099	1.047	1.391
1.011							0.731
0.979	1.056	1.153	1.120	1.226	0.989	1.054	1.150
1.127	0.810	0.768	0.818	0.729	1.142	0.882	
1.109							
0.849							1.011
	1.345	1.275	1.191	1.132	1.136	0.934	1.185
1.020	0.828	0.878	0.866	0.873	0.967	0.984	0.797
0.958	1.183	1.330	1.248	1.361	0.957	1.058	0.756
1.012	0.886	0.826	0.784	0.859	1.019	0.979	0.781
1.040	0.641	0.693	0.645	0.699	1.000	1.063	0.746
0.936	1.344	1.330	1.282	1.272	1.055	0.974	1.066
0.995	1.344	1.223	1.315	1.200	1.028	0.896	1.261
0.989	0.906	0.873	0.916	0.906	0.943	1.057	0.986
0.998							
1.143							0.847
1.014	0.602	0.612	0.595	0.606	1.035	1.022	0.764
1.010	1.214	1.198	1.261	1.249	0.968	0.972	1.194
1.034							1.003
							0.876
1.049	1.038	0.984	1.097	0.957	1.013	0.937	1.120
1.086	1.004	1.095	1.017	1.138	1.036	1.094	0.873
1.109	0.886	0.812	0.842	0.795	0.982	0.932	0.851
1.007	1.118	1.095	1.203	1.152	0.958	1.080	1.089
	1.133	1.094	0.962	0.967	1.099	0.966	0.783
0.966	1.018	1.103	1.048	1.165	0.996	1.064	0.979
0.991							
	1.327	1.251	1.128	1.067	1.183	0.928	1.231
1.057	0.824	0.821	0.863	0.830	1.006	0.960	0.851
0.998							0.822
1.090							0.790
1.057	0.943	0.894	0.868	0.826	1.092	0.934	1.034
	1.130	1.161	1.132	1.165	1.004	1.010	1.181
0.944	1.299	1.350	1.372	1.325	0.982	1.035	1.279
1.030	0.849	0.867	0.870	0.805	1.028	0.954	0.980
1.046	0.917	0.870	0.763	0.804	1.065	0.934	0.908
0.971	1.101	1.042	1.180	0.929	1.169	0.901	0.858
1.047							1.255
1.041							0.742
1.000	1.584	1.567	1.429	1.427	1.082	1.014	1.134
							0.973

1.003	0.697	0.781	0.639	0.684	1.058	1.060	0.759
1.076	1.161	1.144	1.115	1.145	1.007	1.044	1.107
0.993	0.988	0.928	0.906	0.971	1.029	0.976	0.824
1.180	1.079	1.012	0.896	0.843	1.211	0.923	0.701
0.928	1.210	1.317	1.120	1.231	1.070	1.035	0.978
1.094	0.873	0.936	0.885	0.926	1.009	1.058	0.928
0.975	0.953	0.847	0.909	0.881	1.010	0.925	0.874
1.073	0.885	1.103	0.968	1.210	0.919	1.226	0.869
							1.266
	0.684	0.662	0.674	0.655	1.064	1.006	0.715
1.003							0.956
	1.141	1.014	0.913	0.896	1.235	0.874	1.027
1.179							0.913
1.055	0.614	0.630	0.617	0.618	0.952	1.048	0.582
0.949							1.174
	0.943	0.915	0.984	0.958	0.963	0.955	
1.021	1.199	1.087	1.068	1.055	1.121	0.985	0.977
1.031							0.906
	0.941	0.719	1.019	0.754	0.928	0.811	1.118
							0.751
0.982	0.755	0.725	0.814	0.783	0.933	1.020	0.882
0.964	1.118	1.157	1.242	1.184	0.905	0.963	
0.970	0.964	0.953	0.931	0.883	1.041	0.914	
1.000	0.860	0.961	0.950	0.947	0.931	1.002	0.833
1.029	0.822	0.793	0.803	0.777	1.022	0.949	0.957
0.938	1.289	1.327	1.228	1.290	1.049	1.033	1.102
							0.677
1.059	0.990	1.040	1.019	1.074	1.003	1.027	0.952
1.017	1.348	1.308	1.249	1.143	0.974	1.043	0.699
1.023							1.063
0.939	1.117	1.015	1.118	1.038	0.944	0.995	1.272
0.930	1.115	1.094	1.089	1.125	1.007	0.964	1.362
0.950	1.095	1.089	1.138	1.200	0.983	0.977	1.200
0.984							1.318
1.013							
1.016	1.655	1.713	1.638	1.598	1.057	0.965	1.204
1.028							
1.050							
0.973	0.788	0.725	0.788	0.763	0.968	0.944	0.691
0.935	1.106	1.098	1.196	1.156	0.916	0.948	1.157
							1.086
1.057	1.269	1.352	1.171	1.224	1.060	1.026	1.314
	1.068	1.164	1.094	1.195	0.982	1.072	0.943
0.987							
0.966							
1.025	0.993	0.935	1.228	1.002	0.935	0.915	1.000
0.995	1.472	1.559	1.536	1.571	1.040	1.018	1.101
							1.380
0.987							0.717
	1.543	1.146	1.367	1.018	1.135	0.731	1.005
							0.816
							1.005
							1.579
	0.858	0.840	0.940	0.922	0.918	0.963	0.935

1.023							
1.056							
							1.145
0.696							
1.061	0.753	0.809	0.661	0.712	1.147	1.057	0.776
							0.986
1.085	0.901	0.715	0.800	0.636	1.133	0.780	0.836
1.007							
0.954	0.909	0.936	0.922	0.956	0.969	0.974	0.989
1.001	0.424	0.470	0.454	0.531	0.891	1.126	
1.068	1.177	1.209	1.181	1.159	1.052	0.979	1.472
0.917	1.333	1.271	1.343	1.284	0.999	0.938	1.264
							1.068
							0.938
1.160	0.995	1.012	0.983	1.002	1.018	1.000	1.615
1.015	1.258	1.165	1.131	1.050	1.119	0.911	
							1.291
0.939							
1.127	0.780	0.746	0.799	0.730	1.030	0.861	0.808
							1.009
1.001	0.556	0.558	0.821	0.624	0.997	0.988	
1.133							0.845
0.853							
1.036	0.776	0.897	0.927	1.074	0.842	1.137	1.110
	0.805	0.788	0.767	0.753	1.053	0.963	0.818
1.022							
0.816							
1.062	1.349	1.315	1.168	1.229	1.074	0.959	1.388
0.960							
1.179							
1.052	1.379	1.259	1.017	1.065	1.203	0.899	
1.080							0.615
1.063	1.275	1.287	1.196	1.211	1.072	0.993	
1.061	1.546	1.337	1.440	1.263	1.084	0.890	1.069
	1.050	1.311	1.227	1.536	0.861	1.229	
0.947	0.931	0.948	0.927	0.916	1.009	0.936	0.987
							0.738
1.011	1.242	1.352	1.143	1.248	1.092	1.071	
							1.003
							0.965
0.951							0.874
1.036	0.882	0.928	0.892	0.941	0.995	1.035	
0.936							
							1.130
							1.123
0.960							1.053
							1.145
							0.641
	1.620	1.426	2.007	1.773	0.811	0.866	1.119
0.929							
0.931	1.557	1.668	1.586	1.541	0.995	0.997	1.278
1.128	0.814	0.682	0.844	0.710	0.970	0.825	
0.983	0.971	1.021	1.026	0.998	1.017	0.997	0.893
							1.174

0.927							1.435
							0.815
1.195							1.165
1.081	1.042	0.943	0.904	0.723	1.081	0.890	1.220
1.091	1.029	0.972	0.981	0.929	1.055	0.929	
0.975	1.306	1.240	1.241	1.241	1.014	1.016	1.751
							0.919
0.947	1.475	1.688	1.458	1.486	1.054	1.029	1.241
0.965	0.823	0.844	0.837	0.861	0.988	1.009	1.151
1.046	0.367	0.342	0.397	0.372	0.928	0.987	0.419
							0.970
0.963	1.398	1.371	1.355	1.337	1.086	1.010	1.233
1.059							
1.213							
0.982							
							1.150
							0.963
0.857							1.113
	1.247	1.285	1.308	1.352	0.958	1.014	1.314
							0.976
1.282							
							1.092
	1.436	1.362	1.653	1.573	0.873	0.934	1.206
1.036							
	0.630	0.640	0.630	0.641	1.006	0.999	0.611
0.913	0.665	0.781	0.726	0.848	0.958	1.135	0.719
1.138							1.381
1.010							
							1.051
0.823							
0.929	0.939	0.897	0.931	0.891	1.014	0.939	
	0.634	0.665	0.622	0.671	1.065	0.902	
0.956	0.686	0.693	0.737	0.746	0.937	0.993	0.540
							1.055
0.916							1.185
1.016	1.128	1.004	1.044	0.996	1.051	0.963	1.177
							1.132
1.004							1.178
0.969	1.290	1.155	1.212	1.088	1.070	0.946	0.915
0.906	1.022	1.002	1.011	1.011	1.017	0.982	1.467
1.150							
	1.004	1.018	1.046	1.113	1.039	0.903	
	0.969	0.936	0.995	0.965	0.979	0.951	0.920
0.979							
1.045							
0.920							
							0.710
1.113							
0.910	0.866	0.764	0.768	0.708	1.079	0.904	0.837
0.940							
							0.799
1.155	1.520	1.547	1.635	1.669	0.935	1.002	1.246
1.028	0.710	0.649	0.762	0.699	0.937	0.899	0.551

	1.314	1.275	1.312	1.439	1.007	0.971	0.908
	1.221	0.981	1.147	0.924	1.070	0.790	1.022
	1.142	1.090	1.119	1.071	1.026	0.939	
							1.255
	0.762	0.759	0.789	0.788	0.971	0.980	
							0.795
1.013							1.186
	0.630	0.704	0.596	0.668	1.063	1.100	
							0.633
							0.745
1.131	1.100	1.096	1.093	1.092	1.012	0.980	1.197
							1.493
0.939	1.459	1.245	1.044	0.894	1.405	0.840	0.993
1.008							
1.013	0.933	0.854	0.963	0.869	0.974	0.880	1.171
							1.014
1.028							1.035
							1.344
	0.461	0.445	0.544	0.526	0.853	0.948	
							1.340
0.937							
							1.413
							1.106
0.978	1.074	0.993	0.860	0.798	1.256	0.910	0.719
	0.518	0.532	0.462	0.476	1.128	1.010	
							1.500
							1.644
0.912							
1.023							

0.827	0.791	0.822	1.027	0.998	1001.60	83.22
1.331	1.207	1.241	1.045	1.057	150.39	57.72
1.480	1.223	1.409	1.090	1.134	3204.72	59.62
0.885	0.922	0.887	1.022	0.982	1351.69	51.78
1.012	0.954	0.936	1.067	1.020	1511.06	57.07
0.829	0.737	0.753	1.085	1.044	1688.35	59.86
1.089	1.006	1.042	1.058	1.012	4065.48	56.36
1.268	1.152	1.259	1.039	1.025	522.78	52.24
1.328	1.158	1.275	1.050	1.063	2831.70	52.57
					142.11	37.72
0.402	**0.351**	**0.373**	1.098	1.028	815.26	43.72
0.723	0.790	0.777	0.999	0.971	782.95	42.69
1.017	0.956	0.983	1.037	1.044	825.42	47.04
1.647	0.993	1.171	1.188	1.273	938.93	41.24
1.037	0.928	0.988	1.067	1.053	2729.98	47.01
1.067	0.984	1.017	1.019	1.028	1132.40	41.85
0.938	0.884	0.906	1.036	1.021	3488.28	46.32
0.721	0.784	0.683	1.122	1.051	411.23	50.00
1.470	1.354	1.431	1.033	1.060	2463.79	49.08
0.606	**0.578**	**0.589**	1.010	1.014	2183.03	48.79
1.263	1.125	1.211	1.023	1.054	2513.18	43.79
1.188	1.052	1.125	1.055	1.057	1269.60	38.89
1.015	0.950	1.042	1.132	1.054	1111.35	34.74
0.857	0.927	0.919	1.000	0.975	781.73	37.39
0.629	**0.660**	**0.617**	1.046	0.946	396.48	38.28
0.532	**0.554**	**0.527**	1.019	0.975	908.74	44.28
0.729	0.700	0.720	1.075	1.060	669.28	43.89
0.917	0.850	0.894	1.032	1.030	327.65	43.23
0.800	0.748	0.803	1.018	1.061	1060.06	38.99
1.019	0.921	0.967	1.014	1.043	744.55	33.83
0.650	**0.640**	**0.625**	0.964	0.965	397.54	37.08
1.384	1.373	1.414	1.019	0.973	439.20	32.23
0.814	0.771	0.806	1.066	1.036	1372.94	33.72
1.266	1.218	1.246	1.030	1.051	1784.56	41.57
1.165	1.018	1.123	1.059	1.086	76.88	25.84
1.440	1.240	1.324	1.068	0.991	476.23	37.13
					37.96	40.91
1.066	1.010	1.060	1.011	1.034		
1.109	1.107	1.100	1.032	1.035	690.43	31.64
0.876	0.783	0.799	1.059	1.031	2076.45	30.28
1.162	0.910	1.032	1.132	1.116		
1.021	0.995	0.994	1.056	1.032	476.78	33.70
0.816	0.861	0.858	0.977	0.985	437.66	26.68
1.061	0.953	0.995	1.026	1.039	736.90	32.19
0.899	0.935	0.891	0.937	0.984	705.21	30.51
0.757	0.924	0.832	0.910	0.929	166.96	25.21
1.207	0.968	1.067	1.137	1.085	613.83	30.79
1.026	1.102	1.115	0.933	0.971	705.53	27.09
0.690	0.751	0.666	1.022	0.983	701.77	36.03
1.193	1.122	1.205	1.025	1.042	860.10	34.02
0.716	0.688	0.712	1.053	1.021	2552.82	34.92
0.819	0.748	0.743	1.035	1.003	283.98	30.68
1.175	1.053	1.089	1.060	1.073	726.38	32.33

0.623	0.663	0.602	1.010	0.951	567.58	28.12
1.006	0.956	0.985	1.048	1.010	321.15	21.84
0.820	0.891	0.923	0.991	0.933	468.41	27.46
0.841	0.788	0.790	1.047	0.934	92.01	25.95
0.736	0.692	0.662	1.053	0.985	62.16	27.49
0.786	0.744	0.755	1.044	0.993	1356.32	32.54
0.762	0.640	0.674	1.100	1.052	704.20	28.94
1.039	1.179	1.108	0.947	0.977	682.58	25.77
					71.64	34.07
0.961	0.883	0.924	1.043	1.028	274.73	25.97
0.623	0.597	0.599	1.019	1.011	158.18	29.55
1.067	1.030	1.084	1.035	1.020	473.45	29.65
0.753	0.684	0.709	1.081	1.002	1358.38	31.93
0.724	0.757	0.733	1.001	0.996	1246.53	30.06
1.109	0.999	1.039	1.065	1.057	1346.21	27.92
1.116	1.068	1.062	1.044	1.027	781.37	29.68
1.122	1.136	1.109	0.993	0.974	346.63	18.38
0.890	0.972	0.923	0.974	0.966	512.93	26.00
0.681	0.795	0.719	0.989	0.983	424.96	18.68
1.259	1.235	1.251	0.959	0.977	617.77	21.30
0.977	0.923	0.957	1.029	1.028	971.61	26.98
0.843	0.821	0.815	1.038	0.987	799.81	26.70
1.318	1.299	1.378	0.960	1.022	556.51	25.38
					271.11	28.98
1.081	1.038	1.015	1.067	0.998	228.49	24.80
1.088	1.252	1.215	0.944	0.936	216.78	21.40
0.749	0.664	0.692	1.092	1.004	233.33	16.93
0.973	1.036	0.999	0.952	0.958	161.76	22.70
1.597	1.496	1.616	1.004	1.054	1238.82	21.50
0.747	0.661	0.690	0.984	1.027	475.05	20.57
0.779	0.806	0.707	0.992	0.937	271.12	20.91
0.960	1.042	1.019	0.987	0.968	667.30	20.53
1.066	1.092	1.109	1.046	1.004	594.48	13.48
0.960	0.951	0.985	1.039	1.013	99.27	27.56
1.152	1.084	1.091	1.085	1.045	254.96	18.26
0.492	0.564	0.528	0.910	0.943	82.63	20.52
1.211	1.133	1.172	1.030	1.012	1068.15	22.71
0.920	0.926	0.957	1.000	1.020	144.54	11.51
0.898	0.936	0.913	0.988	0.949	345.97	18.47
1.206	1.087	1.195	1.022	1.082	183.71	24.11
1.118	1.031	1.082	1.055	1.019	725.00	18.86
0.923	1.131	1.037	0.863	0.933	293.77	20.59
0.914	0.824	0.899	1.051	1.027	343.49	26.47
1.141	1.089	1.168	1.033	1.050	442.75	20.74
1.107	1.182	1.158	0.960	0.991	135.18	26.14
1.123	1.050	1.118	0.988	1.014	30.26	10.50
1.005	0.991	1.042	0.986	0.993	557.21	21.86
0.835	1.061	1.007	1.009	0.922	339.00	22.06
1.160	1.309	1.248	0.934	0.939		
1.010	0.862	0.919	1.124	1.077	572.07	23.81
0.564	0.688	0.644	0.901	0.972	53.01	13.54
1.011	1.033	1.038	1.024	1.013	266.88	16.86
1.099	1.165	1.099	0.996	0.961	516.42	25.25
1.428	1.443	1.500	0.947	1.055	139.85	25.24

1.095	1.413	1.319	0.835	0.918	70.27	25.14
0.714	0.712	0.723	1.077	0.994	351.93	17.74
0.675	0.850	0.763	0.889	0.883	166.42	25.00
0.932	0.899	0.944	0.980	0.996	223.15	15.79
1.138	1.122	1.164	0.983	1.021	269.56	21.22
0.785	0.873	0.807	0.925	0.926	118.75	13.72
0.502	0.634	0.572	0.914	0.899	553.82	21.28
1.137	1.077	1.112	0.999	1.033	181.95	16.48
1.065	1.196	1.115	0.984	0.989	168.60	14.22
0.947	0.910	0.963	0.987	1.056	149.84	22.08
1.309	1.317	1.344	0.964	1.060	123.60	17.99
1.353	1.102	1.062	1.059	1.026	85.86	17.65
1.123	1.072	1.128	1.002	1.036	525.60	23.62
					130.83	23.53
1.068	1.191	1.169	0.959	0.992	227.39	18.97
0.875	0.803	0.878	1.037	1.022	192.89	21.45
0.937	0.902	0.911	1.063	1.015	198.83	16.74
0.782	0.773	0.828	0.990	1.043	222.50	13.79
0.997	1.030	0.999	1.008	1.024	226.13	18.64
0.653	0.669	0.627	1.046	0.923	209.22	22.69
0.804	0.850	0.808	1.002	0.964	297.24	18.55
0.960	0.986	1.043	0.950	0.975	490.77	15.65
1.110	1.126	1.150	0.989	1.013	272.69	16.12
0.895	0.864	0.907	0.984	1.018	553.90	18.87
0.661	0.910	0.868	0.803	0.904	122.99	22.27
1.255	1.262	1.280	0.948	0.964	596.69	17.75
1.632	1.581	1.531	1.007	1.017	1096.21	17.51
0.668	0.771	0.871	0.865	0.991	153.68	15.58
1.625	1.554	1.639	1.007	1.011	403.20	16.56
1.645	1.306	1.456	1.070	1.129	153.65	11.06
1.112	1.033	1.087	1.053	1.060	40.86	7.73
1.112	1.064	1.093	1.050	1.000	429.01	14.73
1.029	0.892	0.967	1.056	1.068	490.20	15.31
0.796	0.882	0.779	0.938	0.936	169.94	12.21
					31.80	20.59
0.710	0.785	0.764	0.984	0.997		
0.985	0.922	0.990	1.015	1.083	83.22	20.55
0.876	0.906	0.960	0.968	1.028	300.28	18.65
0.857	0.949	0.869	0.991	0.902	61.55	20.51
1.150	1.126	1.114	0.978	0.974	125.28	13.05
					70.42	20.00
0.889	1.143	1.058	0.944	0.976	101.15	10.21
1.155	1.020	1.070	1.047	1.000	280.21	20.00
					205.59	19.95
1.415	1.214	1.305	1.007	1.024	144.15	8.69
1.300	1.159	1.255	1.041	1.066	96.65	10.23
1.209	1.113	1.138	0.978	1.007	261.97	19.77
0.827	0.886	0.900	0.923	1.000	80.26	10.98
1.488	1.547	1.660	0.920	1.036	221.02	13.95
1.076	1.093	1.089	0.960	0.996	250.62	10.99
0.773	0.915	0.850	1.009	0.920	177.72	19.35
1.333	1.350	1.309	1.003	0.967	304.70	12.73
1.216	1.134	1.191	0.967	0.980	235.34	14.86
0.763	0.694	0.740	1.055	1.026	87.75	7.88

0.802	1.006	0.847	0.952	0.829	70.75	19.06
1.126	1.197	1.308	0.965	0.976	151.25	11.11
1.167	1.098	1.174	0.979	1.042	637.71	15.04
1.063	0.850	1.006	1.018	0.999	77.49	17.20
1.169	0.957	1.114	1.120	1.067	303.32	18.93
0.846	0.995	0.899	0.946	0.982	76.55	9.22
					134.20	18.82
1.455	1.449	1.484	1.004	1.014	539.62	12.07
0.740	0.771	0.750	1.040	0.957	88.46	7.14
0.655	0.756	0.672	1.007	0.897	43.41	5.34
0.857	0.890	0.883	0.995	1.014	86.58	16.33
1.452	1.180	1.419	1.033	1.081	68.87	13.89
1.233	1.232	1.311	1.020	1.106	30.91	17.31
1.506	1.303	1.500	0.984	1.056	90.24	11.08
0.822	0.867	0.842	1.006	0.993	388.41	15.83
0.770	0.793	0.775	1.004	0.973	172.75	9.02
1.078	1.119	1.128	0.966	0.996	154.74	11.13
1.304	1.209	1.391	1.000	1.084		
1.047	1.118	1.132	0.934	1.009	192.71	6.70
0.930	0.990	0.965	0.957	0.957	104.02	10.61
0.943	1.033	1.001	0.987	0.960	87.21	10.45
0.766	0.775	0.741	1.013	0.951	118.97	8.63
2.193	1.650	1.952	1.144	1.175	217.41	11.64
0.626	0.662	0.709	0.951	1.017	124.47	16.15
1.041	1.080	1.098	0.953	1.001	109.45	11.30
					80.60	16.10
0.961	0.932	0.914	0.890	0.954		
					57.27	16.08
0.591	0.468	0.538	0.993	1.008	166.36	14.25
0.764	0.726	0.734	1.008	1.050	303.09	14.18
					138.84	15.90
0.833	0.877	0.857	1.011	0.971	383.04	10.64
1.577	1.402	1.423	1.114	0.999		
1.225	1.356	1.336	0.913	0.939	124.40	8.28
1.092	1.135	1.101	1.005	0.982	181.84	6.17
1.093	1.004	1.049	1.021	1.040	104.38	5.76
1.508	1.509	1.521	0.996	0.992		
0.901	0.869	0.900	0.959	0.997	118.37	7.43
1.026	0.888	0.942	1.093	1.071	135.60	8.52
0.970	1.171	1.161	0.882	0.974	82.13	15.25
1.002	0.939	0.979	1.016	1.029	281.51	6.58
1.269	1.195	1.296	0.976	1.068	236.81	13.82
0.961	1.256	1.064	0.961	0.882	60.01	9.81
0.910	0.934	0.941	0.973	1.004	144.91	12.20
0.607	0.722	0.656	0.946	0.919	45.56	12.35
1.187	1.168	1.186	0.962	1.029	214.04	12.77
1.730	1.653	1.724	1.031	0.998	339.32	11.67
0.726	0.718	0.714	1.026	0.989	542.23	13.00
0.934	0.904	0.933	1.036	1.015	124.05	14.22
0.739	0.712	0.738	0.959	1.027	43.10	6.75
1.262	1.208	1.310	1.009	1.059	456.05	10.77
1.059	1.290	1.174	0.951	0.933		
1.020	1.026	1.041	0.978	0.969	88.67	5.38

1.269	1.225	1.272	1.018	1.009	256.53	7.98
0.982	1.026	1.032	0.957	0.990	75.89	9.09
1.127	0.988	1.061	1.067	1.057	54.71	5.45
1.271	1.255	1.338	0.954	1.050		
1.424	1.482	1.358	0.958	0.951	42.82	13.48
0.745	0.946	0.990	0.893	1.012	30.87	7.24
1.037	1.133	1.129	0.928	0.894	269.97	11.71
1.235	1.099	1.200	1.054	1.081	85.65	8.49
1.425	1.380	1.422	1.007	1.014	98.73	7.31
0.761	0.806	0.844	0.906	1.031	34.72	10.37
1.158	1.157	1.155	1.061	1.034	168.88	11.38
					105.17	12.50
					33.13	12.50
1.120	0.979	1.090	1.033	1.096	27.28	9.77
1.212	1.314	1.369	0.895	1.049		
0.772	0.761	0.768	1.041	0.980	94.21	4.46
0.825	0.733	0.835	1.020	1.038	160.66	10.52
0.829	0.743	0.762	1.051	1.063	320.67	8.20
0.700	0.735	0.759	0.936	0.957	0.00	5.26
1.094	1.002	1.034	1.063	1.016	63.28	8.79
1.270	1.473	1.457	0.963	0.997	37.65	6.50
0.970	0.900	0.988	1.076	1.061	140.22	10.54
0.771	0.833	0.764	1.015	0.902	54.27	11.83
0.841	0.811	0.805	1.034	0.987	69.93	6.24
1.184	1.226	1.199	0.975	0.956	143.01	9.25
0.905	1.000	0.908	1.002	0.894	28.97	8.63
0.845	0.879	0.852	1.061	0.955		
1.070	1.089	1.090	0.984	0.955	86.88	6.69
0.944	0.781	0.878	1.081	1.062	76.75	9.31
0.795	0.916	0.899	0.929	0.966	100.34	5.64
1.083	1.039	1.051	1.047	0.984	170.92	9.88
0.772	0.836	0.825	0.940	0.953		
1.023	0.960	0.992	1.068	1.077	812.76	10.06
					78.34	6.60
1.218	1.249	1.257	0.951	0.986		
0.920	0.868	0.880	1.007	1.028	127.74	4.63
0.714	0.962	0.841	0.961	0.948	58.88	5.21
0.730	0.841	0.817	0.945	0.949	76.76	10.49
1.008	1.071	1.037	0.973	0.965	53.41	2.71
1.335	1.050	1.178	1.123	1.119		
1.362	1.247	1.305	1.025	1.031	186.58	8.38
0.903	1.052	0.991	0.929	0.957	205.28	10.40
0.873	0.872	0.901	1.011	1.006	181.21	5.99
0.861	0.827	0.837	1.020	0.991	192.67	8.90
1.242	1.144	1.208	1.096	0.967	63.89	10.07
0.715	0.822	0.797	0.928	0.876		
1.140	1.138	1.187	0.993	1.028	147.17	3.48
0.994	1.059	1.088	0.918	1.011		

0.811	0.767	0.810	0.986	1.031	34.70	3.28
1.238	1.277	1.212	0.981	1.107	68.40	9.85
0.798	0.850	0.814	0.966	0.934	95.03	3.16
0.734	0.729	0.769	1.022	1.005	63.74	5.74
0.803	1.069	0.943	0.899	0.877	55.10	5.76
0.887	0.913	0.902	1.019	0.997	52.95	3.97
0.840	0.971	0.948	0.944	0.961	133.54	7.38
0.853	0.771	0.761	1.057	0.982	55.92	9.60
1.557	1.188	1.469	1.065	1.218		
0.714	0.775	0.777	0.942	0.976		
0.981	1.194	1.233	0.800	1.016	21.07	4.24
0.992	1.029	0.986	1.021	1.009		
1.004	0.906	1.011	1.027	1.047	54.19	6.28
0.618	0.570	0.582	1.013	1.027	313.11	5.63
1.093	1.180	1.210	0.962	1.012	47.72	4.51
0.916	0.950	0.894	0.994	0.946	118.15	2.77
0.971	0.814	0.878	1.112	1.062	88.76	6.27
0.898	1.214	0.981	0.920	0.795		
0.691	0.870	0.804	0.863	0.911		
0.905	0.955	0.962	1.004	0.978	122.05	7.44
					77.19	8.61
					197.39	8.60
0.907	0.940	0.951	0.967	1.045	107.62	6.88
0.904	0.968	0.853	1.016	0.868	38.86	2.25
1.142	0.999	1.114	1.042	1.027	191.17	6.81
0.659	0.732	0.670	0.989	0.929		
1.006	1.034	1.078	0.997	1.050		
0.735	0.653	0.703	0.988	1.037	62.18	1.60
1.012	1.074	1.068	0.981	0.998		
1.407	1.119	1.239	1.045	1.058	65.56	8.13
1.328	1.289	1.573	1.021	1.081	233.53	6.52
1.259	1.195	1.346	0.983	1.039	164.87	7.96
1.444	1.467	1.617	0.898	1.085	75.22	6.00
					98.10	7.78
1.084	1.270	1.176	1.008	0.959	377.98	6.17
					81.41	7.73
					28.72	7.63
0.648	0.732	0.691	0.956	0.950	100.21	5.14
1.253	1.090	1.182	1.086	1.072	67.50	5.18
1.190	1.226	1.352	0.884	1.057		
1.214	1.464	1.361	0.897	0.915	103.20	7.51
0.888	0.897	0.896	0.976	0.933		
					40.08	7.19
					26.97	7.18
0.876	1.142	1.007	0.875	0.868	95.93	5.18
1.139	1.112	1.158	0.997	1.025	92.93	7.06
1.250	1.307	1.115	1.185	0.897		
0.753	0.679	0.717	1.027	0.976	41.75	4.48
0.892	1.189	1.061	0.845	0.879		
0.741	0.851	0.752	0.889	0.920		
1.078	0.892	0.975	1.171	1.079		
1.560	1.518	1.509	1.039	0.979		
0.939	0.960	0.971	0.973	0.995		

					40.89	6.79
					49.97	6.78
1.231	0.909	0.976	1.259	1.064		
					47.35	6.60
0.680	0.846	0.857	0.915	0.867	51.83	6.55
1.094	0.941	1.050	1.047	1.098		
0.808	0.831	0.868	0.946	0.967	89.30	6.46
					101.51	6.46
0.948	1.065	1.053	0.909	0.898	24.28	2.55
					63.36	6.37
1.346	1.487	1.432	0.953	0.929	53.35	3.76
1.270	1.251	1.282	0.996	0.953	110.74	4.51
0.965	1.258	1.143	0.848	0.895		
1.054	1.083	1.224	0.865	1.112		
1.515	1.984	1.830	0.904	0.930	85.68	6.27
					62.03	6.26
1.254	1.214	1.186	1.062	0.962		
					89.18	6.18
0.797	0.871	0.868	1.002	0.977	36.85	2.30
1.010	1.039	1.047	0.970	0.991		
					54.32	6.10
0.763	0.872	0.792	0.968	0.894	48.26	4.59
					72.69	6.03
1.010	1.116	1.022	0.993	0.901	62.46	6.01
0.738	0.886	0.856	0.971	0.997		
					82.62	5.88
					37.77	5.84
1.322	1.422	1.363	0.975	0.943	52.07	4.22
					30.99	5.77
					57.49	5.74
					60.84	4.16
0.584	0.710	0.679	0.864	0.941	39.88	4.46
					78.82	3.92
1.166	1.124	1.156	0.994	0.984	109.92	2.53
0.986	0.880	0.912	1.086	0.935	147.04	3.39
0.738	0.776	0.781	0.951	0.991		
					35.59	3.11
1.061	1.047	1.125	0.967	1.046		
0.885	0.881	0.813	1.094	0.908		
0.941	0.885	1.008	0.914	1.131	58.12	1.66
					44.96	5.07
					27.37	5.07
1.387	1.171	1.447	0.963	1.216		
1.235	1.129	1.166	1.020	1.055		
1.203	0.953	1.096	1.017	1.106	33.35	5.01
1.142	1.123	1.113	1.029	0.994		
0.640	0.613	0.617	1.044	0.989		
1.146	1.066	1.078	1.145	1.035		
					41.23	4.83
1.224	1.478	1.267	1.031	1.000	145.58	4.81
					28.36	4.77
0.912	0.840	0.830	1.061	1.008	97.60	1.95
1.166	1.400	1.246	0.851	0.944		

1.415	1.571	1.558	0.923	0.963		
0.813	0.832	0.834	0.915	0.937		
1.141	1.172	1.155	0.993	0.970	28.49	4.62
1.122	1.376	1.222	0.889	0.946	147.02	4.57
					113.72	4.46
1.983	1.612	1.976	1.009	1.075	340.76	4.41
0.827	0.909	0.823	1.010	0.891		
1.222	1.344	1.349	0.967	0.988	117.35	2.15
1.001	1.028	0.899	1.119	0.861	63.66	2.92
0.399	0.505	0.484	0.895	0.954	34.79	2.11
0.909	1.115	1.051	0.869	0.928		
1.270	1.250	1.244	0.994	1.039	47.92	1.90
					114.77	2.99
					25.21	4.12
1.275	1.104	1.177	1.038	1.025		
1.036	0.900	0.960	1.020	1.052		
1.032	1.133	1.009	1.028	0.983	71.42	3.90
1.388	1.278	1.358	1.028	1.046		
1.136	1.041	1.146	0.996	1.083		
					28.72	3.79
0.871	1.569	1.260	0.695	0.790		
1.265	1.214	1.281	0.992	1.039		
0.518	0.539	0.459	1.134	0.839		
0.695	0.664	0.627	1.078	0.974	76.67	3.59
1.465	1.351	1.481	0.962	0.998	39.29	2.57
1.091	1.023	1.060	0.988	1.028		
					48.26	2.71
0.429	0.562	0.488	0.871	0.980	76.36	2.20
0.807	1.167	0.897	0.904	0.757		
1.274	1.196	1.293	0.990	1.065	75.96	2.63
1.098	1.423	1.354	0.969	0.937	82.35	1.02
1.072	1.095	1.044	0.943	0.951		
1.163	1.086	1.095	1.060	0.980	50.23	2.10
0.944	0.942	0.944	0.975	0.986	159.99	3.21
1.717	1.315	1.458	1.114	1.159	35.33	3.21
					74.55	3.20
0.942	0.889	0.948	1.000	1.049		
					39.73	2.87
0.687	0.870	0.848	0.952	0.959		
					38.06	2.74
0.792	0.778	0.735	1.083	0.938	118.30	2.74
0.775	0.764	0.746	1.044	0.961		
1.138	1.217	1.161	1.034	0.955	30.49	1.12
0.573	0.598	0.623	0.903	1.033	27.75	2.60

0.819	0.980	0.889	0.926	0.893		
1.269	1.327	1.473	0.769	1.153		
1.428	1.349	1.543	0.930	1.126		
0.705	0.836	0.746	0.950	0.878		
1.212	0.997	1.025	1.189	1.012		
0.479	0.636	0.484	0.995	0.749		
0.769	0.860	0.893	0.952	1.024		
1.235	1.107	1.149	1.044	1.014	27.93	0.94
1.733	1.526	1.782	0.978	1.073		
1.061	0.861	0.925	1.152	1.058	86.24	1.69
					20.82	1.60
1.078	1.218	1.167	0.931	0.943	45.02	0.78
0.946	1.028	0.965	0.985	0.924		
1.004	1.081	1.062	0.954	1.006		
1.129	1.360	1.150	0.987	0.832		
1.401	1.362	1.432	0.983	1.035		
1.488	1.230	1.303	1.148	1.043		
1.137	1.024	1.060	1.078	1.018		
0.709	0.837	0.830	0.858	0.977	78.43	0.75
1.604	1.419	1.526	1.056	1.058		
2.406	1.416	2.084	1.160	1.449		
					31.76	0.50
					20.68	0.37

8	50	144.32	83.22	8	56
4	8	19.81	57.72	4	9
37	134	409.94	58.22	37	142
22	78	192.86	51.78	22	84
18	78	220.51	55.47	17	83
16	75	208.32	56.99	15	78
42	214	588.13	57.03	42	236
14	30	92.25	52.24	14	35
31	124	373.14	51.71	31	139
3	5	14.30	56.14	4	7
17	53	149.75	43.96	18	68
15	44	124.95	40.69	14	47
21	48	129.98	48.89	22	53
14	37	112.89	42.56	15	36
25	129	368.13	47.01	25	135
29	68	189.10	42.54	30	84
47	168	488.10	46.41	48	182
6	29	89.94	50.00	6	32
16	131	314.73	49.08	16	128
16	92	250.31	47.33	15	94
31	115	340.40	45.65	33	124
22	72	197.67	39.94	23	79
11	67	162.38	34.74	11	71
13	40	121.71	39.41	14	45
8	13	44.83	38.28	8	15
16	50	141.37	44.28	16	60
19	51	130.76	43.89	19	59
11	27	67.76	43.23	11	36
13	63	156.97	38.99	14	75
16	50	122.94	35.55	17	57
6	13	47.93	37.08	6	14
12	27	61.93	34.64	13	32
22	80	222.82	35.66	25	89
21	78	209.17	41.57	21	85
4	6	18.20	25.84	4	7
10	24	67.30	39.52	11	31
2	3	5.79	40.91	2	3
12	50	143.32	37.44	16	61
21	134	307.95	31.06	22	141
12	26	75.51	34.59	13	29
12	23	55.19	22.51	10	26
17	51	116.76	33.27	18	59
16	43	102.03	34.11	17	47
7	12	32.01	25.21	7	13
11	32	102.76	32.81	12	37
16	35	102.08	27.09	16	41
12	40	117.72	34.64	11	43
26	46	137.01	34.02	26	60
25	165	428.13	34.11	24	193
8	15	44.88	30.68	8	18
9	40	120.75	34.96	10	57

15	40	90.26	28.12	15	46
5	11	30.96	21.84	5	12
10	20	65.35	27.46	10	22
4	7	26.84	25.95	4	8
5	5	14.31	27.49	5	9
32	96	266.95	32.54	32	112
15	48	115.17	30.24	16	62
16	32	85.15	25.77	16	35
3	4	10.29	34.07	3	4
7	19	57.09	25.97	7	24
5	10	31.52	29.55	5	12
10	23	64.91	30.95	11	26
17	73	210.19	31.93	17	79
17	48	146.72	29.05	16	49
19	62	186.74	27.92	19	67
14	39	100.74	29.49	14	42
12	23	62.85	18.38	12	33
11	33	89.10	26.00	11	38
7	16	41.48	18.68	7	15
16	40	106.87	22.98	18	53
17	40	125.04	27.99	18	51
15	31	99.28	25.81	14	36
14	23	74.50	25.69	14	27
6	17	36.20	28.98	6	18
6	18	37.44	24.80	6	18
11	11	38.00	22.34	12	12
8	22	43.26	16.93	8	23
10	13	16.78	11.96	5	9
39	60	187.49	21.37	39	66
10	28	69.90	20.57	10	31
8	16	41.83	20.91	8	16
21	36	103.18	21.63	21	46
13	23	72.73	14.76	15	29
7	10	24.85	27.56	7	13
5	13	36.62	20.36	6	17
7	11	33.58	20.52	7	18
31	52	135.94	21.50	30	56
4	8	24.61	11.51	4	12
10	22	50.29	18.47	10	26
5	8	24.48	24.11	5	11
22	48	127.33	18.86	22	56
4	23	61.29	23.11	5	28
8	14	45.26	24.18	7	15
13	28	87.35	21.75	15	40
6	8	20.30	26.14	6	10
2	3	5.55	10.50	2	3
17	37	94.29	22.85	18	46
10	16	53.11	22.06	10	19
12	25	72.63	24.10	13	28
3	3				
8	14	39.07	15.24	7	14
21	34	101.23	25.08	20	42
6	9	17.20	16.72	4	8

3	3	6.09	25.14	3	3
9	23	61.48	19.24	10	26
6	13	34.49	25.00	6	13
7	14	35.34	16.30	7	15
5	18	34.10	21.22	5	17
5	6	17.48	13.72	5	5
17	33	99.59	21.10	16	41
7	11	33.01	18.08	8	14
3	4	16.02	15.66	4	5
5	11	33.80	22.08	5	12
5	7	14.91	15.17	4	8
6	10	25.56	17.65	6	12
8	25	78.65	23.62	8	24
3	6	12.24	23.53	3	5
6	10	31.38	18.97	6	10
6	10	29.76	21.45	6	12
8	15	33.33	16.74	8	17
3	13	35.00	13.79	3	14
8	18	48.48	18.64	8	19
4	8	23.44	22.69	4	7
9	19	46.57	14.31	8	24
17	36	96.69	15.65	17	43
10	17	41.52	14.50	9	18
12	18	50.73	19.61	13	21
4	7	17.61	22.27	4	8
15	25	75.10	17.75	15	29
31	65	168.14	17.21	30	71
4	7	16.03	15.58	4	6
12	19	58.58	16.56	12	25
4	9	21.33	12.44	5	11
2	5	10.54	7.73	2	5
11	30	67.49	15.80	12	38
11	29	75.55	15.31	11	28
4	7	20.74	16.79	5	9
2	4	5.82	20.59	2	3
		5.86	7.65	2	2
4	4	14.98	20.55	4	5
7	15	52.83	18.65	7	18
2	3	8.80	20.51	2	5
8	8	28.99	13.05	8	9
2	3	4.40	20.00	2	3
4	5	19.05	14.26	6	8
6	15	40.17	20.00	6	17
8	12				
7	10	27.91	9.53	8	12
3	4	17.09	10.23	3	5
12	22	51.84	19.77	12	22
2	5	12.22	10.98	2	5
7	8	22.63	13.95	7	8
4	20	51.88	10.99	4	22
3	7	22.87	19.35	3	9
6	18	48.97	12.73	6	18
6	13	32.84	14.86	6	14
2	4	11.10	7.88	2	4

5	7	9.60	19.06	5	7
3	7	16.35	11.11	3	6
17	33	86.01	16.62	18	39
4	6	25.94	18.95	5	9
4	24	53.49	18.93	4	26
2	3	6.46	9.22	2	3
4	8	16.50	18.82	4	7
10	33	82.77	12.84	11	38
6	10	28.91	11.03	8	12
2	2	3.71	5.34	2	2
6	10	22.50	18.12	7	14
3	3	9.48	13.89	3	6
2	3	5.68	17.31	2	3
3	3	10.87	11.08	3	4
7	19	55.32	15.83	7	22
7	15	29.97	9.02	7	17
7	10	24.17	11.13	7	10
4	5	20.16	7.64	5	9
4	5	17.43	13.97	5	11
3	3	7.95	7.71	2	2
2	4	14.61	8.63	2	6
8	22	45.16	11.64	8	30
3	8	21.96	16.15	3	9
3	5	12.43	11.30	3	4
2	2	8.04	16.10	2	2
2	3	11.52	16.08	2	4
4	9	21.54	15.95	5	14
8	15	36.77	14.18	8	21
4	5	15.38	15.90	4	6
10	15	50.49	11.27	11	18
		31.23	15.82	3	14
7	9	22.54	8.28	7	11
6	10	22.88	6.17	6	8
5	8	17.59	7.47	7	11
4	6	19.64	7.43	4	9
2	6	18.83	8.52	2	7
2	6	13.97	15.25	2	6
8	17	49.37	6.58	8	20
8	11	37.50	13.82	8	15
4	4	8.85	6.26	3	4
7	9	23.34	11.21	6	10
4	6	14.81	12.35	4	7
8	11	29.85	12.77	8	13
6	17	47.63	11.67	6	22
6	31	71.22	13.00	6	32
6	10	25.37	14.22	6	11
3	4	5.13	4.96	2	4
8	14	53.57	11.51	9	20
4	7	16.72	5.38	4	9

15	25	63.22	7.98	15	25
2	3	7.92	9.09	2	4
2	3	8.49	5.45	2	3
2	2	4.47	13.48	2	2
2	2	5.76	7.24	2	3
4	9	25.12	13.21	5	15
5	8	20.85	8.49	5	10
2	3	9.31	7.31	2	3
3	3	7.25	10.37	3	3
7	15	35.82	11.38	7	15
3	6	15.69	12.50	3	6
2	2	6.37	12.50	2	2
2	2	5.77	9.77	2	2
4	8	15.19	4.46	4	9
9	13	32.87	10.52	9	17
9	18	40.23	7.55	8	20
2	5	6.72	8.31	3	8
2	3	3.24	8.79	2	4
3	6	11.50	6.50	3	6
4	5	19.76	10.54	4	6
		3.11	11.86	2	2
3	3	10.57	11.83	3	4
4	5	13.59	7.33	5	7
3	6	13.76	9.25	3	5
4	4	6.66	7.11	3	4
4	7	20.59	6.69	4	10
4	6	11.56	9.31	4	7
4	5	10.43	5.64	4	5
7	10	33.77	11.01	9	16
7	40	105.18	10.06	7	42
3	3	12.88	6.60	3	5
2	7	17.99	4.63	2	9
2	2	6.24	5.21	2	2
4	4	11.38	10.49	4	6
2	3	10.39	2.71	2	3
7	11	29.77	8.38	7	14
5	7	26.80	10.40	5	8
4	7	23.38	5.99	4	7
6	6	21.17	8.90	6	7
2	2	7.32	10.07	2	2
		4.70	6.47	2	2
5	8	20.75	4.04	6	10

2	2	5.47	3.28	2	2
3	4	6.91	9.85	3	4
4	6	14.74	3.16	4	6
4	4	14.06	7.06	5	7
3	3	10.29	5.76	3	4
2	6	15.66	5.19	3	9
3	7	17.23	9.62	4	9
2	6	5.86	9.60	2	4
2	2	7.36	6.23	3	4
2	2	6.21	6.28	2	3
5	11	33.82	5.63	5	10
3	4	6.47	2.97	2	3
5	7	20.21	2.77	5	8
2	2	8.85	6.27	2	3
4	5	17.95	7.44	4	5
2	4	16.53	8.61	2	7
3	5	16.97	8.60	3	5
4	6	15.60	6.88	4	7
2	2				
3	9	26.12	8.45	4	12
		3.49	2.71	2	3
2	2	8.10	2.80	3	3
		7.61	5.15	2	5
4	5	14.96	8.13	4	6
8	11	29.79	7.27	8	13
4	7	23.37	7.96	4	8
2	5	11.53	6.00	2	5
3	5				
18	33	70.11	5.92	17	35
3	3	10.16	7.73	3	3
3	4	5.18	6.14	2	2
4	6	17.79	5.14	4	6
2	3	9.09	5.18	2	5
3	6	15.70	7.51	3	6
2	2	7.20	7.19	2	2
2	4	9.07	7.18	2	7
3	5	14.93	5.18	3	5
4	7	19.96	7.06	4	9
2	3	5.65	4.48	2	3

2	2	5.88	6.79	2	3
3	5	12.55	6.78	3	6
2	3	5.86	6.60	2	2
3	3	11.86	6.55	3	5
3	6	8.53	6.46	3	5
2	2	8.28	6.46	2	4
2	3	7.31	3.15	3	4
3	6	14.97	6.37	3	7
3	6	13.59	3.76	3	6
7	10	22.57	4.51	7	11
3	6	9.54	6.27	3	7
2	4	9.37	6.26	2	4
2	2	9.62	6.18	2	2
2	2				
2	2	7.03	6.10	2	2
2	2	5.94	4.59	2	2
2	3	9.44	6.03	2	3
3	3	8.77	6.01	3	3
2	2	7.76	5.88	2	3
2	2	3.43	5.84	2	2
3	5	5.96	2.11	2	3
2	2	6.41	5.77	2	3
2	3				
2	5	9.57	4.16	2	6
2	3	6.18	4.46	2	4
2	2	6.61	3.92	2	2
6	8	17.03	2.05	5	8
4	4	13.73	3.39	4	7
2	2	9.27	5.18	3	3
2	3	4.90	1.66	2	2
2	2	6.49	5.07	2	3
2	2	5.80	5.07	2	4
2	2				
2	2	6.71	4.83	2	2
2	6	19.47	4.81	2	7
3	3	2.89	2.17	2	3
6	8	19.71	1.95	6	10
		4.95	2.62	2	2

		0.00	1.56	2	2
2	2	5.60	4.62	2	2
3	7	17.96	4.57	3	7
2	3	9.07	4.46	2	3
7	25	48.45	4.41	7	25
4	5	13.51	2.15	4	5
2	3	6.67	2.92	2	3
2	2	5.62	2.11	2	4
2	3	6.83	1.90	2	4
2	5	16.83	4.14	3	6
2	2	6.71	4.12	2	2
		6.04	3.99	2	2
2	4	13.49	3.90	2	5
2	2	6.85	3.79	2	2
		22.38	3.61	2	14
4	7	20.34	3.59	4	6
2	2				
		4.96	3.52	2	3
		8.20	3.43	2	4
2	7	8.67	3.42	3	7
2	2	8.13	2.20	2	2
2	4	13.49	2.63	2	4
2	3	9.07	1.02	2	3
4	5	8.35	2.02	4	4
11	17	35.37	2.94	10	19
2	2	8.28	3.21	2	5
2	4	10.23	3.20	2	5
		0.00	2.99	2	2
		3.05	2.88	2	2
2	3				
2	3	8.09	2.74	2	4
2	3	10.95	2.74	2	3
		6.07	2.74	2	2
2	2	5.02	1.48	3	3
2	3	5.80	2.60	2	4

		2.95	2.36	2	2
		2.26	2.15	2	2
		5.85	2.11	2	2
2	2	6.13	0.94	2	3
2	2	7.84	1.69	2	2
2	2				
3	4	7.61	0.78	3	6
		0.00	0.59	2	2
		2.14	1.30	2	2
		6.59	1.25	2	2
3	3	9.82	0.75	3	4
2	3	5.74	0.50	2	3
2	2				

1095.91	67.83	8	53	164.67	67.83
109.59	36.24	3	7	15.45	44.30
2392.85	47.73	32	106	299.23	46.32
1641.66	59.07	25	104	267.87	60.14
1391.07	51.73	16	76	196.82	51.73
1679.25	51.97	14	77	218.70	51.97
4009.92	50.74	39	208	529.88	49.00
188.23	22.12	7	13	34.01	24.68
2509.35	47.26	29	105	325.18	48.46
94.02	26.32	2	3	9.87	26.32
604.67	44.93	18	58	147.83	44.93
714.78	47.28	15	35	103.14	44.41
692.96	46.30	21	52	114.53	43.89
486.04	30.70	12	27	69.14	30.70
2400.04	44.10	23	126	327.57	44.96
805.16	29.97	23	51	130.67	30.94
4161.44	48.29	53	220	602.78	47.18
300.06	50.00	7	27	69.04	50.00
1799.56	46.19	15	112	263.22	46.19
2508.61	49.03	17	99	264.01	49.03
2694.02	41.77	30	122	342.30	42.70
1170.53	32.58	22	66	188.57	31.53
987.93	39.29	11	60	151.52	39.29
306.32	23.65	9	18	60.49	23.65
480.87	41.80	9	16	49.21	41.80
732.41	33.58	13	39	113.42	33.58
566.23	22.90	12	38	86.04	22.90
393.49	42.90	10	25	62.36	43.23
724.55	36.48	14	46	119.32	34.59
732.87	39.83	20	53	133.40	38.54
462.25	37.08	6	18	63.04	37.08
384.48	34.04	13	24	55.61	34.04
1390.69	29.97	20	78	222.73	30.62
1415.14	30.02	17	56	161.78	30.02
42.36	19.48	3	5	9.20	19.48
327.72	26.35	8	16	44.44	30.54
325.53	25.12	12	31	76.15	25.36
2590.98	37.48	27	169	370.81	37.48
522.55	34.37	13	35	78.19	34.37
335.54	24.83	11	19	47.40	23.20
511.01	27.52	16	37	87.53	28.60
459.80	21.82	12	28	73.71	22.03
269.38	25.48	8	15	40.72	25.48
359.39	20.59	11	20	57.25	20.59
617.83	33.95	12	32	110.66	33.95
591.70	28.01	22	40	92.43	29.37
3181.86	37.24	27	198	485.35	36.43
242.37	33.92	9	14	39.75	33.92
771.44	34.21	10	42	127.09	36.84

451.33	21.35	11	28	77.01	22.83
146.65	17.06	4	8	20.02	17.06
249.11	20.40	7	16	45.42	20.40
109.63	35.44	5	9	28.25	35.44
64.35	24.17	5	7	15.74	24.17
1394.80	29.87	32	100	275.33	29.87
639.09	27.21	15	44	99.74	24.41
399.88	19.29	13	24	57.65	19.29
191.96	19.74	6	14	35.57	19.74
178.82	21.86	4	10	34.34	33.60
327.61	20.78	8	18	48.44	20.78
1259.57	31.58	17	75	199.01	31.58
1138.22	27.17	15	51	129.50	27.60
1375.91	27.70	18	69	204.42	29.36
483.03	25.71	14	28	74.42	24.39
231.67	15.88	11	17	44.36	15.88
523.99	23.71	10	28	70.73	23.71
166.99	13.16	5	7	25.52	13.16
483.18	17.60	14	41	107.51	18.95
861.90	23.81	17	36	100.11	23.81
771.82	22.27	13	30	94.58	22.27
161.47	12.39	7	9	23.00	12.39
280.00	19.92	5	16	37.55	15.85
221.95	11.57	8	12	26.96	11.57
303.34	21.38	10	26	57.83	21.38
135.47	19.94	9	17	32.51	15.95
1197.72	20.00	37	67	198.54	20.60
263.02	16.19	8	21	48.83	14.33
234.65	13.18	5	10	31.84	13.18
489.62	13.99	15	30	80.09	15.27
770.98	17.58	16	35	95.46	18.17
69.35	21.26	5	8	14.43	21.26
244.03	22.46	6	15	35.47	22.46
143.54	20.20	6	16	33.38	20.20
831.13	16.49	24	41	109.30	16.49
202.01	18.42	5	9	32.31	18.42
286.23	17.09	9	14	37.65	17.09
91.00	13.39	3	6	17.76	13.39
590.26	20.96	26	45	118.45	19.41
244.42	23.95	5	15	41.05	20.59
125.73	12.75	4	7	17.32	10.46
321.88	19.74	13	24	76.23	19.74
100.20	20.75	5	6	14.13	18.26
52.41	18.00	3	4		
757.14	20.08	16	40	103.72	20.08
119.11	10.29	5	9	20.54	10.29
41.56	16.25	2	2	6.73	25.62
545.04	25.25	13	33	72.15	25.25
36.00	13.02	3	4	7.70	9.38
275.88	22.63	10	18	38.37	21.02
321.83	15.42	12	22	58.65	15.42
71.69	13.56	3	3	11.28	17.98

48.83	13.71	2	3	6.82	13.71
222.78	15.59	8	19	44.04	16.58
163.93	25.00	6	10	29.21	25.00
142.65	9.68	5	7	19.72	11.04
175.75	16.73	5	14	21.45	13.88
201.31	19.70	7	10	32.88	19.70
427.08	16.49	12	28	73.58	16.49
130.67	10.98	5	9	20.60	10.98
26.92	9.40	3	3	7.03	9.40
47.30	12.30	3	8	19.04	12.30
125.05	13.11	4	7	18.08	13.11
166.63	15.35	5	9	28.67	15.35
336.60	15.10	5	14	43.20	15.10
168.54	17.24	6	8	23.35	17.24
197.99	19.24	7	12	30.78	19.24
104.35	12.45	6	13	24.12	12.45
291.56	16.81	4	16	37.49	16.81
221.31	13.65	5	13	35.92	13.65
161.81	12.70	7	10	24.51	12.70
281.13	10.31	11	17	45.30	10.31
246.72	13.46	9	19	50.37	14.64
422.71	17.03	11	18	43.05	16.91
56.73	12.73	3	6	10.50	10.00
336.14	12.33	10	20	52.46	12.65
791.74	14.43	25	42	112.28	14.43
95.58	13.51	3	3	10.37	13.51
215.49	11.08	8	11	31.12	12.58
188.94	15.90	5	8	25.92	17.28
69.88	5.80	2	3	3.73	5.80
323.20	11.76	9	28	66.22	11.76
464.09	11.96	9	27	62.55	11.96
86.84	8.65	3	3	11.11	8.65
67.86	13.83	3	3	9.87	13.83
279.15	18.65	7	18	51.89	18.65
				3.40	20.51
121.93	4.55	4	5	15.40	4.55
156.25	10.43	4	5	14.26	10.64
201.58	13.11	4	9	29.76	15.41
197.05	8.90	8	16	38.52	10.06
45.77	5.94	2	3	7.56	5.94
113.66	9.46	5	8	17.80	7.88
76.26	8.33	2	4	11.93	8.33
83.09	5.07	3	3	12.02	5.07
182.55	17.03	6	20	50.03	17.03
122.64	19.35	3	6	20.15	19.35
212.92	16.18	6	11	33.28	16.18
34.92	5.14	3	3	4.84	4.86
30.99	6.64	2	3	6.94	11.62

				4.98	7.69
179.85	19.01	5	10	22.45	19.01
498.76	11.58	15	29	66.09	11.58
48.78	6.71	2	5	9.34	6.71
364.71	18.93	4	30	66.72	18.93
421.11	13.61	11	35	85.27	13.61
150.47	8.00	7	13	27.96	8.00
55.62	11.41	4	5	11.50	11.41
53.78	8.80	2	2	6.34	8.80
71.37	17.31	2	6	9.96	17.31
174.27	15.24	4	5	19.09	15.24
240.14	13.13	6	14	40.61	14.37
148.44	11.16	8	15	37.03	12.40
148.31	10.47	7	12	24.35	7.85
32.07	8.75	2	5	14.65	8.75
148.35	5.90	3	6	20.22	6.84
39.94	5.03	2	3	5.31	8.38
64.64	6.22	2	4	11.74	6.22
286.64	16.16	9	29	58.67	16.16
78.68	11.46	2	6	15.00	11.46
37.81	8.17	2	2	6.17	8.17
123.67	14.25	4	9	23.52	15.95
200.99	12.64	6	15	30.35	12.64
67.68	8.38	2	3	6.28	8.38
264.75	7.87	8	14	33.28	7.87
83.10	5.66	5	6	13.28	4.58
69.03	15.79	2	2	6.75	15.79
331.18	9.84	13	17	33.95	8.73
95.07	6.40	5	6	19.77	6.40
133.25	4.80	3	6	20.60	6.97
119.40	8.52	2	4	9.65	8.52
461.81	10.40	11	30	86.02	10.40
160.59	5.97	4	5	14.02	5.97
32.56	6.09	2	2	6.02	6.09
160.85	10.50	6	7	21.71	10.50
60.54	9.64	3	8	27.50	9.64
153.48	8.56	5	7	23.11	10.05
388.37	11.67	6	16	50.95	14.32
473.07	11.73	6	27	70.56	11.73
130.19	10.78	4	10	25.84	10.78
34.94	5.75	3	4	9.18	5.75
349.76	13.18	11	19	57.41	13.18
94.51	7.54	5	7	18.50	7.54
89.96	6.30	4	5	15.98	7.37

				8.99	13.75
177.68	4.83	11	17	44.54	4.83
63.01	13.61	5	7	16.04	13.61
92.43	13.24	2	3	9.27	13.24
163.56	8.71	3	7	21.77	10.21
44.93	13.10	2	2	5.54	13.10
55.38	13.04	2	3	6.00	13.04
83.98	9.53	7	10	23.52	9.01
90.71	9.03	3	5	13.15	9.03
				8.32	12.77
35.70	4.34	3	4	8.60	4.34
75.14	9.69	2	4	3.11	9.69
97.50	9.68	2	3	9.48	9.68
159.32	8.23	6	12	35.59	8.23
98.83	6.66	7	7	21.72	6.66
355.21	7.27	10	22	39.34	6.19
				4.39	5.26
33.45	8.79	2	3	2.96	8.79
28.73	4.44	2	3	6.99	4.44
105.16	8.20	3	4	12.26	9.60
46.87	6.24	4	6	8.88	6.24
77.88	6.17	2	4	8.59	6.17
134.46	8.39	5	8	15.76	8.39
87.61	9.31	4	7	14.18	7.64
120.31	6.61	6	9	22.08	6.61
69.92	4.63	3	3	10.83	5.45
52.53	7.89	2	4		
811.23	10.06	7	45	118.63	10.06
84.14	7.51	6	9		
137.17	4.63	2	8	14.37	4.63
43.33	4.34	2	2	6.50	4.34
0.00	3.64	2	2	5.86	3.64
176.13	9.20	8	10	33.29	9.20
230.33	10.40	5	8	28.53	10.40
70.23	3.61	3	4	10.89	3.61
145.45	2.65	2	3	11.09	2.65
203.80	3.54	4	7	20.04	3.54

65.29	7.16	2	4	12.80	7.16
66.28	9.85	3	5	7.93	9.85
169.01	5.35	6	8	21.01	4.84
				8.55	3.24
31.30	6.52	3	3	8.63	6.52
137.44	7.94	4	9	22.21	7.94
95.38	9.62	4	10	20.44	9.62
33.82	9.60	2	3		
105.19	5.58	4	5	10.64	4.69
88.67	4.16	2	4	11.41	4.16
250.21	3.27	4	10	29.47	2.78
28.60	8.97	4	4	5.02	5.90
71.46	3.42	5	5	14.69	4.01
45.58	5.47	2	2	6.84	5.47
113.14	4.25	2	5	13.28	4.25
56.71	8.61	2	4	11.81	8.61
60.31	4.42	2	3	9.08	4.42
70.43	3.44	2	3	10.36	4.81
110.38	5.57	3	4	10.74	5.57
230.92	8.45	4	11	31.26	8.45
40.53	5.15	3	3	7.55	6.37
99.44	6.01	6	7	18.44	6.01
62.12	8.13	4	7	16.70	8.13
226.68	7.06	7	10	26.41	6.42
112.93	7.96	4	6	17.68	7.96
152.54	4.39	13	21	47.83	4.39
113.71	4.47	4	7	19.20	4.47
48.65	5.18	2	4	7.13	5.18
104.94	4.86	2	3		
				8.71	2.52
65.74	3.37	2	3	8.85	3.37
112.11	7.06	3	6	13.32	7.06
				2.52	5.05
39.98	5.20	2	3	8.12	5.20

53.38	6.55	3	5	8.51	6.55
				3.53	4.79
28.95	2.67	2	5	8.48	2.67
50.51	3.50	2	4	10.12	3.50
57.67	4.15	3	4	6.27	2.98
43.56	1.28	2	3	11.80	1.28
69.58	4.10	2	3	5.22	4.10
29.63	6.26	2	2	5.53	6.26
63.71	3.59	3	3	5.55	2.44
42.98	6.10	2	2		
34.82	3.74	2	2	5.56	3.74
83.09	1.26	2	4	13.78	1.57
50.85	3.72	3	4	8.75	3.72
52.93	3.24	2	2	5.42	3.24
28.42	3.51	2	2		
137.60	2.69	6	6	19.88	2.69
				20.29	5.51
101.51	2.54	3	4	8.19	2.54
30.65	3.11	2	2		
36.66	5.07	2	2	6.54	5.07
				2.82	2.00
155.46	4.81	2	7	20.70	4.81
				6.19	2.17
84.04	1.54	5	6	18.02	1.54

98.37	3.20	2	3	10.08	3.20
100.30	4.46	2	2	5.78	4.46
239.01	3.93	6	19	45.33	3.93
45.42	1.71	3	3	6.26	1.75
55.20	2.40	2	2	7.70	2.40
0.00	2.11	2	3	5.37	2.77
39.00	1.90	2	5	8.34	1.90
				4.00	3.89
24.09	1.92	2	2	5.01	1.92
38.14	3.60	2	2	5.23	3.60
87.35	3.59	4	8	21.33	3.59
0.00	2.00	2	2	2.14	2.00
33.76	3.42	2	2	2.47	3.42
52.58	1.78	2	2	7.02	1.78
61.17	1.74	3	3	8.17	1.74
36.99	0.68	2	3	5.92	0.68
27.63	3.21	2	3	9.65	3.21
53.06	3.13	2	4	8.66	3.13
52.82	2.38	2	3	4.81	2.38
116.64	2.74	2	4	10.79	2.74
36.69	1.12	2	2	4.69	1.12
45.42	2.60	2	3	5.94	2.60

121.88	2.57	3	4	12.89	2.57
36.26	2.54	2	2	4.35	2.54
45.99	2.44	2	3	7.27	2.44
				2.76	2.32
0.00	2.03	2	2		
0.00	0.94	2	2	2.34	0.94
65.90	1.69	2	2	5.75	1.69
53.83	0.66	3	4	11.49	0.66
39.56	1.51	2	2	5.20	1.51
				4.86	0.44
				0.00	0.74

8	57	708.23	65.73	7	34
4	9	153.15	57.72	4	8
31	111	2471.50	51.17	32	95
26	120	1336.44	51.96	23	83
16	85	1141.35	45.87	17	66
14	81	1631.26	49.10	14	77
37	215	3819.35	54.35	39	178
8	15	230.23	27.88	8	16
30	122	1919.93	39.38	27	92
2	4				
18	72	679.39	41.06	18	53
14	40	825.91	51.58	17	40
19	52	708.47	45.93	22	48
12	27	764.58	46.14	19	37
23	125	2116.56	47.01	23	114
24	63	952.93	38.12	26	54
49	228	3387.12	43.93	50	190
7	27	220.06	50.00	7	17
15	108	1456.43	41.73	14	98
17	100	2308.64	48.79	16	105
31	136	2078.34	38.35	30	108
21	78	1516.69	36.04	22	79
11	62	776.83	36.36	11	48
9	24	450.41	26.58	10	29
9	17	228.02	29.30	7	9
13	45	866.21	33.58	13	46
12	41	593.43	29.01	14	39
11	35	240.44	32.34	9	22
13	54	834.19	38.99	14	48
19	62	659.23	41.76	21	54
6	18	400.84	36.25	6	16
13	25	335.46	30.72	11	21
21	88	1416.97	31.78	25	72
17	64	1253.00	36.92	19	53
3	5	48.58	16.48	3	5
9	18	287.05	29.94	9	18
		719.36	40.49	19	37
12	36	598.76	33.09	14	44
27	167	2207.34	35.52	26	147
		453.20	37.20	7	20
13	39	419.84	26.83	10	25
10	22	446.59	35.73	16	23
17	42	769.05	30.58	17	48
12	34	540.60	25.21	15	35
8	17	250.66	22.74	8	15
		402.73	26.52	10	27
11	27	587.28	34.98	20	35
12	39	662.07	32.10	11	40
23	45	768.60	28.55	22	44
26	211	2372.45	35.61	25	159
9	16	235.91	27.43	7	13
11	56	711.13	34.21	10	44

12	34	675.36	27.91	16	42
4	8	327.97	31.06	7	16
7	19	338.96	32.75	13	21
5	10	70.85	35.44	5	7
5	7	171.80	35.07	7	13
32	115	1357.85	28.73	31	81
13	47	577.70	30.24	15	40
14	28	629.62	32.70	22	37
6	17	277.05	28.83	10	24
6	15	137.96	21.86	4	9
8	21	394.34	19.91	8	17
17	83	1104.84	31.93	17	72
15	45	745.50	20.52	11	31
20	74	1115.35	25.83	18	55
13	32	413.40	23.63	13	28
11	23	385.94	23.54	14	28
10	32	585.82	21.99	10	30
5	7	411.22	19.53	8	17
15	46	557.22	21.19	18	39
17	41	721.11	26.84	18	39
13	35	581.43	29.06	18	33
7	11	376.48	23.85	14	18
4	17	235.75	26.02	6	18
8	12	506.01	22.07	13	20
10	29	250.95	25.84	12	23
7	14	183.35	24.23	9	13
39	79	1797.78	26.70	49	91
7	21	277.40	25.97	13	22
5	10	219.65	17.95	6	10
17	39	727.54	21.71	24	38
17	41	1216.60	26.62	24	55
5	10	163.55	22.44	5	7
6	15	215.90	21.26	6	11
6	20	156.38	27.36	8	18
24	41	1163.23	19.44	28	57
5	15	217.22	24.34	6	10
9	16	558.99	26.92	14	34
3	7	82.58	13.39	3	6
25	48	1008.95	24.48	30	66
4	16	251.01	23.95	5	15
3	9	193.05	20.59	7	13
13	30	310.68	20.17	12	23
4	5	90.92	14.94	3	5
		81.20	18.50	4	4
16	42	830.46	23.34	19	46
5	10	200.91	18.91	8	11
3	3	79.63	16.25	2	3
13	32	652.89	20.49	12	32
2	6	57.70	21.35	4	4
9	17	274.82	21.25	10	18
12	28	348.36	21.36	16	27
4	6	82.28	21.14	5	12

2	2	54.02	13.71	2	2
9	23	267.62	21.56	11	22
6	12	89.17	10.42	3	5
6	10	221.57	15.28	9	12
4	12	220.50	16.73	4	13
7	10	127.26	17.46	7	11
12	33	410.98	20.92	15	28
5	12	169.63	20.59	9	13
3	3	135.36	15.90	5	6
3	9	89.12	12.62	3	6
4	7	154.59	22.62	6	11
5	12	90.05	10.23	4	8
5	15	429.38	23.62	8	18
6	9	210.50	19.70	7	11
7	14	186.44	17.35	5	7
6	13	334.02	19.53	9	24
4	16	340.63	19.83	4	16
5	16	260.91	22.83	9	19
		92.73	11.04	2	3
7	14	461.11	17.14	9	24
11	19	586.31	16.78	18	36
10	22	241.86	8.88	7	14
11	19	651.81	22.30	15	27
2	5	61.52	12.73	3	4
11	21	383.72	16.15	14	21
25	45	1042.71	18.39	32	65
3	3	98.80	8.31	3	8
9	15	461.44	20.05	14	26
6	10	192.93	12.67	6	11
2	2	109.02	13.81	4	5
9	34	393.92	18.76	13	29
9	27	444.38	14.86	11	25
3	4	119.09	12.47	4	8
		96.05	17.68	6	8
3	3	53.03	13.83	3	4
7	20	329.69	20.27	8	21
2	4				
4	7	180.66	9.44	8	11
4	5	173.72	14.89	6	7
5	13	181.69	20.00	6	12
9	18	359.00	14.83	14	26
2	4	76.33	7.76	2	3
4	8	110.68	7.45	4	5
2	5	59.94	8.71	2	2
3	4	181.45	12.86	7	8
6	19	215.44	19.51	7	15
3	6	149.86	19.35	3	6
6	13	227.00	14.55	6	10
2	2	91.14	13.78	5	8
3	3	107.24	15.35	4	7

2	4				
5	10	176.81	13.45	4	10
15	29	520.63	13.88	18	33
2	5	115.82	17.20	4	7
4	31	231.40	18.93	4	15
		124.79	15.67	3	5
11	36	477.24	17.23	14	36
7	13	272.31	14.38	13	18
		87.19	18.20	6	7
4	8	59.37	10.51	4	7
2	4	92.09	18.06	4	5
2	6	82.16	17.31	2	6
4	7	172.93	17.17	5	6
7	23	341.37	13.13	6	19
9	17	161.63	10.94	9	18
5	10	187.38	11.78	9	15
2	7	46.37	16.73	4	6
4	7	178.79	7.64	6	9
3	5	166.93	13.13	5	8
2	6	81.27	12.19	5	6
		81.01	8.04	2	4
9	29	243.95	11.64	8	20
2	7	96.84	11.46	2	7
2	3	54.36	6.01	2	2
		39.85	16.09	2	4
5	13	120.67	14.25	4	10
6	15	194.09	12.84	6	11
2	2				
8	18	453.94	14.58	13	23
4	4	220.31	9.37	9	12
2	2				
11	18	344.78	14.40	20	23
5	10	251.44	12.91	10	18
4	10	254.29	13.16	7	13
2	4	184.00	15.25	3	8
		65.75	15.25	2	3
11	34	520.42	12.27	15	34
4	6	260.22	10.75	7	10
2	2	63.92	7.28	3	3
6	8	107.33	8.23	6	10
3	10	98.57	11.75	4	10
6	9	207.52	11.68	7	10
7	19	295.87	9.03	5	13
6	30	199.29	13.00	7	19
4	12	127.77	13.99	5	9
3	8	59.56	11.31	5	6
11	21	314.64	12.87	11	17
5	8	64.90	7.54	5	7
5	7	137.93	12.75	8	10

2	4				
11	19	333.90	11.20	21	34
		78.91	8.08	2	2
5	7	54.49	6.93	2	4
		85.46	13.57	3	4
		63.38	13.48	2	3
		44.26	9.19	3	4
2	3				
4	11	193.24	8.71	3	8
2	3				
2	3				
7	12	98.03	9.71	7	12
3	4	57.26	5.38	2	3
3	3				
3	5	71.06	5.56	4	8
2	3				
		20.24	6.25	2	2
2	5	111.63	12.50	3	5
6	14	236.98	10.80	9	15
7	11	178.69	10.14	9	13
8	21	462.40	9.06	11	25
2	5	53.40	12.19	4	5
2	3	49.12	5.86	2	2
2	3	78.44	7.52	4	5
4	7	116.78	10.54	4	6
		51.09	6.51	2	3
4	5	147.54	9.91	7	11
2	4	73.27	11.57	4	5
		30.84	4.31	2	2
		21.93	8.83	2	3
5	10	159.25	9.53	6	11
3	7	97.60	9.55	4	5
6	10	197.38	8.17	7	14
4	7	52.07	1.75	2	2
		54.51	6.14	2	4
7	42	597.58	10.06	7	34
		95.70	10.75	8	11
2	10	206.44	10.73	4	13
		27.05	7.81	3	3
		94.47	8.86	4	7
2	2	186.45	10.49	6	8
2	3	94.96	10.45	3	4
8	13	294.40	9.20	8	15
5	8	196.17	10.40	5	5
3	4	166.99	7.98	6	8
2	3	276.10	7.10	5	9
		89.01	10.07	2	3
		23.39	6.47	2	3
4	8	299.28	7.21	10	15
		31.30	9.88	2	3

2	4	103.24	9.85	4	5
3	5	46.96	7.30	2	4
5	7	203.77	8.12	9	10
2	3	82.98	6.62	5	7
3	3	53.46	7.88	4	4
4	9	91.78	6.87	4	11
4	10	149.25	9.62	4	10
		47.24	9.60	2	4
		59.66	9.50	2	3
3	4	252.21	8.49	6	10
2	5	128.55	9.07	5	7
		73.93	5.28	2	3
3	10	278.92	5.70	8	15
		110.08	7.47	5	7
2	4				
6	7	172.15	7.63	12	15
		35.92	6.51	2	2
2	3	68.40	6.08	2	2
		56.86	6.44	2	5
2	6	133.95	5.46	3	9
2	4				
2	3				
3	4	55.76	5.09	3	6
3	3	175.25	8.47	5	5
4	13	72.50	6.81	3	3
		86.20	8.41	2	4
4	6	52.97	4.74	3	3
6	8	174.65	7.69	8	12
		63.29	8.25	3	4
4	8	87.95	6.10	3	7
7	10	206.08	5.88	6	9
4	7	135.42	7.96	4	6
		79.22	4.08	2	3
13	23	218.70	4.35	13	19
4	9	152.90	7.61	7	10
2	4	76.26	7.53	3	4
		0.00	7.53	2	3
		63.38	4.86	2	2
3	4	76.28	7.44	8	10
2	3	79.19	5.30	3	4
3	6	86.91	7.06	3	5
		37.03	7.03	2	2
		46.10	7.00	3	4
2	2	34.16	4.00	2	2
		63.14	6.92	3	4
		37.46	6.83	2	4
		35.32	6.82	2	2
2	3	34.06	4.20	2	3

		0.00	6.71	2	2
3	5	35.77	6.55	3	5
2	3	96.87	6.46	3	6
2	4	36.78	4.36	3	5
2	6				
2	4	78.10	5.19	4	6
2	5	135.01	5.13	7	10
		36.69	6.34	2	2
		35.73	6.30	2	2
2	3	90.83	6.27	3	6
2	2				
		23.45	6.21	2	2
2	2	82.20	3.88	3	3
		37.03	6.16	2	2
		32.95	3.55	2	2
2	2	24.03	3.74	2	2
3	6	219.49	5.92	9	13
3	4	36.72	2.11	2	3
2	2				
		24.40	3.39	2	3
6	8	206.14	3.77	9	10
2	8				
3	5	240.69	5.37	6	9
		57.44	5.29	2	2
		73.90	5.18	4	4
		50.08	5.11	2	2
		83.41	4.50	3	3
2	2				
		32.96	5.07	2	2
		77.68	5.04	4	5
		40.04	5.01	2	2
		19.86	4.93	2	4
		68.87	4.89	2	3
2	2	82.98	4.09	5	6
2	9	133.89	4.81	2	8
2	2				
5	9	246.36	4.38	14	22
		83.14	4.70	4	4

		43.64	3.12	4	4
		42.94	4.67	3	4
		26.44	4.62	2	2
2	3	132.85	4.57	3	5
2	2				
6	19	241.95	3.93	6	17
		35.07	4.38	2	2
3	3	124.52	2.83	5	6
2	2	51.49	2.40	2	3
3	3	34.08	4.22	4	5
		40.61	4.19	2	2
2	4	73.27	4.17	4	6
		98.43	3.99	5	6
		143.52	3.98	2	4
		74.69	3.90	2	3
2	4	28.09	3.89	2	3
		22.42	3.85	2	3
2	2	0.00	2.62	2	2
2	2	24.57	3.60	2	2
4	8	106.54	2.50	3	8
		52.47	3.54	3	3
		22.44	1.99	2	2
2	2				
2	3				
2	2	50.23	2.29	3	5
		70.29	2.00	2	2
3	3	104.43	2.22	3	5
		76.16	3.28	3	3
		92.06	2.51	5	6
2	4	83.61	1.75	6	8
2	6	26.29	3.21	2	2
2	4				
2	3	60.89	3.05	3	5
		63.04	2.79	2	2
2	3	247.63	2.74	2	7
		45.56	2.72	2	2
2	2	57.68	2.35	4	4
2	3	43.01	2.60	2	5

3	4	77.52	1.96	2	3
2	2	51.11	2.54	2	2
2	3				
2	2				
		41.10	2.17	3	3
		25.44	2.11	2	2
		40.05	2.01	2	3
		72.54	1.91	2	3
2	2	38.11	1.78	3	3
		65.96	1.11	2	2
2	2	57.76	1.69	2	2
3	4	64.97	1.37	6	7
		70.72	1.56	2	3
		49.04	0.63	3	4
		67.07	1.54	2	2
2	2				
		49.71	1.32	2	3
2	2	47.81	0.53	2	2
2	2				
		36.19	0.57	2	3

118.90	65.73	7	42	143	16.0
21.82	65.77	5	9	149	16.8
292.29	51.64	33	102	639	65.4
196.96	49.64	23	96	562	62.9
171.20	45.87	17	73	375	41.7
216.77	49.10	14	83	279	28.8
516.85	54.35	39	199	747	82.5
38.72	28.21	9	21	312	35.2
273.10	41.95	30	104	584	58.8
				114	13.2
143.44	41.06	18	68	414	46.9
115.69	51.58	18	48	349	38.1
109.99	44.63	21	54	540	60.6
104.99	46.14	19	39	531	57.9
311.67	47.01	23	127	585	65.3
158.39	40.75	29	71	724	83.2
512.29	44.02	49	205	1170	129.3
56.32	50.00	7	23	148	16.2
204.46	41.73	14	88	381	41.9
277.06	48.79	16	107	412	44.5
299.42	39.29	31	119	644	66.0
227.63	36.94	23	93	666	74.8
120.98	36.36	11	53	308	35.0
88.83	26.58	11	34	444	49.6
29.08	29.30	7	10	256	28.8
129.50	33.58	13	54	402	45.0
99.06	30.15	15	50	524	58.1
57.79	32.34	9	30	303	33.8
121.60	41.19	15	59	318	35.9
126.75	41.54	21	61	467	54.0
53.61	36.25	6	18	240	25.8
49.88	33.13	12	26	332	36.7
223.91	32.56	26	85	774	86.7
136.11	34.99	18	52	623	62.0
12.74	16.48	3	4	267	30.1
45.49	31.74	10	22	334	36.6
				44	5.0
				531	58.0
119.25	37.68	17	53	414	47.7
349.50	32.90	25	160	763	86.9
60.80	40.10	8	22	207	22.4
61.08	26.83	10	26	451	50.1
62.09	35.73	16	28	431	49.6
128.55	32.73	19	62	556	63.1
89.25	26.69	16	44	472	51.5
45.85	22.74	8	18	365	40.9
79.53	26.52	11	29	445	49.8
95.10	34.98	20	42	646	70.9
123.07	32.10	11	48	433	49.4
116.13	28.55	23	57	732	84.6
389.48	36.43	26	183	733	82.9
37.17	27.43	7	16	339	37.8
113.82	32.33	9	48	266	28.7

112.41	31.92	18	53	473	51.2
31.59	31.06	7	16	293	31.5
50.78	28.21	12	26	397	44.0
23.49	35.44	5	8	158	17.6
41.09	35.07	7	18	211	24.1
229.32	29.45	32	103	971	108.6
91.63	30.24	15	47	463	51.8
84.78	32.70	21	37	679	75.9
				135	14.4
60.99	28.83	10	30	385	43.7
27.76	21.86	4	10	247	27.6
41.38	19.91	8	16	462	50.1
175.43	31.93	17	80	570	63.6
78.16	21.97	12	33	692	74.2
154.20	25.83	18	59	906	101.2
72.61	24.76	14	30	529	57.9
61.40	20.06	13	32	718	82.2
70.82	19.12	9	36	523	58.9
41.72	21.66	9	18	471	51.9
102.69	23.21	20	53	892	103.0
102.64	26.84	18	43	693	76.9
94.37	29.06	18	36	678	74.9
55.96	26.15	16	24	654	72.3
				245	27.7
42.59	26.02	6	19	246	27.3
66.16	22.07	13	23	743	82.2
60.42	25.84	12	33	449	50.3
39.23	26.38	10	16	326	35.8
273.81	27.00	50	106	2330	256.3
54.92	25.97	13	27	593	63.5
31.22	19.77	7	13	440	49.9
99.49	22.31	25	49	1179	134.5
143.32	27.30	25	63	1172	129.9
22.51	25.20	6	14	254	29.2
28.64	21.26	6	13	334	37.6
44.87	27.36	8	23	307	35.8
161.63	20.18	30	67	1898	211.6
33.99	26.97	7	16	304	35.0
82.27	26.92	14	41	509	58.4
9.97	16.07	4	7	224	25.4
157.32	24.81	31	71	1479	165.2
44.60	23.95	5	19	238	26.7
29.43	20.59	7	15	306	34.2
74.03	21.17	13	28	699	79.5
13.75	14.94	3	5	241	26.9
12.30	18.50	4	7	200	23.0
118.76	24.04	20	58	1011	113.7
29.79	18.91	8	13	476	54.1
9.41	16.25	2	3	160	17.8
91.68	20.78	13	42	693	76.4
12.38	21.35	4	6	192	21.8
42.48	21.25	10	18	433	47.9
62.71	20.00	15	30	590	62.3
25.42	21.14	5	12	317	35.6

7.39	13.71	2	2	175	20.0
44.94	22.55	12	28	603	68.9
17.37	10.42	3	6	240	25.3
27.31	15.28	9	16	589	65.4
26.55	16.73	4	13	245	27.7
31.22	17.46	8	16	401	46.0
70.12	20.92	15	33	564	60.0
34.00	20.59	9	15	437	50.1
10.89	15.90	5	6	415	47.1
18.37	14.83	4	8	317	35.9
29.03	21.34	6	12	389	41.4
20.75	10.23	4	11	391	44.2
66.13	23.62	8	19	563	61.2
				153	16.5
26.50	19.70	7	11	406	46.1
29.78	19.24	7	11	317	34.8
64.87	19.53	9	30	466	53.7
43.17	22.84	5	17	232	25.8
46.38	22.83	9	21	381	42.0
9.08	11.04	2	3	335	37.0
67.09	18.35	10	29	496	55.8
97.06	16.78	18	45	1144	131.1
49.80	16.27	12	22	676	75.1
76.53	21.45	14	31	816	89.7
9.72	10.00	2	4	220	24.1
60.52	15.73	14	26	941	107.2
162.53	18.39	32	69	2045	214.7
14.24	8.05	3	10	385	42.5
67.17	18.80	13	30	803	92.4
28.69	14.06	7	14	434	47.1
15.23	13.81	4	8	362	41.8
72.14	19.83	14	36	842	92.3
67.26	14.86	11	28	895	97.4
15.32	12.47	4	6	393	45.5
				102	11.7
20.33	17.68	6	9	379	41.7
12.96	13.83	3	4	253	28.9
61.28	20.54	9	24	370	42.8
5.90	20.51	2	5	117	13.0
30.71	8.39	7	13	858	95.3
				110	11.3
26.22	18.09	8	11	470	52.7
25.28	20.00	6	12	305	33.6
				381	44.3
70.19	15.15	14	29	944	106.8
9.51	7.76	2	3	606	66.2
15.02	7.45	4	6	698	77.5
6.72	8.71	2	4	264	28.8
21.09	12.86	7	11	552	62.0
45.75	19.51	7	19	364	39.3
21.48	19.35	3	7	155	17.0
28.13	14.55	6	11	550	61.8
19.83	13.78	5	10	370	41.8
13.51	15.35	4	5	241	26.1

5.06	7.69	2	4	299	34.4
22.86	13.45	4	10	342	39.5
81.01	14.32	19	37	1390	155.4
22.53	17.20	4	10	343	39.1
36.34	18.93	4	18	206	22.7
9.72	15.67	3	6	217	24.8
				255	29.2
93.16	17.23	14	43	911	104.8
46.84	14.38	13	20	925	104.9
13.23	12.86	4	7	412	46.6
17.11	12.30	5	10	447	51.5
12.70	18.06	4	8	216	23.7
12.54	17.31	2	5	104	11.7
18.86	17.17	5	9	361	39.3
46.33	14.37	7	23	480	54.4
35.66	9.81	8	21	887	98.7
35.88	11.78	9	16	764	85.5
18.00	16.73	4	8	263	29.5
23.31	10.59	8	15	746	86.2
28.15	16.48	6	16	358	41.5
15.78	12.19	5	6	402	45.8
8.31	11.61	3	5	336	38.0
39.67	11.64	8	23	464	52.6
15.41	11.46	2	9	192	21.9
6.65	6.01	2	3	416	44.8
				205	22.9
9.51	16.09	2	4	174	20.0
				199	22.5
25.29	15.95	5	18	351	39.6
32.47	12.84	6	14	522	57.9
				346	38.7
61.33	15.21	14	28	1118	122.2
4.67	12.03	2	2	158	17.6
34.17	11.87	10	14	918	103.5
				133	15.3
61.88	12.96	19	28	1798	195.9
38.99	13.66	11	23	937	104.7
3.78	15.49	2	2	142	15.2
34.62	13.16	7	15	646	71.6
21.47	15.25	3	8	223	25.0
7.41	15.25	2	3	590	60.5
99.75	12.27	15	43	1231	139.0
31.71	10.75	7	13	586	63.9
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25.64	7.23	5	12	705	80.1
22.21	11.75	4	12	332	37.8
28.34	11.68	7	10	736	83.3
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47.80	14.26	8	25	554	60.1
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12.19	9.72	4	8	504	54.5
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9.11	13.57	3	5	199	22.1
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				274	31.5
2.46	4.61	2	3	347	41.0
19.79	5.56	4	8	738	84.7
				320	35.9
				184	21.1
				256	29.5
12.59	12.50	3	5	248	27.6
47.64	10.80	9	19	1009	113.9
40.17	10.14	9	17	1036	113.7
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15.75	10.54	4	8	427	48.5
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24.18	8.68	5	13	703	81.1
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23.69	9.22	5	9	553	62.8
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47.90	9.82	9	18	967	105.3
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34.48	8.49	6	12	789	87.4
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37.86	7.03	11	17	2019	220.7
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6.96	5.13	2	4	390	43.3
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P04004
Q6PCB0
O75083
P13010
F5H1I8
Q9H1B5

14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 - [1433E_HUMAN]
14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 - [1433T_HUMAN]
14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 - [1433Z_HUMAN]
26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3 - [PSD11_HUMAN]
26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=4 SV=1 - [J3KNQ3_HUMAN]
26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=2 SV=1 - [E9PCS3_HUMAN]
26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1 - [PSMD6_HUMAN]
35 kDa inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=2 SV=1 - [F5GXQ1_HUMAN]
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=2 SV=1 - [E9PQX2_HUMAN]
45 kDa calcium-binding protein OS=Homo sapiens GN=SDF4 PE=1 SV=1 - [CAB45_HUMAN]
5'-nucleotidase OS=Homo sapiens GN=NT5E PE=2 SV=1 - [Q96B60_HUMAN]
60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 - [RL10A_HUMAN]
78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]
A disintegrin and metalloproteinase with thrombospondin motifs 1 OS=Homo sapiens GN=ADAMTS1 PE=1 SV=4 - [ATS1_HUMAN]
Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=2 SV=1 - [E7EMM4_HUMAN]
Acid sphingomyelinase-like phosphodiesterase 3a OS=Homo sapiens GN=SMPDL3A PE=2 SV=1 - [B7Z729_HUMAN]
Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]
ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2 - [ARF3_HUMAN]
Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Homo sapiens GN=MGAT2 PE=1 SV=1 - [MGAT2_HUMAN]
Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1 - [FETUA_HUMAN]
Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]
Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 - [ACTN1_HUMAN]
Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 - [ACTN4_HUMAN]
Alpha-amylase 2B OS=Homo sapiens GN=AMY2B PE=2 SV=1 - [B3KTI1_HUMAN]
Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]
Alpha-galactosidase A OS=Homo sapiens GN=GLA PE=1 SV=1 - [AGAL_HUMAN]
Alpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2 - [MA2A1_HUMAN]
Alpha-N-acetylglucosaminidase OS=Homo sapiens GN=NAGLU PE=1 SV=2 - [ANAG_HUMAN]
Amphoterin-induced protein 2 OS=Homo sapiens GN=AMIGO2 PE=1 SV=1 - [AMGO2_HUMAN]
Amyloid-like protein 1 OS=Homo sapiens GN=APLP1 PE=2 SV=1 - [F5GZ08_HUMAN]
Amyloid-like protein 2 OS=Homo sapiens GN=APLP2 PE=1 SV=2 - [APLP2_HUMAN]
Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=2 SV=1 - [H0YN42_HUMAN]
Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 - [ANXA1_HUMAN]
Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]
Annexin OS=Homo sapiens GN=ANXA3 PE=2 SV=1 - [D6RA82_HUMAN]
Anosmin-1 OS=Homo sapiens GN=KAL1 PE=1 SV=3 - [KALM_HUMAN]
Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1 - [ANT3_HUMAN]
Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=2 SV=1 - [F5H3T8_HUMAN]
Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DKFZp781B11202 PE=2 SV=1 - [Q68CR9_HUMAN]
Aspartyl aminopeptidase (Fragment) OS=Homo sapiens GN=DNPEP PE=2 SV=2 - [C9JRG3_HUMAN]
ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=2 SV=1 - [B4E3P0_HUMAN]
ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]
Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2 - [BCAM_HUMAN]
Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4 - [PGBM_HUMAN]
Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase OS=Homo sapiens GN=GCNT1 PE=2 SV=2 - [GCNT1_HUMA
Beta-1,3-galactosyltransferase 6 OS=Homo sapiens GN=B3GALT6 PE=2 SV=2 - [B3GT6_HUMAN]
Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe OS=Homo sapiens GN=LFNG PE=1 SV=2 - [LFNG_HUMAN]
Beta-1,4-galactosyltransferase 5 OS=Homo sapiens GN=B4GALT5 PE=2 SV=1 - [B4GT5_HUMAN]
Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=4 SV=1 - [J3KS17_HUMAN]
Beta-glucuronidase OS=Homo sapiens GN=GUSB PE=1 SV=2 - [BGLR_HUMAN]
Beta-hexosaminidase OS=Homo sapiens GN=HEXA PE=2 SV=1 - [H3BS10_HUMAN]
Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3 - [HEXB_HUMAN]

Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 OS=Homo sapiens GN=NDST1 PE=2 SV=1 - [E7EVJ3_HUMAN]
Biotinidase OS=Homo sapiens GN=BTD PE=2 SV=1 - [F8W1Q3_HUMAN]
Bis(5'-adenosyl)-triphosphatase ENPP4 OS=Homo sapiens GN=ENPP4 PE=1 SV=3 - [ENPP4_HUMAN]
BRI2, membrane form OS=Homo sapiens GN=ITM2B PE=2 SV=1 - [Q5W0A2_HUMAN]
CAD protein OS=Homo sapiens GN=CAD PE=2 SV=1 - [F8VPD4_HUMAN]
Calsyntenin-3 OS=Homo sapiens GN=CLSTN3 PE=1 SV=1 - [CSTN3_HUMAN]
Carbohydrate sulfotransferase 12 OS=Homo sapiens GN=CHST12 PE=1 SV=2 - [CHSTC_HUMAN]
Carbohydrate sulfotransferase 14 OS=Homo sapiens GN=CHST14 PE=2 SV=1 - [H0YN65_HUMAN]
Carbohydrate sulfotransferase 15 OS=Homo sapiens GN=CHST15 PE=1 SV=1 - [CHSTF_HUMAN]
Carbohydrate sulfotransferase 3 OS=Homo sapiens GN=CHST3 PE=1 SV=3 - [CHST3_HUMAN]
Carboxypeptidase A4 OS=Homo sapiens GN=CPA4 PE=2 SV=1 - [B7Z5J4_HUMAN]
Cartilage-associated protein OS=Homo sapiens GN=CRTAP PE=2 SV=1 - [C9JP16_HUMAN]
Casein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=2 SV=1 - [E7EU96_HUMAN]
Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]
Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]
Cathepsin L1 OS=Homo sapiens GN=CTSL1 PE=1 SV=2 - [CATL1_HUMAN]
Cathepsin L2 OS=Homo sapiens GN=CTSL2 PE=1 SV=2 - [CATL2_HUMAN]
Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]
Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3 - [MPRI_HUMAN]
CD44 antigen OS=Homo sapiens GN=CD44 PE=2 SV=2 - [H0YD13_HUMAN]
Cell adhesion molecule 4 OS=Homo sapiens GN=CADM4 PE=1 SV=1 - [CADM4_HUMAN]
Cell surface glycoprotein MUC18 OS=Homo sapiens GN=MCAM PE=1 SV=2 - [MUC18_HUMAN]
Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens GN=CLN5 PE=1 SV=2 - [CLN5_HUMAN]
Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 - [CLIC1_HUMAN]
Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 - [CLIC4_HUMAN]
CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase 1 OS=Homo sapiens GN=ST3GAL1 PE=2 SV=1 - [SIA4A_HUMAN]
CMP-N-acetylneuraminate-poly-alpha-2,8-sialyltransferase OS=Homo sapiens GN=ST8SIA4 PE=1 SV=1 - [SIA8D_HUMAN]
Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3 - [COPB_HUMAN]
Coiled-coil domain-containing protein 80 OS=Homo sapiens GN=CCDC80 PE=1 SV=1 - [CCD80_HUMAN]
Collagen alpha-1(V) chain OS=Homo sapiens GN=COL5A1 PE=1 SV=3 - [CO5A1_HUMAN]
Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3 - [CO6A1_HUMAN]
Collagen alpha-1(VIII) chain OS=Homo sapiens GN=COL8A1 PE=1 SV=2 - [CO8A1_HUMAN]
Collagen and calcium-binding EGF domain-containing protein 1 OS=Homo sapiens GN=CCBE1 PE=1 SV=1 - [CCBE1_HUMAN]
Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2 - [C1R_HUMAN]
Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2 - [CO3_HUMAN]
Complement decay-accelerating factor (Fragment) OS=Homo sapiens GN=CD55 PE=4 SV=1 - [H3BLV0_HUMAN]
Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2 - [CFAB_HUMAN]
Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4 - [CFAH_HUMAN]
Connective tissue growth factor OS=Homo sapiens GN=CTGF PE=1 SV=2 - [CTGF_HUMAN]
C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2 - [MRC2_HUMAN]
Cysteine-rich motor neuron 1 protein OS=Homo sapiens GN=CRIM1 PE=1 SV=1 - [CRIM1_HUMAN]
Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]
Deoxyribonuclease-2-alpha OS=Homo sapiens GN=DNASE2 PE=2 SV=1 - [B7Z4K6_HUMAN]
Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN]
Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2 - [DSG2_HUMAN]
D-glucuronyl C5-epimerase OS=Homo sapiens GN=GLCE PE=2 SV=1 - [H0YNP1_HUMAN]
Dickkopf-related protein 1 OS=Homo sapiens GN=DKK1 PE=1 SV=1 - [DKK1_HUMAN]
Di-N-acetylchitobiase OS=Homo sapiens GN=CTBS PE=1 SV=1 - [DIAC_HUMAN]
Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]
Dipeptidyl peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=3 - [DPP2_HUMAN]
Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens GN=ADAM9 PE=2 SV=1 - [F8WC54_HUMAN]
Dynein heavy chain 5, axonemal OS=Homo sapiens GN=DNAH5 PE=1 SV=3 - [DYH5_HUMAN]
Dystroglycan OS=Homo sapiens GN=DAG1 PE=1 SV=2 - [DAG1_HUMAN]
Ectonucleotide pyrophosphatase/phosphodiesterase family member 1 OS=Homo sapiens GN=ENPP1 PE=1 SV=2 - [ENPP1_HUMAN]

Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]
Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN]
Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]
Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=ERAP1 PE=1 SV=3 - [ERAP1_HUMAN]
Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase OS=Homo sapiens GN=MAN1B1 PE=1 SV=2 - [MA1B1_HUMAN]
Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [ENPL_HUMAN]
Endothelial protein C receptor OS=Homo sapiens GN=PROCR PE=1 SV=1 - [EPCR_HUMAN]
Endothelin-converting enzyme 1 OS=Homo sapiens GN=ECE1 PE=2 SV=1 - [B4DKB2_HUMAN]
Ephrin type-A receptor 4 OS=Homo sapiens GN=EPHA4 PE=2 SV=1 - [E9PG71_HUMAN]
Ephrin-A5 OS=Homo sapiens GN=EFNA5 PE=1 SV=1 - [EFNA5_HUMAN]
Ephrin-B2 OS=Homo sapiens GN=EFNB2 PE=1 SV=1 - [EFNB2_HUMAN]
Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=4 SV=1 - [J3KMY5_HUMAN]
Epididymis-specific alpha-mannosidase OS=Homo sapiens GN=MAN2B2 PE=1 SV=4 - [MA2B2_HUMAN]
Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 - [IF4A1_HUMAN]
Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=2 SV=1 - [F5H335_HUMAN]
Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=2 SV=1 - [B0QY90_HUMAN]
Eukaryotic translation initiation factor 3 subunit M (Fragment) OS=Homo sapiens GN=EIF3M PE=2 SV=1 - [E9PN86_HUMAN]
Exostosin-1 OS=Homo sapiens GN=EXT1 PE=1 SV=2 - [EXT1_HUMAN]
Exostosin-2 OS=Homo sapiens GN=EXT2 PE=1 SV=1 - [EXT2_HUMAN]
Exportin-2 OS=Homo sapiens GN=CSE1L PE=2 SV=1 - [F8W904_HUMAN]
Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2 - [ECM1_HUMAN]
Extracellular matrix protein FRAS1 (Fragment) OS=Homo sapiens GN=FRAS1 PE=4 SV=1 - [H0Y930_HUMAN]
Extracellular serine/threonine protein kinase FAM20C OS=Homo sapiens GN=FAM20C PE=1 SV=2 - [DMP4_HUMAN]
Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2 - [SODE_HUMAN]
Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]
FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1 - [SSRP1_HUMAN]
Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FAS_HUMAN]
FERM and PDZ domain-containing protein 1 OS=Homo sapiens GN=FRMPD1 PE=1 SV=1 - [FRPD1_HUMAN]
Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]
Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=3 - [FBN1_HUMAN]
Fibroblast growth factor receptor-like 1 OS=Homo sapiens GN=FGFRL1 PE=1 SV=1 - [FGRL1_HUMAN]
Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4 - [FBLN1_HUMAN]
Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3 - [FILA_HUMAN]
Filamin-A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q5HY54_HUMAN]
Filamin-B OS=Homo sapiens GN=FLNB PE=2 SV=1 - [E7EN95_HUMAN]
Follistatin-related protein 1 OS=Homo sapiens GN=FSTL1 PE=1 SV=1 - [FSTL1_HUMAN]
Four-jointed box protein 1 OS=Homo sapiens GN=FJX1 PE=2 SV=1 - [FJX1_HUMAN]
Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOA PE=2 SV=1 - [H3BQN4_HUMAN]
Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 - [LG3BP_HUMAN]
Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 - [GGH_HUMAN]
Gamma-interferon-inducible lysosomal thiol reductase OS=Homo sapiens GN=IFI30 PE=1 SV=3 - [GILT_HUMAN]
Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Homo sapiens GN=G6PD PE=2 SV=1 - [E9PD92_HUMAN]
Glucosylceramidase OS=Homo sapiens GN=GBA PE=4 SV=1 - [J3KQG4_HUMAN]
Glutaminyl-peptide cyclotransferase OS=Homo sapiens GN=QPCT PE=1 SV=1 - [QPCT_HUMAN]
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=2 SV=1 - [E7EUT4_HUMAN]
Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 - [SYG_HUMAN]
Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]
Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=2 - [GPC1_HUMAN]
Glypican-6 OS=Homo sapiens GN=GPC6 PE=1 SV=1 - [GPC6_HUMAN]
Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2 - [GSLG1_HUMAN]
Granulins OS=Homo sapiens GN=GRN PE=1 SV=2 - [GRN_HUMAN]
Group XV phospholipase A2 OS=Homo sapiens GN=PLA2G15 PE=1 SV=2 - [PAG15_HUMAN]
GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=2 SV=1 - [F5H018_HUMAN]
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=2 SV=1 - [E7EP32_HUMAN]

Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment) OS=Homo sapiens GN=GNB2L1 PE=4 SV=1 - [H0YAF8_HUMAN]
Heat shock 70 kDa protein 13 OS=Homo sapiens GN=HSPA13 PE=1 SV=1 - [HSP13_HUMAN]
Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 - [HSP74_HUMAN]
Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]
Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN]
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]
Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 - [HBA_HUMAN]
Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=2 SV=1 - [E9PFT6_HUMAN]
Heparan sulfate glucosamine 3-O-sulfotransferase 1 OS=Homo sapiens GN=HS3ST1 PE=1 SV=1 - [HS3S1_HUMAN]
Heparan sulfate glucosamine 3-O-sulfotransferase 3B1 OS=Homo sapiens GN=HS3ST3B1 PE=1 SV=1 - [HS3SB_HUMAN]
Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3 - [HEP2_HUMAN]
Hepatocyte growth factor receptor OS=Homo sapiens GN=MET PE=1 SV=4 - [MET_HUMAN]
Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=2 SV=1 - [D6RAF8_HUMAN]
Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=2 SV=1 - [Q5T6W1_HUMAN]
HLA class I histocompatibility antigen, A-2 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 - [1A02_HUMAN]
HLA-B associated transcript 1 OS=Homo sapiens GN=DDX39B PE=4 SV=2 - [Q5STU3_HUMAN]
Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2 - [HORN_HUMAN]
Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=3 SV=1 - [E9PL22_HUMAN]
Iduronate 2-sulfatase OS=Homo sapiens GN=IDS PE=1 SV=1 - [IDS_HUMAN]
Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]
Importin-5 OS=Homo sapiens GN=IPO5 PE=2 SV=1 - [B4E0R6_HUMAN]
Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 - [IPO7_HUMAN]
Inhibin beta B chain OS=Homo sapiens GN=INHBB PE=1 SV=2 - [INHBB_HUMAN]
Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=2 SV=1 - [B4E351_HUMAN]
Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1 - [IBP6_HUMAN]
Insulin-like growth factor-binding protein-like 1 OS=Homo sapiens GN=IGFBPL1 PE=2 SV=1 - [IBPL1_HUMAN]
Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1 - [ITA2_HUMAN]
Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5 - [ITA3_HUMAN]
Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2 - [ITA5_HUMAN]
Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=4 SV=1 - [Q5T985_HUMAN]
Interleukin-1 receptor accessory protein (Fragment) OS=Homo sapiens GN=IL1RAP PE=2 SV=1 - [C9J1D9_HUMAN]
Interleukin-6 receptor subunit beta OS=Homo sapiens GN=IL6ST PE=1 SV=2 - [IL6RB_HUMAN]
Isoform 10 of Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH - [ASPH_HUMAN]
Isoform 13 of Fibroblast growth factor receptor 1 OS=Homo sapiens GN=FGFR1 - [FGFR1_HUMAN]
Isoform 17 of Fibronectin OS=Homo sapiens GN=FN1 - [FINC_HUMAN]
Isoform 2 of 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 - [4F2_HUMAN]
Isoform 2 of 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP - [K6PP_HUMAN]
Isoform 2 of Adenosylhomocysteinase OS=Homo sapiens GN=AHCY - [SAHH_HUMAN]
Isoform 2 of Cadherin-11 OS=Homo sapiens GN=CDH11 - [CAD11_HUMAN]
Isoform 2 of Cadherin-4 OS=Homo sapiens GN=CDH4 - [CADH4_HUMAN]
Isoform 2 of Calsyntenin-1 OS=Homo sapiens GN=CLSTN1 - [CSTN1_HUMAN]
Isoform 2 of Carbohydrate sulfotransferase 11 OS=Homo sapiens GN=CHST11 - [CHSTB_HUMAN]
Isoform 2 of Carboxypeptidase E OS=Homo sapiens GN=CPE - [CBPE_HUMAN]
Isoform 2 of CD166 antigen OS=Homo sapiens GN=ALCAM - [CD166_HUMAN]
Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC - [CLH1_HUMAN]
Isoform 2 of CUB domain-containing protein 1 OS=Homo sapiens GN=CDCP1 - [CDCP1_HUMAN]
Isoform 2 of Cullin-4A OS=Homo sapiens GN=CUL4A - [CUL4A_HUMAN]
Isoform 2 of EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 - [FBLN3_HUMAN]
Isoform 2 of EGF-like repeat and discoidin I-like domain-containing protein 3 OS=Homo sapiens GN=EDIL3 - [EDIL3_HUMAN]
Isoform 2 of Epithelial discoidin domain-containing receptor 1 OS=Homo sapiens GN=DDR1 - [DDR1_HUMAN]
Isoform 2 of Epsilon-sarcoglycan OS=Homo sapiens GN=SGCE - [SGCE_HUMAN]
Isoform 2 of Follistatin OS=Homo sapiens GN=FST - [FST_HUMAN]
Isoform 2 of Glia-derived nexin OS=Homo sapiens GN=SERPINE2 - [GDN_HUMAN]
Isoform 2 of Glucoside xylosyltransferase 1 OS=Homo sapiens GN=GXYLT1 - [GXLT1_HUMAN]

Isoform 2 of Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL - [PYGL_HUMAN]
Isoform 2 of Golgi membrane protein 1 OS=Homo sapiens GN=GOLM1 - [GOLM1_HUMAN]
Isoform 2 of Growth arrest-specific protein 6 OS=Homo sapiens GN=GAS6 - [GAS6_HUMAN]
Isoform 2 of Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A - [HSP71_HUMAN]
Isoform 2 of Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 - [IBP7_HUMAN]
Isoform 2 of Lactadherin OS=Homo sapiens GN=MFGE8 - [MFGM_HUMAN]
Isoform 2 of Laminin subunit alpha-4 OS=Homo sapiens GN=LAMA4 - [LAMA4_HUMAN]
Isoform 2 of Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA - [LICH_HUMAN]
Isoform 2 of MAM domain-containing protein 2 OS=Homo sapiens GN=MAMDC2 - [MAMC2_HUMAN]
Isoform 2 of Neogenin OS=Homo sapiens GN=NEO1 - [NEO1_HUMAN]
Isoform 2 of Neuroligin-1 OS=Homo sapiens GN=NLGN1 - [NLGN1_HUMAN]
Isoform 2 of Oncostatin-M-specific receptor subunit beta OS=Homo sapiens GN=OSMR - [OSMR_HUMAN]
Isoform 2 of Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 - [PSA3_HUMAN]
Isoform 2 of Protein KIAA1199 OS=Homo sapiens GN=KIAA1199 - [K1199_HUMAN]
Isoform 2 of Protocadherin gamma-B1 OS=Homo sapiens GN=PCDHGB1 - [PCDGD_HUMAN]
Isoform 2 of Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens GN=PTPRF - [PTPRF_HUMAN]
Isoform 2 of Receptor-type tyrosine-protein phosphatase gamma OS=Homo sapiens GN=PTPRG - [PTPRG_HUMAN]
Isoform 2 of Receptor-type tyrosine-protein phosphatase S OS=Homo sapiens GN=PTPRS - [PTPRS_HUMAN]
Isoform 2 of Roundabout homolog 4 OS=Homo sapiens GN=ROBO4 - [ROBO4_HUMAN]
Isoform 2 of Seizure 6-like protein 2 OS=Homo sapiens GN=SEZ6L2 - [SE6L2_HUMAN]
Isoform 2 of Semaphorin-4B OS=Homo sapiens GN=SEMA4B - [SEM4B_HUMAN]
Isoform 2 of Syndecan-4 OS=Homo sapiens GN=SDC4 - [SDC4_HUMAN]
Isoform 2 of Transportin-2 OS=Homo sapiens GN=TNPO2 - [TNPO2_HUMAN]
Isoform 2 of Tumor necrosis factor ligand superfamily member 15 OS=Homo sapiens GN=TNFSF15 - [TNF15_HUMAN]
Isoform 2 of UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2 OS=Homo sapiens GN=B3GNT2 - [B3GN2_HUMAN]
Isoform 3 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 - [RO60_HUMAN]
Isoform 3 of Attractin OS=Homo sapiens GN=ATRN - [ATRN_HUMAN]
Isoform 3 of Clusterin OS=Homo sapiens GN=CLU - [CLUS_HUMAN]
Isoform 3 of KDEL motif-containing protein 2 OS=Homo sapiens GN=KDELC2 - [KDEL2_HUMAN]
Isoform 3 of Latrophilin-2 OS=Homo sapiens GN=LPHN2 - [LPHN2_HUMAN]
Isoform 3 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR - [LDLR_HUMAN]
Isoform 3 of Matrilin-2 OS=Homo sapiens GN=MATN2 - [MATN2_HUMAN]
Isoform 3 of Netrin-4 OS=Homo sapiens GN=NTN4 - [NET4_HUMAN]
Isoform 3 of Neural cell adhesion molecule L1 OS=Homo sapiens GN=L1CAM - [L1CAM_HUMAN]
Isoform 3 of Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 - [NDKB_HUMAN]
Isoform 3 of Phospholipid transfer protein OS=Homo sapiens GN=PLTP - [PLTP_HUMAN]
Isoform 3 of Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 - [PSB5_HUMAN]
Isoform 3 of Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 - [SPTN1_HUMAN]
Isoform 3 of Transportin-1 OS=Homo sapiens GN=TNPO1 - [TNPO1_HUMAN]
Isoform 3 of Tubulointerstitial nephritis antigen-like OS=Homo sapiens GN=TINAGL1 - [TINAL_HUMAN]
Isoform 3 of Ubiquitin-protein ligase E3B OS=Homo sapiens GN=UBE3B - [UBE3B_HUMAN]
Isoform 4 of Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 - [COCA1_HUMAN]
Isoform 4 of Epidermal growth factor receptor OS=Homo sapiens GN=EGFR - [EGFR_HUMAN]
Isoform 4 of Galactocerebrosidase OS=Homo sapiens GN=GALC - [GALC_HUMAN]
Isoform 4 of Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 - [RBBP4_HUMAN]
Isoform 4 of Peptidyl-glycine alpha-amidating monooxygenase OS=Homo sapiens GN=PAM - [AMD_HUMAN]
Isoform 4 of Sushi repeat-containing protein SRPX OS=Homo sapiens GN=SRPX - [SRPX_HUMAN]
Isoform 5 of Inactive tyrosine-protein kinase 7 OS=Homo sapiens GN=PTK7 - [PTK7_HUMAN]
Isoform 6 of Agrin OS=Homo sapiens GN=AGRN - [AGRIN_HUMAN]
Isoform 6 of Roundabout homolog 1 OS=Homo sapiens GN=ROBO1 - [ROBO1_HUMAN]
Isoform 7 of Plectin OS=Homo sapiens GN=PLEC - [PLEC_HUMAN]
Isoform 8 of Maternal embryonic leucine zipper kinase OS=Homo sapiens GN=MELK - [MELK_HUMAN]
Isoform 8 of Pro-neuregulin-1, membrane-bound isoform OS=Homo sapiens GN=NRG1 - [NRG1_HUMAN]
Isoform Alpha of Poliovirus receptor-related protein 2 OS=Homo sapiens GN=PVRL2 - [PVRL2_HUMAN]

Isoform B0 of Neuropilin-2 OS=Homo sapiens GN=NRP2 - [NRP2_HUMAN]
Isoform Beta-1B of Integrin beta-1 OS=Homo sapiens GN=ITGB1 - [ITB1_HUMAN]
Isoform Gamma of Poliovirus receptor OS=Homo sapiens GN=PVR - [PVR_HUMAN]
Isoform L-APP733 of Amyloid beta A4 protein OS=Homo sapiens GN=APP - [A4_HUMAN]
Isoform M1 of Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM - [KPYM_HUMAN]
Isoform Short of Beta-1,4-galactosyltransferase 1 OS=Homo sapiens GN=B4GALT1 - [B4GT1_HUMAN]
Isoform Short of Tyrosine-protein kinase receptor UFO OS=Homo sapiens GN=AXL - [UFO_HUMAN]
Isoform Short of Very low-density lipoprotein receptor OS=Homo sapiens GN=VLDLR - [VLDLR_HUMAN]
Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=2 SV=1 - [J3KR24_HUMAN]
Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]
Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN]
Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN]
Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]
Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]
Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN]
Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN]
Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1 - [KPRP_HUMAN]
Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8 - [LAMA5_HUMAN]
Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=2 SV=1 - [E7EPA6_HUMAN]
Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2 - [LAMB2_HUMAN]
Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3 - [LAMC1_HUMAN]
Legumain OS=Homo sapiens GN=LGMN PE=1 SV=1 - [LGMN_HUMAN]
Leucine-rich repeat transmembrane protein FLRT2 OS=Homo sapiens GN=FLRT2 PE=1 SV=1 - [FLRT2_HUMAN]
Lipolysis-stimulated lipoprotein receptor OS=Homo sapiens GN=LSR PE=2 SV=1 - [B4DKL4_HUMAN]
L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 - [LDHA_HUMAN]
L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]
Low-density lipoprotein receptor-related protein 5 OS=Homo sapiens GN=LRP5 PE=1 SV=2 - [LRP5_HUMAN]
Low-density lipoprotein receptor-related protein 6 (Fragment) OS=Homo sapiens GN=LRP6 PE=4 SV=1 - [H0YGW5_HUMAN]
Lumican OS=Homo sapiens GN=LUM PE=1 SV=2 - [LUM_HUMAN]
Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]
Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]
Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3 - [MA2B1_HUMAN]
Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2 - [PPGB_HUMAN]
Lysosomal Pro-X carboxypeptidase OS=Homo sapiens GN=PRCP PE=1 SV=1 - [PCP_HUMAN]
Lysosomal thioesterase PPT2 OS=Homo sapiens GN=PPT2 PE=1 SV=4 - [PPT2_HUMAN]
Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]
Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=2 SV=1 - [B4E2S7_HUMAN]
Lysyl oxidase homolog 2 (Fragment) OS=Homo sapiens GN=LOXL2 PE=4 SV=1 - [H0YAR1_HUMAN]
Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1 - [LOXL2_HUMAN]
Lysyl oxidase homolog 4 OS=Homo sapiens GN=LOXL4 PE=1 SV=1 - [LOXL4_HUMAN]
Macrophage colony-stimulating factor 1 OS=Homo sapiens GN=CSF1 PE=1 SV=2 - [CSF1_HUMAN]
Mammalian ependymin-related protein 1 OS=Homo sapiens GN=EPDR1 PE=1 SV=2 - [EPDR1_HUMAN]
Mannosyl-oligosaccharide glucosidase (Fragment) OS=Homo sapiens GN=MOGS PE=2 SV=1 - [C9J8D4_HUMAN]
Matrix metalloproteinase-19 OS=Homo sapiens GN=MMP19 PE=2 SV=1 - [F8W1C3_HUMAN]
Matrix-remodeling-associated protein 8 OS=Homo sapiens GN=MXRA8 PE=2 SV=1 - [B3KTR6_HUMAN]
Membrane-bound transcription factor site-1 protease OS=Homo sapiens GN=MBTPS1 PE=1 SV=1 - [MBTP1_HUMAN]
Mesothelin (Fragment) OS=Homo sapiens GN=MSLN PE=2 SV=2 - [H3BMA1_HUMAN]
Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=2 SV=1 - [Q5H9A7_HUMAN]
Metalloproteinase inhibitor 2 OS=Homo sapiens GN=TIMP2 PE=1 SV=2 - [TIMP2_HUMAN]
Metalloproteinase inhibitor 3 OS=Homo sapiens GN=TIMP3 PE=1 SV=2 - [TIMP3_HUMAN]
Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=2 SV=1 - [B3KVK7_HUMAN]
MHC class I polypeptide-related sequence A OS=Homo sapiens GN=MICA PE=2 SV=1 - [Q96QC4_HUMAN]
MHC class I polypeptide-related sequence B OS=Homo sapiens GN=MICB PE=1 SV=1 - [MICB_HUMAN]

Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN]
Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens GN=MINPP1 PE=1 SV=1 - [MINP1_HUMAN]
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]
N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase (Fragment) OS=Homo sapiens GN=AGA PE=2 SV=1 - [H0Y9C7_HUMAN]
N-acetylgalactosamine-6-sulfatase OS=Homo sapiens GN=GALNS PE=2 SV=1 - [F5H325_HUMAN]
N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3 - [GNS_HUMAN]
N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase OS=Homo sapiens GN=B3GNT1 PE=1 SV=1 - [B3GN1_HUMAN]
N-acetyllactosaminide beta-1,6-N-acetylglucosaminyl-transferase, isoform A OS=Homo sapiens GN=GCNT2 PE=2 SV=1 - [GNT2A_HUMAN]
Neuron navigator 3 OS=Homo sapiens GN=NAV3 PE=2 SV=2 - [E7EUA9_HUMAN]
Neuroserpin OS=Homo sapiens GN=SERPINI1 PE=1 SV=1 - [NEUS_HUMAN]
Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 - [GANAB_HUMAN]
Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2 - [AAAT_HUMAN]
NKG2D ligand 2 OS=Homo sapiens GN=ULBP2 PE=1 SV=1 - [N2DL2_HUMAN]
Nodal modulator 3 OS=Homo sapiens GN=NOMO3 PE=2 SV=1 - [F5H826_HUMAN]
Noggin OS=Homo sapiens GN=NOG PE=1 SV=1 - [NOGG_HUMAN]
N-sulphoglucosamine sulphohydrolase OS=Homo sapiens GN=SGSH PE=2 SV=1 - [F5H6A3_HUMAN]
Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4 - [NUCB1_HUMAN]
Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=3 SV=1 - [H0YH88_HUMAN]
Nucleotide exchange factor SIL1 OS=Homo sapiens GN=SIL1 PE=1 SV=1 - [SIL1_HUMAN]
Out at first protein homolog OS=Homo sapiens GN=OAF PE=2 SV=1 - [OAF_HUMAN]
Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1 - [PPT1_HUMAN]
Pantetheinase OS=Homo sapiens GN=VNN1 PE=1 SV=2 - [VNN1_HUMAN]
Pappalysin-1 OS=Homo sapiens GN=PAPPA PE=1 SV=3 - [PAPP1_HUMAN]
Pentraxin-related protein PTX3 OS=Homo sapiens GN=PTX3 PE=1 SV=3 - [PTX3_HUMAN]
Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2 - [PPIB_HUMAN]
Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2 - [PXDN_HUMAN]
Peroxiredoxin 2, isoform CRA_a OS=Homo sapiens GN=PRDX2 PE=2 SV=2 - [A6NIW5_HUMAN]
Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]
Peroxiredoxin-4 (Fragment) OS=Homo sapiens GN=PRDX4 PE=4 SV=1 - [H7C3T4_HUMAN]
Phosphoglycerate kinase OS=Homo sapiens GN=PGK1 PE=2 SV=1 - [B7Z7A9_HUMAN]
Phosphoribosylaminoimidazole carboxylase OS=Homo sapiens GN=PAICS PE=2 SV=1 - [D6RF62_HUMAN]
Phosphoribosylaminoimidazolecarboxamide formyltransferase OS=Homo sapiens GN=ATIC PE=2 SV=1 - [E9PBU3_HUMAN]
Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4 - [PEDF_HUMAN]
Plasma alpha-L-fucosidase OS=Homo sapiens GN=FUCA2 PE=1 SV=2 - [FUCO2_HUMAN]
Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]
Plastin-3 OS=Homo sapiens GN=PLS3 PE=2 SV=1 - [B7Z6M1_HUMAN]
Platelet-derived growth factor D OS=Homo sapiens GN=PDGFD PE=1 SV=1 - [PDGFD_HUMAN]
Plexin domain-containing protein 2 OS=Homo sapiens GN=PLXDC2 PE=1 SV=1 - [PXDC2_HUMAN]
Polypeptide N-acetylgalactosaminyltransferase 10 OS=Homo sapiens GN=GALNT10 PE=1 SV=2 - [GLT10_HUMAN]
Polypeptide N-acetylgalactosaminyltransferase 18 OS=Homo sapiens GN=GALNT18 PE=2 SV=2 - [GLT18_HUMAN]
Polypeptide N-acetylgalactosaminyltransferase 5 OS=Homo sapiens GN=GALNT5 PE=1 SV=1 - [GALT5_HUMAN]
Polyubiquitin-C (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=1 - [F5H265_HUMAN]
Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2 - [SAP_HUMAN]
Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2 - [CPVL_HUMAN]
Pro-cathepsin H OS=Homo sapiens GN=CTSH PE=1 SV=4 - [CATH_HUMAN]
Processed exostosin-like 2 OS=Homo sapiens GN=EXTL2 PE=2 SV=1 - [F5GZK1_HUMAN]
Procollagen galactosyltransferase 1 OS=Homo sapiens GN=COLGALT1 PE=1 SV=1 - [GT251_HUMAN]
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2 - [PLOD1_HUMAN]
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens GN=PLOD2 PE=2 SV=1 - [E7ETU9_HUMAN]
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1 - [PLOD3_HUMAN]
Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2 - [LRP1_HUMAN]
Prolyl 3-hydroxylase 1 OS=Homo sapiens GN=LEPRE1 PE=1 SV=2 - [P3H1_HUMAN]
Proprotein convertase subtilisin/kexin type 9 OS=Homo sapiens GN=PCSK9 PE=1 SV=3 - [PCSK9_HUMAN]
Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 - [PSA1_HUMAN]

Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2 - [PSB3_HUMAN]
Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4 - [PSB4_HUMAN]
Protein CREG1 OS=Homo sapiens GN=CREG1 PE=1 SV=1 - [CREG1_HUMAN]
Protein CutA OS=Homo sapiens GN=CUTA PE=2 SV=1 - [C9IZG4_HUMAN]
Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1 - [CYR61_HUMAN]
Protein disulfide-isomerase (Fragment) OS=Homo sapiens GN=P4HB PE=2 SV=1 - [I3L398_HUMAN]
Protein kinase C-binding protein NELL1 OS=Homo sapiens GN=NRP1 PE=2 SV=2 - [E9PEP6_HUMAN]
Protein NAMPTL (Fragment) OS=Homo sapiens GN=NAMPTL PE=2 SV=1 - [Q5SYT8_HUMAN]
Protein NOV homolog OS=Homo sapiens GN=NOV PE=1 SV=1 - [NOV_HUMAN]
Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1 - [S10A9_HUMAN]
Protocadherin Fat 1 OS=Homo sapiens GN=FAT1 PE=1 SV=2 - [FAT1_HUMAN]
Putative phospholipase B-like 2 OS=Homo sapiens GN=PLBD2 PE=1 SV=2 - [PLBL2_HUMAN]
Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]
Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]
Receptor-type tyrosine-protein phosphatase kappa OS=Homo sapiens GN=PTPRK PE=1 SV=2 - [PTPRK_HUMAN]
Receptor-type tyrosine-protein phosphatase mu OS=Homo sapiens GN=PTPRM PE=2 SV=2 - [E7EPS8_HUMAN]
Ribonuclease T2 (Fragment) OS=Homo sapiens GN=RNASET2 PE=2 SV=1 - [D6RHI9_HUMAN]
Semaphorin-3A OS=Homo sapiens GN=SEMA3A PE=1 SV=1 - [SEM3A_HUMAN]
Semaphorin-4D OS=Homo sapiens GN=SEMA4D PE=4 SV=1 - [E9PFD9_HUMAN]
Semaphorin-7A OS=Homo sapiens GN=SEMA7A PE=1 SV=1 - [SEM7A_HUMAN]
Septin-2 (Fragment) OS=Homo sapiens GN=SEPT2 PE=2 SV=1 - [C9J2Q4_HUMAN]
Serglycin OS=Homo sapiens GN=SRGN PE=1 SV=3 - [SRGN_HUMAN]
Serine protease 23 OS=Homo sapiens GN=PRSS23 PE=2 SV=1 - [B4E2J3_HUMAN]
Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1 - [HTRA1_HUMAN]
Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP1CA PE=2 SV=1 - [E9PMD7_HUMAN]
Serum albumin (Fragment) OS=Homo sapiens GN=ALB PE=4 SV=1 - [H0YA55_HUMAN]
Sialidase-1 OS=Homo sapiens GN=NEU1 PE=1 SV=1 - [NEUR1_HUMAN]
SLIT and NTRK-like protein 1 OS=Homo sapiens GN=SLITRK1 PE=1 SV=2 - [SLIK1_HUMAN]
SLIT and NTRK-like protein 5 OS=Homo sapiens GN=SLITRK5 PE=2 SV=2 - [SLIK5_HUMAN]
Soluble calcium-activated nucleotidase 1 OS=Homo sapiens GN=CANT1 PE=1 SV=1 - [CANT1_HUMAN]
Solute carrier family 2, facilitated glucose transporter member 1 (Fragment) OS=Homo sapiens GN=SLC2A1 PE=2 SV=1 - [C9JIM8_HUMAN]
Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3 - [SORT_HUMAN]
Stanniocalcin-1 OS=Homo sapiens GN=STC1 PE=1 SV=1 - [STC1_HUMAN]
Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3 - [QSOX1_HUMAN]
Sulfhydryl oxidase 2 OS=Homo sapiens GN=QSOX2 PE=1 SV=3 - [QSOX2_HUMAN]
Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=2 - [SBSN_HUMAN]
Sushi domain-containing protein 5 OS=Homo sapiens GN=SUSD5 PE=1 SV=3 - [SUSD5_HUMAN]
Sushi repeat-containing protein SRPX2 OS=Homo sapiens GN=SRPX2 PE=1 SV=1 - [SRPX2_HUMAN]
Talin-1 OS=Homo sapiens GN=TLN1 PE=2 SV=1 - [Q5TCU6_HUMAN]
T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=2 SV=1 - [F8VQ14_HUMAN]
T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=2 SV=1 - [B7Z9L0_HUMAN]
T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1 - [B4DYD8_HUMAN]
T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=2 SV=1 - [B4DUR8_HUMAN]
T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=2 SV=1 - [B4DQH4_HUMAN]
Tenascin OS=Homo sapiens GN=TNC PE=4 SV=1 - [J3QSU6_HUMAN]
Testican-1 OS=Homo sapiens GN=SPOCK1 PE=1 SV=1 - [TICN1_HUMAN]
Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=2 SV=1 - [F5H780_HUMAN]
Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2 - [TSP1_HUMAN]
Thrombospondin-2 OS=Homo sapiens GN=THBS2 PE=1 SV=2 - [TSP2_HUMAN]
Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2 - [THBG_HUMAN]
Tissue alpha-L-fucosidase OS=Homo sapiens GN=FUCA1 PE=1 SV=4 - [FUCO_HUMAN]
Tissue factor pathway inhibitor OS=Homo sapiens GN=TFPI PE=1 SV=1 - [TFPI1_HUMAN]
Tissue-type plasminogen activator OS=Homo sapiens GN=PLAT PE=1 SV=1 - [TPA_HUMAN]
Torsin-1B OS=Homo sapiens GN=TOR1B PE=1 SV=2 - [TOR1B_HUMAN]

Torsin-3A (Fragment) OS=Homo sapiens GN=TOR3A PE=2 SV=1 - [Q5W0C6_HUMAN]
Transferrin receptor (P90, CD71), isoform CRA_c OS=Homo sapiens GN=TFRC PE=4 SV=1 - [G3V0E5_HUMAN]
Transforming growth factor beta-1 OS=Homo sapiens GN=TGFB1 PE=1 SV=2 - [TGFB1_HUMAN]
Transforming growth factor beta-2 OS=Homo sapiens GN=TGFB2 PE=1 SV=1 - [TGFB2_HUMAN]
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN]
Transmembrane protein 132A OS=Homo sapiens GN=TMEM132A PE=2 SV=1 - [T132A_HUMAN]
Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2 - [TPP1_HUMAN]
Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 - [TBA1B_HUMAN]
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]
Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]
Tumor necrosis factor receptor superfamily member 11B OS=Homo sapiens GN=TNFRSF11B PE=1 SV=3 - [TR11B_HUMAN]
Tumor necrosis factor receptor superfamily member 21 OS=Homo sapiens GN=TNFRSF21 PE=1 SV=1 - [TNR21_HUMAN]
Twisted gastrulation protein homolog 1 OS=Homo sapiens GN=TWSG1 PE=2 SV=1 - [TWSG1_HUMAN]
Urokinase plasminogen activator surface receptor OS=Homo sapiens GN=PLAUR PE=1 SV=1 - [UPAR_HUMAN]
Urokinase-type plasminogen activator chain B OS=Homo sapiens GN=PLAU PE=2 SV=1 - [E7ET40_HUMAN]
Vascular endothelial growth factor C OS=Homo sapiens GN=VEGFC PE=1 SV=1 - [VEGFC_HUMAN]
Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1 - [VASN_HUMAN]
Vesicular integral-membrane protein VIP36 (Fragment) OS=Homo sapiens GN=LMAN2 PE=2 SV=1 - [D6RIU4_HUMAN]
Vimentin OS=Homo sapiens GN=VIM PE=2 SV=1 - [B0YJC4_HUMAN]
Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1 - [PROS_HUMAN]
Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1 - [VTNC_HUMAN]
von Willebrand factor A domain-containing protein 1 OS=Homo sapiens GN=VWA1 PE=2 SV=1 - [VWA1_HUMAN]
WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 - [WDR1_HUMAN]
X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 - [XRCC5_HUMAN]
X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=2 SV=1 - [F5H1I8_HUMAN]
Xylosyltransferase 2 OS=Homo sapiens GN=XYLT2 PE=2 SV=2 - [XYLT2_HUMAN]

1.08	1.19	1.13	1.26	0.95	1.14
1.39	1.01	1.24	0.90	1.09	0.70
0.96	1.00	1.12	1.06	0.87	1.02
1.30	1.30	1.26	1.28	0.94	1.04
1.23	1.13	1.34	1.22	0.95	1.01
1.15	0.94	1.13	0.99	0.99	0.91
1.14	1.41	1.10	1.36	1.04	1.27
1.65	**1.59**	**1.61**	**1.55**	1.03	0.99
0.85	0.99	0.79	0.79	1.16	1.09
1.28	1.27	1.19	1.18	1.08	1.02
1.30	1.27	1.16	1.22	1.05	1.01
1.31	1.22	1.32	1.26	0.95	0.94
1.08	1.13	0.99	0.92	1.05	1.04
1.10	1.13	1.16	1.08	0.95	0.93
1.20	1.21	1.16	1.17	1.04	1.03
1.18	1.08	1.21	1.13	0.99	0.97
0.99	0.94	0.97	0.96	1.03	1.04
1.11	1.08	1.25	1.20	0.91	0.94
1.32	1.23	1.40	1.22	1.00	0.98
1.10	1.12	0.98	1.07	1.08	1.10
1.34	1.32	1.29	1.26	1.00	1.07
1.26	1.20	1.24	1.16	1.03	1.00
0.82	0.74	0.77	0.71	0.99	1.09
1.20	1.13	1.21	1.14	1.01	0.99
1.11	1.16	1.06	1.20	1.04	1.05
0.73	**0.66**	**0.67**	**0.63**	1.02	0.99
1.08	1.12	0.91	1.00	1.11	1.06
0.73	0.68	0.70	**0.67**	0.92	0.98
0.77	0.83	0.77	0.79	1.05	1.06
0.98	1.00	0.98	1.00	1.11	1.02
1.06	1.10	1.12	0.99	0.98	1.13
0.91	1.06	0.76	0.89	1.09	1.18
1.88	**1.53**	**2.19**	**1.78**	0.88	0.83
1.20	1.16	1.04	1.02	1.02	1.00
1.84	1.30	**1.87**	1.32	0.99	0.73
1.11	1.16	1.16	1.19	1.03	1.03
1.62	**1.72**	**1.53**	**1.53**	1.02	0.97
N]					
0.81	0.75	0.91	0.85	0.90	0.96
1.20	1.20	1.11	1.11	1.09	1.03
0.93	0.86	0.87	0.82	1.03	0.98
0.80	0.87	0.77	0.81	1.07	1.08
0.83	0.79	0.86	0.85	1.05	1.00

0.98	0.90	0.91	0.89	0.93	0.95
0.92	0.87	0.96	0.91	0.97	0.98
1.41	1.43	**1.52**	**1.54**	1.01	1.06
1.20	1.16	1.06	1.13	1.01	0.98
0.95	0.96	1.03	1.04	0.92	1.04
0.59	**0.62**	**0.53**	**0.56**	1.12	1.08
1.23	1.16	1.09	1.04	1.12	1.02
1.23	0.95	1.18	1.13	1.06	0.99
0.92	0.84	0.95	0.85	0.99	1.01
0.56	**0.56**	**0.60**	**0.57**	0.93	0.94
0.77	0.90	0.75	0.79	0.99	1.02
0.78	0.84	0.77	0.83	1.05	1.01
0.70	**0.67**	0.73	0.73	0.95	1.01
1.04	1.07	1.00	1.02	1.06	1.06
1.44	1.29	**1.50**	1.32	0.94	0.93
1.05	1.23	1.04	1.05	1.01	1.02
0.75	0.73	0.77	0.77	0.94	0.94
1.31	1.40	**1.81**	**1.67**	1.07	1.04
1.63	**1.65**	1.25	1.27	1.30	1.04
0.58	**0.54**	**0.56**	**0.52**	1.03	0.95
1.44	1.07	1.21	1.08	1.33	0.92
0.63	**0.56**	0.68	**0.61**	0.91	0.91
0.84	0.94	0.95	1.02	1.05	1.11
1.78	**1.58**	**1.57**	**1.62**	1.13	0.86
1.04	0.93	0.97	0.90	1.09	0.97
0.93	1.11	0.95	1.01	1.00	1.02
1.03	1.03	0.94	1.00	1.03	1.08
0.96	0.97	0.97	0.97	0.96	1.02
0.90	0.91	0.95	0.94	1.04	1.00
0.69	0.69	0.71	0.74	1.02	1.01
0.95	0.90	0.86	0.81	1.05	0.96
1.68	1.48	**1.73**	**1.54**	0.97	0.91
0.75	0.74	0.77	0.74	1.01	1.02
1.15	1.03	1.23	1.22	1.05	1.02
0.92	0.99	0.85	0.89	1.02	1.07
0.88	1.01	1.04	1.13	0.90	1.06
0.98	0.89	1.02	0.92	0.94	0.94
0.77	0.78	0.81	0.80	0.96	1.01
0.52	**0.51**	**0.58**	**0.55**	0.95	0.96
1.24	0.98	1.19	1.01	1.05	0.94
0.54	**0.53**	**0.56**	**0.53**	1.00	1.00
0.97	0.91	0.99	0.95	1.00	0.95
0.67	0.72	0.70	**0.64**	1.08	0.99

1.17	1.12	1.17	1.12	1.00	0.99
1.16	1.33	1.17	1.16	1.04	1.02
1.21	1.15	1.10	1.19	1.00	0.97
1.28	1.25	1.25	1.19	0.99	0.97
1.06	1.03	1.12	1.03	1.04	1.00
1.48	1.38	**1.54**	1.44	1.02	1.02
0.96	0.92	1.16	1.05	0.91	0.98
0.95	0.97	0.96	0.99	0.99	1.06
0.69	**0.61**	0.73	**0.65**	0.94	0.91
0.78	0.74	0.94	0.87	0.89	0.93
0.80	0.84	0.79	0.82	1.03	1.02
1.60	1.42	1.42	1.37	1.03	1.01
1.23	1.11	1.27	1.14	0.97	0.93
1.41	1.29	1.43	1.32	0.98	1.03
1.55	1.36	**1.86**	**1.57**	0.86	0.88
1.18	1.05	1.25	1.17	0.96	0.93
1.06	1.07	1.01	0.99	1.02	1.01
0.93	0.89	0.93	0.90	1.00	1.00
1.13	1.25	0.99	1.09	1.15	1.13
0.57	**0.60**	**0.63**	**0.65**	0.99	1.03
1.76	**1.51**	**1.73**	1.45	1.00	0.95
0.66	1.08	**0.62**	0.93	1.04	1.16
1.48	**1.55**	**1.67**	**1.63**	1.00	1.02
0.75	0.80	0.80	0.81	0.94	1.00
1.17	1.16	1.09	1.08	1.08	1.02
1.28	1.29	1.21	1.26	1.02	1.05
0.86	0.89	0.78	0.84	0.98	0.94
1.38	0.92	1.35	0.88	1.04	0.94
1.54	**1.55**	1.41	1.41	1.08	1.03
0.82	0.79	0.89	0.85	0.93	0.97
0.70	0.72	0.77	0.76	0.94	1.00
0.99	1.11	0.96	1.08	1.07	1.07
1.35	1.11	1.37	1.13	0.98	0.85
0.60	**0.59**	**0.58**	**0.59**	0.97	0.99
0.70	0.70	0.73	0.73	0.96	1.04
1.58	**1.59**	1.35	1.31	1.04	1.02
0.92	0.90	1.20	1.17	0.77	1.01
1.37	1.26	**1.54**	1.43	0.89	0.95
1.79	**2.11**	1.30	**1.54**	1.38	1.21
1.11	1.04	1.00	0.93	1.12	0.96
1.38	1.27	1.29	1.17	1.05	0.96
0.72	0.76	**0.63**	0.68	0.99	1.07
1.00	0.92	0.93	0.86	1.07	0.95
1.38	1.33	**1.61**	**1.60**	0.81	0.99
0.85	0.87	0.74	0.83	1.19	1.18

1.44	1.32	1.31	1.21	1.10	0.96
0.73	0.79	0.73	0.69	1.03	1.09
1.07	0.98	0.98	0.90	1.09	0.94
1.08	1.05	1.10	1.07	1.00	1.03
1.16	1.13	1.14	1.17	1.01	1.01
1.03	0.98	1.00	1.02	0.98	1.03
1.52	**2.05**	1.23	**1.66**	1.24	1.39
0.56	**0.60**	**0.52**	**0.58**	1.05	1.12
1.25	1.25	1.24	1.25	1.01	1.04
1.15	1.11	1.18	1.16	1.01	0.99
1.39	1.33	1.45	1.39	0.96	0.99
0.98	1.00	0.97	0.97	1.03	1.04
1.38	1.23	1.38	1.32	0.93	0.94
1.17	1.15	1.10	1.09	1.05	1.01
1.13	1.02	1.06	1.00	1.07	0.95
1.24	1.22	1.27	1.31	1.04	0.95
1.28	**1.50**	1.46	1.41	0.93	1.08
1.53	1.48	**1.50**	1.34	1.03	1.01
1.14	1.01	**1.53**	1.49	0.77	1.06
0.93	0.88	0.92	0.86	1.01	0.97
0.68	**0.62**	0.75	0.68	0.95	1.02
0.86	0.89	0.93	0.87	1.01	0.95
1.03	1.05	1.00	1.02	1.03	1.05
0.97	0.90	0.92	0.86	1.05	0.96
0.73	0.89	**0.65**	0.78	1.03	0.97
1.15	1.08	1.23	1.09	1.00	0.93
1.27	1.23	1.40	1.21	0.98	1.02
1.90	**1.51**	**1.88**	**1.51**	1.01	0.82
1.37	1.34	1.27	1.31	1.01	1.03
1.09	1.07	1.13	1.04	0.98	1.00
1.18	1.18	1.12	1.12	1.05	1.03
0.87	0.86	0.84	0.87	1.00	1.01
0.91	0.89	0.90	0.87	1.02	1.02
0.85	0.82	0.81	0.79	0.99	0.98
0.86	0.93	0.96	0.88	0.95	1.01
0.71	0.71	0.70	0.77	1.03	1.03
0.80	0.73	0.86	0.78	0.94	0.94
1.51	**1.50**	**1.60**	**1.63**	0.94	0.92
0.76	0.76	0.84	0.83	0.99	1.05
1.58	**1.60**	1.42	1.44	1.12	1.05
0.87	0.90	0.80	0.82	1.10	1.06
0.86	0.82	0.90	0.90	0.96	0.93
0.68	**0.67**	**0.67**	0.68	0.99	1.11
0.87	0.82	0.87	0.83	1.03	0.99
0.87	0.91	0.91	0.89	0.99	0.98
0.96	0.84	0.94	0.87	1.07	0.98

1.12	1.34	1.35	**1.63**	0.83	1.15
1.18	1.10	1.27	1.17	0.97	1.01
0.76	0.75	0.72	0.72	1.04	1.03
1.39	1.33	1.49	1.40	0.97	0.93
0.68	**0.64**	0.72	0.74	0.94	0.99
1.05	1.02	1.11	1.11	0.92	1.00
0.83	0.77	0.82	0.77	1.01	0.98
1.20	1.20	1.24	1.24	0.94	1.00
1.51	1.42	1.41	1.45	1.02	1.00
1.01	0.95	1.04	0.93	1.01	0.95
0.86	0.86	0.85	0.85	1.01	1.03
1.15	1.08	1.23	1.16	0.93	0.96
0.80	0.74	0.81	0.79	0.95	1.01
5.62	**4.43**	**5.15**	**4.07**	1.09	1.00
0.40	**0.39**	**0.39**	**0.38**	1.02	1.02
0.74	0.73	0.70	0.68	1.03	0.98
1.33	1.20	1.41	1.28	0.95	0.93
0.78	0.84	**0.63**	0.83	1.06	1.08
2.66	**1.79**	**2.85**	**1.93**	0.93	0.70
0.98	0.97	1.05	0.99	0.97	1.02
0.85	0.71	0.93	0.71	1.04	1.02
1.22	1.16	1.05	1.02	1.06	1.00
0.71	0.81	**0.66**	0.76	1.07	1.18
1.02	0.93	1.02	0.93	1.01	0.93
0.88	0.99	1.03	1.01	1.08	1.07
0.76	0.68	0.78	0.70	0.98	0.92
1.32	1.32	1.44	1.31	1.00	0.95
0.99	0.91	0.98	0.94	1.03	0.98
1.03	1.20	0.98	1.14	1.06	1.20
0.85	0.82	0.78	0.78	1.07	1.01
0.88	0.82	0.88	0.82	1.00	0.96
0.89	0.85	0.91	0.88	0.99	1.00
2.64	**2.35**	**2.56**	**2.32**	1.01	0.89
0.82	0.88	0.85	0.82	1.09	0.99
1.42	1.25	1.44	1.27	0.99	1.01
0.81	0.77	0.87	0.83	0.93	0.98
0.61	**0.56**	0.74	0.69	0.83	0.95
0.87	0.95	0.78	0.86	1.11	1.13

0.89	0.94	0.97	1.02	0.98	1.05
1.13	1.03	1.14	1.05	0.99	0.92
0.72	**0.66**	0.77	0.73	0.97	0.98
0.86	**0.67**	0.91	0.86	0.94	0.95
1.07	1.00	1.11	1.03	0.95	0.97
1.20	1.09	1.10	1.00	1.09	0.94
2.59	**2.14**	**2.81**	**2.34**	0.93	0.85
1.83	**1.59**	1.49	1.45	1.07	0.94
1.79	**1.67**	**1.55**	**1.52**	1.07	0.96
1.48	1.38	**1.51**	1.45	1.01	0.97
1.86	**1.65**	**1.95**	**1.72**	0.94	0.90
2.50	**2.05**	**2.46**	**2.26**	0.96	0.86
1.78	**1.68**	**1.68**	**1.64**	1.02	0.94
2.59	**2.71**	**2.39**	**2.10**	1.05	1.02
1.09	1.22	1.34	**1.50**	0.87	1.01
1.08	1.10	1.13	1.11	1.00	0.98
1.08	1.13	1.04	1.18	0.96	1.07
1.04	0.98	1.07	0.99	1.00	1.00
0.56	**0.57**	**0.50**	**0.57**	1.01	1.06
0.92	0.97	0.95	1.06	0.92	0.93
1.29	1.36	1.13	1.20	1.10	1.09
1.57	1.48	1.42	1.47	1.06	1.01
1.59	1.43	1.44	1.39	1.09	0.92
0.80	0.81	**0.66**	0.74	1.11	1.14
0.89	0.87	0.91	0.89	0.99	1.00
0.74	0.72	0.75	0.74	1.01	1.02
0.61	**0.62**	**0.62**	**0.57**	1.01	1.01
1.20	1.13	1.23	1.11	0.98	0.96
1.58	**1.51**	1.47	1.37	1.00	0.98
0.90	0.84	0.96	0.91	0.94	0.96
0.67	**0.61**	**0.66**	**0.62**	0.99	0.97
0.98	1.02	0.91	0.96	1.08	1.02
0.95	0.94	0.96	1.01	1.00	1.02
0.91	1.00	0.89	0.91	1.05	1.06
0.87	0.88	0.86	0.90	0.94	1.05
1.09	1.27	1.07	1.12	1.00	1.06
0.78	0.76	0.83	0.81	0.96	0.97
0.77	0.79	0.72	0.72	1.14	1.13
0.85	0.87	0.79	0.82	1.03	1.09
0.72	0.72	0.79	0.78	0.92	1.02

1.16	1.33	0.90	1.00	1.34	1.14
1.06	1.08	0.90	1.10	0.99	1.06
1.36	**1.52**	1.03	1.15	0.92	1.15
0.89	0.97	0.80	0.82	0.98	1.00
0.84	0.77	0.85	0.81	0.96	0.98
1.34	1.42	1.26	1.37	1.06	1.09
0.80	0.77	0.89	0.72	1.00	0.98
1.04	0.86	0.96	1.12	0.94	1.02
0.77	0.75	0.72	0.74	1.01	1.06
1.34	1.35	1.36	1.29	1.01	0.94
0.71	0.69	**0.61**	**0.59**	1.16	1.00
0.91	0.85	0.85	0.87	0.98	1.06
0.80	0.78	0.77	0.80	0.99	0.99
1.04	1.07	1.04	1.00	1.07	0.98
1.04	1.01	0.92	0.89	1.14	1.00
0.48	**0.47**	0.87	0.85	**0.55**	1.00
0.96	1.06	1.17	1.15	0.93	1.13
0.90	0.87	0.90	0.85	1.00	0.94
0.67	**0.63**	**0.63**	**0.61**	0.96	1.02
0.95	0.93	1.02	0.93	0.94	0.94
1.41	1.31	1.46	1.37	0.94	0.96
1.33	1.23	1.24	1.18	1.04	0.97
0.99	0.98	0.99	0.96	0.98	1.01
1.56	1.43	**1.55**	**1.58**	0.92	0.99
1.37	1.44	1.37	**1.56**	0.92	1.15
1.27	1.24	1.26	1.23	1.01	1.01
0.81	0.78	0.88	0.82	0.99	0.98
0.52	**0.55**	**0.59**	**0.58**	0.98	1.05
1.02	1.03	0.96	0.94	1.03	1.00
0.98	0.98	0.92	0.98	1.01	1.01
0.64	**0.67**	**0.59**	**0.62**	1.08	1.00
0.82	1.02	**0.64**	0.80	1.27	1.28
1.44	1.41	1.12	1.10	1.28	1.01
1.37	1.36	1.39	1.40	0.97	1.02
0.67	0.70	0.69	0.74	0.94	1.02
0.75	0.73	0.78	0.81	0.97	0.97
0.80	0.78	0.77	0.75	1.04	1.00
0.94	1.02	1.05	1.03	0.89	1.01
1.26	1.09	1.30	0.99	0.97	1.14
0.98	0.99	1.05	0.98	0.98	1.00
0.92	0.93	0.91	0.93	1.02	1.05
1.17	1.09	1.11	1.08	0.98	0.98
0.84	0.74	0.94	0.85	0.89	0.98
1.02	0.92	1.04	0.99	0.96	0.98
0.67	0.70	**0.66**	0.69	0.97	1.00

1.43	**1.64**	1.32	**1.52**	1.08	1.18
0.64	0.69	**0.64**	**0.65**	1.00	1.04
1.42	1.46	1.41	1.44	1.02	1.05
0.95	0.99	1.06	1.00	1.04	1.00
1.09	**1.63**	0.91	1.37	1.20	**1.54**
1.11	1.03	1.17	1.08	0.95	0.94
1.62	**1.60**	1.04	1.10	1.46	1.05
0.72	0.69	0.72	0.69	1.01	0.99
0.81	0.79	0.76	0.78	1.09	1.06
1.12	1.12	1.12	1.13	1.00	1.03
0.84	0.89	0.81	0.90	0.98	1.02
1.17	1.04	1.15	1.09	0.95	0.97
1.09	0.99	1.00	0.91	1.09	0.94
0.69	0.70	0.75	0.78	1.00	1.05
0.91	0.92	0.90	0.91	1.01	1.01
0.76	0.81	0.81	0.81	0.98	0.98
0.88	0.92	0.89	0.92	1.00	1.07
0.88	0.81	0.91	0.84	0.96	0.97
1.14	1.23	1.19	1.29	0.95	1.11
11.85	**5.17**	**12.51**	**5.53**	0.95	**0.45**
0.53	**0.56**	**0.53**	**0.57**	1.01	1.03
0.80	0.85	0.77	0.81	1.04	1.09
1.29	1.19	1.26	1.12	1.01	0.99
1.69	**1.52**	**1.73**	**1.55**	0.96	0.87
0.81	0.81	0.93	0.93	0.88	1.03
0.78	0.85	**0.67**	0.74	1.16	1.13
1.00	0.94	0.98	0.92	1.02	0.97
0.88	0.77	0.74	**0.65**	1.11	0.97
0.48	**0.47**	**0.47**	**0.47**	1.03	0.99
0.99	0.93	1.07	1.00	0.94	0.97
1.30	1.15	1.21	1.15	1.00	0.98
1.17	1.13	1.17	1.14	1.00	1.00
1.36	1.24	1.29	1.18	1.05	0.94
0.96	0.95	0.90	0.92	1.06	1.00
1.32	0.98	1.13	0.91	1.15	0.93
1.26	0.94	1.40	1.16	0.81	0.85
1.32	1.27	1.31	1.28	1.02	0.99
1.03	1.06	1.16	1.18	0.95	1.02
2.09	**1.89**	**2.19**	**2.02**	0.95	1.00
1.07	1.06	0.99	0.99	1.07	1.02
0.90	0.88	0.93	0.89	0.98	0.98
1.03	0.98	1.02	0.98	1.02	0.99
0.95	1.18	0.96	1.06	1.08	1.16
0.67	**0.65**	0.68	**0.66**	1.00	0.97
1.27	1.17	1.18	1.15	1.06	0.96
0.82	0.80	0.84	0.85	0.95	0.97
0.92	1.04	0.94	1.07	0.97	0.93

0.95	0.95	0.90	0.93	1.01	1.02
1.14	0.97	1.23	1.06	0.93	0.94
1.56	**1.98**	1.43	1.42	1.35	1.06
1.23	1.13	1.41	1.24	0.94	0.95
0.83	0.79	0.84	0.80	0.94	0.99
1.12	1.10	1.15	1.04	1.10	0.94
1.47	1.13	**1.58**	1.40	0.98	1.00
1.61	**1.90**	**1.55**	**1.83**	1.04	1.21
1.01	0.93	0.82	0.93	0.96	1.15
0.82	0.87	0.73	0.79	1.05	1.09
0.64	**0.62**	**0.65**	**0.63**	0.99	1.01
0.47	**0.47**	**0.47**	**0.47**	1.01	1.03
0.35	**0.33**	**0.36**	**0.35**	0.98	0.97
0.93	0.93	0.96	0.96	1.02	1.09
1.05	0.95	1.05	1.02	0.98	1.03
0.77	0.74	0.77	0.70	1.02	0.96
0.89	0.95	0.89	0.97	1.03	1.08
1.04	1.04	1.10	1.12	0.94	1.02
2.69	**2.21**	**2.57**	**2.33**	0.95	0.93
1.60	1.26	1.36	1.08	1.18	0.82
1.14	1.19	1.30	1.20	0.90	0.94
0.66	**0.66**	**0.64**	**0.64**	1.03	1.03
0.34	**0.32**	**0.34**	**0.33**	0.98	0.98

1.16	0.08	6.76			
1.14	0.22	19.27			
1.03	0.07	6.54	1.39	1.41	**1.56**
#DIV/0!	#DIV/0!	#DIV/0!			
#DIV/0!	#DIV/0!	#DIV/0!			
1.28	0.02	1.37	0.78	0.90	0.93
1.23	0.09	7.11	1.21	1.20	1.26
1.05	0.10	9.46	1.02	1.00	1.01
1.25	0.15	12.35			
1.60	0.04	2.73	1.21	1.35	1.14
0.85	0.09	10.97	0.84	0.84	0.86
1.23	0.05	4.22			
1.24	0.06	4.99	1.20	1.22	1.07
1.28	0.05	3.57	1.30	1.35	1.37
1.03	0.10	9.34	0.94	0.76	1.12
#DIV/0!	#DIV/0!	#DIV/0!			
1.12	0.03	3.08	1.10	1.05	1.02
1.18	0.02	2.01			
1.15	0.06	4.82			
0.96	0.02	2.29	0.84	0.87	0.91
1.16	0.08	6.58	1.29	1.33	1.23
1.29	0.09	6.63	1.31	1.24	1.24
1.07	0.06	5.65	1.25	1.19	1.12
1.30	0.03	2.65	1.37	1.34	1.35
#DIV/0!	#DIV/0!	#DIV/0!			
1.22	0.04	3.51	1.21	1.37	1.34
0.76	0.05	6.17			
1.17	0.04	3.71	1.06	1.00	1.04
1.13	0.06	5.15	1.16	1.11	1.12
0.67	0.04	6.26	0.78	0.75	0.81
1.03	0.09	9.12	0.75	0.81	**0.66**
0.70	0.02	3.45	1.09	1.16	1.13
0.79	0.03	3.39	**0.64**	**0.60**	**0.60**
0.99	0.01	1.30	**0.52**	**0.52**	**0.50**
1.07	0.06	5.35	0.81	0.77	0.82
#DIV/0!	#DIV/0!	#DIV/0!			
0.91	0.12	13.79	1.08	1.01	0.90
1.85	0.27	14.68	1.36	**1.55**	1.42
#DIV/0!	#DIV/0!	#DIV/0!			
1.11	0.09	8.01			
1.58	0.31	19.87	0.98	0.89	1.10
1.16	0.03	2.73	0.99	0.94	1.23
#DIV/0!	#DIV/0!	#DIV/0!	1.14	1.09	1.12
#DIV/0!	#DIV/0!	#DIV/0!			
1.60	0.09	5.68	1.29	1.15	1.21
#DIV/0!	#DIV/0!	#DIV/0!			
#DIV/0!	#DIV/0!	#DIV/0!	0.94	0.72	1.02
0.83	0.06	7.69			
#DIV/0!	#DIV/0!	#DIV/0!			
1.15	0.05	4.66	1.25	1.41	1.25
0.87	0.05	5.63	0.92	0.88	0.93
0.81	0.04	5.18	0.77	0.77	0.83
0.83	0.03	3.70	0.85	0.91	0.92

0.92	0.04	4.33	0.91	0.94	0.92
0.91	0.04	3.96	0.94	0.92	0.97
1.48	0.06	4.39	1.27	1.35	1.17
#DIV/0!	#DIV/0!	#DIV/0!	0.77	0.78	0.78
#DIV/0!	#DIV/0!	#DIV/0!			
1.14	0.06	5.16	1.24	1.16	1.15
1.00	0.05	4.89	0.88	0.93	0.89
#DIV/0!	#DIV/0!	#DIV/0!			
0.57	0.04	6.97			
1.13	0.08	7.33	1.26	1.17	1.13
1.12	0.12	10.92	1.14	1.20	1.08
#DIV/0!	#DIV/0!	#DIV/0!			
#DIV/0!	#DIV/0!	#DIV/0!			
0.89	0.05	6.06	0.74	0.86	0.73
0.57	0.02	3.11	**0.46**	**0.50**	**0.50**
0.80	0.06	8.00	0.95	0.96	0.90
0.81	0.03	3.88			
0.71	0.03	3.98	0.74	0.76	0.78
1.03	0.03	3.01	**1.55**	1.34	1.44
1.39	0.10	7.25	1.12	1.15	1.17
#DIV/0!	#DIV/0!	#DIV/0!			
1.09	0.09	8.24	0.77	0.87	0.83
0.75	0.02	2.34	0.77	0.81	0.78
1.55	0.23	14.90	1.11	1.14	1.07
#DIV/0!	#DIV/0!	#DIV/0!			
1.45	0.22	15.19			
0.55	0.03	4.72			
#DIV/0!	#DIV/0!	#DIV/0!			
1.20	0.17	14.32			
0.62	0.05	7.91	**0.67**	0.78	0.73
0.94	0.07	7.88	0.89	0.81	0.84
1.64	0.10	5.95			
#DIV/0!	#DIV/0!	#DIV/0!			
0.96	0.06	6.56	0.94	0.91	0.94
1.00	0.08	7.96	1.13	1.00	1.04
1.00	0.04	4.08	1.20	1.23	1.18
0.97	0.01	0.80	1.14	1.15	1.03
0.93	0.03	2.76	**1.54**	**1.65**	**1.55**
0.71	0.02	3.07	1.00	1.04	1.03
#DIV/0!	#DIV/0!	#DIV/0!	1.31	1.28	1.31
0.88	0.06	6.77	1.18	1.33	1.25
1.61	0.12	7.24			
0.75	0.02	2.13	0.95	1.00	0.98
1.16	0.09	7.68			
0.91	0.06	6.69	0.78	0.79	0.74
1.01	0.10	10.17	0.94	0.89	0.87
0.95	0.06	6.19	1.42	**1.65**	**1.55**
0.79	0.02	2.00	0.95	0.94	1.01
0.54	0.03	5.46	**0.56**	**0.62**	**0.63**
1.10	0.13	11.69	1.12	1.01	1.12
0.54	0.01	2.55	**0.42**	**0.47**	**0.45**
#DIV/0!	#DIV/0!	#DIV/0!	**0.52**	**0.53**	**0.46**
0.96	0.03	3.52	0.81	0.83	0.84
0.68	0.03	4.94	0.68	0.74	0.71

1.15	0.03	2.27	1.03	1.14	1.04
1.21	0.08	6.69	1.10	1.05	1.04
1.16	0.05	3.91	1.08	1.09	0.95
1.25	0.04	2.93	1.25	1.16	1.31
1.06	0.04	3.99	1.14	1.11	1.11
1.46	0.07	4.48	1.29	1.21	1.20
1.02	0.11	10.55	0.98	0.92	0.90
0.97	0.02	1.78	0.99	1.04	1.02
0.67	0.05	7.87	0.87	0.76	0.77
#DIV/0!	#DIV/0!	#DIV/0!	1.13	1.09	0.96
#DIV/0!	#DIV/0!	#DIV/0!			
0.83	0.09	10.62	0.79	0.88	0.83
0.81	0.02	2.70	0.83	0.88	0.87
1.45	0.10	6.84	1.20	1.09	1.00
1.19	0.07	6.23			
1.36	0.07	5.13			
1.59	0.20	12.91			
1.16	0.08	7.07	1.11	1.03	1.04
1.03	0.04	3.55	0.99	0.98	0.98
#DIV/0!	#DIV/0!	#DIV/0!			
0.92	0.02	2.02	1.01	1.06	1.02
1.12	0.11	9.47	1.10	1.10	1.09
#DIV/0!	#DIV/0!	#DIV/0!	**0.63**	**0.66**	**0.62**
0.61	0.04	6.03	**0.54**	**0.54**	**0.55**
#DIV/0!	#DIV/0!	#DIV/0!	1.33	1.25	1.13
#DIV/0!	#DIV/0!	#DIV/0!			
1.61	0.15	9.61	1.48	**1.69**	1.46
#DIV/0!	#DIV/0!	#DIV/0!			
0.82	0.22	26.88	0.97	0.90	0.90
1.58	0.08	5.29	**1.66**	**1.71**	**1.64**
0.79	0.03	3.31	0.80	0.81	0.84
#DIV/0!	#DIV/0!	#DIV/0!	1.00	1.02	1.05
1.13	0.05	4.28			
1.26	0.03	2.55	1.37	1.34	1.31
#DIV/0!	#DIV/0!	#DIV/0!			
0.84	0.05	5.46	1.21	1.30	1.18
1.13	0.27	23.76			
1.48	0.08	5.20	1.44	1.32	1.33
0.84	0.04	5.22	0.81	0.92	0.88
0.74	0.03	4.18	0.73	0.81	0.76
1.04	0.07	6.80	0.88	1.10	0.97
1.24	0.14	11.17			
0.59	0.01	1.59	**0.57**	**0.62**	**0.61**
0.71	0.02	2.29	**0.64**	0.69	**0.65**
1.46	0.15	10.17	1.10	1.12	1.09
1.05	0.16	15.14			
1.40	0.12	8.41			
1.68	0.35	20.53			
1.02	0.08	7.44			
1.28	0.08	6.46	1.31	1.30	1.27
0.70	0.06	8.06	0.90	0.93	0.85
0.93	0.06	6.01			
1.48	0.15	9.94			
0.82	0.06	7.32			

1.32	0.09	7.18			
0.74	0.04	5.59	**0.65**	0.69	0.71
0.98	0.07	7.29			
1.08	0.02	1.99	0.95	0.99	1.01
1.15	0.02	1.57	1.12	1.09	1.05
1.01	0.02	1.91	0.87	0.94	0.90
#DIV/0!	#DIV/0!	#DIV/0!			
1.62	0.34	21.07			
0.57	0.03	5.97	**0.53**	**0.48**	**0.50**
#DIV/0!	#DIV/0!	#DIV/0!			
1.25	0.01	0.60			
1.15	0.03	2.51	1.06	1.08	1.03
#DIV/0!	#DIV/0!	#DIV/0!			
1.39	0.05	3.50			
0.98	0.02	1.64	0.86	0.87	0.76
1.33	0.07	5.46	1.11	1.10	1.20
1.13	0.04	3.12			
1.05	0.06	5.42	1.05	1.08	1.03
1.26	0.04	2.97	1.16	1.25	1.16
1.41	0.09	6.67	1.04	0.94	0.90
1.46	0.08	5.75	1.12	1.09	1.20
1.29	0.26	20.00			
0.90	0.04	3.99	0.96	0.95	0.93
0.68	0.05	7.55	0.92	0.93	0.91
0.89	0.03	3.76	1.29	1.31	1.22
1.02	0.02	1.68			
0.91	0.05	4.98	0.69	0.69	0.74
0.76	0.10	13.34	0.79	0.73	0.79
#DIV/0!	#DIV/0!	#DIV/0!	0.97	0.94	1.00
1.14	0.07	6.34	1.12	1.09	1.09
#DIV/0!	#DIV/0!	#DIV/0!	1.13	1.09	1.19
1.28	0.09	6.83	1.30	1.23	1.19
1.70	0.22	12.84			
#DIV/0!	#DIV/0!	#DIV/0!	0.86	0.84	0.94
1.32	0.04	3.28	**1.88**	**1.87**	**1.80**
1.08	0.04	3.55	0.86	0.91	0.88
#DIV/0!	#DIV/0!	#DIV/0!	0.76	0.76	0.79
1.15	0.03	2.92	1.04	1.15	1.13
0.86	0.01	1.45	0.75	0.79	0.80
0.89	0.02	1.91	0.81	0.89	0.85
0.82	0.02	2.68	0.76	0.84	0.81
0.91	0.05	5.00			
0.72	0.03	4.68	0.71	**0.65**	**0.64**
0.79	0.05	6.70	**0.64**	0.74	0.73
1.56	0.06	4.06	1.33	1.27	1.34
0.80	0.04	5.57	1.38	1.26	1.02
1.51	0.09	6.27			
0.85	0.05	5.56	1.28	1.29	1.20
0.87	0.04	4.44	0.85	0.87	0.91
0.68	0.01	1.10			
0.85	0.02	2.88	0.91	0.87	0.92
0.90	0.02	1.96	1.01	1.06	0.95
0.90	0.06	6.53	0.81	0.85	0.82
#DIV/0!	#DIV/0!	#DIV/0!			

1.36	0.21	15.44			
1.18	0.07	5.98	1.09	1.12	1.05
0.74	0.02	2.62	0.73	0.75	0.71
1.40	0.06	4.60	0.91	0.89	0.90
0.69	0.04	6.37	0.81	0.89	0.85
1.07	0.04	3.89	0.98	1.06	1.00
#DIV/0!	#DIV/0!	#DIV/0!			
0.80	0.03	3.87	0.70	0.82	0.79
#DIV/0!	#DIV/0!	#DIV/0!	**1.56**	1.39	**1.51**
#DIV/0!	#DIV/0!	#DIV/0!			
#DIV/0!	#DIV/0!	#DIV/0!			
1.22	0.02	1.75	1.18	1.13	1.22
#DIV/0!	#DIV/0!	#DIV/0!	1.35	1.28	1.19
#DIV/0!	#DIV/0!	#DIV/0!	1.44	1.36	**1.65**
#DIV/0!	#DIV/0!	#DIV/0!			
1.45	0.04	3.04	1.04	1.07	1.05
0.98	0.05	5.41	0.93	0.95	0.93
#DIV/0!	#DIV/0!	#DIV/0!	0.81	0.79	0.77
0.86	0.00	0.42	0.82	0.79	0.80
1.15	0.06	5.51	1.40	1.37	1.35
0.79	0.03	3.62	**0.60**	**0.61**	**0.59**
4.82	0.70	14.51			
#DIV/0!	#DIV/0!	#DIV/0!	**0.63**	0.70	**0.60**
0.39	0.01	1.88	0.71	0.70	0.68
0.71	0.03	4.16	0.83	0.88	0.89
1.31	0.09	6.78			
#DIV/0!	#DIV/0!	#DIV/0!	**1.62**	1.43	**2.01**
0.77	0.10	12.36	1.16	1.14	1.12
2.31	0.52	22.66			
#DIV/0!	#DIV/0!	#DIV/0!	**0.46**	**0.44**	**0.54**
1.00	0.04	3.58	1.01	1.05	1.01
#DIV/0!	#DIV/0!	#DIV/0!			
#DIV/0!	#DIV/0!	#DIV/0!	1.25	1.28	1.31
0.80	0.11	13.43	1.35	1.31	1.25
1.11	0.09	8.26	0.91	0.94	1.00
0.74	0.06	8.80			
#DIV/0!	#DIV/0!	#DIV/0!	**1.52**	1.26	1.25
#DIV/0!	#DIV/0!	#DIV/0!			
0.97	0.05	5.54	0.94	0.90	0.93
0.98	0.07	6.73	0.76	0.78	0.73
0.73	0.05	6.59			
#DIV/0!	#DIV/0!	#DIV/0!			
1.35	0.06	4.44	1.10	1.09	1.14
0.95	0.04	3.80	0.75	0.72	0.81
1.09	0.10	9.17			
0.81	0.03	4.28	0.72	0.83	0.73
0.85	0.03	3.99			
0.88	0.03	2.93	0.76	0.82	0.79
2.47	0.16	6.40	1.46	**1.51**	1.40
0.84	0.03	3.55	0.99	0.93	0.91
1.34	0.10	7.18	0.93	0.85	0.96
0.82	0.04	5.33			
0.65	0.08	12.67	0.99	1.12	1.04
0.86	0.07	8.29			

0.95	0.06	5.89	**0.37**	**0.34**	**0.40**
#DIV/0!	#DIV/0!	#DIV/0!	0.68	**0.66**	**0.67**
1.09	0.06	5.24	0.91	0.95	0.96
0.72	0.04	5.94	0.77	0.81	0.77
#DIV/0!	#DIV/0!	#DIV/0!			
0.83	0.11	13.21	**0.52**	**0.52**	0.77
1.05	0.05	4.76	1.02	1.10	1.05
#DIV/0!	#DIV/0!	#DIV/0!			
1.10	0.08	7.27			
2.47	0.29	11.72	1.19	1.27	1.20
1.59	0.17	10.87	**1.63**	**1.50**	1.46
1.63	0.12	7.44	**1.88**	**1.91**	**1.83**
1.46	0.06	3.99	1.38	1.48	1.44
1.79	0.13	7.43	1.24	1.32	1.25
2.32	0.20	8.82	1.18	1.31	1.22
1.70	0.06	3.52	1.48	**1.57**	1.41
2.45	0.27	10.96	**2.06**	**1.91**	**1.81**
1.29	0.17	13.56	1.24	1.35	1.14
1.10	0.02	1.89	0.97	1.02	1.03
#DIV/0!	#DIV/0!	#DIV/0!			
1.11	0.06	5.42	1.31	1.36	1.31
1.02	0.04	4.13	**1.58**	**1.57**	1.43
0.55	0.03	5.70	0.73	0.79	0.75
0.97	0.06	6.04	1.21	1.32	1.12
1.24	0.10	8.08	1.03	0.97	0.98
1.48	0.06	4.35	1.24	1.27	1.26
1.46	0.09	6.01	1.37	1.33	1.39
#DIV/0!	#DIV/0!	#DIV/0!			
#DIV/0!	#DIV/0!	#DIV/0!			
0.75	0.07	9.33			
#DIV/0!	#DIV/0!	#DIV/0!			
#DIV/0!	#DIV/0!	#DIV/0!			
0.89	0.02	1.80	0.92	0.94	0.94
0.74	0.01	1.70	0.87	0.92	0.93
0.61	0.02	3.68	0.72	0.75	0.76
1.17	0.06	4.75	1.12	1.16	1.24
1.48	0.09	5.82			
#DIV/0!	#DIV/0!	#DIV/0!	1.05	1.31	1.23
#DIV/0!	#DIV/0!	#DIV/0!			
0.90	0.05	5.24	0.94	1.03	1.01
#DIV/0!	#DIV/0!	#DIV/0!	1.37	1.21	1.18
0.64	0.03	4.92	0.84	0.86	0.88
0.97	0.05	4.98	1.00	0.98	1.08
#DIV/0!	#DIV/0!	#DIV/0!			
0.97	0.03	3.03			
0.93	0.05	5.43	1.07	1.01	1.03
0.88	0.02	2.16	0.92	0.87	0.76
1.14	0.09	8.07	1.02	0.99	0.93
0.79	0.03	3.61	0.91	0.97	0.90
#DIV/0!	#DIV/0!	#DIV/0!	1.13	1.16	1.13
0.75	0.04	4.70	0.82	0.85	0.83
#DIV/0!	#DIV/0!	#DIV/0!			
0.83	0.03	4.11	0.88	0.80	0.86
0.75	0.04	5.02			

1.10	0.19	17.27	1.06	1.03	1.04
1.03	0.09	8.58			
1.27	0.22	17.43	**1.52**	**1.55**	**1.63**
0.87	0.07	8.57	1.14	0.96	0.86
0.82	0.04	4.71	0.95	0.85	0.91
1.35	0.07	4.87	1.48	1.35	1.36
0.80	0.07	8.91	0.88	0.93	0.87
1.00	0.11	11.08	0.85	0.83	0.83
#DIV/0!	#DIV/0!	#DIV/0!			
0.75	0.02	2.67	0.82	0.82	0.86
1.33	0.03	2.46	1.38	1.34	1.25
0.65	0.06	8.73	**0.56**	**0.56**	0.82
0.87	0.03	3.41	0.83	0.90	0.88
#DIV/0!	#DIV/0!	#DIV/0!			
0.79	0.01	1.90	0.90	0.97	0.85
1.04	0.03	2.94	1.44	1.00	1.29
0.97	0.07	7.45			
0.67	0.22	33.59			
1.09	0.10	8.93	0.81	0.68	0.84
0.88	0.03	3.20	1.34	1.33	1.28
0.63	0.02	3.65	**0.65**	0.72	0.71
0.96	0.04	4.28			
#DIV/0!	#DIV/0!	#DIV/0!	1.07	1.16	1.09
1.39	0.06	4.51	1.29	1.38	1.32
1.24	0.06	4.99	0.93	1.00	1.09
0.98	0.01	1.36	1.07	1.09	1.09
#DIV/0!	#DIV/0!	#DIV/0!	0.80	0.94	1.19
#DIV/0!	#DIV/0!	#DIV/0!			
#DIV/0!	#DIV/0!	#DIV/0!	0.69	0.76	0.93
1.53	0.07	4.43	1.21	1.21	1.27
#DIV/0!	#DIV/0!	#DIV/0!			
1.43	0.09	6.44	1.05	1.32	0.99
1.25	0.02	1.39			
0.82	0.04	5.42	0.89	0.91	0.94
0.56	0.03	5.67	**0.41**	**0.42**	**0.44**
0.99	0.04	4.47	1.34	1.22	1.31
0.96	0.03	2.94	0.92	0.98	0.95
#DIV/0!	#DIV/0!	#DIV/0!	1.14	1.01	0.91
0.63	0.04	5.63	**0.66**	0.68	**0.65**
0.82	0.15	18.70			
1.26	0.18	14.34			
1.38	0.02	1.48	1.21	1.31	1.30
0.70	0.03	4.26	0.74	0.80	0.81
0.77	0.04	4.72	0.84	1.06	0.88
0.77	0.02	2.46	0.70	0.78	**0.64**
1.01	0.05	4.80	0.80	0.88	0.86
1.16	0.14	12.41			
1.00	0.03	3.35	0.86	0.96	0.95
0.92	0.01	0.97	1.04	0.98	1.10
1.12	0.04	3.66	1.06	1.15	1.12
0.84	0.08	9.81	1.07	0.99	0.86
0.99	0.05	5.34	0.95	1.05	0.97
0.68	0.02	2.44	0.70	**0.67**	0.69
#DIV/0!	#DIV/0!	#DIV/0!	1.29	1.27	1.18

1.47	0.13	9.08			
#DIV/0!	#DIV/0!	#DIV/0!			
0.66	0.02	3.16	**0.64**	**0.66**	**0.66**
1.43	0.02	1.71			
1.00	0.05	4.63	1.22	1.25	1.22
1.25	0.32	25.26	1.28	1.10	0.99
1.10	0.06	5.28	0.98	1.05	1.03
1.34	0.31	23.37			
0.71	0.02	2.48			
0.79	0.02	2.83	1.15	1.26	1.26
1.12	0.00	0.23			
0.86	0.04	4.86	0.97	0.89	0.93
1.12	0.06	5.42	1.31	1.34	**1.52**
1.00	0.07	7.27	1.46	1.25	1.04
0.73	0.04	5.59	**0.61**	**0.63**	**0.62**
0.91	0.01	1.18	0.89	0.83	0.78
0.80	0.03	3.40	0.83	0.84	0.81
0.90	0.02	2.20	1.18	1.21	1.18
#DIV/0!	#DIV/0!	#DIV/0!			
0.86	0.04	5.06	1.04	1.10	1.05
1.21	0.06	5.16			
8.77	3.96	45.14			
0.55	0.02	3.41	**0.66**	0.72	0.68
0.81	0.03	4.19	0.90	0.71	0.80
1.21	0.08	6.24	1.22	1.23	0.99
1.62	0.11	6.53	0.91	0.79	0.75
0.87	0.07	7.72			
0.76	0.07	9.77	0.78	0.75	0.80
0.96	0.04	3.80	0.82	0.84	0.84
#DIV/0!	#DIV/0!	#DIV/0!			
#DIV/0!	#DIV/0!	#DIV/0!	**0.63**	**0.64**	**0.63**
0.76	0.09	12.16	1.10	1.04	1.18
0.47	0.00	0.81	**0.50**	**0.54**	**0.51**
1.00	0.06	6.09	0.95	1.00	1.00
1.20	0.07	5.89	0.94	0.90	1.03
1.15	0.02	1.91			
#DIV/0!	#DIV/0!	#DIV/0!			
1.27	0.07	5.90	**1.56**	**1.63**	1.37
0.93	0.03	2.73			
1.09	0.18	16.62	1.27	0.94	**1.52**
#DIV/0!	#DIV/0!	#DIV/0!			
1.19	0.19	16.08			
1.29	0.03	1.96			
#DIV/0!	#DIV/0!	#DIV/0!	**1.54**	1.15	1.37
1.10	0.07	6.76	1.20	1.09	1.07
2.05	0.13	6.19	1.47	**1.56**	**1.54**
1.03	0.04	3.98			
0.90	0.02	2.56	**1.51**	**1.54**	1.49
1.00	0.03	2.83	**1.94**	**1.86**	**1.88**
1.04	0.11	10.48	1.00	1.01	0.98
0.66	0.01	2.18	0.87	0.90	0.88
1.19	0.05	4.37	1.06	1.11	1.17
0.83	0.02	2.42	1.15	1.21	1.17
0.99	0.08	7.59			

#DIV/0!	#DIV/0!	#DIV/0!			
0.93	0.02	2.41	0.90	0.86	0.95
#DIV/0!	#DIV/0!	#DIV/0!	0.94	0.91	0.98
1.10	0.11	10.08	1.06	1.17	1.11
1.60	0.26	16.35	1.35	1.32	1.17
1.25	0.11	9.10			
0.81	0.03	3.10	0.87	0.90	0.82
1.10	0.05	4.19	0.88	0.95	0.89
1.39	0.19	13.95	0.95	0.97	0.88
1.72	0.17	9.72			
0.92	0.08	8.48	0.87	0.85	0.78
0.80	0.06	7.59	0.87	0.94	0.88
0.63	0.01	1.77	0.92	0.97	0.94
0.47	0.00	0.31			
0.35	0.01	3.99	**0.39**	**0.41**	**0.42**
0.95	0.02	2.09	1.00	1.09	1.02
1.02	0.05	4.70	0.85	0.87	0.87
0.74	0.03	4.39	**0.65**	**0.65**	**0.66**
0.93	0.04	4.31	0.83	0.86	0.82
1.08	0.04	3.73	0.97	1.00	0.96
2.45	0.22	8.94	**1.56**	**1.67**	**1.59**
1.32	0.22	16.30			
1.21	0.06	5.29	1.07	1.12	1.07
0.65	0.01	1.72	0.71	**0.65**	0.76
0.33	0.01	2.91			
#DIV/0!	#DIV/0!	#DIV/0!	1.22	0.98	1.15

			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.59	0.92	0.99	1.49	0.10	6.96
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.07	0.84	1.14	0.92	0.12	13.35
1.25	0.97	0.97	1.23	0.03	2.39
1.01	1.02	0.98	1.01	0.01	0.80
			#DIV/0!	#DIV/0!	#DIV/0!
1.28	1.07	1.10	1.25	0.09	7.33
0.86	1.08	0.98	0.85	0.01	1.49
			#DIV/0!	#DIV/0!	#DIV/0!
1.13	1.12	0.99	1.16	0.07	5.97
1.33	0.98	1.03	1.34	0.03	2.37
0.95	0.82	0.97	0.94	0.15	15.63
			#DIV/0!	#DIV/0!	#DIV/0!
1.03	0.99	1.03	1.05	0.04	3.57
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
0.95	0.96	1.01	0.89	0.05	5.42
1.29	1.05	1.03	1.28	0.04	3.20
1.24	1.01	1.02	1.26	0.03	2.59
1.12	1.07	0.98	1.17	0.06	5.25
1.32	1.02	0.97	1.34	0.02	1.47
			#DIV/0!	#DIV/0!	#DIV/0!
1.45	0.91	1.12	1.34	0.10	7.52
			#DIV/0!	#DIV/0!	#DIV/0!
1.06	0.95	0.90	1.04	0.03	2.68
1.01	0.96	0.91	1.10	0.07	5.94
0.81	0.96	0.98	0.79	0.03	3.88
0.71	1.15	1.06	0.73	0.06	8.59
1.19	0.97	1.05	1.14	0.04	3.71
0.62	1.05	1.04	**0.62**	0.02	3.21
0.51	1.03	1.00	**0.51**	0.01	1.80
0.73	1.14	0.88	0.78	0.04	5.27
			#DIV/0!	#DIV/0!	#DIV/0!
0.84	1.21	0.92	0.96	0.11	11.21
1.63	0.95	1.10	1.49	0.12	8.35
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.01	0.90	0.90	0.99	0.08	8.50
1.00	0.94	0.91	1.04	0.13	12.42
1.07	1.03	0.94	1.11	0.03	2.82
			#DIV/0!	#DIV/0!	#DIV/0!
1.09	1.07	0.95	1.19	0.09	7.22
			#DIV/0!	#DIV/0!	#DIV/0!
0.75	0.93	0.81	0.86	0.15	16.89
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.42	1.00	1.05	1.34	0.10	7.15
0.96	0.99	1.01	0.92	0.03	3.28
0.78	0.98	0.92	0.79	0.03	3.67
0.98	0.96	1.04	0.92	0.05	5.72

0.96	0.97	0.97	0.93	0.02	2.13
0.91	1.01	0.93	0.93	0.02	2.68
1.22	1.06	1.03	1.25	0.08	6.12
0.80	0.98	1.00	0.78	0.01	1.86
			#DIV/0!	#DIV/0!	#DIV/0!
1.11	1.07	0.99	1.17	0.06	4.78
0.94	0.99	1.04	0.91	0.03	3.10
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.05	1.12	0.91	1.15	0.09	7.48
1.15	1.07	0.99	1.14	0.05	4.57
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
0.83	0.99	1.02	0.79	0.06	7.88
0.57	0.88	1.09	**0.51**	0.05	9.05
0.87	1.07	0.99	0.92	0.04	4.58
			#DIV/0!	#DIV/0!	#DIV/0!
0.81	0.97	1.04	0.77	0.03	3.68
1.26	1.08	0.89	1.40	0.12	8.81
1.21	0.95	1.05	1.16	0.04	3.29
			#DIV/0!	#DIV/0!	#DIV/0!
0.92	0.96	1.02	0.85	0.07	7.70
0.77	1.00	0.98	0.78	0.02	2.25
1.12	1.01	0.98	1.11	0.03	2.84
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
0.85	0.96	1.13	0.76	0.08	10.32
0.80	0.98	0.93	0.83	0.04	4.76
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
0.91	0.98	0.95	0.92	0.02	2.05
1.00	1.05	0.96	1.04	0.06	5.82
1.18	1.04	0.99	1.20	0.02	2.04
1.06	1.02	1.10	1.09	0.06	5.32
1.52	1.02	1.01	**1.57**	0.05	3.41
1.05	0.97	0.99	1.03	0.02	2.24
1.44	1.01	0.97	1.34	0.07	5.37
1.36	0.96	1.06	1.28	0.08	6.31
			#DIV/0!	#DIV/0!	#DIV/0!
1.04	0.97	1.05	0.99	0.04	4.04
			#DIV/0!	#DIV/0!	#DIV/0!
0.78	1.03	0.97	0.77	0.02	2.95
0.83	1.09	0.93	0.88	0.05	5.52
1.71	0.95	1.06	**1.58**	0.13	7.93
0.98	0.96	0.94	0.97	0.03	3.18
0.67	0.90	1.02	**0.62**	0.05	7.61
1.04	0.94	0.99	1.07	0.05	4.98
0.53	0.89	1.13	**0.47**	0.05	9.66
0.48	1.13	1.01	**0.50**	0.03	6.70
0.91	0.94	1.03	0.85	0.04	5.01
0.78	0.96	1.03	0.73	0.04	5.73

1.16	0.98	1.08	1.09	0.07	6.07
1.09	1.05	0.99	1.07	0.03	2.74
1.03	1.06	1.01	1.04	0.06	6.13
1.14	1.01	0.91	1.22	0.08	6.54
1.07	1.04	0.97	1.11	0.03	2.74
1.15	1.09	0.97	1.21	0.06	4.66
0.86	1.03	0.91	0.92	0.05	5.28
1.07	1.00	1.03	1.03	0.04	3.40
0.71	1.08	0.90	0.78	0.07	8.47
0.97	1.10	0.97	1.04	0.09	8.41
			#DIV/0!	#DIV/0!	#DIV/0!
0.94	0.94	1.09	0.86	0.06	7.40
0.87	0.97	0.98	0.86	0.02	2.64
0.90	1.08	0.98	1.05	0.13	12.36
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
0.97	1.04	0.90	1.04	0.06	5.58
1.04	1.03	0.97	1.00	0.03	3.16
			#DIV/0!	#DIV/0!	#DIV/0!
1.05	0.98	1.03	1.03	0.02	2.36
1.09	1.01	0.98	1.10	0.00	0.34
0.67	1.06	0.90	**0.65**	0.02	3.67
0.57	0.98	0.99	**0.55**	0.01	2.59
1.07	1.18	0.93	1.19	0.12	9.86
			#DIV/0!	#DIV/0!	#DIV/0!
1.49	1.05	1.03	**1.53**	0.11	7.06
			#DIV/0!	#DIV/0!	#DIV/0!
0.83	1.09	0.91	0.90	0.06	6.32
1.60	1.06	0.97	**1.65**	0.05	2.90
0.79	1.01	0.99	0.81	0.02	2.57
1.11	1.04	0.90	1.05	0.05	4.65
			#DIV/0!	#DIV/0!	#DIV/0!
1.32	1.02	0.95	1.34	0.03	1.95
			#DIV/0!	#DIV/0!	#DIV/0!
1.32	1.00	1.05	1.25	0.07	5.66
			#DIV/0!	#DIV/0!	#DIV/0!
1.32	1.00	0.96	1.35	0.06	4.19
1.00	0.95	1.08	0.90	0.08	8.69
0.85	0.96	1.03	0.79	0.05	6.49
1.21	0.92	1.23	1.04	0.14	13.83
			#DIV/0!	#DIV/0!	#DIV/0!
0.66	0.95	1.06	**0.62**	0.04	6.10
0.70	1.00	1.06	**0.67**	0.03	4.57
1.11	1.03	0.99	1.11	0.01	1.15
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.21	1.02	0.96	1.27	0.05	3.78
0.91	1.03	1.02	0.90	0.03	3.64
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!

			#DIV/0!	#DIV/0!	#DIV/0!
0.76	0.93	1.01	0.70	0.04	6.20
			#DIV/0!	#DIV/0!	#DIV/0!
1.05	1.01	1.01	1.00	0.04	4.28
0.98	1.10	0.96	1.06	0.06	5.52
0.93	0.98	1.05	0.91	0.03	3.68
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
0.49	1.09	0.99	**0.50**	0.02	4.75
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.05	1.03	1.01	1.05	0.02	2.05
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
0.81	1.07	1.01	0.82	0.05	6.28
1.16	0.92	0.95	1.14	0.05	4.00
			#DIV/0!	#DIV/0!	#DIV/0!
1.10	1.07	0.99	1.07	0.03	2.86
1.27	0.98	0.97	1.21	0.06	4.71
0.72	1.08	0.89	0.90	0.13	14.78
1.15	0.96	1.08	1.14	0.05	4.11
			#DIV/0!	#DIV/0!	#DIV/0!
0.88	1.04	0.91	0.93	0.04	3.83
0.93	1.00	1.01	0.92	0.01	1.01
1.32	1.02	1.07	1.28	0.05	3.72
			#DIV/0!	#DIV/0!	#DIV/0!
0.75	0.94	0.99	0.72	0.03	4.22
0.76	0.97	0.94	0.77	0.03	3.86
0.96	0.98	0.95	0.97	0.02	2.51
1.13	1.01	0.96	1.11	0.02	1.54
1.15	0.96	0.95	1.14	0.04	3.61
1.21	1.02	1.04	1.23	0.05	3.74
			#DIV/0!	#DIV/0!	#DIV/0!
0.92	0.92	0.96	0.89	0.05	5.45
1.83	1.08	0.98	**1.85**	0.04	2.01
0.97	0.97	1.05	0.90	0.05	5.14
0.79	0.97	0.98	0.77	0.02	2.09
1.17	1.00	1.02	1.12	0.06	5.08
0.82	0.96	1.05	0.79	0.03	3.62
0.92	0.97	1.07	0.87	0.05	5.60
0.85	0.95	1.04	0.82	0.04	4.77
			#DIV/0!	#DIV/0!	#DIV/0!
0.68	1.12	1.02	**0.67**	0.03	4.85
0.85	0.89	1.09	0.74	0.09	12.03
1.28	1.00	0.94	1.31	0.04	2.72
1.07	1.20	0.90	1.18	0.17	14.30
			#DIV/0!	#DIV/0!	#DIV/0!
1.21	1.07	0.99	1.24	0.05	3.65
0.91	0.96	1.04	0.88	0.03	3.69
			#DIV/0!	#DIV/0!	#DIV/0!
0.91	0.94	1.06	0.90	0.02	2.08
1.01	1.01	1.04	1.01	0.04	4.30
0.85	1.05	0.97	0.83	0.02	2.66
			#DIV/0!	#DIV/0!	#DIV/0!

			#DIV/0!	#DIV/0!	#DIV/0!
1.17	0.98	1.07	1.11	0.05	4.64
0.81	0.97	1.02	0.75	0.04	5.97
0.83	1.02	0.90	0.88	0.04	4.45
0.95	0.92	1.08	0.87	0.06	6.66
1.05	1.01	1.03	1.02	0.04	3.92
			#DIV/0!	#DIV/0!	#DIV/0!
0.93	0.90	1.07	0.81	0.09	11.73
1.36	1.03	0.88	1.46	0.09	6.43
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.16	0.97	0.95	1.17	0.04	3.18
1.13	1.14	0.93	1.24	0.09	7.56
1.57	0.87	0.93	**1.51**	0.13	8.71
			#DIV/0!	#DIV/0!	#DIV/0!
1.10	1.01	1.01	1.07	0.03	2.54
0.92	1.01	0.94	0.93	0.01	1.43
0.75	1.05	0.96	0.78	0.02	2.96
0.78	1.02	0.95	0.80	0.02	2.36
1.34	1.09	1.01	1.37	0.03	1.90
0.61	1.03	1.02	**0.60**	0.01	1.17
			#DIV/0!	#DIV/0!	#DIV/0!
0.67	1.06	1.10	**0.65**	0.05	7.23
0.68	1.05	0.96	0.69	0.01	1.96
0.89	0.94	0.99	0.87	0.03	3.44
			#DIV/0!	#DIV/0!	#DIV/0!
1.77	0.81	0.87	**1.71**	0.25	14.39
1.14	1.01	1.04	1.14	0.02	1.67
			#DIV/0!	#DIV/0!	#DIV/0!
0.53	0.85	0.95	**0.49**	0.05	9.78
1.09	1.00	1.02	1.04	0.04	3.56
			#DIV/0!	#DIV/0!	#DIV/0!
1.35	0.96	1.01	1.30	0.04	3.39
1.14	0.97	1.04	1.26	0.09	7.08
1.03	0.92	1.03	0.97	0.06	5.67
			#DIV/0!	#DIV/0!	#DIV/0!
1.32	1.06	0.93	1.34	0.13	9.44
			#DIV/0!	#DIV/0!	#DIV/0!
0.89	1.01	0.94	0.91	0.02	2.64
0.78	0.96	1.04	0.76	0.02	3.07
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.20	0.98	0.98	1.13	0.05	4.52
0.78	0.93	1.02	0.77	0.04	4.95
			#DIV/0!	#DIV/0!	#DIV/0!
0.83	0.99	1.01	0.78	0.06	7.98
			#DIV/0!	#DIV/0!	#DIV/0!
0.85	0.96	1.06	0.81	0.04	4.82
1.47	1.05	0.99	1.46	0.04	3.07
0.97	1.03	0.98	0.95	0.04	3.97
0.87	0.97	0.88	0.90	0.05	5.74
			#DIV/0!	#DIV/0!	#DIV/0!
1.15	0.94	1.12	1.07	0.08	7.08
			#DIV/0!	#DIV/0!	#DIV/0!

0.37	0.93	0.99	**0.37**	0.02	6.06
0.65	1.06	1.01	**0.67**	0.01	1.94
0.99	0.95	1.04	0.95	0.03	3.43
0.85	0.95	1.07	0.80	0.04	4.93
			#DIV/0!	#DIV/0!	#DIV/0!
0.58	0.91	0.84	**0.60**	0.12	19.88
1.16	1.00	1.06	1.08	0.06	5.97
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.35	0.97	1.06	1.25	0.07	5.88
1.34	1.10	0.98	1.48	0.12	8.00
1.77	0.92	1.00	**1.85**	0.06	3.32
1.51	0.99	1.04	1.45	0.06	4.02
1.34	1.00	1.04	1.29	0.05	4.02
1.35	0.99	1.05	1.27	0.08	6.19
1.51	1.13	1.03	1.49	0.07	4.38
1.68	1.14	0.91	**1.87**	0.16	8.49
1.25	1.09	1.07	1.25	0.09	6.85
1.00	1.02	1.00	1.00	0.02	2.49
			#DIV/0!	#DIV/0!	#DIV/0!
1.25	1.06	0.98	1.31	0.05	3.56
1.43	1.08	1.01	**1.50**	0.09	5.69
0.78	1.00	1.04	0.76	0.03	3.54
1.23	1.07	1.04	1.22	0.08	6.63
0.93	1.06	0.93	0.98	0.04	4.20
1.31	0.98	0.97	1.27	0.03	2.25
1.31	1.00	1.01	1.35	0.04	2.76
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
0.96	0.99	0.98	0.94	0.02	1.63
1.00	0.97	1.01	0.93	0.05	5.53
0.77	0.98	0.99	0.75	0.02	2.66
1.18	0.91	0.96	1.18	0.05	4.43
			#DIV/0!	#DIV/0!	#DIV/0!
1.54	0.86	1.23	1.28	0.20	15.76
			#DIV/0!	#DIV/0!	#DIV/0!
1.06	0.95	1.07	1.01	0.05	4.97
0.98	1.25	0.88	1.19	0.16	13.48
0.98	0.95	1.12	0.89	0.06	6.97
0.97	1.02	0.95	1.01	0.05	4.83
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.03	1.07	0.96	1.03	0.02	2.31
0.80	1.06	0.93	0.84	0.07	8.14
0.96	1.04	1.02	0.97	0.04	3.89
0.98	0.97	1.04	0.94	0.04	4.24
1.17	1.00	1.01	1.15	0.02	1.62
0.88	1.00	0.99	0.84	0.03	2.98
			#DIV/0!	#DIV/0!	#DIV/0!
0.69	0.99	0.89	0.81	0.09	10.87
			#DIV/0!	#DIV/0!	#DIV/0!

1.03	1.01	0.97	1.04	0.01	1.36
			#DIV/0!	#DIV/0!	#DIV/0!
1.67	0.93	1.00	**1.59**	0.07	4.45
0.96	1.12	1.03	0.98	0.12	11.99
0.88	1.01	0.92	0.90	0.04	4.99
1.24	1.09	0.91	1.36	0.10	7.31
0.97	1.01	1.04	0.91	0.05	5.37
0.87	0.96	0.96	0.84	0.02	2.23
			#DIV/0!	#DIV/0!	#DIV/0!
0.83	1.01	0.96	0.83	0.02	2.32
1.30	1.02	0.99	1.32	0.06	4.28
0.62	1.00	0.99	**0.64**	0.12	19.54
0.93	0.99	1.02	0.88	0.04	4.77
			#DIV/0!	#DIV/0!	#DIV/0!
0.97	1.04	1.07	0.92	0.06	6.49
0.90	1.12	0.68	1.16	0.25	21.95
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
0.71	0.97	0.82	0.76	0.08	10.33
1.27	1.05	0.97	1.31	0.04	2.72
0.79	0.93	1.09	0.72	0.06	8.25
			#DIV/0!	#DIV/0!	#DIV/0!
1.19	0.98	1.07	1.13	0.06	5.23
1.37	1.02	1.03	1.34	0.04	3.06
1.18	0.86	1.06	1.05	0.11	10.28
1.08	1.03	0.99	1.08	0.01	1.13
1.27	0.80	1.02	1.05	0.22	21.03
			#DIV/0!	#DIV/0!	#DIV/0!
1.02	0.75	1.08	0.85	0.15	17.71
1.22	0.98	0.95	1.23	0.03	2.16
			#DIV/0!	#DIV/0!	#DIV/0!
1.25	1.07	1.24	1.16	0.16	13.67
			#DIV/0!	#DIV/0!	#DIV/0!
0.94	0.99	1.04	0.92	0.03	2.85
0.50	0.91	1.01	**0.44**	0.04	9.36
1.20	1.03	0.90	1.27	0.07	5.47
0.98	0.96	1.04	0.96	0.03	2.75
0.90	1.24	0.87	0.99	0.11	11.38
0.67	1.04	1.01	**0.66**	0.01	2.03
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.36	0.99	1.00	1.30	0.06	4.81
0.89	0.91	1.09	0.81	0.06	7.62
0.93	1.11	1.02	0.92	0.10	10.61
0.68	1.06	1.06	0.70	0.06	8.47
0.96	1.00	1.14	0.88	0.06	7.33
			#DIV/0!	#DIV/0!	#DIV/0!
0.95	0.93	1.00	0.93	0.05	5.00
0.96	1.01	0.94	1.02	0.06	6.08
1.23	0.99	1.05	1.14	0.07	6.20
0.80	1.26	0.91	0.93	0.13	13.47
1.01	1.05	0.97	1.00	0.04	4.21
0.74	1.00	1.03	0.70	0.03	4.15
1.20	1.05	0.98	1.24	0.06	4.57

			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
0.67	1.01	1.00	**0.66**	0.01	1.62
			#DIV/0!	#DIV/0!	#DIV/0!
1.19	1.03	0.99	1.22	0.02	1.96
0.85	1.30	0.84	1.05	0.18	17.31
1.10	0.95	1.07	1.04	0.05	4.85
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.38	0.92	1.08	1.26	0.10	7.55
			#DIV/0!	#DIV/0!	#DIV/0!
0.91	0.99	0.97	0.92	0.04	4.12
1.16	1.12	0.71	1.33	0.14	10.85
0.89	1.41	0.84	1.16	0.25	21.17
0.62	0.95	1.05	**0.62**	0.01	1.18
0.86	1.02	0.98	0.84	0.04	5.23
0.82	1.00	1.03	0.82	0.01	1.31
1.16	1.05	0.98	1.18	0.02	1.74
			#DIV/0!	#DIV/0!	#DIV/0!
1.09	0.95	1.03	1.07	0.03	2.94
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
0.67	0.94	1.07	0.68	0.03	3.93
0.64	1.13	0.78	0.76	0.11	14.94
1.01	0.93	1.02	1.11	0.13	11.77
0.86	0.95	1.06	0.82	0.07	8.55
			#DIV/0!	#DIV/0!	#DIV/0!
0.73	1.03	0.86	0.76	0.03	4.08
0.86	0.99	1.01	0.84	0.02	1.88
			#DIV/0!	#DIV/0!	#DIV/0!
0.64	1.01	1.00	**0.64**	0.01	0.98
0.93	1.17	0.90	1.06	0.11	9.96
0.53	0.98	1.02	**0.52**	0.02	3.25
1.06	0.95	1.05	1.00	0.05	4.86
0.98	0.90	0.95	0.96	0.05	5.63
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.50	1.10	1.05	**1.51**	0.11	7.32
			#DIV/0!	#DIV/0!	#DIV/0!
1.13	0.84	0.73	1.22	0.24	20.13
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
			#DIV/0!	#DIV/0!	#DIV/0!
1.02	1.14	0.73	1.27	0.23	18.37
1.05	1.12	0.99	1.10	0.07	5.96
1.57	1.04	1.02	**1.53**	0.04	2.88
			#DIV/0!	#DIV/0!	#DIV/0!
1.57	0.98	1.04	**1.53**	0.04	2.32
1.79	1.02	0.93	**1.87**	0.06	3.36
1.00	1.02	1.00	1.00	0.01	1.20
0.94	0.99	1.05	0.90	0.03	3.58
1.04	1.04	0.98	1.09	0.06	5.24
1.20	0.98	0.99	1.18	0.03	2.44
			#DIV/0!	#DIV/0!	#DIV/0!

			#DIV/0!	#DIV/0!	#DIV/0!
0.86	1.01	0.94	0.89	0.04	4.39
0.96	0.96	0.95	0.95	0.03	3.06
1.26	0.96	1.04	1.15	0.09	7.51
1.23	1.07	0.96	1.27	0.08	6.49
			#DIV/0!	#DIV/0!	#DIV/0!
0.83	1.06	0.98	0.86	0.04	4.26
0.93	0.99	1.04	0.91	0.03	3.58
0.85	1.05	0.97	0.91	0.06	6.33
			#DIV/0!	#DIV/0!	#DIV/0!
0.81	1.06	0.98	0.83	0.04	4.92
0.93	1.01	1.06	0.91	0.03	3.42
0.99	0.99	1.04	0.95	0.03	3.28
			#DIV/0!	#DIV/0!	#DIV/0!
0.47	0.88	1.05	**0.42**	0.03	7.93
1.14	1.04	1.09	1.06	0.06	6.01
0.81	1.03	0.95	0.85	0.03	3.52
0.70	0.90	1.02	**0.67**	0.02	3.43
0.90	0.96	1.01	0.85	0.03	3.96
1.02	0.99	1.03	0.99	0.03	3.00
1.54	1.00	1.00	**1.59**	0.06	3.57
			#DIV/0!	#DIV/0!	#DIV/0!
1.00	1.13	0.91	1.07	0.05	4.60
0.70	0.94	0.90	0.71	0.05	6.60
			#DIV/0!	#DIV/0!	#DIV/0!
0.92	1.07	0.79	1.07	0.14	13.04

						#DIV/0!
						#DIV/0!
1.10	1.14	1.12	1.16	0.98	1.02	1.13
1.01	1.01	1.04	1.05	0.97	0.99	1.03
0.94	1.05	1.08	1.22	0.87	1.11	1.07
1.11	1.01	1.12	1.02	0.99	0.90	1.06
1.19	1.18	1.23	1.20	0.97	0.96	1.20
1.47	**1.72**	1.31	1.46	1.11	1.16	1.49
						#DIV/0!
1.07	1.11	1.03	1.09	1.05	1.06	1.08
0.82	0.83	0.89	0.90	0.92	1.00	0.86
0.94	0.85	1.00	0.90	0.95	0.98	0.92
1.30	1.32	1.30	1.38	0.96	1.02	1.32
1.28	1.36	1.25	1.31	1.02	1.03	1.30
1.14	1.22	1.13	1.19	0.97	0.98	1.17
1.01	1.08	0.89	0.98	1.17	1.08	0.99
0.98	1.01	0.95	0.94	1.07	1.02	0.97
1.00	0.91	1.00	0.91	1.00	0.89	0.95
						#DIV/0!
0.86	0.86	0.89	0.88	1.00	1.01	0.87
1.10	1.14	1.00	1.11	1.04	1.03	1.09
1.75	**1.98**	**1.61**	**1.98**	1.01	1.07	**1.83**
1.17	1.26	1.23	1.25	0.96	0.98	1.23
1.52	1.45	1.45	1.48	1.00	1.01	1.48
1.38	1.25	1.31	1.11	1.18	0.90	1.26
1.44	**1.64**	1.31	1.46	1.07	1.13	1.46
0.79	0.73	0.84	0.82	0.95	0.95	0.79
1.00	0.96	0.99	1.04	0.95	0.98	1.00
1.19	1.09	1.25	1.21	0.94	0.94	1.19
0.76	0.76	0.73	0.73	1.01	1.05	0.75
0.78	0.68	0.85	0.86	0.92	0.87	0.79
0.86	0.88	0.78	0.80	1.06	1.03	0.83
0.67	**0.63**	**0.66**	**0.62**	1.05	0.95	**0.64**
						#DIV/0!
						#DIV/0!
1.07	0.96	1.26	1.14	0.85	0.89	1.11
0.70	0.73	0.73	0.77	1.02	1.00	0.73
1.93	**2.19**	**1.65**	**1.95**	1.14	1.18	**1.93**
1.13	1.39	1.17	1.45	0.96	1.22	1.28
0.96	0.98	1.19	1.23	0.80	1.02	1.09
0.94	0.86	0.95	0.87	0.99	0.90	0.90
1.00	0.88	1.14	1.01	0.87	0.87	1.01
						#DIV/0!
0.96	1.04	0.90	0.96	1.02	1.05	0.96
0.92	0.94	0.94	0.94	0.97	0.99	0.94
0.82	0.81	0.83	0.83	0.91	0.94	0.82
1.12	0.90	1.21	0.98	0.92	0.80	1.05
0.72	0.71	0.78	0.76	0.98	1.00	0.75
0.75	0.69	0.87	0.80	0.86	0.91	0.78
1.17	1.23	1.23	1.31	1.02	1.11	1.24
1.00	1.02	1.03	1.04	0.98	0.97	1.02
0.91	0.90	0.94	0.91	0.99	0.95	0.91
1.01	1.06	0.95	0.99	1.03	1.04	1.00

0.99	0.95	1.07	1.05	0.91	0.90	1.01
0.89	0.89	0.97	0.92	0.97	0.97	0.92
1.31	1.21	1.46	1.36	0.90	0.92	1.34
						#DIV/0!
1.49	**1.73**	**1.53**	**1.78**	0.98	1.07	**1.63**
1.24	1.26	1.21	1.31	1.01	1.06	1.25
						#DIV/0!
0.88	0.84	0.88	0.85	1.06	0.95	0.86
0.61	**0.58**	0.71	0.68	0.86	0.94	**0.65**
						#DIV/0!
1.35	1.43	1.44	**1.50**	0.95	1.05	1.43
0.97	0.91	1.12	1.05	0.87	0.93	1.01
1.09	1.19	1.23	1.35	0.88	1.06	1.21
0.83	0.82	0.75	0.74	1.04	1.00	0.79
0.58	**0.61**	**0.58**	**0.59**	1.01	1.01	**0.59**
1.11	1.04	1.13	1.13	0.93	0.89	1.10
						#DIV/0!
0.88	0.92	0.85	0.89	1.03	1.03	0.89
1.07	1.17	1.12	1.16	0.99	0.98	1.13
1.08	1.17	0.96	1.11	1.12	1.07	1.08
0.92	0.83	0.91	0.82	1.01	0.89	0.87
0.88	0.90	0.87	0.90	0.96	1.00	0.89
0.93	0.93	0.99	0.96	0.96	0.96	0.95
1.14	1.11	1.18	1.16	0.96	0.99	1.15
0.97	0.99	1.06	1.09	0.92	1.01	1.03
0.74	0.71	0.82	0.80	0.93	0.88	0.77
0.87	0.75	0.95	0.99	0.89	1.01	0.89
1.05	1.09	1.02	1.06	0.99	1.03	1.06
1.18	1.27	1.20	1.29	0.99	1.06	1.24
0.72	0.70	**0.66**	**0.63**	1.08	0.97	0.68
0.85	0.80	0.92	0.90	0.93	0.97	0.87
1.11	1.03	1.13	1.01	1.03	0.98	1.07
1.15	1.14	1.12	1.11	1.03	0.99	1.13
0.94	0.91	0.93	0.94	0.97	1.00	0.93
1.18	1.10	1.42	1.35	0.97	0.94	1.26
0.95	0.97	1.04	1.00	0.95	0.96	0.99
1.02	1.08	1.12	1.13	0.97	1.00	1.09
0.95	1.00	0.94	0.98	1.02	1.03	0.97
0.78	0.72	0.79	0.78	1.00	0.97	0.77
0.91	0.82	0.98	0.89	0.93	0.89	0.90
0.76	0.83	0.73	0.84	1.02	1.04	0.79
						#DIV/0!
1.09	1.16	1.02	1.07	1.05	1.00	1.08
						#DIV/0!
0.86	0.83	0.88	0.86	1.01	0.97	0.86
1.03	1.01	1.07	1.04	0.97	0.97	1.04
1.07	1.17	1.05	1.09	1.06	1.07	1.10
0.93	0.96	0.88	0.92	1.04	1.03	0.92
0.73	0.76	**0.64**	**0.67**	1.10	1.05	0.70
1.27	1.41	1.12	1.24	1.04	1.06	1.26
						#DIV/0!
						#DIV/0!
0.99	1.03	0.89	0.97	1.06	1.07	0.97
0.73	0.74	0.77	0.75	1.04	0.96	0.75

1.08	1.07	1.03	1.08	1.03	1.02	1.06
1.03	1.14	1.08	1.11	1.00	1.03	1.09
1.15	1.15	1.13	1.11	0.98	0.97	1.13
1.22	1.25	1.26	1.28	0.95	0.96	1.25
1.14	1.14	1.09	1.17	1.03	1.05	1.14
1.61	**1.62**	**1.55**	**1.64**	1.01	1.01	**1.61**
0.98	0.92	1.13	1.04	0.86	0.93	1.02
0.95	1.01	1.03	1.08	1.00	1.05	1.02
0.84	0.79	0.78	0.74	1.08	0.94	0.79
0.78	0.77	0.84	0.82	0.94	0.95	0.80
0.68	**0.66**	0.73	**0.67**	0.99	0.93	0.68
0.72	0.72	0.78	0.68	1.12	1.05	0.73
0.80	0.77	0.76	0.77	1.04	0.98	0.77
1.12	1.07	1.19	1.17	0.96	0.99	1.14
1.43	1.41	**1.57**	**1.56**	0.92	0.96	1.49
						#DIV/0!
						#DIV/0!
1.06	1.05	1.12	1.13	0.93	1.01	1.09
1.13	1.12	1.14	1.11	0.99	0.97	1.12
1.13	1.07	1.09	1.04	0.94	0.95	1.09
1.02	1.02	0.96	0.98	1.04	1.04	0.99
1.20	1.24	1.11	1.15	1.04	1.01	1.17
						#DIV/0!
0.65	**0.65**	**0.64**	**0.62**	0.96	0.96	**0.64**
1.23	1.22	1.25	1.26	0.95	0.99	1.24
1.06	0.81	1.17	0.90	0.90	0.76	0.98
1.24	1.22	1.34	1.35	0.97	0.99	1.29
1.11	1.14	1.02	1.06	1.08	1.02	1.08
1.18	1.10	1.41	1.32	0.83	0.92	1.25
1.20	1.08	1.27	1.18	1.01	0.96	1.18
0.69	0.74	0.71	0.74	0.96	1.03	0.72
						#DIV/0!
						#DIV/0!
1.27	1.27	1.22	1.27	1.02	1.01	1.26
1.34	1.13	1.36	1.15	0.99	0.83	1.25
1.02	1.02	0.95	1.04	1.13	1.05	1.01
						#DIV/0!
1.39	**1.51**	1.30	**1.50**	0.98	1.06	1.42
1.01	1.04	0.93	0.99	1.07	1.05	0.99
0.76	0.80	0.75	0.80	1.02	1.06	0.78
0.87	0.85	0.77	0.76	1.06	0.98	0.81
1.01	1.12	0.98	1.09	1.03	1.10	1.05
0.73	0.75	**0.66**	0.69	1.09	1.00	0.71
0.75	0.70	0.74	0.76	0.94	0.96	0.73
0.97	1.01	0.96	0.99	1.05	1.01	0.98
						#DIV/0!
1.17	1.09	1.18	1.21	0.96	1.01	1.16
						#DIV/0!
						#DIV/0!
1.00	0.96	1.04	1.02	0.99	0.97	1.01
0.71	0.75	**0.66**	0.69	0.98	1.03	0.70
0.72	**0.66**	0.76	**0.67**	1.01	0.90	0.70
						#DIV/0!
						#DIV/0!

0.98	0.98	1.03	1.03	0.96	0.99	1.01
0.73	0.68	0.79	0.72	0.99	0.98	0.73
						#DIV/0!
1.03	1.03	1.10	1.12	0.93	0.97	1.07
1.17	1.19	1.12	1.20	1.02	1.04	1.17
1.04	1.07	0.98	1.02	1.02	1.03	1.03
1.51	**1.51**	**1.51**	**1.52**	1.00	0.99	**1.51**
1.42	1.42	1.48	1.36	0.96	0.95	1.42
0.52	**0.49**	**0.56**	**0.53**	0.91	0.94	**0.52**
0.82	0.74	0.85	0.75	0.89	0.92	0.79
						#DIV/0!
1.11	1.17	1.10	1.17	0.98	1.04	1.14
1.27	**1.56**	1.19	1.47	1.07	1.22	1.37
						#DIV/0!
0.85	0.76	0.92	0.83	0.91	0.93	0.84
1.16	1.25	1.09	1.18	1.09	1.07	1.17
1.19	1.21	1.00	1.02	1.19	1.01	1.11
1.03	1.09	1.00	1.05	1.02	1.04	1.04
1.45	1.33	1.35	1.31	1.00	0.97	1.36
1.22	1.12	1.38	1.22	0.89	0.95	1.23
1.09	1.08	1.04	1.05	1.05	0.98	1.07
						#DIV/0!
						#DIV/0!
0.86	0.84	0.79	0.79	1.05	0.93	0.82
0.76	**0.67**	0.85	0.76	0.89	0.88	0.76
1.25	1.24	1.14	1.21	1.10	0.97	1.21
0.54	**0.43**	**0.56**	**0.49**	0.87	0.98	**0.50**
0.69	**0.65**	0.73	0.69	0.96	0.95	0.69
0.92	0.94	0.89	0.95	1.00	1.05	0.92
1.36	1.33	1.29	**1.57**	1.02	1.08	1.39
						#DIV/0!
1.28	1.23	1.36	1.34	0.91	0.94	1.30
						#DIV/0!
0.93	0.94	0.96	0.97	0.97	1.00	0.95
1.55	**1.60**	**1.50**	**1.62**	1.00	1.05	**1.56**
1.04	1.12	1.07	1.06	1.04	1.03	1.07
						#DIV/0!
1.06	1.13	0.99	1.06	1.07	1.06	1.06
0.93	1.01	0.86	0.92	1.12	1.08	0.93
1.12	1.11	1.06	1.09	1.05	1.00	1.10
0.80	0.79	0.74	0.75	1.04	0.99	0.77
0.73	0.76	0.81	0.84	0.91	1.03	0.79
0.83	0.78	0.81	0.71	0.99	0.94	0.78
0.73	0.75	0.68	0.71	1.08	1.00	0.72
1.26	1.27	1.25	1.28	1.00	0.95	1.27
						#DIV/0!
						#DIV/0!
						#DIV/0!
0.96	0.89	1.14	1.06	0.94	0.98	1.01
						#DIV/0!
0.99	0.97	0.90	0.99	1.08	1.06	0.96
0.86	0.87	0.80	0.88	1.04	1.02	0.85
0.87	0.82	0.89	0.92	0.99	0.93	0.88
0.64	**0.64**	**0.61**	**0.62**	1.04	0.99	**0.63**

						#DIV/0!
1.23	1.35	1.10	1.06	1.06	1.03	1.19
0.84	0.84	0.82	0.82	1.04	0.99	0.83
1.12	1.27	1.20	1.30	0.98	1.07	1.22
0.83	0.83	0.74	0.75	1.09	1.04	0.79
1.21	1.27	1.15	1.26	1.04	1.02	1.22
1.34	1.40	1.36	1.43	0.98	1.04	1.38
0.96	1.06	0.85	1.01	1.02	1.00	0.97
						#DIV/0!
1.01	0.95	1.03	0.97	0.99	0.92	0.99
0.71	0.69	0.87	0.85	0.95	0.96	0.78
1.13	1.13	1.20	1.31	0.96	0.98	1.19
1.18	1.21	1.31	1.37	0.89	1.05	1.27
1.21	1.27	1.21	1.28	0.99	1.04	1.24
0.80	0.77	0.76	0.75	1.04	0.96	0.77
1.15	1.21	1.13	1.17	1.03	1.01	1.17
0.99	0.99	0.88	0.91	1.09	0.93	0.94
0.82	0.74	0.89	0.86	0.97	1.00	0.82
0.96	0.90	0.97	0.85	1.02	0.87	0.92
1.23	1.27	1.25	1.24	0.99	1.04	1.25
0.76	0.84	0.81	0.80	1.03	0.99	0.81
						#DIV/0!
						#DIV/0!
0.61	**0.56**	0.69	**0.64**	0.90	0.97	**0.63**
0.84	0.80	0.88	0.78	0.94	0.94	0.82
						#DIV/0!
1.12	1.15	1.07	1.08	1.15	1.04	1.10
1.11	1.24	1.28	1.21	0.98	1.11	1.21
						#DIV/0!
						#DIV/0!
0.98	0.98	0.92	0.96	1.03	1.03	0.96
1.17	1.17	1.40	1.25	0.85	0.94	1.25
1.31	1.39	1.28	1.36	1.03	1.05	1.33
0.70	0.74	**0.65**	0.70	0.99	1.04	0.70
1.05	1.17	1.02	1.12	1.06	1.09	1.09
0.91	1.00	0.91	1.01	1.03	1.05	0.96
1.22	1.16	1.31	1.25	0.93	0.94	1.23
1.50	**1.60**	1.42	**1.53**	1.06	1.06	**1.51**
						#DIV/0!
0.91	0.93	0.90	0.93	1.04	1.02	0.92
						#DIV/0!
1.64	**2.41**	1.42	**2.08**	1.16	1.45	**1.89**
1.20	1.26	1.20	1.35	0.98	1.04	1.25
0.88	0.91	0.96	0.96	1.00	0.98	0.93
1.16	1.14	1.17	1.15	0.99	0.97	1.16
0.74	0.77	0.79	0.78	1.00	0.97	0.77
1.05	1.20	0.95	1.10	1.02	1.11	1.08
0.88	0.90	0.86	0.91	0.98	1.02	0.89
1.64	**1.63**	**1.58**	**1.53**	1.01	1.02	**1.60**
0.82	0.80	0.85	0.81	0.97	0.93	0.82
1.17	1.08	1.22	1.17	0.93	0.94	1.16
						#DIV/0!
0.72	0.76	0.69	0.74	1.05	1.03	0.73
0.84	0.76	0.87	0.79	0.97	0.89	0.82

0.42	**0.40**	**0.51**	**0.48**	0.90	0.95	**0.45**
0.72	0.71	0.77	0.78	0.94	0.98	0.75
1.10	1.08	1.09	1.09	0.96	1.00	1.09
0.71	0.72	0.69	0.71	1.05	1.02	0.71
1.02	1.07	1.01	1.06	1.01	1.03	1.04
0.77	**0.67**	0.77	0.87	0.86	0.99	0.77
0.98	1.02	0.96	0.99	1.07	1.08	0.99
0.63	**0.48**	**0.64**	**0.48**	1.00	0.75	**0.56**
						#DIV/0!
1.29	1.33	1.16	1.27	1.05	1.06	1.26
0.85	0.90	0.94	0.89	0.94	0.98	0.89
0.72	**0.62**	**0.66**	**0.60**	1.01	0.95	**0.65**
1.23	1.27	1.22	1.25	1.03	1.05	1.24
1.20	1.26	1.13	1.21	1.02	1.05	1.20
1.38	1.48	1.22	1.41	1.09	1.13	1.37
1.20	1.10	1.17	1.10	1.00	0.96	1.14
0.56	**0.50**	**0.63**	**0.57**	0.91	0.90	**0.57**
						#DIV/0!
0.89	0.91	0.84	0.83	1.06	1.01	0.87
1.00	1.06	1.05	1.12	0.97	1.05	1.06
1.10	1.09	1.14	1.10	1.01	0.98	1.11
1.13	1.14	1.14	1.19	0.99	1.03	1.15
0.70	0.69	0.75	**0.67**	1.02	0.98	0.70
0.98	0.80	1.07	0.94	0.90	0.88	0.95
						#DIV/0!
1.35	1.38	1.37	1.41	1.02	0.97	1.38
1.28	1.44	1.24	1.32	1.07	0.99	1.32
0.80	0.71	0.84	0.75	0.95	0.88	0.77
1.15	1.28	1.10	1.18	1.04	1.02	1.18
0.85	0.77	0.83	0.76	1.01	0.90	0.80
1.26	1.43	1.35	**1.54**	0.93	1.13	1.39
1.12	1.24	1.13	1.17	1.02	1.05	1.16
1.01	1.01	0.99	1.04	0.99	0.99	1.01
0.86	0.82	0.87	0.84	1.01	0.99	0.85
0.83	0.80	0.85	0.81	1.00	0.96	0.82
						#DIV/0!
1.32	1.44	1.47	**1.62**	0.90	1.09	1.46
						#DIV/0!
1.03	1.16	0.91	1.03	1.13	1.12	1.03
0.84	0.81	0.77	0.81	1.07	1.04	0.81
1.21	1.06	1.29	1.17	0.95	0.93	1.18
0.67	0.73	0.72	0.71	1.03	0.99	0.71
1.17	1.21	1.09	1.20	1.02	1.08	1.16
1.15	1.23	0.91	0.98	1.26	1.06	1.07
1.06	1.01	1.07	1.07	0.98	1.00	1.05
1.05	1.01	1.03	1.04	1.02	1.01	1.03
0.91	0.87	0.87	0.90	1.01	1.01	0.89
1.11	1.15	1.08	1.09	1.09	1.05	1.11
0.75	0.83	0.79	0.82	1.03	1.00	0.80
1.18	1.33	1.05	1.18	1.12	1.12	1.19
0.72	0.74	0.69	**0.66**	1.05	0.99	0.70
0.98	1.14	1.04	1.15	1.00	1.08	1.07
0.64	**0.61**	0.72	**0.66**	0.95	0.92	**0.66**
						#DIV/0!

1.16	1.24	1.10	1.20	1.05	1.08	1.17
						#DIV/0!
1.25	1.14	1.22	1.16	1.03	0.96	1.19
0.92	0.77	0.92	0.85	1.01	0.92	0.87
0.87	0.84	0.97	0.95	0.94	0.96	0.91
1.47	1.49	**1.55**	**1.66**	0.92	1.04	**1.54**
1.04	1.06	1.20	1.11	0.98	0.99	1.10
0.98	0.94	1.03	1.00	0.99	0.96	0.99
1.41	1.49	1.23	1.30	1.15	1.04	1.36
0.85	0.92	0.87	0.88	1.01	1.03	0.88
1.32	1.41	1.21	1.31	1.01	1.02	1.31
						#DIV/0!
1.02	1.08	1.04	1.01	1.07	1.00	1.04
0.75	0.77	0.86	0.89	0.95	1.02	0.82
0.83	0.78	0.77	0.83	0.99	1.04	0.80
0.96	0.80	1.01	0.85	0.95	0.83	0.90
0.82	0.71	0.96	0.84	0.96	0.95	0.83
						#DIV/0!
						#DIV/0!
1.07	1.09	1.00	1.03	1.06	1.02	1.05
0.89	0.91	0.82	0.90	1.05	1.03	0.88
						#DIV/0!
0.94	0.89	0.90	0.90	0.98	0.93	0.91
1.42	1.47	1.35	1.43	1.03	1.06	1.42
1.32	1.45	1.18	1.42	1.03	1.08	1.34
1.09	1.12	1.03	1.08	1.05	1.02	1.08
						#DIV/0!
1.20	1.27	1.25	1.34	0.95	1.05	1.27
						#DIV/0!
1.38	1.31	1.32	1.34	0.96	1.06	1.34
0.96	0.88	0.88	0.81	1.09	0.91	0.89
1.18	0.96	1.26	1.06	0.96	0.88	1.11
						#DIV/0!
0.94	1.02	0.92	0.97	1.01	1.04	0.96
0.53	**0.53**	**0.55**	**0.53**	1.02	0.98	**0.54**
1.26	1.27	1.47	1.46	0.96	1.00	1.37
0.84	0.88	0.91	0.96	0.97	1.03	0.90
1.03	0.99	1.03	0.99	1.02	1.01	1.01
0.70	0.71	0.71	0.72	1.08	0.99	0.71
						#DIV/0!
						#DIV/0!
1.25	1.33	1.21	1.24	1.05	1.06	1.26
0.70	0.73	0.70	0.72	1.07	1.06	0.71
0.98	0.83	1.06	1.01	1.01	0.92	0.97
0.76	0.81	0.77	0.81	0.99	1.03	0.79
0.90	0.95	0.91	0.96	0.99	1.06	0.93
1.38	1.47	1.35	1.48	0.96	1.00	1.42
0.83	0.91	0.94	0.95	0.97	1.04	0.91
1.12	1.07	1.09	1.09	0.98	0.96	1.09
1.15	1.16	1.16	1.15	1.06	1.03	1.15
0.72	0.71	0.84	0.83	0.86	0.98	0.77
1.12	1.19	1.17	1.19	0.96	1.03	1.17
0.77	0.72	0.76	0.73	1.00	1.00	0.75
1.19	1.30	1.21	1.39	1.00	1.08	1.27

						#DIV/0!
1.58	**1.56**	**1.52**	**1.51**	1.04	0.98	**1.54**
0.71	**0.66**	0.91	0.87	0.80	0.90	0.79
						#DIV/0!
1.03	1.00	1.03	1.00	1.01	1.02	1.01
1.10	1.12	1.05	1.12	0.99	1.01	1.10
1.07	1.11	1.00	1.04	1.06	1.06	1.05
						#DIV/0!
0.72	0.75	0.68	0.72	1.03	0.98	0.72
						#DIV/0!
1.04	1.00	1.08	1.06	0.95	1.01	1.05
1.00	0.93	0.90	0.94	0.98	1.00	0.94
1.28	**1.65**	0.99	1.17	1.19	1.27	1.27
0.99	1.06	0.86	0.93	1.15	1.06	0.96
0.58	**0.62**	**0.57**	**0.58**	1.01	1.03	**0.59**
0.78	0.83	0.74	0.76	1.05	1.06	0.78
0.91	0.96	0.95	0.98	1.04	1.01	0.95
1.47	1.35	1.49	1.43	0.95	0.93	1.43
0.74	0.74	0.78	0.78	0.95	0.99	0.76
1.12	1.19	1.05	1.12	1.06	1.06	1.12
						#DIV/0!
1.56	**1.58**	1.40	1.42	1.11	1.00	1.49
0.56	**0.59**	**0.47**	**0.54**	0.99	1.01	**0.54**
0.84	0.81	0.83	0.87	0.95	0.97	0.84
0.90	0.98	0.92	0.99	1.02	1.08	0.95
1.67	**1.73**	**1.65**	**1.72**	1.03	1.00	**1.69**
0.91	0.97	0.81	0.88	1.11	1.06	0.89
0.81	0.80	0.87	0.87	1.00	0.98	0.84
1.15	1.00	1.03	0.90	1.12	0.86	1.02
0.99	1.09	0.94	1.05	1.05	1.10	1.02
0.61	**0.52**	**0.54**	**0.46**	1.13	0.84	**0.53**
0.86	0.86	0.83	0.84	1.02	0.99	0.85
0.59	**0.62**	**0.60**	**0.60**	1.02	1.01	**0.60**
1.10	1.09	1.01	1.04	1.06	1.01	1.06
1.19	1.21	1.11	1.14	0.98	1.01	1.16
1.02	0.97	1.17	1.16	0.88	0.97	1.08
1.09	0.87	**1.57**	1.26	0.70	0.79	1.20
1.39	1.42	1.38	1.42	1.01	1.01	1.40
1.18	1.16	1.09	1.09	1.06	0.98	1.13
1.03	1.04	1.08	1.10	0.95	1.00	1.06
1.29	1.25	1.21	1.19	1.06	0.96	1.24
						#DIV/0!
						#DIV/0!
1.01	0.89	1.19	1.06	0.84	0.88	1.04
0.98	0.92	0.95	0.89	0.99	0.95	0.93
1.10	1.14	1.11	1.16	1.00	1.02	1.13
						#DIV/0!
0.94	0.94	0.88	0.91	1.04	1.02	0.92
1.11	1.07	1.09	1.11	1.05	1.00	1.09
1.62	**1.51**	**1.98**	**1.83**	0.90	0.93	**1.74**
0.94	0.94	0.90	0.91	1.06	1.02	0.92
0.88	0.92	0.93	0.96	1.00	1.02	0.92
0.92	0.88	0.92	0.89	1.02	0.98	0.90
0.82	0.77	0.78	0.74	1.01	0.95	0.78

0.99	0.96	0.93	0.91	0.89	0.95	0.95
1.07	1.04	1.18	1.11	0.95	0.98	1.10
						#DIV/0!
1.15	1.11	1.11	1.10	1.03	1.03	1.12
1.39	1.32	1.42	1.36	0.98	0.94	1.37
0.87	0.94	0.88	1.01	0.91	1.13	0.93
1.10	1.12	1.07	1.13	1.00	1.04	1.11
1.01	1.02	1.00	0.99	1.06	1.03	1.01
0.93	0.86	0.93	0.92	1.00	0.98	0.91
1.10	1.21	0.97	1.07	1.14	1.09	1.09
0.82	0.79	0.87	0.81	0.92	0.93	0.82
0.93	0.89	0.91	0.90	1.02	1.00	0.91
0.97	1.03	0.89	0.94	1.09	1.07	0.96
0.70	**0.65**	**0.67**	**0.63**	1.05	0.92	**0.66**
0.39	**0.40**	**0.35**	**0.37**	1.10	1.03	**0.38**
0.87	0.94	0.78	0.88	1.08	1.06	0.87
0.98	0.90	1.05	0.99	0.93	0.96	0.98
0.59	**0.63**	**0.66**	0.71	0.95	1.02	**0.65**
0.83	0.82	0.86	0.86	0.98	0.98	0.84
1.08	1.11	1.13	1.15	0.99	1.01	1.12
1.28	1.22	1.48	1.27	1.03	1.00	1.31
						#DIV/0!
1.21	1.30	1.16	1.26	1.04	1.07	1.23
0.55	**0.57**	**0.60**	**0.62**	0.90	1.03	**0.59**
						#DIV/0!
1.02	1.27	1.33	1.47	0.77	1.15	1.27

[redacted]	[redacted]
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!
0.03	2.26
0.02	1.91
0.12	10.93
0.06	5.30
0.02	1.49
0.17	11.23
#DIV/0!	#DIV/0!
0.03	3.07
0.04	4.79
0.06	6.87
0.04	2.87
0.05	3.74
0.04	3.32
0.08	7.77
0.03	3.46
0.05	5.74
#DIV/0!	#DIV/0!
0.02	2.02
0.06	5.72
0.18	9.90
0.04	3.42
0.03	2.12
0.11	8.89
0.14	9.55
0.05	6.02
0.03	3.50
0.07	5.91
0.02	2.53
0.08	10.32
0.05	5.53
0.02	3.85
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!
0.12	11.14
0.03	3.80
0.22	11.51
0.16	12.21
0.14	13.06
0.05	5.27
0.11	10.78
#DIV/0!	#DIV/0!
0.06	5.77
0.01	1.48
0.01	1.34
0.14	13.37
0.03	4.67
0.08	9.78
0.06	4.84
0.01	1.47
0.02	1.72
0.04	4.47

0.06	5.43
0.04	4.17
0.10	7.74
#DIV/0!	#DIV/0!
0.15	8.90
0.04	3.45
#DIV/0!	#DIV/0!
0.02	1.99
0.06	8.95
#DIV/0!	#DIV/0!
0.06	4.27
0.09	8.97
0.11	9.06
0.05	5.99
0.01	2.26
0.04	4.04
#DIV/0!	#DIV/0!
0.03	3.12
0.04	3.86
0.09	8.30
0.05	5.92
0.02	1.72
0.03	3.02
0.03	2.80
0.05	5.27
0.05	6.40
0.11	12.05
0.03	2.65
0.05	4.42
0.04	5.91
0.05	6.27
0.06	5.67
0.02	1.35
0.01	1.49
0.15	11.97
0.04	3.63
0.05	4.48
0.03	2.89
0.03	3.98
0.07	7.36
0.05	6.43
#DIV/0!	#DIV/0!
0.06	5.19
#DIV/0!	#DIV/0!
0.02	2.08
0.03	2.50
0.05	4.91
0.03	3.45
0.05	7.75
0.12	9.40
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!
0.06	5.89
0.02	2.28

0.02	2.24
0.05	4.42
0.02	1.50
0.02	1.99
0.03	2.91
0.04	2.33
0.09	8.69
0.05	5.18
0.04	5.32
0.03	3.90
0.03	4.72
0.04	5.78
0.02	2.02
0.05	4.80
0.08	5.44
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!
0.04	3.96
0.01	1.03
0.04	3.43
0.03	3.17
0.06	4.77
#DIV/0!	#DIV/0!
0.01	1.99
0.02	1.44
0.16	16.34
0.07	5.18
0.05	4.59
0.14	11.31
0.08	6.52
0.02	3.34
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!
0.02	1.81
0.12	9.90
0.04	3.93
#DIV/0!	#DIV/0!
0.10	6.88
0.05	4.66
0.03	3.71
0.06	6.79
0.07	6.28
0.04	5.52
0.03	3.43
0.02	2.18
#DIV/0!	#DIV/0!
0.05	4.29
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!
0.03	3.46
0.04	5.12
0.05	6.58
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!

0.03	2.68
0.05	6.48
#DIV/0!	#DIV/0!
0.05	4.46
0.04	3.12
0.04	3.42
0.01	0.46
0.05	3.58
0.03	5.79
0.05	6.65
#DIV/0!	#DIV/0!
0.04	3.45
0.17	12.56
#DIV/0!	#DIV/0!
0.07	8.16
0.07	5.74
0.11	9.93
0.04	3.63
0.06	4.71
0.10	8.49
0.02	2.28
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!
0.03	4.26
0.07	9.40
0.05	4.07
0.06	11.73
0.03	4.96
0.03	2.90
0.13	9.13
#DIV/0!	#DIV/0!
0.06	4.59
#DIV/0!	#DIV/0!
0.02	1.78
0.05	3.41
0.03	3.01
#DIV/0!	#DIV/0!
0.06	5.35
0.06	6.53
0.03	2.29
0.03	3.49
0.05	6.37
0.05	6.71
0.03	4.05
0.01	1.02
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!
0.11	10.94
#DIV/0!	#DIV/0!
0.04	4.30
0.04	4.13
0.04	4.95
0.01	2.37

#DIV/0!	#DIV/0!
0.13	11.12
0.01	1.53
0.08	6.55
0.05	6.12
0.05	4.38
0.04	2.97
0.09	9.28
#DIV/0!	#DIV/0!
0.04	3.95
0.09	12.00
0.08	7.07
0.09	6.81
0.04	3.00
0.02	2.86
0.03	2.85
0.05	5.70
0.06	7.77
0.05	5.74
0.02	1.26
0.03	3.94
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!
0.05	8.44
0.05	5.60
#DIV/0!	#DIV/0!
0.04	3.34
0.07	6.01
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!
0.03	2.67
0.11	8.71
0.05	3.65
0.03	4.82
0.07	6.27
0.06	5.93
0.06	4.98
0.08	5.03
#DIV/0!	#DIV/0!
0.01	1.58
#DIV/0!	#DIV/0!
0.44	23.46
0.07	5.61
0.04	4.18
0.01	1.18
0.02	2.88
0.10	9.64
0.02	2.16
0.05	3.25
0.02	2.65
0.06	5.04
#DIV/0!	#DIV/0!
0.03	4.07
0.05	6.05

0.05	11.32
0.04	4.75
0.01	0.84
0.01	1.80
0.03	2.70
0.08	10.81
0.03	2.71
0.09	15.82
#DIV/0!	#DIV/0!
0.07	5.76
0.03	3.85
0.05	8.02
0.02	1.76
0.06	4.73
0.11	7.90
0.05	4.57
0.05	9.54
#DIV/0!	#DIV/0!
0.04	4.61
0.05	4.77
0.02	1.71
0.02	2.15
0.04	5.10
0.11	11.67
#DIV/0!	#DIV/0!
0.03	1.86
0.09	6.52
0.06	7.42
0.07	6.14
0.04	5.29
0.12	8.76
0.05	4.43
0.02	2.15
0.02	2.45
0.02	2.65
#DIV/0!	#DIV/0!
0.12	8.40
#DIV/0!	#DIV/0!
0.10	9.95
0.03	3.71
0.10	8.10
0.03	3.79
0.05	4.62
0.15	13.96
0.03	2.73
0.02	1.66
0.02	2.11
0.03	2.73
0.04	4.45
0.12	9.81
0.03	4.68
0.08	7.51
0.05	7.52
#DIV/0!	#DIV/0!

0.06	5.00
#DIV/0!	#DIV/0!
0.05	4.18
0.07	8.08
0.06	6.78
0.09	5.63
0.07	6.38
0.04	3.86
0.11	8.45
0.03	3.34
0.08	6.24
#DIV/0!	#DIV/0!
0.03	2.89
0.07	8.68
0.03	3.57
0.09	10.49
0.10	12.16
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!
0.04	3.79
0.04	4.49
#DIV/0!	#DIV/0!
0.02	2.73
0.05	3.39
0.12	9.13
0.04	3.38
#DIV/0!	#DIV/0!
0.06	4.53
#DIV/0!	#DIV/0!
0.03	2.50
0.06	7.02
0.13	11.60
#DIV/0!	#DIV/0!
0.04	4.44
0.01	2.18
0.12	8.46
0.05	5.62
0.02	2.25
0.01	1.05
#DIV/0!	#DIV/0!
#DIV/0!	#DIV/0!
0.05	4.20
0.01	2.01
0.10	9.96
0.03	3.53
0.03	3.19
0.06	4.49
0.05	5.85
0.02	1.89
0.00	0.28
0.07	8.95
0.03	2.51
0.02	2.99
0.09	7.26

#DIV/0!	#DIV/0!
0.03	2.17
0.12	15.28
#DIV/0!	#DIV/0!
0.02	1.85
0.03	3.04
0.05	4.42
#DIV/0!	#DIV/0!
0.03	4.17
#DIV/0!	#DIV/0!
0.03	3.21
0.04	4.36
0.28	21.68
0.09	8.97
0.02	3.53
0.04	4.75
0.03	3.19
0.06	4.41
0.02	3.05
0.06	4.98
#DIV/0!	#DIV/0!
0.09	6.16
0.05	9.71
0.02	2.95
0.04	4.72
0.04	2.27
0.07	7.33
0.04	4.67
0.10	10.17
0.07	6.64
0.06	11.86
0.02	1.91
0.02	2.58
0.04	4.04
0.04	3.79
0.10	9.40
0.29	24.54
0.02	1.60
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Description
Urokinase-type plasminogen activator chain B OS=Homo sapiens GN=PLAU PE=2 SV=1 - [E7ET40_HUMAN]
Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens GN=ADAM9 PE=2 SV=1 - [F8WC54
Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]
Stanniocalcin-1 OS=Homo sapiens GN=STC1 PE=1 SV=1 - [STC1_HUMAN]
Heparan sulfate glucosamine 3-O-sulfotransferase 1 OS=Homo sapiens GN=HS3ST1 PE=1 SV=1 - [HS3S1_HUMAN]
Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]
Urokinase plasminogen activator surface receptor OS=Homo sapiens GN=PLAUR PE=1 SV=1 - [UPAR_HUMAN]
Isoform 2 of Tumor necrosis factor ligand superfamily member 15 OS=Homo sapiens GN=TNFSF15 - [TNF15_HUMAN
Solute carrier family 2, facilitated glucose transporter member 1 (Fragment) OS=Homo sapiens GN=SLC2A1 PE=2 SV
Serine protease 23 OS=Homo sapiens GN=PRSS23 PE=2 SV=1 - [B4E2J3_HUMAN]
Isoform B0 of Neuropilin-2 OS=Homo sapiens GN=NRP2 - [NRP2_HUMAN]
Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2 - [SODE_HUMAN]
Carbohydrate sulfotransferase 15 OS=Homo sapiens GN=CHST15 PE=1 SV=1 - [CHSTF_HUMAN]
Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [CATC_HUMAN]
Glucosylceramidase OS=Homo sapiens GN=GBA PE=4 SV=1 - [J3KQG4_HUMAN]
Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2 - [AAAT_HUMAN]
Receptor-type tyrosine-protein phosphatase kappa OS=Homo sapiens GN=PTPRK PE=1 SV=2 - [PTPRK_HUMAN]
X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 - [XRCC5_HUMAN]
Polypeptide N-acetylgalactosaminyltransferase 10 OS=Homo sapiens GN=GALNT10 PE=1 SV=2 - [GLT10_HUMAN]
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Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=2 SV=1 - [H0YN42_HUMAN]
Collagen alpha-1(V) chain OS=Homo sapiens GN=COL5A1 PE=1 SV=3 - [CO5A1_HUMAN]
Vesicular integral-membrane protein VIP36 (Fragment) OS=Homo sapiens GN=LMAN2 PE=2 SV=1 - [D6RIU4_HUMA
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Glutaminyl-peptide cyclotransferase OS=Homo sapiens GN=QPCT PE=1 SV=1 - [QPCT_HUMAN]
Isoform Beta-1B of Integrin beta-1 OS=Homo sapiens GN=ITGB1 - [ITB1_HUMAN]
Proprotein convertase subtilisin/kexin type 9 OS=Homo sapiens GN=PCSK9 PE=1 SV=3 - [PCSK9_HUMAN]
Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1 - [ITA2_HUMAN]
Protein NOV homolog OS=Homo sapiens GN=NOV PE=1 SV=1 - [NOV_HUMAN]
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Isoform 2 of Carboxypeptidase E OS=Homo sapiens GN=CPE - [CBPE_HUMAN]
Heat shock 70 kDa protein 13 OS=Homo sapiens GN=HSPA13 PE=1 SV=1 - [HSP13_HUMAN]
Lysosomal Pro-X carboxypeptidase OS=Homo sapiens GN=PRCP PE=1 SV=1 - [PCP_HUMAN]
Isoform Short of Beta-1,4-galactosyltransferase 1 OS=Homo sapiens GN=B4GALT1 - [B4GT1_HUMAN]
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Amphoterin-induced protein 2 OS=Homo sapiens GN=AMIGO2 PE=1 SV=1 - [AMGO2_HUMAN]
Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5 - [ITA3_HUMAN]
Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2 - [SAP_HUMAN]
Isoform L-APP733 of Amyloid beta A4 protein OS=Homo sapiens GN=APP - [A4_HUMAN]
Ephrin type-A receptor 4 OS=Homo sapiens GN=EPHA4 PE=2 SV=1 - [E9PG71_HUMAN]
Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1 - [PPT1_HUMAN]
Macrophage colony-stimulating factor 1 OS=Homo sapiens GN=CSF1 PE=1 SV=2 - [CSF1_HUMAN]
Isoform 2 of CD166 antigen OS=Homo sapiens GN=ALCAM - [CD166_HUMAN]
Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 - [ANXA1_HUMAN]
Pro-cathepsin H OS=Homo sapiens GN=CTSH PE=1 SV=4 - [CATH_HUMAN]
MHC class I polypeptide-related sequence A OS=Homo sapiens GN=MICA PE=2 SV=1 - [Q96QC4_HUMAN]
Granulins OS=Homo sapiens GN=GRN PE=1 SV=2 - [GRN_HUMAN]
Metalloproteinase inhibitor 3 OS=Homo sapiens GN=TIMP3 PE=1 SV=2 - [TIMP3_HUMAN]

Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 - [GGH_HUMAN]
Isoform 2 of Growth arrest-specific protein 6 OS=Homo sapiens GN=GAS6 - [GAS6_HUMAN]
Fibroblast growth factor receptor-like 1 OS=Homo sapiens GN=FGFRL1 PE=1 SV=1 - [FGRL1_HUMAN]
Alpha-galactosidase A OS=Homo sapiens GN=GLA PE=1 SV=1 - [AGAL_HUMAN]
Lumican OS=Homo sapiens GN=LUM PE=1 SV=2 - [LUM_HUMAN]
Isoform 2 of Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 - [IBP7_HUMAN]
Isoform 4 of Peptidyl-glycine alpha-amidating monooxygenase OS=Homo sapiens GN=PAM - [AMD_HUMAN]
SLIT and NTRK-like protein 1 OS=Homo sapiens GN=SLITRK1 PE=1 SV=2 - [SLIK1_HUMAN]
Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe OS=Homo sapiens GN=LFNG PE=1 SV=2 - [LFNG_HUMAN]
Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]
Isoform 2 of Receptor-type tyrosine-protein phosphatase S OS=Homo sapiens GN=PTPRS - [PTPRS_HUMAN]
Isoform 2 of Calsyntenin-1 OS=Homo sapiens GN=CLSTN1 - [CSTN1_HUMAN]
Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1 - [HTRA1_HUMAN]
Isoform 2 of UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2 OS=Homo sapiens GN=B3GNT2 - [B3
Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=4 SV=1 - [J3KMY5_HUMAN]
Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=2 SV=1 - [B4E351_HUMAN]
Group XV phospholipase A2 OS=Homo sapiens GN=PLA2G15 PE=1 SV=2 - [PAG15_HUMAN]
Epididymis-specific alpha-mannosidase OS=Homo sapiens GN=MAN2B2 PE=1 SV=4 - [MA2B2_HUMAN]
Isoform 8 of Pro-neuregulin-1, membrane-bound isoform OS=Homo sapiens GN=NRG1 - [NRG1_HUMAN]
Neuroserpin OS=Homo sapiens GN=SERPINI1 PE=1 SV=1 - [NEUS_HUMAN]
Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]
Tissue alpha-L-fucosidase OS=Homo sapiens GN=FUCA1 PE=1 SV=4 - [FUCO_HUMAN]
Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens GN=CLN5 PE=1 SV=2 - [CLN5_HUMAN]
Connective tissue growth factor OS=Homo sapiens GN=CTGF PE=1 SV=2 - [CTGF_HUMAN]
Noggin OS=Homo sapiens GN=NOG PE=1 SV=1 - [NOGG_HUMAN]
Beta-hexosaminidase OS=Homo sapiens GN=HEXA PE=2 SV=1 - [H3BS10_HUMAN]
Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2 - [PPGB_HUMAN]
Isoform Alpha of Poliovirus receptor-related protein 2 OS=Homo sapiens GN=PVRL2 - [PVRL2_HUMAN]
Receptor-type tyrosine-protein phosphatase mu OS=Homo sapiens GN=PTPRM PE=2 SV=2 - [E7EPS8_HUMAN]
Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=2 SV=1 - [Q5H9A7_HUMAN]
Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2 - [DSG2_HUMAN]
Isoform 3 of Phospholipid transfer protein OS=Homo sapiens GN=PLTP - [PLTP_HUMAN]
Isoform 2 of Carbohydrate sulfotransferase 11 OS=Homo sapiens GN=CHST11 - [CHSTB_HUMAN]
Twisted gastrulation protein homolog 1 OS=Homo sapiens GN=TWSG1 PE=2 SV=1 - [TWSG1_HUMAN]
Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2 - [LRP1_HUMAN]
Amyloid-like protein 1 OS=Homo sapiens GN=APLP1 PE=2 SV=1 - [F5GZ08_HUMAN]
5'-nucleotidase OS=Homo sapiens GN=NT5E PE=2 SV=1 - [Q96B60_HUMAN]
Ribonuclease T2 (Fragment) OS=Homo sapiens GN=RNASET2 PE=2 SV=1 - [D6RHI9_HUMAN]
Tumor necrosis factor receptor superfamily member 11B OS=Homo sapiens GN=TNFRSF11B PE=1 SV=3 - [TR11B_
Isoform 5 of Inactive tyrosine-protein kinase 7 OS=Homo sapiens GN=PTK7 - [PTK7_HUMAN]
Isoform 2 of Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA - [LICH_HUMAN]
Isoform 2 of Roundabout homolog 4 OS=Homo sapiens GN=ROBO4 - [ROBO4_HUMAN]
Isoform 2 of Cadherin-11 OS=Homo sapiens GN=CDH11 - [CAD11_HUMAN]
Anosmin-1 OS=Homo sapiens GN=KAL1 PE=1 SV=3 - [KALM_HUMAN]
Membrane-bound transcription factor site-1 protease OS=Homo sapiens GN=MBTPS1 PE=1 SV=1 - [MBTP1_HUMA
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Isoform 6 of Roundabout homolog 1 OS=Homo sapiens GN=ROBO1 - [ROBO1_HUMAN]
Tumor necrosis factor receptor superfamily member 21 OS=Homo sapiens GN=TNFRSF21 PE=1 SV=1 - [TNR21_HU
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N-acetylgalactosamine-6-sulfatase OS=Homo sapiens GN=GALNS PE=2 SV=1 - [F5H325_HUMAN]
Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3 - [CO6A1_HUMAN]
HLA class I histocompatibility antigen, A-2 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 - [1A02_HUMAN]
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Torsin-1B OS=Homo sapiens GN=TOR1B PE=1 SV=2 - [TOR1B_HUMAN]
Isoform 4 of Galactocerebrosidase OS=Homo sapiens GN=GALC - [GALC_HUMAN]
Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2 - [CPVL_HUMAN]
Isoform 3 of Tubulointerstitial nephritis antigen-like OS=Homo sapiens GN=TINAGL1 - [TINAL_HUMAN]
Amyloid-like protein 2 OS=Homo sapiens GN=APLP2 PE=1 SV=2 - [APLP2_HUMAN]

Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3 - [SORT_HUMAN]
Di-N-acetylchitobiase OS=Homo sapiens GN=CTBS PE=1 SV=1 - [DIAC_HUMAN]
Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4 - [NUCB1_HUMAN]
Plasma alpha-L-fucosidase OS=Homo sapiens GN=FUCA2 PE=1 SV=2 - [FUCO2_HUMAN]
Isoform 2 of Epsilon-sarcoglycan OS=Homo sapiens GN=SGCE - [SGCE_HUMAN]
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Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1 - [LOXL2_HUMAN]
Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Homo sapiens GN=MGAT2 PE=1 SV=1
Putative phospholipase B-like 2 OS=Homo sapiens GN=PLBD2 PE=1 SV=2 - [PLBL2_HUMAN]
Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 - [LG3BP_HUMAN]
Inhibin beta B chain OS=Homo sapiens GN=INHBB PE=1 SV=2 - [INHBB_HUMAN]
Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3 - [HEXB_HUMAN]
Isoform 3 of Neural cell adhesion molecule L1 OS=Homo sapiens GN=L1CAM - [L1CAM_HUMAN]
Isoform 2 of Follistatin OS=Homo sapiens GN=FST - [FST_HUMAN]
Isoform 13 of Fibroblast growth factor receptor 1 OS=Homo sapiens GN=FGFR1 - [FGFR1_HUMAN]
Ephrin-A5 OS=Homo sapiens GN=EFNA5 PE=1 SV=1 - [EFNA5_HUMAN]
Isoform 2 of EGF-like repeat and discoidin I-like domain-containing protein 3 OS=Homo sapiens GN=EDIL3 - [EDIL3_H
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Nucleotide exchange factor SIL1 OS=Homo sapiens GN=SIL1 PE=1 SV=1 - [SIL1_HUMAN]
Dystroglycan OS=Homo sapiens GN=DAG1 PE=1 SV=2 - [DAG1_HUMAN]
Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]
Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2 - [TPP1_HUMAN]
NKG2D ligand 2 OS=Homo sapiens GN=ULBP2 PE=1 SV=1 - [N2DL2_HUMAN]
N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase OS=Homo sapiens GN=B3GNT1 PE=1 SV=1 - [B3GN
Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2 - [C1R_HUMAN]
Processed exostosin-like 2 OS=Homo sapiens GN=EXTL2 PE=2 SV=1 - [F5GZK1_HUMAN]
Beta-glucuronidase OS=Homo sapiens GN=GUSB PE=1 SV=2 - [BGLR_HUMAN]
Platelet-derived growth factor D OS=Homo sapiens GN=PDGFD PE=1 SV=1 - [PDGFD_HUMAN]
SLIT and NTRK-like protein 5 OS=Homo sapiens GN=SLITRK5 PE=2 SV=2 - [SLIK5_HUMAN]
Cell surface glycoprotein MUC18 OS=Homo sapiens GN=MCAM PE=1 SV=2 - [MUC18_HUMAN]
N-acetyllactosaminide beta-1,6-N-acetylglucosaminyl-transferase, isoform A OS=Homo sapiens GN=GCNT2 PE=2 SV
Deoxyribonuclease-2-alpha OS=Homo sapiens GN=DNASE2 PE=2 SV=1 - [B7Z4K6_HUMAN]
Cathepsin L1 OS=Homo sapiens GN=CTSL1 PE=1 SV=2 - [CATL1_HUMAN]
Isoform 3 of Transportin-1 OS=Homo sapiens GN=TNPO1 - [TNPO1_HUMAN]
Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2 - [ITA5_HUMAN]
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2 - [PLOD1_HUMAN]
Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3 - [MA2B1_HUMAN]
Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1 - [VASN_HUMAN]
Isoform 2 of Receptor-type tyrosine-protein phosphatase gamma OS=Homo sapiens GN=PTPRG - [PTPRG_HUMAN]
Isoform 2 of Cadherin-4 OS=Homo sapiens GN=CDH4 - [CADH4_HUMAN]
Carbohydrate sulfotransferase 12 OS=Homo sapiens GN=CHST12 PE=1 SV=2 - [CHSTC_HUMAN]
Beta-1,3-galactosyltransferase 6 OS=Homo sapiens GN=B3GALT6 PE=2 SV=2 - [B3GT6_HUMAN]
Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 OS=Homo sapiens GN=NDST1 PE=2 SV=1 - [E7EVJ
Vascular endothelial growth factor C OS=Homo sapiens GN=VEGFC PE=1 SV=1 - [VEGFC_HUMAN]
Isoform 4 of Sushi repeat-containing protein SRPX OS=Homo sapiens GN=SRPX - [SRPX_HUMAN]
Gamma-interferon-inducible lysosomal thiol reductase OS=Homo sapiens GN=IFI30 PE=1 SV=3 - [GILT_HUMAN]
Tissue-type plasminogen activator OS=Homo sapiens GN=PLAT PE=1 SV=1 - [TPA_HUMAN]
Transferrin receptor (P90, CD71), isoform CRA_c OS=Homo sapiens GN=TFRC PE=4 SV=1 - [G3V0E5_HUMAN]
Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1 - [IBP6_HUMAN]
D-glucuronyl C5-epimerase OS=Homo sapiens GN=GLCE PE=2 SV=1 - [H0YNP1_HUMAN]
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]
Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2 - [ECM1_HUMAN]
Cysteine-rich motor neuron 1 protein OS=Homo sapiens GN=CRIM1 PE=1 SV=1 - [CRIM1_HUMAN]
Endothelial protein C receptor OS=Homo sapiens GN=PROCR PE=1 SV=1 - [EPCR_HUMAN]
Isoform 2 of CUB domain-containing protein 1 OS=Homo sapiens GN=CDCP1 - [CDCP1_HUMAN]
Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]
Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8 - [LAMA5_HUMAN]
Matrix-remodeling-associated protein 8 OS=Homo sapiens GN=MXRA8 PE=2 SV=1 - [B3KTR6_HUMAN]

Isoform 3 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR - [LDLR_HUMAN]
Plexin domain-containing protein 2 OS=Homo sapiens GN=PLXDC2 PE=1 SV=1 - [PXDC2_HUMAN]
Endothelin-converting enzyme 1 OS=Homo sapiens GN=ECE1 PE=2 SV=1 - [B4DKB2_HUMAN]
Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 - [TBA1B_HUMAN]
Matrix metalloproteinase-19 OS=Homo sapiens GN=MMP19 PE=2 SV=1 - [F8W1C3_HUMAN]
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens GN=PLOD2 PE=2 SV=1 - [E7ETU9_HUMAN]
Semaphorin-7A OS=Homo sapiens GN=SEMA7A PE=1 SV=1 - [SEM7A_HUMAN]
Pappalysin-1 OS=Homo sapiens GN=PAPPA PE=1 SV=3 - [PAPP1_HUMAN]
Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3 - [QSOX1_HUMAN]
Isoform 2 of 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 - [4F2_HUMAN]
Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1 - [S10A9_HUMAN]
Talin-1 OS=Homo sapiens GN=TLN1 PE=2 SV=1 - [Q5TCU6_HUMAN]
N-sulphoglucosamine sulphohydrolase OS=Homo sapiens GN=SGSH PE=2 SV=1 - [F5H6A3_HUMAN]
Follistatin-related protein 1 OS=Homo sapiens GN=FSTL1 PE=1 SV=1 - [FSTL1_HUMAN]
Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]
Isoform 3 of Clusterin OS=Homo sapiens GN=CLU - [CLUS_HUMAN]
Isoform Short of Tyrosine-protein kinase receptor UFO OS=Homo sapiens GN=AXL - [UFO_HUMAN]
Isoform Gamma of Poliovirus receptor OS=Homo sapiens GN=PVR - [PVR_HUMAN]
Isoform 2 of EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 - [FBLN3_HUM
Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
Mammalian ependymin-related protein 1 OS=Homo sapiens GN=EPDR1 PE=1 SV=2 - [EPDR1_HUMAN]
Tenascin OS=Homo sapiens GN=TNC PE=4 SV=1 - [J3QSU6_HUMAN]
Leucine-rich repeat transmembrane protein FLRT2 OS=Homo sapiens GN=FLRT2 PE=1 SV=1 - [FLRT2_HUMAN]
Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]
Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2 - [PXDN_HUMAN]
Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=2 SV=1 - [E7EMM4_HUMAN]
Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2 - [CFAB_HUMAN]
Exostosin-2 OS=Homo sapiens GN=EXT2 PE=1 SV=1 - [EXT2_HUMAN]
Prolyl 3-hydroxylase 1 OS=Homo sapiens GN=LEPRE1 PE=1 SV=2 - [P3H1_HUMAN]
Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=3 SV=1 - [E9PL22_HUMAN]
Isoform 3 of Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 - [NDKB_HUMAN]
Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1 - [PROS_HUMAN]
Complement decay-accelerating factor (Fragment) OS=Homo sapiens GN=CD55 PE=4 SV=1 - [H3BLV0_HUMAN]
Protein kinase C-binding protein NELL1 OS=Homo sapiens GN=NRP1 PE=2 SV=2 - [E9PEP6_HUMAN]
ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=2 SV=1 - [B4E3P0_HUMAN]
Tissue factor pathway inhibitor OS=Homo sapiens GN=TFPI PE=1 SV=1 - [TFPI1_HUMAN]
Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]
Alpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2 - [MA2A1_HUMAN]
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]
Mesothelin (Fragment) OS=Homo sapiens GN=MSLN PE=2 SV=2 - [H3BMA1_HUMAN]
60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 - [RL10A_HUMAN]
Out at first protein homolog OS=Homo sapiens GN=OAF PE=2 SV=1 - [OAF_HUMAN]
Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1 - [CYR61_HUMAN]
Protocadherin Fat 1 OS=Homo sapiens GN=FAT1 PE=1 SV=2 - [FAT1_HUMAN]
26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=2 SV=1 - [E9PCS3_HUMAN]
Transmembrane protein 132A OS=Homo sapiens GN=TMEM132A PE=2 SV=1 - [T132A_HUMAN]
Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP1CA PE=2 SV=1 - [E9PMD7_HUMAN]
Exostosin-1 OS=Homo sapiens GN=EXT1 PE=1 SV=2 - [EXT1_HUMAN]
Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DKFZp781B11202 PE=2 SV=1 - [Q68CR9_HUMAN]
Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase OS=Homo sapiens GN=MAN1B1 PE=1 SV=
Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]
Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2 - [CO3_HUMAN]
Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN]
Isoform 2 of Lactadherin OS=Homo sapiens GN=MFGE8 - [MFGM_HUMAN]
Sulfhydryl oxidase 2 OS=Homo sapiens GN=QSOX2 PE=1 SV=3 - [QSOX2_HUMAN]
Isoform 2 of Adenosylhomocysteinase OS=Homo sapiens GN=AHCY - [SAHH_HUMAN]
CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase 1 OS=Homo sapiens GN=ST3GAL1 PE=2
Lipolysis-stimulated lipoprotein receptor OS=Homo sapiens GN=LSR PE=2 SV=1 - [B4DKL4_HUMAN]

Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]
Hepatocyte growth factor receptor OS=Homo sapiens GN=MET PE=1 SV=4 - [MET_HUMAN]
Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2 - [TSP1_HUMAN]
Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2 - [HORN_HUMAN]
Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=2 - [SBSN_HUMAN]
C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2 - [MRC2_HUMAN]
Insulin-like growth factor-binding protein-like 1 OS=Homo sapiens GN=IGFBPL1 PE=2 SV=1 - [IBPL1_HUMAN]
T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=2 SV=1 - [F8VQ14_HUMAN]
Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN]
Transforming growth factor beta-2 OS=Homo sapiens GN=TGFB2 PE=1 SV=1 - [TGFB2_HUMAN]
Isoform 4 of Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 - [RBBP4_HUMAN]
Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN]
Extracellular matrix protein FRAS1 (Fragment) OS=Homo sapiens GN=FRAS1 PE=4 SV=1 - [H0Y930_HUMAN]
Protein disulfide-isomerase (Fragment) OS=Homo sapiens GN=P4HB PE=2 SV=1 - [I3L398_HUMAN]
Isoform 7 of Plectin OS=Homo sapiens GN=PLEC - [PLEC_HUMAN]
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1 - [PLOD3_HUMAN]
Alpha-N-acetylglucosaminidase OS=Homo sapiens GN=NAGLU PE=1 SV=2 - [ANAG_HUMAN]
Carbohydrate sulfotransferase 3 OS=Homo sapiens GN=CHST3 PE=1 SV=3 - [CHST3_HUMAN]
Dipeptidyl peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=3 - [DPP2_HUMAN]
Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Homo sapiens GN=G6PD PE=2 SV=1 - [E9PD92_HUMAN]
T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=2 SV=1 - [B4DQH4_HUMAN]
Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4 - [CFAH_HUMAN]
Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 - [ACTN1_HUMAN]
Isoform 2 of Golgi membrane protein 1 OS=Homo sapiens GN=GOLM1 - [GOLM1_HUMAN]
Aspartyl aminopeptidase (Fragment) OS=Homo sapiens GN=DNPEP PE=2 SV=2 - [C9JRG3_HUMAN]
Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment) OS=Homo sapiens GN=GNB2L1 PE=4 SV=1 - [H
Metalloproteinase inhibitor 2 OS=Homo sapiens GN=TIMP2 PE=1 SV=2 - [TIMP2_HUMAN]
WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 - [WDR1_HUMAN]
Isoform 2 of Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A - [HSP71_HUMAN]
Xylosyltransferase 2 OS=Homo sapiens GN=XYLT2 PE=2 SV=2 - [XYLT2_HUMAN]
Lysosomal thioesterase PPT2 OS=Homo sapiens GN=PPT2 PE=1 SV=4 - [PPT2_HUMAN]
Semaphorin-3A OS=Homo sapiens GN=SEMA3A PE=1 SV=1 - [SEM3A_HUMAN]
Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2 - [LAMB2_HUMAN]
Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1 - [FETUA_HUMAN]
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=2 SV=1 - [E7EUT4_HUMAN]
Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]
Lysyl oxidase homolog 4 OS=Homo sapiens GN=LOXL4 PE=1 SV=1 - [LOXL4_HUMAN]
35 kDa inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=2 SV=1 - [F5GXQ1_HUMAN]
Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2 - [GSLG1_HUMAN]
Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3 - [MPRI_HUMAN]
Calsyntenin-3 OS=Homo sapiens GN=CLSTN3 PE=1 SV=1 - [CSTN3_HUMAN]
Isoform 2 of Oncostatin-M-specific receptor subunit beta OS=Homo sapiens GN=OSMR - [OSMR_HUMAN]
Plastin-3 OS=Homo sapiens GN=PLS3 PE=2 SV=1 - [B7Z6M1_HUMAN]
CD44 antigen OS=Homo sapiens GN=CD44 PE=2 SV=2 - [H0YD13_HUMAN]
Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=4 SV=1 - [Q5T985_HUMAN]
Dickkopf-related protein 1 OS=Homo sapiens GN=DKK1 PE=1 SV=1 - [DKK1_HUMAN]
Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2 - [PPIB_HUMAN]
HLA-B associated transcript 1 OS=Homo sapiens GN=DDX39B PE=4 SV=2 - [Q5STU3_HUMAN]
Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 - [IF4A1_HUMAN]
Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]
14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 - [1433Z_HUMAN]
Coiled-coil domain-containing protein 80 OS=Homo sapiens GN=CCDC80 PE=1 SV=1 - [CCD80_HUMAN]
26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1 - [PSMD6_HUMAN]
Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3 - [LAMC1_HUMAN]
Importin-5 OS=Homo sapiens GN=IPO5 PE=2 SV=1 - [B4E0R6_HUMAN]
Isoform 2 of Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens GN=PTPRF - [PTPRF_HUMAN]
Carboxypeptidase A4 OS=Homo sapiens GN=CPA4 PE=2 SV=1 - [B7Z5J4_HUMAN]
Phosphoribosylaminoimidazolecarboxamide formyltransferase OS=Homo sapiens GN=ATIC PE=2 SV=1 - [E9PBU3_H

78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]
Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=ERAP1 PE=1 SV=3 - [ERAP1_HUMAN]
Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]
Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4 -
Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=4 SV=1 - [J3KS17_HUMAN]
Isoform 4 of Epidermal growth factor receptor OS=Homo sapiens GN=EGFR - [EGFR_HUMAN]
Isoform 2 of Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 - [PSA3_HUMAN]
Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 - [PSA1_HUMAN]
Isoform 2 of Seizure 6-like protein 2 OS=Homo sapiens GN=SEZ6L2 - [SE6L2_HUMAN]
Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2 - [THBG_HUMAN]
Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1 - [KPRP_HUMAN]
Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 - [CLIC1_HUMAN]
Interleukin-6 receptor subunit beta OS=Homo sapiens GN=IL6ST PE=1 SV=2 - [IL6RB_HUMAN]
Iduronate 2-sulfatase OS=Homo sapiens GN=IDS PE=1 SV=1 - [IDS_HUMAN]
Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]
Filamin-A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q5HY54_HUMAN]
Isoform 3 of Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 - [PSB5_HUMAN]
Procollagen galactosyltransferase 1 OS=Homo sapiens GN=COLGALT1 PE=1 SV=1 - [GT251_HUMAN]
A disintegrin and metalloproteinase with thrombospondin motifs 1 OS=Homo sapiens GN=ADAMTS1 PE=1 SV=4 - [AT
45 kDa calcium-binding protein OS=Homo sapiens GN=SDF4 PE=1 SV=1 - [CAB45_HUMAN]
Polyubiquitin-C (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=1 - [F5H265_HUMAN]
Isoform 3 of Netrin-4 OS=Homo sapiens GN=NTN4 - [NET4_HUMAN]
Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 - [GANAB_HUMAN]
Thrombospondin-2 OS=Homo sapiens GN=THBS2 PE=1 SV=2 - [TSP2_HUMAN]
Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN]
Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]
Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=2 SV=1 - [F5H335_HUMAN]
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]
Collagen alpha-1(VIII) chain OS=Homo sapiens GN=COL8A1 PE=1 SV=2 - [CO8A1_HUMAN]
Bis(5'-adenosyl)-triphosphatase ENPP4 OS=Homo sapiens GN=ENPP4 PE=1 SV=3 - [ENPP4_HUMAN]
Phosphoglycerate kinase OS=Homo sapiens GN=PGK1 PE=2 SV=1 - [B7Z7A9_HUMAN]
Isoform 2 of Protein KIAA1199 OS=Homo sapiens GN=KIAA1199 - [K1199_HUMAN]
Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 - [ACTN4_HUMAN]
L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]
L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 - [LDHA_HUMAN]
Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN]
Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC - [CLH1_HUMAN]
Serum albumin (Fragment) OS=Homo sapiens GN=ALB PE=4 SV=1 - [H0YA55_HUMAN]
Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]
Pentraxin-related protein PTX3 OS=Homo sapiens GN=PTX3 PE=1 SV=3 - [PTX3_HUMAN]
Sushi repeat-containing protein SRPX2 OS=Homo sapiens GN=SRPX2 PE=1 SV=1 - [SRPX2_HUMAN]
Isoform 3 of Attractin OS=Homo sapiens GN=ATRN - [ATRN_HUMAN]
Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN]
N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3 - [GNS_HUMAN]
Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOA PE=2 SV=1 - [H3BQN4_HUMAN]
Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [ENPL_HUMAN]
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]
Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN]
Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]
Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3 - [LAMP1_HUMAN]
Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=3 - [FBN1_HUMAN]

Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FAS_HUMAN]
Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=2 SV=1 - [E9PFT6_HUMAN]
Testican-1 OS=Homo sapiens GN=SPOCK1 PE=1 SV=1 - [TICN1_HUMAN]
Isoform 17 of Fibronectin OS=Homo sapiens GN=FN1 - [FINC_HUMAN]
Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN]
Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]
Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]
Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1 - [ANT3_HUMAN]
Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1 - [VTNC_HUMAN]
Isoform 6 of Agrin OS=Homo sapiens GN=AGRN - [AGRIN_HUMAN]
Serglycin OS=Homo sapiens GN=SRGN PE=1 SV=3 - [SRGN_HUMAN]
X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=2 SV=1 - [F5H1I8_HUMAN]
Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=3 SV=1 - [H0YH88_HUMAN]
Isoform 2 of Epithelial discoidin domain-containing receptor 1 OS=Homo sapiens GN=DDR1 - [DDR1_HUMAN]
Isoform 3 of Ubiquitin-protein ligase E3B OS=Homo sapiens GN=UBE3B - [UBE3B_HUMAN]
MHC class I polypeptide-related sequence B OS=Homo sapiens GN=MICB PE=1 SV=1 - [MICB_HUMAN]
Cathepsin L2 OS=Homo sapiens GN=CTSL2 PE=1 SV=2 - [CATL2_HUMAN]
Polypeptide N-acetylgalactosaminyltransferase 18 OS=Homo sapiens GN=GALNT18 PE=2 SV=2 - [GLT18_HUMAN]
Isoform 8 of Maternal embryonic leucine zipper kinase OS=Homo sapiens GN=MELK - [MELK_HUMAN]
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=2 SV=1 - [E7EP3
Pantetheinase OS=Homo sapiens GN=VNN1 PE=1 SV=2 - [VNN1_HUMAN]
Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 - [HSP74_HUMAN]
Glypican-6 OS=Homo sapiens GN=GPC6 PE=1 SV=1 - [GPC6_HUMAN]
Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=2 SV=1 - [F5H780_HUMAN]
Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens GN=MINPP1 PE=1 SV=1 - [MINP1_HUMAN]
Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 - [SYG_HUMAN]
Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=2 SV=1 - [J3KR24_HUMAN]
Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3 - [FILA_HUMAN]
Four-jointed box protein 1 OS=Homo sapiens GN=FJX1 PE=2 SV=1 - [FJX1_HUMAN]
14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 - [1433T_HUMAN]
ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2 - [ARF3_HUMAN]
Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN]
14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 - [1433E_HUMAN]
T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1 - [B4DYD8_HUMAN]
Septin-2 (Fragment) OS=Homo sapiens GN=SEPT2 PE=2 SV=1 - [C9J2Q4_HUMAN]
Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3 - [HEP2_HUMAN]
Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4 - [PEDF_HUMAN]
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=2 SV=1 - [E9PQX2_HUMAN]
Polypeptide N-acetylgalactosaminyltransferase 5 OS=Homo sapiens GN=GALNT5 PE=1 SV=1 - [GALT5_HUMAN]
Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 - [IPO7_HUMAN]
T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=2 SV=1 - [B4DUR8_HUMAN]
Isoform 3 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 - [RO60_HUMAN]
von Willebrand factor A domain-containing protein 1 OS=Homo sapiens GN=VWA1 PE=2 SV=1 - [VWA1_HUMAN]
Protein NAMPTL (Fragment) OS=Homo sapiens GN=NAMPTL PE=2 SV=1 - [Q5SYT8_HUMAN]
Isoform 2 of Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL - [PYGL_HUMAN]
Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=2 SV=1 - [B0QY90_HUMAN]
Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=2 SV=1 - [Q5T6W1_HUMAN]
Protein CutA OS=Homo sapiens GN=CUTA PE=2 SV=1 - [C9IZG4_HUMAN]
Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2 - [PSB3_HUMAN]
GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=2 SV=1 - [F5H018_HUMAN]
Isoform 2 of Cullin-4A OS=Homo sapiens GN=CUL4A - [CUL4A_HUMAN]
Eukaryotic translation initiation factor 3 subunit M (Fragment) OS=Homo sapiens GN=EIF3M PE=2 SV=1 - [E9PN86_H
Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]
Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=2 - [GPC1_HUMAN]
Isoform 10 of Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH - [ASPH_HUMAN]
Isoform 3 of KDEL motif-containing protein 2 OS=Homo sapiens GN=KDELC2 - [KDEL2_HUMAN]

Isoform 2 of Syndecan-4 OS=Homo sapiens GN=SDC4 - [SDC4_HUMAN]
Isoform 3 of Latrophilin-2 OS=Homo sapiens GN=LPHN2 - [LPHN2_HUMAN]
Dynein heavy chain 5, axonemal OS=Homo sapiens GN=DNAH5 PE=1 SV=3 - [DYH5_HUMAN]
Extracellular serine/threonine protein kinase FAM20C OS=Homo sapiens GN=FAM20C PE=1 SV=2 - [DMP4_HUMAN
Isoform 2 of Transportin-2 OS=Homo sapiens GN=TNPO2 - [TNPO2_HUMAN]
Isoform 2 of 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP - [K6PP_HUMAN]
BRI2, membrane form OS=Homo sapiens GN=ITM2B PE=2 SV=1 - [Q5W0A2_HUMAN]
Peroxiredoxin-4 (Fragment) OS=Homo sapiens GN=PRDX4 PE=4 SV=1 - [H7C3T4_HUMAN]
Transforming growth factor beta-1 OS=Homo sapiens GN=TGFB1 PE=1 SV=2 - [TGFB1_HUMAN]
Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4 - [FBLN1_HUMAN]
Peroxiredoxin 2, isoform CRA_a OS=Homo sapiens GN=PRDX2 PE=2 SV=2 - [A6NIW5_HUMAN]
ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]
Interleukin-1 receptor accessory protein (Fragment) OS=Homo sapiens GN=IL1RAP PE=2 SV=1 - [C9J1D9_HUMAN]
Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=2 SV=1 - [B4E2S7_HUMAN]
Isoform 2 of MAM domain-containing protein 2 OS=Homo sapiens GN=MAMDC2 - [MAMC2_HUMAN]
26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3 - [PSD11_HUMAN]
26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=4 SV=1 - [J3KNQ3_HUMAN
Acid sphingomyelinase-like phosphodiesterase 3a OS=Homo sapiens GN=SMPDL3A PE=2 SV=1 - [B7Z729_HUMAN
Alpha-amylase 2B OS=Homo sapiens GN=AMY2B PE=2 SV=1 - [B3KTI1_HUMAN]
Annexin OS=Homo sapiens GN=ANXA3 PE=2 SV=1 - [D6RA82_HUMAN]
Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=2 SV=1 - [F5H3T8_HUMAN]
Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2 - [BCAM_HUMAN]
Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase OS=Homo sapiens GN=GCNT1
Beta-1,4-galactosyltransferase 5 OS=Homo sapiens GN=B4GALT5 PE=2 SV=1 - [B4GT5_HUMAN]
CAD protein OS=Homo sapiens GN=CAD PE=2 SV=1 - [F8VPD4_HUMAN]
Carbohydrate sulfotransferase 14 OS=Homo sapiens GN=CHST14 PE=2 SV=1 - [H0YN65_HUMAN]
Cartilage-associated protein OS=Homo sapiens GN=CRTAP PE=2 SV=1 - [C9JP16_HUMAN]
Casein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=2 SV=1 - [E7EU96_HUMAN]
Cell adhesion molecule 4 OS=Homo sapiens GN=CADM4 PE=1 SV=1 - [CADM4_HUMAN]
Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 - [CLIC4_HUMAN]
Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3 - [COPB_HUMAN]
Collagen and calcium-binding EGF domain-containing protein 1 OS=Homo sapiens GN=CCBE1 PE=1 SV=1 - [CCBE1
Ephrin-B2 OS=Homo sapiens GN=EFNB2 PE=1 SV=1 - [EFNB2_HUMAN]
Exportin-2 OS=Homo sapiens GN=CSE1L PE=2 SV=1 - [F8W904_HUMAN]
FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1 - [SSRP1_HUMAN]
FERM and PDZ domain-containing protein 1 OS=Homo sapiens GN=FRMPD1 PE=1 SV=1 - [FRPD1_HUMAN]
Filamin-B OS=Homo sapiens GN=FLNB PE=2 SV=1 - [E7EN95_HUMAN]
Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 - [HBA_HUMAN]
Heparan sulfate glucosamine 3-O-sulfotransferase 3B1 OS=Homo sapiens GN=HS3ST3B1 PE=1 SV=1 - [HS3SB_HU
Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=2 SV=1 - [D6RAF8_HU
Isoform 2 of Glucoside xylosyltransferase 1 OS=Homo sapiens GN=GXYLT1 - [GXLT1_HUMAN]
Isoform 2 of Laminin subunit alpha-4 OS=Homo sapiens GN=LAMA4 - [LAMA4_HUMAN]
Isoform 2 of Neogenin OS=Homo sapiens GN=NEO1 - [NEO1_HUMAN]
Isoform 2 of Neuroligin-1 OS=Homo sapiens GN=NLGN1 - [NLGN1_HUMAN]
Isoform 2 of Protocadherin gamma-B1 OS=Homo sapiens GN=PCDHGB1 - [PCDGD_HUMAN]
Isoform 3 of Matrilin-2 OS=Homo sapiens GN=MATN2 - [MATN2_HUMAN]
Isoform 3 of Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 - [SPTN1_HUMAN]
Isoform 4 of Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 - [COCA1_HUMAN]
Isoform M1 of Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM - [KPYM_HUMAN]
Isoform Short of Very low-density lipoprotein receptor OS=Homo sapiens GN=VLDLR - [VLDLR_HUMAN]
Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=2 SV=1 - [E7EPA6_HUMAN]
Low-density lipoprotein receptor-related protein 5 OS=Homo sapiens GN=LRP5 PE=1 SV=2 - [LRP5_HUMAN]
Low-density lipoprotein receptor-related protein 6 (Fragment) OS=Homo sapiens GN=LRP6 PE=4 SV=1 - [H0YGW5_H
Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]
Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]
Lysyl oxidase homolog 2 (Fragment) OS=Homo sapiens GN=LOXL2 PE=4 SV=1 - [H0YAR1_HUMAN]
Mannosyl-oligosaccharide glucosidase (Fragment) OS=Homo sapiens GN=MOGS PE=2 SV=1 - [C9J8D4_HUMAN]
Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=2 SV=1 - [B3KVK7_HUMAN]

Neuron navigator 3 OS=Homo sapiens GN=NAV3 PE=2 SV=2 - [E7EUA9_HUMAN]
Nodal modulator 3 OS=Homo sapiens GN=NOMO3 PE=2 SV=1 - [F5H826_HUMAN]
Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]
Phosphoribosylaminoimidazole carboxylase OS=Homo sapiens GN=PAICS PE=2 SV=1 - [D6RF62_HUMAN]
Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4 - [PSB4_HUMAN]
Semaphorin-4D OS=Homo sapiens GN=SEMA4D PE=4 SV=1 - [E9PFD9_HUMAN]
Soluble calcium-activated nucleotidase 1 OS=Homo sapiens GN=CANT1 PE=1 SV=1 - [CANT1_HUMAN]
Sushi domain-containing protein 5 OS=Homo sapiens GN=SUSD5 PE=1 SV=3 - [SUSD5_HUMAN]
T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=2 SV=1 - [B7Z9L0_HUMAN]
Torsin-3A (Fragment) OS=Homo sapiens GN=TOR3A PE=2 SV=1 - [Q5W0C6_HUMAN]

R1 Media (I/NI)	SD (I/	CV% (I	R2 Media (I/NI)	SD (I/	CV% (I	R3 Media (I/NI)	SD (I/	CV% (I	Media delle Medie (I/NI)
0.35	0.01	3.99	**0.42**	0.03	7.93	**0.38**	0.02	5.99	**0.38**
0.54	0.01	2.55	**0.47**	0.05	9.66	#DIV/0!	###	###	**0.50**
0.56	0.03	5.67	**0.44**	0.04	9.36	**0.54**	0.01	2.18	**0.51**
0.47	0.00	0.81	**0.52**	0.02	3.25	**0.60**	0.02	2.58	**0.53**
0.57	0.03	5.97	**0.50**	0.02	4.75	**0.52**	0.03	5.79	**0.53**
0.57	0.02	3.11	**0.51**	0.05	9.05	**0.59**	0.01	2.26	**0.56**
0.47	0.00	0.31	#DIV/0!	####	####	**0.66**	0.03	4.63	**0.56**
0.39	0.01	1.88	0.69	0.01	1.96	**0.63**	0.05	8.44	**0.57**
#DIV/0!	####	###	**0.64**	0.01	0.98	**0.53**	0.06	###	**0.58**
0.55	0.02	3.41	0.68	0.03	3.93	**0.54**	0.05	9.71	**0.59**
0.95	0.06	5.89	**0.37**	0.02	6.06	**0.45**	0.05	###	**0.59**
0.61	0.04	6.03	**0.55**	0.01	2.59	**0.64**	0.01	1.99	**0.60**
0.57	0.04	6.97	#DIV/0!	####	####	**0.65**	0.06	8.95	**0.61**
0.54	0.03	5.46	**0.62**	0.05	7.61	0.70	0.05	7.75	**0.62**
0.59	0.01	1.59	**0.62**	0.04	6.10	0.71	0.04	5.52	**0.64**
0.65	0.06	8.73	**0.64**	0.12	####	#DIV/0!	###	###	**0.65**
0.73	0.04	5.59	**0.62**	0.01	1.18	**0.59**	0.02	3.53	**0.65**
0.65	0.01	1.72	0.71	0.05	6.60	**0.59**	0.03	5.35	**0.65**
0.63	0.04	5.63	**0.66**	0.01	2.03	0.71	0.01	1.05	**0.67**
0.55	0.03	5.70	0.76	0.03	3.54	0.70	0.04	5.10	**0.67**
0.79	0.03	3.39	**0.62**	0.02	3.21	**0.64**	0.02	3.85	0.68
0.62	0.05	7.91	0.76	0.08	####	0.68	0.04	5.91	0.68
0.74	0.03	4.39	**0.67**	0.02	3.43	**0.65**	0.05	7.96	0.69
0.66	0.02	3.16	**0.66**	0.01	1.62	0.79	0.12	###	0.70
0.71	0.02	2.29	**0.67**	0.03	4.57	0.73	0.03	3.43	0.71
#DIV/0!	####	###	**0.67**	0.01	1.94	0.75	0.04	4.75	0.71
0.68	0.02	2.44	0.70	0.03	4.15	0.75	0.02	2.99	0.71
0.91	0.05	4.98	0.72	0.03	4.22	**0.50**	0.06	###	0.71
0.71	0.02	2.48	#DIV/0!	####	####	0.72	0.03	4.17	0.71
0.55	0.03	4.72	#DIV/0!	####	####	0.89	0.11	###	0.72
0.68	0.03	4.94	0.73	0.04	5.73	0.75	0.02	2.28	0.72
0.72	0.03	4.68	**0.67**	0.03	4.85	0.78	0.05	6.71	0.72
0.74	0.04	5.59	0.70	0.04	6.20	0.73	0.05	6.48	0.72
0.61	0.02	3.68	0.75	0.02	2.66	0.82	0.02	2.65	0.73
0.83	0.11	###	**0.60**	0.12	####	0.77	0.08	###	0.73
0.79	0.03	3.62	**0.60**	0.01	1.17	0.81	0.03	3.94	0.73
0.67	0.04	6.26	0.79	0.03	3.88	0.75	0.02	2.53	0.74
0.76	0.10	###	0.77	0.03	3.86	0.69	0.03	4.96	0.74
0.70	0.03	4.26	0.81	0.06	7.62	0.71	0.01	2.01	0.74
0.72	0.04	5.94	0.80	0.04	4.93	0.71	0.01	1.80	0.74
0.67	0.05	7.87	0.78	0.07	8.47	0.79	0.04	5.32	0.74
0.63	0.02	3.65	0.72	0.06	8.25	0.88	0.04	4.49	0.74
0.64	0.03	4.92	0.89	0.06	6.97	0.71	0.03	3.79	0.75
0.79	0.05	6.70	0.74	0.09	####	0.72	0.03	4.05	0.75
0.99	0.01	1.30	**0.51**	0.01	1.80	#DIV/0!	###	###	0.75
0.77	0.02	2.46	0.70	0.06	8.47	0.79	0.03	3.53	0.75
0.83	0.03	4.11	0.81	0.09	####	**0.66**	0.05	7.52	0.76
0.70	0.06	8.06	0.90	0.03	3.64	0.70	0.04	5.12	0.77
0.75	0.04	4.70	0.84	0.03	2.98	0.70	0.03	4.68	0.77

0.74	0.03	4.18	0.79	0.05	6.49	0.78	0.03	3.71	0.77
0.74	0.02	2.62	0.75	0.04	5.97	0.83	0.01	1.53	0.77
0.79	0.03	3.31	0.81	0.02	2.57	0.72	0.02	3.34	0.77
0.76	0.05	6.17	#DIV/0!	####	####	0.79	0.05	6.02	0.78
0.75	0.07	9.33	#DIV/0!	####	####	0.80	0.04	5.29	0.78
0.69	0.04	6.37	0.87	0.06	6.66	0.79	0.05	6.12	0.78
0.81	0.03	4.28	0.78	0.06	7.98	0.77	0.02	2.88	0.79
0.76	0.07	9.77	0.76	0.03	4.08	0.84	0.04	4.67	0.79
0.83	0.06	7.69	#DIV/0!	####	####	0.75	0.03	4.67	0.79
0.71	0.03	3.98	0.77	0.03	3.68	0.89	0.03	3.12	0.79
#DIV/0!	####	###	0.78	0.02	2.96	0.82	0.06	7.77	0.80
0.82	0.02	2.68	0.82	0.04	4.77	0.77	0.03	3.49	0.80
0.81	0.03	4.19	0.76	0.11	####	0.84	0.02	2.95	0.80
0.71	0.03	4.16	0.87	0.03	3.44	0.82	0.05	5.60	0.80
0.83	0.09	###	0.86	0.06	7.40	0.73	0.04	5.78	0.81
0.68	0.05	7.55	0.92	0.01	1.01	0.82	0.03	4.26	0.81
0.93	0.06	6.01	#DIV/0!	####	####	0.70	0.05	6.58	0.82
0.81	0.02	2.70	0.86	0.02	2.64	0.77	0.02	2.02	0.82
0.65	0.08	###	1.07	0.08	7.08	0.73	0.03	4.07	0.82
0.75	0.02	2.67	0.83	0.02	2.32	0.88	0.03	3.34	0.82
0.89	0.05	6.06	0.79	0.06	7.88	0.79	0.05	5.99	0.82
0.66	0.01	2.18	0.90	0.03	3.58	0.92	0.02	1.93	0.83
0.75	0.02	2.34	0.78	0.02	2.25	0.95	0.03	3.02	0.83
0.71	0.02	3.07	1.03	0.02	2.24	0.77	0.03	3.98	0.83
0.79	0.01	1.90	0.92	0.06	6.49	0.80	0.03	3.57	0.84
0.81	0.04	5.18	0.79	0.03	3.67	0.91	0.02	1.72	0.84
0.74	0.01	1.70	0.93	0.05	5.53	0.85	0.02	2.45	0.84
0.86	0.07	8.29	#DIV/0!	####	####	0.82	0.05	6.05	0.84
0.91	0.01	1.18	0.84	0.04	5.23	0.78	0.04	4.75	0.84
0.79	0.03	3.61	0.94	0.04	4.24	0.80	0.04	4.45	0.84
0.91	0.06	6.69	0.77	0.02	2.95	0.86	0.02	2.08	0.85
0.74	0.06	8.80	#DIV/0!	####	####	0.96	0.06	5.93	0.85
0.91	0.05	5.00	#DIV/0!	####	####	0.79	0.05	6.37	0.85
0.63	0.01	1.77	0.95	0.03	3.28	0.96	0.06	5.99	0.85
0.84	0.08	9.81	0.93	0.13	####	0.77	0.07	8.95	0.85
1.03	0.09	9.12	0.73	0.06	8.59	0.79	0.08	###	0.85
0.85	0.09	###	0.85	0.01	1.49	0.86	0.04	4.79	0.85
0.80	0.03	3.40	0.82	0.01	1.31	0.95	0.03	3.19	0.86
0.92	0.08	8.48	0.83	0.04	4.92	0.82	0.04	4.55	0.86
0.88	0.03	2.93	0.81	0.04	4.82	0.89	0.02	2.16	0.86
0.80	0.03	3.87	0.81	0.09	####	0.97	0.09	9.28	0.86
0.86	0.00	0.42	0.80	0.02	2.36	0.92	0.05	5.74	0.86
0.86	0.01	1.45	0.79	0.03	3.62	0.93	0.06	6.53	0.86
0.91	0.12	###	0.96	0.11	####	0.73	0.03	3.80	0.87
0.88	0.02	2.16	0.84	0.07	8.14	0.89	0.02	2.11	0.87
0.90	0.06	6.53	0.83	0.02	2.66	0.88	0.04	4.95	0.87
0.84	0.03	3.55	0.95	0.04	3.97	0.82	0.02	2.65	0.87
0.80	0.06	7.59	0.91	0.03	3.42	0.91	0.02	1.94	0.87
0.93	0.04	4.31	0.85	0.03	3.96	0.84	0.02	2.68	0.87
0.82	0.04	4.71	0.90	0.04	4.99	0.91	0.06	6.78	0.87
0.94	0.07	7.88	0.83	0.04	4.76	0.87	0.05	6.27	0.88
0.98	0.02	1.64	0.82	0.05	6.28	0.84	0.07	8.16	0.88
0.87	0.07	7.72	#DIV/0!	####	####	0.89	0.07	7.33	0.88
0.99	0.08	7.59	#DIV/0!	####	####	0.78	0.03	4.14	0.88
0.95	0.04	3.80	0.77	0.04	4.95	0.93	0.04	4.18	0.88
0.77	0.04	4.72	0.92	0.10	####	0.97	0.10	9.96	0.89
0.98	0.07	6.73	0.76	0.02	3.07	0.92	0.01	1.58	0.89
0.70	0.02	3.45	1.14	0.04	3.71	0.83	0.05	5.53	0.89

0.76	0.09	###	1.06	0.11	9.96	0.85	0.02	1.91	0.89
0.79	0.02	2.00	0.97	0.03	3.18	0.92	0.03	3.45	0.89
0.97	0.07	7.45	#DIV/0!	####	####	0.83	0.10	###	0.90
0.82	0.04	5.42	0.92	0.03	2.85	0.96	0.04	4.44	0.90
0.85	0.02	2.88	0.90	0.02	2.08	0.96	0.04	4.30	0.90
0.87	0.07	8.57	0.98	0.12	####	0.87	0.07	8.08	0.90
0.90	0.05	5.24	1.01	0.05	4.97	0.81	0.03	3.71	0.91
0.96	0.02	2.29	0.89	0.05	5.42	0.87	0.02	2.02	0.91
0.86	0.04	4.86	0.92	0.04	4.12	0.94	0.04	4.36	0.91
0.84	0.04	5.22	0.90	0.08	8.69	0.99	0.05	4.66	0.91
0.90	0.04	3.99	0.93	0.04	3.83	#DIV/0!	###	###	0.91
0.83	0.03	3.70	0.92	0.05	5.72	1.00	0.04	4.47	0.92
0.80	0.11	###	1.26	0.09	7.08	0.70	0.03	4.82	0.92
0.90	0.02	1.96	1.01	0.04	4.30	0.85	0.04	4.13	0.92
#DIV/0!	####	###	0.89	0.05	5.45	0.95	0.02	1.78	0.92
#DIV/0!	####	###	1.04	0.09	8.41	0.80	0.03	3.90	0.92
0.87	0.04	4.44	0.88	0.03	3.69	1.01	0.11	###	0.92
0.91	0.04	3.96	0.93	0.02	2.68	0.92	0.04	4.17	0.92
1.09	0.10	8.93	0.76	0.08	####	#DIV/0!	###	###	0.92
0.96	0.03	3.52	0.85	0.04	5.01	0.97	0.06	5.89	0.92
1.07	0.06	5.35	0.78	0.04	5.27	#DIV/0!	###	###	0.93
0.81	0.03	3.10	0.86	0.04	4.26	1.11	0.03	2.31	0.93
0.87	0.03	3.41	0.88	0.04	4.77	1.04	0.03	2.89	0.93
0.80	0.07	8.91	0.91	0.05	5.37	1.10	0.07	6.38	0.94
0.96	0.06	6.56	0.92	0.02	2.05	0.93	0.01	1.49	0.94
1.01	0.05	4.80	0.88	0.06	7.33	0.93	0.03	3.19	0.94
0.87	0.05	5.63	0.92	0.03	3.28	1.02	0.01	1.47	0.94
0.96	0.03	2.94	0.96	0.03	2.75	0.90	0.05	5.62	0.94
0.96	0.04	3.80	0.84	0.02	1.88	1.02	0.10	###	0.94
1.09	0.09	8.24	0.85	0.07	7.70	0.89	0.02	1.72	0.94
1.00	0.11	###	0.84	0.02	2.23	0.99	0.04	3.86	0.94
0.75	0.02	2.13	0.99	0.04	4.04	1.08	0.06	5.19	0.94
0.80	0.06	8.00	0.92	0.04	4.58	1.10	0.04	4.04	0.94
0.97	0.05	5.54	0.91	0.02	2.64	#DIV/0!	###	###	0.94
#DIV/0!	####	###	0.97	0.02	2.51	0.92	0.03	2.90	0.95
1.00	0.03	3.35	0.93	0.05	5.00	0.91	0.05	5.85	0.95
0.89	0.02	1.80	0.94	0.02	1.63	1.01	0.02	2.15	0.95
1.02	0.05	4.70	0.85	0.03	3.52	0.98	0.06	6.21	0.95
0.98	0.05	5.41	0.93	0.01	1.43	0.94	0.05	5.70	0.95
0.89	0.02	1.91	0.87	0.05	5.60	1.10	0.03	2.29	0.95
1.00	0.05	4.89	0.91	0.03	3.10	#DIV/0!	###	###	0.95
#DIV/0!	####	###	0.86	0.15	####	1.05	0.14	###	0.96
0.92	0.04	4.33	0.93	0.02	2.13	1.01	0.06	5.43	0.96
0.95	0.02	2.09	1.06	0.06	6.01	0.87	0.07	7.71	0.96
0.85	0.03	3.99	#DIV/0!	####	####	1.08	0.10	9.64	0.96
1.04	0.07	6.80	1.04	0.14	####	0.81	0.06	6.79	0.96
0.83	0.02	2.42	1.18	0.03	2.44	0.90	0.02	2.10	0.97
0.93	0.02	2.41	0.89	0.04	4.39	1.10	0.06	5.42	0.98
0.89	0.03	3.76	1.28	0.05	3.72	0.76	0.07	9.40	0.98
1.01	0.10	###	0.88	0.05	5.52	1.04	0.03	2.50	0.98
1.01	0.02	1.91	0.91	0.03	3.68	1.03	0.04	3.42	0.98
0.92	0.02	2.02	1.03	0.02	2.36	0.99	0.03	3.17	0.98
0.88	0.06	6.77	1.28	0.08	6.31	0.79	0.05	6.43	0.98
1.02	0.11	###	0.92	0.05	5.28	1.02	0.09	8.69	0.99
0.80	0.04	5.57	1.18	0.17	####	#DIV/0!	###	###	0.99
0.82	0.22	###	0.90	0.06	6.32	1.25	0.14	###	0.99
1.10	0.02	1.89	1.00	0.02	2.49	0.87	0.04	4.61	0.99
0.93	0.05	5.43	1.03	0.02	2.31	1.03	0.02	1.66	1.00

1.00	0.04	3.58	1.04	0.04	3.56	0.96	0.03	2.67	1.00
#DIV/0!	####	###	0.99	0.11	####	1.01	0.02	2.25	1.00
0.97	0.02	1.78	1.03	0.04	3.40	1.02	0.05	5.18	1.00
1.10	0.05	4.19	0.91	0.03	3.58	1.01	0.01	1.27	1.01
0.97	0.03	3.03	#DIV/0!	####	####	1.05	0.03	2.73	1.01
0.92	0.01	0.97	1.02	0.06	6.08	1.09	0.02	1.89	1.01
0.86	0.04	5.06	1.07	0.03	2.94	1.12	0.06	4.98	1.02
#DIV/0!	####	###	1.13	0.06	5.23	0.91	0.02	2.73	1.02
1.00	0.06	6.09	1.00	0.05	4.86	1.06	0.04	4.04	1.02
1.08	0.04	3.55	0.90	0.05	5.14	1.07	0.03	3.01	1.02
0.79	0.02	2.83	1.26	0.10	7.55	#DIV/0!	###	###	1.02
0.93	0.03	2.73	#DIV/0!	####	####	1.13	0.05	4.15	1.03
1.04	0.03	2.94	1.16	0.25	####	0.90	0.09	###	1.03
0.84	0.05	5.46	1.25	0.07	5.66	1.01	0.04	3.93	1.03
1.00	0.07	7.27	1.16	0.25	####	0.96	0.09	8.97	1.04
0.77	0.10	###	1.14	0.02	1.67	1.21	0.07	6.01	1.04
1.05	0.05	4.76	1.08	0.06	5.97	0.99	0.03	2.71	1.04
1.09	0.06	5.24	0.95	0.03	3.43	1.09	0.01	0.84	1.04
0.85	0.05	5.56	1.24	0.05	3.65	#DIV/0!	###	###	1.04
1.12	0.03	3.08	1.05	0.04	3.57	0.97	0.03	3.46	1.05
0.97	0.05	4.98	1.01	0.05	4.83	1.16	0.05	4.62	1.05
1.10	0.07	6.76	1.10	0.07	5.96	0.93	0.04	3.94	1.05
0.97	0.06	6.04	1.22	0.08	6.63	0.95	0.11	###	1.05
1.08	0.02	1.99	1.00	0.04	4.28	1.07	0.05	4.46	1.05
0.98	0.01	1.36	1.08	0.01	1.13	1.08	0.04	3.38	1.05
1.03	0.10	9.34	0.94	0.15	####	1.17	0.04	3.32	1.05
0.97	0.01	0.80	1.09	0.06	5.32	1.09	0.05	4.48	1.05
1.03	0.04	3.55	1.00	0.03	3.16	1.12	0.01	1.03	1.05
0.99	0.05	5.34	1.00	0.04	4.21	1.17	0.03	2.51	1.05
1.05	0.06	5.42	1.07	0.03	2.86	1.04	0.04	3.63	1.05
1.11	0.09	8.26	0.97	0.06	5.67	1.09	0.07	6.27	1.06
1.08	0.04	3.73	0.99	0.03	3.00	1.12	0.03	2.53	1.06
1.00	0.04	4.08	1.20	0.02	2.04	0.99	0.04	3.63	1.06
1.10	0.06	5.28	1.04	0.05	4.85	1.05	0.05	4.42	1.06
1.16	0.03	2.73	1.04	0.13	####	1.01	0.11	###	1.07
1.19	0.05	4.37	1.09	0.06	5.24	0.92	0.03	3.44	1.07
1.18	0.02	2.01	#DIV/0!	####	####	0.95	0.05	5.74	1.07
1.17	0.04	3.71	1.04	0.03	2.68	1.00	0.03	3.50	1.07
1.39	0.19	###	0.91	0.06	6.33	0.91	0.03	3.74	1.07
1.14	0.09	8.07	0.97	0.04	3.89	1.11	0.03	2.73	1.07
1.23	0.05	4.22	#DIV/0!	####	####	0.92	0.06	6.87	1.07
0.88	0.03	3.20	1.31	0.04	2.72	1.05	0.04	3.79	1.08
1.00	0.05	4.63	1.22	0.02	1.96	1.01	0.02	1.85	1.08
1.12	0.00	0.23	#DIV/0!	####	####	1.05	0.03	3.21	1.08
1.28	0.02	1.37	0.92	0.12	####	1.06	0.06	5.30	1.09
1.25	0.11	9.10	#DIV/0!	####	####	0.93	0.06	6.64	1.09
1.21	0.08	6.24	1.11	0.13	####	0.95	0.04	4.72	1.09
1.16	0.08	7.07	1.04	0.06	5.58	1.09	0.04	3.96	1.10
1.11	0.09	8.01	#DIV/0!	####	####	1.09	0.14	###	1.10
1.06	0.04	3.99	1.11	0.03	2.74	1.14	0.03	2.91	1.10
1.15	0.03	2.27	1.09	0.07	6.07	1.06	0.02	2.24	1.10
1.00	0.08	7.96	1.04	0.06	5.82	1.26	0.15	###	1.10
1.10	0.19	###	1.04	0.01	1.36	1.17	0.06	5.00	1.10
1.07	0.04	3.89	1.02	0.04	3.92	1.22	0.05	4.38	1.11
1.20	0.07	5.89	0.96	0.05	5.63	1.16	0.04	3.79	1.11
1.15	0.03	2.92	1.12	0.06	5.08	1.06	0.06	5.35	1.11
1.45	0.22	###	#DIV/0!	####	####	0.77	0.05	6.40	1.11
1.24	0.10	8.08	0.98	0.04	4.20	#DIV/0!	###	###	1.11

1.16	0.05	3.91	1.04	0.06	6.13	1.13	0.02	1.50	1.11
1.15	0.03	2.51	1.05	0.02	2.05	1.14	0.04	3.45	1.11
0.90	0.02	2.56	**1.53**	0.04	2.32	0.92	0.03	2.93	1.12
1.13	0.04	3.12	#DIV/0!	####	####	1.11	0.11	9.93	1.12
1.15	0.02	1.91	#DIV/0!	####	####	1.08	0.10	9.40	1.12
#DIV/0!	####	###	1.34	0.07	5.37	0.90	0.07	7.36	1.12
1.02	0.02	1.68	#DIV/0!	####	####	1.21	0.05	4.07	1.12
1.09	0.18	###	1.22	0.24	####	1.06	0.03	2.98	1.12
1.21	0.08	6.69	1.07	0.03	2.74	1.09	0.05	4.42	1.12
1.10	0.11	###	1.15	0.09	7.51	1.12	0.02	1.84	1.12
1.09	0.10	9.17	#DIV/0!	####	####	1.16	0.01	1.18	1.12
1.15	0.02	1.57	1.06	0.06	5.52	1.17	0.04	3.12	1.13
1.12	0.11	9.47	1.10	0.00	0.34	1.17	0.06	4.77	1.13
1.25	0.32	###	1.05	0.18	####	1.10	0.03	3.04	1.13
1.34	0.10	7.18	0.90	0.05	5.74	1.16	0.06	5.04	1.14
1.12	0.04	3.66	1.14	0.07	6.20	1.15	0.00	0.28	1.14
1.13	0.06	5.15	1.10	0.07	5.94	1.19	0.07	5.91	1.14
1.13	0.08	7.33	1.15	0.09	7.48	#DIV/0!	###	###	1.14
1.10	0.13	###	1.07	0.05	4.98	1.26	0.12	9.40	1.14
1.24	0.14	###	#DIV/0!	####	####	1.05	0.07	6.28	1.14
#DIV/0!	####	###	1.27	0.23	####	1.04	0.12	###	1.15
0.93	0.03	2.76	**1.57**	0.05	3.41	0.97	0.03	2.89	1.15
1.07	0.06	5.65	1.17	0.06	5.25	1.23	0.04	3.42	1.16
1.18	0.07	5.98	1.11	0.05	4.64	1.19	0.13	###	1.16
1.58	0.31	###	0.99	0.08	8.50	0.90	0.05	5.27	1.16
1.32	0.09	7.18	#DIV/0!	####	####	1.01	0.03	2.68	1.16
#DIV/0!	####	###	1.15	0.02	1.62	1.19	0.12	9.81	1.17
1.21	0.06	5.29	1.07	0.05	4.60	1.23	0.06	4.93	1.17
1.40	0.06	4.60	0.88	0.04	4.45	1.22	0.08	6.55	1.17
#DIV/0!	####	###	1.07	0.14	####	1.27	0.19	###	1.17
1.17	0.06	4.75	1.18	0.05	4.43	#DIV/0!	###	###	1.17
0.90	0.02	2.20	1.18	0.02	1.74	1.43	0.06	4.41	1.17
1.11	0.06	5.42	1.31	0.05	3.56	1.11	0.02	1.71	1.17
1.16	0.08	6.58	1.28	0.04	3.20	1.09	0.06	5.72	1.18
1.46	0.15	###	1.11	0.01	1.15	0.98	0.02	2.18	1.18
1.41	0.09	6.67	0.90	0.13	####	1.23	0.10	8.49	1.18
#DIV/0!	####	###	1.19	0.16	####	1.18	0.10	8.10	1.18
1.05	0.10	9.46	1.01	0.01	0.80	1.49	0.17	###	1.18
1.28	0.08	6.46	1.27	0.05	3.78	1.01	0.03	3.46	1.19
1.03	0.03	3.01	1.40	0.12	8.81	1.13	0.04	3.86	1.19
1.14	0.06	5.16	1.17	0.06	4.78	1.25	0.04	3.45	1.19
1.22	0.02	1.75	1.17	0.04	3.18	1.19	0.08	7.07	1.20
0.99	0.04	4.47	1.27	0.07	5.47	1.37	0.12	8.46	1.21
1.39	0.10	7.25	1.16	0.04	3.29	1.08	0.09	8.30	1.21
1.14	0.07	6.34	1.11	0.02	1.54	1.39	0.13	9.13	1.21
0.95	0.06	6.19	**1.58**	0.13	7.93	1.10	0.05	4.91	1.21
1.24	0.06	4.99	1.05	0.11	####	1.34	0.12	9.13	1.21
1.33	0.07	5.46	1.14	0.05	4.00	1.17	0.07	5.74	1.21
1.45	0.10	6.84	1.05	0.13	####	1.14	0.05	4.80	1.21
#DIV/0!	####	###	1.19	0.12	9.86	1.24	0.02	1.44	1.22
1.03	0.07	6.54	1.49	0.10	6.96	1.13	0.03	2.26	1.22
1.20	0.17	###	#DIV/0!	####	####	1.24	0.05	4.42	1.22
1.23	0.09	7.11	1.23	0.03	2.39	1.20	0.02	1.49	1.22
1.02	0.04	4.13	**1.50**	0.09	5.69	1.15	0.02	2.15	1.22
1.46	0.08	5.75	1.14	0.05	4.11	1.07	0.02	2.28	1.22
1.45	0.04	3.04	1.07	0.03	2.54	1.17	0.03	2.85	1.23
1.12	0.12	###	1.14	0.05	4.57	1.43	0.06	4.27	1.23
1.43	0.09	6.44	1.16	0.16	####	1.11	0.13	###	1.23

1.24	0.06	4.99	1.16	0.07	5.97	1.32	0.04	2.87	1.24
1.25	0.04	2.93	1.22	0.08	6.54	1.25	0.02	1.99	1.24
1.12	0.06	5.42	1.33	0.14	####	1.27	0.28	###	1.24
1.60	0.09	5.68	1.19	0.09	7.22	0.94	0.01	1.48	1.24
1.15	0.05	4.66	1.34	0.10	7.15	1.24	0.06	4.84	1.24
1.35	0.06	4.44	1.13	0.05	4.52	1.25	0.07	5.61	1.24
#DIV/0!	####	###	1.24	0.09	7.56	1.27	0.09	6.81	1.25
#DIV/0!	####	###	1.24	0.06	4.57	1.27	0.09	7.26	1.25
1.15	0.06	5.51	1.37	0.03	1.90	1.25	0.02	1.26	1.26
1.04	0.11	###	1.00	0.01	1.20	**1.74**	0.21	###	1.26
1.29	0.17	###	1.25	0.09	6.85	#DIV/0!	###	###	1.27
1.55	0.23	###	1.11	0.03	2.84	1.15	0.03	2.80	1.27
1.28	0.09	6.83	1.23	0.05	3.74	1.30	0.06	4.59	1.27
1.26	0.04	2.97	1.21	0.06	4.71	1.36	0.06	4.71	1.28
1.40	0.12	8.41	#DIV/0!	####	####	1.16	0.05	4.29	1.28
1.26	0.03	2.55	1.34	0.03	1.95	1.26	0.02	1.81	1.28
#DIV/0!	####	###	1.34	0.13	9.44	1.23	0.06	4.98	1.29
1.16	0.14	###	#DIV/0!	####	####	1.42	0.06	4.49	1.29
1.28	0.05	3.57	1.34	0.03	2.37	1.30	0.05	3.74	1.30
1.60	0.04	2.73	1.25	0.09	7.33	1.08	0.03	3.07	1.31
1.38	0.02	1.48	1.30	0.06	4.81	1.26	0.05	4.20	1.31
#DIV/0!	####	###	1.30	0.04	3.39	1.33	0.05	3.65	1.32
1.33	0.03	2.46	1.32	0.06	4.28	1.31	0.08	6.24	1.32
1.00	0.03	2.83	**1.87**	0.06	3.36	1.09	0.02	1.76	1.32
1.59	0.17	###	1.48	0.12	8.00	0.89	0.03	3.85	1.32
1.22	0.04	3.51	1.34	0.10	7.52	1.46	0.14	9.55	1.34
1.19	0.07	6.23	#DIV/0!	####	####	1.49	0.08	5.44	1.34
1.27	0.22	###	**1.59**	0.07	4.45	1.19	0.05	4.18	1.35
1.64	0.10	5.95	#DIV/0!	####	####	1.07	0.06	5.67	1.36
1.48	0.06	4.39	1.25	0.08	6.12	1.34	0.10	7.74	1.36
1.53	0.07	4.43	1.23	0.03	2.16	1.34	0.03	2.50	1.37
#DIV/0!	####	###	**1.51**	0.13	8.71	1.24	0.04	3.00	1.37
1.30	0.03	2.65	1.34	0.02	1.47	1.48	0.03	2.12	1.38
1.46	0.09	6.01	1.35	0.04	2.76	1.32	0.09	6.52	1.38
1.48	0.06	4.35	1.27	0.03	2.25	1.38	0.03	1.86	1.38
1.63	0.12	7.44	**1.85**	0.06	3.32	**0.65**	0.05	8.02	1.38
1.56	0.06	4.06	1.31	0.04	2.72	1.27	0.01	1.02	1.38
1.62	0.11	6.53	0.82	0.07	8.55	**1.69**	0.04	2.27	1.38
1.46	0.06	3.99	1.45	0.06	4.02	1.24	0.02	1.76	1.38
1.39	0.06	4.51	1.34	0.04	3.06	1.42	0.05	3.39	1.38
1.27	0.07	5.90	**1.51**	0.11	7.32	1.40	0.02	1.60	1.40
#DIV/0!	####	###	**1.71**	0.25	####	1.10	0.04	3.34	1.40
1.72	0.17	9.72	#DIV/0!	####	####	1.09	0.10	9.08	1.40
1.60	0.26	###	1.27	0.08	6.49	1.37	0.04	3.06	1.41
1.35	0.07	4.87	1.36	0.10	7.31	**1.54**	0.09	5.63	1.42
1.48	0.08	5.20	1.35	0.06	4.19	1.42	0.10	6.88	1.42
1.46	0.07	4.48	1.21	0.06	4.66	**1.61**	0.04	2.33	1.43
1.79	0.13	7.43	1.29	0.05	4.02	1.20	0.06	4.73	1.43
1.70	0.06	3.52	1.49	0.07	4.38	1.14	0.05	4.57	1.44
1.29	0.09	6.63	1.26	0.03	2.59	**1.83**	0.18	9.90	1.46
1.48	0.09	5.82	#DIV/0!	####	####	1.46	0.12	8.40	1.47
1.58	0.08	5.29	**1.65**	0.05	2.90	1.18	0.08	6.52	1.47

1.61	0.15	9.61	**1.53**	0.11	7.06	1.29	0.07	5.18	1.48
1.62	0.34	###	#DIV/0!	####	####	1.42	0.05	3.58	**1.52**
2.05	0.13	6.19	**1.53**	0.04	2.88	1.13	0.03	2.28	**1.57**
1.32	0.04	3.28	**1.85**	0.04	2.01	**1.56**	0.05	3.41	**1.58**
2.45	0.27	###	**1.87**	0.16	8.49	**0.57**	0.05	9.54	**1.63**
2.32	0.20	8.82	1.27	0.08	6.19	1.37	0.11	7.90	**1.65**
2.47	0.29	###	1.25	0.07	5.88	1.26	0.07	5.76	**1.66**
1.85	0.27	###	1.49	0.12	8.35	**1.93**	0.22	###	**1.76**
2.45	0.22	8.94	**1.59**	0.06	3.57	1.31	0.11	8.64	**1.78**
2.47	0.16	6.40	1.46	0.04	3.07	**1.60**	0.05	3.25	**1.84**
8.77	3.96	###	#DIV/0!	####	####	1.49	0.09	6.16	**5.13**
0.33	0.01	2.91	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
0.67	0.22	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
0.68	0.01	1.10	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
0.73	0.05	6.59	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
0.75	0.04	5.02	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
0.81	0.03	3.88	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
0.82	0.15	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
0.82	0.04	5.33	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
0.82	0.06	7.32	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
0.96	0.04	4.28	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
0.98	0.07	7.29	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.02	0.08	7.44	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.03	0.04	3.98	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.03	0.09	8.58	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.05	0.16	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.10	0.08	7.27	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.13	0.05	4.28	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.13	0.27	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.14	0.22	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.15	0.06	4.82	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.16	0.09	7.68	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.16	0.08	6.76	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.19	0.19	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.21	0.06	5.16	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.25	0.01	0.60	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.25	0.02	1.39	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.25	0.15	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.26	0.18	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.29	0.26	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.29	0.03	1.96	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.31	0.09	6.78	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.32	0.22	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.34	0.31	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.36	0.21	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.36	0.07	5.13	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.39	0.05	3.50	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.43	0.02	1.71	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.47	0.13	9.08	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.48	0.15	9.94	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.51	0.09	6.27	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.59	0.20	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.61	0.12	7.24	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.68	0.35	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
1.70	0.22	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
2.31	0.52	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!

4.82	0.70	###	#DIV/0!	####	####	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	**0.49**	0.05	9.78	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	**0.50**	0.03	6.70	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	**0.65**	0.02	3.67	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	**0.65**	0.05	7.23	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	0.77	0.02	2.09	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	0.78	0.01	1.86	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	0.85	0.15	####	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	0.95	0.03	3.06	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	1.05	0.05	4.65	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	1.05	0.22	####	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	1.11	0.03	2.82	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	1.14	0.04	3.61	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	1.28	0.20	####	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	1.46	0.09	6.43	#DIV/0!	###	###	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.03	0.02	1.91	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.07	0.12	###	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.99	0.08	7.77	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.26	0.11	8.89	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.11	0.12	###	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.28	0.16	###	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.96	0.06	5.77	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.82	0.01	1.34	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.78	0.08	9.78	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	**1.63**	0.15	8.90	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.86	0.02	1.99	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.01	0.09	8.97	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.21	0.11	9.06	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.87	0.05	5.92	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.03	0.05	5.27	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.06	0.03	2.65	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.13	0.02	1.35	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.68	0.03	4.72	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.09	0.04	3.43	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.98	0.16	###	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.08	0.05	4.59	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.25	0.12	9.90	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	**1.51**	0.01	0.46	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.79	0.05	6.65	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.37	0.17	###	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	**0.63**	0.01	2.37	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.38	0.04	2.97	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.99	0.04	3.95	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.78	0.09	###	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.77	0.02	2.86	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.25	0.11	8.71	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	**1.51**	0.08	5.03	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	**1.89**	0.44	###	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.04	0.03	2.70	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	**0.56**	0.09	###	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.06	0.05	4.77	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.77	0.06	7.42	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.18	0.07	6.14	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.39	0.12	8.76	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.16	0.05	4.43	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.03	0.10	9.95	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.07	0.15	###	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.07	0.08	7.51	#DIV/0!

#DIV/0!	####	###	#DIV/0!	####	####	1.36	0.11	8.45	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.82	0.07	8.68	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.27	0.06	4.53	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.89	0.06	7.02	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	**1.54**	0.03	2.17	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.76	0.02	3.05	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.02	0.07	6.64	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.20	0.29	###	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	1.24	0.05	3.72	#DIV/0!
#DIV/0!	####	###	#DIV/0!	####	####	0.95	0.03	3.39	#DIV/0!

SD delle Medie (I/NI)	CV% delle Medie (I/NI)
0.04	9.8
0.05	9.8
0.06	12.4
0.07	12.4
0.03	6.1
0.04	7.8
0.14	24.4
0.16	27.8
0.07	12.6
0.08	13.6
0.32	53.4
0.05	7.7
0.05	8.4
0.08	13.1
0.06	10.0
0.01	1.2
0.07	11.6
0.06	9.2
0.04	6.4
0.11	16.4
0.09	13.3
0.07	9.8
0.05	7.5
0.08	10.8
0.03	4.7
0.05	7.6
0.03	4.8
0.20	28.6
0.01	1.1
0.24	33.3
0.03	4.5
0.06	7.6
0.02	2.5
0.11	15.3
0.12	16.1
0.11	15.2
0.06	7.9
0.04	5.8
0.06	8.2
0.05	6.7
0.07	8.9
0.13	17.0
0.13	17.2
0.04	5.0
0.34	45.0
0.05	6.2
0.10	12.5
0.11	14.8
0.07	9.4

0.03	3.3
0.05	6.4
0.05	6.1
0.03	3.2
0.04	4.6
0.09	11.4
0.02	2.6
0.04	5.5
0.06	7.6
0.09	11.4
0.03	4.1
0.03	3.3
0.04	4.6
0.08	10.2
0.07	8.8
0.12	14.8
0.16	19.8
0.04	5.3
0.23	27.6
0.07	8.3
0.06	7.0
0.14	17.2
0.11	13.1
0.17	20.5
0.07	8.9
0.07	8.0
0.10	11.7
0.03	4.0
0.07	7.8
0.08	9.9
0.07	8.3
0.16	18.6
0.09	10.4
0.19	21.8
0.08	9.3
0.16	18.3
0.00	0.6
0.08	9.7
0.06	6.5
0.04	5.0
0.10	11.3
0.06	7.1
0.07	8.2
0.12	13.6
0.03	3.1
0.03	4.0
0.07	7.8
0.06	6.8
0.05	5.3
0.05	5.7
0.05	6.1
0.09	9.8
0.01	1.6
0.15	17.2
0.10	11.3
0.11	12.0
0.11	12.6
0.23	25.8

0.16	17.5
0.09	10.6
0.09	10.3
0.07	8.0
0.06	6.2
0.06	7.0
0.10	11.1
0.05	5.4
0.05	5.0
0.08	8.3
0.03	2.8
0.09	9.3
0.30	32.7
0.08	8.6
0.04	4.7
0.17	18.0
0.08	8.6
0.01	1.1
0.23	24.8
0.07	7.0
0.20	22.1
0.16	17.0
0.09	9.9
0.15	16.5
0.02	2.0
0.07	7.1
0.08	8.2
0.04	4.0
0.09	9.7
0.13	13.9
0.09	9.0
0.17	18.3
0.15	16.0
0.04	4.4
0.03	3.1
0.05	5.2
0.06	6.4
0.09	9.5
0.03	2.9
0.13	13.3
0.06	6.3
0.14	14.4
0.05	5.3
0.10	10.2
0.16	16.5
0.13	13.5
0.19	19.2
0.11	11.2
0.27	28.0
0.08	8.5
0.06	6.3
0.06	6.2
0.26	26.7
0.06	6.1
0.27	27.5
0.23	23.1
0.12	11.9
0.06	6.1

0.04	4.1
0.01	1.2
0.03	3.4
0.10	9.5
0.06	6.2
0.08	8.3
0.14	13.5
0.16	15.6
0.03	3.4
0.10	9.8
0.34	32.8
0.14	13.6
0.13	12.3
0.21	19.9
0.11	10.2
0.24	22.6
0.05	4.6
0.08	7.7
0.28	26.7
0.07	7.0
0.10	9.9
0.10	9.3
0.15	14.3
0.04	4.0
0.06	5.6
0.11	10.9
0.07	6.7
0.07	6.2
0.10	9.4
0.01	1.0
0.07	7.0
0.07	6.2
0.12	10.9
0.03	2.8
0.08	7.4
0.14	12.8
0.16	15.3
0.09	8.4
0.28	26.1
0.09	8.1
0.22	20.3
0.21	19.9
0.12	11.4
0.05	5.1
0.18	16.9
0.23	21.1
0.13	12.2
0.06	5.7
0.01	0.9
0.04	3.6
0.04	3.8
0.14	12.7
0.07	6.0
0.10	9.3
0.13	11.6
0.05	4.2
0.48	43.4
0.19	16.9

0.06	5.8
0.05	4.7
0.36	32.2
0.01	1.3
0.05	4.7
0.31	27.6
0.13	11.8
0.08	7.4
0.07	6.6
0.03	2.3
0.05	4.4
0.06	5.3
0.04	3.5
0.10	9.1
0.22	19.4
0.02	1.7
0.04	3.8
0.01	1.3
0.10	8.8
0.13	11.7
0.16	14.2
0.36	31.1
0.08	7.0
0.04	3.6
0.37	31.7
0.22	19.0
0.03	2.3
0.09	7.6
0.26	22.6
0.14	12.3
0.00	0.4
0.27	22.7
0.12	9.9
0.10	8.4
0.25	21.0
0.26	21.9
0.00	0.2
0.26	22.3
0.16	13.1
0.19	15.9
0.06	5.0
0.02	2.0
0.20	16.2
0.16	13.1
0.15	12.8
0.33	27.2
0.15	12.2
0.10	8.3
0.21	17.7
0.03	2.7
0.24	19.6
0.03	2.2
0.02	1.4
0.25	20.4
0.21	17.3
0.20	16.1
0.17	14.0
0.17	14.1

0.08	6.8
0.02	1.6
0.11	9.0
0.34	27.1
0.09	7.3
0.11	8.8
0.02	1.9
0.03	2.1
0.11	8.4
0.42	33.1
0.03	2.4
0.24	19.2
0.03	2.7
0.08	6.0
0.17	13.1
0.04	3.4
0.07	5.5
0.18	14.2
0.03	2.3
0.27	20.5
0.06	4.8
0.03	2.0
0.01	0.8
0.48	36.0
0.37	28.3
0.12	9.2
0.22	16.2
0.21	15.9
0.40	29.6
0.11	8.2
0.15	11.2
0.19	13.6
0.09	6.5
0.07	5.4
0.11	7.8
0.64	46.3
0.16	11.5
0.48	35.0
0.12	9.0
0.04	2.9
0.12	8.8
0.43	30.4
0.45	32.1
0.17	12.0
0.11	7.6
0.06	4.4
0.20	14.0
0.32	22.4
0.28	19.4
0.32	22.0
0.01	1.0
0.25	17.2

0.17	11.3
0.14	9.0
0.46	29.4
0.26	16.7
0.96	59.2
0.58	35.0
0.70	42.2
0.23	13.3
0.60	33.4
0.55	29.6
5.14	100.3
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E7ET40	Urokinase-type plasminogen activator chain B OS=Homo sapiens G	**0.354**	**0.329**	**0.361**
O60462-4	Isoform B0 of Neuropilin-2 OS=Homo sapiens GN=NRP2 - [NRP2_H	0.888	0.937	0.966
O14792	Heparan sulfate glucosamine 3-O-sulfotransferase 1 OS=Homo sap	0.561	0.600	0.520
P05121	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1	**0.523**	**0.546**	**0.590**
P17301	Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1 - [ITA2	0.967	0.897	0.923
P13010	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=	0.664	0.662	0.643
P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=	2.595	2.715	2.387
B4E2J3	Serine protease 23 OS=Homo sapiens GN=PRSS23 PE=2 SV=1 - [B	0.530	0.558	0.531
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HU	**0.561**	**0.561**	**0.599**
Q15262	Receptor-type tyrosine-protein phosphatase kappa OS=Homo sapie	0.692	0.700	0.750
P52823	Stanniocalcin-1 OS=Homo sapiens GN=STC1 PE=1 SV=1 - [STC1_	0.475	0.469	0.475
D6RIU4	Vesicular integral-membrane protein VIP36 (Fragment) OS=Homo	0.766	0.737	0.770
O95150-2	Isoform 2 of Tumor necrosis factor ligand superfamily member 15	0.399	0.387	0.392
C9JIM8	Solute carrier family 2, facilitated glucose transporter member 1 (Fragment) OS=Homo sapiens GN=SLC2A1 PE=2 SV=1 -			
Q7LFX5	Carbohydrate sulfotransferase 15 OS=Homo sapiens GN=CHST15	0.592	0.621	0.529
P98155-2	Isoform Short of Very low-density lipoprotein receptor OS=Homo sapiens GN=VLDLR - [VLDLR_HUMAN]			
Q96QC4	MHC class I polypeptide-related sequence A OS=Homo sapiens GN=	0.851	0.870	0.794
Q4G148-2	Isoform 2 of Glucoside xylosyltransferase 1 OS=Homo sapiens GN=GXYLT1 - [GXLT1_HUMAN]			
P08294	Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=	**0.569**	**0.599**	**0.630**
P09603	Macrophage colony-stimulating factor 1 OS=Homo sapiens GN=CS	0.675	0.611	0.662
H0YN42	Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=2 SV=1 - [	0.770	0.825	0.767
P52799	Ephrin-B2 OS=Homo sapiens GN=EFNB2 PE=1 SV=1 - [EFNB2_HUMAN]			
Q8N441	Fibroblast growth factor receptor-like 1 OS=Homo sapiens GN=FG	0.753	0.805	0.803
P26006	Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5 - [ITA3	0.727	0.894	0.652
P32004-3	Isoform 3 of Neural cell adhesion molecule L1 OS=Homo sapiens G	0.848	0.708	0.927
Q03405	Urokinase plasminogen activator surface receptor OS=Homo sapien	0.469	0.467	0.466
Q99538	Legumain OS=Homo sapiens GN=LGMN PE=1 SV=1 - [LGMN_HUM	0.557	0.571	0.503
P23352	Anosmin-1 OS=Homo sapiens GN=KAL1 PE=1 SV=3 - [KALM_HUM	0.913	1.064	0.759
P07602	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2 -	**0.666**	0.703	0.693
Q86SR1	Polypeptide N-acetylgalactosaminyltransferase 10 OS=Homo sapien	0.644	0.668	0.586
P28799	Granulins OS=Homo sapiens GN=GRN PE=1 SV=2 - [GRN_HUMAN]	0.725	0.763	0.633
Q8N2Q7-2	Isoform 2 of Neuroligin-1 OS=Homo sapiens GN=NLGN1 - [NLGN1_HUMAN]			
O75629	Protein CREG1 OS=Homo sapiens GN=CREG1 PE=1 SV=1 - [CREG	0.645	0.686	0.642
P05067-7	Isoform L-APP733 of Amyloid beta A4 protein OS=Homo sapiens G	0.717	0.664	0.766
P05556-2	Isoform Beta-1B of Integrin beta-1 OS=Homo sapiens GN=ITGB1 - [ITB1_HUMAN]			
P48745	Protein NOV homolog OS=Homo sapiens GN=NOV PE=1 SV=1 - [N	0.725	0.694	0.716
J3KMY5	Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=4	0.778	0.740	0.936
Q02297-8	Isoform 8 of Pro-neuregulin-1, membrane-bound isoform OS=Hom	0.606	0.559	0.743
Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sap	0.841	0.738	0.940
P20908	Collagen alpha-1(V) chain OS=Homo sapiens GN=COL5A1 PE=1 S	0.633	0.565	0.683
P35625	Metalloproteinase inhibitor 3 OS=Homo sapiens GN=TIMP3 PE=1 S	0.768	0.794	0.721
P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1	1.788	1.674	1.551
Q8NES3	Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe OS=Homo	0.813	0.755	0.907
Q8NCC3	Group XV phospholipase A2 OS=Homo sapiens GN=PLA2G15 PE=1	1.000	0.922	0.934
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2 - [	0.519	0.511	0.575
Q13740-2	Isoform 2 of CD166 antigen OS=Homo sapiens GN=ALCAM - [CD1	0.798	0.728	0.857
Q9NPF2-2	Isoform 2 of Carbohydrate sulfotransferase 11 OS=Homo sapiens	0.863	0.929	0.964
P22413	Ectonucleotide pyrophosphatase/phosphodiesterase family member	0.673	0.722	0.700
P48723	Heat shock 70 kDa protein 13 OS=Homo sapiens GN=HSPA13 PE=	0.732	0.793	0.730
J3KQG4	Glucosylceramidase OS=Homo sapiens GN=GBA PE=4 SV=1 - [J3K	0.599	0.589	0.576
E9PFD9	Semaphorin-4D OS=Homo sapiens GN=SEMA4D PE=4 SV=1 - [E9PFD9_HUMAN]			
P19021-4	Isoform 4 of Peptidyl-glycine alpha-amidating monooxygenase OS=	0.852	0.822	0.780
Q11201	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltrans	1.633	1.649	1.251

F5H826	Nodal modulator 3 OS=Homo sapiens GN=NOMO3 PE=2 SV=1 - [F5H826_HUMAN]			
Q16769	Glutaminyl-peptide cyclotransferase OS=Homo sapiens GN=QPCT P	0.696	0.703	0.727
Q5H9A7	Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=2 S	0.779	0.762	0.825
O43286	Beta-1,4-galactosyltransferase 5 OS=Homo sapiens GN=B4GALT5 PE=2 SV=1 - [B4GT5_HUMAN]			
Q9NZV1	Cysteine-rich motor neuron 1 protein OS=Homo sapiens GN=CRIM1	0.949	0.896	0.858
P24592	Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=	0.858	0.893	0.932
Q92820	Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=	0.704	0.725	0.771
P09668	Pro-cathepsin H OS=Homo sapiens GN=CTSH PE=1 SV=4 - [CATH_	0.797	0.775	0.769
Q86SJ2	Amphoterin-induced protein 2 OS=Homo sapiens GN=AMIGO2 PE=	0.731	0.658	0.670
Q9NPR2-2	Isoform 2 of Semaphorin-4B OS=Homo sapiens GN=SEMA4B - [SE	0.799	0.744	0.808
P15291-2	Isoform Short of Beta-1,4-galactosyltransferase 1 OS=Homo sapien	0.860	0.666	0.914
Q8NBP7	Proprotein convertase subtilisin/kexin type 9 OS=Homo sapiens GN	0.675	0.698	0.660
F5GZ08	Amyloid-like protein 1 OS=Homo sapiens GN=APLP1 PE=2 SV=1 -	1.080	1.121	0.910
E7EPS8	Receptor-type tyrosine-protein phosphatase mu OS=Homo sapiens	0.909	0.921	0.896
P29279	Connective tissue growth factor OS=Homo sapiens GN=CTGF PE=1	0.694	0.686	0.710
P52803	Ephrin-A5 OS=Homo sapiens GN=EFNA5 PE=1 SV=1 - [EFNA5_HUMAN]			
P06280	Alpha-galactosidase A OS=Homo sapiens GN=GLA PE=1 SV=1 - [A	0.819	0.735	0.771
O75197	Low-density lipoprotein receptor-related protein 5 OS=Homo sapiens GN=LRP5 PE=1 SV=2 - [LRP5_HUMAN]			
Q9Y2E5	Epididymis-specific alpha-mannosidase OS=Homo sapiens GN=MAN	0.802	0.841	0.791
Q9Y5G3-2	Isoform 2 of Protocadherin gamma-B1 OS=Homo sapiens GN=PCDHGB1 - [PCDGD_HUMAN]			
O94985-2	Isoform 2 of Calsyntenin-1 OS=Homo sapiens GN=CLSTN1 - [CSTN	0.846	0.820	0.811
Q96PX8	SLIT and NTRK-like protein 1 OS=Homo sapiens GN=SLITRK1 PE=1	0.776	0.848	0.671
Q02742	Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase OS=Homo sapiens GN=GCNT1 PE=			
Q9Y662	Heparan sulfate glucosamine 3-O-sulfotransferase 3B1 OS=Homo sapiens GN=HS3ST3B1 PE=1 SV=1 - [HS3SB_HUMAN]			
Q13332-6	Isoform 2 of Receptor-type tyrosine-protein phosphatase S OS=Homo sapiens GN=PTPRS - [PTPRS_HUMAN]			
O14657	Torsin-1B OS=Homo sapiens GN=TOR1B PE=1 SV=2 - [TOR1B_HU	0.916	1.040	0.937
Q96B60	5'-nucleotidase OS=Homo sapiens GN=NT5E PE=2 SV=1 - [Q96B6	0.851	0.989	0.785
O00300	Tumor necrosis factor receptor superfamily member 11B OS=Homo	1.012	0.930	0.822
Q02818	Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4 - [NUCB	1.043	1.010	0.918
Q9Y6N7-6	Isoform 6 of Roundabout homolog 1 OS=Homo sapiens GN=ROBO1	0.819	0.883	0.849
Q13253	Noggin OS=Homo sapiens GN=NOG PE=1 SV=1 - [NOGG_HUMAN]	0.798	0.778	0.770
Q16270-2	Isoform 2 of Insulin-like growth factor-binding protein 7 OS=Homo	0.684	**0.637**	0.720
P16870-2	Isoform 2 of Carboxypeptidase E OS=Homo sapiens GN=CPE - [CB	0.711	0.709	0.698
B0YJC4	Vimentin OS=Homo sapiens GN=VIM PE=2 SV=1 - [B0YJC4_HUMA	0.890	0.955	0.894
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapie	0.983	0.990	1.052
P42785	Lysosomal Pro-X carboxypeptidase OS=Homo sapiens GN=PRCP PE	0.613	0.620	0.617
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HU	0.922	0.837	0.947
Q14393-2	Isoform 2 of Growth arrest-specific protein 6 OS=Homo sapiens GN	0.756	0.752	0.718
Q92743	Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1	0.802	0.852	0.769
E9PG71	Ephrin type-A receptor 4 OS=Homo sapiens GN=EPHA4 PE=2 SV=	0.687	0.607	0.729
Q9NY97-2	Isoform 2 of UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltra	0.740	0.735	0.696
Q9GZP0	Platelet-derived growth factor D OS=Homo sapiens GN=PDGFD PE=	0.978	0.979	0.921
Q9Y4K0	Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1	0.901	0.841	0.956
Q92692-2	Isoform Alpha of Poliovirus receptor-related protein 2 OS=Homo sa	0.868	0.954	0.779
P01892	HLA class I histocompatibility antigen, A-2 alpha chain OS=Homo sa	0.980	1.004	0.966
P51884	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2 - [LUM_HUMAN]	0.804	0.809	0.659
Q99574	Neuroserpin OS=Homo sapiens GN=SERPINI1 PE=1 SV=1 - [NEUS	0.772	0.746	0.724
P12109	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 S	0.843	0.942	0.948
P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1	1.833	1.594	1.488
Q10469	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransf	0.990	0.937	0.966
B4E351	Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=	0.681	0.624	0.750
Q99523	Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3 - [SORT_HUMA	0.876	0.774	0.742
Q14126	Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2 - [DSG2_H	0.921	0.990	0.847
Q06481	Amyloid-like protein 2 OS=Homo sapiens GN=APLP2 PE=1 SV=2 -	0.726	0.681	0.703

P10619	Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV	0.740	0.719	0.748
P19883-2	Isoform 2 of Follistatin OS=Homo sapiens GN=FST - [FST_HUMAN]	0.873	0.913	0.906
P13284	Gamma-interferon-inducible lysosomal thiol reductase OS=Homo sa	0.992	1.114	0.964
Q92187	CMP-N-acetylneuraminate-poly-alpha-2,8-sialyltransferase OS=Hom	0.579	0.536	0.562
P07093-2	Isoform 2 of Glia-derived nexin OS=Homo sapiens GN=SERPINE2 -	0.960	0.837	0.942
P49767	Vascular endothelial growth factor C OS=Homo sapiens GN=VEGFC	0.928	0.928	0.960
Q24JP5	Transmembrane protein 132A OS=Homo sapiens GN=TMEM132A P	1.228	1.134	1.408
F5H325	N-acetylgalactosamine-6-sulfatase OS=Homo sapiens GN=GALNS P	0.841	0.768	0.855
H0YN65	Carbohydrate sulfotransferase 14 OS=Homo sapiens GN=CHST14 PE=2 SV=1 - [H0YN65_HUMAN]			
Q13308-5	Isoform 5 of Inactive tyrosine-protein kinase 7 OS=Homo sapiens G	0.887	0.848	0.910
P10646	Tissue factor pathway inhibitor OS=Homo sapiens GN=TFPI PE=1 S	1.268	1.173	1.177
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUN	0.695	0.674	0.728
P54803-4	Isoform 4 of Galactocerebrosidase OS=Homo sapiens GN=GALC - [	0.992	0.914	0.977
P43121	Cell surface glycoprotein MUC18 OS=Homo sapiens GN=MCAM PE=	1.053	1.227	1.038
P50897	Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1	0.666	0.627	0.626
F8W1Q3	Biotinidase OS=Homo sapiens GN=BTD PE=2 SV=1 - [F8W1Q3_HU	0.918	0.872	0.960
O15230	Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	1.079	1.104	1.130
F5GZK1	Processed exostosin-like 2 OS=Homo sapiens GN=EXTL2 PE=2 SV=	0.940	1.019	1.050
E9PMD7	Serine/threonine-protein phosphatase (Fragment) OS=Homo sapien	1.288	1.191	1.259
Q99519	Sialidase-1 OS=Homo sapiens GN=NEU1 PE=1 SV=1 - [NEUR1_HU	0.813	0.814	0.928
Q14703	Membrane-bound transcription factor site-1 protease OS=Homo sap	0.866	0.880	0.863
Q9UBG0	C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2 - [MRC2_HUMAN]			
H3BS10	Beta-hexosaminidase OS=Homo sapiens GN=HEXA PE=2 SV=1 - [H	0.801	0.871	0.770
D6RHI9	Ribonuclease T2 (Fragment) OS=Homo sapiens GN=RNASET2 PE=	0.756	0.806	0.811
P55058-3	Isoform 3 of Phospholipid transfer protein OS=Homo sapiens GN=P	0.709	0.812	0.661
Q9GZM7-3	Isoform 3 of Tubulointerstitial nephritis antigen-like OS=Homo sapi	0.884	0.988	1.034
P00750	Tissue-type plasminogen activator OS=Homo sapiens GN=PLAT PE=	0.822	0.804	0.843
P98160	Basement membrane-specific heparan sulfate proteoglycan core pro	1.622	1.721	1.532
Q8NFZ8	Cell adhesion molecule 4 OS=Homo sapiens GN=CADM4 PE=1 SV=1 - [CADM4_HUMAN]			
P08648	Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2 - [ITA5_HUMAN]			
H0Y9C7	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase (Fragment) OS=H	0.889	0.968	0.803
P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB	1.468	1.126	**1.584**
O75509	Tumor necrosis factor receptor superfamily member 21 OS=Homo s	0.824	0.874	0.730
Q01459	Di-N-acetylchitobiase OS=Homo sapiens GN=CTBS PE=1 SV=1 - [D	0.771	0.780	0.806
O75503	Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens GN=CLN	0.755	0.729	0.766
P55287-2	Isoform 2 of Cadherin-11 OS=Homo sapiens GN=CDH11 - [CAD11_	0.874	0.862	0.845
P11362-13	Isoform 13 of Fibroblast growth factor receptor 1 OS=Homo sapiens GN=FGFR1 - [FGFR1_HUMAN]			
P00736	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1	1.041	0.925	0.972
P04066	Tissue alpha-L-fucosidase OS=Homo sapiens GN=FUCA1 PE=1 SV=	0.674	0.646	0.678
J3KNQ3	26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=4 SV=1 - [J3KNQ3_HUMAN]			
Q9BTY2	Plasma alpha-L-fucosidase OS=Homo sapiens GN=FUCA2 PE=1 SV	0.806	0.777	0.882
P07996	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2 - [TS	0.901	0.877	0.930
C9JRG3	Aspartyl aminopeptidase (Fragment) OS=Homo sapiens GN=DNPEP	1.840	1.298	1.866
P62906	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 S	1.279	1.268	1.187
Q13219	Pappalysin-1 OS=Homo sapiens GN=PAPPA PE=1 SV=3 - [PAPP1_HUMAN]			
B4DKB2	Endothelin-converting enzyme 1 OS=Homo sapiens GN=ECE1 PE=2	0.948	0.975	0.956
P08603	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4 - [CF	0.901	0.907	0.954
H3BLV0	Complement decay-accelerating factor (Fragment) OS=Homo sapie	1.032	1.028	0.943
Q68CR9	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DKFZp7	1.197	1.165	1.042
Q8WZ75-2	Isoform 2 of Roundabout homolog 4 OS=Homo sapiens GN=ROBO4	0.860	0.858	0.853
F5H6A3	N-sulphoglucosamine sulphohydrolase OS=Homo sapiens GN=SGSH	1.041	1.073	1.040
P38571-2	Isoform 2 of Lysosomal acid lipase/cholesteryl ester hydrolase OS=	0.825	0.770	0.821
P50895	Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2 - [BCAM_HUMAN]			
O43854-2	Isoform 2 of EGF-like repeat and discoidin I-like domain-containing	0.859	0.818	0.899

D6RF62	Phosphoribosylaminoimidazole carboxylase OS=Homo sapiens GN=PAICS PE=2 SV=1 - [D6RF62_HUMAN]			
Q9GZX9	Twisted gastrulation protein homolog 1 OS=Homo sapiens GN=TW	0.637	0.623	0.648
C9JP16	Cartilage-associated protein OS=Homo sapiens GN=CRTAP PE=2 SV=1 - [C9JP16_HUMAN]			
E7EUT4;P04406-2	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN	1.577	1.594	1.355
Q9Y696	Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 - [CLIC4_HUMAN]			
B3KVK7	Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=2 SV=1 - [B3KVK7_HUMAN]			
Q9H3G5	Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPV	0.752	0.726	0.782
J3QSU6	Tenascin OS=Homo sapiens GN=TNC PE=4 SV=1 - [J3QSU6_HUMA	1.028	1.055	1.155
P01130-3	Isoform 3 of Low-density lipoprotein receptor OS=Homo sapiens G	0.980	0.968	1.048
Q8N0V5	N-acetyllactosaminide beta-1,6-N-acetylglucosaminyl-transferase, is	1.045	0.859	0.963
O43155	Leucine-rich repeat transmembrane protein FLRT2 OS=Homo sapie	0.923	0.971	0.946
P30530-2	Isoform Short of Tyrosine-protein kinase receptor UFO OS=Homo s	1.072	0.996	1.110
Q6EMK4	Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1 - [VASN_HUMAN	1.051	0.949	1.049
Q9UNN8	Endothelial protein C receptor OS=Homo sapiens GN=PROCR PE=1	0.958	0.920	1.163
H0YAF8	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment	1.436	1.320	1.306
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [A	1.103	1.126	1.161
Q14118	Dystroglycan OS=Homo sapiens GN=DAG1 PE=1 SV=2 - [DAG1_H	0.970	0.911	0.990
O43556-3	Isoform 2 of Epsilon-sarcoglycan OS=Homo sapiens GN=SGCE - [S	0.866	0.823	0.874
Q8WVQ1	Soluble calcium-activated nucleotidase 1 OS=Homo sapiens GN=CANT1 PE=1 SV=1 - [CANT1_HUMAN]			
Q5W0C6	Torsin-3A (Fragment) OS=Homo sapiens GN=TOR3A PE=2 SV=1 - [Q5W0C6_HUMAN]			
P23470-2	Isoform 2 of Receptor-type tyrosine-protein phosphatase gamma O	1.013	0.948	1.041
E7EVJ3	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 OS	0.982	0.903	0.913
P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=	1.092	0.994	1.000
Q8NHP8	Putative phospholipase B-like 2 OS=Homo sapiens GN=PLBD2 PE=	0.835	0.887	0.809
B4E3P0	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=2 SV=1 - [B	1.115	1.160	1.163
Q16706	Alpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2	1.202	1.129	1.214
P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 -	1.204	1.207	1.161
E7EPA6	Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=2 SV=1 - [E7EPA6_HUMAN]			
Q92896	Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2	1.375	1.272	1.292
P08236	Beta-glucuronidase OS=Homo sapiens GN=GUSB PE=1 SV=2 - [BG	0.934	0.858	0.874
B7Z729	Acid sphingomyelinase-like phosphodiesterase 3a OS=Homo sapiens GN=SMPDL3A PE=2 SV=1 - [B7Z729_HUMAN]			
B4DQH4	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=2 SV=1 - [B4DQH4_HUMAN]			
O00754	Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE	0.891	0.874	0.913
O00231	26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3 - [PSD11_HUMAN]			
Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1	0.820	0.793	0.894
P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	1.122	1.096	1.154
P07686	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE	0.828	0.792	0.861
E9PD92	Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Homo sapie	1.345	1.107	1.373
Q92859-2	Isoform 2 of Neogenin OS=Homo sapiens GN=NEO1 - [NEO1_HUMAN]			
Q6UWP8	Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=2 - [SBSN_HUM	1.175	1.134	1.171
Q12841	Follistatin-related protein 1 OS=Homo sapiens GN=FSTL1 PE=1 SV	0.860	0.891	0.782
Q9BZM5	NKG2D ligand 2 OS=Homo sapiens GN=ULBP2 PE=1 SV=1 - [N2DL	0.914	0.853	0.849
P14618-2	Isoform M1 of Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM - [KPYM_HUMAN]			
P00751	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2 - [CF	0.957	0.974	0.973
Q9H1B5	Xylosyltransferase 2 OS=Homo sapiens GN=XYLT2 PE=2 SV=2 - [XYLT2_HUMAN]			
Q16610	Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 S	0.929	0.895	0.932
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV	1.163	1.328	1.175
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8	1.081	1.054	1.104
Q6UX71	Plexin domain-containing protein 2 OS=Homo sapiens GN=PLXDC2 PE=1 SV=1 - [PXDC2_HUMAN]			
E9PL22	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=	1.130	1.023	1.058
F8VQ14	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=	1.318	0.978	1.134
O00622	Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1 - [CYR61	0.950	0.991	1.062
H0YAR1	Lysyl oxidase homolog 2 (Fragment) OS=Homo sapiens GN=LOXL2 PE=4 SV=1 - [H0YAR1_HUMAN]			
H0YNP1	D-glucuronyl C5-epimerase OS=Homo sapiens GN=GLCE PE=2 SV=	0.883	1.006	1.036

O43505	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase OS	0.797	0.772	0.893
Q14517	Protocadherin Fat 1 OS=Homo sapiens GN=FAT1 PE=1 SV=2 - [FA	1.123	1.120	1.125
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1	1.028	0.983	1.002
P08195-2	Isoform 2 of 4F2 cell-surface antigen heavy chain OS=Homo sapien	1.088	1.072	1.130
P22392-2	Isoform 3 of Nucleoside diphosphate kinase B OS=Homo sapiens G	1.216	1.156	1.049
P53618	Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3 - [COPB_HUMAN]			
B3KTR6	Matrix-remodeling-associated protein 8 OS=Homo sapiens GN=MXR	0.906	1.002	0.889
P78539-4	Isoform 4 of Sushi repeat-containing protein SRPX OS=Homo sapie	0.880	0.820	0.882
Q08945	FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1 - [SSRP1_HUMAN]			
P23526-2	Isoform 2 of Adenosylhomocysteinase OS=Homo sapiens GN=AHC	1.175	1.177	1.115
Q16394	Exostosin-1 OS=Homo sapiens GN=EXT1 PE=1 SV=2 - [EXT1_HUM	1.178	1.051	1.249
F8W1C3	Matrix metalloproteinase-19 OS=Homo sapiens GN=MMP19 PE=2 S	0.950	0.942	0.963
Q86UD1	Out at first protein homolog OS=Homo sapiens GN=OAF PE=2 SV=	0.902	0.869	0.904
D6RA82	Annexin OS=Homo sapiens GN=ANXA3 PE=2 SV=1 - [D6RA82_HUMAN]			
P11717	Cation-independent mannose-6-phosphate receptor OS=Homo sapi	1.035	1.075	1.002
E9PEP6	Protein kinase C-binding protein NELL1 OS=Homo sapiens GN=NRP	1.110	1.027	1.167
O94907	Dickkopf-related protein 1 OS=Homo sapiens GN=DKK1 PE=1 SV=	0.985	0.891	1.020
Q9BRK5	45 kDa calcium-binding protein OS=Homo sapiens GN=SDF4 PE=1	1.655	1.586	1.612
G3V0E5	Transferrin receptor (P90, CD71), isoform CRA_c OS=Homo sapien	0.946	0.951	0.901
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 S	1.168	1.124	1.170
P07225	Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1	1.039	1.043	1.105
H0YD13	CD44 antigen OS=Homo sapiens GN=CD44 PE=2 SV=2 - [H0YD13_	1.443	1.286	1.497
E7EU96	Casein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=2 SV=1 - [E7EU96_HUMAN]			
B4E0R6	Importin-5 OS=Homo sapiens GN=IPO5 PE=2 SV=1 - [B4E0R6_HU	1.533	1.476	1.503
O60279	Sushi domain-containing protein 5 OS=Homo sapiens GN=SUSD5 PE=1 SV=3 - [SUSD5_HUMAN]			
Q92626	Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2 - [P	0.985	0.976	0.995
B7Z4K6	Deoxyribonuclease-2-alpha OS=Homo sapiens GN=DNASE2 PE=2 S	0.755	0.741	0.772
I3L398	Protein disulfide-isomerase (Fragment) OS=Homo sapiens GN=P4H	1.090	1.630	0.911
O00391	Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3 - [	0.988	0.926	1.074
P15151-3	Isoform Gamma of Poliovirus receptor OS=Homo sapiens GN=PVR	1.132	1.032	1.144
Q08629	Testican-1 OS=Homo sapiens GN=SPOCK1 PE=1 SV=1 - [TICN1_H	2.091	1.891	2.193
P68371	Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	1.613	1.899	1.551
P02765	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	1.114	1.078	1.246
P55268	Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2	1.083	1.126	1.036
P63104	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=	0.961	1.001	1.116
O14773	Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2 -	0.834	0.788	0.836
Q5SYB0	FERM and PDZ domain-containing protein 1 OS=Homo sapiens GN=FRMPD1 PE=1 SV=1 - [FRPD1_HUMAN]			
P35442	Thrombospondin-2 OS=Homo sapiens GN=THBS2 PE=1 SV=2 - [T	1.031	0.983	1.024
H3BMA1	Mesothelin (Fragment) OS=Homo sapiens GN=MSLN PE=2 SV=2 -	1.094	1.271	1.065
P10909-3	Isoform 3 of Clusterin OS=Homo sapiens GN=CLU - [CLUS_HUMAN	0.779	0.842	0.634
P08581	Hepatocyte growth factor receptor OS=Homo sapiens GN=MET PE=	1.148	1.108	1.177
E9PCS3	26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapien	1.296	1.303	1.265
P07711	Cathepsin L1 OS=Homo sapiens GN=CTSL1 PE=1 SV=2 - [CATL1_	0.771	0.896	0.752
P27658	Collagen alpha-1(VIII) chain OS=Homo sapiens GN=COL8A1 PE=1	1.781	1.576	1.573
O75326	Semaphorin-7A OS=Homo sapiens GN=SEMA7A PE=1 SV=1 - [SEM	0.878	0.809	0.910
P08107-2	Isoform 2 of Heat shock 70 kDa protein 1A/1B OS=Homo sapiens G	1.391	1.334	1.490
Q96L58	Beta-1,3-galactosyltransferase 6 OS=Homo sapiens GN=B3GALT6 PE=2 SV=2 - [B3GT6_HUMAN]			
O75882-3	Isoform 3 of Attractin OS=Homo sapiens GN=ATRN - [ATRN_HUMAN]			
E7ETU9	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Homo sapie	0.921	0.931	0.914
P55283-2	Isoform 2 of Cadherin-4 OS=Homo sapiens GN=CDH4 - [CADH4_H	0.911	0.887	0.904
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=	1.597	1.422	1.425
P10253	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]			
Q32P28	Prolyl 3-hydroxylase 1 OS=Homo sapiens GN=LEPRE1 PE=1 SV=2	1.020	0.919	1.040
Q93063	Exostosin-2 OS=Homo sapiens GN=EXT2 PE=1 SV=1 - [EXT2_HUM	1.056	1.069	1.013

F5H3T8	Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=2 SV=1 - [F5H3T8_HUMAN]			
F8W904;P55060-4	Exportin-2 OS=Homo sapiens GN=CSE1L PE=2 SV=1 - [F8W904_HUMAN]			
Q99650-2	Isoform 2 of Oncostatin-M-specific receptor subunit beta OS=Homo	1.203	1.203	1.238
P11047	Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV	1.039	0.980	1.070
O00299	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLI	1.312	1.404	1.811
E7EMM4	Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=2 SV=1 - [E7E	1.079	1.134	0.990
Q9UKM7	Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannos	1.059	1.027	1.116
C9J8D4	Mannosyl-oligosaccharide glucosidase (Fragment) OS=Homo sapiens GN=MOGS PE=2 SV=1 - [C9J8D4_HUMAN]			
Q6UXH8	Collagen and calcium-binding EGF domain-containing protein 1 OS=Homo sapiens GN=CCBE1 PE=1 SV=1 - [CCBE1_HUM			
P61812	Transforming growth factor beta-2 OS=Homo sapiens GN=TGFB2	1.140	0.970	1.231
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2	1.206	1.149	1.103
H0YGW5	Low-density lipoprotein receptor-related protein 6 (Fragment) OS=Homo sapiens GN=LRP6 PE=4 SV=1 - [H0YGW5_HUM			
O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapie	1.174	1.094	1.112
O94991	SLIT and NTRK-like protein 5 OS=Homo sapiens GN=SLITRK5 PE=	1.000	0.937	0.983
P10586-2	Isoform 2 of Receptor-type tyrosine-protein phosphatase F OS=Ho	1.509	1.421	1.410
Q5STU3	HLA-B associated transcript 1 OS=Homo sapiens GN=DDX39B PE=	1.380	1.227	1.380
P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN]	1.164	1.333	0.899
Q09028-4	Isoform 4 of Histone-binding protein RBBP4 OS=Homo sapiens GN=	1.034	1.199	0.978
J3KS17	Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE	1.200	1.199	1.105
P12814	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 - [ACTN	1.101	1.118	0.983
Q9UM22	Mammalian ependymin-related protein 1 OS=Homo sapiens GN=EP	0.979	1.023	0.907
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1	1.156	1.132	1.135
Q15149-7	Isoform 7 of Plectin OS=Homo sapiens GN=PLEC - [PLEC_HUMAN]	1.418	1.251	1.436
P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB	1.372	1.262	1.545
O00339-3	Isoform 3 of Matrilin-2 OS=Homo sapiens GN=MATN2 - [MATN2_HUMAN]			
P01024	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2 - [CO3_HU	0.934	1.112	0.953
Q5TCU6	Talin-1 OS=Homo sapiens GN=TLN1 PE=2 SV=1 - [Q5TCU6_HUM	0.961	0.945	0.904
E9PBU3	Phosphoribosylaminoimidazolecarboxamide formyltransferase OS=	1.366	1.438	1.369
P16035	Metalloproteinase inhibitor 2 OS=Homo sapiens GN=TIMP2 PE=1 SV=2 - [TIMP2_HUMAN]			
P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_	0.659	1.078	0.616
P25788-2	Isoform 2 of Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 - [PSA3_HUMAN]			
Q76M96	Coiled-coil domain-containing protein 80 OS=Homo sapiens GN=C	1.436	1.066	1.213
P54802	Alpha-N-acetylglucosaminidase OS=Homo sapiens GN=NAGLU PE=	1.106	1.157	1.063
Q86YZ3	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2 - [HORN_HUM	1.166	1.145	1.105
Q6ZRP7	Sulfhydryl oxidase 2 OS=Homo sapiens GN=QSOX2 PE=1 SV=3 - [	1.297	1.148	1.214
P25786	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 - [PSA1_HUMAN]			
Q15008	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapie	1.234	1.126	1.340
H0Y930	Extracellular matrix protein FRAS1 (Fragment) OS=Homo sapiens	1.134	1.245	0.990
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]			
P00533-4	Isoform 4 of Epidermal growth factor receptor OS=Homo sapiens	1.322	1.324	1.437
P35555	Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=3 - [FBN1_HUMA	1.483	1.553	1.673
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1	**1.859**	**1.650**	**1.945**
P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1	1.782	1.677	1.685
Q08431-2	Isoform 2 of Lactadherin OS=Homo sapiens GN=MFGE8 - [MFGM_	1.055	1.025	1.109
Q8WUJ3-2	Isoform 2 of Protein KIAA1199 OS=Homo sapiens GN=KIAA1199 - [K1199_HUMAN]			
O75083	WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=	1.143	1.192	1.296
Q96JB6	Lysyl oxidase homolog 4 OS=Homo sapiens GN=LOXL4 PE=1 SV=1 - [LOXL4_HUMAN]			
Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	1.283	1.500	1.459
Q9NZ08	Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=E	1.282	1.250	1.255
P28074-3	Isoform 3 of Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 - [PSB5_HUMAN]			
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 S	1.485	1.379	**1.513**
Q8NBJ4-2	Isoform 2 of Golgi membrane protein 1 OS=Homo sapiens GN=GO	1.176	1.100	1.271
P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]			
Q6UXD5-2	Isoform 2 of Seizure 6-like protein 2 OS=Homo sapiens GN=SEZ6L	1.152	1.076	1.232

Q9BQT9	Calsyntenin-3 OS=Homo sapiens GN=CLSTN3 PE=1 SV=1 - [CSTN	1.202	1.164	1.063
P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FA	1.757	1.513	1.732
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMA	1.361	1.524	1.026
F5H265	Polyubiquitin-C (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=	1.368	1.360	1.391
Q8WX77	Insulin-like growth factor-binding protein-like 1 OS=Homo sapiens	1.029	1.045	1.003
Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]			
B7Z6M1	Plastin-3 OS=Homo sapiens GN=PLS3 PE=2 SV=1 - [B7Z6M1_HUM	1.023	1.030	0.965
Q00610-2	Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC -	1.511	1.500	1.601
D6RAF8	Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=2 SV=1 - [D6RAF8_HUMAN			
Q5HY54	Filamin-A OS=Homo sapiens GN=FLNA PE=2 SV=1 - [Q5HY54_HU	1.277	1.286	1.214
Q9UHL4	Dipeptidyl peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=3 - [	1.236	0.980	1.190
P40189	Interleukin-6 receptor subunit beta OS=Homo sapiens GN=IL6ST P	1.268	1.226	1.405
P04004	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1 - [VTNC_HUMA	2.694	2.215	2.572
Q9UHI8	A disintegrin and metalloproteinase with thrombospondin motifs 1	1.306	1.224	1.325
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=	**1.588**	1.427	1.445
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=	1.174	1.041	1.153
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1	**2.590**	**2.142**	**2.805**
B7Z9L0	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=2 SV=1 - [B7Z9L0_HUMAN]			
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE	1.300	1.271	1.160
Q9Y6X5	Bis(5'-adenosyl)-triphosphatase ENPP4 OS=Homo sapiens GN=ENP	1.411	1.430	1.519
Q9HB63-3	Isoform 3 of Netrin-4 OS=Homo sapiens GN=NTN4 - [NET4_HUMAN]			
P23284	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB P	1.326	1.233	1.240
Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1	1.343	1.351	1.356
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens	1.580	1.508	1.470
Q16363-2	Isoform 2 of Laminin subunit alpha-4 OS=Homo sapiens GN=LAMA4 - [LAMA4_HUMAN]			
E7EN95	Filamin-B OS=Homo sapiens GN=FLNB PE=2 SV=1 - [E7EN95_HUMAN]			
B7Z5J4	Carboxypeptidase A4 OS=Homo sapiens GN=CPA4 PE=2 SV=1 - [B	1.226	0.946	1.178
P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=	**1.570**	1.481	1.415
Q5T985	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=	1.147	1.076	1.234
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KR	**2.496**	**2.052**	**2.457**
B3KTI1	Alpha-amylase 2B OS=Homo sapiens GN=AMY2B PE=2 SV=1 - [B3KTI1_HUMAN]			
Q8NBJ5	Procollagen galactosyltransferase 1 OS=Homo sapiens GN=COLGAL	1.260	1.092	1.300
B7Z7A9	Phosphoglycerate kinase OS=Homo sapiens GN=PGK1 PE=2 SV=1	1.560	1.429	1.547
H3BQN4	Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOA PE=	1.540	1.546	1.412
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=	1.564	1.977	1.425
O60687	Sushi repeat-containing protein SRPX2 OS=Homo sapiens GN=SRP	1.358	1.238	1.293
E7EUA9	Neuron navigator 3 OS=Homo sapiens GN=NAV3 PE=2 SV=2 - [E7EUA9_HUMAN]			
P26022	Pentraxin-related protein PTX3 OS=Homo sapiens GN=PTX3 PE=1	1.415	1.312	1.457
E9PFT6	Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=2 SV=1	1.520	2.049	1.230
F5H335	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapien	1.231	1.108	1.265
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_	1.259	1.198	1.240
P22304	Iduronate 2-sulfatase OS=Homo sapiens GN=IDS PE=1 SV=1 - [ID	1.238	1.223	1.273
P15586	N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1	1.342	1.420	1.263
F5GXQ1	35 kDa inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapie	1.148	0.944	1.127
Q14563	Semaphorin-3A OS=Homo sapiens GN=SEMA3A PE=1 SV=1 - [SEM	0.884	0.916	0.888
F8VPD4	CAD protein OS=Homo sapiens GN=CAD PE=2 SV=1 - [F8VPD4_HUMAN]			
Q13813-3	Isoform 3 of Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 - [SPTN1_HUMAN]			
P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 - [HBA_HUMAN]			
O43707	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 - [ACTN	1.341	1.324	1.289
P02751-17	Isoform 17 of Fibronectin OS=Homo sapiens GN=FN1 - [FINC_HUM	1.367	1.344	1.267
P10124	Serglycin OS=Homo sapiens GN=SRGN PE=1 SV=3 - [SRGN_HUMA	11.855	5.169	12.512
P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4 - [PSB4_HUMAN]			
P14625	Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [ENPL	1.480	1.384	1.539
P05543	Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1	0.946	1.181	0.959

O00468-6	Isoform 6 of Agrin OS=Homo sapiens GN=AGRN - [AGRIN_HUMAN	2.645	2.348	2.555
Q99715-4	Isoform 4 of Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 - [COCA1_HUMAN]			
H0YA55	Serum albumin (Fragment) OS=Homo sapiens GN=ALB PE=4 SV=1	1.692	1.516	1.734
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [	1.322	1.227	1.400
P01008	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1 - [	1.881	1.532	2.188
F8WC54	Disintegrin and metalloproteinase domain-containing protein 9 OS=	0.545	0.528	0.557
O95490-3	Isoform 3 of Latrophilin-2 OS=Homo sapiens GN=LPHN2 - [LPHN2_HUMAN]			
P04083	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 - [ANXA1_H	0.982	1.000	0.978
Q8TE73	Dynein heavy chain 5, axonemal OS=Homo sapiens GN=DNAH5 PE=1 SV=3 - [DYH5_HUMAN]			
Q15758	Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A	0.710	0.689	0.610
O14787-2	Isoform 2 of Transportin-2 OS=Homo sapiens GN=TNPO2 - [TNPO2_HUMAN]			
Q8IXL6	Extracellular serine/threonine protein kinase FAM20C OS=Homo sapiens GN=FAM20C PE=1 SV=2 - [DMP4_HUMAN]			
H7C3T4	Peroxiredoxin-4 (Fragment) OS=Homo sapiens GN=PRDX4 PE=4 SV=1 - [H7C3T4_HUMAN]			
Q01813-2	Isoform 2 of 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP - [K6PP_HUMAN]			
Q5W0A2	BRI2, membrane form OS=Homo sapiens GN=ITM2B PE=2 SV=1 - [Q5W0A2_HUMAN]			
A6NIW5	Peroxiredoxin 2, isoform CRA_a OS=Homo sapiens GN=PRDX2 PE=2 SV=2 - [A6NIW5_HUMAN]			
P08758	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_H	1.057	1.103	1.123
Q9H173	Nucleotide exchange factor SIL1 OS=Homo sapiens GN=SIL1 PE=1	0.960	1.063	1.171
Q9NRB3	Carbohydrate sulfotransferase 12 OS=Homo sapiens GN=CHST12	0.952	0.956	1.034
Q92973-3	Isoform 3 of Transportin-1 OS=Homo sapiens GN=TNPO1 - [TNPO	1.024	0.926	1.017
P01137	Transforming growth factor beta-1 OS=Homo sapiens GN=TGFB1 PE=1 SV=2 - [TGFB1_HUMAN]			
P09529	Inhibin beta B chain OS=Homo sapiens GN=INHBB PE=1 SV=2 - [I	0.933	0.878	0.920
P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4 - [FBLN1_HUMAN]			
B4DKL4	Lipolysis-stimulated lipoprotein receptor OS=Homo sapiens GN=LS	1.292	1.355	1.128
B4E2S7	Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=2 SV=1 - [B4E2S7_HUMAN]			
Q9UMR5	Lysosomal thioesterase PPT2 OS=Homo sapiens GN=PPT2 PE=1 S	1.201	1.134	1.230
C9J1D9	Interleukin-1 receptor accessory protein (Fragment) OS=Homo sapiens GN=IL1RAP PE=2 SV=1 - [C9J1D9_HUMAN]			
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]			
P06702	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1 - [S10	0.811	0.793	0.758
Q5T749	Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1	1.093	1.217	1.344
Q7LGC8	Carbohydrate sulfotransferase 3 OS=Homo sapiens GN=CHST3 PE=	1.230	1.161	1.095
Q12805-2	Isoform 2 of EGF-containing fibulin-like extracellular matrix protein	0.872	0.899	0.795
Q9H5V8-2	Isoform 2 of CUB domain-containing protein 1 OS=Homo sapiens G	0.756	0.760	0.838
Q7Z304-2	Isoform 2 of MAM domain-containing protein 2 OS=Homo sapiens GN=MAMDC2 - [MAMC2_HUMAN]			
F5H1I8	X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=	0.337	0.321	0.343
H0YH88	Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapien	0.480	0.465	0.872
Q08345-2	Isoform 2 of Epithelial discoidin domain-containing receptor 1 OS=	0.685	0.673	0.671
Q29980	MHC class I polypeptide-related sequence B OS=Homo sapiens GN=	0.722	0.716	0.786
Q7Z3V4-3	Isoform 3 of Ubiquitin-protein ligase E3B OS=Homo sapiens GN=U	0.761	0.680	0.779
O60911	Cathepsin L2 OS=Homo sapiens GN=CTSL2 PE=1 SV=2 - [CATL2_	0.783	0.835	0.774
Q14680-8	Isoform 8 of Maternal embryonic leucine zipper kinase OS=Homo s	0.809	0.769	0.873
Q6P9A2	Polypeptide N-acetylgalactosaminyltransferase 18 OS=Homo sapien	0.817	1.016	0.642
E7EP32	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	0.847	0.873	0.735
P41250	Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 - [S	0.920	0.901	1.195
O95497	Pantetheinase OS=Homo sapiens GN=VNN1 PE=1 SV=2 - [VNN1_H	0.951	0.934	1.016
Q9UNW1	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens G	1.057	1.083	0.904
F5H780	Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNR	1.066	1.056	0.994
P34932	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 S	1.073	0.978	0.982
P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	1.076	1.195	1.129
Q9Y625	Glypican-6 OS=Homo sapiens GN=GPC6 PE=1 SV=1 - [GPC6_HUM	1.112	1.036	0.996
P06737-2	Isoform 2 of Glycogen phosphorylase, liver form OS=Homo sapiens	1.116	1.343	1.349
O95373	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 - [IPO7_HUM	1.136	1.010	1.531
C9J2Q4	Septin-2 (Fragment) OS=Homo sapiens GN=SEPT2 PE=2 SV=1 - [	1.140	1.227	1.195
E9PQX2	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=2 SV=1	1.144	1.411	1.099

P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN	1.155	1.033	1.226
P20930	Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3 - [FILA_HUMAN]	1.174	1.165	1.089
P61204	ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2	1.179	1.084	1.209
J3KR24	Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS P	1.197	1.088	1.098
P05546	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3 -	1.248	1.254	1.236
B4DYD8	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 P	1.255	0.942	1.398
P36955	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF	1.273	1.244	1.259
B4DUR8	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3	1.317	1.265	1.312
P10155-3	Isoform 3 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens	1.334	1.202	1.411
Q86VR8	Four-jointed box protein 1 OS=Homo sapiens GN=FJX1 PE=2 SV=1	1.378	0.918	1.351
F5H018	GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN	1.382	1.326	1.607
P27348	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 -	1.386	1.013	1.241
Q5T6W1	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=	1.386	1.327	1.446
B0QY90	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapien	1.408	1.289	1.433
C9IZG4	Protein CutA OS=Homo sapiens GN=CUTA PE=2 SV=1 - [C9IZG4_	1.417	1.464	1.409
P49720	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=	1.429	1.636	1.319
Q7Z7M9	Polypeptide N-acetylgalactosaminyltransferase 5 OS=Homo sapiens	1.437	1.406	1.119
E9PN86	Eukaryotic translation initiation factor 3 subunit M (Fragment) OS=	1.550	1.361	1.857
Q13619-2	Isoform 2 of Cullin-4A OS=Homo sapiens GN=CUL4A - [CUL4A_HU	1.581	1.603	1.417
Q6PCB0	von Willebrand factor A domain-containing protein 1 OS=Homo sap	1.597	1.264	1.357
Q5SYT8	Protein NAMPTL (Fragment) OS=Homo sapiens GN=NAMPTL PE=2	1.622	1.597	1.039
Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1	1.677	1.483	1.731
P35052	Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=2 - [GPC1_HUM	1.790	2.107	1.301
Q12797-10	Isoform 10 of Aspartyl/asparaginyl beta-hydroxylase OS=Homo sap	1.896	1.514	1.880
Q7Z4H8-3	Isoform 3 of KDEL motif-containing protein 2 OS=Homo sapiens G	2.655	1.793	2.846
P31431-2	Isoform 2 of Syndecan-4 OS=Homo sapiens GN=SDC4 - [SDC4_HU	5.624	4.430	5.148
Q58FF8	Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens GN=HSP90AB2P PE=1 SV=2 - [H90B2_HUMAN]			
H0Y3Z3	Protein disulfide-isomerase (Fragment) OS=Homo sapiens GN=P4HB PE=3 SV=1 - [H0Y3Z3_HUMAN]			
P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 - [TCPA_HUMAN]			
Q02487-2	Isoform 2B of Desmocollin-2 OS=Homo sapiens GN=DSC2 - [DSC2_HUMAN]			
Q70JA7	Chondroitin sulfate synthase 3 OS=Homo sapiens GN=CHSY3 PE=2 SV=3 - [CHSS3_HUMAN]			
Q5D862	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1 - [FILA2_HUMAN]			

0.354	0.976	0.974	**0.393**	**0.410**	**0.422**	**0.472**	0.883
1.023	0.981	1.046	0.367	0.342	0.397	0.372	0.928
0.578	1.054	1.118	0.535	0.479	0.499	0.493	1.095
0.584	0.976	1.048	**0.407**	**0.418**	**0.438**	**0.499**	0.912
0.859	1.048	0.956	0.686	0.693	0.737	0.746	0.937
0.644	1.032	1.028	0.710	0.649	0.762	0.699	0.937
2.102	1.050	1.019	2.058	1.912	1.809	1.685	1.144
0.567	1.014	1.032	0.658	0.720	0.679	0.671	0.940
0.574	0.926	0.941	**0.456**	**0.501**	**0.503**	**0.568**	0.877
0.778	0.997	1.055	0.614	0.630	0.617	0.618	0.952
0.468	1.029	0.990	0.501	0.535	0.506	0.528	0.979
0.700	1.022	0.956	0.650	0.651	0.663	0.699	0.901
0.382	1.018	1.021	0.705	0.696	0.682	0.675	1.053
[C9JIM8_HUMAN]			0.630	0.640	0.630	0.641	1.006
0.556	1.119	1.080					
0.815	1.033	1.093	0.878	0.796	0.863	0.686	0.988
0.654	0.989	1.027	**0.538**	**0.543**	**0.552**	**0.571**	0.976
0.619	0.990	0.968	0.840	0.858	0.877	0.978	0.946
0.787	1.052	1.059	**0.644**	**0.601**	**0.604**	**0.623**	1.054
0.809	0.938	1.001	0.803	0.806	0.836	0.786	1.011
0.780	1.025	0.973	0.788	0.725	0.788	0.763	0.968
0.712	1.035	1.017	1.348	1.308	1.249	1.143	0.974
0.466	1.007	1.027					
0.565	1.010	1.055	0.733	0.791	0.747	0.779	0.999
0.888	1.094	1.180	1.079	1.012	0.896	0.843	1.211
0.738	0.937	1.017	0.738	0.804	0.814	0.889	0.905
0.617	1.083	1.000	0.658	0.677	0.645	0.668	1.035
0.678	0.993	1.070	0.901	0.928	0.851	0.906	1.025
0.649	1.003	1.038	0.645	0.660	0.658	0.671	1.012
0.732	0.966	0.983	0.769	0.808	0.768	0.851	0.951
			0.684	0.662	0.674	0.655	1.064
0.688	1.012	0.987					
0.867	0.885	0.925	0.795	0.878	0.834	0.944	0.937
0.688	0.826	0.951	0.985	1.117	1.038	1.153	0.941
0.850	0.894	0.978	1.074	0.993	0.860	0.798	1.256
0.608	0.908	0.913	0.665	0.781	0.726	0.848	0.958
0.725	1.143	1.131	0.822	0.847	0.828	0.878	1.003
1.524	1.072	0.958	1.879	1.909	1.832	1.769	0.916
0.846	0.895	0.957					
0.864	1.071	0.950					
0.548	0.950	0.957	0.557	0.621	0.632	0.670	0.904
0.783	0.938	0.938	0.636	0.740	0.731	0.853	0.889
0.883	0.954	1.011					
0.644	1.079	0.988	0.683	0.737	0.708	0.780	0.965
0.693	1.030	1.090	0.653	0.690	0.713	0.757	0.933
0.590	0.972	0.994	0.571	0.623	0.607	0.661	0.947
0.782	1.073	1.009	0.722	0.832	0.728	0.834	0.989
1.268	1.305	1.041					

0.728	0.957	1.040	0.641	0.693	0.645	0.699	1.000
0.809	0.963	0.970	0.912	0.972	0.900	0.976	0.967
0.808	1.050	0.958	1.183	1.330	1.248	1.361	0.957
0.865	1.011	0.950	1.293	1.313	1.215	1.319	1.021
0.760	0.943	1.001	0.734	0.809	0.760	0.849	0.958
0.751	1.036	1.003	0.697	0.781	0.639	0.684	1.058
0.632	1.021	0.991	0.775	0.750	0.814	0.811	0.962
0.790	0.946	1.014	0.602	0.612	0.595	0.606	1.035
0.862	0.945	0.954	0.519	0.524	0.773	0.581	0.909
0.687	0.975	0.999	0.699	0.673	0.689	0.741	0.997
0.998	1.110	1.061	0.753	0.809	0.661	0.712	1.147
0.914	1.006	1.012	0.886	0.826	0.784	0.859	1.019
0.735	1.021	1.012	0.996	1.039	1.033	1.049	0.972
			1.133	1.094	0.962	0.967	1.099
0.711	0.987	1.090					
0.818	1.029	1.020	0.828	0.878	0.866	0.873	0.967
0.793	0.988	0.978	0.764	0.839	0.809	0.852	0.953
0.737	1.156	1.127	0.780	0.746	0.799	0.730	1.030
2 SV=2 - [GCNT1_HUMAN]							
			0.805	0.788	0.767	0.753	1.053
1.068	0.966	0.928					
0.795	1.162	1.092	0.835	0.840	0.860	0.859	1.081
0.926	0.964	1.154	0.872	0.852	0.781	0.812	1.059
0.893	1.136	0.998					
0.820	1.085	0.993	0.988	0.928	0.906	0.971	1.029
0.800	0.992	0.987	0.897	0.974	0.849	0.968	1.043
0.738	0.940	0.993	0.808	0.889	0.852	0.945	0.924
0.773	1.028	1.026	0.707	0.650	0.635	0.684	1.118
0.966	1.030	1.078	0.832	0.856	0.823	0.899	0.962
0.984	0.980	1.000	0.860	0.961	0.950	0.947	0.931
0.573	1.006	1.013	0.721	0.747	0.759	0.766	0.976
0.850	0.988	1.008	0.745	0.862	0.734	0.825	0.988
0.724	1.038	1.029	0.729	0.755	0.706	0.810	0.968
0.806	1.043	1.085	0.901	0.715	0.800	0.636	1.133
0.646	0.944	0.910	0.866	0.764	0.768	0.708	1.079
0.679	1.032	0.983	0.828	0.877	0.886	0.895	0.935
0.977	1.008	1.014	0.923	0.979	0.953	0.977	0.957
0.911	0.938	0.963	0.942	1.029	1.005	1.060	0.945
0.859	1.114	1.133					
0.974	1.035	1.045	0.864	0.867	0.758	0.807	1.067
0.740	1.108	1.143					
0.743	1.008	1.057	0.824	0.821	0.863	0.830	1.006
1.024	1.049	1.109	0.886	0.812	0.842	0.795	0.982
1.447	1.074	0.940	1.628	1.502	1.459	1.341	1.102
0.960	1.025	1.044	0.836	0.868	0.905	0.948	0.960
0.682	0.952	1.015	0.921	0.925	0.910	0.932	1.001
0.652	1.112	0.971	1.101	1.042	1.180	0.929	1.169
0.887	1.017	1.067	0.781	0.790	0.739	0.777	1.035
0.672	0.924	0.980	1.094	1.162	1.126	1.191	0.967

0.738	1.008	1.019	0.874	0.925	0.929	0.999	0.965
0.893	0.987	0.980	1.007	1.059	0.953	1.013	1.013
1.079	1.068	1.073	0.885	1.103	0.968	1.210	0.919
0.521	1.031	0.953					
0.867	1.074	0.980	0.809	0.854	0.819	0.850	1.048
0.964	1.018	1.086	1.004	1.095	1.017	1.138	1.036
1.242	0.942	0.951					
0.806	0.964	0.975	0.953	0.847	0.909	0.881	1.010
0.876	0.990	0.999	0.764	0.825	0.793	0.854	0.959
1.149	1.060	0.962	1.057	1.106	1.169	1.042	1.037
0.734	0.947	1.011	0.741	0.765	0.780	0.809	0.973
0.936	1.033	0.982	0.755	0.725	0.814	0.783	0.933
1.050	1.014	1.024	0.766	0.870	0.830	0.921	0.959
0.613	0.962	1.015	0.646	0.720	0.714	0.791	0.935
0.907	0.972	0.976	0.940	0.919	0.967	0.911	1.007
1.105	1.003	0.983	0.971	1.021	1.026	0.998	1.017
1.029	0.888	1.006	0.803	0.882	0.862	0.959	1.000
1.118	1.008	0.992	1.221	1.235	0.994	1.008	0.935
0.932	0.876	1.031					
0.905	0.940	1.046	0.917	0.870	0.763	0.804	1.065
			1.314	1.275	1.312	1.439	1.007
0.815	1.073	1.079	0.768	0.769	0.828	0.778	0.980
0.813	0.978	0.982	0.826	0.837	0.812	0.820	0.998
0.759	1.073	1.179					
1.009	1.079	1.068	0.762	0.775	0.731	0.784	0.964
0.848	0.954	0.969	1.150	1.213	1.170	1.200	0.984
1.530	1.025	0.969	1.290	1.155	1.212	1.088	1.070
			0.969	0.936	0.995	0.965	0.979
0.823	0.979	1.000	1.138	0.963	0.856	0.956	1.118
1.400	0.983	1.004	0.949	0.971	0.876	0.850	1.047
0.786	1.048	1.094	0.873	0.936	0.885	0.926	1.009
0.797	0.964	1.010	0.948	0.941	1.006	0.984	0.960
0.767	0.939	0.944	0.769	0.807	0.776	0.772	1.001
0.867	1.004	1.014	0.753	0.792	0.796	0.822	0.962
			0.858	0.840	0.940	0.922	0.918
0.897	1.095	0.974	0.938	0.907	0.942	0.908	0.983
0.661	0.997	0.969	0.869	0.902	0.885	0.944	0.993
0.821	0.987	0.977	0.892	0.905	0.942	0.944	0.988
0.889	0.979	0.981	**1.509**	**1.543**	1.493	**1.572**	0.978
1.321	0.986	0.727	0.979	0.894	1.099	1.006	0.896
1.181	1.077	1.022					
			1.068	1.164	1.094	1.195	0.982
0.986	0.992	1.059	0.990	1.040	1.019	1.074	1.003
0.940	1.039	1.000	1.544	1.645	1.554	1.524	1.020
1.001	1.034	1.080	1.200	1.229	1.180	1.176	1.038
1.018	1.020	1.003					
0.854	1.009	1.029	0.822	0.793	0.803	0.777	1.022
0.998	1.073	0.977	1.441	0.996	1.291	0.895	1.123
0.770	1.011	0.981	0.695	0.818	0.794	0.926	0.899
0.899	0.955	0.933	0.846	0.870	0.913	0.910	0.961

0.627	0.991	1.008	0.919	0.968	0.935	0.988	0.988
1.307	1.037	1.016	1.101	1.123	1.094	1.112	1.027
0.809	0.968	0.973	0.836	1.061	0.876	0.927	1.105
1.181	0.954	1.021	1.199	1.087	1.068	1.055	1.121
0.991	0.974	1.018	1.012	1.049	1.011	1.089	1.000
1.115	0.940	1.016	0.850	0.832	0.828	0.869	0.962
1.057	0.923	0.928	1.210	1.317	1.120	1.231	1.070
1.028	0.950	0.966	1.018	1.103	1.048	1.165	0.996
1.025	0.979	1.030	0.849	0.867	0.870	0.805	1.028
1.050	0.912	0.984	0.977	0.924	0.905	0.860	1.032
1.205	1.099	0.957					
1.081	0.946	0.935	1.099	1.046	1.016	1.026	0.991
0.951	0.999	0.951	0.814	0.831	0.844	0.911	0.944
0.834	1.032	0.989	0.906	0.873	0.916	0.906	0.943
0.929	1.009	0.947	0.931	0.948	0.927	0.916	1.009
0.895	0.925	0.954	0.909	0.936	0.922	0.956	0.969
0.914	1.092	0.939	1.459	1.245	1.044	0.894	1.405
0.897	0.980	1.022	0.974	0.886	0.931	0.906	0.989
1.191	1.032	1.025	0.993	0.935	1.228	1.002	0.935
1.139	1.012	0.990	1.063	1.002	1.044	1.059	0.955
1.168	1.037	1.034					
1.174	1.047	0.958	1.312	1.303	1.273	1.205	1.019
0.815	1.027	0.979	0.921	0.884	0.931	0.958	0.991
			1.543	1.146	1.367	1.018	1.135
0.889	0.987	0.996	0.919	0.935	0.943	0.955	0.990
0.854	0.931	0.969	0.809	0.925	0.879	0.996	0.946
1.044	1.097	0.945	0.882	0.949	0.888	0.930	0.990
0.852	1.055	1.003	0.852	0.911	0.921	0.980	0.964
1.134	0.980	0.849					
1.136	0.998	0.996					
0.840	0.980	0.936	1.205	1.302	1.180	1.324	1.000
0.871	0.984	1.061	0.827	0.903	0.883	0.926	0.992
0.969	0.956	1.016	1.138	1.146	1.029	1.059	1.015
			1.221	0.981	1.147	0.924	1.070
0.904	0.997	0.998	1.010	1.060	1.017	1.049	0.979
1.163	1.039	1.018	1.104	1.049	1.043	1.086	1.049
1.066	0.997	1.029	0.947	0.988	1.014	1.049	1.008
			1.141	1.014	0.913	0.896	1.235
0.999	1.068	0.948	1.049	1.077	1.033	1.102	1.069
0.913	1.147	0.930	1.271	0.940	1.521	1.129	0.840
1.001	1.042	1.000	1.217	1.250	1.224	1.192	1.032
1.134	0.896	1.057	0.943	0.894	0.868	0.826	1.092

0.724	1.002	0.977	0.879	0.933	0.868	0.973	1.013
1.126	0.998	1.028					
1.015	0.977	1.030	0.869	0.940	0.897	0.935	0.981
1.037	0.981	1.002	0.857	0.909	0.885	0.967	0.968
1.019	1.063	0.998	0.910	0.944	1.000	1.033	0.915
0.915	1.046	1.056	1.067	1.010	1.028	1.033	1.071
0.825	0.997	0.960					
1.121	1.054	1.032	1.040	1.145	1.131	1.171	0.998
1.170	0.955	0.929	1.111	1.031	1.042	0.970	1.041
1.007	1.000	1.023					
0.846	0.997	0.936	1.344	1.330	1.282	1.272	1.055
1.019	1.058	1.061	1.546	1.337	1.440	1.263	1.084
1.084	0.952	0.938	0.981	1.046	1.028	1.103	0.949
0.919	0.945	0.942	1.420	1.650	1.551	1.706	0.952
1.551	1.026	0.988	1.210	1.354	1.141	1.280	1.066
0.934	1.007	1.017	0.904	0.865	0.946	0.864	1.012
1.124	0.997	0.986	1.033	1.139	1.036	1.157	0.980
1.115	0.938	1.015	0.971	1.000	0.958	1.024	0.993
1.317	0.939	0.927	1.120	1.148	1.172	1.210	0.950
1.342	1.028	1.007	1.118	1.095	1.203	1.152	0.958
0.963	0.982	1.013	1.067	1.094	1.089	1.079	1.029
0.736	1.008	1.024	0.945	1.003	0.984	1.042	0.967
1.367	1.197	1.541	1.282	1.097	0.989	0.849	1.303
0.998	0.939	0.967	0.946	0.997	0.996	1.065	0.954
1.048	0.986	0.920	0.909	0.946	0.956	0.988	0.950
2.023	0.954	0.995	1.472	1.559	1.536	1.571	1.040
1.832	1.040	1.213					
1.195	0.908	0.938	1.289	1.327	1.228	1.290	1.049
1.177	0.960	1.075	1.314	1.359	1.308	1.246	1.059
1.059	0.869	1.020	1.390	1.405	1.565	1.587	0.924
0.796	0.941	0.989	0.868	0.905	0.824	0.834	1.060
0.975	1.025	0.989	1.943	1.864	1.879	1.790	1.016
1.117	1.003	1.058	1.020	0.988	0.934	0.955	1.043
0.831	1.061	1.076	1.161	1.144	1.115	1.145	1.007
1.158	1.005	0.987	1.058	1.079	1.028	1.047	1.027
1.276	0.941	1.036	0.776	0.897	0.927	1.074	0.842
0.792	0.991	1.017	0.954	0.965	0.905	0.874	1.073
1.623	1.132	0.857					
0.844	0.963	0.972	1.036	1.099	1.047	1.091	0.951
1.401	0.965	0.931	0.913	0.889	0.904	0.826	1.016
			0.941	0.719	1.019	0.754	0.928
			1.620	1.426	2.007	1.773	0.811
0.933	1.017	1.049	1.038	0.984	1.097	0.957	1.013
0.873	1.022	1.019	0.806	0.888	0.851	0.919	0.972
1.369	1.030	1.005	1.198	1.091	0.996	0.896	1.080
0.991	0.963	0.977	0.954	1.050	0.975	1.006	1.053
0.990	1.020	1.011	0.987	0.982	0.976	1.044	1.030

1.242	0.940	0.996	1.179	1.133	1.221	1.160	0.967
0.991	0.999	1.000	1.584	1.567	1.429	1.427	1.082
1.667	1.069	1.043	1.114	1.142	1.067	1.116	1.010
0.916	1.055	1.036	0.944	0.760	1.122	0.950	0.820
1.027	1.041	0.995	1.139	1.108	1.109	1.065	1.039
AN]							
1.063	0.929	0.937	1.060	1.170	1.112	1.261	0.963
1.186	1.005	0.971	1.082	1.089	0.951	1.031	1.063
AN]							
1.082	0.976	0.979	1.056	1.153	1.120	1.226	0.989
0.924	1.018	0.965	0.823	0.844	0.837	0.861	0.988
1.448	1.018	0.997	1.044	1.068	1.050	1.104	1.006
1.318	0.934	0.935	1.106	1.098	1.196	1.156	0.916
1.001	1.336	1.144	1.062	1.034	1.040	1.031	1.005
1.139	1.057	1.195					
1.108	1.086	1.030	1.253	1.411	1.253	1.425	0.999
1.070	1.079	1.105	1.248	1.188	1.120	1.121	1.072
0.960	1.081	1.022	1.005	0.984	1.079	0.970	1.022
1.170	1.013	1.011	1.118	1.086	1.054	0.982	1.096
1.271	0.988	1.013	0.933	0.854	0.963	0.869	0.974
1.428	0.888	0.949					
1.010	1.001	1.016	1.128	1.004	1.044	0.996	1.051
0.920	1.063	1.004					
1.564	0.923	1.151	1.052	1.324	0.993	1.253	1.065
			1.130	1.161	1.132	1.165	1.004
0.926	1.035	1.163	0.974	0.901	0.901	0.835	1.088
			1.345	1.275	1.191	1.132	1.136
1.080	1.326	0.916					
1.196	1.041	1.052	1.165	1.105	1.116	1.009	0.960
1.090	1.055	1.013					
1.149	0.996	0.982	0.939	0.900	1.026	0.980	0.905
			1.295	1.274	1.179	1.197	1.054
1.223	0.949	1.010	1.214	1.198	1.261	1.249	0.968
1.091	1.146	1.131	1.100	1.096	1.093	1.092	1.012
1.309	1.001	0.950	1.095	1.089	1.138	1.200	0.983
1.628	0.998	1.016	1.655	1.713	1.638	1.598	1.057
1.720	0.937	0.898	1.243	1.324	1.246	1.343	0.998
1.644	1.024	0.943	1.482	1.568	1.411	1.512	1.133
1.109	0.918	1.002	0.979	1.063	1.000	1.051	1.006
			1.436	1.362	1.653	1.573	0.873
1.197	0.897	0.939	1.073	1.119	1.075	1.000	1.128
			1.370	1.208	1.184	0.980	1.247
1.414	0.934	1.081	1.042	0.943	0.904	0.723	1.081
1.195	0.993	0.973	1.254	1.165	1.309	1.137	1.009
			1.519	1.258	1.248	1.318	1.056
1.446	1.011	0.970	1.378	1.479	1.440	**1.514**	0.990
1.165	0.971	1.008	1.088	1.125	1.053	1.174	0.984
			1.327	1.251	1.128	1.067	1.183
1.156	0.935	0.963	1.398	1.371	1.355	1.337	1.086

1.133	1.015	0.983	1.244	1.162	1.150	1.111	1.075
1.448	0.999	0.947	1.475	1.688	1.458	1.486	1.054
1.152	0.917	1.155	1.520	1.547	1.635	1.669	0.935
1.404	0.972	1.018	1.214	1.313	1.305	1.364	0.994
1.022	1.026	1.047					
0.940	1.027	0.995	1.344	1.223	1.315	1.200	1.028
1.625	0.942	0.917	1.333	1.271	1.343	1.284	0.999
]							
1.261	1.019	1.047	1.372	1.337	1.313	1.321	1.021
1.006	1.047	0.939	1.117	1.015	1.118	1.038	0.944
1.215	0.979	1.020	1.296	1.234	1.189	1.212	1.016
2.331	0.951	0.931	1.557	1.668	1.586	1.541	0.995
1.259	0.946	0.944	1.299	1.350	1.372	1.325	0.982
1.386	1.093	0.924	1.367	1.328	1.388	1.306	1.000
1.093	0.946	0.965	1.310	1.337	**1.515**	1.163	1.120
2.339	0.930	0.847	1.190	1.269	1.196	1.347	0.972
1.218	1.052	1.008	1.198	1.224	1.071	1.129	1.123
1.542	1.006	1.057	1.269	1.352	1.171	1.224	1.060
			1.247	1.285	1.308	1.352	0.958
1.175	1.043	0.967	0.930	1.001	1.092	1.178	0.857
1.286	1.007	0.941	1.384	1.337	1.249	1.305	1.021
1.373	0.998	0.984					
1.131	1.063	0.994	1.140	1.204	1.077	1.155	1.072
1.465	1.056	1.014	1.238	1.265	1.262	1.307	0.977
1.088	1.001	0.930	1.115	1.094	1.089	1.125	1.007
2.259	0.965	0.858	1.182	1.310	1.218	1.350	0.993
0.992	0.969	1.138					
1.580	0.925	0.989	1.214	1.212	1.267	1.217	0.980
1.409	1.085	1.025	1.438	1.324	1.326	1.323	1.001
1.424	1.347	1.062	1.349	1.315	1.168	1.229	1.074
1.183	1.050	0.940	1.556	1.633	1.370	1.498	1.099
1.367	0.941	0.964	1.290	1.376	1.324	1.373	1.022
1.664	1.236	1.389					
1.142	0.973	0.927					
1.164	1.027	1.002	1.205	1.369	1.341	1.447	0.912
1.307	1.041	0.953	1.163	1.248	1.164	1.273	0.978
1.371	1.059	1.090	1.485	1.348	1.359	1.242	1.091
0.994	0.987	0.906	1.022	1.002	1.011	1.011	1.017
0.923	0.996	1.068	1.177	1.209	1.181	1.159	1.052
1.264	0.999	1.067	1.366	1.341	1.352	1.319	1.019
1.310	1.013	1.029	1.885	1.871	1.804	1.831	1.075
5.531	0.952	0.449					
1.440	1.021	1.025	1.288	1.206	1.199	1.152	1.088
1.059	1.082	1.160	0.995	1.012	0.983	1.002	1.018

2.321	1.012	0.895	1.463	1.509	1.401	1.473	1.051
1.551	0.960	0.867	0.907	0.792	0.746	0.855	0.948
1.221	1.002	0.975	1.306	1.240	1.241	1.241	1.014
1.783	0.884	0.826	1.357	1.550	1.423	1.634	0.947
0.530	1.000	1.001	0.424	0.470	0.454	0.531	0.891
			0.461	0.445	0.544	0.526	0.853
1.004	1.110	1.019	0.516	0.524	0.502	0.511	1.034
			0.518	0.532	0.462	0.476	1.128
0.595	1.163	1.001	0.556	0.558	0.821	0.624	0.997
			0.630	0.704	0.596	0.668	1.063
			0.634	0.665	0.622	0.671	1.065
			0.694	0.763	0.928	1.024	0.752
			0.762	0.759	0.789	0.788	0.971
			0.767	0.783	0.785	0.803	0.984
			0.797	0.937	1.188	1.273	0.802
0.994	0.983	1.127	0.810	0.768	0.818	0.729	1.142
1.153	0.925	1.128	0.814	0.682	0.844	0.710	0.970
1.042	0.921	1.036	0.882	0.928	0.892	0.941	0.995
0.928	1.011	0.929	0.939	0.897	0.931	0.891	1.014
			0.943	0.915	0.984	0.958	0.963
0.856	1.014	0.970	0.964	0.953	0.931	0.883	1.041
			1.004	1.018	1.046	1.113	1.039
1.198	1.103	1.091	1.029	0.972	0.981	0.929	1.055
			1.050	1.311	1.227	1.536	0.861
1.111	0.980	0.964	1.118	1.157	1.242	1.184	0.905
			1.130	1.090	1.189	1.151	0.956
			1.142	1.090	1.119	1.071	1.026
0.785	1.086	1.063	1.148	1.257	1.258	1.381	0.918
1.501	0.874	1.011	1.242	1.352	1.143	1.248	1.092
1.038	1.123	1.015	1.258	1.165	1.131	1.050	1.119
0.823	1.097	1.063	1.275	1.287	1.196	1.211	1.072
0.832	0.987	1.052	1.379	1.259	1.017	1.065	1.203
			1.556	1.394	1.515	1.361	1.033
0.328	0.983	0.982					
0.848	0.551	0.998					
0.685	0.986	1.113					
0.782	0.919	1.023					
0.698	0.977	0.920					
0.829	1.049	1.013					
0.832	0.927	0.979					
0.802	1.272	1.282					
0.831	1.188	1.179					
1.175	0.770	1.010					
0.926	0.936	0.936					
1.096	0.992	1.056					
0.988	1.073	1.022					
0.898	1.093	0.940					
1.257	0.953	1.144					
0.931	1.117	0.960					
1.628	0.828	1.150					
1.489	0.770	1.059					
1.290	0.954	1.109					
1.361	1.041	1.271					

1.216	1.053	1.019					
1.084	1.079	1.023					
1.127	0.988	0.966					
1.002	1.090	0.937					
1.247	1.010	1.036					
1.160	0.810	0.853					
1.234	1.012	1.007					
1.278	1.015	0.991					
1.276	0.945	0.929					
0.882	1.045	0.939					
1.604	0.814	0.989					
0.901	1.086	0.701					
1.390	0.959	0.987					
1.317	0.983	1.028					
1.436	1.023	1.049					
1.516	1.083	1.180					
1.098	1.285	1.008					
1.574	0.860	0.878					
1.442	1.116	1.045					
1.078	1.177	0.816					
1.099	1.458	1.050					
1.536	0.969	0.912					
1.537	1.376	1.213					
1.507	1.009	0.823					
1.929	0.933	0.696					
4.072	1.092	0.998					

1.051	**0.392**	**0.402**	**0.351**	**0.373**	1.098	1.028
0.987	0.419	0.399	0.505	0.484	0.895	0.954
0.987	0.515	0.492	0.564	0.528	0.910	0.943
1.015	**0.535**	**0.532**	**0.554**	**0.527**	1.019	0.975
0.993	0.540	0.429	0.562	0.488	0.871	0.980
0.899	0.551	0.573	0.598	0.623	0.903	1.033
0.914	0.560	0.502	0.634	0.572	0.914	0.899
1.069	0.561	0.591	0.468	0.538	0.993	1.008
1.089	**0.578**	**0.606**	**0.578**	**0.589**	1.010	1.014
1.048	0.582	0.618	0.570	0.582	1.013	1.027
1.024	0.586	0.623	0.597	0.599	1.019	1.011
1.023	0.588	0.626	0.662	0.709	0.951	1.017
0.961	0.607	0.564	0.688	0.644	0.901	0.972
0.999	0.611	0.518	0.539	0.459	1.134	0.839
	0.615	0.584	0.710	0.679	0.864	0.941
	0.633	0.479	0.636	0.484	0.995	0.749
0.886	0.635	0.607	0.722	0.656	0.946	0.919
	0.641	0.640	0.613	0.617	1.044	0.989
0.989	**0.653**	**0.650**	**0.640**	**0.625**	0.964	0.965
1.122	0.666	0.726	0.718	0.714	1.026	0.989
1.037	0.670	**0.629**	**0.660**	**0.617**	1.046	0.946
	0.677	0.659	0.732	0.670	0.989	0.929
0.987	0.689	0.739	0.712	0.738	0.959	1.027
0.944	0.691	0.648	0.732	0.691	0.956	0.950
1.043	0.699	0.735	0.653	0.703	0.988	1.037
	0.700	0.653	0.669	0.627	1.046	0.923
1.038	0.701	0.690	0.751	0.666	1.022	0.983
0.923	0.701	0.734	0.729	0.769	1.022	1.005
1.094	0.702	0.729	0.700	0.720	1.075	1.060
1.012	0.704	0.714	0.712	0.723	1.077	0.994
1.016	0.707	0.747	0.661	0.690	0.984	1.027
	0.710	0.687	0.870	0.848	0.952	0.959
1.001	0.710	0.661	0.910	0.868	0.803	0.904
1.067	0.711	0.716	0.688	0.712	1.053	1.021
1.006	0.715	0.714	0.775	0.777	0.942	0.976
	0.717	0.753	0.679	0.717	1.027	0.976
1.094	0.718	0.721	0.784	0.683	1.122	1.051
1.124	0.718	0.763	0.694	0.740	1.055	1.026
0.910	0.719	0.709	0.837	0.830	0.858	0.977
1.135	0.719	0.695	0.664	0.627	1.078	0.974
0.994	0.721	0.736	0.692	0.662	1.053	0.985
1.000	0.721	0.623	0.663	0.602	1.010	0.951
	0.723	0.710	0.785	0.764	0.984	0.997
	0.723	0.655	0.756	0.672	1.007	0.897
1.020	0.726	0.762	0.640	0.674	1.100	1.052
1.093	0.727	0.753	0.684	0.709	1.081	1.002
	0.731	0.761	0.806	0.844	0.906	1.031
1.027	0.732	0.740	0.771	0.750	1.040	0.957
1.009	0.733	0.681	0.795	0.719	0.989	0.983
1.065	0.735	0.749	0.664	0.692	1.092	1.004
	0.738	0.738	0.776	0.781	0.951	0.991
1.012	0.740	0.770	0.793	0.775	1.004	0.973
	0.742	0.715	0.822	0.797	0.928	0.876

	0.745	0.769	0.860	0.893	0.952	1.024
1.063	0.746	0.700	0.735	0.759	0.936	0.957
1.039	0.750	0.827	0.791	0.822	1.027	0.998
	0.751	0.691	0.870	0.804	0.863	0.911
1.058	0.756	0.825	0.733	0.835	1.020	1.038
1.066	0.756	0.675	0.850	0.763	0.889	0.883
1.033	0.757	0.800	0.748	0.803	1.018	1.061
1.060	0.759	0.811	0.767	0.810	0.986	1.031
0.976	0.760	0.764	0.726	0.734	1.008	1.050
1.022	0.764	0.841	0.811	0.805	1.034	0.987
0.837	0.766	0.668	0.771	0.871	0.865	0.991
1.031	0.773	0.724	0.757	0.733	1.001	0.996
1.057	0.776	0.680	0.846	0.857	0.915	0.867
0.979	0.781	0.829	0.743	0.762	1.051	1.063
0.994	0.781	0.723	0.790	0.777	0.999	0.971
0.966	0.783	0.772	0.836	0.825	0.940	0.953
	0.790	0.730	0.841	0.817	0.945	0.949
	0.795	0.705	0.836	0.746	0.950	0.878
0.984	0.797	0.772	0.761	0.768	1.041	0.980
	0.799	0.775	0.764	0.746	1.044	0.961
1.039	0.802	0.786	0.744	0.755	1.044	0.993
0.861	0.808	0.797	0.871	0.868	1.002	0.977
	0.815	0.813	0.832	0.834	0.915	0.937
	0.816	0.741	0.851	0.752	0.889	0.920
0.963	0.818	0.738	0.886	0.856	0.971	0.997
	0.818	0.766	0.775	0.741	1.013	0.951
0.981	0.819	0.827	0.886	0.900	0.923	1.000
0.981	0.821	0.785	0.873	0.807	0.925	0.926
	0.822	0.714	0.962	0.841	0.961	0.948
0.976	0.824	0.798	0.850	0.814	0.966	0.934
1.072	0.826	0.782	0.773	0.828	0.990	1.043
1.081	0.826	0.829	0.737	0.753	1.085	1.044
1.022	0.827	0.779	0.806	0.707	0.992	0.937
1.010	0.827	0.816	0.861	0.858	0.977	0.985
1.002	0.833	0.907	0.940	0.951	0.967	1.045
0.989	0.834	0.804	0.850	0.808	1.002	0.964
1.021	0.834	0.819	0.748	0.743	1.035	1.003
1.019	0.836	0.843	0.821	0.815	1.038	0.987
0.780	0.836	0.808	0.831	0.868	0.946	0.967
0.904	0.837	0.792	0.778	0.735	1.083	0.938
0.991	0.839	0.796	0.882	0.779	0.938	0.936
1.045	0.841	0.876	0.906	0.960	0.968	1.028
1.066	0.844	0.814	0.771	0.806	1.066	1.036
	0.845	0.763	0.872	0.792	0.968	0.894
1.006	0.845	0.757	0.924	0.832	0.910	0.929
	0.847	0.771	0.833	0.764	1.015	0.902
0.960	0.851	0.920	0.868	0.880	1.007	1.028
0.932	0.851	0.795	0.916	0.899	0.929	0.966
0.981	0.851	0.899	0.935	0.891	0.937	0.984
1.014	0.856	0.857	0.890	0.883	0.995	1.014
1.014	0.856	0.841	0.788	0.790	1.047	0.934
0.901	0.858	0.861	0.827	0.837	1.020	0.991
0.975	0.859	0.833	0.877	0.857	1.011	0.971
1.052	0.863	0.876	0.783	0.799	1.059	1.031

1.007	0.864	0.822	0.867	0.842	1.006	0.993
1.035	0.864	0.875	0.803	0.878	1.037	1.022
1.226	0.869	0.853	0.771	0.761	1.057	0.982
	0.871	0.745	0.946	0.990	0.893	1.012
0.968	0.872	0.820	0.891	0.923	0.991	0.933
1.094	0.873	0.944	0.781	0.878	1.081	1.062
	0.874	0.941	0.885	1.008	0.914	1.131
0.925	0.874	0.840	0.971	0.948	0.944	0.961
	0.876	0.845	0.879	0.852	1.061	0.955
1.056	0.877	0.895	0.864	0.907	0.984	1.018
0.982	0.880	0.920	0.926	0.957	1.000	1.020
1.040	0.882	0.917	0.850	0.894	1.032	1.030
1.020	0.882	0.905	0.955	0.962	1.004	0.978
1.024	0.883	0.901	0.869	0.900	0.959	0.997
1.092	0.892	0.914	0.824	0.899	1.051	1.027
0.927	0.892	0.890	0.972	0.923	0.974	0.966
0.997	0.893	0.912	0.840	0.830	1.061	1.008
1.136	0.900	0.947	0.910	0.963	0.987	1.056
1.019	0.901	0.985	0.922	0.990	1.015	1.083
	0.906	0.971	0.814	0.878	1.112	1.062
0.934	0.908	0.873	0.872	0.901	1.011	1.006
0.971	0.908	0.819	0.980	0.889	0.926	0.893
0.922	0.909	0.898	0.936	0.913	0.988	0.949
1.031	0.912	0.960	0.951	0.985	1.039	1.013
	0.913	1.004	0.906	1.011	1.027	1.047
1.040	0.913	0.934	0.904	0.933	1.036	1.015
0.989	0.915	0.885	0.922	0.887	1.022	0.982
0.946	0.915	0.944	0.942	0.944	0.975	0.986
	0.919	0.827	0.909	0.823	1.010	0.891
0.951	0.920	0.942	0.889	0.948	1.000	1.049
1.025	0.924	0.773	0.915	0.850	1.009	0.920
0.971	0.928	0.857	0.927	0.919	1.000	0.975
1.058	0.928	0.887	0.913	0.902	1.019	0.997
0.939	0.932	0.961	0.883	0.924	1.043	1.028
0.981	0.932	0.930	0.990	0.965	0.957	0.957
1.051	0.934	1.010	0.862	0.919	1.124	1.077
0.963	0.935	0.939	0.960	0.971	0.973	0.995
0.951	0.937	0.910	0.934	0.941	0.973	1.004
1.051	0.937	0.937	0.902	0.911	1.063	1.015
	0.938	1.054	1.083	1.224	0.865	1.112
1.036	0.939	1.019	0.921	0.967	1.014	1.043
1.040	0.940	0.938	0.884	0.906	1.036	1.021
0.898	0.941	0.857	0.949	0.869	0.991	0.902
	0.942	0.846	0.995	0.899	0.946	0.982
1.072	0.943	0.888	0.897	0.896	0.976	0.933
1.027	0.952	1.006	1.034	1.078	0.997	1.050
1.007	0.953	1.002	0.939	0.979	1.016	1.029
0.992	0.953	0.973	1.036	0.999	0.952	0.958
	0.956	0.981	1.194	1.233	0.800	1.016
0.949	0.957	0.904	0.968	0.853	1.016	0.868
0.680	0.958	0.802	1.006	0.847	0.952	0.829
1.069	0.961	1.063	0.850	1.006	1.018	0.999
	0.963	1.036	0.900	0.960	1.020	1.052
1.040	0.963	0.889	1.143	1.058	0.944	0.976

	0.965	0.885	0.881	0.813	1.094	0.908
1.037	0.969	1.026	0.888	0.942	1.093	1.071
	0.970	0.909	1.115	1.051	0.869	0.928
0.990	0.971	1.006	0.956	0.985	1.048	1.010
	0.973	0.994	1.059	1.088	0.918	1.011
	0.976	1.136	1.041	1.146	0.996	1.083
1.021	0.977	0.835	1.061	1.007	1.009	0.922
0.985	0.977	0.916	0.950	0.894	0.994	0.946
1.019	0.978	0.977	0.923	0.957	1.029	1.028
0.964	0.978	0.943	1.033	1.001	0.987	0.960
1.035	0.978	0.803	1.069	0.943	0.899	0.877
1.064	0.979	1.023	0.960	0.992	1.068	1.077
0.954	0.980	0.903	1.052	0.991	0.929	0.957
0.908	0.980	0.923	1.131	1.037	0.863	0.933
	0.982	0.982	1.026	1.032	0.957	0.990
1.027	0.984	1.012	0.954	0.936	1.067	1.020
1.029	0.986	1.029	0.892	0.967	1.056	1.068
1.057	0.986	0.970	0.900	0.988	1.076	1.061
	0.986	1.094	0.941	1.050	1.047	1.098
	0.986	0.961	0.932	0.914	0.890	0.954
0.936	0.987	0.986	0.880	0.912	1.086	0.935
0.974	0.989	0.948	1.065	1.053	0.909	0.898
0.840	0.993	1.061	0.861	0.925	1.152	1.058
0.973	0.998	0.932	0.899	0.944	0.980	0.996
0.915	1.000	0.876	1.142	1.007	0.875	0.868
0.900	1.000	0.960	0.986	1.043	0.950	0.975
	1.003	0.905	1.000	0.908	1.002	0.894
	1.003	1.061	1.047	1.125	0.967	1.046
0.957	1.003	0.960	1.042	1.019	0.987	0.968
1.006	1.004	1.020	1.026	1.041	0.978	0.969
	1.005	1.078	0.892	0.975	1.171	1.079
0.731	1.005	0.892	1.189	1.061	0.845	0.879
0.981	1.009	1.005	0.991	1.042	0.986	0.993
	1.009	1.010	1.039	1.047	0.970	0.991
1.083	1.010	1.037	0.928	0.988	1.067	1.053
1.037	1.010	1.021	0.995	0.994	1.056	1.032
1.037	1.011	1.061	0.953	0.995	1.026	1.039
	1.011	1.120	0.979	1.090	1.033	1.096
	1.014	0.946	1.028	0.965	0.985	0.924
	1.016	0.970	1.171	1.161	0.882	0.974
1.050	1.019	1.015	0.950	1.042	1.132	1.054
1.023	1.020	1.081	1.038	1.015	1.067	0.998
	1.021	1.066	1.010	1.060	1.011	1.034
1.096	1.021	1.078	1.119	1.128	0.966	0.996
0.790	1.022	1.269	1.327	1.473	0.769	1.153
1.027	1.024	1.017	0.956	0.983	1.037	1.044
0.991	1.026	1.137	1.077	1.112	0.999	1.033
1.012	1.027	1.026	1.102	1.115	0.933	0.971
0.874	1.027	0.992	1.029	0.986	1.021	1.009
0.988	1.027	1.093	1.004	1.049	1.021	1.040
0.728	1.030	1.041	1.080	1.098	0.953	1.001
0.992	1.031	0.997	1.030	0.999	1.008	1.024
	1.032	1.162	0.910	1.032	1.132	1.116
0.934	1.034	1.008	1.071	1.037	0.973	0.965

1.044	1.035	1.065	1.196	1.115	0.984	0.989
	1.035	1.004	1.081	1.062	0.954	1.006
1.054	1.038	1.067	0.984	1.017	1.019	1.028
1.050	1.040	1.116	1.068	1.062	1.044	1.027
1.026	1.045	1.165	1.018	1.123	1.059	1.086
	1.051	1.091	1.023	1.060	0.988	1.028
0.963	1.053	1.011	1.033	1.038	1.024	1.013
	1.053	1.203	0.953	1.096	1.017	1.106
	1.055	0.807	1.167	0.897	0.904	0.757
1.016	1.055	1.127	0.988	1.061	1.067	1.057
0.904	1.056	1.047	1.118	1.132	0.934	1.009
	1.063	1.012	1.074	1.068	0.981	0.998
0.974	1.066	1.094	1.002	1.034	1.063	1.016
	1.068	0.965	1.258	1.143	0.848	0.895
0.890	1.069	1.166	1.124	1.156	0.994	0.984
1.072	1.070	1.109	0.999	1.039	1.065	1.057
1.064	1.072	1.175	1.053	1.089	1.060	1.073
1.101	1.073	1.112	1.033	1.087	1.053	1.060
0.937	1.074	1.039	1.179	1.108	0.947	0.977
1.080	1.076	1.067	1.030	1.084	1.035	1.020
1.025	1.082	1.110	1.126	1.150	0.989	1.013
1.052	1.084	1.169	0.957	1.114	1.120	1.067
	1.086	1.190	1.226	1.352	0.884	1.057
1.080	1.089	1.083	1.039	1.051	1.047	0.984
	1.092	0.871	1.569	1.260	0.695	0.790
0.986	1.093	1.118	1.031	1.082	1.055	1.019
1.051	1.095	1.155	1.020	1.070	1.047	1.000
0.842	1.097	1.123	1.050	1.118	0.988	1.014
1.048	1.098	1.089	1.006	1.042	1.058	1.012
1.039	1.098	1.076	1.093	1.089	0.960	0.996
1.018	1.101	1.139	1.112	1.158	0.997	1.025
	1.101	1.207	0.968	1.067	1.137	1.085
1.033	1.102	1.142	0.999	1.114	1.042	1.027
0.979	1.102	1.092	1.135	1.101	1.005	0.982
0.995	1.103	1.138	1.122	1.164	0.983	1.021
0.983	1.103	1.123	1.072	1.128	1.002	1.036
	1.106	1.137	1.024	1.060	1.078	1.018
0.929	1.106	1.066	1.092	1.109	1.046	1.004
1.022	1.107	1.152	1.084	1.091	1.085	1.045
1.044	1.107	1.238	1.277	1.212	0.981	1.107
1.009	1.108	1.167	1.098	1.174	0.979	1.042
1.137	1.110	1.010	1.116	1.022	0.993	0.901
0.994	1.111	1.037	1.133	1.129	0.928	0.894
	1.113	1.032	1.133	1.009	1.028	0.983
1.029	1.118	1.188	1.052	1.125	1.055	1.057
0.897	1.118	1.269	1.195	1.296	0.976	1.068
0.811	1.118	0.898	1.214	0.981	0.920	0.795
0.866	1.119	1.146	1.066	1.078	1.145	1.035
0.937	1.120	1.070	1.089	1.090	0.984	0.955
1.067	1.121	1.112	1.064	1.093	1.050	1.000
0.983	1.121	1.068	1.191	1.169	0.959	0.992
	1.123	1.235	1.129	1.166	1.020	1.055
0.973	1.125	1.187	1.168	1.186	0.962	1.029
0.966	1.129	1.122	1.136	1.109	0.993	0.974

	1.130	1.387	1.171	1.447	0.963	1.216
	1.132	1.072	1.095	1.044	0.943	0.951
0.952	1.134	1.126	1.197	1.308	0.965	0.976
1.014	1.134	1.140	1.138	1.187	0.993	1.028
0.980	1.136	1.107	1.182	1.158	0.960	0.991
0.973	1.144	1.216	1.134	1.191	0.967	0.980
0.969	1.144	1.141	1.089	1.168	1.033	1.050
	1.145	1.231	0.909	0.976	1.259	1.064
	1.145	1.142	1.123	1.113	1.029	0.994
1.040	1.146	1.109	1.107	1.100	1.032	1.035
1.006	1.146	1.150	1.126	1.114	0.978	0.974
	1.150	1.275	1.104	1.177	1.038	1.025
1.054	1.150	1.158	1.157	1.155	1.061	1.034
1.009	1.151	1.001	1.028	0.899	1.119	0.861
1.007	1.152	1.211	1.133	1.172	1.030	1.012
0.948	1.157	1.253	1.090	1.182	1.086	1.072
0.974	1.159	1.235	1.099	1.200	1.054	1.081
	1.165	1.141	1.172	1.155	0.993	0.970
1.052	1.165	1.233	1.232	1.311	1.020	1.106
0.977	1.167	1.259	1.235	1.251	0.959	0.977
0.949	1.170	1.206	1.087	1.195	1.022	1.082
0.962	1.171	1.193	1.122	1.205	1.025	1.042
0.880	1.171	1.078	1.218	1.167	0.931	0.943
	1.174	1.093	1.180	1.210	0.962	1.012
	1.174	1.166	1.400	1.246	0.851	0.944
0.963	1.177	1.098	1.423	1.354	0.969	0.937
	1.178	1.163	1.086	1.095	1.060	0.980
1.238	1.179	0.961	1.256	1.064	0.961	0.882
1.010	1.181	1.335	1.050	1.178	1.123	1.119
0.909	1.181	1.095	1.413	1.319	0.835	0.918
0.934	1.185	1.212	1.314	1.369	0.895	1.049
	1.185	1.274	1.196	1.293	0.990	1.065
0.905	1.186	1.088	1.252	1.215	0.944	0.936
	1.186	1.212	0.997	1.025	1.189	1.012
0.945	1.187	1.209	1.113	1.138	0.978	1.007
0.983	1.191	1.304	1.209	1.391	1.000	1.084
0.972	1.194	1.184	1.226	1.199	0.975	0.956
0.980	1.197	1.235	1.107	1.149	1.044	1.014
	1.199	1.271	1.255	1.338	0.954	1.050
0.977	1.200	1.259	1.195	1.346	0.983	1.039
0.965	1.204	1.084	1.270	1.176	1.008	0.959
1.040	1.205	1.263	1.125	1.211	1.023	1.054
1.027	1.205	1.099	1.165	1.099	0.996	0.961
1.034	1.205	1.268	1.152	1.259	1.039	1.025
0.934	1.206	1.265	1.214	1.281	0.992	1.039
0.913	1.208	1.300	1.159	1.255	1.041	1.066
0.882	1.208	1.059	1.290	1.174	0.951	0.933
0.890	1.220	1.122	1.376	1.222	0.889	0.946
0.907	1.220	1.255	1.262	1.280	0.948	0.964
0.927	1.223	1.160	1.309	1.248	0.934	0.939
1.045	1.226	1.266	1.218	1.246	1.030	1.051
1.067	1.229	1.353	1.102	1.062	1.059	1.026
0.928	1.231	1.218	1.249	1.257	0.951	0.986
1.010	1.233	1.270	1.250	1.244	0.994	1.039

0.988	1.239	1.262	1.208	1.310	1.009	1.059
1.029	1.241	1.222	1.344	1.349	0.967	0.988
1.002	1.246	1.138	1.217	1.161	1.034	0.955
1.000	1.248	1.331	1.207	1.241	1.045	1.057
	1.255	1.242	1.144	1.208	1.096	0.967
	1.255	1.428	1.349	1.543	0.930	1.126
0.896	1.261	1.270	1.473	1.457	0.963	0.997
0.938	1.264	1.270	1.251	1.282	0.996	0.953
	1.266	1.557	1.188	1.469	1.065	1.218
0.952	1.270	1.269	1.225	1.272	1.018	1.009
0.995	1.272	1.407	1.119	1.239	1.045	1.058
1.040	1.277	1.225	1.356	1.336	0.913	0.939
0.997	1.278	1.224	1.478	1.267	1.031	1.000
1.035	1.279	1.362	1.247	1.305	1.025	1.031
1.011	1.281	1.440	1.240	1.324	1.068	0.991
0.711	1.281	**1.647**	0.993	1.171	1.188	1.273
1.061	1.287	1.328	1.158	1.275	1.050	1.063
	1.291	1.254	1.214	1.186	1.062	0.962
0.986	1.297	1.318	1.299	1.378	0.960	1.022
1.026	1.314	1.214	1.464	1.361	0.897	0.915
1.014	1.314	1.388	1.278	1.358	1.028	1.046
1.059	1.315	1.452	1.180	1.419	1.033	1.081
0.989	1.315	1.415	1.214	1.305	1.007	1.024
	1.318	1.444	1.467	1.617	0.898	1.085
	1.340	1.401	1.362	1.432	0.983	1.035
	1.344	1.129	1.360	1.150	0.987	0.832
0.988	1.352	1.428	1.443	1.500	0.947	1.055
0.974	1.352	1.384	1.373	1.414	1.019	0.973
0.964	1.362	1.328	1.289	1.573	1.021	1.081
1.054	1.376	1.480	1.223	1.409	1.090	1.134
	1.380	1.250	1.307	1.115	1.185	0.897
	1.381	1.465	1.351	1.481	0.962	0.998
0.953	1.383	1.309	1.317	1.344	0.964	1.060
0.957	1.385	1.506	1.303	1.500	0.984	1.056
0.959	1.388	1.322	1.422	1.363	0.975	0.943
1.047	1.391	1.425	1.380	1.422	1.007	1.014
	1.413	1.488	1.230	1.303	1.148	1.043
1.029	1.422	1.470	1.354	1.431	1.033	1.060
	1.425	1.424	1.482	1.358	0.958	0.951
	1.435	1.415	1.571	1.558	0.923	0.963
1.124	1.436	1.645	1.306	1.456	1.070	1.129
0.965	1.455	1.333	1.350	1.309	1.003	0.967
0.908	1.466	1.488	1.547	1.660	0.920	1.036
0.982	1.467	1.717	1.315	1.458	1.114	1.159
0.979	1.472	1.346	1.487	1.432	0.953	0.929
	1.493	1.733	1.526	1.782	0.978	1.073
	1.500	1.604	1.419	1.526	1.056	1.058
	1.505	1.508	1.509	1.521	0.996	0.992
0.970	1.517	1.455	1.449	1.484	1.004	1.014
0.981	1.552	1.597	1.496	1.616	1.004	1.054
	1.564	1.577	1.402	1.423	1.114	0.999
	1.579	1.560	1.518	1.509	1.039	0.979
0.972	1.610	1.625	1.554	1.639	1.007	1.011
1.000	1.615	1.515	1.984	1.830	0.904	0.930

0.988	1.644	1.632	1.581	1.531	1.007	1.017
	1.644	2.406	1.416	2.084	1.160	1.449
1.060	1.669	1.730	1.653	1.724	1.031	0.998
1.016	1.751	1.983	1.612	1.976	1.009	1.075
1.104	1.933	2.193	1.650	1.952	1.144	1.175
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3	0.399016137	-1.325481002	0.3873349	-1.368346596	0.391820496
4	0.468878398	-1.092714281	0.465107531	-1.104363793	0.465818008
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9	0.530342383	-0.915004046	0.535748828	-0.900371305	0.530647006
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14	0.56932239	-0.812682255	0.564982504	-0.823721903	0.585853431
15	0.579307546	-0.787598638	0.571172165	-0.808002421	0.589814246
16	0.592310804	-0.755573694	0.588958391	-0.763762381	0.598941515
17	0.599129182	-0.739060989	0.598699812	-0.740095277	0.610340105
18	0.605997398	-0.722616496	0.600100847	-0.736723128	0.616062293
19	0.613034094	-0.705960783	0.606995019	-0.720243417	0.617285244
20	0.632661016	-0.660495394	0.610570538	-0.711770119	0.626007149
21	0.637265722	-0.650033033	0.620113914	-0.689394834	0.630036293
22	0.644475927	-0.633801624	0.620579468	-0.688312129	0.633078719
23	0.644879512	-0.632898459	0.623223793	-0.682177782	0.634434997
24	0.658547281	-0.60264107	0.623820856	-0.680796308	0.641757248
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26	0.665625845	-0.587216642	0.637370661	-0.649795482	0.643317355
27	0.666460442	-0.585408849	0.645914613	-0.630584635	0.648201159
28	0.672619018	-0.572138525	0.65794036	-0.603971281	0.651803582
29	0.674372124	-0.568383194	0.661957378	-0.595189766	0.658887887
30	0.67460608	-0.567882774	0.663667534	-0.591467395	0.659619989
31	0.674979374	-0.567084678	0.666340672	-0.58566814	0.661194808
32	0.680986175	-0.554302585	0.667748433	-0.582623409	0.661701535
33	0.684397774	-0.547093028	0.67254811	-0.572290622	0.66965089
34	0.684725295	-0.546402786	0.673724803	-0.569768682	0.671032618
35	0.687430066	-0.540715143	0.679842378	-0.5567278	0.671220384
36	0.692219034	-0.530699484	0.680916689	-0.554449802	0.677720918
37	0.694107882	-0.526768184	0.686055956	-0.543601845	0.682704568
38	0.695474374	-0.523930738	0.686086059	-0.543538542	0.693325597
39	0.696141128	-0.522548283	0.688729267	-0.53799111	0.696351017
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41	0.709380911	-0.495367587	0.698410938	-0.517851941	0.700411478
42	0.70951256	-0.495099872	0.700489612	-0.513564438	0.702963335
43	0.711152802	-0.491768517	0.703329582	-0.507727196	0.710332214
44	0.71659572	-0.480768668	0.703338113	-0.507709697	0.715991396
45	0.721504028	-0.470920647	0.707760327	-0.4986672	0.717823782
46	0.724652459	-0.464638846	0.709232813	-0.49566881	0.720304194
47	0.72497901	-0.463988868	0.715736681	-0.482499176	0.720903154
48	0.725950351	-0.462057212	0.718509746	-0.476920369	0.723893721
49	0.726733803	-0.460501081	0.721616261	-0.470696246	0.727217681
50	0.731280116	-0.451503961	0.724507132	-0.464928203	0.727774016
51	0.732171736	-0.449746012	0.725779007	-0.462397767	0.7285405
52	0.73974605	-0.434898007	0.727930147	-0.458128081	0.729841665
53	0.739951684	-0.434497024	0.729209161	-0.455595409	0.730053638

54	0.751771924	-0.411633059	0.734972352	-0.444238115	0.735256156
55	0.753422445	-0.408469083	0.735254353	-0.443684675	0.742087752
56	0.754784762	-0.405862798	0.736609848	-0.441027409	0.743022895
57	0.754968018	-0.405512565	0.738336579	-0.43764946	0.748127881
58	0.755877075	-0.40377646	0.740275534	-0.433865746	0.749677519
59	0.756155334	-0.403245463	0.740885455	-0.432677584	0.750031471
60	0.756350623	-0.402872913	0.744324151	-0.425997047	0.75241399
61	0.761391676	-0.393289298	0.745926137	-0.422895315	0.757769828
62	0.766096669	-0.384401646	0.752281703	-0.410655094	0.759106804
63	0.767754104	-0.381283776	0.754715546	-0.405995103	0.766334213
64	0.770203119	-0.376689129	0.759949326	-0.396024873	0.766341498
65	0.770849643	-0.37547861	0.761970208	-0.392193504	0.766931195
66	0.770867735	-0.37544475	0.762860221	-0.390509358	0.769153673
67	0.772352168	-0.372669274	0.768342663	-0.380178231	0.769434776
68	0.775704611	-0.366420718	0.768611577	-0.379673388	0.769905253
69	0.777841251	-0.362452349	0.769761409	-0.37751675	0.770110004
70	0.77857761	-0.361087238	0.771997998	-0.373330989	0.770253693
71	0.779143643	-0.360038766	0.773651718	-0.370243854	0.771261523
72	0.782551991	-0.353741491	0.775026151	-0.367683103	0.771347215
73	0.796705234	-0.327882042	0.776910638	-0.364179428	0.771631124
74	0.796850053	-0.327619824	0.777715075	-0.362686392	0.774228354
75	0.798090695	-0.325375392	0.779934676	-0.3585748	0.778643637
76	0.798470701	-0.324688625	0.788247655	-0.343279121	0.779154395
77	0.799395807	-0.32301809	0.792314182	-0.335855469	0.779848014
78	0.801482415	-0.319257228	0.792559937	-0.335408052	0.781861589
79	0.801763519	-0.318751321	0.792612665	-0.335312075	0.782483987
80	0.802454082	-0.317509253	0.792642277	-0.335258177	0.785062387
81	0.804357352	-0.314091504	0.794211485	-0.332404871	0.785542468
82	0.805843442	-0.311428514	0.804496197	-0.313842493	0.790749436
83	0.80946132	-0.304965951	0.804710851	-0.313457608	0.794288562
84	0.811475958	-0.301379744	0.805566354	-0.311924667	0.795210347
85	0.812559778	-0.299454142	0.808987846	-0.305810067	0.80295575
86	0.813481185	-0.297819117	0.809042001	-0.305713494	0.803356716
87	0.817340786	-0.290990366	0.811621698	-0.301120661	0.805772645
88	0.818570851	-0.288820801	0.81369961	-0.297431796	0.808062135
89	0.819157822	-0.287786661	0.818320557	-0.289262001	0.809374814
90	0.820348609	-0.285690978	0.81961285	-0.286985491	0.810959147
91	0.82211894	-0.282580964	0.820377198	-0.285640702	0.811430056
92	0.824215578	-0.278906364	0.82244372	-0.282011136	0.821304164
93	0.825469137	-0.276713818	0.823331077	-0.280455412	0.8215294
94	0.827589406	-0.273012917	0.825058014	-0.277432528	0.825206029
95	0.834104549	-0.261699868	0.835045425	-0.260073415	0.836415758
96	0.835291196	-0.259648863	0.836532231	-0.257506967	0.837837207
97	0.840718745	-0.250304854	0.836701867	-0.257214441	0.842945384
98	0.840866359	-0.250051568	0.840856311	-0.250068808	0.844588748
99	0.8433346	-0.24582295	0.841103012	-0.249645594	0.846701047
100	0.84602389	-0.241229691	0.841639774	-0.248725211	0.849070256
101	0.84705	-0.239480964	0.84752517	-0.238671881	0.849146512
102	0.847597254	-0.23854918	0.848245468	-0.237446277	0.852511891
103	0.85084002	-0.233040201	0.851784603	-0.231439443	0.854593576
104	0.851396467	-0.232096992	0.853286516	-0.228897845	0.856906983
105	0.851624206	-0.231711138	0.858142099	-0.220711534	0.858348379
106	0.858183309	-0.220642252	0.858237026	-0.220551952	0.861413565
107	0.858527879	-0.220063111	0.858733505	-0.219717612	0.86334724

108	0.859819496	-0.217894272	0.862033585	-0.214184017	0.87198196
109	0.859978957	-0.217626737	0.869293099	-0.202085403	0.873342399
110	0.860195975	-0.217262714	0.870028109	-0.200866082	0.873506258
111	0.86269453	-0.213078286	0.871163791	-0.198984103	0.873955541
112	0.866109932	-0.207377943	0.872459328	-0.196840218	0.882013906
113	0.866407654	-0.206882108	0.873074356	-0.195823568	0.882441307
114	0.867639344	-0.20483262	0.874175543	-0.194005079	0.887790949
115	0.872325362	-0.19706176	0.874498441	-0.193472283	0.889372745
116	0.872851434	-0.196191978	0.876563491	-0.190069502	0.892630903
117	0.873517349	-0.195091739	0.878262101	-0.187276545	0.8942307
118	0.875980996	-0.191028524	0.87958334	-0.185107817	0.894435082
119	0.877856478	-0.187943004	0.882745441	-0.179930629	0.895724587
120	0.879724108	-0.184876947	0.886891448	-0.17317056	0.898535911
121	0.883063692	-0.179410597	0.886925065	-0.173115876	0.899378397
122	0.883811791	-0.178188917	0.89108785	-0.166360424	0.901152918
123	0.884273959	-0.177434692	0.891209606	-0.166163311	0.903711409
124	0.886502183	-0.173803911	0.89322853	-0.162898764	0.903945349
125	0.888387208	-0.170739475	0.893773879	-0.162018213	0.903986462
126	0.889137207	-0.16952203	0.894562177	-0.160746333	0.904316324
127	0.890004487	-0.168115485	0.896028307	-0.158383785	0.905951408
128	0.890675903	-0.167027531	0.896451182	-0.157703074	0.90686048
129	0.900563032	-0.151100839	0.897452052	-0.156093233	0.90741636
130	0.900966846	-0.150454077	0.899428988	-0.152918713	0.909515337
131	0.901432414	-0.149708767	0.90146939	-0.149649591	0.909776821
132	0.901998339	-0.148803318	0.903187873	-0.14690198	0.910165793
133	0.905682721	-0.142922362	0.90732909	-0.14030218	0.910815288
134	0.908646412	-0.138209097	0.911117874	-0.134290383	0.913031265
135	0.910749652	-0.134873557	0.9126583	-0.13185328	0.913078337
136	0.912535461	-0.132047472	0.913922992	-0.129855487	0.913764423
137	0.914258568	-0.129325852	0.916495413	-0.125800435	0.914296157
138	0.915546431	-0.127295042	0.917747512	-0.123830797	0.918442525
139	0.91823151	-0.123070154	0.918872992	-0.122062631	0.920495517
140	0.920214652	-0.119957667	0.920315963	-0.119798842	0.921393942
141	0.920502651	-0.119506218	0.921063867	-0.118626898	0.923198421
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144	0.922695322	-0.116073752	0.925596869	-0.111544111	0.930313252
145	0.927977022	-0.107839012	0.926286133	-0.110470179	0.931707752
146	0.929123467	-0.106057772	0.928141342	-0.107583572	0.9321547
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148	0.933711229	-0.098951662	0.929544346	-0.105404401	0.935776182
149	0.934128427	-0.098307185	0.930926513	-0.103260809	0.936930633
150	0.939506749	-0.09002457	0.933984387	-0.098529662	0.940459645
151	0.945986569	-0.080108395	0.936674461	-0.094380365	0.941508119
152	0.946250785	-0.079705503	0.936841536	-0.094123054	0.943342473
153	0.948280574	-0.076614113	0.936874404	-0.09407244	0.945711178
154	0.948827034	-0.075782979	0.941588722	-0.086831054	0.946739685
155	0.949502815	-0.074755818	0.941882749	-0.086380619	0.948064182
156	0.95029479	-0.073552975	0.942306177	-0.085732193	0.953480949
157	0.950977718	-0.072516556	0.944319553	-0.082652953	0.953833079
158	0.951518668	-0.071696133	0.945051442	-0.081535233	0.955724141
159	0.956907618	-0.063548445	0.946462742	-0.07938238	0.956089297
160	0.958373601	-0.061339926	0.947799919	-0.077345557	0.959064573
161	0.959675151	-0.059381957	0.948705833	-0.075967278	0.96043322

162	0.9597922	-0.059206005	0.951300886	-0.072026373	0.960485983
163	0.960703759	-0.057836462	0.953895951	-0.068096187	0.962660835
164	0.961229145	-0.057047703	0.954972308	-0.066469197	0.963312859
165	0.967485626	-0.047687867	0.956331427	-0.064417409	0.96396064
166	0.970314589	-0.04347553	0.967949275	-0.04699665	0.96435271
167	0.978319957	-0.031621723	0.968206199	-0.046613764	0.964869878
168	0.979248444	-0.030253165	0.969949087	-0.044019073	0.966135403
169	0.979542027	-0.029820702	0.971097808	-0.042311485	0.966298995
170	0.980062505	-0.029054333	0.973955421	-0.038072355	0.966371149
171	0.982093576	-0.0260676	0.974612739	-0.037099016	0.972407745
172	0.982131695	-0.026011604	0.976468172	-0.034355074	0.972691228
173	0.983189661	-0.02445835	0.97793842	-0.032184472	0.977257912
174	0.984694003	-0.022252624	0.978469415	-0.031401339	0.97839768
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177	0.990472534	-0.013811125	0.979990481	-0.029160359	0.98252163
178	0.992129184	-0.011400111	0.982872258	-0.02492417	0.983265271
179	0.992453804	-0.010928145	0.982935188	-0.024831803	0.990010995
180	1	0	0.988263932	-0.017031707	0.990257812
181	1.000476147	0.000686772	0.988505048	-0.016679761	0.990485097
182	1.012477924	0.017890451	0.990083922	-0.014377278	0.993501915
183	1.013363885	0.019152319	0.990417263	-0.013891634	0.994729635
184	1.020125356	0.028746446	0.991362189	-0.012515861	0.995688625
185	1.023162771	0.033035677	0.994144014	-0.008473235	1.000372288
186	1.023989547	0.034200988	0.9956554	-0.006281588	1.001639502
187	1.027809233	0.039572517	1	0	1.002410714
188	1.028241232	0.04017877	1.001320018	0.001903128	1.003388906
189	1.029351451	0.041735645	1.001815362	0.002616639	1.01309541
190	1.031226217	0.044360847	1.003525505	0.005077283	1.016080172
191	1.032210914	0.045737791	1.006032462	0.008676858	1.01678744
192	1.034230171	0.048557298	1.009561587	0.013728924	1.019946037
193	1.035377727	0.050157188	1.010056597	0.014436135	1.02387185
194	1.038636537	0.054690882	1.013188405	0.018902472	1.026285734
195	1.039316542	0.055635119	1.016435114	0.023518121	1.033555383
196	1.040656501	0.057493943	1.01913609	0.027346714	1.033561061
197	1.041142278	0.058167235	1.023019543	0.032833705	1.03582872
198	1.042969457	0.060696909	1.023079755	0.032918615	1.03638734
199	1.044503379	0.06281716	1.024544857	0.03498315	1.037958526
200	1.050818455	0.071513443	1.026678316	0.037984221	1.039413627
201	1.05288111	0.074342538	1.027334349	0.038905788	1.03968636
202	1.054696778	0.076828289	1.027502764	0.039142275	1.040007774
203	1.055806928	0.078346038	1.030465534	0.043296251	1.041132873
204	1.056996294	0.079970318	1.031948742	0.045371313	1.042380261
205	1.057434387	0.080568148	1.032778497	0.046530868	1.048299809
206	1.058705352	0.082301129	1.03589296	0.050874936	1.048689078
207	1.065893755	0.092063642	1.039567496	0.055983431	1.04917433
208	1.07201026	0.100318714	1.040817127	0.057716607	1.050437946
209	1.073457195	0.102264663	1.043074564	0.060842292	1.052410503
210	1.076281008	0.106054803	1.045022911	0.063534572	1.05751601
211	1.078685829	0.109274736	1.050651686	0.071284463	1.062495933
212	1.078728443	0.109331729	1.053957614	0.075816849	1.062903515
213	1.080443639	0.111623817	1.055074262	0.077344547	1.063362027
214	1.080873891	0.11219821	1.05638319	0.079133249	1.065451301
215	1.082932573	0.114943419	1.063171207	0.088373939	1.070037597

216	1.087838595	0.121464516	1.063633008	0.089000454	1.073772769
217	1.09023029	0.124632909	1.065644081	0.091725666	1.088691093
218	1.091907758	0.126850986	1.068573377	0.095685978	1.094980366
219	1.093118593	0.128449928	1.072429428	0.100882713	1.098030517
220	1.093572082	0.129048317	1.072585378	0.101092491	1.099479223
221	1.100954268	0.138754543	1.074967405	0.104292915	1.102618229
222	1.102958438	0.141378428	1.075694883	0.105268921	1.103703031
223	1.105737845	0.145009383	1.076474633	0.106314323	1.104571425
224	1.110382975	0.151057353	1.0782872	0.108741489	1.104937571
225	1.111910575	0.153040764	1.078363284	0.108843282	1.10536728
226	1.114273988	0.15610402	1.083020625	0.115060718	1.108741032
227	1.114551093	0.156462754	1.083692532	0.115955489	1.110178353
228	1.115906056	0.158215577	1.088191894	0.121932986	1.111743228
229	1.121711474	0.165701634	1.092122165	0.127134246	1.115322536
230	1.123006376	0.167366119	1.09429531	0.13000212	1.11599076
231	1.129631978	0.175852835	1.095650698	0.131787929	1.116070897
232	1.132471315	0.179474508	1.100198053	0.137763255	1.118773665
233	1.134337692	0.181850195	1.103290039	0.141812105	1.12320745
234	1.13597802	0.183934921	1.103732916	0.142391108	1.124910666
235	1.140020354	0.189059583	1.107395004	0.147169918	1.127454259
236	1.140247942	0.189347566	1.107575415	0.147404935	1.128118582
237	1.143373466	0.193296715	1.108272686	0.148312894	1.12891251
238	1.144118706	0.194236745	1.111817997	0.152920641	1.129649645
239	1.147020944	0.197891734	1.114092588	0.155869135	1.129901108
240	1.147851186	0.198935615	1.118098708	0.161047558	1.13416915
241	1.148405455	0.199632089	1.119832666	0.163283169	1.13502341
242	1.151797238	0.203886768	1.120993252	0.164777593	1.143541315
243	1.154899518	0.207767336	1.123664956	0.16821193	1.153124328
244	1.156143584	0.20932058	1.125976261	0.171176412	1.153972485
245	1.163197796	0.218096441	1.125984959	0.171187556	1.155384899
246	1.163515363	0.21849026	1.12600204	0.171209441	1.159856444
247	1.165553419	0.221015126	1.126218468	0.171486714	1.160777644
248	1.167642282	0.223598358	1.128687703	0.174646361	1.161181269
249	1.173936989	0.231354974	1.132145583	0.179059487	1.162563109
250	1.174142134	0.231607062	1.133745093	0.181096307	1.162579532
251	1.174333834	0.231842589	1.134041678	0.181473663	1.166604429
252	1.174989461	0.232647817	1.134067919	0.181507046	1.17019555
253	1.175202537	0.232909415	1.134327835	0.181837658	1.171274359
254	1.176460538	0.234452929	1.145356743	0.195797022	1.171284396
255	1.178149268	0.236522336	1.148070698	0.199211486	1.174943689
256	1.178794564	0.237312313	1.149185938	0.200612244	1.17657778
257	1.196689872	0.259049319	1.156330517	0.209553826	1.176683093
258	1.196887587	0.259287659	1.157202092	0.210640836	1.178221541
259	1.200387694	0.263500434	1.159649032	0.21368824	1.187087124
260	1.201297433	0.264593396	1.161090401	0.215480303	1.189878961
261	1.201852576	0.26525994	1.164483964	0.219690773	1.194518725
262	1.202301325	0.265798515	1.164863227	0.22016057	1.195098855
263	1.202905996	0.266523904	1.164869701	0.220168588	1.208858396
264	1.203566407	0.267315745	1.172671094	0.229798428	1.212539982
265	1.20598921	0.270216999	1.176649096	0.234684139	1.213748834
266	1.215576195	0.281640327	1.18052109	0.239423816	1.214122998
267	1.226089305	0.294064065	1.191210897	0.252428857	1.214494392
268	1.228406398	0.296787931	1.191770521	0.253106467	1.225925646
269	1.229518357	0.298093275	1.194628542	0.256562096	1.229722476

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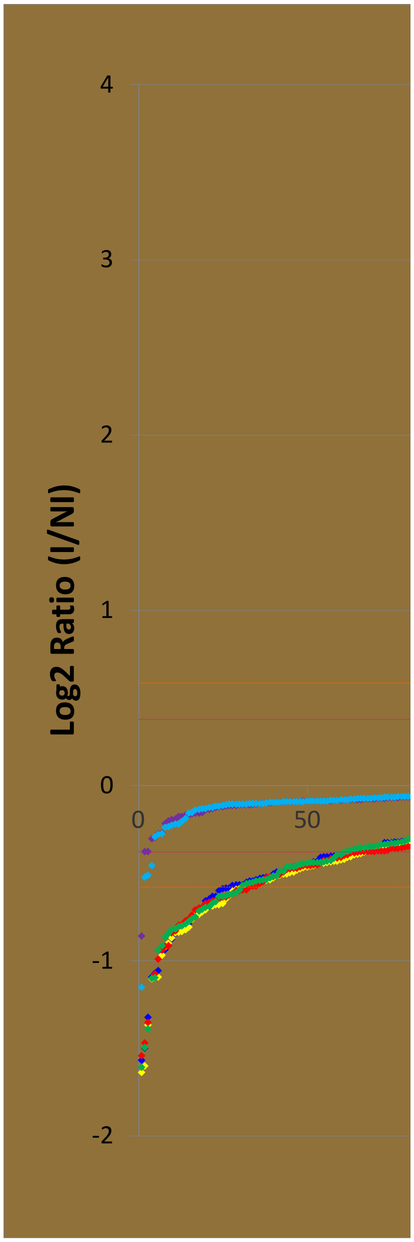

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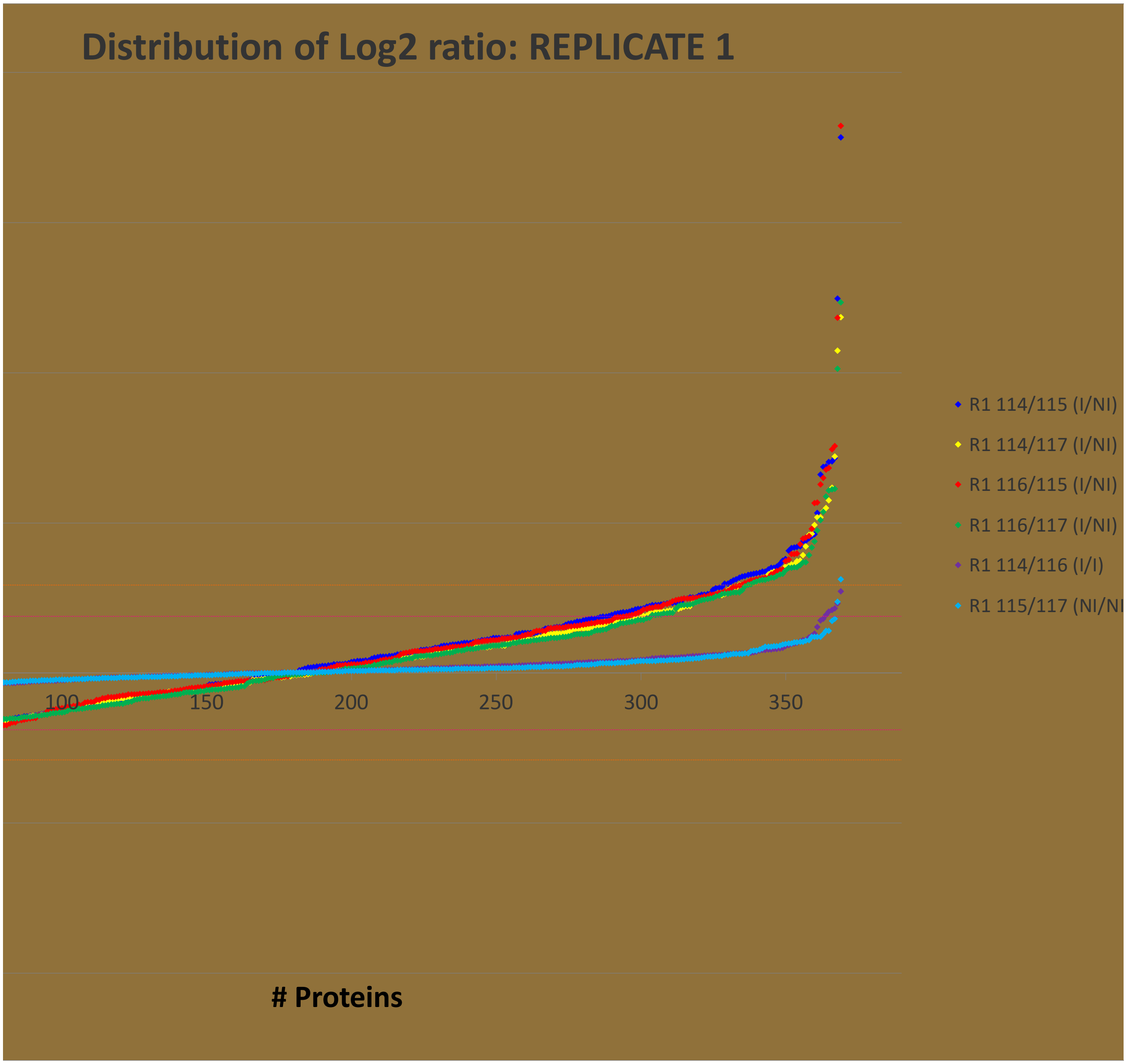

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11	0.535	-0.902415121	0.535	-0.901148387	0.552
12	0.538	-0.893717267	0.543	-0.880041049	0.595
13	0.556	-0.847889517	0.558	-0.842171627	0.596
14	0.557	-0.845454341	0.601	-0.734981488	0.604
15	0.571	-0.809132007	0.612	-0.708608333	0.607
16	0.602	-0.731149017	0.621	-0.687300302	0.617
17	0.614	-0.703837998	0.623	-0.681606163	0.622
18	0.630	-0.667612684	0.630	-0.665435829	0.630
19	0.630	-0.666425531	0.640	-0.643959422	0.632
20	0.634	-0.657925758	0.649	-0.623825568	0.635
21	0.636	-0.653803152	0.650	-0.622080599	0.639
22	0.641	-0.640838139	0.651	-0.619287417	0.645
23	0.644	-0.635050136	0.660	-0.599958395	0.645
24	0.645	-0.632921257	0.662	-0.594396882	0.658
25	0.646	-0.630469959	0.665	-0.588846362	0.661
26	0.650	-0.621696133	0.673	-0.571790708	0.663
27	0.653	-0.615880873	0.677	-0.562924964	0.674
28	0.658	-0.604304815	0.682	-0.551232767	0.679
29	0.658	-0.603118173	0.690	-0.535063947	0.682
30	0.665	-0.588191683	0.693	-0.530041125	0.689
31	0.683	-0.550968629	0.693	-0.52905761	0.706
32	0.684	-0.547591681	0.696	-0.52287173	0.708
33	0.686	-0.542804584	0.704	-0.506180974	0.713
34	0.694	-0.527401027	0.715	-0.484944546	0.714
35	0.695	-0.524668078	0.719	-0.475213483	0.726
36	0.697	-0.521396648	0.720	-0.473997115	0.728
37	0.699	-0.516143783	0.720	-0.472970014	0.731
38	0.705	-0.503433373	0.725	-0.464576466	0.731
39	0.707	-0.500220493	0.725	-0.463159041	0.734
40	0.710	-0.494036765	0.737	-0.440060675	0.737
41	0.721	-0.472400695	0.740	-0.434051966	0.739
42	0.722	-0.469426213	0.746	-0.422802947	0.746
43	0.729	-0.456688672	0.747	-0.421037195	0.747
44	0.733	-0.448821242	0.750	-0.41477584	0.758
45	0.734	-0.445929108	0.755	-0.405853307	0.759
46	0.738	-0.438648	0.759	-0.398107189	0.760
47	0.741	-0.431492081	0.760	-0.395319657	0.762
48	0.745	-0.425582177	0.763	-0.389350912	0.763
49	0.753	-0.409520788	0.764	-0.388608244	0.767
50	0.753	-0.408551758	0.765	-0.386939166	0.768
51	0.755	-0.405553343	0.768	-0.381520194	0.768
52	0.762	-0.392705645	0.769	-0.379683586	0.773
53	0.762	-0.39237047	0.775	-0.367575803	0.776

54	0.764	-0.388362322	0.781	-0.357162246	0.780
55	0.764	-0.387536104	0.781	-0.35698037	0.781
56	0.766	-0.383781382	0.783	-0.35240632	0.784
57	0.767	-0.381897903	0.788	-0.343521553	0.785
58	0.768	-0.381512054	0.790	-0.340093149	0.788
59	0.769	-0.379213737	0.791	-0.338555681	0.789
60	0.769	-0.378991624	0.792	-0.33702513	0.793
61	0.775	-0.36688835	0.792	-0.336691879	0.794
62	0.776	-0.365923275	0.793	-0.334567647	0.796
63	0.780	-0.358645695	0.796	-0.329986315	0.799
64	0.781	-0.356471996	0.804	-0.315454364	0.800
65	0.788	-0.344187908	0.806	-0.311429976	0.803
66	0.795	-0.331401705	0.807	-0.30965958	0.809
67	0.797	-0.327737705	0.808	-0.307600823	0.812
68	0.803	-0.316233294	0.809	-0.305346155	0.814
69	0.803	-0.316176131	0.809	-0.305198064	0.814
70	0.805	-0.312900199	0.812	-0.300011133	0.814
71	0.806	-0.311255571	0.818	-0.290273179	0.818
72	0.808	-0.307676531	0.821	-0.283852141	0.819
73	0.809	-0.305662058	0.825	-0.277771499	0.821
74	0.809	-0.305048022	0.826	-0.275294062	0.823
75	0.810	-0.304132752	0.831	-0.26632753	0.824
76	0.814	-0.297634374	0.832	-0.265740328	0.828
77	0.814	-0.296219207	0.832	-0.265592376	0.828
78	0.822	-0.282669125	0.837	-0.255899744	0.828
79	0.822	-0.282296834	0.839	-0.252965215	0.830
80	0.823	-0.281081511	0.840	-0.252056313	0.834
81	0.824	-0.27847077	0.840	-0.250962494	0.836
82	0.826	-0.275311931	0.844	-0.244702504	0.837
83	0.827	-0.273637461	0.847	-0.239858012	0.842
84	0.828	-0.272888647	0.847	-0.239535273	0.844
85	0.828	-0.27243894	0.852	-0.230461607	0.844
86	0.832	-0.265291307	0.854	-0.228460325	0.849
87	0.835	-0.259477851	0.854	-0.227062976	0.851
88	0.836	-0.259141833	0.856	-0.224633164	0.851
89	0.836	-0.257897752	0.858	-0.22152201	0.852
90	0.840	-0.251231488	0.862	-0.214233458	0.856
91	0.846	-0.241804146	0.865	-0.209832258	0.860
92	0.849	-0.236175897	0.867	-0.205623506	0.860
93	0.850	-0.233779733	0.867	-0.205386821	0.862
94	0.852	-0.231825014	0.868	-0.203682905	0.863
95	0.857	-0.222024748	0.870	-0.201541377	0.863
96	0.858	-0.22102972	0.870	-0.200815795	0.866
97	0.860	-0.216910053	0.870	-0.200774421	0.868
98	0.864	-0.211530007	0.873	-0.195216948	0.868
99	0.866	-0.207068147	0.877	-0.189090878	0.870
100	0.868	-0.204605786	0.878	-0.187830404	0.876
101	0.869	-0.202392822	0.878	-0.18724447	0.876
102	0.869	-0.202085317	0.882	-0.180632857	0.877
103	0.872	-0.197623818	0.884	-0.177309036	0.879
104	0.873	-0.196094687	0.886	-0.174590427	0.883
105	0.874	-0.194033109	0.888	-0.171841008	0.885
106	0.878	-0.188041745	0.889	-0.170529591	0.885
107	0.879	-0.186244071	0.889	-0.169989077	0.885

108	0.882	-0.18188517	0.894	-0.162319606	0.886
109	0.882	-0.180399516	0.894	-0.161142109	0.888
110	0.885	-0.176900663	0.897	-0.157495558	0.892
111	0.886	-0.174878739	0.897	-0.156884063	0.896
112	0.886	-0.174173023	0.900	-0.151681421	0.897
113	0.892	-0.164913825	0.901	-0.151083282	0.900
114	0.897	-0.15699107	0.902	-0.14926428	0.901
115	0.901	-0.150174882	0.903	-0.147796305	0.904
116	0.901	-0.149937478	0.905	-0.14420562	0.904
117	0.904	-0.14607146	0.905	-0.143298425	0.905
118	0.906	-0.141784657	0.907	-0.141515764	0.905
119	0.907	-0.141593717	0.909	-0.138417288	0.905
120	0.909	-0.137807583	0.911	-0.134144131	0.906
121	0.909	-0.137115572	0.915	-0.128762992	0.909
122	0.910	-0.136027051	0.919	-0.122373753	0.910
123	0.912	-0.132481925	0.924	-0.114109057	0.913
124	0.913	-0.13149595	0.925	-0.113068109	0.913
125	0.917	-0.125488778	0.925	-0.113032224	0.916
126	0.919	-0.122327884	0.925	-0.112058628	0.921
127	0.919	-0.122111081	0.928	-0.108559365	0.922
128	0.921	-0.118780713	0.928	-0.108241829	0.927
129	0.921	-0.118644556	0.928	-0.107034943	0.927
130	0.923	-0.116255314	0.933	-0.100532159	0.928
131	0.930	-0.104284682	0.935	-0.09690874	0.929
132	0.931	-0.10382161	0.935	-0.096211782	0.931
133	0.933	-0.099584305	0.936	-0.095024274	0.931
134	0.938	-0.091608749	0.936	-0.09490744	0.931
135	0.939	-0.091371407	0.936	-0.094707606	0.931
136	0.939	-0.090405264	0.937	-0.093842275	0.934
137	0.940	-0.089202153	0.940	-0.088826564	0.935
138	0.941	-0.087949295	0.940	-0.088500465	0.940
139	0.942	-0.08640405	0.941	-0.087821256	0.942
140	0.943	-0.085379183	0.943	-0.084543158	0.942
141	0.943	-0.085130288	0.944	-0.082385618	0.943
142	0.944	-0.082570694	0.946	-0.080016178	0.946
143	0.945	-0.080975755	0.948	-0.077185358	0.950
144	0.946	-0.079816896	0.949	-0.075458183	0.951
145	0.947	-0.078156519	0.953	-0.070154698	0.953
146	0.948	-0.077740019	0.961	-0.057606428	0.953
147	0.949	-0.075033655	0.963	-0.054265896	0.956
148	0.953	-0.069904568	0.965	-0.051697484	0.958
149	0.954	-0.068278466	0.968	-0.046875239	0.962
150	0.954	-0.068146386	0.971	-0.043116924	0.963
151	0.964	-0.0525092	0.972	-0.040579244	0.967
152	0.969	-0.045523095	0.972	-0.040295077	0.968
153	0.971	-0.043143459	0.974	-0.038498369	0.975
154	0.971	-0.041968279	0.979	-0.030245247	0.976
155	0.974	-0.037490573	0.981	-0.028059975	0.981
156	0.974	-0.037266881	0.982	-0.026210704	0.983
157	0.977	-0.033237751	0.984	-0.023348036	0.984
158	0.979	-0.031220353	0.984	-0.022797765	0.984
159	0.979	-0.030827367	0.988	-0.017859995	0.989
160	0.981	-0.027974932	0.988	-0.017435703	0.993
161	0.985	-0.021412753	0.993	-0.009444185	0.994

162	0.987	-0.018401249	0.996	-0.005198477	0.995
163	0.988	-0.018096105	0.997	-0.004919752	0.996
164	0.990	-0.013829507	1.000	-9.2636E-05	0.996
165	0.993	-0.009691373	1.001	0.001226917	1.000
166	0.995	-0.006834292	1.002	0.002917304	1.000
167	0.996	-0.005584073	1.002	0.003578982	1.005
168	1.004	0.005584073	1.003	0.00484646	1.006
169	1.004	0.005662777	1.004	0.005178897	1.011
170	1.005	0.006481274	1.010	0.013642747	1.011
171	1.007	0.009920826	1.012	0.016650565	1.014
172	1.010	0.014401295	1.012	0.017402935	1.016
173	1.012	0.017844379	1.014	0.019631886	1.017
174	1.018	0.025606414	1.015	0.020984364	1.017
175	1.020	0.028917195	1.018	0.026260087	1.017
176	1.022	0.031737792	1.021	0.030427471	1.019
177	1.029	0.041727501	1.029	0.041883896	1.019
178	1.033	0.046864754	1.031	0.043489765	1.026
179	1.036	0.050747634	1.034	0.048201395	1.026
180	1.038	0.053772858	1.039	0.054828356	1.028
181	1.040	0.056941902	1.040	0.057244484	1.028
182	1.042	0.059834161	1.042	0.059362499	1.028
183	1.044	0.062189195	1.046	0.064512002	1.029
184	1.049	0.069263639	1.046	0.065073084	1.033
185	1.050	0.070351958	1.049	0.069162175	1.033
186	1.052	0.073382144	1.049	0.069211949	1.036
187	1.056	0.078996863	1.050	0.071001907	1.038
188	1.057	0.080190426	1.059	0.083206442	1.040
189	1.058	0.080919575	1.060	0.084227408	1.042
190	1.060	0.083533512	1.061	0.085251925	1.043
191	1.062	0.087239091	1.063	0.087624854	1.044
192	1.063	0.088528161	1.068	0.09531803	1.044
193	1.067	0.092983048	1.077	0.106879794	1.044
194	1.067	0.093266587	1.079	0.110134885	1.046
195	1.068	0.095173665	1.086	0.119098324	1.047
196	1.073	0.101198824	1.087	0.120788035	1.048
197	1.074	0.103003577	1.089	0.122548967	1.050
198	1.079	0.109076864	1.089	0.123228018	1.053
199	1.082	0.113549651	1.090	0.124829711	1.054
200	1.088	0.121470711	1.090	0.124981261	1.067
201	1.094	0.128991417	1.091	0.125985192	1.068
202	1.095	0.131230316	1.094	0.129321239	1.071
203	1.099	0.136797042	1.094	0.129678479	1.075
204	1.100	0.137553381	1.094	0.129974214	1.077
205	1.101	0.138336285	1.095	0.130573092	1.079
206	1.101	0.139022564	1.095	0.130733838	1.089
207	1.104	0.14289969	1.096	0.131703884	1.089
208	1.106	0.145973373	1.097	0.133948582	1.092
209	1.111	0.15181081	1.098	0.13518681	1.093
210	1.114	0.156185874	1.099	0.135984905	1.094
211	1.115	0.157514421	1.103	0.140885581	1.094
212	1.117	0.159674817	1.103	0.141004472	1.097
213	1.118	0.161296232	1.105	0.144197569	1.099
214	1.118	0.161381533	1.106	0.14473075	1.109
215	1.118	0.16146429	1.108	0.148205439	1.112

216	1.120	0.163518639	1.117	0.159424194	1.115
217	1.128	0.174288819	1.119	0.161668197	1.116
218	1.130	0.176176843	1.123	0.166938764	1.118
219	1.130	0.176843345	1.125	0.169356782	1.119
220	1.133	0.179950552	1.133	0.179805097	1.120
221	1.138	0.186500298	1.139	0.188378429	1.120
222	1.138	0.187133173	1.142	0.191687556	1.120
223	1.139	0.187407133	1.144	0.193829901	1.122
224	1.140	0.18904491	1.145	0.195892226	1.126
225	1.141	0.190629146	1.146	0.196361044	1.128
226	1.142	0.191758957	1.146	0.196684065	1.131
227	1.148	0.199379726	1.148	0.19897659	1.131
228	1.150	0.201717609	1.153	0.205338611	1.132
229	1.161	0.215262538	1.155	0.207795014	1.138
230	1.163	0.217342518	1.157	0.210033265	1.141
231	1.165	0.220067732	1.161	0.215016047	1.143
232	1.177	0.235529251	1.162	0.216588557	1.147
233	1.179	0.23756533	1.162	0.216674018	1.150
234	1.182	0.241527627	1.164	0.218683285	1.164
235	1.183	0.241935636	1.165	0.219802743	1.168
236	1.190	0.251361833	1.165	0.220486442	1.169
237	1.198	0.26019037	1.170	0.225939035	1.170
238	1.198	0.260214788	1.188	0.248471849	1.171
239	1.199	0.261472702	1.198	0.261030322	1.172
240	1.200	0.262696289	1.204	0.267739423	1.179
241	1.205	0.26923186	1.206	0.270460644	1.180
242	1.205	0.269387056	1.208	0.272757855	1.180
243	1.210	0.274885078	1.209	0.273899039	1.180
244	1.210	0.275469883	1.212	0.277747241	1.181
245	1.214	0.279287504	1.213	0.279154714	1.184
246	1.214	0.279742479	1.223	0.290736966	1.188
247	1.214	0.280185332	1.224	0.291400917	1.189
248	1.217	0.282923926	1.229	0.297628722	1.189
249	1.221	0.287647117	1.234	0.303414352	1.191
250	1.221	0.288613407	1.235	0.304470123	1.196
251	1.238	0.30783752	1.240	0.310261357	1.196
252	1.242	0.312606527	1.245	0.316593537	1.196
253	1.243	0.314010691	1.248	0.320042514	1.199
254	1.244	0.314615837	1.250	0.322466738	1.203
255	1.247	0.318285261	1.251	0.323505118	1.212
256	1.248	0.320093641	1.257	0.329691998	1.215
257	1.253	0.324828951	1.258	0.331189331	1.218
258	1.254	0.326218887	1.259	0.332840137	1.221
259	1.258	0.331340049	1.265	0.339205569	1.224
260	1.269	0.343827182	1.269	0.343929739	1.227
261	1.271	0.345600389	1.271	0.345936374	1.228
262	1.275	0.350561853	1.274	0.349212659	1.228
263	1.282	0.357910291	1.275	0.350688472	1.241
264	1.288	0.364640257	1.275	0.350711608	1.242
265	1.289	0.366507896	1.285	0.361683084	1.246
266	1.290	0.367109622	1.287	0.364121615	1.248
267	1.290	0.36756472	1.302	0.380468425	1.248
268	1.293	0.370473643	1.303	0.381413594	1.249
269	1.295	0.372523497	1.308	0.3868276	1.249

270	1.296	0.374432251	1.310	0.389310167	1.253
271	1.299	0.377003165	1.311	0.390639507	1.258
272	1.306	0.384746627	1.313	0.392393155	1.261
273	1.310	0.389787497	1.313	0.392853646	1.262
274	1.312	0.391534684	1.315	0.395168658	1.267
275	1.314	0.393453504	1.317	0.396709616	1.273
276	1.314	0.394214696	1.324	0.404761441	1.282
277	1.327	0.407631104	1.324	0.40487206	1.291
278	1.333	0.41476356	1.324	0.405334561	1.305
279	1.344	0.426281597	1.327	0.408074703	1.308
280	1.344	0.426714107	1.328	0.409625131	1.308
281	1.345	0.42797026	1.330	0.411315881	1.309
282	1.348	0.431023876	1.330	0.41164194	1.312
283	1.349	0.431649066	1.337	0.418705263	1.313
284	1.357	0.440521675	1.337	0.419088163	1.315
285	1.366	0.449774711	1.337	0.419241255	1.324
286	1.367	0.451232358	1.337	0.419391908	1.326
287	1.370	0.453774149	1.341	0.422999884	1.341
288	1.372	0.456025234	1.348	0.431178094	1.343
289	1.378	0.462144759	1.350	0.433168534	1.352
290	1.379	0.463582761	1.352	0.435053393	1.355
291	1.384	0.468442725	1.352	0.435536125	1.359
292	1.390	0.47483894	1.354	0.436758771	1.367
293	1.398	0.48369986	1.359	0.442901828	1.370
294	1.420	0.505535328	1.362	0.446232342	1.372
295	1.436	0.521654424	1.369	0.452922927	1.388
296	1.438	0.523825568	1.371	0.454849773	1.401
297	1.441	0.527328296	1.376	0.460069374	1.411
298	1.459	0.54478397	1.394	0.479004512	1.423
299	1.463	0.549333883	1.405	0.490845025	1.429
300	1.472	0.557870682	1.411	0.497032068	1.440
301	1.475	0.560775927	1.426	0.512274363	1.440
302	1.482	0.567817754	1.479	0.564596184	1.458
303	1.485	0.569991888	1.502	0.587031013	1.459
304	1.509	0.593159363	1.509	0.593612943	1.493
305	1.519	0.603236425	1.543	0.6254749	1.515
306	1.520	0.603652398	1.547	0.629747678	1.515
307	1.543	0.62589575	1.550	0.631884148	1.521
308	1.544	0.626748486	1.559	0.640808795	1.536
309	1.546	0.628258708	1.567	0.647679565	1.551
310	1.556	0.637502771	1.568	0.649151476	1.554
311	1.556	0.637933974	1.633	0.707680026	1.565
312	1.557	0.638698872	1.645	0.718119125	1.586
313	1.584	0.663379138	1.650	0.722103083	1.635
314	1.620	0.695791668	1.668	0.738537798	1.638
315	1.628	0.703499178	1.688	0.75490373	1.653
316	1.655	0.727128375	1.713	0.776909411	1.804
317	1.879	0.909871084	1.864	0.8986731	1.809
318	1.885	0.914397463	1.871	0.903664008	1.832
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0.046311566	1.038	0.053822678	1.012	0.017250312	1.010
0.046746607	1.042	0.059034903	1.012	0.017528934	1.011
0.05083511	1.042	0.059673295	1.012	0.017749032	1.012
0.053390975	1.044	0.062179213	1.013	0.018635878	1.012
0.056711987	1.047	0.066837112	1.013	0.018782542	1.012
0.059403081	1.049	0.068536236	1.013	0.01922884	1.014
0.060859564	1.049	0.069127777	1.014	0.019602301	1.014
0.0616143	1.049	0.069191054	1.014	0.020564604	1.014
0.061903984	1.050	0.070788926	1.015	0.021850443	1.014
0.062305415	1.051	0.072029598	1.016	0.022234869	1.015
0.064717117	1.055	0.076642153	1.016	0.022583675	1.016
0.066209984	1.059	0.082199108	1.016	0.022777408	1.016
0.067205856	1.059	0.08241389	1.017	0.023797916	1.016
0.069809235	1.060	0.084191742	1.017	0.024631127	1.018
0.074977833	1.065	0.090285881	1.018	0.025844046	1.019
0.075853955	1.065	0.09098205	1.019	0.02701564	1.019
0.093016619	1.065	0.091336219	1.019	0.027556379	1.019
0.09514528	1.067	0.09310627	1.019	0.027672095	1.020
0.098934491	1.071	0.09939838	1.020	0.029159368	1.020
0.103843236	1.074	0.102602461	1.021	0.029709495	1.021
0.107219151	1.074	0.10323458	1.021	0.02973925	1.021
0.110157037	1.079	0.109768668	1.021	0.030399164	1.022
0.123478733	1.086	0.119401353	1.022	0.030915303	1.022
0.123650323	1.088	0.121844164	1.022	0.031702638	1.022
0.127050447	1.089	0.123540413	1.022	0.031936271	1.023
0.128301638	1.091	0.125334947	1.025	0.036327448	1.023
0.129246643	1.092	0.126491186	1.026	0.037620495	1.023
0.12928315	1.102	0.140190212	1.027	0.038442251	1.024
0.133209006	1.103	0.141050422	1.027	0.038527945	1.024
0.13590056	1.104	0.14278277	1.028	0.039704091	1.025
0.149422165	1.111	0.151894243	1.028	0.040169623	1.025
0.152600426	1.112	0.152531324	1.029	0.040650766	1.026

0.157195895	1.113	0.155016142	1.029	0.041042179	1.026
0.158496605	1.116	0.158698585	1.030	0.042617357	1.027
0.160322959	1.121	0.164703078	1.030	0.042979243	1.027
0.162137031	1.125	0.170252012	1.032	0.045180142	1.027
0.163095846	1.129	0.175303204	1.032	0.045417034	1.027
0.163506297	1.129	0.175513378	1.033	0.046458133	1.027
0.16413946	1.132	0.179420491	1.034	0.048135222	1.029
0.165491803	1.137	0.18549655	1.035	0.049221166	1.029
0.170944435	1.138	0.186442251	1.035	0.049389036	1.029
0.173193211	1.143	0.192218792	1.035	0.049794504	1.029
0.177603488	1.145	0.19518379	1.036	0.051550621	1.031
0.177956836	1.151	0.202526604	1.037	0.052963945	1.031
0.178720228	1.152	0.203541936	1.038	0.053713915	1.033
0.18699765	1.152	0.204475498	1.039	0.055404183	1.033
0.190406951	1.153	0.205818734	1.039	0.055484622	1.034
0.193168149	1.155	0.207582872	1.040	0.05699298	1.035
0.198328311	1.156	0.208691244	1.041	0.058175186	1.035
0.202032315	1.157	0.211004064	1.041	0.058200263	1.035
0.218916492	1.159	0.213117342	1.043	0.060441548	1.035
0.223947377	1.160	0.213612297	1.043	0.061260535	1.036
0.225851009	1.163	0.218293746	1.047	0.06583463	1.037
0.22589849	1.165	0.220132666	1.048	0.067130705	1.037
0.227464545	1.165	0.220931975	1.049	0.069308081	1.037
0.228469486	1.171	0.228234188	1.049	0.069628702	1.037
0.238107168	1.174	0.231049399	1.051	0.071407364	1.038
0.238233634	1.176	0.233893834	1.051	0.072257892	1.039
0.238508374	1.178	0.236601091	1.052	0.07281931	1.039
0.238853998	1.184	0.244107128	1.053	0.073854019	1.039
0.240220966	1.191	0.25195395	1.053	0.074174337	1.040
0.243653531	1.192	0.253734887	1.053	0.075136059	1.040
0.248966366	1.195	0.256831815	1.054	0.075297335	1.040
0.249810164	1.197	0.259816578	1.054	0.075717176	1.040
0.249834692	1.200	0.262449859	1.054	0.076271999	1.040
0.252640098	1.200	0.263070489	1.055	0.076642263	1.040
0.257782767	1.200	0.26353833	1.055	0.077483408	1.040
0.257965678	1.205	0.269525313	1.056	0.078883712	1.043
0.258621041	1.210	0.275162617	1.057	0.080393083	1.044
0.261600467	1.210	0.275326407	1.058	0.081738413	1.044
0.266481396	1.211	0.276219847	1.059	0.082433931	1.045
0.277119728	1.212	0.277627137	1.059	0.082656528	1.045
0.281168417	1.217	0.283848741	1.060	0.083622363	1.047
0.284220411	1.224	0.29144469	1.060	0.083741788	1.048
0.28857721	1.226	0.29388709	1.063	0.087723098	1.048
0.291511887	1.229	0.297361363	1.063	0.088636831	1.050
0.294889762	1.231	0.299957412	1.064	0.088828446	1.050
0.296138854	1.241	0.311263049	1.065	0.09028167	1.051
0.296180021	1.242	0.312468128	1.065	0.090771162	1.051
0.311676403	1.246	0.317351798	1.065	0.091115414	1.051
0.312874285	1.248	0.320136791	1.066	0.092476696	1.051
0.317686215	1.249	0.320462363	1.067	0.093153173	1.052
0.31924663	1.253	0.325683641	1.069	0.095640499	1.052
0.320178377	1.261	0.334817433	1.070	0.096995311	1.052
0.320867472	1.263	0.337069041	1.070	0.097988463	1.054
0.321180388	1.272	0.34703729	1.070	0.098283665	1.054

0.325313487	1.273	0.348133952	1.071	0.098924758	1.054
0.331507215	1.273	0.348796673	1.072	0.099939381	1.056
0.334680501	1.280	0.356319689	1.072	0.100565133	1.057
0.335334184	1.284	0.361159432	1.072	0.100866434	1.057
0.341961002	1.290	0.367637011	1.073	0.101346344	1.058
0.347868459	1.305	0.383970588	1.074	0.103282992	1.058
0.358070412	1.306	0.385169425	1.075	0.104275744	1.059
0.368556291	1.307	0.385709909	1.075	0.104749011	1.060
0.383688852	1.318	0.398673468	1.079	0.10927049	1.060
0.387404756	1.319	0.399530958	1.080	0.110685877	1.061
0.387551852	1.319	0.399743646	1.081	0.11285919	1.063
0.388824594	1.321	0.401416282	1.081	0.112980291	1.064
0.3918627	1.323	0.403882687	1.082	0.113365525	1.064
0.393068675	1.324	0.404897518	1.084	0.116939819	1.065
0.394576075	1.325	0.406371522	1.086	0.118407298	1.066
0.405428065	1.337	0.419399758	1.088	0.121403104	1.066
0.407601591	1.341	0.423584686	1.088	0.121560359	1.067
0.422794892	1.343	0.425238275	1.091	0.125904656	1.067
0.425947573	1.347	0.429306643	1.092	0.126338216	1.067
0.435366369	1.350	0.433372958	1.092	0.127436947	1.069
0.438111691	1.352	0.43498872	1.095	0.130532537	1.069
0.442296064	1.361	0.444583992	1.096	0.132402126	1.071
0.450894047	1.361	0.44485693	1.099	0.135755441	1.072
0.454546077	1.364	0.448277909	1.099	0.136484235	1.072
0.456492549	1.373	0.456898088	1.102	0.139641408	1.072
0.473331423	1.381	0.465858532	1.105	0.144182112	1.077
0.486761461	1.425	0.510535533	1.118	0.160924177	1.080
0.496688291	1.427	0.512671518	1.118	0.16146297	1.080
0.509089157	1.439	0.52531646	1.119	0.16173513	1.081
0.514654314	1.447	0.533195771	1.120	0.163986371	1.083
0.525942973	1.473	0.559114682	1.121	0.164213303	1.083
0.52642786	1.486	0.571034764	1.123	0.166770574	1.089
0.544377304	1.498	0.583233404	1.123	0.167432213	1.092
0.54518846	1.512	0.596202793	1.128	0.173133482	1.093
0.578277462	1.514	0.598341275	1.128	0.173578345	1.094
0.599043207	1.524	0.608329122	1.133	0.180156126	1.094
0.599685852	1.536	0.619216356	1.133	0.180293093	1.094
0.605365014	1.541	0.624110478	1.135	0.183000272	1.096
0.618825919	1.571	0.651781501	1.136	0.18332873	1.100
0.633048928	1.572	0.653040296	1.142	0.191503195	1.101
0.636132686	1.573	0.653610397	1.144	0.194487948	1.104
0.645985631	1.587	0.666030762	1.147	0.197404263	1.122
0.665677957	1.598	0.676173733	1.169	0.225850312	1.124
0.709258662	1.634	0.708744797	1.183	0.242436461	1.124
0.712160425	1.669	0.739392986	1.203	0.267034037	1.126
0.724993434	1.685	0.752446696	1.211	0.275737106	1.135
0.85089113	1.706	0.770465346	1.235	0.304749601	1.136
0.855019609	1.769	0.822594889	1.247	0.31889352	1.137
0.873100459	1.773	0.825869262	1.256	0.328799673	1.226
0.909762404	1.790	0.839853341	1.303	0.382086637	1.229
1.005347521	1.831	0.872398312	1.405	0.490878555	1.238

[redacted]		R2 log2 115/116 (I/NI)	R2 log2 115/114 (I/NI)	R2 log2 117/116 (I/NI)
-0.555910842	1	-1.448089751	-1.545833582	-1.332592913
-0.492879285	2	-1.346848135	-1.285134189	-1.244056793
-0.457484923	3	-1.297007771	-1.258201107	-1.190373626
-0.452595753	4	-1.239470056	-1.169064866	-1.138562084
-0.358153732	5	-1.132083671	-1.090440664	-1.112776619
-0.34005745	6	-1.115654672	-1.062152827	-1.002911931
-0.301401742	7	-0.997904285	-0.998251667	-0.995133906
-0.278397628	8	-0.954997253	-0.93337405	-0.992101166
-0.256054866	9	-0.947641706	-0.932029213	-0.983628448
-0.251574501	10	-0.947578896	-0.91048445	-0.878238006
-0.247345778	11	-0.902415121	-0.901148387	-0.856744042
-0.215921369	12	-0.893717267	-0.880041049	-0.749042489
-0.206901373	13	-0.847889517	-0.842171627	-0.747337214
-0.194381328	14	-0.845454341	-0.734981488	-0.726617465
-0.183899732	15	-0.809132007	-0.708608333	-0.721025875
-0.181882327	16	-0.731149017	-0.687300302	-0.696589807
-0.181017761	17	-0.703837998	-0.681606163	-0.685806879
-0.180332928	18	-0.667612684	-0.665435829	-0.667040894
-0.174323762	19	-0.666425531	-0.643959422	-0.66151273
-0.168037391	20	-0.657925758	-0.623825568	-0.65434146
-0.167761387	21	-0.653803152	-0.622080599	-0.64658402
-0.158928699	22	-0.640838139	-0.619287417	-0.632227033
-0.157524474	23	-0.635050136	-0.599958395	-0.631589372
-0.154483321	24	-0.632921257	-0.594396882	-0.604716756
-0.154126692	25	-0.630469959	-0.588846362	-0.597957452
-0.153172872	26	-0.621696133	-0.571790708	-0.591838844
-0.152059564	27	-0.615880873	-0.562924964	-0.568203429
-0.151022496	28	-0.604304815	-0.551232767	-0.558503647
-0.148292553	29	-0.603118173	-0.535063947	-0.551176241
-0.146673241	30	-0.588191683	-0.530041125	-0.537442486
-0.146005708	31	-0.550968629	-0.52905761	-0.502846804
-0.14510253	32	-0.547591681	-0.52287173	-0.498080332
-0.143935713	33	-0.542804584	-0.506180974	-0.487209145
-0.140952782	34	-0.527401027	-0.484944546	-0.485838737
-0.139796301	35	-0.524668078	-0.475213483	-0.461119495
-0.139166095	36	-0.521396648	-0.473997115	-0.457242618
-0.136976777	37	-0.516143783	-0.472970014	-0.452697318
-0.13583183	38	-0.503433373	-0.464576466	-0.45249112
-0.134237675	39	-0.500220493	-0.463159041	-0.44684539
-0.131138883	40	-0.494036765	-0.440060675	-0.440346128
-0.129996027	41	-0.472400695	-0.434051966	-0.437314397
-0.129036325	42	-0.469426213	-0.422802947	-0.422984654
-0.128584373	43	-0.456688672	-0.421037195	-0.419899167
-0.117185579	44	-0.448821242	-0.41477584	-0.399151206
-0.115057998	45	-0.445929108	-0.405853307	-0.397210753
-0.112917501	46	-0.438648	-0.398107189	-0.396239121
-0.109998727	47	-0.431492081	-0.395319657	-0.391419836
-0.109504983	48	-0.425582177	-0.389350912	-0.389684556
-0.107510055	49	-0.409520788	-0.388608244	-0.382952488
-0.106102772	50	-0.408551758	-0.386939166	-0.380606898
-0.105690813	51	-0.405553343	-0.381520194	-0.380397679
-0.101098751	52	-0.392705645	-0.379683586	-0.372117046
-0.099146994	53	-0.39237047	-0.367575803	-0.366707034

-0.098820734	54	-0.388362322	-0.357162246	-0.3577226
-0.09880615	55	-0.387536104	-0.35698037	-0.356456875
-0.098669712	56	-0.383781382	-0.35240632	-0.350621238
-0.09615251	57	-0.381897903	-0.343521553	-0.350023305
-0.094624472	58	-0.381512054	-0.340093149	-0.343528801
-0.094095822	59	-0.379213737	-0.338555681	-0.342602811
-0.092211254	60	-0.378991624	-0.33702513	-0.335378779
-0.090474362	61	-0.36688835	-0.336691879	-0.332732712
-0.090272054	62	-0.365923275	-0.334567647	-0.328838203
-0.090161764	63	-0.358645695	-0.329986315	-0.324168839
-0.082691626	64	-0.356471996	-0.315454364	-0.322469407
-0.081497485	65	-0.344187908	-0.311429976	-0.315979579
-0.080660357	66	-0.331401705	-0.30965958	-0.30495149
-0.076794262	67	-0.327737705	-0.307600823	-0.300853169
-0.076697547	68	-0.316233294	-0.305346155	-0.297552328
-0.075282591	69	-0.316176131	-0.305198064	-0.296769755
-0.074933453	70	-0.312900199	-0.300011133	-0.296131544
-0.074731201	71	-0.311255571	-0.290273179	-0.290631576
-0.072768413	72	-0.307676531	-0.283852141	-0.288464134
-0.072520968	73	-0.305662058	-0.277771499	-0.284787098
-0.070829722	74	-0.305048022	-0.275294062	-0.280414157
-0.070511555	75	-0.304132752	-0.26632753	-0.279281326
-0.069623138	76	-0.297634374	-0.265740328	-0.272796562
-0.067236921	77	-0.296219207	-0.265592376	-0.272184996
-0.067016773	78	-0.282669125	-0.255899744	-0.271483511
-0.063221789	79	-0.282296834	-0.252965215	-0.268488777
-0.063213006	80	-0.281081511	-0.252056313	-0.261627117
-0.059864476	81	-0.27847077	-0.250962494	-0.258518598
-0.058393218	82	-0.275311931	-0.244702504	-0.256388115
-0.056647686	83	-0.273637461	-0.239858012	-0.247982011
-0.056305092	84	-0.272888647	-0.239535273	-0.244537723
-0.055114726	85	-0.27243894	-0.230461607	-0.244047116
-0.054788706	86	-0.265291307	-0.228460325	-0.235927321
-0.054410662	87	-0.259477851	-0.227062976	-0.233487963
-0.054005423	88	-0.259141833	-0.224633164	-0.231968467
-0.053653231	89	-0.257897752	-0.22152201	-0.231242439
-0.053123614	90	-0.251231488	-0.214233458	-0.224996532
-0.052901036	91	-0.241804146	-0.209832258	-0.218345399
-0.0513862	92	-0.236175897	-0.205623506	-0.217797527
-0.051143598	93	-0.233779733	-0.205386821	-0.213745032
-0.050392744	94	-0.231825014	-0.203682905	-0.212060743
-0.049323773	95	-0.222024748	-0.201541377	-0.21194579
-0.047265058	96	-0.22102972	-0.200815795	-0.207499663
-0.045704078	97	-0.216910053	-0.200774421	-0.204476521
-0.043581916	98	-0.211530007	-0.195216948	-0.20371883
-0.043136067	99	-0.207068147	-0.189090878	-0.201695318
-0.042339459	100	-0.204605786	-0.187830404	-0.191215221
-0.041641251	101	-0.202392822	-0.18724447	-0.190404802
-0.04111264	102	-0.202085317	-0.180632857	-0.18936861
-0.03974491	103	-0.197623818	-0.177309036	-0.185860814
-0.039333544	104	-0.196094687	-0.174590427	-0.178716009
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-0.027421872	125	-0.125488778	-0.113032224	-0.12580978
-0.02716351	126	-0.122327884	-0.112058628	-0.119508972
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-0.024919498	131	-0.104284682	-0.09690874	-0.105768839
-0.023347013	132	-0.10382161	-0.096211782	-0.102971299
-0.021438739	133	-0.099584305	-0.095024274	-0.102752015
-0.021026557	134	-0.091608749	-0.09490744	-0.102710894
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-0.017666179	140	-0.085379183	-0.084543158	-0.085937036
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-0.013536452	149	-0.068278466	-0.046875239	-0.055491395
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0.008743293	173	0.017844379	0.019631886	0.023770979
0.009272962	174	0.025606414	0.020984364	0.023994456
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0.010107286	176	0.031737792	0.030427471	0.027489424
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0.013773188	181	0.056941902	0.057244484	0.039251009
0.014164291	182	0.059834161	0.059362499	0.039443587
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0.015905562	185	0.070351958	0.069162175	0.046746607
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0.019361417	189	0.080919575	0.084227408	0.059403081
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0.036557032	215	0.16146429	0.148205439	0.152600426

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0.038496431	219	0.176843345	0.169356782	0.162137031
0.038668576	220	0.179950552	0.179805097	0.163095846
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0.050298744	234	0.241527627	0.218683285	0.218916492
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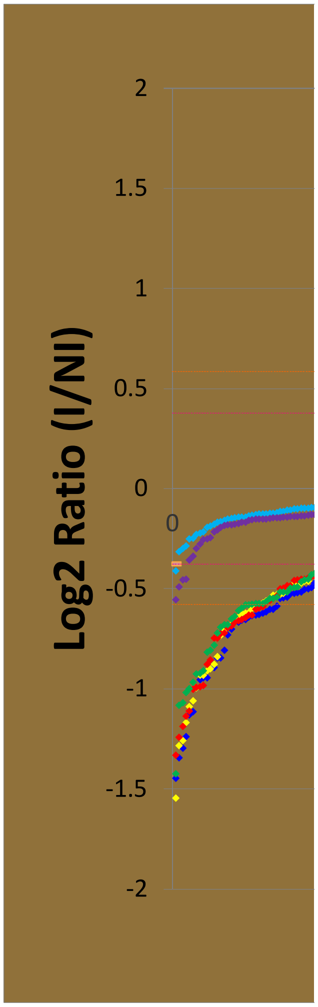

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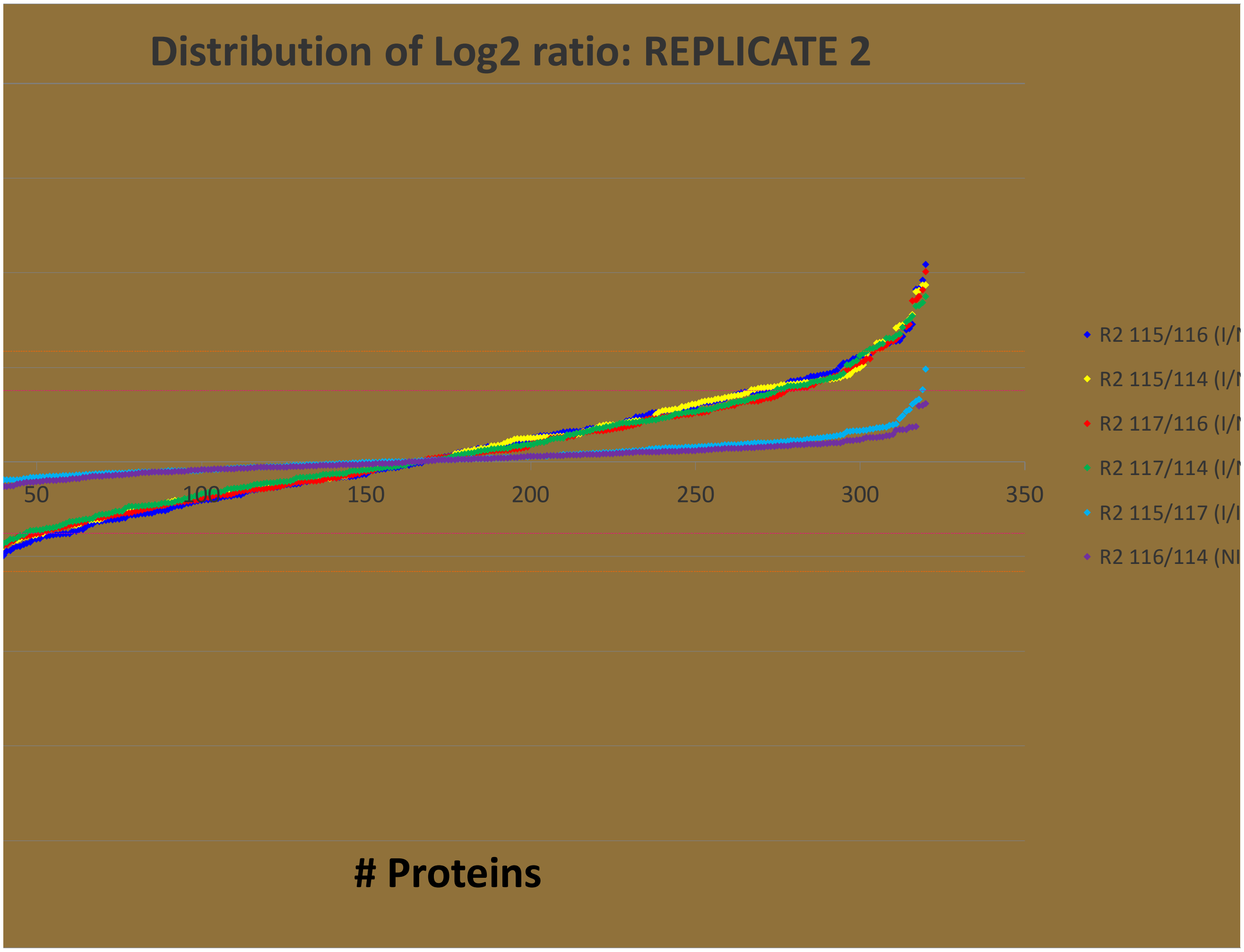

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71	0.795	-0.330	0.770	-0.377	0.795
72	0.797	-0.327	0.771	-0.375	0.803
73	0.799	-0.325	0.772	-0.374	0.806
74	0.802	-0.319	0.772	-0.374	0.806
75	0.808	-0.308	0.773	-0.372	0.811
76	0.815	-0.294	0.775	-0.368	0.814
77	0.816	-0.294	0.779	-0.360	0.821
78	0.818	-0.290	0.782	-0.355	0.822
79	0.818	-0.290	0.785	-0.349	0.824
80	0.819	-0.288	0.786	-0.348	0.827
81	0.821	-0.285	0.792	-0.336	0.831
82	0.822	-0.284	0.795	-0.331	0.832
83	0.824	-0.279	0.796	-0.329	0.833
84	0.826	-0.276	0.797	-0.327	0.836
85	0.826	-0.275	0.798	-0.326	0.836
86	0.827	-0.274	0.800	-0.321	0.837
87	0.827	-0.274	0.802	-0.318	0.840
88	0.833	-0.263	0.803	-0.317	0.841
89	0.834	-0.262	0.804	-0.316	0.846
90	0.834	-0.261	0.807	-0.309	0.850
91	0.836	-0.259	0.808	-0.307	0.850
92	0.836	-0.258	0.811	-0.302	0.850
93	0.837	-0.257	0.813	-0.299	0.850
94	0.839	-0.253	0.814	-0.297	0.850
95	0.841	-0.250	0.816	-0.294	0.851
96	0.844	-0.244	0.819	-0.288	0.860
97	0.845	-0.243	0.819	-0.288	0.861
98	0.845	-0.242	0.820	-0.287	0.861
99	0.847	-0.240	0.822	-0.283	0.862
100	0.851	-0.233	0.825	-0.277	0.864
101	0.851	-0.233	0.827	-0.274	0.867
102	0.851	-0.232	0.827	-0.274	0.868
103	0.856	-0.224	0.827	-0.274	0.869
104	0.856	-0.224	0.829	-0.270	0.870
105	0.858	-0.220	0.829	-0.270	0.870
106	0.859	-0.219	0.833	-0.263	0.871
107	0.863	-0.213	0.835	-0.261	0.872

108	0.864	-0.212	0.840	-0.252	0.872
109	0.864	-0.211	0.841	-0.250	0.873
110	0.869	-0.203	0.841	-0.250	0.877
111	0.871	-0.199	0.843	-0.247	0.879
112	0.872	-0.198	0.845	-0.244	0.880
113	0.873	-0.196	0.846	-0.241	0.881
114	0.874	-0.194	0.853	-0.230	0.882
115	0.874	-0.194	0.857	-0.223	0.883
116	0.876	-0.191	0.857	-0.223	0.884
117	0.877	-0.190	0.857	-0.222	0.885
118	0.880	-0.184	0.861	-0.217	0.886
119	0.882	-0.181	0.871	-0.198	0.886
120	0.882	-0.181	0.873	-0.196	0.888
121	0.883	-0.179	0.875	-0.193	0.889
122	0.892	-0.165	0.876	-0.192	0.890
123	0.892	-0.164	0.876	-0.192	0.891
124	0.893	-0.163	0.876	-0.190	0.892
125	0.900	-0.152	0.885	-0.176	0.892
126	0.901	-0.151	0.885	-0.176	0.897
127	0.906	-0.143	0.887	-0.174	0.899
128	0.908	-0.139	0.888	-0.171	0.900
129	0.908	-0.139	0.889	-0.170	0.900
130	0.909	-0.137	0.890	-0.168	0.902
131	0.912	-0.133	0.892	-0.165	0.904
132	0.913	-0.131	0.895	-0.160	0.906
133	0.913	-0.131	0.898	-0.155	0.906
134	0.915	-0.127	0.898	-0.155	0.909
135	0.915	-0.127	0.899	-0.153	0.909
136	0.919	-0.122	0.901	-0.150	0.910
137	0.920	-0.120	0.903	-0.147	0.910
138	0.924	-0.114	0.904	-0.145	0.910
139	0.928	-0.107	0.905	-0.144	0.913
140	0.928	-0.107	0.905	-0.143	0.915
141	0.932	-0.102	0.907	-0.140	0.916
142	0.932	-0.101	0.909	-0.138	0.921
143	0.934	-0.098	0.910	-0.136	0.922
144	0.935	-0.097	0.912	-0.132	0.922
145	0.937	-0.094	0.914	-0.130	0.923
146	0.937	-0.094	0.916	-0.127	0.924
147	0.938	-0.092	0.917	-0.126	0.926
148	0.939	-0.090	0.920	-0.120	0.927
149	0.940	-0.089	0.920	-0.120	0.928
150	0.941	-0.088	0.923	-0.115	0.932
151	0.942	-0.086	0.930	-0.105	0.934
152	0.943	-0.085	0.932	-0.102	0.935
153	0.952	-0.071	0.934	-0.099	0.936
154	0.953	-0.070	0.937	-0.094	0.939
155	0.953	-0.070	0.938	-0.093	0.940
156	0.956	-0.065	0.939	-0.090	0.941
157	0.957	-0.063	0.941	-0.087	0.942
158	0.958	-0.062	0.942	-0.086	0.946
159	0.961	-0.057	0.943	-0.085	0.949
160	0.963	-0.055	0.944	-0.084	0.950
161	0.963	-0.055	0.944	-0.083	0.950

162	0.965	-0.052	0.946	-0.080	0.951
163	0.969	-0.045	0.947	-0.079	0.953
164	0.970	-0.045	0.948	-0.076	0.953
165	0.971	-0.042	0.960	-0.059	0.954
166	0.973	-0.040	0.960	-0.059	0.955
167	0.976	-0.034	0.960	-0.058	0.956
168	0.977	-0.033	0.961	-0.058	0.956
169	0.977	-0.033	0.961	-0.057	0.957
170	0.978	-0.033	0.961	-0.057	0.960
171	0.978	-0.033	0.965	-0.052	0.960
172	0.978	-0.031	0.970	-0.044	0.962
173	0.979	-0.030	0.970	-0.043	0.968
174	0.980	-0.030	0.971	-0.042	0.968
175	0.980	-0.029	0.973	-0.040	0.971
176	0.982	-0.025	0.977	-0.034	0.972
177	0.984	-0.024	0.981	-0.027	0.979
178	0.986	-0.021	0.982	-0.026	0.980
179	0.986	-0.021	0.985	-0.022	0.984
180	0.986	-0.020	0.986	-0.021	0.986
181	0.986	-0.020	0.992	-0.011	0.988
182	0.987	-0.019	0.994	-0.009	0.990
183	0.989	-0.016	0.997	-0.004	0.991
184	0.993	-0.010	1.001	0.001	0.993
185	0.998	-0.003	1.002	0.003	0.995
186	1.000	0.000	1.004	0.006	0.995
187	1.000	0.001	1.004	0.006	0.997
188	1.003	0.004	1.005	0.008	0.999
189	1.003	0.004	1.006	0.009	0.999
190	1.003	0.005	1.006	0.009	1.000
191	1.004	0.006	1.008	0.011	1.002
192	1.005	0.007	1.010	0.014	1.004
193	1.005	0.008	1.010	0.014	1.006
194	1.009	0.012	1.010	0.015	1.006
195	1.009	0.013	1.011	0.016	1.010
196	1.010	0.014	1.012	0.017	1.018
197	1.010	0.014	1.012	0.018	1.020
198	1.011	0.015	1.015	0.022	1.023
199	1.011	0.016	1.017	0.024	1.024
200	1.014	0.020	1.019	0.027	1.026
201	1.016	0.023	1.020	0.028	1.026
202	1.019	0.026	1.021	0.030	1.028
203	1.020	0.028	1.023	0.033	1.028
204	1.021	0.030	1.026	0.037	1.029
205	1.021	0.030	1.026	0.038	1.030
206	1.022	0.031	1.029	0.042	1.030
207	1.024	0.034	1.032	0.045	1.031
208	1.026	0.037	1.036	0.051	1.033
209	1.027	0.038	1.037	0.052	1.033
210	1.027	0.038	1.037	0.053	1.033
211	1.027	0.039	1.039	0.055	1.034
212	1.030	0.043	1.041	0.058	1.036
213	1.031	0.044	1.047	0.066	1.038
214	1.032	0.045	1.054	0.075	1.039
215	1.034	0.049	1.059	0.082	1.039

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217	1.035
218	1.038
219	1.040
220	1.045
221	1.051
222	1.053
223	1.053
224	1.055
225	1.055
226	1.056
227	1.063
228	1.066
229	1.068
230	1.069
231	1.070
232	1.072
233	1.073
234	1.074
235	1.076
236	1.082
237	1.084
238	1.086
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242	1.095
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244	1.098
245	1.098
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251	1.103
252	1.106
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254	1.107
255	1.107
256	1.108
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258	1.111
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260	1.118
261	1.118
262	1.118
263	1.119
264	1.120
265	1.121
266	1.121
267	1.123
268	1.125
269	1.129

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0.050	1.061
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0.056	1.063
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0.072	1.066
0.074	1.066
0.074	1.067
0.077	1.067
0.078	1.068
0.078	1.070
0.089	1.072
0.092	1.076
0.094	1.078
0.096	1.078
0.098	1.078
0.100	1.081
0.102	1.083
0.104	1.084
0.106	1.088
0.114	1.089
0.116	1.091
0.119	1.092
0.123	1.093
0.127	1.093
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0.131	1.094
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0.161	1.136
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0.165	1.138
0.168	1.139
0.169	1.140
0.176	1.141

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0.092	1.052
0.093	1.052
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0.094	1.059
0.095	1.061
0.098	1.064
0.101	1.065
0.106	1.066
0.108	1.068
0.108	1.069
0.109	1.071
0.112	1.072
0.115	1.074
0.116	1.077
0.122	1.080
0.123	1.081
0.126	1.083
0.127	1.084
0.129	1.086
0.129	1.087
0.129	1.089
0.130	1.089
0.131	1.090
0.135	1.092
0.136	1.093
0.146	1.095
0.149	1.098
0.150	1.099
0.151	1.102
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0.154	1.104
0.159	1.107
0.161	1.107
0.163	1.112
0.166	1.113
0.167	1.115
0.167	1.116
0.168	1.118
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0.172	1.119
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0.190	1.131

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315	1.208
316	1.208
317	1.220
318	1.220
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321	1.229
322	1.231
323	1.233

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0.179	1.142
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0.181	1.146
0.184	1.150
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0.195	1.155
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0.196	1.162
0.197	1.163
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0.202	1.166
0.203	1.166
0.204	1.167
0.211	1.169
0.212	1.175
0.220	1.184
0.221	1.187
0.222	1.188
0.227	1.190
0.227	1.193
0.228	1.203
0.232	1.206
0.232	1.207
0.235	1.209
0.236	1.211
0.237	1.212
0.239	1.212
0.240	1.214
0.244	1.216
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0.246	1.222
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0.247	1.225
0.252	1.231
0.256	1.233
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0.263	1.235
0.267	1.238
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0.269	1.253
0.270	1.254
0.273	1.255
0.273	1.259
0.287	1.259
0.287	1.262
0.291	1.263
0.294	1.265
0.298	1.266
0.299	1.268
0.302	1.269

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0.192	1.133
0.196	1.134
0.202	1.135
0.204	1.136
0.208	1.138
0.211	1.142
0.214	1.143
0.217	1.144
0.218	1.152
0.221	1.157
0.221	1.158
0.222	1.159
0.223	1.165
0.225	1.167
0.233	1.168
0.244	1.171
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0.249	1.172
0.251	1.179
0.254	1.180
0.267	1.180
0.270	1.182
0.271	1.188
0.274	1.189
0.276	1.191
0.277	1.194
0.278	1.195
0.280	1.195
0.282	1.196
0.284	1.196
0.290	1.197
0.291	1.207
0.293	1.208
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0.302	1.214
0.305	1.214
0.305	1.214
0.305	1.214
0.308	1.217
0.312	1.218
0.322	1.218
0.326	1.223
0.326	1.225
0.327	1.226
0.332	1.226
0.333	1.230
0.335	1.232
0.337	1.235
0.339	1.240
0.341	1.247
0.342	1.249
0.343	1.250

324	1.239	0.309	1.269	0.343	1.251
325	1.241	0.312	1.269	0.344	1.252
326	1.246	0.317	1.270	0.345	1.255
327	1.248	0.319	1.270	0.345	1.256
328	1.255	0.328	1.270	0.345	1.258
329	1.255	0.328	1.271	0.345	1.262
330	1.261	0.335	1.274	0.349	1.270
331	1.264	0.338	1.275	0.351	1.277
332	1.266	0.340	1.300	0.379	1.278
333	1.270	0.345	1.304	0.383	1.289
334	1.272	0.347	1.309	0.388	1.290
335	1.277	0.353	1.318	0.398	1.299
336	1.278	0.354	1.322	0.403	1.303
337	1.279	0.355	1.328	0.409	1.306
338	1.281	0.357	1.328	0.409	1.307
339	1.281	0.357	1.331	0.413	1.309
340	1.287	0.364	1.333	0.414	1.314
341	1.291	0.369	1.335	0.416	1.315
342	1.297	0.375	1.346	0.429	1.317
343	1.314	0.394	1.353	0.437	1.327
344	1.314	0.394	1.362	0.446	1.344
345	1.315	0.396	1.384	0.469	1.349
346	1.315	0.396	1.387	0.472	1.350
347	1.318	0.398	1.388	0.474	1.351
348	1.340	0.422	1.401	0.486	1.354
349	1.344	0.426	1.407	0.493	1.356
350	1.352	0.435	1.415	0.500	1.360
351	1.352	0.436	1.415	0.501	1.362
352	1.362	0.446	1.424	0.510	1.373
353	1.376	0.460	1.425	0.511	1.376
354	1.380	0.465	1.428	0.514	1.380
355	1.381	0.466	1.428	0.514	1.400
356	1.383	0.468	1.440	0.526	1.402
357	1.385	0.470	1.444	0.530	1.413
358	1.388	0.473	1.452	0.538	1.416
359	1.391	0.476	1.455	0.541	1.419
360	1.413	0.499	1.465	0.551	1.422
361	1.422	0.508	1.470	0.556	1.423
362	1.425	0.510	1.480	0.566	1.443
363	1.435	0.521	1.488	0.573	1.449
364	1.436	0.522	1.488	0.574	1.464
365	1.455	0.541	1.506	0.591	1.467
366	1.466	0.552	1.508	0.592	1.473
367	1.467	0.553	1.515	0.599	1.478
368	1.472	0.558	1.557	0.639	1.482
369	1.493	0.578	1.560	0.642	1.487
370	1.500	0.585	1.577	0.658	1.496
371	1.505	0.590	1.597	0.675	1.509
372	1.517	0.601	1.604	0.681	1.518
373	1.552	0.634	1.625	0.700	1.526
374	1.564	0.645	1.632	0.707	1.547
375	1.579	0.659	1.645	0.718	1.554
376	1.610	0.687	1.647	0.720	1.569
377	1.615	0.692	1.717	0.780	1.571

378	1.644	0.717	1.730	0.791	1.581
379	1.644	0.717	1.733	0.794	1.612
380	1.669	0.739	1.983	0.988	1.650
381	1.751	0.808	2.193	1.133	1.653
382	1.933	0.951	2.406	1.266	1.984

-1.512	0.373	-1.423	0.695	-0.524	0.749
-1.095	0.459	-1.124	0.769	-0.378	0.757
-0.984	0.484	-1.047	0.800	-0.322	0.790
-0.893	0.484	-1.047	0.803	-0.316	0.795
-0.853	0.488	-1.034	0.835	-0.261	0.829
-0.831	0.527	-0.925	0.845	-0.243	0.832
-0.825	0.528	-0.920	0.848	-0.238	0.839
-0.811	0.538	-0.895	0.851	-0.233	0.861
-0.790	0.572	-0.805	0.858	-0.221	0.867
-0.745	0.582	-0.782	0.863	-0.213	0.868
-0.741	0.589	-0.763	0.863	-0.213	0.868
-0.705	0.599	-0.739	0.864	-0.210	0.876
-0.657	0.602	-0.733	0.865	-0.209	0.877
-0.654	0.617	-0.698	0.865	-0.208	0.878
-0.645	0.617	-0.696	0.869	-0.203	0.879
-0.643	0.623	-0.682	0.871	-0.200	0.882
-0.614	0.625	-0.679	0.875	-0.193	0.883
-0.601	0.627	-0.674	0.882	-0.182	0.891
-0.596	0.627	-0.674	0.884	-0.177	0.893
-0.596	0.644	-0.635	0.889	-0.170	0.894
-0.593	0.656	-0.607	0.889	-0.169	0.894
-0.591	0.662	-0.596	0.889	-0.169	0.894
-0.590	0.666	-0.585	0.890	-0.169	0.895
-0.581	0.670	-0.577	0.893	-0.164	0.897
-0.558	0.672	-0.573	0.895	-0.160	0.897
-0.548	0.674	-0.570	0.895	-0.159	0.898
-0.540	0.679	-0.559	0.897	-0.157	0.899
-0.539	0.683	-0.550	0.898	-0.156	0.901
-0.532	0.690	-0.535	0.899	-0.153	0.902
-0.528	0.691	-0.533	0.901	-0.150	0.902
-0.515	0.692	-0.532	0.903	-0.148	0.904
-0.494	0.703	-0.509	0.904	-0.146	0.908
-0.491	0.707	-0.501	0.904	-0.146	0.911
-0.489	0.709	-0.497	0.906	-0.143	0.915
-0.478	0.709	-0.496	0.909	-0.138	0.918
-0.469	0.712	-0.490	0.910	-0.137	0.919
-0.462	0.714	-0.487	0.910	-0.137	0.920
-0.457	0.717	-0.481	0.913	-0.131	0.920
-0.450	0.719	-0.476	0.914	-0.130	0.922
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0.252	1.200	0.263	1.045	0.064	1.044
0.256	1.205	0.269	1.046	0.065	1.044
0.257	1.208	0.273	1.046	0.065	1.045
0.257	1.210	0.275	1.046	0.066	1.045
0.258	1.211	0.276	1.047	0.066	1.046
0.258	1.212	0.277	1.047	0.066	1.046
0.260	1.215	0.281	1.047	0.066	1.047
0.271	1.222	0.289	1.047	0.067	1.049
0.272	1.224	0.291	1.048	0.068	1.049
0.274	1.233	0.302	1.050	0.071	1.050
0.280	1.239	0.309	1.050	0.071	1.050
0.280	1.241	0.312	1.051	0.071	1.050
0.280	1.244	0.315	1.051	0.071	1.050
0.280	1.246	0.317	1.053	0.074	1.051
0.283	1.246	0.318	1.053	0.075	1.051
0.284	1.248	0.320	1.053	0.075	1.052
0.285	1.251	0.323	1.054	0.075	1.052
0.291	1.255	0.328	1.055	0.077	1.053
0.293	1.257	0.330	1.055	0.077	1.054
0.294	1.259	0.332	1.055	0.078	1.054
0.294	1.260	0.333	1.056	0.078	1.054
0.298	1.267	0.342	1.056	0.079	1.055
0.300	1.272	0.347	1.056	0.079	1.055
0.304	1.275	0.350	1.057	0.080	1.056
0.311	1.280	0.356	1.058	0.081	1.056
0.319	1.281	0.357	1.059	0.083	1.057
0.321	1.282	0.358	1.059	0.083	1.057
0.322	1.293	0.371	1.059	0.083	1.057

0.323	1.296
0.324	1.303
0.328	1.305
0.329	1.305
0.331	1.308
0.335	1.309
0.345	1.310
0.352	1.311
0.353	1.319
0.366	1.324
0.367	1.336
0.377	1.338
0.382	1.344
0.385	1.346
0.386	1.349
0.388	1.352
0.394	1.354
0.395	1.358
0.398	1.358
0.408	1.361
0.427	1.363
0.432	1.369
0.433	1.378
0.434	1.391
0.437	1.409
0.440	1.414
0.444	1.419
0.446	1.422
0.457	1.423
0.460	1.431
0.464	1.432
0.486	1.432
0.488	1.447
0.499	1.456
0.502	1.457
0.505	1.458
0.508	1.469
0.509	1.473
0.529	1.481
0.535	1.484
0.550	1.500
0.553	1.500
0.559	1.509
0.564	1.521
0.568	1.526
0.572	1.531
0.581	1.543
0.594	1.558
0.602	1.573
0.610	1.616
0.629	1.617
0.636	1.639
0.650	1.660
0.652	1.724

0.374	1.060
0.381	1.060
0.384	1.061
0.384	1.061
0.387	1.061
0.389	1.062
0.390	1.063
0.391	1.063
0.399	1.065
0.405	1.065
0.418	1.066
0.420	1.067
0.427	1.067
0.428	1.067
0.432	1.067
0.435	1.068
0.437	1.068
0.441	1.070
0.441	1.075
0.445	1.076
0.446	1.077
0.453	1.078
0.463	1.078
0.476	1.081
0.495	1.081
0.500	1.083
0.505	1.085
0.508	1.085
0.509	1.086
0.517	1.086
0.518	1.090
0.518	1.092
0.533	1.093
0.542	1.094
0.543	1.096
0.544	1.098
0.555	1.100
0.559	1.112
0.567	1.114
0.570	1.114
0.585	1.119
0.585	1.120
0.593	1.122
0.605	1.123
0.610	1.124
0.614	1.132
0.626	1.132
0.640	1.134
0.653	1.137
0.692	1.144
0.693	1.145
0.713	1.148
0.731	1.152
0.786	1.160

0.084	1.057
0.085	1.057
0.086	1.058
0.086	1.058
0.086	1.058
0.087	1.059
0.088	1.060
0.088	1.060
0.090	1.060
0.091	1.060
0.092	1.061
0.093	1.061
0.093	1.062
0.094	1.062
0.094	1.063
0.095	1.063
0.095	1.064
0.098	1.065
0.104	1.066
0.106	1.067
0.107	1.068
0.109	1.068
0.109	1.071
0.112	1.072
0.112	1.073
0.115	1.073
0.118	1.075
0.118	1.077
0.119	1.077
0.119	1.079
0.124	1.081
0.127	1.081
0.128	1.081
0.130	1.082
0.132	1.083
0.135	1.083
0.137	1.084
0.153	1.085
0.155	1.085
0.156	1.086
0.162	1.096
0.164	1.098
0.166	1.106
0.167	1.106
0.169	1.107
0.178	1.112
0.179	1.116
0.182	1.119
0.185	1.126
0.195	1.129
0.195	1.131
0.199	1.134
0.205	1.153
0.214	1.159

0.661	1.782	0.834	1.171	0.228	1.175
0.689	1.830	0.872	1.185	0.244	1.216
0.722	1.952	0.965	1.188	0.248	1.218
0.725	1.976	0.983	1.189	0.249	1.273
0.989	2.084	1.060	1.259	0.332	1.449

[redacted]		R3 log2 116/117 (I/NI)	R3 log2 116/115 (I/NI)	R3 log2 114/117 (I/NI)
-0.416	1	-1.352	-1.327	-1.512
-0.401	2	-1.256	-1.314	-1.095
-0.340	3	-0.957	-1.221	-0.984
-0.331	4	-0.903	-1.062	-0.893
-0.271	5	-0.890	-1.024	-0.853
-0.265	6	-0.861	-0.993	-0.831
-0.254	7	-0.837	-0.949	-0.825
-0.216	8	-0.835	-0.911	-0.811
-0.206	9	-0.792	-0.826	-0.790
-0.204	10	-0.781	-0.803	-0.745
-0.204	11	-0.770	-0.776	-0.741
-0.191	12	-0.766	-0.758	-0.705
-0.190	13	-0.721	-0.722	-0.657
-0.188	14	-0.710	-0.721	-0.654
-0.187	15	-0.702	-0.695	-0.645
-0.181	16	-0.660	-0.683	-0.643
-0.179	17	-0.655	-0.682	-0.614
-0.166	18	-0.642	-0.675	-0.601
-0.163	19	-0.615	-0.669	-0.596
-0.162	20	-0.585	-0.643	-0.596
-0.162	21	-0.579	-0.625	-0.593
-0.161	22	-0.562	-0.622	-0.591
-0.160	23	-0.538	-0.616	-0.590
-0.157	24	-0.533	-0.609	-0.581
-0.156	25	-0.516	-0.601	-0.558
-0.155	26	-0.514	-0.597	-0.548
-0.154	27	-0.513	-0.583	-0.540
-0.150	28	-0.512	-0.568	-0.539
-0.149	29	-0.511	-0.557	-0.532
-0.149	30	-0.505	-0.555	-0.528
-0.145	31	-0.500	-0.541	-0.515
-0.139	32	-0.495	-0.536	-0.494
-0.135	33	-0.494	-0.534	-0.491
-0.128	34	-0.491	-0.524	-0.489
-0.123	35	-0.483	-0.514	-0.478
-0.121	36	-0.480	-0.504	-0.469
-0.121	37	-0.477	-0.497	-0.462
-0.120	38	-0.477	-0.494	-0.457
-0.118	39	-0.477	-0.486	-0.450
-0.116	40	-0.476	-0.486	-0.450
-0.114	41	-0.473	-0.485	-0.448
-0.111	42	-0.472	-0.484	-0.444
-0.108	43	-0.468	-0.483	-0.439
-0.107	44	-0.468	-0.471	-0.429
-0.106	45	-0.462	-0.469	-0.427
-0.106	46	-0.460	-0.466	-0.419
-0.104	47	-0.453	-0.463	-0.419
-0.101	48	-0.451	-0.455	-0.412
-0.100	49	-0.449	-0.454	-0.404
-0.100	50	-0.445	-0.446	-0.402
-0.100	51	-0.438	-0.444	-0.393
-0.099	52	-0.435	-0.442	-0.388
-0.098	53	-0.431	-0.438	-0.383

-0.097	54	-0.424	-0.437	-0.376
-0.096	55	-0.423	-0.436	-0.376
-0.095	56	-0.415	-0.434	-0.375
-0.095	57	-0.413	-0.433	-0.375
-0.095	58	-0.404	-0.424	-0.371
-0.094	59	-0.403	-0.420	-0.368
-0.092	60	-0.402	-0.417	-0.368
-0.091	61	-0.398	-0.410	-0.366
-0.090	62	-0.397	-0.410	-0.362
-0.088	63	-0.389	-0.402	-0.357
-0.085	64	-0.385	-0.394	-0.353
-0.084	65	-0.372	-0.393	-0.351
-0.084	66	-0.365	-0.391	-0.350
-0.083	67	-0.357	-0.391	-0.343
-0.080	68	-0.356	-0.388	-0.340
-0.080	69	-0.353	-0.385	-0.339
-0.079	70	-0.340	-0.379	-0.334
-0.078	71	-0.330	-0.377	-0.331
-0.075	72	-0.327	-0.375	-0.317
-0.075	73	-0.325	-0.374	-0.312
-0.074	74	-0.319	-0.374	-0.311
-0.073	75	-0.308	-0.372	-0.302
-0.073	76	-0.294	-0.368	-0.298
-0.073	77	-0.294	-0.360	-0.285
-0.073	78	-0.290	-0.355	-0.283
-0.070	79	-0.290	-0.349	-0.279
-0.069	80	-0.288	-0.348	-0.273
-0.067	81	-0.285	-0.336	-0.268
-0.067	82	-0.284	-0.331	-0.265
-0.067	83	-0.279	-0.329	-0.263
-0.066	84	-0.276	-0.327	-0.259
-0.066	85	-0.275	-0.326	-0.258
-0.064	86	-0.274	-0.321	-0.257
-0.064	87	-0.274	-0.318	-0.251
-0.064	88	-0.263	-0.317	-0.249
-0.064	89	-0.262	-0.316	-0.241
-0.063	90	-0.261	-0.309	-0.235
-0.062	91	-0.259	-0.307	-0.235
-0.061	92	-0.258	-0.302	-0.235
-0.060	93	-0.257	-0.299	-0.234
-0.059	94	-0.253	-0.297	-0.234
-0.058	95	-0.250	-0.294	-0.232
-0.058	96	-0.244	-0.288	-0.217
-0.057	97	-0.243	-0.288	-0.216
-0.057	98	-0.242	-0.287	-0.216
-0.055	99	-0.240	-0.283	-0.214
-0.053	100	-0.233	-0.277	-0.210
-0.053	101	-0.233	-0.274	-0.206
-0.052	102	-0.232	-0.274	-0.204
-0.051	103	-0.224	-0.274	-0.202
-0.051	104	-0.224	-0.270	-0.202
-0.050	105	-0.220	-0.270	-0.201
-0.049	106	-0.219	-0.263	-0.198
-0.048	107	-0.213	-0.261	-0.198

-0.048	108	-0.212	-0.252	-0.198
-0.047	109	-0.211	-0.250	-0.196
-0.045	110	-0.203	-0.250	-0.190
-0.044	111	-0.199	-0.247	-0.185
-0.043	112	-0.198	-0.244	-0.184
-0.042	113	-0.196	-0.241	-0.183
-0.042	114	-0.194	-0.230	-0.181
-0.041	115	-0.194	-0.223	-0.179
-0.040	116	-0.191	-0.223	-0.178
-0.040	117	-0.190	-0.222	-0.176
-0.039	118	-0.184	-0.217	-0.174
-0.038	119	-0.181	-0.198	-0.174
-0.038	120	-0.181	-0.196	-0.171
-0.037	121	-0.179	-0.193	-0.170
-0.036	122	-0.165	-0.192	-0.168
-0.036	123	-0.164	-0.192	-0.166
-0.036	124	-0.163	-0.190	-0.165
-0.036	125	-0.152	-0.176	-0.164
-0.036	126	-0.151	-0.176	-0.156
-0.035	127	-0.143	-0.174	-0.154
-0.035	128	-0.139	-0.171	-0.152
-0.034	129	-0.139	-0.170	-0.151
-0.034	130	-0.137	-0.168	-0.149
-0.034	131	-0.133	-0.165	-0.145
-0.033	132	-0.131	-0.160	-0.143
-0.032	133	-0.131	-0.155	-0.143
-0.031	134	-0.127	-0.155	-0.138
-0.030	135	-0.127	-0.153	-0.137
-0.029	136	-0.122	-0.150	-0.136
-0.029	137	-0.120	-0.147	-0.136
-0.029	138	-0.114	-0.145	-0.136
-0.027	139	-0.107	-0.144	-0.131
-0.027	140	-0.107	-0.143	-0.128
-0.026	141	-0.102	-0.140	-0.126
-0.026	142	-0.101	-0.138	-0.118
-0.025	143	-0.098	-0.136	-0.117
-0.025	144	-0.097	-0.132	-0.117
-0.024	145	-0.094	-0.130	-0.116
-0.023	146	-0.094	-0.127	-0.114
-0.023	147	-0.092	-0.126	-0.111
-0.023	148	-0.090	-0.120	-0.109
-0.022	149	-0.089	-0.120	-0.107
-0.021	150	-0.088	-0.115	-0.102
-0.020	151	-0.086	-0.105	-0.099
-0.020	152	-0.085	-0.102	-0.097
-0.019	153	-0.071	-0.099	-0.096
-0.019	154	-0.070	-0.094	-0.090
-0.017	155	-0.070	-0.093	-0.090
-0.016	156	-0.065	-0.090	-0.087
-0.015	157	-0.063	-0.087	-0.087
-0.015	158	-0.062	-0.086	-0.080
-0.015	159	-0.057	-0.085	-0.076
-0.013	160	-0.055	-0.084	-0.075
-0.013	161	-0.055	-0.083	-0.073

-0.013	162	-0.052	-0.080	-0.072
-0.013	163	-0.045	-0.079	-0.070
-0.013	164	-0.045	-0.076	-0.069
-0.012	165	-0.042	-0.059	-0.068
-0.012	166	-0.040	-0.059	-0.066
-0.011	167	-0.034	-0.058	-0.066
-0.010	168	-0.033	-0.058	-0.065
-0.010	169	-0.033	-0.057	-0.064
-0.010	170	-0.033	-0.057	-0.060
-0.009	171	-0.033	-0.052	-0.059
-0.009	172	-0.031	-0.044	-0.056
-0.007	173	-0.030	-0.043	-0.047
-0.006	174	-0.030	-0.042	-0.047
-0.006	175	-0.029	-0.040	-0.042
-0.005	176	-0.025	-0.034	-0.041
-0.005	177	-0.024	-0.027	-0.031
-0.005	178	-0.021	-0.026	-0.029
-0.005	179	-0.021	-0.022	-0.023
-0.004	180	-0.020	-0.021	-0.020
-0.004	181	-0.020	-0.011	-0.017
-0.004	182	-0.019	-0.009	-0.014
-0.004	183	-0.016	-0.004	-0.013
-0.003	184	-0.010	0.001	-0.010
-0.003	185	-0.003	0.003	-0.007
-0.003	186	0.000	0.006	-0.007
-0.002	187	0.001	0.006	-0.004
-0.002	188	0.004	0.008	-0.002
-0.002	189	0.004	0.009	-0.001
0.000	190	0.005	0.009	0.000
0.000	191	0.006	0.011	0.002
0.000	192	0.007	0.014	0.006
0.001	193	0.008	0.014	0.008
0.001	194	0.012	0.015	0.009
0.003	195	0.013	0.016	0.014
0.004	196	0.014	0.017	0.025
0.005	197	0.014	0.018	0.028
0.006	198	0.015	0.022	0.033
0.006	199	0.016	0.024	0.035
0.007	200	0.020	0.027	0.037
0.008	201	0.023	0.028	0.037
0.008	202	0.026	0.030	0.039
0.010	203	0.028	0.033	0.040
0.011	204	0.030	0.037	0.041
0.012	205	0.030	0.038	0.043
0.013	206	0.031	0.042	0.043
0.013	207	0.034	0.045	0.044
0.014	208	0.037	0.051	0.047
0.015	209	0.038	0.052	0.047
0.015	210	0.038	0.053	0.047
0.016	211	0.039	0.055	0.048
0.016	212	0.043	0.058	0.051
0.017	213	0.044	0.066	0.053
0.017	214	0.045	0.075	0.055
0.017	215	0.049	0.082	0.056

0.018	216	0.050	0.085	0.058
0.018	217	0.050	0.086	0.060
0.018	218	0.054	0.086	0.066
0.019	219	0.056	0.088	0.071
0.019	220	0.064	0.091	0.071
0.019	221	0.072	0.092	0.073
0.019	222	0.074	0.093	0.073
0.020	223	0.074	0.094	0.075
0.020	224	0.077	0.094	0.083
0.021	225	0.078	0.095	0.086
0.021	226	0.078	0.098	0.090
0.022	227	0.089	0.101	0.091
0.022	228	0.092	0.106	0.092
0.023	229	0.094	0.108	0.095
0.023	230	0.096	0.108	0.096
0.024	231	0.098	0.109	0.099
0.025	232	0.100	0.112	0.100
0.025	233	0.102	0.115	0.103
0.026	234	0.104	0.116	0.107
0.027	235	0.106	0.122	0.111
0.028	236	0.114	0.123	0.113
0.029	237	0.116	0.126	0.115
0.029	238	0.119	0.127	0.117
0.030	239	0.123	0.129	0.119
0.030	240	0.127	0.129	0.121
0.030	241	0.128	0.129	0.123
0.032	242	0.131	0.130	0.123
0.032	243	0.134	0.131	0.125
0.034	244	0.135	0.135	0.128
0.034	245	0.135	0.136	0.128
0.035	246	0.139	0.146	0.131
0.035	247	0.139	0.149	0.134
0.035	248	0.140	0.150	0.136
0.035	249	0.140	0.151	0.140
0.037	250	0.142	0.154	0.141
0.038	251	0.142	0.154	0.143
0.038	252	0.145	0.159	0.147
0.038	253	0.145	0.161	0.147
0.039	254	0.146	0.163	0.154
0.039	255	0.147	0.166	0.154
0.039	256	0.148	0.167	0.157
0.039	257	0.151	0.167	0.159
0.039	258	0.152	0.168	0.161
0.039	259	0.155	0.171	0.162
0.039	260	0.161	0.172	0.163
0.040	261	0.161	0.175	0.166
0.040	262	0.161	0.184	0.166
0.040	263	0.162	0.185	0.168
0.040	264	0.163	0.185	0.169
0.040	265	0.165	0.186	0.170
0.041	266	0.165	0.186	0.171
0.042	267	0.168	0.188	0.172
0.043	268	0.169	0.189	0.175
0.044	269	0.176	0.190	0.177

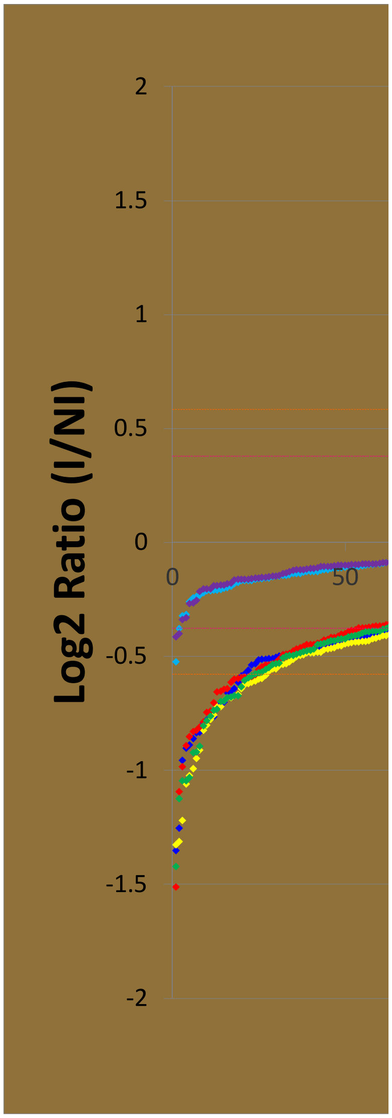
0.044	270	0.176	0.190	0.180
0.044	271	0.179	0.192	0.180
0.044	272	0.181	0.192	0.181
0.045	273	0.181	0.196	0.182
0.047	274	0.184	0.202	0.183
0.047	275	0.193	0.204	0.184
0.048	276	0.195	0.208	0.186
0.048	277	0.196	0.211	0.192
0.049	278	0.196	0.214	0.193
0.050	279	0.196	0.217	0.194
0.050	280	0.197	0.218	0.204
0.051	281	0.202	0.221	0.210
0.051	282	0.202	0.221	0.212
0.052	283	0.203	0.222	0.213
0.053	284	0.204	0.223	0.220
0.054	285	0.211	0.225	0.222
0.055	286	0.212	0.233	0.224
0.055	287	0.220	0.244	0.228
0.056	288	0.221	0.248	0.228
0.056	289	0.222	0.249	0.229
0.057	290	0.227	0.251	0.237
0.059	291	0.227	0.254	0.238
0.059	292	0.228	0.267	0.239
0.060	293	0.232	0.270	0.241
0.061	294	0.232	0.271	0.248
0.061	295	0.235	0.274	0.250
0.062	296	0.236	0.276	0.252
0.062	297	0.237	0.277	0.256
0.063	298	0.239	0.278	0.257
0.064	299	0.240	0.280	0.257
0.065	300	0.244	0.282	0.258
0.065	301	0.245	0.284	0.258
0.067	302	0.246	0.290	0.260
0.069	303	0.247	0.291	0.271
0.069	304	0.247	0.293	0.272
0.070	305	0.252	0.300	0.274
0.070	306	0.256	0.302	0.280
0.070	307	0.260	0.305	0.280
0.070	308	0.261	0.305	0.280
0.071	309	0.263	0.305	0.280
0.072	310	0.267	0.308	0.283
0.073	311	0.269	0.312	0.284
0.074	312	0.269	0.322	0.285
0.075	313	0.269	0.326	0.291
0.075	314	0.270	0.326	0.293
0.075	315	0.273	0.327	0.294
0.076	316	0.273	0.332	0.294
0.077	317	0.287	0.333	0.298
0.077	318	0.287	0.335	0.300
0.078	319	0.291	0.337	0.304
0.078	320	0.294	0.339	0.311
0.079	321	0.298	0.341	0.319
0.080	322	0.299	0.342	0.321
0.080	323	0.302	0.343	0.322

0.080	324	0.309	0.343	0.323
0.081	325	0.312	0.344	0.324
0.081	326	0.317	0.345	0.328
0.082	327	0.319	0.345	0.329
0.082	328	0.328	0.345	0.331
0.083	329	0.328	0.345	0.335
0.084	330	0.335	0.349	0.345
0.084	331	0.338	0.351	0.352
0.084	332	0.340	0.379	0.353
0.085	333	0.345	0.383	0.366
0.085	334	0.347	0.388	0.367
0.085	335	0.353	0.398	0.377
0.087	336	0.354	0.403	0.382
0.087	337	0.355	0.409	0.385
0.088	338	0.357	0.409	0.386
0.088	339	0.357	0.413	0.388
0.090	340	0.364	0.414	0.394
0.090	341	0.369	0.416	0.395
0.092	342	0.375	0.429	0.398
0.094	343	0.394	0.437	0.408
0.094	344	0.394	0.446	0.427
0.095	345	0.396	0.469	0.432
0.099	346	0.396	0.472	0.433
0.100	347	0.398	0.474	0.434
0.101	348	0.422	0.486	0.437
0.101	349	0.426	0.493	0.440
0.104	350	0.435	0.500	0.444
0.106	351	0.436	0.501	0.446
0.107	352	0.446	0.510	0.457
0.110	353	0.460	0.511	0.460
0.112	354	0.465	0.514	0.464
0.113	355	0.466	0.514	0.486
0.113	356	0.468	0.526	0.488
0.114	357	0.470	0.530	0.499
0.115	358	0.473	0.538	0.502
0.115	359	0.476	0.541	0.505
0.116	360	0.499	0.551	0.508
0.118	361	0.508	0.556	0.509
0.118	362	0.510	0.566	0.529
0.119	363	0.521	0.573	0.535
0.133	364	0.522	0.574	0.550
0.135	365	0.541	0.591	0.553
0.145	366	0.552	0.592	0.559
0.145	367	0.553	0.599	0.564
0.147	368	0.558	0.639	0.568
0.154	369	0.578	0.642	0.572
0.158	370	0.585	0.658	0.581
0.163	371	0.590	0.675	0.594
0.172	372	0.601	0.681	0.602
0.175	373	0.634	0.700	0.610
0.177	374	0.645	0.707	0.629
0.181	375	0.659	0.718	0.636
0.206	376	0.687	0.720	0.650
0.213	377	0.692	0.780	0.652

0.233	378	0.717	0.791	0.661
0.282	379	0.717	0.794	0.689
0.284	380	0.739	0.988	0.722
0.348	381	0.808	1.133	0.725
0.535	382	0.951	1.266	0.989

R3 log2 114/115 (I/NI)	R3 log2 116/114 (I/I)	R3 log2 117/115 (NI/NI)
-1.423	-0.524	-0.416
-1.124	-0.378	-0.401
-1.047	-0.322	-0.340
-1.047	-0.316	-0.331
-1.034	-0.261	-0.271
-0.925	-0.243	-0.265
-0.920	-0.238	-0.254
-0.895	-0.233	-0.216
-0.805	-0.221	-0.206
-0.782	-0.213	-0.204
-0.763	-0.213	-0.204
-0.739	-0.210	-0.191
-0.733	-0.209	-0.190
-0.698	-0.208	-0.188
-0.696	-0.203	-0.187
-0.682	-0.200	-0.181
-0.679	-0.193	-0.179
-0.674	-0.182	-0.166
-0.674	-0.177	-0.163
-0.635	-0.170	-0.162
-0.607	-0.169	-0.162
-0.596	-0.169	-0.161
-0.585	-0.169	-0.160
-0.577	-0.164	-0.157
-0.573	-0.160	-0.156
-0.570	-0.159	-0.155
-0.559	-0.157	-0.154
-0.550	-0.156	-0.150
-0.535	-0.153	-0.149
-0.533	-0.150	-0.149
-0.532	-0.148	-0.145
-0.509	-0.146	-0.139
-0.501	-0.146	-0.135
-0.497	-0.143	-0.128
-0.496	-0.138	-0.123
-0.490	-0.137	-0.121
-0.487	-0.137	-0.121
-0.481	-0.131	-0.120
-0.476	-0.130	-0.118
-0.475	-0.129	-0.116
-0.468	-0.128	-0.114
-0.448	-0.128	-0.111
-0.446	-0.124	-0.108
-0.444	-0.121	-0.107
-0.439	-0.120	-0.106
-0.433	-0.115	-0.106
-0.432	-0.115	-0.104
-0.428	-0.113	-0.101
-0.423	-0.111	-0.100
-0.422	-0.109	-0.100
-0.415	-0.107	-0.100
-0.411	-0.107	-0.099
-0.409	-0.106	-0.098

x	y
0	0.378512
400	0.378512
0	0.584963
400	0.584963



-0.406	-0.105	-0.097
-0.398	-0.103	-0.096
-0.394	-0.101	-0.095
-0.392	-0.099	-0.095
-0.391	-0.098	-0.095
-0.389	-0.095	-0.094
-0.389	-0.094	-0.092
-0.382	-0.092	-0.091
-0.379	-0.089	-0.090
-0.367	-0.086	-0.088
-0.364	-0.085	-0.085
-0.363	-0.084	-0.084
-0.360	-0.083	-0.084
-0.357	-0.083	-0.083
-0.341	-0.081	-0.080
-0.337	-0.081	-0.080
-0.327	-0.081	-0.079
-0.324	-0.080	-0.078
-0.316	-0.079	-0.075
-0.314	-0.078	-0.075
-0.313	-0.077	-0.074
-0.312	-0.075	-0.073
-0.309	-0.074	-0.073
-0.308	-0.073	-0.073
-0.304	-0.073	-0.073
-0.299	-0.072	-0.070
-0.297	-0.072	-0.069
-0.294	-0.071	-0.067
-0.292	-0.071	-0.067
-0.283	-0.071	-0.067
-0.280	-0.070	-0.066
-0.278	-0.070	-0.066
-0.272	-0.069	-0.064
-0.269	-0.068	-0.064
-0.269	-0.067	-0.064
-0.266	-0.064	-0.064
-0.262	-0.064	-0.063
-0.260	-0.063	-0.062
-0.256	-0.062	-0.061
-0.249	-0.061	-0.060
-0.247	-0.061	-0.059
-0.244	-0.060	-0.058
-0.240	-0.060	-0.058
-0.238	-0.059	-0.057
-0.234	-0.059	-0.057
-0.230	-0.059	-0.055
-0.229	-0.057	-0.053
-0.224	-0.057	-0.053
-0.223	-0.056	-0.052
-0.222	-0.055	-0.051
-0.220	-0.055	-0.051
-0.205	-0.054	-0.050
-0.204	-0.054	-0.049
-0.204	-0.053	-0.048

-0.202	-0.053	-0.048
-0.199	-0.052	-0.047
-0.188	-0.050	-0.045
-0.188	-0.050	-0.044
-0.188	-0.049	-0.043
-0.185	-0.049	-0.042
-0.179	-0.048	-0.042
-0.172	-0.048	-0.041
-0.170	-0.047	-0.040
-0.166	-0.047	-0.040
-0.164	-0.046	-0.039
-0.162	-0.044	-0.038
-0.162	-0.043	-0.038
-0.158	-0.040	-0.037
-0.156	-0.040	-0.036
-0.154	-0.039	-0.036
-0.154	-0.038	-0.036
-0.154	-0.037	-0.036
-0.153	-0.037	-0.036
-0.152	-0.036	-0.035
-0.152	-0.036	-0.035
-0.150	-0.035	-0.034
-0.148	-0.033	-0.034
-0.143	-0.033	-0.034
-0.140	-0.032	-0.033
-0.139	-0.032	-0.032
-0.134	-0.032	-0.031
-0.133	-0.031	-0.030
-0.131	-0.029	-0.029
-0.130	-0.028	-0.029
-0.122	-0.027	-0.029
-0.122	-0.025	-0.027
-0.116	-0.025	-0.027
-0.115	-0.025	-0.026
-0.114	-0.024	-0.026
-0.112	-0.023	-0.025
-0.101	-0.023	-0.025
-0.095	-0.023	-0.024
-0.088	-0.023	-0.023
-0.085	-0.023	-0.023
-0.084	-0.022	-0.023
-0.084	-0.020	-0.022
-0.083	-0.020	-0.021
-0.077	-0.019	-0.020
-0.077	-0.019	-0.020
-0.072	-0.019	-0.019
-0.063	-0.019	-0.019
-0.063	-0.018	-0.017
-0.060	-0.018	-0.016
-0.059	-0.017	-0.015
-0.056	-0.017	-0.015
-0.055	-0.017	-0.015
-0.052	-0.016	-0.013
-0.051	-0.016	-0.013

-0.048	-0.015	-0.013
-0.048	-0.014	-0.013
-0.043	-0.013	-0.013
-0.036	-0.013	-0.012
-0.035	-0.012	-0.012
-0.030	-0.011	-0.011
-0.028	-0.011	-0.010
-0.025	-0.010	-0.010
-0.022	-0.010	-0.010
-0.022	-0.010	-0.009
-0.021	-0.010	-0.009
-0.017	-0.009	-0.007
-0.017	-0.009	-0.006
-0.015	-0.009	-0.006
-0.014	-0.007	-0.005
-0.013	-0.007	-0.005
-0.011	-0.006	-0.005
-0.008	-0.005	-0.005
-0.008	-0.005	-0.004
-0.001	-0.005	-0.004
-0.001	-0.005	-0.004
0.001	-0.004	-0.004
0.009	-0.002	-0.003
0.010	-0.001	-0.003
0.010	0.000	-0.003
0.012	0.000	-0.002
0.012	0.000	-0.002
0.015	0.000	-0.002
0.021	0.001	0.000
0.024	0.002	0.000
0.028	0.002	0.000
0.031	0.002	0.001
0.036	0.003	0.001
0.045	0.004	0.003
0.045	0.005	0.004
0.048	0.005	0.005
0.053	0.006	0.006
0.053	0.006	0.006
0.053	0.008	0.007
0.056	0.009	0.008
0.057	0.009	0.008
0.059	0.010	0.010
0.059	0.010	0.011
0.060	0.010	0.012
0.061	0.010	0.013
0.061	0.011	0.013
0.066	0.011	0.014
0.069	0.011	0.015
0.071	0.012	0.015
0.072	0.012	0.016
0.072	0.012	0.016
0.075	0.013	0.017
0.081	0.013	0.017
0.084	0.014	0.017

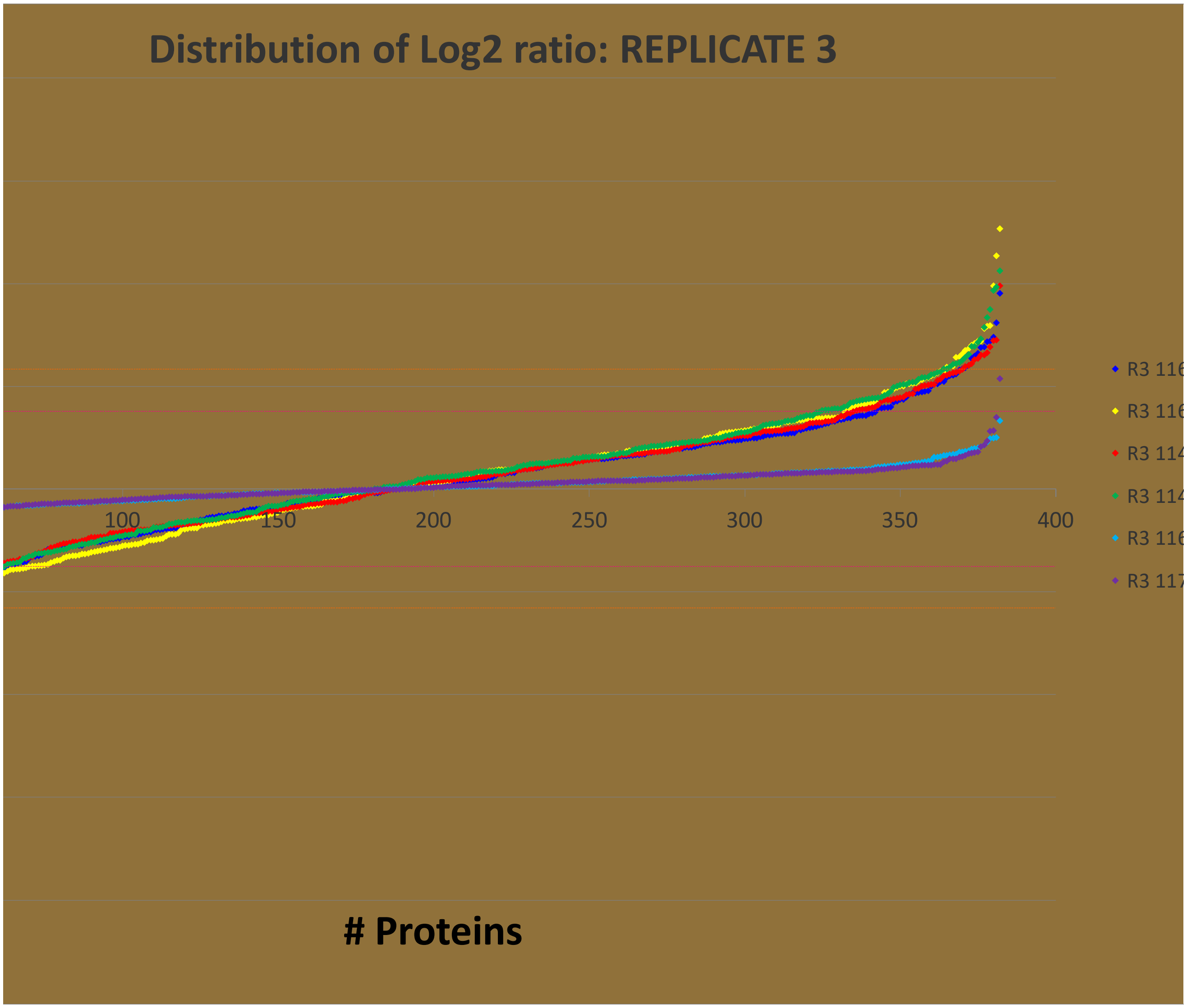
0.084	0.014	0.018
0.084	0.014	0.018
0.085	0.015	0.018
0.085	0.015	0.019
0.087	0.016	0.019
0.087	0.019	0.019
0.087	0.019	0.019
0.090	0.020	0.020
0.093	0.021	0.020
0.095	0.022	0.021
0.098	0.023	0.021
0.108	0.023	0.022
0.109	0.025	0.022
0.114	0.025	0.023
0.116	0.026	0.023
0.121	0.026	0.024
0.122	0.027	0.025
0.123	0.027	0.025
0.124	0.027	0.026
0.124	0.028	0.027
0.124	0.028	0.028
0.125	0.028	0.029
0.128	0.029	0.029
0.131	0.029	0.030
0.132	0.029	0.030
0.134	0.029	0.030
0.136	0.030	0.032
0.138	0.030	0.032
0.139	0.030	0.034
0.148	0.031	0.034
0.149	0.031	0.035
0.149	0.031	0.035
0.153	0.032	0.035
0.155	0.033	0.035
0.155	0.034	0.037
0.156	0.035	0.038
0.156	0.036	0.038
0.157	0.036	0.038
0.157	0.037	0.039
0.157	0.038	0.039
0.161	0.038	0.039
0.167	0.038	0.039
0.170	0.039	0.039
0.170	0.040	0.039
0.174	0.041	0.039
0.174	0.041	0.040
0.175	0.042	0.040
0.178	0.042	0.040
0.187	0.044	0.040
0.193	0.044	0.040
0.196	0.045	0.041
0.200	0.045	0.042
0.201	0.046	0.043
0.201	0.047	0.044

0.207	0.047	0.044
0.208	0.047	0.044
0.209	0.049	0.044
0.211	0.049	0.045
0.212	0.050	0.047
0.215	0.050	0.047
0.215	0.051	0.048
0.219	0.051	0.048
0.221	0.052	0.049
0.222	0.052	0.050
0.223	0.053	0.050
0.225	0.054	0.051
0.228	0.055	0.051
0.229	0.055	0.052
0.231	0.055	0.053
0.231	0.056	0.054
0.234	0.058	0.055
0.235	0.058	0.055
0.236	0.059	0.056
0.241	0.061	0.056
0.246	0.062	0.057
0.246	0.062	0.059
0.247	0.062	0.059
0.253	0.062	0.060
0.257	0.062	0.061
0.261	0.063	0.061
0.263	0.064	0.062
0.269	0.065	0.062
0.273	0.065	0.063
0.275	0.066	0.064
0.276	0.066	0.065
0.277	0.066	0.065
0.281	0.066	0.067
0.289	0.067	0.069
0.291	0.068	0.069
0.302	0.071	0.070
0.309	0.071	0.070
0.312	0.071	0.070
0.315	0.071	0.070
0.317	0.074	0.071
0.318	0.075	0.072
0.320	0.075	0.073
0.323	0.075	0.074
0.328	0.077	0.075
0.330	0.077	0.075
0.332	0.078	0.075
0.333	0.078	0.076
0.342	0.079	0.077
0.347	0.079	0.077
0.350	0.080	0.078
0.356	0.081	0.078
0.357	0.083	0.079
0.358	0.083	0.080
0.371	0.083	0.080

0.374	0.084	0.080
0.381	0.085	0.081
0.384	0.086	0.081
0.384	0.086	0.082
0.387	0.086	0.082
0.389	0.087	0.083
0.390	0.088	0.084
0.391	0.088	0.084
0.399	0.090	0.084
0.405	0.091	0.085
0.418	0.092	0.085
0.420	0.093	0.085
0.427	0.093	0.087
0.428	0.094	0.087
0.432	0.094	0.088
0.435	0.095	0.088
0.437	0.095	0.090
0.441	0.098	0.090
0.441	0.104	0.092
0.445	0.106	0.094
0.446	0.107	0.094
0.453	0.109	0.095
0.463	0.109	0.099
0.476	0.112	0.100
0.495	0.112	0.101
0.500	0.115	0.101
0.505	0.118	0.104
0.508	0.118	0.106
0.509	0.119	0.107
0.517	0.119	0.110
0.518	0.124	0.112
0.518	0.127	0.113
0.533	0.128	0.113
0.542	0.130	0.114
0.543	0.132	0.115
0.544	0.135	0.115
0.555	0.137	0.116
0.559	0.153	0.118
0.567	0.155	0.118
0.570	0.156	0.119
0.585	0.162	0.133
0.585	0.164	0.135
0.593	0.166	0.145
0.605	0.167	0.145
0.610	0.169	0.147
0.614	0.178	0.154
0.626	0.179	0.158
0.640	0.182	0.163
0.653	0.185	0.172
0.692	0.195	0.175
0.693	0.195	0.177
0.713	0.199	0.181
0.731	0.205	0.206
0.786	0.214	0.213

0.834	0.228	0.233
0.872	0.244	0.282
0.965	0.248	0.284
0.983	0.249	0.348
1.060	0.332	0.535

x	y
0	-0.37707
400	-0.37707
0	-0.57777
400	-0.57777



6/117 (I/NI)
6/115 (I/NI)
4/117 (I/NI)
4/115 (I/NI)
6/114 (I/I)
7/115 (NI/NI)

0.337	0.328
0.354	0.354
0.399	0.382
0.469	0.466
0.475	0.468
0.480	0.848
0.519	0.548
0.523	0.584
0.530	0.567
0.545	0.530
0.557	0.565
0.561	0.574
0.561	0.578
0.569	0.654
0.579	0.521
0.592	0.556
0.599	0.590
0.606	0.688
0.613	0.573
0.633	0.608
0.637	0.627
0.644	0.617
0.645	0.649
0.659	0.926
0.664	0.644
0.666	0.738
0.666	0.613
0.673	0.644
0.674	0.661
0.675	0.687
0.675	0.619
0.681	0.682
0.684	0.738
0.685	0.685
0.687	0.646
0.692	0.778
0.694	0.735
0.695	0.734
0.696	0.728
0.704	0.760
0.709	0.759
0.710	0.595
0.711	0.773
0.717	0.732
0.722	0.782
0.725	0.688
0.725	0.678
0.726	0.672
0.727	0.780
0.731	0.632
0.732	0.693
0.740	0.738
0.740	0.679

0.367	0.372
0.393	0.472
0.407	0.499
0.424	0.531
0.456	0.568
0.461	0.526
0.501	0.528
0.516	0.511
0.518	0.476
0.519	0.581
0.535	0.493
0.538	0.571
0.556	0.624
0.557	0.670
0.571	0.661
0.602	0.606
0.614	0.618
0.630	0.668
0.630	0.641
0.634	0.671
0.636	0.853
0.641	0.699
0.644	0.623
0.645	0.671
0.646	0.791
0.650	0.699
0.653	0.757
0.658	0.671
0.658	0.668
0.665	0.848
0.683	0.780
0.684	0.655
0.686	0.746
0.694	1.024
0.695	0.926
0.697	0.684
0.699	0.741
0.705	0.675
0.707	0.684
0.710	0.699
0.721	0.766
0.722	0.834
0.729	0.810
0.733	0.779
0.734	0.849
0.738	0.889
0.741	0.809
0.745	0.825
0.753	0.822
0.753	0.712
0.755	0.783
0.762	0.788
0.762	0.784

0.392
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0.515
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0.740
0.742

0.752	0.809
0.753	0.809
0.755	0.767
0.755	0.736
0.756	0.724
0.756	0.813
0.756	0.832
0.761	0.698
0.766	0.700
0.768	0.725
0.770	0.787
0.771	0.797
0.771	0.792
0.772	0.743
0.776	0.737
0.778	0.867
0.779	0.831
0.779	0.809
0.783	0.829
0.797	0.724
0.797	0.751
0.798	0.783
0.798	0.800
0.799	0.790
0.801	0.815
0.802	0.818
0.802	0.806
0.804	0.740
0.806	0.821
0.809	0.832
0.811	0.785
0.813	0.846
0.813	0.932
0.817	0.802
0.819	0.711
0.819	0.820
0.820	0.854
0.822	0.848
0.824	0.786
0.825	0.770
0.828	0.852
0.834	0.796
0.835	0.897
0.841	0.806
0.841	0.850
0.843	1.024
0.846	0.793
0.847	0.831
0.848	0.712
0.851	0.815
0.851	0.795
0.852	0.782
0.858	0.865
0.859	0.899

0.764	0.854
0.764	0.852
0.766	0.921
0.767	0.803
0.768	0.778
0.769	0.772
0.769	0.851
0.775	0.811
0.776	1.074
0.780	0.730
0.781	0.777
0.788	0.763
0.795	0.944
0.797	1.273
0.803	0.786
0.803	0.959
0.805	0.753
0.806	0.919
0.808	0.945
0.809	0.996
0.809	0.850
0.810	0.729
0.814	0.911
0.814	0.710
0.822	0.777
0.822	0.878
0.823	0.861
0.824	0.830
0.826	0.820
0.827	0.926
0.828	0.895
0.828	0.873
0.832	0.899
0.835	0.859
0.836	0.927
0.836	0.948
0.840	0.978
0.846	0.910
0.849	0.805
0.850	0.869
0.852	0.980
0.857	0.967
0.858	0.922
0.860	0.947
0.864	0.807
0.866	0.708
0.868	0.834
0.869	0.944
0.869	0.935
0.872	0.812
0.873	0.926
0.874	0.999
0.878	0.686
0.879	0.973

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0.860	0.862
0.860	0.854
0.860	0.840
0.863	0.883
0.866	0.834
0.866	0.905
0.868	0.859
0.872	0.823
0.873	0.893
0.874	0.867
0.876	0.652
0.878	0.844
0.880	0.825
0.883	1.134
0.884	1.009
0.884	0.923
0.887	0.876
0.888	1.023
0.889	0.823
0.890	0.966
0.891	0.889
0.901	0.940
0.901	0.889
0.901	0.911
0.902	0.846
0.906	0.915
0.909	0.914
0.911	0.873
0.913	0.888
0.914	0.871
0.916	1.068
0.918	0.907
0.920	1.175
0.921	0.887
0.921	0.933
0.922	0.850
0.923	1.057
0.928	0.964
0.929	0.904
0.933	0.856
0.934	0.815
0.934	1.010
0.940	1.029
0.946	0.934
0.946	1.059
0.948	0.986
0.949	0.808
0.950	1.007
0.950	1.001
0.951	0.926
0.952	1.042
0.957	0.969
0.958	1.050
0.960	1.153

0.882	0.930
0.882	0.941
0.885	1.210
0.886	0.795
0.886	0.859
0.892	0.944
0.897	0.968
0.901	0.636
0.901	0.906
0.904	0.864
0.906	0.906
0.907	0.855
0.909	0.988
0.909	0.956
0.910	1.033
0.912	0.976
0.913	0.826
0.917	0.804
0.919	0.955
0.919	0.988
0.921	0.932
0.921	0.958
0.923	0.977
0.930	1.178
0.931	0.916
0.933	0.869
0.938	0.908
0.939	0.980
0.939	0.891
0.940	0.911
0.941	0.754
0.942	1.060
0.943	0.826
0.943	0.958
0.944	0.950
0.945	1.042
0.946	1.065
0.947	1.049
0.948	0.984
0.949	0.850
0.953	0.881
0.954	0.874
0.954	1.006
0.964	0.883
0.969	0.965
0.971	1.024
0.971	0.998
0.974	0.835
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0.979	1.006
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0.960	0.867
0.961	0.920
0.961	1.059
0.967	0.859
0.970	0.951
0.978	0.977
0.979	0.960
0.980	0.991
0.980	0.974
0.982	1.004
0.982	0.895
0.983	0.984
0.985	0.919
0.985	0.963
0.988	0.998
0.990	0.960
0.992	0.936
0.992	1.079
1.000	0.864
1.000	0.924
1.012	0.926
1.013	0.929
1.020	0.991
1.023	0.940
1.024	0.928
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1.029	1.022
1.031	0.975
1.032	1.001
1.034	1.139
1.035	1.019
1.039	1.115
1.039	0.991
1.041	0.998
1.041	0.897
1.043	0.893
1.045	1.115
1.051	1.025
1.053	1.050
1.055	1.109
1.056	0.990
1.057	1.096
1.057	0.994
1.059	1.027
1.066	0.988
1.072	1.028
1.073	0.898
1.076	1.257
1.079	1.105
1.079	0.916
1.080	0.998
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1.083	1.177

0.987	1.044
0.988	0.971
0.990	1.074
0.993	1.002
0.995	1.002
0.996	1.049
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1.004	1.113
1.005	0.970
1.007	1.013
1.010	1.049
1.012	1.089
1.018	1.165
1.020	0.955
1.022	1.011
1.029	0.929
1.033	1.157
1.036	1.091
1.038	0.957
1.040	1.171
1.042	0.723
1.044	1.104
1.049	1.102
1.050	1.536
1.052	1.253
1.056	1.226
1.057	1.042
1.058	1.047
1.060	1.261
1.062	1.031
1.063	1.059
1.067	1.079
1.067	1.033
1.068	1.195
1.073	1.000
1.074	0.798
1.079	0.843
1.082	1.031
1.088	1.174
1.094	1.191
1.095	1.200
1.099	1.026
1.100	1.092
1.101	1.112
1.101	0.929
1.104	1.086
1.106	1.156
1.111	0.970
1.114	1.116
1.115	1.125
1.117	1.038
1.118	1.152
1.118	1.184
1.118	0.982

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1.092	0.914
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1.101	1.070
1.103	1.081
1.106	1.196
1.110	1.084
1.112	0.931
1.114	1.195
1.115	1.191
1.116	1.628
1.122	1.044
1.123	1.126
1.130	0.999
1.132	1.048
1.134	1.091
1.136	1.489
1.140	1.290
1.140	1.063
1.143	1.197
1.144	1.361
1.147	1.088
1.148	0.994
1.148	1.158
1.152	1.156
1.155	1.216
1.156	1.170
1.163	1.163
1.164	1.001
1.166	1.090
1.168	1.124
1.174	1.082
1.174	1.084
1.174	1.093
1.175	1.136
1.175	1.121
1.176	1.165
1.178	1.170
1.179	1.127
1.197	1.002
1.197	1.018
1.200	1.108
1.201	1.111
1.202	1.133
1.202	1.139
1.203	1.242
1.204	1.168
1.206	1.186
1.216	1.019
1.226	1.131
1.228	1.242
1.230	1.038

1.120	1.210
1.128	0.996
1.130	1.151
1.130	1.165
1.133	0.967
1.138	0.956
1.138	1.059
1.139	1.065
1.140	1.155
1.141	0.896
1.142	1.071
1.148	1.381
1.150	1.200
1.161	1.145
1.163	1.273
1.165	1.009
1.177	1.159
1.179	1.160
1.182	1.350
1.183	1.361
1.190	1.347
1.198	1.129
1.198	0.896
1.199	1.055
1.200	1.176
1.205	1.324
1.205	1.447
1.210	1.280
1.210	1.231
1.214	1.249
1.214	1.364
1.214	1.217
1.217	1.192
1.221	1.008
1.221	0.924
1.238	1.307
1.242	1.248
1.243	1.343
1.244	1.111
1.247	1.352
1.248	1.121
1.253	1.425
1.254	1.137
1.258	1.050
1.269	1.224
1.271	1.129
1.275	1.211
1.282	0.849
1.288	1.152
1.289	1.290
1.290	1.088
1.290	1.373
1.293	1.319
1.295	1.197

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1.234	1.223
1.236	1.006
1.238	1.307
1.248	1.247
1.255	1.160
1.259	1.164
1.260	0.992
1.268	1.149
1.268	1.215
1.273	1.234
1.277	1.261
1.279	1.181
1.282	1.195
1.283	1.414
1.288	1.118
1.292	1.198
1.296	1.276
1.297	1.149
1.300	1.218
1.306	1.259
1.312	1.667
1.317	1.278
1.318	0.913
1.322	1.221
1.322	1.309
1.326	1.175
1.334	1.276
1.341	1.264
1.342	1.371
1.343	1.286
1.345	1.134
1.358	1.183
1.361	1.152
1.366	1.564
1.367	1.310
1.368	1.404
1.372	1.428
1.375	1.174
1.378	0.882
1.380	1.318
1.382	1.604
1.386	0.901
1.386	1.390
1.391	1.401
1.408	1.317
1.411	1.542
1.415	1.367
1.417	1.436
1.418	1.271
1.429	1.516
1.436	1.080
1.436	1.205
1.437	1.098

1.296	1.212
1.299	1.325
1.306	1.241
1.310	1.163
1.312	1.205
1.314	1.439
1.314	1.246
1.327	1.067
1.333	1.284
1.344	1.200
1.344	1.272
1.345	1.132
1.348	1.143
1.349	1.229
1.357	1.634
1.366	1.319
1.367	1.306
1.370	0.980
1.372	1.321
1.378	1.514
1.379	1.065
1.384	1.305
1.390	1.587
1.398	1.337
1.420	1.706
1.436	1.573
1.438	1.323
1.441	0.895
1.459	0.894
1.463	1.473
1.472	1.571
1.475	1.486
1.482	1.512
1.485	1.242
1.509	1.572
1.519	1.318
1.520	1.669
1.543	1.018
1.544	1.524
1.546	1.263
1.556	1.361
1.556	1.498
1.557	1.541
1.584	1.427
1.620	1.773
1.628	1.341
1.655	1.598
1.879	1.769
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1.943	1.790
2.058	1.685

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1.443	1.317
1.468	1.400
1.480	1.440
1.483	1.628
1.485	1.446
1.509	1.448
1.511	1.625
1.520	1.664
1.533	1.342
1.540	1.409
1.550	1.574
1.560	1.580
1.564	1.424
1.570	1.465
1.577	1.307
1.580	1.373
1.581	1.442
1.588	1.386
1.597	1.078
1.597	1.369
1.613	1.832
1.622	1.530
1.622	1.099
1.633	1.268
1.655	1.551
1.677	1.536
1.692	1.551
1.757	1.448
1.781	1.623
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1.788	1.524
1.790	1.537
1.833	1.447
1.840	1.321
1.859	1.720
1.881	1.783
1.896	1.507
2.091	2.023
2.496	2.259
2.590	2.339
2.595	2.102
2.645	2.321
2.655	1.929
2.694	2.331
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11.855	5.531

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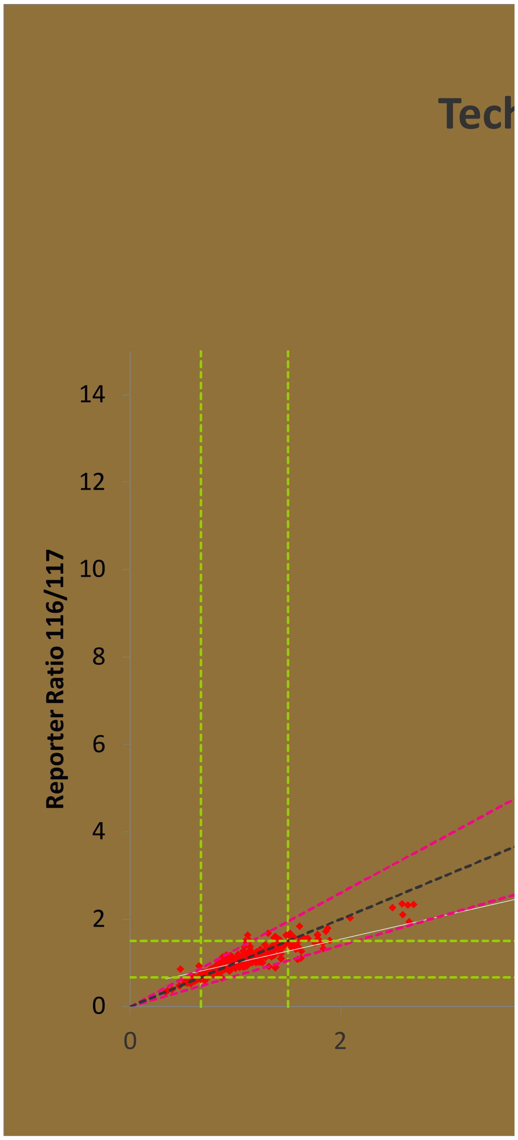

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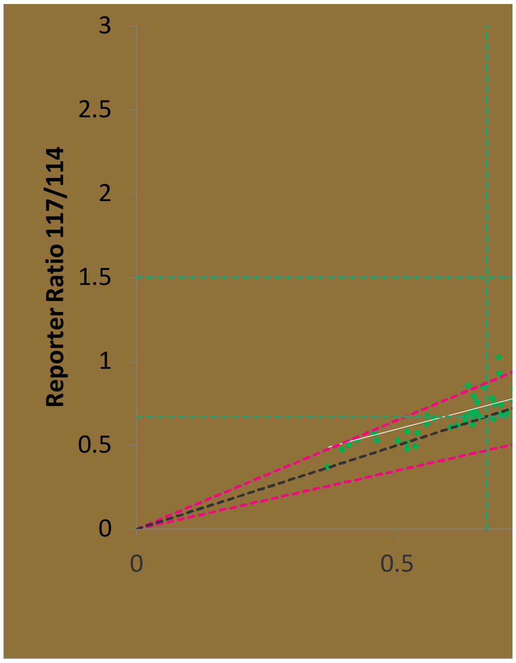

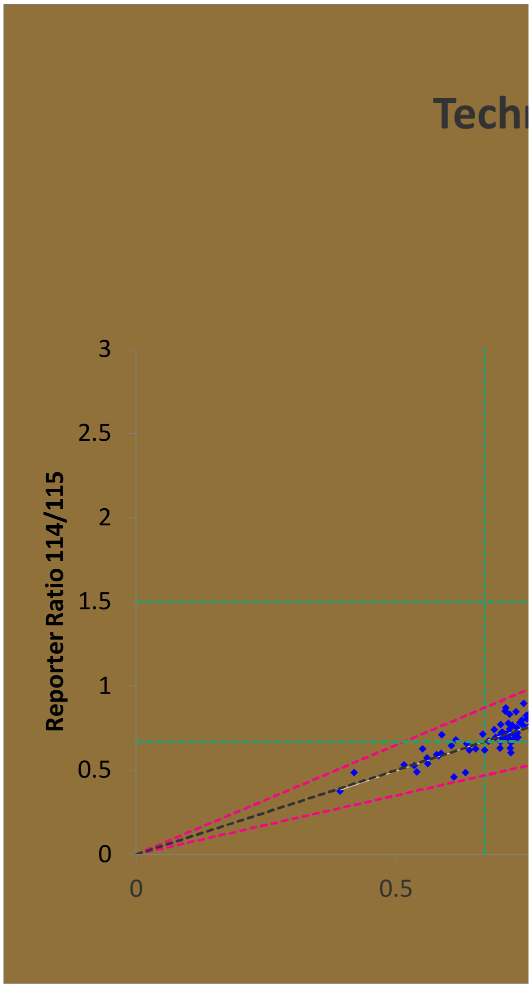

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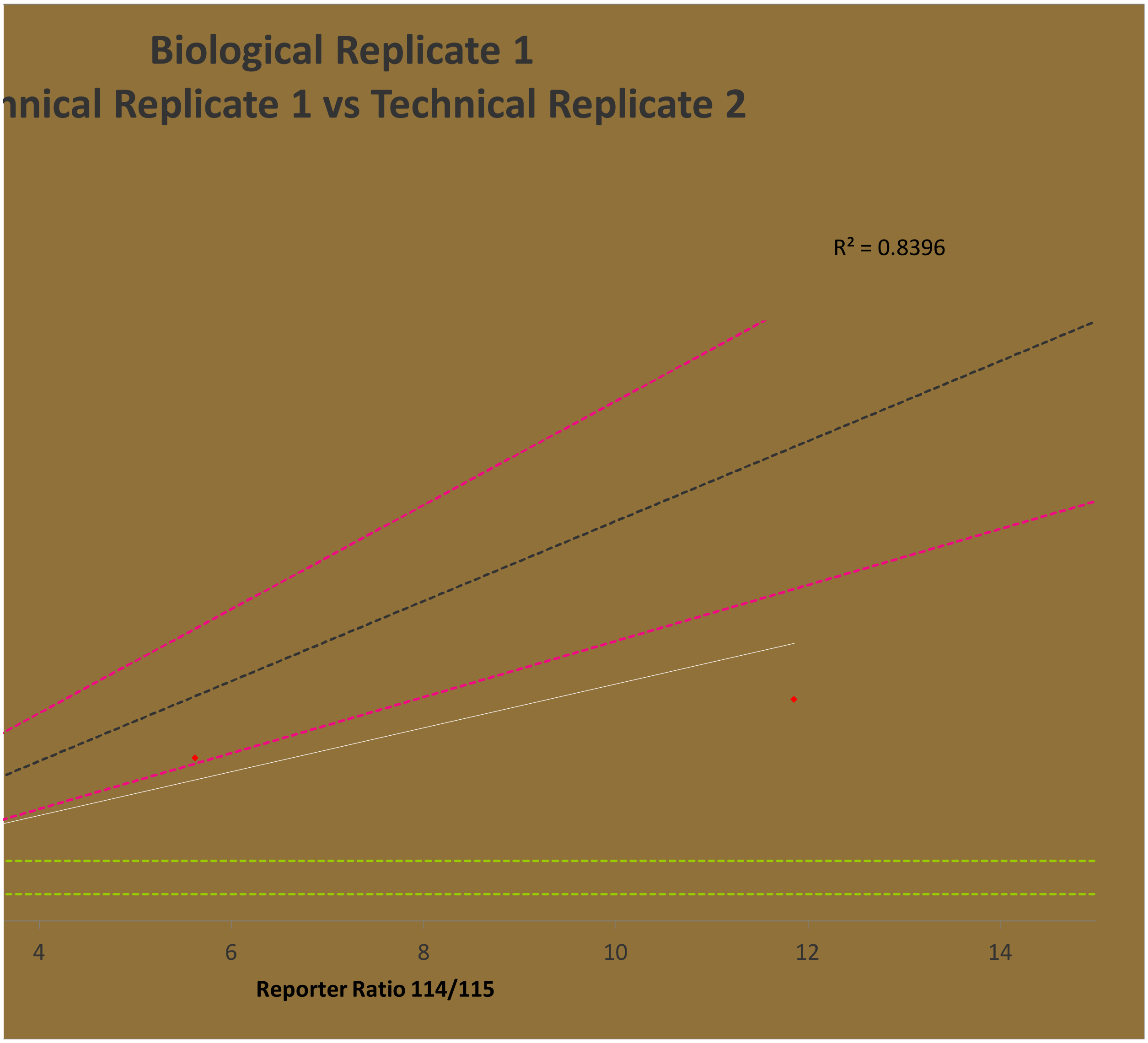

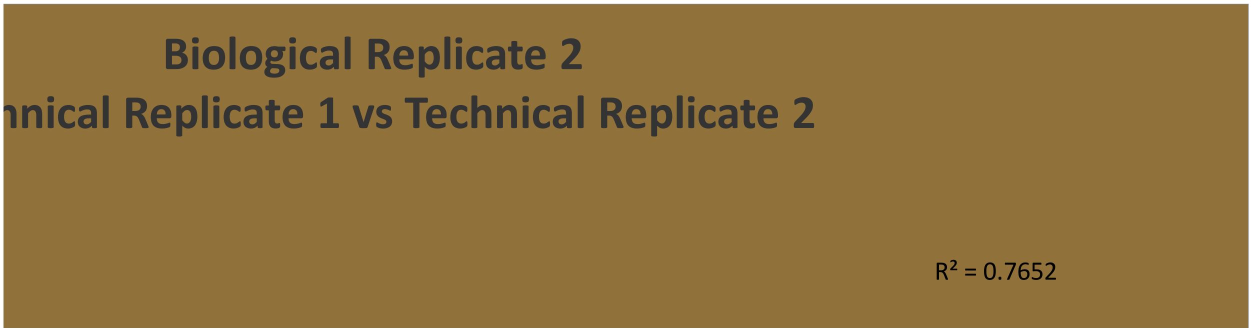

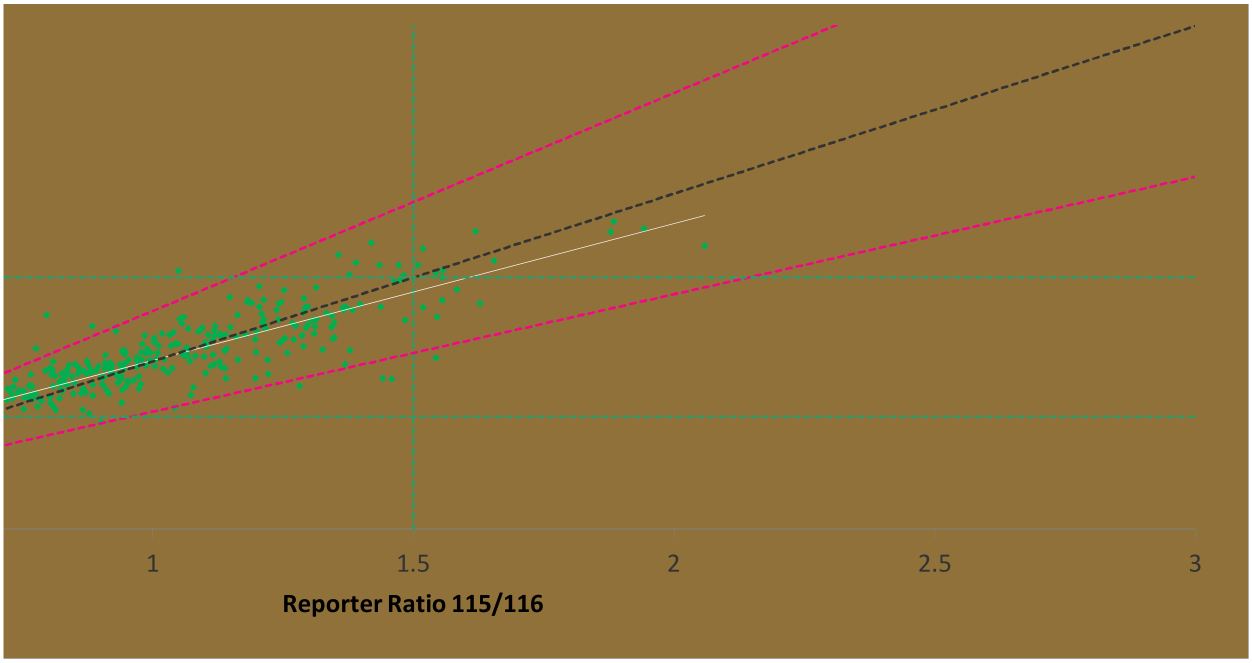
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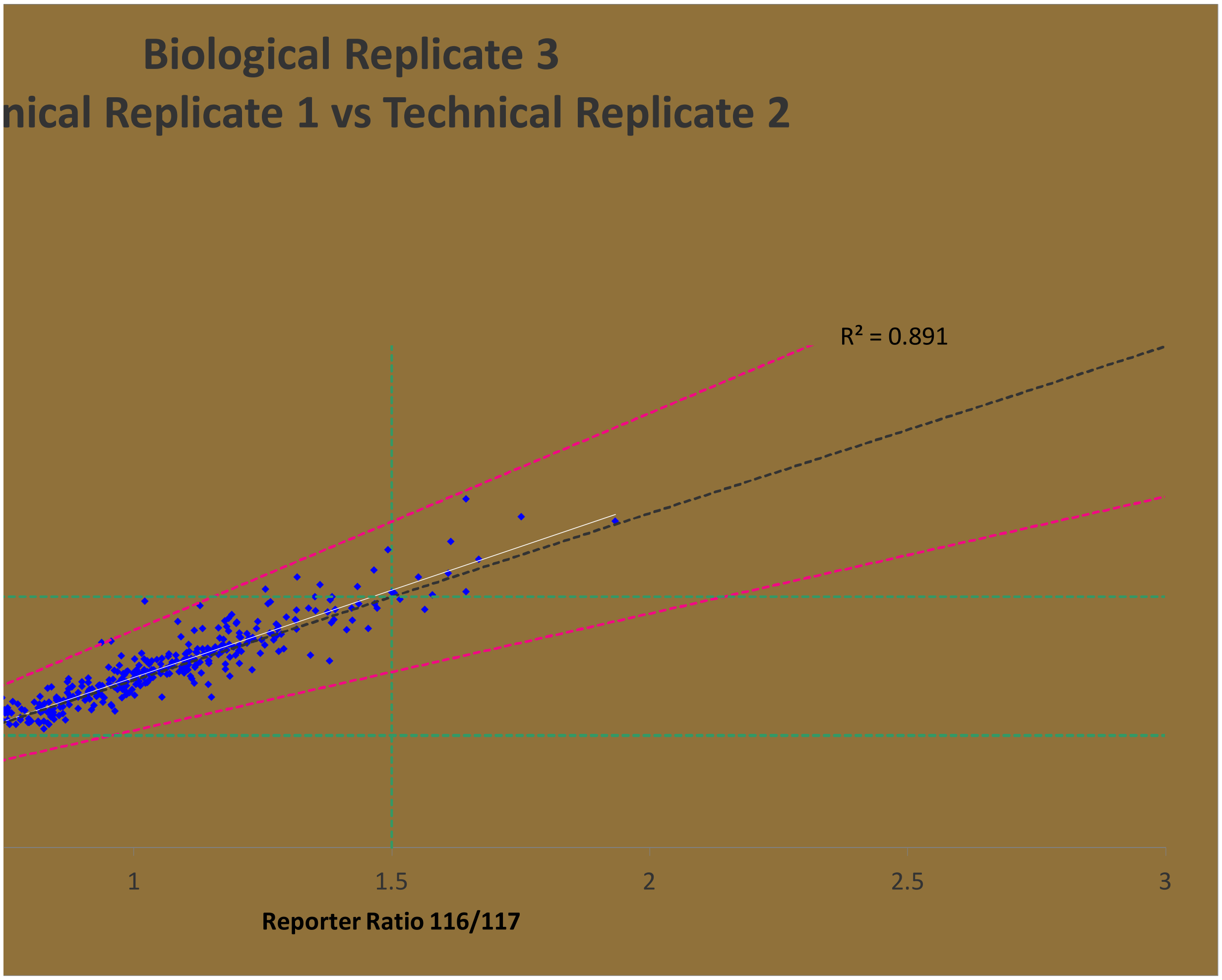
2
2.5
3
Reporter Ratio 115/116


Biological Replicate 3
nical Replicate 1 vs Technical Replicate 2
R² = 0.891
1
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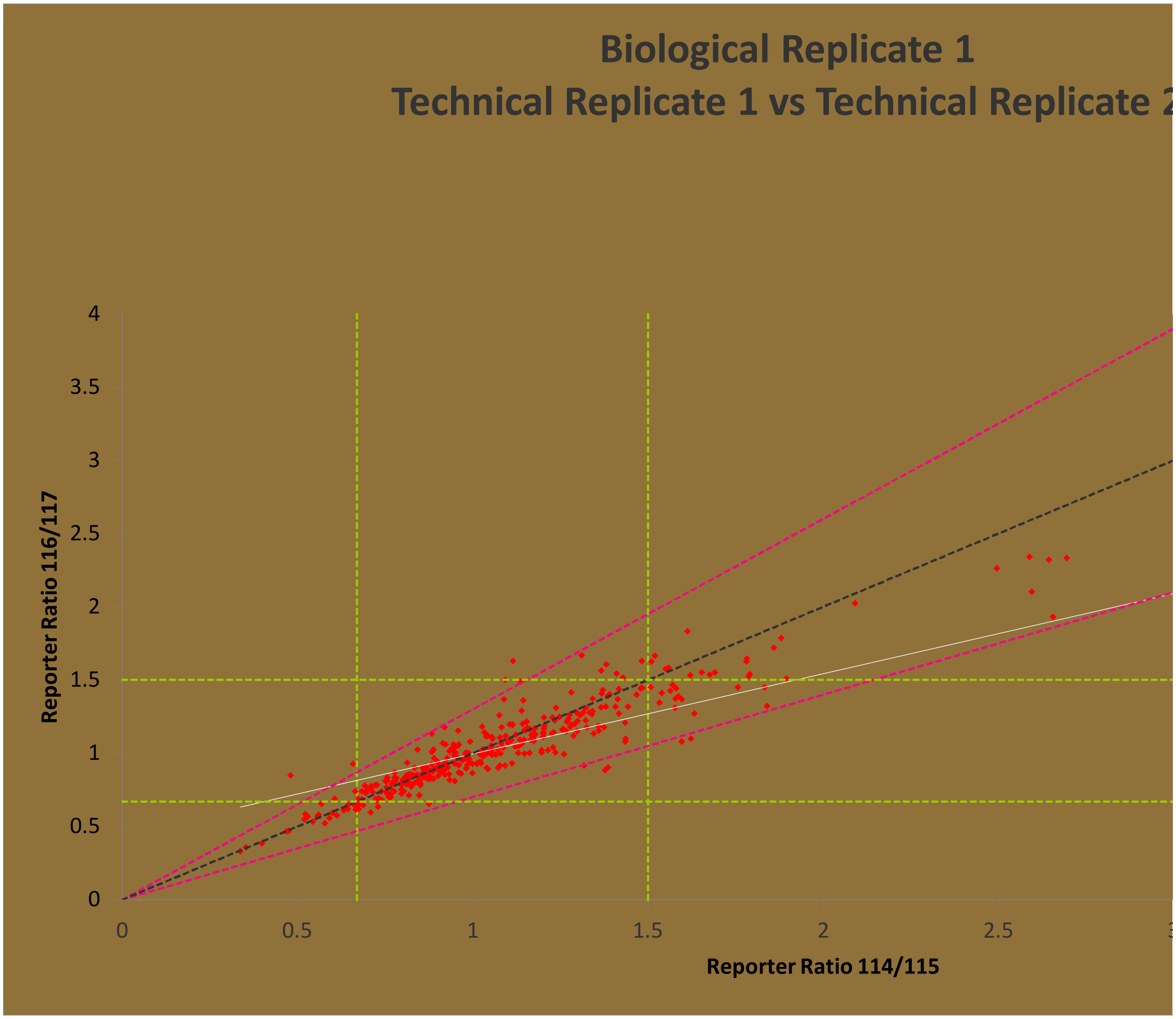
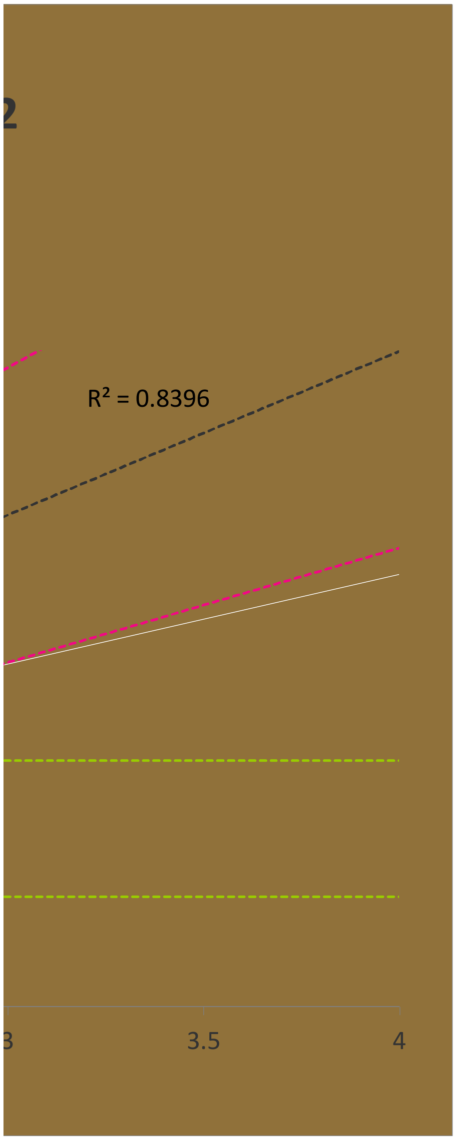
2
2.5
3
Reporter Ratio 116/117


Biological Replicate 1
Technical Replicate 1 vs Technical Replicate 2
Reporter Ratio 116/117
0
0.5
1
1.5
2
2.5
3
3.5
4
0
0.5
1
1.5
2
2.5
Reporter Ratio 114/115


2
R² = 0.8396
3
3.5
4

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0.47	0.52		0.47	0.66		0.44	0.54
0.54	0.62		0.47	0.60		0.50	0.52
0.54	0.47		0.54	0.70		0.51	0.59
0.55	0.68		0.55	0.54		0.52	0.60
0.55	0.76		0.55	0.70		0.55	0.64
0.56	0.44		0.55	0.89		0.60	0.77
0.57	0.50		0.56	0.54		0.60	0.81
0.57	0.51		0.57	0.52		0.62	0.71
0.59	0.62		0.57	0.59		0.62	0.64
0.61	0.75		0.57	0.65		0.62	0.59
0.61	0.55		0.59	0.71		0.62	0.70
0.62	0.76		0.61	0.82		0.64	0.53
0.63	0.66		0.61	0.64		0.66	0.79
0.63	0.72		0.62	0.68		0.66	0.71
0.63	0.95		0.63	0.71		0.67	0.65
0.64	0.89		0.63	0.88		0.67	0.75
0.65	1.07		0.63	0.96		0.67	0.78
0.65	0.64		0.64	0.71		0.67	0.73
0.65	0.71		0.65	0.73		0.68	0.54
0.66	0.66		0.65	0.59		0.69	0.63
0.66	0.90		0.66	0.79		0.70	0.79
0.67	0.78		0.66	0.92		0.70	0.75
0.67	0.79		0.67	0.79		0.70	0.73
0.68	0.70		0.67	0.75		0.71	0.59
0.68	0.92		0.68	0.75		0.72	0.50
0.68	0.73		0.68	0.82		0.72	0.88
0.69	0.87		0.68	0.75		0.73	0.75
0.70	1.14		0.69	0.79		0.73	0.79
0.70	0.90		0.70	0.83		0.74	0.72
0.70	0.81		0.70	0.70		0.75	0.82
0.71	1.03		0.70	0.71		0.75	0.83
0.71	0.77		0.71	0.72		0.76	0.68
0.71	0.87		0.71	0.77		0.76	0.70
0.71	0.67		0.71	0.89		0.76	0.84
0.72	0.80		0.71	0.82		0.76	0.92
0.72	0.67		0.71	0.73		0.76	0.84
0.73	0.62		0.72	0.71		0.77	0.69
0.74	0.93		0.72	0.78		0.77	0.93
0.74	0.70		0.73	0.59		0.77	0.86
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0.74	0.67		0.74	0.73		0.78	0.82
0.75	0.83		0.74	0.83		0.78	0.77
0.75	0.99		0.74	0.78		0.78	0.95
0.75	0.84		0.74	0.65		0.79	0.91
0.75	0.78		0.75	0.88		0.79	0.75
0.76	0.76		0.75	1.08		0.79	0.78
0.76	1.06		0.75	0.70		0.79	0.93
0.76	0.77		0.75	0.80		0.79	0.79
0.77	0.92		0.75	0.95		0.80	0.92
0.77	1.14		0.76	0.84		0.80	0.71

0.77	0.70	0.76	0.79	0.81	0.66
0.79	0.60	0.76	0.85	0.81	0.72
0.79	0.92	0.76	0.69	0.81	0.97
0.79	1.26	0.77	0.97	0.81	0.89
0.79	0.62	0.77	1.21	0.81	0.71
0.79	0.97	0.77	0.79	0.82	0.77
0.79	0.74	0.79	0.81	0.82	0.95
0.79	0.81	0.79	0.80	0.82	0.84
0.79	0.94	0.79	0.64	0.82	1.69
0.80	0.91	0.79	0.92	0.83	0.82
0.80	1.18	0.79	0.72	0.83	0.88
0.80	0.82	0.79	0.72	0.83	0.87
0.80	0.81	0.79	0.80	0.83	0.88
0.80	1.26	0.80	1.10	0.84	0.89
0.80	0.92	0.80	0.95	0.84	0.78
0.80	0.91	0.80	0.97	0.84	1.02
0.81	0.76	0.80	0.70	0.84	0.70
0.81	0.78	0.80	1.10	0.84	0.99
0.81	0.86	0.80	0.91	0.85	0.89
0.81	0.86	0.81	0.84	0.85	0.98
0.81	0.79	0.81	0.77	0.85	0.86
0.82	0.90	0.81	0.77	0.85	0.97
0.82	0.82	0.81	1.11	0.85	0.84
0.82	0.90	0.81	0.91	0.86	1.11
0.82	0.92	0.82	0.91	0.86	1.05
0.83	0.60	0.82	0.77	0.86	0.77
0.83	1.18	0.82	1.25	0.86	0.73
0.83	0.86	0.82	0.96	0.87	1.10
0.83	0.81	0.83	0.77	0.87	0.82
0.83	0.92	0.83	0.90	0.87	0.79
0.84	0.90	0.83	0.75	0.88	0.93
0.84	0.93	0.83	0.73	0.88	1.22
0.84	0.95	0.83	0.66	0.88	1.04
0.84	1.25	0.83	1.00	0.88	1.01
0.85	1.24	0.84	0.99	0.88	1.04
0.85	0.90	0.84	0.77	0.89	0.71
0.85	0.85	0.84	0.82	0.89	0.87
0.86	0.80	0.84	1.01	0.89	0.95
0.86	0.92	0.85	0.96	0.89	1.10
0.86	1.07	0.85	1.08	0.90	0.70
0.86	0.79	0.85	0.86	0.90	0.91
0.87	0.88	0.86	0.92	0.90	0.92
0.87	0.92	0.86	0.94	0.90	0.96
0.87	0.98	0.86	1.12	0.90	0.99
0.87	0.88	0.86	0.93	0.90	1.25
0.88	1.28	0.86	0.82	0.90	1.23
0.88	0.84	0.87	1.01	0.90	1.07
0.88	0.81	0.87	1.02	0.90	1.16
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0.89	1.28	0.87	0.89	0.91	1.03
0.89	0.79	0.87	1.04	0.91	0.91
0.89	0.94	0.88	0.79	0.91	1.01
0.89	0.87	0.88	0.89	0.91	1.10
0.90	1.01	0.88	0.89	0.92	1.00

0.90	0.93	0.88	1.05	0.92	1.02
0.90	1.53	0.89	0.76	0.92	1.06
0.90	0.83	0.89	0.79	0.92	0.96
0.90	1.01	0.89	1.01	0.92	0.80
0.90	1.18	0.89	1.10	0.92	0.82
0.91	0.96	0.90	0.85	0.92	1.02
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0.91	0.72	0.90	0.81	0.92	0.94
0.91	0.93	0.90	1.43	0.92	0.97
0.92	1.03	0.91	0.73	0.93	0.91
0.92	0.83	0.91	0.79	0.93	0.94
0.92	0.93	0.91	0.78	0.93	1.01
0.92	1.02	0.91	0.86	0.93	0.77
0.93	1.57	0.91	0.50	0.93	0.85
0.93	0.85	0.91	0.92	0.93	0.92
0.93	1.03	0.92	0.99	0.94	1.01
0.93	0.89	0.92	0.82	0.94	0.80
0.94	0.83	0.92	1.01	0.94	1.17
0.95	1.06	0.92	1.09	0.95	0.82
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1.03	0.94	1.00	1.09	1.04	1.17
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1.06	1.11	1.03	1.12	1.06	0.87
1.07	1.17	1.03	1.13	1.07	1.04
1.07	0.78	1.03	1.13	1.07	1.17
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1.09	1.22	1.05	1.04	1.07	1.26
1.09	0.76	1.05	1.49	1.07	0.73
1.09	0.95	1.06	1.14	1.08	1.08
1.09	0.85	1.07	1.23	1.08	0.99
1.10	1.04	1.07	1.22	1.09	1.06
1.10	1.04	1.08	1.12	1.09	1.09
1.10	1.15	1.08	1.07	1.09	0.92
1.10	1.07	1.08	1.07	1.10	1.17
1.10	0.91	1.09	1.06	1.10	1.19
1.10	1.00	1.09	1.16	1.10	0.93
1.10	1.10	1.09	1.09	1.11	1.14
1.11	1.31	1.09	0.89	1.11	1.39
1.11	0.97	1.10	1.05	1.11	0.98
1.12	1.10	1.10	1.17	1.11	1.15
1.12	1.33	1.10	1.12	1.11	1.19
1.12	1.14	1.10	1.26	1.11	0.95
1.12	1.05	1.10	1.01	1.12	1.06
1.12	1.14	1.10	0.87	1.13	0.91
1.13	1.10	1.10	0.93	1.13	1.25
1.13	1.15	1.11	1.09	1.14	1.15
1.14	1.11	1.11	1.11	1.14	1.17
1.14	0.97	1.11	1.09	1.14	1.21
1.14	1.17	1.12	1.17	1.14	1.07
1.15	1.09	1.12	1.27	1.14	0.83
1.15	1.12	1.12	1.15	1.14	1.43
1.15	1.05	1.12	0.97	1.15	1.19
1.15	1.06	1.12	1.43	1.15	1.12
1.15	1.34	1.12	1.05	1.16	1.32
1.15	1.37	1.13	1.11	1.16	1.11
1.16	1.04	1.13	1.19	1.16	0.90
1.16	1.28	1.14	1.39	1.16	0.96
1.16	1.04	1.14	1.11	1.16	1.08
1.16	1.04	1.14	1.25	1.17	1.25
1.17	1.18	1.15	1.06	1.17	1.23

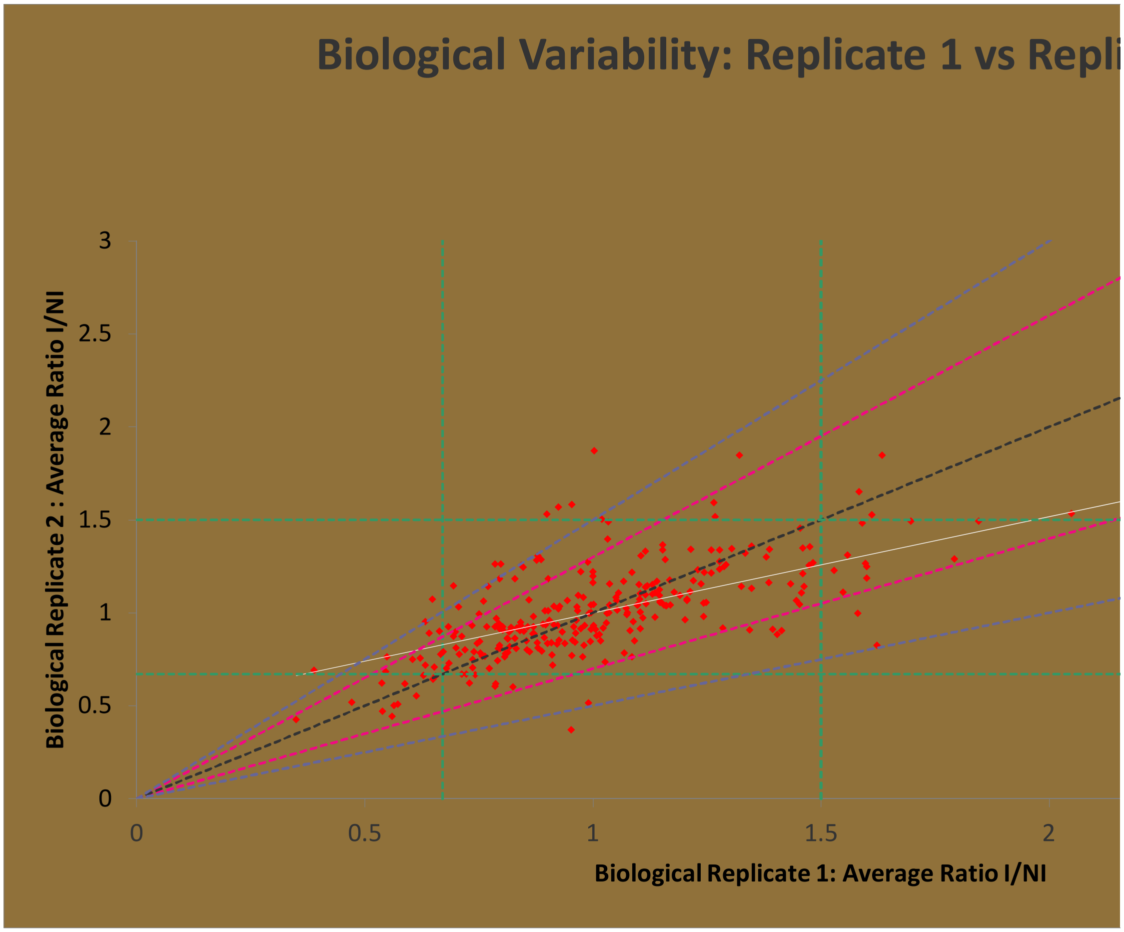
1.17	1.04	1.15	1.06	1.17	1.19
1.18	1.11	1.15	1.14	1.18	1.43
1.19	1.09	1.15	1.17	1.18	0.90
1.20	0.96	1.15	1.24	1.19	1.18
1.21	1.07	1.15	1.25	1.19	0.94
1.21	1.07	1.15	1.08	1.19	1.24
1.21	1.11	1.16	1.01	1.20	0.99
1.22	1.34	1.16	1.09	1.21	1.61
1.22	1.17	1.16	1.13	1.21	1.36
1.23	1.23	1.16	1.42	1.22	1.06
1.24	1.16	1.16	1.09	1.22	1.25
1.24	0.98	1.17	1.00	1.22	0.95
1.24	1.05	1.18	1.19	1.22	1.01
1.25	1.22	1.18	0.95	1.23	1.34
1.25	1.05	1.19	1.49	1.23	1.20
1.26	1.34	1.19	0.92	1.23	1.30
1.26	1.21	1.20	1.24	1.24	1.27
1.27	1.59	1.20	1.16	1.24	1.27
1.27	1.51	1.21	1.23	1.25	1.08
1.28	1.27	1.21	1.09	1.25	1.26
1.28	1.34	1.21	0.95	1.25	1.01
1.28	1.23	1.22	1.46	1.25	1.34
1.28	0.92	1.22	1.19	1.26	1.83
1.29	1.25	1.23	0.92	1.26	0.70
1.29	1.26	1.23	1.20	1.27	1.37
1.30	1.34	1.24	1.32	1.27	1.37
1.32	1.85	1.24	1.05	1.27	1.38
1.33	1.14	1.24	1.34	1.27	1.04
1.33	1.32	1.25	1.25	1.27	1.37
1.34	0.90	1.25	1.10	1.27	1.01
1.35	1.13	1.25	0.93	1.28	0.79
1.35	1.36	1.26	1.26	1.28	1.09
1.38	1.30	1.26	1.36	1.28	0.76
1.39	1.16	1.27	1.19	1.29	1.20
1.39	1.34	1.27	1.40	1.30	1.33
1.39	0.91	1.28	1.01	1.30	1.26
1.40	0.88	1.28	1.30	1.31	1.11
1.41	0.90	1.28	1.30	1.31	1.05
1.43	1.16	1.28	1.06	1.31	1.27
1.45	1.07	1.29	1.83	1.32	1.31
1.45	1.05	1.30	1.48	1.33	1.27
1.46	1.45	1.32	1.01	1.34	0.90
1.46	1.11	1.32	1.56	1.34	1.24
1.46	1.21	1.33	1.17	1.34	1.26
1.46	1.35	1.33	1.31	1.34	1.23
1.46	1.14	1.34	1.16	1.34	1.30
1.48	1.25	1.35	1.25	1.34	1.46
1.48	1.35	1.35	1.54	1.34	1.42
1.48	1.27	1.38	1.26	1.34	1.48
1.53	1.23	1.39	1.08	1.35	1.32
1.55	1.11	1.39	1.42	1.35	1.42
1.56	1.31	1.39	0.91	1.36	1.54
1.58	0.99	1.40	1.16	1.37	1.25
1.58	1.65	1.40	1.22	1.40	1.13

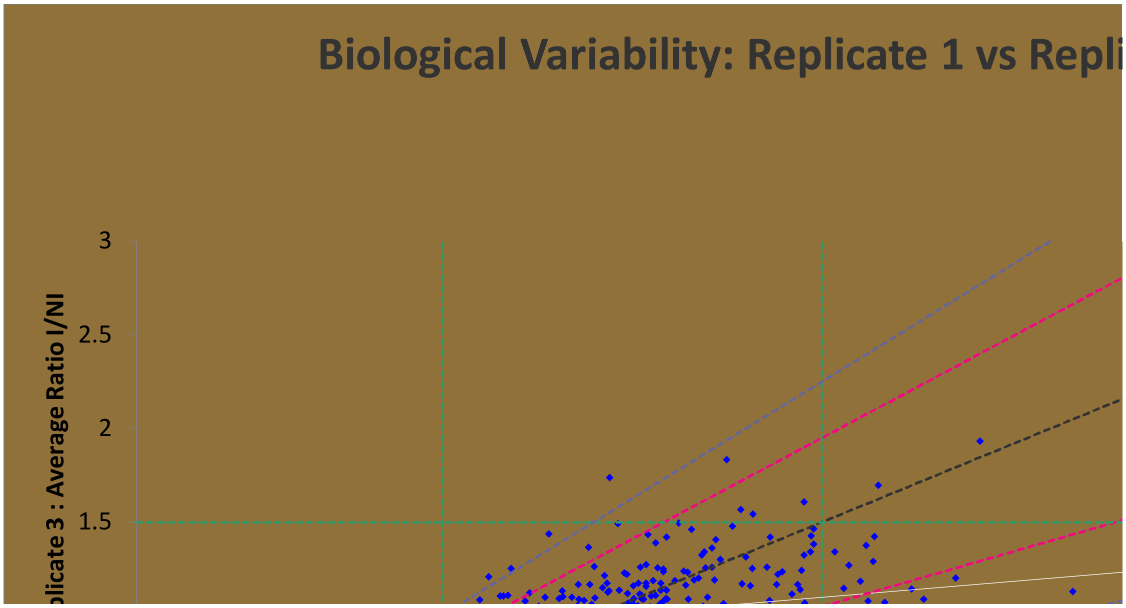
1.59	1.48
1.60	1.27
1.60	1.25
1.60	1.19
1.61	1.53
1.62	0.82
1.63	1.85
1.70	1.49
1.79	1.29
1.85	1.49
2.05	1.53
2.32	1.27
2.45	1.87
2.45	1.59
2.47	1.46
2.47	1.25

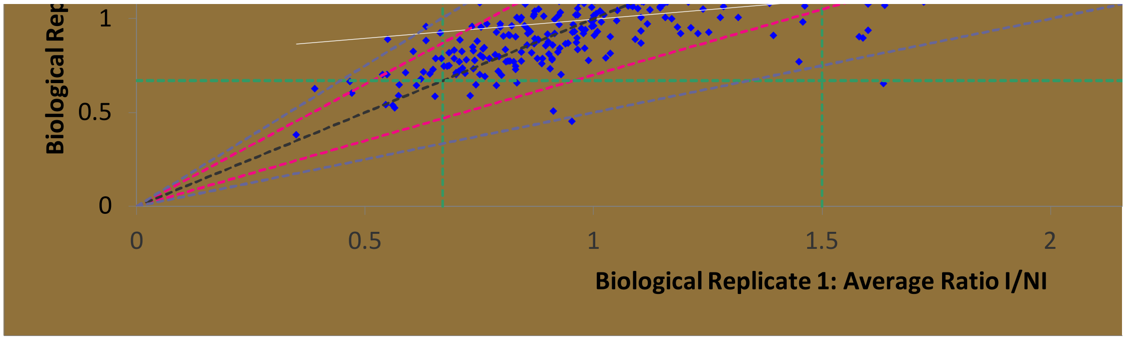
1.41	1.23
1.43	1.11
1.45	1.17
1.45	0.77
1.45	1.14
1.46	1.24
1.46	0.98
1.46	1.61
1.46	1.32
1.46	1.07
1.48	1.34
1.48	1.42
1.48	1.46
1.48	1.38
1.53	1.34
1.55	1.15
1.56	1.27
1.58	0.90
1.58	1.18
1.59	0.89
1.60	1.37
1.60	1.08
1.60	0.94
1.61	1.29
1.62	1.42
1.62	1.69
1.63	0.65
1.64	1.07
1.70	1.14
1.72	1.09
1.79	1.20
1.85	1.93
2.05	1.13
2.32	1.37
2.45	0.57
2.45	1.31
2.47	1.60
2.47	1.26
8.77	1.49

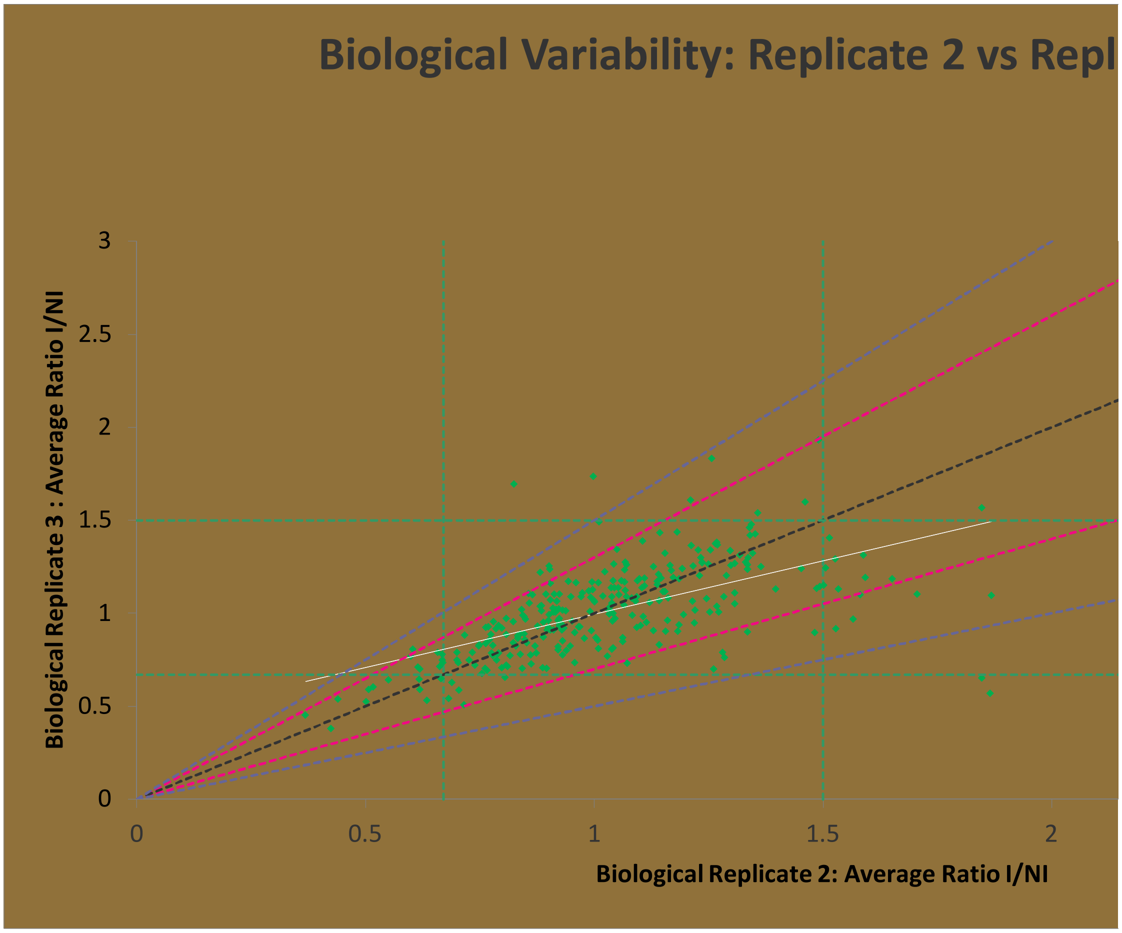
1.45	1.24
1.46	1.60
1.48	0.89
1.49	1.13
1.49	1.93
1.49	1.14
1.50	1.15
1.51	1.24
1.51	1.40
1.53	1.29
1.53	0.92
1.53	1.13
1.57	0.97
1.58	1.10
1.59	1.31
1.59	1.19
1.65	1.18
1.71	1.10
1.85	0.65
1.85	1.56
1.87	0.57
1.87	1.09

0	0	0	0	0	0	0	1.5	0
15	10.5	15	19.5	15	15	15	1.5	15
						1.5	0	
						1.5	15	



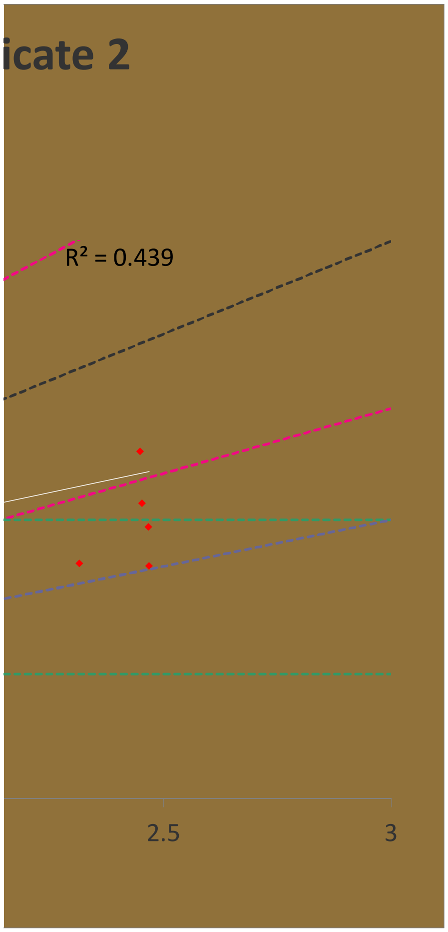


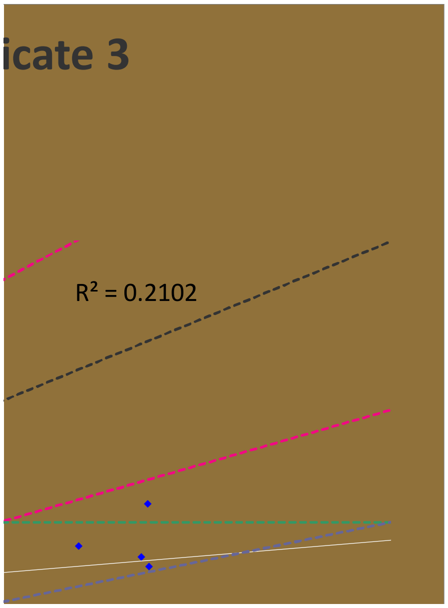

Biological Rep
1
0.5
0
0
0.5
1
1.5
2
Biological Replicate 1: Average Ratio I/NI

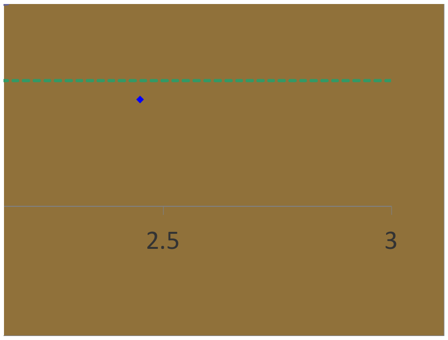

Biological Variability: Replicate 2 vs Repl
Biological Replicate 3 : Average Ratio I/NI
3
2.5
2
1.5
1
0.5
0
0
0.5
1
1.5
2
Biological Replicate 2: Average Ratio I/NI

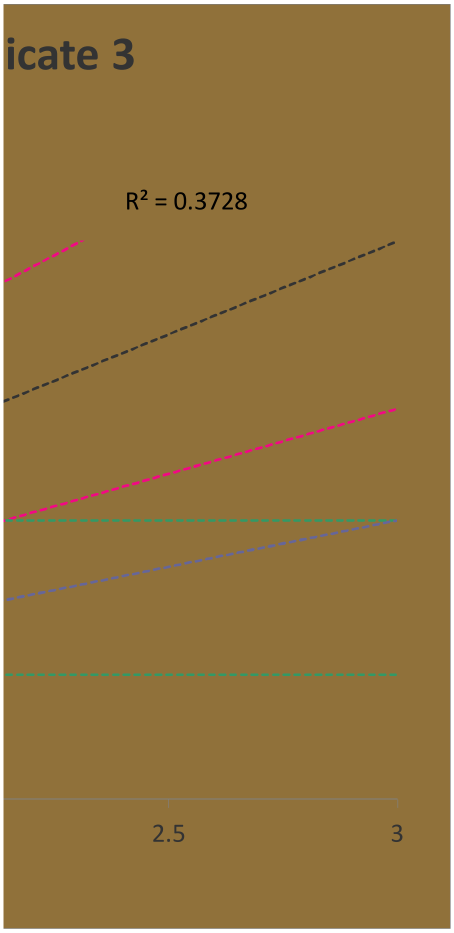
[redacted]

0.67	0.67	0	0	0	0	0
0.67	0.67	15	15	22.5	15	7.5






2.5
3


icate 3
R² = 0.3728
2.5
3