

Protein Name	Accession Numbers	Sequence	Prob	Ion Score	Identity Score	11443	11444	11445	11446	11447	11448	11449	11450	11443 Raw	11444 Raw	11445 Raw	11446 Raw	11447 Raw	11448 Raw	11449 Raw	11450 Raw	Obs	Actual Mass	Charge	Delta AMU	Delta PPM
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	aEFV EVTk	87%	40.1	52.04993	Ref	0.91	0.39	1.1	0.88	0.54	1.3	0.7	3E+05	514000	4E+05	721000	679000	5E+05	8E+05	540000	765.9	1529.9	2	0.015	9.786
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	aEFV EVTk	91%	42.9	52.04993	Ref	0.9	0.49	1.1	0.96	0.37	1.3	0.6	3E+05	715000	6E+05	1E+06	1000000	6E+05	1E+06	703000	765.9	1529.9	2	0.015	9.786
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	aEFV EVTk	72%	35.8	52.03914	Ref	0.83	0.63	0.85	0.84	0.25	1.5	0.94	6E+05	1300000	1E+06	2E+06	1760000	1E+06	3E+06	1700000	511	1529.9	3	0.0143	9.359
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	aEFV EVTk	73%	35.7	51.71135	Ref	0.87	0.62	0.64	0.95	0.77	1.1	0.75	7920	10800	9910	11200	15400	11900	15800	12100	511	1529.9	3	0.0034	2.245
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	aEFV EVTk	90%	42.3	51.88397	Ref	0.9	0.56	0.99	0.91	0.5	1.3	0.71	17400	30900	26500	39900	41700	27400	48800	32900	765.9	1529.9	2	0.0083	5.409
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	aTEE QLk	58%	32.7	52.30544	Ref	0.88	0.55	1	0.92	0.42	1.4	0.61	7E+05	1310000	1E+06	2E+06	1800000	1E+06	2E+06	1310000	713.9	1425.8	2	0.0151	10.6

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	aTEE QLk	56%	32.2	52.02589	Ref	0.87	0.76	1.1	0.9	0.44	1.3	0.56	48100	103000	1E+05	151000	142000	89400	2E+05	101000	713.9	1425.8	2	0.0049	3.407
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	aTEE QLk	55%	32.1	52.10661	Ref	0.94	0.67	1.1	0.88	0.44	1.3	0.53	11600	23200	20900	32000	30000	19300	35700	21300	713.9	1425.8	2	0.0025	1.781
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	ccAA DDk EAcF AVE GPK	86%	38.1	51.13385	Ref	0.63	0.51	1.1	0.8	0.17	1.5	0.92	16600	22100	22100	36400	33600	18900	48200	33000	702.6	2806.3	4	0.0275	9.79
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	ccAA DDk EAcF AVE GPK	84%	37.3	51.08206	Ref	0.5	0.56	1.3	0.87	0.27	1.5	0.62	9240	12400	14000	25600	21500	12500	30200	16400	702.6	2806.3	4	0.0284	10.13
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	ccAA DDk EAcF AVE GPK	70%	34.4	51.13161	Ref	0.71	0.56	1.1	0.93	0.39	1.4	0.6	7200	11200	11000	18500	17600	10600	21900	12600	936.4	2806.3	3	0.0274	9.76
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	ccTE SLVN R	72%	28.1	44.90085	Ref	0.83	0.5	1.1	0.63	0.34	1.3	0.72	20600	24100	20800	35800	28200	20100	40400	27200	710.8	1419.6	2	0.0167	11.76
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	ccTE SLVN R	90%	35.8	45.49077	Ref	0.89	0.59	1.1	0.73	0.31	1.2	0.68	59100	72500	63800	102000	86900	56900	1E+05	75900	710.8	1419.6	2	0.0094	6.605

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dAFL GSFL YEYS R	95%	54	52.39011	Ref	No Values (0.98610616)	No Values (0.86841273)	No Values (0.701818)	No Values (0.5613388)	No Values (0.7572113)	No Values (0.6944446)	No Values (0.7053185)	No Values (0.78371626)	No Values (0.98610616)	No Values (0.86841273)	No Values (0.701818)	No Values (0.5613388)	No Values (0.7572113)	No Values (0.6944446)	No Values (0.7053185)	624.7	1870.9	3	0.0112	5.965
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dAFL GSFL YEYS R	95%	51.1	52.48946	Ref	0.83	0.47	1	0.94	0.41	1.4	0.79	1630	3570	3030	5000	5180	3140	6630	4250	936.5	1870.9	2	0.0106	5.662
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dAFL GSFL YEYS R	95%	48.2	52.66937	Ref	0.87	0.57	0.95	0.96	0.43	1.4	0.77	1170	2570	2280	3320	3680	2230	4530	2910	936.5	1870.9	2	0.0034	1.816
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dAFL GSFL YEYS R	95%	57	52.60599	Ref	0.93	0.51	0.91	0.95	0.48	1.4	0.64	470	958	777	1150	1310	825	1650	957	936.5	1870.9	2	0.0057	3.056
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dAFL GSFL YEYS R	74%	36.5	52.72009	Ref	1.1	0.41	1	1	0.26	1.3	0.74	302	755	514	883	957	499	1090	721	936.5	1870.9	2	#####	0.449
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dAFL GSFL YEYS R	90%	44.1	54.32471	Ref	0.91	0.52	1.1	1	0.22	1.4	0.54	540	977	808	1330	1400	706	1650	918	1089	2175.1	2	0.0115	5.266
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dAFL GSFL YEYS R	81%	41.1	54.32349	Ref	0.8	0.42	1.1	0.95	0.35	1.4	0.48	3910	5370	4490	8140	8010	4600	9940	5230	726.1	2175.1	3	0.0141	6.473

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dDP HAcY STVF Dk	84%	38.5	50.69591	Ref	1.1	0.54	0.84	0.74	0.52	1.2	0.67	4210	5740	4380	6040	6190	4660	7580	5370	718	2151	3	0.0265	12.31
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dDP HAcY STVF Dk	60%	31.8	50.79575	Ref	0.96	0.54	0.95	0.76	0.62	1	0.75	9410	12800	10400	15500	15000	11800	16600	13400	718	2151	3	0.0239	11.11
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dDP HAcY STVF Dk	89%	41.9	50.79152	Ref	0.97	0.42	0.95	0.81	0.51	1.3	0.62	5470	7500	5580	9010	9010	6390	11300	7150	718	2151	3	0.0235	10.94
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dDP HAcY STVF Dk	95%	52.1	50.88696	Ref	0.97	0.48	1	0.76	0.63	1.2	0.56	12900	20000	15400	25200	23200	18400	29600	18300	718	2151	3	0.021	9.756
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dDP HAcY STVF Dk	74%	35.2	50.93071	Ref	1	0.56	0.9	0.79	0.62	1.3	0.4	3970	6630	5160	7290	7480	5800	9860	5170	718	2151	3	0.0202	9.407
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dDP HAcY STVF Dk	78%	36.5	51.06895	Ref	0.97	0.65	0.98	0.83	0.58	1.1	0.56	11700	17400	15100	21300	21200	15600	23400	15900	718	2151	3	0.0171	7.958
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	dDP HAcY STVF Dk	83%	38.6	51.23558	Ref	0.98	0.43	1.1	0.88	0.45	1.2	0.37	4660	6310	4680	8360	7910	5120	9230	5030	718	2151	3	0.014	6.522

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	dDP HAcY STVF Dk	95%	51.1	51.3952	Ref	0.8	0.52	0.97	0.88	0.45	1.5	0.67	38700	65200	58200	89300	92600	60200	1E+05	72500	718	2151	3	0.0107	4.988
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	dDP HAcY STVF Dk	92%	45.6	50.88646	Ref	0.79	0.8	1.1	0.86	0.4	1.3	0.52	6650	10800	11900	16400	15300	9710	18900	11000	718	2151	3	0.0215	10.01
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	dDP HAcY STVF Dk	92%	45.7	50.92984	Ref	0.85	0.41	0.92	0.86	0.65	1	0.8	7850	9060	7240	11600	12300	9270	12700	10600	718	2151	3	0.0204	9.491
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	dDP HAcY STVF Dk	88%	42	51.52496	Ref	0.91	0.68	0.84	0.71	0.57	0.99	0.84	4150	4810	4450	5560	5590	4430	6220	5550	718	2151	3	0.0065	3.023
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	dDSP DLpk	53%	32.3	52.34795	Ref	0.89	0.71	0.9	0.88	0.51	1.1	0.57	42800	51800	49600	63800	69200	46800	73000	50600	498.9	1493.8	3	0.0161	10.75
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	dTHk SEIA HR	51%	27.4	53.15834	Ref	0.73	0.47	1.1	0.6	1.1	1.2	0.79	17400	32500	29500	50500	39800	49300	53700	41100	361.2	1801	5	0.0104	5.781
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	eAcF AVE Gpk	52%	31.9	52.11136	Ref	1.1	0.69	1	0.79	0.38	1	0.71	10600	16300	13700	19100	18200	11900	19500	15600	569	1703.9	3	0.0174	10.23

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eAcFAVE GPK	83%	40	52.35488	Ref	1	0.71	0.89	0.85	0.38	0.94	0.82	13100	18400	16100	20500	22000	13900	21400	19500	569	1703.9	3	0.0103	6.04
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eAcFAVE GPK	69%	35.5	52.44712	Ref	0.96	0.81	0.89	0.7	0.61	0.92	0.55	6830	7610	7460	8800	8520	6980	9050	6950	569	1703.9	3	0.0072	4.21
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eccHGDLL EcADDR	95%	47.3	35.84444	Ref	1.4	0.99	0.79	0.62	0.36	0.92	0.45	1470	2870	2380	2320	2270	1660	2550	1830	1011	2019.7	2	0.0108	5.368
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eccHGDLL EcADDR	95%	52.4	36.88509	Ref	0.92	0.68	1	0.73	0.46	1.1	0.62	16300	19900	18300	26300	23400	17000	27000	19600	674.3	2019.8	3	#####	0.393
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eccHGDLL EcADDR	95%	74.1	35.74147	Ref	0.76	0.79	0.92	0.77	0.51	1	0.77	6080	6430	7120	8780	8680	6330	9450	7890	674.3	2019.7	3	0.0114	5.648
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eccHGDLL EcADDR	95%	54.3	35.83765	Ref	1.2	0.67	0.95	0.89	0.23	1.2	0.53	3040	5930	4560	6190	6580	3620	7500	4640	1011	2019.7	2	0.0111	5.487
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eccHGDLL EcADDR	95%	50.4	35.84897	Ref	0.93	0.59	1	0.75	0.6	1.1	0.6	1300	1670	1430	2130	1970	1550	2260	1610	674.3	2019.7	3	0.0107	5.277

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	eccH GDLL EcAD DR	95%	35.2	36.40282	Ref	0.68	0.56	0.91	0.76	0.43	1	1.1	2070	2110	2100	3020	3010	2090	3340	3450	674.3	2019.8	3	0.0055	2.738
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	eccH GDLL EcAD DR	95%	46	36.58775	Ref	1	0.66	0.95	0.68	0.7	0.92	0.63	559	698	597	822	748	661	804	657	674.3	2019.8	3	0.003	1.476
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	eccH GDLL EcAD DR	95%	38.2	36.41772	Ref	0.73	0.94	0.81	0.66	0.62	0.95	0.75	266	256	320	329	327	278	365	315	674.3	2019.8	3	0.0048	2.382
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	eTYG DMA DccE k	95%	49	42.44549	Ref	0.55	0.58	1	0.95	0.43	1.4	0.9	4680	6980	7700	11800	12400	7540	15000	10800	1033	2063.8	2	0.029	14.05
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	eTYG DMA DccE k	95%	46.6	42.75173	Ref	0.74	0.67	1	0.85	0.24	1.4	0.67	72200	93000	95500	136000	134000	76800	2E+05	108000	689	2063.8	3	0.025	12.11
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	eTYG DMA DccE k	95%	51.1	42.86007	Ref	0.55	0.52	1.2	0.91	0.58	1.4	0.57	1E+05	229000	2E+05	433000	396000	3E+05	5E+05	282000	689	2063.8	3	0.0239	11.59
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	eTYG DMA DccE k	74%	26.7	43.19564	Ref	0.72	0.45	1.2	1.1	0.51	1.3	0.52	21000	41300	37100	71800	73300	41900	74700	43700	1033	2063.8	2	0.0183	8.852

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eTYG DMA DccEk	95%	45.4	43.26377	Ref	0.71	0.56	1.2	0.97	0.34	1.3	0.74	9540	16300	15900	27400	26100	14700	29900	20100	689	2063.8	3	0.018	8.739
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eTYG DMA DccEk	83%	29.8	43.26377	Ref	0.67	0.59	1.1	0.91	0.31	1.4	0.7	4970	6480	6650	10300	10200	5890	12800	8040	1033	2063.8	2	0.018	8.736
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eTYG DMA DccEk	89%	34.9	43.53301	Ref	0.7	0.75	0.81	0.98	0.45	1.3	0.62	13100	16000	18000	21100	26200	15800	30100	18400	689	2063.8	3	0.015	7.243
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eTYG DMA DccEk	93%	38.3	42.53919	Ref	0.57	0.77	1	0.92	0.41	1.2	0.77	22100	25200	31400	41700	43100	26400	48100	35100	689	2063.8	3	0.0276	13.36
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eTYG DMA DccEk	75%	26.9	42.8769	Ref	0.59	0.54	1	1	0.37	1.4	0.6	2590	3360	3530	5620	6100	3400	7420	4140	1033	2063.8	2	0.0232	11.22
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eTYG DMA DccEk	84%	32.2	44.00624	Ref	0.91	0.7	0.95	0.52	0.61	1.1	0.71	726	819	773	1030	844	784	1120	866	689	2063.9	3	0.0078	3.785
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eTYG DmA DccEk	95%	44.2	41.96508	Ref	0.94	0.48	1.1	0.89	0.5	1.1	0.63	32800	44400	34800	58900	57200	38200	59700	43500	694.3	2079.8	3	0.0168	8.087

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eTYG DmA DccE k	93%	37.3	41.74641	Ref	0.88	0.64	0.93	0.81	0.47	1.1	0.8	5190	6830	6280	8600	8740	6020	9940	7850	694.3	2079.8	3	0.0187	8.967
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eYEA TLEE ccAk	95%	54.2	49.08844	Ref	0.73	0.63	1.1	0.89	0.59	1.3	0.63	37400	63400	64400	99300	95600	67400	1E+05	72100	697	2087.9	3	0.0192	9.199
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eYEA TLEE ccAk	95%	44.7	49.13077	Ref	0.84	0.62	1.1	0.86	0.45	1.4	0.46	2340	3890	3620	5500	5280	3490	7100	3630	1045	2087.9	2	0.0185	8.871
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eYEA TLEE ccAk	95%	55.3	49.20671	Ref	0.69	0.53	1.1	0.92	0.42	1.4	0.72	21000	31300	30400	50500	49300	30500	61000	38900	697	2087.9	3	0.0166	7.964
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eYEA TLEE ccAk	87%	39.9	49.76964	Ref	0.82	0.73	0.73	0.79	0.67	0.98	0.88	12300	13800	14100	15900	18200	14700	19000	17500	697	2087.9	3	0.0051	2.45
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eYEA TLEE ccAk	95%	45.4	49.79821	Ref	0.86	0.57	1	0.86	0.48	1.5	0.48	2560	4500	4010	6170	6040	4070	8320	4220	1045	2087.9	2	0.0049	2.322
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eYEA TLEE ccAk	95%	48.1	49.13586	Ref	0.99	0.67	1.2	0.55	0.41	1.2	0.63	2170	3330	2890	4590	3300	2610	4710	3160	697	2087.9	3	0.0185	8.84

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eYEATLEeccAk	95%	56.4	49.36634	Ref	0.94	0.51	0.89	0.76	0.59	1.3	0.67	1260	1780	1430	2090	2100	1640	2740	1790	697	2087.9	3	0.0137	6.571
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eYEATLEeccAk	95%	57.4	49.60576	Ref	0.89	0.55	1.1	0.9	0.54	1.4	0.49	631	1200	1030	1640	1630	1110	2070	1110	1045	2087.9	2	0.0085	4.074
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eYEATLEeccAk	95%	48.5	49.23327	Ref	0.89	0.68	0.98	0.82	0.41	1.1	0.73	757	981	923	1270	1250	827	1390	1070	697	2087.9	3	0.0157	7.533
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eYEATLEeccAk	95%	57.8	49.76139	Ref	1	0.68	0.82	0.81	0.5	1.2	0.74	465	832	712	885	963	678	1190	832	697	2087.9	3	0.0057	2.708
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	eYEATLEeccAk	88%	39.6	49.23959	Ref	0.62	0.63	1.1	0.84	0.68	1.2	0.35	224	210	228	359	327	255	371	211	697	2087.9	3	0.0156	7.447
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	fkDLGEEHfK	61%	34.4	53.47572	Ref	0.72	0.51	1.1	0.96	0.38	1.5	0.42	1110	1770	1660	2850	2800	1640	3730	1750	1082	2161.2	2	0.0175	8.114
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	gLVLIAFSQYLq qcPF DEH VK	62%	37.1	55.74331	Ref	No Values (0.98610616)	No Values (0.8684126)	No Values (0.70181787)	No Values (0.5613388)	No Values (0.75721127)	No Values (0.6944445)	No Values (0.7053185)	No Values (0.78371614)	No Values (0.98610616)	No Values (0.8684126)	No Values (0.70181787)	No Values (0.5613388)	No Values (0.75721127)	No Values (0.6944445)	No Values (0.7053185)	1031	3090.6	3	0.007	2.277

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ NLIK	83%	37.7	52.22807	Ref	0.6	1.5	0.95	0.84	0.23	1.3	0.36	75600	162000	3E+05	252000	257000	1E+05	3E+05	167000	479.3	1913.1	4	0.0182	9.512
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ NLIK	81%	38.9	52.18593	Ref	0.71	1	0.93	0.89	0.56	0.91	0.41	9710	9410	12700	13300	14400	9940	13200	9290	638.7	1913.1	3	0.0171	8.924
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ NLIK	90%	44.3	52.16857	Ref	0.93	1.1	1.1	0.88	0.24	1.2	0.61	1E+05	327000	4E+05	440000	422000	2E+05	5E+05	317000	638.7	1913.1	3	0.016	8.344
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ NLIK	95%	62.5	52.0275	Ref	0.82	0.59	1.1	0.93	0.47	1.4	0.63	13900	27400	25500	39600	39700	25300	49500	29200	957.6	1913.1	2	0.0151	7.897
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ NLIK	89%	43.9	52.23369	Ref	0.85	0.96	0.83	0.96	0.44	1.4	0.41	35300	66000	77100	79300	95500	58000	1E+05	58800	638.7	1913.1	3	0.0191	9.974
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ NLIK	95%	60.3	52.19972	Ref	0.86	0.54	0.96	1	0.36	1.4	0.58	13900	25500	22200	33300	37600	21100	46500	25500	957.6	1913.1	2	0.018	9.422
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ NLIK	95%	60.2	52.23369	Ref	0.84	0.48	1	0.97	0.61	1.3	0.58	1430	2470	2090	3390	3630	2480	4210	2510	957.6	1913.1	2	0.019	9.934

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ nLlk	88%	42.2	51.90813	Ref	0.77	1	0.88	0.8	0.32	1.3	0.7	1010	1590	2030	2080	2180	1360	2790	1840	638.7	1913.1	3	0.0092	4.802
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ nLlk	83%	39.6	51.91853	Ref	0.94	0.99	0.75	0.77	0.49	1.1	0.69	641	959	1080	1020	1140	822	1310	976	638.7	1913.1	3	0.0129	6.729
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ nLlk	55%	32.9	52.7001	Ref	0.73	0.9	0.95	0.82	0.6	1.1	0.52	10300	11800	14400	16700	16900	12600	18700	12400	639	1914.1	3	0.0149	7.764
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ nLlk	95%	50.2	52.81315	Ref	0.82	0.61	1	0.89	0.36	1.4	0.66	2570	4560	4290	6300	6470	3890	8590	4990	958	1914.1	2	0.0184	9.61
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ nLlk	95%	61.1	52.79393	Ref	0.95	0.48	1	0.95	0.43	1.4	0.61	3260	6590	5170	8560	8880	5410	10700	6320	958.1	1914.1	2	0.0172	8.973
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ nLlk	62%	32.4	52.7836	Ref	0.85	1.2	1	0.73	0.098	1.3	0.5	23900	47500	65900	65900	58600	33000	79200	45000	479.5	1914.1	4	0.0166	8.676
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hLVD EPQ nLlk	95%	55.7	52.79163	Ref	0.66	1.2	0.84	0.79	0.37	1.3	0.67	15100	26300	41900	36200	38500	25200	50100	32100	639	1914.1	3	0.0158	8.25

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hPEY AVS VLLR	86%	41.1	52.10171	Ref	0.97	0.7	1.2	0.74	0.6	0.79	0.72	13600	19600	17600	27400	22400	17700	21200	20000	530	1586.9	3	0.0099	6.223
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hPEY AVS VLLR	90%	43.9	52.03275	Ref	1	0.72	1	0.76	0.48	1.3	0.55	22700	49000	43500	60900	55100	39600	73800	43100	530	1586.9	3	0.0049	3.106
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hPEY AVS VLLR	60%	32.7	51.96764	Ref	0.9	0.56	0.99	0.7	0.59	1.3	0.78	4050	6630	5670	8560	7750	6260	10400	7400	794.5	1586.9	2	0.0028	1.748
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hPEY AVS VLLR	88%	42.1	51.80086	Ref	0.97	0.69	1.1	0.73	0.5	1.3	0.56	22100	38900	34600	50000	44000	32800	58100	35500	530	1586.9	3	#####	0.215
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hPEY AVS VLLR	90%	44.3	52.07912	Ref	0.82	0.68	0.78	0.76	0.55	1.2	0.74	2370	2610	2560	3090	3350	2530	4030	2990	530	1586.9	3	0.0068	4.258
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hPEY AVS VLLR	91%	44.7	52.0356	Ref	0.85	0.71	0.89	0.75	0.68	1.1	0.68	928	1160	1150	1460	1450	1210	1680	1250	530	1586.9	3	0.0075	4.711
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	hPEY AVS VLLR	91%	45.1	52.06966	Ref	0.87	0.7	0.9	0.62	0.59	0.99	0.77	672	700	674	874	792	676	932	795	530	1586.9	3	0.0066	4.145

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	78%	29.8	46.19656	Ref	0.75	0.54	0.98	0.95	0.42	1.4	0.74	6680	12000	11200	17100	18500	11100	23500	14500	514.6	2054.3	4	0.0375	18.23
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	93%	40.2	44.80209	Ref	0.8	0.57	1	0.96	0.38	1.4	0.73	98100	194000	2E+05	278000	292000	2E+05	4E+05	224000	685.8	2054.3	3	0.0232	11.27
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	85%	31.2	44.40437	Ref	0.79	0.33	1.1	0.92	0.27	1.6	0.77	86000	217000	2E+05	334000	318000	2E+05	5E+05	259000	514.6	2054.3	4	0.0197	9.565
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	95%	40.9	43.59323	Ref	0.83	0.61	1.1	0.94	0.38	1.4	0.52	2370	4450	4150	6540	6440	3830	8120	4350	1028	2054.3	2	0.0105	5.092
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	83%	28	42.5358	Ref	0.97	0.47	0.96	0.87	0.45	0.98	0.66	2320	2600	2000	3150	3260	2130	3200	2540	514.6	2054.3	4	#####	0.186
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	59%	26.6	45.7066	Ref	1.2	0.87	0.69	0.68	0.47	1	0.75	1550	2740	2360	2350	2580	1940	2990	2450	685.8	2054.3	3	0.0336	16.35
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	92%	34.4	45.4893	Ref	0.64	0.44	1.2	0.88	0.66	1.4	0.63	3510	6120	5790	10900	9720	7320	12800	7430	411.9	2054.3	5	0.0309	15.06

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQTLVLLk	90%	38	45.44031	Ref	0.66	1.7	-0.19	-0.28	-0.05	0.027	2.1	2750	6590	15200	4480	4620	4740	5220	22300	685.8	2054.3	3	0.0292	14.22
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQTLVLLk	94%	40.3	45.4382	Ref	0.44	1.9	-0.43	-0.84	0.011	-0.09	2.3	2210	5370	15500	3580	2970	4670	4550	23300	514.6	2054.3	4	0.0285	13.85
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQTLVLLk	89%	36.3	44.80366	Ref	0.81	0.42	1.2	1	0.4	1.3	0.63	2E+05	350000	3E+05	540000	545000	3E+05	6E+05	375000	685.8	2054.3	3	0.0234	11.36
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQTLVLLk	95%	44.1	44.41679	Ref	0.79	0.46	0.98	0.9	0.48	1.5	0.69	77900	157000	1E+05	218000	227000	1E+05	3E+05	178000	514.6	2054.3	4	0.0189	9.214
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQTLVLLk	77%	29.1	43.92011	Ref	0.62	0.4	1.2	0.95	0.47	1.5	0.6	15100	25600	23900	45100	43100	27100	58300	30700	685.8	2054.3	3	0.0138	6.735
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQTLVLLk	95%	42.8	42.89053	Ref	0.8	0.53	1.1	0.94	0.41	1.4	0.68	2230	3960	3580	5770	5890	3560	7270	4440	514.6	2054.3	4	0.0021	1.001
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQTLVLLk	87%	32.8	42.89053	Ref	0.81	0.67	0.91	0.92	0.52	1.1	0.73	3790	5060	4960	6570	7310	4840	7810	5800	685.8	2054.3	3	0.0019	0.94

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	87%	30.6	42.89053	Ref	0.82	0.59	0.9	0.86	0.55	1.2	0.7	1260	1540	1420	1970	2120	1490	2440	1720	514.6	2054.3	4	0.0018	0.885
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	94%	39	42.53144	Ref	0.96	0.44	0.97	0.76	0.56	1.1	0.86	2740	4040	3070	4960	4730	3600	5560	4600	685.8	2054.3	3	#####	0.05
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	85%	34	45.68894	Ref	0.73	0.62	1.1	0.94	0.42	1.3	0.63	5610	8130	8170	12600	12600	7720	14800	9250	685.8	2054.3	3	0.0316	15.38
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	88%	30.5	45.43981	Ref	0.73	0.43	1.1	0.9	0.63	1.4	0.66	3360	5580	4900	8830	8420	6090	10500	6480	411.9	2054.3	5	0.0289	14.08
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	94%	40.1	44.80596	Ref	0.85	0.66	0.89	0.75	0.48	1.2	0.72	1910	2360	2250	2960	2970	2150	3770	2620	514.6	2054.3	4	0.0241	11.71
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	93%	40	44.1956	Ref	0.65	0.41	1.1	0.78	0.44	1.5	0.76	4330	6720	6170	11400	9880	6820	14800	8800	685.8	2054.3	3	0.0173	8.428
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	91%	35.3	44.02055	Ref	0.87	0.53	1	0.92	0.36	1.3	0.73	3260	5380	4610	7370	7480	4430	8830	5960	514.6	2054.3	4	0.015	7.307

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	90%	35.5	43.24879	Ref	0.78	0.37	1.1	0.96	0.42	1.5	0.75	2590	5080	4130	7500	7710	4630	9920	6050	685.8	2054.3	3	0.0104	5.042
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	90%	35.2	42.89634	Ref	0.75	0.57	1.1	0.98	0.44	1.2	0.7	770	1080	1030	1620	1690	1020	1820	1270	685.8	2054.3	3	0.0023	1.13
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	83%	33.1	45.68894	Ref	0.76	0.51	0.94	0.94	0.51	1.4	0.66	503	849	775	1170	1290	835	1670	962	685.8	2054.3	3	0.0316	15.38
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kQT ALVE LLk	91%	35	43.92011	Ref	0.88	0.53	0.94	0.96	0.42	1.3	0.84	786	1510	1280	1920	2150	1280	2460	1780	514.6	2054.3	4	0.0138	6.704
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kVP QVS TPTL VEVS R	95%	51.2	51.16856	Ref	0.95	0.53	1	0.81	0.37	1.4	0.61	34200	56100	45600	71600	68200	43900	92300	53800	750.1	2247.3	3	0.0195	8.686
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kVP QVS TPTL VEVS R	95%	59.4	50.87217	Ref	0.96	0.57	0.95	0.85	0.51	1.1	0.74	12500	18900	15600	22800	23500	16200	26000	19700	750.1	2247.3	3	0.0157	6.978
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kVP QVS TPTL VEVS R	95%	49.8	51.43028	Ref	0.78	1.4	0.4	0.33	0.41	0.65	1.4	5010	7530	12800	7040	7410	6830	8420	14400	750.1	2247.3	3	0.0235	10.47

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kVP QVS TPTL VEVS R	95%	53.9	51.02228	Ref	0.64	0.51	1.1	1.1	0.31	1.4	0.64	2E+05	415000	4E+05	718000	744000	4E+05	9E+05	505000	750.1	2247.3	3	0.0173	7.698
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kVP QVS TPTL VEVS R	77%	35.9	50.90649	Ref	0.77	0.55	0.92	0.93	0.39	1.4	0.71	6960	9370	8730	12700	14000	8430	17200	10900	750.1	2247.3	3	0.0168	7.458
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kVP QVS TPTL VEVS R	94%	45.8	50.90477	Ref	No Values (0.32350382)	No Values (0.2058105)	Reference Missing (1.3668486)	Reference Missing (0.95956725)	No Values (0.09460898)	Reference Missing (1.444081)	Reference Missing (0.8192463)	No Values (0.12111389)	No Values (0.32350382)	No Values (0.2058105)	Reference Missing (1.3668486)	Reference Missing (0.95956725)	No Values (0.09460898)	Reference Missing (1.444081)	Reference Missing (0.8192463)	562.8	2247.3	4	0.0162	7.225
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kVP QVS TPTL VEVS R	95%	55.7	50.90579	Ref	0.84	0.62	1.1	0.93	0.6	1.1	0.63	35500	53000	49300	75000	75600	52500	77700	55600	750.1	2247.3	3	0.016	7.138
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kVP QVS TPTL VEVS R	58%	32.2	51.47089	Ref	0.77	1.1	0.67	0.54	0.59	0.67	1.3	6230	7380	9810	8420	8490	7680	8440	12600	750.1	2247.3	3	0.0257	11.45
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kVP QVS TPTL VEVS R	95%	57.2	51.09008	Ref	0.69	0.33	1.3	0.98	0.44	1.4	0.62	36700	59700	50400	109000	98200	58800	1E+05	69000	750.1	2247.3	3	0.019	8.432
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kVP QVS TPTL VEVS R	85%	37.6	51.02207	Ref	0.53	1.1	0.89	0.43	0.67	1.1	0.72	40000	36400	59200	57200	45700	47300	66300	50500	562.8	2247.3	4	0.0172	7.652

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kVP QVS TPTL VEVS R	95%	63.6	51.05183	Ref	0.92	0.55	0.9	0.94	0.53	1.3	0.65	3360	5500	4610	6590	7490	4900	8510	5540	750.1	2247.3	3	0.0179	7.952
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	kVPq VSTP TLVE VSR	95%	59.4	52.02581	Ref	0.86	0.66	0.82	0.74	0.67	1.2	0.71	13500	17000	16100	20100	21100	17400	25900	18600	750.4	2248.3	3	0.0236	10.5
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	lcVL HEK	55%	31.8	51.93169	Ref	0.88	0.53	0.92	0.87	0.6	1.2	0.8	711	1130	966	1420	1510	1090	1740	1300	748.4	1494.9	2	#####	0.067
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IFTF HADI cTLP DTEK	86%	44	54.90481	Ref	0.83	0.52	1	0.95	0.46	1.4	0.59	693	1350	1180	1890	1970	1230	2530	1390	835.8	2504.3	3	0.0022	0.862
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IFTF HADI cTLP DTEK	77%	40	54.728	Ref	0.85	0.58	1.1	0.91	0.29	1.4	0.7	727	1500	1350	2130	2100	1200	2760	1640	835.8	2504.3	3	0.016	6.383
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IFTF HADI cTLP DTEK	91%	48	54.6712	Ref	0.89	0.51	1	0.85	0.32	1.4	0.75	749	1440	1200	1950	1870	1130	2510	1580	835.8	2504.3	3	0.0185	7.401
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IFTF HADI cTLP DTEK	73%	38.7	54.65477	Ref	0.81	0.35	1.2	0.87	0.27	1.4	0.84	303	595	468	925	829	479	1120	734	835.8	2504.3	3	0.0204	8.131

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	95%	52.5	53.22249	Ref	0.88	0.52	1.1	0.79	0.39	1.4	0.69	54700	111000	94500	157000	141000	93100	2E+05	119000	892.5	1783	2	0.0116	6.488
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	74%	36.9	53.19976	Ref	0.71	0.59	1	0.96	0.46	1.4	0.65	32000	52400	52500	78100	83700	51900	1E+05	61500	892.5	1783	2	0.0111	6.208
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	95%	65.6	53.21735	Ref	1.4	0.47	0.98	0.81	Value Missing (-0.30085948)	1.3	0.34	8420	16300	9280	14800	14500	Value Missing (-0.30085948)	19200	9500	595.3	1783	3	0.0106	5.914
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	69%	35.7	53.22517	Ref	0.88	0.52	0.88	0.74	0.28	1.5	0.88	501	819	695	998	995	632	1500	993	892.5	1783	2	0.0145	8.125
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	92%	44.5	53.28184	Ref	0.82	0.51	1.1	0.84	0.37	1.4	0.73	1790	2970	2610	4260	4050	2550	5460	3390	892.5	1783	2	0.0073	4.089
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	95%	59.4	53.23446	Ref	0.88	0.39	1	0.98	0.37	1.4	0.72	1080	1890	1450	2510	2720	1550	3220	2050	892.5	1783	2	0.0072	4.021
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	95%	52.1	53.1702	Ref	0.67	0.5	0.77	0.74	0.63	1.3	0.68	367	309	299	404	437	354	575	380	595.3	1783	3	0.0069	3.862

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	54%	33	53.23644	Ref	0.7	0.52	1.2	0.81	0.36	1.4	0.68	1190	1670	1600	2840	2410	1540	3290	2000	1045	2087.2	2	0.0171	8.169
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	95%	50.1	53.40767	Ref	0.86	0.62	0.9	0.82	0.54	1.3	0.81	7290	12700	11700	15900	16600	11900	20900	14900	893	1784	2	0.0146	8.192
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	92%	45	53.41001	Ref	0.78	0.36	1.1	0.87	0.54	1.4	0.71	16100	28000	22700	42100	40100	27700	53300	32400	893	1784	2	0.0068	3.811
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	92%	45.5	53.39336	Ref	0.97	0.54	0.9	0.89	0.49	1.3	0.77	12300	22100	17900	25600	28200	18700	33100	23400	893	1784	2	0.0033	1.828
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	92%	44.8	53.4132	Ref	1.1	0.44	0.97	0.92	0.3	1.4	0.74	2680	6540	4640	7530	8010	4550	10100	6400	893	1784	2	0.0139	7.778
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	94%	47.1	53.36818	Ref	0.94	0.52	0.97	0.93	0.34	1.4	0.74	3110	6140	4990	7650	8200	4760	10100	6520	893	1784	2	0.0125	7.027
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	I GEY GFQ NALI VR	69%	35.8	53.38203	Ref	1	0.57	0.94	0.77	0.37	1.3	0.79	618	1040	832	1210	1180	784	1530	1090	893	1784	2	0.0095	5.324

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IGFY GFQ nALI VR	74%	37	53.40855	Ref	0.81	0.57	0.96	0.81	0.35	1.3	1	477	853	787	1150	1150	730	1490	1180	893	1784	2	0.0083	4.64
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IkHL VDE PQN LIK	86%	36.9	48.00456	Ref	0.41	0.088	1	1.1	0.63	1.4	1.1	1050	2130	1840	3910	4610	2890	5300	4230	820.5	2458.5	3	0.0162	6.567
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVNE LTEF Ak	95%	55.6	52.42387	Ref	0.77	0.48	1.1	0.93	0.42	1.4	0.7	19100	35200	31200	52600	53000	32500	68400	40700	886.5	1771	2	0.0165	9.29
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVNE LTEF Ak	81%	38.9	52.423	Ref	0.75	0.42	0.95	0.96	0.33	1.4	1	1E+05	254000	2E+05	357000	394000	2E+05	5E+05	371000	591.3	1771	3	0.0144	8.153
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVNE LTEF Ak	78%	37.4	51.72209	Ref	0.68	0.5	0.97	0.79	0.65	1.1	1	741	961	920	1430	1390	1100	1570	1500	591.4	1771	3	0.0051	2.902
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVNE LTEF Ak	94%	45.6	52.28657	Ref	0.82	0.49	1	0.96	0.38	1.4	0.66	7580	13100	11400	18700	19500	11300	23900	14300	886.5	1771	2	0.0123	6.942
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVNE LTEF Ak	91%	45.6	52.40067	Ref	0.81	0.52	0.99	0.88	0.45	1.3	0.8	2030	2980	2630	4100	4200	2710	4990	3600	591.3	1771	3	0.0154	8.678

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVNE LTEF AK	95%	50.3	52.15368	Ref	0.79	0.54	1.1	0.93	0.38	1.4	0.59	1180	2140	1950	3310	3170	1890	3990	2260	886.5	1771	2	0.0095	5.362
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVNE LTEF AK	91%	45.8	52.21043	Ref	0.87	0.45	0.93	0.86	0.43	1.3	0.9	2640	4230	3430	5360	5630	3660	6960	5270	591.3	1771	3	0.0104	5.884
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVNE LTEF AK	95%	64.7	52.15973	Ref	0.86	0.36	1.1	0.95	0.39	1.4	0.69	855	1550	1190	2200	2210	1310	2730	1660	886.5	1771	2	0.0085	4.809
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVNE LTEF AK	95%	64.5	52.40072	Ref	0.78	0.52	1.1	0.88	0.35	1.4	0.72	623	1060	956	1570	1520	920	2010	1230	886.5	1771	2	0.0151	8.533
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVNE LTEF AK	91%	45.4	52.19307	Ref	1	0.58	0.9	0.79	0.27	1.2	0.91	1280	2310	1830	2570	2620	1590	3250	2570	591.3	1771	3	0.0111	6.291
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVNE LTEF AK	83%	40	52.44465	Ref	0.88	0.59	0.92	0.76	0.6	1.2	0.8	351	501	442	626	616	482	755	574	591.3	1771	3	0.0159	8.983
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVNE LTEF AK	93%	47.7	52.19645	Ref	0.93	0.41	0.9	0.67	0.47	1.4	0.85	446	705	535	845	792	603	1200	815	591.3	1771	3	0.0108	6.088

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVnE LTEF AK	87%	41	52.80025	Ref	0.58	0.53	0.88	0.99	0.69	1.5	0.7	2910	5140	5390	7710	9200	6530	12000	6800	887	1772	2	0.0183	10.32
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVnE LTEF AK	73%	36.6	52.6997	Ref	Reference Missing (1.0361656)	Refer ence Missi ng (0.7830933)	Refer ence Missi ng (1.3054217)	Refer ence Missi ng (0.9954354)	Refer ence Missi ng (0.1316004)	Refer ence Missi ng (1.2851745)	Refer ence Missi ng (0.51667255)	No Values (-1.43654)	Reference Missing (1.0361656)	Refer ence Missi ng (0.7830933)	Refer ence Missi ng (1.3054217)	Reference Missing (0.9954354)	Refer ence Missi ng (0.1311600)	Refer ence Missi ng (1.2851745)	Reference Missing (0.51667255)	591.7	1772	3	0.0172	9.693
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVnE LTEF AK	55%	32.9	52.74675	Ref	0.93	0.45	0.94	0.93	0.34	1.2	1.1	55600	122000	94600	149000	163000	94600	2E+05	166000	591.7	1772	3	0.0159	8.983
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVnE LTEF AK	88%	43.3	52.5629	Ref	0.8	0.43	1.1	0.79	0.31	1.1	0.93	17400	20500	17200	31900	27400	17200	30500	27200	591.7	1772	3	0.0108	6.089
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVnE LTEF AK	95%	48.1	52.37061	Ref	0.91	0.68	0.93	0.96	0.39	1.2	0.58	2420	3490	3230	4310	4840	2850	5220	3370	887	1772	2	0.0014	0.807
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVnE LTEF AK	84%	40.9	52.64005	Ref	0.76	0.46	1.1	0.82	0.41	1.2	1	4460	6560	5800	9820	9160	6010	10900	9540	591.7	1772	3	0.0132	7.426
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVTD LTk	55%	28.3	48.07583	Ref	0.88	0.61	0.94	0.74	0.59	1.1	0.71	2150	2720	2450	3460	3300	2610	3980	2930	466.6	1396.9	3	0.0013	0.92

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVTD LTKV Hk	82%	32.5	47.62446	Ref	0.91	0.49	1	0.65	0.81	0.92	0.74	5660	6690	5400	8730	7500	7290	8210	7200	441.3	1761.1	4	0.0033	1.878
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVVS TQT ALA	95%	46.3	51.57248	Ref	No Values (0.98610616)	No Values (0.86841273)	No Values (0.701818)	No Values (0.56133866)	No Values (0.7521127)	No Values (0.6944444)	No Values (0.7053185)	No Values (0.78371614)	No Values (0.98610616)	No Values (0.86841273)	No Values (0.701818)	No Values (0.56133866)	No Values (0.75721127)	No Values (0.6944444)	No Values (0.7053185)	653.9	1305.8	2	0.004	3.068
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVVS TQT ALA	95%	49.5	51.91283	Ref	Reference Missing (1.2446446)	Reference Missing (1.1587112)	Reference Missing (1.0462523)	No Values (-0.7110696)	Reference Missing (0.9308845)	Reference Missing (0.9685484)	No Values (-0.6845649)	Reference Missing (1.2446446)	Reference Missing (1.1587112)	Reference Missing (1.0462523)	Reference Missing (0.8524033)	No Values (-0.7110696)	Reference Missing (0.9308845)	Reference Missing (0.9685484)	653.9	1305.8	2	0.014	10.72	
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	IVVS TQT ALA	95%	72.8	51.73297	Ref	No Values (0.7177577)	No Values (0.60006434)	No Values (0.43346944)	No Values (0.29299024)	No Values (0.48886272)	Reference Missing (1.8665931)	No Values (0.43696997)	No Values (0.51536745)	No Values (0.7177577)	No Values (0.60006434)	No Values (0.43346944)	No Values (0.29299024)	No Values (0.48886272)	Reference Missing (1.8665931)	No Values (0.43696997)	653.9	1305.8	2	0.0099	7.553
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	mPc TEDY LSLIL NR	95%	52.1	52.31426	Ref	0.88	0.6	0.97	0.73	0.48	1.2	0.64	2100	2460	2200	3190	2990	2190	3750	2530	673.3	2017	3	0.0133	6.582
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	mPc TEDY LSLIL NR	95%	62.7	52.55974	Ref	0.89	0.61	1	0.92	0.33	1.4	0.71	5560	11300	10100	14800	15500	9010	19600	12100	1010	2017	2	0.0044	2.164
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	mPc TEDY LSLIL NR	91%	45.8	52.42484	Ref	0.92	0.39	1	0.71	0.41	1.1	0.78	227	251	188	324	291	206	353	276	673.3	2017	3	0.0098	4.858

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	mPc TEDY LSLIL NR	95%	59.8	52.46391	Ref	0.88	0.45	1	0.98	0.17	1.4	0.78	643	1270	1020	1700	1830	910	2270	1440	1010	2017	2	0.0086	4.285
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	mPc TEDY LSLIL NR	77%	36.9	52.44057	Ref	0.99	0.38	1.1	1.1	0.14	1.3	0.69	320	641	456	821	922	420	997	634	1010	2017	2	0.0096	4.771
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	mPc TEDY LSLIL NR	64%	34.2	52.46169	Ref	1	0.5	1	0.76	0.84	1	0.39	139	197	150	244	222	205	246	156	673.3	2017	3	0.008	3.951
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	mPc TEDY LSLIL NR	95%	81	52.28716	Ref	0.73	0.68	0.95	0.92	0.54	1.2	0.72	2050	2700	2840	3850	4150	2780	4580	3270	1017	2033	2	0.0103	5.085
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	mPc TEDY LSLIL NR	95%	66.6	51.81706	Ref	0.75	0.64	0.84	0.72	0.28	1.5	0.58	895	999	1000	1300	1310	845	2080	1080	678.7	2033	3	0.0135	6.627
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	mPc TEDY LSLIL NR	95%	66.2	52.4192	Ref	0.89	0.47	0.97	0.92	0.39	1.4	0.83	1270	2540	2060	3270	3490	2110	4350	2970	1018	2033	2	0.0045	2.204
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	mPc TEDY LSLIL NR	95%	85.7	52.32025	Ref	0.82	0.61	0.94	0.93	0.28	1.5	0.75	669	1420	1340	1880	2060	1150	2790	1650	1018	2033	2	0.0086	4.249

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	mPc TEDY LSLIL NR	73%	36.4	52.49724	Ref	0.9	0.44	0.74	0.7	0.55	1.5	0.6	394	500	394	547	586	460	918	495	678.7	2033	3	0.0021	1.051
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	nEcF LSHK	67%	34.7	52.07096	Ref	1.1	0.81	0.84	0.69	0.55	1.1	0.55	23600	32900	30200	34400	34200	27100	40900	28200	544.6	1630.8	3	0.0105	6.46
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	nEcF LSHK	61%	33	52.12297	Ref	0.74	1.1	0.78	0.81	0.36	1.3	0.3	2770	2980	4210	3710	4200	2670	5210	2660	816.4	1630.8	2	0.0069	4.244
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	qNc DQF Ek	79%	27.9	42.92212	Ref	0.9	0.59	1.1	0.86	0.36	1.5	0.38	1720	3440	3010	4920	4490	2770	6370	2930	672.8	1343.6	2	0.0134	9.973
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	qNc DQF Ek	52%	22.7	43.16578	Ref	1.3	0.39	0.81	0.39	0.1	1.2	0.63	395	455	260	390	323	230	500	343	672.8	1343.6	2	0.0117	8.694
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	qNc DQF Ek	83%	29	42.48047	Ref	0.87	0.51	0.98	1	0.34	1.4	0.73	4000	7710	6510	10100	11300	6220	13400	8480	672.8	1343.6	2	0.0178	13.23
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	qNc DQF Ek	82%	28.8	42.68601	Ref	0.69	0.28	0.72	0.62	0.2	1.1	0.48	3920	1960	1600	2440	2500	1630	3250	2060	672.8	1343.6	2	0.0168	12.52

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qNc DQF Ek	65%	24.4	42.76209	Ref	0.91	0.61	1	0.74	0.13	1.4	0.61	2290	3360	2960	4490	4010	2280	5900	3310	672.8	1343.6	2	0.0146	10.88
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qNc DQF Ek	61%	23.8	42.91769	Ref	1	0.59	1.1	0.84	0.61	1.2	0.5	8500	16300	13000	20000	19100	14200	22000	13700	672.8	1343.6	2	0.013	9.691
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qNc DQF Ek	58%	23.7	43.34615	Ref	0.91	0.42	0.52	0.82	0.59	1.3	0.77	476	501	387	466	635	471	783	555	672.8	1343.6	2	0.0096	7.147
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qNc DQF Ek	95%	45.2	50.30393	Ref	0.75	0.53	1.1	0.98	0.37	1.4	0.66	31600	52100	48700	80700	82400	47000	98400	59600	833.4	1664.8	2	0.0154	9.223
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qNc DQF Ek	67%	32.5	50.39973	Ref	0.83	0.36	1.1	0.92	0.42	1.3	0.77	18000	30300	23700	43600	43200	26700	52400	35300	833.4	1664.8	2	0.0138	8.262
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qNc DQF Ek	88%	39	50.32373	Ref	0.82	0.44	1.1	1	0.47	1.4	0.71	17500	36600	30700	52800	55800	33600	66400	41400	833.4	1664.8	2	0.0151	9.067
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qTAL VELL k	86%	37.3	49.69709	Ref	1.4	0.51	0.76	0.77	0.18	1.2	0.79	419	959	570	761	845	489	1040	773	651.4	1300.8	2	0.0072	5.515

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qTALVELLk	86%	37.4	49.65192	Ref	0.97	0.64	0.99	0.81	0.37	1.4	0.68	3200	6320	5470	7840	7590	4880	10100	6280	651.4	1300.8	2	0.0111	8.511
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qTALVELLk	62%	30.3	49.10763	Ref	1	0.54	0.96	0.87	0.48	1.1	0.75	3470	5550	4250	6400	6630	4430	6970	5530	812	1622	2	0.0234	14.43
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qTALVELLk	91%	41.7	48.77585	Ref	0.76	0.65	1	0.9	0.4	1.4	0.74	16700	31500	31600	46800	46700	28700	58900	37700	541.7	1622	3	0.018	11.12
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qTALVELLk	95%	56.8	48.53978	Ref	1	0.49	1	0.93	0.34	1.3	0.37	10000	15200	11400	18600	19100	11000	22200	11700	812	1622	2	0.013	8.03
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qTALVELLk	95%	49.3	48.53558	Ref	0.88	0.52	0.85	0.87	0.51	1.4	0.65	1E+05	180000	2E+05	215000	240000	2E+05	3E+05	188000	541.7	1622	3	0.0118	7.295
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qTALVELLk	95%	50.3	48.12914	Ref	0.8	0.44	1.1	1	0.23	1.4	0.68	33800	56400	47800	83700	89500	44800	1E+05	63400	812	1622	2	0.0091	5.627
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qTALVELLk	94%	41.9	48.58068	Ref	0.87	0.4	1.1	0.87	0.33	1.5	0.63	6340	12500	9740	17800	16700	10000	23500	12800	812	1622	2	0.015	9.238

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qTALVELLk	95%	48.6	48.34885	Ref	0.77	0.53	0.92	0.91	0.48	1.4	0.61	5970	8060	7370	10800	11900	7720	15200	8720	541.7	1622	3	0.0109	6.721
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qTALVELLk	91%	42.1	48.68451	Ref	0.79	0.61	0.88	0.75	0.37	1.1	0.73	2160	1960	1880	2550	2560	1720	3010	2280	541.7	1622	3	0.0204	12.6
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qTALVELLk	95%	46.8	48.64298	Ref	0.84	0.82	0.82	0.88	0.54	1.3	0.63	307	505	543	606	697	482	850	533	812	1622	2	0.0188	11.57
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qTALVELLk	87%	37.8	47.91361	Ref	0.86	0.61	1	0.79	0.53	1.1	0.57	901	985	900	1360	1270	920	1400	979	541.7	1622	3	0.0056	3.45
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	qTALVELLk	52%	27.6	47.91361	Ref	0.57	0.29	1	1	0.62	1.2	0.49	360	293	260	483	542	354	542	337	541.7	1622	3	0.0052	3.228
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPEYAVSVLLR	86%	40.3	53.05336	Ref	No Values (0.75839525)	Reference Missing (0.7803382)	Reference Missing (1.2528954)	No Values (0.33362803)	No Values (0.52950037)	Reference Missing (1.14460773)	No Values (0.47760773)	No Values (0.5560053625)	No Values (0.75839525)	Reference Missing (0.7803382)	Reference Missing (1.2528954)	No Values (0.33362803)	No Values (0.52950037)	Reference Missing (1.14460773)	No Values (0.47760773)	436.8	1743	4	0.0156	8.957
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPEYAVSVLLR	88%	43.7	52.96286	Ref	0.99	0.62	0.72	0.76	0.78	0.9	0.89	23100	31400	26300	31800	35900	31900	36100	35500	582	1743	3	0.0123	7.027

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	55%	32.8	52.89486	Ref	0.81	0.52	0.73	0.77	0.62	1.2	0.89	1750	2080	1840	2380	2700	2140	3400	2660	872.5	1743	2	0.0114	6.565	
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	87%	40.7	52.91511	Ref	Reference Missing (0.9471342)	No Values (0.51765895)	Reference Missing (1.02036)	Reference Missing (0.78121823)	No Values (0.40645728)	Reference Missing (1.1659675)	Reference Missing (0.625999)	No Values (0.43296224)	Reference Missing (0.9471342)	Reference Missing (0.51765895)	Reference Missing (1.02036)	Reference Missing (0.78121823)	No Values (0.40645728)	Reference Missing (1.1659675)	Reference Missing (0.625999)		436.8	1743	4	0.0107	6.159
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	95%	53.1	52.89618	Ref	0.75	0.55	0.99	0.79	0.52	1.2	0.92	65700	89600	84700	129000	124000	89400	2E+05	123000	582	1743	3	0.0119	6.821	
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	86%	40.7	52.89455	Ref	0.92	0.38	1.1	0.59	0.52	1.4	0.87	3420	6150	4600	8380	6590	5480	10300	7220	872.5	1743	2	0.0111	6.359	
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	94%	49.6	52.89555	Ref	0.74	0.76	0.93	0.84	0.74	1.2	0.59	70100	95400	1E+05	133000	138000	1E+05	2E+05	105000	582	1743	3	0.011	6.288	
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	91%	44	52.90636	Ref	1.14	Value Missing (0.2982515)	1	0.58	0.76	0.7	0.8	7290	8110	Value Missing (0.2982515)	9650	7750	7650	7710	8210	436.8	1743	4	0.0105	6.021	
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	86%	40.2	52.86834	Ref	No Values (0.78805345)	No Values (0.6703601)	Reference Missing (1.307878)	No Values (0.36328605)	No Values (0.5591585)	Reference Missing (1.0659491)	No Values (0.507266)	No Values (0.58566344)	No Values (0.78805345)	No Values (0.6703601)	Reference Missing (1.307878)	No Values (0.36328605)	No Values (0.5591585)	Reference Missing (1.0659491)	No Values (0.507266)	436.8	1743	4	0.0097	5.54	

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	95%	53.3	53.05193	Ref	0.98	0.67	0.89	0.59	0.69	1.3	0.82	13500	28300	24900	32400	29000	27100	43000	30800	582	1743	3	0.0154	8.816
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	89%	44.6	52.96573	Ref	0.87	0.81	0.77	0.67	0.76	0.95	0.72	3660	4100	4270	4670	4800	4470	5310	4500	582	1743	3	0.0134	7.664
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	93%	46.1	52.96097	Ref	0.66	0.65	1.2	0.7	0.78	0.94	0.74	9140	10000	10800	17100	13700	12800	14900	12800	436.8	1743	4	0.012	6.87
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	89%	42.2	52.89455	Ref	1.1	0.47	1.1	0.73	0.42	1.2	0.7	1020	2330	1590	2830	2360	1650	3000	2090	872.5	1743	2	0.0111	6.359
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	95%	53.3	52.915	Ref	0.86	0.73	0.9	0.6	0.63	0.97	0.71	5130	5180	5160	6500	5820	5200	6860	5690	582	1743	3	0.0106	6.081
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	90%	42.9	52.88569	Ref	No Values (0.95521045)	No Values (0.83751696)	No Values (0.67092234)	No Values (0.53044313)	No Values (0.72631556)	Refer ence Missi ng (0.90417475)	No Values (0.6744229)	No Values (0.7528204)	No Values (0.95521045)	No Values (0.83751696)	No Values (0.67092234)	No Values (0.53044313)	No Values (0.72631556)	Refer ence Missi ng (0.90417475)	No Values (0.6744229)	436.8	1743	4	0.0104	5.953
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	95%	51.5	52.84954	Ref	0.88	0.68	0.95	0.61	0.67	0.87	0.76	2410	2500	2360	3210	2790	2540	3050	2810	436.8	1743	4	0.0091	5.242

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	62%	34	52.84952	Ref	1	0.58	1.2	0.74	0.58	1	0.62	893	1470	1170	1990	1610	1270	1760	1350	872.5	1743	2	0.009	5.166
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	95%	51.2	52.84785	Ref	0.83	0.76	0.97	0.72	0.51	1.2	0.59	8180	9720	10100	13100	12100	9090	15100	10000	582	1743	3	0.0088	5.032
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	91%	44.1	52.7987	Ref	0.96	0.57	1.3	0.42	0.74	0.78	0.52	3390	3880	3220	6100	3570	3900	4200	3470	436.8	1743	4	0.0072	4.141
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	90%	43	52.96808	Ref	0.68	0.57	1.2	0.88	0.7	1	0.72	3890	4970	5000	8420	7680	5910	7820	6210	436.8	1743	4	0.0128	7.352
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	64%	34.9	52.96286	Ref	0.87	0.76	0.77	0.78	0.66	0.9	0.68	983	978	985	1120	1230	990	1220	1040	582	1743	3	0.0123	7.027
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	90%	45.5	52.84945	Ref	0.96	0.78	0.76	0.52	0.61	1.2	0.87	939	1310	1250	1390	1300	1210	1830	1490	582	1743	3	0.0095	5.445
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	95%	50	52.79676	Ref	1	0.27	1.3	0.45	0.64	0.93	0.74	798	1000	641	1430	899	896	1140	997	436.8	1743	4	0.0077	4.416

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	88%	43.4	52.79644	Ref	0.84	0.74	0.97	0.63	0.61	1.1	0.76	1190	1410	1440	1890	1650	1420	2010	1630	582	1743	3	0.0073	4.189
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	60%	33.8	52.80619	Ref	0.77	0.62	0.85	0.76	0.62	1	0.9	3150	3310	3250	4280	4430	3500	4790	4400	582	1743	3	0.0071	4.086
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	95%	55.6	52.80642	Ref	1.1	0.61	1.3	0.63	0.29	1.4	0.4	3540	9580	7410	13100	9310	6430	14800	7150	582	1743	3	0.0069	3.982
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	91%	44.2	52.80394	Ref	No Values (0.8931405)	No Values (0.77544725)	Reference Missing (1.246015)	No Values (0.4683732)	No Values (0.66424567)	No Values (0.60147905)	No Values (0.61235315)	No Values (0.6907506)	No Values (0.8931405)	No Values (0.77544725)	Reference Missing (1.246015)	No Values (0.4683732)	No Values (0.66424567)	No Values (0.60147905)	No Values (0.61235315)	436.8	1743	4	0.0066	3.774
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	94%	50.6	53.05336	Ref	0.63	0.48	0.88	0.61	0.97	1.1	0.87	833	806	787	1170	1070	1200	1320	1150	582	1743	3	0.0156	8.919
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	95%	52.3	52.88381	Ref	0.99	0.47	1.1	0.74	0.4	1.4	0.82	1540	3930	2970	5280	4420	3070	6200	4240	582	1743	3	0.0101	5.771
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	65%	34.9	52.86834	Ref	0.75	0.85	0.82	0.55	0.74	1	0.88	670	734	855	938	859	853	1070	976	582	1743	3	0.0097	5.565

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	92%	44.3	52.79676	Ref	No Values (0.84973884)	No Values (0.7320455)	Reference Missing (1.0015075)	No Values (0.4249715)	No Values (0.620844)	Reference Missing (1.1202927)	No Values (0.56895137)	No Values (0.64734876)	No Values (0.84973884)	No Values (0.7320455)	Reference Missing (1.0015075)	No Values (0.4249715)	No Values (0.620844)	Reference Missing (1.1202927)	No Values (0.56895137)	No Values (0.64734876)	436.8	1743	4	0.0077	4.416
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	90%	42.5	52.80619	Ref	0.85	0.93	1.3	0.39	0.51	0.85	0.63	352	418	479	697	407	387	512	435	436.8	1743	4	0.0071	4.049	
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	90%	42.6	52.80642	Ref	0.73	0.8	1	0.56	0.99	0.56	0.56	263	221	251	329	263	308	239	238	436.8	1743	4	0.0069	3.98	
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	85%	34.4	51.48344	Ref	0.98	0.69	0.65	0.77	0.88	0.98	0.63	618	785	698	759	914	858	960	751	410.4	2047.2	5	0.0141	6.903	
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	86%	35.3	51.48344	Ref	0.82	0.67	1.2	0.89	0.26	1.2	0.58	54600	77600	76100	122000	109000	61700	1E+05	80100	410.4	2047.2	5	0.0141	6.903	
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	61%	27.4	51.46615	Ref	0.84	0.45	1.2	0.91	0.68	1	0.69	1850	2880	2370	4410	4040	3010	4020	3130	410.4	2047.2	5	0.0137	6.684	
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	66%	28.1	51.4014	Ref	0.81	0.52	1.2	0.9	0.42	1.2	0.66	8590	14000	12500	22400	20100	12500	23300	15400	410.4	2047.2	5	0.0121	5.927	

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPE YAVS VLLR	73%	29.9	51.3963	Ref	0.68	0.57	1.3	0.59	0.94	1.1	0.56	654	893	898	1620	1120	1250	1490	995	410.4	2047.2	5	0.0088	4.291
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPY FYAP ELLY YANK	74%	33.7	55.08855	Ref	0.77	0.52	0.85	0.79	0.41	1.6	0.59	755	1180	1080	1510	1610	1070	2630	1260	531.5	2652.4	5	0.02	7.556
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	rHPY FYAP ELLY YANK	71%	32.9	55.04578	Ref	0.88	0.92	0.6	0.65	0.35	1.7	0.39	522	885	989	893	1020	718	1910	770	531.5	2652.4	5	0.0121	4.56
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	RHPy FYAP ELLY YANK	76%	39.8	55.09037	Ref	0.91	0.53	0.81	0.77	0.62	1.3	0.77	424	661	551	749	802	631	1070	727	885.1	2652.4	3	0.0162	6.115
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	RHPy FYAP ELLY YANK	55%	35.2	55.00051	Ref	1.1	0.76	1	0.57	0.48	1.1	0.65	148	250	211	286	229	189	297	220	885.1	2652.4	3	0.0056	2.113
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	RHPy FYAP ELLY YANK	52%	32.9	55.08255	Ref	0.89	0.54	1	0.58	0.4	1.2	0.85	207	266	227	356	287	222	411	313	664.1	2652.4	4	0.016	6.02
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	sHcl AEVE k	77%	37.7	52.59061	Ref	0.92	0.63	0.87	0.87	0.37	1.3	0.51	24600	30000	26700	35300	38900	23900	46400	27400	557.3	1668.9	3	0.0133	7.991

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	sHCl AEVE k	95%	51.4	52.27771	Ref	0.99	0.76	0.88	0.63	0.43	1.2	0.67	2590	3560	3290	4020	3730	2830	5020	3460	835.4	1668.9	2	0.0233	13.95
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	sHCl AEVE k	95%	47.7	52.47995	Ref	0.99	0.72	0.86	0.84	0.41	1.2	0.62	2650	3990	3600	4440	4830	3130	5690	3760	835.4	1668.9	2	0.0215	12.86
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	sHCl AEVE k	84%	40.9	52.59781	Ref	1.1	0.61	1.1	0.9	0.39	1.2	0.47	49300	96400	74200	116000	112000	68700	1E+05	75000	557.3	1668.9	3	0.0139	8.332
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	sHCl AEVE k	89%	41.4	52.58592	Ref	0.97	0.63	0.96	0.74	0.5	1.3	0.53	11300	17600	15200	21300	20200	14900	27600	15800	418.2	1668.9	4	0.0132	7.905
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	sHCl AEVE k	60%	33.7	52.61831	Ref	0.97	0.79	0.85	0.75	0.4	1.1	0.53	56700	66500	63400	74200	76700	52500	90500	59600	557.3	1668.9	3	0.0126	7.56
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	sLHT LFGD ELck	73%	37.9	53.93122	Ref	0.76	0.43	0.96	0.88	0.6	1.2	0.86	13900	19700	17100	27700	28800	20600	33600	25700	673	2016	3	0.0182	9.011
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	sLHT LFGD ELck	95%	57.4	53.91089	Ref	0.98	0.4	1.1	0.79	0.47	1.4	0.66	1950	4280	3110	5880	5030	3520	6920	4190	1009	2016	2	0.0163	8.101

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	sLHT LFGD ELck	94%	51.9	53.93924	Ref	0.82	0.57	1.1	0.75	0.52	1.3	0.73	3150	5490	5010	8060	7010	5220	9650	6250	673	2016	3	0.0172	8.55
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	sLHT LFGD ELck	95%	64.3	53.90707	Ref	1.1	0.37	1	0.72	0.38	1.4	0.81	1300	3040	1970	3480	3110	2140	4470	3010	1009	2016	2	0.0167	8.28
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	sLHT LFGD ELck	94%	52	53.99186	Ref	0.91	0.5	1.1	0.83	0.5	1.3	0.67	4640	7730	6310	10700	9820	6800	12000	7950	673	2016.1	3	0.0121	6.022
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	sLHT LFGD ELck	94%	51.4	54.00526	Ref	0.86	0.58	1	0.87	0.56	1.2	0.67	1240	1880	1680	2520	2540	1790	2930	1990	673	2016.1	3	0.0127	6.29
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	TcVA DES HAG cEk	95%	58.9	41.81758	Ref	0.83	0.45	0.97	0.98	0.57	1.4	0.63	2290	4250	3560	5720	6340	4170	7710	4490	873.4	1744.7	2	0.0134	7.681
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tcVA DES HAG cEk	95%	56.9	47.82473	Ref	0.86	0.68	1	0.87	0.49	1.3	0.57	5750	10300	9930	14100	14000	9420	17800	10300	1025	2048.9	2	0.0177	8.62
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tcVA DES HAG cEk	95%	61.5	47.40568	Ref	0.72	0.57	1.1	0.96	0.45	1.4	0.61	9270	15900	15500	25100	25200	15400	30800	17800	1025	2048.9	2	0.0245	11.96

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tcVA DES HAG cEk	92%	42.1	47.69111	Ref	0.87	0.61	1.1	0.99	0.092	1.3	0.71	35700	63900	57800	91100	93200	43700	1E+05	69200	684	2048.9	3	0.0197	9.609
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tcVA DES HAG cEk	95%	47.4	47.75836	Ref	0.87	0.44	0.99	0.88	0.54	1.2	0.78	12100	17800	14400	23600	24200	16600	27600	20400	684	2048.9	3	0.0188	9.169
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tcVA DES HAG cEk	91%	41	47.76745	Ref	0.72	0.66	1.1	0.87	0.5	1.3	0.58	21500	29800	31100	47000	44400	29900	54100	32900	684	2048.9	3	0.0184	8.979
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tcVA DES HAG cEk	89%	38.9	47.95971	Ref	0.89	0.51	1	0.89	0.38	1.3	0.74	15900	26100	21700	34400	35100	21500	42800	28500	684	2048.9	3	0.0153	7.472
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tVM ENFV AFV Dk	95%	70.8	53.95416	Ref	0.76	0.5	1.1	0.92	0.39	1.4	0.75	7830	13300	12100	19900	20000	12100	25400	16100	1005	2007.1	2	0.0198	9.836
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tVM ENFV AFV Dk	95%	68.1	53.92815	Ref	0.68	0.68	1.1	1	0.19	1.4	0.69	2230	3920	4260	6390	6700	3290	7980	4820	1005	2007.1	2	0.0166	8.252
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tVM ENFV AFV Dk	95%	54.7	53.96498	Ref	0.88	0.58	1.1	0.97	0.23	1.4	0.7	373	761	672	1060	1080	567	1310	818	1005	2007.1	2	0.015	7.465

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	tVM ENFV AFV Dk	95%	66.9	53.90158	Ref	0.87	0.53	1.1	0.92	0.29	1.3	0.66	544	988	848	1440	1370	776	1680	1040	1005	2007.1	2	0.0123	6.131
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	tVM ENFV AFV Dk	64%	35.3	53.91274	Ref	0.88	0.49	1.1	0.79	0.42	1.4	0.52	197	287	237	411	362	244	492	272	1005	2007.1	2	0.0107	5.334
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	tVM ENFV AFV Dk	95%	53.2	53.8483	Ref	0.73	0.8	0.6	0.78	0.53	1	1.2	278	356	407	397	495	364	542	595	670	2007.1	3	0.006	2.977
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	tVm ENFV AFV Dk	95%	54.4	53.89095	Ref	0.88	0.6	0.92	0.85	0.34	1.2	0.99	14900	25200	22600	31700	33200	20300	38900	33100	675.4	2023.1	3	0.0169	8.37
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	tVm ENFV AFV Dk	95%	66.7	53.953	Ref	0.83	0.52	0.99	0.9	0.28	1.3	1	11300	22100	19300	30000	31100	17700	37000	31200	675.4	2023.1	3	0.0131	6.473
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	tVm ENFV AFV Dk	91%	45.2	53.96895	Ref	0.92	0.54	0.89	0.85	0.66	1.2	0.76	1630	2700	2240	3200	3440	2630	4010	2940	1013	2023.1	2	0.01	4.934
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	tVm ENFV AFV Dk	67%	36.4	53.94495	Ref	0.63	0.56	0.99	0.87	0.38	1.2	1.2	1380	1890	1960	2970	3010	1870	3340	3300	675.4	2023.1	3	0.0111	5.48

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tVm ENFV AFV Dk	65%	36	53.93235	Ref	0.9	0.45	0.97	0.8	0.67	0.83	0.94	2960	3590	2850	4590	4480	3580	4180	4480	675.4	2023.1	3	0.0124	6.117
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tVm ENFV AFV Dk	89%	45.4	53.92243	Ref	0.83	0.57	0.93	0.78	0.67	1	0.87	1900	2360	2130	3070	3050	2470	3230	2930	675.4	2023.1	3	0.0106	5.213
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tVM EnFV AFV Dk	95%	60.6	53.82523	Ref	0.72	0.59	0.96	1	0.53	1.2	0.64	9610	12000	11900	17200	19700	12300	20300	13800	1005	2008.1	2	0.0232	11.53
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tVM EnFV AFV Dk	95%	53.6	53.8184	Ref	0.76	0.71	1	0.95	0.39	1.2	0.8	18200	29600	31000	43300	45400	27000	50000	37100	670.4	2008.1	3	0.0163	8.132
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tVM EnFV AFV Dk	84%	41.8	53.8488	Ref	0.72	0.43	0.96	0.77	0.46	1.1	1.2	5020	6410	5690	9240	8960	6290	10600	10500	670.4	2008.1	3	0.0121	6.042
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	tVm EnFV AFV Dk	84%	41.8	53.89836	Ref	0.95	0.77	0.8	0.5	0.75	0.8	0.76	3840	3880	3710	4250	3800	3950	4280	4140	675.7	2024.1	3	0.0129	6.385
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P0276 9 ALBU_B OVIN	vHkE ccHG DLLE cAD DR	66%	28.5	48.09345	Ref	0.7	0.48	0.87	0.87	0.58	1.1	0.91	9570	9580	8920	13200	14500	10300	15300	13500	673	2688.2	4	0.0194	7.211

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylcD NQD TISSk	90%	44.6	52.43891	Ref	0.89	0.24	0.86	1.3	0.44	1.3	0.74	58600	106000	73500	127000	184000	91000	2E+05	116000	681	2040	3	0.0173	8.462
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylcD NQD TISSk	95%	51.1	52.42701	Ref	0.98	0.46	1.1	0.95	0.13	1.5	0.56	4E+05	1120000	8E+05	2E+06	1470000	7E+05	2E+06	1010000	681	2040	3	0.0156	7.653
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylcD NQD TISSk	95%	57.6	52.38565	Ref	0.93	0.51	0.94	0.97	0.51	1.2	0.77	47000	87300	70500	107000	121000	76400	1E+05	94600	681	2040	3	0.0196	9.623
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylcD NQD TISSk	95%	52.8	52.41185	Ref	0.84	0.59	0.96	0.79	0.59	1.1	0.77	2370	2920	2660	3860	3770	2870	4230	3380	681	2040	3	0.0158	7.742
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylcD NQD TISSk	95%	60.7	52.34008	Ref	0.97	0.52	0.85	0.95	0.35	1.5	0.7	25200	54900	43500	61500	72300	41700	94400	55300	1021	2040	2	0.0169	8.302
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylcD NQD TISSk	95%	71.5	52.34649	Ref	0.66	0.56	1.1	0.99	0.33	1.5	0.71	77300	152000	2E+05	254000	259000	1E+05	3E+05	192000	1021	2040	2	0.0167	8.185
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylcD NQD TISSk	83%	38.8	52.42506	Ref	0.7	0.8	0.88	0.9	0.48	1.3	0.66	6740	8520	9910	11800	13200	8550	15400	10100	1021	2040	2	0.0149	7.283

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylcD nQD TISSk	95%	71.5	52.34024	Ref	0.75	0.63	1.1	0.93	0.29	1.3	0.68	4150	6800	6810	10800	10400	5790	12600	7910	1021	2040	2	0.0171	8.361
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylcD nQD TISSk	65%	36.5	54.46487	Ref	0.82	0.56	1	0.83	0.38	1.3	0.6	11600	14300	12900	19700	19200	12300	24800	14800	782.4	2344.2	3	0.0201	8.56
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylcD nQD TISSk	95%	61.6	51.75628	Ref	1.1	0.59	1.1	1.1	-0.03	1.3	0.66	31500	80100	60500	93100	106000	42200	1E+05	70900	681.3	2041	3	0.0165	8.095
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylcD nQD TISSk	52%	31.5	51.75137	Ref	0.84	0.94	0.83	0.72	0.48	0.93	0.69	11100	11300	13100	13600	14000	10300	14800	12400	681.3	2041	3	0.0163	8.007
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylcD nQD TISSk	91%	42.2	51.74458	Ref	0.87	0.39	1.1	1.1	0.24	1.4	0.66	10100	21900	17000	31600	34100	16600	39000	23100	1021	2041	2	0.0191	9.37
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylcD nQD TISSk	95%	56.7	51.81303	Ref	0.91	0.18	1	0.97	0.083	1.5	0.9	14100	30500	20000	40500	42600	20200	57100	36900	1021	2041	2	0.0176	8.596
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ylYEI AR	55%	30.9	50.63187	Ref	1	0.69	1	0.67	0.39	1.4	0.56	3500	6400	5560	7920	6760	4880	9980	5670	411.2	1230.7	3	0.0093	7.523

Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ynG VFQ EccQ AEDk	76%	32	47.09533	Ref	0.9	0.83	0.91	0.73	0.5	1.1	0.62	963	1200	1240	1470	1430	1070	1680	1200	779	2334	3	0.0145	6.195
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	sp P02769 ALBU_BOVIN	ynG VFQ EccQ AEDk	52%	27.5	47.84503	Ref	1.2	0.3	1.2	0.73	0.34	0.94	0.6	387	521	310	645	515	343	546	428	779	2334	3	0.0024	1.018
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	aHY DLR	54%	29.7	49.66695	Ref	0.55	0.34	0.86	0.036	0.51	0.73	0.088	2E+05	336000	3E+05	508000	317000	4E+05	5E+05	297000	360.2	1077.6	3	0.0086	7.985
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	aHY DLR	53%	29.6	49.73585	Ref	0.43	0.39	0.73	0.23	0.5	0.66	0.14	14200	18600	19700	27900	21800	22900	26800	18500	360.2	1077.6	3	0.0116	10.79
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	aLG GED VR	69%	32.4	49.9174	Ref	0.65	0.24	0.61	0.42	0.037	0.86	0.07	27300	39200	32000	46100	44800	29900	55400	31800	560.8	1119.6	2	0.0097	8.696
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	aLG GED VR	69%	32.3	49.91695	Ref	0.48	0.28	0.54	0.32	0.08	0.92	0.3	3E+06	4170000	4E+06	5E+06	5010000	4E+06	7E+06	4450000	560.8	1119.6	2	0.0099	8.803

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	aLGED VR	95%	66.2	50.15787	Ref	0.53	Value Missing (-0.9150124)	0.49	0.86	0.33	0.98	0.023	1E+05	154000	Value Missing (-0.9150124)	181000	258000	2E+05	3E+05	131000	374.2	1119.6	3	0.0087	7.764
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	aLGED VR	57%	30.6	50.36601	Ref	0.54	0.43	0.6	0.49	-0.05	0.8	0.14	3E+06	4040000	4E+06	5E+06	5260000	3E+06	6E+06	3720000	560.8	1119.6	2	0.0086	7.714
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	aLGED VR	89%	41.2	50.21764	Ref	-0.005	Value Missing (-1.0064844)	0.81	0.5	0.26	1.3	0.37	87600	93200	Value Missing (-1.0064844)	200000	178000	1E+05	3E+05	147000	374.2	1119.6	3	0.008	7.175
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	aLGED VR	92%	41.9	49.98482	Ref	0.52	0.32	0.53	0.54	0.11	0.67	0.3	1E+05	158000	1E+05	194000	216000	1E+05	2E+05	166000	560.8	1119.6	2	0.0103	9.231
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	aLGED VR	95%	53	49.97295	Ref	0.56	Value Missing (-1.3799417)	0.48	0.49	0.6	0.79	0.46	22300	24000	Value Missing (-1.3799417)	27700	30800	28900	34600	27300	374.2	1119.6	3	0.0091	8.085
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	aQF VPLP VSVS VEFA VAA TDcl Ak	84%	43.1	55.16493	Ref	-0.073	0.58	0.47	0.71	0.067	1.1	0.082	145	149	254	264	343	192	400	201	1040	3115.7	3	0.0135	4.323

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VR	95%	51.7	41.04692	Ref	0.57	0.15	0.67	0.43	-0.08	0.79	0.046	398	413	336	539	502	308	588	349	815.8	1629.7	2	0.0397	24.32
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VR	95%	37.5	41.90948	Ref	0.73	-0.1	0.5	0.073	-0.07	0.87	0.26	547	552	337	574	470	370	744	485	815.8	1629.7	2	0.0307	18.85
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VR	83%	29.8	43.53416	Ref	0.52	0.58	0.38	0.21	0.35	0.48	0.042	281	252	284	277	272	262	299	219	815.8	1629.7	2	0.0102	6.277
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VR	95%	41	43.88581	Ref	0.72	0.25	0.54	0.058	0.17	0.63	0.36	413	495	388	533	421	396	570	468	815.9	1629.7	2	0.0054	3.285
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VR	95%	48.5	44.52553	Ref	0.67	0.25	0.48	0.25	0.011	0.76	0.26	2140	2430	1970	2610	2450	1810	3170	2230	815.9	1629.7	2	#####	0.395
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VR	95%	45.5	43.23314	Ref	0.44	0.25	0.55	0.19	-0.17	0.93	0.38	2E+05	180000	2E+05	237000	203000	1E+05	3E+05	209000	815.8	1629.7	2	0.0146	8.963

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VR	95%	61.3	43.35638	Ref	0.66	0.34	0.64	0.31	-0.09	0.51	0.11	1E+05	119000	1E+05	142000	125000	82600	1E+05	98000	544.2	1629.7	3	0.0126	7.71
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VR	95%	42.8	43.36359	Ref	0.59	0.34	0.66	0.26	-0.01	0.62	0.13	44500	45100	41000	57400	48100	34700	56200	39800	815.8	1629.7	2	0.0126	7.7
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VR	83%	30	43.44412	Ref	0.46	0.44	0.35	0.25	-0.02	0.9	0.17	14900	13800	14700	15500	16000	11600	22800	13700	815.8	1629.7	2	0.0124	7.626
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VRk	81%	33.7	46.90878	Ref	0.31	0.55	0.47	0.5	0.21	0.69	0.41	41300	52100	66900	71000	80000	56800	83100	67900	586.9	1757.8	3	0.0124	7.069
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VRk	58%	27.7	47.01516	Ref	0.51	0.33	0.48	0.57	0.2	0.74	0.3	22200	31900	30700	38200	44700	30300	45800	33500	586.9	1757.8	3	0.0106	6.029
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VRk	95%	46.8	47.05547	Ref	0.51	0.37	0.3	0.66	0.2	0.78	0.29	4110	6010	5900	6320	8930	5650	8860	6230	879.9	1757.8	2	0.01	5.678

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VRk	95%	44.2	47.99657	Ref	0.51	0.58	0.04	0.71	0.17	0.77	0.25	2750	3920	4460	3440	6030	3630	5730	3970	879.9	1757.8	2	0.0042	2.373
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VRk	52%	27.7	48.01164	Ref	0.14	0.74	0.056	0.61	0.17	0.62	0.38	33800	27600	45100	31600	51200	32900	46900	39400	586.9	1757.8	3	0.0046	2.602
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cDSS PDS AED VRk	66%	33	51.15301	Ref	0.32	0.24	0.77	0.45	-0.08	0.76	0.33	16000	16300	16700	27200	24000	14500	27200	19900	1032	2062	2	0.0186	9.04
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	cNLL AEk	84%	38.7	51.99138	Ref	0.47	0.15	0.48	0.38	-0.07	0.98	0.32	2E+05	216000	2E+05	265000	272000	2E+05	4E+05	236000	722.9	1443.8	2	0.0165	11.39
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	ePac DDP DTE QAA LAAV DYIN k	93%	48.7	53.65533	Ref	0.54	0.33	0.63	0.67	0.18	0.49	0.11	1670	2110	1980	2730	3090	1930	2480	1910	1002	3002.4	3	0.0234	7.802
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	ePac DDP DTE QAA LAAV DYIN k	95%	64	53.84248	Ref	0.33	6E-04	0.65	0.48	0.14	0.43	0.017	2030	1240	1070	1890	1850	1280	1630	1210	1002	3002.4	3	0.0172	5.724

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	gSVI Qk	56%	31.8	51.76529	Ref	0.58	0.34	0.52	0.47	0.049	0.75	0.19	9E+05	1060000	1E+06	1E+06	1330000	9E+05	1E+06	989000	620.4	1238.8	2	0.013	10.52
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	gSVI Qk	57%	32	51.77254	Ref	0.5	0.18	0.57	0.39	0.19	0.81	0.33	95600	120000	1E+05	154000	150000	1E+05	2E+05	130000	620.4	1238.8	2	0.0161	12.97
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	gSVI Qk	57%	32.1	51.76529	Ref	0.51	0.32	0.49	0.46	0.074	0.83	0.3	2E+06	2410000	2E+06	3E+06	3130000	2E+06	4E+06	2540000	620.4	1238.8	2	0.0129	10.41
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	gSVI Qk	57%	31.4	51.17619	Ref	0.56	0.31	0.45	0.43	0.16	0.67	0.39	38700	47700	43600	54000	58700	42500	63000	51600	620.4	1238.8	2	0.0024	1.956
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	gSVI Qk	53%	30.7	51.17619	Ref	0.36	0.39	0.49	0.45	0.18	0.74	0.32	15700	16600	18300	22000	23700	17200	26400	19600	620.4	1238.8	2	0.0036	2.941
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTFS GVA SVES SSGE AFH VGK	95%	62.6	55.1526	Ref	0.83	-0.08	0.5	0.019	-0.02	1.1	0.29	1680	2620	1520	2540	2010	1710	3830	2190	910.1	2727.4	3	0.0231	8.472

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTFS GVA SVES SSGE AFH VGk	95%	61.1	55.18517	Ref	0.68	0.17	0.58	0.28	0.24	0.78	0.4	4280	7240	5520	8190	7340	6230	9470	7210	682.9	2727.4	4	0.0216	7.921
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTFS GVA SVES SSGE AFH VGk	95%	65	55.18517	Ref	0.62	0.2	0.58	0.29	0.3	0.54	0.36	7690	9260	7520	11000	9940	8690	10700	9420	682.9	2727.4	4	0.0216	7.921
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTFS GVA SVES SSGE AFH VGk	95%	61.6	55.18056	Ref	0.58	-0.1	0.51	0.12	0.2	1.2	0.3	4120	6480	4400	7560	6330	5830	12400	6500	910.1	2727.4	3	0.0189	6.933
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTFS GVA SVES SSGE AFH VGk	81%	36.3	55.22731	Ref	0.48	0.22	0.44	0.49	-0	0.7	0.54	11300	12800	11600	15100	17300	10700	18200	16100	546.5	2727.4	5	0.0168	6.164
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTFS GVA SVES SSGE AFH VGk	84%	37.6	55.18842	Ref	0.26	0.03	0.43	0.48	0.36	0.74	0.39	3140	2630	2430	3600	4120	3290	4480	3510	546.5	2727.4	5	0.0205	7.501
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTFS GVA SVES SSGE AFH VGk	95%	55.1	55.21788	Ref	0.64	0.24	0.61	0.34	0.083	0.74	0.28	2840	3870	3180	4610	4220	3080	5070	3670	682.9	2727.4	4	0.0177	6.484

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTFS GVA SVES SSGE AFH VGk	95%	81.1	55.26102	Ref	0.79	0.052	0.52	0.26	0.12	0.87	0.27	883	1400	913	1420	1310	1040	1810	1190	910.1	2727.4	3	0.0143	5.25
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	90%	42.9	52.56662	Ref	0.43	0.28	0.63	0.48	0.07	0.79	0.24	20500	23700	23300	33300	33000	21700	37300	25200	882	1762	2	0.0151	8.577
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	81%	39.7	53.03248	Ref	0.39	0.39	0.57	0.42	0.1	0.83	0.31	2E+05	204000	2E+05	282000	280000	2E+05	3E+05	235000	588.3	1762	3	0.0274	15.55
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	95%	50.9	52.57093	Ref	0.5	0.19	0.54	0.52	0.15	0.76	0.22	62800	73900	64600	92600	101000	67900	1E+05	73700	588.3	1762	3	0.0153	8.688
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	94%	45.9	52.50462	Ref	0.59	0.24	0.55	0.52	0.088	0.75	0.19	8260	11000	9320	13000	14000	9060	15000	10100	882	1762	2	0.0121	6.841
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	95%	48.3	52.7392	Ref	0.36	0.27	0.53	0.51	0.13	0.77	0.32	2990	3120	3180	4270	4640	3120	5090	3680	882	1762	2	0.0199	11.28

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	65%	34.8	52.7392	Ref	0.47	0.85	0.11	0.054	0.12	0.2	0.89	9880	11100	15600	10500	11200	10200	11300	18100	588.3	1762	3	0.0199	11.27
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	88%	43.2	52.63096	Ref	0.41	0.27	0.59	0.43	0.11	0.95	0.21	4E+05	555000	5E+05	763000	755000	5E+05	1E+06	586000	588.3	1762	3	0.0162	9.199
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	68%	35.3	52.57093	Ref	0.69	0.2	0.76	0.33	-0.04	0.67	0.21	37700	50400	38800	64300	52600	35700	61000	43800	588.3	1762	3	0.0153	8.688
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	93%	44.7	52.51962	Ref	0.6	0.13	0.49	0.56	0.025	0.86	0.34	15300	23000	18100	25900	30000	18100	33800	23300	882	1762	2	0.0141	8.021
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	95%	68.7	52.43294	Ref	0.39	0.33	0.66	0.43	-0.02	0.82	0.21	3500	3720	3850	5440	5110	3280	6110	3990	882	1762	2	0.0104	5.877
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	82%	38.7	52.7392	Ref	0.4	0.36	0.59	0.51	0.05	0.83	0.18	11300	13100	13800	18100	18900	12000	21500	13600	882	1762	2	0.0199	11.28

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	91%	45.4	52.51794	Ref	0.32	0.43	0.68	0.37	-0.01	0.95	0.095	8E+05	887000	1E+06	1E+06	1240000	8E+05	2E+06	924000	588.3	1762	3	0.0146	8.263
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	93%	45.7	52.51295	Ref	0.37	0.084	0.59	0.48	0.12	0.85	0.45	7430	8560	7650	12200	12400	8460	14600	11100	882	1762	2	0.0123	6.977
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	95%	51.4	52.4638	Ref	0.48	0.35	0.58	0.56	0.17	0.64	0.18	4960	5830	5790	7630	8280	5520	7980	5770	882	1762	2	0.0134	7.601
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	95%	51	52.41053	Ref	0.39	0.37	0.6	0.43	0.13	0.74	0.26	41500	45300	48500	63500	62400	44200	70300	50100	588.3	1762	3	0.0098	5.574
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	81%	38.9	52.43294	Ref	0.56	0.42	0.37	0.4	0.23	0.58	0.3	5490	6170	6080	6580	7400	5740	7670	6240	588.3	1762	3	0.0104	5.88
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLN QIDS Vk	88%	42.5	52.28174	Ref	0.45	0.31	0.5	0.38	0.43	0.46	0.31	2620	2640	2600	3310	3360	3040	3230	2910	588.3	1762	3	0.006	3.379

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTLn QIDS Vk	94%	50.9	52.88073	Ref	0.49	0.21	0.6	0.56	0.16	0.81	0.014	73800	87400	78000	114000	123000	81100	1E+05	76100	588.7	1763	3	0.0146	8.263
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTLn QIDS Vk	80%	38.4	52.88527	Ref	0.45	0.39	0.46	0.53	0.11	0.77	0.22	10100	11800	12300	14500	16800	10900	18000	12300	882.5	1763	2	0.0134	7.602
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTLn QIDS Vk	95%	53.9	52.99928	Ref	0.48	0.65	0.23	0.34	0.094	0.56	0.79	1910	2900	3540	2970	3540	2600	3760	4370	882.5	1763	2	0.0206	11.68
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTLn QIDS Vk	91%	46.5	53.0113	Ref	0.38	0.7	0.24	0.31	0.007	0.66	0.64	29300	33700	45600	37100	43000	30400	49800	48700	588.7	1763	3	0.0199	11.27
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTLn QIDS Vk	89%	44.4	52.95429	Ref	0.38	0.35	0.42	0.58	0.084	0.85	0.33	88000	105000	1E+05	132000	162000	1E+05	2E+05	124000	588.7	1763	3	0.0171	9.709
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTLn QIDS Vk	94%	50.9	52.94773	Ref	0.46	0.41	0.48	0.32	0.2	0.77	0.46	19200	25600	26800	31500	31300	25000	38700	31100	588.7	1763	3	0.0166	9.403

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLn QIDS Vk	88%	43.4	52.94636	Ref	0.29	0.35	0.5	0.46	0.17	0.76	0.42	56500	58500	66000	82100	88500	63100	99200	77400	588.7	1763	3	0.0162	9.199
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLn QIDS Vk	92%	47.2	52.93714	Ref	0.39	0.37	0.49	0.42	0.32	0.66	0.36	26500	30000	32200	39300	41300	33600	44400	35900	588.7	1763	3	0.016	9.096
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLn QIDS Vk	95%	48	52.88059	Ref	0.45	0.35	0.55	0.52	0.089	0.76	0.34	9760	12800	13000	16800	18000	11700	19400	14400	882.5	1763	2	0.0145	8.226
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLn QIDS Vk	79%	36.7	52.87598	Ref	0.47	0.43	0.39	0.46	-0.07	0.7	0.43	92000	98400	1E+05	114000	132000	79700	1E+05	117000	441.8	1763	4	0.0144	8.164
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLn QIDS Vk	94%	46.3	52.89317	Ref	0.43	0.38	0.6	0.64	0.18	0.8	0.15	7670	11800	12400	16300	18300	11700	18700	11800	882.5	1763	2	0.0128	7.251
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	hTLn QIDS Vk	95%	49.3	52.88935	Ref	0.41	0.27	0.47	0.57	0.13	0.82	0.34	6490	7900	7770	10100	11900	7640	12800	9170	882.5	1763	2	0.0122	6.911

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	hTLN QIDS VKV WPR	94%	51.6	53.69789	Ref	0.7	0.42	0.32	0.16	0.24	0.55	0.45	4340	5460	4870	5110	5020	4650	6000	5570	666.4	1996.1	3	0.0206	10.32
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	QDG QFS VLFT k	81%	38.3	52.48976	Ref	0.58	0.48	0.32	0.42	0.18	0.66	0.18	3990	4510	4550	4590	5420	4010	5810	4150	787.4	1572.8	2	0.0057	3.625
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	82%	38.2	52.07257	Ref	0.49	0.33	0.33	0.5	0.24	0.8	0.3	443	543	529	595	737	536	824	579	778.9	1555.8	2	0.0112	7.203
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	93%	49.4	53.66753	Ref	0.4	0.051	0.48	0.4	-0.02	0.86	0.76	4E+05	476000	4E+05	611000	640000	4E+05	8E+05	742000	626.7	1877	3	0.0261	13.87
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	86%	42.5	53.60344	Ref	0.55	0.23	0.47	0.31	0.15	0.54	0.66	10400	12700	11000	14600	14400	11300	15400	16600	626.7	1877	3	0.0213	11.33
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	95%	49.2	53.59869	Ref	0.49	0.24	0.52	0.47	0.11	0.82	0.32	20000	25400	23200	31400	33600	22800	39000	27300	939.5	1877	2	0.0207	11.04

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	90%	45.3	53.60576	Ref	0.17	0.69	0.34	0.07	-0.02	0.51	1.1	8340	10300	15900	14100	12800	10500	15900	24400	626.7	1877	3	0.0206	10.95
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	95%	50.6	53.59485	Ref	0.43	0.19	0.44	0.48	0.078	0.88	0.43	61200	71500	65600	87900	99600	65800	1E+05	86800	939.5	1877	2	0.02	10.64
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	57%	33.8	53.57746	Ref	0.49	0.26	0.59	0.5	0.12	0.75	0.26	38500	48300	44500	62800	65100	43600	70500	49900	939.5	1877	2	0.0179	9.546
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	95%	62.5	53.5705	Ref	0.63	0.094	0.61	0.44	0.071	0.8	0.1	63300	77300	57800	92500	90800	61400	1E+05	65100	939.5	1877	2	0.0173	9.216
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	95%	57.6	53.50783	Ref	0.35	0.2	0.68	0.44	-0.02	0.78	0.4	51000	52500	51200	80200	75200	47600	86500	66100	626.7	1877	3	0.016	8.505
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	83%	38.9	53.50248	Ref	0.37	-0.07	0.35	0.3	0.25	0.79	0.74	13200	13200	10500	15800	16800	14200	21500	20600	470.3	1877	4	0.0155	8.264

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	95%	61.7	53.50248	Ref	0.37	0.2	0.74	0.56	0.13	0.78	0.19	61700	74300	71600	117000	114000	73700	1E+05	79800	939.5	1877	2	0.0155	8.246
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	94%	50.6	53.492	Ref	0.56	0.15	0.54	0.53	-0.21	0.91	0.49	80700	124000	1E+05	149000	162000	85200	2E+05	143000	626.7	1877	3	0.0153	8.122
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	92%	48.4	53.51864	Ref	0.58	0.069	0.56	0.3	0.34	0.52	0.36	437	457	349	550	507	454	537	479	626.7	1877	3	0.0141	7.531
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	63%	35	53.41053	Ref	0.39	0.26	0.49	0.36	0.1	0.6	0.54	21300	19800	19700	25800	26100	19000	28000	26800	626.7	1877	3	0.011	5.87
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	95%	52	53.43515	Ref	0.52	0.23	0.39	0.35	-0.12	0.85	0.7	5E+05	613000	5E+05	679000	731000	5E+05	9E+05	844000	626.7	1877	3	0.0099	5.294
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	92%	47.3	53.36504	Ref	0.59	0.01	0.42	0.39	0.33	0.77	0.41	3820	4920	3570	5310	5750	4820	6800	5270	626.7	1877	3	0.0074	3.921

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri qDG QFS VLFT B0JYN6 B0JYN6_BOVIN	k	92%	47.2	53.35506	Ref	0.64	0.24	0.4	0.39	0.005	0.54	0.63	2440	2990	2470	3100	3400	2270	3420	3620	626.7	1877	3	0.0072	3.825
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri qDG QFS VLFT B0JYN6 B0JYN6_BOVIN	k	88%	41.9	53.32513	Ref	0.26	0.15	0.48	0.52	0.19	0.7	0.7	4850	5370	5410	7640	8610	5980	8920	8860	470.3	1877	4	0.0051	2.726
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri qDG QFS VLFT B0JYN6 B0JYN6_BOVIN	k	74%	37	53.27263	Ref	0.42	0.19	0.64	0.45	0.047	0.77	0.33	9610	10500	9730	14900	14400	9500	16400	12000	939.5	1877	2	0.0047	2.517
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri qDG QFS VLFT B0JYN6 B0JYN6_BOVIN	k	94%	51.4	53.2107	Ref	0.7	0.54	-0.15	0.14	0.11	0.85	0.41	143	170	165	115	154	132	230	169	626.7	1877	3	0.0015	0.806
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri qDG QFS VLFT B0JYN6 B0JYN6_BOVIN	k	95%	57.8	53.51864	Ref	0.36	0.19	0.58	0.47	0.092	0.76	0.32	93900	91300	88000	129000	132000	88600	1E+05	107000	626.7	1877	3	0.014	7.435
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri qDG QFS VLFT B0JYN6 B0JYN6_BOVIN	k	95%	57.3	53.5188	Ref	0.33	0.2	0.46	0.45	-0.09	0.81	0.7	12100	13300	13100	17600	19400	11600	22600	20800	626.7	1877	3	0.0145	7.723

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	95%	67	53.4335	Ref	0.47	0.22	0.51	0.49	-0.02	0.87	0.3	1360	1580	1440	1980	2150	1320	2560	1700	939.5	1877	2	0.0116	6.159
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	94%	51.2	53.45707	Ref	0.58	0.083	0.55	0.29	0.2	0.58	0.6	2440	2960	2280	3530	3260	2660	3630	3640	626.7	1877	3	0.0125	6.652
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	95%	53.9	53.27682	Ref	0.39	0.18	0.59	0.59	0.084	0.79	0.29	683	775	727	1080	1190	735	1260	882	939.5	1877	2	0.0049	2.592
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	95%	54	53.49746	Ref	0.65	0.26	0.52	0.32	-0.04	0.86	0.31	524	718	594	801	771	523	1020	693	939.5	1877	2	0.0132	7.011
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qDG QFS VLFT k	95%	54.4	53.43572	Ref	0.43	0.091	0.51	0.55	-0.06	0.76	0.54	1230	1360	1170	1750	1980	1130	2090	1780	626.7	1877	3	0.0096	5.103
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qDG QFSV LFTk	95%	53.6	53.5566	Ref	0.51	0.33	0.32	0.21	0.26	0.66	0.38	3450	3230	3080	3440	3520	3180	4380	3580	627	1878	3	0.0158	8.41

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	67%	34.1	51.66264	Ref	0.41	0.23	0.67	0.35	-0.02	1.1	0.2	25900	36300	34900	52800	46700	31600	71600	38200	752	2253.1	3	0.0252	11.18
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	95%	71.8	51.69918	Ref	0.58	0.4	0.49	0.32	0.12	0.73	0.36	918	1200	1150	1380	1350	1030	1630	1260	1128	2253.1	2	0.0249	11.04
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	79%	37.6	51.87977	Ref	0.59	0.16	0.5	0.41	0.07	0.88	0.32	22800	31400	25200	35900	37100	25600	46900	31600	752	2253.1	3	0.0202	8.981
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	78%	37.7	52.06699	Ref	0.59	0.16	0.4	0.65	-0.29	0.87	0.48	15900	22600	18200	24000	31500	14400	33600	25300	752	2253.1	3	0.0153	6.785
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	95%	54	52.24727	Ref	0.48	0.24	0.23	0.32	0.29	0.89	0.4	12400	14000	12900	14300	16800	14400	22900	16100	752	2253.1	3	0.0111	4.922
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	76%	37.6	52.59266	Ref	0.4	0.33	0.49	0.37	0.011	1	0.14	27700	30600	31600	39600	40300	27400	58100	31000	752	2253.1	3	0.0025	1.102

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	95%	60.7	52.66269	Ref	0.7	0.11	0.62	0.38	-0.16	0.85	0.18	659	846	609	975	911	549	1160	718	1128	2253.1	2	#####	0.227
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	75%	37.4	52.73932	Ref	0.52	0.1	0.48	0.41	0.2	0.92	0.31	12900	16800	13700	20000	21100	15900	27400	17700	752	2253.1	3	0.0017	0.761
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	88%	42.3	52.01037	Ref	0.43	0.16	0.4	0.54	-0.05	1.1	0.25	54200	68100	61300	81200	98800	57400	1E+05	73400	752	2253.1	3	0.0169	7.517
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	95%	64.3	52.25299	Ref	0.46	0.12	0.53	0.29	0.28	0.99	0.46	153	240	206	306	286	248	425	290	1128	2253.1	2	0.0112	4.972
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	86%	41.1	52.1786	Ref	0.6	0.28	0.43	0.41	0.22	0.72	0.37	3820	5260	4550	5700	6170	4710	6960	5430	752	2253.1	3	0.0126	5.574
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	61%	33.3	52.08511	Ref	0.62	0.22	0.4	0.29	0.16	0.96	0.25	1900	2610	2150	2730	2780	2220	4040	2460	752	2253.1	3	0.0142	6.306

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	80%	38.7	52.24349	Ref	0.47	0.32	0.55	0.39	0.073	0.92	0.35	605	863	847	1120	1090	769	1440	963	752	2253.1	3	0.0109	4.842
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	81%	39	52.24248	Ref	0.64	0.39	0.3	0.47	0.094	0.74	0.33	387	530	485	512	632	426	697	520	752	2253.1	3	0.0107	4.762
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	92%	48.8	54.71951	Ref	0.3	0.21	0.54	0.43	0.25	0.92	0.31	16300	18300	18700	26300	26700	20600	34300	22300	859.1	2574.3	3	0.0228	8.841
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	67%	35.5	54.76033	Ref	0.26	0.25	0.59	0.52	0.11	0.77	0.42	22700	23300	25100	35700	37400	24500	40600	31500	644.6	2574.3	4	0.0209	8.105
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	91%	48.3	54.67944	Ref	0.53	-0.2	0.53	0.53	0.16	1	0.13	6670	8170	5370	9980	11000	7440	14100	7570	859.1	2574.3	3	0.0189	7.338
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	87%	44.6	54.73937	Ref	0.52	0.29	0.58	0.48	-0.09	0.82	0.37	4230	5720	5290	7260	7510	4410	8660	6280	859.1	2574.3	3	0.0217	8.41

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6_BOJYN6_BOVIN	qQT QHA VEG DcDI HVLk	76%	39.7	54.73328	Ref	0.69	0.11	0.67	0.36	0.23	0.9	-0.11	2970	4410	3200	5290	4700	3760	6250	3090	859.1	2574.3	3	0.0215	8.34
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6_BOJYN6_BOVIN	qQT QHA VEG DcDI HVLk	95%	54.5	54.75751	Ref	0.52	0.22	0.69	0.42	0.094	0.67	0.13	1E+05	159000	1E+05	218000	199000	1E+05	2E+05	147000	859.1	2574.3	3	0.02	7.769
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6_BOJYN6_BOVIN	qQT QHA VEG DcDI HVLk	95%	69.4	54.75767	Ref	0.37	0.23	0.62	0.5	-0.05	0.92	0.35	4660	5730	5640	8300	8390	5000	10200	6830	1288	2574.3	2	0.02	7.767
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6_BOJYN6_BOVIN	qQT QHA VEG DcDI HVLk	71%	36.4	54.78819	Ref	0.57	0.29	0.42	0.43	0.091	0.83	0.4	2E+05	237000	2E+05	259000	288000	2E+05	3E+05	256000	644.6	2574.3	4	0.0194	7.53
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6_BOJYN6_BOVIN	qQT QHA VEG DcDI HVLk	81%	39.3	54.71949	Ref	0.44	0.35	0.61	0.6	0.053	0.77	0.19	3E+05	398000	4E+05	542000	594000	4E+05	6E+05	406000	644.6	2574.3	4	0.0177	6.878
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6_BOJYN6_BOVIN	qQT QHA VEG DcDI HVLk	73%	36.9	54.79026	Ref	0.47	0.13	0.56	0.5	0.016	0.8	0.33	18600	20400	17500	26400	27900	17500	31500	22500	644.6	2574.3	4	0.0131	5.076

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	56%	33.2	54.78946	Ref	0.52	0.44	0.37	0.38	0.03	0.93	-0.13	201	200	205	219	244	167	326	154	644.6	2574.3	4	0.0128	4.983
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	65%	34.9	54.63872	Ref	0.43	0.15	0.59	0.43	0.013	0.94	0.34	2E+05	286000	3E+05	389000	383000	3E+05	5E+05	327000	644.6	2574.3	4	0.0262	10.19
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	91%	45.5	54.7189	Ref	0.66	0.28	0.6	0.31	-0.17	0.71	0.67	612	1040	870	1230	1100	691	1330	1280	1288	2574.3	2	0.0229	8.9
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	95%	53.7	54.71872	Ref	0.44	0.35	0.48	0.52	0.092	0.78	0.29	3300	3870	3930	4850	5500	3560	5980	4240	859.1	2574.3	3	0.0224	8.689
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	89%	43.6	54.71789	Ref	0.42	0.21	0.5	0.46	0.12	0.85	0.33	25800	28800	27100	37100	39700	27500	47700	33100	644.6	2574.3	4	0.0172	6.676
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	71%	36.4	54.72563	Ref	0.45	0.096	0.57	0.53	0.28	0.69	0.25	1630	1790	1520	2380	2540	1870	2600	1900	644.6	2574.3	4	0.017	6.583

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	95%	59	54.73845	Ref	0.49	0.19	0.54	0.53	-0.09	0.93	0.2	865	1020	902	1290	1410	799	1690	1020	859.1	2574.3	3	0.016	6.208
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	66%	35.2	54.7384	Ref	0.36	0.2	0.62	0.55	0.037	0.92	0.16	2000	2200	2140	3230	3390	2070	3980	2340	644.6	2574.3	4	0.016	6.21
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	80%	41.3	54.82409	Ref	0.62	0.24	0.81	0.34	-0.03	0.79	0.21	263	408	340	568	451	305	563	374	859.1	2574.3	3	0.0103	4.006
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT QHA VEG DcDI HVLk	59%	35.8	54.82409	Ref	0.51	0.15	0.58	0.38	0.26	0.92	0.2	250	342	290	438	419	336	554	334	859.1	2574.3	3	0.0103	4.006
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT qHA VEG DcDI HVLk	74%	38.8	54.4576	Ref	0.37	0.14	0.56	0.43	0.19	0.94	0.39	5140	6600	6090	9160	9220	6790	12000	8110	859.4	2575.3	3	0.0201	7.792
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN,tri B0JYN6 B0JYN6_BOVIN	qQT qHA VEG DcDI HVLk	87%	43.9	54.42578	Ref	0.53	0.24	0.53	0.39	0.19	0.91	0.095	3200	4020	3560	4890	4900	3710	6400	3610	859.4	2575.3	3	0.0219	8.502

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	68%	35.1	52.28708	Ref	0.22	-0.29	0.53	0.32	-0.06	0.55	0.56	1700	905	690	1360	1310	872	1390	1390	593.7	1778	3	0.0095	5.346	
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	88%	40.9	52.39079	Ref	0.31	0.3	0.55	0.53	0.064	0.72	0.48	7330	7910	8520	11300	12400	7800	12800	10800	890	1778	2	0.0184	10.35	
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	88%	41	52.33521	Ref	0.55	0.31	0.48	0.38	0.24	0.59	0.32	5240	5820	5360	6770	6970	5510	7320	6050	890	1778	2	0.0141	7.945	
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	90%	44.3	52.29999	Ref	No Values (-0.15175138)	No Values (-0.2694445678216)	Reference Missing (0.567186)	No Values (-0.5765186)	Reference Missing (0.8969834)	Reference Missing (0.93136525455)	Reference Missing (1.024455413)	No Values (-0.35410.15175138)	No Values (-0.2694445678216)	Reference Missing (0.56778216)	No Values (-0.5765186)	Reference Missing (0.8969834)	Reference Missing (0.93136525455)	Reference Missing (1.0244555)							
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	95%	57.1	52.21289	Ref	0.63	0.23	0.39	0.53	0.16	0.89	0.2	4E+05	646000	5E+05	668000	813000	5E+05	9E+05	584000	890	1778	2	0.0132	7.394	
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	95%	50.2	52.21289	Ref	0.53	0.36	0.64	0.49	-0.05	0.83	0.081	92100	119000	1E+05	157000	155000	93100	2E+05	106000	890	1778	2	0.0132	7.394	

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	95%	54.7	52.22797	Ref	0.65	0.2	0.44	0.5	0.14	0.82	0.38	28500	48600	38600	51200	58400	39800	66900	48800	890	1778	2	0.008	4.516
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	93%	45.5	52.25369	Ref	0.44	0.21	0.38	0.52	0.095	0.84	0.29	4470	4660	4310	5430	6610	4290	7530	5080	890	1778	2	0.0134	7.529
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	85%	40.8	52.21949	Ref	No Values (0.10951202)	No Values (-0.008181496)	Reference Missing (0.8136926)	Reference Missing (0.5631437)	No Values (-0.11938308)	Reference Missing (0.7397987)	Reference Missing (0.7064825)	No Values (-0.092878185)	No Values (0.10951202)	No Values (-0.008181496)	Reference Missing (0.8136926)	Reference Missing (0.5631437)	No Values (-0.11938308)	Reference Missing (0.7397987)	Reference Missing (0.7064825)	593.7	1778	3	0.0126	7.1
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	83%	38.7	52.18701	Ref	0.49	0.28	0.6	0.38	-0.13	0.86	0.45	7800	10100	9460	13300	12600	7690	16000	12000	890	1778	2	0.0122	6.843
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	95%	50.2	52.25369	Ref	0.47	0.32	0.55	0.43	-0.07	0.89	0.22	4030	4620	4530	5960	6030	3740	7580	4730	890	1778	2	0.0134	7.529
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	95%	49.4	52.22456	Ref	0.55	0.4	0.45	0.41	0.09	0.86	0.19	4000	5270	5170	6000	6430	4490	8000	4990	890	1778	2	0.0133	7.462

Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	85%	39.2	52.1218	Ref	0.39	0.39	0.46	0.47	0.047	0.83	0.4	938	1110	1210	1420	1580	1030	1850	1360	890	1778	2	0.0111	6.225
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	81%	37.9	52.18105	Ref	0.16	0.22	0.48	0.68	-0.34	1.1	0.31	247	246	276	372	470	203	585	331	890	1778	2	0.0089	5
Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	sp P12763 FETUA_BOVIN, tr B0JYN6 B0JYN6_BOVIN	tPIV GQP SIPG GPV R	82%	38	52.12505	Ref	0.4	0.34	0.73	0.31	0.06	0.78	0.25	215	236	246	360	299	219	375	259	890	1778	2	0.0105	5.888
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA6 A4ZYA6_SHEEP	dNLA EDI MR	72%	33.5	50.3841	Ref	-0.26	-0	-0.96	-0.42	-1	-0.23	-1.1	2E+05	99700	1E+05	74800	119000	69800	1E+05	69000	690.9	1379.7	2	0.0157	11.38
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA6 A4ZYA6_SHEEP	dNLA EDI MR	72%	33.7	50.5214	Ref	-0.28	-0.03	-0.82	-0.42	-0.86	-0.27	-0.97	67600	45000	58200	37700	54800	35300	55300	33900	690.9	1379.7	2	0.0108	7.847
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA6 A4ZYA6_SHEEP	dNLA EDI MR	70%	33.4	50.6405	Ref	-0.31	0.006	-0.92	-0.4	-0.81	-0.27	-1	1E+05	69700	93900	55300	87800	57400	87500	50800	690.9	1379.7	2	0.0086	6.254

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	dNLA EDI MR	53%	30.5	50.62285	Ref	-0.33	-0.27	-0.66	-0.49	-0.6	-0.29	-0.42	6860	5300	6000	5140	6390	5150	6690	6030	460.9	1379.7	3	0.0085	6.12
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eEAE STLQ SFR	94%	44.9	51.12048	Ref	-0.3	0.15	-1.2	-0.43	-1.1	-0.1	-1.2	3E+05	159000	2E+05	103000	195000	1E+05	2E+05	104000	800.9	1599.8	2	0.0126	7.841
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eEAE STLQ SFR	90%	40.9	51.12263	Ref	-0.58	0.029	-0.98	-0.16	-1.1	-0.2	-1.2	82400	39800	65900	36700	71700	33700	63600	32000	800.9	1599.8	2	0.0121	7.528
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eEAE STLQ SFR	95%	55	51.13432	Ref	-0.38	-0.26	-0.4	-0.64	-0.68	-0.31	-0.73	45000	28300	33400	34200	31700	27100	36300	26900	534.3	1599.8	3	0.0116	7.232
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSL LVDT HSK	95%	52.3	54.52961	Ref	-0.066	-0.22	-1	-0.37	-0.45	-0.22	-0.91	9890	9230	9010	5790	10100	8290	10200	6240	570.1	2276.2	4	0.028	12.28
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSL LVDT HSK	93%	50.4	54.54472	Ref	-0.062	-0.04	-0.79	-0.44	-0.97	-0.07	-0.91	13600	13300	14600	9710	13700	8250	16100	8940	759.7	2276.2	3	0.0248	10.88

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSLPLVDT HSK	89%	45.5	54.48412	Ref	-0.24	-0.09	-0.8	-0.36	-0.84	-0.06	-0.89	14000	11500	13900	9500	14200	8920	15900	8910	759.7	2276.2	3	0.0209	9.19
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSLPLVDT HSK	91%	47.9	54.45655	Ref	-0.25	-0.25	-0.94	-0.47	-0.63	-0.19	-0.62	9570	7030	7590	5300	8060	6310	8910	6590	759.7	2276.2	3	0.0198	8.703
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSLPLVDT HSK	95%	59.3	54.45718	Ref	-0.59	-0.19	-1	-0.28	-0.81	0.13	-0.93	13900	7720	11100	6990	12900	7780	15600	7420	759.7	2276.2	3	0.0196	8.624
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSLPLVDT HSK	95%	60.2	54.46396	Ref	-0.41	-0.02	-1	-0.29	-0.88	-0.06	-1.2	99100	57600	82300	45300	84000	48800	90300	39500	759.8	2276.2	3	0.0193	8.466
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSLPLVDT HSK	90%	46.2	54.4377	Ref	-0.52	-0.21	-0.67	-0.32	-0.56	-0.22	-0.81	14500	8740	11700	9580	13400	9950	13100	8660	759.8	2276.2	3	0.0183	8.057
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSLPLVDT HSK	95%	59.6	54.43298	Ref	-0.27	-0.28	-0.89	-0.39	-0.77	-0.17	-0.88	19900	12800	13800	10200	15900	10600	16800	10200	759.8	2276.2	3	0.018	7.899

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSL LP LVDT HSK	93%	47.6	54.43013	Ref	-0.21	-0.24	-1	-0.34	-0.9	-0.05	-0.54	3890	3210	3400	2250	3930	2330	4380	3100	570.1	2276.2	4	0.0175	7.665
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSL LP LVDT HSK	95%	55.2	54.43366	Ref	-0.5	-0.07	-1.2	-0.27	-0.91	0.051	-1.2	3E+05	162000	2E+05	118000	253000	1E+05	3E+05	122000	759.8	2276.2	3	0.0167	7.333
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSL LP LVDT HSK	95%	59.6	54.43366	Ref	-0.38	-0.34	-0.97	-0.22	-0.72	-0.15	-0.71	13200	8460	9390	6820	12600	7790	12100	8140	759.8	2276.2	3	0.0167	7.333
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSL LP LVDT HSK	95%	59.7	54.43375	Ref	-0.4	-0.09	-0.88	-0.35	-0.89	0.011	-0.87	7330	4970	6680	4340	6890	4130	8070	4350	759.8	2276.2	3	0.0165	7.254
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSL LP LVDT HSK	95%	50.2	54.40609	Ref	-0.35	-0.44	-0.82	-0.19	-0.94	-0.15	-0.73	13000	8030	8220	7060	12000	6280	11300	7520	570.1	2276.2	4	0.0163	7.138
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSL LP LVDT HSK	91%	45.3	54.39604	Ref	-0.11	-0.36	-0.89	-0.47	-0.9	-0.02	-0.93	45100	33700	30600	23800	35200	22800	43700	23200	570.1	2276.2	4	0.016	7.015

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSLPLVDT HSK	78%	39.9	54.39545	Ref	-0.24	-0.22	-0.84	-0.27	-0.9	-0.34	-0.29	12700	10800	11900	8690	14200	8030	12400	12700	759.8	2276.2	3	0.0156	6.859
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSLPLVDT HSK	74%	36.7	54.39246	Ref	-0.41	-0.19	-0.82	-0.14	-0.77	-0.32	-0.79	7660	4870	6180	4480	7920	4470	6380	4550	570.1	2276.2	4	0.0143	6.277
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSLPLVDT HSK	95%	63.5	54.40098	Ref	-0.32	-0.21	-1.1	-0.32	-0.59	-0.09	-0.83	6640	4620	5400	3280	6190	4480	6660	3940	759.8	2276.2	3	0.013	5.726
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSLPLVDT HSK	95%	57.5	54.35376	Ref	-0.57	-0.01	-1.1	-0.3	-0.86	-0.08	-0.95	18500	9530	15300	8130	15500	9180	16400	8920	759.8	2276.2	3	0.0127	5.567
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSLPLVDT HSK	89%	45.7	54.27036	Ref	-0.28	-0.29	-0.83	-0.4	-0.65	-0.23	-0.65	7590	5380	5770	4480	6620	4870	6820	5040	759.8	2276.2	3	0.0079	3.473
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSLPLVDT HSK	95%	57.7	54.23169	Ref	-0.31	-0.39	-0.79	-0.45	-0.58	-0.13	-0.39	4160	3350	3430	2920	4070	3260	4630	3860	570.1	2276.2	4	0.0057	2.518

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSL LP LVDT Hsk	95%	62.6	54.27145	Ref	-0.59	0.018	-1.2	-0.19	-1	0.012	-1.2	5690	2800	4640	2190	4970	2430	5220	2300	1139	2276.2	2	0.0053	2.346
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSL LP LVDT Hsk	64%	36	54.48148	Ref	-0.54	-0.08	-1.3	-0.19	-1.1	0.12	-0.87	1610	869	1300	614	1490	672	1690	842	1139	2276.2	2	0.0234	10.29
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSL LP LVDT Hsk	95%	63.4	54.39663	Ref	-0.43	-0.16	-0.99	-0.22	-0.82	0.017	-0.91	26400	17300	22600	14200	26800	15500	28800	15100	759.8	2276.2	3	0.0141	6.213
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSL LP LVDT Hsk	95%	61.5	54.35376	Ref	-0.48	-0.24	-0.75	-0.28	-0.7	0.007	-0.77	6890	4710	6010	4750	7230	4720	8070	4660	759.8	2276.2	3	0.0127	5.567
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTnL DSL LP LVDT Hsk	93%	50.7	54.54487	Ref	-0.32	-0.24	-0.65	-0.47	-0.78	-0.19	-0.55	12500	9230	10600	8960	11100	7830	12300	9560	760.1	2277.2	3	0.0316	13.88
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eTNL DSL LP LVDT HskR	58%	33.3	54.5118	Ref	-0.51	-0.37	-0.93	0.028	-0.57	0.053	-0.62	18300	15800	18900	14400	30700	17700	28500	17800	609.1	2432.3	4	0.0223	9.176

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eYQ DLLN Vk	95%	52.6	52.87851	Ref	-0.45	-0.08	-1.3	-0.23	-0.9	-0.06	-0.89	1E+05	71700	1E+05	47800	112000	61500	1E+05	64200	577.3	1729	3	0.0178	10.27
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eYQ DLLN Vk	95%	60.5	52.87271	Ref	-0.54	0.013	-1	-0.21	-0.88	-0.15	-0.93	1E+05	62000	98400	53200	104000	57200	99400	57400	865.5	1729	2	0.0164	9.507
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eYQ DLLN Vk	71%	36.5	52.88964	Ref	-0.67	-0.08	-1.1	-0.11	-0.67	-0.04	-0.81	44700	25900	42300	24000	51400	30400	49100	28600	577.3	1729	3	0.0152	8.776
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eYQ DLLN Vk	79%	38.8	52.88964	Ref	-0.48	-0.03	-1.1	-0.13	-0.78	-0.18	-1.1	3E+05	192000	3E+05	156000	331000	2E+05	3E+05	152000	577.3	1729	3	0.0152	8.776
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eYQ DLLN Vk	95%	64	52.81265	Ref	-0.56	-0.09	-0.97	-0.12	-0.94	-0.01	-0.98	34800	19900	29900	18300	36400	18000	35600	18100	865.5	1729	2	0.0135	7.819
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eYQ DLLN Vk	95%	63.5	52.93533	Ref	-0.45	-0.17	-0.95	-0.26	-0.84	0.065	-0.93	10700	6920	9120	5960	10600	6180	12100	6020	865.5	1729	2	0.0189	10.92

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	eYQ DLLN Vk	95%	52.4	52.89317	Ref	-0.37	-0.08	-0.8	-0.36	-0.89	-0.08	-0.93	33500	22400	29800	20200	30300	18300	33600	18400	577.3	1729	3	0.0168	9.73
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	fADL SEAA NR	94%	44.9	51.06316	Ref	-0.38	-0.07	-0.93	-0.34	-0.87	-0	-0.98	4E+05	276000	4E+05	230000	382000	2E+05	4E+05	222000	699.4	1396.7	2	0.0116	8.273
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	gTNE SLER	94%	48.1	50.07863	Ref	-0.38	-0.15	-0.37	-0.54	-0.38	-0.44	-0.65	19500	16000	20300	19600	19100	18700	18800	16100	403.9	1208.6	3	0.0082	6.796
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL k	95%	51.5	49.08775	Ref	-0.26	-0	-1.1	-0.3	-1	-0.13	-1	22200	15100	19600	10500	19800	10500	20300	11000	593.4	1777.1	3	0.0306	17.19
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL k	89%	40.6	48.9805	Ref	-0.42	0.34	-1.2	-0.39	-1.1	-0.32	-0.59	1390	944	1730	660	1290	676	1240	1020	593.4	1777.1	3	0.0258	14.51
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL k	95%	45.9	48.77849	Ref	-0.38	0.066	-1.2	-0.25	-1.1	-0.1	-1.1	6870	3980	5900	2680	5850	2810	5940	3000	889.6	1777.1	2	0.0204	11.45

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL k	95%	47	48.07549	Ref	-0.36	-0.21	-0.79	-0.39	-0.76	-0.18	-0.71	29000	19200	23100	17400	25300	17000	26500	18300	593.4	1777.1	3	0.0124	6.998
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL k	95%	51.2	47.95943	Ref	-0.49	0.019	-1.1	-0.19	-1.1	-0.11	-1.1	2270	1190	1840	926	1970	900	1900	974	889.6	1777.1	2	0.0104	5.825
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL k	69%	30.9	47.8651	Ref	-0.21	-0.22	-0.32	-0.29	-0.93	-0.38	-1.1	470	354	383	400	451	253	387	232	593.4	1777.1	3	0.0097	5.446
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL k	90%	40.6	48.62585	Ref	-0.27	-0.02	-1.2	-0.41	-0.96	-0.08	-1.1	2250	1410	1810	926	1710	1020	1960	948	593.4	1777.1	3	0.0192	10.81
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL k	75%	32.4	47.95943	Ref	-0.027	-0.7	-0.97	-0.48	-0.62	-0.51	-0.59	522	357	242	226	350	278	313	294	593.4	1777.1	3	0.0106	5.969
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL k	91%	40.8	47.46378	Ref	-0.45	-0.16	-0.96	-0.26	-1.1	-0.04	-0.95	3540	1960	2600	1680	2990	1490	3180	1670	593.4	1777.1	3	0.006	3.388

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL k	89%	37	47.38361	Ref	-0.24	-0.22	-0.98	-0.18	-1.1	0.15	-1.4	789	555	609	403	775	350	889	300	889.6	1777.1	2	0.0036	2.046
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL k	92%	41.5	47.42049	Ref	-0.4	-0.09	-0.54	-0.57	-0.9	-0.31	-0.6	562	357	482	395	425	296	465	379	593.4	1777.1	3	0.0025	1.431
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL k	86%	36.6	47.46369	Ref	-0.46	-0.13	-1	-0.26	-0.71	-0.3	-0.99	508	268	368	226	414	266	367	227	593.4	1777.1	3	0.0053	2.983
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL kGQ Gk	95%	52	47.88366	Ref	-0.82	-0.27	-1	0.041	-0.63	0.077	-0.4	1980	1350	2140	1420	3290	1800	3070	2190	613.9	2451.5	4	0.0326	13.29
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL kGQ Gk	95%	52.1	47.70322	Ref	-1	-0.31	-0.85	-0.018	-0.73	0.26	-0.57	4440	2430	4320	3340	6560	3510	7270	4040	613.9	2451.5	4	0.0279	11.4
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iLLAE LEQL kGQ Gk	60%	27.5	46.53309	Ref	-0.94	-0.21	-1	3E-04	-0.67	0.22	-0.41	1430	973	1750	1130	2510	1370	2660	1710	818.2	2451.5	3	0.0141	5.746

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	iSLPL PNFS SLNL R	83%	38.6	52.03019	Ref	-0.34	-0.11	-1.1	-0.26	-0.94	-0.03	-0.89	25500	17200	21800	12800	24400	13200	26100	14200	938.1	1874.1	2	#####	0.44
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	kVES LQEE IAFL k	80%	35.2	50.85922	Ref	-0.61	-0.07	-0.8	-0.33	-0.83	-0.14	-0.58	33700	19700	31000	21000	32100	19900	33400	24500	612.4	2445.4	4	0.0253	10.33
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	kVES LQEE IAFL k	92%	44.8	50.66404	Ref	-0.45	-0.05	-0.84	-0.35	-0.84	-0.08	-0.99	1650	1000	1430	928	1440	892	1580	836	816.2	2445.4	3	0.0211	8.629
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	kVES LQEE IAFL k	95%	52.1	50.47104	Ref	-0.59	-0.21	-1.1	-0.24	-0.93	-0.08	-0.41	7340	4110	5810	3450	7030	3790	7130	5640	612.4	2445.4	4	0.0172	7.03
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	kVES LQEE IAFL k	95%	55.8	50.2375	Ref	-0.52	-0.17	-0.76	-0.28	-0.91	-0.04	-0.69	1800	1120	1540	1150	1770	998	1910	1200	612.4	2445.4	4	0.0123	5.035
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	IGDL YEEE MR	91%	40.3	49.7064	Ref	-0.48	-0.07	-1	-0.25	-0.92	-0.07	-0.84	87700	52100	75100	43900	81900	45200	85100	49400	779.9	1557.7	2	0.0189	12.13

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	IGDL YEEE MR	95%	48	49.97264	Ref	-0.5	-0.1	-1.2	-0.2	-0.82	-0.09	-0.89	13400	7450	10700	5630	12300	7010	12100	6890	779.9	1557.8	2	0.014	8.996
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	IGDL YEEE MR	95%	48.6	50.02015	Ref	-0.46	0.06	-1.1	-0.22	-0.92	-0.1	-0.94	1E+05	68800	1E+05	53500	110000	58800	1E+05	60200	779.9	1557.8	2	0.0113	7.264
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	IGDL YEEE MR	95%	45.9	50.18139	Ref	-0.51	0.074	-1.2	-0.15	-1	-0.04	-0.93	16300	9960	16200	7600	17100	8240	16900	9010	779.9	1557.8	2	0.0101	6.481
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	IGDL YEEE MR	95%	44.9	50.20697	Ref	0.18	0.26	-1.1	-0.58	-1	-0.25	-0.9	2000	2570	2940	1290	2030	1320	2330	1480	779.9	1557.8	2	0.0091	5.853
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	IGDL YEEE mR	87%	37.8	49.53837	Ref	-0.39	0.063	-1.1	-0.22	-0.98	-0.13	-0.9	31400	20800	30900	15700	31300	16200	30500	17800	787.9	1573.7	2	0.0122	7.732
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	IGDL YEEE mR	70%	32.2	49.51988	Ref	-0.4	0.15	-1	-0.31	-0.94	-0.16	-0.91	20500	13900	22100	11100	19800	11200	20100	11900	787.9	1573.7	2	0.0115	7.275

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	ILQD SVDF SLAD AINT EFk	95%	75.3	55.47047	Ref	-0.48	-0.14	-0.87	-0.32	-0.63	-0.28	-0.43	3580	2450	3360	2280	3680	2600	3450	3090	912.2	2733.4	3	0.0267	9.753
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	ILQD SVDF SLAD AINT EFk	95%	65	55.41734	Ref	-0.37	-0.03	-1.3	-0.17	-1.1	-0.15	-0.78	450	274	375	170	422	198	389	251	912.2	2733.5	3	0.0157	5.727
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	ILQD SVDF SLAD AINT EFk	75%	40	55.39436	Ref	Value Missing (- 2.3710 272)	0.38	Value Missi ng (- 2.655 3156)	0.018	Value Missin g (- 2.5999 224)	0.74	Value Missin g (- 2.6518 15)	132	Value Missing (- 2.371027 2)	113	Value Missin g (- 2.6553 156)	109	Value Missi ng (- 2.599 9224)	163	Value Missing (- 2.651815)	912.2	2733.5	3	0.0116	4.257
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	ILQD SVDF SLAD AINT EFk	73%	39.4	55.42504	Ref	0.15	-0.31	Value Missi ng (- 2.978 3185)	0.028	Value Missin g (- 2.9229 252)	0.36	Value Missin g (- 2.9748 18)	205	132	Value Missing (- 2.9783 185)	105	Value Missi ng (- 2.922 9252)	163	Value Missi ng (- 2.974818)	187	912.2	2733.5	3	0.0135	4.926
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	83%	39.2	52.62214	Ref	-0.39	-0.18	-0.51	-0.38	-0.74	-0.23	-0.57	3510	2730	3420	3070	3700	2520	3730	2930	800.4	1598.8	2	0.0163	10.2
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	94%	49.8	52.4976	Ref	-0.51	-0.12	-0.5	-0.54	-0.61	-0.34	-0.46	8020	5450	7720	6660	7160	5950	7460	6830	534	1598.9	3	0.0142	8.877

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	70%	35.3	52.564	Ref	-0.36	-0.08	-0.86	-0.27	-0.89	-0.07	-0.91	27900	19700	26000	17000	28200	16000	29400	16300	800.4	1598.9	2	0.0132	8.229
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	80%	38	52.6261	Ref	-0.48	-0.17	-0.87	-0.38	-0.75	-0.05	-0.74	16700	10300	13900	9570	14900	10100	17000	10400	800.4	1598.8	2	0.0152	9.517
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	95%	52.5	52.68982	Ref	-0.29	-0.24	-0.79	-0.18	-0.7	-0.16	-0.78	5910	4840	5440	4170	7020	4260	6490	4170	534	1598.9	3	0.0109	6.814
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	89%	44.4	52.63477	Ref	-0.33	-0.24	-0.64	-0.42	-0.68	-0.18	-0.53	1540	1230	1420	1210	1560	1130	1670	1310	534	1598.9	3	0.008	4.995
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	63%	34	52.74075	Ref	-0.48	-0.05	-0.97	-0.27	-1	-0.04	-0.82	16100	9680	14200	8440	15100	7920	16200	9300	800.4	1598.9	2	0.0064	4.029
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	86%	42	52.7426	Ref	-0.23	-0.29	-0.57	-0.37	-0.55	-0.3	-0.72	1130	958	996	924	1170	900	1120	833	534	1598.9	3	0.0067	4.189

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	67%	34.9	52.78097	Ref	-0.55	-0.04	-0.93	-0.22	-0.96	-0.03	-0.87	3980	2320	3600	2170	3910	2040	4090	2260	800.4	1598.9	2	0.0045	2.804
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	95%	55.7	52.74366	Ref	-0.58	-0.45	-0.9	-0.23	-0.69	0.13	-0.74	731	429	507	416	733	466	856	464	534	1598.9	3	0.0069	4.302
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	52%	32.4	52.73129	Ref	-0.35	-0.62	-0.49	-0.28	-0.23	-0.59	-0.28	256	226	203	250	318	286	234	288	534	1598.9	3	0.0062	3.851
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	84%	40.7	52.53457	Ref	-0.39	-0.37	-0.5	-0.33	-0.57	-0.47	-0.28	2910	2320	2540	2620	3250	2400	2690	3030	539.3	1614.8	3	0.0102	6.292
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	58%	33.2	52.48993	Ref	-0.45	-0.17	-0.32	-0.44	-0.74	-0.35	-0.37	3950	3210	4230	4270	4360	3070	4230	4140	539.3	1614.9	3	0.0082	5.048
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	73%	35.6	52.36867	Ref	-0.36	-0.14	-0.93	-0.22	-0.81	-0.19	-0.67	2160	1550	1950	1270	2280	1320	2120	1520	808.4	1614.8	2	0.0147	9.123

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	79%	38.3	52.53263	Ref	-0.48	-0.24	-0.55	-0.62	-0.52	-0.24	-0.22	1080	845	1090	980	1030	965	1220	1230	539.3	1614.9	3	0.0093	5.735
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	66%	34.8	52.50271	Ref	0.36	0.31	-0.78	-0.85	-0.92	-0.62	-0.71	1990	3430	3580	1890	1990	1650	2120	1980	539.3	1614.9	3	0.0083	5.159
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	88%	42.9	52.67019	Ref	0.13	0.13	-0.53	-0.63	-0.64	-0.54	-0.83	2290	3240	3510	2490	2550	2230	2480	2010	539.3	1614.9	3	#####	0.039
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	94%	49.6	52.50527	Ref	-0.38	-0.15	-0.44	-0.17	-0.74	-0.31	-0.67	580	511	650	599	794	468	658	509	539.3	1614.9	3	0.0067	4.157
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATYR	54%	32.5	52.52647	Ref	-0.13	-0.61	-0.44	-0.35	-0.2	-0.67	-0.36	307	335	262	330	388	376	282	347	539.3	1614.9	3	0.0063	3.916
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATyR	82%	40.5	53.46388	Ref	-0.31	-0.3	-0.64	-0.36	-0.77	-0.17	-0.71	6400	4640	5090	4520	6040	3970	6300	4300	635.4	1903.1	3	0.0103	5.386

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	mAL DIEI ATyR	77%	39.1	53.73356	Ref	-0.41	-0.29	-0.62	-0.36	-0.72	-0.23	-0.66	18800	12400	14500	13000	17100	11700	17100	12600	640.7	1919.1	3	0.0138	7.176
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	nLQE AEE WYK	72%	36.9	53.31047	Ref	-0.38	-0.13	-1.1	-0.21	-0.9	-0.18	-0.77	2E+05	107000	1E+05	81800	162000	87500	2E+05	99500	640	1917	3	0.0165	8.622
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	nLQE AEE WYK	95%	56.1	53.3668	Ref	-0.49	0.026	-1.2	-0.3	-0.88	-0.19	-0.84	59700	32400	50200	24000	49500	28800	48700	30800	959.5	1917	2	0.015	7.811
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	nLQE AEE WYK	66%	33.8	53.42168	Ref	-0.4	-0.32	-0.86	-0.42	-0.6	-0.02	-0.68	7890	5350	6140	4740	7120	5480	8580	5360	480.3	1917	4	0.0027	1.404
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	nLQE AEE WYK	95%	67.6	53.35897	Ref	-0.52	0.081	-1.1	-0.22	-0.92	0.048	-0.95	8910	5730	9440	4580	9490	5110	10400	5180	959.5	1917	2	0.0132	6.862
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	nLQE AEE WYK	90%	45.1	53.15548	Ref	-0.57	-0.22	-0.84	-0.35	-0.52	-0.26	-0.77	11400	6110	8410	6130	9520	7380	9250	6450	640.3	1918	3	0.0183	9.56

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	nLQE AEE WYK	81%	40	53.1534	Ref	-0.35	-0.34	-0.77	0.005	-0.8	-0.21	-0.65	5410	4360	4740	3950	7460	3730	5860	4300	640.3	1918	3	0.0149	7.747
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qQYE SVA Ak	90%	41.4	51.01558	Ref	-0.53	-0.07	-1.2	-0.27	-0.7	-0.09	-1.1	6100	3150	4680	2350	5040	3280	5230	2600	655.8	1309.7	2	0.0107	8.172
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qQYE SVA Ak	68%	33.3	51.0149	Ref	-0.5	0.025	-0.69	-0.11	-1.1	-0.12	-1.2	5930	3550	5540	3790	6240	2670	5660	2570	655.8	1309.7	2	0.0106	8.08
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qQYE SVA Ak	61%	33.8	52.67028	Ref	-0.5	0.2	-1	-0.17	-0.96	-0.03	-1.2	3E+05	183000	3E+05	156000	309000	2E+05	3E+05	140000	544.6	1630.9	3	0.0143	8.787
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qQYE SVA Ak	94%	45.9	52.6167	Ref	-0.45	0.032	-1.2	-0.18	-0.91	-0.1	-0.94	21900	13600	20600	10100	22000	11600	21300	11800	816.5	1630.9	2	0.0095	5.824
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qQYE SVA Ak	93%	45.4	52.60422	Ref	-0.53	-0.02	-0.99	-0.2	-0.91	-0.04	-0.86	17300	10400	16200	9240	17600	9420	18000	10100	816.5	1630.9	2	0.0183	11.2

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVD QLT NDk	55%	30.3	50.3887	Ref	-0.68	0.41	-1.1	-0.57	-0.29	-0.44	-0.89	1190	708	1630	626	1020	1090	1020	743	674.4	1346.7	2	0.0132	9.759
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVD QLTn Dk	94%	47.3	52.93915	Ref	-0.35	0.034	-0.93	-0.39	-0.96	-0.19	-1.1	33700	20300	28700	16500	26400	15600	27600	14800	835.5	1668.9	2	0.0173	10.37
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVD QLTn Dk	95%	53.5	52.87598	Ref	-0.37	0.089	-0.92	-0.26	-1.1	-0.18	-0.99	13000	8420	12600	7020	12200	6070	11800	6700	835.5	1668.9	2	0.01	5.985
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVD QLTn Dk	95%	48.9	53.02164	Ref	-0.22	-0.02	-0.95	-0.4	-0.98	-0.19	-0.87	14700	10600	13200	7710	12500	7310	13200	8150	835.5	1668.9	2	0.0043	2.548
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVD QLTn DKA R	75%	38	53.50376	Ref	-0.47	-0.03	-1	-0.36	-0.97	0.11	-0.81	2E+05	125000	2E+05	102000	180000	1E+05	2E+05	119000	633	1896	3	0.0177	9.327
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVD QLTn DKA R	54%	33.2	53.41397	Ref	-0.22	0.081	-1.2	-0.19	-1	-0.12	-1	20500	15900	21200	9910	21800	10600	20800	11000	949	1896	2	0.0155	8.159

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVQ SLTc EVD ALK	95%	82	54.04866	Ref	-0.37	-0.16	-1.1	-0.2	-1	-0.1	-1	7910	4510	5650	3370	6840	3310	6660	3490	1045	2087.1	2	0.0202	9.688
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVQ SLTc EVD ALK	95%	67.9	54.01311	Ref	-0.47	-0.23	-1.2	-0.24	-1.1	0.01	-1.1	56900	28000	36000	20900	44100	22000	47900	22200	696.7	2087.1	3	0.0177	8.47
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVQ SLTc EVD ALK	95%	68	54.0431	Ref	-0.47	-0.07	-1.1	-0.22	-0.97	0.13	-1.3	40700	23300	33300	18300	37200	19300	43200	16100	696.7	2087.1	3	0.0171	8.211
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVQ SLTc EVD ALK	86%	43.3	54.06	Ref	-0.48	-0.37	-0.52	-0.32	-0.33	-0.12	-0.96	4360	3070	3590	3630	4600	3990	4830	2680	696.7	2087.1	3	0.0126	6.013
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVQ SLTc EVD ALK	95%	72.4	54.06801	Ref	-0.38	-0.03	-1	-0.3	-1.1	-0.11	-1	3890	2230	3080	1710	3160	1540	3300	1760	1045	2087.1	2	0.0107	5.129
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVQ SLTc EVD ALK	95%	64.4	54.0636	Ref	-0.19	-0.13	-0.76	-0.34	-0.96	-0.21	-0.76	7590	6020	6780	4920	7250	4120	7260	4900	696.7	2087.1	3	0.0122	5.841

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVQ SLTc EVD ALK	95%	53.7	54.08389	Ref	-0.25	-0.36	-0.37	-0.41	-0.59	-0.27	-0.6	629	575	578	648	691	534	694	548	696.7	2087.1	3	0.0062	2.953
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVQ SLTc EVD ALK	92%	48	54.04149	Ref	-0.39	-0.24	-1.3	-0.24	-0.79	0.059	-0.67	360	242	290	151	360	214	403	242	696.7	2087.1	3	0.0164	7.852
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	qVQ SLTc EVD ALK	51%	33.5	54.05199	Ref	-0.54	-0.09	-0.72	-0.55	-0.76	-0.06	-0.6	367	227	337	245	303	228	387	264	696.7	2087.1	3	0.0137	6.545
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	rQV QSLT cEVD ALK	65%	34.8	54.5845	Ref	-0.26	-0.36	-0.83	-0.19	-0.74	-0.02	-0.72	3480	2980	3020	2440	4210	2510	4310	2640	561.8	2243.2	4	0.0167	7.449
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	tLYT SSPG GVY ATR	95%	51.6	52.65897	Ref	-0.28	-0.12	-0.97	-0.28	-0.83	-0.06	-0.89	16100	12000	14600	9090	16100	9650	17100	9590	889	1775.9	2	0.0147	8.295
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	tLYT SSPG GVY ATR	74%	36.3	52.68816	Ref	-0.41	-0.2	-0.98	-0.18	-0.83	-0.02	-0.98	27300	17400	21800	14200	27300	15200	27900	14200	889	1775.9	2	0.0129	7.27

Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	tLYT SSPG GVY ATR	94%	46.9	52.64763	Ref	-0.33	-0.17	-1	-0.3	-0.89	-0.03	-0.97	6470	4150	5020	3090	5680	3290	6270	3230	889	1775.9	2	0.0167	9.398
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	tLYT SSPG GVY ATR	52%	32.1	52.67883	Ref	-0.53	-0.15	-1.1	-0.25	-0.78	-0.13	-0.83	13400	7180	10200	6000	11700	7110	11600	7110	889	1775.9	2	0.0128	7.203
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	tNEK VELQ ELnD R	87%	42.1	54.42526	Ref	-0.24	-0.37	-0.68	-0.36	-0.85	-0.1	-0.74	56800	42600	42100	38300	52700	32800	57500	36700	550	2196.2	4	0.0158	7.168
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	tNEK VELQ ELnD R	65%	36.6	54.45825	Ref	-0.5	0.054	-0.99	-0.26	-0.95	0.013	-0.98	50300	31600	50400	27400	50200	27200	55300	27700	733.1	2196.2	3	0.0168	7.666
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	vEVE RDN LAED IMR	78%	38.8	53.37497	Ref	-0.44	0.026	-1.3	-0.1	-0.92	0.074	-0.84	1E+05	82000	1E+05	53600	139000	68600	1E+05	75300	665	1992	3	0.0134	6.734
Vimentin (Fragment) OS=Ovis aries PE=2 SV=1	tr A4ZYA 6 A4ZYA6 _SHEEP	vEVE RDN LAED IMR	95%	66.9	53.41515	Ref	-0.45	-0.12	-0.64	-0.15	-0.84	-0.07	-0.56	1460	1310	1790	1400	2160	1170	2080	1480	997	1992	2	0.0124	6.239

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	aALTI DEK	60%	32.8	51.67911	Ref	0.58	-0.13	0.61	0.45	-0.15	0.86	-0.03	1E+06	1850000	1E+06	2E+06	2260000	1E+06	3E+06	1470000	490.3	1467.9	3	0.0104	7.09
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	aALTI DEK	76%	36.3	52.06899	Ref	0.38	0.18	0.48	0.41	0.13	0.63	0.087	18800	21500	20300	28000	29600	21200	31200	21300	734.9	1467.9	2	0.0241	16.43
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	aALTI DEK	57%	32.4	51.82403	Ref	0.58	0.22	0.58	0.38	-0.1	0.79	-0.05	43700	73700	62600	89900	86100	54000	1E+05	57800	490.3	1467.9	3	0.0143	9.725
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	aALTI DEK	75%	36.2	51.65852	Ref	0.47	0.16	0.68	0.32	-0.16	0.79	-0.04	31400	42400	37100	59900	51300	32100	64900	36200	490.3	1467.9	3	0.0095	6.477
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	aDLS GITK	88%	40.1	51.5687	Ref	0.52	0.15	0.42	0.28	0.048	0.63	0.22	33700	41300	34600	46900	47000	34900	54400	40800	706.9	1411.8	2	0.0248	17.52
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	aDLS GITK	82%	37.6	51.59182	Ref	0.48	0.059	0.41	0.35	-0.15	0.8	0.26	3E+05	344000	3E+05	399000	422000	3E+05	5E+05	358000	706.9	1411.8	2	0.0179	12.68

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	aDLS GITk	69%	34.3	51.28593	Ref	0.55	-0.03	0.53	0.23	-0.13	0.88	0.14	3E+05	444000	3E+05	533000	477000	3E+05	7E+05	403000	471.6	1411.8	3	0.0131	9.273
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	aDLS GITk	87%	41.2	51.61296	Ref	0.49	0.22	0.37	0.39	-0.14	0.74	0.15	28100	34200	30600	38100	42600	25800	49600	32600	471.6	1411.8	3	0.0253	17.89
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	aDLS GITk	92%	42.5	51.11618	Ref	0.42	0.18	0.46	0.37	0.098	0.57	0.2	17500	20400	18600	25500	26300	19000	27600	21100	706.9	1411.8	2	0.0046	3.267
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	aDLS GITk	72%	35.2	51.61296	Ref	0.44	0.45	0.31	0.25	-0.03	0.48	0.35	9030	9930	10800	11100	11700	8400	12500	11300	471.6	1411.8	3	0.0253	17.89
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	dFH VDE QTT Vk	92%	47.8	53.62837	Ref	0.64	0.23	0.58	0.4	-0.14	0.63	-0.08	2E+05	247000	2E+05	290000	282000	2E+05	3E+05	183000	643	1926	3	0.0153	7.916
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	dFH VDE QTT Vk	95%	48.7	53.60932	Ref	0.62	0.27	0.5	0.4	-0.3	0.72	-0.13	15500	20800	17600	23300	23900	12900	27200	15000	964	1926	2	0.0147	7.653

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	dFH VDE QTT Vk	95%	54.8	53.57169	Ref	0.45	0.25	0.56	0.43	-0.09	0.6	-0.14	20800	22000	20800	28900	29200	17700	29800	17800	964	1926	2	0.0166	8.598
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	gNT HTEI Lk	86%	39.5	51.9071	Ref	0.56	0.24	0.46	0.41	-0.18	0.77	0.019	24600	34800	30300	39600	42100	24400	49200	29100	811	1619.9	2	0.0141	8.725
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	gNT HTEI Lk	80%	37.2	51.79911	Ref	0.47	0.14	0.5	0.34	0.092	0.65	0.058	22500	26500	22900	33100	32700	24000	36800	24300	811	1619.9	2	0.0121	7.442
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	gnTH TEILk	94%	46.8	52.59847	Ref	0.57	0.13	0.48	0.41	-0.23	0.79	0.056	8630	12100	9680	13800	14600	8160	17300	10300	811.5	1620.9	2	0.0231	14.21
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	gnTH TEILk	95%	50.5	52.50683	Ref	0.58	0.13	0.47	0.36	-0.08	0.81	0.024	10900	15700	12500	17700	18100	11700	22600	13000	811.5	1620.9	2	0.0184	11.35
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	InDY VEk	50%	29.2	50.00134	Ref	0.28	0.34	0.17	0.36	0.17	0.52	0.23	24100	20500	23200	23100	29100	22300	29800	24100	593.3	1184.6	2	0.0083	6.978

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	IGMFDLH YcDk	63%	33.9	52.27102	Ref	0.67	0.046	0.5	0.32	-0.07	0.76	-0.03	5750	8320	5870	9020	8760	5830	10900	6250	666	1995	3	0.0089	4.451
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	IGMFDLH YcDk	57%	32.9	52.34363	Ref	0.56	0.085	0.37	0.26	-0.03	0.63	0.18	951	1030	806	1100	1130	803	1320	962	666	1995	3	0.0054	2.723
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	INNE LLAK	51%	29	49.44389	Ref	0.79	0.28	0.4	0.062	-0.05	0.53	-0.15	31500	38700	29400	35800	31200	25300	39400	24400	508.3	1521.9	3	0.0097	6.343
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	INNE LLAK	83%	35.9	49.33836	Ref	0.7	0.23	0.37	0.24	0.012	0.59	-0.07	11600	14700	11600	14300	14400	10700	16700	10500	762	1521.9	2	0.0064	4.231
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	IQQL EDkL NNE LLAK	54%	28	49.84932	Ref	0.61	-0.02	0.35	0.61	-0.09	0.4	0.16	232	263	184	267	352	189	277	234	671.2	2680.6	4	0.0079	2.958
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	ISISE TYDL k	93%	45.9	53.07855	Ref	0.58	0.035	0.47	0.32	-0.1	0.87	0.16	59200	94600	70100	106000	106000	69200	1E+05	85800	889	1776	2	0.0207	11.66

Alpha-1- antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_B OVIN	ISISE TYDL k	95%	49.2	53.0488	Ref	0.5	0.025	0.53	0.42	0.024	0.84	0.015	66300	97800	76600	122000	124000	82600	2E+05	85100	889	1776	2	0.0191	10.77
Alpha-1- antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_B OVIN	ISISE TYDL k	87%	42.6	53.02355	Ref	0.45	-0.08	0.43	0.39	-0.12	1.1	0.16	1E+05	214000	2E+05	257000	275000	2E+05	4E+05	212000	593	1776	3	0.0163	9.157
Alpha-1- antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_B OVIN	ISISE TYDL k	89%	44.5	53.01841	Ref	0.47	-0.32	0.55	0.32	-0.2	0.97	0.16	53100	62800	39600	80700	76200	46400	1E+05	61500	593	1776	3	0.0159	8.954
Alpha-1- antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_B OVIN	ISISE TYDL k	89%	42	52.9848	Ref	0.46	0.1	0.59	0.31	-0.22	0.92	0.19	14200	21800	18500	29100	26400	16000	36800	22000	889	1776	2	0.0156	8.782
Alpha-1- antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_B OVIN	ISISE TYDL k	95%	48.7	52.98517	Ref	0.63	0.13	0.43	0.43	-0.13	0.79	0.01	68000	104000	79700	110000	121000	71700	1E+05	82100	889	1776	2	0.0152	8.568
Alpha-1- antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_B OVIN	ISISE TYDL k	94%	49.7	52.98517	Ref	0.51	-0.03	0.59	0.32	-0.13	0.95	-0.03	2E+05	347000	3E+05	447000	409000	3E+05	6E+05	292000	593	1776	3	0.0152	8.549

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	ISISE TYDL k	87%	42.7	52.99643	Ref	0.2	0.21	0.53	0.55	-0.04	0.78	0.19	44800	55000	59700	83800	93900	54300	1E+05	66100	593	1776	3	0.0148	8.346
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	ISISE TYDL k	87%	42.6	53.01913	Ref	0.46	-0.24	0.47	0.43	-0.08	1	0.11	3E+05	373000	2E+05	457000	490000	3E+05	7E+05	355000	593	1776	3	0.0143	8.026
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	ISISE TYDL k	85%	41.4	52.97787	Ref	0.41	0.17	0.45	0.5	-0.12	0.82	0.11	8510	11300	10400	14300	16200	9230	18500	11200	593	1776	3	0.0123	6.894
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	ISISE TYDL k	76%	37	52.8582	Ref	0.63	0.025	0.32	0.44	0.043	0.7	0.2	6550	10000	7150	9870	11800	7820	12900	9050	889	1776	2	0.0114	6.441
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	ISISE TYDL k	91%	43.4	52.80043	Ref	0.61	0.24	0.4	0.43	-0.07	0.69	0.012	5560	8170	6870	8650	9740	6020	10600	6580	889	1776	2	0.0092	5.203
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	ISISE TYDL k	84%	41.1	52.79792	Ref	0.47	0.32	0.37	0.27	0.24	0.5	0.12	5890	6790	6670	7740	7970	6780	8490	6460	593	1776	3	0.0079	4.43

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	ISISE TYDL k	84%	40.8	52.76197	Ref	0.46	0.16	0.39	0.33	0.058	0.68	0.29	3690	4770	4210	5540	5860	4240	6830	5170	593	1776	3	0.0069	3.906
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	ISISE TYDL k	54%	32.9	52.82128	Ref	0.42	0.24	0.34	0.32	0.082	0.69	0.12	3540	3860	3690	4450	4810	3570	5670	3790	593	1776	3	0.0068	3.805
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	ISISE TYDL k	89%	42.4	53.09193	Ref	0.35	0.15	0.43	0.43	0.15	0.69	0.12	9050	10200	9630	13200	14500	10400	15800	10600	889	1776	2	0.0228	12.83
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	ISISE TYDL k	83%	40.3	52.81831	Ref	0.39	0.21	0.42	0.34	0.095	0.61	0.22	13400	15000	14400	18700	19500	14400	21500	16200	593	1776	3	0.0086	4.835
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	ISISE TYDL k	91%	43.8	52.80098	Ref	0.45	-0	0.43	0.38	-0.03	0.86	0.22	2770	3710	2950	4480	4770	3120	6060	3850	889	1776	2	0.0097	5.484
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	ISISE TYDL k	85%	41.2	52.76197	Ref	0.43	0.16	0.47	0.39	0.013	0.79	0.15	6910	9480	8510	11800	12400	8320	14900	9460	593	1776	3	0.0069	3.906

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_Bk	ISISE TYDL	85%	41.7	52.81229	Ref	0.5	0.28	0.39	0.43	0.1	0.51	-0	670	761	709	859	977	680	942	655	593	1776	3	0.0084	4.733
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_Bk	ISISE TYDL	90%	45.5	52.8583	Ref	0.29	0.39	0.43	0.3	0.027	0.76	0.15	645	741	860	989	1000	722	1250	813	593	1776	3	0.0112	6.287
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_Bk	IVDT FLED	86%	40.3	52.50993	Ref	0.62	0.028	0.44	0.31	-0.21	0.88	0.079	24200	34700	24900	37200	37600	22800	50800	28900	894	1786	2	0.0143	7.979
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_Bk	IVDT FLED	90%	44.3	52.37931	Ref	0.38	0.056	0.57	0.16	-0.29	0.75	0.48	41900	46300	40200	64500	53300	34100	73100	60400	596.3	1786	3	0.0118	6.589
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_Bk	IVDT FLED	89%	44.2	52.82493	Ref	0.62	0.027	0.3	0.37	-0.34	0.65	0.4	2620	3200	2300	3120	3620	1930	4000	3340	596.3	1786	3	0.0261	14.58
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_Bk	IVDT FLED	95%	52	52.5099	Ref	0.51	0.17	0.44	0.27	-0.16	0.85	0.059	3620	4490	3840	5220	5100	3310	6920	3980	894	1786	2	0.0171	9.546

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	IVDT FLED Vk	95%	51.3	52.39635	Ref	0.53	0.33	0.29	0.12	-0.15	0.46	0.6	2300	2770	2620	2860	2800	2020	3220	3530	596.3	1786	3	0.0108	6.069
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	IVDT FLED Vk	86%	41.7	52.26136	Ref	0.5	0.096	0.37	0.21	-0.22	0.76	0.4	1320	1550	1270	1720	1690	1100	2270	1760	596.4	1786	3	0.005	2.795
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	IVDT FLED Vk	92%	46.4	51.91962	Ref	0.55	0.22	0.37	0.028	-0.09	0.76	0.35	804	1030	885	1100	956	770	1450	1080	596.4	1786	3	0.0023	1.301
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	IVDT FLED Vk	71%	35.4	51.98621	Ref	0.66	0.3	0.28	0.11	-0.1	0.56	0.28	545	665	563	623	609	460	757	619	596.4	1786	3	#####	0.377
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	IVDT FLED Vk	90%	42.8	52.51195	Ref	0.59	0.23	0.5	0.37	-0.42	0.93	0.008	318	506	428	581	585	295	783	411	894	1786	2	0.0145	8.114
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	IVDT FLED Vk	74%	36.6	52.32356	Ref	0.55	-0.06	0.31	0.16	0.008	0.73	0.02	421	383	272	395	391	308	529	322	596.3	1786	3	0.0099	5.565

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	IVDT FLED Vk	67%	34.6	52.09684	Ref	0.44	0.27	0.45	-0.009	0.085	0.68	0.12	432	432	417	532	425	396	627	420	596.4	1786	3	#####	0.328
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	IVDT FLED Vk	85%	41.4	52.62017	Ref	0.21	-0.01	0.59	0.28	-0.16	0.59	0.32	278	209	195	332	294	189	334	274	596.3	1786	3	0.0237	13.24
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLYH SEAF SINF R	81%	39.5	52.87137	Ref	0.78	0.1	0.46	0.13	-0.3	0.75	0.075	21000	29700	20100	28900	25300	16400	35500	22100	634.7	1901	3	0.0143	7.536
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLYH SEAF SINF R	57%	33.3	52.74359	Ref	0.75	-0.23	0.6	0.19	-0.09	0.39	0.098	4720	5120	2820	5640	4660	3360	4900	3970	634.7	1901	3	0.018	9.46
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLYH SEAF SINF R	94%	46.3	52.85874	Ref	0.44	-0.03	0.74	0.23	0.048	0.69	0.1	3970	4870	3810	7310	5640	4350	7070	4680	951.5	1901	2	0.0128	6.728
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLYH SEAF SINF R	75%	37.6	53.08389	Ref	0.7	0.036	0.58	0.16	Value Missing (-0.21525963)	0.73	0.14	47000	68300	46800	76500	63000	Value Missing (-0.21525963)	85300	56300	634.7	1901	3	0.0021	1.085

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLYH SEAF SINF R	89%	44	52.85089	Ref	0.53	0.1	0.44	0.19	0.12	0.6	0.24	2760	3240	2610	3700	3430	2870	4160	3210	634.7	1901	3	0.0127	6.668
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLYH SEAF SINF R	95%	54.8	52.9477	Ref	0.66	0.089	0.43	0.19	Value Missing (-0.10983529)	0.77	0.099	17300	23200	17000	24100	22500	Value Missing (-0.10983529)	30800	19100	634.7	1901	3	0.0094	4.933
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLYH SEAF SINF R	95%	59.1	52.97408	Ref	0.62	0.051	0.57	0.23	-0.17	0.82	-0.03	2520	3380	2480	3980	3460	2290	4770	2610	951.5	1901	2	0.0085	4.478
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLYH SEAF SINF R	88%	43.6	52.95875	Ref	0.55	0.25	0.28	0.12	0.18	0.47	0.25	2720	2900	2560	2940	2890	2640	3370	2870	634.7	1901	3	0.0083	4.365
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLYH SEAF SINF R	65%	33.1	53.00852	Ref	-0.012	0.71	0.21	0.11	-0.18	0.34	0.68	4070	2840	5090	4020	4150	2960	4440	5570	476.2	1901	4	0.007	3.664
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLYH SEAF SINF R	60%	34	52.95684	Ref	0.28	0.28	0.44	0.23	0.28	0.12	0.54	1190	1090	1190	1490	1420	1280	1200	1590	634.7	1901	3	0.0081	4.255

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLYH SEAF SINF R	83%	40.5	53.14101	Ref	Reference Missing (0.4888076)	Reference Missing (0.16716973)	Reference Missing (0.5435641)	Reference Missing (0.15380296)	No Values (-0.121602334)	Reference Missing (0.84506625)	Reference Missing (0.14607329)	No Values (-0.09509742)	Reference Missing (0.4888076)	Reference Missing (0.16716973)	Reference Missing (0.5435641)	Reference Missing (0.15380296)	No Values (-0.121602334)	Reference Missing (0.84506625)	Reference Missing (0.14607329)	634.7	1901	3	#####	0.367
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLYH SEAF SINF R	71%	36.4	52.95684	Ref	0.62	0.31	0.4	0.38	0.098	0.43	0.27	291	472	412	492	537	385	507	450	634.7	1901	3	0.0081	4.255
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLYH SEAF SINF R	53%	32.9	52.98731	Ref	0.6	0.1	0.24	0.4	-0.09	0.62	0.23	458	547	420	519	639	395	678	513	634.7	1901	3	0.0087	4.555
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLyH SEAF SINF R	73%	36.4	54.38919	Ref	0.6	0.14	0.58	0.29	-0.2	0.59	0.11	5910	7300	5750	8790	7930	4910	8870	6320	552.3	2205.2	4	0.0141	6.369
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLyH SEAF SINF R	95%	51.5	54.37319	Ref	0.57	0.32	0.51	0.28	-0.06	0.64	0.12	6600	9610	8810	11300	10600	7270	12300	8590	552.3	2205.2	4	0.0138	6.26
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLyH SEAF SINF R	85%	41	54.38477	Ref	0.64	0.068	0.65	0.17	-0.14	0.61	0.11	50400	66100	48200	80800	64200	45200	79200	55700	552.3	2205.2	4	0.0133	6.024

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLyH SEAF SINF R	95%	56.4	54.37492	Ref	0.47	0.14	0.52	0.27	-0.14	0.84	-0.04	1330	1520	1310	1910	1780	1170	2400	1300	1104	2205.2	2	0.0034	1.541
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLyH SEAF SINF R	68%	35.2	54.38998	Ref	0.46	0.14	0.38	0.19	0.21	0.54	0.3	2820	3090	2680	3550	3440	3040	4000	3360	552.3	2205.2	4	0.0128	5.807
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLyH SEAF SINF R	72%	36.2	54.3893	Ref	0.54	0.001	0.55	0.29	-0.03	0.68	0.11	4160	4970	3720	6110	5610	3940	6700	4490	552.3	2205.2	4	0.0119	5.372
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLyH SEAF SINF R	86%	41.3	54.37273	Ref	0.67	-0.07	0.51	0.25	-0.15	0.93	0.035	73700	117000	75800	127000	117000	77700	2E+05	91300	552.3	2205.2	4	0.0116	5.263
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLyH SEAF SINF R	95%	55.9	54.38968	Ref	0.53	0.006	0.66	0.2	-0.33	0.82	0.13	6110	7520	5670	9990	8020	4870	11200	6930	552.3	2205.2	4	0.005	2.271
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLyH SEAF SINF R	84%	40.5	54.3647	Ref	0.55	0.13	0.43	0.26	-0.07	0.72	0.18	1460	1850	1500	2070	2040	1410	2550	1740	552.3	2205.2	4	0.0131	5.916

Alpha-1- antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P3495 5 A1AT_B OVIN	nLyH SEAF SINF R	73%	36.6	54.41387	Ref	0.52	0.33	0.35	0.39	-0.11	0.73	-0.07	2790	3340	3160	3620	4100	2530	4720	2690	552.3	2205.2	4	0.0075	3.377
Alpha-1- antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P3495 5 A1AT_B OVIN	nLyH SEAF SINF R	95%	50	54.38968	Ref	0.51	0.096	0.35	0.23	0.076	0.69	0.18	949	1050	857	1150	1160	913	1460	1020	552.3	2205.2	4	0.005	2.271
Alpha-1- antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P3495 5 A1AT_B OVIN	nLyH SEAF SINF R	76%	37.3	54.3647	Ref	0.5	0.12	0.36	0.38	-0.01	0.65	0.29	953	1180	981	1310	1460	972	1600	1240	552.3	2205.2	4	0.0131	5.916
Alpha-1- antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P3495 5 A1AT_B OVIN	nLYH SEAF SInF R	93%	48.7	52.38056	Ref	0.51	0.53	0.36	0.018	-0.49	0.74	-0.15	6710	5900	6510	6470	5630	3460	8460	4540	635	1901.9	3	0.0118	6.181
Alpha-1- antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P3495 5 A1AT_B OVIN	nLYH SEAF SInF R	94%	49.3	52.49609	Ref	0.48	0.36	0.68	0.2	-0.11	0.79	-0.04	1930	2950	2950	4130	3250	2300	4480	2500	635	1901.9	3	0.0105	5.503
Alpha-1- antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P3495 5 A1AT_B OVIN	nLYH SEAF SInF R	88%	41.4	52.55118	Ref	0.42	0.18	0.45	0.18	0.12	0.79	0.31	389	545	500	676	615	516	859	610	952	1901.9	2	0.0086	4.543

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	nLyH SEAF SinF R	53%	32.4	54.27721	Ref	0.33	0.14	0.49	0.23	0.13	0.48	0.43	13500	13700	13000	18600	17100	14000	18600	17800	552.5	2206.1	4	0.0162	7.35
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sPLF VGK	65%	30.6	48.86338	Ref	0.48	0.035	0.33	0.37	0.054	0.66	0.29	73900	85300	68000	93800	106000	74400	1E+05	90700	678.4	1354.8	2	0.0061	4.49
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sPLF VGK	80%	35.2	49.86005	Ref	0.5	-0.04	0.48	0.37	-0.11	0.84	0.13	2E+05	294000	2E+05	352000	360000	2E+05	5E+05	276000	678.4	1354.8	2	0.0138	10.15
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sPLF VGK	54%	28.7	48.82695	Ref	0.46	0.15	0.48	0.29	0.14	0.67	0.2	12700	16500	14500	20400	19700	15500	23500	16800	678.4	1354.8	2	0.0034	2.499
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sVLG DVGI TEVF SDR	95%	65.3	53.4818	Ref	No Values (0.524694)	No Values (0.4070006)	No Values (0.24040572)	No Values (0.09992675)	No Values (0.29579893)	No Values (0.23303242)	No Values (0.24390642)	No Values (0.32230407)	No Values (0.524694)	No Values (0.4070006)	No Values (0.24040572)	No Values (0.09992675)	No Values (0.29579893)	No Values (0.23303242)	No Values (0.24390642)	633.3	1897	3	0.0138	7.286
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sVLG DVGI TEVF SDR	95%	53.7	53.49462	Ref	0.54	0.096	0.37	0.43	-0.06	0.73	0.12	5110	6540	5200	7060	8140	5030	9090	5940	949.5	1897	2	0.0137	7.194

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sVLG DVGI TEVF SDR	95%	49.6	53.5093	Ref	0.55	0.16	0.2	0.29	-0	0.94	-0.02	33200	42000	34900	40300	47300	33600	67300	34500	949.5	1897	2	0.0117	6.161
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sVLG DVGI TEVF SDR	87%	41.7	53.49462	Ref	0.67	0.12	0.16	0.36	-0.02	0.8	0.31	2670	4580	3390	3920	4950	3330	6100	4320	949.5	1897	2	0.0137	7.194
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sVLG DVGI TEVF SDR	95%	56.1	53.57792	Ref	0.36	0.34	0.37	-0.014	-0.37	0.73	0.36	1240	1060	1130	1290	1090	746	1670	1280	633.3	1897	3	0.0109	5.753
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sVLG DVGI TEVF SDR	94%	50.6	53.58662	Ref	0.79	0.042	0.63	-0.027	-0.31	0.9	0.072	1340	2370	1530	2580	1810	1290	3120	1750	633.3	1897	3	0.0089	4.694
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sVLG DVGI TEVF SDR	95%	50.3	53.68151	Ref	0.58	0.15	0.45	0.46	-0.06	0.72	0.065	971	1460	1180	1630	1810	1100	1970	1240	949.5	1897	2	0.0056	2.975
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sVLG DVGI TEVF SDR	95%	71.4	53.5905	Ref	0.51	0.11	0.46	0.47	-0.08	0.78	0.15	2520	3850	3150	4510	5000	2980	5670	3640	949.5	1897	2	0.0088	4.623

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sVLG DVGI TEVF SDR	95%	63.9	53.57367	Ref	0.6	0.4	0.27	0.22	-0.12	0.46	0.37	735	916	865	890	948	652	1020	949	633.3	1897	3	0.0073	3.825
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sVLG DVGI TEVF SDR	95%	63.9	53.60754	Ref	0.44	0.4	0.13	0.19	0.31	0.58	0.16	391	416	440	410	471	446	564	418	633.3	1897	3	0.0093	4.884
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sVLG DVGI TEVF SDR	94%	47.4	53.56684	Ref	0.55	0.18	0.37	0.5	-0.06	0.75	0.22	445	751	630	807	978	576	1050	727	949.5	1897	2	0.0082	4.296
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	sVLG DVGI TEVF SDR	95%	52	53.62209	Ref	0.61	0.31	0.4	0.22	-0.06	0.86	0.2	326	618	547	651	634	456	901	566	949.5	1897	2	0.0055	2.884
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	vLDP NTVF ALV NYIS Fk	95%	61.2	53.52725	Ref	0.55	0.13	0.46	0.34	-0.31	0.81	0.31	573	843	683	962	980	546	1230	865	850.2	2547.5	3	#####	0.117
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	vLDP NTVF ALV NYIS Fk	58%	32.9	54.01922	Ref	0.52	-0.16	0.47	0.26	-0.27	0.88	0.4	423	546	370	645	616	373	860	611	637.9	2547.4	4	0.0153	5.994

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	vLDP NTVF ALV NYIS Fk	95%	63.7	53.64153	Ref	0.41	0.02	0.42	0.31	-0.24	0.89	0.44	1690	2210	1830	2710	2770	1650	3770	2740	850.2	2547.5	3	0.0038	1.483
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	vLDP NTVF ALV NYIS Fk	95%	56.9	53.93358	Ref	Reference Missing (0.73411065)	No Values (-1.3572731)	Reference Missing (0.4416717)	No Values (-1.664347)	Reference Missing (0.546101)	Reference Missing (1.5444213)	Reference Missing (0.46680635)	No Values (-1.4419696)	Reference Missing (0.73411065)	No Values (-1.3572731)	Reference Missing (0.4416717)	No Values (-1.664347)	Reference Missing (0.5466101)	Reference Missing (1.5444213)	Reference Missing (0.46680635)	850.2	2547.4	3	0.0127	5.003
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	vLDP NTVF ALV NYIS Fk	89%	45.7	54.01922	Ref	Reference Missing (1.0242769)	No Values (-1.4910004)	Reference Missing (0.6131763)	Reference Missing (1.0058495)	No Values (-1.60202)	Reference Missing (0.8944484)	Reference Missing (0.4893156)	No Values (-1.5756971)	Reference Missing (1.0242769)	No Values (-1.4910004)	Reference Missing (0.6131763)	Reference Missing (1.0058495)	No Values (-1.60202)	Reference Missing (0.8944484)	Reference Missing (0.46893156)	850.2	2547.4	3	0.0153	6.003
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	vLDP NTVF ALV NYIS Fk	77%	36.2	52.9219	Ref	0.62	0.16	0.6	0.032	-0.2	0.85	-0.17	223	271	214	326	242	181	389	191	713.9	2851.6	4	0.0128	4.5
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	vVN PTQ A	78%	35.4	50.72779	Ref	1	0.19	0.18	0.17	-0.46	0.8	0.19	359	830	499	556	608	343	857	558	516.8	1031.6	2	0.0086	8.309
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	yASS ANL HLpk	84%	40.8	52.53992	Ref	0.57	-0.03	0.48	0.32	-0.07	0.86	0.068	55000	76500	54800	87700	86400	57400	1E+05	65600	603.7	1808	3	0.0142	7.853

Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	yASS ANL HLPk	86%	40.4	52.51042	Ref	0.54	0.089	0.5	0.26	0.14	0.6	0.1	2570	3140	2500	3740	3480	2790	4030	2830	905	1808	2	0.0113	6.264
Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	sp P34955 A1AT_BOVIN	yASS ANL HLPk	50%	29.5	51.90343	Ref	0.45	0.005	0.53	0.41	-0.17	0.73	0.19	20400	23600	18900	30400	30900	18000	35300	24000	529.1	2112.2	4	0.0187	8.833
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P63258 ACTG_BOVIN,sp P63259 ACTG_RAT,sp P63260 ACTG_MOUSE,sp P63261 ACTG_HUMAN,tr D2I7P0 D2I7P0_AILME,tr F1PQL8 F1PQL8_CANFA,tr F6TII3 F6TII3_MACMU,tr F7AAK7 F7AAK7_HORSE,tr F7DIB7 F7DIB7_MONDO,tr F7I0	aGF AGD DAP R	77%	34.4	50.00078	Ref	-0.64	0.21	-0.54	-0.16	-0.23	-0.42	-0.17	8140	4280	8390	5620	8030	6690	6110	7220	640.8	1279.6	2	0.0114	8.939

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aGF AGD DAP R	92%	42.3	50.31627	Ref	-0.57	0.14	-0.56	-0.16	-0.14	-0.35	-0.23	2950	1650	2950	2040	2960	2610	2360	2550	640.8	1279.6	2	0.005	3.895
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aGF AGD DAP R	78%	34.6	50.01024	Ref	-0.73	0.093	-0.5	-0.21	-0.05	-0.42	-0.11	5E+06	2500000	5E+06	4E+06	4840000	5E+06	4E+06	4680000	640.8	1279.6	2	0.0118	9.221

Actin, cytoplasmic 2	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR	aGF AGD DAP R	95%	63.6	50.01807	Ref	Value Missing (- 0.1163 93514)	Value Missing (- 0.234 0868)	Value Missing (- 0.400 68176)	Value Missing (- 0.5411 609)	0.24	Value Missing (- 0.408 05507)	Value Missing (- 0.3971 811)	37900	Value Missing (- 0.116393 514)	Value Missing (- 0.234 0868)	Value Missing (- 0.4006 8176)	Value Missing (- 0.541160 9)	44300	Value Missing (- 0.4080 5507)	Value Missing (- 0.397181 1)	427.6	1279.6	3	0.0116	9.085
Actin, cytoplasmic 2	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR	aGF AGD DAP R	58%	30.4	49.98704	Ref	-0.61	0.035	-0.51	-0.034	-0.18	-0.18	-0.26	40100	23500	39800	30600	46900	37000	38600	36400	640.8	1279.6	2	0.0129	10.08

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P O_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aGF AGD DAP R	76%	34.2	50.22734	Ref	-0.57	-0.02	-0.6	-0.07	-0.1	-0.31	-0.11	31600	18600	29500	22200	35300	30100	27400	31100	640.8	1279.6	2	0.0111	8.658
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P O_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aGF AGD DAP R	86%	37.5	49.97954	Ref	-0.33	0.051	-0.41	-0.23	-0.23	-0.24	-0.15	11100	8650	12200	9970	12400	10800	11300	11900	640.8	1279.6	2	0.0128	9.986

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG R	53%	30.7	50.92268	Ref	0.073	0.21	-0.33	-0.073	-0.27	-0.84	582)	2560	1890	2260	1750	2290	1750	1230	2)	417.3	1248.7	3	0.0073	5.876
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	55%	31.4	51.27205	Ref	-0.49	0.024	-0.48	-0.19	-0.17	-0.39	0.13	24200	17400	27000	21400	28800	25500	22800	32700	501.6	1501.9	3	0.0189	12.56

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	83%	38.8	51.35877	Ref	-0.46	-0.07	-0.38	-0.12	-0.01	-0.65	0.12	45300	33900	48300	43700	57700	54400	36400	61600	501.6	1501.9	3	0.0104	6.949
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	90%	43.8	51.15524	Ref	-0.76	0.23	-0.67	-0.08	-0.15	-0.57	0.13	15500	8610	18600	11200	18500	15400	12000	19400	501.6	1501.9	3	0.009	5.991

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	57%	31.7	51.22448	Ref	-0.7	0.041	-0.54	-0.12	-0.07	-0.5	0.17	1E+05	66000	1E+05	89700	133000	1E+05	92900	147000	501.6	1501.9	3	0.0101	6.71
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	79%	34.6	50.79778	Ref	-1	0.13	-0.64	-0.14	-0.11	-0.6	0.48	10800	5770	13700	9080	14100	12600	9350	19700	376.5	1501.9	4	0.0037	2.436

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	81%	38	51.38606	Ref	-0.59	-0.05	-0.45	-0.2	-0.05	-0.37	0.13	33200	22200	35000	29900	39200	37800	31700	44600	501.6	1501.9	3	0.0135	8.966
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	77%	34.7	51.35873	Ref	Value Missing (- 0.8241 942)	-0.2	-0.85	-0.18	-0.08	-0.43	0.68	3110	Value Missing (- 0.824194 2)	3290	2350	4130	3860	3170	6780	376.5	1501.9	4	0.0107	7.146

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	52%	31	51.35769	Ref	-0.59	-0.09	-0.48	-0.048	-0.17	-0.4	0.24	2E+05	136000	2E+05	179000	266000	2E+05	2E+05	294000	501.6	1501.9	3	0.0102	6.77
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	71%	34.8	51.3533	Ref	-0.38	0.069	-0.44	-0.12	-0.22	-0.4	0.007	12700	10300	15200	11900	16500	13400	12400	16300	501.6	1501.9	3	0.011	7.329

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	84%	39.5	51.35877	Ref	-0.77	-0.09	-0.42	0.02	-0.15	-0.63	0.17	8E+05	419000	7E+05	653000	975000	8E+05	6E+05	982000	501.6	1501.9	3	0.0104	6.89
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	53%	29.4	51.31583	Ref	Value Missing (- 0.6964 784)	0.033	-0.96	-0.084	0.052	-0.6	0.34	32300	4)	35600	20200	40700	39000	26000	49200	376.5	1501.9	4	0.0101	6.747

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	54%	29.6	51.35708	Ref	-0.71	-0.07	-0.24	-0.36	-0.11	-0.45	0.32	2810	1780	3000	3010	3030	3150	2600	4400	376.5	1501.9	4	0.011	7.306
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	77%	34.6	51.19249	Ref	-0.51	0.22	-0.28	-0.12	0.098	-0.34	Value Missin g (- 0.8606 791)	3270	2200	3970	3130	3860	3930	3030	Value Missing (- 0.860679 1)	376.5	1501.9	4	0.0076	5.044

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	82%	38.2	51.15174	Ref	-0.43	-0.08	-0.47	-0.2	-0.17	-0.26	0.095	1700	1270	1770	1510	2010	1790	1750	2230	501.6	1501.9	3	0.0091	6.051
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	70%	34.3	51.19246	Ref	-0.6	-0.02	-0.51	-0.27	-0.11	-0.44	0.19	7240	4360	7050	5660	7340	7190	5940	9130	501.6	1501.9	3	0.0074	4.953

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	84%	39.2	51.15174	Ref	-0.64	-0.11	-0.46	-0.23	-0.11	-0.42	0.24	2030	1220	1900	1680	2160	2060	1730	2710	501.6	1501.9	3	0.0091	6.051
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	aVFP SIVG RPR	89%	42.4	51.19351	Ref	-0.3	-0.07	-0.48	-0.15	-0.14	-0.16	-0.17	1040	851	1090	914	1270	1110	1150	1130	501.6	1501.9	3	0.008	5.313

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	cDV DIR	79%	31.8	46.7374	Ref	0.17	-0.43	-0.03	-0.39	-0.72	0.089	-0.76	4E+05	368000	3E+05	389000	335000	2E+05	4E+05	234000	535.8	1069.5	2	0.0105	9.78
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	cDV DIR	53%	26.8	47.22107	Ref	0.11	-0.27	-0.16	-0.32	-0.77	0.14	-0.71	42100	38300	32000	38900	38100	24500	47800	26400	535.8	1069.5	2	0.009	8.416

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	dLTD YLM k	93%	45.9	52.86007	Ref	-0.007	-0.28	-0.35	-0.18	-0.74	0.18	-0.81	54900	41600	37500	39900	49500	29300	58100	29000	803.9	1605.9	2	0.0168	10.47
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	dLTD YLM k	85%	39.9	52.79222	Ref	0.055	-0.21	-0.47	-0.2	-0.7	0.09	-0.83	54600	41400	37400	35000	46700	28700	51900	27300	803.9	1605.9	2	0.0102	6.37

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	dLTD YLM k	81%	38.3	52.77107	Ref	0.025	-0.22	-0.36	-0.16	-0.62	0.026	-0.55	8330	7160	6560	6670	8470	5350	8770	5820	803.9	1605.9	2	0.0082	5.076
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	dLTD YLM k	82%	38.7	52.75512	Ref	0.063	-0.28	-0.35	-0.21	-0.61	0.026	-0.72	16200	13000	11100	11900	14400	9490	15500	9130	804	1605.9	2	#####	0.015

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P O_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	dLTD YLmk	80%	38	52.8512	Ref	0.0029	-0.17	-0.38	-0.18	-0.58	0.11	-0.81	14100	11500	11100	10700	13600	8970	15100	7970	811.9	1621.9	2	0.0092	5.699
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P O_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	dSYV GDE AQS k	95%	55.4	52.0709	Ref	-0.88	1.2	-1.6	-1.4	-0.91	-1.3	1.1	2530	3090	14000	2270	2980	3570	2820	14500	904	1805.9	2	0.0238	13.16

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	dSYV GDE AQS k	95%	56.7	52.29477	Ref	-0.67	-0.02	-0.67	-0.005	-0.11	-0.29	-0.08	4E+05	230000	4E+05	281000	490000	4E+05	4E+05	420000	904	1805.9	2	0.0166	9.178
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	dSYV GDE AQS k	95%	58.7	52.29569	Ref	-0.7	0.21	-0.47	-0.08	-0.02	-0.38	-0.45	2E+05	80200	2E+05	114000	165000	2E+05	1E+05	116000	904	1805.9	2	0.0161	8.901

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	dSYV GDE AQS k	89%	43.8	52.30595	Ref	-0.39	-0.26	-0.93	-0.027	0.12	-0.36	-0.28	4E+05	233000	3E+05	195000	401000	4E+05	3E+05	304000	603	1805.9	3	0.0155	8.567
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	dSYV GDE AQS k	95%	52.1	52.30587	Ref	-0.95	0.09	-0.4	-0.11	-0.03	-0.19	-0.21	6E+05	265000	6E+05	474000	636000	6E+05	6E+05	538000	603	1805.9	3	0.0153	8.467

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7IO	dSYV GDE AQS k	95%	50.3	52.32887	Ref	-0.63	-0.02	-0.52	-0.082	-0.12	-0.23	-0.36	40800	20700	34300	27300	40700	34500	33500	30400	904	1805.9	2	0.0141	7.827
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7IO	dSYV GDE AQS k	95%	54.5	52.24787	Ref	-1	0.088	-0.37	-0.053	0.034	-0.26	-0.31	83900	37300	86800	71000	97400	90300	76800	73700	603	1805.9	3	0.0171	9.48

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	dSYV GDE AQS k	95%	52.3	52.30559	Ref	-0.73	0.13	-0.54	-0.062	-0.05	-0.3	-0.3	11500	6070	11900	8400	12900	11300	9980	9890	904	1805.9	2	0.0154	8.502
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	dSYV GDE AqSk	88%	42	51.83987	Ref	-0.44	-0.1	-0.48	-0.19	-0.17	-0.28	-0.05	58100	37600	51500	44500	59800	53100	51400	59600	603.3	1806.9	3	0.017	9.38

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	eEEI AALV IDnG SGM ck	67%	32.6	50.03473	Ref	-0.49	0.14	0.017	-0.46	-0.71	-0	-0.35	176	109	184	190	150	111	188	147	724.7	2171	3	0.0162	7.467
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	eEEI AALV IDnG SGM ck	95%	68.4	50.39835	Ref	-0.62	-0.04	-0.75	-0.37	-0.33	-0.25	0.048	358	159	259	178	254	228	251	308	724.7	2171	3	0.0093	4.262

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	eEEI AALV IDnG SGM ck	87%	40	50.23668	Ref	-0.062	-0.36	-0.88	-0.41	0.28	-0.65	-0.43	234	150	132	104	158	223	122	141	724.7	2171	3	0.0117	5.367
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	eITA LAPS TMk	93%	48.6	52.72269	Ref	0.067	-0.56	-0.37	-0.086	-0.55	0.19	-0.84	89400	73200	51300	65700	88400	55800	97700	47400	590.7	1769	3	0.0137	7.712

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	eITA LAPS TMk	82%	38.4	52.467	Ref	-0.014	-0.29	-0.3	-0.26	-0.54	0.077	-0.46	10500	9010	8090	9020	10200	7350	11700	8020	885.5	1769	2	0.0062	3.5
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	eITA LAPS TMk	87%	42.8	52.78441	Ref	-0.089	-0.18	-0.26	-0.13	-0.77	0.18	-0.34	29500	28100	28500	30400	36500	20600	41300	28600	590.7	1769	3	0.0161	9.068

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	eITA LAPS Tmk	94%	46.8	52.56145	Ref	-0.03	-0.43	-0.24	-0.16	-0.61	0.076	-0.4	4320	3650	2990	3830	4470	2850	4800	3420	885.5	1769	2	0.0101	5.714
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	eITA LAPS Tmk	80%	39.2	53.07128	Ref	0.014	-0.52	-0.19	-0.16	-0.49	0.13	-0.5	22000	20700	15500	21900	24700	17100	27500	17600	596	1785	3	0.0171	9.6

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	eITA LAPS Tmk	56%	33	52.90153	Ref	0.11	-0.33	-0.38	-0.18	-0.51	0.14	-0.65	7730	7490	5980	6520	8210	5710	9400	5380	893.5	1785	2	0.0125	7.027
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	g LTL k	71%	29.8	46.40968	Ref	-0.53	0.18	-0.35	-0.093	-0.17	-0.44	-0.32	36800	23200	41100	32000	42100	34900	30100	32500	418.3	1251.8	3	0.0014	1.139

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7IO	g LTL k	56%	27.8	47.65691	Ref	-0.44	0.031	-0.33	-0.14	-0.12	-0.38	-0.2	33100	23300	35100	30700	38500	34200	29800	33400	626.9	1251.8	2	0.0256	20.44
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7IO	g LTL k	67%	29	46.40968	Ref	-0.36	-0.11	-0.34	-0.22	-0.16	-0.23	-0.3	5130	3410	4390	4200	5030	4590	4580	4330	418.3	1251.8	3	#####	0.253

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P O_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	gYSF TTTA ER	84%	37.2	50.43276	Ref	0.23	-0.24	-0.3	-0.29	-0.69	0.057	-0.85	4E+05	377000	3E+05	318000	353000	2E+05	4E+05	217000	718.9	1435.7	2	0.0096	6.695
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P O_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	gYSF TTTA ER	85%	37.7	50.40721	Ref	0.033	-0.33	-0.15	-0.29	-0.34	-0.13	-0.33	9190	9090	7650	9740	9750	8230	9940	8620	718.9	1435.7	2	0.0102	7.113

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	92%	47.2	53.37803	Ref	-0.52	-0.19	-0.31	-0.13	-0.32	-0.28	-0.21	37900	19900	27300	28200	35200	27000	29000	30200	594	1779	3	0.0185	10.38
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	95%	55	53.39978	Ref	-0.55	0.041	-0.52	-0.16	-0.23	-0.26	-0.34	78900	40800	66600	50700	72000	59600	61000	57200	594	1779	3	0.0156	8.741

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	95%	62.6	53.37264	Ref	-0.59	-0.01	-0.53	-0.072	-0.17	-0.49	-0.21	64000	31700	51600	40200	61000	49800	41600	50200	594	1779	3	0.0192	10.8
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	59%	32.4	53.38156	Ref	-0.45	-0.1	-0.44	-0.26	-0.15	-0.3	-0.03	23600	15000	20700	18400	22900	21700	20300	24400	445.7	1779	4	0.0169	9.475

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	95%	54.8	53.38156	Ref	-0.67	0.16	-0.52	-0.12	-0.14	-0.28	-0.23	5160	2860	5480	3840	5610	4830	4570	4690	890.5	1779	2	0.0168	9.446
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	91%	44	53.36868	Ref	-0.69	-0.18	-0.53	-0.09	-0.17	-0.29	-0.03	36700	17800	27500	24100	36100	29900	28700	34000	890.5	1779	2	0.0179	10.06

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	93%	49.3	53.41365	Ref	-0.64	-0.26	-0.39	-0.071	-0.22	-0.49	-0.14	2E+05	100000	1E+05	145000	200000	2E+05	1E+05	172000	594	1779	3	0.0161	9.045
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	79%	39.1	53.4127	Ref	-0.63	-0.23	-0.42	-0.06	0.072	-0.52	-0.13	1E+05	56800	81500	80500	114000	1E+05	75200	97500	594	1779	3	0.0159	8.944

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	95%	58.9	53.38793	Ref	-0.91	-0.04	-0.42	-0.008	-0.21	-0.58	-0.09	5E+05	181000	4E+05	309000	454000	3E+05	3E+05	388000	594	1779	3	0.015	8.421
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	95%	53.4	53.36742	Ref	-0.68	0.04	-0.42	-0.018	-0.18	-0.31	-0.28	24300	12800	22800	18600	27100	21100	20200	20500	890.5	1779	2	0.0111	6.232

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	92%	47.5	53.39978	Ref	-0.61	-0	-0.54	-0.043	-0.16	-0.51	-0.36	4E+05	192000	3E+05	246000	383000	3E+05	3E+05	278000	594	1779	3	0.0156	8.741
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	79%	37.2	53.38658	Ref	-0.73	-0.17	-0.69	-0.073	-0.07	-0.21	-0.14	2E+05	98400	2E+05	123000	208000	2E+05	2E+05	181000	445.7	1779	4	0.0149	8.374

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	78%	38.1	53.4347	Ref	-0.63	0.024	-0.42	-0.056	-0.16	-0.36	-0.24	10100	5440	9310	7690	10900	8870	8050	8660	890.5	1779	2	0.0102	5.749
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	91%	46.9	53.31596	Ref	-0.32	-0.13	-0.47	-0.23	-0.08	-0.26	-0.19	6190	4400	5430	4820	6290	6090	5600	5850	594	1779	3	0.0029	1.646

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG Qk	90%	45.2	53.30536	Ref	-0.18	-0.06	-0.51	-0.29	-0.22	-0.43	-0.3	4430	2950	3470	2860	3660	3340	3030	3290	594	1779	3	#####	0.297
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VmV GMG Qk	76%	38.2	53.25544	Ref	-0.67	0.17	-0.8	-0.21	-0.27	-0.38	0.25	58800	33900	65600	37600	62400	52300	50400	77600	599.3	1795	3	0.0191	10.63

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VmV GMG Qk	75%	37.9	53.35187	Ref	-0.92	0.17	-0.49	-0.14	-0.08	-0.42	-0.16	1E+05	57700	1E+05	94900	133000	1E+05	1E+05	119000	599.3	1795	3	0.0167	9.306
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VmV GMG Qk	94%	50.9	53.31217	Ref	-0.75	-0	-0.39	0.059	-0.07	-0.37	-0.45	6E+05	292000	5E+05	454000	685000	5E+05	5E+05	437000	599.3	1795	3	0.0129	7.167

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GmG Qk	83%	40.9	53.25733	Ref	-0.73	0.066	-0.51	-0.088	-0.22	-0.37	-0.01	38800	20200	38000	28500	42200	33600	31700	40400	599.3	1795	3	0.0187	10.42
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GmG Qk	91%	46	53.25745	Ref	-0.62	0.041	-0.34	-0.062	-0.1	-0.4	-0.29	40300	22900	39300	33900	45300	38600	32600	35000	599.3	1795	3	0.0185	10.32

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GmG Qk	84%	41.4	53.35187	Ref	-0.98	0.081	-0.39	-0.059	-0.24	-0.27	-0.17	81000	33100	74800	60700	84000	64700	66000	70500	599.3	1795	3	0.0167	9.306
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GmG Qk	54%	31.6	53.30578	Ref	-0.36	0.017	-0.63	-0.31	0.029	-0.35	-0.36	1E+05	90500	1E+05	92000	127000	1E+05	1E+05	110000	449.7	1795	4	0.0149	8.295

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GmG Qk	89%	44.5	53.28559	Ref	-0.39	0.17	-0.42	-0.36	-0.12	-0.32	-0.18	19300	14100	22500	16800	19400	19900	18100	19800	599.3	1795	3	0.0138	7.668
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GmG Qk	66%	35.2	53.39294	Ref	-0.69	0.16	-0.46	-0.17	-0.09	-0.38	-0.29	8060	4080	7980	5850	7860	7300	6220	6550	898.5	1795	2	0.0091	5.082

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GmG Qk	71%	36.2	53.38518	Ref	-0.77	-0.07	-0.39	-0.11	-0.06	-0.26	-0.25	2790	1330	2330	2100	2820	2540	2310	2310	898.5	1795	2	0.0073	4.068
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	hQG VMV GMG qk	95%	50.2	53.46079	Ref	-0.6	-0.05	-0.39	-0.08	-0.12	-0.32	-0.09	4340	2650	4200	3720	5090	4330	3950	4570	891	1780	2	0.0046	2.595

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	kDLY ANT VLSG GTT MYP GIAD R	76%	38.7	55.58748	Ref	0.024	-0.42	-0.15	-0.4	-0.39	-0.15	-0.2	3230	2940	2340	3180	2940	2580	3200	3070	738.6	2950.5	4	0.0233	7.894
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	kDLY ANT VLSG GTT MYP GIAD R	95%	59.4	55.57691	Ref	0.043	-1.2	-0.14	0.037	-0.73	0.16	-0.79	2600	1890	880	2020	2530	1300	2520	1290	984.5	2950.5	3	0.0204	6.899

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	kDLY AnTV LSGG TTM YPGI ADR	95%	77.3	55.48924	Ref	0.17	-0.56	-0.25	-0.26	-0.26	-0.1	-0.48	2000	2020	1320	1840	2020	1760	2050	1570	984.9	2951.5	3	0.017	5.763
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	kDLY AnTV LSGG TTM YPGI ADR	51%	34.9	55.43742	Ref	0.19	-0.75	-0.07	-0.26	-0.22	-0.14	-0.31	1610	1920	1090	1960	1890	1700	1870	1660	984.9	2951.6	3	0.0015	0.496

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	qEYD ESGP SIVH R	87%	41.6	51.66362	Ref	-0.005	-0.21	-0.26	-0.31	-0.27	-0.17	-0.36	15000	13900	13100	14100	15100	13500	15200	13200	607.6	1819.9	3	0.0136	7.473
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	sYEL PDG QVIT IGNE R	84%	42.1	53.97831	Ref	0.11	-0.7	-0.07	-0.28	-0.11	0.006	-0.62	8910	9520	5900	10200	9740	9560	10800	6990	699	2094.1	3	0.0129	6.171

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	SYEL PDG QVIT IGNE R	93%	46.3	54.06613	Ref	-0.011	-0.29	-0.28	-0.22	-0.47	0.18	-0.62	3850	3540	3170	3570	4110	3020	4930	2820	1048	2094.1	2	0.0061	2.898
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	SYEL PDG QVIT IGNE R	84%	42.1	53.97912	Ref	0.031	-0.28	-0.6	-0.26	-0.3	0.013	-0.05	2590	2860	2500	2260	3140	2660	3460	3290	699	2094.1	3	0.0148	7.044

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	SYEL PDG QVIT IGNE R	95%	58.7	54.02767	Ref	0.13	-0.31	-0.38	-0.27	-0.73	0.13	-0.85	1830	1460	1170	1250	1480	940	1790	897	1048	2094.1	2	0.011	5.227
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	tTGI VMD SGD GVT HTV PIYE GYAL PHAI LR	95%	69.4	55.9806	Ref	0.019	-0.34	-0.66	-0.26	-0.6	0.26	-0.32	2830	2490	2110	1890	2750	1900	3600	2390	872.7	3486.8	4	0.0328	9.416

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	tTGI VMD SGD GVT HTV PIYE GYAL PHAI LR	95%	78.2	55.91866	Ref	0.03	-0.27	-0.11	-0.73	-0.62	0.46	-0.59	402	415	366	459	329	310	687	328	872.7	3486.8	4	0.0162	4.656
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	tTGI VMD SGD GVT HTV PIYE GYAL PHAI LR	63%	31.9	55.7202	Ref	0.1	-0.64	-0.37	-0.23	-0.41	-0.01	-0.28	2660	2440	1580	2130	2600	2000	2760	2270	759.2	3791	5	0.02	5.266

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	tTGI VMD SGD GVT HTV PlyE GYAL PHAI LR	84%	41.3	55.50587	Ref	-0.094	-0.5	-0.18	0.001	-0.67	3E-04	-0.53	418	314	257	361	450	246	411	283	948.8	3791	4	0.0079	2.089
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	tTGI VmD SGD GVT HTV PlyE GYAL PHAI LR	72%	34.1	55.86567	Ref	-0.19	-0.32	0.049	-0.39	-0.39	-0.27	-0.24	583	435	430	624	508	444	503	509	762.4	3807	5	0.0218	5.723

Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	vAPE EHP VLLT EAPL NPK	72%	36.4	52.74303	Ref	-0.19	-0.27	-0.27	-0.26	-0.3	0.005	-0.64	29200	20300	20800	23200	25900	21900	28300	18000	854.8	2561.5	3	0.005	1.946
Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1	7 ACTG_T RIVU,sp P 63258 AC TG_BOVI N,sp P63 259 ACTG _RAT,sp P63260 A CTG_MO USE,sp P6 3261 ACT G_HUMA N,tr D2I7 P0 D2I7P 0_AILME,t r F1PQL8 F1PQL8_ CANFA,tr F6TII3 F6 TII3_MAC MU,tr F7 AAK7 F7A AK7_HOR SE,tr F7DI B7 F7DIB 7_MOND O,tr F7I0	vAPE EHP VLLT EAPL NPK	95%	70.1	53.32305	Ref	-0.22	-0.18	-0.23	-0.16	-0.26	0.008	-0.49	2420	2020	2260	2450	2830	2310	2900	2030	1282	2561.4	2	0.0197	7.704

Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR_SE	aAE DYG VTK	80%	38.6	52.37591	Ref	-0.4	0.42	-0.39	-0.1	-0.36	0.013	-0.77	46300	34400	65500	42200	56600	41200	55900	32200	521.3	1560.8	3	0.016	10.27
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR_SE	aAE DYG VTK	59%	33.2	52.2839	Ref	-0.71	0.16	-0.62	0.081	-0.22	0.43	-0.9	2E+05	108000	2E+05	141000	252000	2E+05	3E+05	116000	521.3	1560.8	3	0.012	7.697
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR_SE	aAE DYG VTK	60%	33.1	52.37438	Ref	-0.68	0.33	-0.45	-0.028	-0.49	0.12	-0.68	21800	11300	24800	16200	23900	15100	24100	13700	781.4	1560.8	2	0.0155	9.915
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR_SE	dLAA VQR	73%	33.8	49.79093	Ref	-0.26	0.7	Value Missing (-1.3385901)	0.26	Value Missing (-1.2831969)	-0.11	-0.58	17500	12900	27100	Value Missing (-1.3385901)	24800	Value Missing (-1.2831969)	17400	12500	359.5	1075.6	3	0.0061	5.631
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR_SE	eFTE SQL QEG k	95%	53.3	53.38516	Ref	-0.99	0.43	-0.44	0.058	-0.61	0.27	-1.1	2E+05	79700	2E+05	142000	221000	1E+05	2E+05	92700	952.5	1903	2	0.0209	10.95
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR_SE	eFTE SQL QEG k	94%	50.4	53.4564	Ref	-0.96	0.55	-0.4	-0.033	-0.57	0.12	-0.82	6E+05	283000	9E+05	510000	724000	4E+05	7E+05	379000	635.3	1903	3	0.0138	7.244
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR_SE	eFTE SQL QEG k	95%	57.8	53.45268	Ref	-0.85	0.53	-0.47	0.055	-0.73	0.16	-0.87	6960	3290	9260	5200	8260	4190	8110	3950	952.5	1903	2	0.0149	7.813
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR_SE	eFTE SQL QEG k	76%	38.2	53.43617	Ref	-0.87	0.31	-0.6	-0.071	-0.42	0.36	-0.61	25900	12700	31300	18600	29700	20300	36400	18500	635.3	1903	3	0.0125	6.566
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR_SE	gAS QAG MTG YGR	90%	40.3	49.95065	Ref	-0.4	0.45	-0.54	-0.051	-0.69	-0.06	-0.85	30200	17500	34000	19300	29800	16800	27100	15500	730.4	1458.7	2	0.0118	8.099

Transgeline OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR SE	gAS QAG MTG YGR	94%	43.6	50.06252	Ref	-0.54	0.38	-0.46	-0.037	-0.45	0.01	-0.91	15200	8340	17200	10800	15900	10400	15000	7840	730.4	1458.7	2	0.0111	7.592
Transgeline OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR SE	gAS QAG mTG YGR	76%	33.4	49.0894	Ref	-0.43	0.48	-0.33	-0.22	-0.54	-0.13	-0.93	10600	6070	12400	7880	9440	6580	9130	5200	738.4	1474.7	2	0.0133	8.996
Transgeline OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR SE	gAS QAG mTG YGR	87%	37.1	49.08324	Ref	-0.76	0.48	-0.59	0.013	-0.66	0.092	-0.98	10600	4590	11700	6280	10500	5770	10100	4770	738.4	1474.7	2	0.0124	8.427
Transgeline OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR SE	gAS QAG MTG YGR	52%	32.4	53.04027	Ref	-0.53	0.42	-0.47	-0.086	-0.87	0.004	-1.1	12200	5490	11500	6950	10000	5060	9720	4620	882.5	1762.9	2	0.0118	6.704
Transgeline OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR SE	gAS QAG MTG YGR PR	60%	33	52.27174	Ref	-0.65	0.39	-0.48	0.058	-0.49	0.22	-0.79	2540	1590	3550	2180	3480	2080	3550	1760	856.9	1711.9	2	0.0121	7.037
Transgeline OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR SE	gAS QAG MTG YGR PR	94%	49.9	52.29664	Ref	-0.64	0.44	-0.54	0.31	-0.91	0.15	-0.89	6E+05	354000	8E+05	461000	914000	3E+05	7E+05	361000	571.6	1711.9	3	0.0115	6.69
Transgeline OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR SE	gAS QAG MTG YGR PR	91%	45.2	52.27326	Ref	-1.1	0.3	-0.67	0.29	-0.64	0.19	-0.68	6E+05	218000	6E+05	346000	746000	3E+05	6E+05	343000	571.6	1711.9	3	0.0127	7.443
Transgeline OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR SE	gAS QAG MTG YGR PR	90%	44.9	52.44631	Ref	-0.5	0.2	-0.58	-0.05	-0.26	-0.1	-0.48	63500	36400	64100	42000	66600	50300	58500	44600	571.6	1711.9	3	0.0107	6.27
Transgeline OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR SE	gDP NWF Mk	56%	32.2	52.07903	Ref	-0.97	0.35	-0.42	0.18	-0.68	0.12	-0.69	98500	41200	1E+05	73600	123000	59300	1E+05	60800	801.9	1601.8	2	0.016	9.955

Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	hVIG LQM GSN R	75%	36.5	52.08535	Ref	-0.4	0.14	-0.17	-0.31	-0.52	0.14	-0.55	17700	11600	18200	16500	16500	12400	20500	12700	505.9	1514.8	3	0.0103	6.8
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	hVIG LQM GSN R	95%	53.6	52.00607	Ref	-0.28	0.17	-0.26	-0.021	-0.61	-0.04	-0.68	34000	23700	34900	29100	37900	22100	34100	21700	505.9	1514.8	3	0.012	7.948
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	hVIG LQM GSN R	93%	48.2	52.07778	Ref	-0.58	0.24	-0.35	-0.14	-0.54	0.095	-0.53	62100	33900	65300	48500	62000	41100	66500	42700	505.9	1514.8	3	0.0109	7.216
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	hVIG LQM GSN R	90%	43.9	51.98814	Ref	-0.54	0.29	-0.31	-0.005	-0.45	0.07	-0.79	1E+05	77400	1E+05	110000	150000	96300	1E+05	79100	505.9	1514.8	3	0.0088	5.83
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	hVIG LQM GSN R	82%	39.2	52.16678	Ref	-0.14	0.3	-0.37	-0.18	-0.47	0.017	-0.62	58300	52900	78000	54700	69000	49100	72100	46000	505.9	1514.8	3	0.0079	5.237
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	hVIG LQM GSN R	91%	44.8	52.01343	Ref	-0.41	0.11	-0.39	-0.15	-0.31	0.13	-0.48	7900	5460	8530	6760	8820	6870	9720	6320	505.9	1514.8	3	0.0093	6.127
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	hVIG LQM GSN R	92%	45.9	52.11313	Ref	-0.22	0.047	-0.32	-0.19	-0.16	-0.14	-0.27	1830	1590	2070	1800	2170	1930	2050	1870	505.9	1514.8	3	0.0073	4.801
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	hVIG LQm GSN R	95%	52.7	52.14748	Ref	-0.67	0.099	-0.29	-0.072	-0.05	-0	-0.59	18900	10800	19900	17100	21900	19400	21000	13800	511.3	1530.8	3	0.0116	7.599
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	hVIG LQm GSN R	86%	41.3	52.16902	Ref	-0.39	-0.08	-0.34	-0.21	-0.08	-0.05	-0.26	44200	31500	42300	39700	47700	45700	48700	41700	511.3	1530.8	3	0.01	6.522

Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	hVIG LQM GSnr	95%	51.1	52.03169	Ref	-0.035	0.021	-0.06	-0.098	-0.45	-0.26	-0.34	24800	25900	29200	31000	33300	22700	27100	25500	506.3	1515.8	3	0.0076	5.041
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	hVIG LQM GSnr	95%	61.2	51.96008	Ref	-0.67	0.29	-0.46	-0.031	-0.48	0.08	-0.39	29700	17000	35900	23900	35500	22800	35000	25000	506.3	1515.8	3	0.0119	7.869
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	hVIG LQM GSnr	95%	56.1	51.9144	Ref	-0.31	0.077	-0.13	-0.15	-0.41	0.16	-0.53	13500	11600	16400	16000	17300	12600	19500	12000	506.3	1515.8	3	0.0111	7.335
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	IGFQ VWLk	84%	36.5	49.76208	Ref	-0.83	0.2	-0.57	0.013	-0.62	0.33	-1.1	10800	4160	9180	6040	10000	5640	11400	4310	800	1598	2	0.0101	6.326
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	IGFQ VWLk	71%	32.9	49.99926	Ref	-0.97	0.29	-0.6	0.047	-0.7	0.34	-1	1260	445	1160	702	1210	632	1350	525	800	1598	2	0.0121	7.539
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	IVNS LYPD GSKP VkvP ENPP SMV Fk	92%	43	51.41798	Ref	-0.69	0.3	-0.24	-0.015	-0.69	0.26	-0.96	973	510	1100	843	1090	594	1210	512	990.6	3958.2	4	0.0289	7.304
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	IVnS LYPD GSKP VkvP ENPP SMV Fk	61%	31.6	52.17039	Ref	-1.2	0.18	-0.47	0.12	-0.02	0.22	-1.3	1950	634	1830	1310	2170	1720	2130	722	990.8	3959.2	4	0.0309	7.799
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	qME QVA QFLk	91%	42.9	52.37551	Ref	-0.6	0.29	-0.39	-0.023	-0.62	0.078	-0.75	727	371	748	522	744	431	728	407	754.9	1507.8	2	0.0101	6.702

Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	qmE QVA QFLK	86%	40.2	52.3125	Ref	-0.37	0.12	-0.52	-0.17	-0.56	0.011	-0.66	4390	2300	3510	2520	3550	2350	3660	2280	754.9	1507.8	2	0.0161	10.67
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	qmE QVA QFLK	88%	42	53.35374	Ref	-0.76	0.22	-0.35	0.008	-0.57	0.14	-0.55	10500	5130	10900	8270	11700	6850	11700	7190	915.5	1829	2	0.0151	8.254
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	qmE QVA QFLK	89%	42.4	53.25341	Ref	-0.53	0.32	-0.53	0.092	-0.64	0.12	-0.81	12900	7400	14400	9010	15300	8010	14200	7400	915.5	1829	2	0.0094	5.117
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	qmE QVA QFLK	90%	43.6	53.31974	Ref	-0.6	0.32	-0.51	0.025	-0.63	0.25	-0.84	6960	3890	8030	5070	8070	4490	8610	4010	915.5	1829	2	0.0145	7.926
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	qmE QVA QFLK	85%	39	51.61784	Ref	-0.36	0.1	-0.61	-0.13	-0.27	-0.17	-0.12	370	254	380	261	399	318	355	365	762.9	1523.8	2	0.015	9.829
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	qmE QVA QFLK	94%	44.8	51.57976	Ref	-0.75	0.35	-0.42	-0.098	-0.34	0.16	-0.54	1020	583	1360	890	1230	904	1340	820	762.9	1523.8	2	0.016	10.47
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	qmE QVA QFLK	95%	48.4	51.64097	Ref	-0.085	-0.06	-0.82	-0.18	-0.82	-0.21	-0.27	750	427	473	311	538	302	479	455	762.9	1523.8	2	0.0134	8.792
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	qmE QVA QFLK	52%	32.8	53.41272	Ref	-0.57	0.41	-0.39	-0.045	-0.56	0.089	-0.72	8020	4840	10400	6690	9370	5740	9380	5330	923.5	1845	2	0.0198	10.7
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	qmE QVA QFLK	71%	37	53.45197	Ref	-0.55	-0.11	-0.39	0.083	-0.55	0.065	0.064	37900	26700	39300	36200	55400	31100	49900	49500	616	1845	3	0.0256	13.88

Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR_SE	tDM FQT VDLF EGk	93%	49.4	54.01931	Ref	-0.69	0.44	-0.66	-0.18	-0.41	0.27	-0.83	62200	32000	76000	39900	61200	45700	76400	35400	713.7	2138.1	3	0.0171	8.015
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR_SE	tDM FQT VDLF EGk	94%	48	54.01821	Ref	-0.85	0.35	-0.34	0.15	-0.71	0.21	-0.96	2860	1330	3320	2300	3570	1720	3390	1500	1070	2138.1	2	0.0146	6.838
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR_SE	tDM FQT VDLF EGk	91%	47.5	54.03055	Ref	-0.53	0.16	-0.48	-0.17	-0.52	0.26	-0.35	7130	4470	7840	5640	7690	5270	9450	6140	713.7	2138.1	3	0.0144	6.724
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR_SE	tDM FQT VDLF EGk	95%	54.6	54.0321	Ref	-0.38	0.17	-0.43	-0.085	-0.53	0.017	-0.36	1790	1200	1910	1420	1980	1270	1940	1480	713.7	2138.1	3	0.0124	5.785
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR_SE	tDM FQT VDLF EGk	95%	54.4	54.09483	Ref	-0.48	0.14	-0.37	-0.19	-0.33	0.044	-0.27	1720	1150	1920	1520	1890	1500	2030	1620	713.7	2138.1	3	0.0063	2.966
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR_SE	tDM FQT VDLF EGk	93%	50.2	54.09483	Ref	-0.41	-0.05	-0.37	-0.12	-0.28	0.089	-0.41	927	609	845	759	998	780	1050	738	713.7	2138.1	3	0.0063	2.966
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR_SE	tDM FQT VDLF EGk	75%	38.4	53.77208	Ref	-0.47	0.097	-0.26	-0.26	-0.42	0.31	-0.75	17500	10900	17500	15400	16900	13200	22800	10900	719	2154.1	3	0.0205	9.506
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR_SE	TLM ALGS LAVT k	95%	50.2	50.93975	Ref	-0.48	0.46	-0.56	-0.012	-0.31	-0.03	-0.62	3660	2680	5590	3080	4980	3530	4500	2970	503.6	1507.9	3	0.0121	8.02
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR_SE	TLM ALGS LAVT k	95%	66	50.37438	Ref	-0.53	0.21	-0.36	-0.087	-0.66	0.27	-0.86	57000	31700	57200	43300	57600	33900	67400	30400	605	1812.1	3	0.0152	8.402

Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HORSE	tLMALGSLAVT	95%	60.5	50.37912	Ref	-0.57	0.26	-0.56	0.014	-0.5	0.25	-0.7	18000	10800	20700	13200	21700	13300	23400	11900	605	1812.1	3	0.0151	8.303
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HORSE	tLMALGSLAVT	95%	68.5	49.79885	Ref	-0.41	0.14	-0.33	-0.065	-0.53	0.058	-0.54	21200	13500	21400	17400	23100	14600	22900	15100	907.1	1812.1	2	0.0059	3.28
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HORSE	tLMALGSLAVT	95%	62.1	50.58027	Ref	-0.66	0.17	-0.38	-0.02	-0.66	0.29	-0.73	10400	5360	10300	7920	11200	6280	12700	6180	907	1812.1	2	0.0173	9.546
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HORSE	tLMALGSLAVT	95%	65.7	49.70021	Ref	-0.4	0.21	-0.42	-0.035	-0.48	0.061	-0.6	5860	3910	6450	4680	6740	4320	6570	4130	605	1812.1	3	0.0046	2.545
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HORSE	tLMALGSLAVT	95%	68.2	50.16745	Ref	-0.53	0.25	-0.34	-0.11	-0.35	-0.07	-0.49	5230	3160	5870	4380	5660	4180	5290	3940	605	1812.1	3	0.0132	7.293
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HORSE	tLMALGSLAVT	95%	52.2	49.98761	Ref	-0.3	0.28	-0.5	-0.21	-0.58	0.12	-0.34	4790	3700	6000	3920	5300	3580	6050	4390	605	1812.1	3	0.0097	5.374
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HORSE	tLMALGSLAVT	95%	71.3	49.9829	Ref	-0.54	0.31	-0.17	-0.093	-0.46	-0.08	-0.46	907	603	1180	949	1100	744	1010	774	605	1812.1	3	0.0092	5.076
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HORSE	tLMALGSLAVT	95%	62.3	49.83396	Ref	-0.32	-0	-0.41	-0.12	-0.5	0.31	-0.5	800	598	809	686	925	618	1130	640	605	1812.1	3	0.0068	3.769
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HORSE	tLMALGSLAVT	72%	34.1	50.45839	Ref	-0.22	-0.1	-0.27	-0.079	-0.33	-0.05	-0.35	3520	2830	3330	3320	4170	3070	3890	3120	610.4	1828.1	3	0.0038	2.078

Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	tLmALGSLAVTK	87%	41.2	51.6348	Ref	-0.16	-0	-0.26	-0.18	-0.41	-0.06	-0.37	3560	2930	3540	3330	3880	2880	3850	3070	610.4	1828.1	3	0.0237	12.95
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	tLmALGSLAVTK	95%	63.3	51.17457	Ref	-0.65	0.22	-0.53	-0.091	-0.55	0.085	-0.53	8020	3740	7420	4960	7410	4720	7640	4950	610.4	1828.1	3	0.0143	7.828
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	tLmALGSLAVTK	76%	36.3	51.44521	Ref	-0.2	-0.22	-0.23	-0.13	-0.23	-0.1	-0.11	1030	919	982	1090	1300	1060	1200	1190	610.4	1828.1	3	0.0185	10.14
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	tLmALGSLAVTK	76%	37.6	54.676	Ref	-0.52	0.18	-0.43	0.077	-0.77	0.3	-0.7	5440	3340	5910	4340	6790	3310	7230	3600	639.9	2555.4	4	0.016	6.253
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	tLmALGSLAVTK	89%	45.7	54.69888	Ref	-0.6	-0.02	-0.28	0.13	-0.47	0.13	-0.33	930	606	979	918	1350	773	1230	886	852.8	2555.4	3	0.0151	5.895
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	tLmALGSLAVTK	61%	33.5	54.03729	Ref	-0.41	-0.16	-0.12	-0.04	-0.26	-0.05	-0.32	6610	4750	6100	7050	8220	6160	7450	6110	715.9	2859.6	4	0.0184	6.442
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	vPENPPSMVFk	75%	38.1	53.42875	Ref	-0.49	0.45	-0.56	-0.3	-0.67	0.046	-0.96	68100	32300	67000	37400	49300	33400	57200	28200	618.3	1852	3	0.0228	12.32
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	vPENPPSMVFk	95%	63.1	53.32596	Ref	-0.39	0.43	-0.52	-0.16	-0.61	-0.11	-0.89	13400	7240	13900	8080	11400	7280	10800	6210	927	1852	2	0.0175	9.469
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN,tr A8J714_HOR SE	vPENPPSMVFk	59%	34.2	53.30773	Ref	-0.68	0.46	-0.63	-0.18	-0.74	-0.01	-1.2	68800	25100	59900	31700	47800	28200	49100	21700	618.3	1852	3	0.0159	8.56

Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR_714_HOR_SE	vPEN PPS MVFk	95%	55.4	53.28506	Ref	-0.78	0.35	-0.57	-0.057	-0.48	-0.03	-0.95	22700	8520	20200	12000	18900	12300	17600	9180	927	1852	2	0.0132	7.105
Transgelin OS=Bos taurus GN=TAGLN PE=1 SV=4	sp Q9TS87 TAGL_BOVIN, tr A8J714_HOR_714_HOR_SE	yDEE LEER	56%	28.2	48.10206	Ref	-0.57	0.39	-0.26	-0.057	-0.48	0.029	-0.83	78000	46900	98800	70700	89900	58600	87000	47700	693.8	1385.6	2	0.0123	8.875
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aDG AEAK	80%	37.1	50.9899	Ref	-0.47	0.016	-0.66	-0.25	-0.21	-0.28	-0.24	17000	9690	14700	10400	15200	13700	13600	13800	423.9	1268.7	3	0.0028	2.219
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aLEE AME Qk	63%	35.1	53.36289	Ref	-0.5	0.39	-0.57	-0.34	-0.63	-0.18	-0.36	36300	21100	42300	24600	31700	22600	32200	28300	553	1655.9	3	0.0216	13.04
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aLEE AME Qk	95%	53.9	53.43412	Ref	-0.41	0.21	-0.82	-0.26	-0.49	0.066	-0.51	15000	9090	15100	8300	13500	10100	15500	10300	828.9	1655.9	2	0.019	11.47
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aLEE AME Qk	95%	50.9	53.37932	Ref	-0.52	0.36	-0.72	-0.21	-0.63	-0.05	-0.51	19900	11200	22400	11900	18700	12200	19100	13700	829	1655.9	2	0.0134	8.094

Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aLEE AME Qk	86%	42.7	53.43792	Ref	-0.52	0.27	-0.68	-0.24	-0.62	0.065	-0.53	84900	48100	90000	52300	78200	52400	88000	57800	553	1655.9	3	0.0126	7.627
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aLEQ QVE EMk	95%	60.9	53.88856	Ref	-0.51	0.36	-0.68	-0.24	-0.64	0.002	-0.59	11700	6630	13200	7160	10700	7090	11600	7600	907	1812	2	0.0177	9.75
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aLEQ QVE EMk	90%	46.4	53.91803	Ref	-0.65	0.38	-0.88	-0.22	-0.78	-0.06	-0.48	54600	24400	53800	25400	44000	26100	44900	33300	605	1812	3	0.0165	9.119
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aLEQ QVE EMk	90%	46.4	53.91803	Ref	-0.51	0.38	-0.6	-0.08	-0.73	-0.19	-0.34	42400	26700	53900	30700	48500	27000	41000	36600	605	1812	3	0.0165	9.119
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aLEQ QVE EMk	68%	36.7	53.98018	Ref	-0.22	0.14	-0.73	-0.16	-0.41	-0.13	-0.65	15200	10400	14500	8910	14500	10700	13500	9370	605	1812	3	0.0154	8.507
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aNL QID QINT DLNL ER	95%	58.4	54.3738	Ref	-0.29	-0.21	-0.13	-0.23	-0.4	-0.09	-0.26	9820	8070	9270	11000	11300	8770	11400	10000	725.4	2173.2	3	0.0111	5.126

Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aNL QID QINT DLNL ER	82%	40.3	54.40805	Ref	-0.33	0.4	-1	-0.28	-0.67	-0.12	-0.38	1810	1150	2070	870	1590	1060	1630	1350	1088	2173.2	2	0.0015	0.681
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aNL QID QINT DLNL ER	95%	65.9	54.38671	Ref	-0.08	-0.09	-0.46	-0.26	-0.49	-0.03	-0.26	4270	4050	4380	3800	4820	3580	5140	4340	725.4	2173.2	3	0.0018	0.849
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aQQ AAD k	95%	44	48.91627	Ref	Value Missing (-2.9482133)	-0.04	-0.41	-0.15	0.16	-0.05	0.33	463	Value Missing (-2.9482133)	562	488	645	700	631	812	539.3	1076.6	2	0.0123	11.42
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aQQ AAD k	95%	44.9	49.01153	Ref	Value Missing (-2.5589364)	0.19	-0.74	-0.068	0.21	-0.58	-0.06	2350	Value Missing (-2.5589364)	2120	1250	2190	2320	1400	1990	539.3	1076.6	2	0.0108	10.07
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aQQ AAD k	95%	49.4	49.01153	Ref	Value Missing (-2.5594263)	0.12	-0.79	0.006	0.28	-0.32	0.068	1380	Value Missing (-2.5594263)	1500	896	1710	1810	1250	1620	539.3	1076.6	2	0.0105	9.715
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aQQ AAD k	89%	38.1	48.91091	Ref	Value Missing (-2.464861)	0.16	-0.73	-0.19	0.11	-0.28	-0.19	1040	Value Missing (-2.464861)	846	515	824	883	703	743	539.3	1076.6	2	0.0079	7.339

Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aQQ AAD	75%	32.7	48.91627	Ref	Value Missing (-3.1708345)	-0.18	-0.37	-0.36	0.2	-0.08	0.33	905	Value Missing (-3.1708345)	802	786	875	1120	967	1280	539.3	1076.6	2	0.0123	11.42
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aQQ AAD	88%	37.5	48.91627	Ref	Value Missing (-2.1018224)	-0.08	-0.6	-0.27	0.082	-0.2	0.24	1500	Value Missing (-2.1018224)	1260	986	1360	1520	1300	1760	539.3	1076.6	2	0.0123	11.42
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aQQ AAD	74%	32.6	49.01153	Ref	Value Missing (-1.6794324)	-0.03	-0.89	-0.12	-0.06	-0.16	0.19	1080	Value Missing (-1.6794324)	908	563	1060	961	935	1190	539.3	1076.6	2	0.0106	9.826
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aSIT ALEA	77%	36.7	51.44198	Ref	-0.38	-0.03	-0.5	-0.096	-0.28	-0.25	-0.24	14600	10300	14400	11600	16900	13000	13800	13800	504.6	1510.9	3	0.0229	15.17
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	aSIT ALEA	95%	53	50.86716	Ref	-0.37	0.096	-0.44	-0.21	-0.35	-0.15	-0.31	18600	13800	20600	15900	20500	16300	19600	17400	756.5	1510.9	2	0.0102	6.768
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	eLED ATET ADA MNR	95%	63.3	49.1494	Ref	-0.71	0.19	-0.97	-0.29	-0.27	-0	-0.24	19500	9560	19400	9740	17100	15200	19100	16100	935.4	1868.9	2	0.0151	8.08

Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	eLED ATET ADA MNR	91%	39.6	49.18119	Ref	-0.45	0.29	-0.79	-0.28	-0.23	-0.39	-0.16	10300	6720	12200	6470	10100	9170	8550	9980	935.4	1868.9	2	0.0144	7.695
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	eME AELE DER	94%	41.4	47.72586	Ref	-0.59	0.4	-0.58	-0.22	-0.57	-0.04	-0.57	54900	31500	67800	38600	54600	37500	56400	38700	777.9	1553.7	2	0.013	8.382
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	eME AELE DER	95%	42.4	47.77644	Ref	-0.37	0.35	-1.1	-0.25	-0.53	-0.08	-0.34	78500	50100	89400	37400	73000	52600	75000	62200	777.9	1553.7	2	0.0122	7.842
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	emE AELE DER	51%	26	46.7408	Ref	-0.71	0.25	-0.34	-0.36	-0.37	-0.17	-0.09	6020	3680	7740	5770	6310	5470	6530	6860	785.9	1569.7	2	0.0123	7.835
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	gALA LEEK	69%	33.6	51.11313	Ref	-0.31	0.11	-0.4	-0.44	-0.4	-0.2	-0.55	2E+05	110000	2E+05	125000	135000	1E+05	1E+05	113000	719.9	1437.8	2	0.018	12.54
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	gALA LEEK	53%	31	51.12132	Ref	-0.25	0.15	-0.59	-0.4	-0.35	-0.43	-0.43	1E+05	61600	88500	59400	74700	67600	66900	66000	480.3	1437.9	3	0.0122	8.469

Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	gALALEEK	95%	45.7	51.13325	Ref	-0.45	0.23	-0.54	-0.24	-0.4	-0.15	-0.39	23900	15400	26700	17600	23800	18700	23200	19400	719.9	1437.8	2	0.026	18.06
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	gALALEEK	85%	39.4	50.82419	Ref	-0.77	0.39	-0.76	-0.13	-0.58	-0.23	-0.29	1E+05	48000	1E+05	58600	99800	64000	85100	81200	480.3	1437.9	3	0.0137	9.554
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	hSQ AVEE LAEQ LEQT k	95%	54	54.8141	Ref	-0.32	0.17	-0.54	-0.099	-0.62	-0.01	-0.41	643	501	767	526	786	479	764	574	816.8	2447.3	3	0.0132	5.378
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	hSQ AVEE LAEQ LEQT kR	74%	37.3	55.02587	Ref	-0.45	0.15	-0.41	-0.24	-0.42	-0.03	-0.29	6550	4810	7910	6020	7490	5770	7890	6570	651.9	2603.4	4	0.0309	11.86
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	hSQ AVEE LAEQ LEQT kR	61%	30.6	54.8427	Ref	-0.41	0.18	-0.49	-0.2	-0.51	-0.1	-0.26	5020	3630	5940	4190	5630	3980	5490	4880	521.7	2603.4	5	0.0102	3.933
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	iAEF TTNL MEE EEK	94%	51.6	54.16091	Ref	-0.2	0.17	-0.56	-0.31	-0.39	-0.21	-0.28	2480	2060	2900	1960	2580	2130	2510	2380	764.7	2291.2	3	0.0184	8.014

Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	iAQL EEQL DNE Tk	92%	48	54.14094	Ref	-0.24	0.22	-0.62	-0.25	-0.43	-0.22	-0.45	6590	4840	7210	4530	6460	4980	6030	5100	713.7	2138.2	3	0.0137	6.42
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	iAQL EEqL DnET k	88%	44.5	54.20136	Ref	-0.21	-0.07	-0.4	-0.28	-0.38	-0.14	-0.24	3440	2800	3350	3000	3600	2930	3610	3350	714.4	2140.1	3	0.0048	2.223
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	kANL QID QINT DLNL ER	87%	44	54.09037	Ref	-0.36	0.19	-0.8	-0.11	-0.49	-0.08	-0.35	14800	10200	16300	9210	16300	11000	15300	12500	869.5	2605.4	3	0.0207	7.933
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	kANL QID QINT DLNL ER	85%	42.6	54.16271	Ref	-0.59	0.44	-0.78	-0.71	-0.49	-0.02	-0.31	14000	7220	16000	7690	8870	9050	13100	10600	869.5	2605.4	3	0.0238	9.13
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	kFD QLLA EEk	66%	34.6	52.21975	Ref	-0.51	0.24	-0.62	-0.2	-0.47	-0.05	-0.47	13600	8040	14700	9110	13400	9700	13500	10100	711.8	2132.2	3	0.0289	13.53
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	kVEA QLQ ELQV k	91%	43.6	49.98843	Ref	-0.42	0.19	-0.55	-0.22	-0.59	-0	-0.36	2700	1810	2990	2000	2780	1870	2950	2280	775.8	2324.4	3	0.0356	15.3

Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	IEVN LQA Mk	61%	33.7	52.34125	Ref	-0.6	0.23	-0.61	-0.39	-0.26	-0	-0.74	10500	5160	9960	6260	8020	7680	9590	5700	552	1653	3	0.0156	9.442
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	IEVN LQA Mk	56%	32.9	52.52484	Ref	-0.56	0.16	-0.77	-0.12	-0.38	0.016	-0.38	21400	12700	22700	13400	23100	16900	23200	17500	552	1653	3	0.0189	11.44
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	IEVN LQA Mk	95%	46.9	52.2273	Ref	-0.33	0.12	-0.68	-0.17	-0.51	0.016	-0.38	6830	4910	7270	4690	7330	5070	7620	5740	827.5	1653	2	0.0069	4.191
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	IEVN LQA mk	85%	39.5	52.32907	Ref	-0.47	0.31	-0.67	-0.27	-0.48	0.087	-0.49	8560	5770	10700	6100	8920	6730	10400	6930	835.5	1669	2	0.0147	8.829
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	IQE MEG TVk	73%	36.7	52.74038	Ref	-0.57	0.43	-0.83	-0.2	-0.46	-0.12	-0.38	2E+05	130000	3E+05	132000	226000	2E+05	2E+05	180000	548.3	1641.9	3	0.0151	9.173
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	IQQE LDDL LVDL DHQ R	95%	65.6	54.5225	Ref	-0.17	0.28	-0.61	-0.12	-0.88	-0.03	-0.8	310	224	331	202	311	161	301	176	752.1	2253.2	3	0.0122	5.404

Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	IQQE LDDL LVDL DHQ R	58%	35.3	54.52676	Ref	No Values (-0.37285936)	Reference Missing (1.1796201)	No Values (-0.6571477)	No Values (-0.7976267)	No Values (-0.6017543)	No Values (-0.6645209)	No Values (-0.65364695)	No Values (-0.5752495)	No Values (-0.37285936)	Reference Missing (1.1796201)	No Values (-0.6571477)	No Values (-0.7976267)	No Values (-0.6017543)	No Values (-0.6645209)	No Values (-0.65364695)	752.1	2253.2	3	0.0102	4.512
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	IQQE LDDL LVDL DHQ R	95%	65.9	54.52717	Ref	-0.2	0.22	Value Missing (-2.2285376)	0.17	Value Missing (-2.1731443)	0.36	-0.32	184	119	173	Value Missing (-2.2285376)	207	Value Missing (-2.1731443)	215	134	752.1	2253.2	3	0.01	4.433
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	IQQE LDDL LVDL DHQ R	93%	50.1	54.50084	Ref	No Values (-1.1854582)	Reference Missing (0.867465)	No Values (-1.4697465)	Reference Missing (0.7789115)	No Values (-1.4143531)	Reference Missing (0.46843225)	No Values (-1.4662458)	No Values (-1.3878485)	No Values (-1.1854582)	Reference Missing (0.86723)	No Values (-1.4697465)	Reference Missing (0.778915)	No Values (-1.4143531)	Reference Missing (0.46843225)	No Values (-1.4662458)	752.1	2253.2	3	0.0017	0.758
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	IQVE LDN VTGL LTQS DSK	95%	84.3	54.23231	Ref	-0.38	0.31	-0.68	-0.26	-0.52	0.14	-0.57	10600	7950	13900	7850	11600	8450	14000	8450	856.8	2567.4	3	0.0107	4.159
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	qAQ QER DELA DEIA NSS Gk	83%	42.6	55.09005	Ref	-0.46	0.021	-0.6	-0.23	-0.37	-0.08	-0.2	5010	3170	4800	3510	5010	3960	5040	4620	899.8	2696.4	3	0.0168	6.24
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	qAQ QER DELA DEIA nSSG k	53%	34.8	54.96609	Ref	-0.57	0.22	-0.56	-0.24	-0.62	0.015	-0.46	18600	10000	18700	12200	16900	11300	18300	13100	900.1	2697.3	3	0.0213	7.886

Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	qLEE AEEE AQR	95%	65	50.37897	Ref	-0.29	0.23	-0.86	-0.31	-0.31	-0.3	-0.22	9670	6750	10500	5550	8950	7810	8190	8630	818.4	1634.8	2	0.0155	9.466
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	qLEE AEEE AQR	81%	36.3	50.47617	Ref	-0.3	0.26	-0.74	-0.24	-0.55	-0.32	-0.29	14900	9630	15400	8630	13500	9490	11600	11800	818.4	1634.8	2	0.0127	7.742
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	qLEE AEEE AQR	95%	65.3	50.51519	Ref	-0.59	0.36	-0.81	-0.24	-0.45	-0.07	-0.36	1E+05	61200	1E+05	63900	104000	78800	1E+05	86800	818.4	1634.8	2	0.0125	7.668
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	qLEE AEEE AQR	94%	47.6	50.62822	Ref	-0.32	0.018	-0.9	-0.13	-0.16	-0.34	-0.31	26400	16900	23200	13800	26000	22000	20400	20600	545.9	1634.8	3	0.009	5.483
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	rGDL PFVV PR	92%	45.5	51.33858	Ref	-0.4	0.38	-0.37	-0.44	-0.46	-0.35	-0.22	2390	1750	3250	2170	2270	1960	2200	2410	487.3	1458.8	3	0.0132	9.063
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	rGDL PFVV PR	79%	37.4	51.45945	Ref	-0.46	0.37	-0.25	-0.29	-0.61	-0.06	-0.43	45200	35300	68000	49500	53100	37300	56900	43600	487.3	1458.8	3	0.0186	12.76

Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	rGDL PFVV PR	81%	38.1	51.32557	Ref	-0.56	0.4	-0.18	-0.27	-0.78	-0.05	-0.52	79200	52200	1E+05	82400	85500	52400	91200	65300	487.3	1458.8	3	0.0116	7.932
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	rGDL PFVV PR	88%	41.8	51.44789	Ref	-0.47	0.21	-0.18	-0.25	-0.59	0.037	-0.27	36900	31600	55000	47200	49500	34200	55200	44200	487.3	1458.8	3	0.0177	12.15
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	rGDL PFVV PR	89%	42.2	51.14971	Ref	-0.36	0.19	-0.4	-0.25	-0.43	-0.13	-0.46	18900	13700	21700	16200	19800	15300	19600	15500	487.3	1458.9	3	0.0089	6.124
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	rGDL PFVV PR	74%	35.3	51.14971	Ref	-0.44	0.078	-0.24	-0.21	-0.44	-0.07	-0.38	1170	854	1330	1200	1340	1000	1350	1080	487.3	1458.9	3	0.009	6.186
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	rQLE EAEE EAQ R	95%	50.8	52.05824	Ref	-0.57	0.3	-0.69	-0.23	-0.22	-0.13	-0.49	1910	1140	2270	1280	1940	1710	1900	1470	896.5	1790.9	2	0.0135	7.544
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	rELA Dk	60%	32.6	51.45174	Ref	-0.67	0.39	-0.89	-0.24	-0.72	0.11	-0.5	27300	13200	29800	13900	23900	14900	27800	18000	428.9	1283.7	3	0.0204	15.86

Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	tQLE ELED ELQA TED Ak	74%	39	54.7837	Ref	-0.18	-0.1	-0.33	-0.21	-0.33	-0.16	-0.46	1670	1350	1560	1490	1780	1430	1680	1360	857.4	2569.3	3	0.0165	6.402
Uncharacterized protein OS=Callithrix jacchus GN=MYH9 PE=4 SV=1	tr F6YYM7 F6YYM7_CALJA, tr F6ZZ90 F6ZZ90_CALJA	vEA QLQ ELQV k	90%	43.9	51.7981	Ref	-0.22	0.65	-0.87	-0.69	-0.84	-0.27	-0.33	5150	3590	7140	2800	3470	2740	4250	4040	631.7	1892.1	3	0.0149	7.893
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	aLEL TGLk	74%	34.1	49.84815	Ref	-0.079	-0.42	-0.18	-0.32	0.2	-0.63	0.032	12000	9730	8320	11100	11100	13900	8100	12800	485	1451.9	3	0.0278	19.13
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	aLEL TGLk	75%	34.6	49.93	Ref	-0.025	-0.6	-0.09	-0.24	0.07	-0.62	0.081	16300	13600	9940	15900	15700	17000	11000	17800	485	1451.9	3	0.0224	15.41
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	aLEL TGLk	85%	37	49.64867	Ref	-0.25	-0.4	0.009	-0.15	0.12	-0.72	-0.03	43400	31200	30400	45300	44800	47200	27600	44000	727	1451.9	2	0.015	10.31

Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	aLEL TGLk	86%	37.4	49.57516	Ref	-0.21	-0.42	-0.06	-0.31	0.18	-0.5	0.019	28900	22300	20900	30100	27700	34000	22300	31600	727	1451.9	2	0.014	9.651
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	aLEL TGLk	69%	32	49.133	Ref	-0.22	-0.37	-0.17	-0.12	0.1	-0.71	0.047	16300	11700	11400	14700	16900	17100	10200	17100	485	1451.9	3	0.0044	3.062
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	aLEL TGLk	77%	34.1	48.91443	Ref	0.076	-0.34	-0.16	-0.33	0.051	-0.79	-0.04	18700	15700	12800	16300	15900	18100	10600	17600	485	1451.9	3	0.0029	1.988
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	aLEL TGLk	91%	40.7	49.62412	Ref	-0.27	-0.49	-0.04	-0.2	0.21	-0.58	0.023	51600	37900	35300	54100	53500	62200	37400	56400	727	1451.9	2	0.0143	9.816
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	aLEL TGLk	77%	34.7	49.59152	Ref	-0.3	-0.38	-0.17	-0.26	0.2	-0.64	0.1	50800	34500	35500	46100	47700	57000	33400	55500	485	1451.9	3	0.013	8.926

Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	aLEL TGLk	86%	37.2	49.54392	Ref	-0.26	-0.48	-0	-0.25	0.18	-0.67	0.087	47100	34400	32000	50200	46700	54800	31900	53300	727	1451.9	2	0.0116	7.958
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	aVVT PGk	51%	27.2	47.60083	Ref	-0.023	-0.29	-0.21	-0.42	-0.13	-0.53	-0.03	28800	20500	18500	21900	20800	22400	17700	24900	427.3	1278.8	3	0.0058	4.504
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	eAM EDG EIDG Nk	95%	62.2	51.80997	Ref	-0.083	-0.35	-0.09	-0.33	0.12	-0.91	-0.04	16100	11500	10400	14000	13000	15600	7980	14500	958.5	1914.9	2	0.0194	10.12
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	eVFE DAV EIR	87%	40.2	51.83014	Ref	0.081	-0.37	-0.15	-0.38	0.028	-0.74	-0.11	15000	11800	9360	12300	11500	13400	8170	12600	755.9	1509.8	2	0.0113	7.492
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	eVFE DAV EIR	92%	43.6	51.93853	Ref	0.031	-0.41	-0.14	-0.45	0.067	-0.75	-0.17	37200	26200	21000	28400	25200	31500	18800	27800	755.9	1509.8	2	0.0111	7.334

Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	eVFE DAV EIR	57%	32.1	51.9011	Ref	0.061	-0.14	-0.19	-0.34	-0.07	-0.63	-0.23	6460	5150	4860	5280	5230	5500	3910	5120	755.9	1509.8	2	0.0097	6.447
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gFGF VDF NSEE DAK	95%	52.4	53.05394	Ref	-0.42	-0.47	0.068	-0.27	0.16	-0.49	0.31	44000	36100	37900	61700	53800	63300	42200	72700	724	2169.1	3	0.0186	8.55
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gFGF VDF NSEE DAK	84%	41.2	53.12491	Ref	-0.16	-0.69	-0.02	-0.17	-0.05	-0.04	-0.07	13400	11200	8480	15100	15000	14200	14900	14600	724	2169.1	3	0.0154	7.112
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gFGF VDF NSEE DAK	95%	51.6	53.01039	Ref	-0.25	-0.35	-0.09	-0.17	0.057	-0.58	0.18	4730	3800	3830	5180	5400	5510	3700	6220	724	2169.1	3	0.0204	9.393
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gFGF VDF NSEE DAK	83%	40.8	53.18243	Ref	0.081	-0.02	-0.31	-0.27	-0.1	-0.56	-0	822	824	832	764	869	854	648	947	724	2169.1	3	0.0145	6.684

Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gIAYI EFk	78%	36.9	52.05183	Ref	-0.34	-0.34	-0.09	-0.18	0.17	-0.62	0.15	9030	6760	7340	9750	10200	11300	6790	11500	775	1547.9	2	0.0245	15.82
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gIAYI EFk	86%	39.3	51.57717	Ref	-0.22	-0.42	-0.14	-0.29	0.22	-0.72	0.15	12200	9210	8660	11800	11800	14600	7930	14400	775	1547.9	2	0.0138	8.885
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gIAYI EFk	85%	38.4	51.33446	Ref	-0.29	-0.44	-0.03	-0.31	0.19	-0.61	0.059	18600	12800	12500	18600	17000	20900	12500	19800	775	1547.9	2	0.0089	5.735
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gIAYI EFk	88%	42	51.39107	Ref	-0.38	-0.7	-0.04	-0.36	0.15	-0.48	0.31	26400	17400	15200	26900	23700	29500	20000	34200	517	1547.9	3	0.0086	5.583
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gIAYI EFk	89%	42.1	51.11766	Ref	-0.37	-0.36	-0.15	-0.089	0.17	-0.74	0.17	19900	14000	15200	19900	22800	23800	13200	24700	517	1547.9	3	0.0052	3.337

Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gIAYI EFk	70%	34.3	51.0911	Ref	-0.27	-0.59	0.1	-0.36	0.17	-0.5	-0.02	24300	16800	14600	26500	21200	26800	17600	24400	517	1547.9	3	0.0037	2.388
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gIAYI EFk	78%	36.3	51.50898	Ref	-0.29	-0.42	-0.03	-0.21	0.27	-0.79	0.083	25200	18800	18700	27400	26700	32500	16200	29600	775	1547.9	2	0.0118	7.633
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gIAYI EFk	88%	42.1	51.43018	Ref	-0.38	-0.51	-0.04	-0.24	0.15	-0.5	0.29	43600	33400	33100	51500	49200	56300	37500	64300	517	1547.9	3	0.0112	7.249
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gIAYI EFk	86%	41	52.06551	Ref	-0.31	-0.43	-0.06	-0.27	0.087	-0.51	0.14	8730	6140	6110	8890	8420	9440	6530	10200	517	1547.9	3	0.024	15.52
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gLSE DTTE ETLk	95%	60.3	53.66912	Ref	-0.073	-0.35	-0.21	-0.29	0.2	-0.36	-0.3	35800	28500	25600	31600	32900	40400	28600	29600	644.3	1930	3	0.0158	8.18

Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gLSE DTTE ETLK	95%	77.6	53.63727	Ref	-0.27	-0.28	0.007	-0.37	0.18	-0.87	-0.39	30200	16300	17500	24100	20500	26200	13200	18300	966	1930	2	0.0127	6.562
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gYAF IEFA SFED AK	89%	45.7	54.15336	Ref	-0.18	-0.4	-0.01	-0.38	-0.05	-0.52	0.33	1490	1300	1210	1780	1520	1670	1260	2250	735.1	2202.1	3	0.0124	5.616
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	gYAF IEFA SFED AK	83%	41.7	54.24183	Ref	-0.29	-0.26	-0.16	-0.35	0.015	-0.44	0.29	866	681	756	907	875	985	751	1230	735.1	2202.1	3	0.0067	3.042
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	GyAF IEFA SFED AK	61%	35.4	54.1572	Ref	-0.073	-0.3	-0.28	-0.43	0.1	-0.56	-0.28	326	207	191	218	217	273	181	217	735.1	2202.1	3	0.0129	5.874
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	kATT TPAK	64%	30	48.26574	Ref	-0.23	-0.33	-0.08	-0.25	0.13	-0.65	-0.01	42500	30100	30500	40800	40000	45400	27600	42700	577.4	1729.1	3	0.0039	2.243

Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	kAV VTP Gkk	83%	29	42.62855	Ref	-0.57	-0.61	-0.12	-0.11	0.52	-0.66	0.13	1090	724	768	1200	1340	1810	832	1430	1073	2143.4	2	0.0451	21.05
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	kFGY VDDE SAED LEK	80%	41.5	55.29611	Ref	-0.038	-0.35	-0.1	-0.089	-0.03	-0.46	-0.1	3330	3010	2630	3520	3900	3530	2750	3500	897.1	2688.4	3	0.028	10.39
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	kFGY VDDE SAED LEK	95%	53.6	55.24596	Ref	-0.4	-0.52	-0.03	-0.39	0.38	-0.67	0.13	7510	4990	4990	7860	6750	10000	5090	8780	897.1	2688.4	3	0.0386	14.34
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	kVA VATP Akk	89%	27.8	36.56865	Ref	-0.52	-0.37	-0.03	-0.17	0.22	-0.47	0.05	10700	6790	8210	11600	11600	13300	8630	12300	743.8	2228.5	3	0.002	0.9
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	IELQ GPR	89%	40.5	49.00198	Ref	-0.19	-0.18	-0.27	-0.49	0.44	-0.42	-0.07	19200	17300	18800	19900	18800	31300	18000	22800	372.9	1115.7	3	0.0078	7.016

Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	nDLA VVD VR	95%	49.6	51.4814	Ref	-0.16	-0.36	0.01	-0.33	0.06	-0.58	0.063	76000	60500	57000	82900	72200	82600	55300	85800	652.9	1303.7	2	0.0107	8.215
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	nDLA VVD VR	56%	31.4	51.34891	Ref	-0.05	-0.32	-0.22	-0.26	0.081	-0.64	0.024	831	678	611	736	786	869	550	867	653.4	1304.7	2	0.0052	4.003
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	qGTE IDGR	85%	37.5	50.25781	Ref	-0.27	-0.23	-0.07	-0.35	0.12	-0.69	0.085	29900	21200	23600	29700	26800	32600	19300	32900	590.3	1178.6	2	0.0119	10.12
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	qGTE IDGR	87%	40.1	50.2037	Ref	-0.33	-0.46	0.016	-0.39	0.25	-0.5	-0.03	17800	11900	11800	18400	15300	20800	12900	17800	393.9	1178.6	3	0.0096	8.117
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	qGTE IDGR	85%	37.4	50.25122	Ref	-0.1	-0.5	-0.02	-0.29	0.16	-0.61	0.017	1E+05	98300	81300	127000	116000	1E+05	84700	130000	590.3	1178.6	2	0.0094	7.951

Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	sISLY YTGE k	85%	40.5	53.20352	Ref	-0.24	-0.15	-0.08	-0.25	0.045	-0.47	-0.06	12900	9840	11400	13500	13200	14100	10300	13500	885	1768	2	0.0141	7.993
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	sISLY YTGE k	93%	45.6	53.18364	Ref	-0.2	-0.28	-0.07	-0.32	0.12	-0.66	0.071	20400	15500	16000	20700	19200	22800	13900	22800	885	1768	2	0.0133	7.507
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	sISLY YTGE k	95%	49.6	53.18257	Ref	-0.31	-0.42	0.002	-0.25	0.17	-0.58	-0.01	11000	7450	7490	11300	10400	12200	7580	11200	885	1768	2	0.0193	10.89
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	tGIS DLFA k	93%	44.5	52.08917	Ref	-0.31	-0.41	-0.01	-0.22	0.12	-0.66	0.055	27800	18900	19000	28200	26900	29700	18100	29400	780.5	1558.9	2	0.0133	8.51
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	tGIS DLFA k	76%	37.1	52.17687	Ref	-0.33	-0.5	0.044	-0.22	-0.03	-0.5	0.32	17900	14000	13500	22200	20400	20300	15300	26900	520.6	1558.9	3	0.0108	6.911

Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	tGIS DLFAk	75%	36.4	51.92891	Ref	-0.11	-0.59	-0.13	-0.37	-0.01	-0.59	0.32	15300	12000	9350	14400	13400	15100	10500	19600	520.6	1558.9	3	0.0038	2.449
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	tGIS DLFAk	76%	37	52.08917	Ref	-0.19	-0.57	0.029	-0.39	0.079	-0.58	0.32	25800	21700	18100	30800	25400	30600	20300	37500	520.6	1558.9	3	0.0134	8.565
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	vAV ATP Ak	78%	32.8	47.23291	Ref	-0.61	-0.34	0.099	-0.25	0.22	-0.7	0.006	58800	31100	40900	62100	53600	64900	35800	58100	455.6	1363.8	3	0.0173	12.69
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	vAV ATP Ak	89%	36.5	46.99768	Ref	-0.2	-0.31	-0.15	-0.23	0.15	-0.68	-0.02	92100	65900	66100	83200	86300	98600	57700	90500	682.9	1363.9	2	0.0103	7.583
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	vAV ATP Ak	87%	34.8	46.57448	Ref	-0.12	-0.24	-0.14	-0.22	0.1	-0.52	-0.05	21500	18300	18400	22200	23000	25200	17100	23600	682.9	1363.9	2	0.0037	2.748

Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	vFG NEIk	72%	34.4	51.2034	Ref	-0.067	-0.37	-0.06	-0.29	-0	-0.24	-0.09	19200	17300	15200	21100	19900	21200	18700	20600	707.9	1413.8	2	0.024	16.98
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	vFG NEIk	83%	36.8	50.52663	Ref	-0.059	-0.33	-0.07	-0.17	-0.1	-0.36	-0.15	21000	17500	15700	21200	21600	19900	17300	19800	707.9	1413.8	2	0.0064	4.552
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	vPQ NQn Gk	79%	37.3	52.38212	Ref	-0.12	-0.27	-0.04	-0.34	-0.03	-0.88	0.024	28100	19200	18800	24700	22100	23900	13900	25800	747.4	1492.8	2	0.0123	8.241
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	vPQn QnG k	84%	39.2	52.3522	Ref	-0.15	0.014	-0.16	-0.35	0.078	-0.83	-0.06	12600	9400	11500	11400	11000	12900	7220	12200	747.9	1493.8	2	0.0193	12.88
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	vPQn QnG k	83%	38.5	52.23078	Ref	-0.13	-0.1	-0.06	-0.35	0.14	-0.89	-0.23	31900	22400	24800	28700	25900	31700	16200	25500	747.9	1493.8	2	0.0084	5.619

Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	vTQ DELK EVFE DAV EIR	73%	39	54.98573	Ref	-0.27	-0.49	-0.05	-0.17	0.11	-0.6	0.16	3330	2510	2330	3560	3600	3820	2430	4110	876.8	2627.4	3	0.0359	13.67
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	vTQ DELK EVFE DAV EIR	68%	37.6	54.85085	Ref	-0.31	-0.36	-0.03	-0.27	0.27	-0.66	0.076	1340	1020	1060	1500	1400	1770	972	1610	876.8	2627.4	3	0.0211	8.025
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	vTQ DELK EVFE DAV EIR	52%	34.5	54.82848	Ref	-0.36	-0.34	-0.2	-0.24	0.28	-0.81	0.16	3130	2080	2280	2820	3030	3790	1860	3610	876.8	2627.4	3	0.0147	5.593
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	vTQ DELK EVFE DAV EIR	72%	38.6	54.82848	Ref	-0.21	-0.49	-0.01	-0.27	0.25	-0.66	0.15	1280	1090	976	1520	1400	1750	973	1690	876.8	2627.4	3	0.0147	5.593
Uncharacterized protein (Fragment) OS=Canis familiaris GN=NCL PE=4 SV=1	tr F1Q0B0 F1Q0B0_CANFA	vTQ DELK EVFE DAV EIR	56%	35.1	54.83219	Ref	-0.32	-0.53	-0.03	-0.18	0.19	-0.57	0.2	1020	804	754	1190	1190	1340	829	1400	876.8	2627.4	3	0.014	5.308

78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	aLSS QHQA AR	80%	37.4	51.08254	Ref	-0.019	0.15	-0.07	-0.21	0.1	0.048	0.25	14100	16000	19500	18900	18800	20500	20600	23500	434.6	1300.7	3	0.0093	7.115
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	dAG TIAG LNV MR	95%	51.8	52.56306	Ref	0.11	0.044	0.16	-0.042	-0.34	0.18	-0.16	64200	63800	66100	80500	77100	54800	81800	64200	761.4	1520.8	2	0.006	3.917
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	dNH LLGT FDLT GIPP APR	95%	63.3	54.68609	Ref	0.23	-0.02	-0.11	-0.075	0.035	-0.1	0.027	4150	4480	4080	4310	4860	4580	4360	4720	746.7	2237.2	3	0.0207	9.238
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	dNH LLGT FDLT GIPP APR	95%	86.6	54.61059	Ref	0.2	-0.18	0.039	-0.14	-0.2	-0.01	0.29	6130	6770	5650	7360	7180	6020	7130	8710	746.7	2237.2	3	#####	0.163
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	dNH LLGT FDLT GIPP APR	95%	104	54.68686	Ref	0.23	0.17	-0.08	-0.15	-0.17	-0.12	0.071	3010	3190	3310	3130	3290	2830	3060	3470	746.7	2237.2	3	0.0205	9.157
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	dNH LLGT FDLT GIPP APR	94%	51.7	54.68027	Ref	0.17	0.22	-0.28	0.094	-0.28	0.3	-0.34	2260	2370	2660	2110	3010	2030	3170	2010	746.7	2237.2	3	0.0159	7.106

78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	eLEEI VQPI Isk	95%	51.7	51.28173	Ref	0.19	0.25	-0.3	-0.17	-0.05	0.055	-0.29	6590	5900	6670	5130	6190	5870	6580	5130	669.4	2005.2	3	0.0062	3.096
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	eTAE AYLG k	74%	37	52.5507	Ref	0.24	0.21	-0.01	-0.22	-0.17	-0.14	-0.52	12200	9830	10400	10100	9610	8680	9270	7040	530.6	1588.9	3	0.0076	4.788
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	fEEL NMD LFR	73%	34.7	51.47444	Ref	0.089	0.1	0.13	-0.19	-0.32	0.029	-0.14	6100	5020	5500	6300	5540	4430	5890	5210	809.4	1616.8	2	0.0068	4.209
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iINEP TAA AIAY GLDk	95%	63.9	53.34247	Ref	0.29	0.44	-0.2	-0.25	-0.12	-0.13	-0.19	12300	13600	16300	11800	12500	12000	12400	11900	756.8	2267.3	3	0.0176	7.772
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iINEP TAA AIAY GLDk	95%	62.5	53.3085	Ref	0.42	-0.14	-0.12	-0.071	0.22	-0.19	-0.4	12400	13800	10200	11600	13200	14100	11100	9520	756.8	2267.3	3	0.0167	7.362
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iINEP TAA AIAY GLDk	95%	52.9	53.3485	Ref	0.26	-0.46	0.2	0.007	-0.2	0.11	-0.23	2500	2420	1590	2830	2720	2060	2660	2100	756.8	2267.3	3	0.018	7.93

78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iINEP TAA AIAY GLDk	59%	31.1	52.16232	Ref	0.06	-0.03	0.099	-0.29	-0.02	-0.09	-0.27	6590	4590	4680	5740	4820	5080	5050	4430	643.9	2571.5	4	0.0218	8.492
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iINEP TAA AIAY GLDk	95%	64.5	53.08693	Ref	-0.083	0.053	0.074	-0.087	-0.25	0.15	0.15	4520	4010	4790	5450	5370	4180	5790	5750	808.8	2423.4	3	0.0226	9.315
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iINEP TAA AIAY GLDk	95%	62.7	52.90123	Ref	0.21	0.044	0.16	-0.17	-0.3	0.23	-0.07	25300	30900	29800	36200	31700	25400	38300	30800	808.8	2423.4	3	0.0178	7.347
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iINEP TAA AIAY GLDk	95%	56.4	52.57669	Ref	0.2	-0.14	0.09	-0.066	-0.33	0.3	-0.01	1030	1180	1010	1330	1320	960	1540	1240	808.8	2423.4	3	0.0097	4.018
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iINEP TAA AIAY GLDk	85%	37.8	51.276	Ref	-0.094	-0.15	0.2	-0.043	-0.19	0.22	-0.05	5210	4250	4440	6340	5910	4650	6460	5340	682.9	2727.6	4	0.0177	6.494
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iINEP TAA AIAY GLDk	78%	35.4	51.97898	Ref	0.096	-0.07	0.092	-0.034	-0.24	0.23	-0.02	4250	4420	4270	5370	5420	4110	5940	4940	682.9	2727.6	4	0.0333	12.21

78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iQQL Vk	64%	27.4	45.90708	Ref	0.074	-0.15	0.17	-0.11	-0.16	0.17	-0.12	36400	32800	30300	42500	38700	32700	42900	34900	668.9	1335.9	2	0.0039	2.902
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iQQL Vk	69%	27.4	44.90647	Ref	0.037	-0.05	0.12	-0.06	-0.07	0.065	-0.06	14900	13800	14200	17900	17400	15100	17300	15700	668.9	1335.9	2	#####	0.254
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iTITn DQNR	82%	37.5	51.53437	Ref	0.12	0.09	0.09	-0.06	-0.13	-0.04	-0.15	68100	64100	68400	76700	76300	63500	70400	65000	690.4	1378.7	2	0.0107	7.774
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iTPS YVAF TPEG ER	95%	56.4	53.13321	Ref	0.099	0.013	0.033	-0.068	-0.12	0.056	-0.02	5480	5330	5450	6200	6370	5360	6340	5980	936	1870	2	0.0236	12.64
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iTPS YVAF TPEG ER	95%	60	53.22157	Ref	0.06	0.13	0.12	-0.1	-0.08	0.074	-0.21	28900	27900	31800	35500	33400	29700	34500	28000	936	1870	2	0.0158	8.471
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iTPS YVAF TPEG ER	95%	60	53.21012	Ref	No Values (0.0086)	No Values (-0.08942)	Reference Missing (0.9241865)	No Values (-0.4161635)	No Values (-0.22029106)	No Values (-0.2830578)	No Values (-0.27210838)	No Values (-0.19378622)	No Values (-0.008603867)	No Values (-0.10908942)	Reference Missing (0.92418655)	No Values (-0.4161635)	No Values (-0.22029106)	No Values (-0.28305788)	No Values (-0.2721838)	624.3	1870	3	0.0154	8.239

78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iTPS YVAF TPEG ER	95%	60.1	53.29902	Ref	0.0024	-0.13	0.02	-0.073	-0.06	0.16	-0.01	8450	7280	7230	8970	9270	8140	9950	8780	936	1870	2	0.0133	7.103
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iTPS YVAF TPEG ER	95%	59.5	53.31539	Ref	0.0031	-0.04	0.005	-0.031	-0.16	0.17	-0.06	6770	5740	6040	6990	7520	6010	7880	6650	936	1870	2	0.0122	6.515
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	iTPS YVAF TPEG ER	87%	41.5	53.25692	Ref	0.1	0.12	0.13	-0.069	-0.16	-0.04	0.039	2800	3010	3300	3730	3590	2940	3330	3500	936	1870	2	0.0107	5.724
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	kELE EIVQ PIISk	83%	33.7	48.24906	Ref	-0.042	-0.08	-0.11	-0.043	0.086	-0.17	0.002	4160	2930	3110	3400	3940	3760	3280	3670	610.4	2437.5	4	0.0177	7.255
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	kkEL EEIV QPII Sk	77%	28.1	43.09098	Ref	-0.48	-0.07	0.11	0.14	0.069	0.12	0.081	1160	787	1140	1450	1630	1350	1460	1410	957.6	2869.8	3	0.0223	7.76
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	kkEL EEIV QPII Sk	83%	28.5	43.06897	Ref	-0.16	-0.18	0.12	-0.005	0.085	0.067	0.06	6720	5520	5880	8140	8230	7650	7890	7790	718.5	2869.8	4	0.0211	7.352

78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	kSDI DEIV LVG GSTR	87%	43.4	53.41625	Ref	0.12	-0.09	0.11	-0.086	-0.14	0.058	-0.09	14400	13200	12400	16000	15400	12900	15500	14000	733.1	2196.2	3	0.0162	7.383
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	kSDI DEIV LVG GSTR	94%	51.7	53.45446	Ref	0.22	-0.1	0.098	-0.004	-0.2	0.063	-0.01	80600	91000	79100	102000	105000	80000	1E+05	94400	733.1	2196.2	3	0.0182	8.298
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	kSDI DEIV LVG GSTR	95%	57.6	53.45656	Ref	0.13	-0.17	0.092	-0.1	-0.27	0.22	-0.03	32900	31200	27300	36900	35600	27600	40500	33900	733.1	2196.2	3	0.0177	8.052
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	kSQI FSTA SDN QPT VTIK	95%	50.1	53.56833	Ref	-0.28	-0.17	0.27	0.07	-0.07	-0	-0.09	8710	5650	6640	10100	9690	7680	8390	7880	720.2	2876.6	4	0.025	8.699
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	kTkP YIQV DVG GGQ Tk	80%	35	50.56265	Ref	0.06	0.11	0.054	-0.15	-0.13	0.25	-0.16	7830	7910	8910	9590	9160	8150	11100	8260	734.7	2934.7	4	0.0448	15.26
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	kVTH AVV TVPA YFN DAQ R	85%	42.6	54.20858	Ref	0.18	-0.18	0.06	-0.067	-0.03	0.18	-0.09	820	901	764	1010	1020	919	1110	912	875.5	2623.5	3	0.0187	7.107

78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	kVTH AVV TVPA YFN DAQ R	59%	35	54.15434	Ref	0.056	-0.05	-0.07	-0.26	-0.11	0.11	0.24	1890	1740	1760	1940	1870	1820	2220	2410	875.5	2623.5	3	0.0166	6.341
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	mKE TAEA YLK	70%	36.5	53.35123	Ref	0.046	-0.12	0.15	-0.049	-0.2	0.16	-0.2	23800	19700	19000	25700	24700	19400	26000	20200	718.4	2152.2	3	0.0147	6.829
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	nELE SYAY SLk	93%	46.4	53.64444	Ref	-0.005	0.009	0.12	-0.11	-0.04	-0.05	-0.04	9860	8250	9040	11000	10300	9460	9810	9810	963	1924	2	0.0178	9.249
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	nELE SYAY SLk	93%	48.7	53.63371	Ref	-0.049	0.005	-0.13	-0.26	0.073	0.28	-0.05	20000	16700	18800	19200	19300	21300	25700	20300	642.3	1924	3	0.016	8.307
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	nELE SYAY SLk	95%	58.8	53.66324	Ref	0.063	-0.02	-0.01	-0.089	-0.07	-0.16	-0.02	5180	4040	4140	4680	4880	4310	4250	4640	963	1924	2	0.0146	7.597
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	nELE SYAY SLk	82%	40.8	53.64481	Ref	-0.15	0.21	-0.12	-0.034	-0.08	0.12	-0.14	5250	3860	5360	4790	5610	4740	5680	4730	642.3	1924	3	0.0131	6.78

78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	nQLT SNPE NTVF DAK	94%	51.6	54.42474	Ref	0.11	0.048	0.068	-0.17	-0.4	-0.16	-0.05	71500	51900	53900	61300	57200	42600	52600	56400	762.7	2285.2	3	0.0164	7.179
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	nQLT SNPE NTVF DAK	84%	42.4	54.39655	Ref	0.23	0.14	0.15	-0.02	-0.4	-0.29	0.069	3460	3630	3710	4190	4110	2750	3110	3950	763.1	2286.2	3	0.0145	6.341
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	nQLT SNPE nTVF DAK	91%	47.3	54.38835	Ref	0.078	-0.05	0.14	-0.13	-0.2	0.12	-0.09	8010	7150	7120	9110	8290	6920	9000	7710	763.1	2286.2	3	0.0158	6.905
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	sDID EIVL VGG STR	95%	54.4	53.39004	Ref	0.13	0.095	0.045	-0.13	-0.28	0.025	-0.03	6880	6370	6730	7300	7130	5590	7230	6930	883	1763.9	2	0.0116	6.562
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	tFAP EEIS AMV LTk	88%	44.6	54.12434	Ref	-0.091	0.17	0.093	-0.11	-0.03	0.12	-0.09	17900	16200	21100	22400	21400	19800	22900	19700	715.7	2144.2	3	0.0222	10.36
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	tFAP EEIS AMV LTk	79%	39.8	53.92667	Ref	0.098	-0.03	0.045	-0.023	-0.05	0.07	-0.02	11100	11500	11400	13500	14200	12200	13900	12900	715.7	2144.2	3	0.014	6.51

78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	tFAP EEIS AMV LTk	76%	38.9	53.95001	Ref	0.18	0.031	-0.12	-0.009	-0.23	0.23	-0.14	2060	2100	2050	2080	2470	1850	2650	2040	715.7	2144.2	3	0.0129	5.993
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	tFAP EEIS AMV LTk	91%	46.9	53.96014	Ref	0.16	0.06	0.007	-0.16	-0.21	0.16	-0.16	750	711	720	779	766	646	869	691	715.7	2144.2	3	0.0132	6.175
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	tkPYI QVD VGG GQT k	76%	36.8	52.01334	Ref	0.14	-0.01	0.1	-0.16	-0.2	0.035	-0.26	8680	7110	6940	8410	7740	6570	8080	6520	835.2	2502.4	3	0.0144	5.749
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	tWN DPS VQQ Dik	84%	41.8	53.95012	Ref	0.062	-0.11	-0.09	0.1	-0.35	0.19	-0.08	87500	71600	69200	78400	98800	63100	96100	78700	680.4	2038.1	3	0.0173	8.501
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	tWN DPS VQQ Dik	92%	45.6	53.9745	Ref	0.12	-0.16	0.15	0.045	-0.44	0.19	-0.14	19700	17800	15800	22100	22600	14100	22800	18000	1020	2038.1	2	0.0145	7.115
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	VEIIA NDQ GNR	89%	41.8	52.29767	Ref	0.2	-0.06	0.12	-0.13	-0.17	-0.25	-0.04	78100	67500	61300	77500	72100	61100	60400	69300	766.9	1531.8	2	0.0115	7.474

78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	vEIIANDQ GnR	85%	39.4	51.95565	Ref	0.15	0.041	-0.04	-0.17	-0.12	-0.19	0.15	14900	13600	13700	14500	14700	13200	13100	16500	767.4	1532.8	2	0.0129	8.426
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	vLED SDLK	51%	31.7	52.42107	Ref	0.1	-0.03	0.053	-0.2	-0.13	0.19	-0.11	27700	25300	25200	29900	27700	25300	33000	26700	763.9	1525.9	2	0.022	14.38
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	vTHAVVT VPAY FND AQR	81%	41.1	54.43728	Ref	0.16	-0.05	0.02	-0.18	-0.25	0.089	0.13	5470	5390	5060	5970	5740	4750	6290	6440	731.4	2191.2	3	0.0123	5.597
78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1	sp Q0VCX2 GRP78_BOVIN	vTHAVVT VPAY FND AQR	89%	46	54.43728	Ref	0.28	-0.04	0.073	-0.079	-0.14	0.098	-0.2	4220	4800	4150	5050	5010	4180	5160	4160	731.4	2191.2	3	0.0123	5.597
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 SV=4 SV=1	tr D2HS92 D2HS92_AILME	aDID ISGP k	89%	41.2	51.56422	Ref	-0.53	-0.31	-0.4	-0.27	-0.08	-0.51	-0.31	18600	12000	15200	16000	19300	19200	15000	17000	762.4	1522.9	2	0.0102	6.706

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	aDID VSG Pk	93%	44.2	51.98503	Ref	-0.72	-0.41	-0.24	-0.035	-0.08	-0.84	-0.4	2E+05	82600	1E+05	141000	178000	2E+05	92800	126000	755.4	1508.9	2	0.0151	10.01
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	aPD VEV QGA DWS Lk	75%	38.7	54.22068	Ref	-0.44	-0.43	-0.3	-0.29	-0.13	-0.44	-0.17	7000	5460	5980	7330	8160	7940	6670	8020	708.4	2122.1	3	0.0246	11.61
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	aPD VEV QGA DWS Lk	88%	44.6	54.20558	Ref	-0.77	-0.25	-0.39	-0.28	0.14	-0.68	-0.35	19600	10700	16600	16900	20100	23400	13800	17300	708.4	2122.1	3	0.0175	8.242

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	aPD VEV QGA DWS Lk	76%	39.2	54.20733	Ref	-0.82	-0.45	-0.28	-0.17	-0.06	-0.45	-0.34	29400	15000	21000	26400	31500	29700	23700	25300	708.4	2122.1	3	0.0146	6.872
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	aPEV Dlk	61%	30.6	49.70663	Ref	-0.63	-0.18	-0.56	-0.21	-0.08	-0.71	-0.73	1E+05	55200	82100	70500	99300	94800	64000	62800	690.4	1378.8	2	0.0052	3.791
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	eVG VDIN FPk	76%	38	53.06406	Ref	-0.73	-0.41	-0.56	-0.19	0.01	-0.87	-0.03	22000	11400	15400	15500	22200	22200	12600	22400	576	1725	3	0.0188	10.89

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	gDF DVS VPk	74%	36.1	52.33116	Ref	-0.72	-0.27	-0.41	-0.2	0.061	-0.67	-0.24	18600	11000	16400	16700	21300	22200	14000	18700	786.4	1570.9	2	0.0049	3.09
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	gDV DVSL Pk	77%	35.6	51.2592	Ref	-0.54	-0.35	-0.48	-0.24	-0.17	-0.53	-0.48	60900	32500	40100	41100	53500	49100	39800	40900	769.4	1536.9	2	0.0132	8.56
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	gDVS ISGP k	85%	39.7	51.33341	Ref	-0.67	-0.28	-0.55	-0.028	-0.06	-0.62	-0.34	27400	15800	22500	21000	33100	28300	20100	24200	490	1466.9	3	0.0039	2.663

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	gEGP DVD VNLP k	95%	63.3	53.45307	Ref	-0.61	-0.27	-0.4	-0.28	-0.06	-0.57	-0.51	15400	8200	11300	11600	13900	14100	10400	10700	924.5	1847	2	0.0129	6.986
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	gEGP EVD VNLP k	95%	63.3	53.4113	Ref	-0.81	-0.27	-0.34	-0.19	-0.07	-0.73	-0.47	24500	10800	17100	18200	22300	21100	14000	16600	931.5	1861	2	0.0152	8.182
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	gEGP EVD VNLP k	95%	67.8	53.44697	Ref	-1.2	-0.28	-0.36	-0.17	0.011	-1.1	-0.5	59700	17300	34400	36500	45900	45500	22000	33100	931.5	1861	2	0.014	7.527

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	gEYD VTVP k	95%	53	52.51765	Ref	-0.73	-0.25	-0.32	-0.19	-0.07	-0.62	-0.46	26100	13400	20300	21700	26100	24700	17600	19600	808.5	1614.9	2	0.0136	8.443
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	gHYE VTGS DDE TGk	88%	43.1	52.43123	Ref	-0.63	-0.14	-0.45	-0.41	-0.05	-0.61	-0.37	3550	1940	2950	2670	3020	3390	2410	2810	701.7	2102	3	0.0258	12.27
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	gPEV DISG Pk	88%	41.1	52.54376	Ref	-0.42	-0.43	-0.46	-0.46	-0.21	-0.6	-0.19	11800	6860	7390	8130	8940	9310	7410	9760	804	1605.9	2	0.0193	11.99

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	gPSL QGD LAVS GDIK	86%	42.4	53.47523	Ref	1	-0.68	-0.7	-0.74	-0.44	-0.75	-0.72	14500	38200	12800	14200	15200	16300	13700	13900	689.1	2064.2	3	0.0152	7.378
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	iSMP DFDL HLK	50%	33	53.55614	Ref	-0.54	-0.21	-0.44	-0.24	-0.06	-0.63	-0.46	4930	2960	4020	3850	4870	4840	3400	3790	642	1923.1	3	0.0162	8.426
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	iSMP DIDL NLkG Pk	66%	31.4	50.98433	Ref	-0.89	-0.44	-0.24	-0.006	-0.08	-0.51	-0.23	13800	7750	11400	14800	19100	15900	12300	14800	614.1	2452.4	4	0.0072	2.934

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	iSMP DIDL nLkG Pk	55%	30.5	52.07734	Ref	-0.61	-0.55	-0.43	-0.14	0.042	-0.34	-0.2	3520	2540	2870	3490	4700	4670	3740	4090	614.4	2453.4	4	0.0167	6.816
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	iSMP DVD LHM k	89%	45.1	53.61063	Ref	-0.74	-0.29	-0.5	-0.11	-0.04	-0.56	-0.34	17500	9290	13800	13400	19300	17700	12900	14900	632	1893	3	0.0149	7.885
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	iSMP DVD LNLk	82%	40.1	53.09705	Ref	-0.63	-0.29	-0.3	-0.28	-0.23	-0.57	-0.44	1E+05	52600	72100	80400	89500	81200	66800	72700	618.4	1852	3	0.0142	7.669

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	iSMP DVD LNLK	94%	49.9	52.97373	Ref	-0.33	-0.36	-0.37	-0.32	-0.27	-0.7	-0.43	19900	12100	12900	14400	16400	14800	11500	13800	618.4	1852	3	0.0102	5.5
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	iSMP DVD LNLK GPK	72%	35.4	51.58848	Ref	-0.79	-0.5	-0.29	0.019	0.12	-0.66	-0.36	12300	7260	9660	12500	17100	16000	9710	11900	813.8	2438.4	3	0.0139	5.681
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	iSMP DVG LNLK	64%	34.2	52.32005	Ref	-0.45	-0.52	-0.24	-0.27	0.016	-0.81	-0.28	12200	8030	8320	11300	12200	13000	7660	11000	599	1794	3	0.0147	8.194

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 _AILME	tPQI SMS DIDL NLk	82%	41.3	54.03853	Ref	-0.26	-0.38	-0.48	-0.34	-0.16	-0.56	-0.47	10200	7020	6980	7330	8910	8800	6960	7360	728.4	2182.2	3	0.0154	7.033
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 _AILME	tPQI SMS DIDL NLkG Pk	75%	35.8	53.18356	Ref	-0.8	0.14	-0.26	-0.17	-0.11	-0.72	-0.41	18200	11700	24400	20800	24400	22100	15100	18600	693.1	2768.6	4	0.0245	8.861
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 _AILME	vDID APD VDV HGP DWH Lk	93%	47.8	55.18826	Ref	-0.5	-0.56	-0.41	-0.16	-0.12	-0.52	-0.58	29300	15800	16500	20500	26800	24100	19100	18100	659.8	2635.4	4	0.0233	8.846

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDID VPD VDV HGP DWH Lk	93%	49.2	55.32871	Ref	-0.76	-0.39	-0.51	-0.14	-0.07	-0.71	-0.21	26300	12600	17700	18200	25900	23800	15900	22300	666.9	2663.4	4	0.0248	9.297
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDID VPD VDV HGP DWH Lk	93%	48.2	55.31913	Ref	-0.95	-0.56	-0.46	-0.16	-0.05	-0.53	-0.04	23100	10300	14700	17600	24000	22500	16900	23600	666.9	2663.4	4	0.0201	7.556
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDID VPD VDV HGP DWH Lk	95%	60.6	55.30541	Ref	-0.66	-0.29	-0.45	-0.076	-0.06	-0.7	-0.37	6710	3770	5260	5280	7550	6670	4480	5590	888.8	2663.4	3	0.0176	6.593

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDID VPD VDV HGP DWH Lk	93%	49	55.3121	Ref	-0.19	-0.06	-0.46	-0.36	-0.28	-0.55	-0.4	915	812	970	821	971	898	776	856	666.9	2663.4	4	0.0182	6.82
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDID VPD VNIE GPD Ak	51%	32.3	54.61552	Ref	-0.54	-0.29	-0.47	-0.33	-0.3	-0.49	-0.42	8430	4300	5570	5510	6670	5940	5460	5680	576.8	2303.2	4	0.025	10.85
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDID VPD VNIE GPD Ak	95%	59.9	54.60561	Ref	-1.5	-0.14	-0.64	-0.071	0.017	-0.69	-0.26	51900	14500	39100	31100	50900	47200	30300	40400	768.8	2303.2	3	0.0181	7.857

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDID VPD VNIE GPD Ak	95%	54.5	54.58472	Ref	-0.76	-0.15	-0.24	-0.061	0.025	-0.99	-0.4	2370	1370	2260	2380	2970	2750	1420	2120	1153	2303.2	2	0.0154	6.665
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDID VPD VNIE GPD Ak	70%	37.7	54.54792	Ref	-0.37	-0.31	-0.16	-0.29	-0.09	-0.71	-0.2	7560	6810	7750	9640	9690	9730	6600	9330	768.8	2303.2	3	0.0111	4.836
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDIE APD VSLE GPE Gk	95%	65.3	54.81418	Ref	-0.53	0.004	-1.1	-0.13	-0.13	-0.89	-0.26	85300	47100	73900	39600	83100	72700	44800	69000	755.1	2262.2	3	0.0178	7.844

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDIE APD VSLE GPE Gk	95%	61.6	54.81418	Ref	-0.63	-0.4	-0.36	-0.089	-0.2	-0.47	-0.29	5580	3360	4260	4910	6550	5310	4580	5140	755.1	2262.2	3	0.0178	7.844
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDIE GPD VNIE GPE Gk	51%	34	54.51963	Ref	-0.38	-0.14	-0.72	-0.24	-0.46	-0.06	-0.72	16400	10400	13400	10100	15500	11600	16000	10000	759.4	2275.2	3	0.0258	11.34
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDIN APD VEV QGk	75%	38.4	53.75225	Ref	-0.38	-0.18	-0.39	-0.43	-0.2	-0.52	-0.43	25700	17200	21500	20800	22300	22800	19100	20100	664.7	1991.1	3	0.0189	9.498

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDIS APDL SLEG PEGk	70%	37.6	54.31232	Ref	-0.03	-0.41	-0.33	-0.42	-0.26	-0.5	-0.5	2470	2230	1860	2210	2290	2220	1980	1960	745.7	2234.2	3	0.0186	8.326
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDIS APDL SLEG PEGk	78%	39.7	54.31232	Ref	-0.027	-0.28	-0.44	-0.35	-0.23	-0.63	-0.41	5100	4890	4460	4460	5260	4980	3930	4550	745.7	2234.2	3	0.0186	8.326
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDIS APDL SLEG PEGk	93%	49.8	54.29207	Ref	-0.68	-0.2	-0.59	-0.35	-0.12	-0.4	-0.13	13600	7880	11900	10200	13300	13600	11700	14000	745.7	2234.2	3	0.017	7.588

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vDV DVP DVD VHG PDW HLk	77%	40.5	55.38118	Ref	-0.68	-0.3	-0.49	-0.3	-0.05	-0.54	-0.38	3250	1640	2310	2280	2850	2970	2200	2450	884.1	2649.4	3	0.0137	5.173
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vEG DLkG PEV DlkG Pk	66%	25.5	48.78079	Ref	-0.93	-0.47	-0.43	-0.097	0.12	-0.28	-0.05	43600	29900	44600	51600	71500	72600	57400	66900	580.4	2896.7	5	0.0126	4.349
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vkGD VDLS LPk	64%	26.3	49.99683	Ref	-0.56	-0.5	-0.43	-0.24	-0.17	-0.36	-0.35	3270	1860	2110	2480	3120	2850	2610	2620	417.5	2082.2	5	0.0327	15.72

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vkGD VDV SLPk	89%	37.7	48.67155	Ref	-1	-0.34	-0.42	-0.042	0.052	-0.58	-0.4	4830	2060	3580	3810	5460	5090	3430	3860	1035	2068.3	2	0.0073	3.526
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014933 PE=4 SV=1	tr D2HS92 D2HS92_AILME	vQTP EVD Vk	90%	41.6	51.48998	Ref	-0.67	-0.46	-0.39	-0.13	-0.1	-0.58	-0.32	33700	17900	22500	26600	35000	31200	23400	27700	812	1621.9	2	0.0119	7.355
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q29443 TRFE_BOVIN	cLM EGA GDV AFVk	95%	56.4	53.08236	Ref	0.99	0.15	0.57	0.32	-0.49	1	0.22	5890	10500	6370	9560	8820	4390	12900	7470	997.5	1993	2	0.0245	12.29
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q29443 TRFE_BOVIN	cLM EGA GDV AFVk	95%	51.8	53.26315	Ref	0.87	0.24	0.43	0.31	0.051	0.77	0.02	19700	23900	16800	21600	21900	15900	27400	16200	665.3	1993	3	0.0157	7.885
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q29443 TRFE_BOVIN	cLM EGA GDV AFVk	95%	69.7	53.07753	Ref	1	-0.09	0.64	0.31	-0.29	0.99	0.32	3340	6560	3330	6210	5440	3130	7940	4950	665.3	1993	3	0.0273	13.68

Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	cLM EGA GDV AFVk	95%	57	53.331	Ref	0.7	0.1	0.63	0.4	0.081	0.76	0.34	1730	2230	1610	2590	2450	1710	2850	2120	665.3	1993	3	0.0143	7.163
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	dNP QTH YYAV AVV k	63%	35.9	54.33354	Ref	0.99	0.21	0.58	0.32	-0.13	1	-0.06	9460	18600	11700	17000	15700	10000	23200	10900	738.4	2212.2	3	0.0192	8.677
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	dNP QTH YYAV AVV k	92%	48.6	54.33035	Ref	1	0.19	0.38	0.4	0.03	0.85	0.21	5770	10800	6700	8570	9560	6470	11900	7630	738.4	2212.2	3	0.0141	6.36
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	dNP QTH YYAV AVV k	69%	37.3	54.32285	Ref	0.75	0.36	0.46	0.37	0.24	0.61	0.37	6650	9460	7850	9430	9770	7770	10500	8850	738.4	2212.2	3	0.0155	7.024
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	ecVP nSNE R	72%	28.5	45.44836	Ref	0.97	0.22	0.57	0.34	-0.24	0.92	0.18	59300	108000	69500	99700	94100	54600	1E+05	75800	699.8	1397.6	2	0.0107	7.661
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	eNFE VLck	95%	48.8	52.52188	Ref	0.74	0.2	0.53	0.42	-0.05	0.98	0.18	7500	10900	8060	11400	11700	7340	15600	8920	818.4	1634.9	2	0.0097	5.958
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	fDEF FSAG cAP GSP R	95%	56.9	47.81985	Ref	1	0.22	0.55	0.33	-0.23	0.84	0.14	4250	7200	4530	6360	6030	3570	7820	4780	969.4	1936.9	2	0.0126	6.477

Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	fDEF FSAG cAP GSP R	95%	62.4	47.8159	Ref	1.1	0.073	0.54	0.47	-0.57	1	-0.03	614	1120	613	952	999	423	1350	639	969.4	1936.9	2	0.0122	6.292
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gDV AFVK	93%	42.5	50.21019	Ref	0.94	0.13	0.62	0.47	-0.27	1	-0.07	1E+05	230000	1E+05	224000	224000	1E+05	3E+05	139000	672.4	1342.8	2	0.0098	7.256
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gEAD AMS LDG GYLY IAGK	61%	35.9	54.52795	Ref	0.82	0.22	0.58	0.37	0.15	0.56	0.22	2610	3370	2400	3470	3300	2480	3440	2700	813.8	2438.2	3	0.0239	9.784
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gEAD AMS LDG GYLY IAGK	65%	36.6	54.61601	Ref	Reference Missing (1.3384 217)	No Value s (- 0.842 44597)	Refer ence Missi ng (1.160 1716)	No Values (- 1.1495 199)	No Values (- 0.9536 475)	Refer ence Missi ng (1.746 6938)	No Values (- 1.0055 403)	No Values (- 0.9271 425)	Reference Missing (1.338421 7)	No Value s (- 0.842 44597)	Refer ence Missi ng (1.1601 716)	No Values (- 1.149519)	No Value s (- 0.953 6475)	Refer ence Missi ng (1.746 6938)	No Values (- 1.005540 3)	813.8	2438.2	3	0.0191	7.828
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gEAD AmS LDG GYLY IAGK	95%	60.2	54.36261	Ref	0.82	0.2	0.41	0.34	0.014	0.88	0.21	4460	5940	4190	5470	5710	3990	7610	4750	819.1	2454.2	3	0.0217	8.845
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gPN HAV VSR	77%	35.1	50.86758	Ref	0.87	0.26	0.62	0.34	-0.04	0.87	0.18	3540	6170	4400	6330	5740	3850	7590	4660	620.9	1239.7	2	0.0105	8.446
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gPN HAV VSR	60%	31.9	50.89619	Ref	0.55	0.36	0.61	0.32	0.32	0.74	0.3	20500	26300	25000	33400	30100	26100	36500	26800	414.2	1239.7	3	0.0093	7.524

Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gPN HAV VSR	84%	37.8	50.96861	Ref	0.79	0.3	0.62	0.35	0.003	0.93	0.12	12000	20000	15400	21700	19800	13600	26900	15300	620.9	1239.7	2	0.011	8.833
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gPN HAV VSR	77%	35.4	50.87143	Ref	0.86	0.17	0.63	0.3	-0.07	0.94	0.094	32000	50000	33700	52000	45500	30800	64600	35700	620.9	1239.7	2	0.01	8.043
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gPN HAV VSR	90%	42.8	50.84222	Ref	0.57	0.29	0.63	0.26	0.19	0.87	0.33	1E+05	142000	1E+05	180000	154000	1E+05	2E+05	146000	414.2	1239.7	3	0.0092	7.379
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gYLA VAV Vk	95%	49.6	47.06086	Ref	1.1	-0.18	0.5	0.4	-0.15	1.1	0.045	15800	34800	15300	27600	28200	16900	40800	20000	510	1527	3	0.0052	3.375
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gYLA VAV Vk	85%	35.6	46.97778	Ref	0.79	0.012	0.45	0.26	0.18	0.91	0.22	3910	4930	3120	4740	4580	3790	6550	4040	510	1527	3	0.0039	2.531
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gYLA VAV Vk	94%	46.5	48.7458	Ref	1.1	0.33	0.49	0.29	-0.24	0.91	-0.04	7840	16300	10300	12900	12300	7480	17400	8930	510	1526.9	3	0.0248	16.26
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gYLA VAV Vk	95%	53.4	47.22634	Ref	0.87	0.29	0.57	0.45	-0.2	0.95	0.043	9400	16200	11700	16000	16200	9030	20900	11100	764.5	1527	2	0.0078	5.093

Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gYLA VAV Vk	92%	40.9	46.54889	Ref	0.68	0.093	0.52	0.47	0.19	0.73	0.28	5930	6990	5050	7620	8090	5830	8860	6420	510	1527	3	0.0021	1.356
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gYLA VAV Vk	74%	31.1	46.8985	Ref	0.67	0.32	0.41	0.34	0.28	0.62	0.36	2160	2510	2140	2550	2670	2240	2950	2460	510	1527	3	#####	0.1
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	GyLA VAV Vk	55%	26.9	46.70237	Ref	0.57	0.2	0.66	0.47	0.25	0.77	0.087	444	516	434	671	647	483	724	449	510	1527	3	0.0012	0.784
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	gyLA VAV Vk	54%	23.1	44.86176	Ref	0.87	-0.03	0.62	0.46	-0.1	0.91	0.066	7770	11300	6550	11600	11400	6770	14200	7860	458.8	1831.2	4	0.0077	4.2
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	hSTV FDNL PNPE DR	90%	44.6	52.08704	Ref	0.77	0.23	0.41	0.37	0.36	0.55	0.26	7030	8530	6400	8140	8730	7560	8980	7290	649	1944	3	0.0135	6.924
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	iLES GPF VScV k	57%	34.2	53.61836	Ref	0.99	0.25	0.78	0.31	-0.57	1	-0.1	13300	25300	16500	26800	21300	10100	31600	14500	645	1932.1	3	0.0164	8.491
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	iLES GPF VScV k	92%	47.5	53.57346	Ref	1.1	-0	0.7	0.35	-0.77	1.1	0.18	3490	7850	3980	7250	6300	2520	9380	5060	645	1932.1	3	0.0104	5.356

Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	iLES GPF VScV k	80%	39.7	53.5998	Ref	0.87	0.038	0.79	0.42	-0.19	0.91	0.11	804	1410	861	1630	1390	797	1780	1010	645	1932.1	3	0.0137	7.063
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	kNYE LLcG DNT R	92%	48.5	53.75581	Ref	1.1	0.028	0.55	0.48	-0.28	0.89	0.11	18200	35400	18700	30200	31700	16400	38300	22200	694	2079.1	3	0.0118	5.693
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	kPVT DAE NcHL AR	95%	93.7	54.21559	Ref	0.75	0.25	0.6	0.44	-0.15	0.92	0.21	1E+05	188000	1E+05	207000	204000	1E+05	3E+05	157000	527.8	2107.1	4	0.016	7.594
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	kPVT DAE ncHL AR	80%	40	53.84613	Ref	0.69	0.28	0.52	0.42	0.18	0.71	0.22	10600	13100	10700	14100	14500	10700	16200	11500	703.7	2108.1	3	0.0197	9.338
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	kSVD DYQ EcYL AMV PSH AVV AR	89%	44.3	55.41418	Ref	0.73	0.34	0.38	0.44	0.098	0.73	0.27	503	635	526	608	696	480	778	562	784.6	3134.6	4	0.0155	4.948
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	kTYD SYLG DDY VR	81%	40.6	54.04171	Ref	0.66	0.36	0.51	0.46	0.33	0.68	0.12	14500	18600	16400	20500	21800	17400	23200	15600	735	2202.1	3	0.0185	8.418
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	kTYD SYLG DDY VR	76%	36.9	54.04002	Ref	0.75	0.34	0.34	0.51	0.12	1.2	0.014	15600	35300	28900	32200	40000	26800	58600	25700	551.5	2202.1	4	0.0182	8.253

Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	kTYD SYLG DDY VR	87%	43.8	54.07889	Ref	0.66	0.33	0.52	0.49	0.019	0.74	0.2	6300	7510	6460	8300	8930	5630	9650	6630	735	2202.1	3	0.0167	7.587
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	lcQL cAGk	75%	35.6	51.65194	Ref	1	0.059	0.63	0.23	-0.2	0.91	0.19	2380	4290	2390	3980	3320	2160	4860	2910	768.4	1534.8	2	0.0089	5.791
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	ILEAc TFHK P	58%	34.5	53.88741	Ref	0.7	0.25	0.71	0.35	-0.1	0.88	0.22	3060	4300	3410	5270	4530	2890	5960	3750	605	1812	3	0.0147	8.102
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	ILEAc TFHK P	92%	46	53.98067	Ref	0.85	0.1	0.75	0.44	-0.18	0.92	0.008	1590	2530	1640	2880	2560	1450	3240	1720	907	1812	2	0.0127	6.99
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	ILEAc TFHK P	60%	35.1	53.98747	Ref	0.64	0.013	0.95	0.3	-0.11	0.93	0.26	56000	83000	58400	126000	88000	58000	1E+05	77700	605	1812	3	0.0125	6.894
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	ILEAc TFHK P	87%	44	53.90485	Ref	0.69	0.28	0.69	0.37	0.025	0.74	0.27	1610	2150	1750	2620	2300	1590	2720	1960	605	1812	3	0.007	3.866
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	ILEAc TFHK P	60%	35	53.96886	Ref	0.71	0.15	0.91	0.32	-0.3	0.91	0.14	12100	16700	12300	23300	17100	9720	23400	13700	605	1812	3	0.0096	5.273

Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	ILEAc TFHK P	91%	44.9	53.9043	Ref	0.76	0.11	0.66	0.4	-0.06	0.98	0.078	1220	1800	1240	2030	1870	1190	2560	1360	907	1812	2	0.0071	3.89
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	ILEAc TFHK P	72%	37.7	53.90621	Ref	0.77	-0.09	0.83	0.5	-0	0.76	-0.04	753	946	568	1200	1060	650	1150	655	605	1812	3	0.003	1.649
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	sVD DYQ EcYL AMV PSH AVV AR	95%	58.1	52.73266	Ref	0.78	0.13	0.22	0.51	0.23	0.92	0.27	933	1390	957	1150	1550	1110	1870	1180	901.8	2702.3	3	0.0043	1.602
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	tSDA NIN WN NLk	64%	35.8	53.90113	Ref	0.96	0.044	0.44	0.51	-0.03	0.83	0.13	15800	25300	14500	21400	24800	14900	28200	17200	666.7	1997.1	3	0.011	5.516
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	tSDA NIN WnN Lk	95%	57.6	53.89657	Ref	1.1	-0.02	0.6	0.33	-0.33	1	-0	10800	23800	11500	19900	18200	10000	26800	13100	1000	1998.1	2	0.0127	6.34
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	tYDS YLGD DYV R	95%	53	49.52396	Ref	0.89	0.26	0.47	0.49	-0.03	0.84	0.25	46000	86700	60800	78600	88000	53400	1E+05	67500	885.9	1769.8	2	0.0152	8.604
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	tYDS YLGD DYV R	95%	44.1	49.40317	Ref	0.62	0.17	0.55	0.5	0.053	0.91	0.3	2010	2720	2160	3160	3370	2150	4060	2650	885.9	1769.8	2	0.0179	10.12

Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	wcAI GHQ ER	67%	31.4	48.88387	Ref	0.84	0.044	0.63	0.25	0.27	0.78	0.2	10900	16300	10200	17100	14600	12900	19200	12700	483.9	1448.7	3	0.0098	6.748
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	wcAI GHQ ER	88%	39.4	48.89134	Ref	1.1	0.002	0.72	0.22	-0.41	1	-0.06	39600	73900	37800	69600	54600	30700	86300	40700	483.9	1448.7	3	0.0093	6.438
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1	sp Q2944 3 TRFE_B OVIN	wcAI GHQ ER	63%	30.7	49.06567	Ref	0.68	0.34	0.56	0.25	0.32	0.57	0.37	5470	6870	5920	7710	6890	6310	7850	6760	483.9	1448.7	3	0.0056	3.851
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME6 5 F1ME6 5_BOVIN	aEES AAH LPEEI R	78%	38.5	52.96837	Ref	-0.13	-0.15	-0.16	-0.29	-0.11	-0.29	-0.12	10100	8290	8890	9910	9970	9850	9100	10200	586	1754.9	3	0.0097	5.526
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME6 5 F1ME6 5_BOVIN	aSVG QVE SDLK	95%	75.7	52.8841	Ref	-0.34	-0.03	0.034	-0.11	-0.19	-0.41	-0.35	19100	12900	17300	20300	20300	16700	15100	15600	871	1740	2	0.0158	9.098
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME6 5 F1ME6 5_BOVIN	dFTS LENT VEER	90%	41.5	51.31795	Ref	-0.009	0.035	-0.23	-0.15	-0.32	-0.4	-0.42	5760	4660	5220	4880	5680	4420	4360	4270	872.4	1742.8	2	0.0136	7.821
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME6 5 F1ME6 5_BOVIN	dFTS LENT VEER	95%	51.4	51.34489	Ref	-0.25	-0.1	-0.1	-0.16	-0.35	-0.28	-0.41	9430	5790	6970	7800	8270	6320	6930	6290	872.4	1742.9	2	0.0123	7.053

Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	eELG QGL QGV EQk	92%	48.2	53.90889	Ref	-0.057	-0.12	-0.2	-0.25	-0.29	-0.16	-0.51	40600	29600	30800	32700	34700	29500	33800	26300	675	2022.1	3	0.0144	7.108
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	eRDF TSLE NTV EER	91%	43.3	52.36499	Ref	-0.38	-0.06	-0.22	-0.027	-0.18	-0.33	-0.29	1510	928	1260	1260	1590	1250	1170	1200	1015	2028	2	0.0176	8.652
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	eSQ GLDS R	72%	32.6	49.33781	Ref	-0.39	-0.09	-0.06	-0.16	-0.23	-0.26	-0.26	94500	59100	79100	90500	93000	77100	79100	78600	598.3	1194.6	2	0.0105	8.757
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	eSQ GLDS R	63%	31	49.41079	Ref	-0.25	-0.13	-0.04	-0.34	0.034	-0.31	-0.15	15100	12300	14400	17300	15500	17500	14400	16000	399.2	1194.6	3	0.0095	7.942
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	gAH PSG GAD DVA k	65%	35.2	53.08426	Ref	-0.3	-0.25	-0.37	-0.12	-0.06	-0.22	0.073	16300	12300	13800	14200	18700	17100	15900	19400	597.3	1788.9	3	0.0249	13.94
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	gGH GAA SPSE k	77%	37.8	52.57295	Ref	-0.1	-0.15	-0.12	-0.19	-0.11	-0.31	-0.17	7930	7140	7480	8600	9000	8310	7570	8260	536	1604.9	3	0.0203	12.65

Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	gGH GAA SPSE k	95%	52.8	52.79649	Ref	-0.13	-0.09	-0.27	-0.083	-0.08	-0.42	-0.23	20300	16500	18300	18100	22800	20000	16500	18700	536	1604.9	3	0.0086	5.348
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	gGH GAA SPSE k	51%	32.3	52.79471	Ref	-0.23	-0.1	-0.33	-0.19	-0.15	-0.36	0.064	12900	9840	11700	11200	13600	12200	11100	14700	536	1604.9	3	0.0084	5.236
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	gLGE AQLS LAG DVD Elk	95%	67.6	54.32064	Ref	-0.36	-0.25	-0.1	-0.1	-0.16	-0.19	-0.18	12300	8170	9600	11900	13100	11000	11300	11300	775.1	2322.3	3	0.0225	9.694
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	gLGE AQLS LAG DVD Elk	95%	57.2	54.28412	Ref	-0.26	-0.26	-0.05	-0.25	0.12	-0.43	-0.2	6070	4540	4930	6400	6110	6900	4940	5720	775.1	2322.3	3	0.0176	7.563
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	gLGE AQLS LAG DVD Elk	87%	43.9	54.18303	Ref	-0.3	-0.38	-0.06	-0.22	-0.09	-0.02	-0.07	1500	1220	1250	1740	1720	1640	1800	1730	775.1	2322.3	3	0.0128	5.51
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	gLGE AQLS LAG DVD Elk	94%	51	54.18764	Ref	-0.35	-0.18	-0.09	-0.062	-0.13	-0.31	-0.28	17600	11500	14000	16800	18900	15800	14500	14700	827.1	2478.4	3	0.0178	7.161

Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	iETN ENN LESA k	95%	73.1	53.9869	Ref	-0.66	-0.17	-0.08	-0.016	-0.1	-0.4	-0.21	25400	12300	18700	22500	25800	21300	18100	20500	985.5	1969	2	0.0129	6.56
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	iETn ENN LESA k	93%	49.7	53.67427	Ref	-0.14	-0.2	-0.18	-0.38	-0.27	-0.03	-0.13	17800	14100	14600	16700	16000	15100	18700	17300	657.7	1970	3	0.0165	8.39
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	iETN EnNL ESAK	95%	55.9	53.6849	Ref	-0.55	-0.1	0.044	-0.048	-0.19	-0.29	-0.36	10900	6050	8980	11100	11500	9090	8850	8410	986	1970	2	0.0148	7.484
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	iETN EnNL ESAK	95%	53.8	53.69086	Ref	-0.39	-0.18	-0.19	-0.028	-0.12	-0.16	-0.18	6500	4530	5670	6320	7810	6400	6500	6380	986	1970	2	0.013	6.612
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	IQNE ILK	80%	35	49.58339	Ref	-0.29	-0.15	0.004	-0.15	-0.18	-0.39	-0.3	52500	35100	41900	52300	51800	44200	39900	42300	733.5	1464.9	2	0.0042	2.893
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	IQNE ILK	84%	37.4	50.63652	Ref	-0.13	-0.18	-0.1	-0.062	-0.15	-0.33	-0.35	14500	11600	12300	14500	16400	13500	12400	12200	733.5	1464.9	2	0.0233	15.88

Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	IQSV EDG VQA AR	79%	37.4	52.32539	Ref	-0.16	-0.15	-0.11	-0.23	-0.28	-0.2	-0.2	11900	9100	9940	11500	11600	9830	10800	10800	788.9	1575.8	2	0.0117	7.419
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	IQSV EDG VQA AR	89%	41.7	52.31457	Ref	-0.42	-0.17	-0.14	-0.35	-0.23	-0.16	-0.07	83700	48300	62500	71900	68200	64800	71300	75200	788.9	1575.8	2	0.008	5.098
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	qGES EINR	82%	37	49.72054	Ref	-0.46	-0.13	-0.17	-0.34	0.34	-0.13	-0.37	11900	8610	11700	12800	12500	17600	13200	11100	412.9	1235.6	3	0.01	8.107
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	qREE LGQ GLQ GVE Qk	51%	33.2	53.86624	Ref	-0.55	-0.14	-0.31	-0.068	-0.16	-0.1	-0.11	17100	9730	14000	13900	18200	14900	16200	16000	993.5	1985	2	0.0152	7.668
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	qREE LGQ GLQ GVE Qk	72%	37.9	54.22436	Ref	-0.47	-0.14	-0.04	-0.04	-0.12	-0.29	-0.29	35700	22200	30300	36500	40100	33200	30800	30600	769.8	2306.3	3	0.0211	9.144
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	qREE LGQ GLQ GVE Qk	60%	35.2	54.1071	Ref	-0.35	-0.17	-0.18	-0.01	-0.2	-0.22	-0.12	7360	5290	6480	7220	8970	6880	7050	7530	769.8	2306.3	3	0.0178	7.714

Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	sIND NIAI FTDV Qk	95%	49	53.99097	Ref	-0.2	-0.41	-0.14	-0.017	-0.35	-0.36	-0.35	5760	3410	3190	4340	5190	3590	3730	3740	1094	2185.2	2	0.0205	9.369
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	sIND NIAI FTDV Qk	95%	59.4	53.91616	Ref	-0.061	-0.3	-0.1	-0.088	-0.2	-0.21	-0.24	1010	916	845	1090	1210	974	1010	983	729.4	2185.2	3	0.013	5.941
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	sIND NIAI FTDV Qk	91%	47.4	53.85202	Ref	-0.034	-0.41	-0.18	0.003	-0.5	0.044	-0.21	586	530	444	582	730	448	684	569	729.4	2185.2	3	0.0086	3.938
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	sIND NIAI FTDV Qk	93%	49.7	54.15179	Ref	-0.047	-0.22	-0.15	-0.21	-0.33	-0.22	-0.07	3730	3270	3130	3700	3900	3130	3550	3900	729.7	2186.2	3	0.0208	9.51
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	sTIQ TME SDVY TEVk	90%	47.2	54.57743	Ref	-0.24	-0.11	-0.41	0.055	-0.31	-0.16	-0.45	22000	13900	16600	15100	23000	15600	18000	14600	780.4	2338.2	3	0.0034	1.462
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	sTIQ TME SDVY TEVk	95%	53.5	54.47431	Ref	-0.25	-0.32	0.083	-0.33	-0.16	-0.25	-0.1	2000	1480	1530	2270	1880	1840	1810	2000	780.4	2338.2	3	0.0157	6.695

Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME6 5 F1ME6 5_BOVIN	tAVD SLVA YSVK	95%	59.7	52.75967	Ref	-0.47	-0.33	-0.07	-0.077	-0.12	-0.1	-0.03	17000	12000	14300	19200	21000	17900	18900	19700	621	1860.1	3	0.0168	9.014
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME6 5 F1ME6 5_BOVIN	tAVD SLVA YSVK	95%	58	52.64334	Ref	-0.26	-0.16	-0.01	-0.1	-0.35	-0.25	-0.17	77400	57300	66600	82600	85500	62800	70400	73700	621	1860.1	3	0.0146	7.837
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME6 5 F1ME6 5_BOVIN	tAVD SLVA YSVK	95%	66	52.64334	Ref	-0.38	-0.24	0.002	0.068	-0.23	-0.27	-0.22	7820	5490	6560	8730	10100	7170	7250	7470	931	1860.1	2	0.0145	7.796
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME6 5 F1ME6 5_BOVIN	tAVD SLVA YSVK	95%	56.7	52.63468	Ref	-0.36	-0.2	-0.16	-0.21	-0.15	-0.3	-0.07	18900	11900	14400	16700	17700	16100	15100	17600	621	1860.1	3	0.0118	6.354
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME6 5 F1ME6 5_BOVIN	tAVD SLVA YSVK	95%	72.3	52.60498	Ref	-0.29	-0.15	-0.25	-0.14	-0.19	-0.25	-0.21	3760	2420	2910	3050	3620	3040	3050	3110	931	1860.1	2	0.0117	6.281
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME6 5 F1ME6 5_BOVIN	vQE QVH TLLG R	85%	39.8	52.35708	Ref	-0.16	-0.16	-0.1	-0.24	-0.1	-0.33	-0.22	9490	7380	8000	9360	9360	9020	8020	8580	792.5	1582.9	2	0.013	8.229

Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	vQE QVH TLLG R	73%	36.3	52.31684	Ref	-0.28	-0.32	0.037	-0.16	-0.22	-0.31	-0.26	9300	6050	6370	9160	8780	7350	7260	7460	528.6	1582.9	3	0.0113	7.115
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	vQE QVH TLLG R	94%	50.6	52.42924	Ref	-0.48	-0.09	-0.28	-0.17	-0.3	-0.14	-0.11	7440	4110	5810	5720	6790	5450	6330	6450	528.6	1582.9	3	0.0164	10.35
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	vQE QVH TLLG R	90%	44.5	52.3005	Ref	-0.3	-0.08	-0.02	-0.32	-0.26	-0.14	-0.24	9930	6890	8720	10200	9130	8270	9380	8710	528.6	1582.9	3	0.0105	6.661
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	vQE QVH TLLG R	95%	48.6	52.48628	Ref	-0.31	-0.18	-0.2	-0.16	-0.15	-0.11	-0.19	5490	3880	4590	5080	5750	5080	5430	5120	792.5	1582.9	2	0.01	6.31
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	vQE QVH TLLG R	90%	42.7	52.46585	Ref	-0.3	-0.15	-0.14	-0.099	-0.24	-0.1	-0.17	5830	4450	5350	6070	6870	5420	6270	5910	792.5	1582.9	2	0.0096	6.07
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	vQE QVH TLLG R	94%	50.7	52.5329	Ref	-0.35	-0.33	0.043	-0.3	-0.2	-0.17	-0.19	28500	17700	19500	28300	24600	23000	24500	24000	528.6	1582.9	3	0.0089	5.619

Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	vQE QVH TLLG R	79%	38.2	52.27961	Ref	0.056	-0.1	-0.41	-0.16	-0.42	-0.06	-0.18	1120	1080	1050	951	1240	906	1220	1110	528.6	1582.9	3	0.0058	3.649
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	vQE QVH TLLG R	59%	33.2	52.31087	Ref	-0.26	-0.03	-0.45	-0.12	-0.01	-0.09	-0.25	815	651	828	693	963	906	899	793	528.6	1582.9	3	0.0067	4.236
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	vQSL QAT FGTF ESLV R	84%	42.3	53.99956	Ref	-0.15	-0.09	-0.2	-0.28	-0.54	0.096	-0.11	1070	900	1010	1060	1100	804	1300	1120	696.4	2086.1	3	0.0024	1.171
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	vQSL QAT FGTF ESLV R	89%	43.6	54.07025	Ref	-0.94	-0.32	0.08	-0.27	-0.05	-0.03	-0.3	326	125	208	308	266	271	287	236	1044	2086.1	2	0.0107	5.136
Uncharacterized protein OS=Bos taurus GN=Bt.3071 PE=4 SV=1	tr F1ME65 F1ME65_BOVIN	vQSL QAT FGTF ESLV R	95%	68.3	54.0557	Ref	-0.21	-0.2	-0.35	-0.66	-0.31	-0.1	0.33	360	271	296	300	266	295	356	479	696.4	2086.1	3	0.0087	4.147
Trypsin - Sus scrofa (Pig).	IPI:CON_Trypsin SWISS-PROT:P00761 TRYP_PIG,sp P00761 TRYP_PIG,tri CS1WV5 CS1WV5_PIG,tri F1RS2 F1RS2_PIG	iITHP NFh GNT LDN DIML lk	62%	34.9	55.21031	Ref	-0.004	-0.01	0.18	-0.072	0.16	0.14	-0.11	23100	20400	22100	28300	26100	26800	27500	23000	723.9	2891.5	4	0.0209	7.221

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	iiTHP NFn GnTL DNDI MLIK	55%	35.4	55.13255	Ref	0.18	0.14	0.14	-0.27	0.13	-0.03	0.003	1380	1410	1490	1680	1390	1600	1490	1520	964.9	2891.6	3	0.016	5.546
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	iiTHP nFn GNT LDN DImL Ik	69%	36.5	55.37371	Ref	0.053	-0.09	0.018	-0.008	0.064	0.17	-0.07	1320	1090	1070	1290	1400	1290	1450	1220	727.9	2907.5	4	0.017	5.831
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	iiTHP NFn GNT LDn DIML Ik	72%	37.1	55.24775	Ref	0.074	-0.07	0.079	-0.035	0.15	0.07	0.024	4910	4540	4450	5550	5650	5620	5550	5330	724.1	2892.5	4	0.0072	2.494

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	iITHP NFn GNT LDn DIML Ik	90%	47.8	55.17055	Ref	0.16	-0.11	0.058	0.052	0.052	0.012	-0.04	1850	1700	1520	1920	2110	1840	1870	1800	965.2	2892.6	3	0.0011	0.395
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	55%	35.6	55.33766	Ref	-0.29	0.005	0.24	-0.038	0.11	-0.1	-0.08	15400	8580	11400	15100	13700	13300	12000	12100	940.5	2818.5	3	0.0337	11.94
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	83%	43	55.28796	Ref	0.029	0.034	0.04	-0.069	0.23	0.027	0.12	2900	2860	3120	3510	3590	3860	3500	3700	940.5	2818.5	3	0.0238	8.441

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	95%	54.9	55.28796	Ref	0.066	-0.16	0.11	0.039	0.13	-0.04	-0	5210	4350	4040	5440	5730	5330	4930	5050	940.5	2818.5	3	0.0238	8.441
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	94%	52.5	55.27961	Ref	0.12	0.088	0.33	0.24	0.078	-0.35	-0.22	29300	30300	32100	42600	44000	34400	26800	29100	940.5	2818.5	3	0.0212	7.526
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	89%	44.1	55.27953	Ref	0.03	-0.07	0.028	-0.23	0.16	-0.08	0.49	20300	20200	20500	24500	22600	25900	22800	33700	705.6	2818.5	4	0.0197	6.974

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	95%	55.6	55.2774	Ref	0.2	-0.26	0.33	-0.12	-0.16	0.19	-0.04	1E+05	142000	1E+05	189000	153000	1E+05	2E+05	145000	705.6	2818.5	4	0.0179	6.364
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	78%	38.9	55.24023	Ref	Referen ce Miss ing (1.4091 66)	No Value s (- 0.624 62616)	No Value s (- 0.791 2209)	Referen ce Miss ing (0.966 0.7358 28785)	No Value s (- 0.7358 2774)	No Value s (- 0.798 5944)	No Value s (- 0.7877 202)	No Value s (- 0.7093 227)	Referen ce Miss ing (1.409166)	No Value s (- 0.624 62616)	No Value s (- 0.7912 209)	Referen ce Miss ing (0.966287 85)	No Value s (- 0.735 82774)	No Value s (- 0.7985 944)	No Value s (- 0.787720 2)	705.6	2818.5	4	0.016	5.669
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	95%	53.8	55.33192	Ref	-0.14	0.32	0.26	-0.13	0.27	-0.25	-0.33	3090	2230	3330	3580	3000	3480	2530	2370	940.5	2818.5	3	0.0348	12.33

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	95%	55.9	55.28259	Ref	0.29	0.016	-0.05	-0.058	-0.04	0.094	0.07	9350	10400	9380	10100	11000	9780	11200	10900	705.6	2818.5	4	0.0248	8.79
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	86%	44.6	55.29058	Ref	-0.1	0.22	0.11	0.032	0.12	0.11	-0.02	1690	1620	2190	2290	2390	2220	2300	2090	940.5	2818.5	3	0.0223	7.919
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	94%	52.7	55.2898	Ref	-0.19	0.36	0.12	-0.41	0.26	-0.06	0.1	85400	66600	1E+05	101000	76600	1E+05	89600	99100	940.5	2818.5	3	0.0203	7.206

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	90%	47.9	55.29619	Ref	0.22	0.093	0.094	0.083	0.29	-0.47	0.025	2910	3310	3300	3710	4060	4080	2520	3530	940.5	2818.5	3	0.0188	6.685
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	95%	56.6	55.26518	Ref	0.37	0.012	-0.01	0.073	-0.18	0.021	-0.21	4E+05	372000	3E+05	349000	406000	3E+05	4E+05	301000	705.6	2818.5	4	0.017	6.024
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	95%	55.5	55.31115	Ref	0.18	-0	-0.01	-0.19	0.009	-0.03	0.33	3090	3160	3030	3380	3290	3300	3350	4270	705.6	2818.5	4	0.0263	9.315

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CS1WV5 C51WV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	76%	40.1	55.25506	Ref	0.084	-0.05	0.32	0.051	0.32	-0.41	-0.13	319	302	300	432	397	418	263	317	940.5	2818.5	3	0.0174	6.164
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CS1WV5 C51WV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	93%	48.1	55.29341	Ref	0.055	0.007	0.081	0.004	-0.09	0.21	0.047	2840	2640	2770	3280	3420	2800	3590	3190	705.6	2818.5	4	0.0255	9.046
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CS1WV5 C51WV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	95%	65.9	55.23403	Ref	-0.11	0.16	0.4	-0.14	0.27	-0.13	-0.14	671	602	790	1050	792	920	729	717	940.5	2818.5	3	0.0135	4.802

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	95%	62	55.19981	Ref	-0.18	0.073	0.014	-0.31	0.21	0.036	0.22	345	239	309	333	292	368	340	382	940.5	2818.5	3	0.0101	3.567
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	89%	44.1	55.26901	Ref	0.25	0.19	-0.11	-0.24	-0.15	0.39	0.011	177	209	217	198	200	184	280	214	705.6	2818.5	4	0.0192	6.804
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA Ak	95%	58.9	55.2525	Ref	0.076	0.17	0.009	-0.02	0.16	0.073	-0.05	288	295	342	343	371	368	361	329	705.6	2818.5	4	0.0155	5.499

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FINA AK	79%	39.1	55.18532	Ref	-0.024	0.33	-0.02	-0.11	0.23	-0.03	-0.04	249	228	317	277	288	317	277	273	705.6	2818.5	4	0.0065	2.293
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEGn EQFI NAA k	86%	42.5	55.32903	Ref	0.035	-0.08	0.082	-0.051	0.064	0.082	0.16	8820	7950	7960	10000	10100	9500	10100	10500	705.9	2819.5	4	0.0209	7.401
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEGn EQFI NAA k	92%	49.5	55.32756	Ref	0.093	-0.02	-0.04	-0.084	0.28	-0.19	0.15	13000	11700	11700	13000	13900	15500	11700	14800	940.8	2819.5	3	0.0147	5.229

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEqF INAA k	94%	50.8	55.34314	Ref	0.32	-0.34	0.077	-0.11	-0.06	-0.07	0.27	20000	20400	14100	21100	20400	18400	19200	24000	705.9	2819.5	4	0.0253	8.961
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	IGEH NIDV LEG NEQ FlnA Ak	78%	38.8	55.33054	Ref	0.076	-0.13	-0.04	-0.029	0.094	-0.22	0.41	10000	8960	8430	10100	11200	10600	8900	13800	705.9	2819.5	4	0.0196	6.962
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	ISSP ATLN SR	91%	42.7	52.03449	Ref	0.23	0.15	0.009	-0.16	-0.03	-0.03	9E-04	1E+06	1070000	1E+06	1E+06	1100000	1E+06	1E+06	1120000	675.4	1348.8	2	0.0104	7.676

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S	ISSP ATLN SR	89%	41.6	52.03735	Ref	0.18	0.035	0.017	-0.17	-0.12	0.1	-0.02	6E+05	532000	5E+05	580000	564000	5E+05	6E+05	563000	675.4	1348.7	2	0.0133	9.839
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S	ISSP ATLN SR	68%	34.5	52.2753	Ref	0.11	0.055	0.092	-0.029	-0.02	0.1	0.017	15900	15400	16100	18600	18800	16600	18800	17600	675.4	1348.8	2	0.0077	5.676
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S	ISSP ATLN SR	59%	32.8	52.27393	Ref	0.21	0.072	0.066	-0.18	-0.09	0.077	0.027	34500	33000	32600	36400	33900	31600	36900	35400	675.4	1348.8	2	0.0085	6.313

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S	ISSP ATLn SR	85%	39.4	52.09574	Ref	0.27	-0.06	0.032	-0.17	-0.1	0.13	0.096	4300	4370	3760	4510	4310	3970	4850	4700	675.9	1349.7	2	0.0307	22.75
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S	ISSP ATLn SR	74%	35.7	52.23991	Ref	0.12	0.04	0.16	-0.14	0.11	-0.04	-0.08	12000	10600	11000	13300	12000	12400	11700	11300	675.9	1349.7	2	0.0117	8.656
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S	ISSP ATLn SR	95%	48.4	52.24522	Ref	0.093	0.002	0.11	-0.042	0.049	-0.05	0.11	1E+05	102000	1E+05	126000	125000	1E+05	1E+05	126000	675.9	1349.7	2	0.0115	8.478

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	ISSP ATLn SR	81%	38.1	52.29767	Ref	0.098	0.26	0.11	-0.1	0.022	-0.04	-0.06	1E+06	931000	1E+06	1E+06	1090000	1E+06	1E+06	1010000	675.9	1349.7	2	0.0108	8.019
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	ISSP ATLn SR	62%	33.4	52.25888	Ref	0.17	0.008	-0.02	-0.084	0.12	-0.04	-0.07	26900	23400	22700	25000	26400	26600	24900	24100	675.9	1349.7	2	0.0107	7.93
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	sSGS SYPS LLQc Lk	73%	38.2	54.19979	Ref	0.13	0.02	0.09	0.098	-0.09	0.1	0.062	707	749	752	886	981	754	896	866	708.7	2123.1	3	0.0123	5.796

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	vATV SLPR	59%	31.2	50.57114	Ref	0.19	0.044	0.22	-0.22	-0.04	0.068	0.007	4E+06	4250000	4E+06	5E+06	4300000	4E+06	5E+06	4540000	573.9	1145.7	2	0.0089	7.745
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	vATV SLPR	70%	33.4	50.57114	Ref	0.16	0.025	0.12	-0.16	0.003	0.14	-0.07	1E+05	111000	1E+05	132000	119000	1E+05	1E+05	115000	573.9	1145.7	2	0.0088	7.64
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	vATV SLPR	95%	50.9	50.57114	Ref	Value Missing (- 1.2373 568)	0.47	0.21	-0.19	-0.07	-0.2	0.046	84100	Value Missing (- 1.237356 8)	72700	68200	57100	54100	51800	60800	382.9	1145.7	3	0.0086	7.524

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	vATV SLPR	95%	57.7	50.56596	Ref	-0.25	-0.07	0.055	0.26	-0.26	0.19	-0.12	55700	31900	39400	48000	60900	37200	53000	42400	382.9	1145.7	3	0.0085	7.445
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	vATV SLPR	73%	33.7	50.19457	Ref	0.17	0.084	0.016	-0.16	0.013	0.07	0.022	2E+06	2260000	2E+06	2E+06	2410000	2E+06	3E+06	2470000	573.9	1145.7	2	0.0068	5.949
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr C5IWV5 C5IWV5_ PIG,tr F1S RS2 F1SR S2_PIG	vATV SLPR	52%	30.1	50.5816	Ref	0.16	0.07	0.076	-0.07	-0.03	0.06	0.01	42000	40700	41600	46900	46700	42000	46600	44700	573.9	1145.7	2	0.0102	8.914

Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	vATV SLPR	78%	36.2	50.56238	Ref	-0.15	0.095	-0.01	-0.1	0.17	-0.16	0.22	5460	3810	4890	5090	5290	5560	4630	5960	382.9	1145.7	3	0.0084	7.367
Trypsin - Sus scrofa (Pig).	IPI:CON_T rypsin S WISS- PROT:P00 761 TRYP _PIG,sp P 00761 TR YP_PIG,tr CSIWV5 CSIWV5_ PIG,tr F1S RS2 F1SR S2_PIG	vATV SLPR	51%	29.9	50.56238	Ref	0.39	0.19	-0	-0.22	0.025	0.085	-0.17	2120	2600	2450	2410	2290	2370	2580	2150	573.9	1145.7	2	0.0082	7.117
Protein disulfide- isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P0530 7 PDIA1_ BOVIN,tr A6H7J6 A 6H7J6_BO VIN	aLAP EYAk	87%	38.9	50.86933	Ref	-0.05	0.089	-0.12	-0.2	-0.15	-0.01	-0.25	18000	15900	19000	18400	19300	17400	20100	16800	735.9	1469.9	2	0.0033	2.22
Protein disulfide- isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P0530 7 PDIA1_ BOVIN,tr A6H7J6 A 6H7J6_BO VIN	gNF DEAL AAH k	95%	59.2	53.43972	Ref	-0.34	0.23	-0.01	-0.2	0.035	-0.33	-0.16	5920	4210	6800	6470	6260	6420	5210	5830	891	1780	2	0.0156	8.762
Protein disulfide- isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P0530 7 PDIA1_ BOVIN,tr A6H7J6 A 6H7J6_BO VIN	gNF DEAL AAH k	95%	52.5	53.39366	Ref	-0.2	-0.17	-0.05	-0.033	0.16	-0.26	-0.16	41000	32600	36000	44000	49000	48800	38300	40500	594.3	1780	3	0.0143	8.018

Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	gnFDEALAAHk	95%	51.7	53.4314	Ref	-0.037	-0.2	0.083	-0.079	-0	-0.33	-0.02	49500	48000	46500	63500	62600	57500	47800	59200	594.3	1780	3	0.0174	9.753
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	gnFDEALAAHk	69%	36.3	53.38158	Ref	-0.066	-0.07	0.048	-0.1	-0.23	0.08	-0.12	14300	14800	16000	19500	19400	15500	20000	17400	594.7	1780.9	3	0.0188	10.58
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	hNQLPLVIEFTEQTAPk	79%	39.7	53.80213	Ref	-0.12	-0.19	0.014	-0.056	-0.21	0.092	-0.23	2030	1700	1750	2270	2390	1870	2410	1910	858.5	2572.4	3	0.0154	5.972
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	hNQLPLVIEFTEQTAPk	87%	41.7	53.85225	Ref	-0.089	-0.05	-0.09	-0.23	-0.44	0.18	-0.15	3000	2390	2670	2900	2910	2200	3530	2780	644.1	2572.4	4	0.0172	6.686
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	iLEFFGLk	88%	40.6	50.15616	Ref	-0.081	-0.09	-0.25	-0.27	-0.47	-0.05	0.31	4010	3200	3450	3460	3760	2870	4010	5090	525.7	1574	3	0.0174	11.04
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	iLEFFGLk	59%	29.9	49.35306	Ref	-0.025	-0.1	-0.09	-0.11	-0.55	0.066	-0.37	2390	1680	1730	1950	2120	1370	2190	1610	788	1574	2	0.0053	3.393

Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	iLEFF GLK	59%	30.2	49.30531	Ref	-0.042	-0.14	-0.14	-0.38	-0.15	-0.22	0.23	782	651	658	741	693	707	707	958	525.7	1574	3	0.0024	1.511
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	iLFIFI DSD HTD NQR	54%	34	53.94569	Ref	0.26	-0.01	-0.57	-0.22	-0.44	0.074	0.092	251	281	253	192	270	203	303	304	713.4	2137.1	3	0.0068	3.161
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	iLFIFI DSD HTD NQR	95%	60.5	53.90458	Ref	0.026	-0.24	0.059	-0.32	-0.02	0.1	-0.43	258	229	206	285	242	259	295	203	713.4	2137.1	3	0.0112	5.223
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	iTEFc HR	72%	32.3	48.60871	Ref	0.08	-0.11	-0.04	-0.34	-0.05	-0.03	-0.28	9870	9140	8720	10200	9170	9770	10300	8650	419.2	1254.6	3	0.0063	5.042
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	iTEFc HR	83%	35.9	48.38541	Ref	0.0073	-0.16	0.074	-0.34	-0.08	0.029	-0.26	7740	7010	6750	8940	7380	7740	8710	7080	419.2	1254.6	3	0.0091	7.24
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	iTEFc HR	79%	34.2	48.38276	Ref	0.012	-0.24	0.11	-0.37	0.088	-0.11	-0.28	10000	8860	8050	11500	9120	10900	9990	8770	419.2	1254.6	3	0.0082	6.499

Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	IITLE EEM Tk	80%	39.4	53.1219	Ref	0.0049	-0.1	-0.08	-0.2	-0.14	-0.04	-0.11	11700	10800	10900	12400	12600	11400	12800	12100	605.7	1814	3	0.022	12.13
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	IITLE EEM Tk	94%	47.4	53.0936	Ref	-0.042	-0.02	-0.06	-0.086	-0.21	-0.04	-0.19	7100	6480	7160	7800	8430	6770	7930	7100	908	1814	2	0.019	10.47
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	IITLE EEM Tk	88%	43.9	53.04566	Ref	-0.066	0.15	-0.18	-0.12	-0.22	-0.14	-0.24	3880	3120	3920	3500	4020	3280	3630	3360	605.7	1814	3	0.0175	9.618
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	IITLE EEM Tk	86%	42.2	52.97237	Ref	0.17	-0.05	-0.11	-0.28	-0.35	0.035	-0.13	1240	1280	1190	1280	1250	1050	1430	1270	605.7	1814	3	0.0092	5.072
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	IITLE EEM Tk	87%	42.5	53.02628	Ref	0.11	-0.23	-0.13	-0.036	-0.18	-0.27	-0.22	800	674	578	693	817	647	634	649	605.7	1814	3	0.0138	7.601
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	ILDFl k	68%	28.2	45.94481	Ref	0.022	-0.12	-0.08	-0.14	-0.3	0.036	-0.33	2320	1900	1870	2170	2290	1790	2350	1810	678.9	1355.9	2	0.0029	2.134

Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	mDSTAN EVEA Vkl	95%	52	53.24254	Ref	-0.28	-0.22	0.041	0.085	-0.14	-0.17	-0.08	1E+05	74700	84700	114000	129000	96300	98300	104000	634.7	1901	3	0.0178	9.371
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	mDSTAN EVEA Vkl	95%	61.4	53.24391	Ref	-0.37	0.13	-0.15	-0.16	0.031	-0.11	-0.21	21700	14100	21600	20000	21900	21900	20700	19200	951.5	1901	2	0.016	8.395
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	mDSTAN E VEA Vkl	95%	71.4	53.07898	Ref	-0.26	0.12	2E-04	-0.2	-0.02	-0.15	-0.08	8610	7110	10100	10400	9960	9880	9450	9830	952	1902	2	0.0143	7.491
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	mDSTAN E VEA Vkl	94%	50.5	53.13304	Ref	-0.18	-0.19	-0.04	-0.2	0.032	-0.22	-0.13	31700	22000	23700	29500	29200	29900	26300	27600	635	1902	3	0.0129	6.754
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	nFEE VAF DEK	90%	43.1	53.00837	Ref	-0.034	0.018	-0.04	-0.13	-0.26	-0.13	-0.46	8330	6170	6940	7480	7750	6200	7090	5600	918.5	1834.9	2	0.0096	5.24
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	nNFE GEV Tk	92%	44.9	52.79092	Ref	0.011	0.017	-0.2	-0.12	-0.33	0.043	-0.32	43100	35400	38500	37200	43400	32700	44200	34000	823.4	1644.9	2	0.0191	11.62

Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	nNFE GEV Tk	64%	34.2	52.68203	Ref	0.046	0.007	-0.02	-0.22	-0.2	-0.09	-0.47	15800	13000	13700	15100	14500	12900	14500	11000	823.9	1645.9	2	0.0128	7.773
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	THIL LFLP k	83%	34.7	48.4279	Ref	-0.14	-0.04	-0.11	-0.095	-0.14	0.1	-0.1	1300	1210	1400	1510	1680	1420	1750	1510	693.4	1384.9	2	0.0072	5.184
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	THIL LFLP k	88%	37.4	48.58796	Ref	-0.021	-0.01	-0.22	-0.12	-0.21	0.21	-0.14	997	1040	1140	1110	1310	1070	1500	1170	693.4	1384.9	2	0.0092	6.67
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	THILL FLPk	90%	37.8	47.4538	Ref	-0.074	-0.39	-0.1	-0.19	-0.15	0.092	0.043	1250	1050	913	1250	1290	1170	1440	1380	423.3	1689.1	4	0.022	13.01
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	THILL FLPk	91%	40	46.61519	Ref	0.094	-0.07	-0.15	-0.16	-0.2	-0.08	-0.25	12400	11200	10800	11500	12600	10700	12200	10700	564	1689.1	3	0.0115	6.825
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	THILL FLPk	95%	44.9	46.61387	Ref	0.051	-0.02	-0.19	-0.16	-0.32	0.066	-0.31	3990	3400	3510	3510	3940	3090	4210	3220	845.5	1689.1	2	0.0106	6.265

Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	tHILL FLPk	94%	44.7	46.45412	Ref	0.093	0.092	-0.24	-0.16	-0.32	0.046	-0.35	12700	11700	12700	11300	13200	10300	13800	10500	564	1689.1	3	0.0091	5.405
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	tHILL FLPk	93%	42.2	47.00418	Ref	0.08	-0.08	-0.15	-0.24	-0.23	-0.05	-0.2	4060	3530	3420	3660	3800	3340	3950	3530	564	1689.1	3	0.0146	8.653
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	tHILL FLPk	95%	45	46.33791	Ref	0.11	0.061	-0.26	-0.19	-0.36	0.12	-0.27	700	675	708	639	738	570	833	632	845.5	1689.1	2	0.008	4.75
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	tHILL FLPk	81%	31	46.33791	Ref	-0.15	-0.04	-0.16	-0.33	-0.29	-0.17	0.23	1800	1330	1560	1600	1570	1410	1600	2100	423.3	1689.1	4	0.0069	4.106
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	tHILL FLPk	53%	24.4	46.26833	Ref	Value Missing (-0.705961)	Value Missing (-0.8236544)	Value Missing (-0.9902493)	Value Missing (-1.1307284)	0.44	0.43	0.38	101	Value Missing (-0.705961)	Value Missing (-0.8236544)	Value Missing (-0.9902493)	Value Missing (-1.1307284)	102	106	101	423.3	1689.1	4	0.0043	2.521
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	tVID YnGER	61%	31.2	50.21019	Ref	-0.18	0.14	-0.06	-0.15	-0.17	-0.19	-0.18	3E+05	199000	3E+05	262000	271000	2E+05	2E+05	242000	686.3	1370.7	2	0.0134	9.776

Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	tVIDYnGE R	87%	40.1	50.21239	Ref	-0.016	-0.28	0.39	-0.21	-0.15	-0.46	-0.18	15400	13200	12000	21300	15600	14200	11900	14400	457.9	1370.7	3	0.0133	9.679
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	vDATEESD LAQ QYG VR	95%	80	52.77208	Ref	-0.11	0.052	-0.27	0.046	-0.22	-0	-0.33	12100	9540	11600	10400	14200	10400	12600	9900	1043	2084	2	0.0139	6.658
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	vDATEESD LAQ QYG VR	69%	37.6	54.60417	Ref	0.032	0.12	-0.23	-0.14	-0.27	-0.08	-0.32	14100	11700	13500	11900	14000	11100	13300	11100	797.1	2388.2	3	0.0221	9.263
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	vHSF PTLK	56%	30.9	50.62826	Ref	-0.23	-0.09	-0.1	-0.078	-0.08	-0.08	-0.15	1E+05	80600	96700	108000	120000	1E+05	1E+05	104000	513	1535.9	3	0.015	9.771
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	vHSF PTLK	60%	31.4	50.62176	Ref	-0.024	-0.03	-0.06	-0.22	-0.12	-0.21	-0.03	8390	7500	8100	8930	8800	8200	8090	9070	769	1535.9	2	0.0145	9.441
Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	vHSF PTLK	62%	31.9	50.5294	Ref	-0.051	-0.23	0.042	-0.17	-0.08	-0.2	-0.01	2E+05	213000	2E+05	276000	263000	2E+05	2E+05	266000	513	1535.9	3	0.0135	8.814

Protein disulfide-isomerase OS=Bos taurus GN=P4HB PE=1 SV=1	sp P05307 PDIA1_BOVIN, tr A6H7J6 A6H7J6_BOVIN	vHSF PTLK	60%	31	50.28738	Ref	-0.14	0.017	-0.1	-0.16	-0.13	-0.09	-0	11500	10000	12200	12600	13400	11800	12800	13500	769	1535.9	2	0.0047	3.078
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_HUMAN, sp P69893 TBB5_CRI GR, sp P69895 TBB5_MACM U, sp P69897 TBB5_RAT, sp P99024 TBB5_MO USE, sp Q2KJD0 TBB5_BOVIN, sp Q5R943 TBB5_PONAB, sp Q767L7 TBB5_PIG, sp Q7JJU6 TBB5_PANTR, tr E2QSF4 E2QSF4_CA NFA, tr F7E0H3 F7E	aLV DLEP GTM DSV R	95%	52.7	53.75987	Ref	-0.06	-0.11	0.057	-0.12	-0.04	-0.18	0.051	10100	8610	9050	11400	11100	10200	9700	11300	960.5	1919	2	0.0132	6.857

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	aiLV DLEP GTM DSV R	74%	37.3	53.72858	Ref	0.21	0.12	-0.07	-0.083	-0.14	-0.19	-0.14	5500	6230	6340	6240	6820	5720	5790	5940	960.5	1919	2	0.0121	6.284
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	aiLV DLEP GTM DSV R	95%	52.5	53.7385	Ref	0.051	-0.03	-0.03	-0.1	-0.17	-0.14	-0.07	8200	7090	7270	8170	8550	7150	7610	7910	960.5	1919	2	0.0112	5.836

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	aLTV PELT QQV FDAK	95%	60	53.49744	Ref	0.41	-0.21	-0.11	-0.17	-0.37	0.18	-0.23	9730	11900	8340	10000	10600	8090	12300	9210	756.8	2267.3	3	0.0224	9.874
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	aLTV PELT QQV FDAK	95%	62.5	53.33862	Ref	0.061	-0.61	0.038	-0.29	-0.05	0.5	-0.03	2790	3110	2120	3730	3280	3370	5140	3560	756.8	2267.3	3	0.0173	7.613

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KJD0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	aLTV PELT QQV FDak	92%	47.4	53.34184	Ref	0.21	-0.1	-0.04	-0.19	-0.28	0.029	-0.15	1450	1410	1230	1450	1430	1180	1520	1330	756.8	2267.3	3	0.0178	7.851
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KJD0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	eIVH IQAG QcG NQI GAK	78%	40.2	54.72711	Ref	0.23	-0.07	-0.28	-0.1	-0.03	-0.09	-0.18	4820	4780	4210	4070	5080	4650	4670	4360	807.4	2419.3	3	0.0182	7.534

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	eIVH IQAG QcG NQi GAK	95%	57.4	54.76372	Ref	-0.16	0.039	0.048	-0.029	0.003	-0.09	-0.27	12700	9810	12200	13800	14400	12900	12600	11100	807.4	2419.3	3	0.0265	10.94
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	eIVH IQAG QcG NQi GAK	78%	40.3	54.7514	Ref	0.057	-0.19	-0.15	0.32	-0.19	-0.32	-0.01	3960	3680	3370	3880	5940	3630	3480	4270	807.4	2419.3	3	0.0234	9.654

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	eIVH IQAG QcG NQi GAK	53%	32.8	54.74505	Ref	-0.11	0.064	0.011	-0.17	0.031	-0.03	-0.21	9300	7580	9310	10100	9810	9830	9820	8620	605.8	2419.3	4	0.0231	9.528
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	eIVH IQAG QcG NQi GAK	71%	36.3	54.72698	Ref	0.16	-0.49	0.1	-0.15	0.18	-0.56	0.11	19400	18400	12700	21500	19900	21800	13700	21500	605.8	2419.3	4	0.0172	7.115

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E	eIVH IQAG QcG NQi	95%	64.7	54.73624	Ref	-0.078	0.015	0.13	-0.091	0.1	-0.28	-0.19	3460	3000	3470	4220	3990	3980	3200	3360	807.4	2419.3	3	0.0162	6.704
	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E	eIVH IQAG qcG NQi	79%	38.5	54.79253	Ref	0.01	-0.1	0.078	0.094	-0.05	-0.15	-0.02	18900	20600	20600	26200	29300	23200	22500	24400	606.1	2420.3	4	0.0221	9.132

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	gHYT EGA ELVD SVLD VVR	95%	62.2	54.35093	Ref	-0.031	0.032	-0.18	-0.57	-0.08	-0.04	0.079	948	682	773	750	631	772	832	895	755.1	2262.2	3	0.0121	5.365
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	gHYT EGA ELVD SVLD VVR	94%	51.9	54.35917	Ref	0.23	-0.21	0.042	0.07	-0.65	0.093	-0.37	430	394	314	420	472	250	437	315	755.1	2262.2	3	0.0142	6.253

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	gHyT EGA ELVD SVLD VVR	82%	42	55.10381	Ref	0.11	-0.22	-0.05	-0.029	-0.14	-0.05	-0.03	1490	1440	1240	1570	1750	1420	1570	1590	856.5	2566.4	3	0.0187	7.27
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	gHyT EGA ELVD SVLD VVR	73%	37.3	55.16132	Ref	-0.053	-0.25	0.17	0.072	-0.14	-0.13	0.1	2050	2050	1940	2920	3000	2250	2370	2770	642.6	2566.4	4	0.0155	6.041

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	gHyT EGA ELVD SVLD VVR	89%	44.6	55.07319	Ref	0.045	-0.1	-0.01	-0.029	-0.26	-0.15	0.27	3140	3380	3330	3970	4310	3220	3630	4780	642.6	2566.4	4	0.0123	4.81
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	gHyT EGA ELVD SVLD VVR	91%	47.8	55.06995	Ref	0.19	0.042	0.07	-0.052	-0.16	-0.04	-0.4	1720	1860	1830	2090	2120	1720	1940	1500	856.5	2566.4	3	0.0115	4.489

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	iMN TFSV VPSP k	89%	42.1	52.88612	Ref	0.4	-0.3	0.06	-0.17	-0.21	-0.11	-0.14	4760	5650	3770	5450	5120	4350	4870	4720	964.6	1927.1	2	0.0125	6.506
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	iMN TFSV VPSP k	95%	49.6	52.95538	Ref	0.21	-0.36	0.051	-0.14	-0.26	-0.01	-0.17	3780	3400	2490	3710	3590	2870	3580	3180	964.6	1927.1	2	0.0169	8.788

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	iREE YPD R	65%	33.4	51.27516	Ref	0.032	0.34	0.35	-0.17	-0.37	-0.37	-0.27	1E+05	125000	2E+05	191000	146000	1E+05	1E+05	123000	461.2	1380.7	3	0.0114	8.271
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	iSEQ FTA MFR	86%	39.5	51.69157	Ref	0.087	-0.21	0.064	-0.26	-0.09	-0.15	-0.13	9170	7320	6450	8770	7740	7570	7590	7640	767.4	1532.8	2	0.0052	3.41

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	iSVY YNE ATG Gk	95%	51.9	53.63629	Ref	0.065	-0.15	0.036	-0.1	0.093	-0.24	-0.18	7120	6360	5960	7590	7600	7600	6290	6530	955.5	1909	2	0.0155	8.101
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	iSVY YNE ATG Gk	95%	52.3	53.58586	Ref	-0.006	-0.15	-0.04	0.16	-0.1	-0.32	-0.15	7510	5910	5800	7030	8870	6480	5800	6500	955.5	1909	2	0.0126	6.572

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	ISVY YNE ATG Gk	91%	46.3	53.578	Ref	0.1	-0.07	-0.03	-0.053	-0.17	-0.13	-0.13	24600	22200	21300	24600	26700	21500	23000	22900	637.4	1909	3	0.0104	5.455
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	ISVY YNE ATG Gk	95%	59.6	53.5379	Ref	-0.13	-0.12	0.014	0.081	-0.09	-0.21	-0.07	5080	3770	4140	5090	5880	4550	4370	4780	955.5	1909	2	0.0157	8.227

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	iSVY YNE ATG Gk	80%	40	53.5894	Ref	-0.055	-0.06	-0.11	-0.07	-0.25	0.014	0.092	4200	3520	3820	4130	4680	3620	4530	4740	637.3	1909	3	0.0205	10.73
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	iSVY YnEA TGG k	86%	42.8	53.45797	Ref	0.039	-0.07	-0.26	-0.075	0.02	-0.18	0.033	15000	13000	13100	12900	16100	15000	13600	15700	637.7	1910	3	0.0212	11.11

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	ISVY YnEA TGG k	95%	58	53.55244	Ref	-0.2	0.13	-0.26	0.065	-0.19	0.002	-0.12	9950	7010	9620	8190	11300	8290	9900	9050	956	1910	2	0.0144	7.526
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	kLAV NMV PFPR	55%	29.7	51.34665	Ref	0.19	0.11	0.03	-0.15	-0.2	-0.1	-0.24	3710	4000	4100	4350	4230	3560	3980	3600	470.8	1879.1	4	0.0234	12.46

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	IAVN MVP FPR	84%	38.5	51.89869	Ref	0.32	-0.22	0.13	-0.25	-0.17	-0.03	-0.29	32500	35100	26300	37600	31800	29300	33800	27900	724.4	1446.8	2	0.0122	8.414
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	IAVn MVP FPR	81%	37.9	52.28172	Ref	0.29	-0.11	-0.06	-0.24	-0.12	-0.22	-0.07	13600	14000	11600	13400	13100	12400	12100	13300	724.9	1447.8	2	0.0104	7.144

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	IHFF MPG FAPL TSR	93%	48.7	53.62568	Ref	0.15	-0.34	-0.27	-0.24	-0.6	-0.19	0.8	1150	1290	995	1170	1310	896	1250	2450	642.3	1924	3	0.0101	5.227
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	IHFF MPG FAPL TSR	94%	50.3	53.75047	Ref	0.044	-0.08	-0.09	-0.23	Value Missin g (- 0.5304 6674)	-0.22	0.51	1450	1340	1330	1490	1490	Value Missi ng (- 0.530 46674)	1370	2250	642.4	1924	3	0.0016	0.847

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	IHFF MPG FAPL TSR	93%	49.1	53.68575	Ref	-0.14	-0.02	0.35	-0.24	-0.46	-0.19	0.069	477	361	424	617	450	339	425	505	642.3	1924	3	0.0075	3.886
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	IHFF mPG FAPL TSR	95%	59.5	53.67796	Ref	0.096	-0.18	-0.17	-0.16	-0.03	-0.11	0.14	1630	1550	1390	1560	1740	1670	1640	1940	647.7	1940	3	0.0085	4.371

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KJD0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	IHFF mPG FAPL TSR	92%	48.4	53.70511	Ref	0.15	-0.21	0.19	-0.28	-0.22	0.14	-0.35	561	519	441	651	518	472	630	447	647.7	1940	3	0.0081	4.17
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KJD0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	IHFF mPG FAPL TSR	95%	59.9	53.69752	Ref	0.16	-0.08	-0.03	-0.12	-0.49	-0.12	0.32	837	929	855	991	1030	695	939	1260	647.7	1940	3	0.0072	3.706

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	nM MAA cDPR	85%	31.3	44.21209	Ref	0.18	-0.05	0.016	-0.11	-0.24	-0.13	-0.14	67600	65600	60700	71300	71800	57400	64900	63700	679.8	1357.6	2	0.0049	3.578
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	nSSY FVE WIP NNV k	62%	36.2	54.62914	Ref	0.034	-0.34	0.14	0.043	-0.44	0.49	-0.19	3960	4700	3950	6160	6350	3980	7900	4900	769.1	2304.2	3	0.0176	7.619

Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	yLTV AAV FR	77%	35.3	50.78294	Ref	0.21	-0.32	0.14	-0.22	-0.39	-0.04	-0.05	6410	5890	4410	6840	5880	4540	6060	5950	672.4	1342.8	2	0.0038	2.804
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	7 TBB5_H UMAN,sp P69893 TBB5_CRI GR,sp P6 9895 TBB 5_MACM U,sp P69 897 TBB5 _RAT,sp P99024 T BB5_MO USE,sp Q 2KID0 TB B5_BOVIN ,sp Q5R9 43 TBB5_ PONAB,sp Q767L7 TBB5_PIG ,sp Q7JJU 6 TBB5_P ANTR,tr E 2QSF4 E2 QSF4_CA NFA,tr F7 E0H3 F7E	yLTV AAV FR	79%	36	50.90808	Ref	0.36	-0.46	0.027	-0.23	-0.16	9E-04	-0.27	1280	1270	785	1240	1140	1050	1220	1000	672.4	1342.8	2	0.007	5.245

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,trans D0G7F7 D0G7F7_PIG,trans E2R662 E2R662_CANF A,trans F7GGJ7 F7GGJ7_MONDO	aEGDVAALNR	94%	45.2	50.80778	Ref	-0.54	-0.02	-0.38	-0.16	0.27	-0.5	0.22	2E+05	128000	2E+05	174000	224000	3E+05	2E+05	263000	660.4	1318.7	2	0.0103	7.839
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,trans D0G7F7 D0G7F7_PIG,trans E2R662 E2R662_CANF A,trans F7GGJ7 F7GGJ7_MONDO	aEVS ELK	51%	31.1	51.71753	Ref	-0.6	-0.05	-0.34	-0.082	0.19	-0.55	0.24	3E+05	139000	2E+05	203000	267000	3E+05	2E+05	302000	692.4	1382.8	2	0.0158	11.45
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,trans D0G7F7 D0G7F7_PIG,trans E2R662 E2R662_CANF A,trans F7GGJ7 F7GGJ7_MONDO	aGLNSLE AVK	95%	60.7	51.53116	Ref	-0.51	0.31	-0.18	-0.21	0.075	-0.9	0.2	1000	615	1180	941	1020	1080	575	1230	674.4	1346.8	2	0.0132	9.767

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tr D0G7F7 D0G7F7_PIG,tr E2R662 E2R662_CANFA,tr F7GGJ7 F7GGJ7_MONDO	aGLNSLEAVk	95%	60	51.54987	Ref	-0.083	-0	-0.48	-0.32	0.18	-0.54	-0.11	2730	1860	2130	1720	2120	2610	1650	2210	674.4	1346.8	2	0.0139	10.3
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tr D0G7F7 D0G7F7_PIG,tr E2R662 E2R662_CANFA,tr F7GGJ7 F7GGJ7_MONDO	aGLnSLEAVk	95%	55.3	51.90029	Ref	0.15	0.17	-0.49	-0.62	-0.19	-0.33	-0.03	1220	1020	1120	798	804	946	894	1100	674.9	1347.7	2	0.0176	13.01
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tr D0G7F7 D0G7F7_PIG,tr E2R662 E2R662_CANFA,tr F7GGJ7 F7GGJ7_MONDO	aGLnSLEAVk	95%	47.6	51.90475	Ref	0.032	0.35	-0.65	-0.62	-0.22	-0.18	-0.02	681	553	749	421	473	546	586	649	674.9	1347.7	2	0.0171	12.66

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	cGDL EEEL k	56%	31.8	51.48902	Ref	-0.07	-0.12	-0.34	-0.12	0.008	-0.34	0.008	42500	34200	35900	34500	44200	42300	34700	43800	564	1688.8	3	0.0169	10
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	cGDL EEEL k	65%	33.1	51.51272	Ref	-0.58	0.019	-0.29	-0.14	0.033	-0.47	0.056	20500	9820	16100	14600	17900	17600	13000	18500	845.4	1688.8	2	0.0157	9.308
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	cGDL EEEL k	74%	35.4	51.69136	Ref	-0.32	-0.13	-0.26	-0.3	0.023	-0.49	0.12	10500	5900	7270	7480	8020	8750	6400	9700	845.4	1688.8	2	0.0097	5.77

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	hIAE EAD R	74%	34.6	50.20245	Ref	-0.44	0.091	-0.17	-0.24	0.22	-0.7	0.11	35000	22000	34500	32300	33900	40700	22500	39300	415.6	1243.6	3	0.0108	8.671
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	hIAE EAD R	78%	35.7	50.20519	Ref	-0.51	0.11	-0.28	-0.18	0.12	-0.51	0.2	37300	23200	38800	33100	39300	42200	28500	46100	415.6	1243.6	3	0.0107	8.599
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	IQAL QQQ ADE AED R	95%	72.1	52.89125	Ref	-0.43	0.091	-0.39	-0.18	0.011	-0.28	0.11	8100	5010	7780	6240	8000	7950	6790	8830	960	1918	2	0.0044	2.281

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,triD0G7F7 D0G7F7_PIG,triE2R662 E2R662_CANFA,triF7GGJ7 F7GGJ7_MONDO	iQLV EEEL DR	94%	46.3	52.39497	Ref	-0.51	0.45	-0.62	-0.062	0.077	-0.45	-0.23	1E+05	81700	2E+05	91900	149000	1E+05	1E+05	120000	774.4	1546.8	2	0.0056	3.617
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,triD0G7F7 D0G7F7_PIG,triE2R662 E2R662_CANFA,triF7GGJ7 F7GGJ7_MONDO	iQLV EEEL DR	95%	49	52.38994	Ref	-0.45	0.35	-0.49	-0.22	-0.09	-0.2	-0.19	2620	1450	2730	1720	2290	2180	2110	2110	774.4	1546.8	2	0.0121	7.79
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,triD0G7F7 D0G7F7_PIG,triE2R662 E2R662_CANFA,triF7GGJ7 F7GGJ7_MONDO	iQLV EEEL DR	94%	46.1	52.33138	Ref	-0.5	0.36	-0.54	-0.22	0.013	-0.18	-0.11	2870	1670	3300	1970	2720	2790	2550	2650	774.4	1546.8	2	0.0116	7.48

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,triD0G7F7 D0G7F7_PIG,triE2R662 E2R662_CANFA,triF7GGJ7 F7GGJ7_MONDO	iQLV EEEL DR	79%	37.3	52.28772	Ref	-0.53	0.3	-0.43	0.024	0.028	-0.3	-0.04	2070	1330	2560	1730	2620	2300	1910	2270	774.4	1546.8	2	0.0083	5.348
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,triD0G7F7 D0G7F7_PIG,triE2R662 E2R662_CANFA,triF7GGJ7 F7GGJ7_MONDO	iQLV EEEL DR	73%	35.9	52.56576	Ref	-0.25	0.2	-0.52	-0.14	-0.01	-0.25	-0.05	1470	1060	1560	1070	1530	1460	1300	1480	774.4	1546.8	2	0.0024	1.562
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,triD0G7F7 D0G7F7_PIG,triE2R662 E2R662_CANFA,triF7GGJ7 F7GGJ7_MONDO	iQLV EEEL DR	95%	53.4	52.41823	Ref	-0.52	0.19	-0.35	-0.19	-0.22	-0.1	-0.1	644	330	587	453	558	477	541	538	774.4	1546.8	2	0.0064	4.159

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,triD0G7F7 D0G7F7_PIG,triE2R662 E2R662_CANF A,triF7GGJ7 F7GGJ7_MOND O	iQLV EEEL DRA QER	52%	33.8	54.10924	Ref	-0.47	0.002	-0.37	-0.047	0.15	-0.14	0.28	654	569	855	739	1020	1020	873	1160	678	2031.1	3	0.0135	6.631
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,triD0G7F7 D0G7F7_PIG,triE2R662 E2R662_CANF A,triF7GGJ7 F7GGJ7_MOND O	kiQA LQQ QAD EAE DR	84%	42.8	54.76839	Ref	-0.32	-0.19	-0.08	-0.13	0.088	-0.31	0.12	5250	3990	4730	5740	6100	6190	4900	6550	784.4	2350.2	3	0.0253	10.77
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,triD0G7F7 D0G7F7_PIG,triE2R662 E2R662_CANF A,triF7GGJ7 F7GGJ7_MOND O	kiQA LQQ QAD EAE DR	95%	72.6	54.7773	Ref	-0.49	0.12	-0.23	-0.29	0.19	-0.49	0.17	7950	5080	8430	7430	7840	9550	6200	9750	784.4	2350.2	3	0.0215	9.126

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tri D0G7F7 D0G7F7_PIG,tri E2R662 E2R662_CANF A,tri F7GGJ7 F7GGJ7_MOND O	KIQA LQQ QAD EAE DR	84%	42.7	54.77318	Ref	-0.27	-0.03	-0.2	-0.19	-0.06	-0.23	0.14	10600	8100	10400	10400	11500	11000	10200	13100	784.4	2350.3	3	0.0206	8.743
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tri D0G7F7 D0G7F7_PIG,tri E2R662 E2R662_CANF A,tri F7GGJ7 F7GGJ7_MOND O	KIQA LQQ QAD EAE DR	92%	48.7	54.78451	Ref	-0.13	0.034	-0.23	-0.24	-0.07	-0.35	0.1	6890	5700	6910	6460	7060	6940	5960	8100	784.4	2350.3	3	0.0202	8.59
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tri D0G7F7 D0G7F7_PIG,tri E2R662 E2R662_CANF A,tri F7GGJ7 F7GGJ7_MOND O	KIQA LQQ QAD EAE DR	95%	73.1	54.74796	Ref	-0.49	-0.01	-0.24	-0.016	-0.03	-0.33	0.14	12500	7820	11800	11300	14600	12600	10700	14700	784.4	2350.3	3	0.0191	8.118

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,triD0G7F7 D0G7F7_PIG,triE2R662 E2R662_CANFA,triF7GGJ7 F7GGJ7_MONDO	KIQA LQQ QAD EAE DR	95%	90.7	54.79657	Ref	-0.7	-0.08	-0.3	-0.08	0.074	-0.44	0.39	51500	28000	46700	44800	57600	56000	40900	72400	784.4	2350.2	3	0.0218	9.292
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,triD0G7F7 D0G7F7_PIG,triE2R662 E2R662_CANFA,triF7GGJ7 F7GGJ7_MONDO	KIQA LQQ QAD EAE DR	95%	58.3	54.77318	Ref	-0.7	0.097	-0.4	-0.061	0.25	-0.6	0.22	34000	18200	34300	27400	38000	41200	23900	41700	784.4	2350.3	3	0.0206	8.743
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,triD0G7F7 D0G7F7_PIG,triE2R662 E2R662_CANFA,triF7GGJ7 F7GGJ7_MONDO	kLVIL EGEL ER	68%	32.1	49.39265	Ref	-0.57	0.41	-0.3	-0.16	0.028	-0.21	-0.14	11800	7550	16200	11100	13500	13400	11800	12300	636.4	1906.2	3	0.0101	5.273

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	kLVILEGELER	79%	35.3	49.57301	Ref	-0.9	0.22	-0.18	0.076	0.046	-0.41	-0.14	11300	4880	11500	9760	12900	11000	8400	10000	636.4	1906.2	3	0.0124	6.516
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	kLVILEGELER	65%	29.4	49.25379	Ref	-0.46	-0.05	-0.25	-0.13	0.006	0.071	-0.02	1420	964	1390	1360	1630	1560	1710	1590	477.5	1906.2	4	0.0074	3.902
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	kLVILEGELER	72%	32.5	48.88337	Ref	-0.17	-0.15	-0.2	-0.11	0.19	-0.21	-0.14	694	586	642	695	818	879	695	726	636.4	1906.2	3	0.002	1.057

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	IVILEGELE	59%	32.2	51.6123	Ref	-0.2	-0.11	-0.45	-0.13	0.2	-0.48	0.14	577	437	503	448	615	673	441	674	737.9	1473.9	2	0.0064	4.365
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	mEI QEM QLk	87%	41.5	53.20975	Ref	-0.98	0.83	-0.86	0.075	-0.47	0.11	-0.85	13000	4900	18700	6480	13700	8200	12800	6530	879.5	1756.9	2	0.0207	11.8
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	mEI QEM QLk	95%	55.2	53.20105	Ref	-0.59	0.071	-0.42	-0.038	0.41	-0.78	-0.02	24400	13100	22500	18000	25800	30700	14100	23700	879.5	1757	2	0.0176	9.987

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	nVTn NLk	67%	33.9	51.81103	Ref	-0.32	-0.03	-0.25	-0.16	0.029	-0.39	0.12	39800	27100	36000	34600	40800	40500	31700	44700	706.4	1410.8	2	0.0057	4.041
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	rIQL VEEE LDR	93%	47.9	52.64631	Ref	-0.26	0.094	-0.07	-0.15	-0.07	-0.15	-0.18	4260	3360	4680	4690	4870	4510	4470	4340	568.7	1703	3	#####	0.553
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANFA,tron F7GGJ7 F7GGJ7_MONDO	rIQL VEEE LDR	93%	48	52.84164	Ref	-0.44	0.42	-0.15	-0.005	-0.22	-0.4	-0.11	17000	12200	24000	18100	22100	16600	15300	18600	568.7	1702.9	3	0.0121	7.088

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tr D0G7F7 D0G7F7_PIG,tr E2R662 E2R662_CANF A,tr F7GGJ7 F7GGJ7_MOND O	rIQLVEEE LDR	86%	42.1	52.78941	Ref	-0.28	-0.05	-0.04	-0.057	-0.02	-0.4	-0.02	8680	6490	8280	9360	10200	9080	7280	9440	568.7	1702.9	3	0.0044	2.564
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tr D0G7F7 D0G7F7_PIG,tr E2R662 E2R662_CANF A,tr F7GGJ7 F7GGJ7_MOND O	rIQLVEEE LDR	66%	34.6	52.71126	Ref	-0.5	0.17	-0.1	-0.047	-0.11	-0.26	-0.25	1450	830	1440	1340	1530	1280	1200	1200	852.5	1702.9	2	0.0027	1.557
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tr D0G7F7 D0G7F7_PIG,tr E2R662 E2R662_CANF A,tr F7GGJ7 F7GGJ7_MOND O	sLEAASEK	93%	44.5	52.04728	Ref	-0.55	-0.09	-0.45	-0.057	0.16	-0.57	0.4	30800	18500	27800	24200	35100	35700	22400	43600	721.9	1441.8	2	0.0251	17.41

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANF A,tron F7GGJ7 F7GGJ7_MONDO	sLEA ASEK	75%	35.9	52.11046	Ref	-0.7	0.024	-0.24	-0.078	0.33	-0.67	0.17	1E+05	74400	1E+05	124000	154000	2E+05	93000	165000	721.9	1441.8	2	0.0185	12.85
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANF A,tron F7GGJ7 F7GGJ7_MONDO	sLEA ASEK	52%	31.5	51.75065	Ref	-0.58	0.02	-0.41	-0.12	0.22	-0.47	0.24	37600	22100	36300	30400	40700	45000	29200	47400	481.6	1441.8	3	0.0044	3.057
Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tron D0G7F7 D0G7F7_PIG,tron E2R662 E2R662_CANF A,tron F7GGJ7 F7GGJ7_MONDO	sLEA ASEK	84%	38.9	52.05313	Ref	-0.67	0.081	-0.33	-0.04	0.21	-0.44	0.049	21600	11500	21000	17700	23900	24800	16500	23000	721.9	1441.8	2	0.0256	17.75

Tropomyosin alpha-4 chain OS=Equus caballus GN=TPM4 PE=1 SV=2	sp P02561 TPM4_HORSE,sp P67936 TPM4_HUMAN,sp P67937 TPM4_PIG,tri D0G7F7 D0G7F7_PIG,tri E2R662 E2R662_CANFA,tri F7GGJ7 F7GGJ7_MONDO	tIDDL	80%	37.8	52.54756	Ref	-0.64	0.13	-0.29	-0.17	0.19	-0.55	0.19	10600	5870	10800	9070	10900	12300	7650	12600	785.9	1569.9	2	0.0193	12.26
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	aAVT SLFA k	91%	43.5	50.68931	Ref	-0.18	0.076	-0.15	0.14	-0.52	0.6	0.24	9690	11300	14700	14100	18900	10500	23800	18400	506	1514.9	3	0.0269	17.74
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	aAVT SLFA k	78%	36.1	50.46905	Ref	-0.31	0.29	-0.23	0.24	-0.58	0.55	0.088	31200	30000	49300	38700	59000	29200	66700	48100	506	1514.9	3	0.0154	10.14
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	aAVT SLFA k	95%	60.4	51.06126	Ref	-0.022	0.22	-0.11	0.13	-0.4	0.56	-0.26	7080	8120	10400	9300	12100	7310	14900	8390	758.5	1514.9	2	0.0252	16.65
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	aAVT SLFA k	78%	36.1	50.47064	Ref	-0.11	0.35	-0.3	0.085	-0.46	0.61	-0.01	46800	57300	85300	61100	87800	52500	1E+05	74300	506	1514.9	3	0.0177	11.64

Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	ILGN VLVV VLAR	95%	60.8	41.3615	Ref	0.084	-0.08	0.03	-0.063	-0.48	0.5	-0.27	994	886	855	1040	1070	701	1450	842	785.5	1569	2	0.0103	6.544
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	ILGN VLVV VLAR	95%	61.6	41.3615	Ref	0.2	-0.03	-0.11	0.11	-0.23	0.22	-0.55	219	191	177	188	241	166	237	139	524	1569	3	0.0119	7.584
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	ILGN VLVV VLAR	95%	65.8	43.56026	Ref	-0.046	-0.33	-0.03	0.24	-0.33	0.096	0.089	228	171	153	212	281	165	232	229	524	1569	3	0.0134	8.505
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	ILGN VLVV VLAR	95%	43.4	42.97279	Ref	0.03	-0.04	0.008	-0.057	-0.49	0.54	-0.19	3170	2900	2990	3470	3660	2370	5060	3020	785.5	1569	2	0.0106	6.743
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	ILGN VLVV VLAR	95%	40.7	42.7358	Ref	-0.088	0.15	-0.02	-0.16	-0.63	0.6	-0.28	1330	1030	1320	1310	1320	827	2030	1100	785.5	1569	2	0.0074	4.73
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	ILGN VLVV VLAR	95%	50	42.71074	Ref	Value Missing (-1.3099478)	Value Missing (-1.4276413)	0.74	Value Missing (-1.7347155)	Value Missing (-1.5388427)	0.64	0.64	221	Value Missing (-1.3099478)	Value Missing (-1.4276413)	Value Missing (-1.7347155)	Value Missing (-1.5388427)	208	206	524	1569	3	0.0071	4.549	

Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	ILGN VLVV VLAR	84%	31	42.97301	Ref	-0.27	-0.14	-0.03	-0.095	0.065	-0.17	0.36	266	173	206	249	263	256	227	327	524	1569	3	0.0093	5.944
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	ILGN VLVV VLAR	95%	47.9	42.5691	Ref	-0.062	-0.14	-0.03	-0.15	-0.35	0.8	-0.29	636	598	616	746	756	575	1330	619	785.5	1569	2	0.0061	3.877
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	ILGN VLVV VLAR	73%	26.6	42.54959	Ref	0.031	0.11	-0.02	-0.31	0.16	-0.51	0.011	276	197	225	232	208	252	166	235	524	1569	3	0.0046	2.906
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	ILGN VLVV VLAR	81%	29.3	42.71074	Ref	0.34	-0.09	-0.39	-0.42	-0.4	0.13	0.24	206	185	149	135	146	129	196	209	524	1569	3	0.0071	4.549
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	ILGN VLVV VLAR	74%	27.1	42.83482	Ref	0.12	-0.1	-0.02	-0.3	0.38	-0.19	-0.19	128	111	103	122	111	155	109	108	524	1569	3	0.0086	5.466
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	ILVV YPW TQR	52%	31.2	51.53592	Ref	-0.35	-0.2	-0.18	0.043	0.11	0.61	-0.32	3210	2190	2630	2990	3850	3530	5200	2720	527	1577.9	3	0.0119	7.522

Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	ILVV yPW TQR	63%	32.6	50.87	Ref	-0.17	0.25	-0.11	0.1	-0.46	0.57	-0.18	4360	4180	6100	5340	6780	4010	8560	5060	628.4	1882.1	3	0.0105	5.596
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	mLS AEEK	63%	30.6	49.4172	Ref	Reference Missing (0.1478204)	Reference Missing (0.5309423)	Reference Missing (0.17302555)	Reference Missing (0.46697262)	No Values (-1.914995)	Reference Missing (0.7086124)	Reference Missing (0.0204946)	Reference Missing (1.8884946)	Reference Missing (0.1478204)	Reference Missing (0.5309423)	Reference Missing (0.17302555)	Reference Missing (0.46697262)	No Values (-1.914995)	Reference Missing (0.7086124)	Reference Missing (0.02046124)	577.3	1152.6	2	0.0099	8.552
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vDEV GGE ALG R	76%	35.6	51.50695	Ref	0.036	0.31	-0.18	0.013	-0.23	0.41	-0.25	54800	61200	80100	64000	80800	59800	97200	61000	703.4	1404.7	2	0.0112	7.976
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vkVD EVG GEAL GR	57%	33.1	52.78962	Ref	-0.22	0.23	0.075	0.33	-0.53	0.6	-0.28	2880	3520	5210	5260	6900	3330	7590	4110	969.1	1936.1	2	0.0197	10.19
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vLDS FcEG Lk	87%	43.1	53.37445	Ref	-0.004	0.11	-0.17	-0.12	-0.45	0.47	-0	2750	2460	2890	2670	3060	2120	4190	2990	589	1763.9	3	#####	0.303
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vLDS FcEG Lk	77%	38.4	53.22582	Ref	0.1	0.16	-0.14	-0.13	-0.48	0.43	-0.25	993	876	986	899	1000	687	1350	831	589	1763.9	3	0.0135	7.663

Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	67.6	51.74688	Ref	0.23	0.023	0.19	-0.071	-0.41	0.19	-0.47	246	231	217	274	252	174	275	173	504.6	1510.9	3	#####	0.225
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	71.4	51.89617	Ref	0.27	-0.18	0.08	-0.15	-0.28	0.35	-0.36	10300	10200	8110	10900	10300	8150	13200	8000	504.6	1510.9	3	0.0114	7.573
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	68	52.02393	Ref	0.33	-0.13	-0.11	-0.1	-0.37	0.33	-0.21	3720	3880	3060	3490	3870	2800	4770	3250	504.6	1510.9	3	0.0077	5.093
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	82%	38	51.90119	Ref	0.15	-0.02	0.052	0.033	-0.42	0.37	-0.09	2270	2610	2520	2970	3230	2060	3730	2680	756.4	1510.9	2	0.0117	7.735
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	71.4	51.63835	Ref	0.26	-0.01	0.058	-0.14	-0.25	0.12	-0.12	4370	4600	4120	4860	4670	3770	5110	4280	504.6	1510.9	3	0.0092	6.065
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	73.3	52.03794	Ref	0.0072	-0.04	0.13	-0.17	-0.47	0.47	-0.16	9720	8320	8720	11000	9880	7010	14000	8990	504.6	1510.9	3	0.0082	5.41

Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	50.7	52.02393	Ref	0.021	0.013	-0	0.017	-0.31	0.47	-0.19	5220	5310	5730	6370	7110	4960	8880	5580	756.4	1510.9	2	0.0079	5.234
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	83.5	52.0584	Ref	-0.087	0.086	0.16	0.057	-0.57	0.37	-0.2	18000	15100	18400	21800	22300	12600	25300	16900	504.6	1510.9	3	0.0064	4.259
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	74.5	51.80258	Ref	0.14	0.008	-0.02	-0.2	-0.3	0.22	-0.14	4970	4190	4150	4590	4460	3610	5410	4190	504.6	1510.9	3	0.0039	2.553
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	67.6	51.63835	Ref	0.2	0.096	-0.03	-0.091	-0.26	0.23	-0.21	1690	1730	1750	1800	1910	1480	2170	1590	504.6	1510.9	3	0.0093	6.125
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	65.6	52.0744	Ref	0.23	-0.09	-0.05	-0.075	-0.18	0.2	-0.2	1660	1600	1390	1610	1740	1410	1920	1440	504.6	1510.9	3	0.0065	4.319
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	73.6	52.06448	Ref	-0.035	-0.13	0.043	-0.16	-0.03	0.098	0.05	563	442	448	568	543	521	593	569	504.6	1510.9	3	0.007	4.617

Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	60.3	51.86863	Ref	-0.24	0.32	-0.07	0.035	-0.29	-0.12	0.096	310	207	331	284	337	235	277	318	504.6	1510.9	3	0.0052	3.466
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	78.4	52.11478	Ref	0.14	0.075	-0.17	-0.031	-0.42	0.35	-0.14	6960	6510	6750	6390	7760	5180	9210	6500	505	1511.9	3	0.013	8.605
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	79.6	52.15053	Ref	0.11	0.22	-0.35	0.05	-0.25	0.38	-0.26	14800	14700	17100	13000	18900	13500	21600	13800	505	1511.9	3	0.0122	8.07
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	91%	43.1	52.16145	Ref	0.42	0.34	-0.2	-0.19	-0.36	0.3	-0.16	4230	6900	7090	5480	6070	4710	7760	5590	756.9	1511.9	2	0.0107	7.088
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	91%	45.5	51.90307	Ref	0.24	-0.12	-0.05	-0.057	-0.15	0.35	-0.12	2290	2710	2300	2710	2970	2430	3590	2570	505	1511.9	3	0.0092	6.067
Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1	sp P02081 HBBF_BOVIN	vVTG VAN ALA HR	95%	70.7	51.98203	Ref	0.25	0.13	-0.14	-0.12	-0.39	0.27	-0.14	2160	2250	2250	2100	2340	1690	2810	2100	505	1511.9	3	0.0059	3.886

Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	aFGP GLQ GGG AGS PAR	95%	52.9	52.75682	Ref	-0.21	-0	-0.29	-0.11	-0.17	-0.27	-0.22	3410	2450	3080	2830	3540	2970	2890	2970	867.5	1732.9	2	0.0107	6.176
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	aGQ SAA GAV LGIG ADT R	95%	76.6	53.45642	Ref	-0.53	0.2	-0.25	-0.19	-0.3	0.074	-0.43	17600	10000	18000	14900	17000	13800	18600	13100	910	1818	2	0.005	2.738
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	aHV VPcF DPSK	95%	55.4	53.42476	Ref	0.036	-0.22	-0.14	-0.24	-0.14	-0.04	-0.41	11100	10500	9590	11400	11700	11000	12200	9420	618.7	1853	3	0.0121	6.517
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	aLTQ TGG PHVk	77%	37.2	52.05502	Ref	-0.18	-0.13	-0.19	-0.13	-0.15	-0.1	-0.25	50900	40700	45400	48900	56200	48500	52500	47100	573	1716	3	0.0122	7.132
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	aLTQ TGG PHVk	88%	42.7	52.05061	Ref	-0.16	-0.08	-0.27	-0.04	-0.1	-0.24	-0.3	69800	55300	63100	62400	80500	67300	63800	60900	573	1716	3	0.0141	8.198
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	aSGP GLN TTG VPAS LPVE FTID Ak	95%	56.3	54.86772	Ref	-6E-04	-0.22	-0.24	-0.12	0.097	-0	-0.63	2360	2310	2150	2380	2850	2900	2820	1810	984.2	2949.6	3	0.0213	7.216

Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	aSGP GLN TTG VPAS LPVE FTID Ak	95%	55.1	54.44304	Ref	-0.37	-0.09	-0.07	-0.16	-0.24	-0.28	-0.18	2880	1740	2300	2620	2710	2240	2270	2420	984.2	2949.6	3	0.0077	2.62
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	dAG EGG LSLAI EGPS k	89%	45.3	54.09065	Ref	-0.13	-0.01	-0.23	-0.16	-0.44	-0.1	-0.41	17700	12300	14500	14000	16200	11700	15400	12300	703.7	2108.1	3	0.0243	11.52
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	dAG EGLL AVQI TDPE GkPk	95%	55.5	53.44032	Ref	-0.25	-0.03	-0.32	-0.12	-0.31	-0.01	-0.34	7790	5260	6670	6120	7740	5940	7600	6010	950.9	2849.6	3	0.0279	9.778
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	dAP QDF HPD R	95%	51.2	49.29025	Ref	-0.47	0.6	-0.49	-0.1	-0.32	-0.07	-0.33	42800	34100	77500	41000	58900	44300	55000	45500	501.2	1500.7	3	0.0115	7.686
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	eAG AGG LAIA VEG PSk	95%	80.6	53.28781	Ref	-0.21	0.024	-0.24	-0.073	-0.41	-0.11	-0.56	5900	3720	4760	4440	5500	3810	4900	3550	1018	2034.1	2	0.0159	7.788
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	eATT EFSV DAR	86%	38.2	50.65565	Ref	0.046	-0.03	-0.18	-0.18	-0.42	-0.11	-0.35	36200	32900	33900	34400	37700	27900	36100	30400	765.4	1528.8	2	0.0135	8.839

Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	eGPY SISV LYGD EEVPR	88%	44.6	53.77803	Ref	0.12	-0.21	-0.3	-0.25	-0.31	-0.28	-0.24	4630	3810	3290	3490	3970	3320	3540	3620	738.7	2213.1	3	0.0041	1.873
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	enGL YLID Vk	51%	32.2	52.61196	Ref	0.4	-0.68	-0.52	-0.6	-0.99	-0.56	-0.74	32300	17300	8890	11100	11600	7750	10900	9510	591.7	1772	3	0.0106	5.955
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	fNEE HIPD SPFV VPV ASPS GDA R	95%	55.8	54.72347	Ref	0.13	0.5	-0.35	-0.26	-0.48	-0.2	-0.68	1650	1770	2490	1540	1810	1370	1720	1230	924.5	2770.4	3	0.0085	3.054
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	gAG TGG LGLA VEG PSEA k	95%	62.3	54.20746	Ref	-0.37	0.054	-0.27	0.18	-0.31	-0.21	-0.43	5400	3470	5070	4540	6850	4250	4760	4050	1090	2178.2	2	0.0215	9.846
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	gQH VPG SPFQ FTVG PLGE GGA Hk	77%	38.8	55.44592	Ref	-0.024	-0.2	-0.24	-0.12	-0.22	-0.15	-0.27	2940	2480	2370	2590	3100	2540	2770	2530	728.9	2911.5	4	0.0136	4.656
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	iVGP SGA AVPc k	76%	37.9	52.88746	Ref	0.2	-0.01	-0.23	-0.062	-0.7	-0.26	-0.18	12800	13800	12900	12400	15400	8610	12200	12800	585	1752	3	0.0112	6.394

Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	IIALL EVLS Qk	95%	47.5	45.52084	Ref	0.22	-0.34	-0.33	-0.2	-0.26	-0	-0.74	366	317	233	262	316	266	331	197	612.4	1834.2	3	0.0075	4.079
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	IIALL EVLS Qk	75%	30.1	45.52206	Ref	0.13	-0.04	-0.04	-0.43	-0.53	-0.46	-0.37	180	137	132	148	124	101	111	118	612.4	1834.2	3	0.0082	4.487
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	IYSV SYLL k	91%	43	50.24502	Ref	-0.016	-0.28	-0.17	-0.2	-0.5	0.24	-0.42	5030	4260	3830	4660	5010	3570	6240	3890	565.3	1693	3	0.0103	6.054
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	rLTV SSLQ ESGL k	66%	33.7	51.32692	Ref	-0.14	-0.04	-0.11	-0.12	-0.28	0.039	-0.44	9610	8370	9690	10400	11400	8880	11600	8240	676.1	2025.2	3	0.017	8.373
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	sPFS VGV SPSP DLSk	95%	53.5	53.51976	Ref	-0.31	-0.05	-0.11	-0.17	-0.36	-0.04	-0.34	12200	7800	10200	10900	11600	8850	11600	9330	710.1	2127.2	3	0.0158	7.444
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	sPFS VGV SPSP DLSk	86%	42.5	53.40361	Ref	0.034	-0.19	-0.26	-0.24	-0.08	-0.16	-0.17	5070	4970	4610	4940	5520	5390	5330	5230	710.1	2127.2	3	0.0098	4.611

Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	sPFS VGV SPSL DLSK	90%	45.2	53.29536	Ref	-0.32	-0.12	-0.29	-0.34	-0.23	-0.25	-0.36	12100	5920	7390	7370	7870	7380	7600	7010	710.1	2127.2	3	0.0067	3.145
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	sPFS VGV SPSL DLSK	90%	45.8	53.52422	Ref	0.42	0.058	-0.32	-0.33	-0.37	-0.32	-0.35	4460	5840	4940	4270	4660	3970	4290	4180	710.1	2127.2	3	0.0155	7.275
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	sPFS VGV SPSL DLSK	79%	39.6	53.65355	Ref	0.038	-0.19	-0.1	-0.32	-0.38	-0.15	-0.19	1300	1120	1040	1240	1170	980	1210	1160	710.1	2127.2	3	0.0212	9.94
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	tFSV WYV PEVT GTH k	95%	55.1	54.59512	Ref	0.19	-0.02	-0.4	-0.2	-0.21	-0.08	-0.65	717	695	651	565	714	617	709	472	787.1	2358.3	3	0.0173	7.313
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	tFSV WYV PEVT GTH k	94%	51.1	54.57061	Ref	-0.068	-0.23	-0.1	-0.069	-0.37	-0.07	-0.28	834	708	689	842	949	675	863	742	787.1	2358.3	3	0.0114	4.833
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	vNV GAG SHP Nk	72%	35.8	52.61971	Ref	-0.17	0.016	-0.16	-0.18	-0.21	-0.24	-0.4	4830	3480	4290	4260	4620	3970	4070	3600	844.5	1687	2	0.0123	7.293

Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	vNV GAG SHP Nk	77%	37.7	52.44445	Ref	-0.11	0.065	-0.29	-0.11	-0.28	-0.21	-0.25	19200	15900	19500	17200	21400	16600	18200	17600	563.3	1687	3	#####	0.43
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	vPVH DVT DASK	61%	34.4	53.2462	Ref	0.24	0.31	-0.34	-0.15	-0.37	-0.43	-0.57	38400	42900	49200	35100	44100	33100	33100	29800	592.7	1775	3	0.0129	7.278
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	vSG QGL HEG HTFE PAEF IIDT R	91%	46	54.93943	Ref	0.033	0.044	-0.16	-0.3	-0.3	-0.11	-0.15	1550	1680	1840	1800	1800	1560	1860	1800	686.9	2743.4	4	0.0133	4.849
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	vTVL FAG QHIA k	95%	63.8	49.66076	Ref	0.037	-0.27	-0.16	-0.12	-0.45	0.011	-0.39	1210	1020	894	1080	1230	854	1230	923	946.6	1891.1	2	0.0085	4.501
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	vTYT PMA PGSY LISik	69%	36.9	53.8133	Ref	0.22	-0.06	-0.31	-0.034	-0.44	-0.28	0.013	895	1220	1090	1030	1370	906	1050	1280	783.8	2348.3	3	0.0175	7.456
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	yGG DEIP FSPY R	91%	42.3	51.50968	Ref	-0.12	-0.05	-0.22	-0.1	-0.27	-0.14	-0.26	6100	5070	5780	5740	6880	5340	6090	5590	852.9	1703.8	2	0.0044	2.566

Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	yGG DEIP FSPY R	61%	32.4	51.55224	Ref	-0.19	0.009	-0.28	-0.1	-0.28	-0.02	-0.26	3440	2790	3480	3200	3990	3070	3840	3240	852.9	1703.8	2	0.0018	1.065
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	yGG PYHI AGS Pfk	53%	33.8	53.93145	Ref	0.026	-0.13	-0.32	-0.13	-0.24	-0.05	-0.11	9310	9910	9670	9480	11900	9630	11500	10900	668	2001.1	3	0.0175	8.748
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	yTPV QQG PVGI NVT YGG DAIP k	95%	58.8	54.98977	Ref	-0.095	-0.05	-0.14	-0.22	-0.06	-0.29	-0.19	2080	1900	2130	2230	2340	2280	2030	2160	961.5	2881.6	3	0.027	9.35
Uncharacterized protein OS=Bos taurus GN=FLNA PE=4 SV=1	tr F1N169 F1N169_BOVIN	yTPV QQG PVGI NVT YGG DAIP k	80%	41.3	54.89337	Ref	0.15	-0.44	-0.24	-0.12	0.14	-0.35	-0.55	1140	1070	772	994	1190	1240	924	801	961.5	2881.6	3	0.0209	7.258
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_CAPHI	aQE DL	64%	30	48.44701	Ref	-0.11	-0.16	0.003	-0.074	0.28	-0.32	0.063	776	603	633	796	832	931	639	828	440.2	878.46	2	0.0048	5.452

Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	aQE DL	60%	29.3	48.56644	Ref	0.14	-0.21	-0.17	-0.082	0.045	-0.09	-0.09	5330	4410	3750	4330	5070	4830	4600	4550	440.2	878.46	2	0.0056	6.362
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	dGEE SGA YDG PR	92%	38.5	46.89211	Ref	0.37	0.17	-0.02	-0.16	-0.13	-0.38	-0.32	13100	13600	12900	12700	12600	11300	9930	10300	778.9	1555.7	2	0.0099	6.33
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	dLFS EAHS EFLK	87%	44	54.20421	Ref	0.25	-0.35	0.16	-0.068	0.085	-0.2	-0.21	63400	64300	46100	73500	69100	67100	57600	56500	677.7	2030.1	3	0.018	8.854
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	dLFS EAHS EFLK	95%	63.5	54.20972	Ref	0.18	-0.2	-0.03	-0.075	0.14	-0.2	-0.11	2090	2020	1680	2120	2260	2300	1890	2000	1016	2030.1	2	0.0168	8.285

Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	dLLI AYY DVD	YEk	95%	62.2	54.60251	Ref	0.081	-0.2	0.12	-0.14	0.11	0.023	-0.09	1130	1140	1010	1420	1310	1360	1340	1230	743.4	2227.2	3	0.0122	5.498
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	dLLI AYY DVD	YEk	95%	65.2	54.55527	Ref	0.14	-0.29	0.077	-0.25	0.073	0.075	-0.08	2360	2260	1830	2640	2320	2530	2650	2350	743.4	2227.2	3	0.0141	6.319
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	dLLI AYY DVD	YEk	94%	52.2	54.59309	Ref	0.38	-0.3	0.14	-0.31	-0.03	-0.03	-0.09	668	801	541	825	665	708	740	700	743.4	2227.2	3	0.0106	4.757
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	dLLI AYY DVD	YEk	95%	55.3	54.5719	Ref	0.27	-0.05	-0.11	-0.26	0.25	-0.1	-0.01	404	508	441	476	473	587	482	508	743.4	2227.2	3	0.0077	3.451

Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C API	dLLI AYY DVD YEK	66%	36.9	54.58197	Ref	0.072	0.031	0.11	-0.021	0.26	-0.24	-0.41	369	361	381	451	454	481	356	315	743.4	2227.2	3	0.0165	7.396
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C API	dPNI VIAK	51%	29	49.48604	Ref	0.18	0.043	0.12	-0.36	0.15	0.031	-0.35	10200	10800	10700	12700	9990	12500	12000	9130	493.3	1476.9	3	0.0243	16.42
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C API	eAT NPP VIQE EkPk	81%	39.1	52.98945	Ref	-0.16	-0.01	0.14	-0.018	0.28	-0.41	-0.15	9550	7290	8780	10900	10800	11600	7520	8910	831.5	2491.4	3	0.0178	7.126
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C API	eLSD FISYL k	70%	36.1	52.98945	Ref	-0.099	0.01	-0.01	-0.079	0.007	-0.04	0.098	1150	996	1170	1290	1360	1260	1270	1390	608.3	1822	3	0.0131	7.199

Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	eLSD FISYL	90%	44.7	52.98925	Ref	-0.2	-0.04	0.014	0.12	0.009	0.047	-0.12	924	720	874	1020	1210	976	1050	925	608.3	1822	3	0.0111	6.08
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	fLED YFD GNlk	94%	50.7	53.83518	Ref	0.18	-0.22	-0.06	-0.15	-0	-0.15	0.11	6280	5980	4930	6190	6410	6180	5840	6940	657	1968	3	0.0123	6.258
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	gFPT IYFS PAN	58%	34.6	53.92202	Ref	-0.075	-0.24	0.086	-0.16	0.2	-0.23	0.097	527	420	406	571	533	597	463	574	650.7	1949.1	3	0.0211	10.83
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	gFPT IYFS PAN	91%	46.7	53.91743	Ref	-0.23	-0.19	-0.02	-0.021	0.15	-0.34	0.32	20200	14800	16400	20900	22900	22500	16800	26300	650.7	1949.1	3	0.0209	10.74

Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	gFPT IYFS PAN	93%	46.1	53.57588	Ref	0.16	-0.06	0.1	-0.11	0.15	-0.42	-0.08	4530	4450	4160	5220	4950	5200	3660	4600	975.5	1949.1	2	0.0106	5.437
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	gFPT IYFS PAN	89%	43.2	53.60177	Ref	0.049	-0.09	0.14	-0.14	0.11	-0.21	-0.07	7470	6770	6670	8770	7960	8250	6920	7600	975.5	1949.1	2	0.0127	6.493
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	gFPT IYFS PAnk	83%	40.1	52.71223	Ref	-0.18	-0.13	0.1	-0.033	0.19	-0.39	0.078	4180	3030	3410	4490	4500	4570	3220	4400	795.1	2382.4	3	0.0108	4.532
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	gIVP LAK	66%	23.6	41.344	Ref	0.022	-0.21	0.072	-0.071	0.003	-0.22	-0.08	47300	35500	32900	44800	44700	41100	36700	40400	436	1304.9	3	0.0064	4.876

Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	gIVP LAK	56%	21.4	41.344	Ref	0.068	-0.1	0.002	0.065	-0.03	-0.24	-0.15	86100	70400	68000	81900	94300	77100	69500	73400	653.4	1304.9	2	0.0049	3.723
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	kDP NIVI AK	71%	26.6	43.72009	Ref	-0.13	-0.08	0.046	-0.12	0.22	-0.23	-0.1	5980	4260	4780	5870	5750	6360	4870	5310	955.6	1909.2	2	0.0012	0.651
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	kQA GPA SVPL k	67%	28.6	46.16958	Ref	0.16	-0.05	-0.01	-0.21	0.037	-0.1	0.042	10500	10800	10100	11600	11200	11600	11000	12100	670.1	2007.3	3	0.0024	1.173
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	kQA GPA SVPL kSEE EFEK	76%	35	52.00941	Ref	-0.18	-0.07	0.22	0.076	0.11	-0.24	-0.04	5020	4210	4920	6750	6740	6040	4930	5620	798.5	3189.8	4	0.0136	4.252

Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	IHFAS	55%	30.1	50.03254	Ref	0.36	0.047	0.013	-0.28	-0.32	-0.32	-0.03	5580	5490	4780	5240	4710	3990	4180	5080	402.2	1203.7	3	0.0108	8.951
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	mDATAN DVP SPYE	95%	51.9	51.34333	Ref	-0.27	-0.07	0.13	-0.081	0.27	-0.48	0.18	13800	10000	12500	16100	15300	17000	10600	16600	985	1967.9	2	0.0146	7.429
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	mDATAN DVP SPYE	95%	74.4	51.26356	Ref	-0.11	0.12	-0.01	-0.13	0.11	-0.18	0.056	3740	3150	4020	4120	4180	4320	3670	4310	993	1983.9	2	0.0108	5.461
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	mDATAN DVP SPYE	95%	71.6	50.59556	Ref	-0.12	0.008	0.028	-0.14	0.16	-0.26	0.11	5450	4470	5280	6010	5890	6340	4960	6350	985.5	1968.9	2	0.0163	8.292

Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	mDAN DVP SPyE	VR	59%	34.8	53.83171	Ref	0.05	-0.07	0.047	-0.12	-0.08	0.025	0.036	10600	10200	10200	12400	12200	11000	12300	12300	758.4	2272.1	3	0.0225	9.909
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	sEPI PESN DGP	Vk	91%	44.8	53.93998	Ref	0.054	-0.08	0.3	-0.057	0.14	-0.31	-0.23	17800	17200	17000	24900	21400	21400	16400	17100	989	1976.1	2	0.0166	8.383
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	sEPI PESn DGP	Vk	86%	41.5	53.77016	Ref	0.18	-0.19	0.17	-0.14	0.15	-0.28	-0.28	11400	10600	8860	12800	11300	12100	9390	9300	989.5	1977	2	0.0169	8.565
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	tAD GIVS	HLk	95%	66.4	51.23068	Ref	0.15	-0.03	0.052	-0.26	0.042	-0.13	-0.16	4210	3790	3610	4300	3810	4110	3810	3690	825	1648	2	0.0106	6.425

Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	tAD GIVS HLK	95%	63.8	51.0779	Ref	0.17	-0.09	0.13	-0.082	-0.05	-0.27	-0.21	5500	4880	4420	5750	5490	4880	4380	4540	825	1648	2	0.0057	3.466
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	tVSY TEQk	78%	37.9	53.18687	Ref	0.2	-0.1	0.19	-0.077	0.023	-0.3	-0.24	30500	29700	26200	35900	32900	30800	25600	26700	782.4	1562.9	2	0.0142	9.111
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	tVSY TEQk	75%	37	53.18153	Ref	0.058	-0.14	0.15	-0.032	0.16	-0.39	-0.01	15800	15000	14200	19500	18900	18900	13500	17300	782.4	1562.9	2	0.0091	5.837
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C	vDcT ANT nTcN k	60%	28.2	47.14925	Ref	-0.02	0.09	-0.08	0.003	-0.08	-0.11	0.004	13200	11400	13300	13300	15500	12800	13100	14000	662.3	1983.9	3	0.0267	13.43

Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C API	yGVS GYPT Lk	64%	34.5	52.52935	Ref	0.13	-0.27	0.14	0.023	0.006	-0.12	0.04	24100	26300	21700	32300	32800	28300	27000	30000	565	1692	3	0.0143	8.462
Protein disulfide isomerase family A member 3 OS=Ovis aries GN=PDIA3 PE=2 SV=1	tr C6JUQ0 C6JUQ0_SHEEP, tr D3K382 D3K382_C API	yGVS GYPT Lk	75%	36.7	52.68611	Ref	0.16	-0.15	-0.09	-0.087	0.02	-0.22	0.042	22400	20400	17900	20900	23100	21700	19200	22800	847	1692	2	0.0189	11.16
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	aAIL EAA Pk	90%	41	49.19941	Ref	-0.011	-0.12	-0.21	-0.34	-0.25	-0.27	-0.36	8900	8000	8050	8480	8550	7960	8200	7610	498	1490.9	3	0.0285	19.09
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	aAIL EAA Pk	62%	28.3	47.25544	Ref	-0.15	-0.19	-0.21	-0.13	-0.15	-0.29	-0.3	16300	14300	15200	16700	19500	16800	15900	15700	746.5	1490.9	2	0.0049	3.262
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	aAIL EAA Pk	53%	26.7	46.78873	Ref	0.11	0.32	-0.44	-0.23	-0.49	-0.35	-0.43	4110	4670	5900	3910	4970	3620	4170	3920	498	1490.9	3	0.0016	1.054
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	aDG TPN QGk	71%	35.7	52.19794	Ref	-0.36	-0.02	-0.35	-0.27	-0.11	-0.5	-0.14	17900	11400	15700	14000	16300	16000	12700	16200	499.3	1494.8	3	0.006	4.023

Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	aEG AQN QGk	63%	33.9	52.28393	Ref	-0.33	-0.09	-0.29	-0.32	-0.1	-0.24	-0.22	23000	16200	20700	20200	21800	22100	21000	21100	504.3	1509.8	3	0.0136	8.988
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	aEG AQN QGk	81%	38	52.35663	Ref	-0.34	-0.14	-0.19	-0.27	0.06	-0.43	-0.32	8690	6020	7460	8080	8440	9270	6890	7400	755.9	1509.8	2	0.0199	13.15
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	aEG AQN QGk	64%	34.1	52.28726	Ref	-0.15	-0.03	-0.23	-0.29	-0.12	-0.48	-0.3	41800	33600	39400	38600	40900	40000	32600	36700	504.3	1509.8	3	0.014	9.286
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	aEG AQn QGk	91%	43.3	52.4612	Ref	-0.45	-0.04	-0.21	-0.16	-0.07	-0.44	-0.45	6960	4040	5820	5820	6610	6160	4980	4890	756.4	1510.8	2	0.0123	8.144
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	aEGT SnQ Gk	92%	43.8	51.78865	Ref	-0.47	-0.04	-0.3	-0.14	-0.14	-0.27	-0.5	4620	2580	3770	3550	4370	3800	3630	3070	750.9	1499.8	2	0.0169	11.29
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	dALN QAT SQV ESk	95%	62.2	53.95279	Ref	-0.022	-0.02	-0.5	-0.47	-0.29	-0.3	-0.19	2510	2010	2190	1760	1970	1950	2020	2170	667	1998.1	3	0.0114	5.698
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	dALN QAT SQV ESk	95%	71.9	53.91692	Ref	-0.2	-0.32	-0.1	-0.16	-0.25	-0.36	-0.27	7560	5570	5580	7310	7730	6340	6140	6480	1000	1998.1	2	0.014	7.01

Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	eQEITAVQAR	57%	32.2	51.9168	Ref	-0.17	-0.23	-0.31	-0.19	-0.26	-0.15	-0.27	28800	22500	23400	24800	29800	24700	28000	25500	724.9	1447.8	2	0.0138	9.501
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	eQQQQMAELHGK	95%	57.8	54.22288	Ref	-0.08	-0.28	-0.74	-0.13	0.036	0.12	-0.95	25100	19300	18200	14900	25000	24500	27300	12800	679	2034.1	3	0.0192	9.435
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	eQQQQmAEELHGK	95%	62.7	53.75638	Ref	-0.26	-0.14	-0.7	-0.042	0.12	-0.36	-0.38	4970	3570	4210	3200	5570	5450	4080	3980	684.4	2050.1	3	0.0222	10.8
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	eSEELQK	72%	35.6	52.51993	Ref	-0.29	-0.27	-0.1	-0.17	-0.11	-0.44	-0.27	20900	14600	16000	20200	21300	19400	16100	18000	771.4	1540.8	2	0.0268	17.41
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	eVPMVVPVSPVGAk	57%	31.9	51.6482	Ref	-0.3	-0.22	-0.2	-0.23	-0.41	0.15	-0.4	3780	2730	3140	3580	3850	2960	4560	3110	960.6	1919.1	2	0.0149	7.747
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	gDPVVILk	88%	34.7	46.11288	Ref	-0.2	-0.1	-0.26	-0.21	-0.22	-0.29	-0.39	43500	31600	36700	36900	42000	36400	36200	33600	725	1447.9	2	0.0078	5.376
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	gEGAQnQGk	91%	43.6	52.46117	Ref	-0.54	-0.22	-0.19	-0.15	-0	-0.38	-0.28	3510	1980	2670	3070	3490	3360	2710	2870	749.4	1496.8	2	0.0011	0.714

Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	gSAP ATSS TQG k	95%	51.3	53.09458	Ref	-0.18	-0.37	-0.22	-0.32	0.092	-0.34	-0.32	7140	5440	5180	6460	6640	7710	5970	6030	850.5	1698.9	2	0.016	9.389
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	gSAP ATSS TQG k	77%	38.1	53.00295	Ref	-0.29	-0.14	-0.32	-0.35	-0.05	-0.18	-0.29	13700	9690	11700	11500	12500	13400	12800	11700	567.3	1698.9	3	0.0227	13.38
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	kAEG AQn QGk	79%	38.8	53.00782	Ref	-0.47	-0.06	-0.11	-0.21	-0.01	-0.51	-0.33	3E+05	202000	3E+05	315000	325000	3E+05	2E+05	269000	648.7	1943.1	3	0.0213	10.95
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	kAEG TPN QGk	57%	32.1	51.51532	Ref	-0.37	-0.02	-0.31	-0.098	-0.02	-0.45	-0.28	12100	8650	12000	11000	14000	13000	10100	11200	648.1	1941.1	3	0.0046	2.345
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	kAEG TPn QGk	59%	34.1	53.1828	Ref	-0.42	-0.22	-0.15	-0.26	0.083	-0.4	-0.31	19700	12600	15800	18500	18900	21000	15700	16600	648.4	1942.1	3	0.0381	19.59
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	ILAT EQE DAA VAK	95%	65.6	53.22463	Ref	-0.25	-0.36	-0.34	-0.082	-0.16	-0.01	-0.41	23100	17200	17300	19700	26000	21500	24900	18700	656.4	1966.1	3	0.0165	8.373
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	ILAT EQE DAA VAK	95%	75.9	53.18739	Ref	-0.18	-0.11	-0.21	-0.12	-0.15	-0.38	-0.5	6980	5340	6080	6360	7470	6370	5680	5200	984.1	1966.1	2	0.0145	7.369

Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	IMEI LADk	58%	31.9	51.09592	Ref	-0.3	-0.31	-0.13	-0.25	-0.22	-0.11	-0.24	8160	5910	6350	8100	8210	7310	8230	7480	514.3	1539.9	3	#####	0.435
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	IMEI LADk	64%	34	52.02259	Ref	-0.29	-0.19	-0.34	-0.33	-0.27	-0.14	-0.38	5450	3250	3770	3800	4230	3860	4400	3700	514.3	1539.9	3	0.0218	14.17
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	nAD MVQ SQE APk	95%	48.7	53.38974	Ref	-0.4	-0.23	-0.18	-0.16	-0.07	-0.3	-0.4	5950	3690	4520	5230	5870	5460	4830	4480	963.5	1925	2	0.0204	10.57
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	qLSL TEA QTk	95%	55.3	52.30513	Ref	-0.44	-0.2	-0.25	-0.082	-0.09	-0.2	-0.44	12100	7480	9580	10400	12900	11200	10800	9120	864	1726	2	0.0156	9.028
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	qVL QLQ ASHk	54%	31.3	51.56685	Ref	-0.37	-0.08	-0.33	-0.14	-0.04	-0.37	-0.3	26200	17700	23600	22100	28000	26100	21600	22500	719.9	1437.8	2	0.0123	8.556
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	qVL QLQ ASHk	95%	60.4	51.34563	Ref	-0.23	-0.31	-0.29	-0.16	-0.15	-0.19	-0.21	30000	22900	23400	26600	32200	28300	28700	28100	587.4	1759	3	0.012	6.79
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	qVL QLQ ASHk	91%	44.4	51.30884	Ref	-0.19	-0.18	-0.29	-0.18	-0.18	-0.19	-0.2	29400	25200	27400	28500	34000	29600	30900	30400	587.4	1759	3	0.0111	6.279

Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	tLQEQLEnGPSAQLAR	95%	70	54.59827	Ref	-0.064	-0.12	-0.22	-0.36	-0.34	-0.32	-0.17	6200	5230	5460	5720	5740	5050	5380	5900	1031	2059.1	2	0.0047	2.297
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	tLVS AVGS MV LSEGEAQR	95%	58	54.05085	Ref	-0.008	-0.04	-0.35	-0.27	-0.27	-0.19	-0.08	4240	4920	5230	4710	5500	4820	5300	5710	713.4	2137.1	3	0.0172	8.039
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	tLVS AVGS MV LSEGEAQR	95%	73.1	54.09299	Ref	-0.18	-0.21	-0.1	-0.29	-0.24	-0.29	-0.28	915	708	753	912	883	793	803	800	713.4	2137.1	3	0.0132	6.159
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	tLVS AVGS MV LSEGEAQR	79%	39.8	54.11519	Ref	-0.24	-0.12	-0.03	-0.25	-0.29	-0.26	-0.13	243	221	260	311	295	250	266	290	713.4	2137.1	3	0.0075	3.507
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	vDAS ANQGk	83%	38.5	52.21394	Ref	-0.28	-0.2	-0.19	-0.29	-0.15	-0.4	-0.17	12000	8220	9460	10600	11000	10500	9280	10800	749.4	1496.8	2	0.0031	2.099
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1MDC1 F1MDC1_BOVIN	vEAD QQAR	95%	64.6	50.64645	Ref	-0.33	-0.08	-0.22	-0.069	-0.08	-0.19	-0.34	17100	14600	18800	19100	23400	20200	19600	17600	450.2	1347.7	3	0.0098	7.285
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGLN2_BOVIN	eNF QNWLK	94%	47.1	53.08963	Ref	0.044	-0.16	0.017	-0.072	-0	-0.46	-0.13	4220	3440	3250	4110	4260	3900	2980	3700	844	1685.9	2	0.0167	9.901

Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	gAS QAG MTG YGM PR	95%	57.7	50.092	Ref	-0.12	-0.34	-0.1	0.03	0.23	-0.47	-0.04	22000	16000	15000	19800	23900	23900	15400	20600	844.4	1686.8	2	0.0124	7.361
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	gAS QAG MTG YGM PR	95%	71.1	50.28531	Ref	-0.074	-0.28	-0.03	-0.066	0.28	-0.49	0.085	9850	8750	8230	11000	11800	13100	8050	11900	844.4	1686.8	2	0.01	5.915
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	gAS QAG mTG YGM PR	86%	36.9	49.23379	Ref	-0.35	-0.23	-0.15	-0.067	0.34	-0.37	0.15	3810	2640	3090	3670	4290	4970	3170	4500	852.4	1702.8	2	0.0154	9.015
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	gAS QAG mTG YGM PR	95%	47.3	49.45606	Ref	-0.29	-0.21	0.003	-0.11	0.31	-0.56	0.27	5720	4560	5230	6800	6960	8100	4620	8160	852.4	1702.8	2	0.0128	7.512
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	gAS QAG MTG YGM PR	59%	33.6	53.04734	Ref	-0.13	-0.38	-0.09	-0.012	0.18	-0.45	0.064	7000	5030	4580	6280	7310	7270	4910	6980	996.5	1991	2	0.0175	8.809
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	gAS QAG MTG YGM PR	95%	48.6	49.58181	Ref	-0.19	-0.21	-0.12	-0.072	0.34	-0.43	0.18	8040	7090	7540	9060	10300	12000	7310	11100	852.4	1702.8	2	0.0104	6.08
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	gAS QAG MTG YGM PR	95%	51.7	49.32606	Ref	-0.17	-0.25	-0.14	-0.026	0.44	-0.49	0.14	3330	3080	3160	3820	4560	5510	3020	4630	852.4	1702.8	2	0.0145	8.51

Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	iQAS TMA Fk	79%	38.3	52.50839	Ref	0.033	-0.31	-0.09	-0.018	0.014	-0.46	-0.08	22100	16500	14100	18400	21400	19100	14300	18500	535.6	1603.9	3	0.017	10.61
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	iQAS TMA Fk	92%	44.4	52.50703	Ref	-0.081	-0.29	0.008	-0.041	0.11	-0.26	-0.03	15000	12300	11500	15900	17000	16400	13300	15400	803	1603.9	2	0.0173	10.79
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	iQAS TMA Fk	82%	39.9	52.61884	Ref	-0.054	-0.33	0.19	-0.094	0.25	-0.46	-0.19	1E+05	105000	93300	151000	136000	2E+05	96400	115000	535.6	1603.9	3	0.0154	9.579
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	iQAS TmA Fk	79%	38.8	52.80588	Ref	0.05	-0.22	-0.18	-0.14	0.14	-0.31	-0.02	29400	25300	22800	26300	29700	31600	24200	29400	541	1619.9	3	0.0132	8.16
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	kiQA STM AFk	93%	47	51.96715	Ref	-0.24	-0.37	-0.02	-0.017	0.27	-0.27	-0.09	1E+05	71300	70700	101000	111000	1E+05	85100	95900	679.7	2036.2	3	0.0374	18.34
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	nVIG LQm GTn R	70%	35.8	52.51446	Ref	0.081	-0.25	-0.19	-0.37	-0.1	0.42	-0.16	9420	9530	8230	9640	9360	9850	14800	9800	508.3	1521.8	3	0.0109	7.129
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	nVIG LOM GTn R	81%	38.4	52.62363	Ref	0.012	-0.24	-0.03	-0.14	0.057	-0.34	0.041	36600	31300	28600	37100	37800	37900	30000	38800	754.4	1506.8	2	0.0112	7.437

Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	qME QISQ FLQA AER	94%	51.1	53.35508	Ref	0.051	-0.19	0.12	-0.29	0.004	-0.21	-0.05	4330	4000	3680	5110	4240	4540	4070	4530	661.7	1982	3	0.0126	6.368
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	qME QISQ FLQA AER	95%	62.4	53.18614	Ref	0.3	0.4	-0.19	-0.25	-0.54	-0.59	-0.42	2750	2340	2730	2040	2160	1530	1550	1730	661.7	1982	3	0.0183	9.227
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	qME QISQ FLQA AER	88%	42.4	53.41179	Ref	-0.003	-0.48	0.043	-0.12	0.21	-0.34	0.033	2000	1750	1360	2200	2170	2370	1700	2180	992	1982	2	0.0108	5.467
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	qME QISQ FLQA AER	82%	40.4	53.38771	Ref	0.25	0.003	-0.32	-0.24	-0.35	0.11	-0.21	426	413	379	340	395	320	459	367	661.7	1982	3	0.0112	5.626
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	qME QISQ FLQA AER	95%	55.9	53.43911	Ref	0.18	-0.24	0.047	-0.26	0.097	-0.18	-0.12	436	473	384	525	466	523	449	465	661.7	1982	3	0.0086	4.341
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	qME QISQ FLQA AER	85%	42	53.43983	Ref	-0.19	-0.25	-0.15	-0.018	0.19	-0.38	0.23	277	224	234	282	340	342	241	366	661.7	1982	3	0.0073	3.69
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	tLM NLG GLA VAR	65%	33.7	51.95706	Ref	-8E-04	-0.37	0.033	-0.088	0.057	-0.36	0.015	89000	73000	61200	91000	92200	89100	69800	89600	760.4	1518.9	2	0.0116	7.613

Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	tLM NLG GLA VAR	95%	50.4	51.99785	Ref	-0.26	-0.9	-0.43	-0.72	-0.61	-0.93	-0.81	15200	3500	2430	3800	3430	3220	2700	2910	507.3	1518.9	3	0.01	6.59
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	tLM NLG GLA VAR	84%	38.6	51.70253	Ref	0.068	-0.41	0.14	-0.13	0.044	-0.37	0.037	43200	40000	31200	51300	46700	46100	36100	47600	760.4	1518.9	2	0.0046	3.033
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	tLM NLG GLA VAR	95%	64.5	51.48451	Ref	0.048	-0.05	0.16	-0.35	0.2	-0.53	-0.12	9680	9040	9180	11900	9200	11800	7410	9770	507.3	1518.9	3	#####	0.141
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	tLM NLG GLA VAR	95%	52.7	51.95562	Ref	0.0067	-0.42	0.072	-0.089	0.038	-0.24	-0.03	34200	29000	23400	36900	36400	34700	29800	34300	760.4	1518.9	2	0.0112	7.376
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	tLM NLG GLA VAR	95%	50.7	51.94243	Ref	0.054	-0.18	0.013	-0.033	-0.33	-0.06	0.059	725	714	661	845	902	642	810	871	507.3	1518.9	3	0.0081	5.327
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	tLM NLG GLA VAR	86%	40.8	51.94243	Ref	0.12	-0.18	0.023	-0.13	-0.17	-0.33	0.002	780	713	627	811	805	684	639	797	507.3	1518.9	3	0.008	5.268
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	tLm NLG GLA VAR	93%	48.5	52.14741	Ref	0.7	-0.21	-0.03	-0.4	-0.51	-0.3	-0.1	1950	2870	1660	2110	1800	1460	1750	2010	512.6	1534.9	3	0.0124	8.054

Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	tLm NLG GLA VAR	59%	32.7	52.19357	Ref	0.2	-0.31	-0	-0.082	0.11	-0.51	-0.03	8260	8550	6540	9050	9450	9440	6410	8880	768.4	1534.9	2	0.0111	7.216
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	yFSD NQL QEG k	76%	38.2	53.44782	Ref	-0.12	-0.43	0.13	0.078	0.23	-0.49	-0.1	2E+05	162000	1E+05	236000	250000	2E+05	2E+05	201000	646.3	1936	3	0.0213	11
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	yFSD NQL QEG k	69%	36.4	53.54022	Ref	-0.098	-0.21	-0.09	0.015	0.25	-0.58	-0.01	29400	23300	23400	28500	33800	34700	20400	30100	646.3	1936	3	0.0154	7.96
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	yFSD NQL QEG k	67%	36.1	53.56821	Ref	0.051	-0.19	-0.05	-0.081	-0.06	-0.16	-0.09	9530	8570	7890	9740	10500	9330	9100	9460	646.3	1936	3	0.0158	8.161
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	yFSD NQL QEG k	92%	45.6	53.51823	Ref	-0.17	-0.16	-0.06	0.011	0.29	-0.58	-0.04	25300	19500	21100	25600	29500	31400	17900	25800	969	1936	2	0.0166	8.561
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	yFSD NQL QEG k	51%	32.9	53.60262	Ref	-0.13	-0.36	0.11	-0.056	0.32	-0.62	0.028	10500	8570	7900	12300	12100	13700	7440	11600	969	1936	2	0.0125	6.475
Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	yFSD NQL QEG k	95%	49.5	53.49138	Ref	-0.19	-0.46	0.034	-0.033	0.21	-0.45	0.079	3290	2330	2100	3320	3490	3610	2390	3420	969	1936	2	0.0202	10.45

Transgelin-2 OS=Bos taurus GN=TAGLN2 PE=2 SV=3	sp Q5E9F5 TAGL2_BOVIN	yFSD nQL QEG k	93%	46.2	53.04376	Ref	-0.2	-0.22	-0.02	-0.042	0.32	-0.44	-0.02	12300	9640	10300	13200	14400	16200	9940	13300	969.5	1937	2	0.0182	9.376
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,trans F1MN08 F1MN08_BOVIN,trans F2Q9A3 F2Q9A3_PIG,trans F2Q9A4 F2Q9A4_PHAAF,trans Q861V5_BOVIN	aLST Gek	55%	30.9	51.00008	Ref	0.053	-0.2	-0.05	-0.19	0.056	-0.26	-0.08	6710	6190	5630	7050	7040	7270	6090	6840	657.4	1312.8	2	0.0083	6.298
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,trans F1MN08 F1MN08_BOVIN,trans F2Q9A3 F2Q9A3_PIG,trans F2Q9A4 F2Q9A4_PHAAF,trans Q861V5_BOVIN	eGM NIVE AME R	69%	32.4	49.97041	Ref	0.2	-0.38	0.13	-0.14	-0.04	-0.26	-0.23	36000	37200	27000	43200	39500	36800	33000	33600	791.9	1581.8	2	0.02	12.63

Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	eGMNIVEAME	R	89%	41.9	50.49137	Ref	-0.086	-0.34	0.39	-0.19	0.036	-0.51	-0.25	3630	2800	2550	4740	3500	3570	2550	3020	528.3	1581.8	3	0.0103	6.517
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	eGMNIVEAmE	R	64%	31.3	49.74539	Ref	0.23	-0.18	0.038	-0.39	0.082	-0.51	-0.14	24100	23800	19500	25400	20800	25200	17500	22500	799.9	1597.8	2	0.0116	7.244
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	fDDENFILk		80%	38.9	53.56148	Ref	0.14	-0.32	0.055	-0.18	0.052	-0.38	-0.23	21500	19300	15200	22100	20800	21300	16500	18100	875	1747.9	2	0.0198	11.3

Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	fDDE NFIL	95%	51.6	53.57506	Ref	0.21	-0.37	0.024	-0.15	-0.01	-0.42	-0.32	54700	48100	34800	51300	50300	48400	37900	40300	875	1748	2	0.0091	5.224
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	fDDE NFIL	87%	41.9	53.52331	Ref	0.35	-0.38	-0.04	-0.29	-0.05	-0.4	-0.28	26800	25200	16400	23400	21700	22400	18300	19700	875	1748	2	0.0033	1.874
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	fDDE NFIL	95%	55	53.32249	Ref	0.23	-0.42	-0.05	-0.1	-0.02	-0.26	-0.33	8300	7640	5280	7670	8130	7500	6650	6270	875	1747.9	2	0.0223	12.76

Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tr F1MN08 F1MN08_BOVIN,tr F2Q9A3 F2Q9A3_PIG,tr F2Q9A4 F2Q9A4_PHAAF,tr Q861V5_BOVIN	hTGP GILS mAN AGP NTN GSqF FicT Ak	82%	40.3	55.00013	Ref	-0.071	-0.57	-0.02	-0.16	0.052	0.082	-0.03	1640	1400	1070	1760	1770	1790	1900	1750	852.2	3404.7	4	0.0233	6.845
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tr F1MN08 F1MN08_BOVIN,tr F2Q9A3 F2Q9A3_PIG,tr F2Q9A4 F2Q9A4_PHAAF,tr Q861V5_BOVIN	iIPGF McQ GGD FTR	95%	56.8	51.17096	Ref	0.21	-0.23	0.021	-0.19	-0.09	-0.23	-0.18	7350	7540	6020	8070	7710	7180	6800	7030	946.5	1890.9	2	0.0055	2.894
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tr F1MN08 F1MN08_BOVIN,tr F2Q9A3 F2Q9A3_PIG,tr F2Q9A4 F2Q9A4_PHAAF,tr Q861V5_BOVIN	iIPGF McQ GGD FTR	93%	43.3	50.93467	Ref	0.22	-0.31	0.073	-0.26	-0.04	-0.21	-0.22	1870	1890	1420	2080	1830	1850	1720	1700	946.5	1890.9	2	0.0105	5.537

Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	iIPGF mcQ GGD	92%	42.2	50.52571	Ref	0.19	-0.39	-0.06	-0.057	-0.03	-0.3	-0.03	5910	6150	4460	6290	6950	6180	5370	6410	954.5	1906.9	2	0.0033	1.715
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	kITIA DcG QI	65%	34.9	52.9209	Ref	0.15	-0.44	-0.03	-0.1	0.071	-0.28	-0.14	33100	31800	22900	34000	35800	35200	28900	31600	572.7	1714.9	3	0.0146	8.523
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	kITIA DcG QI	65%	34.6	52.9764	Ref	0.1	-0.39	0.11	-0.19	0.087	-0.33	-0.17	32200	29600	22800	36200	32600	34400	27000	29800	858.5	1714.9	2	0.0134	7.809

Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	kITIA DcG QI	77%	38.3	52.96066	Ref	0.0039	-0.36	0.15	-0.21	0.16	-0.42	-0.1	62800	54700	46100	73500	63200	71400	50000	61800	572.7	1714.9	3	0.0126	7.352
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	kITIA DcG QI	55%	32.9	52.98359	Ref	0.065	-0.21	-0.05	-0.12	-0.15	-0.22	0.027	3580	3350	3000	3750	3960	3390	3360	3960	858.5	1715	2	0.0056	3.263
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	kITIA DcG QI	87%	41.1	53.04089	Ref	-0.037	-0.36	0.12	-0.11	0.11	-0.32	-0.14	20100	17100	14800	23300	21900	22300	17300	19300	858.5	1714.9	2	0.0168	9.802

Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	kITIA DcG QI	83%	39.5	52.97566	Ref	0.015	-0.41	0.13	-0.058	0.18	-0.25	-0.09	576	626	507	827	798	824	637	709	858.5	1714.9	2	0.013	7.599
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	kITIA DcG QI	63%	34.6	53.01271	Ref	0.04	-0.12	-0.07	-0.12	-0.17	-0.13	-0.09	2320	2110	2050	2370	2530	2140	2300	2350	572.7	1715	3	0.006	3.523
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	kITIA DcG QI	74%	36.6	52.97022	Ref	0.55	-0.68	0.065	-0.27	-0.08	-0.7	-0.58	1760	1650	763	1440	1260	1250	851	916	859	1715.9	2	0.01	5.817

Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,trans F1MN08 F1MN08_BOVIN,trans F2Q9A3 F2Q9A3_PIG,trans F2Q9A4 F2Q9A4_PHAAF,trans Q861V5 Q861V5_BOVIN	tEWL DGk	53%	31.9	52.26528	Ref	0.029	-0.48	0.26	-0.15	0.006	-0.26	-0.18	81900	73300	56000	105000	86700	84500	73400	76800	728.9	1455.8	2	0.0089	6.098
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,trans F1MN08 F1MN08_BOVIN,trans F2Q9A3 F2Q9A3_PIG,trans F2Q9A4 F2Q9A4_PHAAF,trans Q861V5 Q861V5_BOVIN	vkEG MNI VEA MER	81%	38.8	54.23726	Ref	0.14	-0.5	0.16	-0.34	-0.06	-0.3	-0.19	4510	3640	2540	4500	3510	3720	3290	3530	529.3	2113.1	4	0.0141	6.647
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,trans F1MN08 F1MN08_BOVIN,trans F2Q9A3 F2Q9A3_PIG,trans F2Q9A4 F2Q9A4_PHAAF,trans Q861V5 Q861V5_BOVIN	vNPT VFFD IAVD GEPL GR	95%	69.6	54.556	Ref	0.42	Value Missing (-1.303)	0.049	-0.17	-0.19	0.07	-0.1	2430	2790	Value Missing (-1.303)	2620	2470	2140	2670	2360	750.7	2249.2	3	0.0112	4.982

Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PH	VNPT VFFD IAVD GEPL	GR	95%	74.6	54.54981	Ref	0.45	-0.63	0.044	-0.28	0.13	-0.61	0.12	2510	3550	1820	3260	2860	3330	2090	3420	1126	2249.2	2	0.0075	3.349
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PH	VNPT VFFD IAVD GEPL	GR	95%	66.2	54.53005	Ref	0.41	-0.73	-0.1	-0.04	0.23	-0.17	0.083	144	282	138	241	277	291	230	273	1126	2249.2	2	0.0158	7.037
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PH	VNPT VFFD IAVD GEPL	GR	95%	62	54.55037	Ref	0.32	-0.29	0.032	-0.54	0.15	-0.19	-0.54	303	301	214	300	222	314	259	202	750.7	2249.2	3	0.0136	6.049

Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5_BOVIN	VNPT VFFD IAVD GEPL	GR	95%	59.7	54.57341	Ref	0.14	0.16	-0.19	0.013	-0.2	0.15	-0.73	167	184	202	178	226	171	228	122	750.7	2249.2	3	0.011	4.902
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5_BOVIN	VNPT VFFD IAVD GEPL	GR	95%	59.6	54.54981	Ref	-0.33	-0.38	-0.13	0.037	0.001	-0.69	0.69	474	401	422	561	695	592	383	988	750.7	2249.2	3	0.0076	3.356
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5_BOVIN	VNPT VFFD IAVD GEPL	GR	95%	58.7	54.56849	Ref	-0.12	-0.28	-0.28	-0.45	0.15	Value Missing (-0.9248733)	0.8	275	251	243	272	267	352	Value Missing (-0.9248733)	573	750.7	2249.2	3	0.0085	3.769

Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5_BOVIN	VNPTVFFDIADVGEPLGR	95%	63.4	54.54697	Ref	-0.18	Value Missing (-0.5912971)	-0.56	-0.4	0.31	-0.05	0.67	130	130	Value Missing (-0.5912971)	121	150	214	174	283	750.7	2249.2	3	0.0096	4.249
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5_BOVIN	VNPTVFFDIADVGEPLGR	95%	67.2	54.55296	Ref	No Values (-0.35357106)	No Values (-0.4712644)	Reference Missing (0.6258415)	Reference Missing (0.31834987)	Reference Missing (0.36871627)	No Values (-0.6452326)	No Values (-0.63435876)	No Values (-0.5559613)	No Values (-0.35357106)	No Values (-0.4712644)	Reference Missing (0.6258415)	Reference Missing (0.31834987)	Reference Missing (0.36871627)	No Values (-0.6452326)	No Values (-0.63435876)	750.7	2249.2	3	0.0109	4.822
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5_BOVIN	VSFELFADK	90%	42.5	52.60265	Ref	0.12	-0.31	0.07	-0.16	0.023	-0.28	-0.31	66200	59000	47300	69200	65100	64500	54600	53200	832.5	1662.9	2	0.0126	7.547

Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	vSFE LFAD	94%	46	52.61037	Ref	0.31	-0.33	-0.08	-0.2	-0.11	-0.33	-0.17	11300	11300	7850	10500	10600	9820	8810	9790	832.5	1662.9	2	0.0078	4.686
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	vSFE LFAD	90%	42.7	52.61938	Ref	0.21	-0.23	0.055	-0.18	-0.05	-0.32	-0.32	12500	11800	9480	13000	12100	11600	10100	9950	832.5	1662.9	2	0.0089	5.335
Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,tron F1MN08 F1MN08_BOVIN,tron F2Q9A3 F2Q9A3_PIG,tron F2Q9A4 F2Q9A4_PHAAF,tron Q861V5 Q861V5_BOVIN	vSFE LFAD	92%	43.8	52.58309	Ref	0.11	-0.4	0.041	-0.2	-0	-0.22	-0.23	1220	1040	789	1200	1120	1120	1010	996	832.5	1662.9	2	0.0094	5.636

Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus GN=PPIA PE=1 SV=2	sp P62935 PPIA_BOVIN,sp P62936 PPIA_PIG,trans F1MN08 F1MN08_BOVIN,trans F2Q9A3 F2Q9A3_PIG,trans F2Q9A4 F2Q9A4_PHAAF,trans Q861V5 Q861V5_BOVIN	vSFE LFAD kVPK	66%	31	50.7088	Ref	-0.25	-0.62	0.14	-0.016	0.096	-0.23	0.49	20700	23300	19600	37200	36800	34700	28900	47200	573.8	2291.4	4	0.0119	5.173
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	dLcQ VQG VPL QTM k	74%	38.6	54.38572	Ref	0.73	0.79	0.87	0.8	0.29	1.5	0.88	6930	8700	9820	11600	12200	7480	18100	11700	738.7	2213.2	3	0.0213	9.638
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	dLcQ VQG VPL QTM k	83%	42	54.36705	Ref	0.72	0.63	0.89	1	-0.23	1.8	0.68	13700	18200	18500	25000	30000	11100	45600	21500	738.7	2213.2	3	0.0204	9.231
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	dVLT IIEkP TGSK	65%	30.3	48.32113	Ref	0.58	0.87	0.96	0.87	0.4	1.5	0.69	5600	6380	8450	10200	10500	6600	14800	8360	771.8	2312.4	3	0.0049	2.134
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	eSSL LNQ HicA VMG k	89%	45.5	54.36015	Ref	0.49	0.61	0.92	0.91	0.31	1.6	1	5440	6690	7900	11000	12100	6920	17900	11600	762.1	2283.2	3	0.0219	9.588

Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	eSSL LNQ HicA VMG k	87%	44.1	54.37208	Ref	0.82	0.75	0.77	0.95	0.49	1.4	0.69	1070	1300	1350	1530	1920	1210	2380	1450	762.1	2283.2	3	0.0228	9.982
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	eSSL LNQ HicA VMG k	88%	45.3	54.46677	Ref	0.62	0.73	0.89	0.99	0.34	1.6	0.85	1430	2120	2470	3110	3680	2040	5040	3010	762.1	2283.2	3	0.0151	6.62
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	eSSL LNQ HicA VmG k	78%	39.7	54.16504	Ref	0.82	0.88	0.86	0.82	0.53	1.3	0.85	2050	2890	3260	3610	3870	2760	4990	3570	767.4	2299.2	3	0.0243	10.58
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	gNVL EcLQ DGE R	73%	33.5	50.08455	Ref	0.79	0.66	0.85	0.77	0.069	1.8	0.71	8140	11400	11300	14500	15100	8110	27700	13100	841.9	1681.8	2	0.0096	5.712
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	gNVL EcLQ DGE R	65%	31.5	49.90192	Ref	0.76	0.78	0.8	0.92	0.24	1.6	0.72	1850	2700	2960	3380	4040	2200	6070	3180	841.9	1681.8	2	0.0138	8.184
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	gYQE LLEk	95%	49.2	52.15614	Ref	0.29	0.66	0.92	1	0.21	1.7	0.97	24800	30800	43200	58100	68900	34300	1E+05	60100	794.5	1586.9	2	0.0183	11.52

Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	gYQELLEK	95%	48.9	52.30572	Ref	0.46	0.56	0.86	0.92	0.2	1.8	0.96	5040	7090	8210	11400	13100	6920	21900	12200	794.5	1586.9	2	0.025	15.75
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	gYQELLEK	67%	34.6	52.16665	Ref	0.28	0.55	0.99	1.1	0.14	1.8	0.85	11300	15600	20500	31100	36600	16700	55900	28200	530	1586.9	3	0.0175	10.99
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	hPVL YAPT ILSV ANQ YNk	78%	37.1	53.66459	Ref	0.85	0.83	0.81	0.82	0.35	1.3	0.88	1170	1440	1550	1710	1910	1200	2480	1790	659.9	2635.5	4	0.016	6.071
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	kAP QLTS PEL MAL TR	95%	66.1	52.86025	Ref	0.31	0.69	0.88	1.1	0.32	1.7	0.83	7620	10400	14700	18700	24900	12300	33700	18100	755.4	2263.3	3	0.0209	9.214
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	kAP QLTS PEL MAL TR	85%	39.3	52.84036	Ref	0.81	0.58	0.95	0.8	0.84	1.1	0.85	3750	4280	3960	5730	5690	5130	6440	5340	566.8	2263.3	4	0.0201	8.894
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	kAP QLTS PEL MAL TR	95%	61.6	52.63821	Ref	0.57	0.79	0.91	0.9	0.41	1.6	0.86	2480	3620	4570	5570	6100	3780	8980	5350	755.4	2263.3	3	0.0143	6.299

Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	kAP QLTS PEL MAL TR	68%	35.3	52.51266	Ref	0.5	0.83	0.91	0.9	0.32	1.6	0.82	3610	4560	6210	7380	8080	4700	12100	6890	755.4	2263.3	3	0.0114	5.014
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	IAVPI ILR	55%	16.9	36.93199	Ref	0.62	0.75	0.96	0.96	0.086	1.6	0.86	8070	11900	14000	18200	20100	9600	29500	17000	599.9	1197.8	2	0.0077	6.398
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	IAVPI ILR	94%	34.1	36.03253	Ref	0.46	0.86	0.97	0.88	-0.21	1.8	1	695	1130	1620	1970	2040	833	3400	2040	400.3	1197.8	3	0.0019	1.573
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	IAVPI ILR	92%	34	40.04579	Ref	0.41	0.6	1.1	1	0.026	1.8	0.8	1530	2260	2800	4380	4710	2030	7130	3610	400.3	1197.8	3	0.0129	10.73
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	IGEY YLQ NAFL VAYT k	91%	47.4	54.70852	Ref	0.6	0.5	0.83	0.71	0.46	1.8	0.88	190	286	289	409	412	304	817	420	834.5	2500.4	3	0.0313	12.49
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	IVM DVA HIHE Ecck	89%	43.6	52.48402	Ref	0.62	0.68	0.96	1	0.3	1.6	0.84	552	855	963	1310	1520	800	2030	1210	776.4	2326.1	3	0.0083	3.566

Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	Ivm DVA HIHE Eckc	89%	41.2	52.30191	Ref	0.57	0.89	0.83	0.82	0.36	1.5	0.83	1490	1680	2290	2450	2690	1710	4040	2440	586.5	2342.1	4	0.0062	2.651
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	qQFL INLV k	63%	32.3	50.91252	Ref	0.76	0.6	0.85	0.83	0.32	1.2	1	294	275	267	355	386	237	468	396	695.4	1388.8	2	0.008	5.785
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	qQFL INLV k	95%	59.7	48.85571	Ref	0.37	0.74	0.95	0.98	0.24	1.7	0.92	1860	2450	3430	4480	5040	2620	7440	4370	856	1710.1	2	0.0149	8.693
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	qQFL INLV k	56%	29	48.62083	Ref	0.81	0.65	0.73	0.66	0.44	1.1	0.69	4160	2700	2630	3110	3280	2460	4020	3030	571	1710.1	3	0.0121	7.048
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	qQFL INLV k	78%	34.5	48.9477	Ref	0.41	0.64	0.85	0.93	0.3	1.6	1.1	1690	1820	2320	3000	3520	1970	5050	3480	571	1710	3	0.0166	9.731
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	qQFL INLV k	64%	30.4	48.61588	Ref	0.68	0.71	0.8	0.89	0.4	1.4	0.91	1470	1590	1760	2100	2480	1540	3260	2260	571	1710.1	3	0.0132	7.697

Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	qQFLINLVk	80%	35.3	48.95754	Ref	0.67	0.72	0.8	0.67	0.58	1.3	0.85	929	801	899	1070	1070	884	1560	1100	571	1710	3	0.0185	10.8
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	rHPVLYAPTILSVANQYNk	87%	41.2	53.19081	Ref	0.61	0.65	0.8	0.84	0.53	1.5	1.1	693	855	953	1180	1340	949	1900	1410	698.9	2791.6	4	0.0158	5.643
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	rHPVLYAPTILSVANQYNk	83%	38.2	52.64719	Ref	0.62	0.59	1	0.91	0.36	1.7	0.88	979	1700	1800	2740	2790	1670	4260	2470	698.9	2791.6	4	0.004	1.446
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	rHPVLYAPTILSVANQYNk	65%	32.6	52.43601	Ref	0.84	0.62	0.78	0.98	0.68	1.3	0.8	471	622	580	730	920	655	1060	735	698.9	2791.6	4	0.0014	0.487
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	yGLSDccSR	72%	25.1	41.95041	Ref	0.48	0.71	0.85	0.99	0.12	1.8	0.95	14400	22400	28600	35300	42900	20500	66700	37900	700.3	1398.6	2	0.0132	9.405
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	yIQESQALAk	95%	56.2	52.78518	Ref	0.53	0.71	1	0.94	0.097	1.7	0.78	8210	13200	16200	22800	23500	11400	37400	19000	880	1758	2	0.0255	14.49

Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	YIQE SQAL AK	95%	57.3	52.70577	Ref	0.41	0.88	0.94	0.86	0.29	1.7	0.76	4320	5700	8570	10000	10400	6140	17300	8810	880	1758	2	0.02	11.37
Alpha-fetoprotein OS=Bos taurus GN=AFP PE=2 SV=1	sp Q3SZ57 FETA_BOVIN	YIQE SQAL AK	58%	31.1	52.17318	Ref	0.84	0.59	0.82	0.81	0.39	1.3	0.86	11100	10900	9970	13100	14300	9410	18500	13500	516.6	2062.2	4	0.0266	12.9
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	aATA SQA k	84%	38.4	51.72142	Ref	-0.018	0.22	-0.09	-0.23	-0.2	0.1	-0.52	19400	16500	21000	19100	19200	17000	22000	14200	678.4	1354.8	2	0.029	21.4
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	aVAI SLPk	93%	37.3	44.18152	Ref	0.25	-0.18	-0.13	-0.17	-0.35	0.19	-0.2	18600	20600	16600	19300	20600	16000	24200	18300	704	1405.9	2	0.0033	2.322
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	dQA VENI LLSP VVV ASSL GLVS LGGk	95%	60.8	49.84815	Ref	0.014	-0.08	0.055	-0.03	-0.3	0.3	Value Missing (-1.9946213)	178	118	120	148	153	111	176	Value Missing (-1.9946213)	1059	3172.9	3	#####	0.244
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	dQA VENI LLSP VVV ASSL GLVS LGGk	95%	71.8	49.73423	Ref	0.014	0.38	-0.5	-0.3	0.055	0.18	-0.68	157	143	201	122	155	172	196	107	1059	3172.9	3	0.0011	0.332

Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	dQAVENILLSPVVV ASLLGLVSLGGk	81%	37.4	50.75919	Ref	No Values (0.14849877)	No Values (0.030805526)	No Values (-0.13578948)	No Values (-0.27626854)	No Values (-0.0803162859612)	No Values (-0.143162858878)	No Values (-0.05389126)	No Values (-0.14849877)	No Values (0.030805526)	No Values (-0.13578948)	No Values (-0.27626854)	No Values (-0.0803162859612)	No Values (-0.143162858878)	No Values (-0.13228878)	1059	3172.8	3	0.0165	5.207	
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	dQAVENILLSPVVV ASLLGLVSLGGk	90%	42.4	50.37984	Ref	No Values (0.14849861)	No Values (0.030805526)	No Values (-0.13578929)	No Values (-0.27626854)	No Values (-0.0803162859612)	No Values (-0.143162858887)	No Values (-0.05389135)	No Values (-0.14849861)	No Values (0.030805526)	No Values (-0.13578929)	No Values (-0.27626854)	No Values (-0.0803162859612)	No Values (-0.14316285887)	No Values (-0.13228887)	1059	3172.8	3	0.0096	3.014	
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	gVVEVTHDLQk	95%	71.2	52.66605	Ref	0.059	-0	-0.09	-0.28	-0.47	0.42	-0.64	9860	8230	8540	9050	8710	6690	12900	6170	917	1832	2	0.015	8.178
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	gVVEVTHDLQk	92%	47.4	52.66045	Ref	0.1	0.038	-0.18	-0.076	-0.51	0.26	-0.57	30800	26400	27400	26400	31400	20300	36100	20200	611.7	1832	3	0.0142	7.751
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	hLAGLGLTEAIDk	66%	32.5	52.10856	Ref	0.16	0.002	-0.14	-0.29	-0.36	0.13	-0.36	8680	7690	7470	7600	7520	6280	9210	6520	487.3	1945.1	4	0.0161	8.289
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	hLAGLGLTEAIDk	95%	63.6	51.97859	Ref	0.3	0.013	0.038	-0.41	-0.31	0.026	-0.63	14500	14100	12500	14300	11600	10800	14300	8970	649.4	1945.1	3	0.0129	6.611

Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	hLAG LGLT EAID knk	82%	36.9	49.99178	Ref	0.046	-0.05	-0.13	-0.11	-0.44	0.49	-0.37	4140	4410	4480	4760	5300	3680	7350	4010	831.5	2491.5	3	0.0113	4.549
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	IFYA DHP FIFL VR	88%	44.4	53.58592	Ref	0.058	0.14	0.023	-0.28	-0.6	0.41	-0.49	2980	2950	3390	3510	3130	2190	4610	2450	648	1941.1	3	0.0124	6.4
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	IFYA DHP FIFL VR	64%	35.3	53.46953	Ref	0.25	-0.01	-0.04	-0.46	-0.45	0.46	-0.63	550	601	545	598	492	434	851	397	648	1941.1	3	0.0071	3.666
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	IQM VEM PLAH k	91%	46.4	53.12626	Ref	0.16	-0.12	-0.13	-0.27	-0.38	0.21	-0.37	11300	9760	8730	9770	9730	7870	12400	8210	635.7	1904.1	3	0.0086	4.536
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	IQM VEM PLAH k	77%	36	52.76368	Ref	0.11	-0.07	-0.04	-0.1	-0.45	0.18	-0.6	5820	4860	4660	5310	5620	3860	6240	3610	477	1904.1	4	0.0044	2.311
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	IQM VEM PLAH k	89%	44.7	53.23372	Ref	0.25	-0.11	-0.09	-0.27	-0.39	0.2	-0.59	21200	19300	16300	18700	18100	14500	22900	13100	635.7	1904.1	3	0.0129	6.757

Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	IQM VEM PLAHk	95%	60.3	53.24387	Ref	0.17	-0.14	-0.07	-0.14	-0.32	0.19	-0.39	4120	4060	3530	4180	4380	3370	5010	3330	635.7	1904.1	3	0.0116	6.08
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	ISSLII IMP HHV EPLER	95%	59.9	53.33061	Ref	0.17	-0.11	-0.05	-0.23	-0.41	0.22	-0.37	1520	1430	1280	1500	1460	1130	1820	1200	763.4	2287.3	3	0.0094	4.125
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	ISSLII IMP HHV EPLER	87%	40.8	53.32651	Ref	0.034	-0.01	0.086	-0.44	-0.68	0.14	-0.49	2310	1530	1620	1930	1480	1100	2010	1300	572.8	2287.3	4	0.0094	4.105
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	ISSLII IMP HHV EPLER	54%	33.2	53.15929	Ref	0.18	-0.35	0.041	-0.002	-0.14	-0.1	-0.14	249	274	205	302	323	256	274	266	763.4	2287.3	3	0.0043	1.883
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	ISSLII Imp HHV EPLER	94%	51.6	53.67085	Ref	0.11	-0.24	-0.06	-0.24	-0.25	0.16	-0.21	1080	974	828	1060	1030	891	1240	946	768.8	2303.3	3	0.0092	3.971
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	ISSLII Imp HHV EPLER	69%	34.7	53.71666	Ref	0.037	-0.18	-0.1	0.024	-0.28	0.085	-0.16	541	506	472	562	673	476	640	536	576.8	2303.3	4	0.0113	4.924

Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	IYGP SSVS FAED FVR	93%	46	52.95712	Ref	0.091	0.12	-0.14	-0.053	-0.57	0.35	-0.31	2760	3150	3500	3280	3830	2340	4640	2900	989.5	1977	2	0.022	11.1
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	IYGP SSVS FAED FVR	95%	57.5	53.04109	Ref	0.081	0.074	-0.18	-0.22	-0.36	0.29	-0.45	5400	4920	5310	4980	5370	4240	6960	4130	989.5	1977	2	0.0188	9.493
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	sAGL AFSL YQA MAK	91%	46.7	53.89813	Ref	No Values (-1.1003441)	Reference Missing (0.98178023)	No Values (-1.3846321)	No Values (-1.525114)	Reference Missing (0.87586626446)	No Values (-1.3811318)	No Values (-1.3027343)	No Values (-1.1003441)	Reference Missing (0.98178023)	No Values (-1.3846321)	No Values (-1.525114)	Reference Missing (0.875446)	Reference Missing (0.845866268)	No Values (-1.3811318)		689.4	2065.1	3	0.0159	7.704
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	sAGL AFSL YQA MAK	95%	89.7	53.80544	Ref	-0.23	0.14	-0.03	-0.25	-0.44	0.2	-0.25	2160	1470	2070	2070	1960	1490	2430	1760	1034	2065.1	2	0.006	2.881
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	sAGL AFSL YQA MAK	95%	60.1	53.84361	Ref	-0.16	0.1	-0.18	-0.2	-0.34	0.31	-0.21	1600	1280	1660	1540	1670	1320	2160	1500	689.4	2065.1	3	0.0139	6.731
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	sAGL AFSL YQA MAK	95%	64.3	53.81323	Ref	0.047	-0.01	-0.24	-0.29	-0.23	0.37	-0.35	1920	1770	1850	1760	1880	1720	2700	1640	689.4	2065.1	3	0.0115	5.584

Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	sAGL AFSL YQA MAK	79%	39.8	53.95391	Ref	-0.38	-0.14	-0.09	-0.041	-0.19	0.43	-0	374	319	408	477	542	426	687	504	689.4	2065.1	3	0.0223	10.81
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	sAGL AFSL YQA mAk	95%	60.5	53.94545	Ref	-0.039	0.18	-0.26	-0.17	-0.41	0.17	-0.19	10800	9070	11500	9480	11100	8230	12900	9910	694.7	2081.1	3	0.0183	8.79
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	sAGL AFSL YQA mAk	95%	57.9	53.93593	Ref	0.077	-0.09	-0.32	-0.045	-0.18	0.28	-0.15	957	1050	1020	972	1300	1030	1480	1090	694.7	2081.1	3	0.0163	7.825
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	sYTV GVT MM HR	71%	34.9	51.34897	Ref	0.055	-0.33	0.19	-0.19	-0.27	0.22	-0.09	24400	27400	22800	36700	31000	25600	37700	30100	529.3	1584.8	3	0.0095	5.989
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	sYTV GVT MM HR	77%	35.8	51.35034	Ref	0.26	-0.07	-0.13	-0.33	-0.42	0.29	-0.38	5450	5630	4870	5230	5040	4120	7060	4390	793.4	1584.8	2	0.0096	6.061
Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH6 SERPH_BOVIN	syTV GVT MM HR	66%	33.6	53.28412	Ref	0.34	0.11	-0.08	-0.39	-0.48	0.19	-0.53	30700	34400	31800	31200	27800	22700	38000	22800	473.3	1889	4	0.0183	9.696

Serpin H1 OS=Bos taurus GN=SERPINH1 PE=2 SV=1	sp Q2KJH 6 SERPH_ BOVIN	tGLY NYY DDE kEk	69%	37.9	55.04219	Ref	0.2	0.16	-0.25	-0.039	-0.63	0.38	-0.81	11100	11100	11800	9980	12700	7380	15500	6740	850.8	2549.3	3	0.0185	7.245
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	aDD ANV VR	66%	32	49.75721	Ref	-0.11	0.24	-0.1	-0.3	-0.06	0.046	-0.14	9980	8370	11600	10200	9860	10200	11400	9930	388.5	1162.6	3	0.0128	11.02
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	aDD ANV VR	51%	29	49.60495	Ref	-1.9	1.3	-1.8	0.028	-1.9	1.1	-2	89800	22300	2E+05	27300	111000	25300	2E+05	23900	582.3	1162.6	2	0.0112	9.627
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	dGE AGA QGP PGP AGP AGE R	50%	30.6	51.18652	Ref	0.43	0.74	-0.57	-0.58	-0.39	-0.12	-0.43	1690	2130	2840	1300	1410	1400	1780	1420	665.7	1993.9	3	0.0265	13.3
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	dGE AGA QGP PGP AGP AGE R	94%	49.7	51.66229	Ref	-0.16	0.33	-0.3	0.007	-0.22	0.013	-0.15	9500	7620	11700	8450	11500	8610	10500	9360	665.7	1994	3	0.0148	7.433
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	dGE AGA QGP PGP AGP AGE R	95%	90.1	51.71047	Ref	-2.1	1.5	-2	-0.1	-1.7	1	-2.1	11500	2490	33100	3180	13500	3780	26600	2950	998	1994	2	0.0143	7.149

Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	eGA PGA EGSP GR	90%	42	50.04085	Ref	-0.81	0.56	-0.73	-0.015	-0.58	0.41	-0.41	17700	6620	18600	8530	15400	9120	18900	10600	463.6	1387.7	3	0.0125	8.988
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	gAA GEP GK	50%	30.9	51.7376	Ref	-0.88	1.1	-1.3	-0.11	-1.1	0.84	-1.4	14400	6120	25600	5470	14000	6270	24600	5050	647.9	1293.7	2	0.0241	18.65
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	gAn GAP GIAG APG FPG AR	95%	79.7	53.21725	Ref	-1.8	1.4	-1.4	-0.16	-1.2	0.87	-1.7	11700	3000	28600	4620	12200	5040	22700	3670	922	1842	2	0.0133	7.207
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	gAn GAP GND GAK	89%	43.8	52.2627	Ref	-1.1	1.2	-1.4	0.003	-1.3	0.82	-1.6	18500	6720	35500	6630	19500	6950	31300	5650	546.6	1636.8	3	0.024	14.64
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	gAn GAP GND GAK	79%	37.4	52.27257	Ref	-1.8	1.4	-2.3	0.025	-2	1.1	-2.6	4870	1130	11700	1020	5510	1160	10300	781	819.4	1636.8	2	0.0215	13.1
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	gDk GET GEQ GDR	90%	43	52.72584	Ref	-1.2	0.78	-0.81	0.098	-0.78	0.78	-1.2	6580	2130	9140	3410	7030	3350	10300	2620	465	1855.9	4	0.0143	7.684

Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P02453 CO1A1_BOVIN	gEPG PPG PAG AAG PAG NPG ADG QPG Ak	81%	41.8	55.13622	Ref	Value Missing (- 1.8960 222)	Value Missi ng (- 2.180 3102)	Value Missin g (- 2.1249 168)	Value Missin g (- 2.1768 095)	267	Value Missing (- 1.896022 2)	626	Value Missing (- 2.1803 102)	182	Value Missi ng (- 2.124 9168)	610	Value Missing (- 2.176809 5)	954.2	2859.4	3	0.0312	10.9			
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P02453 CO1A1_BOVIN	gEPG PPG PAG AAG PAG NPG ADG QPG Ak	55%	35.3	55.16452	Ref	Value Missing (- 2.1065 753)	Value Missi ng (- 2.390 8637)	Value Missin g (- 2.3354 702)	Value Missin g (- 2.3873 63)	2000	Value Missing (- 2.106575 3)	9250	Value Missing (- 2.3908 637)	3130	Value Missi ng (- 2.335 4702)	7330	Value Missing (- 2.387363)	954.2	2859.4	3	0.0282	9.873			
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P02453 CO1A1_BOVIN	gEPG PTGI QGP PGP AGE EGk	79%	40.6	54.8339	Ref	-0.42	0.96	-1	-0.14	-0.86	0.62	-0.94	5330	3380	9550	2680	5520	2930	8510	2860	814.1	2439.3	3	0.0245	10.05
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P02453 CO1A1_BOVIN	gEPG PTGI QGP PGP AGE EGkR	90%	47.5	55.1129	Ref	-1.7	1.3	-2.1	-0.079	-1.7	1.1	-2	2770	704	5940	651	2810	811	5630	687	866.1	2595.4	3	0.0251	9.682
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P02453 CO1A1_BOVIN	gETG PAG PAG PIGP VGA R	95%	68.3	53.59234	Ref	-1.2	1.1	-1.3	-0.12	-1.3	0.77	-1.3	4790	1480	8140	1720	4220	1670	7130	1640	933	1864	2	0.0137	7.321
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P02453 CO1A1_BOVIN	gFPG LPGP SGEP Gk	86%	41.2	53.61441	Ref	-0.84	1.2	-1.2	-0.078	-1.1	0.81	-1.4	4710	2420	10600	2270	5530	2390	9340	2000	953	1904	2	0.0223	11.71

Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P02453 CO1A1_BOVIN	gFSG LQG PPG PPGS PGE QGP SGAS GPA GPR	95%	81.7	54.13789	Ref	-0.59	0.69	-0.32	-0.069	-0.18	0.4	-0.43	1170	905	2380	1330	1750	1410	2200	1230	987.8	2960.4	3	0.0372	12.57
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P02453 CO1A1_BOVIN	gnSG EPG APG Sk	51%	31.8	52.49453	Ref	-2.1	1.6	-2.5	-0.23	-1.9	1.1	Value Missing (-2.9182823)	4220	834	11800	813	4200	1140	9380	Value Missing (-2.9182823)	833.9	1665.9	2	0.0229	13.75
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P02453 CO1A1_BOVIN	gPA GPP GR	93%	45.6	49.63259	Ref	-0.63	0.73	-0.3	-0.25	-0.44	0.52	-0.89	6350	3420	9480	5230	5980	4560	9300	3470	338.2	1011.6	3	0.0093	9.16
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P02453 CO1A1_BOVIN	gPSG PQG PSGP PGPk	92%	45.8	53.79316	Ref	-2.2	1.4	Value Missing (-3.1089942)	0.14	-2.1	1.2	Value Missing (-3.1054938)	5230	921	11700	Value Missing (-3.1089942)	6090	1120	11300	Value Missing (-3.1054938)	963	1924	2	0.0229	11.91
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P02453 CO1A1_BOVIN	gPSG PQG PSGP PGPk	87%	43.4	53.79356	Ref	-0.9	1.1	-0.97	-0.15	-0.7	0.65	-0.81	18400	9310	39600	10800	21000	12600	33500	12000	642.4	1924	3	0.0223	11.56
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P02453 CO1A1_BOVIN	gQA GVM GFP GPK	95%	53.9	53.07106	Ref	-0.42	0.61	-0.55	-0.014	-0.51	0.4	-0.63	13600	8020	17800	8950	14300	8830	17400	8470	585.3	1753	3	0.0158	9.005

Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	gQA GVM GFP GPK	95%	51.1	52.95145	Ref	-0.89	0.95	-1.2	0.046	-1	0.73	-1.1	3140	1310	5090	1310	3350	1400	4930	1400	877.5	1753	2	0.0169	9.657
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	gRP GAP GPA GAR	87%	41.8	51.6714	Ref	-1.5	1.4	-0.84	-0.19	-1.5	0.86	-2.2	4E+05	121000	9E+05	229000	395000	1E+05	7E+05	91800	456.6	1366.8	3	0.0137	10.04
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	gSAG PPG ATG FPG AAG R	95%	80.6	52.57976	Ref	-1.7	1.4	-2	-0.33	-1.9	1.2	-2.3	9040	2420	22500	2430	8410	2470	21500	2000	866.5	1730.9	2	0.0128	7.392
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	gSEG PQG VR	88%	40	49.81792	Ref	-1.3	1.3	-0.64	-0.048	-0.78	0.56	-1.9	8880	3480	22500	6600	11000	5750	15200	2830	397.5	1189.6	3	0.0097	8.159
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	gVP GPP GAV GPA Gk	95%	52.9	52.20573	Ref	-1.2	1.4	-2.1	-0.14	-1.6	1	-2.3	6680	2800	18800	1870	7810	2410	15700	1570	885	1768	2	0.0199	11.24
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	gVQ GPP GPA GPR	76%	36.4	52.28662	Ref	-1.1	1.3	-1.5	-0.07	-1	0.93	-1.8	19300	8750	48500	7830	24000	10700	43800	6600	697.4	1392.8	2	0.0138	9.874

Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	gVQ GPP GPA GPR	76%	36.4	52.22425	Ref	-1.3	1.2	-1.4	0.022	-1.1	0.84	-1.5	11700	4210	25900	4750	14000	5450	22400	4360	697.4	1392.8	2	0.014	10.06
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	sGD RGET GPA GPIG PVG AR	95%	62.1	54.47682	Ref	-1.6	1.2	-1.4	-0.13	-1.1	0.96	-1.1	10100	2940	21200	3980	10700	4700	20800	4910	760.7	2279.2	3	0.0181	7.916
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	sLSQ QIEN IR	58%	33	52.65033	Ref	-0.9	0.86	-0.97	-0.027	-0.97	0.9	-1.1	33800	15300	56200	17800	37700	17100	65500	16300	746.4	1490.8	2	0.0133	8.903
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	sLSQ QIEN IR	76%	36.7	52.65316	Ref	-0.51	0.66	-0.79	-0.098	-0.59	0.76	-0.67	9090	5980	14600	5980	10700	6620	17600	6490	746.4	1490.8	2	0.0138	9.225
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3	sp P0245 3 CO1A1 _BOVIN	sTGI SVP GPM GPS GPR	95%	59.2	52.95345	Ref	-1.6	1.3	-1.8	0.13	-1.4	0.94	-1.7	13100	3860	29500	4110	16800	5030	26900	4380	901	1799.9	2	0.0149	8.257

Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tr D2H4P3 D2H4P3_AILME,tr E2RG49 E2RG49_CANFA,tr F7DXG8 F7DXG8_HORSE,tr F7GPI9 F7GPI9_CALJAK	aSGV AVS DGVI	65%	33.9	52.22332	Ref	-0.11	-0.3	0.62	0.74	-0.16	-0.46	-0.66	135	143	136	290	346	162	137	119	724.9	1447.8	2	0.0149	10.27
Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tr D2H4P3 D2H4P3_AILME,tr E2RG49 E2RG49_CANFA,tr F7DXG8 F7DXG8_HORSE,tr F7GPI9 F7GPI9_CALJAK	aSGV AVS DGVI	89%	41.7	52.24551	Ref	-0.25	0.25	0.15	-0.039	0.084	-0.18	-0.06	189	148	227	238	230	219	190	205	724.9	1447.8	2	0.0069	4.786

Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,triD2H4P3 D2H4P3_AILME,triE2RG49 E2RG49_CANFA,triF7DXG8 F7DXG8_HORSE,triF7GPI9 F7GPI9_CALJAK	aSGV AVS DGVI	95%	62	52.22927	Ref	Value Missing (- 1.423038)	-0.22	0.33	0.15	0.26	-0.15	0.31	2050	Value Missing (- 1.423038)	1630	2690	2600	2460	1930	2640	724.9	1447.8	2	0.0152	10.51
Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,triD2H4P3 D2H4P3_AILME,triE2RG49 E2RG49_CANFA,triF7DXG8 F7DXG8_HORSE,triF7GPI9 F7GPI9_CALJAK	aSGV AVS DGVI	95%	57.4	52.28172	Ref	0.23	-0.88	-0.46	-0.6	-0.26	-0.83	-0.36	11800	4520	2260	3410	3400	3770	2640	3630	724.9	1447.8	2	0.0129	8.913

Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tron D2H4P3 D2H4P3_AILME,tron E2RG49 E2RG49_CANFA,tron F7DXG8 F7DXG8_HORSE,tron F7GPI9 F7GPI9_CALJADK	aVLF cLSE DK	91%	45.8	52.93581	Ref	0.1	-0.26	0.066	-0.15	0.18	-0.31	0.23	7480	7100	5970	8430	8000	8770	6510	9420	593.6	1777.9	3	0.0334	18.76
Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tron D2H4P3 D2H4P3_AILME,tron E2RG49 E2RG49_CANFA,tron F7DXG8 F7DXG8_HORSE,tron F7GPI9 F7GPI9_CALJADK	aVLF cLSE DK	51%	32.8	53.35283	Ref	0.093	-0.05	-0.1	-0.05	-0.08	-0.01	-0.03	3720	3150	3090	3360	3830	3270	3590	3520	593.7	1777.9	3	0.0096	5.384

Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tr D2H4P3 D2H4P3_AILME,tr E2RG49 E2RG49_CANFA,tr F7DXG8 F7DXG8_HORSE,tr F7GPI9 F7GPI9_CALJAEiLVGDV GQTVDDPYATFVk	95%	70.5	55.17763	Ref	0.11	-0.01	-0.02	-0.074	-0.08	0.037	-0.03	3980	3810	3810	4240	4490	3910	4420	4200	925.5	2773.5	3	0.0203	7.322
Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tr D2H4P3 D2H4P3_AILME,tr E2RG49 E2RG49_CANFA,tr F7DXG8 F7DXG8_HORSE,tr F7GPI9 F7GPI9_CALJAEiLVGDV GQTVDDPYATFVk	95%	58.9	55.12124	Ref	0.4	0.14	0.044	-0.34	-0.11	-0.03	-0.15	3380	4260	3850	4060	3420	3500	3870	3530	925.5	2773.5	3	0.0183	6.597

Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tron D2H4P3 D2H4P3_AILME,tron E2RG49 E2RG49_CANFA,tron F7DXG8 F7DXG8_HORSE,tron F7GPI9 F7GPI9_CALJAEVKhELQANcY	86%	42.3	53.06541	Ref	0.19	-0.2	0.05	0.002	0.025	-0.27	0.012	8690	8350	6910	9190	9800	8700	7430	8930	706.4	2116	3	0.0155	7.34
Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tron D2H4P3 D2H4P3_AILME,tron E2RG49 E2RG49_CANFA,tron F7DXG8 F7DXG8_HORSE,tron F7GPI9 F7GPI9_CALJAEVKhELQANcY	74%	35.6	53.19315	Ref	0.085	-0.21	0.12	-0.077	0.16	-0.08	-0.02	14800	14500	12900	18100	17400	17900	15900	16500	597.8	2387.2	4	0.0213	8.939

<p>Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3</p>	<p>sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,triD2H4P3 D2H4P3_AILME,triE2RG49 E2RG49_CANFA,triF7DXG8 F7DXG8_HORSE,triF7GPI9 F7GPI9_CALJADR</p>	<p>hELQ ANcY EEVK</p>	83%	40.8	53.25306	Ref	0.012	-0.12	0.19	-0.013	0.052	-0.3	-0.02	7500	6210	6130	8530	8200	7490	6130	7400	796.7	2387.2	3	0.0196	8.225
<p>Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3</p>	<p>sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,triD2H4P3 D2H4P3_AILME,triE2RG49 E2RG49_CANFA,triF7DXG8 F7DXG8_HORSE,triF7GPI9 F7GPI9_CALJADR</p>	<p>kLTG</p>	59%	23.6	44.55225	Ref	0.054	-0.39	0.28	-0.097	0.3	-0.39	-0.13	78200	64800	51600	92200	78300	90200	58400	69000	393.8	1571	4	0.0095	6.063

Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,triD2H4P3 D2H4P3_AILME,triE2RG49 E2RG49_CANFA,triF7DXG8 F7DXG8_HORSE,triF7GPI9 F7GPI9_CALJAPL	IGGS AVIS LEGK PL	62%	32	50.63048	Ref	-0.27	-0.22	0.36	0.02	0.25	-0.16	-0.13	42900	32100	36000	60400	52500	53600	42300	42800	650.4	1948.2	3	0.0152	7.791
Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,triD2H4P3 D2H4P3_AILME,triE2RG49 E2RG49_CANFA,triF7DXG8 F7DXG8_HORSE,triF7GPI9 F7GPI9_CALJAPL	IGGS AVIS LEGK PL	95%	63.3	50.41274	Ref	-0.023	-0.53	0.19	-0.061	0.28	-0.21	0.14	13700	11700	8930	16600	15300	17000	12600	15900	975.1	1948.2	2	0.0101	5.187

Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tron D2H4P3 D2H4P3_AILME,tron E2RG49 E2RG49_CANFA,tron F7DXG8 F7DXG8_HORSE,tron F7GPI9 F7GPI9_CALJIA	IGGS AVIS LEGK PL	95%	52.5	50.2419	Ref	0.057	-0.32	0.11	-0.15	0.31	-0.35	0.099	70300	61600	51300	77500	71600	86100	57000	77000	650.4	1948.2	3	0.0089	4.59
Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tron D2H4P3 D2H4P3_AILME,tron E2RG49 E2RG49_CANFA,tron F7DXG8 F7DXG8_HORSE,tron F7GPI9 F7GPI9_CALJIA	IGGS AVIS LEGK PL	95%	65.3	49.81279	Ref	0.026	-0.28	0.12	0.005	0.2	-0.23	0.033	7890	7050	6180	9190	9330	9330	7210	8610	975.1	1948.2	2	0.0016	0.806

Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,triD2H4P3 D2H4P3_AILME,triE2RG49 E2RG49_CANFA,triF7DXG8 F7DXG8_HORSE,triF7GPI9 F7GPI9_CALJAPL	IGGS AVIS LEGK PL	95%	56.4	50.70942	Ref	-0.15	-0.18	0.29	-0.05	0.26	-0.38	-0.02	15400	11900	12600	19500	17000	18400	12400	15700	650.4	1948.2	3	0.0165	8.453
Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,triD2H4P3 D2H4P3_AILME,triE2RG49 E2RG49_CANFA,triF7DXG8 F7DXG8_HORSE,triF7GPI9 F7GPI9_CALJAPL	IGGS AVIS LEGK PL	95%	70.2	50.63048	Ref	-0.033	-0.15	0.1	0.009	0.18	-0.3	0.027	6070	5000	4990	6670	6900	6780	5070	6330	975.1	1948.2	2	0.0152	7.814

<p>Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3</p>	<p>sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,triD2H4P3 D2H4P3_AILME,triE2RG49 E2RG49_CANFA,triF7DXG8 F7DXG8_HORSE,triF7GPI9 F7GPI9_CALJAPL</p>	<p>IGGS AVIS LEGK</p>	<p>79%</p>	<p>36.4</p>	<p>50.56299</p>	<p>Ref</p>	<p>0.03</p>	<p>-0.03</p>	<p>-0.04</p>	<p>-0.002</p>	<p>0.12</p>	<p>-0.14</p>	<p>-0.02</p>	<p>1710</p>	<p>1520</p>	<p>1580</p>	<p>1760</p>	<p>1990</p>	<p>1890</p>	<p>1650</p>	<p>1780</p>	<p>650.4</p>	<p>1948.2</p>	<p>3</p>	<p>0.0134</p>	<p>6.853</p>
<p>Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3</p>	<p>sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,triD2H4P3 D2H4P3_AILME,triE2RG49 E2RG49_CANFA,triF7DXG8 F7DXG8_HORSE,triF7GPI9 F7GPI9_CALJAniILEEGK</p>	<p>nILE EGK</p>	<p>57%</p>	<p>30.8</p>	<p>50.51504</p>	<p>Ref</p>	<p>0.14</p>	<p>-0.12</p>	<p>0.11</p>	<p>-0.13</p>	<p>0.1</p>	<p>-0.37</p>	<p>-0.18</p>	<p>52200</p>	<p>41800</p>	<p>37800</p>	<p>49700</p>	<p>46500</p>	<p>47600</p>	<p>35700</p>	<p>40600</p>	<p>762.5</p>	<p>1522.9</p>	<p>2</p>	<p>0.0102</p>	<p>6.716</p>

Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tron D2H4P3 D2H4P3_AILME,tron E2RG49 E2RG49_CANFA,tron F7DXG8 F7DXG8_HORSE,tron F7GP19 F7GPI9_CALJAEgk	nILE	61%	32	50.7501	Ref	0.19	-0.31	0.041	-0.13	0.094	-0.2	0.028	32500	29100	22400	32100	31400	32000	27300	31700	508.6	1522.9	3	0.019	12.49
Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tron D2H4P3 D2H4P3_AILME,tron E2RG49 E2RG49_CANFA,tron F7DXG8 F7DXG8_HORSE,tron F7GP19 F7GPI9_CALJAVk	nILE EGkE ILVG DVG QTV DDP YATF	73%	36.2	54.28234	Ref	No Values (-794)	No Values (-1.676073)	No Values (-1.8426678)	Reference Missing (1.0280646)	Reference Missing (1.39013763)	Reference Missing (0.8331839167)	No Values (-1.7607696)	No Values (-1.5583794)	No Values (-1.676073)	No Values (-1.842678)	Reference Missing (1.0280646)	Reference Missing (1.3905867)	Reference Missing (0.83313763)	No Values (-1.839167)	994.6	3974.2	4	0.0304	7.65	

Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tron D2H4P3 D2H4P3_AILME,tron E2RG49 E2RG49_CANFA,tron F7DXG8 F7DXG8_HO RSE,tron F7GPI9 F7GPI9_CALJAVk	nHILE EGkE ILVG DVG QTV DDP YATF	89%	42.1	53.18314	Ref	Value Missing (- 2.8399 367)	-0.44	0.18	0.45	0.34	-0.2	0.41	194	Value Missing (- 2.839936 7)	122	211	279	226	163	247	994.6	3974.2	4	0.0028	0.702
Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tron D2H4P3 D2H4P3_AILME,tron E2RG49 E2RG49_CANFA,tron F7DXG8 F7DXG8_HO RSE,tron F7GPI9 F7GPI9_CALJAVk	nHILE EGkE ILVG DVG QTV DDP YATF	95%	52.6	53.56573	Ref	0.061	-0.54	0.25	-0.19	0.49	-0.35	0.21	208	234	167	325	263	369	215	314	994.6	3974.2	4	0.0082	2.055

Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tr D2H4P3 D2H4P3_AILME,tr E2RG49 E2RG49_CANFA,tr F7DXG8 F7DXG8_HORSE,tr F7GPI9 F7GPI9_CALJAVk	nHLE EGkE ILVG DVG qTV DDP YATF	84%	39.9	53.81712	Ref	-0.38	-0.38	0.37	-0.14	0.36	-0.21	0.24	181	136	148	279	216	266	187	255	994.8	3975.2	4	#####	0.035
Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tr D2H4P3 D2H4P3_AILME,tr E2RG49 E2RG49_CANFA,tr F7DXG8 F7DXG8_HORSE,tr F7GPI9 F7GPI9_CALJAYALY DAT YETK		94%	51.7	53.79905	Ref	0.059	-0.44	0.027	-0.024	0.09	0.12	-0	1E+05	112000	86000	134000	142000	1E+05	1E+05	131000	649.3	1945	3	0.0157	8.062

Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tr D2H4P3 D2H4P3_AILME,tr E2RG49 E2RG49_CANFA,tr F7DXG8 F7DXG8_HORSE,tr F7GPI9 F7GPI9_CALJA	yALY DAT YETK	88%	44.6	53.79639	Ref	-0.098	-0.11	0.077	-0.027	-0.09	-0.16	0.054	11700	8090	8730	11100	11400	9570	9500	10900	649.3	1945	3	0.0155	7.954
Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tr D2H4P3 D2H4P3_AILME,tr E2RG49 E2RG49_CANFA,tr F7DXG8 F7DXG8_HORSE,tr F7GPI9 F7GPI9_CALJA	yALY DAT YETK	73%	37.8	53.8072	Ref	0.026	-0.63	0.29	0.028	0.11	0.005	0.12	73200	74000	50800	108000	99500	91700	89300	96200	649.3	1945	3	0.0148	7.584

<p>Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3</p>	<p>sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,triD2H4P3 D2H4P3_AILME,triE2RG49 E2RG49_CANFA,triF7DXG8 F7DXG8_HORSE,triF7GPI9 F7GPI9_CALJAYETK</p>	<p>yALY DAT</p>	<p>93%</p>	<p>49.1</p>	<p>53.79567</p>	<p>Ref</p>	<p>0.011</p>	<p>0.07</p>	<p>0.046</p>	<p>-0.18</p>	<p>0.013</p>	<p>-0.1</p>	<p>0.083</p>	<p>5340</p>	<p>4810</p>	<p>5440</p>	<p>6010</p>	<p>5660</p>	<p>5650</p>	<p>5480</p>	<p>6150</p>	<p>649.3</p>	<p>1945</p>	<p>3</p>	<p>0.0094</p>	<p>4.855</p>
<p>Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3</p>	<p>sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,triD2H4P3 D2H4P3_AILME,triE2RG49 E2RG49_CANFA,triF7DXG8 F7DXG8_HORSE,triF7GPI9 F7GPI9_CALJAYETK</p>	<p>yALY DAT</p>	<p>95%</p>	<p>69.4</p>	<p>53.76858</p>	<p>Ref</p>	<p>-0.074</p>	<p>-0.34</p>	<p>0.14</p>	<p>0.046</p>	<p>0.29</p>	<p>-0.33</p>	<p>-0</p>	<p>42300</p>	<p>33000</p>	<p>29700</p>	<p>46600</p>	<p>48100</p>	<p>49900</p>	<p>33800</p>	<p>42100</p>	<p>973.5</p>	<p>1945</p>	<p>2</p>	<p>0.0151</p>	<p>7.761</p>

Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tr D2H4P3 D2H4P3_AILME,tr E2RG49 E2RG49_CANFA,tr F7DXG8 F7DXG8_HORSE,tr F7GPI9 F7GPI9_CALJA	yALY DAT YETK	95%	56.3	53.85313	Ref	0.029	-0.24	0.14	0.024	0.26	-0.39	0.012	15600	13800	12500	18200	18500	19000	12700	16600	973.5	1945	2	0.0084	4.318
Cofilin-1 OS=Sus scrofa GN=CFL1 PE=1 SV=3	sp P10668 COF1_PIG,sp P23528 COF1_HUMAN,sp Q4R5C0 COF1_MACFA,sp Q5E9F7 COF1_BOVIN,sp Q6B7M7 COF1_SHEEP,tr B0JYL8 B0JYL8_BOVIN,tr D2H4P3 D2H4P3_AILME,tr E2RG49 E2RG49_CANFA,tr F7DXG8 F7DXG8_HORSE,tr F7GPI9 F7GPI9_CALJA	yALY DAT YETK	95%	70.1	53.73537	Ref	-0.11	-0.29	0.15	0.13	0.32	-0.4	0.09	3490	3050	2910	4430	4840	4820	3050	4250	973.5	1945	2	0.0189	9.714

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	eAG GGG VGG PGA k	95%	62.7	52.87445	Ref	-0.49	-0.42	0.061	-0.14	0.39	-0.93	0.11	22100	13500	15400	24100	23100	29100	12200	24900	811.5	1620.9	2	0.0139	8.562
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	eETQ PPV Alk	95%	51.4	52.39877	Ref	-0.22	-0.33	0.024	-0.28	0.2	-0.64	-0.15	20500	13400	13500	19300	17200	21000	12300	17100	860.5	1719	2	0.0051	2.961

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	eMT LDE Wk	55%	32.7	52.4718	Ref	-0.65	-0.39	-0.04	-0.21	0.37	-0.61	0.16	22700	12200	15800	22700	22200	29100	15300	25900	554	1658.9	3	0.0194	11.71
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	eMT LDE Wk	55%	32.6	52.64835	Ref	-0.34	-0.44	-0.05	-0.2	0.25	-0.63	0.069	8440	5340	5400	7980	7930	9430	5360	8630	830.4	1658.9	2	0.0091	5.5

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	fDQL FDD ESDP FEVL	95%	62	54.60533	Ref	-0.21	-0.35	0.21	-0.29	0.057	-0.58	0.003	2250	1680	1650	2730	2130	2370	1590	2360	851.4	2551.3	3	0.014	5.477
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	gFVL HK	61%	29.4	48.04555	Ref	-0.66	-0.35	-0.05	-0.14	0.38	-0.9	0.17	1E+05	58000	78300	108000	111000	1E+05	60300	125000	436.9	1307.8	3	0.004	3.067

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	gFVL HK	77%	32.1	47.6003	Ref	-0.43	-0.4	-0.04	-0.12	0.25	-0.41	0.085	31500	21800	24100	34600	36200	40800	27000	37700	654.9	1307.8	2	0.0029	2.222
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	gFVL HK	60%	29.3	48.26955	Ref	-0.42	-0.43	-0.13	-0.11	0.31	-0.76	0.11	3E+05	180000	2E+05	269000	299000	4E+05	2E+05	315000	436.9	1307.8	3	0.0128	9.784

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	gFVL HK	60%	29.3	48.16745	Ref	-0.65	-0.37	0.098	-0.2	0.45	-0.96	0.15	3E+05	182000	2E+05	373000	335000	5E+05	2E+05	385000	436.9	1307.8	3	0.0119	9.096
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	gFVL HK	65%	29.4	47.65147	Ref	-0.44	-0.4	-0.08	-0.14	0.41	-0.89	0.036	64400	37700	42000	59100	62300	79600	33800	63800	654.9	1307.8	2	0.0016	1.199

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	gFVL HK	52%	28.5	48.82297	Ref	-0.57	-0.32	-0.04	-0.23	0.46	-0.75	0.058	2130	1210	1570	2130	2060	2900	1310	2280	436.9	1307.8	3	0.0187	14.25
	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	kEAG GGG VGG PGA k	95%	51.9	53.00028	Ref	-0.68	-0.38	-0.06	-0.078	0.25	-0.55	0.31	7910	4680	6230	8750	9500	10500	6230	11200	685.4	2053.2	3	0.0371	18.08

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	KNPL PPSV GVV Dkk	59%	27.5	48.38093	Ref	-0.15	-0.3	-0.21	-0.14	0.16	-0.69	-0.03	28500	19800	19300	23100	26700	28800	16600	26100	566.4	2261.4	4	0.0082	3.621
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	KNPL PPSV GVV Dkk	55%	21.6	46.68684	Ref	-0.25	-0.3	0.023	-0.13	0.17	-0.47	-0.03	18400	14500	15200	21400	21100	22800	15200	20600	539.7	2693.6	5	0.0507	18.83

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	kPA NDIT SQLE INFG DLG R	95%	56	54.89431	Ref	-0.15	0.068	-0.17	-0.25	0.085	-0.5	-0.09	4610	3770	4770	4540	4720	5210	3630	4770	899.5	2695.5	3	0.0242	8.981
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	kPA NDIT SQLE INFG DLG R	74%	39.2	54.87273	Ref	-0.33	-0.06	0.046	-0.37	-0.01	-0.37	0.09	2280	1670	2190	2640	2180	2440	1990	2720	899.5	2695.5	3	0.0227	8.435

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	kPANDITSQLFINFGDLGR	95%	60.5	54.85212	Ref	-0.23	-0.46	0.27	-0.14	0.18	-0.79	-0.3	6570	4370	4040	7530	6260	6830	3620	5060	899.5	2695.5	3	0.0222	8.235
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	kPANDITSQLFINFGDLGR	94%	49.4	54.69044	Ref	-0.035	-0.24	-0.02	-0.4	0.099	-0.61	0.036	4300	3610	3390	4450	3760	4640	2980	4610	674.9	2695.5	4	0.0128	4.748

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	kPAn DITS QLEI NFG DLG R	91%	48	55.12865	Ref	0.066	-0.04	-0.11	-0.094	0.018	-0.7	-0.16	833	822	831	885	988	932	593	856	899.8	2696.4	3	0.0249	9.226
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	kPnE GAD GQ Wk	69%	37	53.97997	Ref	-0.36	-0.36	0.017	-0.16	0.29	-0.91	0.097	23000	14800	16100	23500	22800	27300	12400	24800	715.1	2142.2	3	0.0083	3.89

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	pGH LQE GFG cVVT NR	95%	57.5	52.10037	Ref	-0.15	-0.44	0.14	-0.22	0.13	-0.48	-0.13	9250	7180	6390	10700	9220	10300	6990	8830	655.3	1963	3	0.0113	5.744
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	pGH LQE GFG cVVT NR	58%	33	52.21907	Ref	-0.014	-0.22	-0.11	-0.21	-0.18	-0.1	-0.06	13500	12800	12000	14500	15000	13400	14800	15000	655.3	1963	3	0.0087	4.43

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	SAA QAA AQT NSN AAG k	95%	56.8	54.20263	Ref	-0.83	-0.24	0.15	-0.13	0.46	-1.2	0.17	6220	3140	5130	7550	6870	8980	3000	7640	1035	2068.1	2	0.03	14.5
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_HUMAN, tr Q63HR1 Q63HR1_HUMAN	SAA QAA AQT NSN AAG k	95%	58.9	54.10244	Ref	-0.35	0.06	-0.12	-0.27	0.2	-0.79	0.14	5110	3780	5450	5390	5370	6480	3420	6470	690.4	2068.1	3	0.0137	6.636

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	sAA QAA AQT nSN AAG k	95%	66.9	53.94951	Ref	0.14	-0.35	-0.12	-0.37	-0.07	-0.53	0.14	1720	1640	1280	1670	1550	1670	1260	2000	690.7	2069.1	3	0.0224	10.84
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	sAA QAA AQT nSN AAG k	95%	61.8	53.99403	Ref	-0.61	-0.43	-0.1	-0.28	0.22	-0.48	0.57	16000	11200	13800	19400	18900	23400	15000	30900	690.7	2069.1	3	0.0164	7.928

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	sAA QAA AQT nSN AAG k	95%	63.2	53.98856	Ref	-0.59	0.094	-0.02	-0.22	0.26	-0.81	0.099	35300	22100	38500	39900	38200	46700	23200	43300	690.7	2069.1	3	0.0161	7.754
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	sAA QAA AQT nSN AAG k	85%	42.6	54.01128	Ref	0.042	0.78	-0.59	-0.29	-0.3	-0.54	-0.32	6320	7070	12800	5560	7560	6540	5780	6670	690.7	2069.1	3	0.0149	7.218

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	sAA QAA AQT NSn AAG k	95%	86.8	53.97509	Ref	-0.28	-0.26	-0.16	-0.38	0.15	-0.15	0.059	1980	1480	1620	1960	1850	2340	1980	2270	690.7	2069.1	3	0.027	13.06
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	sAA QAA AQT NSn AAG k	95%	59.2	53.95194	Ref	-0.37	-0.08	0.027	-0.37	0.26	-0.71	0.084	11500	8120	10800	13000	10900	14700	7870	13500	690.7	2069.1	3	0.0221	10.67

Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	sAA QAA AQT nSnA AGk	88%	44.2	53.63858	Ref	-0.34	-0.06	-0.13	-0.1	0.18	-0.59	-0.1	33800	23200	30500	32500	36500	38900	23800	33100	691	2070.1	3	0.0179	8.652
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp Q8NC51 PAIRB_HUMAN, tr A1L5B7 A1L5B7_BOVIN, tr F1MFK6 F1MFK6_BOVIN, tr F6WZG6 F6WZG6_MACMU, tr F7EEX7 F7EEX7_C ALJA, tr Q4R9B0 Q4R9B0_M ACFA, tr Q4R9B2 Q4R9B2_M ACFA, tr Q5VU21 Q5VU21_H UMAN, tr Q63HR1 Q63HR1_HUMAN	sAA QAA AQT nSnA AGk	95%	58	53.6523	Ref	-0.54	-0.15	-0.07	-0.14	0.29	-0.5	0.18	22000	16000	22800	27000	28400	33200	20100	32000	691	2070.1	3	0.0168	8.13

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,transcript B0FZM4 B0FZM4_SHEEP,transcript B2GV99 B2GV99_RAT,transcript B7Z6Z4 B7Z6Z4_HUMAN,transcript D2H345 D2H345_AILME,transcript D3	aLGEVlk	72%	36.7	52.86564	Ref	-0.66	0.028	-0.25	-0.22	-0.09	-0.33	-0.31	3E+05	179000	3E+05	290000	325000	3E+05	3E+05	276000	655	1962.1	3	0.0231	11.78
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,transcript B0FZM4 B0FZM4_SHEEP,transcript B2GV99 B2GV99_RAT,transcript B7Z6Z4 B7Z6Z4_HUMAN,transcript D2H345 D2H345_AILME,transcript D3	aLGEVlk	95%	51.9	52.3979	Ref	-0.79	0.026	-0.44	-0.051	0.011	-0.39	-0.15	15900	8510	16300	13200	19100	17400	13800	16100	982.1	1962.1	2	0.0056	2.848

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,transcript B0FZM4 B0FZM4_SHEEP,transcript B2GV99 B2GV99_RAT,transcript B7Z6Z4 B7Z6Z4_HUMAN,transcript D2H345 D2H345_AILME,transcript D3	aLGNPNA	95%	64	52.909	Ref	-0.56	0.048	-0.58	-0.027	0.12	-0.3	-0.49	5650	3580	5900	4280	6930	6710	5230	4560	982.1	1962.1	2	0.0184	9.378
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,transcript B0FZM4 B0FZM4_SHEEP,transcript B2GV99 B2GV99_RAT,transcript B7Z6Z4 B7Z6Z4_HUMAN,transcript D2H345 D2H345_AILME,transcript D3	aLGNPNA	93%	48.4	52.82026	Ref	-0.35	-0.09	-0.62	-0.12	-0.1	-0.2	-0.28	44000	30300	39600	30800	47800	42500	41300	38700	655	1962.1	3	0.018	9.167

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3	aLGNPnAE	94%	50.3	53.15777	Ref	-0.59	-0.07	-0.55	-0.2	-0.09	-0.21	-0.09	29300	17100	26600	21400	30000	28300	27200	29300	655.4	1963.1	3	0.0151	7.67
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3	aLGNPnAE	95%	52.1	53.09547	Ref	-0.71	0.046	-0.54	-0.06	-0.04	-0.31	-0.21	6030	3290	6020	4490	6920	6140	5310	5630	982.6	1963.1	2	0.0136	6.944

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,sp B0FZM4 B0FZM4_SHEEP,sp B2GV99 B2GV99_RAT,sp B7Z6Z4 B7Z6Z4_HUMAN,sp D2H345 D2H345_AILME,sp D3GLR	dQG TYED YVE	95%	49.4	50.61615	Ref	-0.27	0.18	-0.61	-0.24	-0.19	-0.49	-0.52	18600	11600	17200	11200	15800	14300	12200	11800	924.9	1847.9	2	0.0127	6.85
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,sp B0FZM4 B0FZM4_SHEEP,sp B2GV99 B2GV99_RAT,sp B7Z6Z4 B7Z6Z4_HUMAN,sp D2H345 D2H345_AILME,sp D3QLF	eAF QLF	90%	43.3	51.12109	Ref	Value Missing (-0.403940)	-0.01	Value Missing (-0.6882284)	-0.049	-0.08	-0.6	0.12	75404	Value Missing (-0.403940)	8070	Value Missing (-0.6882284)	9700	8300	6050	9870	443.9	1328.7	3	0.0098	7.336

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3k	hVLV TLGE	56%	28.6	50.03223	Ref	-0.39	0.097	-0.71	-0.1	-0.02	-0.34	-0.45	13200	8560	13000	8350	14000	12900	10800	9950	401.7	1603	4	0.025	15.61
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3k	hVLV TLGE	83%	36.3	49.81094	Ref	-0.4	0.087	-0.47	-0.2	-0.03	-0.42	-0.32	9810	6660	10200	7750	10300	10100	8070	8560	802.5	1603	2	0.0168	10.49

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3k	hVLV TLGE	94%	47	49.48384	Ref	-0.36	0.12	-0.58	-0.12	-0.19	-0.41	-0.33	86100	56700	85300	59200	89700	74500	67000	70100	535.3	1603	3	0.0156	9.703
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3k	hVLV TLGE	82%	36.2	50.00235	Ref	-0.52	0.049	-0.62	-0.18	-0.05	-0.3	-0.22	13700	8240	13200	9320	14000	13400	11700	12300	802.5	1603	2	0.0206	12.85

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,tr B0FZM4 B0FZM4_SHEEP,tr B2GV99 B2GV99_RAT,tr B7Z6Z4 B7Z6Z4_HUMAN,tr D2H345 D2H345_AILME,tr D3	hVLV TLGE	95%	49.5	49.3862	Ref	-0.58	-0.02	-0.51	-0.2	-0.13	-0.21	-0.09	33900	20300	32500	25900	35400	32400	32000	34700	535.3	1603	3	0.0128	7.982
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,tr B0FZM4 B0FZM4_SHEEP,tr B2GV99 B2GV99_RAT,tr B7Z6Z4 B7Z6Z4_HUMAN,tr D2H345 D2H345_AILME,tr D3	hVLV TLGE	78%	32.4	48.70819	Ref	-0.49	0.033	-0.56	-0.17	0.008	-0.26	-0.43	20400	12300	19100	14200	20500	20300	17500	15500	401.8	1603	4	0.004	2.518

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3k	hVLV TLGE	87%	37.1	48.86045	Ref	-0.48	0.047	-0.56	-0.11	-0.06	-0.32	-0.33	16000	9960	15600	11400	17200	15700	13600	13400	802.5	1603	2	0.0072	4.481
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3k	hVLV TLGE	69%	29.9	48.7505	Ref	-0.36	0.013	-0.59	-0.17	-0.04	-0.47	-0.38	26700	16300	22900	16900	25000	23900	18500	19500	401.8	1603	4	0.003	1.895

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3k	hVLV TLGE	90%	40.3	49.96394	Ref	-0.3	-0.06	-0.34	-0.3	-0.12	-0.39	-0.33	5260	3490	4470	4130	4700	4650	4010	4160	401.8	1603	4	0.0182	11.35
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3k	iLYS QcG DVM R	75%	33.9	50.08788	Ref	-0.4	0.098	-0.47	-0.14	-0.23	-0.34	-0.37	51100	32300	49400	37500	51700	42500	41000	39900	817.9	1633.8	2	0.0119	7.303

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,sp B0FZM4 B0FZM4_SHEEP,sp B2GV99 B2GV99_RAT,sp B7Z6Z4 B7Z6Z4_HUMAN,sp D2H345 D2H345_AILME,sp D3	iLYS QcG DVM	R	95%	45	50.09562	Ref	-0.43	0.051	-0.46	-0.25	-0.14	-0.34	-0.23	7390	4670	7070	5580	7090	6670	6080	6500	817.9	1633.8	2	0.0115	7.009
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,sp B0FZM4 B0FZM4_SHEEP,sp B2GV99 B2GV99_RAT,sp B7Z6Z4 B7Z6Z4_HUMAN,sp D2H345 D2H345_AILME,sp D3	iLYS QcG DVM	R	93%	42.7	50.24945	Ref	-0.27	-0.19	-0.48	-0.16	-0.19	-0.16	-0.26	1410	1040	1190	1090	1490	1280	1360	1270	817.9	1633.8	2	0.0064	3.939

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,transcript B7Z6Z4 B7Z6Z4_HUMAN,transcript D2H345 D2H345_AILME,transcript D3	nkD QGT YEDY VEGL R	85%	43	54.43546	Ref	-0.35	-0.07	-0.55	-0.15	0.056	-0.47	-0.26	26900	18400	24200	19400	28300	28500	20800	23700	799.1	2394.2	3	0.0219	9.14
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,transcript B7Z6Z4 B7Z6Z4_HUMAN,transcript D2H345 D2H345_AILME,transcript D3	nkD QGT YEDY VEGL R	51%	34	54.44819	Ref	-0.036	0.16	-0.39	-0.31	-0.37	-0.2	-0.43	10900	10700	13300	10200	11900	9980	11700	9880	799.1	2394.2	3	0.0204	8.527

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,transcript B7Z6Z4 B7Z6Z4_HUMAN,transcript D2H345 D2H345_AILME,transcript D3R	nkD QGT YEDY VEGL	57%	32.7	54.07868	Ref	-0.17	-0.36	-0.41	-0.17	-0.04	-0.13	-0.17	7210	6720	6370	6900	8980	8580	8410	8120	599.8	2395.2	4	0.0221	9.219
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,transcript B7Z6Z4 B7Z6Z4_HUMAN,transcript D2H345 D2H345_AILME,transcript D3R	nkD QGT YEDY VEGL	54%	34.2	54.1572	Ref	-0.42	0.066	-0.7	-0.2	0.023	-0.3	-0.35	60700	38700	58800	38900	60400	61600	51400	49200	799.4	2395.2	3	0.0189	7.889

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3k	sDE MNV	91%	42.5	51.61904	Ref	-0.63	0.052	-0.46	-0.19	-0.04	-0.3	-0.28	1E+05	73400	1E+05	101000	133000	1E+05	1E+05	113000	715.9	1429.8	2	0.0174	12.19
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3k	sDE mNV	68%	34	51.32208	Ref	-0.55	-0.01	-0.38	-0.2	-0.04	-0.34	-0.18	39300	24400	38500	33500	41900	41000	34600	38400	482.9	1445.7	3	0.0214	14.82

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3	sDE MnV	55%	31.4	51.4129	Ref	-0.48	-0.04	-0.34	-0.13	-0.05	-0.46	-0.16	19800	13300	19500	17800	22700	20900	16500	20100	716.4	1430.8	2	0.0034	2.365
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,trans B0FZM4 B0FZM4_SHEEP,trans B2GV99 B2GV99_RAT,trans B7Z6Z4 B7Z6Z4_HUMAN,trans D2H345 D2H345_AILME,trans D3	vFDK EGn GTV MGA EIR	52%	34.3	54.62952	Ref	-0.63	0.13	-0.54	-0.19	0.031	-0.32	-0.33	25300	14300	26500	18600	26200	26600	21800	21500	778.1	2331.2	3	0.0237	10.15

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,transcript B0FZM4 B0FZM4_SHEEP,transcript B2GV99 B2GV99_RAT,transcript B7Z6Z4 B7Z6Z4_HUMAN,transcript D2H345 D2H345_AILME,transcript D3	vLDF EHFL PML QTV AK	88%	44.5	53.77323	Ref	-0.46	-0.05	-0.59	-0.097	-0.05	-0.29	-0.31	892	548	794	609	948	856	758	739	832.8	2495.4	3	0.0125	5.01
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,transcript B0FZM4 B0FZM4_SHEEP,transcript B2GV99 B2GV99_RAT,transcript B7Z6Z4 B7Z6Z4_HUMAN,transcript D2H345 D2H345_AILME,transcript D3	vLDF EHFL PmL QTV AK	91%	47.6	54.28543	Ref	-0.45	-0.06	-0.51	-0.26	0.047	-0.36	-0.35	660	388	550	453	595	642	507	505	838.1	2511.4	3	0.019	7.55

Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	0 MYL6_HUMAN,sp P60661 MYL6_BOVIN,sp P60662 MYL6_PIG,sp Q5R844 MYL6_PONAB,sp Q60605 MYL6_MOUSE,sp Q64119 MYL6_RAT,tr B0FZM4 B0FZM4_SHEEP,tr B2GV99 B2GV99_RAT,tr B7Z6Z4 B7Z6Z4_HUMAN,tr D2H345 D2H345_AILME,tr D3	vLDF EHFL PmL QTV AK	95%	53.8	54.32613	Ref	-0.66	0.006	-0.63	0.008	-0.18	-0.31	-0.25	514	260	447	324	554	426	406	418	838.1	2511.4	3	0.0206	8.207
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1MLW0 F1MLW0_BOVIN,tr Q8HY3 Q8HY3_BOVIN	aAkP TkPA ASDL PVP AEG VR	74%	33.3	51.0152	Ref	-0.52	0.13	-0.59	-0.11	-0.47	-0.18	-0.38	15700	9780	16700	11300	17400	11900	15100	13100	722.7	2886.7	4	0.0309	10.69
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1MLW0 F1MLW0_BOVIN,tr Q8HY3 Q8HY3_BOVIN	aAkP TkPA ASDL PVP AEG VR	95%	52.5	50.68182	Ref	-1.1	0.48	-0.9	-0.094	-0.7	-0.08	-0.38	77400	29400	95100	41100	79200	45300	73200	58700	722.7	2886.7	4	0.0258	8.917

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	aAkP TkPA ASDL PVP AEG VR	95%	56.6	49.90166	Ref	-0.63	0.26	-0.64	-0.1	-0.37	-0.2	-0.42	12700	7770	15600	9410	15000	10900	12800	10900	722.7	2886.7	4	0.0116	4.014
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	aEFL Nk	59%	31.5	50.9332	Ref	-0.79	0.41	-0.78	-0.17	-0.57	-0.11	-0.51	33500	16100	40100	19700	33100	22000	31500	23600	665.4	1328.8	2	0.0246	18.52
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	eAE GTS QVE AGk	74%	37.2	53.05605	Ref	-0.24	-0.19	-0.59	-0.05	-0.31	-0.45	-0.36	10000	6990	7840	6680	10700	7790	7400	7800	605.3	1812.9	3	0.0228	12.57
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	eAE GTS QVE AGk	94%	51.2	53.05964	Ref	-0.88	0.45	-0.72	-0.28	-0.46	-0.16	-0.49	37500	16700	45500	22700	33900	26200	33700	26500	605.3	1812.9	3	0.0226	12.47
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	eAE GTS QVE AGk	95%	62.4	53.08445	Ref	-0.83	0.56	-0.95	-0.17	-0.48	-0.18	-0.7	28800	13100	37200	14700	27900	19600	25300	17400	907.5	1813	2	0.0165	9.074

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	gETE SEEF Ek	86%	40.8	51.7376	Ref	-0.84	0.5	-1	-0.12	-0.8	-0.26	-0.33	89900	38200	1E+05	41100	84100	46000	69600	66100	598.3	1791.9	3	0.0149	8.301
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	gETE SEEF Ek	91%	42.3	51.83403	Ref	-1.1	0.58	-0.9	-0.13	-0.62	-0.07	-0.66	21600	8330	28200	11300	21300	13300	20300	13400	897	1791.9	2	0.0125	6.999
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	IEQY TSAI EGTk	95%	59.3	53.73842	Ref	-1.1	0.31	-0.96	-0.11	-0.57	0.19	-0.41	31500	12900	36600	17000	33900	21400	38000	24700	650	1947.1	3	0.0194	9.961
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	IEQY TSAI EGTk	91%	44.7	53.7644	Ref	-0.77	0.17	-0.72	-0.23	-0.55	0.08	-0.23	10400	5500	11400	6900	10700	7500	12100	9680	974.5	1947.1	2	0.0174	8.952
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	IEQY TSAI EGTk	95%	57.1	53.6549	Ref	-0.69	0.27	-0.84	-0.28	-0.6	0.053	-0.16	5270	3060	6480	3350	5440	3830	6270	5390	974.5	1947.1	2	0.0071	3.623

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	IEQY TSAI EGTk	93%	49.5	53.72918	Ref	-0.53	0.34	-0.7	-0.24	-0.63	-0.12	-0.39	8990	5590	11100	6040	9150	6110	9080	7480	650	1947.1	3	0.017	8.729
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	mQN DTT DnET AEk	85%	39.7	51.04347	Ref	-0.83	0.4	-0.88	-0.18	-0.45	-0.11	-0.66	18700	8040	20500	9490	17000	12300	16200	11000	702.7	2105	3	0.023	10.92
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	nDD DEEE AAR	95%	41.3	45.50827	Ref	-0.97	0.65	-0.78	-0.22	-0.54	-0.12	-0.62	10200	4730	15700	6550	10700	7450	10400	7290	734.3	1466.6	2	0.0079	5.387
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	nDD DEEE AAR	95%	57.1	45.5234	Ref	-0.85	0.45	-0.36	-0.29	-0.44	-0.27	-0.37	3440	1900	5070	3240	3770	2970	3470	3220	489.9	1466.6	3	0.0077	5.234
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	nDW MEA EEk	95%	51.7	51.47942	Ref	-0.87	0.36	-0.87	-0.15	-0.55	-0.05	-0.46	12600	5560	14200	6810	12300	8180	12100	9030	880.4	1758.8	2	0.0242	13.72

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	qkEF DPTI TDAS LSLS SR	79%	41.1	55.05836	Ref	-0.49	0.13	-0.6	-0.19	-0.26	-0.21	-0.28	6760	4860	8090	5470	8020	6650	7210	6820	868.5	2602.4	3	0.0247	9.485
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	qkEF DPTI TDAS LSLS SR	59%	36	55.0268	Ref	-0.76	0.25	-0.71	-0.26	-0.45	-0.01	-0.44	5280	2610	5690	3290	4960	3780	5360	3940	868.5	2602.4	3	0.0188	7.238
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	qkEF DPTI TDAS LSLS SR	95%	54.1	55.0276	Ref	-0.73	0.42	-0.65	-0.2	-0.41	-0.02	-0.52	4080	2550	6130	3270	4940	3710	5100	3580	868.5	2602.4	3	0.0196	7.526
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	qkQE EEAL GQV TDQ VEV NTQ NSV PDEE Vk	72%	34.4	56.21809	Ref	-0.49	-0.03	-0.54	-0.34	-0.23	-0.11	-0.35	1790	1110	1660	1310	1660	1570	1770	1500	837.4	4182.1	5	0.0549	13.13
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	qkQE EEAL GQV TDQ VEV NTQ NSV PDEE Vk	58%	35.2	56.21319	Ref	No Values (-0.025164016)	No Value s (-0.14285748)	No Value s (-0.30945227)	No Values (-0.4499314)	No Values (-0.25405902)	No Value s (-0.3168257)	No Values (-0.30595154)	No Values (-0.22755413)	No Values (-0.025164016)	No Value s (-0.14285748)	No Values (-0.30945227)	No Values (-0.4499314)	No Value s (-0.25405902)	No Values (-0.3168257)	No Values (-0.30595154)	1047	4182.1	4	0.0367	8.781

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	qkQE EEAL GQV TDQ VEV NTQ NSV PDEE Vk	78%	39.7	56.2077	Ref	No Values (-0.025164278)	No Value s (-0.14285767)	No Value s (-0.30945247)	No Values (-0.4499315)	No Values (-0.25405923)	No Value s (-0.31682578)	No Values (-0.30595186)	No Values (-0.22755413)	No Values (-0.025164278)	No Value s (-0.14285767)	No Values (-0.309452475)	No Value s (-0.25405923)	No Values (-0.316825786)	No Values (-0.30595186)	1047	4182.1	4	0.0265	6.333	
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	qkQE EEAL GQV TDQ VEV NTQ nSVP DEEV k	82%	41.5	56.23902	Ref	No Values (-0.025164103)	No Value s (-0.14285748)	No Value s (-0.30945247)	No Values (-0.4499315)	No Value s (-0.316825785902)	No Values (-0.30595186)	No Values (-0.22755413)	No Values (-0.025164103)	No Value s (-0.14285748)	No Values (-0.309452475)	No Value s (-0.25405902)	No Values (-0.316825786)	No Values (-0.30595186)	1047	4183.1	4	0.0294	7.033		
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	qQE AALE LEEL k	77%	38.5	53.32109	Ref	-0.27	-0.05	-0.3	-0.18	-0.6	0.18	-0.43	55900	56900	71900	68200	81700	53100	95400	62100	670.4	2008.1	3	0.0081	4.031
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	qQE AALE LEEL k	61%	34.4	53.13992	Ref	-0.2	-0.09	-0.34	-0.29	-0.36	-0.07	-0.34	6900	6570	7720	7300	8300	6930	8800	7250	670.4	2008.1	3	0.0046	2.299
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	qQE AALE LEEL kk	52%	33.2	53.59551	Ref	-0.58	0.24	-0.65	-0.24	-0.4	-0.13	-0.28	17000	11000	21100	12700	18600	14600	18400	16400	707.4	2119.2	3	0.0178	8.4

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	sQn GEF MTH k	84%	40.3	52.43576	Ref	-0.7	0.33	-0.92	-0.15	-0.58	-0.14	-0.32	39200	20000	44400	20900	39400	25500	36200	31600	596.6	1786.9	3	0.0176	9.827
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	tTTT NTQ AEG DDE AALL ER	95%	48.3	52.40147	Ref	-1.1	0.5	-1	-0.073	-0.57	-0	-0.47	9140	3700	12200	4760	10100	6250	9640	6930	1171	2339.1	2	0.021	8.962
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	vLEE EEQ ER	81%	36.4	50.61203	Ref	-0.91	0.4	-0.73	-0.23	-0.42	-0	-0.49	54400	25900	69800	35800	55700	42600	59600	42000	668.4	1334.7	2	0.0115	8.572
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.59726 PE=4 SV=1	tr F1ML W0 F1ML W0_BOVI N,tr Q8H YY3 Q8HY Y3_BOVIN	vLEE EEQ R	68%	32.9	50.75365	Ref	-0.92	0.43	-0.74	-0.19	-0.52	-0.1	-0.51	1E+05	60900	2E+05	83900	136000	94300	1E+05	98200	668.4	1334.7	2	0.0104	7.749
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P1041 2 H14_H UMAN,tr A3R0T8 A 3R0T8_H UMAN,tr Q4VB24 Q4VB24_ HUMAN	aLAA AGY DVEk	95%	72.8	52.92502	Ref	-1.2	0.2	-1.5	-0.25	-0.47	-0.36	-0.45	29500	10800	30600	10500	27800	20800	23400	21800	858.5	1715	2	0.0208	12.15

Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	aLAAAGYDVEK	67%	35.5	52.93102	Ref	-1.4	0.2	-1.9	-0.45	-0.36	-0.25	-0.28	1E+05	38400	1E+05	33200	101000	93000	1E+05	102000	572.7	1715	3	0.0189	10.99
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	aSGP PVSE LITk	94%	49.5	51.77	Ref	-1.3	0.23	-1.5	-0.21	-0.51	-0.35	-0.32	1E+05	36700	1E+05	39200	106000	75300	87900	89600	603	1806	3	0.0214	11.84
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	aSGP PVSE LITk	95%	58.8	51.47642	Ref	-1.6	0.41	-2.4	-0.2	-0.5	-0.4	-0.54	31600	7970	34400	5660	27900	19700	22100	19900	904	1806.1	2	0.0151	8.363
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	aSGP PVSE LITk	93%	43.7	51.47642	Ref	-1.6	0.36	-2.2	-0.16	-0.49	-0.31	-0.43	16700	4630	19400	3730	16700	11600	13800	12500	904	1806.1	2	0.0151	8.363
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	aSGP PVSE LITk	93%	47.6	51.25943	Ref	-1	-0.06	-0.72	-0.4	-0.62	-0.23	-0.41	10700	4680	9930	7090	9710	7310	9940	8730	603	1806.1	3	0.0089	4.952

Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	aSGP PVSE LITk	92%	45.6	51.75314	Ref	-0.69	-0.03	-0.93	-0.26	-0.64	-0.31	-0.44	17700	10600	18300	10900	19300	12900	16900	15400	603	1806.1	3	0.021	11.64
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	gTG ASGS Fk	90%	42.3	52.11967	Ref	-1.4	0.47	-2	-0.29	-0.64	-0.29	-0.47	44300	14500	56700	11400	41300	28400	37800	33000	710.4	1418.8	2	0.024	16.91
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	gTG ASGS Fk	95%	50.6	52.10888	Ref	-1.4	0.27	-1.7	-0.13	-0.61	-0.26	-0.32	50200	17200	60800	17800	56700	35500	47400	45000	473.9	1418.8	3	0.0225	15.82
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	gTG ASGS Fk	95%	54.9	52.13353	Ref	-1.6	0.5	-2	-0.23	-0.59	-0.32	-0.53	20200	5820	26100	5230	19500	13300	16700	14300	710.4	1418.8	2	0.0245	17.27
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	gTLV Qtk	86%	38.7	51.03071	Ref	-1.3	0.39	-1.6	-0.26	-0.61	-0.34	-0.49	28500	9910	35300	10200	27800	19100	24000	21400	677.9	1353.8	2	0.023	17.01

Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	gTLV QTK	84%	38.3	51.40637	Ref	-0.99	0.19	-1.4	-0.28	-0.6	-0.38	-0.42	32400	14000	34400	12700	30600	21400	26200	25200	677.9	1353.8	2	0.0205	15.12
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	kALA AAG YDVE k	87%	39.7	52.1765	Ref	-1.3	0.16	-1.6	-0.086	-0.49	-0.17	-0.4	54200	21500	64200	21800	67100	44200	57700	48700	537.8	2147.2	4	0.0262	12.21
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	kASG PPVS ELITk	92%	44.7	50.22738	Ref	-1.2	0.096	-1.3	-0.052	-0.59	-0.24	-0.37	16700	6950	18900	7990	21000	12700	16800	15300	747.1	2238.3	3	0.0399	17.82
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	kATG AAT Pk	71%	32.9	49.5789	Ref	-1.3	0.22	-1.5	-0.17	-0.6	-0.34	-0.39	2E+05	79800	2E+05	87700	235000	2E+05	2E+05	182000	586.4	1756.1	3	0.0263	14.96
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	kPAA AAG Ak	87%	36	48.5091	Ref	-1	0.16	-1.3	-0.23	-0.48	-0.38	-0.49	34000	15100	37200	15500	35100	25800	28900	26500	425	1696	4	0.0319	18.78

Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	kPAA AAG Ak	81%	32.5	45.92654	Ref	-1.4	0.2	-1.3	-0.21	-0.55	-0.42	-0.34	77200	24900	81800	33200	76300	52700	60300	63000	566.4	1696.1	3	0.0037	2.184
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	kPA GAA k	51%	24.4	46.72966	Ref	-1.8	0.4	-2	-0.11	-0.81	-0.22	-0.45	6E+05	150000	7E+05	152000	632000	3E+05	5E+05	454000	389.5	1554	4	0.0221	14.21
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	sETA PAA PAA PAP AEk	63%	34.4	53.15775	Ref	Value Missing (-0.9699349)	Value Missing (-1.2542233)	0.42	Value Missing (-1.1988299)	Value Missing (-1.2615968)	Value Missing (-1.2507226)	Value Missing (-0.9699349)	112	9)	Value Missing (-1.2542119)	233)	149	Value Missing (-1.1988299)	Value Missing (-1.2615968)	Value Missing (-1.2507226)	913	1823.9	2	0.0188	10.29
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	sETA PAA PAA PAP AEk	65%	36.2	54.12311	Ref	-0.6	-0.09	-1.4	-0.34	-0.56	-0.51	-0.17	2380	1370	2110	964	2190	1640	1770	2240	696.4	2086.1	3	0.0256	12.25
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	sGVS LAAL k	95%	47.9	49.78212	Ref	-0.96	0.23	-1.4	-0.29	-0.64	-0.43	-0.49	1E+05	57000	1E+05	49500	122000	83500	1E+05	96000	727.5	1452.9	2	0.0075	5.186

Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	sGVS LAAL k	95%	48.3	50.8147	Ref	-0.93	0.32	-1.6	-0.33	-0.56	-0.32	-0.62	37000	16900	43600	13400	34300	25700	31600	25500	727.5	1452.9	2	0.0229	15.76
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	sGVS LAAL k	95%	58.2	50.43056	Ref	-1.7	0.52	-2.6	-0.2	-0.61	-0.35	-0.42	4E+05	89500	5E+05	57300	343000	2E+05	3E+05	266000	485.3	1452.9	3	0.0152	10.44
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	sGVS LAAL kk	71%	29.2	47.59396	Ref	-0.89	0.037	-0.93	-0.29	-0.44	-0.35	-0.35	7130	4040	8330	4770	8220	6440	7180	7150	472.3	1885.2	4	0.0332	17.59
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	sGVS LAAL kk	93%	40.6	47.89087	Ref	-2	0.25	-1.8	-0.064	-0.44	-0.08	-0.23	3950	1050	5410	1480	5370	3600	4840	4320	943.6	1885.2	2	0.0375	19.86
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3ROT8 A3ROT8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	sGVS LAAL kk	59%	27.6	46.83047	Ref	-1.6	0.13	-1.9	-0.082	-0.42	-0.13	-0.15	52000	17400	64000	17900	68200	47200	60300	58800	629.4	1885.2	3	0.0228	12.1

Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3R0T8 A3R0T8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	sGVS LAAL kk	92%	38.8	46.70923	Ref	-2.1	0.25	-2.1	0.03	-0.4	-0.08	-0.15	1E+05	32900	2E+05	41400	195000	1E+05	2E+05	155000	472.3	1885.2	4	0.0206	10.94
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3R0T8 A3R0T8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	sGVS LAAL kk	84%	35.5	47.67482	Ref	-1.1	0.055	-1.1	-0.11	-0.62	-0.22	-0.23	29200	16000	37800	19700	41600	25700	35400	34700	629.4	1885.2	3	0.0355	18.79
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp P10412 H14_HUMAN, tr A3R0T8 A3R0T8_HUMAN, tr Q4VB24 Q4VB24_HUMAN	sGVS LAAL kk	94%	39.8	45.39741	Ref	-1.7	0.19	-1.8	0.011	-0.48	-0.13	-0.28	7640	2460	9700	2710	10600	6600	8770	7870	943.6	1885.2	2	0.0058	3.093
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	aPLN VQF SSPG PGD AVk	56%	34.5	54.08703	Ref	0.62	-0.89	-1.2	0.16	0.43	-0.84	-1.3	23700	25300	9660	8750	24700	26000	11200	8370	764.8	2291.3	3	0.0147	6.392
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	aTQT GDA Sk	86%	41.3	52.39197	Ref	0.21	-0.62	-0.14	-0.25	0.14	-0.27	-0.39	27100	28100	17200	26900	27400	31400	24700	22600	496.3	1485.8	3	0.0113	7.574
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	aTQT GDA Sk	51%	31.5	52.27966	Ref	0.23	-0.54	-0.1	-0.26	0.2	-0.85	-0.21	20700	20700	13100	19900	19600	23600	11900	18400	743.9	1485.8	2	0.0085	5.727

Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	aWG PGL HGGL VGR	95%	57.2	52.42424	Ref	0.37	-0.52	-0.22	-0.25	-0.12	-0.29	-0.27	26800	31600	18500	25600	27500	26400	24400	24600	527.6	1579.9	3	0.0097	6.13
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	dAG EGLL AVQI TDQ EGkP k	83%	39	53.3101	Ref	-0.045	-0.43	-0.04	-0.093	0.062	-0.43	-0.25	9030	7870	6550	9650	10200	9940	7360	8280	721.2	2880.6	4	0.0126	4.369
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	dAG YGGI SLAV EGPS k	95%	68.9	54.18816	Ref	0.087	-0.27	-0.29	-0.064	0.052	-0.75	-0.3	14600	12200	10400	11400	14800	14000	8380	11400	710.4	2128.2	3	0.0126	5.921
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	dLDII DNY DYS HTVk	79%	40.4	54.44479	Ref	0.12	-0.17	-0.18	-0.21	-0.07	-0.48	-0.15	6350	6530	5790	6470	6970	6690	5290	6580	807.1	2418.2	3	0.0172	7.105
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	eAG AGG LSIA VEG PSK	95%	82	53.56882	Ref	0.3	-0.37	-0.1	-0.4	-0.37	-0.37	-0.22	9060	8660	5920	7980	7190	6390	6700	7360	684.4	2050.1	3	0.0158	7.727
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	eATT DFTV DSR	88%	39	50.26386	Ref	0.39	-0.43	-0.09	-0.28	-0.11	-0.77	-0.38	23000	23400	14400	20400	19700	19300	12800	16700	773.4	1544.7	2	0.0128	8.279

Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	fNDE HIPE SPVV VPVI APS DDA R	92%	48.5	54.71384	Ref	Reference Missing (0.1466588)	Reference Missing (0.0182687)	Reference Missing (0.38146585)	No Values (-1.2688136)	Reference Missing (0.2994485)	No Values (-1.1357077)	Reference Missing (0.273898)	Reference Missing (0.0182687)	Reference Missing (0.38146585)	No Values (-1.2688136)	Reference Missing (0.2994485)	No Values (-1.1357077)	Reference Missing (0.273898)	957.8	2870.4	3	0.0218	7.607		
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	gAG TGG LGLT VEG PcEA k	83%	41.9	54.37994	Ref	-0.16	-0.17	-0.07	-0.038	-0.17	-0.82	-0.19	5720	3810	4100	4920	5550	4410	2940	4520	757.7	2270.2	3	0.014	6.181
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	gLHV VEVY YDD VPV PNSP Fk	95%	63.8	55.05881	Ref	0.23	-0.5	-0.33	-0.25	0.14	-0.46	-0.11	787	846	552	702	815	933	643	810	940.8	2819.5	3	0.0213	7.567
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	hVG NQQ YNV TYVV k	90%	46.3	54.32761	Ref	0.21	-0.59	-0.06	-0.25	-0.01	-0.42	-0.07	7690	8610	5360	8710	8380	8670	6800	8600	753.1	2256.2	3	0.0166	7.349
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	rLTV LSLQ ESGL k	87%	36.9	49.29557	Ref	0.19	-0.19	-0.34	-0.23	-0.21	-0.39	-0.02	5100	5400	4510	4540	5410	4810	4430	5650	513.8	2051.2	4	0.0129	6.298
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	sPFE VNV DK	91%	43.8	52.7114	Ref	0.48	-0.48	-0.11	-0.31	0.035	-0.96	-0.37	25500	29400	16400	23800	22800	25300	13300	19800	822	1641.9	2	0.0134	8.159

Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	sPFT VGV AAPL DLSR	95%	55.2	53.29502	Ref	0.35	-0.37	-0.12	-0.28	-0.07	-0.56	-0.24	5740	6740	4420	5920	5850	5890	4380	5410	917.5	1833	2	0.0061	3.315
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	tFEM SDFI VDT R	90%	41.4	51.63212	Ref	0.3	-0.26	-0.12	-0.25	-0.04	-0.58	-0.16	9370	11700	8650	10700	10800	10900	7830	10300	882.9	1763.9	2	0.0091	5.174
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	tGEE VGF VVD AK	88%	43.9	53.5306	Ref	0.16	-0.55	0.13	-0.44	0.028	-1	-0.2	33200	27100	17900	32100	23900	28900	14800	25600	620.3	1858	3	0.0171	9.217
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	vDIQ TEDL EDG Tck	95%	59.2	52.59549	Ref	0.27	-0.45	-0.12	-0.12	-0.09	-0.44	-0.52	20700	20600	13600	19100	21100	18700	15300	14400	740.7	2219.1	3	0.0187	8.409
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	vEPA VDTS R	74%	34.5	50.89035	Ref	0.26	-0.39	-0.22	-0.21	-0.06	-0.68	-0.2	8690	8420	5790	7310	8140	7890	5360	7410	639.3	1276.7	2	0.0107	8.388
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKK7 E1BKK7_BOVIN	VLPT VDAS k	80%	37.2	52.02191	Ref	0.2	-0.49	-0.2	-0.1	0.079	-0.69	-0.2	28100	28000	18900	25900	30500	30200	18500	25800	801.5	1600.9	2	0.0148	9.209

Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKX7 E1BKX7_BOVIN	vLQS FTVD SSk	93%	48.5	53.11067	Ref	0.14	-0.38	-0.28	-0.35	-0.1	-0.6	0.17	4880	4550	3440	4160	4370	4510	3330	5650	607	1818	3	0.0127	7.004
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKX7 E1BKX7_BOVIN	vQA QGP GLk	78%	35.1	49.45936	Ref	0.12	-0.4	-0.1	-0.064	0.013	-0.39	-0.17	22800	26400	19900	27600	31100	28700	22600	26200	502.6	1504.9	3	0.0062	4.119
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKX7 E1BKX7_BOVIN	vTGL HK	52%	27.7	48.08332	Ref	0.31	-0.62	-0.02	-0.35	0.13	-0.64	-0.26	44600	48900	27900	47300	41600	50800	31000	40200	421.6	1261.8	3	0.0046	3.653
Uncharacterized protein OS=Bos taurus GN=Bt.24937 PE=4 SV=1	tr E1BKX7 E1BKX7_BOVIN	yADE EIPR	76%	34.4	50.34376	Ref	0.25	-0.44	-0.09	-0.26	0.059	-0.77	-0.17	92700	95900	64500	92400	90700	98500	57800	87200	648.8	1295.7	2	0.01	7.703
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	eVY QQQ QYG SGG R	92%	45.7	51.18906	Ref	-0.1	0.16	-0.17	-0.28	0.22	-0.51	0.28	10100	8150	10600	9470	9670	12000	7550	12900	602	1802.9	3	0.0152	8.453

Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	eVY QQQ QYG SGG R	59%	31.8	51.23231	Ref	-0.1	0.058	-0.06	-0.25	0.34	-0.51	0.22	8220	7050	8570	8860	8580	11300	6520	10700	902.4	1802.9	2	0.0129	7.163
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	fGEV VDcT lk	85%	41.8	53.23683	Ref	-0.22	-0.28	0.085	-0.18	0.28	-0.35	0.25	29900	21600	22500	32500	29800	35900	24300	36400	589	1763.9	3	0.0137	7.782
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	fGEV VDcT lk	88%	43.9	53.25087	Ref	0.063	-0.37	0.054	-0.083	0.24	-0.47	0.014	14400	11600	9280	14000	14000	15300	9800	13600	589	1763.9	3	0.0128	7.255
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	fGEV VDcT lk	87%	41.6	53.2035	Ref	-4E-04	-0.09	-0.11	-0.061	0.13	-0.36	0.21	3490	3050	3120	3450	3930	3910	2910	4290	883	1763.9	2	0.0164	9.319

Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	fGEV VDcT lk	93%	49	53.24663	Ref	-0.16	-0.01	-0.32	-0.14	0.19	-0.19	0.19	8350	5910	7150	6470	8030	8820	7090	9140	589	1763.9	3	0.0113	6.422
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	fGEV VDcT lk	70%	36.5	53.23327	Ref	0.082	-0.38	-0.02	-0.17	0.19	-0.29	0.035	6400	5060	3990	5750	5710	6370	4770	5950	589	1763.9	3	0.011	6.218
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	fGEV VDcT lk	83%	40.8	53.23683	Ref	-0.081	-0.16	-0.13	-0.049	0.007	-0.11	0.21	3070	2440	2500	2880	3350	3040	2930	3630	589	1763.9	3	0.0137	7.782
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	gFGF lLFk	54%	30.4	50.43103	Ref	-0.31	0.082	-0.31	-0.29	0.23	-0.35	0.21	14400	8170	11600	9940	11100	13900	9710	14200	513	1535.9	3	0.0153	9.953

Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	gFGF ILFk	87%	38.4	50.40741	Ref	-0.44	0.07	-0.09	-0.13	0.3	-0.42	0.27	39900	24900	38500	38700	41400	48700	30900	49600	769	1535.9	2	0.0136	8.876
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	gFGF ILFk	61%	31.6	50.40741	Ref	-0.47	-0.13	-0.17	-0.2	0.29	-0.46	0.65	27100	18200	25100	27500	29600	36200	22500	48300	513	1535.9	3	0.014	9.133
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	gFGF ILFk	87%	38.6	50.40741	Ref	-0.33	0.071	-0.1	-0.15	0.27	-0.34	0.25	2400	1690	2420	2410	2560	2990	2050	3060	769	1535.9	2	0.0138	8.954
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	gFGF ILFk	63%	31.5	49.92845	Ref	-0.41	-0.05	-0.19	-0.19	0.077	-0.32	0.65	4390	3030	4200	4300	4720	4970	3940	7680	513	1535.9	3	0.0027	1.735

Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	gFGF ILFk	62%	31.6	50.52948	Ref	-0.2	0.11	-0.17	-0.13	0.36	-0.44	0.11	1100	841	1130	1050	1180	1450	869	1260	769	1535.9	2	0.0179	11.66
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	gSG GGG GSG GQG STNy Gk	95%	85.9	52.28167	Ref	-0.36	0.26	-0.05	-0.084	0.31	-0.49	0.085	5060	3560	5940	5370	5800	6640	3980	5900	698.3	2092	3	0.022	10.52
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	gSG GGG GSG GQG STNy Gk	95%	71.4	51.87811	Ref	-0.26	0.14	0.005	-0.15	0.29	-0.38	0.077	10400	7840	11200	11500	11300	13500	8870	12100	698.7	2093	3	0.017	8.095
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	gSG GGG GSG GQG STNy Gk	95%	51.9	54.4576	Ref	-0.26	0.39	-0.14	-0.33	0.28	-0.51	0.19	5530	4250	7260	5660	5440	7290	4390	7060	600.1	2396.2	4	0.0219	9.116

Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	gSG GGG GSG GQG STNy Gk	95%	56.6	54.39514	Ref	-0.21	0.43	-0.04	-0.48	0.16	-0.46	0.23	11400	9250	15700	12700	10300	14000	9530	15300	600.1	2396.2	4	0.0275	11.45
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	iFVG GLN PEAT EEk	89%	45.4	54.02774	Ref	-0.27	-0.01	-0.12	-0.14	0.27	-0.37	0.28	30000	21700	28100	29100	31800	36700	24700	38300	704.7	2111.1	3	0.0333	15.77
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	iFVG GLN PEAT EEk	95%	48.7	54.00593	Ref	-0.37	0.077	4E-04	-0.18	0.27	-0.49	0.26	2450	1610	2390	2540	2470	2950	1820	3040	1057	2111.2	2	0.0207	9.815
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	iFVG GLN PEAT EEk	92%	48.2	53.96759	Ref	0.0039	-0.02	0.048	-0.23	0.17	-0.3	-0.07	10300	8340	8930	10500	9540	11000	8300	9640	704.7	2111.2	3	0.0196	9.264

Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	iFVG GLN PEAT EEk	95%	55.1	53.9909	Ref	-0.28	-0.02	-0.26	-0.093	0.14	-0.14	0.25	36600	24400	31700	30000	37300	38300	32900	42900	704.7	2111.2	3	0.0188	8.923
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	iFVG GLN PEAT EEk	79%	38.8	53.97575	Ref	-0.2	0.28	-0.28	-0.33	0.29	-0.43	0.079	3210	2150	3240	2480	2650	3540	2240	3170	1057	2111.2	2	0.0188	8.887
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	iFVG GLN PEAT EEk	86%	43	53.976801	Ref	-0.19	-0.07	-0.11	-0.16	0.22	-0.29	0.23	12800	9420	11100	12100	12900	14700	10700	15300	704.7	2111.2	3	0.008	3.81
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	iFVG GLN PEAT EEk	67%	36.4	53.97971	Ref	-0.22	-0.34	-0.15	-0.021	0.05	0.33	0.32	7960	7610	7630	9740	11800	10800	13600	13500	704.7	2111.2	3	0.0203	9.619

Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	kIFV GGL NPE ATEE k	64%	33.2	53.13467	Ref	-0.18	-0.15	0.024	-0.13	0.25	-0.08	0.011	8890	6880	7600	9650	9560	10900	9050	9540	636.9	2543.4	4	0.0294	11.57
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	kIFV GGL NPE ATEE k	89%	43.5	52.11211	Ref	-0.12	-0.13	0.08	-0.007	0.13	-0.19	0.055	5450	4560	4940	6400	6640	6350	5340	6270	848.8	2543.5	3	0.0051	2.004
Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus GN=HNRNPAB PE=2 SV=1	tr Q3ZC44 Q3ZC44_BOVIN	mDP nTG R	53%	25.8	46.08494	Ref	-0.4	0.059	-0.23	-0.088	0.34	-0.47	0.34	1280	845	1260	1160	1400	1650	984	1710	556.3	1110.5	2	0.0058	5.258
Triosephosphate isomerase OS=Bos taurus GN=TP11 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	dLGA TWV VLG HSER	91%	46.8	53.50758	Ref	0.0034	-0.07	-0.08	-0.037	-0.07	0.068	-0.1	2270	2140	2210	2460	2800	2380	2740	2420	615.3	1843	3	0.0054	2.935
Triosephosphate isomerase OS=Bos taurus GN=TP11 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	dLGA TWV VLG HSER	95%	63.4	53.48922	Ref	0.38	-0.33	0.086	-0.069	-0.13	0.029	-0.53	5250	6030	4000	5980	5920	4970	5780	3910	615.3	1843	3	0.0131	7.116

Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPI5_BOVIN	dLGA TWV VLG HSER	95%	71.6	53.42774	Ref	-0.099	0.032	-0.19	-0.089	0.036	0.11	-0.24	2320	1850	2200	2120	2510	2390	2610	2040	922.5	1843	2	0.0107	5.817
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPI5_BOVIN	dLGA TWV VLG HSER	95%	51.8	53.48889	Ref	0.074	0.065	-0.14	-0.045	-0.26	0.19	-0.23	2280	2260	2430	2370	2790	2090	3000	2220	615.3	1843	3	0.0129	7.018
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPI5_BOVIN	dLGA TWV VLG HSER	95%	56.7	53.42713	Ref	-0.022	-0.29	0.047	-0.078	-0.08	0.052	0.042	1890	1730	1570	2220	2240	1950	2230	2200	615.3	1843	3	0.0098	5.326
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPI5_BOVIN	dLGA TWV VLG HSER	77%	38.5	53.46799	Ref	0.24	-0.32	0.095	-0.21	-0.12	-0.06	-0.09	4920	5040	3710	5560	4960	4610	5020	4880	615.3	1843	3	0.0084	4.529
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPI5_BOVIN	dLGA TWV VLG HSER	90%	46.1	53.42713	Ref	0.14	-0.25	0.029	-0.16	-0.17	-0.13	-0.27	1670	1300	1070	1460	1410	1230	1320	1180	615.3	1843	3	0.0098	5.326
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPI5_BOVIN	dLGA TWV VLG HSER	60%	34.6	53.45207	Ref	0.14	0.17	-0.4	-0.26	-0.11	-0.05	0.11	289	295	327	247	300	291	318	351	615.3	1843	3	0.0093	5.017

Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	dLGA TWV VLG HSER	60%	34.6	53.44286	Ref	-0.31	0.18	-0.03	-0.2	-0.01	-0.09	-0.14	382	243	370	359	352	351	346	331	615.3	1843	3	0.0058	3.13
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	iiYG GSVT GATc k	95%	53.3	53.77747	Ref	0.12	-0	-0.06	-0.07	-0.13	-0.05	-0.18	9080	8830	8830	9520	10400	8730	9640	8720	642	1923	3	0.0165	8.556
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	iiYG GSVT GATc k	95%	55.4	53.7897	Ref	0.11	0.012	0.027	-0.18	-0.11	0.099	-0.31	4260	4270	4330	4910	4690	4300	5180	3870	962.5	1923	2	0.0151	7.856
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	kNNL GELI NTL NAA k	90%	39.2	49.18329	Ref	0.041	-0.01	-0.07	-0.077	-0.38	0.052	-0.16	1430	1160	1210	1310	1430	1010	1430	1220	632.1	2524.5	4	0.0033	1.312
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	nNL GELI NTL NAA k	94%	51	52.79206	Ref	0.13	-0.01	3E-04	-0.056	-0.15	-0.18	-0.28	3730	3330	3280	3700	3920	3210	3280	3030	698.4	2092.2	3	0.0139	6.638
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	sNVS DAV AQS AR	89%	41.6	52.19731	Ref	0.072	0.093	-0.35	-0.051	-0.05	-0.1	-0.28	5650	4530	4990	4130	5590	4870	4930	4330	754.9	1507.8	2	0.0117	7.751

Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	sNVS DAV AQS AR	81%	37.6	52.02687	Ref	0.076	0.1	-0.13	-0.089	-0.28	0.03	-0.22	30300	26600	29400	28000	31800	24400	31500	26400	754.9	1507.8	2	0.0141	9.368
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	sNVS DAV AQS AR	74%	35.7	52.19731	Ref	0.11	0.025	-0.19	-0.093	-0.1	0.036	-0.12	6520	6550	6690	6470	7630	6650	7610	6800	754.9	1507.8	2	0.0117	7.751
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	tATP QQA QEV HEK	95%	60	54.1061	Ref	-0.016	0.42	-0.17	-0.19	-0.28	0.061	-0.36	22600	19600	28900	21400	23300	19100	25300	18800	692.4	2074.1	3	0.0174	8.401
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	vAH ALAE GLG VIAcl GEK	95%	51	53.84876	Ref	0.21	0.075	0.16	0.25	-0.5	Value Missing (-1.8477726)	-0.04	244	195	193	230	269	140	Value Missing (-1.8477726)	200	602.1	2404.3	4	0.0055	2.277
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	vAn GAF TGEI SPG MIK	95%	75.2	54.36276	Ref	-0.067	-0.01	-0.12	-0.094	-0.11	0.054	-0.09	29500	24000	27200	28200	31700	27300	32000	28800	734.4	2200.2	3	0.0261	11.84
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	vAn GAF TGEI SPG MIK	95%	69.7	54.30511	Ref	0.0054	-0.29	-0.08	0.056	-0.02	-0.01	-0.18	4740	3890	3450	4470	5410	4480	4710	4150	734.4	2200.2	3	0.0204	9.251

Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	vAn GAF TGEI SPG MIK	95%	58.9	54.30511	Ref	0.16	-0.21	-0.14	0.069	-0.16	-0.05	-0.13	6710	6430	5390	6320	8070	5990	6800	6350	734.4	2200.2	3	0.0204	9.251
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	vAn GAF TGEI SPG MIK	57%	34.4	54.25427	Ref	0.066	-0.03	-0.13	-0.051	0.088	-0.1	-0.12	790	792	804	842	980	942	863	847	1101	2200.2	2	0.0183	8.303
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	vAn GAF TGEI SPG mik	95%	54.6	54.46769	Ref	0.036	-0.05	-0.19	-0.13	0.015	-0.08	-0.17	10800	8710	8870	9060	10400	10100	9830	9200	739.7	2216.2	3	0.0188	8.473
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	vVLA YEPV WAI GTG k	95%	53.2	52.74162	Ref	0.056	0.2	-0.09	-0.036	-0.15	-0.36	0.15	674	731	875	805	920	742	672	949	737.8	2210.3	3	0.0269	12.14
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	vVLA YEPV WAI GTG k	95%	56.9	52.48299	Ref	0.039	-0.11	-0.08	-0.16	0.034	0.017	-0.14	2270	2040	2000	2290	2390	2390	2460	2200	737.8	2210.3	3	0.0204	9.239
Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	vVLA YEPV WAI GTG k	52%	32	52.28041	Ref	-0.012	-0.03	-0.22	-0.24	-0.04	-0.04	-0.12	806	590	634	623	678	679	711	663	737.8	2210.3	3	0.0157	7.082

Triosephosphate isomerase OS=Bos taurus GN=TP11 PE=2 SV=3	sp Q5E956 TPIS_BOVIN	vVLAyEPVWAI GTGk	52%	28.1	50.17459	Ref	-0.16	-0.01	-0.11	-0.16	-0.19	0.14	0.061	1100	858	1030	1080	1150	983	1290	1210	629.6	2514.5	4	0.0087	3.442
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	eHAL LAYT LGVk	66%	32	51.68934	Ref	0.47	-0.19	-0.05	-0.14	-0.46	0.17	-0.28	1070	1140	785	968	1000	703	1130	823	481.5	1922.1	4	0.0189	9.837
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	eHAL LAYT LGVk	85%	38.4	51.59354	Ref	0.61	-0.49	0.073	-0.3	-0.47	0.26	-0.29	4950	6010	3040	5030	4280	3310	5760	3910	481.5	1922.1	4	0.015	7.798
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	eHAL LAYT LGVk	95%	52.2	51.60246	Ref	0.4	-0.2	0.029	-0.049	-0.35	0.19	-0.26	3150	3620	2590	3400	3560	2520	3830	2780	641.7	1922.1	3	0.0137	7.14
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	eHAL LAYT LGVk	95%	60.5	51.57967	Ref	0.46	-0.33	-0.06	-0.052	-0.33	0.34	-0.31	1080	1320	828	1130	1250	899	1490	945	962.1	1922.1	2	0.0144	7.48

Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	eHAL LAYT LGVk	90%	43.8	51.17043	Ref	0.42	-0.06	0.021	0.037	-0.62	0.29	-0.36	4160	5080	3950	4700	5230	2900	5700	3590	641.7	1922.1	3	0.0055	2.85
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	eHAL LAYT LGVk	88%	39.2	51.02018	Ref	0.44	-0.07	-0.1	-0.15	-0.35	0.13	-0.39	2950	3020	2300	2540	2690	2050	2990	2060	481.5	1922.1	4	0.003	1.579
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	eHAL LAYT LGVk	71%	33.4	51.82383	Ref	0.35	-0.11	-0.04	-0.22	-0.37	0.076	-0.15	822	767	606	713	694	548	779	663	481.5	1922.1	4	0.0199	10.36
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	iGGI GTV PVG R	83%	36.2	49.91248	Ref	0.54	-0.39	0.12	-0.15	-0.21	-0.07	-0.14	95800	120000	68600	109000	99900	83900	96500	90900	665.4	1328.8	2	0.0116	8.705
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	iGGI GTV PVG R	79%	35	50.01937	Ref	0.33	-0.26	0.064	-0.16	-0.16	0.23	-0.11	31300	37500	27000	37900	35800	31100	42600	33500	665.4	1328.8	2	0.0173	13.02

Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	IPLQ DVK	74%	34.2	50.69202	Ref	0.54	-0.24	0.11	-0.3	-0.08	-0.07	-0.38	18500	21600	13700	19500	16200	16500	17400	13900	792.5	1582.9	2	0.0084	5.298
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	qLIV GVN k	89%	38	48.40301	Ref	0.68	-0.13	-0.19	-0.29	-0.54	-0.06	0.012	2140	2780	1720	1860	1910	1400	2040	2120	579.4	1156.7	2	0.0096	8.313
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	qLIV GVN k	89%	37.9	48.36862	Ref	0.51	-0.43	-0.12	-0.56	-0.4	0.49	-0	1140	1410	794	1100	900	874	1700	1200	579.4	1156.7	2	0.0084	7.259
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	qLIV GVN k	83%	33.7	47.31573	Ref	0.57	-0.22	0.024	-0.016	-0.44	0.031	-0.22	17900	23800	15000	19900	21300	13900	20100	16800	740	1477.9	2	0.0052	3.528
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	qLIV GVN k	71%	30.9	47.38773	Ref	0.31	-0.06	0.023	0.006	-0.08	-0.16	-0.13	4770	5270	4430	5270	5740	4720	4680	4720	493.7	1477.9	3	0.0059	3.978

Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	qTVA VGVI k	73%	31.9	48.52663	Ref	0.24	-0.28	-0.02	-0.27	-0.22	0.21	0.023	1180	1120	846	1140	1060	952	1340	1170	601.4	1200.7	2	0.0095	7.896
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	qTVA VGVI k	95%	43.6	48.8377	Ref	0.51	-0.33	0.13	-0.31	-0.1	-0.01	-0.43	1590	1690	1020	1580	1280	1300	1450	1070	601.4	1200.7	2	0.0136	11.36
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	qTVA VGVI k	95%	43.7	48.61254	Ref	0.69	-0.28	0.021	-0.33	-0.13	-0.15	-0.41	1550	1930	1070	1480	1280	1280	1320	1090	601.4	1200.7	2	0.0113	9.427
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	qTVA VGVI k	95%	50.4	47.92889	Ref	0.32	-0.25	0.12	-0.095	-0.1	0.023	-0.07	40700	47600	34700	50400	48000	41900	47500	44200	762	1522	2	0.0122	7.999
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	tHINI VVIG HVn SGk	95%	48.5	52.60355	Ref	0.36	-0.3	0.037	-0.16	-0.14	0.042	-0.08	13200	14200	9770	13800	13300	11800	13900	12700	550.1	2196.3	4	0.0226	10.28

Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	tHINI VVIG HVn SGk	95%	53.5	52.36031	Ref	0.21	-0.02	-0.1	-0.087	-0.18	0.19	-0.09	13800	14400	13300	14000	15700	12800	17300	14100	550.1	2196.3	4	0.0175	7.951
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	tHINI VVIG HVn SGk	93%	47.4	52.38896	Ref	0.18	-0.17	0.085	-0.059	-0.13	0.013	4E-04	2550	2600	2220	2960	2950	2450	2830	2780	733.1	2196.3	3	0.0178	8.103
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	tHINI VVIG HVn SGk	84%	38.5	52.30602	Ref	0.16	-0.08	0.048	-0.14	-0.15	0.12	-0.03	7880	7970	7320	8980	8710	7520	9520	8520	550.1	2196.3	4	0.015	6.841
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	tHINI VVIG HVn SGk	95%	53.6	52.09413	Ref	0.3	-0.12	0.025	0.036	-0.12	0.14	-0.38	2400	2690	2180	2710	3010	2350	2950	2050	550.1	2196.3	4	0.0104	4.729
Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	tHINI VVIG HVn SGk	95%	54.2	52.14682	Ref	0.42	-0.19	0.016	-0.1	-0.2	0.023	-0.16	1440	1670	1190	1540	1560	1270	1550	1360	550.1	2196.3	4	0.0106	4.838

Elongation factor 1-alpha OS=Canis familiaris GN=LOC476546 PE=3 SV=1	tr E2RGE2 E2RGE2_CANFA	yYVT IIDA PGH R	84%	39.7	53.07464	Ref	0.66	-0.27	0.032	-0.23	-0.33	0.071	-0.29	2230	3080	1750	2430	2240	1820	2510	1940	855	1707.9	2	0.014	8.201
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3 F6S2X3_MACMU	aDID ISAP k	93%	44.1	51.04357	Ref	-0.38	-0.2	-0.31	-0.11	-0.06	-0.48	-0.3	22000	14900	18300	19000	24100	21800	16900	19100	769.5	1536.9	2	0.0083	5.387
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3 F6S2X3_MACMU	aDID VSG Pk	93%	44.2	51.98503	Ref	-0.64	-0.32	-0.15	0.049	0.006	-0.76	-0.31	2E+05	82600	1E+05	141000	178000	2E+05	92800	126000	755.4	1508.9	2	0.0151	10.01
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3 F6S2X3_MACMU	aDLD ISGP k	89%	41.2	51.56422	Ref	-0.45	-0.23	-0.32	-0.19	9E-04	-0.42	-0.23	18600	12000	15200	16000	19300	19200	15000	17000	762.4	1522.9	2	0.0102	6.706
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3 F6S2X3_MACMU	gEVD VSLP NVE GDLk	94%	52	54.22237	Ref	-0.34	-0.4	-0.29	-0.15	-0.07	-0.5	-0.26	7080	4420	4620	5580	6790	6260	4850	5680	727.1	2178.2	3	0.0112	5.118

Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_1 F6S2X3_1 MACMU	iSMP DIDL NLkG Pk	66%	31.4	50.98433	Ref	-0.8	-0.36	-0.15	0.079	0.007	-0.42	-0.15	13800	7750	11400	14800	19100	15900	12300	14800	614.1	2452.4	4	0.0072	2.934
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_2 F6S2X3_2 MACMU	iSMP DIDL nLkG Pk	55%	30.5	52.07734	Ref	-0.52	-0.46	-0.35	-0.058	0.13	-0.26	-0.12	3520	2540	2870	3490	4700	4670	3740	4090	614.4	2453.4	4	0.0167	6.816
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_3 F6S2X3_3 MACMU	vDID APD VDV HGP DWH Lk	93%	47.8	55.18826	Ref	-0.42	-0.47	-0.32	-0.074	-0.03	-0.43	-0.5	29300	15800	16500	20500	26800	24100	19100	18100	659.8	2635.4	4	0.0233	8.846
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_4 F6S2X3_4 MACMU	vDID TPDI DIHG PEGk	95%	53.4	54.66536	Ref	-0.81	-0.05	-0.31	-0.082	0.082	-0.73	-0.27	30200	13900	25500	23900	30900	30200	18000	24500	777.1	2328.2	3	0.0205	8.799
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_5 F6S2X3_5 MACMU	vDID TPDI DIHG PEGk	94%	52.7	54.64451	Ref	-0.62	-0.22	-0.35	-0.15	0.14	-0.63	-0.11	8480	4880	6970	7130	9070	9650	5920	8410	777.1	2328.2	3	0.0196	8.4

Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_1 F6S2X3_MACMU	vDID TPDI DIHG PEGk	93%	51.1	54.67808	Ref	-0.76	-0.25	-0.34	0.043	-0.03	-0.39	-0.22	6020	3100	4770	5020	7230	6000	4900	5450	777.1	2328.2	3	0.0185	7.936
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_2 F6S2X3_MACMU	vDID TPDI DIHG PEGk	95%	53.1	54.68169	Ref	-0.63	-0.14	-0.29	-0.15	0.15	-0.62	-0.18	3710	2220	3380	3420	4150	4480	2740	3670	777.1	2328.2	3	0.0145	6.21
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_3 F6S2X3_MACMU	vDID VPD VDV QGP DWH Lk	95%	62.3	55.13693	Ref	-0.57	-0.32	-0.18	-0.044	-0	-0.81	-0.15	5840	3260	4200	5200	6290	5660	3380	5300	885.8	2654.4	3	0.0237	8.941
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_4 F6S2X3_MACMU	vDID VPD VDV QGP DWH Lk	95%	62.4	55.13592	Ref	-0.63	-0.5	-0.15	-0.044	0.058	-0.67	-0.05	3090	1730	2060	2950	3500	3270	2060	3150	885.8	2654.4	3	0.016	6.038
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_5 F6S2X3_MACMU	vDIE GPD VNIE GPD Gk	95%	59.2	54.45906	Ref	-0.33	-0.1	-0.41	-0.088	-0.02	-0.38	-0.5	5900	4190	5330	4840	6670	6120	4960	4540	754.7	2261.2	3	0.0234	10.36

Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_1 F6S2X3_1 MACMU	vDIE GPD VNIE GPD Gk	95%	63.1	54.52889	Ref	-0.45	-0.25	-0.13	-0.25	0.09	-0.72	-0.27	35500	22100	27500	33500	34000	37500	22400	30300	754.7	2261.2	3	0.0155	6.869
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_2 F6S2X3_2 MACMU	vDV DVP DVD VQG PDW Hlk	84%	43.3	55.07481	Ref	-0.47	-0.35	-0.2	-0.18	-0.15	-0.52	-0.03	8540	5260	6190	7710	8640	7690	6210	8680	881.1	2640.4	3	0.009	3.416
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_3 F6S2X3_3 MACMU	vDV DVP DVD VqG PDW Hlk	93%	50.7	55.0189	Ref	-0.19	-0.31	-0.33	-0.33	-0.29	-0.34	-0.12	2420	1760	1750	1950	2140	1930	1940	2250	881.5	2641.4	3	0.0154	5.814
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_4 F6S2X3_4 MACMU	vDVS VPD VSIE GPE Gk	90%	46.3	54.3183	Ref	-0.19	-0.04	-0.51	-0.22	-0.44	-0.26	-0.46	14800	9850	11800	9560	12900	9650	11500	9880	745.7	2234.2	3	0.0202	9.035
Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3_5 F6S2X3_5 MACMU	vDVS VPD VSIE GPE Gk	89%	46	54.3058	Ref	-0.21	-0.2	-0.32	-0.16	-0.08	-0.5	-0.26	7730	6220	6810	7060	8690	7980	6250	7340	745.7	2234.2	3	0.0171	7.639

Uncharacterized protein (Fragment) OS=Macaca mulatta GN=AHNAK PE=4 SV=1	tr F6S2X3 F6S2X3_MACMU	vSAP GVQ GDV k	95%	59.2	52.09539	Ref	-0.55	-0.24	-0.22	-0.035	-0.05	-0.41	-0.35	31000	18700	25200	28800	36000	31100	25300	26300	833	1664	2	0.0146	8.786
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6_BOVIN	eQFL DGD GWT ER	95%	50.6	51.62511	Ref	0.11	-0.08	0.059	-0.15	-0.09	-0.1	-0.16	10600	9310	8910	11000	10500	9520	9880	9410	878.9	1755.8	2	0.0157	8.95
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6_BOVIN	eQFL DGD GWT ER	92%	46.6	51.66913	Ref	-0.12	-0.04	-0.32	-0.011	-0.34	0.018	0.27	7360	5320	6090	5650	7700	5360	7160	8460	586.3	1755.8	3	0.0145	8.254
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6_BOVIN	eQFL DGD GWT ER	80%	37.1	51.66951	Ref	0.045	-0.26	-0.05	0.043	0.081	-0.09	-0.03	11100	10400	9130	11800	13900	12500	11500	11900	878.9	1755.8	2	0.014	7.971
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6_BOVIN	eQFL DGD GWT ER	87%	40	51.71341	Ref	0.12	-0.07	-0.02	0.031	-0.11	-0.08	-0.13	20600	20100	19100	22100	25300	20000	21400	20400	878.9	1755.8	2	0.0129	7.357
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6_BOVIN	eQFL DGD GWT ER	59%	32.3	51.76685	Ref	0.068	-0.08	-0.02	-0.058	-0	0.01	-0.17	4650	4390	4290	5040	5400	4890	5160	4520	878.9	1755.8	2	0.0119	6.799
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6_BOVIN	eQFL DGD GWT ER	77%	36.9	51.7942	Ref	-0.048	-0.05	-0.29	-0.042	-0.33	0.091	0.046	8610	6090	6600	6280	8210	5870	8210	7900	586.3	1755.8	3	0.0118	6.7

Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	eQFL DGD GWT ER	78%	36.5	51.82794	Ref	0.11	-0.05	0.096	-0.09	-0.1	-0.06	-0.26	3260	3010	2920	3630	3510	3040	3280	2840	878.9	1755.8	2	0.0105	5.956
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	eQFL DGD GWT ER	79%	37.1	51.97316	Ref	0.036	-0.1	0.031	-0.06	0.035	-0.19	-0.25	25000	20000	19700	24200	25100	23400	20900	19900	878.9	1755.8	2	0.005	2.837
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	gQTL VVQ FTVK	87%	40.9	50.93257	Ref	0.059	-0.09	-0.09	0.16	-0.22	-0.12	-0.02	15500	14000	13700	15400	20100	13500	15200	16100	610	1827.1	3	0.0243	13.28
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	gQTL VVQ FTVK	85%	38.7	50.19444	Ref	0.14	0.033	0.11	0.016	-0.27	-0.11	-0.27	12100	11600	11700	13900	14300	10300	12000	10600	610	1827.1	3	0.0124	6.779
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	gQTL VVQ FTVK	78%	35.6	50.08307	Ref	0.14	-0.06	-0.09	0.045	-0.12	-0.12	0.002	10500	11000	10400	11400	13700	10700	11200	12100	610	1827.1	3	0.0091	4.974
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	gQTL VVQ FTVK	95%	65.6	50.0552	Ref	0.14	-0.14	0.058	-0.071	-0.09	-0.1	-0.21	3850	3470	3110	3990	4030	3470	3610	3310	914.6	1827.1	2	0.0078	4.265
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	gQTL VVQ FTVK	95%	74	50.54356	Ref	0.03	-0.13	0.12	0.018	-0.09	-0.06	-0.17	8240	7510	7290	9740	10000	8100	8660	7960	914.6	1827.1	2	0.0162	8.87

Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	gQTL VVQ FTVk	63%	31.7	50.0512	Ref	-0.075	-0.23	0.13	0.12	-0.09	0.084	0.059	8600	9080	8820	12700	14000	10500	12400	12100	610	1827.1	3	0.0067	3.661
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	gQTL VVQ FTVk	88%	40.6	50.08302	Ref	0.15	-0	-0.04	0.065	-0.32	-0.13	-0.04	2190	2140	2090	2280	2710	1810	2160	2280	610	1827.1	3	0.0095	5.17
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	gQTL VVQ FTVk	89%	41.6	50.07031	Ref	0.095	-0.09	-0.04	0.29	-0.27	-0.12	-0.24	1830	1690	1610	1880	2610	1540	1780	1630	610	1827.1	3	0.0087	4.76
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	hEQ NIDc GGG YVvk	95%	51.1	52.3148	Ref	0.28	0.02	-0.02	-0.084	-0.01	-0.28	-0.21	30200	33300	30100	32800	34600	31800	27600	28600	692	2073	3	0.0184	8.885
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	hEQ NIDc GGG YVvk	95%	59.1	52.15357	Ref	-0.039	-0.24	0.17	-0.015	-0.05	-0.02	-0.17	3170	2620	2460	3690	3570	3040	3260	2910	1038	2073	2	0.0229	11.05
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	hEQ NIDc GGG YVvk	89%	43.5	52.29836	Ref	0.1	0.15	-0	-0.14	-0.09	-0.19	-0.12	9740	9330	10400	10600	10600	9600	9300	9740	692	2073	3	0.0193	9.319
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	kVH VIFN Yk	56%	27.4	48.9161	Ref	0.081	-0.2	0.098	-0.068	-0.03	0.015	-0.2	2E+05	180000	2E+05	222000	218000	2E+05	2E+05	180000	515.8	2059.3	4	0.0185	8.956

Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	qIDN PEyK	73%	36.2	52.89101	Ref	-0.11	0.01	0.083	-0.086	0.034	-0.22	-0.19	82400	60100	70700	83500	81900	77700	67900	69100	807.9	1613.9	2	0.013	8.072
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	vHVI FNYK	75%	35.5	50.85983	Ref	0.12	-0.13	0.12	-0.1	-0.18	-0	-0.15	16800	15800	14400	19300	18200	15100	17800	15900	543.3	1627	3	0.0037	2.279
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	vHVI FNYK	83%	37.8	51.28567	Ref	0.063	-0	0.16	-0.12	-0.14	0.014	-0.24	3410	3230	3340	4200	3810	3280	3820	3180	814.5	1627	2	0.0125	7.706
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	vHVI FNYK	92%	43.6	51.48251	Ref	0.12	-0.22	0.015	-0.027	-0.13	0.012	-0.11	1820	1690	1450	1910	2050	1670	1920	1750	814.5	1627	2	0.0172	10.56
Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2	sp P52193 CALR_BOVIN, tr A5D7J6 A5D7J6_BOVIN	vHVI FNYK	54%	30.6	50.57955	Ref	-0.1	-0.33	-0	-0.096	0.11	-0.11	0.029	839	609	565	796	822	829	741	811	543.3	1627	3	#####	0.3
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr B0JYQ0 B0JYQ0_BOVIN	eTYG DMA DccA k	53%	23.8	43.94522	Ref	1.3	0.79	1.1	0.93	0.73	1.3	0.84	3740	5120	4030	5450	5500	4170	6320	4680	669.6	2005.8	3	0.0189	9.419
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr B0JYQ0 B0JYQ0_BOVIN	eTYG DMA DccA k	88%	32.5	44.03258	Ref	1.2	0.54	1.3	0.93	0.8	1.5	0.89	4810	11300	7770	15200	12700	10100	17200	11200	1004	2005.8	2	0.0171	8.504

ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_ BOVIN	eTYG DMA DccA k	65%	25.8	44.11081	Ref	1.5	0.47	1.2	1.1	0.71	1.3	0.77	5270	11800	6270	11500	11900	7980	12300	8610	1004	2005.8	2	0.016	7.956
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_ BOVIN	eTYG DMA DccA k	95%	52.3	44.16973	Ref	1.5	0.6	1.3	0.97	0.83	1.4	0.67	8200	30800	17500	32100	28100	22300	33900	20700	669.6	2005.8	3	0.0156	7.774
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_ BOVIN	eTYG DMA DccA k	50%	23.3	43.94522	Ref	1.1	1	0.96	0.87	0.82	1.4	0.79	6550	8210	8410	9120	9470	7990	12200	8100	669.6	2005.8	3	0.0189	9.419
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_ BOVIN	IGFY GFQ NELI VR	89%	44.6	53.45001	Ref	0.98	0.74	0.86	0.94	1.1	1	1.2	8220	8230	7600	9270	10800	10200	10300	11700	614.7	1841	3	0.0027	1.484
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_ BOVIN	IGFY GFQ NELI VR	95%	48.8	53.48095	Ref	1.5	0.46	1.2	0.92	0.78	1.5	0.91	7930	24500	13100	24300	22200	17600	29300	20000	921.5	1841	2	0.0018	0.981
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_ BOVIN	IGFY GFQ NELI VR	95%	52.9	53.42257	Ref	1.5	0.55	1.2	0.86	0.83	1.4	0.9	765	2120	1210	2080	1860	1590	2490	1730	921.5	1841	2	0.0114	6.215
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_ BOVIN	IGFY GFQ NELI VR	74%	37	53.45382	Ref	1.4	0.5	1.2	0.85	0.87	1.3	0.93	632	1490	836	1520	1330	1170	1670	1270	921.5	1841	2	0.0069	3.761

ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	mPc AED YLSLI LNR	84%	40.5	52.50937	Ref	1.2	0.59	0.98	1.2	0.68	1.3	0.8	198	266	184	271	339	211	347	238	663.3	1987	3	0.0114	5.732
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	mPc AED YLSLI LNR	95%	59.5	52.50639	Ref	1.9	Value Missing (-0.29801834)	0.92	0.97	0.61	1.2	0.85	142	370	Value Missing (-0.29801834)	222	253	172	276	210	663.3	1987	3	0.0116	5.823
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	mPc AED YLSLI LNR	93%	49	52.71635	Ref	1.3	0.46	0.98	0.88	0.75	1.3	1.2	190	257	160	257	264	211	315	293	663.3	1987	3	0.0055	2.789
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	mPc AED YLSLI LNR	95%	73	51.97187	Ref	Reference Missing (1.3602957)	Reference Missing (0.3364616)	Reference Missing (0.8699256)	Reference Missing (0.8374492)	Reference Missing (0.8517555)	Reference Missing (1.7116258)	Reference Missing (0.8637019)	No Values (0.16747573)	Reference Missing (1.3602957)	Reference Missing (0.3364616)	Reference Missing (0.8699256)	Reference Missing (0.8374492)	Reference Missing (0.8517555)	Reference Missing (1.7116258)	Reference Missing (0.8637019)	668.7	2003	3	0.0129	6.456
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	mPc AED YLSLI LNR	95%	72.4	51.99604	Ref	1.7	0.34	1.2	0.89	0.82	1.6	0.68	370	1550	678	1350	1220	1020	1770	961	1002	2003	2	0.0124	6.199
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	mPc AED YLSLI LNR	95%	70.2	52.00364	Ref	Reference Missing (1.3924317)	No Values (0.4325374)	Reference Missing (0.96123844)	Reference Missing (0.61458147)	Reference Missing (0.7273222)	Reference Missing (1.7556298)	Reference Missing (0.77350223)	No Values (0.34784085)	Reference Missing (1.3924317)	No Values (0.4325374)	Reference Missing (0.96123844)	Reference Missing (0.61458147)	Reference Missing (0.7273222)	Reference Missing (1.7556298)	Reference Missing (0.77350223)	668.7	2003	3	0.0118	5.902
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	mPc AED YLSLI LNR	90%	42.3	52.02848	Ref	1.5	0.37	1.2	0.99	0.64	1.5	0.91	300	924	474	952	898	616	1200	771	1002	2003	2	0.011	5.47

ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	tVM ENFV AFV Gk	95%	56.1	53.55158	Ref	1.3	0.3	1	0.92	0.6	1.4	1.5	11400	30300	16000	29400	30400	21300	38400	41200	650.7	1949.1	3	0.0158	8.104
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	tVM ENFV AFV Gk	95%	63.9	53.47038	Ref	1.3	0.41	1.3	1	0.75	1.5	0.79	2160	5140	3000	6430	5620	4090	7050	4350	975.6	1949.1	2	0.0047	2.43
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	tVM ENFV AFV Gk	95%	73.6	53.67102	Ref	1.3	0.4	1.2	0.87	0.74	1.6	0.84	631	1610	919	1840	1570	1260	2440	1390	975.5	1949.1	2	0.021	10.76
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	tVM ENFV AFV Gk	92%	47.7	53.56707	Ref	Reference Missing (1.3318381)	Missing (0.36775294)	Reference Missing (1.1719851)	Reference Missing (0.8815356)	Reference Missing (0.6959952)	Reference Missing (1.4182385)	Reference Missing (1.318014)	No Values (-0.36153835)	Reference Missing (1.3318381)	Reference Missing (0.36775294)	Reference Missing (1.1719851)	Reference Missing (0.8815356)	Reference Missing (0.6959952)	Reference Missing (1.4182385)	Reference Missing (1.318014)	650.7	1949.1	3	0.0132	6.781
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	tVM ENFV AFV Gk	94%	50.4	53.58319	Ref	Reference Missing (1.4688914)	Missing (0.46078658)	Reference Missing (1.1742151)	Reference Missing (0.8275526)	Reference Missing (0.5245116)	Reference Missing (1.3839763)	Reference Missing (1.2986054)	No Values (-0.34859362)	Reference Missing (1.4688914)	Reference Missing (0.46078658)	Reference Missing (1.1742151)	Reference Missing (0.8275526)	Reference Missing (0.5245116)	Reference Missing (1.3839763)	Reference Missing (1.2986054)	650.7	1949.1	3	0.0138	7.074
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	tVM ENFV AFV Gk	93%	49.7	53.69023	Ref	1.3	0.34	1.1	0.72	0.79	1.4	1.4	1010	2040	1130	2120	1820	1670	2590	2550	650.7	1949.1	3	0.0184	9.412
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQO BOJYQO_BOVIN	tVM ENFV AFV Gk	92%	47.7	53.57466	Ref	1.3	0.3	1.2	0.76	0.64	1.4	1.4	629	1470	769	1600	1310	1050	1800	1870	650.7	1949.1	3	0.0149	7.627

ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQ0 BOJYQ0_BOVIN	tVM ENFV AFV Gk	95%	58.3	53.51967	Ref	1.2	0.4	1.2	1	0.77	1.1	1.4	239	468	298	593	557	416	552	675	650.7	1949.1	3	0.0105	5.381
ALB protein OS=Bos taurus GN=ALB PE=2 SV=1	tr BOJYQ0 BOJYQ0_BOVIN	tVm EnFV AFV Gk	84%	41.8	53.73578	Ref	1.1	0.87	0.88	0.92	0.85	1.1	1.1	5300	6110	5490	6240	7040	5880	7270	7110	656.4	1966.1	3	0.0134	6.826
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF8 F1MNF8_BOVIN	aVc MLS NTT AIAE AWA R	95%	65.7	53.13211	Ref	0.84	Value Missing (-1.9129511)	0.024	-0.41	-0.27	-0.02	-0.38	289	346	Value Missing (-1.9129511)	240	196	189	234	181	720	2157.1	3	0.0052	2.402
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF8 F1MNF8_BOVIN	aVc MLS NTT AIAE AWA R	73%	37.1	53.01521	Ref	0.091	Value Missing (-2.881796)	0.34	-0.045	-0.04	0.24	-0.29	164	118	Value Missing (-2.881796)	171	144	126	160	110	720	2157.1	3	0.0101	4.696
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF8 F1MNF8_BOVIN	aVFV DLEP TVID EVR	95%	60.1	53.84327	Ref	0.31	0.36	-0.14	-0.29	-0.38	-0.01	-0.11	4960	6980	7820	6200	6180	5080	6830	6340	669.4	2005.1	3	0.0155	7.748
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF8 F1MNF8_BOVIN	aVFV DLEP TVID EVR	95%	49.4	53.71812	Ref	0.2	0.081	-0.16	-0.075	-0.25	0.11	-0.28	2610	2860	2860	2720	3180	2470	3290	2500	1004	2005.1	2	0.0016	0.782

Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	dVN AAIA TIk	95%	68.3	51.04702	Ref	0.11	-0.32	0.054	-0.062	-0	-0.07	-0.29	32300	28700	23000	33600	34200	31100	31000	26400	812.5	1623	2	0.0168	10.35
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	dVN AAIA TIk	95%	51.8	50.94128	Ref	0.19	-0.21	0.082	-0.1	-0.11	-0.07	-0.29	66300	65400	53800	73800	71600	62300	66900	56700	542	1623	3	0.0114	7.05
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	dVn AAIA TIk	95%	58.4	51.43646	Ref	0.23	-0.27	-0.05	-0.006	-0.08	-0.12	-0.18	15300	15800	12100	15900	18100	15000	15300	14500	813	1624	2	0.0072	4.42
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	iHFP LATY APVI SAEK	67%	35.5	53.08163	Ref	0.2	-0.26	0.056	-0.11	-0.18	0.043	-0.14	1390	1490	1180	1640	1610	1340	1640	1430	789.1	2364.3	3	0.0211	8.92
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	iHFP LATY APVI SAEK	92%	44.5	52.86187	Ref	0.34	-0.19	-0.05	-0.25	-0.33	-0.03	-0.18	7750	7800	5880	7240	6980	5740	7410	6610	592.1	2364.4	4	0.0165	6.965
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	iHFP LATY APVI SAEK	93%	45.9	52.8658	Ref	-0.015	-0.41	0.049	-0.35	-0.23	0.3	-0.15	6230	4640	3830	5910	4930	4700	7080	5130	592.1	2364.4	4	0.0167	7.067

Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	iHFP LATY APVI SAEK	94%	50.5	52.84128	Ref	0.21	-0.17	-0	-0.18	-0.32	0.073	-0.17	1070	1030	862	1090	1060	836	1150	961	789.1	2364.4	3	0.0161	6.827
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	iHFP LATY APVI SAEK	93%	45.3	52.67172	Ref	0.23	-0.37	0.18	-0.098	-0.4	0.12	-0.24	9190	9350	6690	11000	10000	7110	10600	8190	592.1	2364.4	4	0.0114	4.801
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	iHFP LATY APVI SAEK	94%	50.2	52.59245	Ref	0.24	-0.22	0.11	-0.12	-0.25	0.014	-0.17	683	754	594	842	789	628	790	691	789.1	2364.4	3	0.0098	4.126
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	iHFP LATY APVI SAEK	91%	41.5	51.02365	Ref	0.25	-0.26	0.13	-0.2	-0.28	0.047	-0.14	4310	4750	3620	5330	4670	3840	5040	4410	668.1	2668.6	4	0.0155	5.813
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	iHFP LATY APVI SAEK	81%	36.2	51.37234	Ref	-0.055	-0.32	0.19	-0.15	-0.33	0.2	-0.02	2450	2110	1900	3040	2640	2040	3080	2620	668.1	2668.6	4	0.0211	7.91
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	qLFH PEQL ISGK	61%	33.9	52.64986	Ref	0.21	-0.17	-0.05	-0.14	-0.38	0.1	-0.13	3060	3000	2510	3070	3180	2340	3420	2890	669.1	2004.1	3	0.0122	6.082

Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	tIGG GDD SFNT FFSE TGA Gk	95%	56	53.7495	Ref	0.23	-0.53	-0.04	-0.096	-0.3	-0.04	-0.08	2430	2070	1330	2100	2220	1680	2110	2030	872.8	2615.3	3	0.0259	9.888
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	tIGG GDD SFNT FFSE TGA Gk	95%	66.6	53.94405	Ref	0.1	-0.22	-0.03	-0.2	0.03	-0.12	0.15	5670	6100	5280	6750	6630	6790	6390	7650	872.8	2615.3	3	0.0193	7.366
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	tIGG GDD SFNT FFSE TGA Gk	95%	85.3	53.95564	Ref	0.21	-0.15	-0.17	-0.21	-0.43	-0.05	0.13	9540	8880	7500	8310	8920	6670	9090	10200	872.8	2615.3	3	0.0184	7.022
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	tIGG GDD SFNT FFSE TGA Gk	95%	62.1	53.29884	Ref	-0.23	0.042	0.24	-0.19	-0.14	-0.37	0.33	1740	1550	2030	2620	2140	1930	1720	2780	873.1	2616.3	3	0.0229	8.743
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	vGIN YQP PTVV PGG DLAK	92%	47.7	53.42247	Ref	0.56	-0.63	0.007	-0.25	-0.36	-0.46	-0	6230	6430	3060	5350	4930	3980	3880	5310	811.8	2432.4	3	0.0177	7.27
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF 8 F1MNF 8_BOVIN	vGIN YQP PTVV PGG DLAK	86%	42.8	53.42247	Ref	0.53	-0.34	0.13	-0.027	-0.28	-0.29	-0.34	8820	11600	6860	10600	10500	7730	7990	7670	811.8	2432.4	3	0.0177	7.27

Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF8 F1MNF8_BOVIN	vGIN YQP PTVV PGG DLAK	77%	36.6	53.43231	Ref	0.31	-0.57	0.16	-0.31	-0.07	-0.02	-0.11	19100	20600	12100	22600	18000	18500	20000	18700	609.1	2432.4	4	0.0175	7.174
Uncharacterized protein OS=Bos taurus GN=LOC787568 PE=3 SV=1	tr F1MNF8 F1MNF8_BOVIN	vGIN YQP PTVV PGG DLAK	79%	37.2	53.10394	Ref	0.39	-0.32	0.1	-0.076	-0.19	0.084	-0.35	9260	12500	8300	12500	12100	9800	12400	9080	609.1	2432.4	4	0.0072	2.965
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE, tr F1RQU2 F1RQU2_PIG, tr F4NAS1 F4NAS1_BOVIN, tr F7GST0 F7GSTO_MAC	aDH GEPI GR	66%	32.8	50.5182	Ref	-0.037	-0.04	-0.08	-0.2	-0.06	-0.29	-0.12	22000	17500	19000	20700	21000	20200	18000	20000	419.2	1254.7	3	0.0104	8.255

Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BO SIN,tr F7GSTO F7GSTO_MAC	aLLFI PR	53%	28.5	48.80516	Ref	0.19	-0.4	0.069	-0.21	-0.48	0.071	-0.22	21400	19400	14100	21800	19900	14400	22000	17900	567.4	1132.7	2	0.0105	9.246
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BO SIN,tr F7GSTO F7GSTO_MAC	eDQ TEYL EER	81%	34.4	48.92162	Ref	0.24	-0.2	0.056	-0.14	-0.17	-0.22	-0.41	22900	23000	18400	24600	23700	20300	20400	17800	808.4	1614.8	2	0.0134	8.3

Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BOVIN,tr F7GST0 F7GST0_MAC	eLIS NAS DAL Dk	95%	55.7	53.42047	Ref	-0.013	-0.12	-0.27	-0.096	-0.24	-0.23	-0.29	27700	17900	18000	18200	22700	17900	18900	18000	628.7	1883	3	0.013	6.892
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BOVIN,tr F7GST0 F7GST0_MAC	eLIS NAS DAL DKIR	51%	33	53.48887	Ref	0.12	-0.11	0.022	-0.1	-0.2	-0.14	-0.38	8980	8350	7740	9490	9580	7810	8540	7170	718.4	2152.2	3	0.0196	9.1

Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BOVIN,tr F7GSTO F7GSTO_MACR	eQVANS AFVE	93%	44.9	52.10915	Ref	0.031	-0.26	-0.14	-0.023	-0.35	0.064	-0.15	8680	7360	6550	7950	9510	6630	9210	7870	777.4	1552.8	2	0.0091	5.874
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BOVIN,tr F7GSTO F7GSTO_MACR	eQVAnSA FVER	67%	33.8	51.65236	Ref	0.082	-0.23	-0.11	-0.021	-0.36	-0.06	-0.15	10500	9090	7960	9700	11400	7850	10100	9380	777.9	1553.8	2	0.0124	7.999

Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BOVIN,tr F7GST0 F7GST0_MAC	gVV DSE DLPL NISR	67%	35.3	53.3027	Ref	0.14	-0.4	-0.14	0.37	-0.4	0.022	-0.37	4160	4310	3210	4300	6780	3460	4850	3660	909.5	1817	2	0.017	9.324
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BOVIN,tr F7GST0 F7GST0_MAC	gVV DSE DLPL NISR	95%	49.9	53.42202	Ref	0.15	-0.29	-0.11	0.023	-0.47	0.076	-0.36	8920	7810	6260	7930	9580	5940	9070	6640	909.5	1817	2	0.0124	6.838

Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BOVIN,tr F7GST0 F7GSTO_MAC	hLEI NPD HPIV ETLR	95%	54.3	53.99609	Ref	0.079	-0.09	-0.06	-0.16	-0.2	-0.02	-0.03	5210	5730	5520	6360	6530	5550	6560	6480	696.4	2086.1	3	0.0145	6.928
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BOVIN,tr F7GST0 F7GSTO_MAC	hLEI NPD HPIV ETLR	95%	60.5	53.99823	Ref	0.31	0.044	-0.09	-0.23	-0.25	-0.28	-0.09	6580	8260	7430	7620	7580	6540	6710	7570	696.4	2086.1	3	0.0143	6.841

Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BOVIN,tr F7GST0 F7GST0_MAC	hLEI NPD HPIV ETLR	95%	57.7	53.93677	Ref	-0.24	-0.52	0.3	-0.15	0.097	-0.21	-0.01	26700	21400	19100	37900	30500	31600	26700	30500	522.5	2086.1	4	0.0121	5.79
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BOVIN,tr F7GST0 F7GST0_MAC	hLEI NPD HPIV ETLR	95%	73.5	54.04345	Ref	0.081	0.048	-0.01	-0.18	-0.22	-0.12	-0.12	4360	4670	4950	5320	5240	4440	4980	4940	696.4	2086.1	3	0.0172	8.236

Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,trl F1RQU2 F1RQU2_PIG,trl F4NAS1 F4NAS1_BOVIN,trl F7GSTO F7GSTO_MAC	hSQF IGYPI TLYL Ek	76%	38.5	53.70395	Ref	-0.058	-0.24	0.13	-0.27	-0.2	-0.01	-0.06	796	679	648	939	787	719	861	821	806.5	2416.3	3	0.0124	5.149
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,trl F1RQU2 F1RQU2_PIG,trl F4NAS1 F4NAS1_BOVIN,trl F7GSTO F7GSTO_MAC	kHLE INPD HPIV ETLR	77%	32.6	52.89022	Ref	-0.21	-0.39	0.16	-0.066	0.042	-0.41	0.24	28200	24400	23500	38400	36300	34200	26200	40800	504.7	2518.4	5	0.0159	6.309

Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BOVIN,tr F7GST0 F7GST0_MAC	ETLR	92%	46.6	52.77525	Ref	-0.14	-0.43	0.047	-0.11	0.21	-0.49	0.067	4070	3220	2850	4450	4390	4810	3080	4500	840.5	2518.4	3	0.0137	5.45
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,tr F1RQU2 F1RQU2_PIG,tr F4NAS1 F4NAS1_BOVIN,tr F7GST0 F7GST0_MAC	ETLR	92%	46.9	52.91591	Ref	-0.17	-0.27	0.11	-0.022	0.052	-0.31	0.028	3910	3390	3430	5010	5050	4640	3770	4730	840.5	2518.4	3	0.0163	6.463

Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,trl F1RQU2 F1RQU2_PIG,trl F4NAS1 F4NAS1_BOVIN,trl F7GST0 F7GST0_MAC	ETLR	78%	32.8	52.77242	Ref	-0.21	-0.53	0.05	0.014	0.12	-0.43	0.094	76700	55900	48800	81600	87800	82600	58900	84000	504.7	2518.4	5	0.0136	5.416
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_HUMAN,sp P11499 HS90B_MOUSE,sp P34058 HS90B_RAT,sp Q4R4T5 HS90B_MACFA,sp Q5R710 HS90B_PONAB,sp Q76LV1 HS90B_BOVIN,sp Q9GKX8 HS90B_HORSE,trl F1RQU2 F1RQU2_PIG,trl F4NAS1 F4NAS1_BOVIN,trl F7GST0 F7GST0_MAC	VLHLk	81%	26	39.42703	Ref	0.17	-0.24	0.17	-0.18	-0.22	-0.24	-0.56	44700	37300	30600	45500	39300	33400	34400	27300	444.3	1329.9	3	0.0037	2.759

Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_	VIDQ EELN k	94%	46.8	53.12691	Ref	0.31	-0.22	0.012	-0.22	-0.28	-0.08	-0.21	21500	25100	18800	24900	23400	19600	23500	21200	880.5	1758.9	2	0.0147	8.381
	HUMAN,s p P11499 HS90B_ MOUSE,s p P34058 HS90B_R AT,sp Q4 R4T5 HS9 OB_MACF A,sp Q5R 710 HS90 B_PONAB ,sp Q76L V1 HS90B _BOVIN,s p Q9GKX 8 HS90B_ HORSE,tr F1RQU2 F1RQU2_ PIG,tr F4 NAS1 F4 NAS1_BO SIN,tr F7 GST0 F7G STO_MAC																									
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	8 HS90B_	VIDQ EELn k	58%	34	53.20192	Ref	0.27	-0.05	-0.19	-0.12	-0.15	-0.27	-0.28	16700	17600	15300	15600	17900	15400	14800	14500	587.7	1759.9	3	0.0067	3.779
	HUMAN,s p P11499 HS90B_ MOUSE,s p P34058 HS90B_R AT,sp Q4 R4T5 HS9 OB_MACF A,sp Q5R 710 HS90 B_PONAB ,sp Q76L V1 HS90B _BOVIN,s p Q9GKX 8 HS90B_ HORSE,tr F1RQU2 F1RQU2_ PIG,tr F4 NAS1 F4 NAS1_BO SIN,tr F7 GST0 F7G STO_MAC																									

Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	eIAE AYLG k	82%	38	51.83162	Ref	0.1	-0.04	0.017	-0.2	-0.37	-0.17	-0.3	19500	15000	14700	17200	16400	12700	15200	13700	801.5	1600.9	2	0.0062	3.866
Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	fDDA VVQ SDM k	82%	40.4	53.16599	Ref	0.05	-0.17	-0.39	-0.11	-0.14	-0.02	0.15	10600	9530	8900	8530	11500	9770	11100	12400	621.7	1862	3	0.0104	5.556

Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	FEEL NAD	LFR	84%	38.8	51.8608	Ref	0.1	-0.39	0.22	-0.21	-0.25	-0.06	-0.17	5190	4530	3500	5970	4900	4170	4960	4550	779.4	1556.8	2	0.0117	7.506
Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	hWP FMV VND AGR	Pk	91%	45.6	54.40098	Ref	0.084	-0.43	0.11	-0.1	-0.23	0.2	-0.07	17800	19300	14600	23900	22700	18100	25600	21100	566.3	2261.2	4	0.0067	2.974

Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_	hWP	84%	40.3	54.46125	Ref	0.081	-0.3	0.14	-0.3	-0.17	0.053	-0.16	10300	9380	7810	11900	9670	9240	11300	9660	566.3	2261.2	4	0.013	5.768
	HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr																									
Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_	hWP	70%	35.7	54.44828	Ref	-0.1	-0.22	0.13	-0.1	-0.2	0.14	-0.02	9330	8930	8910	12800	12000	9760	12900	11500	570.3	2277.2	4	0.0087	3.81
	HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr																									

Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_	hWP	94%	49.8	54.77962	Ref	0.23	-0.07	0.045	-0.2	-0.25	-0.07	-0.18	9970	11100	9770	11900	11100	9350	11100	10100	566.6	2262.2	4	0.0179	7.924
	HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr																									
Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_	hWP	95%	53.2	54.70037	Ref	0.075	-0.28	0.013	-0.11	-0.12	-0.1	-0.03	2760	2610	2220	3040	3090	2670	2830	2950	755.1	2262.2	3	0.0067	2.982
	HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr																									

Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	iINEP TAA AIAY GLDk	93%	44.4	51.14281	Ref	-0.075	-0.63	0.03	-0.002	0.045	0.086	-0.26	44900	34400	25500	45100	48600	43900	47100	36700	675.9	2699.6	4	0.0228	8.449
Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	iINEP TAA AIAY GLDk	95%	53.9	50.89082	Ref	-0.006	-0.43	0.18	-0.016	-0.14	-0.23	-0.09	5550	4530	3660	6260	6040	4850	4730	5190	900.9	2699.6	3	0.0176	6.525

Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	IDkS QIH DIVL VGG STR	88%	43.3	52.45293	Ref	-0.06	-0.28	0.099	-0.08	-0.18	0.083	0.003	3030	2880	2680	3920	3820	3110	3900	3660	816.1	2445.4	3	0.0117	4.765
Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	nQV AMN PTNT VFD Ak	95%	60.5	54.44956	Ref	-0.18	-0.25	0.074	0.026	-0.32	0.033	-0.14	15600	11000	11300	15900	16900	11600	15500	13600	753.4	2257.2	3	0.0187	8.27

Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	nSLE SYAF NMk	82%	40.4	53.3997	Ref	-0.054	-0.31	-0.01	-0.19	-0.16	-0.18	0.49	4120	4340	3940	5460	5300	4740	4860	7670	638	1911	3	0.0174	9.118
Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	nSLE SYAF NMk	87%	43	53.06103	Ref	-0.17	-0.2	-0.06	-0.088	0.042	-0.27	0.031	8820	6300	6700	8260	8950	8550	7190	8800	638.3	1912	3	0.0186	9.698

Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	nSLE SYAF NMc	73%	37.4	53.29447	Ref	-0.18	-0.21	-0.13	-0.24	-0.06	-0.15	0.086	7070	4540	4850	5740	5850	5810	5670	6650	638.3	1912	3	0.0074	3.848
Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	sFYP EEVS SMV LTK	92%	48.9	54.43473	Ref	0.18	-0.35	0.2	0.029	-0.33	-0.09	-0.24	29700	30800	23100	37900	37200	25300	31200	27900	742.4	2224.2	3	0.017	7.621

Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	sFYP EEVS SMV LTK	84%	42.7	54.49525	Ref	0.19	-0.17	0.045	0.005	-0.26	-0.23	-0.2	7900	7800	6620	8620	9240	6710	7150	7250	742.4	2224.2	3	0.0151	6.798
Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	sFYP EEVS SmV LTK	65%	36.6	54.48235	Ref	0.052	-0.41	-0.14	-0.19	-0.26	0.42	-0.12	7310	6920	5440	7390	7830	6520	10900	7470	747.7	2240.2	3	0.007	3.13

Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	STAG DTHL GGE DFD NR	76%	34.2	49.24677	Ref	0.36	-0.11	-0.09	-0.27	-0.16	-0.2	0.074	36600	49000	38500	43700	42600	40200	40700	49000	666	1994.9	3	0.0131	6.567
Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_ HORSE,sp P11142 HSP7C_H UMAN,sp P19120 HSP7C_B OVIN,sp P19378 H SP7C_CRI GR,sp P6 3017 HSP 7C_MOUS E,sp P630 18 HSP7C _RAT,sp Q71U34 HSP7C_SA GOE,tr B2 KI81 B2KI 81_RHIFE, tr D2GYC 0 D2GYC 0_AILME,t r E2R0T6 E2R0T6_ CANFA,tr	TPS YVAF TDTE R	95%	70.7	51.89122	Ref	0.11	-0.43	0.081	-0.21	-0.1	-0.18	0.005	3780	3350	2510	4010	3610	3420	3370	3800	896.5	1790.9	2	0.0124	6.94

Heat shock cognate 71 kDa protein OS=Equus caballus GN=HSPA8 PE=2 SV=1	1 HSP7C_HORSE,sp P11142 HSP7C_HUMAN,sp P19120 HSP7C_BOVIN,sp P19378 HSP7C_CRIGR,sp P63017 HSP7C_MOUSE,sp P63018 HSP7C_RAT,sp Q71U34 HSP7C_SAGO,sp B2KI81 B2KI81_RHIFE,sp D2GYC0 D2GYC0_AILME,sp E2R0T6 E2R0T6_CANFA,sp	vcNP	63%	33.8	52.13396	Ref	-0.3	-0.33	-0.08	0.13	-0.01	-0.19	0.15	39300	27900	29800	39600	50700	40100	36900	46600	514.6	1540.9	3	0.0129	8.351
60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,sp E2QUU5 E2QUU5_CANFA,sp E2REN7 E2REN7_CANFA,sp F1MUZ9 F1MUZ9_BOVIN,sp F1SMZ7 F1SMZ7_PIG,sp F6Z587 F6Z587_HORSE,sp F7BGB7 F7BGB7_MACMU,sp F7I3J9 F7I3J9_CALI	aLM LQG VDLL ADA VAV TmG	95%	55.5	54.10176	Ref	No Values (-0.35774875)	No Values (-0.47544202)	Reference Missing (-1.3617414)	No Values (-0.7825161)	No Values (-0.58664364)	No Values (-0.649362)	No Values (-0.6385387)	No Values (-0.56013875)	No Values (-0.35774875)	No Values (-0.47544202)	Reference Missing (-1.3617414)	No Values (-0.7825161)	No Values (-0.58664364)	No Values (-0.649362)	No Values (-0.6385387)	913.2	2736.5	3	0.0203	7.401

60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALIA	aLM LQG VDLL ADA VAV TmG Pk	53%	33.7	53.83576	Ref	No Values (0.08678025)	No Values (-0.0304)	No Values (-0.1975078)	No Values (-0.3379871)	No Values (-0.1421446)	No Values (-0.20488144)	No Values (-0.1940734)	No Values (-0.11560978)	No Values (-0.08678025)	No Values (-0.0304)	No Values (-0.1975078)	No Values (-0.3379871)	No Values (-0.1421446)	No Values (-0.20488144)	No Values (-0.1940734)	913.2	2736.5	3	0.0104	3.784
60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALIA	aLM LQG VDLL ADA VAV TmG Pk	95%	53.9	53.95089	Ref	No Values (0.08678025)	No Values (-0.0306)	No Values (-0.1979)	No Values (-0.3379871)	No Values (-0.1421474)	No Values (-0.20488136)	No Values (-0.1940723)	No Values (-0.11560978)	No Values (-0.08678025)	No Values (-0.0306)	No Values (-0.19750799)	No Values (-0.3379871)	No Values (-0.1421474)	No Values (-0.20488136)	No Values (-0.1940723)	913.2	2736.5	3	0.0153	5.593

60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJAK	aLmL QGV DLLA DAV AVT mGPK	79%	40.5	54.39454	Ref	Value Missing (-1.5297354)	Value Missing (-1.6474285)	0.7	1.1	Value Missing (-1.7586304)	Value Missing (-1.8213968)	Value Missing (-1.8105226)	121	Value Missing (-1.5297354)	Value Missing (-1.6474285)	105	153	Value Missing (-1.7586304)	Value Missing (-1.8213968)	Value Missing (-1.8105226)	918.5	2752.5	3	0.0172	6.251
60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJAK	gVM LAV DAVI AELK	95%	61.9	51.28047	Ref	-0.17	-0.24	-0.08	-0.43	-0.02	-0.12	-0.67	344	202	208	262	226	263	255	173	679.7	2036.2	3	0.0159	7.821

60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJ A	gVm LAV DAVI AELK	94%	49	51.79736	Ref	0.13	-0.28	-0.12	-0.36	-0.58	0.07	-0.43	433	347	283	356	332	248	407	286	685.1	2052.2	3	0.009	4.363
60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJ A	gVm LAV DAVI AELK	69%	34.6	51.69077	Ref	0.025	-0.36	-0.02	-0.44	-0.33	0.13	-0.19	256	230	191	271	224	211	302	240	685.1	2052.2	3	0.0068	3.296

60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALI	gYIS PYFI	64%	35.7	53.78607	Ref	-0.032	-0.17	-0.1	-0.46	-0.32	-0.06	0.023	4540	3970	3920	4610	3950	3800	4760	5010	666.7	1997.1	3	0.0199	9.953
60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALI	iSSV QsIV PALE IANA HR	95%	67.9	53.3654	Ref	0.36	-0.16	-0.1	-0.23	-0.22	-0.45	-0.18	1210	1610	1220	1430	1440	1270	1130	1350	737.1	2208.2	3	0.0112	5.08

60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJANA	ISSV QSIV PALE IANA	95%	53.9	52.58412	Ref	0.32	-0.28	-0.05	-0.27	-0.14	-0.46	-0.07	1220	1620	1160	1530	1440	1390	1150	1510	737.1	2208.3	3	0.0163	7.358
60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJANA	KISS VQSI VPAL EIAAn AHR	95%	52.9	52.13411	Ref	-0.12	-0.19	-0.04	-0.25	-0.21	-0.12	-0.16	1140	929	956	1200	1140	1020	1130	1090	661.4	2641.5	4	0.0194	7.347

60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJ A	IkVG LQV VAV k	75%	19.5	36.74677	Ref	-0.15	-0.33	-0.04	-0.16	-0.15	-0.03	-0.12	3020	2590	2480	3400	3450	3040	3460	3210	517.4	2065.4	4	0.0012	0.593
60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJ A	ISDG VAVL k	95%	45.6	49.97513	Ref	0.039	-0.16	-0.18	-0.29	-0.24	-0.17	-0.27	12600	10400	9820	10800	11100	9990	11000	10200	755.5	1508.9	2	0.0039	2.574

60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJ A	nAG VEGS LIVE k	95%	63	52.45152	Ref	-0.14	-0.24	-0.05	-0.044	-0.36	-0.11	-0.35	9490	6810	6870	8820	9770	6840	8490	7170	912.5	1823	2	0.0151	8.281
60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJ A	tVIIIE QSW GSPK	91%	46	53.18796	Ref	-0.17	0.037	-0	-0.49	0.004	-0.35	-0.24	13800	10600	13200	14400	11400	13900	11400	12200	651.7	1952.1	3	0.0153	7.835

60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJA	tVIIIEQSW	95%	54.2	53.1212	Ref	-0.006	-0.16	-0.01	-0.32	-0.17	-0.3	-0.15	2900	2550	2480	3080	2750	2650	2550	2810	977.1	1952.1	2	0.0123	6.301
60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJA	vGEVIVTK	90%	39.2	49.26569	Ref	0.0053	-0.07	-0.12	-0.29	-0.27	-0.15	-0.44	37000	29100	30000	32500	31700	28100	32000	25900	727	1451.9	2	0.0046	3.181

60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJ A	VGG TSDV EVN Ek	95%	55.8	53.49526	Ref	0.04	-0.21	0.059	-0.23	-0.41	-0.14	-0.37	11600	9760	8900	12100	10900	8390	10600	8900	921.5	1841	2	0.0095	5.152
60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJ A	VGL QVV AVk	62%	25.2	43.83869	Ref	-0.022	-0.16	-0.08	-0.27	-0.2	-0.12	-0.2	12200	10900	10800	12800	12300	11300	12500	11700	507.7	1520	3	0.0016	1.038

60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJ A	VGL QVV AVk	93%	37.8	44.84983	Ref	0.038	-0.19	-0.12	-0.24	-0.36	0.005	-0.18	10400	9830	9130	10700	10900	8730	11800	10300	761	1520	2	0.0078	5.123
60 kDa heat shock protein, mitochondrial OS=Cricetulus griseus GN=HSPD1 PE=2 SV=1	7 CH60_C RIGR,sp P63038 CH60_MOUSE,sp P63039 CH60_RAT,tr E2QUU5 E2QUU5_CANFA,tr E2REN7 E2REN7_CANFA,tr F1MUZ9 F1MUZ9_BOVIN,tr F1SMZ7 F1SMZ7_PIG,tr F6Z587 F6Z587_HORSE,tr F7BGB7 F7BGB7_MACMU,tr F713J9 F713J9_CALJ A	VGL QVV AVk	80%	30.2	44.00987	Ref	0.06	-0.24	-0.06	-0.26	-0.31	-0.09	-0.3	14500	12600	11100	14200	13600	11500	13900	11900	507.7	1520	3	0.0027	1.768

Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	aAVP SGAS TGIY EALE LR	95%	48.8	54.15155	Ref	0.062	0.1	-0.17	0.014	0.063	-0.07	-0.37	3240	3040	3390	3160	3950	3570	3400	2740	1055	2108.1	2	0.0151	7.166
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	aAVP SGAS TGIY EALE LR	95%	70.8	54.15476	Ref	0.22	0.39	-0.24	-0.27	-0.15	-0.05	-0.11	1420	1750	2140	1550	1670	1590	1790	1690	703.7	2108.1	3	0.0152	7.226
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	aVEH INK	65%	32.5	50.76393	Ref	0.13	0.12	-0.24	-0.077	-0.2	0.22	-0.33	9030	9090	9800	8580	10600	8450	11900	8040	709.9	1417.8	2	0.0074	5.232
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	dAT NVG DEG GFA PNIL ENK	95%	80.1	54.8605	Ref	-0.18	0.069	-0.25	0.12	-0.27	0.029	-0.36	6060	3680	4730	4260	6070	4050	5200	3930	857.1	2568.3	3	0.0205	7.982
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	eALE LLk	74%	32.7	49.00143	Ref	0.18	0.12	-0.17	-0.2	-0.25	0.13	-0.61	48700	40300	42100	38500	41600	35100	47800	28300	712.5	1422.9	2	0.0051	3.589
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	fGA NAIL GVSL AVck	95%	58.7	54.19308	Ref	0.073	-0.04	-0.17	-0.059	-0.34	0.37	-0.42	1240	1070	1070	1100	1310	939	1610	922	706.4	2116.2	3	0.0219	10.35
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	fGA NAIL GVSL AVck	95%	53	53.97222	Ref	0.3	0.16	-0.21	-0.2	-0.46	0.1	-0.56	502	449	442	384	425	312	480	302	706.4	2116.2	3	0.0118	5.586

Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSL4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	fGA NAIL GVSL AVck	90%	45.8	54.02721	Ref	0.33	0.093	-0.09	-0.089	-0.28	-0.06	-0.53	315	318	293	290	320	245	298	213	706.4	2116.2	3	0.0144	6.805
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSL4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	fTAS AGIQ VVG DDL VTN Pk	92%	49.6	54.60375	Ref	0.093	0.21	0.17	-0.37	-0.38	0.11	-0.34	3460	3230	3800	4160	3150	2730	4010	2910	881.2	2640.4	3	0.0228	8.634
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSL4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	gNPT VEV DLFT Ak	95%	73.3	53.622	Ref	0.023	0.063	-0.22	-0.067	-0.12	0.21	-0.49	4790	3860	4310	3980	4870	4090	5390	3280	1000	1998.1	2	0.0216	10.79
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSL4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	gNPT VEV DLFT Ak	83%	41	53.48247	Ref	-0.21	0.35	-0.32	-0.11	-0.12	0.094	-0.42	1E+05	67100	1E+05	75500	96200	83900	1E+05	70300	667	1998.1	3	0.0157	7.871
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSL4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	gNPT VEV DLFT Ak	63%	34.9	53.25243	Ref	-0.17	-0.11	-0.1	-0.11	0.059	0.044	-0.08	3950	2890	3260	3670	4040	3960	4090	3740	667	1998.1	3	0.0049	2.469
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSL4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	gNPT VEV DLFT Ak	53%	33.3	53.34448	Ref	0.27	-0.28	0.018	-0.19	-0.11	0.18	-0.16	292	344	255	353	336	311	396	312	667	1998.1	3	0.0073	3.654
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSL4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	iGAE VYH NLk	57%	32.7	52.08288	Ref	0.056	0.16	-0.05	-0.12	-0.46	0.23	-0.25	6870	6330	7380	7150	7510	5180	8740	6210	584.7	1751	3	0.0127	7.233

Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	IAQSnGWGVMVSHR	53%	32.7	52.81347	Ref	0.18	0.22	-0.08	0.004	-0.36	0.24	-0.23	2100	2990	3320	3040	3550	2410	3820	2740	616.3	1845.9	3	0.0108	5.846
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	vVIGMDVAASEFYR	95%	57.5	53.10704	Ref	0.15	0.012	-0.21	-0.013	-0.39	0.3	-0.35	8290	8000	7890	7600	9590	6450	10900	6850	931	1860	2	0.0188	10.09
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	vVIGMDVAASEFYR	95%	49.8	53.33066	Ref	0.091	0.13	-0.19	0.036	-0.36	0.22	-0.57	2160	1860	2070	1860	2400	1590	2480	1420	931	1860	2	0.0097	5.229
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	vVIGMDVAASEFYR	81%	41	54.37075	Ref	0.049	-0.03	-0.2	-0.006	-0.34	0.24	-0.24	1300	1100	1140	1130	1420	985	1540	1090	722.4	2164.2	3	0.0165	7.631
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	yITPDELAnLYk	80%	40.5	54.11433	Ref	0.19	0.005	-0.14	-0.009	-0.32	0.17	-0.23	10500	11200	10700	10800	13100	9240	13500	10200	683.7	2048.1	3	0.0116	5.647
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	yITPDELAnLYk	82%	41.4	54.1152	Ref	0.15	-0.08	-0.05	-0.053	-0.23	0.13	-0.23	4470	4470	4130	4730	5200	4010	5400	4170	683.7	2048.1	3	0.0178	8.693
Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4	sp Q9XSJ4 ENOA_BOVIN, tr F1MB08 F1MB08_BOVIN	yITPDELAnLYk	92%	45.8	54.09443	Ref	0.17	0.045	-0.06	-0.078	-0.21	0.21	-0.55	5510	5390	5380	5600	6110	4870	6780	3990	1025	2048.1	2	0.0123	6.001

Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ QNR	eAFn MID	94%	43.3	49.72767	Ref	-0.48	0.36	-0.62	-0.084	0.3	-0.17	0.018	24400	13100	25400	14500	23100	26300	19900	22500	771.9	1541.7	2	0.013	8.453
Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ DR	eLLT TMG	74%	34.8	51.05231	Ref	-0.45	0.49	-0.41	0.085	0.12	-0.28	-0.1	3E+05	177000	4E+05	223000	346000	3E+05	2E+05	276000	670.4	1338.7	2	0.0094	7.003

Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HKK5 D2HKK5_ AILME,tr D2HKK6 D2HKK6_ LYR	fTDE EVDE	95%	56.5	50.15419	Ref	-0.67	0.33	-0.59	0.2	0.33	-0.27	0.1	42600	22700	49200	29300	55600	53000	36500	47000	860.4	1718.8	2	0.014	8.148
Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HKK5 D2HKK5_ AILME,tr D2HKK6 D2HKK6_ LYR	fTDE EVDE	95%	47.2	50.21243	Ref	-0.54	0.4	-0.51	0.13	0.38	-0.43	0.082	20500	12600	26200	15700	26900	28000	16700	23600	860.4	1718.8	2	0.0133	7.717

Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ LYR	fTDE EVDE	94%	46.8	50.29408	Ref	-0.21	0.17	-0.45	-0.075	0.36	-0.24	-0.11	8810	5690	8020	5850	8390	9890	6820	7390	573.9	1718.8	3	0.0106	6.162
Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ LYR	fTDE EVDE	95%	58.2	50.35302	Ref	-0.91	0.34	-0.67	0.3	0.4	-0.42	-0.07	42200	16200	41800	23300	50300	47100	27900	35300	860.4	1718.8	2	0.0096	5.589

Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ LYR	fTDE EVDE	95%	46.3	50.35582	Ref	-0.29	0.37	-0.5	0.056	0.25	-0.29	0.022	4310	3080	5250	3220	5230	5230	3760	4630	860.4	1718.8	2	0.0095	5.519
Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ LYR	fTDE EVDE	95%	47.4	50.53539	Ref	-0.59	0.37	-0.49	0.084	0.34	-0.52	0.083	42700	21700	45700	28400	46500	48400	27900	42100	860.4	1718.8	2	0.0051	2.973

Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ LYR	fTDE EVDE	95%	46.1	49.8867	Ref	-0.43	0.37	-0.35	0.055	0.24	-0.28	0.024	6670	4270	8080	5520	8040	7980	5810	7120	860.4	1718.8	2	0.019	11.05
Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ FTR	gNF NYIE	88%	39.9	51.36689	Ref	-0.79	0.42	-0.65	0.2	0.31	-0.27	0.12	64100	31500	79200	42400	83700	78900	55300	72000	782.9	1563.8	2	0.0127	8.097

Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ FTR	gNF NYIE	82%	37.4	51.409	Ref	-0.66	0.35	-0.56	0.18	0.35	-0.31	0.18	12700	7390	16100	9630	17700	17500	11500	16000	782.9	1563.8	2	0.0114	7.317
Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ FTR	gNF NYIE	87%	39.7	51.48229	Ref	-0.53	0.32	-0.59	0.062	0.35	-0.18	0.14	8130	4990	9770	5840	10100	10800	7780	9680	782.9	1563.8	2	0.0107	6.844

Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_	gNF NYIE FTR	81%	37.2	51.48229	Ref	-0.48	0.25	-0.4	0.087	0.23	-0.18	0.15	5210	3260	5880	4190	6490	6250	4920	6140	782.9	1563.8	2	0.0107	6.844
Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_	gNF NYIE FTR	72%	34.7	51.49271	Ref	-0.47	0.35	-0.45	0.11	0.24	-0.36	0.17	9940	6290	12000	7740	12600	12000	8310	11800	782.9	1563.8	2	0.0099	6.307

Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ FTR	gNF NYIE	64%	32.6	51.08886	Ref	-0.5	0.29	-0.33	0.078	0.26	-0.18	0.15	12300	8280	15500	11300	16600	16400	12700	15700	782.9	1563.8	2	0.0194	12.39
Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ FTR	gNF NYIE	67%	33.3	51.30121	Ref	-0.34	0.23	-0.42	0.051	0.26	-0.25	0.15	5050	3540	5720	4080	6230	6280	4620	6050	782.9	1563.8	2	0.0142	9.107

Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ FTR	gNF NYIE	64%	33.1	51.67873	Ref	-0.46	0.18	-0.41	0.085	0.29	-0.14	0.2	2760	1880	3180	2370	3680	3720	2870	3600	782.9	1563.8	2	0.0042	2.716
Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ TR	gNFn YIEF	72%	33.6	50.47684	Ref	-0.49	0.16	-0.45	0.089	0.33	-0.32	0.28	7100	4470	7610	5610	8960	9260	6140	9270	783.4	1564.8	2	0.0184	11.75

Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ TR	gNFn YIEF	55%	30.5	50.47668	Ref	-0.41	0.15	-0.24	0.067	0.28	-0.21	0.11	3740	2520	4040	3450	4720	4770	3540	4410	783.4	1564.8	2	0.0182	11.6
Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19 105 ML1 2A_HUM AN,sp Q3 THE2 ML 12B_MOU SE,sp Q5E 9E2 MYL9 _BOVIN,s p Q5RC3 4 ML12A _PONAB,t r B9VH05 B9VH05_ SHEEP,tr D2HXX5 D2HXX5_ AILME,tr D2HXX6 D2HXX6_ TR	gNFn YIEF	87%	38.9	50.71289	Ref	-0.44	0.28	-0.5	0.13	0.24	-0.25	0.078	15000	9050	16200	10600	18100	17000	12700	15800	783.4	1564.8	2	0.0115	7.318

Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1	ML12B_ BOVIN,sp O14950 ML12B_H UMAN,sp P18666 ML12B_R AT,sp P19105 ML12A_HUMAN,sp Q3THE2 ML12B_MOUSE,sp Q5E9E2 MYL9_BOVIN,sp Q5RC34 ML12A_PONAB, tr B9VH05 B9VH05_SHEEP, tr D2HXK5 D2HXK5_AILME, tr D2HXK6 D2HXK6_R	nAFA cFDE EAT GTIQ EDYL	84%	37.7	49.70333	Ref	-0.27	0.22	Value Missing (-3.0083933)	-0.025	0.25	0.32	0.007	212	114	174	Value Missing (-3.0083933)	181	191	210	168	881.7	2642.2	3	0.014	5.302
Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,sp Q4R4M6 HNRPK_MACFA,sp Q5R5H8 HNRPK_PONAB, tr B2M1R6 B2M1R6_MOUSE, tr F6WZ02 F6WZ02_MACMU, tr F6WZ20 F6WZ20_MACMU, tr F7BUQ2 F7BUQ2_MONDO, tr F7BUZ6 F7BUZ6_MONDO, tr F7IK44 F7IK44_CALA, tr Q3TL	dLAG SIIGK	69%	33.9	51.01537	Ref	-0.073	-0.24	-0.16	-0.12	0.12	-0.38	-0.23	33500	32200	31200	36900	41900	43100	31900	35100	494.6	1480.9	3	0.0058	3.895

Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	eNT QTTI	83%	38.5	51.97818	Ref	0.2	-0.26	-0.15	-0.24	-0.11	-0.4	-0.39	23200	23000	18200	22000	22900	21800	18600	18700	771.9	1541.9	2	0.0065	4.184
	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	eNT QTTI	89%	41.3	52.01053	Ref	0.17	-0.27	-0.11	-0.3	-0.09	-0.46	-0.24	8870	8840	7070	8840	8590	8630	7010	8060	771.9	1541.9	2	0.0088	5.674

Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	gGDL MAY DR	85%	35.8	48.69918	Ref	0.12	-0.28	-0.06	-0.28	-0.04	-0.52	-0.17	71400	72900	60100	78400	74100	76600	57000	72100	651.3	1300.6	2	0.0104	7.959
	Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	gSDF DcEL R	95%	46.1	45.12804	Ref	0.09	-0.27	-0.08	-0.24	-0.16	-0.22	-0.29	97800	97700	82300	106000	104000	96300	96300	91200	696.3	1390.6	2	0.0067

Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	gSYG DLG GPIIT TQV	95%	49.8	53.00776	Ref	0.16	-0.56	-0.45	-0.17	-0.05	-0.48	-0.07	748	645	425	512	686	651	504	668	1263	2524.4	2	#####	0.375
	Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	iDEP LEGS EDR	73%	33.9	50.48718	Ref	-0.02	-0.3	-0.05	-0.16	0.054	-0.55	-0.2	32200	29600	26400	35200	36000	36500	25100	31700	782.4	1562.8	2	0.0117

Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	iLSIS ADIE TIGEI	Lk	95%	54.8	50.0843	Ref	0.63	-0.18	-0.46	-0.022	Value Missing (-1.8316)	-0.19	-0.39	162	194	120	111	166	Value Missing (-1.8316469)	134	116	775.1	2322.4	3	0.0067	2.88
	Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	ILIH QSLA GGII	Gvk	87%	34.5	46.60999	Ref	0.026	-0.21	-0.15	-0.33	-0.2	-0.24	-0.23	2710	2340	2160	2530	2450	2350	2380	2390	532.6	2126.3	4	0.0175

Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	ILIH QSLA GGII	95%	60.5	46.36187	Ref	0.22	-0.34	-0.22	-0.13	-0.13	-0.34	-0.11	1720	2130	1570	1910	2250	1960	1760	2060	709.8	2126.3	3	0.0145	6.798
	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	ILIH QSLA GGII	90%	34.9	45.1403	Ref	-0.03	-0.37	-0.15	-0.041	-0.28	-0.12	-0.28	820	700	601	782	932	688	803	714	532.6	2126.3	4	0.0045	2.119

Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	ILIH QSLA GGII	93%	41.2	45.14016	Ref	0.035	-0.49	-0.06	-0.24	-0.23	-0.15	-0.21	715	624	471	713	690	606	674	640	709.8	2126.3	3	0.0038	1.806
	Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	nAG AVIG	77%	33.3	49.01856	Ref	-0.09	-0.29	-0.17	-0.28	-0.09	-0.37	-0.05	24300	19200	18200	22100	22600	22500	19400	24100	669.4	1336.8	2	0.0014

Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	nLPL PPPP	95%	46.9	51.23329	Ref	0.058	-0.26	-0.17	-0.25	-0.3	-0.13	-0.19	15700	14600	12700	15200	15800	13400	15700	15000	749.9	1497.9	2	0.0141	9.426
	Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	nLPL PPPP	83%	37.6	51.2237	Ref	-0.077	-0.27	-0.23	-0.16	-0.29	-0.1	-0.27	26200	20100	19200	22000	25500	20400	24300	21500	750	1497.9	2	0.0118

Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	nTDE MVE LR	87%	38.7	50.56966	Ref	-0.01	-0.41	-0.02	-0.29	-0.2	-0.36	0.027	1E+05	92900	76500	113000	103000	95500	89400	116000	705.9	1409.7	2	0.0093	6.559
	Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	qYA DVE GF	95%	55.9	48.47468	Ref	-0.076	-0.28	-0.34	-0.28	-0.03	-0.09	-0.42	408	299	280	303	348	361	363	286	616.8	1231.6	2	0.01

Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	qYA DVE	95%	56.3	48.2893	Ref	-0.07	Value Missing (-1.3238099)	0.05	-0.32	0.32	-0.24	-0.24	1830	1440	Value Missing (-1.3238099)	1910	1630	2220	1570	1560	616.8	1231.6	2	0.0133	10.78
	0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U,tr F6WZ20 F6WZ20_MAC MU,tr F7BUQ2 F7BUQ2_M ONDO,tr F7BUZ6 F7BUZ6_M ONDO,tr F7IK44 F7IK44_CALJ A,tr Q3TL	qYA DVE	95%	55.2	48.67909	Ref	0.12	-0.45	-0.36	-0.72	-0.07	0.21	-0.06	439	456	334	398	343	469	594	488	616.8	1231.6	2	0.0086	7.015

<p>Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus GN=HNRNPK PE=2 SV=1</p>	<p>0 HNRPK_BOVIN,s p Q4R4M6 HNRPK_MACFA,s p Q5R5H8 HNRPK_PONAB,t r B2M1R6 B2M1R6_MOUSE ,tr F6WZ02 F6WZ02_MACM U, tr F6WZ20 F6WZ20_MAC MU, tr F7BUQ2 F7BUQ2_M ONDO, tr F7BUZ6 F7BUZ6_M ONDO, tr F7IK44 F7IK44_CALJ A, tr Q3TL</p>	<p>tDYN ASVS VPD SSGP ER</p>	<p>95%</p>	<p>66.4</p>	<p>51.41704</p>	<p>Ref</p>	<p>-0.002</p>	<p>-0.28</p>	<p>-0.39</p>	<p>-0.15</p>	<p>0.002</p>	<p>-0.29</p>	<p>-0.25</p>	<p>6650</p>	<p>5610</p>	<p>5020</p>	<p>5240</p>	<p>6820</p>	<p>6590</p>	<p>5640</p>	<p>5730</p>	<p>1043</p>	<p>2084</p>	<p>2</p>	<p>0.0119</p>	<p>5.727</p>
<p>Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3</p>	<p>0 YBOX1_MOUSE,s p P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,s p Q28618 YBOX1_RABIT, tr A2BGG7 A2BGG7_MOUSE, tr A4UTS9 A4UTS9_SHEEP, tr D2HX94 D2HX94_AILME, tr D3ZEV0 D3ZEV0_RAT, tr E2R1A0 E2R1A0_CANFA, tr E</p>	<p>gAEA ANV TGP GGV PVQ GSK</p>	<p>95%</p>	<p>64.3</p>	<p>54.45651</p>	<p>Ref</p>	<p>Value Missing (-0.94642276)</p>	<p>0.31</p>	<p>0.29</p>	<p>0.18</p>	<p>1.1</p>	<p>-0.55</p>	<p>0.67</p>	<p>19100</p>	<p>Value Missing (-0.94642276)</p>	<p>22300</p>	<p>24500</p>	<p>25100</p>	<p>41300</p>	<p>13800</p>	<p>32000</p>	<p>768.8</p>	<p>2303.3</p>	<p>3</p>	<p>0.0195</p>	<p>8.45</p>

Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,sp P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,sp Q28618 YBOX1_RABIT,tr A2BGG7 A2BGG7_MOUSE,tr A4UTS9 A4UTS9_SHEEP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_CANFA,tr E	gAEA ANV TGP GGV PVQ GSK	95%	51.6	54.38155	Ref	Value Missing (-2.9491067)	0.39	0.39	0.37	1.1	-0.81	0.98	2500	Value Missing (-2.9491067)	4170	4680	5100	7620	2060	7030	1153	2303.3	2	0.0149	6.455
Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,sp P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,sp Q28618 YBOX1_RABIT,tr A2BGG7 A2BGG7_MOUSE,tr A4UTS9 A4UTS9_SHEEP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_CANFA,tr E	gAEA ANV TGP GGV PVQ GSK	95%	71.9	54.48881	Ref	-0.029	0.23	-0.09	0.022	0.69	-0.08	0.77	5850	4380	5700	5110	6090	8450	5180	9260	768.8	2303.2	3	0.0211	9.166

Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,sp P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,sp Q28618 YBOX1_RABIT,tr A2BGG7 A2BGG7_MOUSE,tr A4UTS9 A4UTS9_SHEEP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_CANFA,tr E	gAEA AnVT GPG GVP VQG Sk	95%	61.5	54.55586	Ref	0.0033	0.12	0.38	0.31	0.54	-0.25	0.71	9600	8650	10200	13700	14400	14700	8870	17100	769.1	2304.2	3	0.0227	9.844
Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,sp P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,sp Q28618 YBOX1_RABIT,tr A2BGG7 A2BGG7_MOUSE,tr A4UTS9 A4UTS9_SHEEP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_CANFA,tr E	nEGS ESAP EGQ AQQ R	93%	46.3	50.31441	Ref	0.12	0.39	0.052	-0.021	0.52	-0.14	0.41	5770	3830	5010	4450	4660	5930	3910	5690	631.3	1890.9	3	0.0123	6.475

Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,sp P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,sp Q28618 YBOX1_RABIT,tr A2BGG7 A2BGG7_MOUSE,tr A44UTS9 A4UTS9_SHEEP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_CANFA,tr E	nEGS ESAP EGQ AQQ R	95%	52.1	50.30373	Ref	-0.64	0.26	0.39	0.17	0.7	-0.41	0.73	4610	2120	4310	5270	4980	6310	3040	6660	946.5	1890.9	2	0.0118	6.25
Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,sp P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,sp Q28618 YBOX1_RABIT,tr A2BGG7 A2BGG7_MOUSE,tr A44UTS9 A4UTS9_SHEEP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_CANFA,tr E	nYQ QNY QNS ESGE kNE GSES APE GQA QQR	71%	34.2	52.76211	Ref	Value Missing (-0.9304516)	0.018	0.39	0.11	0.65	-0.52	1.2	6626	650	946	857	1090	505	1690	967.2	3864.8	4	0.0258	6.668	

Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,sp P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,sp Q28618 YBOX1_RABIT,tr A2BGG7 A2BGG7_MOUSE,tr A44UTS9 A4EP,tr D2HX94 D2HX94_AILM E,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_C ANFA,tr E	nYQ QNY QnSE SGEK NEG SESA PEG QAQ QR	73%	34.4	52.17479	Ref	-0.41	0.28	0.18	0.36	0.81	-0.75	0.79	1060	653	1150	1200	1490	1790	632	1820	967.4	3865.8	4	0.0289	7.486
Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,sp P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,sp Q28618 YBOX1_RABIT,tr A2BGG7 A2BGG7_MOUSE,tr A44UTS9 A4EP,tr D2HX94 D2HX94_AILM E,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_C ANFA,tr E	rPQY SNPP VqG EVM EGA DNQ GAG EQG R	95%	52.5	53.16285	Ref	(0.42246917)	(0.30477577)	(0.13818116)	(0.0022981418)	(0.19357438)	(0.130807614789)	Reference Missing (0.52907921)	No Values (0.22007921)	No Values (0.422469477577)	No Values (0.30477578116)	No Values (0.1381418)	No Values (0.002298357438)	No Values (0.130807619)	Reference Missing (0.529478)	1060	3175.5	3	0.0036	1.126	

Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,sp P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,sp Q28618 YBOX1_RABIT,tr A2BGG7 A2BGG7_MOUSE,tr A44UTS9 A4EP,tr D2HX94 D2HX94_AILM, E, tr D3ZEV0 D3ZEV0_RAT, tr E2R1A0 E2R1A0_C2R1A0_C ANFA, tr E	rPQY SNPP VQG EVM EGA DnQ GAG EQG	84%	41.5	53.3309	Ref	No Values (0.4749647)	No Values (0.3572713)	No Values (0.19067651)	No Values (0.0501974)	No Values (0.2406977)	No Values (0.18317717)	No Values (0.1945747)	Values (0.2725747)	No Values (0.4749647)	No Values (0.3572713)	No Values (0.19067651)	No Values (0.0501974)	No Values (0.2406977)	No Values (0.18330327)	No Values (0.19417717)	1060	3175.5	3	0.0012	0.366
	0 YBOX1_MOUSE,sp P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,sp Q28618 YBOX1_RABIT,tr A2BGG7 A2BGG7_MOUSE,tr A44UTS9 A4EP,tr D2HX94 D2HX94_AILM, E, tr D3ZEV0 D3ZEV0_RAT, tr E2R1A0 E2R1A0_C2R1A0_C ANFA, tr E	rPQY SNPP VQG EVM EGA DnQ GAG EQG RPV	68%	35.7	54.96185	Ref	No Values (0.2878737)	No Values (0.17018013)	No Values (0.003585335)	Reference Missing (0.27372235)	No Values (0.05897882)	Reference Missing (0.89778798)	No Values (0.0859959)	No Values (0.287873483647)	No Values (0.17018013)	No Values (0.003585335)	Reference Missing (0.27372226)	No Values (0.05897882)	No Values (0.00379959)	Reference Missing (0.8979959)	882.7	3526.7	4	0.0192	5.432	

<p>Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3</p>	<p>0 YBOX1_MOUSE,sp P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,sp Q28618 YBOX1_RABIT,tr A2BGG7 A2BGG7_MOUSE,tr A44UTS9 A4UTS9_SHEP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_CANFA,tr E</p>	<p>rPQy SNPP VQG EVM EGA DNQ GAG EQG RPV R</p>	<p>57%</p>	<p>30.8</p>	<p>55.67691</p>	<p>Ref</p>	<p>0.14</p>	<p>0.13</p>	<p>0.28</p>	<p>0.19</p>	<p>0.56</p>	<p>0.066</p>	<p>0.52</p>	<p>2070</p>	<p>1960</p>	<p>2110</p>	<p>2620</p>	<p>2730</p>	<p>3080</p>	<p>2280</p>	<p>3100</p>	<p>767.2</p>	<p>3830.9</p>	<p>5</p>	<p>0.0433</p>	<p>11.3</p>		
<p>Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3</p>	<p>0 YBOX1_MOUSE,sp P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,sp Q28618 YBOX1_RABIT,tr A2BGG7 A2BGG7_MOUSE,tr A44UTS9 A4UTS9_SHEP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_CANFA,tr E</p>	<p>rPQY SNPP VQG EVM EGA DNQ GAG EQG RPV R</p>	<p>64%</p>	<p>34.9</p>	<p>54.93355</p>	<p>Ref</p>	<p>0.0947</p>	<p>0.21</p>	<p>0.086</p>	<p>0.190</p>	<p>0.446</p>	<p>0.582</p>	<p>0.8369</p>	<p>49204</p>	<p>38708</p>	<p>35522</p>	<p>35522</p>	<p>0.0860</p>	<p>0.190789</p>	<p>63870</p>	<p>63870</p>	<p>0.582</p>	<p>0.838492</p>	<p>882.9</p>	<p>3527.7</p>	<p>4</p>	<p>0.0057</p>	<p>1.625</p>

Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,s p P62961 YBOX1_R AT,sp P67808 YBOX1_BOVIN, sp P67809 YBOX1_HUMAN,s p Q28618 YBOX1_R ABIT,tr A2BGG7 A2BGG7_MOUSE,tr A44UTS9 A4UTS9_SHE EP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_C ANFA,tr E	SVG DGE TVEF DVV EG EK	95%	50.5	54.10469	Ref	-0.74	0.23	0.28	0.22	0.86	-0.44	0.92	2280	1280	2720	3150	3340	4520	1920	4910	1203	2403.2	2	0.0212	8.822
Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,s p P62961 YBOX1_R AT,sp P67808 YBOX1_BOVIN, sp P67809 YBOX1_HUMAN,s p Q28618 YBOX1_R ABIT,tr A2BGG7 A2BGG7_MOUSE,tr A44UTS9 A4UTS9_SHE EP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_C ANFA,tr E	SVG DGE TVEF DVV EG EK	83%	41.6	54.12408	Ref	-0.29	0.34	0.045	0.22	0.96	-0.14	0.5	5210	3800	6390	5840	7250	10600	5180	7980	802.1	2403.2	3	0.0204	8.475

Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,s p P62961 YBOX1_R AT,sp P67808 YBOX1_BOVIN, sp P67809 YBOX1_HUMAN,s p Q28618 YBOX1_R ABIT,tr A2BGG7 A2BGG7_MOUSE,tr A4UTS9 A4UTS9_SHEP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_C ANFA,tr E	SVG DGE TVEF DVV EGEK	73%	38.2	54.12506	Ref	-0.29	0.3	0.34	0.28	0.67	-0.5	0.97	44700	43300	71000	81600	86700	99200	45900	126000	802.1	2403.2	3	0.0197	8.176
Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,s p P62961 YBOX1_R AT,sp P67808 YBOX1_BOVIN, sp P67809 YBOX1_HUMAN,s p Q28618 YBOX1_R ABIT,tr A2BGG7 A2BGG7_MOUSE,tr A4UTS9 A4UTS9_SHEP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_C ANFA,tr E	SVG DGE TVEF DVV EGEK	91%	47.4	54.0917	Ref	-0.087	0.4	0.32	0.37	0.43	0.26	0.24	2890	2380	3620	3830	4370	3990	3710	3640	802.1	2403.2	3	0.0226	9.386

Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,s p P62961 YBOX1_R AT,sp P67808 YBOX1_BOVIN, sp P67809 YBOX1_HUMAN,s p Q28618 YBOX1_R ABIT,tr A2BGG7 A2BGG7_MOUSE,tr A4UTS9 A4UTS9_SHE EP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_C ANFA,tr E	SVG DGE TVEF DVV EG EK	81%	40.8	54.19119	Ref	0.15	0.21	-0.03	0.13	0.45	0.19	0.74	743	716	812	772	949	1030	902	1310	802.1	2403.2	3	0.0162	6.728
Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,s p P62961 YBOX1_R AT,sp P67808 YBOX1_BOVIN, sp P67809 YBOX1_HUMAN,s p Q28618 YBOX1_R ABIT,tr A2BGG7 A2BGG7_MOUSE,tr A4UTS9 A4UTS9_SHE EP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_C ANFA,tr E	SVG DGE TVEF DVV EG EK	76%	39.1	54.30971	Ref	-0.34	0.22	0.29	0.18	0.44	0.18	0.73	406	262	421	494	504	529	462	670	802.1	2403.2	3	0.0109	4.52

Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	0 YBOX1_MOUSE,sp P62961 YBOX1_RAT,sp P67808 YBOX1_BOVIN,sp P67809 YBOX1_HUMAN,sp Q28618 YBOX1_RABIT,tr A2BGG7 A2BGG7_MOUSE,tr A44UTS9 A44UTS9_SHEEP,tr D2HX94 D2HX94_AILME,tr D3ZEV0 D3ZEV0_RAT,tr E2R1A0 E2R1A0_CANFA,tr E	SVG DGE TVEF DVV EGEK	95%	55.7	54.07326	Ref	No Values (-2.7551253)	Reference Missing (0.5045076)	Reference Missing (0.991224)	Reference Missing (0.881822)	Reference Missing (1.209106)	No Values (-3.046787)	Reference Missing (0.64344174)	No Values (-2.9575152)	No Values (-2.7551253)	Reference Missing (0.5045076)	Reference Missing (0.99124)	Reference Missing (0.881822)	No Values (-3.046787)	Reference Missing (0.64344174)	802.1	2403.2	3	0.0227	9.461	
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8 F1SEV8_PIG	aTNF LVHE	80%	37.5	52.04454	Ref	0.41	-0.31	0.083	-0.17	0.091	-0.55	-0.13	1E+05	125000	82300	121000	112000	1E+05	78400	105000	702.9	1403.8	2	0.0111	7.893
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8 F1SEV8_PIG	aTnF LVHE	77%	36	51.68321	Ref	0.12	-0.16	0.036	-0.11	0.033	-0.1	-0.01	14200	15400	13700	17700	17700	17000	16300	17200	703.4	1404.7	2	0.0128	9.103
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=1 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8 F1SEV8_PIG	gVV QDL QQA VSK	95%	87.7	52.18165	Ref	0.027	-0.29	0.1	-0.11	0.21	-0.31	-0.05	9840	8730	7600	11200	10700	11600	8450	10000	940.5	1879.1	2	0.0144	7.649

Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8_PIG	iASL EVE NQS LR	95%	48.1	53.09268	Ref	-0.036	-0.29	0.15	-0.089	0.13	-0.42	-0.03	8710	6760	6160	9350	8740	8860	6320	8270	832	1661.9	2	0.0157	9.453
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8_PIG	iASL EVE NQS LR	95%	49.7	52.9414	Ref	-0.014	-0.22	0.068	-0.061	0.17	-0.4	0.049	25200	22100	20800	28400	28700	29400	20600	28000	832	1661.9	2	0.0119	7.179
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8_PIG	iASL EVE NQS LR	95%	60.9	52.94078	Ref	-0.035	-0.2	0.057	-0.069	-0.04	-0.48	0.11	18700	13900	13500	18100	18200	16200	12600	18700	555	1661.9	3	0.0099	5.968
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8_PIG	iASL EVE NQS LR	90%	43.1	52.85931	Ref	0.069	-0.27	0.098	-0.16	0.081	-0.59	0.16	4240	3610	3100	4480	4130	4260	2800	4670	832	1661.9	2	0.0045	2.705
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8_PIG	iASL EVE NQS LR	95%	47.6	52.97944	Ref	0.1	-0.2	0.017	-0.2	0.099	-0.27	0.034	5330	4960	4380	5700	5410	5810	4710	5760	832	1661.9	2	0.0105	6.302
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8_PIG	kFYE QMn GPV AGSS R	95%	55.1	54.31509	Ref	-0.086	-0.06	0.13	0.059	0.022	-0.42	-0.02	14200	12100	13300	17100	17900	15200	11700	15400	760.7	2279.2	3	0.0194	8.513

Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8_PIG	kFYE QMn GPV AGSS R	94%	50.9	54.33714	Ref	-0.13	-0.2	0.13	-0.043	-0.02	0.045	-0.05	11000	9540	9800	13900	13600	12000	13100	12200	760.7	2279.2	3	0.0168	7.382
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8_PIG	kFYE QMn GPV AGSS R	89%	45.7	54.3028	Ref	-0.16	-0.12	-0	-0.028	-0.04	0.005	0.072	5330	4470	4980	6070	6570	5700	6130	6370	760.7	2279.2	3	0.0198	8.671
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8_PIG	kFYE QMn GPV AGSS R	95%	56.6	54.31759	Ref	-0.11	-0.21	-0	-0.083	0.15	-0.16	0.12	6680	5770	5840	7570	7900	8130	6850	8230	760.7	2279.2	3	0.0183	8.026
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8_PIG	kFYE QMn GPV AGSS R	93%	50.2	54.41391	Ref	-0.028	-0.1	-0.01	-0.081	0.25	-0.2	0.016	5160	5270	5430	6500	6820	7490	5740	6600	760.7	2279.2	3	0.0139	6.092
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8_PIG	kFYE QMn GPV AGSS R	72%	38.1	54.41391	Ref	-0.093	-0.25	0.012	0.023	0.083	-0.04	0.069	5850	5500	5350	7200	8000	7280	7010	7470	760.7	2279.2	3	0.0139	6.092
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_SHEEP,tr F1SEV8_PIG	kFYE Qm n GPV AGSS R	82%	41.2	54.08566	Ref	-0.17	-0.37	0.17	0.022	0.2	-0.49	0.12	8020	6190	5860	9590	9510	9390	6100	9240	766.1	2295.2	3	0.0147	6.395

Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_S HEEP,tr F1SEV8_PIG	kPAL VAK	84%	26.4	38.37525	Ref	-0.12	-0.05	0.025	-0.16	0.19	-0.42	-0.11	49300	34600	39500	46700	45500	50500	34500	42500	547	1638.1	3	0.0076	4.618
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_S HEEP,tr F1SEV8_PIG	kPAL VAK	52%	20.7	40.93702	Ref	-0.25	-0.2	0.11	-0.14	0.33	-0.49	0.02	1E+06	725000	8E+05	1E+06	1050000	1E+06	8E+05	1060000	547	1638.1	3	0.0189	11.54
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_S HEEP,tr F1SEV8_PIG	kPAL VAK	69%	21.3	38.35183	Ref	-0.3	-0.25	0.084	-0.12	0.27	-0.28	0.076	33500	22900	25800	36300	34800	39700	28400	36000	547	1638.1	3	0.0063	3.831
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_S HEEP,tr F1SEV8_PIG	kPAL VAK	87%	28.1	38.3512	Ref	-0.24	-0.06	-0.05	-0.076	0.25	-0.29	-0.01	30500	21500	26500	29900	32300	35300	25400	30500	547	1638.1	3	0.0059	3.611
Elongation factor 1-delta OS=Ovis aries GN=EEF1D PE=2 SV=1	sp Q717R8 EF1D_S HEEP,tr F1SEV8_PIG	qEnG ASVI LR	75%	36.1	52.22326	Ref	-0.002	-0.21	0.009	-0.084	0.14	-0.39	0.026	1E+05	98200	92100	121000	125000	1E+05	92100	122000	696.4	1390.8	2	0.0088	6.295
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	fMET ATES LAK	86%	42.6	53.53012	Ref	0.61	0.15	0.38	0.28	-0.03	0.66	0.19	3350	3700	2920	3820	3950	2780	4680	3350	612.7	1835	3	0.0191	10.4
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	fMET ATES LAK	92%	45	53.5107	Ref	0.33	0.36	0.42	0.38	-0.11	0.79	0.31	3860	4230	4700	5480	5880	3670	7130	5070	918.5	1835	2	0.0141	7.699

Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	fMETATES LAK	95%	62.7	53.49064	Ref	0.56	0.044	0.46	0.32	0.031	0.85	0.21	5640	7680	5810	8730	8730	6220	11500	7300	918.5	1835	2	0.0132	7.165
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	fMETATES LAK	81%	40	53.51118	Ref	0.41	0.006	0.47	0.45	-0.14	0.8	0.29	23300	24800	20300	31500	34200	19800	39700	27700	612.7	1835	3	0.0123	6.706
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	fMETATES LAK	92%	47.7	53.51118	Ref	0.54	0.061	0.44	0.53	-0.21	0.82	0.38	4050	6110	4750	6930	8110	4240	9040	6650	612.7	1835	3	0.0123	6.706
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	gSVQYLP DWDk	70%	36.8	53.52032	Ref	0.59	0.23	0.47	0.32	-0.01	0.72	-0.03	32600	37300	31500	41700	41400	28900	49900	29500	639.3	1915	3	0.0171	8.946
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	gSVQYLP DWDk	81%	39.3	53.51812	Ref	0.38	0.16	0.32	0.47	0.15	0.82	0.24	2900	3410	3170	3990	4880	3410	5660	3770	958.5	1915	2	0.0169	8.839
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	gSVQYLP DWDk	89%	43.1	53.55724	Ref	0.44	0.23	0.45	0.48	0.043	0.79	0.044	6480	7880	7370	9650	10900	7000	12300	7260	958.5	1915	2	0.0144	7.503
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	gSVQYLP DWDk	94%	47.4	53.56647	Ref	0.51	0.15	0.43	0.42	-0.03	0.68	0.22	5610	6410	5420	7380	8040	5160	8800	6350	958.5	1915	2	0.0141	7.377
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	sAecPGP AQk	86%	39.7	52.03952	Ref	0.33	0.28	0.56	0.38	0.008	0.78	0.23	16800	20100	21100	28700	28000	18900	33700	22800	821.4	1640.8	2	0.0152	9.282
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	sAecPGP AQk	83%	39.7	52.07834	Ref	0.46	-0.11	0.48	0.47	0.082	0.75	0.37	1E+05	168000	1E+05	207000	226000	2E+05	3E+05	191000	548	1640.8	3	0.0136	8.311

Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	sAec PGP Aqk	81%	37.5	51.92907	Ref	0.39	0.24	0.43	0.37	0.21	0.68	0.22	7810	8650	8450	10800	11500	8970	13000	9330	821.4	1640.8	2	0.02	12.18
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	vVVL PFPS k	90%	39.2	49.28677	Ref	0.38	0.21	0.52	0.42	0.088	0.74	0.14	16000	18000	17300	24200	24800	17200	28300	18600	797.5	1593	2	0.0254	15.91
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	vVVL PFPS k	95%	47.2	48.41404	Ref	0.37	0.053	0.58	0.42	0.15	0.88	0.16	20300	27400	23800	38500	38000	27500	47900	28700	532	1593	3	0.0127	7.951
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	vVVL PFPS k	85%	36.8	48.19636	Ref	0.25	0.27	0.57	0.29	-0.25	0.98	0.13	22600	22100	24300	33500	30500	18400	44800	24700	532	1593	3	0.0101	6.352
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	vVVL PFPS k	57%	25.7	47.04803	Ref	0.23	0.019	0.71	0.28	0.17	0.55	0.23	753	613	572	1040	850	686	931	740	399.3	1593	4	0.0052	3.281
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	vVVL PFPS k	92%	39.4	48.14873	Ref	0.47	0.34	0.43	0.51	0.1	0.67	0.12	5960	8080	7990	9600	11200	7350	11300	7730	797.5	1593	2	0.0086	5.419
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	vVVL PFPS k	83%	34.6	47.19961	Ref	0.29	0.23	0.46	0.41	0.056	0.63	0.32	1670	1570	1640	2150	2290	1560	2430	1950	532	1593	3	#####	0.254
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	vVVL PFPS k	68%	29.9	47.21266	Ref	0.36	0.21	0.38	0.39	0.077	0.54	0.36	1980	1820	1770	2240	2480	1740	2510	2190	532	1593	3	0.0045	2.833
Fetuin-B OS=Bos taurus GN=FETUB PE=2 SV=1	sp Q58D62 FETUB_BOVIN	yNSE SPSk	66%	34	52.14298	Ref	0.45	0.18	0.5	0.42	-0.15	0.92	0.2	4310	5890	5290	7460	7730	4550	10000	6020	760.4	1518.8	2	0.0058	3.834

40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	aLAA Flk	69%	28.3	45.38712	Ref	-0.19	-0.07	0.48	0.088	0.35	-0.37	0.71	3970	3130	3690	6080	5090	5330	3370	7090	448	1340.9	3	0.0038	2.821
40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	aLAA Flk	70%	28.5	45.38712	Ref	-0.63	-0.03	0.25	0.24	0.47	-0	0.69	3880	2280	3750	5080	5600	5700	4300	6880	448	1340.9	3	0.0031	2.329

40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	aLAA Flk	55%	28.5	48.23285	Ref	-0.57	-0.03	0.28	0.27	0.42	-0.23	0.76	17400	10300	16200	22700	24700	23900	16000	31400	448	1340.8	3	0.0224	16.73
40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	aLAA Flk	70%	28.6	45.40329	Ref	-0.47	-0.04	0.36	0.16	0.53	-0.34	0.74	15600	10400	15200	22400	21600	24200	13900	29200	448	1340.9	3	0.0059	4.386

40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE, tr B0ZBD0 B0ZBD0_HUMAN, tr B7SBG1 B7SBG1_AILME, tr D4A6G6 D4A6G6_RAT, tr F1P680 F1P680_CANFA, tr F1RGG1 F1RGG1_PIG, tr F6YV	aLAA Flk	89%	34.9	45.39578	Ref	-0.34	-0.03	0.41	0.27	0.5	-0.17	0.36	23200	15000	20100	30700	30700	31400	20600	29600	671.4	1340.9	2	0.005	3.711
40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE, tr B0ZBD0 B0ZBD0_HUMAN, tr B7SBG1 B7SBG1_AILME, tr D4A6G6 D4A6G6_RAT, tr F1P680 F1P680_CANFA, tr F1RGG1 F1RGG1_PIG, tr F6YV	gGA GVG SMT k	93%	44.5	52.04524	Ref	-0.21	0.19	0.32	0.23	0.42	-0.13	0.34	20300	15100	21600	26500	27400	27400	19500	26800	736.9	1471.8	2	0.0241	16.39

40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	gGA GVG SMT k	83%	39.5	52.09236	Ref	0.099	0.26	0.36	0.039	0.43	-0.27	0.19	58800	51700	62500	75300	66500	76000	48900	67000	491.6	1471.8	3	0.0083	5.629
40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	gGA GVG SMT k	95%	48	52.06853	Ref	-0.33	0.12	0.4	0.25	0.49	-0.13	0.31	9610	6640	9860	13400	13300	13700	9330	12600	736.9	1471.8	2	0.0055	3.71

40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	hkEL APY DEN WFY TR	95%	53.5	54.83075	Ref	-0.22	0.14	0.16	0.21	0.44	-0.08	0.5	10900	8130	11300	12900	14700	15100	11000	16300	645.1	2576.3	4	0.015	5.823
40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	iAGQ VAA ANK	95%	66.8	50.51731	Ref	-0.34	-0.02	0.41	0.12	0.44	0.032	0.33	17200	10500	14200	21500	19400	21100	16600	20300	776	1549.9	2	0.0147	9.509

40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	iAGQ VAA ANK	94%	47.3	50.55562	Ref	0.03	0.41	0.27	0.15	0.13	0.093	0.23	80000	74700	1E+05	107000	109000	93700	95600	104000	517.6	1549.9	3	0.0161	10.38
40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	iAGQ VAA ANK	95%	65	50.1728	Ref	-0.29	0.16	0.31	0.1	0.43	-0.02	0.41	8370	5780	8560	10700	10200	11200	8550	11400	776	1549.9	2	0.0077	4.944

40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	rVLQ ALEG Lk	69%	30.5	47.51756	Ref	-0.14	0.028	0.29	0.26	0.46	-0.1	0.43	1780	1490	1810	2440	2620	2630	1860	2670	579	1734.1	3	0.012	6.921
40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	rVLQ ALEG Lk	51%	25	47.21531	Ref	-0.5	0.15	0.43	0.27	0.49	-0.07	0.33	5670	3640	6210	8460	8330	8480	5990	7870	434.5	1734.1	4	0.0087	4.999

40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE, tr B0ZBD0 B0ZBD0_HUMAN, tr B7SBG1 B7SBG1_AILM E, tr D4A6G6 D4A6G6_RAT, tr F1P680 F1P680_C ANFA, tr F1RGG1 F1RGG1_PIG, tr F6YV	rVLQ ALEGLk	60%	28.6	47.60121	Ref	-0.036	-0.03	0.12	0.17	0.75	-0.14	0.24	363	304	332	412	471	615	347	446	579	1734.1	3	0.0148	8.511
40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE, tr B0ZBD0 B0ZBD0_HUMAN, tr B7SBG1 B7SBG1_AILM E, tr D4A6G6 D4A6G6_RAT, tr F1P680 F1P680_C ANFA, tr F1RGG1 F1RGG1_PIG, tr F6YV	vLQA LEGLk	92%	40.3	49.00689	Ref	-0.13	0.13	0.37	0.18	0.27	-0	0.18	2900	1940	2520	3360	3230	3020	2600	2930	790	1578	2	0.0134	8.491

40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	k	91%	42.4	48.6828	Ref	-0.12	-0.01	0.36	0.1	0.21	0.33	0.23	1610	1170	1370	1980	1830	1720	1960	1810	527	1578	3	0.0095	5.987
40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_R AT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	k	59%	29.3	48.31761	Ref	0.31	-0.5	0.3	0.11	0.46	0.19	0.35	282	339	209	409	395	438	381	423	527	1578	3	0.0049	3.08

40S ribosomal protein S19 OS=Rattus norvegicus GN=Rps19 PE=2 SV=3	4 RS19_RAT,sp P39019 RS19_HUMAN,sp Q32PD5 RS19_BOVIN,sp Q5R8M9 RS19_PONAB,sp Q9CZX8 RS19_MOUSE,tr B0ZBD0 B0ZBD0_HUMAN,tr B7SBG1 B7SBG1_AILME,tr D4A6G6 D4A6G6_RAT,tr F1P680 F1P680_CANFA,tr F1RGG1 F1RGG1_PIG,tr F6YV	VPE WVD TVk	95%	52.6	52.75763	Ref	-0.27	0.13	0.34	0.13	0.42	-0.13	0.34	16400	10400	14800	19300	18400	19600	14000	19200	841	1680	2	0.0103	6.157
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1	2 ROA2_RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,tr B7ZP22 B7ZP22_MOUSE,tr D2GVC7 D2GVC7_AILME,tr E2QXD3 E2QXD3_CANFA,tr F1LM82 F1LM82_RAT,tr F	eDTE EHHL R	62%	30.6	49.49209	Ref	0.48	-0.14	-0.4	-0.36	-0.01	-0.58	-0.14	2910	3070	2160	2040	2310	2570	1800	2430	735.4	1468.7	2	0.0129	8.789

Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1	2 ROA2_RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,tr B7ZP22 B7ZP22_MOUSE,SE,tr D2GVC7 D2GVC7_AILME,tr E2QXD3 E2QXD3_CANFA,tr E2QXF7 E2QXF7_CANFA,tr F1LM82 F1LM82_RAT,tr F	eDTE EHHL	93%	42.4	49.68996	Ref	0.77	0.23	2623)	-0.23	692)	-0.24	0.026	9740	11800	8860	623)	7960	8692)	7210	8600	368.2	1468.7	4	0.0096	6.565
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1	2 ROA2_RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,tr B7ZP22 B7ZP22_MOUSE,SE,tr D2GVC7 D2GVC7_AILME,tr E2QXD3 E2QXD3_CANFA,tr E2QXF7 E2QXF7_CANFA,tr F1LM82 F1LM82_RAT,tr F	gFGF VTFD DHD PVDK	95%	56.1	53.77512	Ref	0.4	-0.05	-0.38	-0.2	-0.08	-0.23	-0.25	12200	14200	11300	9990	12500	11900	11200	11000	768.7	2303.1	3	0.0226	9.818

<p>Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1</p>	<p>2 ROA2_RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,transcript B7ZP22 B7ZP22_MOUSE,transcript D2GVC7 D2GVC7_AILME,transcript E2QXD3 E2QXD3_CANFA,transcript E2QXF7 E2QXF7_CANFA,transcript F1LM82 F1LM82_RAT,transcript F</p>	<p>gFGF VTFD DHD PVDk</p>	95%	61.5	53.87883	Ref	0.16	0.073	-0.3	-0.34	-0.14	-0.19	-0.03	7390	7040	7170	6230	6670	6690	6730	7450	768.7	2303.1	3	0.0194	8.398
<p>Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1</p>	<p>2 ROA2_RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,transcript B7ZP22 B7ZP22_MOUSE,transcript D2GVC7 D2GVC7_AILME,transcript E2QXD3 E2QXD3_CANFA,transcript E2QXF7 E2QXF7_CANFA,transcript F1LM82 F1LM82_RAT,transcript F</p>	<p>gGG GNF GPG PGS NFR</p>	64%	32.3	50.81297	Ref	0.0002	-0.05	-0.19	-0.23	0.076	-0.23	-0.03	8300	7400	7760	7920	8470	9140	7740	8810	841.4	1680.8	2	0.014	8.337

Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1	2 ROA2_ RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,tr B7ZP22 B7ZP22_MOUSE,tr D2GVC7 D2GVC7_AILME,tr E2QXD3 E2QXD3_CANFA,tr E2QXF7 E2QXF7_CANFA,tr F1LM82 F1LM82_RAT,tr F	gGN FGF GDS R	91%	39.5	48.59222	Ref	0.18	0.045	-0.37	-0.23	-0.12	-0.2	-0.08	19100	18100	17900	15100	18300	17200	17100	18400	659.3	1316.6	2	0.0121	9.157
			95%	75.7	54.07671	Ref	0.38	-0.18	-0.46	-0.27	0.012	-0.18	-0.14	6810	7550	5530	5110	6420	6830	6260	6360	845.8	2534.4	3	0.0175	6.904

Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1	2 ROA2_RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,tr B7ZP22 B7ZP22_MOUSE,SE,tr D2GVC7 D2GVC7_AILME,tr E2QXD3 E2QXD3_CANFA,tr E2QXF7 E2QXF7_CANFA,tr F1LM82 F1LM82_RAT,tr F	KLFI GGLS FETT EESL	95%	62	54.01361	Ref	0.27	-0.06	-0.26	-0.31	0.11	-0.22	-0.1	486	585	505	492	525	611	510	550	845.8	2534.4	3	0.0142	5.602
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1	2 ROA2_RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,tr B7ZP22 B7ZP22_MOUSE,SE,tr D2GVC7 D2GVC7_AILME,tr E2QXD3 E2QXD3_CANFA,tr E2QXF7 E2QXF7_CANFA,tr F1LM82 F1LM82_RAT,tr F	KLFI GGLS FETT EESL	95%	64.5	54.01361	Ref	0.26	-0.23	-0.29	-0.23	0.005	-0.08	-0.03	595	680	525	564	648	667	658	673	845.8	2534.4	3	0.0142	5.602

Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1	2 ROA2_RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,tr B7ZP22 B7ZP22_MOUSE,SE,tr D2GVC7 D2GVC7_AILME,tr E2QXD3 E2QXD3_CANFA,tr E2QXF7 E2QXF7_CANFA,tr F1LM82 F1LM82_RAT,tr F	KLF1 GGLS FETT EESL	95%	64.6	53.95838	Ref	0.12	-0.06	-0.07	-0.11	-0.26	-0.19	-0.21	1100	974	934	1040	1120	876	963	941	845.8	2534.4	3	0.0107	4.23
	2 ROA2_RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,tr B7ZP22 B7ZP22_MOUSE,SE,tr D2GVC7 D2GVC7_AILME,tr E2QXD3 E2QXD3_CANFA,tr E2QXF7 E2QXF7_CANFA,tr F1LM82 F1LM82_RAT,tr F	KLFV GGIK EDTE EHHL	94%	45.1	53.01317	Ref	0.3	-0.14	-0.53	-0.22	-0.04	-0.01	-0.13	30500	32900	26400	22500	30800	30400	32400	29500	584.9	2919.6	5	0.0216	7.385

Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1	2 ROA2_																																												
	RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,tr B7ZP22 B7ZP22_MOUSE,SE,tr D2GVC7 D2GVC7_AILME,tr E2QXD3 E2QXD3_CANFA,tr E2QXF7 E2QXF7_CANFA,tr F1LM82 F1LM82_RAT,tr F	IFIG GLSF ETTE ESLR	79%	39.9	54.06739	Ref	0.15	-0.4	0.021	-0.082	-0.16	-0.31	0.16	3100	3250	2410	3620	3710	3070	2880	3980	701.7	2102.1		3	0.0169	8.055																		
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1	2 ROA2_																																												
	RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,tr B7ZP22 B7ZP22_MOUSE,SE,tr D2GVC7 D2GVC7_AILME,tr E2QXD3 E2QXD3_CANFA,tr E2QXF7 E2QXF7_CANFA,tr F1LM82 F1LM82_RAT,tr F	IFVG Gik	68%	27.6	45.00676	Ref	0.45	-0.13	-0.4	-0.41	-0.14	-0.4	-0.26	13600	12600	9140	8500	9310	9830	8550	9360	448	1340.9		3	0.0027	2.018																		

<p>Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1</p>	<p>2 ROA2_RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,transcript B7ZP22 B7ZP22_MOUSE,transcript D2GVC7 D2GVC7_AILME,transcript E2QXD3 E2QXD3_CANFA,transcript E2QXF7 E2QXF7_CANFA,transcript F1LM82 F1LM82_RAT,transcript F</p>	<p>nYYE QW Gk</p>	<p>54%</p>	<p>32.4</p>	<p>52.53088</p>	<p>Ref</p>	<p>0.26</p>	<p>-0.04</p>	<p>-0.39</p>	<p>-0.29</p>	<p>0.058</p>	<p>-0.23</p>	<p>-0.1</p>	<p>6680</p>	<p>7010</p>	<p>6200</p>	<p>5440</p>	<p>6440</p>	<p>7150</p>	<p>6100</p>	<p>6630</p>	<p>848.4</p>	<p>1694.9</p>	<p>2</p>	<p>0.0202</p>	<p>11.93</p>
<p>Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1</p>	<p>2 ROA2_RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,transcript B7ZP22 B7ZP22_MOUSE,transcript D2GVC7 D2GVC7_AILME,transcript E2QXD3 E2QXD3_CANFA,transcript E2QXF7 E2QXF7_CANFA,transcript F1LM82 F1LM82_RAT,transcript F</p>	<p>qEM QEV QSSR</p>	<p>79%</p>	<p>34.9</p>	<p>50.06411</p>	<p>Ref</p>	<p>0.24</p>	<p>-0.09</p>	<p>-0.51</p>	<p>-0.044</p>	<p>0.001</p>	<p>-0.31</p>	<p>-0.07</p>	<p>4510</p>	<p>4640</p>	<p>3980</p>	<p>3350</p>	<p>5090</p>	<p>4590</p>	<p>3870</p>	<p>4540</p>	<p>763.4</p>	<p>1524.7</p>	<p>2</p>	<p>0.0112</p>	<p>7.34</p>

<p>Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1</p>	<p>2 ROA2_RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,tr B7ZP22 B7ZP22_MOUSE,SE,tr D2GVC7 D2GVC7_AILME,tr E2QXD3 E2QXD3_CANFA,tr E2QXF7 E2QXF7_CANFA,tr F1LM82 F1LM82_RAT,tr F</p>	<p>yHTInGHNAEVR</p>	<p>95%</p>	<p>50.4</p>	<p>51.96179</p>	<p>Ref</p>	<p>0.091</p>	<p>-0.25</p>	<p>-0.41</p>	<p>-0.032</p>	<p>0.002</p>	<p>-0.05</p>	<p>-0.06</p>	<p>2710</p>	<p>2510</p>	<p>2150</p>	<p>2170</p>	<p>3100</p>	<p>2770</p>	<p>2800</p>	<p>2740</p>	<p>858.4</p>	<p>1714.9</p>	<p>2</p>	<p>0.0106</p>	<p>6.17</p>
<p>Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Rattus norvegicus GN=Hnrnpa2b1 PE=1 SV=1</p>	<p>2 ROA2_RAT,sp O88569 ROA2_MOUSE,sp P22626 ROA2_HUMAN,sp Q2HJ60 ROA2_BOVIN,sp Q9TTV2 ROA2_SAGOE,tr B7ZP22 B7ZP22_MOUSE,SE,tr D2GVC7 D2GVC7_AILME,tr E2QXD3 E2QXD3_CANFA,tr E2QXF7 E2QXF7_CANFA,tr F1LM82 F1LM82_RAT,tr F</p>	<p>yHTInGHNAEVR</p>	<p>85%</p>	<p>40.4</p>	<p>53.94537</p>	<p>Ref</p>	<p>0.08</p>	<p>-0.13</p>	<p>-0.35</p>	<p>-0.18</p>	<p>0.013</p>	<p>-0.06</p>	<p>-0.06</p>	<p>49900</p>	<p>45800</p>	<p>42800</p>	<p>41400</p>	<p>51300</p>	<p>51200</p>	<p>50800</p>	<p>50700</p>	<p>505.8</p>	<p>2019.1</p>	<p>4</p>	<p>0.0159</p>	<p>7.862</p>

14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POB,sp D0PNI1 D0PNI1_HUMAN,sp D2GY30 D2GY30_AILME,sp F1PBL1 F1PBL1_CANFA,sp F2Z558 F2Z558_PIG,sp F1LLEK	dicNDVLS	82%	41.2	53.94707	Ref	0.57	-0.24	-0.09	-0.31	-0.1	-0.23	-0.66	498	478	297	369	349	354	336	249	672.7	2015.1	3	0.0157	7.801
14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POB,sp D0PNI1 D0PNI1_HUMAN,sp D2GY30 D2GY30_AILME,sp F1PBL1 F1PBL1_CANFA,sp F2Z558 F2Z558_PIG,sp F1LLEK	dicNDVLS	67%	36.4	53.98743	Ref	0.61	Value Missing (-1.586)	0.3	-0.39	0.22	0.085	-0.47	280	Value Missing (-1.586)	359	352	240	320	304	205	672.7	2015.1	3	0.002	0.986

14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POB,sp D00PNI1 D00PNI1_HUMAN,sp D02GY30 D2GY30_AILME,sp F1PBL1 F1PBL1_CANFAL1,sp F2Z558 F2Z558_PIG,sp F1R	dSTLI MQL LR	95%	54	51.78658	Ref	0.44	-0.07	0.11	-0.22	-0.12	-0.23	-0.24	956	1150	878	1120	976	914	885	873	498.6	1492.8	3	0.0153	10.22
14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POB,sp D00PNI1 D00PNI1_HUMAN,sp D02GY30 D2GY30_AILME,sp F1PBL1 F1PBL1_CANFAL1,sp F2Z558 F2Z558_PIG,sp F1R	eMQ PTHP IR	77%	37	51.75558	Ref	0.3	-0.3	0.12	-0.009	0.16	-0.39	-0.05	41000	51300	36700	55000	55400	54500	38900	48800	471.6	1411.7	3	0.0125	8.858

14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_ SHEEP,sp P63101 1 433Z_MO USE,sp P6 3102 143 3Z_RAT,s p P63103 1433Z_B OVIN,sp P63104 1 433Z_HU MAN,sp Q5R651 1 433Z_PO NAB,tr D OPNI1 D0 PNI1_HU MAN,tr D 2GY30 D2 GY30_AIL ME,tr F1P BL1 F1PB L1_CANFA ,tr F2Z55 8 F2Z558 _PIG,tr F	g VD QSQ QAY QEA FEISk	95%	79.8	55.18247	Ref	0.28	-0.1	0.054	0.086	0.22	-0.56	-0.33	11500	12700	10500	13200	14900	14200	8640	10100	883.8	2648.4	3	0.0179	6.767
14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_ SHEEP,sp P63101 1 433Z_MO USE,sp P6 3102 143 3Z_RAT,s p P63103 1433Z_B OVIN,sp P63104 1 433Z_HU MAN,sp Q5R651 1 433Z_PO NAB,tr D OPNI1 D0 PNI1_HU MAN,tr D 2GY30 D2 GY30_AIL ME,tr F1P BL1 F1PB L1_CANFA ,tr F2Z55 8 F2Z558 _PIG,tr F	g VD QSQ QAY QEA FEISk	95%	70.6	55.19369	Ref	0.24	-0.19	-0.21	-0.16	0.024	-0.01	0.064	10300	10900	8810	9730	11100	11000	11200	11700	663.1	2648.4	4	0.017	6.403

14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_ SHEEP,sp P63101 1 433Z_MO USE,sp P6 3102 143 3Z_RAT,s p P63103 1433Z_B OVIN,sp P63104 1 433Z_HU MAN,sp Q5R651 1 433Z_PO NAB,tr D OPNI1 D0 PNI1_HU MAN,tr D 2GY30 D2 GY30_AIL ME,tr F1P BL1 F1PB L1_CANFA ,tr F2Z55 8 F2Z558 _PIG,tr F	gIVD QSQ QAY QEA FEISK	k	82%	40.5	55.15419	Ref	-0.19	-0.3	0.016	0.12	0.27	0.074	0.081	2660	2740	2750	3850	4560	4400	4020	4020	771.2	3080.7	4	0.0311	10.1
14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_ SHEEP,sp P63101 1 433Z_MO USE,sp P6 3102 143 3Z_RAT,s p P63103 1433Z_B OVIN,sp P63104 1 433Z_HU MAN,sp Q5R651 1 433Z_PO NAB,tr D OPNI1 D0 PNI1_HU MAN,tr D 2GY30 D2 GY30_AIL ME,tr F1P BL1 F1PB L1_CANFA ,tr F2Z55 8 F2Z558 _PIG,tr F	kGIV DQS QQA YQE AFEI	Sk	91%	46.4	55.05591	Ref	0.13	-0.3	-0.1	0.13	-0.04	-0.11	-0.09	2950	2650	2120	2750	3550	2760	2740	2770	771.2	3080.7	4	0.0265	8.599

14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POONAB,tr DOPNI1 DOPNI1_HUMAN,tr D2GY30 D2GY30_AILME,tr F1PBL1 F1PBL1_CANFA,tr F2Z558 F2Z558_PIG,tr F	nLLS	70%	33.9	50.6875	Ref	0.097	-0.39	0.14	-0.14	0.33	-0.3	-0.11	1E+05	126000	97300	157000	143000	2E+05	1E+05	133000	506	1514.9	3	0.018	11.88
14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POONAB,tr DOPNI1 DOPNI1_HUMAN,tr D2GY30 D2GY30_AILME,tr F1PBL1 F1PBL1_CANFA,tr F2Z558 F2Z558_PIG,tr F	nLLS	65%	33.1	51.06181	Ref	0.23	-0.37	0.082	-0.06	0.12	-0.06	-0.31	3960	3980	2850	4370	4360	4320	3980	3330	506	1514.9	3	0.0255	16.85

14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POONAB,tr DOPNI1 DOPNI1_HUMAN,tr D2GY30 D2GY30_AILME,tr F1PBL1 F1PBL1_CANFA,tr F2Z558 F2Z558_PIG,tr F	nLLS VAYk	79%	36.1	50.20879	Ref	0.11	-0.23	0.019	-0.2	0.072	-0.04	0.063	4180	4090	3510	4690	4440	4680	4540	4820	506	1514.9	3	0.0043	2.837
14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POONAB,tr DOPNI1 DOPNI1_HUMAN,tr D2GY30 D2GY30_AILME,tr F1PBL1 F1PBL1_CANFA,tr F2Z558 F2Z558_PIG,tr F	nLLS VAYk	67%	33.7	51.08906	Ref	0.076	-0.27	-0.08	-0.082	0.32	-0.11	-0.09	11600	11100	9500	12200	13400	15500	12000	12100	506.3	1515.9	3	0.0018	1.199

14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POONAB,tr D0PNI1 D0PNI1_HUMAN,tr D2GY30 D2GY30_AILME,tr F1PBL1 F1PBL1_CANFA,tr F2Z558 F2Z558_PIG,tr F	nLLS VAYK NVV GAR	93%	47.3	51.8956	Ref	0.13	-0.1	-0.15	-0.25	0.09	-0.11	-0	832	735	678	738	759	837	759	813	603.4	1807.1	3	0.0083	4.587
14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POONAB,tr D0PNI1 D0PNI1_HUMAN,tr D2GY30 D2GY30_AILME,tr F1PBL1 F1PBL1_CANFA,tr F2Z558 F2Z558_PIG,tr F	nLLS VAYK NVV GAR	95%	62.5	51.7232	Ref	-0.084	-0.05	-0	-0.18	0.1	-0.03	0.13	2080	1890	2100	2440	2380	2520	2400	2670	603.4	1807.1	3	0.0059	3.26

14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POONAB,tr D0PNI1 D0PNI1_HUMAN,MAN,tr D2GY30 D2GY30_AILME,tr F1PBL1 F1PBL1_CANFA,tr F2Z558 F2Z558_PIG,tr F	svTE QGA ELSN EER	95%	64.1	51.42246	Ref	0.14	-0.04	-0.15	0.021	0.12	-0.14	-0.23	22800	21900	21000	21800	27000	25300	22100	20600	927	1851.9	2	0.0129	6.965
14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POONAB,tr D0PNI1 D0PNI1_HUMAN,MAN,tr D2GY30 D2GY30_AILME,tr F1PBL1 F1PBL1_CANFA,tr F2Z558 F2Z558_PIG,tr F	svTE QGA ELSN EER	95%	59	51.47095	Ref	0.42	-0.17	-0.27	-0.018	-0.14	0.24	-0.77	28400	29300	21100	22100	29100	23400	31600	15700	618.3	1851.9	3	0.0121	6.547

14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POB,sp D00PNI1 D00PNI1_HUMAN,sp D02GY30 D2GY30_AILME,sp F1PBL1 F1PBL1_CANFAL1 F22558 F22558_PIG,sp F1	yDD MAA cMk	87%	38.4	48.35552	Ref	0.28	0.14	-0.12	-0.15	0.003	-0.33	-0.16	7340	7690	7560	7080	7630	7410	6130	6870	567.9	1700.8	3	0.0124	7.313
14-3-3 protein zeta/delta OS=Ovis aries GN=YWHAZ PE=1 SV=1	1 1433Z_SHEEP,sp P63101 1433Z_MOUSE,sp P63102 1433Z_RAT,sp P63103 1433Z_BOVIN,sp P63104 1433Z_HUMAN,sp Q5R651 1433Z_POB,sp D00PNI1 D00PNI1_HUMAN,sp D02GY30 D2GY30_AILME,sp F1PBL1 F1PBL1_CANFAL1 F22558 F22558_PIG,sp F1	yDD MAA cMk	68%	31.4	48.79263	Ref	0.078	-0.22	0.033	-0.11	-0.03	0.076	-0.22	3660	3110	2740	3670	3670	3380	3800	3080	567.9	1700.8	3	0.0062	3.646

Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	aPLD IPVP DPV k	54%	29.4	49.31956	Ref	-0.41	-0.55	0.057	-0.23	0.12	-1.1	-0.22	12200	7960	7830	13400	12200	13500	5930	11000	810.8	2429.5	3	0.0163	6.72
Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	iEDG NNF GVA VQE k	90%	46.7	54.09481	Ref	-0.002	-0.43	-0.09	-0.34	-0.39	-0.77	-0.1	11600	10400	8340	11900	11000	9290	7450	11700	710	2127.1	3	0.0175	8.223
Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	iEDG nNF GVA VQE k	95%	55.1	54.12956	Ref	0.098	-0.64	-0.27	-0.24	-0.06	-0.69	-0.5	13600	12000	7810	11400	12800	12700	8540	9630	710.4	2128.1	3	0.0189	8.887
Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	iEDG nNF GVA VQE k	87%	44	54.15619	Ref	-0.22	-0.57	-0.16	-0.25	-0.25	-0.32	-0.12	14800	12300	10500	15600	16200	14200	14100	16100	710.4	2128.1	3	0.0163	7.675
Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	ivVL LQR	95%	50.7	44.57185	Ref	-0.42	-0.88	-0.14	-0.28	0.09	-0.82	-0.28	1820	947	747	1390	1390	1580	878	1260	382.3	1143.8	3	0.0084	7.371

Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	kISELDAFLk	53%	28.4	48.56433	Ref	-0.31	-0.67	-0.03	-0.29	0.11	-0.92	-0.2	4710	3230	2730	4800	4400	5060	2600	4240	692.8	2075.3	3	0.0038	1.844
Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	kISELDAFLk	80%	32.5	48.22076	Ref	-0.29	-1.1	0.006	-0.41	0.1	-1.2	0.028	6400	3990	2490	5950	4920	6120	2640	6020	519.8	2075.3	4	#####	0.181
Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	nAYAVLYDIILk	89%	42.1	50.95078	Ref	0.22	-0.35	0.06	-0.4	-0.2	-1	-0.82	787	762	555	829	666	668	392	451	668.7	2003.2	3	0.0051	2.545
Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	nAYAVLYDIILk	81%	38	51.37135	Ref	0.14	-0.82	-0.04	-0.32	-0.18	-0.9	-0.44	404	344	191	369	334	322	205	279	668.7	2003.2	3	0.0134	6.661
Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	nAYAVLYDIILk	86%	40.1	51.07244	Ref	-0.52	-0.32	-0.08	-0.29	-0.01	-0.97	-0.11	568	330	409	543	517	549	294	530	668.7	2003.2	3	0.0066	3.278

Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	nAY AVLY DIILK	85%	39.7	51.2919	Ref	0.11	-0.49	-0.13	-0.13	-0.13	-0.34	-0.32	159	245	174	251	277	243	219	220	668.7	2003.2	3	0.0102	5.104
Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	qLVH ELDE AEYR	93%	48.7	52.46326	Ref	-0.47	Value Missing (-1.1260751)	0.057	-0.43	0.41	-0.71	-0.15	9290	6300	Value Missing (-1.1260751)	11100	8710	13500	6530	9580	602.6	1804.9	3	0.0148	8.173
Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	qPH VGD YR	79%	36.4	50.59885	Ref	-0.33	-0.37	-0.24	-0.3	-0.04	-0.62	-0.13	3220	2310	2430	3000	3160	3300	2310	3230	425.9	1274.7	3	0.0082	6.397
Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	qPH VGD YR	80%	36.8	50.60781	Ref	-0.38	-0.51	-0.08	-0.32	0.17	-1.1	-0.07	37200	25900	25600	38700	36100	44300	19700	39000	425.9	1274.7	3	0.0084	6.609
Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	vFEL MTA LHTK	95%	53.7	52.53699	Ref	-0.2	-0.74	-0.04	-0.46	-0.17	-0.83	-0.34	4130	2380	1780	3240	2660	2830	1880	2610	633.4	1897.1	3	0.0078	4.116

Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	VLPE AQA k	79%	34.1	49.00738	Ref	-0.44	-0.9	-0.02	-0.18	0.29	-1.2	0.013	57800	40800	32100	66400	65600	79300	30200	67800	732.5	1462.9	2	0.0068	4.655
Proteasome activator complex subunit 1 OS=Bos taurus GN=PSME1 PE=1 SV=1	sp Q4U5R3 PSME1_BOVIN, tr Q2KJE7 Q2KJE7_BOVIN	VLPE AQA k	82%	35.2	49.00738	Ref	-0.36	-0.7	-0.11	-0.18	0.11	-0.84	-0.01	9720	7420	6370	10700	11300	12100	6490	11500	732.5	1462.9	2	0.0071	4.819
cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1	tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PIG	aGIT TIEA Vk	95%	52.7	52.09013	Ref	-0.24	-0.23	-0.47	-0.36	0.14	-0.88	-0.1	450	299	326	310	368	455	234	399	674.9	1347.8	2	0.0139	10.3

<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>cLSA AEK</p>	<p>87%</p>	<p>39.6</p>	<p>51.52998</p>	<p>Ref</p>	<p>-0.23</p>	<p>-0.32</p>	<p>-0.36</p>	<p>-0.35</p>	<p>0.03</p>	<p>-0.51</p>	<p>-0.03</p>	<p>9110</p>	<p>6930</p>	<p>7090</p>	<p>7760</p>	<p>8580</p>	<p>9750</p>	<p>6990</p>	<p>9670</p>	<p>752.9</p>	<p>1503.8</p>	<p>2</p>	<p>0.0106</p>	<p>7.043</p>
<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>eQA EAEV ASLN R</p>	<p>92%</p>	<p>44</p>	<p>51.99429</p>	<p>Ref</p>	<p>-0.42</p>	<p>-0.37</p>	<p>-0.37</p>	<p>-0.25</p>	<p>0.26</p>	<p>-0.75</p>	<p>0.002</p>	<p>64500</p>	<p>43800</p>	<p>49400</p>	<p>55500</p>	<p>66200</p>	<p>82200</p>	<p>42900</p>	<p>71400</p>	<p>810.9</p>	<p>1619.8</p>	<p>2</p>	<p>0.0124</p>	<p>7.666</p>

<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>eQA EAEV ASLn R</p>	<p>95%</p>	<p>57.6</p>	<p>51.54558</p>	<p>Ref</p>	<p>-0.32</p>	<p>-0.26</p>	<p>-0.42</p>	<p>-0.27</p>	<p>0.15</p>	<p>-0.73</p>	<p>0.027</p>	<p>13600</p>	<p>10100</p>	<p>11400</p>	<p>11500</p>	<p>14000</p>	<p>16400</p>	<p>9260</p>	<p>15600</p>	<p>811.4</p>	<p>1620.8</p>	<p>2</p>	<p>0.0124</p>	<p>7.667</p>
<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>eQA EAEV ASLn R</p>	<p>95%</p>	<p>51.2</p>	<p>51.56416</p>	<p>Ref</p>	<p>-0.34</p>	<p>-0.43</p>	<p>-0.3</p>	<p>-0.086</p>	<p>0.083</p>	<p>-0.73</p>	<p>0.019</p>	<p>10200</p>	<p>7540</p>	<p>7640</p>	<p>9410</p>	<p>12000</p>	<p>11800</p>	<p>7000</p>	<p>11700</p>	<p>811.4</p>	<p>1620.8</p>	<p>2</p>	<p>0.0117</p>	<p>7.21</p>

<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>iQVL QQQ ADD</p>	<p>AEER</p>	<p>95%</p>	<p>70.6</p>	<p>53.09409</p>	<p>Ref</p>	<p>-0.31</p>	<p>-0.28</p>	<p>-0.39</p>	<p>-0.27</p>	<p>0.1</p>	<p>-0.63</p>	<p>-0.05</p>	<p>4220</p>	<p>3040</p>	<p>3370</p>	<p>3500</p>	<p>4190</p>	<p>4740</p>	<p>2980</p>	<p>4410</p>	<p>974</p>	<p>1946</p>	<p>2</p>	<p>0.0145</p>	<p>7.451</p>
<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>iQVL QQQ ADD</p>	<p>AEER</p>	<p>95%</p>	<p>66.6</p>	<p>53.20537</p>	<p>Ref</p>	<p>-0.29</p>	<p>-0.28</p>	<p>-0.44</p>	<p>-0.45</p>	<p>0.16</p>	<p>-0.95</p>	<p>0.03</p>	<p>6050</p>	<p>3870</p>	<p>4230</p>	<p>4250</p>	<p>4660</p>	<p>6210</p>	<p>3000</p>	<p>5870</p>	<p>974</p>	<p>1946</p>	<p>2</p>	<p>0.0114</p>	<p>5.879</p>

<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>KIQV LQQ QAD DAE ER</p>	<p>95%</p>	<p>69.7</p>	<p>54.47338</p>	<p>Ref</p>	<p>-0.48</p>	<p>-0.35</p>	<p>-0.4</p>	<p>-0.28</p>	<p>0.089</p>	<p>-0.74</p>	<p>0.29</p>	<p>6110</p>	<p>4120</p>	<p>4880</p>	<p>5290</p>	<p>6340</p>	<p>7160</p>	<p>4200</p>	<p>8520</p>	<p>793.8</p>	<p>2378.3</p>	<p>3</p>	<p>0.0149</p>	<p>6.257</p>
<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>KIQV LQQ QAD DAE ER</p>	<p>89%</p>	<p>43.5</p>	<p>54.53375</p>	<p>Ref</p>	<p>-0.36</p>	<p>-0.15</p>	<p>-0.16</p>	<p>-0.22</p>	<p>-0.13</p>	<p>-0.61</p>	<p>-0.07</p>	<p>5710</p>	<p>4200</p>	<p>5250</p>	<p>5870</p>	<p>6210</p>	<p>5770</p>	<p>4320</p>	<p>6220</p>	<p>595.6</p>	<p>2378.3</p>	<p>4</p>	<p>0.0179</p>	<p>7.537</p>

cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1	tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA,tr F1RFX8 F1RFX8_PI G,tr F6VQW8 F6VQW8_MAC MU,tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN,tr Q6QA25 Q6QA25_PI G	klQV LQQ QAD DAE ER	95%	75	54.45844	Ref	-0.48	-0.15	-0.54	-0.36	0.11	-0.6	0.023	13100	7850	10700	9180	11400	13800	8830	13500	793.8	2378.3	3	0.0161	6.787
	cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1	tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA,tr F1RFX8 F1RFX8_PI G,tr F6VQW8 F6VQW8_MAC MU,tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G	mEL QEIQ Lk	52%	32.1	52.65002	Ref	-0.43	-0.08	-0.56	-0.24	0.036	-0.54	-0.1	6570	4140	5720	4590	6360	6700	4690	6330	870.5	1739	2	0.0215

<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>mEL QEIQ Lk</p>	<p>83%</p>	<p>39</p>	<p>52.67197</p>	<p>Ref</p>	<p>-0.42</p>	<p>-0.28</p>	<p>-0.44</p>	<p>-0.33</p>	<p>0.17</p>	<p>-0.65</p>	<p>-0.09</p>	<p>9520</p>	<p>5690</p>	<p>6810</p>	<p>6870</p>	<p>8170</p>	<p>10100</p>	<p>5970</p>	<p>8710</p>	<p>870.5</p>	<p>1739</p>	<p>2</p>	<p>0.0211</p>	<p>12.12</p>
<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>mEL QEIQ Lk</p>	<p>83%</p>	<p>39.9</p>	<p>52.44351</p>	<p>Ref</p>	<p>-0.48</p>	<p>-0.21</p>	<p>-0.56</p>	<p>-0.38</p>	<p>0.18</p>	<p>-0.78</p>	<p>0.11</p>	<p>28800</p>	<p>17000</p>	<p>22200</p>	<p>19600</p>	<p>24500</p>	<p>31500</p>	<p>16900</p>	<p>31100</p>	<p>580.7</p>	<p>1739</p>	<p>3</p>	<p>0.0158</p>	<p>9.07</p>

<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>mEL QEIQ Lk</p>	<p>95%</p>	<p>50.6</p>	<p>52.61841</p>	<p>Ref</p>	<p>-0.95</p>	<p>0.6</p>	<p>-1.1</p>	<p>0.072</p>	<p>-0.6</p>	<p>0.009</p>	<p>-0.66</p>	<p>6330</p>	<p>2780</p>	<p>8800</p>	<p>3130</p>	<p>7570</p>	<p>4160</p>	<p>6610</p>	<p>4120</p>	<p>870.5</p>	<p>1739</p>	<p>2</p>	<p>0.0135</p>	<p>7.768</p>
<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>mEL QEIQ Lk</p>	<p>95%</p>	<p>47.7</p>	<p>52.67817</p>	<p>Ref</p>	<p>-0.71</p>	<p>0.1</p>	<p>-0.75</p>	<p>-0.046</p>	<p>-0.15</p>	<p>-0.21</p>	<p>-0.25</p>	<p>7080</p>	<p>3630</p>	<p>6930</p>	<p>4320</p>	<p>7740</p>	<p>6270</p>	<p>6300</p>	<p>6090</p>	<p>870.5</p>	<p>1739</p>	<p>2</p>	<p>0.0129</p>	<p>7.423</p>

<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>mEL QEIQ Lk</p>	<p>54%</p>	<p>32.5</p>	<p>52.46843</p>	<p>Ref</p>	<p>-0.83</p>	<p>0.59</p>	<p>-1.2</p>	<p>0.034</p>	<p>-0.48</p>	<p>-0.07</p>	<p>-0.4</p>	<p>27500</p>	<p>14500</p>	<p>42300</p>	<p>13900</p>	<p>35500</p>	<p>21700</p>	<p>30200</p>	<p>23800</p>	<p>580.7</p>	<p>1739</p>	<p>3</p>	<p>0.0076</p>	<p>4.346</p>
<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F7IC11 F7IC11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>mEL QEIQ Lk</p>	<p>65%</p>	<p>34</p>	<p>52.38749</p>	<p>Ref</p>	<p>-0.92</p>	<p>0.34</p>	<p>-0.64</p>	<p>-0.029</p>	<p>-0.34</p>	<p>-0.02</p>	<p>-0.14</p>	<p>5630</p>	<p>3270</p>	<p>8480</p>	<p>4810</p>	<p>8120</p>	<p>5700</p>	<p>7440</p>	<p>6790</p>	<p>870.5</p>	<p>1739</p>	<p>2</p>	<p>0.0028</p>	<p>1.596</p>

<p>cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1</p>	<p>tr B2RDE1 B2RDE1_HUMAN, tr E2RB38 E2RB38_CANFA, tr F1RFX8 F1RFX8_PI G, tr F6VQW8 F6VQW8_MAC MU, tr F71C11 F71C11_CALJA, tr Q5HYB6 Q5HYB6_HUMAN, tr Q5VU59 Q5VU59_HUMAN, tr Q6QA25 Q6QA25_PI G</p>	<p>tIDD LEDK</p>	<p>79%</p>	<p>37.4</p>	<p>52.49502</p>	<p>Ref</p>	<p>-0.32</p>	<p>-0.18</p>	<p>-0.62</p>	<p>-0.26</p>	<p>0.16</p>	<p>-0.87</p>	<p>-0.08</p>	<p>20600</p>	<p>12800</p>	<p>15300</p>	<p>12700</p>	<p>18000</p>	<p>21000</p>	<p>10800</p>	<p>18400</p>	<p>778.9</p>	<p>1555.8</p>	<p>2</p>	<p>0.0102</p>	<p>6.575</p>
<p>Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3</p>	<p>4 H2B1K_HUMAN, sp P10853 H2B1F_MOUSE, sp P10854 H2B1M_MOUSE, sp P57053 H2BFS_HUMAN, sp P58876 H2B1D_HUMAN, sp P62807 H2B1C_HUMAN, sp P62808 H2B1_BOVIN, sp Q00715 H2B1_RAT, sp Q2M2T1 H2B1K_BOVIN, sp Q5QNW6 H2B2F</p>	<p>aMG IMN SFVN DIFE R</p>	<p>65%</p>	<p>34.7</p>	<p>52.69569</p>	<p>Ref</p>	<p>0.067</p>	<p>-0.58</p>	<p>-0.86</p>	<p>-0.62</p>	<p>-0.32</p>	<p>-0.21</p>	<p>-0.23</p>	<p>237</p>	<p>167</p>	<p>116</p>	<p>107</p>	<p>139</p>	<p>150</p>	<p>168</p>	<p>165</p>	<p>683.3</p>	<p>2047</p>	<p>3</p>	<p>0.0124</p>	<p>6.037</p>

Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,sp P10853 H2B1F_MOUSE,s P10854 H2B1M_MOUSE,s P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,sp Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F_k	eSYS VVYVY	95%	49.6	53.15968	Ref	-0.49	-0.05	-1.4	-0.05	-0.15	-0.19	-0.14	47500	29100	42900	18700	53000	43200	43900	45200	873.5	1744.9	2	0.0167	9.569
Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,sp P10853 H2B1F_MOUSE,s P10854 H2B1M_MOUSE,s P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,sp Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F_k	eSYS VVYVY	61%	34.4	53.10185	Ref	-0.43	0.01	0.0667	-0.33	-0.14	0.13	-0.28	1E+05	72700	1E+05	667	105000	1E+05	1E+05	98000	582.7	1744.9	3	0.0156	8.937

Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,s p P10853 H2B1F_MOUSE,s p P10854 H2B1M_MOUSE,s p P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,s p Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F_k	eSYS VYVY	95%	49.2	53.10296	Ref	-0.63	-0.1	-1.5	-0.018	-0.02	-0.26	0.086	20500	12400	19500	8150	25500	22300	19600	24800	873.5	1744.9	2	0.0157	9.008
	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,s p P10853 H2B1F_MOUSE,s p P10854 H2B1M_MOUSE,s p P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,s p Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F_k	hAVS EGTK	95%	56.1	52.16359	Ref	-0.5	-0.07	-1.3	-0.23	-0.04	-0.22	-0.09	18500	11000	16100	7760	17900	17700	16300	17800	479.6	1435.8	3	0.0232

Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,s p P10853 H2B1F_MOUSE,s p P10854 H2B1M_MOUSE,s p P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,s p Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F	hAVS	90%	44	52.07295	Ref	-0.33	-0.03	-1.4	-0.23	-0.04	-0.16	-0.19	1E+05	82800	1E+05	47700	120000	1E+05	1E+05	111000	479.6	1435.8	3	0.0268	18.68
Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,s p P10853 H2B1F_MOUSE,s p P10854 H2B1M_MOUSE,s p P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,s p Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F	kESY SVYV Yk	85%	40.8	53.52993	Ref	-0.6	0.016	-1.8	0.083	-0.25	-0.26	0.012	3000	1690	2820	907	3650	2530	2630	3150	1090	2177.2	2	0.0273	12.54

Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,s p P10853 H2B1F_MOUSE,s p P10854 H2B1M_MOUSE,s p P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,s p Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F_k	ILLP GELA k	88%	35.2	46.58355	Ref	-0.5	0.097	-2	-0.1	-0.08	-0.21	-0.06	96300	60300	99100	26800	107000	95000	90300	99400	781.5	1561	2	0.0166	10.61
Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,s p P10853 H2B1F_MOUSE,s p P10854 H2B1M_MOUSE,s p P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,s p Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F_k	ILLP GELA k	80%	32.9	46.44321	Ref	-0.66	0.028	-1.8	-0.11	-0.05	-0.17	0.069	4E+05	219000	4E+05	123000	432000	4E+05	4E+05	442000	521.3	1561	3	0.013	8.317

Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,s p P10853 H2B1F_MOUSE,s p P10854 H2B1M_MOUSE,s p P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,s p Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F_k	ILLP GELAK	70%	28.3	45.66284	Ref	-0.45	-0.16	-1.3	-0.16	-0.13	-0.18	-0.14	25000	14300	18900	9370	23400	20900	21100	21500	781.5	1561	2	0.0069	4.44
	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,s p P10853 H2B1F_MOUSE,s p P10854 H2B1M_MOUSE,s p P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,s p Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F_k	ILLP GELAK	82%	33.2	47.08412	Ref	-0.53	-0.01	-1.6	-0.12	-0.14	-0.17	-0.08	15400	8950	13900	5360	15900	13700	14100	14900	781.5	1561	2	0.0224

Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,s p P10853 H2B1F_MOUSE,s p P10854 H2B1M_MOUSE,s p P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,s p Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F_k	ILLP GELAK	73%	30.5	46.57056	Ref	-0.4	0.052	-1.2	-0.13	-0.19	-0.19	-0.13	7280	5280	7810	3610	8530	7150	7470	7710	521.3	1561	3	0.0157	10.07
	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,s p P10853 H2B1F_MOUSE,s p P10854 H2B1M_MOUSE,s p P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,s p Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F_k	ILLP GELAK	71%	30.4	47.04794	Ref	-0.47	-0.12	-1	-0.19	-0.22	-0.11	-0.07	5140	3340	4620	2840	5480	4670	5250	5390	521.3	1561	3	0.0205

Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,sp P10853 H2B1F_MOUSE,s P10854 H2B1M_MOUSE,s P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,s P Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F_k	qVH PDT GISS k	59%	32	51.52047	Ref	-0.35	-0.1	-0.78	-0.23	-0.25	-0.17	-0.06	4300	3340	4310	3030	4870	4200	4640	4950	728.4	1454.8	2	0.0115	7.871
Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,sp P10853 H2B1F_MOUSE,s P10854 H2B1M_MOUSE,s P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,s P Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F_k	qVH PDT GISS k	88%	42	53.3284	Ref	-0.29	-0.11	-1.8	-0.12	-0.11	-0.22	-0	5890	4320	5320	1910	6550	5750	5560	6420	889	1776	2	0.0228	12.84

Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	4 H2B1K_HUMAN,sp P10853 H2B1F_MOUSE,sp P10854 H2B1M_MOUSE,sp P57053 H2BFS_HUMAN,sp P58876 H2B1D_HUMAN,sp P62807 H2B1C_HUMAN,sp P62808 H2B1_BOVIN,sp Q00715 H2B1_RAT,sp Q2M2T1 H2B1K_BOVIN,sp Q5QNW6 H2B2F_k	qVH PDT GISS	87%	41.6	53.2677	Ref	-0.7	0.043	-1.3	-0.12	-0.13	-0.25	-0.14	4740	2310	4210	1820	4640	4040	3880	4140	889	1776	2	0.0182	10.22
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ49 MOES_BOVIN,tr F1MZW0 F1MZW0_BOVIN,tr F6PUX2 F6PUX2_HORSE	aQM VQE DLEK	90%	45.3	53.19312	Ref	-0.39	-0.04	-0.15	-0.23	0.075	-0.55	-0.2	24000	16400	22600	23500	24500	26500	17900	22700	600.3	1798	3	0.0189	10.52
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ49 MOES_BOVIN,tr F1MZW0 F1MZW0_BOVIN,tr F6PUX2 F6PUX2_HORSE	aQM VQE DLEK	95%	61.6	53.23046	Ref	-0.26	-0.06	-0.22	-0.16	-0.05	-0.45	-0.34	14800	10300	12900	12900	14900	14000	11100	11900	900	1798	2	0.0163	9.078

Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	aQM VQE DLEK	95%	62.2	53.21062	Ref	-0.37	-0.18	-0.36	-0.007	0.079	-0.41	-0.3	24300	16200	19900	19800	27800	25800	19200	20600	900	1798	2	0.0133	7.378
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	aQm VQE DLEK	77%	38.2	53.16928	Ref	-0.2	-0.07	-0.15	-0.081	-0.1	-0.53	-0.23	27200	22400	26700	28200	32700	28200	21900	26800	605.7	1814	3	0.0155	8.53
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	aQm VQE DLEK	87%	41.2	53.16224	Ref	-0.18	-0.3	-0.24	-0.039	0.19	-0.6	-0.34	9410	7540	7490	8800	11100	11400	6860	8150	908	1814	2	0.0094	5.16
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	aQQ ELEEE QTR	95%	53.8	51.46903	Ref	-0.09	-0.21	-0.12	-0.29	-0.13	-0.37	-0.38	39200	30100	30100	35800	35100	34400	30300	29800	768.4	1534.8	2	0.013	8.486
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	eALL QAS QDQ k	94%	50.5	53.01336	Ref	-0.007	-0.29	-0.11	-0.22	-0.12	-0.25	-0.6	17200	14300	12800	16200	16600	15500	14800	11500	613.7	1838	3	0.0139	7.553

Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	eALL QAS QDQ k	95%	54.5	53.01369	Ref	-0.27	-0.23	-0.06	-0.19	-0.05	-0.5	-0.24	14500	10100	11300	14100	14200	13700	10500	12400	920	1838	2	0.0137	7.425
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	eRQ EAEE Ak	51%	30.8	53.08761	Ref	-0.074	-0.3	-0.28	0.045	-0.05	-0.43	-0.44	32500	26800	24900	28300	39100	32100	25700	25200	425.2	1696.9	4	0.0095	5.6
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	eSEA VEW Qqk	95%	59.4	53.42114	Ref	-0.32	-0.31	-0.17	-0.074	0.035	-0.53	-0.15	10300	7230	7860	9740	11500	10800	7650	9870	921.5	1841	2	0.0139	7.542
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	iDEF ESm	88%	34	45.37995	Ref	-1	-0.55	-0.05	-0.59	0.23	0.75	-0.32	1240	867	1320	2090	1580	2440	3670	1730	595.8	1189.5	2	0.0124	10.43
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	kTQE QLAL EMA ELTA R	95%	55.6	54.2453	Ref	-0.016	-0.2	-0.18	-0.095	-0.04	-0.4	-0.45	11100	10400	9880	11300	13200	12000	9680	9290	814.1	2439.3	3	0.0168	6.879

Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	KTQE QLAL EMA ELTA R	89%	45.5	54.1288	Ref	0.052	-0.41	-0.13	-0.19	-0.09	-0.39	-0.26	2540	2410	1900	2590	2730	2560	2170	2370	814.1	2439.3	3	0.0131	5.367
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	KTQE QLAL EMA ELTA R	92%	48.6	54.07641	Ref	0.058	-0.32	-0.21	-0.22	-0.16	-0.13	-0.32	608	617	515	625	683	621	663	579	814.1	2439.4	3	0.0104	4.248
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	IFFL QVk	50%	28	48.76201	Ref	0.33	-0.55	-0.16	-0.2	-0.46	-0.13	-0.64	8590	8720	5150	7550	8100	5920	7760	5390	752	1501.9	2	0.004	2.665
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	IFFL QVk	50%	27.6	48.20747	Ref	0.29	-0.57	-0.24	-0.39	-0.42	-0.18	-0.11	2470	2630	1570	2220	2210	1880	2320	2420	501.7	1501.9	3	0.0023	1.545
Moesin OS=Bos taurus GN=MSN PE=2 SV=3	sp Q2HJ4 9 MOES_ BOVIN,tr F1MZW0 F1MZW0_ BOVIN,tr F6PUX2 F 6PUX2_H ORSE	qEAE EAk	52%	31.4	51.96494	Ref	-0.037	-0.16	-0.15	-0.25	-0.11	-0.47	-0.54	11400	8630	8570	9710	9980	9600	7840	7400	706.9	1411.8	2	0.0046	3.27

Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	eAG EQG DVE PR	95%	49.1	49.8913	Ref	0.18	-0.11	0.41	-0.071	0.21	-0.55	0.22	15600	15700	14000	22400	17700	18900	11600	19600	745.9	1489.7	2	0.0116	7.764
Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	eAG EQG DVE PR	94%	47.8	49.97605	Ref	0.067	-0.01	0.43	-0.22	0.28	-0.22	0.17	30600	32100	33100	50200	35400	43600	32200	41800	497.6	1489.7	3	0.0111	7.425
Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	fMQ TFVL APE GSV Ank	78%	40.2	54.48298	Ref	0.39	-0.31	-0.06	-0.013	-0.07	0.23	0.064	854	902	601	801	914	768	990	873	783.1	2346.3	3	0.0126	5.381
Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	fYVH NDIF R	64%	33.6	51.86538	Ref	0.2	-0.15	0.4	-0.23	0.14	-0.18	0.19	6570	6770	5760	9420	6710	7580	6350	8160	505.6	1513.8	3	0.0113	7.479
Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	fYVH NDIF R	81%	38.7	51.91359	Ref	0.15	-0.27	0.37	-0.18	0.077	-0.13	0.35	11500	11600	9390	16400	12400	12900	11700	16200	505.6	1513.8	3	0.0093	6.152

Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	kVM SQN FTNc HTk	83%	40.5	54.87616	Ref	0.19	-0.21	0.29	0.004	0.11	-0.05	0.08	25400	25500	20800	33100	30000	28100	26300	28600	624.8	2495.3	4	0.0336	13.46
Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	nLPP SGA VPVT GIPP HVV k	95%	52.6	50.53989	Ref	0.14	0.038	0.029	-0.12	-0	0.054	0.16	1350	1190	1200	1340	1330	1260	1370	1460	829.8	2486.5	3	0.0193	7.768
Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	nLPP SGA VPVT GIPP HVV k	95%	49.3	50.45499	Ref	0.34	-0.21	0.18	-0.12	0.18	-0.17	0.11	1340	1430	1060	1560	1390	1490	1220	1470	829.8	2486.5	3	0.0181	7.261
Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	qYYT LLNQ APD MLH R	95%	68.4	53.90262	Ref	0.27	-0.02	-0.06	0.13	-0.2	0.053	0.077	4200	4000	3560	3880	4870	3390	4210	4250	723	2166.1	3	0.0145	6.697
Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	qYYT LLNQ APD MLH R	95%	62.5	53.94289	Ref	0.4	0.079	0.008	0.076	0.029	-0.16	0.063	781	980	849	907	1050	885	812	940	723	2166.1	3	0.0136	6.282

Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	qYYT LLNQ APD MLH R	89%	45.5	53.97194	Ref	0.45	0.15	-0.05	0.002	-0.28	-0.02	0.16	858	1080	955	933	1060	765	957	1070	723	2166.1	3	0.0107	4.925
Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	qYYT LLNQ APD MLH R	78%	38.4	54.85584	Ref	0.33	-0.21	0.23	-0.19	-0.12	0.078	0.21	1140	1240	924	1410	1160	1060	1270	1390	618.6	2470.3	4	0.0155	6.268
Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	qYYT LLNQ APD MLH R	94%	52	54.81725	Ref	0.28	-0.25	0.37	-0.15	-0.04	-0.17	0.22	1040	1060	790	1360	1050	987	944	1220	824.4	2470.3	3	0.0092	3.705
Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	sEPV LEET APE DVQ k	94%	51.2	54.59955	Ref	0.19	-0.13	0.26	-0.14	0.27	-0.23	0.11	9810	9570	8310	12200	10200	11900	8760	11000	760.4	2278.2	3	0.0107	4.675
Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	tFSW ASVT Sk	95%	59.2	52.8693	Ref	0.18	-0.35	0.48	-0.14	0.1	-0.29	0.17	5880	5380	4050	8110	5800	5990	4750	6510	861.5	1720.9	2	0.0172	9.977

Ras GTPase-activating protein-binding protein 1 OS=Bos taurus GN=G3BP PE=2 SV=1	sp Q32LC7 G3BP1_BOVIN, tr F1MQ98 F1MQ98_BOVIN	tFSW ASVT Sk	58%	33.5	52.84679	Ref	0.15	0.06	0.082	-0.12	0.12	-0.08	0.25	4630	4630	4730	5390	5150	5330	4860	6050	574.7	1721	3	0.0098	5.671
Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN, sp P62158 CALM_HUMAN, sp P62160 CALM_RABBIT, sp P62161 CALM_RAT, sp P62204 CALM_MOUSE, sp Q5RAD2 CALM_PONAB, sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	aDQ LTEE QIAE Fk	95%	70.3	52.67719	Ref	Value Missing (-1.7200047)	0.54	0.16	0.48	1.1	-0.23	0.7	233	Value Missing (-1.7200047)	406	349	480	646	267	507	934.5	1866.9	2	0.0162	8.677

Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	aDQ LTEE QIAE	95%	56.1	52.66805	Ref	Value Missing (-1.7627269)	0.44	0.27	0.79	1.1	-0.25	0.31	1889)	257	258	406	426	180	263	934.5	1866.9	2	0.0151	8.088	
Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	dGD GTIT Tk	86%	39.6	52.07411	Ref	-0.44	0.41	0.29	0.27	0.74	-0.3	0.43	36900	17400	34100	35200	38300	46400	23500	38600	758.4	1514.8	2	0.0216	14.24

Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	dTDS EEEI R	55%	28	48.02486	Ref	-0.58	0.57	0.34	0.27	0.67	0.16	0.42	40700	23800	57200	54600	57400	66200	48300	57400	699.3	1396.7	2	0.0108	7.757
Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	eAFS LFDK DGD GTIT TK	90%	47.7	55.19257	Ref	-1.1	0.33	0.36	0.45	0.91	-0.2	0.58	79700	30900	89500	103000	120000	1E+05	69600	119000	919.8	2756.5	3	0.0367	13.3

Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	eAFSLFDK DGD GTIT Tk	74%	37.2	54.93047	Ref	-0.72	0.28	0.25	0.6	0.66	0.081	0.55	59100	29600	64500	70900	99400	90700	63300	86700	690.1	2756.5	4	0.016	5.795
Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	eAFSLFDK DGD GTIT Tk	64%	35.2	55.15113	Ref	-0.2	0.34	0.25	0.33	0.55	0.17	0.57	5430	4020	6350	6690	7770	7900	6340	8350	690.1	2756.5	4	0.0348	12.61

Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	eAFS LFDK DGD GTIT Tk	89%	46.1	55.03033	Ref	-0.77	0.42	0.42	0.42	0.76	-0.04	0.55	7730	4140	10200	11500	12700	14000	8400	12500	919.8	2756.5	3	0.0242	8.785
Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	eAFS LFDK DGD GTIT Tk	67%	37.4	55.02775	Ref	-0.63	0.19	0.21	0.46	0.91	0.019	0.52	964	526	1010	1150	1510	1790	1010	1420	919.8	2756.5	3	0.0237	8.589

Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	kMk DTD SEEE IR	52%	29	54.66858	Ref	-0.72	0.17	0.34	0.44	0.96	0.041	0.68	36400	25700	51600	65300	76900	96100	53200	82300	479.5	2392.3	5	0.032	13.36
Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	mkD TDSE EEIR	55%	32.7	52.86337	Ref	-1.1	0.34	0.37	0.45	0.75	-0.1	0.6	4790	1720	4960	5680	6630	7110	4130	6650	981	1960	2	0.0188	9.578

Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	mkD TDSE EEIR	76%	37.1	52.87388	Ref	-0.85	0.63	0.31	0.45	0.77	-0.24	0.45	4320	1980	6010	5390	6530	7160	3710	5920	981	1960	2	0.0187	9.517
Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	vFDK DGn GYIS AAEL R	51%	34.4	54.82635	Ref	-1.3	0.27	0.28	0.45	0.82	0.22	0.84	20300	9360	29900	33900	41900	47400	32700	49700	788.8	2363.2	3	0.0232	9.83

Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	vFDK DGn GYIS AAEL R	73%	37.1	54.94635	Ref	-0.82	0.34	0.19	0.48	0.87	0.12	0.61	12400	6930	16800	17000	23000	26300	16400	22700	591.8	2363.2	4	0.018	7.595
Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	vFDK DGn GYIS AAEL R	56%	35.3	54.94844	Ref	-0.82	0.24	0.099	0.5	0.83	0.002	0.69	99900	46600	1E+05	107000	156000	2E+05	1E+05	161000	788.8	2363.3	3	0.0066	2.788

Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	vFDK DGn GYIS AAEL R	74%	37.3	54.94664	Ref	-0.81	0.38	0.24	0.45	0.74	-0	0.73	6430	3390	8400	8550	10900	11600	7270	12000	591.8	2363.3	4	0.0033	1.403
Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2	7 CALM_BOVIN,sp P62158 CALM_HUMAN,sp P62160 CALM_RABIT,sp P62161 CALM_RAT,sp P62204 CALM_MOUSE,sp Q5RAD2 CALM_PONAB,sp Q6YNX6 CALM_SHEEP, tr A5A6L2 A5A6L2_PANTR, tr B2RDW0 B2RDW0_HUMAN, tr B2ZPE9 B2ZPE9_CAVPO, tr	vFDK DGn GYIS AAEL R	64%	36.7	54.94772	Ref	-0.48	0.24	0.33	0.39	0.69	0.089	0.68	1740	1150	2060	2460	2820	3040	2090	3120	788.8	2363.2	3	0.0117	4.957

Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK 2 F1MCK 2_BOVIN	aDID ISGP k	89%	41.2	51.56422	Ref	-0.5	-0.28	-0.37	-0.24	-0.05	-0.48	-0.28	18600	12000	15200	16000	19300	19200	15000	17000	762.4	1522.9	2	0.0102	6.706
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK 2 F1MCK 2_BOVIN	aDID VSAP k	93%	44.5	51.5122	Ref	-0.65	-0.32	-0.4	-0.24	-0.01	-0.67	-0.15	28500	15400	20900	22300	27300	28100	18500	26300	762.4	1522.9	2	0.0084	5.511
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK 2 F1MCK 2_BOVIN	aDID VSG Pk	93%	44.2	51.98503	Ref	-0.69	-0.38	-0.21	-0.006	-0.05	-0.82	-0.37	2E+05	82600	1E+05	141000	178000	2E+05	92800	126000	755.4	1508.9	2	0.0151	10.01
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK 2 F1MCK 2_BOVIN	aEGP DMA VDLP k	90%	43.8	53.61519	Ref	-1	-0.18	-0.48	-0.082	-0.17	-0.53	-0.49	14400	4800	9410	8570	12500	10200	8350	8510	926	1850	2	0.0161	8.689
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK 2 F1MCK 2_BOVIN	aEGP DMA VDLP k	91%	46.5	53.63033	Ref	-0.59	-0.25	-0.3	-0.1	0.064	-0.66	0.067	8660	8030	11000	11900	15000	14800	9310	15300	617.7	1850	3	0.015	8.098
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK 2 F1MCK 2_BOVIN	iSMP DIDL NLkG Pk	66%	31.4	50.98433	Ref	-0.86	-0.41	-0.21	0.023	-0.05	-0.48	-0.2	13800	7750	11400	14800	19100	15900	12300	14800	614.1	2452.4	4	0.0072	2.934

Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK 2 F1MCK 2_BOVIN	iSMP DIDL nLkG Pk	55%	30.5	52.07734	Ref	-0.58	-0.52	-0.41	-0.11	0.071	-0.31	-0.17	3520	2540	2870	3490	4700	4670	3740	4090	614.4	2453.4	4	0.0167	6.816
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK 2 F1MCK 2_BOVIN	mDIE GPE Vk	83%	39.1	52.61085	Ref	-0.65	-0.25	-0.4	-0.15	0.009	-0.61	-0.35	49500	27000	38800	39300	51300	50100	34100	40600	813.4	1624.9	2	0.0228	14.02
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK 2 F1MCK 2_BOVIN	mDIE GPE Vk	64%	34.5	52.54983	Ref	-0.13	-0.07	-0.43	-0.38	-0.49	-0.57	-0.35	14900	11300	12800	11200	12800	10300	10200	11800	542.6	1624.9	3	0.006	3.704
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK 2 F1MCK 2_BOVIN	vDID APD VNV HGP DWH Lk	95%	55.9	55.29953	Ref	-0.7	-0.43	-0.54	-0.065	-0.04	-0.3	-0.28	6750	3650	4770	4970	7610	6780	5880	5940	879.1	2634.4	3	0.0185	7.037
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK 2 F1MCK 2_BOVIN	vDID APD VnV HGP DWH Lk	93%	47.8	55.18826	Ref	-0.47	-0.53	-0.38	-0.13	-0.09	-0.49	-0.55	29300	15800	16500	20500	26800	24100	19100	18100	659.8	2635.4	4	0.0231	8.754
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK 2 F1MCK 2_BOVIN	vDIE GPD VHLE GPE Gk	92%	49	54.47679	Ref	-0.66	-0.2	-0.28	-0.18	-0.22	-0.53	-0.17	10600	6160	9150	9740	11500	9780	8230	10500	767.1	2298.2	3	0.0198	8.626

Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK2 F1MCK2_BOVIN	vDIE GPD VHLE GPE Gk	95%	53.5	54.48454	Ref	-0.5	-0.44	-0.39	-0.059	-0.15	-0.49	-0.34	16500	9880	11200	13000	18000	14700	12100	13400	767.1	2298.2	3	0.014	6.069
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MCK2 F1MCK2_BOVIN	vkGE VDV SLPN VEG DLk	67%	32.8	52.25149	Ref	-0.31	-0.34	-0.41	-0.24	-0.25	-0.16	-0.24	5150	4440	4720	5040	6230	5420	6010	5670	678.4	2709.6	4	0.0123	4.551
Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4 F7AJD4_HORSE	aDID ISGP k	89%	41.2	51.56422	Ref	-0.46	-0.24	-0.33	-0.2	-0.01	-0.43	-0.24	18600	12000	15200	16000	19300	19200	15000	17000	762.4	1522.9	2	0.0102	6.706
Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4 F7AJD4_HORSE	aDID VSG Pk	93%	44.2	51.98503	Ref	-0.65	-0.33	-0.16	0.039	-0	-0.77	-0.32	2E+05	82600	1E+05	141000	178000	2E+05	92800	126000	755.4	1508.9	2	0.0151	10.01
Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4 F7AJD4_HORSE	gPQ VTG Elk	72%	34.4	51.25227	Ref	-0.55	0.037	-0.38	-0.25	-0.09	-0.56	-0.25	27100	15600	25400	21400	25800	25200	18900	23200	769	1535.9	2	0.0237	15.39

Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4_1 F7AJD4_1 HORSE	iSLP DVD LHLk	59%	31.4	50.88667	Ref	-0.34	-0.33	-0.44	-0.21	0.002	-0.23	-0.22	1920	1460	1600	1660	2140	2170	1930	1930	929.6	1857.1	2	0.0138	7.414
Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4_2 F7AJD4_2 HORSE	iSLP DVD LHLk	82%	38	50.88717	Ref	-0.37	-0.34	-0.25	-0.24	-0.12	-0.39	-0.17	2260	1560	1730	2070	2290	2180	1890	2180	620	1857.1	3	0.0126	6.766
Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4_3 F7AJD4_3 HORSE	iSMP DIDL NLkG Pk	66%	31.4	50.98433	Ref	-0.81	-0.37	-0.16	0.069	-0	-0.43	-0.16	13800	7750	11400	14800	19100	15900	12300	14800	614.1	2452.4	4	0.0072	2.934
Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4_4 F7AJD4_4 HORSE	iSMP DIDL nLkG Pk	55%	30.5	52.07734	Ref	-0.53	-0.47	-0.36	-0.068	0.12	-0.27	-0.13	3520	2540	2870	3490	4700	4670	3740	4090	614.4	2453.4	4	0.0167	6.816
Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4_5 F7AJD4_5 HORSE	vDID APD VDV HGP DWH Lk	93%	47.8	55.18826	Ref	-0.43	-0.48	-0.33	-0.084	-0.04	-0.44	-0.51	29300	15800	16500	20500	26800	24100	19100	18100	659.8	2635.4	4	0.0233	8.846

Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4 F7AJD4_ HORSE	vDID APD VNIE GPE Gk	95%	88.6	54.56036	Ref	-0.48	-0.08	-0.85	0.009	0.17	-0.41	-0.76	3000	1670	2410	1590	3160	3090	2150	1680	1139	2275.2	2	0.0163	7.173
Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4 F7AJD4_ HORSE	vDID APD VNIE GPE Gk	94%	51.6	54.60773	Ref	-0.31	-0.28	-0.41	-0.15	-0.11	-0.27	-0.42	26300	18100	20000	20500	27100	24400	22700	20300	759.4	2275.2	3	0.0134	5.871
Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4 F7AJD4_ HORSE	vDID VPD VNIE GPD Ak	70%	37.7	54.54792	Ref	-0.3	-0.23	-0.08	-0.21	-0.01	-0.64	-0.12	7560	6810	7750	9640	9690	9730	6600	9330	768.8	2303.2	3	0.0111	4.836
Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4 F7AJD4_ HORSE	vDVE VPD VNIE GPn Ak	86%	43.7	54.59988	Ref	-0.59	-0.31	-0.37	-0.18	-0.1	-0.32	-0.18	10000	5420	7160	7680	9700	8970	8010	8790	768.8	2303.2	3	0.017	7.36
Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4 F7AJD4_ HORSE	vDVE VPD VNIE GPn Ak	90%	47.1	54.58472	Ref	-0.39	-0.38	-0.18	-0.3	0.17	-0.53	-0.22	9690	7030	7680	9960	10100	12200	7810	9620	768.8	2303.2	3	0.0151	6.566

Uncharacterized protein (Fragment) OS=Equus caballus GN=AHNAK PE=4 SV=1	tr F7AJD4 F7AJD4_HORSE	vTAP DIDL HLk	57%	30.7	52.07333	Ref	-0.42	-0.23	-0.18	-0.16	-0.11	-0.51	-0.37	15600	9820	12200	14200	15800	14300	11300	12400	458.3	1829.1	4	0.0183	9.999
40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_CAPHI,sp P62269 RS18_HUMAN,sp P62270 RS18_MOUSE,sp P62271 RS18_RAT,sp P62272 RS18_PIG,sp Q3TOR1 RS18_BOVIN,sp Q5TJE9 RS18_CANFA,tr D3ZM33 D3ZM33_RAT,tr F2X217 F2X217_AILME,tr F5H8M6 F5H8M6_MOUSE,tr F6TQC9 F6T	aGEL TEDE VER	95%	46	50.62586	Ref	0.3	-0.04	0.35	-0.14	0.31	-0.13	0.37	40600	40500	34800	51300	40000	48000	36800	51800	776.4	1550.8	2	0.0117	7.538

40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C APHI,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	iAFAI TAlk	73%	29.3	45.19303	Ref	0.28	0.16	0.24	0.013	0.22	-0.13	0.17	5060	4490	4480	5340	5020	5060	4140	5050	519.3	1555	3	0.003	1.908
40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C APHI,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	iAFAI TAlk	70%	29.3	45.97136	Ref	0.22	-0.06	0.38	-0.031	0.22	-0.11	0.39	16500	15300	13700	20800	17200	17800	14800	20900	519.3	1555	3	0.011	7.095

40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C APHI,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	kiAF AITA Ik	95%	51.1	44.27372	Ref	0.11	-0.05	0.45	0.076	0.35	-0.02	0.3	2670	2620	2550	4050	3450	3650	2940	3650	663.4	1987.3	3	0.0322	16.2
40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C APHI,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	kiAF AITA Ik	89%	30.1	41.00922	Ref	0.11	0.025	0.43	0.054	0.37	-0.04	0.29	1710	1720	1760	2610	2220	2420	1890	2370	497.8	1987.3	4	0.0038	1.911

40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C APHI,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	kiAF AITA ik	78%	23.6	40.10682	Ref	0.13	-0.07	0.37	0.049	0.31	0.006	0.38	1890	1810	1710	2600	2300	2400	2030	2610	497.8	1987.3	4	0.0017	0.865
40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C APHI,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	kiAF AITA ik	94%	40.6	44.07442	Ref	0.24	-0.18	0.4	0.08	0.27	0.021	0.32	4000	4100	3340	5600	4940	4930	4320	5270	663.4	1987.3	3	0.0307	15.46

40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C APHI,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	klAF AITA Ik	87%	30	42.49321	Ref	-0.063	-0	0.47	0.1	0.34	-0.13	0.39	9550	7960	9000	14000	12000	12300	9280	13200	497.8	1987.3	4	0.019	9.576
40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C APHI,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	klAF AITA Ik	95%	39.9	41.00543	Ref	0.13	0.012	0.35	0.11	0.29	0.076	0.22	3800	3630	3620	5160	4790	4760	4270	4700	663.4	1987.3	3	0.0025	1.28

40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C APHI,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	klAF AITA Ik	57%	22.7	44.07408	Ref	-0.008	0.37	-0.12	0.17	0.13	0.028	0.34	937	679	956	763	1030	878	852	1050	497.8	1987.3	4	0.0303	15.23
40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C APHI,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	sLVIP Ek	69%	31.7	49.30164	Ref	-0.13	0.16	0.12	-0.15	0.002	0.24	0.84	1570	1350	1800	1960	1790	1740	2140	3210	566.3	1130.7	2	0.0152	13.46

40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C API,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	VITI MQ NPR	53%	31.5	51.79928	Ref	0.3	-0.11	0.41	-0.081	0.22	0.083	0.16	1E+05	101000	81800	132000	104000	1E+05	1E+05	111000	688.4	1374.8	2	0.0101	7.344
40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C API,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	VITI MQ NPR	69%	34.8	51.79862	Ref	0.39	-0.07	0.14	-0.014	0.22	-0.01	0.2	7620	7080	5580	7230	7160	7380	6570	7540	459.3	1374.8	3	0.0097	7.043

40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C APHI,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	yAH	94%	48.8	51.76982	Ref	0.053	0.14	0.6	-0.096	0.46	-0.09	0.046	57700	53800	61900	95500	65100	83600	59700	65000	387.9	1160.7	3	0.0076	6.554
40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1	6 RS18_C APHI,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T	yAH VVLR	81%	38.3	51.74415	Ref	0.094	0.16	0.54	-0.095	0.44	-0.18	0.11	5760	5350	6080	8900	6300	7960	5420	6580	387.9	1160.7	3	0.0052	4.514

<p>40S ribosomal protein S18 OS=Capra hircus GN=RPS18 PE=2 SV=1</p>	<p>6 RS18_C APHI,sp P 62269 RS 18_HUMA N,sp P62 270 RS18 _MOUSE, sp P6227 1 RS18_R AT,sp P62 272 RS18 _PIG,sp Q 3TOR1 RS 18_BOVIN ,sp Q5TJE 9 RS18_C ANFA,tr D3ZM33 D3ZM33_ RAT,tr F2 X217 F2X 217_AILM E,tr F5H8 M6 F5H8 M6_MOU SE,tr F6T QC9 F6T</p>	<p>ySQV LAnG</p>	<p>LDNk</p>	<p>95%</p>	<p>49.1</p>	<p>53.56643</p>	<p>Ref</p>	<p>0.14</p>	<p>-0.03</p>	<p>0.45</p>	<p>0.014</p>	<p>0.37</p>	<p>-0.14</p>	<p>0.3</p>	<p>17900</p>	<p>16700</p>	<p>16200</p>	<p>25200</p>	<p>20600</p>	<p>23000</p>	<p>16900</p>	<p>22700</p>	<p>966</p>	<p>1930.1</p>	<p>2</p>	<p>0.009</p>	<p>4.67</p>
<p>Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2</p>	<p>3 RL40_ MACFA,sp POC275 RL40_PO NPY,sp P 0C276 RL 40_SHEEP ,sp POCG 47 UBB_ HUMAN,s p POCG48 UBC_HU MAN,sp P 0CG49 U BB_MOUS E,sp POC G50 UBC _MOUSE, sp POCG5 1 UBB_R AT,sp PO CG53 UB B_BOVIN, sp POCG5 4 UBB_C AVPO,sp POCG55 </p>	<p>eSTL HLVL</p>	<p>R</p>	<p>95%</p>	<p>52.7</p>	<p>51.67982</p>	<p>Ref</p>	<p>-0.26</p>	<p>-0.07</p>	<p>0.048</p>	<p>-0.25</p>	<p>0.12</p>	<p>-0.53</p>	<p>-0.17</p>	<p>12700</p>	<p>8990</p>	<p>11100</p>	<p>13500</p>	<p>12100</p>	<p>13600</p>	<p>9110</p>	<p>11600</p>	<p>457.9</p>	<p>1370.8</p>	<p>3</p>	<p>0.0099</p>	<p>7.186</p>

Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2	3 RL40_MACFA,sp POC275 RL40_PONPY,sp POC276 RL40_SHEEP,sp POCG47 UBB_HUMAN,sp POCG48 UBC_HUMAN,sp POCG49 UBB_MOUSE,sp POCG50 UBC_MOUSE,sp POCG51 UBB_RAT,sp POCG53 UBB_BOVIN,sp POCG54 UBB_CAVPO,sp POCG55	eSTLHLVL	R	95%	55.5	51.60496	Ref	-0.47	-0.15	0.064	-0.11	0.086	-0.56	-0.13	12500	7050	9560	12400	12100	12100	8110	10900	457.9	1370.8	3	0.0122	8.913
Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2	3 RL40_MACFA,sp POC275 RL40_PONPY,sp POC276 RL40_SHEEP,sp POCG47 UBB_HUMAN,sp POCG48 UBC_HUMAN,sp POCG49 UBB_MOUSE,sp POCG50 UBC_MOUSE,sp POCG51 UBB_RAT,sp POCG53 UBB_BOVIN,sp POCG54 UBB_CAVPO,sp POCG55	eSTLHLVL	R	95%	55.8	51.66351	Ref	-0.33	0.12	0.11	-0.35	0.033	-0.41	-0	9970	8120	12000	13400	10800	12200	9370	12400	457.9	1370.8	3	0.0094	6.836

Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2	3 RL40_ MACFA,sp POC275 RL40_PO NPY,sp P OC276 RL 40_SHEEP ,sp POCG 47 UBB_ HUMAN,s p POCG48 UBC_HU MAN,sp P OCG49 U BB_MOUS E,sp POC G50 UBC _MOUSE, sp POCG5 1 UBB_R AT,sp PO CG53 UB B_BOVIN, sp POCG5 4 UBB_C AVPO,sp POCG55	eSTL HLVL R	93%	46.7	51.67982	Ref	-0.25	0.042	-0.02	-0.4	-0.02	-0.54	-0.05	8000	5290	7020	7570	6380	7270	5280	7400	457.9	1370.8	3	0.0099	7.251
Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2	3 RL40_ MACFA,sp POC275 RL40_PO NPY,sp P OC276 RL 40_SHEEP ,sp POCG 47 UBB_ HUMAN,s p POCG48 UBC_HU MAN,sp P OCG49 U BB_MOUS E,sp POC G50 UBC _MOUSE, sp POCG5 1 UBB_R AT,sp PO CG53 UB B_BOVIN, sp POCG5 4 UBB_C AVPO,sp POCG55	eSTL HLVL R	95%	52.8	51.70704	Ref	-0.28	0.022	0.037	-0.29	-0.02	-0.12	-0.12	16000	13400	17800	20200	17800	18700	18300	18000	457.9	1370.8	3	0.0087	6.377

Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2	3 RL40_ MACFA,sp POC275 RL40_PO NPY,sp P OC276 RL 40_SHEEP ,sp POCG 47 UBB_ HUMAN,s p POCG48 UBC_HU MAN,sp P OCG49 U BB_MOUS E,sp POC G50 UBC _MOUSE, sp POCG5 1 UBB_R AT,sp PO CG53 UB B_BOVIN, sp POCG5 4 UBB_C AVPO,sp POCG55	eSTL HLVLR	88%	42.4	51.67979	Ref	-0.27	-0.08	-0.02	-0.22	-0.03	-0.49	0.14	8530	6410	7940	9270	8920	8850	6720	10300	457.9	1370.8	3	0.0096	6.967
Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2	3 RL40_ MACFA,sp POC275 RL40_PO NPY,sp P OC276 RL 40_SHEEP ,sp POCG 47 UBB_ HUMAN,s p POCG48 UBC_HU MAN,sp P OCG49 U BB_MOUS E,sp POC G50 UBC _MOUSE, sp POCG5 1 UBB_R AT,sp PO CG53 UB B_BOVIN, sp POCG5 4 UBB_C AVPO,sp POCG55	eSTL HLVLR	62%	33	51.53949	Ref	-0.063	-0.03	-0.2	-0.32	0.14	-0.38	-0.16	1130	947	1050	1050	1060	1270	933	1070	457.9	1370.8	3	0.0055	4.037

Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2	3 RL40_ MACFA,sp POC275 RL40_PO NPY,sp P OC276 RL 40_SHEEP ,sp POCG 47 UBB_ HUMAN,s p POCG48 UBC_HU MAN,sp P OCG49 U BB_MOUS E,sp POC G50 UBC _MOUSE, sp POCG5 1 UBB_R AT,sp PO CG53 UB B_BOVIN, sp POCG5 4 UBB_C AVPO,sp POCG55	eSTL HLVL	81%	38.4	51.70704	Ref	-0.052	0.16	-0.2	-0.29	-0.14	-0.39	0.018	613	563	708	618	639	621	547	718	457.9	1370.8	3	0.0087	6.377
Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2	3 RL40_ MACFA,sp POC275 RL40_PO NPY,sp P OC276 RL 40_SHEEP ,sp POCG 47 UBB_ HUMAN,s p POCG48 UBC_HU MAN,sp P OCG49 U BB_MOUS E,sp POC G50 UBC _MOUSE, sp POCG5 1 UBB_R AT,sp PO CG53 UB B_BOVIN, sp POCG5 4 UBB_C AVPO,sp POCG55	TITLE VEPS DTIE NVK	85%	43	54.54953	Ref	-0.43	-0.5	-0.5	0.2	0.55	-0.35	-0.08	33400	24700	25600	28700	51200	57000	32000	38200	799.4	2395.3	3	0.0228	9.519

Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2	3 RL40_MACFA,sp POC275 RL40_PO NPY,sp POC276 RL40_SHEEP,sp POCG47 UBB_HUMAN,sp POCG48 UBC_HUMAN,sp POCG49 UBB_MOUSE,sp POCG50 UBC_MOUSE,sp POCG51 UBB_RAT,sp POCG53 UBB_BOVIN,sp POCG54 UBB_CAVPO,sp POCG55	TITLE VEPS DTIE NVK	95%	56.6	54.49151	Ref	-0.79	-0.36	-0.16	-0.24	0.21	-0.46	0.35	4240	1920	2800	3630	3760	4500	2950	5130	1199	2395.3	2	0.0178	7.426
Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2	3 RL40_MACFA,sp POC275 RL40_PO NPY,sp POC276 RL40_SHEEP,sp POCG47 UBB_HUMAN,sp POCG48 UBC_HUMAN,sp POCG49 UBB_MOUSE,sp POCG50 UBC_MOUSE,sp POCG51 UBB_RAT,sp POCG53 UBB_BOVIN,sp POCG54 UBB_CAVPO,sp POCG55	TITLE VEPS DTIE NVK	85%	43.2	54.41326	Ref	-0.3	-0.21	-0.34	-0.048	0.34	-0.72	0.28	16400	13900	16000	16500	22200	25400	12700	25200	799.4	2395.3	3	0.0146	6.089

Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2	3 RL40_ MACFA,sp POC275 RL40_PO NPY,sp P OC276 RL 40_SHEEP ,sp POCG 47 UBB_ HUMAN,s p POCG48 UBC_HU MAN,sp P OCG49 U BB_MOUS E,sp POC G50 UBC _MOUSE, sp POCG5 1 UBB_R AT,sp PO CG53 UB B_BOVIN, sp POCG5 4 UBB_C AVPO,sp POCG55	tITLE VEPS DTIE NVk	78%	39.9	54.40193	Ref	-0.33	-0.15	-0.28	0.025	0.17	-0.23	-0.31	5350	3550	4370	4450	6080	5860	4630	4360	799.4	2395.3	3	0.0142	5.926
Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2	3 RL40_ MACFA,sp POC275 RL40_PO NPY,sp P OC276 RL 40_SHEEP ,sp POCG 47 UBB_ HUMAN,s p POCG48 UBC_HU MAN,sp P OCG49 U BB_MOUS E,sp POC G50 UBC _MOUSE, sp POCG5 1 UBB_R AT,sp PO CG53 UB B_BOVIN, sp POCG5 4 UBB_C AVPO,sp POCG55	tITLE VEPS DTIE NVk	87%	42.4	54.384	Ref	-0.59	-0	0.17	-0.042	-0.05	-0.83	0.02	1020	552	903	1140	1090	945	573	1030	1199	2395.3	2	0.0137	5.698

<p>Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2</p>	<p>3 RL40_ MACFA,sp POC275 RL40_PO NPY,sp P OC276 RL 40_SHEEP ,sp POCG 47 UBB_ HUMAN,s p POCG48 UBC_HU MAN,sp P OCG49 U BB_MOUS E,sp POC G50 UBC _MOUSE, sp POCG5 1 UBB_R AT,sp PO CG53 UB B_BOVIN, sp POCG5 4 UBB_C AVPO,sp POCG55 </p>	<p>tITLE VEPS DTIE NVk</p>	<p>86%</p>	<p>43.8</p>	<p>54.44958</p>	<p>Ref</p>	<p>-0.39</p>	<p>-0.21</p>	<p>-0.08</p>	<p>-0.22</p>	<p>0.18</p>	<p>-0.38</p>	<p>0.037</p>	<p>2340</p>	<p>1540</p>	<p>1900</p>	<p>2320</p>	<p>2330</p>	<p>2690</p>	<p>1910</p>	<p>2520</p>	<p>799.4</p>	<p>2395.3</p>	<p>3</p>	<p>0.0159</p>	<p>6.614</p>
<p>Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2</p>	<p>3 RL40_ MACFA,sp POC275 RL40_PO NPY,sp P OC276 RL 40_SHEEP ,sp POCG 47 UBB_ HUMAN,s p POCG48 UBC_HU MAN,sp P OCG49 U BB_MOUS E,sp POC G50 UBC _MOUSE, sp POCG5 1 UBB_R AT,sp PO CG53 UB B_BOVIN, sp POCG5 4 UBB_C AVPO,sp POCG55 </p>	<p>tLSD YNIQ k</p>	<p>81%</p>	<p>38.5</p>	<p>52.99886</p>	<p>Ref</p>	<p>-0.27</p>	<p>-0.09</p>	<p>-0.14</p>	<p>-0.1</p>	<p>0.13</p>	<p>-0.5</p>	<p>-0.1</p>	<p>29000</p>	<p>20400</p>	<p>25100</p>	<p>27200</p>	<p>30800</p>	<p>31500</p>	<p>21300</p>	<p>28000</p>	<p>845.5</p>	<p>1688.9</p>	<p>2</p>	<p>0.0089</p>	<p>5.264</p>

Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=UBA52 PE=2 SV=2	3 RL40_MACFA,sp POC275 RL40_PONPY,sp POC276 RL40_SHEEP,sp POCG47 UBB_HUMAN,sp POCG48 UBC_HUMAN,sp POCG49 UBB_MOUSE,sp POCG50 UBC_MOUSE,sp POCG51 UBB_RAT,sp POCG53 UBB_BOVIN,sp POCG54 UBB_CAVPO,sp POCG55	tLSDYNIQkESTLHLVLR	87%	41.2	53.32661	Ref	-0.086	-0.32	-0.06	-0.093	0.095	-0.04	-0.11	2020	2180	2010	2710	2910	2900	2760	2600	685.4	2737.5	4	0.0163	5.935
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P50413 THIO_SHEEP	IEATINELI	95%	62.9	51.53248	Ref	0.15	-0.29	-0.23	-0.37	-0.2	-0.21	-0.62	246	261	210	245	244	241	251	187	660.4	1318.8	2	0.0049	3.683
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P50413 THIO_SHEEP	IEATINELI	95%	63.4	51.48229	Ref	-0.1	-0.51	-0.18	-0.17	-0.45	-0.58	-0.43	267	167	137	194	214	154	147	162	660.4	1318.8	2	0.0052	3.956
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P50413 THIO_SHEEP	IEATINELI	88%	40.3	51.53544	Ref	0.64	0.9	0.34	Value Missing (-3.0499606)	Value Missing (-2.8540883)	Value Missing (-2.9168549)	Value Missing (-2.905981)	125	103	134	102	Value Missing (-3.0499606)	Value Missing (-2.8540883)	Value Missing (-2.9168549)	Value Missing (-2.905981)	660.4	1318.8	2	0.0051	3.865

Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P5041 3 THIO_S HEEP	vSEF SGA Nk	66%	34.1	52.3474	Ref	-0.25	-0.33	-0.18	-0.14	-0.06	-0.54	-0.45	24300	17100	17500	21800	24800	22800	17100	18100	773.9	1545.9	2	0.0092	5.978
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P5041 3 THIO_S HEEP	vSEF SGA Nk	80%	37.5	52.31824	Ref	-0.28	-0.27	-0.29	-0.086	-0.1	-0.55	-0.33	11700	8230	8990	9900	12600	10900	8340	9650	773.9	1545.8	2	0.024	15.53
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P5041 3 THIO_S HEEP	yAF QEAL NSA Gek	95%	61.6	53.7751	Ref	-0.31	-0.42	-0.1	0.071	-0.32	-0.64	-0.16	28200	20400	20500	28700	35700	23800	20000	27500	679.4	2035.1	3	0.0212	10.42
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P5041 3 THIO_S HEEP	yAF QEAL NSA Gek	95%	52.2	53.7751	Ref	-0.33	-0.36	-0.3	-0.055	-0.15	-0.37	-0.27	29600	20600	21800	25600	33500	27300	24600	26200	679.4	2035.1	3	0.0212	10.42
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P5041 3 THIO_S HEEP	yAF QEAL NSA Gek	94%	51.3	53.78222	Ref	-0.24	-0.53	-0.07	-0.29	-0.1	-0.37	-0.31	31900	22900	20400	31300	29600	29500	25500	26500	679.4	2035.1	3	0.0176	8.627
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P5041 3 THIO_S HEEP	yAF QEAL NSA Gek	90%	45.6	53.79298	Ref	-0.053	-0.31	-0.05	-0.11	-0.33	-0.32	-0.51	19400	18500	16800	22600	23800	17900	18800	16300	679.4	2035.1	3	0.0166	8.171
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P5041 3 THIO_S HEEP	yAF QEAL NSA Gek	94%	51	53.84499	Ref	-0.036	-0.26	-0.33	-0.21	-0.18	-0.39	-0.26	4430	4190	3880	4160	4970	4440	4020	4350	679.4	2035.1	3	0.0057	2.778

Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P5041 3 THIO_S HEEP	yAF QEAL NSA Gek	95%	64.9	53.75737	Ref	-0.22	-0.43	-0.25	-0.11	-0.07	-0.62	-0.29	4300	3040	2850	3630	4400	3950	2820	3520	1019	2035.1	2	0.0202	9.941
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P5041 3 THIO_S HEEP	yAF QEAL NSA Gek	95%	52.5	53.75859	Ref	-0.33	-0.32	-0.45	-0.24	-0.21	-0.57	0.18	4670	3200	3510	3590	4570	4080	3320	5530	1019	2035.1	2	0.0178	8.742
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P5041 3 THIO_S HEEP	yAF QEAL NSA Gek	93%	47.6	54.36692	Ref	-0.37	-0.27	-0.14	-0.21	-0.23	-0.21	-0.24	8680	6480	7530	9240	9700	8370	8840	8570	585.8	2339.3	4	0.0287	12.25
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P5041 3 THIO_S HEEP	yAF QEAL nSA Gek	61%	35	53.67697	Ref	0.17	-0.09	-0.28	-0.37	-0.6	-0.25	-0.52	34900	34800	31400	31000	32000	23900	31700	26200	679.7	2036.1	3	0.0176	8.628
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P5041 3 THIO_S HEEP	yAF QEAL nSA Gek	95%	54.5	53.67147	Ref	-0.25	-0.3	-0.25	-0.15	-0.04	-0.42	-0.45	17300	12800	13400	15600	18500	17400	14000	13600	1019	2036.1	2	0.0169	8.32
Thioredoxin OS=Ovis aries GN=TXN PE=1 SV=2	sp P5041 3 THIO_S HEEP	yAF QEAL nSA Gek	89%	45.4	54.50312	Ref	-0.24	-0.32	-0.05	-0.084	-0.25	-0.5	-0.55	10600	7420	7630	10300	11100	8670	7610	7300	781.1	2340.2	3	0.0244	10.42
Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D 1 ACTN4_ BOVIN,tr E2R5T9 E 2R5T9_CA NFA,tr F1 PLA7 F1P LA7_CANF A	dGLA FNAL IHR	95%	59	52.38701	Ref	-0.11	-0.4	-0.33	-0.33	-0.55	-0.26	0.022	3070	2820	2500	2960	3240	2440	3110	3760	511	1529.9	3	0.0084	5.489

Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1 PLA7 F1P LA7_CANF A	eLPP DQA EYcl AR	84%	37.6	50.75554	Ref	-0.21	-0.21	-0.61	-0.18	-0.27	-0.22	-0.45	5180	3880	4210	3600	5340	4360	4710	4000	927.9	1853.9	2	0.0166	8.939
Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1 PLA7 F1P LA7_CANF A	eLPP DQA EYcl AR	65%	32.4	50.75284	Ref	-0.21	-0.01	-0.58	-0.29	-0.4	-0.22	-0.65	9020	6240	7800	5910	7970	6440	7610	5620	927.9	1853.9	2	0.0163	8.809
Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1 PLA7 F1P LA7_CANF A	fAIQ DISV EETS Ak	95%	57.8	54.15826	Ref	-0.065	-0.36	-0.52	-0.35	-0.67	0.005	-0.53	9400	6870	6090	6110	7590	5290	8820	6040	716.1	2145.2	3	0.0126	5.852
Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1 PLA7 F1P LA7_CANF A	gISQ EQM QEF R	95%	46.7	51.03161	Ref	-0.18	-0.05	-0.62	-0.23	-0.3	-0.31	-0.5	19800	15100	17900	13600	19600	16300	16900	14700	828.9	1655.8	2	0.0124	7.5
Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1 PLA7 F1P LA7_CANF A	hTNY TME HIR	95%	71.8	50.82645	Ref	-0.055	0.014	-0.23	-0.55	-0.24	-0.36	-0.72	2E+05	147000	2E+05	158000	140000	2E+05	1E+05	112000	402.2	1604.8	4	0.0117	7.302
Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1 PLA7 F1P LA7_CANF A	hTNY TME HIR	66%	32.8	50.89693	Ref	-0.28	-0.24	-0.53	-0.26	-0.37	-0.11	-0.48	16900	11300	12700	11600	15400	12500	15600	12000	803.4	1604.8	2	0.0096	5.986

Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1PLA7 F1PLA7_CANF A	mAP YQG PDA VPG ALDY k	58%	35.3	54.64251	Ref	-0.17	-0.54	-0.35	-0.21	-0.05	-0.16	-0.75	5140	3960	3320	4270	5170	5040	4860	3230	801.1	2400.2	3	0.0243	10.14
Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1PLA7 F1PLA7_CANF A	qLETI DQL HLEY Ak	95%	59.9	53.8433	Ref	-0.18	-0.2	-0.62	-0.11	-0.31	-0.23	-0.37	9070	7590	8120	6780	10700	8110	8950	8060	770.4	2308.3	3	0.0065	2.829
Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1PLA7 F1PLA7_CANF A	rDH ALLE EQSk	51%	33.6	54.11472	Ref	-0.29	-0.07	-0.47	-0.23	-0.22	-0.32	-0.39	13500	10500	13200	11200	14700	12900	12500	11900	645.4	1933.1	3	0.0212	10.95
Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1PLA7 F1PLA7_CANF A	tINE VEN QILT R	73%	37.1	53.0418	Ref	-0.16	-0.35	-0.19	-0.23	-0.33	-0.17	-0.33	8560	8410	8020	10100	10700	8740	10300	9080	578.7	1732.9	3	0.0171	9.854
Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1PLA7 F1PLA7_CANF A	tINE VEN QILT R	70%	35.8	53.00008	Ref	-0.26	-0.32	-0.33	-0.17	-0.47	-0.08	-0.45	11300	8480	8840	9830	12100	8570	11800	9010	867.5	1733	2	0.0099	5.692
Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1PLA7 F1PLA7_CANF A	vGW EQLL TTIA R	89%	43.7	52.71153	Ref	-0.19	-0.13	-0.48	-0.22	-0.37	-0.03	-0.78	1180	911	1040	911	1200	942	1250	738	564.3	1690	3	0.0119	7.036

Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1PLA7 F1PLA7_CANF A	vGW EQLL TTIA R	91%	43.6	52.82695	Ref	-0.19	-0.09	-0.73	-0.14	-0.44	-0.15	-0.63	1500	1060	1230	890	1470	1050	1330	953	846	1690	2	0.0099	5.838
Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	sp A5D7D1 ACTN4_BOVIN, tr E2R5T9 E2R5T9_CA NFA, tr F1PLA7 F1PLA7_CANF A	vGW EQLL TTIA R	90%	42.5	52.48574	Ref	-0.25	-0.3	-0.65	0.085	-0.51	-0.04	-0.59	1200	873	917	810	1480	855	1240	842	846	1690	2	#####	0.492
Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_C AMBA, sp B0FY4 ITB1_SHEEP, sp P53712 ITB1_BOVIN, sp Q9GLP0 ITB1_PIG, tr C7AR56 C7AR56_LITWA, tr E2RT52 E2RT52_CA NFA, tr F1RVE7 F1RVE7_PIG ck	dkLP QPG QVD PLSH ck	51%	34.2	54.64542	Ref	-0.34	0.046	0.13	0.055	-0.28	0.11	-0.1	1310	889	1260	1500	1570	1090	1490	1270	907.5	2719.5	3	0.0139	5.112

Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_CAMBA,sp B0FY4 ITB1_SHEEP,sp P53712 ITB1_BOVIN,sp Q9GLP0 ITB1_PIG,tr C7AR56 C7AR56_LITWA,tr E2RT52 E2RT52_CANFA,tr F1RVE7 F1RVE7_PIG	dNT NEIY SGk	95%	52.2	52.73615	Ref	-0.76	0.24	-0.01	0.14	-0.03	0.098	-0.08	13800	7500	16200	15400	18800	14600	16600	14600	875	1747.9	2	0.0201	11.5
Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_CAMBA,sp B0FY4 ITB1_SHEEP,sp P53712 ITB1_BOVIN,sp Q9GLP0 ITB1_PIG,tr C7AR56 C7AR56_LITWA,tr E2RT52 E2RT52_CANFA,tr F1RVE7 F1RVE7_PIG	dNT NEIY SGk	56%	33.1	52.84372	Ref	-0.42	0.23	-0.19	0.04	-0.26	0.31	-0.15	95100	61200	1E+05	87800	113000	80400	1E+05	90200	583.6	1747.9	3	0.0167	9.564

Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_CAMBA,sp B0FY4 ITB1_SHEEP,sp P53712 ITB1_BOVIN,sp Q9GLP0 ITB1_PIG,tr C7AR56 C7AR56_LITWA,tr E2RT52 E2RT52_CANFA,tr F1RVE7 F1RVE7_PIG	dNTn EIYS Gk	94%	46	52.33189	Ref	-0.66	0.3	-0.12	0.096	-0.12	0.12	-0.11	5130	2750	5820	4880	6250	4700	5790	4890	875.4	1748.9	2	0.0205	11.7
Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_CAMBA,sp B0FY4 ITB1_SHEEP,sp P53712 ITB1_BOVIN,sp Q9GLP0 ITB1_PIG,tr C7AR56 C7AR56_LITWA,tr E2RT52 E2RT52_CANFA,tr F1RVE7 F1RVE7_PIG	iGFG SFVE k	61%	33	52.04996	Ref	-0.54	0.3	-0.03	0.055	-0.13	0.12	-0.13	5930	3720	7220	6420	7530	5780	7190	5990	796.5	1590.9	2	0.0077	4.812

Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_CAMBA,sp B0FYY4 ITB1_SHEEP,sp P53712 ITB1_BOVIN,sp Q9GLP0 ITB1_PIG,tra C7AR56 C7AR56_LITWA,tra E2RT52 E2RT52_CAF1RVE7 F1RVE7_PIG	ILVFS TDA GFH FAG DGk	90%	47	54.81507	Ref	-0.54	0.067	-0	-0.024	0.061	0.25	-0.02	1590	1080	1790	1920	2080	1930	2300	1890	797.4	2389.3	3	0.0121	5.057
Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_CAMBA,sp B0FYY4 ITB1_SHEEP,sp P53712 ITB1_BOVIN,sp Q9GLP0 ITB1_PIG,tra C7AR56 C7AR56_LITWA,tra E2RT52 E2RT52_CAF1RVE7 F1RVE7_PIG	ILVFS TDA GFH FAG DGk	59%	35.5	54.63171	Ref	-0.24	0.24	-0.03	-0.12	-0.22	0.057	-0.21	641	423	639	594	616	500	635	523	797.4	2389.3	3	0.004	1.68

Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_C AMBA,sp B0FY4 IT B1_SHEEP ,sp P5371 2 ITB1_B OVIN,sp Q9GLP0 TB1_PIG,t r C7AR56 C7AR56_ LITWA,tr E2RT52 E 2RT52_CA NFA,tr F1 RVE7 F1R VE7_PIG	IPEG VTIN Yk	81%	37.9	52.32289	Ref	-0.36	0.38	-0.12	-0.079	-0.17	-0.09	-0.16	14000	8380	15100	12100	13600	11200	12400	11700	871.5	1741	2	0.0196	11.26
Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_C AMBA,sp B0FY4 IT B1_SHEEP ,sp P5371 2 ITB1_B OVIN,sp Q9GLP0 TB1_PIG,t r C7AR56 C7AR56_ LITWA,tr E2RT52 E 2RT52_CA NFA,tr F1 RVE7 F1R VE7_PIG	nVLS LTDK GEVF NELV Gk	69%	33.7	52.58621	Ref	-0.45	0.11	0.065	-0.005	-0.15	0.2	0.054	907	660	1060	1150	1210	952	1270	1140	719.4	2873.6	4	0.027	9.386

Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_C AMBA,sp B0FYY4 IT B1_SHEEP ,sp P5371 2 ITB1_B OVIN,sp Q9GLP0 TB1_PIG,t r C7AR56 C7AR56_ LITWA,tr E2RT52 E 2RT52_CA NFA,tr F1 RVE7 F1R VE7_PIG	sAVT TVV NPK	95%	55.7	50.9626	Ref	-0.51	0.31	-0.07	0.061	-0.1	6E-04	-0.12	8700	5280	10100	8720	10500	8210	9180	8360	812.5	1623	2	0.0143	8.776
Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_C AMBA,sp B0FYY4 IT B1_SHEEP ,sp P5371 2 ITB1_B OVIN,sp Q9GLP0 TB1_PIG,t r C7AR56 C7AR56_ LITWA,tr E2RT52 E 2RT52_CA NFA,tr F1 RVE7 F1R VE7_PIG	sGEP QTFT Lk	81%	38.7	52.90645	Ref	-0.59	0.25	-0.13	0.02	-0.18	0.17	0.032	20100	11600	22600	19400	23800	18100	24000	21700	858.5	1714.9	2	0.0221	12.86

Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_C AMBA,sp B0FYY4 IT B1_SHEEP ,sp P5371 2 ITB1_B OVIN,sp Q9GLP0 TB1_PIG,t r C7AR56 C7AR56_ LITWA,tr E2RT52 E 2RT52_CA NFA,tr F1 RVE7 F1R VE7_PIG	SLGT DLM NEM R	94%	44	50.45124	Ref	-0.35	0.41	-0.19	-0.081	-0.16	0.17	-0.1	23000	17000	31300	23200	27500	22800	29800	24500	785.9	1569.8	2	0.0141	8.996
Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_C AMBA,sp B0FYY4 IT B1_SHEEP ,sp P5371 2 ITB1_B OVIN,sp Q9GLP0 TB1_PIG,t r C7AR56 C7AR56_ LITWA,tr E2RT52 E 2RT52_CA NFA,tr F1 RVE7 F1R VE7_PIG	SLGT DLM NEM R	59%	31.4	50.87817	Ref	-0.29	0.17	-0.01	-0.009	-0.24	0.21	-0.04	13800	10900	16300	16100	17800	13200	18800	15700	785.9	1569.8	2	0.0041	2.63

Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_CAMBA,sp B0FYY4 ITB1_SHEEP,sp P53712 ITB1_BOVIN,sp Q9GLP0 ITB1_PIG,tra C7AR56 C7AR56_LITWA,tra E2RT52 E2RT52_CANFA,tra F1RVE7 F1RVE7_PIG	tVM PYIS TTPA	90%	43.4	53.23743	Ref	-0.67	0.24	-0.1	0.046	-0.09	0.17	-0.03	17900	9870	20000	17700	21700	17200	21600	18700	959	1916.1	2	0.0205	10.68
Integrin beta-1 OS=Camelus bactrianus GN=ITGB1 PE=2 SV=1	sp A5Z1X6 ITB1_CAMBA,sp B0FYY4 ITB1_SHEEP,sp P53712 ITB1_BOVIN,sp Q9GLP0 ITB1_PIG,tra C7AR56 C7AR56_LITWA,tra E2RT52 E2RT52_CANFA,tra F1RVE7 F1RVE7_PIG	wDT GEN PIYK	95%	53.6	53.30576	Ref	-0.68	0.36	-0.02	0.04	-0.12	0.12	-0.2	20600	11100	24800	21300	24600	19200	23700	18800	916	1830	2	0.0211	11.52
LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT,tra D3ZIA3 D3ZIA3_RAT,tra F1LN56 F1LN56_RAT,tra F6PSB8 F6PSB8_HORSE	gFSV VAD TPEL QR	95%	53.4	52.97977	Ref	-0.86	0.13	-1.1	-0.076	-0.32	-0.27	-0.72	37200	18100	38800	18900	41800	30800	33300	24100	862	1721.9	2	0.0125	7.279

LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	gFSV VAD TPEL QR	94%	46.6	53.06238	Ref	-0.95	0.11	-0.85	-0.073	-0.35	-0.19	-0.79	18300	8810	19900	11500	21700	15700	18300	12000	862	1721.9	2	0.0124	7.209
LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	gFSV VAD TPEL QR	93%	45.8	53.07318	Ref	-1	0.08	-0.86	-0.053	-0.32	-0.28	-0.82	19000	7890	18300	10700	20700	15000	16100	11000	862	1721.9	2	0.0122	7.07
LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	gFSV VAD TPEL QR	95%	62.9	53.03337	Ref	-0.6	0.16	-1.1	-0.27	-0.26	-0.4	-0.64	16400	9810	18000	8730	16600	14600	13800	11600	575	1721.9	3	0.0112	6.476
LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	kPYc nAH YPk	67%	36.9	54.37817	Ref	-0.67	-0.13	-0.57	-0.18	-0.32	-0.26	-0.52	15500	9810	15500	12800	18500	14700	16000	13300	727.4	2179.1	3	0.0303	13.88

LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	mGPGGGEGIEPER	89%	39.2	49.67806	Ref	-1	0.18	-1.1	-0.15	-0.26	-0.34	-0.71	17400	7070	17500	7950	17300	14000	13800	10600	818.4	1634.8	2	0.0132	8.049
LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	mGPGGGEGIEPER	54%	31.9	52.09252	Ref	-0.73	0.15	-0.96	-0.18	-0.38	-0.14	-0.78	2450	1380	2760	1440	2720	2060	2550	1630	888.4	1774.9	2	0.0117	6.581
LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	qQSE LQS QVR	56%	32.6	52.57827	Ref	-1.1	0.11	-0.98	-0.093	-0.46	-0.14	-0.86	1E+05	36800	93000	49200	100000	67900	88400	53100	753.9	1505.8	2	0.0125	8.328
LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	qSFT MVA DTPE NLR	95%	73.7	52.41793	Ref	-0.74	-0.03	-0.81	-0.11	-0.33	-0.18	-0.7	7750	4380	7790	5070	9080	6820	7930	5470	957	1911.9	2	0.0211	11.03

LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	qSFT MVA DTPE NLR	95%	56.3	52.67944	Ref	-0.73	-0.03	-0.8	-0.15	-0.26	-0.26	-0.83	23800	12500	22000	14400	25000	20300	21200	14200	957	1912	2	0.0127	6.618		
LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	qSFT mVA DTPE NLR	93%	44.4	52.12704	Ref	-0.96	-0.15	-0.85	-0.093	-0.32	-0.17	-0.53	12400	5510	10500	7240	13500	10100	11700	9040	965	1927.9	2	0.0123	6.384		
LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	tGDT GML PAN YVEA I	52%	31.8	52.35094	Ref	Reference Missing (-0.21663873)	Reference Missing (-0.147758161.5612414)	Reference Missing (-0.46005102)	Reference Missing (-0.036757550.5646718)	Reference Missing (-0.564032019907)	Reference Missing (-0.32011.479343)	Reference Missing (-0.21663873)	Reference Missing (-0.147758161.5612414)	Reference Missing (-0.46005102)	Reference Missing (-0.036757550.5646718)	Reference Missing (-0.564032019907)	Reference Missing (-0.32011.479343)	Reference Missing (-0.21663873)	Reference Missing (-0.147758161.5612414)	Reference Missing (-0.46005102)	Reference Missing (-0.036757550.5646718)	Reference Missing (-0.564032019907)	928.5	1854.9	2	0.016	8.604
LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	tQD QISN ik	87%	43	53.46515	Ref	-1.1	0.021	-1.1	-0.26	-0.16	-0.14	-0.78	2E+05	60400	1E+05	71000	142000	1E+05	1E+05	90000	552.3	1653.9	3	0.0163	9.875		

LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	tQD QISN ik	95%	49.7	53.45889	Ref	-0.98	0.086	-0.88	0.014	-0.37	-0.25	-0.94	23600	10100	22800	13100	26900	17900	20400	12500	828	1653.9	2	0.0138	8.324
LIM and SH3 domain protein 1 OS=Rattus norvegicus GN=Lasp1 PE=1 SV=1	sp Q99MZ8 LASP1_RAT, tr D3ZIA3 D3ZIA3_RAT, tr F1LN56 F1LN56_RAT, tr F6PSB8 F6PSB8_HORSE	tQD QISN ik	94%	47.6	53.42906	Ref	-1.1	-0.09	-0.75	-0.079	-0.34	-0.27	-0.69	6910	2570	5600	3960	6960	5060	5560	4130	828	1653.9	2	0.019	11.49
Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS B0FYYS_SHEEP	aGT QLLA GLR	67%	31.8	49.64962	Ref	0.23	-0.06	0.4	-0.09	-0.2	-0.09	0.3	24400	25400	22700	35000	27400	22100	25000	32400	652.4	1302.8	2	0.0085	6.541
Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS B0FYYS_SHEEP	aLFL HNR	89%	41.5	50.05948	Ref	0.18	-0.1	0.3	-0.32	0.038	-0.33	0.71	4240	4950	4430	6570	4700	5260	4260	8700	392.2	1173.7	3	0.0055	4.686
Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS B0FYYS_SHEEP	aLFL HNR	83%	37.6	50.25425	Ref	0.04	-0.23	0.24	-0.036	0.05	-0.32	0.72	6670	6710	6040	9400	8540	7910	6400	13000	392.2	1173.7	3	0.0138	11.79
Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS B0FYYS_SHEEP	aLFL HNR	77%	35.4	50.13154	Ref	0.25	-0.1	0.39	-0.24	-0	-0.37	0.66	12500	17000	14400	22700	16200	16700	13500	27400	392.2	1173.7	3	0.0097	8.287

Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS B0FYYS_ SHEEP	aML HLQ WPK	57%	33.4	52.96002	Ref	0.12	-0.11	0.22	0.014	-0.08	0.094	0.098	3140	2610	2410	3410	3250	2650	3140	3120	632.4	1894.1	3	0.0068	3.605
Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS B0FYYS_ SHEEP	aSG DFQ TIK	69%	34.8	52.32831	Ref	0.13	-0.04	0.52	-0.22	-0.2	-0.18	0.41	23200	22600	21800	36000	23800	21100	22400	33300	787.9	1573.9	2	0.0073	4.637
Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS B0FYYS_ SHEEP	iLAc APly HWR	95%	56.7	52.65422	Ref	0.39	-0.25	0.36	-0.26	-0.12	0.18	0.038	551	602	419	717	515	495	636	571	565	1691.9	3	0.0118	6.955
Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS B0FYYS_ SHEEP	IDFQ VELL LDK	91%	45.2	51.46417	Ref	0.3	-0.18	0.28	-0.21	-0.22	0.086	-0.06	740	596	465	716	563	489	629	565	647.7	1940.1	3	0.0072	3.701
Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS B0FYYS_ SHEEP	IDFQ VELL LDK	95%	50	51.1225	Ref	0.26	-0.4	0.42	-0.019	0.099	-0.1	-0.03	239	216	148	294	239	227	207	214	647.7	1940.1	3	0.0017	0.872
Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS B0FYYS_ SHEEP	IQEV GQV SVAL Qk	95%	60.6	51.13067	Ref	-0.26	-0.44	0.12	-0.28	0.46	0.79	-0	6430	5610	5380	8890	7430	10900	14300	8180	669.7	2006.2	3	0.0168	8.384
Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS B0FYYS_ SHEEP	vDLA VVA AVEI R	88%	39.3	50.41811	Ref	0.19	0.1	0.3	-0.13	-0.1	-0.11	0.055	501	433	442	567	467	414	431	478	780	1557.9	2	0.0064	4.132

Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS_ B0FYYS_ SHEEP	vDLA VVA AVEI R	66%	31.8	49.90174	Ref	0.1	0.18	0.41	0.003	-0.34	-0.3	0.31	322	294	337	443	368	254	273	413	780	1557.9	2	#####	0.166
Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS_ B0FYYS_ SHEEP	vSPV VSYK	57%	30.6	50.12943	Ref	0.33	0.12	0.32	-0.35	-0.07	-0.04	0.11	13300	14000	13100	17000	11700	12400	13300	14600	496.3	1485.9	3	0.0035	2.333
Integrin subunit alphaV OS=Ovis aries PE=2 SV=1	tr B0FYYS_ B0FYYS_ SHEEP	ykEN PETE EDV GPV VQHI YELR	83%	41.3	55.74362	Ref	0.075	-0.2	0.48	-0.073	0.037	-0.05	0.31	1620	1640	1480	2650	1990	1880	1840	2360	813.9	3251.7	4	0.025	7.698
MHC class I antigen OS=Ovis aries GN=ovar PE=2 SV=1	tr A4ZVZ3_ A4ZVZ3_ SHEEP, tr C6K2P4 C6K2P4_SH EEP	dYIA LNED LR	55%	32.4	52.54611	Ref	-0.36	0.67	0.003	0.84	-0.67	0.54	-0.36	20800	7650	17100	12000	23700	7250	17500	9350	763.4	1524.8	2	0.0123	8.067
MHC class I antigen OS=Ovis aries GN=ovar PE=2 SV=1	tr A4ZVZ3_ A4ZVZ3_ SHEEP, tr C6K2P4 C6K2P4_SH EEP	dYIA LNED LR	50%	31.9	52.58055	Ref	0.48	-0.24	0.37	0.49	0.23	0.19	0.22	5230	4400	2890	4970	5930	4330	4400	4450	509.3	1524.8	3	0.011	7.186
MHC class I antigen OS=Ovis aries GN=ovar PE=2 SV=1	tr A4ZVZ3_ A4ZVZ3_ SHEEP, tr C6K2P4 C6K2P4_SH EEP	dYIA LNED LR	85%	40	52.59728	Ref	0.29	-1.2	-0.08	1.1	0.8	-1.4	-0.22	45500	22400	8770	21100	52600	37600	8300	19200	763.4	1524.8	2	0.0097	6.389
MHC class I antigen OS=Ovis aries GN=ovar PE=2 SV=1	tr A4ZVZ3_ A4ZVZ3_ SHEEP, tr C6K2P4 C6K2P4_SH EEP	fIAV GYV DDT QFV R	95%	58.8	54.02602	Ref	0.33	-0.63	0.81	-0.32	1	-0.72	0.98	2510	3390	1900	5770	2910	6430	2010	6460	967.5	1933	2	0.0173	8.952

MHC class I antigen OS=Ovis aries GN=ovar PE=2 SV=1	tr A4ZVZ3 A4ZVZ3_ SHEEP, tr C6K2P4 C 6K2P4_SH EEP	fIAV GYV DDT QFV R	95%	48.9	54.11446	Ref	0.033	-1.3	0.93	-0.26	1.1	-1.1	1.1	257	266	112	603	290	661	144	699	967.5	1933	2	0.0113	5.86
MHC class I antigen OS=Ovis aries GN=ovar PE=2 SV=1	tr A4ZVZ3 A4ZVZ3_ SHEEP, tr C6K2P4 C 6K2P4_SH EEP	fIAV GYV DDT QFV R	95%	62.6	54.14925	Ref	0.045	-1.8	0.98	-0.22	1.2	-1.4	1.1	585	652	201	1520	726	1720	297	1680	967.5	1933	2	0.0078	4.029
MHC class I antigen OS=Ovis aries GN=ovar PE=2 SV=1	tr A4ZVZ3 A4ZVZ3_ SHEEP, tr C6K2P4 C 6K2P4_SH EEP	fIAV GYV DDT QFV R	95%	51.9	54.14343	Ref	0.077	-1.5	0.92	-0.24	1.3	-1.3	1.1	397	480	169	1050	516	1320	226	1160	967.5	1933	2	0.0106	5.477
MHC class I antigen OS=Ovis aries GN=ovar PE=2 SV=1	tr A4ZVZ3 A4ZVZ3_ SHEEP, tr C6K2P4 C 6K2P4_SH EEP	fIAV GYV DDT QFV R	95%	49.6	54.11686	Ref	0.22	Value Missi ng (- 2.908 014)	1	-0.45	1.3	Value Missi ng (- 3.081 9821)	1.2	141	166	Value Missi ng (- 2.908 014)	357	140	412	Value Missi ng (- 3.0819 821)	402	967.5	1933	2	0.0066	3.398
MHC class I antigen OS=Ovis aries GN=ovar PE=2 SV=1	tr A4ZVZ3 A4ZVZ3_ SHEEP, tr C6K2P4 C 6K2P4_SH EEP	sWT AAD TAA QITQ R	95%	57.6	53.00041	Ref	0.64	0.062	0.14	0.18	0.8	7E-04	0.2	12800	15300	11100	13100	14900	20100	12000	13700	608.7	1822.9	3	0.0125	6.847
MHC class I antigen OS=Ovis aries GN=ovar PE=2 SV=1	tr A4ZVZ3 A4ZVZ3_ SHEEP, tr C6K2P4 C 6K2P4_SH EEP	sWT AAD TAA QITQ R	95%	65	53.01405	Ref	0.54	-1.5	0.39	0.056	1.6	-1.5	0.41	9100	10700	2790	11700	10300	25400	3210	11900	912.5	1822.9	2	0.0096	5.275

MHC class I antigen OS=Ovis aries GN=ovar PE=2 SV=1	tr A4ZVZ3 A4ZVZ3_ SHEEP, tr C6K2P4 C 6K2P4_SH EEP	wAA LVVP SGEE QR	71%	36.1	53.16503	Ref	0.31	-0.3	0.32	0.6	0.58	-0.27	0.17	9210	6270	4460	7700	10300	8860	5120	6920	873.5	1744.9	2	0.0083	4.737
MHC class I antigen OS=Ovis aries GN=ovar PE=2 SV=1	tr A4ZVZ3 A4ZVZ3_ SHEEP, tr C6K2P4 C 6K2P4_SH EEP	wVE QEG PEY WDR	91%	40.5	49.55496	Ref	0.43	-1.2	0.95	-0.79	1.2	-0.94	1.1	1230	2380	829	4170	1370	4860	1120	4510	949.4	1896.9	2	0.0232	12.2
MHC class I antigen OS=Ovis aries GN=ovar PE=2 SV=1	tr A4ZVZ3 A4ZVZ3_ SHEEP, tr C6K2P4 C 6K2P4_SH EEP	yTcH VQH EGL QEPL TLR	95%	53.4	55.30998	Ref	0.61	-0.33	0.54	-0.031	0.78	-0.12	0.55	3890	5160	2920	5980	4440	6830	3820	6030	670.4	2677.4	4	0.0187	6.975
Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_ SHEEP	dDN NLcL HFN PR	94%	42.7	49.14402	Ref	-0.46	0.2	-0.56	-0.17	-0.9	0.081	-1.1	3870	2380	4090	2710	3910	2050	4240	1910	904.4	1806.8	2	0.0113	6.269
Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_ SHEEP	dDN NLcL HFN PR	95%	63.5	49.15062	Ref	-0.31	-0.05	-0.39	-0.29	-0.29	-0.22	-0.48	5470	4800	6250	5560	6530	5710	6250	5210	603.3	1806.8	3	0.0122	6.748
Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_ SHEEP	fEAH GDIN TIVc nSk	78%	39.3	53.69943	Ref	-0.45	-0.1	-0.74	-0.25	-0.47	0.22	-0.84	8910	5730	7970	5720	8860	6630	11200	5340	768.4	2302.1	3	0.0165	7.175
Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_ SHEEP	fEAH GDIN TIVc nSk	56%	34	53.64219	Ref	-0.34	-0.04	-0.64	-0.3	-0.61	0.22	-0.66	6110	4830	6450	4770	6660	4670	8680	4700	768.4	2302.1	3	0.0187	8.126
Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_ SHEEP	fEAH GDIN TIVc nSk	87%	41.5	53.63847	Ref	-0.42	7E-04	-0.71	-0.25	-0.37	0.22	-0.85	4620	3540	5150	3540	5360	4300	6750	3210	576.5	2302.1	4	0.0187	8.111

Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_SHEEP	gEVA ADAK	56%	32	51.65007	Ref	-0.78	0.53	-0.63	-0.28	-0.66	-0	-0.73	41100	25500	68500	34500	48500	32500	53600	32100	456.9	1367.8	3	0.024	17.57
Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_SHEEP	gEVA ADAK	76%	36.7	51.64992	Ref	-0.89	0.22	-0.64	-0.48	-0.48	0.2	-0.69	36200	17100	40100	24700	30400	26700	44500	23800	456.9	1367.8	3	0.0237	17.35
Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_SHEEP	gEVA ADAK	95%	46.7	51.74135	Ref	-0.41	0.37	-0.83	-0.3	-0.65	0.06	-1.2	40200	26000	48500	23700	37700	25800	44200	18400	684.9	1367.8	2	0.0036	2.653
Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_SHEEP	INLE AINY LAA GGD Fk	95%	57.4	54.08789	Ref	-0.52	-0	-0.6	-0.25	-0.73	0.21	-0.61	1010	656	1020	753	1060	663	1330	751	773.1	2316.3	3	0.0126	5.453
Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_SHEEP	INLE AINY LAA GGD Fk	94%	52.4	54.1255	Ref	-1.1	0.27	-0.56	-0.077	-0.79	-0.04	-0.9	311	109	305	194	298	159	278	152	773.1	2316.3	3	0.0145	6.242
Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_SHEEP	INLE AINY LAA GGD Fk	81%	37.1	52.43666	Ref	-0.28	0.051	-0.62	-0.28	-0.8	0.22	-1.1	3620	2570	3510	2470	3450	2100	4440	1770	656.1	2620.5	4	0.0026	0.975
Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_SHEEP	IPDG YEFK	54%	32.3	52.47123	Ref	-0.6	0.33	-1.2	-0.2	-0.85	0.37	-1.3	74500	40500	83600	32500	71700	40000	97100	30100	788.9	1575.9	2	0.0156	9.892
Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_SHEEP	sFSL NLGk	76%	35.4	51.29799	Ref	-0.46	0.18	-0.63	-0.23	-0.8	0.1	-0.99	21900	13500	22600	14600	21100	12400	24200	11300	737.4	1472.9	2	0.0221	14.97
Galectin-1 OS=Ovis aries PE=2 SV=1	tr Q6J275 Q6J275_SHEEP	sFSL NLGk	68%	33.5	50.91087	Ref	-0.36	0.29	-1.1	-0.26	-0.75	0.22	-1.4	74800	46300	79000	33900	66800	41300	84400	27200	492	1472.9	3	0.0146	9.93

Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	aVEH LDDL PGAL SELS DLH AHK	92%	44.4	55.36075	Ref	0.48	0.49	0.5	0.81	0.31	1.2	0.44	2370	2960	3210	3650	4960	3070	5930	3490	595.9	2974.6	5	0.0156	5.229
Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	aVEH LDDL PGAL SELS DLH AHK	82%	40.7	55.46075	Ref	0.35	0.68	0.56	0.65	0.55	0.79	0.54	2180	1930	2610	2700	3170	2590	3200	2670	744.6	2974.6	4	0.0316	10.63
Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	aVEH LDDL PGAL SELS DLH AHk	89%	41.3	55.30874	Ref	0.55	0.55	0.54	0.74	0.4	0.96	0.58	1690	2140	2320	2590	3260	2260	3470	2650	595.9	2974.6	5	0.0122	4.103
Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	IRVD PVN Fk	63%	30.4	50.54701	Ref	0.11	0.3	0.51	0.77	0.39	1	0.98	2480	2190	2720	3530	4640	3110	5110	4860	424.8	1695	4	0.0049	2.873
Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	mFLS FPTT k	74%	36.3	52.66653	Ref	0.17	0.86	0.56	0.82	0.32	1.1	0.35	4160	4220	7430	6770	8940	5510	9960	5810	840.5	1678.9	2	0.0172	10.23
Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	vAA ALTK	81%	37.1	50.59473	Ref	0.041	0.74	0.49	0.87	0.32	1.1	0.47	77800	65200	1E+05	109000	156000	92800	2E+05	107000	427.9	1280.8	3	0.0131	10.2

Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	vAA ALTK	81%	37.4	50.58532	Ref	-0.34	0.85	0.52	0.85	0.11	1.3	0.62	71500	50300	1E+05	111000	154000	80300	2E+05	119000	427.9	1280.8	3	0.0122	9.493
Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	vAA ALTK	51%	29.9	50.57156	Ref	0.16	0.76	0.49	0.76	0.38	1.1	0.56	48400	47200	77800	72500	96500	64700	1E+05	75800	641.4	1280.8	2	0.0051	3.981
Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	vGG HAA EYG AEAL ER	95%	56	52.26984	Ref	0.053	0.69	0.56	0.8	0.34	1.2	0.51	4120	3810	6420	6590	8570	5450	10300	6370	917.5	1832.9	2	0.0149	8.112
Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	vGG HAA EYG AEAL ER	95%	58.5	52.27436	Ref	0.21	0.36	0.64	0.67	0.76	0.63	0.75	13900	10600	12800	17400	19500	18200	17300	18700	612	1832.9	3	0.0142	7.717
Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	vGG HAA EYG AEAL ER	95%	56.1	52.24957	Ref	0.67	0.67	0.5	0.73	0.56	0.75	0.71	14200	24700	26800	26800	34600	26900	31900	30900	612	1832.9	3	0.0138	7.521
Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	vGG HAA EYG AEAL ER	95%	52.1	52.29971	Ref	0.16	0.77	0.51	0.83	0.35	1	0.53	2840	2650	4400	4110	5680	3540	5960	4170	917.5	1832.9	2	0.0135	7.37

Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	vGGHAAEYGAERAL	89%	43.5	52.32371	Ref	0.57	0.65	0.56	0.47	0.6	0.61	0.72	9010	9490	10900	11500	11900	11300	12000	12800	612	1832.9	3	0.0129	7.014
Hemoglobin subunit alpha OS=Bos taurus GN=HBA PE=1 SV=2	sp P01966 HBA_BOVIN,sp P01967 HBA1_BOSMU	vGGHAAEYGAERAL	61%	35.1	54.08603	Ref	0.26	0.73	0.63	0.68	0.52	0.99	0.58	1070	1250	1880	1970	2250	1760	2530	1900	1070	2137.1	2	0.0166	7.754
10 kDa heat shock protein, mitochondrial OS=Bos taurus GN=HSPE1 PE=2 SV=2	3 CH10_BOVIN,sp P61604 CH10_HUMAN,tr B8ZZL8_HUMAN,tr D2HDI2 D2HDI2_AILME,tr E2QUS9 E2QUS9_CANFA,tr F6T494 CALJA,tr F6U6U2 F6U6U2_MACMU,tr F6U8E5 F6U8E5_ORNAN,tr F7B G90 F7B G90_MACMU,tr Q6WSP6 Q6	gGIMLP	55%	31.1	51.15887	Ref	-0.26	-0.16	0.003	-0.067	0.2	-0.37	0.049	32500	20600	23900	30000	31500	33100	23300	30900	726.9	1451.8	2	0.0268	18.46

10 kDa heat shock protein, mitochondrial OS=Bos taurus GN=HSPE1 PE=2 SV=2	3 CH10_BOVIN.sp P61604 C H10_HUMAN,tr B8ZZL8 B8ZZL8_HUMAN,tr D2HDI2 D2HDI2_AILME,tr E2QUS9 E2QUS9_CANFA,tr F6T494 F6T494_CALIA,tr F6U6U2 F6U6U2_MACMU,tr F6U8E5 F6U8E5_ORNAN,tr F7BG90 F7BG90_MACMU,tr Q6WSP6 Q6	gGI MLP Ek	72%	34.5	51.23028	Ref	-0.083	-0.05	0.004	-0.13	0.33	-0.44	0.055	16600	14700	16300	19000	19000	22900	14000	19600	726.9	1451.8	2	0.0274	18.89
	3 CH10_BOVIN.sp P61604 C H10_HUMAN,tr B8ZZL8 B8ZZL8_HUMAN,tr D2HDI2 D2HDI2_AILME,tr E2QUS9 E2QUS9_CANFA,tr F6T494 F6T494_CALIA,tr F6U6U2 F6U6U2_MACMU,tr F6U8E5 F6U8E5_ORNAN,tr F7BG90 F7BG90_MACMU,tr Q6WSP6 Q6	sAAE TVTK	88%	40.4	51.49662	Ref	-0.12	-0.04	0.065	0.017	0.23	-0.66	0.063	22300	18100	20800	25100	26700	27100	15200	25000	707.9	1413.8	2	0.0248	17.5

10 kDa heat shock protein, mitochondrial OS=Bos taurus GN=HSPE1 PE=2 SV=2	3 CH10_B OVIN,sp P61604 C H10_HU MAN,tr B 8ZZL8 B8 ZZL8_HU MAN,tr D 2HDI2 D2 HDI2_AIL ME,tr E2 QUS9 E2 QUS9_CA NFA,tr F6 T494 F6T 494_CALJ A,tr F6U6 U2 F6U6 U2_MAC MU,tr F6 U8E5 F6U 8E5_ORN AN,tr F7B G90 F7B G90_MAC MU,tr Q6 WSP6 Q6	VLLP EYG GTK	88%	40.2	51.65265	Ref	-0.19	-0.07	0.092	-0.066	0.32	-0.55	0.091	22800	18400	21800	27300	27000	30900	17600	27300	843	1684	2	0.0188	11.15
	3 CH10_B OVIN,sp P61604 C H10_HU MAN,tr B 8ZZL8 B8 ZZL8_HU MAN,tr D 2HDI2 D2 HDI2_AIL ME,tr E2 QUS9 E2 QUS9_CA NFA,tr F6 T494 F6T 494_CALJ A,tr F6U6 U2 F6U6 U2_MAC MU,tr F6 U8E5 F6U 8E5_ORN AN,tr F7B G90 F7B G90_MAC MU,tr Q6 WSP6 Q6	VLLP EYG GTK	92%	42.8	51.41914	Ref	-0.17	0.007	-0.02	-0.063	0.37	-0.58	0.11	9120	7730	9500	10500	11200	13200	7150	11400	843	1684	2	0.0135	8.024

10 kDa heat shock protein, mitochondrial OS=Bos taurus GN=HSPE1 PE=2 SV=2	3 CH10_BOVIN.sp P61604 C	vLQA TVV AVG SGSk	95%	70.1	51.42933	Ref	-0.26	-0.37	-0	-0.23	0.38	-0.36	0.25	7540	5160	5220	7540	7110	9430	5920	8960	642.1	1923.1	3	0.0256	13.32
	H10_HUMAN,tr B8ZZL8 B8ZZL8_HUMAN,tr D2HDI2 D2HDI2_AILME,tr E2QUS9 E2QUS9_CANFA,tr F6T494 F6T494_CALIA,tr F6U6U2 F6U6U2_MACMU,tr F6U8E5 F6U8E5_ORNAN,tr F7B																									
10 kDa heat shock protein, mitochondrial OS=Bos taurus GN=HSPE1 PE=2 SV=2	G90 F7B	vLQA TVV AVG SGSk	95%	69.8	51.17888	Ref	-0.15	0.058	-0.05	-0.077	0.2	-0.22	-0.13	8730	6800	8490	8860	9570	10100	7910	8360	642.1	1923.1	3	0.0218	11.32
	G90 F7B G90_MAC MU,tr Q6 WSP6 Q6																									

10 kDa heat shock protein, mitochondrial OS=Bos taurus GN=HSPE1 PE=2 SV=2	3 CH10_B OVIN,sp P61604 C H10_HU MAN,tr B 8ZZL8 B8 ZZL8_HU MAN,tr D 2HDI2 D2 HDI2_AIL ME,tr E2 QUS9 E2 QUS9_CA NFA,tr F6 T494 F6T 494_CALJ A,tr F6U6 U2 F6U6 U2_MAC MU,tr F6 U8E5 F6U 8E5_ORN AN,tr F7B G90 F7B G90_MAC MU,tr Q6 WSP6 Q6	VLQA TVV AVG SGSk	95%	57	51.07329	Ref	0.3	-0.33	0.01	-0.14	0.2	-0.52	-0.05	8190	8390	5880	8370	8300	9160	5820	8010	642.1	1923.1	3	0.0203	10.56
	3 CH10_B OVIN,sp P61604 C H10_HU MAN,tr B 8ZZL8 B8 ZZL8_HU MAN,tr D 2HDI2 D2 HDI2_AIL ME,tr E2 QUS9 E2 QUS9_CA NFA,tr F6 T494 F6T 494_CALJ A,tr F6U6 U2 F6U6 U2_MAC MU,tr F6 U8E5 F6U 8E5_ORN AN,tr F7B G90 F7B G90_MAC MU,tr Q6 WSP6 Q6	VLQA TVV AVG SGSk	95%	73.1	50.96093	Ref	-0.39	-0.71	0.094	0.074	0.38	-0.6	0.35	21700	13500	11800	23100	25100	27200	14300	27500	642.1	1923.1	3	0.0176	9.124

10 kDa heat shock protein, mitochondrial OS=Bos taurus GN=HSPE1 PE=2 SV=2	3 CH10_B OVIN,sp P61604 C H10_HU MAN,tr B 8ZZL8 B8 ZZL8_HU MAN,tr D 2HDI2 D2 HDI2_AIL ME,tr E2 QUS9 E2 QUS9_CA NFA,tr F6 T494 F6T 494_CALJ A,tr F6U6 U2 F6U6 U2_MAC MU,tr F6 U8E5 F6U 8E5_ORN AN,tr F7B G90 F7B G90_MAC MU,tr Q6 WSP6 Q6	VLQA TVV AVG SGSK	95%	69	50.90614	Ref	-0.02	-0.07	0.12	-0.31	0.098	-0.32	0.033	10700	8590	8980	11500	9420	10900	8530	10800	642.1	1923.1	3	0.0157	8.173
	3 CH10_B OVIN,sp P61604 C H10_HU MAN,tr B 8ZZL8 B8 ZZL8_HU MAN,tr D 2HDI2 D2 HDI2_AIL ME,tr E2 QUS9 E2 QUS9_CA NFA,tr F6 T494 F6T 494_CALJ A,tr F6U6 U2 F6U6 U2_MAC MU,tr F6 U8E5 F6U 8E5_ORN AN,tr F7B G90 F7B G90_MAC MU,tr Q6 WSP6 Q6	VLQA TVV AVG SGSK	95%	72.7	50.74077	Ref	-0.097	-0.33	0.13	-0.24	0.36	-0.59	0.19	7410	5890	5440	8380	7170	9490	5110	8750	642.1	1923.1	3	0.0141	7.316

10 kDa heat shock protein, mitochondrial OS=Bos taurus GN=HSPE1 PE=2 SV=2	3 CH10_B OVIN.sp P61604 C H10_HU MAN,tr B 8ZZL8 B8 ZZL8_HU MAN,tr D 2HDI2 D2 HDI2_AIL ME,tr E2 QUS9 E2 QUS9_CA NFA,tr F6 T494 F6T 494_CALJ A,tr F6U6 U2 F6U6 U2_MAC MU,tr F6 U8E5 F6U 8E5_ORN AN,tr F7B G90 F7B G90_MAC MU,tr Q6 WSP6 Q6	VLQA TVV AVG SGSk	95%	79.7	50.32562	Ref	-0.1	-0.22	0.024	-0.22	0.28	-0.29	0.15	2870	2390	2380	3180	2970	3650	2570	3470	962.6	1923.2	2	0.0075	3.919
	3 CH10_B OVIN.sp P61604 C H10_HU MAN,tr B 8ZZL8 B8 ZZL8_HU MAN,tr D 2HDI2 D2 HDI2_AIL ME,tr E2 QUS9 E2 QUS9_CA NFA,tr F6 T494 F6T 494_CALJ A,tr F6U6 U2 F6U6 U2_MAC MU,tr F6 U8E5 F6U 8E5_ORN AN,tr F7B G90 F7B G90_MAC MU,tr Q6 WSP6 Q6	VLQA TVV AVG SGSk	95%	58.8	50.97178	Ref	-0.099	-0.16	0.071	-0.09	0.046	-0.08	0.005	8880	7270	7560	9960	9830	9430	9000	9490	642.1	1923.1	3	0.0174	9.031

10 kDa heat shock protein, mitochondrial OS=Bos taurus GN=HSPE1 PE=2 SV=2	3 CH10_BOVIN.sp P61604 C H10_HUMAN,tr B8ZZL8 B8ZZL8_HUMAN,tr D2HDI2 D2HDI2_AILME,tr E2QUS9 E2QUS9_CANFA,tr F6T494 F6T494_CALIA,tr F6U6U2 F6U6U2_MACMU,tr F6U8E5 F6U8E5_ORNAN,tr F7B90 F7B90_MACMU,tr Q6WSP6 Q6	vLQA TVV AVG	95%	75.2	50.74077	Ref	-0.16	-0.02	0.11	-0.27	0.2	-0.41	0.19	5880	4780	5720	7030	5960	7170	4910	7430	642.1	1923.1	3	0.0139	7.222
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	5 LMNA_HUMAN,sp P48678 LMNA_MOUSE,tr A5A6M1 A5A6M1_PANTR,tr B3RH23 B3RH23_MOUSE,tr B3RH24 B3RH24_MOUSE,tr F1MYG5 F1MYG5_BOVIN,tr F1PBJ3 F1PBJ3_CANFA,tr F6ZY40 F6ZY40_HORSE,tr F7GLE9 F7GLE9_MACMU,tr Q3SZI2 Q3S	aAYE AELG DAR	93%	43.6	50.92075	Ref	-0.3	-0.42	-0.68	-0.075	-0.52	-0.48	-0.41	66600	49500	49500	46400	77700	49800	53700	55700	735.4	1468.7	2	0.0107	7.296

Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	5 LMNA_ HUMAN,s p P48678 LMNA_ MOUSE,tr A5A6M1 A5A6M1 _PANTR,tr B3RH23 B3RH23_ MOUSE,tr B3RH24 B3RH24_ MOUSE,tr F1MYG5 F1MYG5 _BOVIN,tr F1PBJ3 F1PBJ3_C ANFA,tr F 6ZY40 F6 ZY40_HO RSE,tr F7 GLE9 F7G LE9_MAC MU,tr Q3 SZ12 Q3S	ITESE EVVS R	72%	35	51.77779	Ref	-0.22	-0.29	-0.75	-0.21	-0.53	-0.44	-0.56	86800	64900	66900	54700	87800	61400	67900	62400	726.9	1451.8	2	0.0141	9.725
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	5 LMNA_ HUMAN,s p P48678 LMNA_ MOUSE,tr A5A6M1 A5A6M1 _PANTR,tr B3RH23 B3RH23_ MOUSE,tr B3RH24 B3RH24_ MOUSE,tr F1MYG5 F1MYG5 _BOVIN,tr F1PBJ3 F1PBJ3_C ANFA,tr F 6ZY40 F6 ZY40_HO RSE,tr F7 GLE9 F7G LE9_MAC MU,tr Q3 SZ12 Q3S	IADA LQEL R	56%	32.6	52.43222	Ref	-0.39	-0.47	-0.64	-0.22	-0.5	-0.37	-0.27	27400	19200	19800	19700	29000	20800	23800	25300	666.9	1331.8	2	0.0111	8.321

Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	5 LMNA_ HUMAN,s p P48678 LMNA_ MOUSE,tr A5A6M1 A5A6M1 _PANTR,tr B3RH23 B3RH23_ MOUSE,tr B3RH24 B3RH24_ MOUSE,tr F1MYG5 F1MYG5 _BOVIN,tr F1PBJ3 F1PBJ3_C ANFA,tr F6ZY40 F6ZY40_HO RSE,tr F7GLE9 F7GLE9_MAC MU,tr Q3SZI2 Q3S	IALD MEI HAY R	86%	41.8	52.67341	Ref	-0.32	-0.53	-0.63	-0.11	-0.6	-0.42	-0.41	9640	6620	6210	6490	10300	6380	7540	7530	546	1634.9	3	0.0136	8.284
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	5 LMNA_ HUMAN,s p P48678 LMNA_ MOUSE,tr A5A6M1 A5A6M1 _PANTR,tr B3RH23 B3RH23_ MOUSE,tr B3RH24 B3RH24_ MOUSE,tr F1MYG5 F1MYG5 _BOVIN,tr F1PBJ3 F1PBJ3_C ANFA,tr F6ZY40 F6ZY40_HO RSE,tr F7GLE9 F7GLE9_MAC MU,tr Q3SZI2 Q3S	IALD MEI HAY R	91%	46.4	52.68272	Ref	-0.096	-0.41	-0.48	-0.32	-0.52	-0.48	-0.5	5950	5290	4620	4940	6090	4620	4960	4860	546	1634.9	3	0.0148	9.055

Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	5 LMNA_ HUMAN,s p P48678 LMNA_ MOUSE,tr A5A6M1 A5A6M1 _PANTR,tr B3RH23 B3RH23_ MOUSE,tr B3RH24 B3RH24_ MOUSE,tr F1MYG5 F1MYG5 _BOVIN,tr F1PBJ3 F1PBJ3_C ANFA,tr F 6ZY40 F6 ZY40_HO RSE,tr F7 GLE9 F7G LE9_MAC MU,tr Q3 SZ12 Q3S	IEAA LGEA k	95%	49.4	51.02471	Ref	-0.26	-0.54	-0.77	-0.17	-0.52	-0.4	-0.54	52400	34200	30600	29300	48900	33500	38100	34300	504	1508.9	3	0.0087	5.738
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	5 LMNA_ HUMAN,s p P48678 LMNA_ MOUSE,tr A5A6M1 A5A6M1 _PANTR,tr B3RH23 B3RH23_ MOUSE,tr B3RH24 B3RH24_ MOUSE,tr F1MYG5 F1MYG5 _BOVIN,tr F1PBJ3 F1PBJ3_C ANFA,tr F 6ZY40 F6 ZY40_HO RSE,tr F7 GLE9 F7G LE9_MAC MU,tr Q3 SZ12 Q3S	IEAA LGEA k	91%	44.7	50.98062	Ref	-0.33	-0.31	-0.8	-0.4	-0.56	-0.41	-0.35	9240	5850	6440	5150	7460	5830	6760	6990	504	1508.9	3	0.0049	3.254

Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	5 LMNA_ HUMAN,s p P48678 LMNA_ MOUSE,tr A5A6M1 A5A6M1 _PANTR,tr B3RH23 B3RH23_ MOUSE,tr B3RH24 B3RH24_ MOUSE,tr F1MYG5 F1MYG5 _BOVIN,tr F1PBJ3 F1PBJ3_C ANFA,tr F6ZY40 F6ZY40_HO RSE,tr F7GLE9 F7GLE9_MAC MU,tr Q3SZI2 Q3S	IRDLEDSL	AR	89%	44.1	52.7434	Ref	-0.19	-0.25	-0.21	-0.35	-0.69	-0.52	-0.47	5060	4620	4810	5540	5550	3810	4490	4620	498	1490.8	3	0.007	4.692
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	5 LMNA_ HUMAN,s p P48678 LMNA_ MOUSE,tr A5A6M1 A5A6M1 _PANTR,tr B3RH23 B3RH23_ MOUSE,tr B3RH24 B3RH24_ MOUSE,tr F1MYG5 F1MYG5 _BOVIN,tr F1PBJ3 F1PBJ3_C ANFA,tr F6ZY40 F6ZY40_HO RSE,tr F7GLE9 F7GLE9_MAC MU,tr Q3SZI2 Q3S	SGA QAS STPL	SPT	95%	60.3	52.82982	Ref	-0.38	-0.4	-1.1	-0.15	-0.48	-0.48	-0.28	27500	17100	18400	13100	27000	18800	19600	22300	832.4	1662.9	2	0.0111	6.661

Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	5 LMNA_ HUMAN,s p P48678 LMNA_ MOUSE,tr A5A6M1 A5A6M1 _PANTR,tr B3RH23 B3RH23_ MOUSE,tr B3RH24 B3RH24_ MOUSE,tr F1MYG5 F1MYG5 _BOVIN,tr F1PBJ3 F1PBJ3_C ANFA,tr F 6ZY40 F6 ZY40_HO RSE,tr F7 GLE9 F7G LE9_MAC MU,tr Q3 SZI2 Q3S	tALI NST GEE VAM R	94%	47	53.01397	Ref	-0.43	-0.21	-0.78	-0.21	-0.59	-0.4	-0.34	5190	3440	4340	3280	5350	3610	4290	4440	898.5	1794.9	2	0.0137	7.603
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	5 LMNA_ HUMAN,s p P48678 LMNA_ MOUSE,tr A5A6M1 A5A6M1 _PANTR,tr B3RH23 B3RH23_ MOUSE,tr B3RH24 B3RH24_ MOUSE,tr F1MYG5 F1MYG5 _BOVIN,tr F1PBJ3 F1PBJ3_C ANFA,tr F 6ZY40 F6 ZY40_HO RSE,tr F7 GLE9 F7G LE9_MAC MU,tr Q3 SZI2 Q3S	tLDS VAK	60%	31	50.3387	Ref	-0.29	-0.52	-0.59	-0.19	-0.56	-0.41	-0.46	45900	31500	29000	31000	45400	30700	35500	33900	671.4	1340.8	2	0.0016	1.166

Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	5 LMNA_ HUMAN,s p P48678 LMNA_ MOUSE,tr A5A6M1 A5A6M1 _PANTR,tr B3RH23 B3RH23_ MOUSE,tr B3RH24 B3RH24_ MOUSE,tr F1MYG5 F1MYG5 _BOVIN,tr F1PBJ3 F1PBJ3_C ANFA,tr F 6ZY40 F6 ZY40_HO RSE,tr F7 GLE9 F7G LE9_MAC MU,tr Q3 SZI2 Q3S	tLEG ELHD LR	95%	64.4	52.39985	Ref	-0.29	-0.37	-0.65	-0.31	-0.45	-0.33	-0.51	23000	16600	17000	15800	22000	17400	19800	17400	496.3	1485.8	3	0.0117	7.883
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	5 LMNA_ HUMAN,s p P48678 LMNA_ MOUSE,tr A5A6M1 A5A6M1 _PANTR,tr B3RH23 B3RH23_ MOUSE,tr B3RH24 B3RH24_ MOUSE,tr F1MYG5 F1MYG5 _BOVIN,tr F1PBJ3 F1PBJ3_C ANFA,tr F 6ZY40 F6 ZY40_HO RSE,tr F7 GLE9 F7G LE9_MAC MU,tr Q3 SZI2 Q3S	vAVE EVDE EGk	95%	53.4	53.88953	Ref	-0.19	-0.43	-0.81	-0.26	-0.66	-0.45	-0.72	29800	18300	16800	14500	23400	15400	18700	15300	906.5	1811	2	0.0112	6.182

Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	sp P08113 ENPL_MOUSE,s p Q66HD0 ENPL_RAT,sp Q95M18 ENPL_BOVIN,tr F1MZ62 F1MZ62_BOVIN,tr Q3UAD6 Q3UAD6_MOUSE,tr Q3UBU0 Q3UBU0_MOUSE,SE,tr Q91V38 Q91V38_MOUSE,SE	dIST NY ASQ k	95%	51.5	53.45017	Ref	-0.3	-0.09	-0.11	-0.15	-0.12	-0.29	-0.37	9920	7060	8840	9780	10500	9350	8720	8180	949.5	1897	2	0.014	7.384
Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	sp P08113 ENPL_MOUSE,s p Q66HD0 ENPL_RAT,sp Q95M18 ENPL_BOVIN,tr F1MZ62 F1MZ62_BOVIN,tr Q3UAD6 Q3UAD6_MOUSE,tr Q3UBU0 Q3UBU0_MOUSE,SE,tr Q91V38 Q91V38_MOUSE,SE	eEAS DYLE LDTI k	83%	41.8	54.22795	Ref	0.032	-0.25	-0.01	-0.21	-0.46	-0.17	-0.54	12100	10200	9100	12100	11600	8510	10900	8330	712	2133.1	3	0.0094	4.424

<p>Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2</p>	<p>sp P08113 ENPL_MOUSE,s p Q66HD0 ENPL_RAT,sp Q95M18 ENPL_BOVIN,tr F1MZ62 F1MZ62_BOVIN,tr Q3UAD6 Q3UAD6_MOUSE,tr Q3UBU0 Q3UBU0_MOUSE,SE,tr Q91V38 Q91V38_MOUSE,SE</p>	<p>eVEE DEYK</p>	<p>50%</p>	<p>31.5</p>	<p>52.08549</p>	<p>Ref</p>	<p>0.12</p>	<p>-0.38</p>	<p>-0.16</p>	<p>-0.2</p>	<p>-0.45</p>	<p>-0.03</p>	<p>-0.53</p>	<p>57900</p>	<p>51800</p>	<p>39900</p>	<p>52100</p>	<p>55800</p>	<p>40800</p>	<p>57100</p>	<p>40200</p>	<p>550.3</p>	<p>1647.8</p>	<p>3</p>	<p>0.0103</p>	<p>6.257</p>
<p>Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2</p>	<p>sp P08113 ENPL_MOUSE,s p Q66HD0 ENPL_RAT,sp Q95M18 ENPL_BOVIN,tr F1MZ62 F1MZ62_BOVIN,tr Q3UAD6 Q3UAD6_MOUSE,tr Q3UBU0 Q3UBU0_MOUSE,SE,tr Q91V38 Q91V38_MOUSE,SE</p>	<p>eVEE DEYK</p>	<p>64%</p>	<p>33.6</p>	<p>52.1459</p>	<p>Ref</p>	<p>0.22</p>	<p>-0.22</p>	<p>-0.15</p>	<p>-0.3</p>	<p>-0.63</p>	<p>-0.11</p>	<p>-0.74</p>	<p>33400</p>	<p>28900</p>	<p>23100</p>	<p>27200</p>	<p>26900</p>	<p>18800</p>	<p>28100</p>	<p>18000</p>	<p>824.9</p>	<p>1647.8</p>	<p>2</p>	<p>0.0084</p>	<p>5.095</p>

Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	sp P08113 ENPL_MOUSE,s p Q66HD0 ENPL_RAT,sp Q95M18 ENPL_BOVIN,tr F1MZ62 F1MZ62_BOVIN,tr Q3UAD6 Q3UAD6_MOUSE,tr Q3UBU0 Q3UBU0_MOUSE,SE,tr Q91V38 Q91V38_MOUSE	gLFD EYGS k	87%	41	52.7231	Ref	0.11	-0.26	-0.27	-0.13	-0.48	-0.02	-0.63	21000	18300	15400	17100	20700	14200	20500	13300	812.4	1622.9	2	0.0074	4.576
Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	sp P08113 ENPL_MOUSE,s p Q66HD0 ENPL_RAT,sp Q95M18 ENPL_BOVIN,tr F1MZ62 F1MZ62_BOVIN,tr Q3UAD6 Q3UAD6_MOUSE,tr Q3UBU0 Q3UBU0_MOUSE,SE,tr Q91V38 Q91V38_MOUSE	gVV DSD DLPL NVS R	95%	52	53.12628	Ref	0.19	-0.18	-0.16	-0.22	-0.68	0.04	-0.55	9750	9960	8400	9520	10100	6410	11000	7240	895.5	1788.9	2	0.0143	7.966

<p>Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2</p>	<p>sp P08113 ENPL_MOUSE,s p Q66HD0 ENPL_RAT,sp Q95M18 ENPL_BOVIN, tr F1MZ62 F1MZ62_BOVIN, tr Q3UAD6 Q3UAD6_MOUSE, tr Q3UBU0 Q3UBU0_MOUSE, tr Q91V38 Q91V38_MOUSE SE</p>	<p>IIINS LYk</p>	<p>88%</p>	<p>36.8</p>	<p>47.88218</p>	<p>Ref</p>	<p>0.025</p>	<p>-0.17</p>	<p>-0.11</p>	<p>-0.25</p>	<p>-0.37</p>	<p>-0.17</p>	<p>-0.7</p>	<p>9630</p>	<p>7480</p>	<p>7070</p>	<p>8270</p>	<p>8270</p>	<p>6670</p>	<p>7980</p>	<p>5480</p>	<p>786.5</p>	<p>1571</p>	<p>2</p>	<p>0.0099</p>	<p>6.278</p>
<p>Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2</p>	<p>sp P08113 ENPL_MOUSE,s p Q66HD0 ENPL_RAT,sp Q95M18 ENPL_BOVIN, tr F1MZ62 F1MZ62_BOVIN, tr Q3UAD6 Q3UAD6_MOUSE, tr Q3UBU0 Q3UBU0_MOUSE, tr Q91V38 Q91V38_MOUSE SE</p>	<p>IISLT DEN ALA GNE ELTV k</p>	<p>95%</p>	<p>73.4</p>	<p>54.34467</p>	<p>Ref</p>	<p>-0.044</p>	<p>-0.3</p>	<p>-0.13</p>	<p>-0.16</p>	<p>-0.11</p>	<p>-0.19</p>	<p>-0.43</p>	<p>4220</p>	<p>3760</p>	<p>3410</p>	<p>4320</p>	<p>4650</p>	<p>4220</p>	<p>4160</p>	<p>3500</p>	<p>880.2</p>	<p>2637.5</p>	<p>3</p>	<p>0.0151</p>	<p>5.731</p>

Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	sp P08113 ENPL_MOUSE,s p Q66HD0 ENPL_RAT,sp Q95M18 ENPL_BOVIN,tr F1MZ62 F1MZ62_BOVIN,tr Q3UAD6 Q3UAD6_MOUSE,tr Q3UBU0 Q3UBU0_MOUSE,tr Q91V38 Q91V38_MOUSE	IISLT DEN ALA GNE ELTV k	95%	88.6	54.4341	Ref	-0.044	-0.01	-0.31	-0.1	-0.22	-0.28	-0.52	631	532	593	539	686	551	552	464	880.2	2637.4	3	0.019	7.186
Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	sp P08113 ENPL_MOUSE,s p Q66HD0 ENPL_RAT,sp Q95M18 ENPL_BOVIN,tr F1MZ62 F1MZ62_BOVIN,tr Q3UAD6 Q3UAD6_MOUSE,tr Q3UBU0 Q3UBU0_MOUSE,tr Q91V38 Q91V38_MOUSE	nLLH VTDT GVG MTR	73%	37.3	53.31139	Ref	-0.16	-0.61	-0.15	-0.24	-0.04	0.075	-0.09	1500	1430	1130	1740	1820	1810	2050	1820	606.7	1817	3	0.0143	7.885

Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	sp P08113 ENPL_MOUSE,s p Q66HD0 ENPL_RAT,sp Q95M18 ENPL_BOVIN,tr F1MZ62 F1MZ62_BOVIN,tr Q3UAD6 Q3UAD6_MOUSE,tr Q3UBU0 Q3UBU0_MOUSE,SE,tr Q91V38 Q91V38_MOUSE,SE	sGTS EFLN k	88%	41.4	52.70598	Ref	-0.075	-0.18	-0.13	-0.16	-0.43	-0.11	-0.37	13900	11500	11600	13500	14500	10500	13700	11300	795.9	1589.9	2	0.0075	4.736
Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	sp P08113 ENPL_MOUSE,s p Q66HD0 ENPL_RAT,sp Q95M18 ENPL_BOVIN,tr F1MZ62 F1MZ62_BOVIN,tr Q3UAD6 Q3UAD6_MOUSE,tr Q3UBU0 Q3UBU0_MOUSE,SE,tr Q91V38 Q91V38_MOUSE,SE	sGTS EFLN k	83%	39.1	52.66605	Ref	-0.03	-0.21	-0.06	-0.2	-0.34	-0.13	-0.4	8140	7340	7040	8740	8760	6930	8370	6890	795.9	1589.9	2	0.0107	6.735

Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	sp P08113 ENPL_MOUSE,sp Q66HD0 ENPL_RAT,sp Q95M18 ENPL_BOVIN, tr F1MZ62 F1MZ62_BOVIN, tr Q3UAD6 Q3UAD6_MOUSE, tr Q3UBU0 Q3UBU0_MOUSE, tr Q91V38 Q91V38_MOUSE	tDDE VVQ R	60%	31.1	50.26476	Ref	0.04	-0.09	-0.2	-0.34	-0.23	-0.47	-0.46	16300	12700	12600	13100	13100	12400	10900	10900	633.3	1264.6	2	0.0101	7.98
Apolipoprotein A-I OS=Bos taurus GN=APOA1 PE=1 SV=3	sp P15497 APOA1_BOVIN	aHVE TLR	74%	34.3	49.93427	Ref	0.17	0.28	0.83	0.023	0.15	0.29	-0.14	82900	81200	94900	156000	98200	93700	1E+05	79300	377.2	1128.6	3	0.0075	6.632
Apolipoprotein A-I OS=Bos taurus GN=APOA1 PE=1 SV=3	sp P15497 APOA1_BOVIN	dYVA QFE ASAL Gk	95%	52.3	53.90911	Ref	-0.066	0.058	0.54	0.11	0.053	0.57	0.52	9760	9080	10700	16800	13800	11600	17300	16600	669.7	2006.1	3	0.0136	6.778
Apolipoprotein A-I OS=Bos taurus GN=APOA1 PE=1 SV=3	sp P15497 APOA1_BOVIN	dYVA QFE ASAL Gk	88%	44.4	53.90937	Ref	0.18	0.13	0.35	0.17	0.3	0.33	0.32	7000	6770	7090	9260	9000	8590	9150	9070	669.7	2006.1	3	0.0116	5.776
Apolipoprotein A-I OS=Bos taurus GN=APOA1 PE=1 SV=3	sp P15497 APOA1_BOVIN	dYVA QFE ASAL Gk	91%	46.8	53.99791	Ref	0.18	0.1	0.32	0.14	0.17	0.36	0.5	6450	6320	6520	8510	8260	7360	8790	9620	669.7	2006.1	3	0.0275	13.71

Apolipoprotein A-I OS=Bos taurus GN=APOA1 PE=1 SV=3	sp P15497 APOA1_BOVIN	dyVA QFE ASAL Gk	69%	37	53.92526	Ref	0.16	0.12	0.3	0.28	0.061	0.57	0.24	1080	1020	1080	1380	1490	1120	1670	1310	771.1	2310.3	3	0.0197	8.527
Apolipoprotein A-I OS=Bos taurus GN=APOA1 PE=1 SV=3	sp P15497 APOA1_BOVIN	ILDN WDT LAST LSk	92%	48.6	53.62766	Ref	0.23	0.31	0.44	0.061	0.13	0.35	0.22	5090	5010	5730	7040	5980	5460	6670	6040	729.1	2184.2	3	0.0118	5.387
Apolipoprotein A-I OS=Bos taurus GN=APOA1 PE=1 SV=3	sp P15497 APOA1_BOVIN	ISPL AQEL R	71%	34	50.6301	Ref	0.015	0.41	0.43	0.35	-0.42	0.75	0.033	7520	6910	9870	11300	11700	6000	14100	8500	444.3	1329.8	3	0.009	6.739
Apolipoprotein A-I OS=Bos taurus GN=APOA1 PE=1 SV=3	sp P15497 APOA1_BOVIN	qQL APYS DDL R	92%	43.6	52.22784	Ref	0.062	0.55	0.16	0.31	-0.25	0.51	-0.17	14600	9680	14800	12600	15400	9110	16100	10000	805.4	1608.8	2	0.0126	7.8
Apolipoprotein A-I OS=Bos taurus GN=APOA1 PE=1 SV=3	sp P15497 APOA1_BOVIN	vkDF ATVY VEAI k	95%	50.1	51.43835	Ref	0.059	0.025	0.51	0.33	0.2	0.59	0.064	1800	1750	1850	2920	2820	2270	3100	2130	799.1	2394.4	3	0.0282	11.79
Apolipoprotein A-I OS=Bos taurus GN=APOA1 PE=1 SV=3	sp P15497 APOA1_BOVIN	vQEL QDk	70%	34.7	52.02406	Ref	0.38	0.26	0.45	0.2	-0.05	0.38	-0.12	21000	20300	20200	26000	24000	17600	24900	17500	734.4	1466.8	2	0.0238	16.2
Apolipoprotein A-I OS=Bos taurus GN=APOA1 PE=1 SV=3	sp P15497 APOA1_BOVIN	vQPY LDEF Qk	56%	33.8	53.47404	Ref	0.25	0.34	0.2	-0.005	0.052	0.51	0.44	24400	26400	30300	31100	29600	26900	38700	36400	625.7	1874	3	0.0196	10.44

Apolipoprotein A-I OS=Bos taurus GN=APOA1 PE=1 SV=3	sp P15497 APOA1_BOVIN	vQPYLDEFQk	80%	38.7	53.41658	Ref	0.21	0.004	0.58	0.3	-0.02	0.56	0.21	13100	15100	14200	23700	21600	15100	23500	18300	938	1874	2	0.0074	3.959
Apolipoprotein A-I OS=Bos taurus GN=APOA1 PE=1 SV=3	sp P15497 APOA1_BOVIN	wHEEVEIYR	73%	35.2	51.30147	Ref	0.28	0.26	0.56	0.21	0.16	0.29	0.13	12100	14000	15000	20700	18000	15100	17300	15300	522.3	1563.8	3	0.0144	9.194
Ubiquitin-associated protein 2 like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp Q14157 UBP2L_HUMAN,sp Q80X50 UBP2L_MOUSE	dGSLASN PYSGDLTK	95%	58.4	54.0303	Ref	-0.25	-0.18	0.085	-0.041	0.1	-0.32	0.056	17200	15200	17300	23300	23600	22700	17700	22800	711.7	2132.1	3	0.0158	7.427
Ubiquitin-associated protein 2 like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp Q14157 UBP2L_HUMAN,sp Q80X50 UBP2L_MOUSE	dGSLASN PYSGDLTK	95%	53.1	54.03939	Ref	-0.51	-0.46	0.23	-0.1	0.37	-0.98	-0.02	5150	2670	2990	5450	4760	5760	2350	4560	1067	2132.1	2	0.0146	6.853
Ubiquitin-associated protein 2 like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp Q14157 UBP2L_HUMAN,sp Q80X50 UBP2L_MOUSE	gFGDVG EAK	80%	38.3	52.95989	Ref	-0.32	-0.21	-0	-0.24	0.28	-0.66	0.063	57400	36800	43100	55800	52100	65200	35400	58200	744.4	1486.8	2	0.0139	9.331

Ubiquitin-associated protein 2 like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp Q14157 UBP2L_HUMAN,sp Q80X50 UBP2L_MOUSE	gGST TGS QFLE QFk	91%	47	54.16777	Ref	-0.19	-0.17	0.007	-0.16	0.17	-0.21	0.083	4890	4760	5250	6660	6550	7170	5780	7010	699	2094.1	3	0.0195	9.312
Ubiquitin-associated protein 2 like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp Q14157 UBP2L_HUMAN,sp Q80X50 UBP2L_MOUSE	gQEn GLD GtK	93%	45	52.51487	Ref	-0.28	-0.12	0.1	-0.26	0.29	-0.73	-0.09	10100	6730	8150	10700	9170	11800	6030	9350	814.4	1626.9	2	0.014	8.612
Ubiquitin-associated protein 2 like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp Q14157 UBP2L_HUMAN,sp Q80X50 UBP2L_MOUSE	IDLA VLLG k	90%	37	45.01771	Ref	-0.3	-0.15	-0.16	-0.15	0.27	-0.64	0.068	3310	2130	2570	2860	3180	3710	2060	3350	517.3	1549	3	0.0031	1.995
Ubiquitin-associated protein 2 like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp Q14157 UBP2L_HUMAN,sp Q80X50 UBP2L_MOUSE	nGFS SVQ ATQL QTT QSV EGA TGS AVk	80%	40.1	55.94271	Ref	-0.033	-0.03	0.046	-0.26	0.022	-0.35	-0.16	2480	2160	2350	2770	2470	2630	2120	2400	802.2	3204.6	4	0.0277	8.641
Ubiquitin-associated protein 2 like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp Q14157 UBP2L_HUMAN,sp Q80X50 UBP2L_MOUSE	nQD EcVI ALH Dcn GDV NR	95%	69.5	44.8193	Ref	-0.18	-0.19	-0.3	-0.19	0.37	-0.15	0.16	4470	4580	4930	5130	6130	7860	5740	7070	804.7	2411	3	0.0211	8.727

Ubiquitin-associated protein 2 like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp Q14157 UBP2L_HUMAN,sp Q80X50 UBP2L_MOUSE	sAYnSYSWGAN	84%	32.9	46.1325	Ref	-0.048	-0.54	-0.26	-0.53	-0.07	-0.17	0.42	234	174	135	183	168	201	196	291	762.8	1523.7	2	0.0112	7.353
Ubiquitin-associated protein 2 like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp Q14157 UBP2L_HUMAN,sp Q80X50 UBP2L_MOUSE	sQTS SIPQkPQT	59%	33.6	52.69957	Ref	-0.41	-0.06	-0.13	-0.1	0.29	-0.45	0.066	2900	2040	2820	3010	3380	3890	2430	3440	819.5	2455.4	3	0.012	4.869
Ubiquitin-associated protein 2 like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp Q14157 UBP2L_HUMAN,sp Q80X50 UBP2L_MOUSE	sSVA TTSGk	93%	44.1	51.75245	Ref	-0.19	-0.38	0.13	-0.11	0.21	-0.66	0.066	6810	5180	4930	7870	7380	8000	4580	7530	723.4	1444.8	2	0.0223	15.44
Ubiquitin-associated protein 2 like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp Q14157 UBP2L_HUMAN,sp Q80X50 UBP2L_MOUSE	tATE EWGTED WNE DLSE Tk	95%	71.3	52.71145	Ref	-0.16	-0.37	-0.05	-0.17	0.52	-0.62	-0.13	2800	2250	2110	2940	2980	4220	1990	2790	950.5	2848.3	3	0.0194	6.804
Ubiquitin-associated protein 2 like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp Q14157 UBP2L_HUMAN,sp Q80X50 UBP2L_MOUSE	tATE EWGTED WNE DLSE Tk	95%	68.3	52.8788	Ref	-0.34	-0.19	-0.28	0.008	0.17	-0.81	0.27	1560	981	1180	1250	1670	1630	862	1820	950.5	2848.3	3	0.0139	4.877

PDIA6 protein (Fragment) OS=Bos taurus GN=PDIA6 PE=2 SV=1	tr A6QNL 5 A6QNL 5_BOVIN	gESP VDY DGG R	95%	43.4	48.66482	Ref	0.01	0.049	-0.22	-0.095	-0.16	-0.15	-0.17	41100	37800	42100	39300	47100	39500	41400	40400	728.3	1454.7	2	0.0108	7.449
PDIA6 protein (Fragment) OS=Bos taurus GN=PDIA6 PE=2 SV=1	tr A6QNL 5 A6QNL 5_BOVIN	gSFS EQGI NEFL R	88%	42.9	52.6205	Ref	0.085	-0.17	-0.17	-0.22	-0.06	-0.23	-0.04	3050	2810	2560	2860	3050	2970	2750	3130	596.6	1786.9	3	0.0159	8.876
PDIA6 protein (Fragment) OS=Bos taurus GN=PDIA6 PE=2 SV=1	tr A6QNL 5 A6QNL 5_BOVIN	gSFS EQGI NEFL R	75%	37	52.56198	Ref	0.018	-0.11	-0.07	-0.17	-0.05	-0.2	-0.12	3750	3510	3500	4020	4140	3920	3690	3890	596.6	1786.9	3	0.0116	6.51
PDIA6 protein (Fragment) OS=Bos taurus GN=PDIA6 PE=2 SV=1	tr A6QNL 5 A6QNL 5_BOVIN	gSFS EQGI NEFL R	92%	44.2	52.62938	Ref	0.052	0.027	-0.19	-0.21	-0.12	0.039	-0.3	9350	9090	9700	9380	10200	9430	11000	8660	894.5	1786.9	2	0.0094	5.243
PDIA6 protein (Fragment) OS=Bos taurus GN=PDIA6 PE=2 SV=1	tr A6QNL 5 A6QNL 5_BOVIN	gSFS EQGI NEFL R	95%	50.8	52.63873	Ref	0.13	-0.02	-0.1	-0.26	-0.09	-0.13	-0.34	6820	6590	6410	6820	6710	6600	6720	5770	894.5	1786.9	2	0.0091	5.108
PDIA6 protein (Fragment) OS=Bos taurus GN=PDIA6 PE=2 SV=1	tr A6QNL 5 A6QNL 5_BOVIN	gSFS EQGI NEFL R	75%	36.5	52.52533	Ref	0.16	-0.23	-0.21	-0.097	-0.11	-0.05	-0.3	3900	3780	3120	3560	4230	3650	4000	3320	894.5	1786.9	2	0.0124	6.954

PDIA6 protein (Fragment) OS=Bos taurus GN=PDIA6 PE=2 SV=1	tr A6QNL 5 A6QNL 5_BOVIN	gSGY SSGk	62%	33.2	52.11766	Ref	-0.11	-0	-0.06	-0.14	-0.05	-0.15	-0.3	20900	16700	19500	21000	21900	20500	19900	17800	675.9	1349.7	2	0.0259	19.14
PDIA6 protein (Fragment) OS=Bos taurus GN=PDIA6 PE=2 SV=1	tr A6QNL 5 A6QNL 5_BOVIN	gSTA PVG GGA FPTI STR	95%	60.9	53.55663	Ref	-0.13	-0.04	-0.11	-0.11	-0.01	0.003	-0.51	11600	8850	10200	11000	12100	11300	11900	8270	940.5	1879	2	0.0112	5.961
PDIA6 protein (Fragment) OS=Bos taurus GN=PDIA6 PE=2 SV=1	tr A6QNL 5 A6QNL 5_BOVIN	IAAV DAT VNQ VLAS R	95%	50	52.88339	Ref	-0.038	-0.03	-0.05	-0.12	0.066	-0.1	-0.4	1120	1040	1140	1260	1320	1320	1230	985	916.5	1831	2	0.005	2.719
PDIA6 protein (Fragment) OS=Bos taurus GN=PDIA6 PE=2 SV=1	tr A6QNL 5 A6QNL 5_BOVIN	nLEP EWA AAA TEVk	88%	45	54.17198	Ref	-0.032	-0.33	0.14	-0.031	-0.2	0.046	-0.53	7580	6220	5480	8500	8350	6490	8030	5350	713.1	2136.2	3	0.0171	8.013
PDIA6 protein (Fragment) OS=Bos taurus GN=PDIA6 PE=2 SV=1	tr A6QNL 5 A6QNL 5_BOVIN	tGEA IVDA ALSA LR	91%	43.6	52.97802	Ref	-0.024	-0.05	-0.21	-0.31	-0.11	-0.02	-0.25	1470	1140	1210	1220	1250	1250	1390	1180	846	1689.9	2	0.0108	6.406
PDIA6 protein (Fragment) OS=Bos taurus GN=PDIA6 PE=2 SV=1	tr A6QNL 5 A6QNL 5_BOVIN	tGEA IVDA ALSA LR	88%	43.2	52.95981	Ref	-0.2	0.13	-0.14	0.1	-0.2	-0.23	-0.33	468	350	478	444	579	410	420	389	564.3	1690	3	0.0058	3.424

PDIA6 protein (Fragment) OS=Bos taurus GN=PDIA6 PE=2 SV=1	tr A6QNL 5 A6QNL 5_BOVIN	tGEA IVDA ALSA	LR	58%	33.6	52.84171	Ref	-0.34	-0.15	-0.13	0.037	-0.28	0.073	0.004	360	255	316	360	444	310	416	393	564.3	1690	3	0.0063	3.743
DPYSL3 protein OS=Bos taurus GN=DPYSL3 PE=2 SV=1	tr A7MBI 5 A7MBI5 _BOVIN, tr B3SXQ8 B3SXQ8_ HUMAN, t r Q6DEN2 Q6DEN2 _HUMAN	eESR EPAP ASPA PAG VEIR		95%	52.7	54.23714	Ref	0.02	-0.64	-0.07	-0.034	0.37	-0.87	0.23	12800	11600	7970	13300	15000	17300	7660	16300	756.4	2266.2	3	0.0214	9.441
DPYSL3 protein OS=Bos taurus GN=DPYSL3 PE=2 SV=1	tr A7MBI 5 A7MBI5 _BOVIN, tr B3SXQ8 B3SXQ8_ HUMAN, t r Q6DEN2 Q6DEN2 _HUMAN	eESR EPAP ASPA PAG VEIR		88%	44.7	54.29266	Ref	-0.14	-0.58	0.11	-0.11	0.46	-0.85	0.2	9020	7800	6230	11200	10600	13800	5800	11900	756.4	2266.2	3	0.0187	8.237
DPYSL3 protein OS=Bos taurus GN=DPYSL3 PE=2 SV=1	tr A7MBI 5 A7MBI5 _BOVIN, tr B3SXQ8 B3SXQ8_ HUMAN, t r Q6DEN2 Q6DEN2 _HUMAN	eVLQ NLG Pk		95%	49.2	50.08707	Ref	-0.01	-0.43	0.19	-0.043	0.28	-0.83	-0.08	14200	12200	9900	17100	16000	17500	8480	14200	803.5	1605	2	0.0088	5.452
DPYSL3 protein OS=Bos taurus GN=DPYSL3 PE=2 SV=1	tr A7MBI 5 A7MBI5 _BOVIN, tr B3SXQ8 B3SXQ8_ HUMAN, t r Q6DEN2 Q6DEN2 _HUMAN	eVLQ NLG Pk		71%	33.2	49.87313	Ref	0.005	-0.39	0.092	-0.17	-0	-0.11	-0.07	4100	3680	3040	4760	4390	4300	4170	4240	536	1605	3	0.0072	4.478

DPYSL3 protein OS=Bos taurus GN=DPYSL3 PE=2 SV=1	tr A7MBI5 A7MBI5_BOVIN, tr B3SXQ8 B3SXQ8_HUMAN, tr Q6DEN2 Q6DEN2_HUMAN	gAPL VVic QGk	92%	47.1	52.22316	Ref	0.37	-0.39	0.096	-0.13	0.055	-0.54	-0.21	5500	6520	4180	6570	6180	6150	4260	5310	580.3	1738	3	0.0071	4.068
DPYSL3 protein OS=Bos taurus GN=DPYSL3 PE=2 SV=1	tr A7MBI5 A7MBI5_BOVIN, tr B3SXQ8 B3SXQ8_HUMAN, tr Q6DEN2 Q6DEN2_HUMAN	gMT TVD DFF QGT k	95%	57.2	53.55955	Ref	0.099	-0.5	-0.03	-0.2	-0.08	-0.67	0.47	8230	7750	5560	8620	8490	8020	5570	12200	685.7	2054	3	0.0137	6.67
DPYSL3 protein OS=Bos taurus GN=DPYSL3 PE=2 SV=1	tr A7MBI5 A7MBI5_BOVIN, tr B3SXQ8 B3SXQ8_HUMAN, tr Q6DEN2 Q6DEN2_HUMAN	gMT TVD DFF QGT k	94%	50.6	53.61958	Ref	0.13	-0.68	0.071	-0.029	0.14	-0.89	0.23	13400	12700	7840	14800	15300	15000	7670	16600	685.7	2054.1	3	0.0106	5.166
DPYSL3 protein OS=Bos taurus GN=DPYSL3 PE=2 SV=1	tr A7MBI5 A7MBI5_BOVIN, tr B3SXQ8 B3SXQ8_HUMAN, tr Q6DEN2 Q6DEN2_HUMAN	iFNL YPR	54%	31.3	51.28767	Ref	0.25	-0.41	0.19	-0.33	-0.48	-0.43	0.14	1330	1210	836	1420	1090	855	926	1370	409.6	1225.7	3	0.0108	8.783
DPYSL3 protein OS=Bos taurus GN=DPYSL3 PE=2 SV=1	tr A7MBI5 A7MBI5_BOVIN, tr B3SXQ8 B3SXQ8_HUMAN, tr Q6DEN2 Q6DEN2_HUMAN	mVIP GGID VHT HFQ MPY k	78%	38.8	55.2617	Ref	0.083	-0.66	9E-04	-0.019	0.34	-0.82	0.008	5330	4650	3010	5350	5810	6530	3040	5360	670.4	2677.4	4	0.0133	4.962

DPYSL3 protein OS=Bos taurus GN=DPYSL3 PE=2 SV=1	tr A7MBI5 A7MBI5_BOVIN, tr B3SXQ8 B3SXQ8_HUMAN, tr Q6DEN2 Q6DEN2_HUMAN	pGTT DQV PR	91%	41.9	50.83004	Ref	0.2	-0.31	0.13	-0.25	-0.07	-0.38	-0.19	64300	58600	44800	68200	57600	57000	48100	54600	637.8	1273.7	2	0.0105	8.21
DPYSL3 protein OS=Bos taurus GN=DPYSL3 PE=2 SV=1	tr A7MBI5 A7MBI5_BOVIN, tr B3SXQ8 B3SXQ8_HUMAN, tr Q6DEN2 Q6DEN2_HUMAN	tIEA nGk	53%	31.1	51.4893	Ref	0.15	-0.54	0.09	-0.16	0.35	-0.82	-0.04	31100	29800	20000	34900	32300	40100	18700	31800	671.4	1340.8	2	0.0025	1.898
DPYSL3 protein OS=Bos taurus GN=DPYSL3 PE=2 SV=1	tr A7MBI5 A7MBI5_BOVIN, tr B3SXQ8 B3SXQ8_HUMAN, tr Q6DEN2 Q6DEN2_HUMAN	tLDF DAL VGQ R	85%	39.7	52.5003	Ref	0.018	-0.58	0.096	-0.26	0.33	-0.88	0.2	14600	12300	8840	15900	13700	17900	8080	17000	813.4	1624.9	2	0.011	6.745
DPYSL3 protein OS=Bos taurus GN=DPYSL3 PE=2 SV=1	tr A7MBI5 A7MBI5_BOVIN, tr B3SXQ8 B3SXQ8_HUMAN, tr Q6DEN2 Q6DEN2_HUMAN	yGG MFc NVE GAF ESk	72%	35	51.21882	Ref	0.25	-0.26	-0.28	-0.033	-0.16	-0.12	-0.06	708	757	576	635	832	666	714	739	765	2292.1	3	0.0222	9.66
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.21712 PE=4 SV=1	tr F1MHR6 F1MHR6_BOVIN	aGLV IGk	74%	29.2	45.07694	Ref	-0.12	-0.2	-0.24	-0.048	0.009	-0.27	-0.13	13900	9730	9950	10900	13700	12400	10700	11700	422.6	1264.8	3	0.0028	2.185

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.21712 PE=4 SV=1	tr F1MHR 6 F1MHR 6_BOVIN	alNQ QTG AFVE ISR	93%	46.5	53.433	Ref	0.035	-0.27	-0.14	-0.29	0.2	-0.61	0.12	7240	6270	5510	6780	6730	8240	4890	8080	919.5	1837	2	0.0111	6.03
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.21712 PE=4 SV=1	tr F1MHR 6 F1MHR 6_BOVIN	gSPQ QID HAK	58%	33.6	52.89226	Ref	-0.085	-0.13	0.014	-0.21	0.14	-0.54	0.01	49700	41800	43800	54500	51400	57200	37400	54200	563.7	1687.9	3	0.0087	5.161
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.21712 PE=4 SV=1	tr F1MHR 6 F1MHR 6_BOVIN	hSV GVVI GR	85%	38.9	50.3454	Ref	-0.18	-0.21	-0.01	-0.2	0.038	-0.22	0.092	26000	21400	22600	29100	28200	29000	25400	31200	409.9	1226.7	3	0.0083	6.746
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.21712 PE=4 SV=1	tr F1MHR 6 F1MHR 6_BOVIN	iGGD AATT VNn STPD FGF GGQ k	67%	37.4	54.94095	Ref	0.028	-0.27	0.011	-0.34	0.028	-0.33	0.068	759	677	598	814	703	793	646	845	921.8	2762.4	3	0.0176	6.355
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.21712 PE=4 SV=1	tr F1MHR 6 F1MHR 6_BOVIN	iGGG IDVP VPR	83%	38.2	51.69733	Ref	-0.007	-0.24	0.002	-0.15	0.077	-0.6	0.081	56800	50000	46300	61300	60900	62100	40700	64600	692.4	1382.8	2	0.011	7.917

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.21712 PE=4 SV=1	tr F1MHR 6 F1MHR 6_BOVIN	iINDL LQSL R	62%	33.2	52.04424	Ref	-0.011	-0.46	0.19	-0.3	-0.04	-0.3	-0.05	1980	1580	1250	2210	1730	1810	1590	1860	745	1487.9	2	0.0065	4.334
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.21712 PE=4 SV=1	tr F1MHR 6 F1MHR 6_BOVIN	KLAS QGD SMS SQL GPIH PPPR	95%	52.3	55.17063	Ref	0.045	0.016	-0.14	-0.19	-0.17	0.066	-0.06	7170	8170	8690	8740	9300	8240	10200	9200	703.6	2810.5	4	0.0292	10.37
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.21712 PE=4 SV=1	tr F1MHR 6 F1MHR 6_BOVIN	mLI QDG SQN TNV DkPL R	52%	34.3	54.64287	Ref	0.028	-0.42	0.047	-0.15	0.018	-0.49	0.007	5440	4520	3600	5570	5360	5250	3870	5400	884.2	2649.5	3	0.0222	8.373
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.21712 PE=4 SV=1	tr F1MHR 6 F1MHR 6_BOVIN	qDD GTG PEK	60%	33.3	52.13818	Ref	0.057	-0.2	-0.26	-0.26	0.12	-0.46	0.14	36500	33000	30000	32300	35600	40500	28200	42300	518.9	1553.8	3	0.0147	9.423
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.21712 PE=4 SV=1	tr F1MHR 6 F1MHR 6_BOVIN	qDD GTG PEK	67%	34.3	52.31054	Ref	-0.12	-0.25	-0.03	-0.12	0.13	-0.63	0.082	10000	7690	7650	10000	10300	10700	6610	10800	777.9	1553.8	2	0.0068	4.377

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.21712 PE=4 SV=1	tr F1MHR6_BOVIN	qLED GDQ PESK	93%	45.2	52.99374	Ref	-0.18	-0.32	0.095	-0.19	0.25	-0.73	0.063	9320	6940	6790	10200	9250	10900	5770	9940	927.5	1852.9	2	0.0206	11.11
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.21712 PE=4 SV=1	tr F1MHR6_BOVIN	sVSL TGA PESV QK	95%	57.7	52.8481	Ref	-0.24	-0.26	0.024	-0.13	0.15	-0.49	0.15	13000	10000	10700	14600	14500	15300	10300	15900	956	1910.1	2	0.0117	6.116
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1N6S9 F1N6S9_BOVIN	aDID ISGP k	89%	41.2	51.56422	Ref	-0.48	-0.25	-0.34	-0.21	-0.03	-0.45	-0.26	18600	12000	15200	16000	19300	19200	15000	17000	762.4	1522.9	2	0.0102	6.706
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1N6S9 F1N6S9_BOVIN	aDID VSAP k	93%	44.5	51.5122	Ref	-0.62	-0.29	-0.37	-0.22	0.022	-0.64	-0.13	28500	15400	20900	22300	27300	28100	18500	26300	762.4	1522.9	2	0.0084	5.511
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1N6S9 F1N6S9_BOVIN	aDID VSG PK	93%	44.2	51.98503	Ref	-0.66	-0.35	-0.18	0.022	-0.02	-0.79	-0.34	2E+05	82600	1E+05	141000	178000	2E+05	92800	126000	755.4	1508.9	2	0.0151	10.01

Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1N6S9_1 F1N6S9_1 BOVIN	aEGP EVN VNLP kPDV DISG Pk	81%	39.2	54.33424	Ref	-0.61	-0.21	-0.43	-0.094	0.054	-0.47	-0.4	6380	3580	5120	4960	6880	6650	4820	5030	772.7	3086.7	4	0.0336	10.87
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1N6S9_2 F1N6S9_2 BOVIN	iSMP DIDL nLkG Pk	66%	31.4	50.98433	Ref	-0.83	-0.38	-0.18	0.051	-0.02	-0.45	-0.18	13800	7750	11400	14800	19100	15900	12300	14800	614.1	2452.4	4	0.0072	2.934
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1N6S9_3 F1N6S9_3 BOVIN	iSMP DIDL nLkG Pk	55%	30.5	52.07734	Ref	-0.55	-0.49	-0.38	-0.085	0.099	-0.28	-0.14	3520	2540	2870	3490	4700	4670	3740	4090	614.4	2453.4	4	0.0167	6.816
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1N6S9_4 F1N6S9_4 BOVIN	vDID APD VDV HGP DWH Lk	93%	47.8	55.18826	Ref	-0.45	-0.5	-0.35	-0.1	-0.06	-0.46	-0.53	29300	15800	16500	20500	26800	24100	19100	18100	659.8	2635.4	4	0.0233	8.846
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1N6S9_5 F1N6S9_5 BOVIN	vDIE GPD VSLE GPE Gk	95%	54.6	54.54023	Ref	-0.15	-0.3	-0.43	-0.39	-0.32	-0.04	-0.28	12800	11000	10800	11000	12500	11500	14600	12300	750.4	2248.2	3	0.0172	7.646
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1N6S9_6 F1N6S9_6 BOVIN	vDV AVP DVD VHG PDW HLk	93%	51.4	55.00023	Ref	-0.53	-0.19	-0.21	-0.29	-0.03	-0.44	-0.34	4120	2540	3490	3870	4040	4210	3310	3520	869.5	2605.4	3	0.0192	7.367

Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1N6S9_1 F1N6S9_1_BOVIN	vDV AVP DVD VHG PDW HLk	51%	32.7	55.00687	Ref	-0.74	-0.36	-0.35	0.034	0.017	-0.88	-0.27	30500	13800	19400	22000	31600	27300	15300	23200	652.4	2605.4	4	0.0192	7.35
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1N6S9_2 F1N6S9_2_BOVIN	vDV DVP DVD VHG PDW Vlk	95%	51.9	53.18072	Ref	-0.41	-0.18	-0.38	-0.18	-0.04	-0.66	-0.25	12400	8230	10500	10200	12900	12400	8460	11100	904.5	1807	2	0.0193	10.66
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1N6S9_3 F1N6S9_3_BOVIN	vDV DVP DVD VHG PDW Vlk	80%	39.5	53.1424	Ref	-0.45	-0.3	-0.23	-0.08	-0.23	-0.61	-0.27	65000	39400	47400	55700	68300	53800	43200	54200	603.3	1807	3	0.0146	8.099
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1N6S9_4 F1N6S9_4_BOVIN	vDV DVP DVD VHG PDW HLk	84%	43.3	55.07481	Ref	-0.5	-0.38	-0.23	-0.21	-0.18	-0.55	-0.06	8540	5260	6190	7710	8640	7690	6210	8680	881.1	2640.4	3	0.0454	17.19
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.27462 PE=3 SV=1	tr F1MK4_4 F1MK4_4_BOVIN, tr F1PY05_1 F1PY05_1_CANFA, tr F1SR53_1 F1SR53_1_PLHR	cELG PLHR	76%	34.9	49.9638	Ref	-0.12	0.16	0.34	-0.25	-0.45	-0.06	-0.16	2090	1660	2190	2770	2030	1550	2120	1970	425.6	1273.6	3	0.0098	7.702

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.27462 PE=3 SV=1	tr F1MK4 4 F1MK4 4_BOVIN, tr F1PY05 F1PY05_ CANFA,tr F1SR53 F 1SR53_P G	cELG PLHR	95%	51	49.86292	Ref	-0.23	-0.21	0.28	-0.28	0.044	0.011	-0.07	6830	5060	5580	8770	6550	7170	7320	6860	425.6	1273.6	3	0.0091	7.137
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.27462 PE=3 SV=1	tr F1MK4 4 F1MK4 4_BOVIN, tr F1PY05 F1PY05_ CANFA,tr F1SR53 F 1SR53_P G	cELG PLHR	95%	48.6	49.85947	Ref	-0.28	-0.07	0.17	-0.16	0.076	-0.04	-0.13	9340	6660	8380	11100	9700	9980	9600	8980	425.6	1273.6	3	0.0086	6.76
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.27462 PE=3 SV=1	tr F1MK4 4 F1MK4 4_BOVIN, tr F1PY05 F1PY05_ CANFA,tr F1SR53 F 1SR53_P G	fTVP HLR	56%	30.3	50.01881	Ref	-0.062	-0.33	0.35	-0.31	0.32	0.078	-0.13	6740	8060	7260	13000	9100	12300	10900	9360	391.9	1172.7	3	0.0068	5.824
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.27462 PE=3 SV=1	tr F1MK4 4 F1MK4 4_BOVIN, tr F1PY05 F1PY05_ CANFA,tr F1SR53 F 1SR53_P G	fTVP HLR	82%	37.5	50.22589	Ref	-0.22	-0.32	0.21	-0.25	-0.01	-0.15	0.28	8880	6730	6790	11000	8840	9090	8640	11500	391.9	1172.7	3	0.0126	10.73
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.27462 PE=3 SV=1	tr F1MK4 4 F1MK4 4_BOVIN, tr F1PY05 F1PY05_ CANFA,tr F1SR53 F 1SR53_P G	fTVP HLR	88%	40.5	49.97718	Ref	-0.27	-0.3	0.22	-0.27	0.053	-0.09	0.2	3590	2630	2790	4500	3540	3860	3650	4440	391.9	1172.7	3	0.005	4.265

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.27462 PE=3 SV=1	tr F1MK4 4 F1MK4 4_BOVIN, tr F1PY05 F1PY05_ CANFA,tr F1SR53 F 1SR53_P IG	kTIQ FDF QILS k	54%	27.6	49.32261	Ref	0.068	-0.32	0.032	-0.079	-0.19	-0.19	0.22	1320	1200	994	1420	1450	1180	1220	1620	595.9	2379.4	4	0.0023	0.983
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.27462 PE=3 SV=1	tr F1MK4 4 F1MK4 4_BOVIN, tr F1PY05 F1PY05_ CANFA,tr F1SR53 F 1SR53_P IG	ILVc DLG NPM k	88%	43.7	53.43024	Ref	-0.19	-0.14	-0.03	-0.13	-0.02	0.074	0.17	9620	8180	9170	11100	11500	10800	12000	12800	619.7	1856	3	0.0289	15.54
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.27462 PE=3 SV=1	tr F1MK4 4 F1MK4 4_BOVIN, tr F1PY05 F1PY05_ CANFA,tr F1SR53 F 1SR53_P IG	qATL TQTL LIQn GAR	85%	40.7	53.28237	Ref	0.049	-0.27	0.22	-0.11	-0.06	-0.24	0.035	2940	2750	2390	3760	3300	2980	2760	3310	967	1932.1	2	0.0118	6.111
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.27462 PE=3 SV=1	tr F1MK4 4 F1MK4 4_BOVIN, tr F1PY05 F1PY05_ CANFA,tr F1SR53 F 1SR53_P IG	sLQ WFG ATV R	61%	33.4	52.11505	Ref	0.34	-0.04	-0.14	-0.11	-0.16	-0.44	-0.09	1810	1800	1510	1580	1770	1490	1290	1630	490.3	1467.8	3	0.0085	5.805
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.27462 PE=3 SV=1	tr F1MK4 4 F1MK4 4_BOVIN, tr F1PY05 F1PY05_ CANFA,tr F1SR53 F 1SR53_P IG	tiQF DFQI LSk	82%	39.9	52.94389	Ref	0.028	-0.11	0.041	-0.099	-0.27	-0.04	0.017	1170	1020	1000	1250	1250	968	1190	1230	650	1947.1	3	0.0209	10.7

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.27462 PE=3 SV=1	tr F1MK44 F1MK44_BOVIN, tr F1PY05 F1PY05_CANFA, tr F1SR53 F1SR53_PIG	tIQFDFQILSK	81%	39.2	52.59506	Ref	0.021	-0.31	-0.05	-0.22	-0.18	-0.03	0.23	1570	1310	1130	1520	1490	1340	1550	1840	650	1947.1	3	0.0093	4.789
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.27462 PE=3 SV=1	tr F1MK44 F1MK44_BOVIN, tr F1PY05 F1PY05_CANFA, tr F1SR53 F1SR53_PIG	vTAPPEAEYSGLVR	94%	50.3	53.36808	Ref	-0.18	-0.15	-0.09	0.14	-0.25	-0.01	0.17	12500	10100	11200	13100	16900	11300	14000	15700	598.3	1792	3	0.0123	6.842
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	sp Q09666 AHNK_HUMAN	aDIDVSGPk	93%	44.2	51.98503	Ref	-0.76	-0.45	-0.28	-0.073	-0.12	-0.88	-0.43	2E+05	82600	1E+05	141000	178000	2E+05	92800	126000	755.4	1508.9	2	0.0151	10.01
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	sp Q09666 AHNK_HUMAN	gEGPDVDVSLPk	95%	63.3	53.26295	Ref	-0.65	-0.29	-0.49	-0.3	-0.21	-0.54	-0.57	19400	9740	13600	13300	16700	15500	12900	12500	911	1820	2	0.0138	7.56

Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	sp Q09666 AHNK_HUMAN	iGIP GVK	56%	22.8	42.39399	Ref	-0.89	-0.28	-0.64	-0.29	-0.01	-0.43	-0.52	19200	8520	14100	12300	17400	18400	14400	13500	431.3	1290.8	3	0.0036	2.804
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	sp Q09666 AHNK_HUMAN	iSMP DIDL NLkG Pk	66%	31.4	50.98433	Ref	-0.92	-0.48	-0.28	-0.043	-0.12	-0.54	-0.27	13800	7750	11400	14800	19100	15900	12300	14800	614.1	2452.4	4	0.0072	2.934
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	sp Q09666 AHNK_HUMAN	iSMP DIDL nLkG Pk	55%	30.5	52.07734	Ref	-0.65	-0.59	-0.47	-0.18	0.004	-0.38	-0.24	3520	2540	2870	3490	4700	4670	3740	4090	614.4	2453.4	4	0.0167	6.816
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	sp Q09666 AHNK_HUMAN	vDID APD VDV HGP DWH Lk	93%	47.8	55.18826	Ref	-0.54	-0.59	-0.45	-0.2	-0.16	-0.56	-0.62	29300	15800	16500	20500	26800	24100	19100	18100	659.8	2635.4	4	0.0233	8.846

Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	sp Q09666 AHNK_HUMAN	vDID TPDI NIEG SEGk	81%	41.3	54.41505	Ref	-0.43	-0.47	-0.37	-0.38	-0.11	-0.28	-0.39	17000	14100	14800	17700	19500	20500	19000	17500	770.7	2309.2	3	0.0192	8.296
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	sp Q09666 AHNK_HUMAN	vDVE GPD VNIE GPE Gk	95%	63.2	54.5351	Ref	-0.72	-0.55	-0.36	-0.5	-0.2	-0.23	-0.4	23400	11800	14400	18500	18500	19900	20300	17900	754.7	2261.2	3	0.0179	7.902
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	sp Q09666 AHNK_HUMAN	vDVE GPD VNIE GPE Gk	95%	73.7	54.52774	Ref	-1.1	-0.27	-0.5	-0.18	0.091	-0.76	-0.39	1920	781	1500	1440	1980	2090	1210	1550	1132	2261.2	2	0.0173	7.656
Peroxisredoxin-1 OS=Bos taurus GN=PRDX1 PE=2 SV=1	sp Q5E947 PRDX1_BOVIN, tr F4YD22 F4YD22_B UBBU	dISL ADYk	68%	35.4	52.58649	Ref	-0.11	-0.11	-0.46	0.26	-0.61	0.059	-0.73	88700	62000	67400	59700	108000	51500	85700	49100	511.6	1531.9	3	0.0143	9.309
Peroxisredoxin-1 OS=Bos taurus GN=PRDX1 PE=2 SV=1	sp Q5E947 PRDX1_BOVIN, tr F4YD22 F4YD22_B UBBU	gLFII DDk	95%	46	50.73546	Ref	-0.11	-0.2	-0.29	0.11	-0.36	0.016	-0.64	39600	29000	29500	31100	45400	28600	38700	24300	765	1527.9	2	0.0089	5.806

Peroxiredoxin-1 OS=Bos taurus GN=PRDX1 PE=2 SV=1	sp Q5E947 PRDX1_BOVIN, tr F4YD22 F4YD22_B UBBU	gLFII DDk	66%	32.7	50.49458	Ref	-0.18	-0.19	-0.76	0.14	-0.29	0.066	-0.57	27200	16700	18100	13600	28000	18200	24400	15600	510.3	1527.9	3	0.0048	3.155
Peroxiredoxin-1 OS=Bos taurus GN=PRDX1 PE=2 SV=1	sp Q5E947 PRDX1_BOVIN, tr F4YD22 F4YD22_B UBBU	gLFII DDk	53%	30.1	50.33657	Ref	-0.26	-0.23	-0.4	0.14	-0.28	0.009	-0.19	13000	9720	10800	10800	17300	11200	14400	12400	510.3	1527.9	3	0.0011	0.741
Peroxiredoxin-1 OS=Bos taurus GN=PRDX1 PE=2 SV=1	sp Q5E947 PRDX1_BOVIN, tr F4YD22 F4YD22_B UBBU	kQG GLG PMN IPLIS DPk	63%	32	52.1318	Ref	-0.07	-0.46	-0.23	0.084	-0.35	0.091	-0.44	4560	3620	2990	3940	5400	3480	4950	3410	670.1	2676.5	4	0.0377	14.09
Peroxiredoxin-1 OS=Bos taurus GN=PRDX1 PE=2 SV=1	sp Q5E947 PRDX1_BOVIN, tr F4YD22 F4YD22_B UBBU	kQG GLG PMN IPLIS DPk	78%	35.5	51.95025	Ref	-0.1	-0.2	-0.16	-0.041	-0.25	-0.06	-0.28	1780	1540	1560	1800	2160	1640	1950	1660	670.1	2676.5	4	0.0338	12.62
Peroxiredoxin-1 OS=Bos taurus GN=PRDX1 PE=2 SV=1	sp Q5E947 PRDX1_BOVIN, tr F4YD22 F4YD22_B UBBU	kQG GLG PMN IPLIS DPkR	72%	32.1	50.40329	Ref	-0.3	-0.35	-0.32	0.23	-0.18	0.14	-0.17	3520	3170	3310	3800	6140	4020	5260	4210	709.2	2832.7	4	0.0196	6.929
Peroxiredoxin-1 OS=Bos taurus GN=PRDX1 PE=2 SV=1	sp Q5E947 PRDX1_BOVIN, tr F4YD22 F4YD22_B UBBU	IVQA FQFT Dk	95%	48.3	52.65726	Ref	-0.2	-0.36	-0.15	0.092	-0.27	-0.03	-0.41	7790	5630	5440	7070	9230	6260	7750	5880	903	1804	2	0.0131	7.285
Peroxiredoxin-1 OS=Bos taurus GN=PRDX1 PE=2 SV=1	sp Q5E947 PRDX1_BOVIN, tr F4YD22 F4YD22_B UBBU	IVQA FQFT Dk	71%	36	52.4707	Ref	-0.15	-0.37	-0.37	0.1	-0.4	-0.1	0.11	31300	26200	24500	27500	42000	25900	33200	38200	602.4	1804	3	0.0056	3.106

Peroxiredoxin-1 OS=Bos taurus GN=PRDX1 PE=2 SV=1	sp Q5E947 PRDX1_BOVIN, tr F4YD22 F4YD22_BUBBU	qITIn DLPV GR	87%	40.3	52.30643	Ref	-0.094	-0.42	-0.32	0.078	-0.17	0.061	-0.28	16100	14100	12200	14700	21400	15700	19300	15100	765.9	1529.9	2	0.0149	9.718
Peroxiredoxin-1 OS=Bos taurus GN=PRDX1 PE=2 SV=1	sp Q5E947 PRDX1_BOVIN, tr F4YD22 F4YD22_BUBBU	tIAQ DYG VLk	80%	38.3	52.13242	Ref	-0.045	-0.36	-0.28	0.09	-0.4	0.037	-0.34	28700	23800	20700	24700	35100	21800	30900	23500	572.7	1715	3	0.0138	8.028
Peroxiredoxin-1 OS=Bos taurus GN=PRDX1 PE=2 SV=1	sp Q5E947 PRDX1_BOVIN, tr F4YD22 F4YD22_BUBBU	tIAQ DYG VLk	95%	55.4	52.06416	Ref	-0.19	-0.18	-0.29	0.24	-0.26	-0.08	-0.54	20900	16000	17400	18100	28700	17800	21000	15200	858.5	1715	2	0.0099	5.746
Peroxiredoxin-1 OS=Bos taurus GN=PRDX1 PE=2 SV=1	sp Q5E947 PRDX1_BOVIN, tr F4YD22 F4YD22_BUBBU	tIAQ DYG VLk	60%	33.1	52.04982	Ref	-0.035	-0.27	-0.18	-0.026	-0.28	0.034	-0.46	45500	39300	36100	43200	53100	38700	50400	35400	572.7	1715	3	0.0092	5.371

Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	5 SET_HUMAN,sp Q63945 SET_RAT,sp Q9EQU5 SET_MOUSE,tr A2BE93 A2BE93_MOUSE,tr A6NGV1 A6NGV1_HUMAN,tr B0BMV1 B0BMV1_RAT,tr B2RCXO B2RCXO_HUMAN,tr B2REB8 B2REB8_HUMAN,tr F1MCF1 F1MCF1_BOVIN,tr F1RR69 F1RR69_PIG,tr	eFHL NES GDP SSk	86%	42.8	53.34162	Ref	0.0043	-0.29	0.27	0.043	0.21	-0.38	0.13	17200	16600	14700	24300	22900	22500	15500	21900	685.7	2054	3	0.019	9.235
Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	5 SET_HUMAN,sp Q63945 SET_RAT,sp Q9EQU5 SET_MOUSE,tr A2BE93 A2BE93_MOUSE,tr A6NGV1 A6NGV1_HUMAN,tr B0BMV1 B0BMV1_RAT,tr B2RCXO B2RCXO_HUMAN,tr B2REB8 B2REB8_HUMAN,tr F1MCF1 F1MCF1_BOVIN,tr F1RR69 F1RR69_PIG,tr	iDFY FDE NPYF ENk	95%	54.9	53.24791	Ref	-0.25	-0.15	0.093	-0.12	0.37	-0.48	0.41	894	709	826	1100	1040	1280	740	1360	817.1	2448.2	3	0.0283	11.53

Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	5 SET_HUMAN,sp Q63945 SET_RAT,sp Q9EQU5 SET_MOUSE,tra2 BE93_MOUSE,tra6 NGV1 NGV1_HUMAN,tra B0BMV1 B0BMV1_RAT,tra B2RCXO B2RCXO_HUMAN,tra B2REB8 B2REB8_HUMAN,tra F1MCF1 F1MCF1_BOVIN,tra F1RR69 F1RR69_PIG,tra	INEQ ASEE ILk	94%	46.7	53.21913	Ref	0.17	-0.2	0.11	-0.25	0.1	-0.68	-0.04	7110	4970	4150	5800	4960	5560	3370	5200	941.5	1881.1	2	0.0141	7.512
Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	5 SET_HUMAN,sp Q63945 SET_RAT,sp Q9EQU5 SET_MOUSE,tra2 BE93_MOUSE,tra6 NGV1 NGV1_HUMAN,tra B0BMV1 B0BMV1_RAT,tra B2RCXO B2RCXO_HUMAN,tra B2REB8 B2REB8_HUMAN,tra F1MCF1 F1MCF1_BOVIN,tra F1RR69 F1RR69_PIG,tra	INEQ ASEE ILkV	91%	45.9	52.99825	Ref	-0.26	-0.39	0.26	-0.098	0.43	-0.47	0.33	4960	3870	3830	6760	5820	7350	4110	7090	890.8	2669.5	3	0.0213	7.967

Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	5 SET_HUMAN,sp Q63945 SET_RAT,sp Q9EQU5 SET_MOUSE,tr A2BE93 A2BE93_MOUSE,tr A6NGV1 A6NGV1_HUMAN,tr B0BMV1 B0BMV1_RAT,tr B2RCXO B2RCXO_HUMAN,tr B2REB8 B2REB8_HUMAN,tr F1MCF1 F1MCF1_BOVIN,tr F1RR69 F1RR69_PIG,tr	IRQP FFQk	52%	28	50.22301	Ref	-0.4	-0.48	-0.04	-0.099	0.26	-0.15	0.85	2660	2500	2580	3920	4140	4630	3650	7250	418.8	1671	4	0.0012	0.738
Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	5 SET_HUMAN,sp Q63945 SET_RAT,sp Q9EQU5 SET_MOUSE,tr A2BE93 A2BE93_MOUSE,tr A6NGV1 A6NGV1_HUMAN,tr B0BMV1 B0BMV1_RAT,tr B2RCXO B2RCXO_HUMAN,tr B2REB8 B2REB8_HUMAN,tr F1MCF1 F1MCF1_BOVIN,tr F1RR69 F1RR69_PIG,tr	sSQT QNK	54%	31.6	51.65025	Ref	-0.25	-0.22	0.02	-0.24	0.49	-0.2	0.25	10100	7660	8500	11200	10300	14900	9670	13200	467.6	1399.8	3	0.0124	8.862

Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	5 SET_HUMAN,sp Q63945 SET_RAT,sp Q9EQU5 SET_MOUSE,tra A2BE93 MOUSE,tra A6NGV1 A6NGV1_HUMAN,tra B0BMV1 B0BMV1_RAT,tra B2RCXO B2RCXO_HUMAN,tra B2REB8 B2REB8_HUMAN,tra F1MCF1 F1MCF1_BOVIN,tra F1RR69 F1RR69_PIG,tra	sSQT Qnk	56%	31.8	51.6249	Ref	-0.078	-0.37	0.1	-0.22	0.44	-0.71	0.48	1010	863	767	1190	1050	1450	682	1540	701.4	1400.8	2	0.0021	1.467
Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	5 SET_HUMAN,sp Q63945 SET_RAT,sp Q9EQU5 SET_MOUSE,tra A2BE93 MOUSE,tra A6NGV1 A6NGV1_HUMAN,tra B0BMV1 B0BMV1_RAT,tra B2RCXO B2RCXO_HUMAN,tra B2REB8 B2REB8_HUMAN,tra F1MCF1 F1MCF1_BOVIN,tra F1RR69 F1RR69_PIG,tra	VEVT EFED Ik	95%	58.3	53.26639	Ref	-0.019	-0.37	0.21	0.077	0.19	-0.54	0.1	4650	3600	3050	5130	5170	4890	3080	4770	909	1816	2	0.02	11.01

Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	5 SET_HU MAN,sp Q63945 S ET_RAT,s p Q9EQU 5 SET_M OUSE,tr A 2BE93 A2 BE93_MO USE,tr A6 NGV1 A6 NGV1_HU MAN,tr B OBMV1 B OBMV1_R AT,tr B2R CX0 B2RC X0_HUMA N,tr B2RE B8 B2REB 8_HUMA N,tr F1M CF1 F1M CF1_BOVI N,tr F1RR 69 F1RR6 9_PIG,tr	VEVT EFED ik	95%	59	53.29506	Ref	-0.31	-0.23	0.27	-0.097	0.41	-0.68	0.29	18100	12700	14600	23100	19700	24500	12000	23400	909	1816	2	0.0179	9.863
Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	5 SET_HU MAN,sp Q63945 S ET_RAT,s p Q9EQU 5 SET_M OUSE,tr A 2BE93 A2 BE93_MO USE,tr A6 NGV1 A6 NGV1_HU MAN,tr B OBMV1 B OBMV1_R AT,tr B2R CX0 B2RC X0_HUMA N,tr B2RE B8 B2REB 8_HUMA N,tr F1M CF1 F1M CF1_BOVI N,tr F1RR 69 F1RR6 9_PIG,tr	VEVT EFED ik	94%	50.1	53.36059	Ref	-0.27	-0.42	0.16	-0.17	0.46	-0.84	0.46	80000	52700	51500	86500	75900	1E+05	43400	106000	606.3	1816	3	0.0172	9.459

Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	5 SET_HUMAN,sp Q63945 SET_RAT,sp Q9EQU5 SET_MOUSE,tra2 BE93_MOUSE,tra6 NGV1 ANGV1_HUMAN,tra B0BMV1 B0BMV1_RAT,tra B2RCXO B2RCXO_HUMAN,tra B2REB8 B2REB8_HUMAN,tra F1MCF1 F1MCF1_BOVIN,tra F1RR69 F1RR69_PIG,tra	VEVTEFEFED	ik	94%	50.1	53.33179	Ref	-0.066	-0.42	0.049	-0.044	0.44	-1.1	0.46	62000	47300	40100	62400	64500	79000	27800	82500	606.3	1816	3	0.0166	9.162
Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	5 SET_HUMAN,sp Q63945 SET_RAT,sp Q9EQU5 SET_MOUSE,tra2 BE93_MOUSE,tra6 NGV1 ANGV1_HUMAN,tra B0BMV1 B0BMV1_RAT,tra B2RCXO B2RCXO_HUMAN,tra B2REB8 B2REB8_HUMAN,tra F1MCF1 F1MCF1_BOVIN,tra F1RR69 F1RR69_PIG,tra	VEVTEFEFED	ik	94%	50	53.30124	Ref	0.0072	-0.31	0.009	-0.13	0.31	-0.76	0.4	21700	17300	15100	21100	21200	25100	12500	27700	606.3	1816	3	0.0161	8.864

Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	5 SET_HUMAN,sp Q63945 SET_RAT,sp Q9EQU5 SET_MOUSE,tr A2BE93 A2BE93_MOUSE,tr A6NGV1 A6NGV1_HUMAN,tr B0BMV1 B0BMV1_RAT,tr B2RCXO B2RCXO_HUMAN,tr B2REB8 B2REB8_HUMAN,tr F1MCF1 F1MCF1_BOVIN,tr F1RR69 F1RR69_PIG,tr	VEVTEFEFDik	59%	34.1	53.29247	Ref	0.021	-0.09	0.11	-0.11	-0.02	-0.12	0.15	2190	1930	1940	2490	2370	2200	2150	2570	606.3	1816	3	0.0146	8.055
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0 RL23A_HUMAN,sp P62751 RL23A_MOUSE,sp P62752 RL23A_RAT,sp Q24JY1 RL23A_BOVIN,tr A8MUS3 A8MUS3_HUMAN,tr A8MXA8 A8MXA8_HUMAN,tr B5DES1 B5DES1_RAT,tr D2GU25 D2GU25_AILME,tr D3YU45 D3YU45_MOUSE,tr D3YWP3 D3YWP	fPLT TESAMk	95%	53.5	53.06095	Ref	0.18	0.61	0.94	0.76	1.2	0.44	1.2	11800	12800	18600	26400	25600	29500	18700	31200	867	1732	2	0.0152	8.794

60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0 RL23A_HUMAN,sp P62751 RL23A_MOUSE,sp P62752 RL23A_RAT,sp Q24JY1 RL23A_BOVIN,tra A8MUS3 A8MUS3_HUMAN,tra A8MXA8 A8MXA8_HUMAN,tra B5DES1 B5DES1_RAT,tra D2GU25 D2GU25_AILME,tra D3YU45 D3YU45_MOUSE,tra D3YWP3 D3YWP	fPLT TESA Mk	95%	50.7	53.18089	Ref	0.14	0.75	0.83	0.78	1.1	0.36	1.2	3030	2910	4810	5710	6070	6840	4140	7240	867	1731.9	2	0.0226	13.02
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0 RL23A_HUMAN,sp P62751 RL23A_MOUSE,sp P62752 RL23A_RAT,sp Q24JY1 RL23A_BOVIN,tra A8MUS3 A8MUS3_HUMAN,tra A8MXA8 A8MXA8_HUMAN,tra B5DES1 B5DES1_RAT,tra D2GU25 D2GU25_AILME,tra D3YU45 D3YU45_MOUSE,tra D3YWP3 D3YWP	iEDN NTLV FIVD Vk	95%	53.9	53.45415	Ref	0.54	0.67	0.73	0.5	1	0.65	1	826	813	964	1130	1060	1340	1080	1400	743.1	2226.3	3	0.0169	7.582

60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0 RL23A_HUMAN,sp P62751 RL23A_MOUSE,sp P62752 RL23A_RAT,sp Q24JY1 RL23A_BOVIN,tra A8MUS3 A8MUS3_HUMAN,tra A8MXA8 A8MXA8_HUMAN,tra B5DES1 B5DES1_RAT,tra D2GU25 D2GU25_AILME,tra D3YU45 D3YU45_MOUSE,tra D3YWP3 D3YWP	iEDN NTLV FIVD Vk	95%	55.9	53.3086	Ref	0.55	0.59	0.8	0.74	1	0.52	0.99	371	394	441	574	603	653	474	649	743.1	2226.3	3	0.0118	5.279
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0 RL23A_HUMAN,sp P62751 RL23A_MOUSE,sp P62752 RL23A_RAT,sp Q24JY1 RL23A_BOVIN,tra A8MUS3 A8MUS3_HUMAN,tra A8MXA8 A8MXA8_HUMAN,tra B5DES1 B5DES1_RAT,tra D2GU25 D2GU25_AILME,tra D3YU45 D3YU45_MOUSE,tra D3YWP3 D3YWP	iEDN NTLV FIVD Vk	67%	35.6	53.17512	Ref	0.95	0.78	0.71	0.59	0.74	0.44	1	206	279	269	289	294	283	241	352	743.1	2226.3	3	0.0088	3.972

60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0 RL23A_HUMAN,sp P62751 RL23A_MOUSE,sp P62752 RL23A_RAT,sp Q24JY1 RL23A_BOVIN,tra A8MUS3 A8MUS3_HUMAN,tra A8MXA8 A8MXA8_HUMAN,tra B5DES1 B5DES1_RAT,tra D2GU25 D2GU25_AILME,tra D3YU45 D3YU45_MOUSE,tra D3YWP3 D3YWP	k	95%	54.2	50.85951	Ref	0.064	0.59	0.97	0.64	1.2	0.32	1.3	1900	1770	2760	4050	3560	4700	2580	4950	887.2	2658.6	3	0.0171	6.426
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0 RL23A_HUMAN,sp P62751 RL23A_MOUSE,sp P62752 RL23A_RAT,sp Q24JY1 RL23A_BOVIN,tra A8MUS3 A8MUS3_HUMAN,tra A8MXA8 A8MXA8_HUMAN,tra B5DES1 B5DES1_RAT,tra D2GU25 D2GU25_AILME,tra D3YU45 D3YU45_MOUSE,tra D3YWP3 D3YWP	k	95%	48	52.12914	Ref	0.28	0.59	0.83	0.61	0.95	0.5	1.3	585	532	716	950	899	993	761	1340	665.9	2659.5	4	0.026	9.779

60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0 RL23A_HUMAN,sp P62751 RL23A_MOUSE,sp P62752 RL23A_RAT,sp Q24JY1 RL23A_BOVIN,trans A8MUS3 A8MUS3_HUMAN,trans A8MXA8 A8MXA8_HUMAN,trans B5DES1 B5DES1_RAT,trans D2GU25 D2GU25_AILME,trans D3YU45 D3YU45_MOUSE,trans D3YWP3 D3YWP	IAPD YDAL DVA Nk	80%	40.1	53.91264	Ref	0.36	0.7	0.53	0.32	1.2	0.48	1.2	11200	8330	11500	11400	10900	17600	11100	17700	671.7	2012.1	3	0.0207	10.28
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0 RL23A_HUMAN,sp P62751 RL23A_MOUSE,sp P62752 RL23A_RAT,sp Q24JY1 RL23A_BOVIN,trans A8MUS3 A8MUS3_HUMAN,trans A8MXA8 A8MXA8_HUMAN,trans B5DES1 B5DES1_RAT,trans D2GU25 D2GU25_AILME,trans D3YU45 D3YU45_MOUSE,trans D3YWP3 D3YWP	IAPD YDAL DVA Nk	80%	40.3	53.87375	Ref	-0.028	0.85	0.97	0.59	1.2	0.25	1.3	26500	25800	51400	63000	53100	71200	38400	77900	671.7	2012.1	3	0.0192	9.545

60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0 RL23A_HUMAN,sp P62751 RL23A_MOUSE,sp P62752 RL23A_RAT,sp Q24JY1 RL23A_BOVIN,trans A8MUS3 A8MUS3_HUMAN,trans A8MXA8 A8MXA8_HUMAN,trans B5DES1 B5DES1_RAT,trans D2GU25 D2GU25_AILME,trans D3YU45 D3YU45_MOUSE,trans D3YWP3 D3YWP	IAPD YDAL DVA Nk	95%	52.9	53.86453	Ref	-0.083	0.69	0.95	0.68	1.3	0.39	1.3	3440	3560	6580	8870	8120	10800	6030	11100	1007	2012.1	2	0.0185	9.205
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0 RL23A_HUMAN,sp P62751 RL23A_MOUSE,sp P62752 RL23A_RAT,sp Q24JY1 RL23A_BOVIN,trans A8MUS3 A8MUS3_HUMAN,trans A8MXA8 A8MXA8_HUMAN,trans B5DES1 B5DES1_RAT,trans D2GU25 D2GU25_AILME,trans D3YU45 D3YU45_MOUSE,trans D3YWP3 D3YWP	IAPD YDAL DVA Nk	95%	63.1	53.87865	Ref	-0.003	0.7	0.87	0.72	1.3	0.35	1.2	4720	4540	8010	10100	10100	12900	7100	13000	1007	2012.1	2	0.0166	8.231

60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0 RL23A_HUMAN,sp P62751 RL23A_MOUSE,sp P62752 RL23A_RAT,sp Q24JY1 RL23A_BOVIN,trans A8MUS3 A8MUS3_HUMAN,trans A8MXA8 A8MXA8_HUMAN,trans B5DES1 B5DES1_RAT,trans D2GU25 D2GU25_AILME,trans D3YU45 D3YU45_MOUSE,trans D3YWP3 D3YWP	YDI DVA k	52%	31.4	51.7149	Ref	0.3	0.75	0.73	0.57	1	0.56	1.1	2800	2130	3150	3480	3440	4070	3120	4400	515.6	1543.9	3	0.0219	14.18
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	0 RL23A_HUMAN,sp P62751 RL23A_MOUSE,sp P62752 RL23A_RAT,sp Q24JY1 RL23A_BOVIN,trans A8MUS3 A8MUS3_HUMAN,trans A8MXA8 A8MXA8_HUMAN,trans B5DES1 B5DES1_RAT,trans D2GU25 D2GU25_AILME,trans D3YU45 D3YU45_MOUSE,trans D3YWP3 D3YWP	YDI DVA k	89%	40.6	51.57871	Ref	0.037	0.79	0.84	0.69	1.2	0.38	1.2	13200	12300	22400	26100	25800	33000	19100	33200	773	1543.9	2	0.0187	12.07

Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	sp P80311 PPIB_BOVIN, tr F7DYN1 F7DYN1_OR	dFMI QGG DFTR	50%	29.3	50.08979	Ref	0.19	0.022	-0.06	-0.28	-0.45	-0.06	-0.79	1370	1240	1200	1270	1200	929	1270	764	795.9	1589.8	2	0.0157	9.882
Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	sp P80311 PPIB_BOVIN, tr F7DYN1 F7DYN1_OR	dTnG SQFF ITTV	92%	49	54.20738	Ref	-0.34	0.022	-0.19	-0.38	-0.5	-0	-0.17	31100	17000	23800	23100	22200	17900	26400	23300	689.7	2066.1	3	0.0162	7.843
Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	sp P80311 PPIB_BOVIN, tr F7DYN1 F7DYN1_OR	dTnG SQFF ITTV	95%	53.1	54.2374	Ref	-0.2	-0.15	-0.13	-0.2	-0.3	0.099	-0.56	2360	1520	1700	1940	2030	1660	2280	1440	1034	2066.1	2	0.0158	7.666
Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	sp P80311 PPIB_BOVIN, tr F7DYN1 F7DYN1_OR	dTnG SQFF ITTV	95%	66.1	54.10729	Ref	0.01	0.085	-0.13	-0.18	-0.39	-0.03	-0.66	2520	2070	2370	2280	2440	1840	2460	1580	1034	2066.1	2	0.0036	1.764
Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	sp P80311 PPIB_BOVIN, tr F7DYN1 F7DYN1_OR	hYGP GWV SMA NAG	90%	46.5	53.84649	Ref	0.18	-0.16	-0.17	-0.083	-0.34	0.007	-0.4	11600	12800	11000	12200	14300	10500	13900	10400	695	2082.1	3	0.0157	7.526

Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	sp P80311 PPIB_BOVIN, tr F7DYN1 F7DYN1_OR	tVDN FVAL ATG Ek	86%	43	53.53995	Ref	-0.15	-0.47	-0.5	0.095	-0.31	0.17	0.001	8150	6580	5740	6310	10500	6910	10100	8890	658.4	1972.1	3	0.0152	7.694
Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	sp P80311 PPIB_BOVIN, tr F7DYN1 F7DYN1_OR	tVDN FVAL ATG Ek	95%	65	53.41892	Ref	0.0073	-0.05	-0.08	-0.2	-0.48	0.078	-0.47	6640	5750	5990	6610	6700	4810	7380	5020	987.1	1972.1	2	0.0148	7.478
Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	sp P80311 PPIB_BOVIN, tr F7DYN1 F7DYN1_OR	tVDn FVAL ATG Ek	94%	51.2	53.70056	Ref	-0.11	-0.24	-0.13	-0.2	-0.25	0.19	-0.25	9100	8020	7900	9630	10100	8490	12100	8790	658.7	1973.1	3	0.0062	3.151
Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	sp P80311 PPIB_BOVIN, tr F7DYN1 F7DYN1_OR	vLEG MDV VR	95%	57.8	52.17926	Ref	-0.14	-0.15	-0.22	-0.27	-0.54	-0.11	-0.39	4360	2410	2590	2770	2960	2150	3000	2450	441.3	1320.7	3	0.0037	2.771
Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	sp P80311 PPIB_BOVIN, tr F7DYN1 F7DYN1_OR	vWIG LFGK	77%	28.5	43.3256	Ref	-0.23	-0.11	-0.24	-0.043	-0.24	0.082	-0.26	5730	4410	5180	5340	6730	5110	6690	5250	481	1439.9	3	#####	0.627

Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	sp P80311 PPIB_BOVIN, tr F7DYN1 F7DYN1_OR	vVIG LFGk	80%	30.7	45.19316	Ref	0.047	-0.07	-0.16	-0.09	-0.4	0.057	-0.55	45800	41100	41000	43300	50200	35400	50600	33000	721	1439.9	2	0.0097	6.76
Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	sp P80311 PPIB_BOVIN, tr F7DYN1 F7DYN1_OR	vVIG LFGk	72%	29.2	45.42714	Ref	-0.18	-0.16	-0.2	-0.14	-0.39	0.031	0.009	78600	63600	70000	76500	87700	64300	90000	88000	481	1439.9	3	0.0092	6.369
Peptidyl-prolyl cis-trans isomerase B OS=Bos taurus GN=PPIB PE=1 SV=4	sp P80311 PPIB_BOVIN, tr F7DYN1 F7DYN1_OR	vVIG LFGk	85%	32.5	45.42714	Ref	0.058	-0.23	-0.1	-0.083	-0.4	0.2	-0.53	31500	30500	27000	33200	37100	26000	41100	24700	721	1439.9	2	0.009	6.247
Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1	sp Q3T149 HSPB1_BOVIN, tr E1BEL7 E1BEL7_BOVIN, tr E9RHW1 E9RHW1_BOVIN	aQL GGP EAGk	89%	43.1	51.9664	Ref	-0.072	0.15	-0.41	-0.055	-0.05	-0.59	-0.82	1E+05	95200	1E+05	91600	129000	1E+05	81200	68800	512.6	1534.9	3	0.0158	10.32
Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1	sp Q3T149 HSPB1_BOVIN, tr E1BEL7 E1BEL7_BOVIN, tr E9RHW1 E9RHW1_BOVIN	aQL GGP EAGk	89%	40.8	51.65289	Ref	-0.12	0.086	-0.5	-0.15	0.025	-0.5	-0.6	33800	23600	29500	22100	31000	30600	22200	20600	768.5	1534.9	2	0.0045	2.922

Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1	sp Q3T149 HSPB1_BOVIN, tr E1BEL7 E1BEL7_BOVIN, tr E9RHW1 E9RHW1_BOVIN	dGV VEIT Gk	95%	48.6	52.15791	Ref	-0.027	-0	-0.37	-0.19	-0.08	-0.39	-0.62	25900	19600	21600	18800	23500	22100	18700	15800	763.5	1524.9	2	0.0053	3.503
Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1	sp Q3T149 HSPB1_BOVIN, tr E1BEL7 E1BEL7_BOVIN, tr E9RHW1 E9RHW1_BOVIN	IFDQ AFGL PR	80%	37.6	52.27427	Ref	0.098	-0.05	-0.38	-0.16	-0.19	-0.29	-0.46	5050	4700	4590	4120	5290	4510	4400	3880	734.4	1466.8	2	0.0123	8.389
Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1	sp Q3T149 HSPB1_BOVIN, tr E1BEL7 E1BEL7_BOVIN, tr E9RHW1 E9RHW1_BOVIN	IFDQ AFGL PR	81%	38	52.18806	Ref	-0.009	0.01	-0.43	-0.069	-0.13	-0.3	-0.69	5900	4730	5190	4300	6090	5110	4730	3580	734.4	1466.8	2	0.0118	8.048
Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1	sp Q3T149 HSPB1_BOVIN, tr E1BEL7 E1BEL7_BOVIN, tr E9RHW1 E9RHW1_BOVIN	IFDQ AFGL PR	60%	32.8	52.15193	Ref	0.075	-0.18	-0.21	-0.19	-0.08	-0.25	-0.4	1200	1210	1100	1210	1350	1280	1180	1060	734.4	1466.8	2	0.01	6.808
Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1	sp Q3T149 HSPB1_BOVIN, tr E1BEL7 E1BEL7_BOVIN, tr E9RHW1 E9RHW1_BOVIN	qDE HGYI SR	52%	29.7	50.12909	Ref	0.054	0.07	-0.7	-0.21	-0.07	-0.42	-0.26	5320	4720	5180	3400	5270	5100	4170	4630	704.9	1407.7	2	0.0113	8.036

Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1	sp Q3T149 HSPB1_BOVIN, tr E1BEL7 E1BEL7_BOVIN, tr E9RHW1 E9RHW1_BOVIN	rVPF SLLR	65%	30.1	48.13221	Ref	-0.36	0.41	-0.05	-0.21	-0.06	-0.55	-0.67	14500	10700	19900	16100	15900	15400	11500	10500	431.3	1290.8	3	0.0053	4.127
Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1	sp Q3T149 HSPB1_BOVIN, tr E1BEL7 E1BEL7_BOVIN, tr E9RHW1 E9RHW1_BOVIN	sATQ SAEI TIPV TFQ AR	95%	53.4	54.21877	Ref	-0.021	-0.02	-0.06	-0.52	-0.06	-0.02	-0.56	8830	8760	9510	10400	8350	10000	10700	7330	708.7	2123.1	3	0.0143	6.724
Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1	sp Q3T149 HSPB1_BOVIN, tr E1BEL7 E1BEL7_BOVIN, tr E9RHW1 E9RHW1_BOVIN	sATQ SAEI TIPV TFQ AR	95%	55.9	54.13891	Ref	-0.36	-0.47	-0.02	-0.11	-0.05	-0.25	-0.28	10900	6880	6950	10700	11000	10000	9090	8840	708.7	2123.1	3	0.0139	6.54
Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1	sp Q3T149 HSPB1_BOVIN, tr E1BEL7 E1BEL7_BOVIN, tr E9RHW1 E9RHW1_BOVIN	sATQ SAEI TIPV TFQ AR	95%	83.3	54.17614	Ref	0.31	0.033	-0.27	-0.092	-0.12	-0.86	-0.5	1400	1650	1480	1340	1670	1440	898	1140	1063	2123.1	2	0.0124	5.855
Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1	sp Q3T149 HSPB1_BOVIN, tr E1BEL7 E1BEL7_BOVIN, tr E9RHW1 E9RHW1_BOVIN	sATQ SAEI TIPV TFQ AR	95%	67.1	54.08016	Ref	-0.027	-0.02	-0.61	-0.1	0.16	-0.34	-0.54	4900	4260	4640	3460	5420	5670	4190	3620	1063	2123.2	2	#####	0.36

Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1	sp Q3T149 HSPB1_BOVIN, tr E1BEL7 E1BEL7_BOVIN, tr E9RHW1 E9RHW1_BOVIN	vSLD vNH FAPE ELTV k	88%	45.1	54.20685	Ref	-0.071	-0.06	-0.4	-0.006	-0.13	-0.12	-0.51	4520	4040	4420	3900	5670	4540	4780	3610	802.8	2405.3	3	0.0188	7.801
Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	69 ANXA2_SHEEP, sp P04272 ANXA2_BOVIN, sp P07355 ANXA2_HUMAN, sp P19620 ANXA2_PIG, sp Q07936 ANXA2_RAT, sp Q2Q1M6 ANXA2_CEREL, sp Q5R5A0 ANXA2_PONAB, sp Q6TEQ7 ANXA2_CANFA, tr D2HKX0 D2HKX0_AILME, tr F1S073 F1S073_PI	dALN IETAI k	94%	45.6	52.02546	Ref	-0.006	-0.21	0.015	0.052	0.08	0.2	-0.49	14400	12400	11700	15400	17400	15500	17600	10800	848.5	1695	2	0.0143	8.404

Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	69 ANXA2_SHEEP,sp P04272 ANXA2_BOVIN,sp P07355 ANXA2_HUMAN,sp P19620 ANXA2_PIG,sp Q07936 ANXA2_RAT,sp Q2Q1M6 ANXA2_CEREL,sp Q5R5A0 ANXA2_PONAB,sp Q6TEQ7 ANXA2_CANFA,tr D2HKX0 D2HKX0_	gVDE VTIV NILT NR	78%	38.9	53.1931	Ref	0.34	-0.52	-0.11	-0.18	-0.47	0.16	-0.19	299	245	147	219	229	164	266	206	616.4	1846	3	0.0092	4.982
Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	69 ANXA2_SHEEP,sp P04272 ANXA2_BOVIN,sp P07355 ANXA2_HUMAN,sp P19620 ANXA2_PIG,sp Q07936 ANXA2_RAT,sp Q2Q1M6 ANXA2_CEREL,sp Q5R5A0 ANXA2_PONAB,sp Q6TEQ7 ANXA2_CANFA,tr D2HKX0 D2HKX0_	gVDE VTIV NILT NR	95%	62.4	53.1895	Ref	0.22	-0.28	0.021	-0.16	-0.03	0.13	-0.09	384	423	324	449	437	417	487	414	616.4	1846	3	0.0079	4.284

Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	69 ANXA2_SHEEP,sp P04272 ANXA2_BOVIN,sp P07355 ANXA2_HUMAN,sp P19620 ANXA2_PIG,sp Q07936 ANXA2_RAT,sp Q2Q1M6 ANXA2_CEREL,sp Q5R5A0 ANXA2_PONAB,sp Q6TEQ7 ANXA2_CANFA,tri D2HXK0 D2HXK0_gVDE	VTIV NILT NR	95%	57.6	53.24558	Ref	0.16	-0.07	0.088	-0.19	-0.07	-0.09	-0.23	330	299	276	346	316	299	308	278	616.4	1846	3	0.0127	6.867
Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	69 ANXA2_SHEEP,sp P04272 ANXA2_BOVIN,sp P07355 ANXA2_HUMAN,sp P19620 ANXA2_PIG,sp Q07936 ANXA2_RAT,sp Q2Q1M6 ANXA2_CEREL,sp Q5R5A0 ANXA2_PONAB,sp Q6TEQ7 ANXA2_CANFA,tri D2HXK0 D2HXK0_gVDE	VTIV NILT NR	72%	37	53.19212	Ref	Refer ence Missing (0.4248 571)	Refer ence Missing (0.03 25855 6)	Refer ence Missing (- 38583)	Refer ence Missing (0.320 3742)	Refer ence Missing (0.042 03137 4)	Refer ence Missing (0.115 13117)	Refer ence Missing (0.489 70968)	No Values (- 2.9402 215)	Refer ence Missing (0.424857 1)	Refer ence Missing (0.03 25855 6)	Refer ence Missing (- 0.4553 8583)	Refer ence Missing (0.320374 2)	Refer ence Missing (0.04 20313 74)	Refer ence Missing (- 0.1151 3117)	Refer ence Missing (0.489709 68)	616.4	1846	3	0.0076	4.089

Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	69 ANXA2_SHEEP,sp P04272 ANXA2_BOVIN,sp P07355 ANXA2_HUMAN,sp P19620 ANXA2_PIG,sp Q07936 ANXA2_RAT,sp Q2Q1M6 ANXA2_CEREL,sp Q5R5A0 ANXA2_PONAB,sp Q6TEQ7 ANXA2_CANFA,triD2HKX0 D2HKX0_AILME,triF15073 F15073_PI	rAED GSVI DYEL IDQ DAR	92%	47.6	52.90684	Ref	0.41	0.039	-0.14	-0.024	-0.21	-0.13	-0.18	1030	1290	1090	1080	1290	985	1090	1040	790.4	2368.1	3	0.0375	15.84
Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	69 ANXA2_SHEEP,sp P04272 ANXA2_BOVIN,sp P07355 ANXA2_HUMAN,sp P19620 ANXA2_PIG,sp Q07936 ANXA2_RAT,sp Q2Q1M6 ANXA2_CEREL,sp Q5R5A0 ANXA2_PONAB,sp Q6TEQ7 ANXA2_CANFA,triD2HKX0 D2HKX0_AILME,triF15073 F15073_PI	rAED GSVI DYEL IDQ DAR	90%	45.1	53.25678	Ref	-0.14	-0.02	0.016	-0.28	-0.28	0.23	0.14	2040	1620	1900	2190	1970	1720	2550	2390	790.4	2368.2	3	0.0253	10.66

Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	69 ANXA2_SHEEP,sp P04272 ANXA2_BOVIN,sp P07355 ANXA2_HUMAN,sp P19620 ANXA2_PIG,sp Q07936 ANXA2_RAT,sp Q2Q1M6 ANXA2_CEREL,sp Q5R5A0 ANXA2_PONAB,sp Q6TEQ7 ANXA2_CANFA,triD2HKX0 D2HKX0_AILME,triF15073 F15073_PI	rAED GSVI DYEL IDQ DAR	94%	51.6	53.40053	Ref	0.052	-0.04	-0.11	-0.16	-0.1	0.26	-0.28	1750	1500	1530	1630	1740	1590	2130	1450	790.4	2368.2	3	0.02	8.421
Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	69 ANXA2_SHEEP,sp P04272 ANXA2_BOVIN,sp P07355 ANXA2_HUMAN,sp P19620 ANXA2_PIG,sp Q07936 ANXA2_RAT,sp Q2Q1M6 ANXA2_CEREL,sp Q5R5A0 ANXA2_PONAB,sp Q6TEQ7 ANXA2_CANFA,triD2HKX0 D2HKX0_AILME,triF15073 F15073_PI	rAED GSVI DYEL IDQ DAR	72%	37.3	53.44856	Ref	0.21	-0.11	-0.11	-0.032	-0.16	-0	-0.16	1820	1720	1490	1680	1960	1570	1820	1620	790.4	2368.2	3	0.019	8.028

Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	69 ANXA2_SHEEP,sp P04272 ANXA2_BOVIN,sp P07355 ANXA2_HUMAN,sp P19620 ANXA2_PIG,sp Q07936 ANXA2_RAT,sp Q2Q1M6 ANXA2_CEREL,sp Q5R5A0 ANXA2_PONAB,sp Q6TEQ7 ANXA2_CANFA,tri D2HKX0 D2HKX0_AILME,tri F15073 F15073_PI	rAED GSVI DYEL IDQ DAR	93%	48.8	53.51808	Ref	-0.16	-0.42	0.44	0.14	-0.07	-0.2	0.007	3320	2880	2600	5300	4760	3600	3420	3930	790.4	2368.2	3	0.0152	6.408
Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	69 ANXA2_SHEEP,sp P04272 ANXA2_BOVIN,sp P07355 ANXA2_HUMAN,sp P19620 ANXA2_PIG,sp Q07936 ANXA2_RAT,sp Q2Q1M6 ANXA2_CEREL,sp Q5R5A0 ANXA2_PONAB,sp Q6TEQ7 ANXA2_CANFA,tri D2HKX0 D2HKX0_AILME,tri F15073 F15073_PI	sEVD MLk	58%	31.8	51.407	Ref	0.15	-0.1	-0.03	-0.043	-0.15	0.24	-0.4	43000	41500	37900	44800	48800	39600	54100	34500	715.4	1428.8	2	0.0046	3.228

Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	69 ANXA2_SHEEP,sp P04272 ANXA2_BOVIN,sp P07355 ANXA2_HUMAN,sp P19620 ANXA2_PIG,sp Q07936 ANXA2_RAT,sp Q2Q1M6 ANXA2_CEREL,sp Q5R5A0 ANXA2_PONAB,sp Q6TEQ7 ANXA2_CANFA,tr D2HKX0 D2HKX0_	tNQELQEINR	71%	35.2	52.26842	Ref	-0.014	-0.04	-0.08	-0.058	-0.06	0.31	-0.39	18600	16100	17200	18700	20900	18200	24600	15000	774.9	1547.8	2	0.0116	7.469
Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	69 ANXA2_SHEEP,sp P04272 ANXA2_BOVIN,sp P07355 ANXA2_HUMAN,sp P19620 ANXA2_PIG,sp Q07936 ANXA2_RAT,sp Q2Q1M6 ANXA2_CEREL,sp Q5R5A0 ANXA2_PONAB,sp Q6TEQ7 ANXA2_CANFA,tr D2HKX0 D2HKX0_	tPAQYDAS	95%	72.7	53.46933	Ref	0.11	-0.11	-0.1	0.14	-0.08	0.23	-0.6	9480	8870	8240	9320	12100	9060	11800	6580	916	1830	2	0.0057	3.123

<p>Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1</p>	<p>sp Q6NZI2 PTRF_HUMAN, tr B3KRY5 B3KRY5_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU</p>	<p>eGQ VEVL k</p>	<p>89%</p>	<p>40.6</p>	<p>50.96827</p>	<p>Ref</p>	<p>0.16</p>	<p>-0.51</p>	<p>0.052</p>	<p>-0.26</p>	<p>-0.05</p>	<p>-0.53</p>	<p>-0.04</p>	<p>12500</p>	<p>12400</p>	<p>8420</p>	<p>14000</p>	<p>12400</p>	<p>12500</p>	<p>9340</p>	<p>13100</p>	<p>755.5</p>	<p>1508.9</p>	<p>2</p>	<p>0.0038</p>	<p>2.495</p>
<p>Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1</p>	<p>sp Q6NZI2 PTRF_HUMAN, tr B3KRY5 B3KRY5_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU</p>	<p>kLEV NEA ELLR</p>	<p>64%</p>	<p>33.3</p>	<p>51.47788</p>	<p>Ref</p>	<p>0.28</p>	<p>-0.7</p>	<p>0.28</p>	<p>-0.36</p>	<p>-0.05</p>	<p>-0.76</p>	<p>-0.11</p>	<p>93500</p>	<p>96700</p>	<p>53500</p>	<p>118000</p>	<p>83300</p>	<p>90300</p>	<p>57900</p>	<p>89800</p>	<p>641.4</p>	<p>1921.1</p>	<p>3</p>	<p>0.0174</p>	<p>9.048</p>

Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1	sp Q6NZI2 PTRF_HUMAN, tr B3KRY5 B3KRY5_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU	kSFTPDHVVYAR	58%	34.1	53.42632	Ref	0.033	-0.39	0.11	-0.34	-0.03	-0.44	0.13	14100	14800	12000	19100	15400	16700	13100	19300	676.7	2027.1	3	0.0141	6.976
Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1	sp Q6NZI2 PTRF_HUMAN, tr B3KRY5 B3KRY5_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU	kVSVNVk	69%	26.2	45.24838	Ref	0.091	-0.81	0.34	-0.25	0.09	-0.91	-0.03	1E+05	109000	63600	159000	116000	1E+05	66700	122000	422.3	1685.1	4	0.0027	1.599

<p>Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1</p>	<p>sp Q6NZI2 PTRF_HUMAN, tr B3KRY5 B3KRY5_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU</p>	<p>qAE MEG AVQ SIQG ELSK</p>	<p>95%</p>	<p>57.8</p>	<p>54.79874</p>	<p>Ref</p>	<p>0.11</p>	<p>-0.49</p>	<p>-0.08</p>	<p>-0.27</p>	<p>-0.17</p>	<p>-0.54</p>	<p>0.14</p>	<p>4820</p>	<p>4200</p>	<p>3000</p>	<p>4490</p>	<p>4340</p>	<p>4050</p>	<p>3290</p>	<p>5220</p>	<p>805.1</p>	<p>2412.3</p>	<p>3</p>	<p>0.0164</p>	<p>6.778</p>
<p>Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1</p>	<p>sp Q6NZI2 PTRF_HUMAN, tr B3KRY5 B3KRY5_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU</p>	<p>qAE MEG AVQ SIQG ELSK</p>	<p>53%</p>	<p>34.7</p>	<p>54.80566</p>	<p>Ref</p>	<p>0.18</p>	<p>-0.3</p>	<p>-0.05</p>	<p>-0.39</p>	<p>-0.49</p>	<p>-0.39</p>	<p>-0.11</p>	<p>2240</p>	<p>1770</p>	<p>1380</p>	<p>1840</p>	<p>1600</p>	<p>1300</p>	<p>1450</p>	<p>1750</p>	<p>805.1</p>	<p>2412.3</p>	<p>3</p>	<p>0.0138</p>	<p>5.708</p>

<p>Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1</p>	<p>sp Q6NZI2 PTRF_HUMAN, tr B3KRY5 B3KRY5_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU</p>	<p>vMIYQDEVk</p>	<p>90%</p>	<p>43.1</p>	<p>53.03522</p>	<p>Ref</p>	<p>0.31</p>	<p>-0.59</p>	<p>0.33</p>	<p>-0.38</p>	<p>-0.15</p>	<p>-0.93</p>	<p>-0.17</p>	<p>17500</p>	<p>17600</p>	<p>10200</p>	<p>21700</p>	<p>14700</p>	<p>15000</p>	<p>9150</p>	<p>15300</p>	<p>867</p>	<p>1732</p>	<p>2</p>	<p>0.0083</p>	<p>4.778</p>
<p>Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1</p>	<p>sp Q6NZI2 PTRF_HUMAN, tr B3KRY5 B3KRY5_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU</p>	<p>vPPFTFHV</p>	<p>74%</p>	<p>35.4</p>	<p>51.13395</p>	<p>Ref</p>	<p>0.018</p>	<p>-0.6</p>	<p>0.098</p>	<p>-0.19</p>	<p>0.021</p>	<p>-0.55</p>	<p>0.031</p>	<p>11500</p>	<p>10300</p>	<p>7290</p>	<p>13300</p>	<p>12000</p>	<p>12100</p>	<p>8530</p>	<p>12700</p>	<p>560.7</p>	<p>1679</p>	<p>3</p>	<p>0.0091</p>	<p>5.442</p>

<p>Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1</p>	<p>sp Q6NZI2 PTRF_HUMAN, tr B3KRY5 B3KRY5_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU</p>	<p>vPPF TFHV</p>	<p>84%</p>	<p>38.9</p>	<p>50.97611</p>	<p>Ref</p>	<p>0.17</p>	<p>-0.78</p>	<p>0.28</p>	<p>-0.42</p>	<p>0.008</p>	<p>-0.93</p>	<p>0.15</p>	<p>30100</p>	<p>29200</p>	<p>16500</p>	<p>38500</p>	<p>26100</p>	<p>30600</p>	<p>16700</p>	<p>35100</p>	<p>560.7</p>	<p>1679</p>	<p>3</p>	<p>0.0066</p>	<p>3.924</p>
<p>Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1</p>	<p>sp Q6NZI2 PTRF_HUMAN, tr B3KRY5 B3KRY5_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU</p>	<p>vPPF TFHV</p>	<p>95%</p>	<p>50.8</p>	<p>51.19991</p>	<p>Ref</p>	<p>0.11</p>	<p>-0.74</p>	<p>0.27</p>	<p>-0.33</p>	<p>-0.09</p>	<p>-0.81</p>	<p>0.084</p>	<p>74700</p>	<p>66000</p>	<p>39700</p>	<p>89400</p>	<p>65300</p>	<p>67100</p>	<p>42500</p>	<p>78600</p>	<p>560.7</p>	<p>1679</p>	<p>3</p>	<p>0.0104</p>	<p>6.21</p>

<p>Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1</p>	<p>sp Q6NZI2 PTRF_HUMAN, tr B3KRY5 B3KRY5_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU</p>	<p>vPPF TFHV k</p>	<p>71%</p>	<p>34.5</p>	<p>51.15574</p>	<p>Ref</p>	<p>0.14</p>	<p>-0.66</p>	<p>0.28</p>	<p>-0.37</p>	<p>-0.11</p>	<p>-0.59</p>	<p>0.1</p>	<p>14400</p>	<p>15000</p>	<p>9340</p>	<p>20000</p>	<p>14100</p>	<p>14700</p>	<p>11000</p>	<p>17700</p>	<p>560.7</p>	<p>1679</p>	<p>3</p>	<p>0.0049</p>	<p>2.942</p>
<p>Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1</p>	<p>sp Q6NZI2 PTRF_HUMAN, tr B3KRY5 B3KRY5_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU</p>	<p>vPPF TFHV k</p>	<p>75%</p>	<p>35.7</p>	<p>51.15574</p>	<p>Ref</p>	<p>0.18</p>	<p>-0.69</p>	<p>0.27</p>	<p>-0.4</p>	<p>0.032</p>	<p>-0.64</p>	<p>0.039</p>	<p>16100</p>	<p>17400</p>	<p>10400</p>	<p>22600</p>	<p>15700</p>	<p>18500</p>	<p>12100</p>	<p>19200</p>	<p>560.7</p>	<p>1679</p>	<p>3</p>	<p>0.0049</p>	<p>2.942</p>

Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1	sp Q6NZI2 PTRF_HUMAN, tr B3KRY5 B3KRY5_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU	vPPF TFHV k	51%	30.1	50.76713	Ref	0.14	-0.6	0.18	-0.39	0.037	-0.62	0.015	2100	2080	1350	2610	1930	2270	1500	2310	840.5	1679	2	0.0036	2.121
40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	3 RS10_HUMAN, sp P63325 RS10_MOUSE, sp P63326 RS10_RAT, sp Q3T0F4 RS10_BOVIN, tr A5JST4 A5JST4_CAPHI, tr E2RGQ5 E2RGQ5_CANFA, tr F1LT36 F1LT36_RAT, tr F1RZ28 F1RZ28_PIG, tr F2X213 F2X213_AILME, tr F6SDA2 F6SDA2_MONDO, tr F6TQP3 F6TQP3_HUMAN, tr E1BNE7 E1BNE7_BOVIN, tr E2RBJ0 E2RBJ0_CANFA, tr F6U9J5 F6U9J5_CALJA, tr F6U9L1 F6U9L1_CALJA, tr F7HJ72 F7HJ72_MACMU	aEAGAG SATE FQFR	95%	53.5	51.76227	Ref	0.16	-0.05	0.18	-0.075	0.32	-0.23	0.16	9480	9420	8810	11600	10700	12300	8770	11400	873.4	1744.9	2	0.0112	6.413

40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	3 RS10_H UMAN,sp P63325 RS10_MO USE,sp P6 3326 RS1 0_RAT,sp Q3T0F4 RS10_BO VIN,tr A5 JST4 A5JS T4_CAPHI ,tr E2RGQ 5 E2RGQ 5_CANFA, tr F1LT36 F1LT36_ RAT,tr F1 RZ28 F1R Z28_PIG,t r F2X213 F2X213_ AILME,tr F6SDA2 F 6SDA2_M ONDO,tr F6TQP3 F	aEA GAG SATE FQFR	80%	38.1	51.84319	Ref	0.074	0.2	0.033	-0.08	-0.01	-0.01	0.28	13700	12900	15300	15200	15500	14200	14900	18100	582.6	1744.9	3	0.0093	5.334
40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	3 RS10_H UMAN,sp P63325 RS10_MO USE,sp P6 3326 RS1 0_RAT,sp Q3T0F4 RS10_BO VIN,tr A5 JST4 A5JS T4_CAPHI ,tr E2RGQ 5 E2RGQ 5_CANFA, tr F1LT36 F1LT36_ RAT,tr F1 RZ28 F1R Z28_PIG,t r F2X213 F2X213_ AILME,tr F6SDA2 F 6SDA2_M ONDO,tr F6TQP3 F	dyLH LPPE IVPA TLR	71%	33.6	52.05994	Ref	0.14	-0.09	0.19	-0.043	0.033	0.048	0.16	927	864	803	1090	1020	942	994	1070	586.3	2341.4	4	0.0079	3.38

40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	3 RS10_H UMAN,sp P63325 RS10_MO USE,sp P6 3326 RS1 0_RAT,sp Q3T0F4 RS10_BO VIN,tr A5 JST4 A5JS T4_CAPHI ,tr E2RGQ 5 E2RGQ 5_CANFA, tr F1LT36 F1LT36_ RAT,tr F1 RZ28 F1R Z28_PIG,t r F2X213 F2X213_ AILME,tr F6SDA2 F 6SDA2_M ONDO,tr F F6TQP3 F	hPEL ADk	57%	32.1	51.88673	Ref	0.093	-0.09	0.28	-0.092	0.25	-0.17	0.19	8760	8310	7960	11500	9810	10900	8480	10800	709.4	1416.8	2	0.028	19.78
40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	3 RS10_H UMAN,sp P63325 RS10_MO USE,sp P6 3326 RS1 0_RAT,sp Q3T0F4 RS10_BO VIN,tr A5 JST4 A5JS T4_CAPHI ,tr E2RGQ 5 E2RGQ 5_CANFA, tr F1LT36 F1LT36_ RAT,tr F1 RZ28 F1R Z28_PIG,t r F2X213 F2X213_ AILME,tr F6SDA2 F 6SDA2_M ONDO,tr F F6TQP3 F	hPEL ADk	67%	34	51.61071	Ref	0.073	-0.23	0.28	0.021	0.27	-0.11	0.17	1E+05	111000	97100	156000	143000	1E+05	1E+05	144000	473.3	1416.8	3	0.016	11.3

40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	3 RS10_H UMAN,sp P63325 RS10_MO USE,sp P6 3326 RS1 0_RAT,sp Q3T0F4 RS10_BO VIN,tr A5 JST4 A5JS T4_CAPHI ,tr E2RGQ 5 E2RGQ 5_CANFA, tr F1LT36 F1LT36_ RAT,tr F1 RZ28 F1R Z28_PIG,t r F2X213 F2X213_ AILME,tr F6SDA2 F 6SDA2_M ONDO,tr F F6TQP3 F	iAIYE LLFk	60%	30.1	49.08233	Ref	0.093	0.034	0.13	-0.073	-0.06	-0.07	-0.18	925	604	629	752	722	637	662	608	573.4	1717	3	0.016	9.298
40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	3 RS10_H UMAN,sp P63325 RS10_MO USE,sp P6 3326 RS1 0_RAT,sp Q3T0F4 RS10_BO VIN,tr A5 JST4 A5JS T4_CAPHI ,tr E2RGQ 5 E2RGQ 5_CANFA, tr F1LT36 F1LT36_ RAT,tr F1 RZ28 F1R Z28_PIG,t r F2X213 F2X213_ AILME,tr F6SDA2 F 6SDA2_M ONDO,tr F F6TQP3 F	iAIYE LLFk	95%	43.6	48.64244	Ref	-0.001	-0.19	0.36	-0.094	0.23	-0.23	0.23	1120	911	865	1420	1150	1260	949	1300	859.5	1717.1	2	0.0111	6.454

40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	3 RS10_H UMAN,sp P63325 RS10_MO USE,sp P6 3326 RS1 0_RAT,sp Q3T0F4 RS10_BO VIN,tr A5 JST4 A5JS T4_CAPHI ,tr E2RGQ 5 E2RGQ 5_CANFA, tr F1LT36 F1LT36_ RAT,tr F1 RZ28 F1R Z28_PIG,t r F2X213 F2X213_ AILME,tr F6SDA2 F 6SDA2_M ONDO,tr F F6TQP3 F	iAIYE LLFk	89%	38.3	48.81042	Ref	-0.03	-0.24	0.27	0.12	0.21	-0.11	0.13	434	350	329	525	521	486	407	474	859.5	1717.1	2	0.0116	6.734
40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	3 RS10_H UMAN,sp P63325 RS10_MO USE,sp P6 3326 RS1 0_RAT,sp Q3T0F4 RS10_BO VIN,tr A5 JST4 A5JS T4_CAPHI ,tr E2RGQ 5 E2RGQ 5_CANFA, tr F1LT36 F1LT36_ RAT,tr F1 RZ28 F1R Z28_PIG,t r F2X213 F2X213_ AILME,tr F6SDA2 F 6SDA2_M ONDO,tr F F6TQP3 F	iAIYE LLFk	55%	28.8	48.93546	Ref	0.045	-0.02	0.32	0.026	0.25	-0.43	0.22	498	458	475	672	606	620	403	627	859.5	1717	2	0.0152	8.864

40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	3 RS10_H UMAN,sp P63325 RS10_MO USE,sp P6 3326 RS1 0_RAT,sp Q3T0F4 RS10_BO VIN,tr A5 JST4 A5JS T4_CAPHI ,tr E2RGQ 5 E2RGQ 5_CANFA, tr F1LT36 F1LT36_ RAT,tr F1 RZ28 F1R Z28_PIG,t r F2X213 F2X213_ AILME,tr F6SDA2 F 6SDA2_M ONDO,tr F F6TQP3 F	iAIYE LLFk	69%	31.4	48.51026	Ref	-0.12	-0.2	0.2	0.058	0.32	-0.01	0.17	1220	967	993	1470	1470	1530	1270	1430	573.4	1717.1	3	0.0074	4.287
40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	3 RS10_H UMAN,sp P63325 RS10_MO USE,sp P6 3326 RS1 0_RAT,sp Q3T0F4 RS10_BO VIN,tr A5 JST4 A5JS T4_CAPHI ,tr E2RGQ 5 E2RGQ 5_CANFA, tr F1LT36 F1LT36_ RAT,tr F1 RZ28 F1R Z28_PIG,t r F2X213 F2X213_ AILME,tr F6SDA2 F 6SDA2_M ONDO,tr F F6TQP3 F	iAIYE LLFk	66%	30.3	47.96935	Ref	0.48	-0.57	0.19	0.006	0.01	-0.75	0.54	205	226	119	226	219	192	118	286	573.4	1717.1	3	0.0013	0.777

40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	3 RS10_H UMAN,sp P63325 RS10_MO USE,sp P6 3326 RS1 0_RAT,sp Q3T0F4 RS10_BO VIN,tr A5 JST4 A5JS T4_CAPHI ,tr E2RGQ 5 E2RGQ 5_CANFA, tr F1LT36 F1LT36_ RAT,tr F1 RZ28 F1R Z28_PIG,t r F2X213 F2X213_ AILME,tr F6SDA2 F 6SDA2_M ONDO,tr F6TQP3 F	kAEA GAG SATE FQFR	76%	39.5	54.50808	Ref	-0.11	0.008	0.32	-0.086	0.35	-0.27	0.25	26100	22500	26400	36800	30600	36200	24600	34900	726.7	2177.1	3	0.0216	9.919
40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	3 RS10_H UMAN,sp P63325 RS10_MO USE,sp P6 3326 RS1 0_RAT,sp Q3T0F4 RS10_BO VIN,tr A5 JST4 A5JS T4_CAPHI ,tr E2RGQ 5 E2RGQ 5_CANFA, tr F1LT36 F1LT36_ RAT,tr F1 RZ28 F1R Z28_PIG,t r F2X213 F2X213_ AILME,tr F6SDA2 F 6SDA2_M ONDO,tr F6TQP3 F	nVP NLH VMK	79%	36.9	51.89619	Ref	0.064	-0.2	0.32	-0.097	0.32	-0.12	0.12	9830	8930	8060	13000	10700	12500	9600	11300	830.5	1659	2	0.0096	5.796

Translocon-associated protein subunit alpha OS=Bos taurus GN=SSR1 PE=2 SV=1	7 SSRA_BOVIN,sp P16967 SRA_CANFA,sp P43307 SSRA_HUMAN,sp Q5R4X4 SSRA_PONAB,sp Q9CY50 SRA_MOUSE,trans B2R6N9 B2R6N9_HUMAN,trans D3ZI03 D3ZI03_RAT,trans E2QRZ8 E2QRZ8_CANFA,trans E9PAL7 E9PAL7_HUMAN,trans E9Q9A7 E9Q9A7_MOUSE,trans F	flVG	79%	35.8	50.73898	Ref	-0.14	0.16	-0.25	-0.2	-0.03	-0.09	-0.01	1720	1510	2020	1710	1960	1910	1920	2010	767.5	1532.9	2	0.0058	3.798
Translocon-associated protein subunit alpha OS=Bos taurus GN=SSR1 PE=2 SV=1	7 SSRA_BOVIN,sp P16967 SRA_CANFA,sp P43307 SSRA_HUMAN,sp Q5R4X4 SSRA_PONAB,sp Q9CY50 SRA_MOUSE,trans B2R6N9 B2R6N9_HUMAN,trans D3ZI03 D3ZI03_RAT,trans E2QRZ8 E2QRZ8_CANFA,trans E9PAL7 E9PAL7_HUMAN,trans E9Q9A7 E9Q9A7_MOUSE,trans F	gEDF PAN NIVK	95%	57.5	53.84551	Ref	-0.26	0.28	-0.22	-0.42	0.09	-0.15	-0.2	28000	19300	30400	24100	23200	28800	25400	24500	906.5	1811	2	0.0161	8.88

Translocon-associated protein subunit alpha OS=Bos taurus GN=SSR1 PE=2 SV=1	7 SSRA_BOVIN,sp P16967 SRA_CANFA,sp P43307 SSRA_HUMAN,sp Q5R4X4 SSRA_PONAB,sp Q9CY50 SRA_MOUSE,trans B2R6N9 B2R6N9_HUMAN,trans D3ZI03 D3ZI03_RAT,trans E2QRZ8 E2QRZ8_CANFA,trans E9PAL7 E9PAL7_HUMAN,trans E9Q9A7 E9Q9A7_MOUSE,trans F	gEDF PAN NIVK	68%	36.5	53.8454	Ref	-0.13	0.15	-0.29	-0.36	-0.09	0.12	-0.15	59900	47500	62700	51700	54600	57200	69300	57000	604.7	1811	3	0.016	8.856
Translocon-associated protein subunit alpha OS=Bos taurus GN=SSR1 PE=2 SV=1	7 SSRA_BOVIN,sp P16967 SRA_CANFA,sp P43307 SSRA_HUMAN,sp Q5R4X4 SSRA_PONAB,sp Q9CY50 SRA_MOUSE,trans B2R6N9 B2R6N9_HUMAN,trans D3ZI03 D3ZI03_RAT,trans E2QRZ8 E2QRZ8_CANFA,trans E9PAL7 E9PAL7_HUMAN,trans E9Q9A7 E9Q9A7_MOUSE,trans F	gEDF PAN NIVK	95%	72.7	53.89375	Ref	-0.29	0.17	-0.16	-0.28	0.092	-0.15	-0.26	10500	6940	10300	9210	9380	10600	9330	8610	907	1812	2	0.0145	7.997

Translocon-associated protein subunit alpha OS=Bos taurus GN=SSR1 PE=2 SV=1	7 SSRA_BOVIN,sp P16967 SRA_CANFA,sp P43307 SSRA_HUMAN,sp Q5R4X4 SSRA_PONAB,sp Q9CY50 SRA_MOUSE,tr B2R6N9 B2R6N9_HUMAN,tr D3ZI03 D3ZI03_RAT, tr E2QRZ8 E2QRZ8_CANFA, tr E9PAL7 E9PAL7_HUMAN, tr E9Q9A7 E9Q9A7_MOUSE, tr F	gTED FIVE SLDA	SFR	95%	64.9	52.65453	Ref	-0.29	0.15	-0.15	-0.25	0.056	-0.16	-0.11	14000	9860	14400	13200	13600	14600	13100	13500	995.5	1989	2	0.0129	6.493
	7 SSRA_BOVIN,sp P16967 SRA_CANFA,sp P43307 SSRA_HUMAN,sp Q5R4X4 SSRA_PONAB,sp Q9CY50 SRA_MOUSE, tr B2R6N9 B2R6N9_HUMAN, tr D3ZI03 D3ZI03_RAT, tr E2QRZ8 E2QRZ8_CANFA, tr E9PAL7 E9PAL7_HUMAN, tr E9Q9A7 E9Q9A7_MOUSE, tr F	gTED FIVE SLDA	SFR	69%	35.7	52.74963	Ref	0.12	-0.07	-0.13	-0.088	-0.02	0.025	-0.34	2020	2230	2120	2270	2590	2380	2550	1970	664	1989	3	0.0086	4.326

Translocon-associated protein subunit alpha OS=Bos taurus GN=SSR1 PE=2 SV=1	7 SSRA_BOVIN,sp P16967 SRA_CANFA,sp P43307 SSRA_HUMAN,sp Q5R4X4 SSRA_PONAB,sp Q9CY50 SRA_MOUSE,trans B2R6N9 B2R6N9_HUMAN,trans D3ZI03 D3ZI03_RAT,trans E2QRZ8 E2QRZ8_CANFA,trans E9PAL7 E9PAL7_HUMAN,trans E9Q9A7 E9Q9A7_MOUSE,trans F	gTED FIVE SLDA	SFR	80%	38.1	52.60518	Ref	-0.076	0.18	-0.2	-0.21	0.068	-0.34	0.035	843	805	1050	898	987	1040	820	1060	995.5	1989	2	0.0138	6.916
Translocon-associated protein subunit alpha OS=Bos taurus GN=SSR1 PE=2 SV=1	7 SSRA_BOVIN,sp P16967 SRA_CANFA,sp P43307 SSRA_HUMAN,sp Q5R4X4 SSRA_PONAB,sp Q9CY50 SRA_MOUSE,trans B2R6N9 B2R6N9_HUMAN,trans D3ZI03 D3ZI03_RAT,trans E2QRZ8 E2QRZ8_CANFA,trans E9PAL7 E9PAL7_HUMAN,trans E9Q9A7 E9Q9A7_MOUSE,trans F	gTED FIVE SLDA	SFR	95%	52.1	52.60518	Ref	-0.12	0.12	-0	-0.31	-0.02	-0.27	-0.09	1420	1160	1490	1530	1360	1460	1280	1440	995.5	1989	2	0.0138	6.916

Translocon-associated protein subunit alpha OS=Bos taurus GN=SSR1 PE=2 SV=1	7 SSRA_BOVIN,sp P16967 SRA_CANFA,sp P43307 SSRA_HUMAN,sp Q5R4X4 SSRA_PONAB,sp Q9CY50 SRA_MOUSE,tr B2R6N9 B2R6N9_HUMAN,tr D3ZI03 D3ZI03_RAT, tr E2QRZ8 E2QRZ8_CANFA, tr E9PAL7 E9PAL7_HUMAN, tr E9Q9A7 E9Q9A7_MOUSE, tr F	gTED FIVE SLDA	95%	52.3	52.70161	Ref	-0.063	0.08	-0.37	-0.32	-0.2	-0.47	0.16	693	459	550	451	514	488	423	650	664	1989	3	0.0119	5.969
Translocon-associated protein subunit alpha OS=Bos taurus GN=SSR1 PE=2 SV=1	7 SSRA_BOVIN,sp P16967 SRA_CANFA,sp P43307 SSRA_HUMAN,sp Q5R4X4 SSRA_PONAB,sp Q9CY50 SRA_MOUSE, tr B2R6N9 B2R6N9_HUMAN, tr D3ZI03 D3ZI03_RAT, tr E2QRZ8 E2QRZ8_CANFA, tr E9PAL7 E9PAL7_HUMAN, tr E9Q9A7 E9Q9A7_MOUSE, tr F	gTED FIVE SLDA	51%	32.2	52.67228	Ref	0.096	0.15	-0.63	0.043	-0.18	0.02	Value Missing (-1.9462475)	370	224	253	166	290	218	261	Value Missing (-1.9462475)	664	1989	3	0.0123	6.165

Translocon-associated protein subunit alpha OS=Bos taurus GN=SSR1 PE=2 SV=1	7 SSRA_BOVIN,sp P16967 SRA_CANFA,sp P43307 SSRA_HUMAN,sp Q5R4X4 SSRA_PONAB,sp Q9CY50 SRA_MOUSE,trans B2R6N9 B2R6N9_HUMAN,trans D3ZI03 D3ZI03_RAT,trans E2QRZ8 E2QRZ8_CANFA,trans E9PAL7 E9PAL7_HUMAN,trans E9Q9A7 E9Q9A7_MOUSE,trans F	gTED FIVE SLDA SFR	95%	63	52.766	Ref	-0.31	0.005	-0.21	-0.15	-0.15	-0.28	0.38	600	446	603	584	671	586	559	875	664	1989	3	0.0088	4.416
Translocon-associated protein subunit alpha OS=Bos taurus GN=SSR1 PE=2 SV=1	7 SSRA_BOVIN,sp P16967 SRA_CANFA,sp P43307 SSRA_HUMAN,sp Q5R4X4 SSRA_PONAB,sp Q9CY50 SRA_MOUSE,trans B2R6N9 B2R6N9_HUMAN,trans D3ZI03 D3ZI03_RAT,trans E2QRZ8 E2QRZ8_CANFA,trans E9PAL7 E9PAL7_HUMAN,trans E9Q9A7 E9Q9A7_MOUSE,trans F	gTED FIVE SLDA SFR	83%	40.5	52.73793	Ref	0.19	0.11	-0.26	-0.054	-0.23	-0	-0.53	174	174	180	155	198	153	187	129	664	1989	3	0.009	4.506

<p>Translocon-associated protein subunit alpha OS=Bos taurus GN=SSR1 PE=2 SV=1</p>	<p>7 SSRA_BOVIN,sp P16967 SRA_CANFA,sp P43307 SSRA_HUMAN,sp Q5R4X4 SSRA_PONAB,sp Q9CY50 SRA_MOUSE,tr B2R6N9 B2R6N9_HUMAN,tr D3ZI03 D3ZI03_RAT, tr E2QRZ8 E2QRZ8_CANFA, tr E9PAL7 E9PAL7_HUMAN, tr E9Q9A7 E9Q9A7_MOUSE, tr F</p>	<p>sVGS DE</p>	<p>92%</p>	<p>36.5</p>	<p>45.00621</p>	<p>Ref</p>	<p>-0.077</p>	<p>0.039</p>	<p>-0.12</p>	<p>-0.26</p>	<p>-0.06</p>	<p>-0.16</p>	<p>-0.1</p>	<p>556</p>	<p>444</p>	<p>522</p>	<p>523</p>	<p>524</p>	<p>525</p>	<p>514</p>	<p>529</p>	<p>449.2</p>	<p>896.42</p>	<p>2</p>	<p>0.0146</p>	<p>16.22</p>
<p>Nucleophosmin OS=Bos taurus GN=NPM1 PE=2 SV=1</p>	<p>sp Q3T160 NPM_BOVIN, tr D2HKP0 D2HKP0_ALME, tr D3U796 D3U796_BOVIN, tr E2R4V7 E2R4V7_CANFA, tr E2RTB1 E2RTB1_CANFA, tr E3SAZ8 E3SAZ8_BOVIN, tr F6X9D3 F6X9D3_HORSE</p>	<p>mQA SIEK</p>	<p>64%</p>	<p>33.6</p>	<p>52.06985</p>	<p>Ref</p>	<p>-0.24</p>	<p>0.085</p>	<p>-0.4</p>	<p>-0.21</p>	<p>-0.11</p>	<p>-0.13</p>	<p>0.015</p>	<p>23400</p>	<p>17200</p>	<p>23400</p>	<p>18700</p>	<p>23600</p>	<p>22100</p>	<p>22800</p>	<p>24900</p>	<p>707.9</p>	<p>1413.8</p>	<p>2</p>	<p>0.0248</p>	<p>17.5</p>

Nucleophosmin OS=Bos taurus GN=NPM1 PE=2 SV=1	sp Q3T160 NPM_BOVIN, tr D2HKP0 D2HKP0_AILME, tr D3U796 D3U796_BOVIN, tr E2R4V7 E2R4V7_CANFA, tr E2RTB1 E2RTB1_CANFA, tr E3SAZ8 E3SAZ8_BOVIN, tr F6X9D3 F6X9D3_HORSE	rSAP GSG Sk	50%	31.5	52.10626	Ref	-0.15	0.044	-0.43	-0.17	-0.11	0.033	-0.04	17000	15000	18600	15000	19900	18100	20800	19600	485.6	1453.8	3	0.0079	5.438
Nucleophosmin OS=Bos taurus GN=NPM1 PE=2 SV=1	sp Q3T160 NPM_BOVIN, tr D2HKP0 D2HKP0_AILME, tr D3U796 D3U796_BOVIN, tr E2R4V7 E2R4V7_CANFA, tr E2RTB1 E2RTB1_CANFA, tr E3SAZ8 E3SAZ8_BOVIN, tr F6X9D3 F6X9D3_HORSE	sAPG SGSk	58%	32.4	51.77023	Ref	-0.16	-0.08	-0.13	-0.16	0.082	-0.49	0.011	18100	14700	16900	18200	19800	20400	14300	20100	433.6	1297.7	3	0.022	16.95

<p>Nucleophosmin OS=Bos taurus GN=NPM1 PE=2 SV=1</p>	<p>sp Q3T160 NPM_BOVIN, tr D2HKP0 D2HKP0_AI LME, tr D3U796 D3U796_BOVIN, tr E2R4V7 E2R4V7_CANFA, tr E2RTB1 E2RTB1_CANFA, tr E3SAZ8 E3SAZ8_BOVIN, tr F6X9D3 F6X9D3_HORSE</p>	<p>tVSL GAG Ak</p>	<p>53%</p>	<p>30.4</p>	<p>50.50716</p>	<p>Ref</p>	<p>-0.042</p>	<p>-0.18</p>	<p>-0.05</p>	<p>-0.26</p>	<p>-0.21</p>	<p>-0.08</p>	<p>-0.15</p>	<p>19400</p>	<p>16300</p>	<p>16100</p>	<p>19800</p>	<p>18900</p>	<p>17100</p>	<p>19500</p>	<p>18400</p>	<p>471.3</p>	<p>1410.9</p>	<p>3</p>	<p>0.0021</p>	<p>1.474</p>
<p>Nucleophosmin OS=Bos taurus GN=NPM1 PE=2 SV=1</p>	<p>sp Q3T160 NPM_BOVIN, tr D2HKP0 D2HKP0_AI LME, tr D3U796 D3U796_BOVIN, tr E2R4V7 E2R4V7_CANFA, tr E2RTB1 E2RTB1_CANFA, tr E3SAZ8 E3SAZ8_BOVIN, tr F6X9D3 F6X9D3_HORSE</p>	<p>tVSL GAG Ak</p>	<p>93%</p>	<p>43.3</p>	<p>50.59313</p>	<p>Ref</p>	<p>-0.013</p>	<p>0.079</p>	<p>-0.39</p>	<p>-0.32</p>	<p>-0.14</p>	<p>-0.27</p>	<p>-0.14</p>	<p>18400</p>	<p>14000</p>	<p>16200</p>	<p>13100</p>	<p>15200</p>	<p>15100</p>	<p>14300</p>	<p>15600</p>	<p>706.4</p>	<p>1410.9</p>	<p>2</p>	<p>0.0062</p>	<p>4.395</p>

<p>Nucleophosmin OS=Bos taurus GN=NPM1 PE=2 SV=1</p>	<p>sp Q3T160 NPM_BOVIN, tr D2HKP0 D2HKP0_AI LME, tr D3U796 D3U796_BOVIN, tr E2R4V7 E2R4V7_CANFA, tr E2RTB1 E2RTB1_CANFA, tr E3SAZ8 E3SAZ8_BOVIN, tr F6X9D3 F6X9D3_HORSE</p>	<p>vDN DEN EHQ LSLR</p>	<p>95%</p>	<p>72.1</p>	<p>51.99744</p>	<p>Ref</p>	<p>-0.068</p>	<p>-0.07</p>	<p>-0.58</p>	<p>-0.24</p>	<p>-0.18</p>	<p>-0.11</p>	<p>-0.16</p>	<p>1E+05</p>	<p>69200</p>	<p>75200</p>	<p>59200</p>	<p>82400</p>	<p>75100</p>	<p>82300</p>	<p>79000</p>	<p>625</p>	<p>1871.9</p>	<p>3</p>	<p>0.013</p>	<p>6.941</p>
<p>Nucleophosmin OS=Bos taurus GN=NPM1 PE=2 SV=1</p>	<p>sp Q3T160 NPM_BOVIN, tr D2HKP0 D2HKP0_AI LME, tr D3U796 D3U796_BOVIN, tr E2R4V7 E2R4V7_CANFA, tr E2RTB1 E2RTB1_CANFA, tr E3SAZ8 E3SAZ8_BOVIN, tr F6X9D3 F6X9D3_HORSE</p>	<p>vDN DEN EHQ LSLR</p>	<p>60%</p>	<p>33</p>	<p>51.87637</p>	<p>Ref</p>	<p>-0.13</p>	<p>-0.01</p>	<p>-0.41</p>	<p>-0.13</p>	<p>0.17</p>	<p>-0.67</p>	<p>0.13</p>	<p>41400</p>	<p>34400</p>	<p>40600</p>	<p>34400</p>	<p>46100</p>	<p>49500</p>	<p>28800</p>	<p>49900</p>	<p>625</p>	<p>1871.9</p>	<p>3</p>	<p>0.0156</p>	<p>8.303</p>

<p>Nucleophosmin OS=Bos taurus GN=NPM1 PE=2 SV=1</p>	<p>sp Q3T160 NPM_BOVIN, tr D2HKP0 D2HKP0_AI LME, tr D3U796 D3U796_BOVIN, tr E2R4V7 E2R4V7_CANFA, tr E2RTB1 E2RTB1_CANFA, tr E3SAZ8 E3SAZ8_BOVIN, tr F6X9D3 F6X9D3_HORSE</p>	<p>vDN DEN EHQ LSLR</p>	<p>93%</p>	<p>45.1</p>	<p>51.97989</p>	<p>Ref</p>	<p>-0.23</p>	<p>0.036</p>	<p>-0.44</p>	<p>-0.12</p>	<p>0.15</p>	<p>-0.32</p>	<p>0.025</p>	<p>6420</p>	<p>5180</p>	<p>6740</p>	<p>5430</p>	<p>7460</p>	<p>7860</p>	<p>5930</p>	<p>7480</p>	<p>937</p>	<p>1871.9</p>	<p>2</p>	<p>0.0138</p>	<p>7.349</p>
<p>Nucleophosmin OS=Bos taurus GN=NPM1 PE=2 SV=1</p>	<p>sp Q3T160 NPM_BOVIN, tr D2HKP0 D2HKP0_AI LME, tr D3U796 D3U796_BOVIN, tr E2R4V7 E2R4V7_CANFA, tr E2RTB1 E2RTB1_CANFA, tr E3SAZ8 E3SAZ8_BOVIN, tr F6X9D3 F6X9D3_HORSE</p>	<p>vDN DEN EHQ LSLR</p>	<p>89%</p>	<p>43</p>	<p>51.88355</p>	<p>Ref</p>	<p>-0.13</p>	<p>0.073</p>	<p>-0.31</p>	<p>-0.13</p>	<p>-0.11</p>	<p>-0.2</p>	<p>-0.08</p>	<p>8500</p>	<p>7020</p>	<p>8780</p>	<p>7540</p>	<p>9440</p>	<p>8330</p>	<p>8210</p>	<p>8830</p>	<p>625</p>	<p>1871.9</p>	<p>3</p>	<p>0.0159</p>	<p>8.495</p>

<p>Nucleophosmin OS=Bos taurus GN=NPM1 PE=2 SV=1</p>	<p>sp Q3T160 NPM_BOVIN, tr D2HKP0 D2HKP0_AI LME, tr D3U796 D3U796_BOVIN, tr E2R4V7 E2R4V7_CANFA, tr E2RTB1 E2RTB1_CANFA, tr E3SAZ8 E3SAZ8_BOVIN, tr F6X9D3 F6X9D3_HORSE</p>	<p>vDn DEN EHQ LSLR</p>	<p>95%</p>	<p>48.2</p>	<p>51.28742</p>	<p>Ref</p>	<p>0.038</p>	<p>0.14</p>	<p>-0.72</p>	<p>-0.18</p>	<p>-0.28</p>	<p>-0.27</p>	<p>-0.1</p>	<p>9160</p>	<p>6920</p>	<p>8040</p>	<p>5000</p>	<p>7970</p>	<p>6510</p>	<p>6860</p>	<p>7620</p>	<p>937.5</p>	<p>1872.9</p>	<p>2</p>	<p>0.0134</p>	<p>7.147</p>
<p>Nucleophosmin OS=Bos taurus GN=NPM1 PE=2 SV=1</p>	<p>sp Q3T160 NPM_BOVIN, tr D2HKP0 D2HKP0_AI LME, tr D3U796 D3U796_BOVIN, tr E2R4V7 E2R4V7_CANFA, tr E2RTB1 E2RTB1_CANFA, tr E3SAZ8 E3SAZ8_BOVIN, tr F6X9D3 F6X9D3_HORSE</p>	<p>vDn DEN EHQ LSLR</p>	<p>95%</p>	<p>68.6</p>	<p>51.28984</p>	<p>Ref</p>	<p>0.043</p>	<p>0.06</p>	<p>-0.68</p>	<p>-0.13</p>	<p>-0.18</p>	<p>-0.11</p>	<p>-0.08</p>	<p>56200</p>	<p>49800</p>	<p>54600</p>	<p>36800</p>	<p>59300</p>	<p>49900</p>	<p>54900</p>	<p>55600</p>	<p>625.3</p>	<p>1872.9</p>	<p>3</p>	<p>0.0132</p>	<p>7.022</p>

<p>Nucleophosmin OS=Bos taurus GN=NPM1 PE=2 SV=1</p>	<p>sp Q3T160 NPM_BOVIN, tr D2HKP0 D2HKP0_AI LME, tr D3U796 D3U796_BOVIN, tr E2R4V7 E2R4V7_CANFA, tr E2RTB1 E2RTB1_CANFA, tr E3SAZ8 E3SAZ8_BOVIN, tr F6X9D3 F6X9D3_HORSE</p>	<p>vDn DEN EHQ LSLR</p>	<p>73%</p>	<p>35</p>	<p>51.08196</p>	<p>Ref</p>	<p>0.097</p>	<p>-0.14</p>	<p>-0.29</p>	<p>-0.27</p>	<p>0.005</p>	<p>-0.2</p>	<p>-0.1</p>	<p>12000</p>	<p>11700</p>	<p>10800</p>	<p>10900</p>	<p>12100</p>	<p>12900</p>	<p>11700</p>	<p>12400</p>	<p>625.3</p>	<p>1872.9</p>	<p>3</p>	<p>0.0176</p>	<p>9.376</p>
<p>Nucleophosmin OS=Bos taurus GN=NPM1 PE=2 SV=1</p>	<p>sp Q3T160 NPM_BOVIN, tr D2HKP0 D2HKP0_AI LME, tr D3U796 D3U796_BOVIN, tr E2R4V7 E2R4V7_CANFA, tr E2RTB1 E2RTB1_CANFA, tr E3SAZ8 E3SAZ8_BOVIN, tr F6X9D3 F6X9D3_HORSE</p>	<p>vTLA TLK</p>	<p>83%</p>	<p>32</p>	<p>45.67191</p>	<p>Ref</p>	<p>-0.11</p>	<p>0.11</p>	<p>-0.44</p>	<p>-0.15</p>	<p>-0.15</p>	<p>-0.24</p>	<p>-0.02</p>	<p>90200</p>	<p>71300</p>	<p>90300</p>	<p>69500</p>	<p>93200</p>	<p>81300</p>	<p>79900</p>	<p>92500</p>	<p>677.4</p>	<p>1352.9</p>	<p>2</p>	<p>0.0022</p>	<p>1.609</p>

40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	8 RS12_H UMAN,sp P46405 RS12_PIG, sp Q7618 1 RS12_B OVIN,tr D 2I741 D2I 741_AILM E,tr D3ZH B3 D3ZH B3_RAT,tr D3ZMD2 D3ZMD2 _RAT,tr E 2R4N7 E2 R4N7_CA NFA,tr F1 M185 F1 M185_RA T,tr F1N5 72 F1N57 2_BOVIN, tr F2X216 F2X216_ AILME,tr F6SIP5 F6	dVIE EYFK	95%	48.5	52.90849	Ref	0.26	0.071	0.26	0.2	0.23	-0.1	0.14	8710	9330	8900	11400	12000	10700	8920	10500	826	1649.9	2	0.0171	10.33
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	8 RS12_H UMAN,sp P46405 RS12_PIG, sp Q7618 1 RS12_B OVIN,tr D 2I741 D2I 741_AILM E,tr D3ZH B3 D3ZH B3_RAT,tr D3ZMD2 D3ZMD2 _RAT,tr E 2R4N7 E2 R4N7_CA NFA,tr F1 M185 F1 M185_RA T,tr F1N5 72 F1N57 2_BOVIN, tr F2X216 F2X216_ AILME,tr F6SIP5 F6	dVIE EYFK	74%	36.4	52.89341	Ref	0.063	-0.03	0.34	0.095	0.31	-0.12	0.15	10900	8790	8960	13000	12100	12200	9490	11400	826	1649.9	2	0.0107	6.494

40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	8 RS12_H UMAN,sp P46405 RS12_PIG, sp Q76I8 1 RS12_B OVIN,tr D 2I741 D2I 741_AILM E,tr D3ZH B3 D3ZH B3_RAT,tr D3ZMD2 D3ZMD2 _RAT,tr E 2R4N7 E2 R4N7_CA NFA,tr F1 M185 F1 M185_RA T,tr F1N5 72 F1N57 2_BOVIN, tr F2X216 F2X216_ AILME,tr F6SIP5 F6	dVIE EYFK	85%	41.3	52.89936	Ref	-0.007	-0.1	0.29	0.19	0.2	0.06	0.37	25500	22500	22900	33700	34600	30500	28800	35500	551	1649.9	3	0.0087	5.244
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	8 RS12_H UMAN,sp P46405 RS12_PIG, sp Q76I8 1 RS12_B OVIN,tr D 2I741 D2I 741_AILM E,tr D3ZH B3 D3ZH B3_RAT,tr D3ZMD2 D3ZMD2 _RAT,tr E 2R4N7 E2 R4N7_CA NFA,tr F1 M185 F1 M185_RA T,tr F1N5 72 F1N57 2_BOVIN, tr F2X216 F2X216_ AILME,tr F6SIP5 F6	dVIE EYFK	85%	41.6	52.86995	Ref	-0.005	-0.1	0.21	0.058	0.24	0.16	0.46	25500	23000	23300	32500	32300	32000	31700	38800	551	1649.9	3	0.0019	1.137

40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	8 RS12_H UMAN,sp P46405 RS12_PIG, sp Q7618 1 RS12_B OVIN,tr D 2I741 D2I 741_AILM E,tr D3ZH B3 D3ZH B3_RAT,tr D3ZMD2 D3ZMD2 _RAT,tr E 2R4N7 E2 R4N7_CA NFA,tr F1 M185 F1 M185_RA T,tr F1N5 72 F1N57 2_BOVIN, tr F2X216 F2X216_ AILME,tr F6SIP5 F6	dVIE EYFK	83%	40.9	53.28212	Ref	-0.033	0.081	0.053	0.12	0.2	0.22	0.38	7260	6300	7400	8140	9420	8700	9190	10200	551	1649.9	3	0.0222	13.46
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	8 RS12_H UMAN,sp P46405 RS12_PIG, sp Q7618 1 RS12_B OVIN,tr D 2I741 D2I 741_AILM E,tr D3ZH B3 D3ZH B3_RAT,tr D3ZMD2 D3ZMD2 _RAT,tr E 2R4N7 E2 R4N7_CA NFA,tr F1 M185 F1 M185_RA T,tr F1N5 72 F1N57 2_BOVIN, tr F2X216 F2X216_ AILME,tr F6SIP5 F6	IVEA LcAE HQI NLIK	94%	52	53.85654	Ref	0.16	-0.28	0.4	0.015	0.2	-0.01	0.12	596	456	365	659	554	549	495	538	783.4	2347.3	3	0.0152	6.493

40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	8 RS12_H UMAN,sp P46405 RS12_PIG, sp Q7618 1 RS12_B OVIN,tr D 2I741 D2I 741_AILM E,tr D3ZH B3 D3ZH B3_RAT,tr D3ZMD2 D3ZMD2 _RAT,tr E 2R4N7 E2 R4N7_CA NFA,tr F1 M185 F1 M185_RA T,tr F1N5 72 F1N57 2_BOVIN, tr F2X216 F2X216_ AILME,tr F6SIP5 F6	IVEA LcAE HQI NLIK	93%	48.8	53.67032	Ref	0.087	0.02	0.33	0.072	0.32	-0.01	0.12	649	567	588	817	754	781	650	704	783.4	2347.3	3	0.0094	4.002
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	8 RS12_H UMAN,sp P46405 RS12_PIG, sp Q7618 1 RS12_B OVIN,tr D 2I741 D2I 741_AILM E,tr D3ZH B3 D3ZH B3_RAT,tr D3ZMD2 D3ZMD2 _RAT,tr E 2R4N7 E2 R4N7_CA NFA,tr F1 M185 F1 M185_RA T,tr F1N5 72 F1N57 2_BOVIN, tr F2X216 F2X216_ AILME,tr F6SIP5 F6	IVEA LcAE HQI NLIK	95%	56	53.82048	Ref	0.018	-0.21	0.4	0.14	0.3	0.003	0.3	410	360	333	571	528	513	437	534	783.4	2347.3	3	0.0151	6.416

40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	8 RS12_H UMAN,sp P46405 RS12_PIG, sp Q7618 1 RS12_B OVIN,tr D 2I741 D2I 741_AILM E,tr D3ZH B3 D3ZH B3_RAT,tr D3ZMD2 D3ZMD2 _RAT,tr E 2R4N7 E2 R4N7_CA NFA,tr F1 M185 F1 M185_RA T,tr F1N5 72 F1N57 2_BOVIN, tr F2X216 F2X216_ tALI AILME,tr HDG F6SIP5 F6 LAR	95%	50.8	51.91636	Ref	0.34	0.079	0.32	0.034	0.065	0.18	0.066	10800	12500	11400	15000	13600	12100	13700	12600	457.6	1369.8	3	0.0129	9.384
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	8 RS12_H UMAN,sp P46405 RS12_PIG, sp Q7618 1 RS12_B OVIN,tr D 2I741 D2I 741_AILM E,tr D3ZH B3 D3ZH B3_RAT,tr D3ZMD2 D3ZMD2 _RAT,tr E 2R4N7 E2 R4N7_CA NFA,tr F1 M185 F1 M185_RA T,tr F1N5 72 F1N57 2_BOVIN, tr F2X216 F2X216_ tALI AILME,tr HDG F6SIP5 F6 LAR	82%	39.1	51.81889	Ref	0.06	-0.35	0.3	-0.06	0.28	0.34	0.27	7150	6130	5020	8820	7570	8350	9080	8630	457.6	1369.8	3	0.0094	6.846

40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	8 RS12_H UMAN,sp P46405 RS12_PIG, sp Q76I8 1 RS12_B OVIN,tr D 2I741 D2I 741_AILM E,tr D3ZH B3 D3ZH B3_RAT,tr D3ZMD2 D3ZMD2 _RAT,tr E 2R4N7 E2 R4N7_CA NFA,tr F1 M185 F1 M185_RA T,tr F1N5 72 F1N57 2_BOVIN, tr F2X216 F2X216_ tALI AILME,tr HDG F6SIP5 F6 LAR	95%	53.5	51.90334	Ref	0.42	-0.06	0.5	-0.11	0.14	-0.11	0.11	15500	17500	13600	22500	16200	16900	14900	17100	457.6	1369.8	3	0.0123	8.99
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	8 RS12_H UMAN,sp P46405 RS12_PIG, sp Q76I8 1 RS12_B OVIN,tr D 2I741 D2I 741_AILM E,tr D3ZH B3 D3ZH B3_RAT,tr D3ZMD2 D3ZMD2 _RAT,tr E 2R4N7 E2 R4N7_CA NFA,tr F1 M185 F1 M185_RA T,tr F1N5 72 F1N57 2_BOVIN, tr F2X216 F2X216_ tALI AILME,tr HDG F6SIP5 F6 LAR	83%	39.3	51.90068	Ref	0.29	-0.07	0.35	-0.025	0.42	-0.25	0.26	16900	18800	15900	23700	20200	24000	15700	22300	457.6	1369.8	3	0.0092	6.714

40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	8 RS12_HUMAN,sp P46405 RS12_PIG,sp Q76181 RS12_BOVIN,triD21741 D21741_AILME,triD32HB3 D32HB3_RAT,triD3ZMD2 D3ZMD2_RAT,triE2R4N7 E2R4N7_CANFA,triF1M185 F1M185_RAT,triF1N572 F1N572_BOVIN,triF2X216 F2X216_AILME,triF651P5 F6	tALI HDG LAR	79%	38.1	52.18449	Ref	0.29	0.16	0.13	0.026	0.09	0.15	0.13	7400	7610	7530	8250	8490	7740	8450	8270	457.6	1369.8	3	0.0139	10.13
Stress-70 protein, mitochondrial OS=Cricetulus griseus GN=HSPA9 PE=2 SV=1	sp O35501 GRP75_CRIGR,sp P38646 GRP75_HUMAN,sp P38647 GRP75_MOUSE,sp Q3ZCH0 GRP75_BOVIN,sp Q5R511 GRP75_PONAB,triB7Z4V2 B7Z4V2_HUMAN,triD2HK99 D2HK99_AILME,triQ7TSZ0 Q7TSZ0_MOUSE,triQ8N1C8 Q8N1C8_HUMAN	aSnG DAW VEA HGK	83%	41	53.35619	Ref	0.23	0.14	0.024	-0.094	-0.2	-0.08	-0.12	16300	16800	17100	17700	18000	14600	16500	15900	651	1950	3	0.0202	10.35

Stress-70 protein, mitochondrial OS=Cricetulus griseus GN=HSPA9 PE=2 SV=1	sp O35501 GRP75_CRIGR,sp P38646 GRP75_HUMAN,sp P38647 GRP75_MOUSE,sp Q3ZCH0 GRP75_BOVIN,sp Q5R511 GRP75_PONAB,trans B7Z4V2 B7Z4V2_HUMAN,trans D2HK99 D2HK99_AILME,trans Q7TSZ0 Q7TSZ0_MOUSE,trans Q8N1C8 Q8N1C8_HUMAN	dAG QISG LNVL	R	95%	48.2	52.41848	Ref	0.2	-0.09	0.12	-0.14	-0.13	0.04	-0.08	19100	19300	17100	22300	20400	18000	21200	19400	773.9	1545.9	2	0.0118	7.641
Stress-70 protein, mitochondrial OS=Cricetulus griseus GN=HSPA9 PE=2 SV=1	sp O35501 GRP75_CRIGR,sp P38646 GRP75_HUMAN,sp P38647 GRP75_MOUSE,sp Q3ZCH0 GRP75_BOVIN,sp Q5R511 GRP75_PONAB,trans B7Z4V2 B7Z4V2_HUMAN,trans D2HK99 D2HK99_AILME,trans Q7TSZ0 Q7TSZ0_MOUSE,trans Q8N1C8 Q8N1C8_HUMAN	dSET GENI	R	80%	35.7	50.49641	Ref	-0.026	-0.04	0.19	-0.18	-0.03	-0.14	0.056	16200	13100	14100	18500	15800	15300	14800	16800	662.8	1323.6	2	0.0111	8.374

Stress-70 protein, mitochondrial OS=Cricetulus griseus GN=HSPA9 PE=2 SV=1	sp O3550 1 GRP75_ CRIGR,sp P38646 G RP75_HU MAN,sp P 38647 GR P75_MOU SE,sp Q3Z CH0 GRP 75_BOVIN ,sp Q5R5 11 GRP75 _PONAB,t r B7Z4V2 B7Z4V2_ HUMAN,t r D2HK99 D2HK99_ AILME,tr Q7TSZ0 Q 7TSZ0_M OUSE,tr Q8N1C8 Q8N1C8_ HUMAN	eGS GSS GTG EQk	95%	54.4	52.20493	Ref	-0.21	-0.08	0.085	0.092	0.023	-0.33	-0.15	21900	12600	14900	18800	20800	17300	14200	15900	578	1730.9	3	0.0123	7.078
Stress-70 protein, mitochondrial OS=Cricetulus griseus GN=HSPA9 PE=2 SV=1	sp O3550 1 GRP75_ CRIGR,sp P38646 G RP75_HU MAN,sp P 38647 GR P75_MOU SE,sp Q3Z CH0 GRP 75_BOVIN ,sp Q5R5 11 GRP75 _PONAB,t r B7Z4V2 B7Z4V2_ HUMAN,t r D2HK99 D2HK99_ AILME,tr Q7TSZ0 Q 7TSZ0_M OUSE,tr Q8N1C8 Q8N1C8_ HUMAN	eGS GSS GTG EQk	93%	45.3	52.25413	Ref	-0.07	0.01	0.19	-0.12	0.074	-0.32	-0.07	4940	3630	4160	5270	4700	4700	3730	4420	866.4	1730.9	2	0.0112	6.474

Stress-70 protein, mitochondrial OS=Cricetulus griseus GN=HSPA9 PE=2 SV=1	sp O3550 1 GRP75_ CRIGR,sp P38646 G RP75_HU MAN,sp P 38647 GR P75_MOU SE,sp Q3Z CH0 GRP 75_BOVIN ,sp Q5R5 11 GRP75 _PONAB,t r B7Z4V2 B7Z4V2_ HUMAN,t r D2HK99 D2HK99_ AILME,tr Q7TSZ0 Q 7TSZ0_M OUSE,tr Q8N1C8 Q8N1C8_ HUMAN	kSQV FSTA ADG QTQ VEIK	95%	52.4	54.36512	Ref	0.037	-0.08	0.1	-0.061	0.1	-0.13	-0.09	12800	11200	11200	14300	14000	13700	12200	12400	713.2	2848.6	4	0.0353	12.37
Stress-70 protein, mitochondrial OS=Cricetulus griseus GN=HSPA9 PE=2 SV=1	sp O3550 1 GRP75_ CRIGR,sp P38646 G RP75_HU MAN,sp P 38647 GR P75_MOU SE,sp Q3Z CH0 GRP 75_BOVIN ,sp Q5R5 11 GRP75 _PONAB,t r B7Z4V2 B7Z4V2_ HUMAN,t r D2HK99 D2HK99_ AILME,tr Q7TSZ0 Q 7TSZ0_M OUSE,tr Q8N1C8 Q8N1C8_ HUMAN	IYSPS QIGA FVL MK	95%	54.9	52.80184	Ref	-0.025	-0.21	0.14	-0.1	-0.22	0.12	0.23	2180	1950	1860	2650	2480	1990	2630	2820	721.4	2161.2	3	0.0099	4.562

Stress-70 protein, mitochondrial OS=Cricetulus griseus GN=HSPA9 PE=2 SV=1	sp O35501 GRP75_CRIGR,sp P38646 GRP75_HUMAN,sp P38647 GRP75_MOUSE,sp Q3ZCH0 GRP75_BOVIN,sp Q5R511 GRP75_PONAB,tra B7Z4V2 B7Z4V2_HUMAN,tra D2HK99 D2HK99_AILME,tra Q7TSZ0 Q7TSZ0_MOUSE,tra Q8N1C8 Q8N1C8_HUMAN	qAAS SLQ QASL k	72%	35.3	52.32582	Ref	0.044	0.036	0.27	-0.26	0.018	-0.44	0.26	255	252	271	359	274	290	220	354	759.9	1517.8	2	0.0117	7.7
Stress-70 protein, mitochondrial OS=Cricetulus griseus GN=HSPA9 PE=2 SV=1	sp O35501 GRP75_CRIGR,sp P38646 GRP75_HUMAN,sp P38647 GRP75_MOUSE,sp Q3ZCH0 GRP75_BOVIN,sp Q5R511 GRP75_PONAB,tra B7Z4V2 B7Z4V2_HUMAN,tra D2HK99 D2HK99_AILME,tra Q7TSZ0 Q7TSZ0_MOUSE,tra Q8N1C8 Q8N1C8_HUMAN	qAAS SLQ QASL k	88%	43.2	52.63485	Ref	0.12	-0.04	-0.12	-0.2	0.15	-0.29	0.22	12400	11600	11200	12000	12400	13900	10700	15100	614	1839.1	3	0.0141	7.682

Stress-70 protein, mitochondrial OS=Cricetulus griseus GN=HSPA9 PE=2 SV=1	sp O3550 1 GRP75_ CRIGR,sp P38646 G RP75_HU MAN,sp P 38647 GR P75_MOU SE,sp Q3Z CH0 GRP 75_BOVIN ,sp Q5R5 11 GRP75 _PONAB,t r B7Z4V2 B7Z4V2_ HUMAN,t r D2HK99 D2HK99_ AILME,tr Q7TSZ0 Q 7TSZ0_M OUSE,tr Q8N1C8 Q8N1C8_ HUMAN	sQVF STAA DGQ, TQV EIk	91%	47.4	54.653	Ref	-0.16	-0.18	0.3	-0.26	0.031	0.021	-0.03	7990	5650	6030	9450	7050	7560	7840	7490	806.4	2416.3	3	0.0175	7.239
Stress-70 protein, mitochondrial OS=Cricetulus griseus GN=HSPA9 PE=2 SV=1	sp O3550 1 GRP75_ CRIGR,sp P38646 G RP75_HU MAN,sp P 38647 GR P75_MOU SE,sp Q3Z CH0 GRP 75_BOVIN ,sp Q5R5 11 GRP75 _PONAB,t r B7Z4V2 B7Z4V2_ HUMAN,t r D2HK99 D2HK99_ AILME,tr Q7TSZ0 Q 7TSZ0_M OUSE,tr Q8N1C8 Q8N1C8_ HUMAN	tTPS VVA FTAD GER	89%	42.3	52.88828	Ref	0.0051	0.071	0.057	-0.22	0.036	-0.04	0.033	10400	9320	10600	11800	10700	11200	11100	11600	878	1753.9	2	0.0103	5.897

Stress-70 protein, mitochondrial OS=Cricetulus griseus GN=HSPA9 PE=2 SV=1	sp O35501 GRP75_CRIGR,sp P38646 GRP75_HUMAN,sp P38647 GRP75_MOUSE,sp Q3ZCH0 GRP75_BOVIN,sp Q5R511 GRP75_PONAB,tr B7Z4V2 B7Z4V2_HUMAN,tr D2HK99 D2HK99_AILME,tr Q7TSZ0 Q7TSZ0_MOUSE,tr Q8N1C8 Q8N1C8_HUMAN	vLEnAEGAR	60%	31.6	50.73392	Ref	0.018	0.009	0.21	-0.15	0.049	-0.18	0.012	29100	27000	29100	37600	32100	32300	28800	32600	632.3	1262.7	2	0.0101	8
Fructose-bisphosphate aldolase OS=Bos taurus GN=ALDOA PE=2 SV=1	tr A6QLL8 A6QLL8_BOVIN	aAQEEYV	84%	38.9	52.18598	Ref	0.15	0.16	0.023	-0.094	0.12	-0.31	0.062	6690	5370	5840	5980	6080	6150	4760	6130	773.4	1544.9	2	0.0114	7.406
Fructose-bisphosphate aldolase OS=Bos taurus GN=ALDOA PE=2 SV=1	tr A6QLL8 A6QLL8_BOVIN	aGA AASE SLFIS NHA y	94%	51.7	54.35293	Ref	0.12	0.01	-0.07	-0.022	0.089	0.093	0.13	9930	8930	8950	9530	10800	10200	10700	10900	739.7	2216.2	3	0.0136	6.128
Fructose-bisphosphate aldolase OS=Bos taurus GN=ALDOA PE=2 SV=1	tr A6QLL8 A6QLL8_BOVIN	aGA AASE SLFIS NHA y	95%	65.3	54.34485	Ref	0.13	0.095	-0.07	-0.01	0.13	-0.05	0.095	8790	7690	8160	8150	9390	9010	8360	9140	739.7	2216.2	3	0.016	7.211

Fructose- biphosphate aldolase OS=Bos taurus GN=ALDOA PE=2 SV=1	tr A6QLL8 A6QLL8_ BOVIN	aLAN SLAc qGk	91%	46.6	53.01392	Ref	0.069	-0.1	0.18	-0.16	0.18	0.052	0.23	1560	1470	1420	1930	1680	1850	1780	1990	577.6	1729.9	3	0.0092	5.286
Fructose- biphosphate aldolase OS=Bos taurus GN=ALDOA PE=2 SV=1	tr A6QLL8 A6QLL8_ BOVIN	aLAn SLAc qGk	90%	44.8	52.99978	Ref	0.11	0.22	0.075	-0.11	0.11	0.18	0.034	567	627	731	744	724	736	805	721	578	1730.9	3	#####	0.317
Fructose- biphosphate aldolase OS=Bos taurus GN=ALDOA PE=2 SV=1	tr A6QLL8 A6QLL8_ BOVIN	aLQA SALK	75%	33.9	49.32245	Ref	0.69	-0.13	0.091	0.022	-0.23	-0.04	-0.11	24600	35800	22000	28800	30300	22100	26400	24900	470.6	1408.9	3	0.0089	6.307
Fructose- biphosphate aldolase OS=Bos taurus GN=ALDOA PE=2 SV=1	tr A6QLL8 A6QLL8_ BOVIN	eLcD IAHR	90%	40.7	48.91247	Ref	0.49	-0.17	0.26	-0.21	0.21	-0.21	-0.13	13400	16000	10900	16500	13200	15300	12000	12600	436.2	1305.6	3	0.0167	12.75
Fructose- biphosphate aldolase OS=Bos taurus GN=ALDOA PE=2 SV=1	tr A6QLL8 A6QLL8_ BOVIN	gGV YGIK	76%	31.3	47.17504	Ref	0.69	-0.24	0.099	-0.15	-0.09	-0.1	-0.1	38500	49800	28400	40400	37500	34000	35500	35200	619.4	1236.8	2	0.0072	5.8
Fructose- biphosphate aldolase OS=Bos taurus GN=ALDOA PE=2 SV=1	tr A6QLL8 A6QLL8_ BOVIN	gLLA ADES TGSi Ak	95%	72.7	53.21721	Ref	0.68	-0.29	0.24	-0.11	0.019	-0.24	0.019	36700	55800	30800	50100	43400	41400	36100	42900	971.1	1940.1	2	0.014	7.218

Fructose- biphosphate aldolase OS=Bos taurus GN=ALDOA PE=2 SV=1	tr A6QLL8 A6QLL8_ BOVIN	iGEH TPSS LAIM ENA NVL AR	87%	44.7	54.85664	Ref	0.57	-0.09	0.4	-0.17	-0.4	-0.08	0.17	718	1080	743	1180	872	650	847	999	809.8	2426.3	3	0.0062	2.538
Fructose- biphosphate aldolase OS=Bos taurus GN=ALDOA PE=2 SV=1	tr A6QLL8 A6QLL8_ BOVIN	pHQ YPAL TPEQ k	52%	33.5	53.82739	Ref	0.31	0.017	0.17	-0.16	-0.04	-0.05	0.1	6640	6940	6150	7650	6720	6390	6630	7310	673	2016.1	3	0.0174	8.625
Fructose- biphosphate aldolase OS=Bos taurus GN=ALDOA PE=2 SV=1	tr A6QLL8 A6QLL8_ BOVIN	ySHE EIA MAT VTAL R	86%	43.5	54.47654	Ref	0.58	-0.05	0.079	-0.073	-0.11	-0.03	-0.07	4570	6110	4280	5240	5200	4430	4890	4720	767.4	2299.2	3	0.0156	6.784
Histone H4 OS=Sus crofa PE=1 SV=2	2 H4_PIG ,sp P6280 3 H4_BO VIN,sp P6 2804 H4_ RAT,sp P 62805 H4 _HUMAN, sp P6280 6 H4_MO USE,sp Q 4R362 H4 _MACFA,s p Q5RCS7 H4_PON AB,tr B2R 4R0 B2R4 RO_HUM AN,tr B2R TM0 B2R TM0_MO USE,tr D2 HWI2 D2 HWI2_AIL ME,tr D2 HWI9 D2 HWI9_AIL	dAVT YTEH AK	92%	47.3	53.02532	Ref	-0.089	0.73	-0.51	0.53	0.84	0.5	0.87	93100	77100	1E+05	69900	159000	2E+05	1E+05	183000	581.6	1741.9	3	0.0182	10.47

Histone H4 OS=Sus scrofa PE=1 SV=2	2 H4_PIG ,sp P6280 3 H4_BO VIN,sp P6 2804 H4_ RAT,sp P 62805 H4 _HUMAN, sp P6280 6 H4_MO USE,sp Q 4R362 H4 _MACFA,s p Q5RCS7 H4_PON AB,tr B2R 4R0 B2R4 R0_HUM AN,tr B2R TM0 B2R TM0_MO USE,tr D2 HWI2 D2 HWI2_AIL ME,tr D2 HWI9 D2 HWI9_AIL	dAVT YTEH AK	95%	55.8	53.02331	Ref	0.056	0.79	-0.75	0.58	0.85	0.45	0.93	4570	4900	8810	3420	9440	9980	7870	10900	872	1741.9	2	0.018	10.36
Histone H4 OS=Sus scrofa PE=1 SV=2	2 H4_PIG ,sp P6280 3 H4_BO VIN,sp P6 2804 H4_ RAT,sp P 62805 H4 _HUMAN, sp P6280 6 H4_MO USE,sp Q 4R362 H4 _MACFA,s p Q5RCS7 H4_PON AB,tr B2R 4R0 B2R4 R0_HUM AN,tr B2R TM0 B2R TM0_MO USE,tr D2 HWI2 D2 HWI2_AIL ME,tr D2 HWI9 D2 HWI9_AIL	iSGLI YEET R	77%	37.3	52.2149	Ref	0.41	0.63	0.22	0.33	0.63	0.44	0.34	1810	1590	2010	1700	2020	2180	1990	1840	495.6	1483.8	3	0.0114	7.664

Histone H4 OS=Sus scrofa PE=1 SV=2	2 H4_PIG ,sp P6280 3 H4_BO VIN,sp P6 2804 H4_ RAT,sp P 62805 H4_ _HUMAN, sp P6280 6 H4_MO USE,sp Q 4R362 H4_ _MACFA,s p Q5RCS7 H4_PON AB,tr B2R 4R0 B2R4 R0_HUM AN,tr B2R TM0 B2R TM0_MO USE,tr D2 HWI2 D2 HWI2_AIL ME,tr D2 HWI9 D2 HWI9_AIL	iSGLI YEET R	84%	39.2	52.42638	Ref	0.34	0.61	-0.12	0.43	0.68	0.5	0.74	1540	1650	2160	1460	2360	2460	2260	2640	742.9	1483.8	2	0.008	5.411
Histone H4 OS=Sus scrofa PE=1 SV=2	2 H4_PIG ,sp P6280 3 H4_BO VIN,sp P6 2804 H4_ RAT,sp P 62805 H4_ _HUMAN, sp P6280 6 H4_MO USE,sp Q 4R362 H4_ _MACFA,s p Q5RCS7 H4_PON AB,tr B2R 4R0 B2R4 R0_HUM AN,tr B2R TM0 B2R TM0_MO USE,tr D2 HWI2 D2 HWI2_AIL ME,tr D2 HWI9 D2 HWI9_AIL	kTVT AMD VYV Alk	79%	35.2	51.30121	Ref	0.037	0.79	Value Missi ng (- 0.516 7658)	0.47	0.78	0.68	0.58	3410	2720	4970	Value Missing (- 0.5167 658)	4920	5340	5180	4820	588.6	2350.4	4	0.0294	12.51

Histone H4 OS=Sus scrofa PE=1 SV=2	2 H4_PIG ,sp P6280 3 H4_BO VIN,sp P6 2804 H4_ RAT,sp P 62805 H4 _HUMAN, sp P6280 6 H4_MO USE,sp Q 4R362 H4 _MACFA,s p Q5RCS7 H4_PON AB,tr B2R 4R0 B2R4 R0_HUM AN,tr B2R TM0 B2R TM0_MO USE,tr D2 HWI2 D2 HWI2_AIL ME,tr D2 HWI9 D2 HWI9_AIL	kTVT AMD VYV ALkR	95%	48.2	50.58764	Ref	-0.18	0.25	-0.3	0.68	0.85	0.7	1.1	1850	2040	2970	2280	4970	4860	4590	6050	627.6	2506.5	4	0.0316	12.61
Histone H4 OS=Sus scrofa PE=1 SV=2	2 H4_PIG ,sp P6280 3 H4_BO VIN,sp P6 2804 H4_ RAT,sp P 62805 H4 _HUMAN, sp P6280 6 H4_MO USE,sp Q 4R362 H4 _MACFA,s p Q5RCS7 H4_PON AB,tr B2R 4R0 B2R4 R0_HUM AN,tr B2R TM0 B2R TM0_MO USE,tr D2 HWI2 D2 HWI2_AIL ME,tr D2 HWI9 D2 HWI9_AIL	tVTA MDV VYAL k	88%	43.8	52.93272	Ref	0.31	0.45	0.41	0.33	0.54	0.67	0.41	2970	2640	3170	3460	3600	3630	4170	3430	640.4	1918.1	3	0.0146	7.601

Histone H4 OS=Sus scrofa PE=1 SV=2	2 H4_PIG ,sp P6280 3 H4_BO VIN,sp P6 2804 H4_ RAT,sp P 62805 H4 _HUMAN, sp P6280 6 H4_MO USE,sp Q 4R362 H4 _MACFA,s p Q5RCS7 H4_PON AB,tr B2R 4R0 B2R4 R0_HUM AN,tr B2R TM0 B2R TM0_MO USE,tr D2 HWI2 D2 HWI2_AIL ME,tr D2 HWI9 D2 HWI9_AIL	tVTA MDV VYAL	k	95%	54.7	53.09752	Ref	0.42	0.33	-0.01	0.22	0.64	0.91	0.37	362	327	333	294	380	444	561	381	640.4	1918.1	3	0.0204	10.65
Histone H4 OS=Sus scrofa PE=1 SV=2	2 H4_PIG ,sp P6280 3 H4_BO VIN,sp P6 2804 H4_ RAT,sp P 62805 H4 _HUMAN, sp P6280 6 H4_MO USE,sp Q 4R362 H4 _MACFA,s p Q5RCS7 H4_PON AB,tr B2R 4R0 B2R4 R0_HUM AN,tr B2R TM0 B2R TM0_MO USE,tr D2 HWI2 D2 HWI2_AIL ME,tr D2 HWI9 D2 HWI9_AIL	tVTA MDV VYAL	k	92%	47.9	53.01772	Ref	0.5	0.7	-0.21	0.37	0.69	0.25	0.81	419	508	632	379	624	681	523	767	640.4	1918.1	3	0.0164	8.555

Histone H4 OS=Sus scrofa PE=1 SV=2	2 H4_PIG ,sp P6280 3 H4_BO VIN,sp P6 2804 H4_ RAT,sp P 62805 H4 _HUMAN, sp P6280 6 H4_MO USE,sp Q 4R362 H4 _MACFA,s p Q5RCS7 H4_PON AB,tr B2R 4R0 B2R4 RO_HUM AN,tr B2R TM0 B2R TM0_MO USE,tr D2 HWI2 D2 HWI2_AIL ME,tr D2 HWI9 D2 HWI9_AIL	tVTA MDV VYAL kR	83%	40.6	53.06654	Ref	-0.39	0.43	-0.58	0.64	0.91	0.61	1.3	3130	3510	6750	3760	9620	10100	8590	13700	692.4	2074.2	3	0.0234	11.25
Histone H4 OS=Sus scrofa PE=1 SV=2	2 H4_PIG ,sp P6280 3 H4_BO VIN,sp P6 2804 H4_ RAT,sp P 62805 H4 _HUMAN, sp P6280 6 H4_MO USE,sp Q 4R362 H4 _MACFA,s p Q5RCS7 H4_PON AB,tr B2R 4R0 B2R4 RO_HUM AN,tr B2R TM0 B2R TM0_MO USE,tr D2 HWI2 D2 HWI2_AIL ME,tr D2 HWI9 D2 HWI9_AIL	tVTA MDV VYAL kR	93%	48	52.93141	Ref	-0.4	0.28	-0.66	0.69	0.97	0.59	1.4	2300	2810	4870	2850	8020	8520	6830	11500	692.4	2074.2	3	0.0186	8.968

Histone H4 OS=Sus scrofa PE=1 SV=2	2 H4_PIG ,sp P6280 3 H4_BO VIN,sp P6 2804 H4_ RAT,sp P 62805 H4 _HUMAN, sp P6280 6 H4_MO USE,sp Q 4R362 H4 _MACFA,s p Q5RCS7 H4_PON AB,tr B2R 4R0 B2R4 R0_HUM AN,tr B2R TM0 B2R TM0_MO USE,tr D2 HWI2 D2 HWI2_AIL ME,tr D2 HWI9 D2 HWI9_AIL	vFLE NVIR	71%	33.5	50.07133	Ref	0.0087	0.72	-0.26	0.32	0.77	0.29	1.2	1340	1370	2440	1380	2280	2720	2040	3740	431.9	1292.8	3	0.011	8.517
Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3	sp Q3SZ6 2 PGAM1 _BOVIN,tr D2H5L1 D2H5L1_ AILME	aLPF WNE EIVP QIk	95%	58.9	52.99357	Ref	-0.2	0.53	0.068	-0.11	-0.11	0.088	-0.1	1360	1030	1860	1510	1470	1280	1540	1340	764.8	2291.3	3	0.0148	6.467
Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3	sp Q3SZ6 2 PGAM1 _BOVIN,tr D2H5L1 D2H5L1_ AILME	aME AVA AQG k	77%	37.8	52.50959	Ref	-0.22	0.5	0.078	0.013	-0.01	0.008	-0.25	96700	70300	1E+05	105000	111000	95400	1E+05	83800	528.6	1582.9	3	0.0148	9.319
Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3	sp Q3SZ6 2 PGAM1 _BOVIN,tr D2H5L1 D2H5L1_ AILME	aME AVA AQG k	61%	33.5	52.61698	Ref	0.024	0.23	0.1	-0.005	0.062	-0.02	-0.18	13700	11700	14600	15000	15300	14000	13900	12300	792.5	1582.9	2	0.0102	6.455

Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3	sp Q3SZ62 PGAM1_BOVIN,triD2H5L1 D2H5L1_AILME	dAGYEFDIcFTSVQk	95%	51.4	52.99588	Ref	0.33	-0.1	0.23	0.045	-0.19	0.19	-0.33	441	480	387	546	530	393	534	371	793.1	2376.1	3	0.0124	5.237
Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3	sp Q3SZ62 PGAM1_BOVIN,triD2H5L1 D2H5L1_AILME	dAGYEFDIcFTSVQk	81%	39.9	53.00909	Ref	0.27	-0.14	0.045	-0.065	0.15	0.065	-0.1	234	240	197	251	256	260	255	226	793.1	2376.1	3	0.0113	4.77
Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3	sp Q3SZ62 PGAM1_BOVIN,triD2H5L1 D2H5L1_AILME	hGES TWN LENR	84%	39.3	51.11168	Ref	0.056	0.11	-0.1	-0.12	-0.01	0.075	0.19	22500	19400	21800	21300	23000	21800	24100	25900	549.6	1645.8	3	0.0099	6.031
Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3	sp Q3SZ62 PGAM1_BOVIN,triD2H5L1 D2H5L1_AILME	hYGLT GLNk	62%	33.3	52.30944	Ref	0.19	0.15	0.37	-0.77	0.16	0.29	0.11	4740	7070	7490	9770	4880	8130	9320	8140	834.5	1667	2	0.0068	4.085
Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3	sp Q3SZ62 PGAM1_BOVIN,triD2H5L1 D2H5L1_AILME	kAMEAVAAQ Gk	53%	29.4	51.41694	Ref	0.033	0.14	-0.03	-0.04	-0.04	0.18	0.088	9820	9110	10700	10600	11600	10100	12400	11500	504.8	2015.2	4	0.0095	4.716
Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3	sp Q3SZ62 PGAM1_BOVIN,triD2H5L1 D2H5L1_AILME	nLkPI kPM QFL GDE ETVR	83%	34.8	52.47801	Ref	0.011	0.045	0.14	-0.15	0.019	0.02	0.22	6430	5770	6410	7690	6950	6800	7110	8080	606.4	3026.7	5	0.0175	5.794

Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3	sp Q3SZ62 PGAM1_BOVIN, tr D2H5L1 D2H5L1_AILME	vLIA AHG nSLR	87%	41.3	51.53763	Ref	0.024	0.15	0.11	-0.12	-0.05	0.19	0.014	26400	24200	28600	31200	29500	27000	33200	29200	485.6	1453.9	3	0.0086	5.909
Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3	sp Q3SZ62 PGAM1_BOVIN, tr D2H5L1 D2H5L1_AILME	vLIA AHG nSLR	95%	66.9	51.91001	Ref	0.093	0.11	0.21	-0.18	-0.13	0.1	0.11	11100	10700	11700	14100	11900	10700	13200	13200	486	1454.8	3	0.01	6.901
Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3	sp Q3SZ62 PGAM1_BOVIN, tr D2H5L1 D2H5L1_AILME	vLIA AHG nSLR	93%	47.5	51.9483	Ref	0.16	0.17	-0.09	-0.2	0.013	0.061	0.005	4660	4110	4500	4210	4300	4350	4700	4490	486	1454.8	3	0.0097	6.653
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.104900 PE=3 SV=1	tr F1MKS3 F1MKS3_BOVIN	aLAP TWE QLAL GLEH SETV k	90%	44.2	54.3908	Ref	0.53	-0.58	0.37	-0.33	0.17	-0.46	-0.07	1430	1740	875	1900	1290	1590	1070	1390	701.1	2800.5	4	0.0157	5.615
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.104900 PE=3 SV=1	tr F1MKS3 F1MKS3_BOVIN	aLAP TWE QLAL GLEH SETV k	95%	68.3	54.29348	Ref	0.36	-0.57	0.39	-0.27	0.48	-0.75	0.073	1150	1430	814	1780	1240	1810	812	1420	934.5	2800.5	3	0.0124	4.413

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.104900 PE=3 SV=1	tr F1MKS 3 F1MKS 3_BOVIN	aLAP TWE QLAL GLEH SETV k	82%	39.2	54.29226	Ref	0.36	-0.31	0.25	-0.36	0.22	-0.39	0.08	345	386	263	436	316	410	282	387	701.1	2800.5	4	0.0123	4.401
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.104900 PE=3 SV=1	tr F1MKS 3 F1MKS 3_BOVIN	dLAP TWE DLSK	70%	36.7	53.54592	Ref	0.48	-0.65	0.31	-0.24	0.2	-0.85	0.088	24300	25900	12800	27900	21100	25000	12600	23900	628.3	1882	3	0.0118	6.249
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.104900 PE=3 SV=1	tr F1MKS 3 F1MKS 3_BOVIN	dLDS LHR	95%	49.4	50.14138	Ref	0.35	-0.38	0.43	-0.37	0.46	-0.74	-0.03	12500	15200	9950	19500	12400	19100	8690	14100	387.2	1158.6	3	0.0094	8.102
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.104900 PE=3 SV=1	tr F1MKS 3 F1MKS 3_BOVIN	gYPT LLLF R	85%	40.2	51.82072	Ref	0.44	-0.5	0.19	-0.28	0.49	-1	0.18	5520	6660	3780	6840	5440	8100	2980	6770	461.9	1382.8	3	0.0069	4.963
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.104900 PE=3 SV=1	tr F1MKS 3 F1MKS 3_BOVIN	gYPT LLW FR	95%	52.4	52.27555	Ref	0.21	-0.55	0.35	-0.16	0.36	-0.52	0.063	1930	1930	1240	2590	2000	2510	1430	2120	486.3	1455.8	3	0.011	7.547

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.104900 PE=3 SV=1	tr F1MKS 3 F1MKS 3_BOVIN	gYPT LLW FR	84%	40.1	52.26749	Ref	0.059	-0.14	0.03	-0.11	0.28	-0.32	0.11	1520	1320	1250	1580	1580	1810	1240	1670	486.3	1455.8	3	0.0092	6.291
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.104900 PE=3 SV=1	tr F1MKS 3 F1MKS 3_BOVIN	vDcT ADSE VcSA QGV R	88%	33.8	45.05354	Ref	0.44	-0.74	0.29	-0.22	0.62	-1	0.14	5280	7210	3480	7930	6160	9610	3240	7160	1018	2034.9	2	0.0183	8.981
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.104900 PE=3 SV=1	tr F1MKS 3 F1MKS 3_BOVIN	vDcT ADSE VcSA QGV R	94%	42.3	45.23915	Ref	0.028	-0.23	0.084	-0.12	0.006	0.18	-0.03	8990	7480	6790	9470	9040	8630	10100	8750	679.3	2034.9	3	0.0153	7.525
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.104900 PE=3 SV=1	tr F1MKS 3 F1MKS 3_BOVIN	vDcT ADSE VcSA QGV R	95%	64.6	45.62043	Ref	0.44	-0.5	0.28	-0.26	0.37	-1.1	0.18	4200	4780	2700	5210	3940	5320	1960	4840	1018	2034.9	2	0.0095	4.668
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.104900 PE=3 SV=1	tr F1MKS 3 F1MKS 3_BOVIN	vDcT QHY ELcS GNQ VR	62%	28.8	47.25103	Ref	0.078	-0.21	0.092	-0.059	0.21	-0.23	0.17	4110	3950	3500	4860	4820	5080	3910	5100	750	2247	3	0.0146	6.505

Glyceraldehyde-3-phosphate dehydrogenase OS=Sus scrofa GN=GAPDH PE=1 SV=4	5 G3P_PI G,sp P10 096 G3P_ BOVIN,sp P46406 G3P_RABI T,sp Q28 554 G3P_ SHEEP,sp Q4KYY3 G3P_SPEC I,tr A0SN U7 A0SN U7_PIG,tr A9YF36 A9YF36_B OSMU,tr D2HMP6 D2HMP6_ AILME,tr D2HNX7 D2HNX7_ AILME,tr D6BQW4 D6BQW4 _AILME,tr D7R7V6	gAA QNII PAST GAA	k	95%	57	52.54908	Ref	0.026	0.36	0.1	0.068	-0.46	0.57	-0.23	11800	10600	14500	13600	14600	8830	18800	10700	989.6	1977.1	2	0.0155	7.823
Glyceraldehyde-3-phosphate dehydrogenase OS=Sus scrofa GN=GAPDH PE=1 SV=4	5 G3P_PI G,sp P10 096 G3P_ BOVIN,sp P46406 G3P_RABI T,sp Q28 554 G3P_ SHEEP,sp Q4KYY3 G3P_SPEC I,tr A0SN U7 A0SN U7_PIG,tr A9YF36 A9YF36_B OSMU,tr D2HMP6 D2HMP6_ AILME,tr D2HNX7 D2HNX7_ AILME,tr D6BQW4 D6BQW4 _AILME,tr D7R7V6	qASE	GPLK	80%	36.6	51.17454	Ref	0.058	0.38	-0.01	0.011	-0.17	0.47	-0.21	59700	54500	73800	63200	70800	54500	88900	55100	719.4	1436.8	2	0.0076	5.253

Glyceraldehyde-3-phosphate dehydrogenase OS=Sus scrofa GN=GAPDH PE=1 SV=4	5 G3P_P1G,sp P10096 G3P_BOVIN,sp P46406 G3P_RABI T,sp Q28554 G3P_SHEEP,sp Q4KYY3 G3P_SPEC I,tr A0SN U7 A0SN U7_PIG,tr A9YF36 A9YF36_B OSMU,tr D2HMP6 D2HMP6_AILME,tr D2HMX7 D2HMX7_AILME,tr D6BQW4 D6BQW4_AILME,tr D7R7V6	vPEL nGk	75%	33.5	49.66883	Ref	0.087	0.34	-0.09	0.11	-0.19	0.35	-0.13	13400	11500	14900	12400	15800	11100	16900	12100	740	1477.9	2	0.0039	2.631
Glyceraldehyde-3-phosphate dehydrogenase OS=Sus scrofa GN=GAPDH PE=1 SV=4	5 G3P_P1G,sp P10096 G3P_BOVIN,sp P46406 G3P_RABI T,sp Q28554 G3P_SHEEP,sp Q4KYY3 G3P_SPEC I,tr A0SN U7 A0SN U7_PIG,tr A9YF36 A9YF36_B OSMU,tr D2HMP6 D2HMP6_AILME,tr D2HMX7 D2HMX7_AILME,tr D6BQW4 D6BQW4_AILME,tr D7R7V6	vPTP NVS VVD LTcR	95%	67.6	53.46018	Ref	0.13	0.36	-0.01	-0.029	-0.25	0.5	-0.13	6660	6590	8380	7280	7920	5930	10400	6680	925.5	1849	2	0.0016	0.849

Glyceraldehyde-3-phosphate dehydrogenase OS=Sus scrofa GN=GAPDH PE=1 SV=4	5 G3P_P1G,sp P10096 G3P_BOVIN,sp P46406 G3P_RABI T,sp Q28554 G3P_SHEEP,sp Q4KYY3 G3P_SPEC I,tr A0SN U7 A0SN U7_PIG,tr A9YF36 A9YF36_B OSMU,tr D2HMP6 D2HMP6_AILME,tr D2HMX7 D2HMX7_AILME,tr D6BQW4 D6BQW4_AILME,tr D7R7V6 k	VVDL MVH MAS	66%	35.3	53.02762	Ref	0.18	0.38	0.027	-0.25	-0.23	0.32	-0.38	1870	1400	1740	1530	1390	1240	1880	1160	613.3	1837	3	0.0177	9.626
Glyceraldehyde-3-phosphate dehydrogenase OS=Sus scrofa GN=GAPDH PE=1 SV=4	5 G3P_P1G,sp P10096 G3P_BOVIN,sp P46406 G3P_RABI T,sp Q28554 G3P_SHEEP,sp Q4KYY3 G3P_SPEC I,tr A0SN U7 A0SN U7_PIG,tr A9YF36 A9YF36_B OSMU,tr D2HMP6 D2HMP6_AILME,tr D2HMX7 D2HMX7_AILME,tr D6BQW4 D6BQW4_AILME,tr D7R7V6 k	VVDL MVH MAS	85%	41.4	52.91935	Ref	0.2	0.23	0.03	0.034	-0.18	0.21	-0.24	940	769	855	832	920	691	949	690	613.4	1837	3	0.0058	3.147

Glyceraldehyde-3-phosphate dehydrogenase OS=Sus scrofa GN=GAPDH PE=1 SV=4	5 G3P_P1G,sp P10096 G3P_BOVIN,sp P46406 G3P_RABI T,sp Q28554 G3P_SHEEP,sp Q4KYY3 G3P_SPEC I,tr A0SN U7 A0SN U7_PIG,tr A9YF36 A9YF36_B OSMU,tr D2HMP6 D2HMP6_AILME,tr D2HMX7 D2HMX7_AILME,tr D6BQW4 D6BQW4_AILME,tr D7R7V6 k	VVDL MVH MAS	70%	36.6	53.4181	Ref	0.2	0.27	0.1	0.051	-0.16	0.24	-0.39	521	443	504	505	536	406	556	357	613.3	1837	3	0.0437	23.78
Glyceraldehyde-3-phosphate dehydrogenase OS=Sus scrofa GN=GAPDH PE=1 SV=4	5 G3P_P1G,sp P10096 G3P_BOVIN,sp P46406 G3P_RABI T,sp Q28554 G3P_SHEEP,sp Q4KYY3 G3P_SPEC I,tr A0SN U7 A0SN U7_PIG,tr A9YF36 A9YF36_B OSMU,tr D2HMP6 D2HMP6_AILME,tr D2HMX7 D2HMX7_AILME,tr D6BQW4 D6BQW4_AILME,tr D7R7V6 kE	VVDL MVH MAS	81%	40.1	53.60285	Ref	-0.048	0.19	0.065	0.098	-0.11	0.44	-0	1400	1210	1550	1590	1790	1350	2080	1520	656.4	1966.1	3	0.009	4.589

Glyceraldehyde-3-phosphate dehydrogenase OS=Sus scrofa GN=GAPDH PE=1 SV=4	5 G3P_P1G,sp P10096 G3P_BOVIN,sp P46406 G3P_RABI T,sp Q28554 G3P_SHEEP,sp Q4KYY3 G3P_SPEC I,tr A0SN U7 A0SN U7_PIG,tr A9YF36 A9YF36_B OSMU,tr D2HMP6 D2HMP6_AILME,tr D2HMX7 D2HMX7_AILME,tr D6BQW4 D6BQW4_AILME,tr D7R7V6	VVDL MVH MAS kE	67%	36.1	53.67833	Ref	-0.065	0.43	-0.17	0.13	-0.04	0.43	-0.11	7070	6200	9460	7040	9520	7380	10700	7320	656.4	1966.1	3	0.0204	10.35
Glyceraldehyde-3-phosphate dehydrogenase OS=Sus scrofa GN=GAPDH PE=1 SV=4	5 G3P_P1G,sp P10096 G3P_BOVIN,sp P46406 G3P_RABI T,sp Q28554 G3P_SHEEP,sp Q4KYY3 G3P_SPEC I,tr A0SN U7 A0SN U7_PIG,tr A9YF36 A9YF36_B OSMU,tr D2HMP6 D2HMP6_AILME,tr D2HMX7 D2HMX7_AILME,tr D6BQW4 D6BQW4_AILME,tr D7R7V6	VVDL MVH MAS kE	81%	40.5	53.6888	Ref	-0.15	0.33	0.04	0.11	-0.09	0.41	-0.18	1860	1380	2080	1910	2210	1670	2490	1630	656.4	1966.1	3	0.0127	6.449

Glyceraldehyde-3-phosphate dehydrogenase OS=Sus scrofa GN=GAPDH PE=1 SV=4	5 G3P_P1G,sp P10096 G3P_BOVIN,sp P46406 G3P_RABI T,sp Q28554 G3P_SHEEP,sp Q4KYY3 G3P_SPEC I,tr A0SN U7 A0SN U7_PIG,tr A9YF36 A9YF36_B OSMU,tr D2HMP6 D2HMP6_AILME,tr D2HMX7 D2HMX7_AILME,tr D6BQW4 D6BQW4_AILME,tr D7R7V6	VVDL MVH MAS kE	69%	36.8	53.70058	Ref	0.056	0.3	-0	0.039	-0.13	0.35	0.011	1220	1110	1430	1300	1480	1150	1670	1310	656.4	1966.1	3	0.0116	5.885
Glyceraldehyde-3-phosphate dehydrogenase OS=Sus scrofa GN=GAPDH PE=1 SV=4	5 G3P_P1G,sp P10096 G3P_BOVIN,sp P46406 G3P_RABI T,sp Q28554 G3P_SHEEP,sp Q4KYY3 G3P_SPEC I,tr A0SN U7 A0SN U7_PIG,tr A9YF36 A9YF36_B OSMU,tr D2HMP6 D2HMP6_AILME,tr D2HMX7 D2HMX7_AILME,tr D6BQW4 D6BQW4_AILME,tr D7R7V6	VVDL MVH MAS kE	71%	37.2	53.60412	Ref	-0.22	0.23	-0.02	0.16	0.019	0.31	0.11	531	393	584	548	687	544	695	601	656.4	1966.1	3	0.0087	4.406

Uncharacterized protein OS=Macaca mulatta GN=LRRC59 PE=4 SV=1	tr F7HBZ3 F7HBZ3_MACMU	aTIL DLSc	Nk	83%	40.8	53.27843	Ref	-0.012	0.049	0.035	-0.1	0.11	-0.16	-0.01	12200	10700	12200	13500	13600	13700	11900	13100	578	1730.9	3	0.0145	8.383
Uncharacterized protein OS=Macaca mulatta GN=LRRC59 PE=4 SV=1	tr F7HBZ3 F7HBZ3_MACMU	dNPL DPVL	Ak	95%	60.9	52.10712	Ref	-0.032	0.03	0.045	-0.038	0.15	-0.25	-0.19	15200	11800	13300	15100	15700	15600	12400	12800	845.5	1689	2	0.0134	7.926
Uncharacterized protein OS=Macaca mulatta GN=LRRC59 PE=4 SV=1	tr F7HBZ3 F7HBZ3_MACMU	IVNL QHL DLLN	NR	65%	34.8	52.67181	Ref	0.089	-0.22	0.17	-0.13	0.067	-0.28	-0.26	3430	2510	2200	3230	2890	2890	2370	2380	622.7	1865.1	3	0.0026	1.405
Uncharacterized protein OS=Macaca mulatta GN=LRRC59 PE=4 SV=1	tr F7HBZ3 F7HBZ3_MACMU	IVNL QHL DLLN	NR	84%	41	52.77618	Ref	-0.082	0.094	0.16	-0.019	-0.1	-0.3	-0.02	2370	1800	2200	2590	2520	2080	1900	2280	622.7	1865.1	3	0.0061	3.27
Uncharacterized protein OS=Macaca mulatta GN=LRRC59 PE=4 SV=1	tr F7HBZ3 F7HBZ3_MACMU	IVNL QHL DLLN	NR	89%	43.6	52.71219	Ref	0.13	-0.27	-0.01	-0.18	0.15	-0.06	0.056	3390	3120	2570	3440	3370	3710	3340	3610	622.7	1865.1	3	0.0085	4.54
Uncharacterized protein OS=Macaca mulatta GN=LRRC59 PE=4 SV=1	tr F7HBZ3 F7HBZ3_MACMU	IVNL QHL DLLN	NR	86%	41.7	52.60691	Ref	-0.003	-0.04	0.031	0.008	-0.17	-0.01	0.085	1600	1400	1480	1750	1900	1470	1710	1810	622.7	1865.1	3	0.0065	3.463

Uncharacterized protein OS=Macaca mulatta GN=LRRC59 PE=4 SV=1	tr F7HBZ3 F7HBZ3_MACMU	IVNL QHL DLLN	NR	93%	48	52.70886	Ref	0.054	-0.11	0.079	0.005	0.021	-0.09	-0.01	823	775	752	961	1010	888	858	903	622.7	1865.1	3	0.0088	4.733
Uncharacterized protein OS=Macaca mulatta GN=LRRC59 PE=4 SV=1	tr F7HBZ3 F7HBZ3_MACMU	IVNL QHL DLLN	NR	83%	40.2	52.71219	Ref	-0.19	0.17	-0.13	0.067	-0.14	0.067	0.003	227	171	238	216	274	207	250	237	622.7	1865.1	3	0.0085	4.54
Uncharacterized protein OS=Macaca mulatta GN=LRRC59 PE=4 SV=1	tr F7HBZ3 F7HBZ3_MACMU	IVNL QHL DLLn	NR	93%	49.4	53.07117	Ref	-0.13	0.035	0.064	-0.059	0.17	-0.13	-0.05	1090	876	1070	1220	1240	1270	1070	1130	623	1866.1	3	0.0114	6.101
Uncharacterized protein OS=Macaca mulatta GN=LRRC59 PE=4 SV=1	tr F7HBZ3 F7HBZ3_MACMU	IVNL QHL DLLn	NR	95%	54.3	52.86014	Ref	-0.42	0.1	-0.09	0.13	-0.06	-0.23	0.051	305	162	252	249	319	244	226	273	623	1866.1	3	0.0067	3.562
Uncharacterized protein OS=Macaca mulatta GN=LRRC59 PE=4 SV=1	tr F7HBZ3 F7HBZ3_MACMU	IVTL PVSF	AQLK	95%	49.9	48.24432	Ref	-0.049	-0.08	-0.05	-0.059	0.22	-0.3	0.2	4230	3650	3860	4440	4860	5130	3770	5260	642.1	1923.2	3	0.0189	9.824
Uncharacterized protein OS=Macaca mulatta GN=LRRC59 PE=4 SV=1	tr F7HBZ3 F7HBZ3_MACMU	IVTL PVSF	AQLK	57%	28.8	48.38364	Ref	-0.059	-0.1	0.082	0.02	0.23	-0.19	-0.02	417	372	391	499	527	531	414	463	642.1	1923.2	3	0.0198	10.31

cDNA FLJ53704, moderately similar to Nascent polypeptide- associated complex subunit alpha OS=Homo sapiens PE=2 SV=1	tr B4DDI8 B4DDI8_ HUMAN	dIEL VMS QAN VSR	60%	33.9	53.09988	Ref	0.11	0.29	0.48	0.19	0.36	-0.12	0.57	3760	3540	4350	5570	5030	4940	3680	5930	883.5	1764.9	2	0.0138	7.801
cDNA FLJ53704, moderately similar to Nascent polypeptide- associated complex subunit alpha OS=Homo sapiens PE=2 SV=1	tr B4DDI8 B4DDI8_ HUMAN	dIEL VMS QAN VSR	86%	42.2	53.19527	Ref	0.19	-0.07	0.18	0.054	0.32	0.024	0.44	17600	10700	9650	12900	13000	13700	11700	15400	589.3	1764.9	3	0.0103	5.834

cDNA FLJ53704, moderately similar to Nascent polypeptide- associated complex subunit alpha OS=Homo sapiens PE=2 SV=1	tr B4DDI8 B4DDI8_ HUMAN	iEDL SQQ AQL AAA Ek	95%	64.7	54.13028	Ref	0.2	0.22	0.11	0.27	0.28	0.28	0.47	2730	2430	2690	2790	3440	3020	3150	3570	741.7	2222.2	3	0.0188	8.455
cDNA FLJ53704, moderately similar to Nascent polypeptide- associated complex subunit alpha OS=Homo sapiens PE=2 SV=1	tr B4DDI8 B4DDI8_ HUMAN	iEDL SQQ AQL AAA Ek	94%	48.4	54.11765	Ref	-0.026	0.27	0.29	0.12	0.51	-0.19	0.75	8860	7270	9670	11000	10800	12300	7930	15200	556.6	2222.2	4	0.018	8.075

cDNA FLJ53704, moderately similar to Nascent polypeptide- associated complex subunit alpha OS=Homo sapiens PE=2 SV=1	tr B4DDI8 B4DDI8_ HUMAN	iEDL SQQ AQL AAA Ek	95%	69.4	54.12163	Ref	0.022	0.11	0.46	0.19	0.49	-0.08	0.68	18600	17400	20000	28700	26300	28200	19900	33400	741.7	2222.2	3	0.0177	7.955
cDNA FLJ53704, moderately similar to Nascent polypeptide- associated complex subunit alpha OS=Homo sapiens PE=2 SV=1	tr B4DDI8 B4DDI8_ HUMAN	iEDL SQQ AQL AAA Ek	95%	59.9	53.8679	Ref	-0.14	0.28	0.46	0.12	0.42	0.1	0.65	4230	3470	5050	6430	5600	5990	5030	7310	741.8	2222.2	3	0.0058	2.598

cDNA FLJ53704, moderately similar to Nascent polypeptide- associated complex subunit alpha OS=Homo sapiens PE=2 SV=1	tr B4DDI8 B4DDI8_ HUMAN	iEDL SQQ AQL AAA Ek	95%	62	53.92561	Ref	0.28	0.33	0.3	0.14	0.25	0.31	0.32	2480	2530	2830	3110	3070	2890	3150	3160	741.7	2222.2	3	0.0093	4.163
cDNA FLJ53704, moderately similar to Nascent polypeptide- associated complex subunit alpha OS=Homo sapiens PE=2 SV=1	tr B4DDI8 B4DDI8_ HUMAN	iEDL SQQ AQL AAA EKFR	93%	46.5	54.13036	Ref	-0.19	-0.2	0.44	0.25	0.55	0.097	0.89	2900	2680	2880	5050	4880	5230	3990	6890	1112	2221.2	2	0.012	5.393

cDNA FLJ53704, moderately similar to Nascent polypeptide- associated complex subunit alpha OS=Homo sapiens PE=2 SV=1	tr B4DDI8 B4DDI8_ HUMAN	sPAS DTYI VFGE Ak	95%	53.4	54.21548	Ref	0.063	-0.12	0.59	0.19	0.48	-0.11	0.66	18600	16800	16100	29500	24600	26200	18200	30900	698.4	2092.1	3	0.0268	12.83
cDNA FLJ53704, moderately similar to Nascent polypeptide- associated complex subunit alpha OS=Homo sapiens PE=2 SV=1	tr B4DDI8 B4DDI8_ HUMAN	sPAS DTYI VFGE Ak	93%	50.4	54.30918	Ref	0.15	-0.03	0.48	0.1	0.55	0.15	0.62	9760	10900	10500	16600	14100	16800	13400	18300	698.4	2092.1	3	0.0224	10.72

cDNA FLJ53704, moderately similar to Nascent polypeptide- associated complex subunit alpha OS=Homo sapiens PE=2 SV=1	tr B4DDI8 B4DDI8_ HUMAN	sPAS DTYI VFGE Ak	95%	57.5	54.32215	Ref	-0.029	0.032	0.54	0.26	0.5	0.033	0.54	10000	8710	9860	15700	14300	14700	11100	15700	698.4	2092.1	3	0.0182	8.713
cDNA FLJ53704, moderately similar to Nascent polypeptide- associated complex subunit alpha OS=Homo sapiens PE=2 SV=1	tr B4DDI8 B4DDI8_ HUMAN	sPAS DTYI VFGE Ak	71%	37.7	54.29166	Ref	0.18	0.3	0.15	0.33	0.34	0.22	0.31	5030	4410	5210	5270	6580	5800	5580	5850	698.4	2092.1	3	0.0232	11.08
PDZ and LIM domain 1 OS=Bos taurus GN=PDLIM1 PE=2 SV=1	tr A6H7E 3 A6H7E3 _BOVIN	aLDH SQLP SGLV IDK	82%	40.1	52.93332	Ref	0.24	-0.29	-0.33	-0.43	0.023	-0.42	-0.12	8850	9830	7360	8030	8270	9880	7610	9260	734.4	2200.3	3	0.0157	7.124
PDZ and LIM domain 1 OS=Bos taurus GN=PDLIM1 PE=2 SV=1	tr A6H7E 3 A6H7E3 _BOVIN	cGT GIVG VFVK	70%	36.1	53.01223	Ref	0.13	-0.44	-0.36	-0.24	-0.04	-0.58	-0.06	19100	16800	12300	14500	17400	17400	12500	17900	578.7	1733	3	0.0159	9.154

PDZ and LIM domain 1 OS=Bos taurus GN=PDLIM1 PE=2 SV=1	tr A6H7E3 A6H7E3_BOVIN	gcTD NMT LTVA R	86%	37.2	49.36725	Ref	0.16	-0.29	-0.42	-0.2	0.05	-0.43	-0.27	19200	18700	14900	15300	19600	20300	15200	16900	816.4	1630.8	2	0.011	6.72
PDZ and LIM domain 1 OS=Bos taurus GN=PDLIM1 PE=2 SV=1	tr A6H7E3 A6H7E3_BOVIN	gcTD NMT LTVA R	89%	39	49.36725	Ref	0.25	-0.32	-0.43	-0.28	0.088	-0.55	-0.26	13900	14100	10300	10700	13100	14700	9880	12000	816.4	1630.8	2	0.0108	6.647
PDZ and LIM domain 1 OS=Bos taurus GN=PDLIM1 PE=2 SV=1	tr A6H7E3 A6H7E3_BOVIN	iWSP LVTE EGkR	93%	49.3	53.11633	Ref	0.21	-0.42	-0.36	-0.2	0.13	-0.69	-0.2	23300	23000	16100	18900	23200	25700	15100	21100	675.1	2022.2	3	0.0183	9.052
PDZ and LIM domain 1 OS=Bos taurus GN=PDLIM1 PE=2 SV=1	tr A6H7E3 A6H7E3_BOVIN	mNL ASEP QEAL HIGS AHN R	76%	39.1	54.2926	Ref	-0.026	-0.15	-0.19	-0.25	-0.09	-0.08	-0.15	508	566	564	614	651	635	668	633	793.7	2378.2	3	0.0142	5.971
PDZ and LIM domain 1 OS=Bos taurus GN=PDLIM1 PE=2 SV=1	tr A6H7E3 A6H7E3_BOVIN	mNL ASEP QEAL HIGS AHN R	92%	46.7	54.39762	Ref	0.056	0.019	-0.5	-0.31	-0.19	-0.25	0.095	3550	4000	4230	3320	4180	3950	3950	5000	595.6	2378.2	4	0.0057	2.405
PDZ and LIM domain 1 OS=Bos taurus GN=PDLIM1 PE=2 SV=1	tr A6H7E3 A6H7E3_BOVIN	qSTS FLVL QEIL ESEK	66%	37.2	54.81617	Ref	0.28	-0.99	-0.13	-0.29	-0.02	-0.66	-0.83	332	230	104	210	207	220	147	130	863.5	2587.4	3	0.0207	8.01

PDZ and LIM domain 1 OS=Bos taurus GN=PDLIM1 PE=2 SV=1	tr A6H7E3 A6H7E3_BOVIN	sAVP FTAS PASS SAPR	95%	69.5	53.20794	Ref	0.26	-0.28	-0.61	-0.09	0.23	-0.63	-0.19	14000	17400	13000	11600	18300	20100	11500	15500	919	1836	2	0.0113	6.165
PDZ and LIM domain 1 OS=Bos taurus GN=PDLIM1 PE=2 SV=1	tr A6H7E3 A6H7E3_BOVIN	vAAS IGnA Qk	95%	46.8	51.37547	Ref	0.094	-0.34	-0.29	-0.27	0.006	-0.46	-0.19	14000	12500	10000	11600	13100	13800	10400	12400	784	1565.9	2	0.0116	7.379
PDZ and LIM domain 1 OS=Bos taurus GN=PDLIM1 PE=2 SV=1	tr A6H7E3 A6H7E3_BOVIN	vAAS IGnA Qk	95%	54.4	51.79819	Ref	0.14	-0.3	-0.4	-0.18	0.22	-0.56	-0.41	23500	22400	18000	18800	24200	27800	17000	18600	784.5	1566.9	2	0.0082	5.199
Heat shock protein HSP 90-alpha OS=Sus scrofa GN=HSP90AA1 PE=2 SV=3	sp O02705 HS90A_PIG,sp P07900 HS90A_HUMAN,sp Q4R4P1 HS90A_MACFA,sp Q76LV2 HS90A_BOVIN,sp Q9GKX7 HS90A_HORSE,tr A8DR93 A8DR93_SHEEP,tr D2HVQ7 D2HVQ7_AI LME,tr F6X099 F6X099_ORN AN	hIYYI TGET k	86%	42.5	53.3802	Ref	0.19	-0.15	0.027	-0.011	-0.26	0.23	-0.17	7790	9000	7690	9770	10500	7720	11300	8490	611.7	1832	3	0.0159	8.679

Heat shock protein HSP 90-alpha OS=Sus scrofa GN=HSP90AA1 PE=2 SV=3	sp O02705 HS90A_PIG,sp P07900 HS90A_HUMAN,sp Q4R4P1 HS90A_MACFA,sp Q76LV2 HS90A_BOVIN,sp Q9GKX7 HS90A_HORSE,trl A8DR93 A8DR93_SHEEP,trl D2HVQ7 D2HVQ7_AILME,trl F6X099 F6X099_ORNAN	hLEI NPD HSIIE TLR	95%	78.8	54.14243	Ref	0.025	-0.13	0.058	0.054	0.009	-0.29	-0.04	6590	5820	5660	7250	7970	6740	5740	6750	697.7	2090.1	3	0.0127	6.06
Heat shock protein HSP 90-alpha OS=Sus scrofa GN=HSP90AA1 PE=2 SV=3	sp O02705 HS90A_PIG,sp P07900 HS90A_HUMAN,sp Q4R4P1 HS90A_MACFA,sp Q76LV2 HS90A_BOVIN,sp Q9GKX7 HS90A_HORSE,trl A8DR93 A8DR93_SHEEP,trl D2HVQ7 D2HVQ7_AILME,trl F6X099 F6X099_ORNAN	hLEI NPD HSIIE TLR	95%	69.4	54.12299	Ref	-0.2	0.17	0.23	-0.15	0.047	-0.39	-0.06	7670	5900	8320	9730	8230	8230	6340	7900	523.5	2090.1	4	0.0123	5.891

Heat shock protein HSP 90-alpha OS=Sus scrofa GN=HSP90AA1 PE=2 SV=3	sp O02705 HS90A_PIG,sp P07900 HS90A_HUMAN,sp Q4R4P1 HS90A_MACFA,sp Q76LV2 HS90A_BOVIN,sp Q9GKX7 HS90A_HORSE,tr A8DR93 A8DR93_SHEEP,tr D2HVQ7 D2HVQ7_AILME,tr F6X099 F6X099_ORNAN	hLEI NPD HSIIE TLR	95%	68.4	54.09599	Ref	0.2	-0.06	0.002	-0.15	0.13	-0.14	-0.07	3300	3860	3500	4110	4060	4320	3750	3890	523.5	2090.1	4	0.0094	4.494
Heat shock protein HSP 90-alpha OS=Sus scrofa GN=HSP90AA1 PE=2 SV=3	sp O02705 HS90A_PIG,sp P07900 HS90A_HUMAN,sp Q4R4P1 HS90A_MACFA,sp Q76LV2 HS90A_BOVIN,sp Q9GKX7 HS90A_HORSE,tr A8DR93 A8DR93_SHEEP,tr D2HVQ7 D2HVQ7_AILME,tr F6X099 F6X099_ORNAN	hSQF IGYPI TLFV Ek	85%	41.9	53.51592	Ref	0.13	-0.19	0.17	-0.19	-0.1	0.15	-0.45	712	640	558	803	687	638	796	519	796.5	2386.3	3	0.0079	3.315

Heat shock protein HSP 90-alpha OS=Sus scrofa GN=HSP90AA1 PE=2 SV=3	sp O02705 HS90A_PIG,sp P07900 HS90A_HUMAN,sp Q4R4P1 HS90A_MACFA,sp Q76LV2 HS90A_BOVIN,sp Q9GKX7 HS90A_HORSE,tr A8DR93 A8DR93_SHEEP,tr D2HVQ7 D2HVQ7_AILME,tr F6X099 F6X099_ORNAN	kHLEINPDHSIIE TLR	90%	43.4	53.35185	Ref	0.064	-0.15	-0.01	-0.14	0.14	-0.23	-0.03	10700	9460	8850	11000	11000	11700	9420	10700	631.6	2522.4	4	0.0189	7.502
Heat shock protein HSP 90-alpha OS=Sus scrofa GN=HSP90AA1 PE=2 SV=3	sp O02705 HS90A_PIG,sp P07900 HS90A_HUMAN,sp Q4R4P1 HS90A_MACFA,sp Q76LV2 HS90A_BOVIN,sp Q9GKX7 HS90A_HORSE,tr A8DR93 A8DR93_SHEEP,tr D2HVQ7 D2HVQ7_AILME,tr F6X099 F6X099_ORNAN	kHLEINPDHSIIE TLR	86%	40.7	53.46869	Ref	-0.1	-0.18	0.078	-0.066	0.22	-0.16	-0.04	39300	33600	34500	46300	46200	49300	39500	42700	631.6	2522.4	4	0.0216	8.564

Heat shock protein HSP 90-alpha OS=Sus scrofa GN=HSP90AA1 PE=2 SV=3	sp O02705 HS90A_PIG,sp P07900 HS90A_HUMAN,sp Q4R4P1 HS90A_MACFA,sp Q76LV2 HS90A_BOVIN,sp Q9GKX7 HS90A_HORSE,tr A8DR93 A8DR93_SHEEP,tr D2HVQ7 D2HVQ7_AILME,tr F6X099 F6X099_ORNAN	kHLE INPD HSIIE TLR	88%	38.9	53.35273	Ref	-0.017	-0.24	-0.06	0.05	0.069	-0.06	-0.16	34800	27800	25800	32900	39000	34500	32900	30600	505.5	2522.4	5	0.0192	7.615
Heat shock protein HSP 90-alpha OS=Sus scrofa GN=HSP90AA1 PE=2 SV=3	sp O02705 HS90A_PIG,sp P07900 HS90A_HUMAN,sp Q4R4P1 HS90A_MACFA,sp Q76LV2 HS90A_BOVIN,sp Q9GKX7 HS90A_HORSE,tr A8DR93 A8DR93_SHEEP,tr D2HVQ7 D2HVQ7_AILME,tr F6X099 F6X099_ORNAN	nPD DITN EEYG EFYK	94%	50.3	52.80344	Ref	0.21	-0.03	0.028	-0.18	-0.25	-0.05	-0.14	7050	6760	6210	7250	6940	5770	6910	6450	814.7	2441.2	3	0.0188	7.692

Heat shock protein HSP 90-alpha OS=Sus scrofa GN=HSP90AA1 PE=2 SV=3	sp O02705 HS90A_PIG,sp P07900 HS90A_HUMAN,sp Q4R4P1 HS90A_MACFA,sp Q76LV2 HS90A_BOVIN,sp Q9GKX7 HS90A_HORSE,tr A8DR93 A8DR93_SHEEP,tr D2HVQ7 D2HVQ7_AILME,tr F6X099 F6X099_ORNAN	rAPFDLFE NR	85%	40.9	52.5465	Ref	0.069	0.037	0.17	-0.14	-0.26	0.2	-0.18	2520	2760	2930	3600	3200	2570	3690	2820	523.6	1567.8	3	0.0116	7.419
Heat shock protein HSP 90-alpha OS=Sus scrofa GN=HSP90AA1 PE=2 SV=3	sp O02705 HS90A_PIG,sp P07900 HS90A_HUMAN,sp Q4R4P1 HS90A_MACFA,sp Q76LV2 HS90A_BOVIN,sp Q9GKX7 HS90A_HORSE,tr A8DR93 A8DR93_SHEEP,tr D2HVQ7 D2HVQ7_AILME,tr F6X099 F6X099_ORNAN	rAPFDLFE NR	91%	45.4	52.47983	Ref	0.096	-0.16	0.16	-0.2	-0.37	0.14	-0.03	6600	6140	5580	7830	6710	5220	7720	6820	523.6	1567.8	3	0.0104	6.615

Heterogeneous nuclear ribonucleoprotein D OS=Bos taurus GN=HNRPD PE=2 SV=1	tr A5D9H5 A5D9H5_BOVIN, tr F1PTP9 F1PTP9_CANFA, tr F7APH2 F7APH2_MACMU	gFGF VLFk	88%	38.7	50.03262	Ref	-0.17	-0.27	-0.09	-0.14	0.29	-0.57	-0.03	4080	3100	3150	3990	4250	5010	2880	4170	762	1521.9	2	0.0035	2.307
Heterogeneous nuclear ribonucleoprotein D OS=Bos taurus GN=HNRPD PE=2 SV=1	tr A5D9H5 A5D9H5_BOVIN, tr F1PTP9 F1PTP9_CANFA, tr F7APH2 F7APH2_MACMU	gFGF VLFk	57%	31.5	50.92924	Ref	-0.13	-0.38	-0.24	-0.28	0.17	-0.65	0.41	5480	4330	3940	4870	5230	6260	3690	7670	508.3	1521.9	3	0.0196	12.85
Heterogeneous nuclear ribonucleoprotein D OS=Bos taurus GN=HNRPD PE=2 SV=1	tr A5D9H5 A5D9H5_BOVIN, tr F1PTP9 F1PTP9_CANFA, tr F7APH2 F7APH2_MACMU	gFGF VLFk	91%	41	50.27749	Ref	0.0012	-0.27	-0.09	-0.25	0.13	-0.53	0.079	2660	2310	2080	2650	2610	2950	1960	2970	762	1521.9	2	0.0079	5.197
Heterogeneous nuclear ribonucleoprotein D OS=Bos taurus GN=HNRPD PE=2 SV=1	tr A5D9H5 A5D9H5_BOVIN, tr F1PTP9 F1PTP9_CANFA, tr F7APH2 F7APH2_MACMU	gFGF VLFk	57%	31.5	50.95086	Ref	-0.2	-0.32	-0.31	-0.18	0.18	-0.41	0.29	1690	1300	1290	1460	1760	1970	1370	2210	508.3	1521.9	3	0.0208	13.64
Heterogeneous nuclear ribonucleoprotein D OS=Bos taurus GN=HNRPD PE=2 SV=1	tr A5D9H5 A5D9H5_BOVIN, tr F1PTP9 F1PTP9_CANFA, tr F7APH2 F7APH2_MACMU	gGD QQS GYG k	63%	33.2	51.80433	Ref	-0.075	-0.55	0.26	-0.36	0.26	-1.1	0.27	3840	3240	2530	4970	3580	4790	1950	5010	802.9	1603.8	2	0.0167	10.41

Heterogeneous nuclear ribonucleoprotein D OS=Bos taurus GN=HNRPD PE=2 SV=1	tr A5D9H5 A5D9H5_BOVIN, tr F1PTP9 F1PTP9_CANFA, tr F7APH2 F7APH2_MACMU	hSEA ATA QR	93%	46	50.25015	Ref	0.37	-0.36	-0.64	-0.3	-0.14	-0.42	0.038	325	294	192	178	248	242	208	283	425.6	1273.7	3	0.0084	6.614
Heterogeneous nuclear ribonucleoprotein D OS=Bos taurus GN=HNRPD PE=2 SV=1	tr A5D9H5 A5D9H5_BOVIN, tr F1PTP9 F1PTP9_CANFA, tr F7APH2 F7APH2_MACMU	iFVG GLSP DTPE Ek	95%	59	53.9311	Ref	-0.079	-0.2	-0.31	-0.25	0.26	-0.42	0.14	15500	13600	13600	14100	16200	20100	13100	19200	699.7	2096.1	3	0.0161	7.682
Heterogeneous nuclear ribonucleoprotein D OS=Bos taurus GN=HNRPD PE=2 SV=1	tr A5D9H5 A5D9H5_BOVIN, tr F1PTP9 F1PTP9_CANFA, tr F7APH2 F7APH2_MACMU	iFVG GLSP DTPE Ek	95%	61.7	53.92507	Ref	-0.045	-0.32	-0.23	-0.6	0.19	-0.29	0.15	28400	21700	19400	23300	19800	29900	22400	30100	699.7	2096.1	3	0.0154	7.325
Heterogeneous nuclear ribonucleoprotein D OS=Bos taurus GN=HNRPD PE=2 SV=1	tr A5D9H5 A5D9H5_BOVIN, tr F1PTP9 F1PTP9_CANFA, tr F7APH2 F7APH2_MACMU	mFIG GLS WDT Tk	89%	45.6	53.91663	Ref	-0.008	-0.32	-0.16	-0.2	-0.17	-0.25	-0.14	4390	3020	2650	3300	3550	3160	3130	3350	655.4	1963.1	3	0.013	6.612
Heterogeneous nuclear ribonucleoprotein D OS=Bos taurus GN=HNRPD PE=2 SV=1	tr A5D9H5 A5D9H5_BOVIN, tr F1PTP9 F1PTP9_CANFA, tr F7APH2 F7APH2_MACMU	yHN VGLS k	72%	36.1	52.44121	Ref	-0.037	-0.26	-0.06	-0.25	0.036	-0.23	-0.04	40400	34400	32000	41200	39700	42400	36800	41800	509.3	1524.9	3	0.0052	3.433

Heterogeneous nuclear ribonucleoprotein D	tr A5D9H5 A5D9H5_BOVIN, tr F1PTP9 F1PTP9_CANFA, tr F7APH2 F7APH2_MACMU	yHN VGLS k	58%	32.9	52.26474	Ref	-0.032	-0.24	-0.11	-0.26	0.085	-0.16	-0.11	11700	10100	9520	11700	11600	12900	11400	11700	509.3	1524.9	3	0.0036	2.352
Tropomyosin 1 (Alpha) isoform 4	tr D9YZV5 D9YZV5_HUMAN, tr E9Q450 E9Q450_MOUSE, tr F6YS84 F6YS84_CALJA, tr F7GV59 F7GV59_MACMU, tr Q2Q1M7 Q2Q1M7_CEREL, tr Q63583 Q63583_RAT	aELS EGQ VR	52%	31.2	51.76777	Ref	-0.74	0.34	-1.1	-0.042	-0.1	-0.21	0.076	89300	46700	1E+05	45000	102000	85400	82400	100000	646.9	1291.7	2	0.0121	9.33
Tropomyosin 1 (Alpha) isoform 4	tr D9YZV5 D9YZV5_HUMAN, tr E9Q450 E9Q450_MOUSE, tr F6YS84 F6YS84_CALJA, tr F7GV59 F7GV59_MACMU, tr Q2Q1M7 Q2Q1M7_CEREL, tr Q63583 Q63583_RAT	aTD AEA DVA SLNR	95%	58.6	51.92314	Ref	-1.4	0.89	-1.4	0.29	-0.63	0.14	-0.83	29000	9690	50500	11700	41300	19100	33900	17200	818.9	1635.8	2	0.0101	6.17

Tropomyosin 1 (Alpha) isoform 4 OS=Homo sapiens GN=TPM1 PE=3 SV=1	tr D9YZV5 D9YZV5_HUMAN, tr E9Q450 E9Q450_MOUSE, tr F6YS84 F6YS84_CALJA, tr F7GV59 F7GV59_MA CMU, tr Q2Q1M7 Q2Q1M7_C EREL, tr Q63583 Q63583_RAT, tr Q63607 Q63607_RAT	hIAE DAD R	72%	33.4	49.82877	Ref	Value Missing (-1.7364192)	0.87	-1.1	0.19	-0.59	0.12	-0.66	1E+05	Value Missing (-1.7364192)	2E+05	68400	187000	95000	2E+05	93700	410.9	1229.6	3	0.0104	8.465
Tropomyosin 1 (Alpha) isoform 4 OS=Homo sapiens GN=TPM1 PE=3 SV=1	tr D9YZV5 D9YZV5_HUMAN, tr E9Q450 E9Q450_MOUSE, tr F6YS84 F6YS84_CALJA, tr F7GV59 F7GV59_MA CMU, tr Q2Q1M7 Q2Q1M7_C EREL, tr Q63583 Q63583_RAT, tr Q63607 Q63607_RAT	hIAE DAD R	61%	31.1	49.84397	Ref	-0.74	0.54	-0.37	-0.053	-0.31	-0.12	-0.51	25400	14100	37300	22300	30600	22400	26700	20200	410.9	1229.6	3	0.0111	9.001

Tropomyosin 1 (Alpha) isoform 4 OS=Homo sapiens GN=TPM1 PE=3 SV=1	tr D9YZV5 D9YZV5_HUMAN, tr E9Q450 E9Q450_MOUSE, tr F6YS84 F6YS84_CALJA, tr F7GV59 F7GV59_MA CMU, tr Q2Q1M7 Q2Q1M7_C EREL, tr Q63583 Q63583_RAT, tr Q63607 Q63607_RAT	IMD QTLK	81%	37.5	51.86773	Ref	-0.98	0.25	-0.79	0.041	-0.02	-0.13	0.2	35100	19500	49700	27100	53100	44400	43000	53500	728.9	1455.8	2	0.0237	16.24
Tropomyosin 1 (Alpha) isoform 4 OS=Homo sapiens GN=TPM1 PE=3 SV=1	tr D9YZV5 D9YZV5_HUMAN, tr E9Q450 E9Q450_MOUSE, tr F6YS84 F6YS84_CALJA, tr F7GV59 F7GV59_MA CMU, tr Q2Q1M7 Q2Q1M7_C EREL, tr Q63583 Q63583_RAT, tr Q63607 Q63607_RAT	kATD AEA DVA SLNR	51%	33.5	53.98428	Ref	-0.32	0.42	-0.8	-0.14	-0.35	0.12	-0.3	15300	12600	22800	11000	19100	14500	20900	15500	690.4	2068.1	3	0.0171	8.279

<p>Tropomyosin 1 (Alpha) isoform 4 OS=Homo sapiens GN=TPM1 PE=3 SV=1</p>	<p>tr D9YZV5 D9YZV5_HUMAN, tr E9Q450 E9Q450_MOUSE, tr F6YS84 F6YS84_CALJA, tr F7GV59 F7GV59_MA CMU, tr Q2Q1M7 Q2Q1M7_C EREL, tr Q63583 Q63583_RAT, tr Q63607 Q63607_RAT</p>	<p>kLVII ESDL ER</p>	<p>79%</p>	<p>36.6</p>	<p>50.5937</p>	<p>Ref</p>	<p>-1.2</p>	<p>0.67</p>	<p>-1.1</p>	<p>0.24</p>	<p>-0.58</p>	<p>0.15</p>	<p>-0.54</p>	<p>5130</p>	<p>1860</p>	<p>7560</p>	<p>2490</p>	<p>6950</p>	<p>3420</p>	<p>5930</p>	<p>3640</p>	<p>641.7</p>	<p>1922.2</p>	<p>3</p>	<p>0.0145</p>	<p>7.545</p>
<p>Tropomyosin 1 (Alpha) isoform 4 OS=Homo sapiens GN=TPM1 PE=3 SV=1</p>	<p>tr D9YZV5 D9YZV5_HUMAN, tr E9Q450 E9Q450_MOUSE, tr F6YS84 F6YS84_CALJA, tr F7GV59 F7GV59_MA CMU, tr Q2Q1M7 Q2Q1M7_C EREL, tr Q63583 Q63583_RAT, tr Q63607 Q63607_RAT</p>	<p>mDA Ik</p>	<p>89%</p>	<p>39.3</p>	<p>50.14025</p>	<p>Ref</p>	<p>Value Missing (-1.6664586)</p>	<p>0.95</p>	<p>Value Missing (-1.9507469)</p>	<p>0.13</p>	<p>-0.98</p>	<p>0.23</p>	<p>-0.23</p>	<p>4470</p>	<p>Value Missing (-1.6664586)</p>	<p>7920</p>	<p>Value Missing (-1.9507469)</p>	<p>5580</p>	<p>2250</p>	<p>5430</p>	<p>3920</p>	<p>462.3</p>	<p>922.5</p>	<p>2</p>	<p>0.0148</p>	<p>15.98</p>

<p>Tropomyosin 1 (Alpha) isoform 4 OS=Homo sapiens GN=TPM1 PE=3 SV=1</p>	<p>tr D9YZV5 D9YZV5_HUMAN, tr E9Q450 E9Q450_MOUSE, tr F6YS84 F6YS84_CALJA, tr F7GV59 F7GV59_MA CMU, tr Q2Q1M7 Q2Q1M7_CEREL, tr Q63583 Q63583_RAT, tr Q63607 Q63607_RAT</p>	<p>mDA lk</p>	<p>88%</p>	<p>38.9</p>	<p>50.07965</p>	<p>Ref</p>	<p>-1.4</p>	<p>0.76</p>	<p>-1.8</p>	<p>0.14</p>	<p>-0.5</p>	<p>0.36</p>	<p>-0.1</p>	<p>1850</p>	<p>840</p>	<p>3940</p>	<p>776</p>	<p>3180</p>	<p>1780</p>	<p>3380</p>	<p>2450</p>	<p>462.3</p>	<p>922.5</p>	<p>2</p>	<p>0.0137</p>	<p>14.85</p>
<p>Tropomyosin 1 (Alpha) isoform 4 OS=Homo sapiens GN=TPM1 PE=3 SV=1</p>	<p>tr D9YZV5 D9YZV5_HUMAN, tr E9Q450 E9Q450_MOUSE, tr F6YS84 F6YS84_CALJA, tr F7GV59 F7GV59_MA CMU, tr Q2Q1M7 Q2Q1M7_CEREL, tr Q63583 Q63583_RAT, tr Q63607 Q63607_RAT</p>	<p>mDA lk</p>	<p>73%</p>	<p>32.7</p>	<p>49.42231</p>	<p>Ref</p>	<p>1.3</p>	<p>0.34</p>	<p>-2.4</p>	<p>-0.36</p>	<p>-1.3</p>	<p>-0.6</p>	<p>-1.5</p>	<p>528</p>	<p>1090</p>	<p>609</p>	<p>103</p>	<p>463</p>	<p>206</p>	<p>357</p>	<p>197</p>	<p>470.3</p>	<p>938.5</p>	<p>2</p>	<p>0.01</p>	<p>10.7</p>

Tropomyosin 1 (Alpha) isoform 4 OS=Homo sapiens GN=TPM1 PE=3 SV=1	tr D9YZV5 D9YZV5_HUMAN, tr E9Q450 E9Q450_MOUSE, tr F6YS84 F6YS84_CALJA, tr F7GV59 F7GV59_MA, tr CMU, tr Q2Q1M7 Q2Q1M7_CEREL, tr Q63583 Q63583_RAT, tr Q63607 Q63607_RAT	siDD LEEK	76%	37.6	52.56576	Ref	-1.6	0.9	-1.6	0.3	-0.74	0.15	-0.72	3E+05	79000	5E+05	91400	390000	2E+05	3E+05	174000	519.6	1555.8	3	0.0149	9.597
Heterogeneous nuclear ribonucleoprotein A1 OS=Pan troglodytes GN=HNRNPA1 PE=2 SV=1	4 ROA1_PANTR, sp P04256 ROA1_RAT, sp P09651 ROA1_HUMAN, sp P09867 ROA1_BOVIN, sp P49312 ROA1_MOUSE, tr D4ACJ7 D4ACJ7_RAT, tr E1BK5 E1BK5_BOVIN, tr E2QYP1 E2QYP1_CANFA, tr F1PP96 F1PP96_CANFA, tr F6YZ44 F6YZ44_HO, tr F7RSE, tr F7RSE	ieVIE IMT DR	85%	39.8	52.50922	Ref	0.67	-0.23	-0.08	-0.32	-0.01	-0.24	0.072	19400	26900	15600	19400	18100	19600	17500	21500	761.9	1521.8	2	0.0138	9.047

Heterogeneous nuclear ribonucleoprotein A1 OS=Pan troglodytes GN=HNRNPA1 PE=2 SV=1	4 ROA1_PANTR,sp P04256 ROA1_RA T,sp P09651 ROA1_HUMAN,sp P09867 ROA1_BOVIN,sp P49312 ROA1_MOUSE,tr D4ACJ7 D4ACJ7_RA T,tr E1KB B5 E1BKB 5_BOVIN, tr E2QYP 1 E2QYP1 _CANFA, tr F1PP96 F1PP96_C ANFA, tr F 6YZ44 F6 YZ44_HO RSE, tr F7	iEVIE IMT DR	86%	40.3	52.51244	Ref	0.63	-0.27	-0.01	-0.35	0.007	-0.14	-0.04	2390	3050	1780	2390	2070	2330	2190	2330	761.9	1521.8	2	0.01	6.551
	4 ROA1_PANTR,sp P04256 ROA1_RA T,sp P09651 ROA1_HUMAN,sp P09867 ROA1_BOVIN,sp P49312 ROA1_MOUSE, tr D4ACJ7 D4ACJ7_RA T,tr E1KB B5 E1BKB 5_BOVIN, tr E2QYP 1 E2QYP1 _CANFA, tr F1PP96 F1PP96_C ANFA, tr F 6YZ44 F6 YZ44_HO RSE, tr F7	iEVIE IMT DR	51%	31.9	52.55272	Ref	0.64	-0.65	0.04	-0.16	-0.07	-0.19	0.26	559	801	357	645	619	577	552	752	761.9	1521.8	2	0.0105	6.88

Heterogeneous nuclear ribonucleoprotein A1 OS=Pan troglodytes GN=HNRNPA1 PE=2 SV=1	4 ROA1_PANTR,sp P04256 ROA1_RA T,sp P09651 ROA1_HUMAN,sp P09867 ROA1_BOVIN,sp P49312 ROA1_MOUSE,tr D4ACJ7 D4ACJ7_RA T,tr E1BKB5 E1BKB5_BOVIN,tr E2QYP1 E2QYP1_CANFA,tr F1PP96 F1PP96_C ANFA,tr F6Y244 F6YZ44_HO RSE,tr F7	R	95%	64.3	54.52406	Ref	0.48	-0.27	-0.16	-0.059	-0.07	-0.16	0.21	7050	8570	5530	6700	7910	6870	6730	8620	841.1	2520.4	3	0.0267	10.58
	4 ROA1_PANTR,sp P04256 ROA1_RA T,sp P09651 ROA1_HUMAN,sp P09867 ROA1_BOVIN,sp P49312 ROA1_MOUSE,tr D4ACJ7 D4ACJ7_RA T,tr E1BKB5 E1BKB5_BOVIN,tr E2QYP1 E2QYP1_CANFA,tr F1PP96 F1PP96_C ANFA,tr F6Y244 F6YZ44_HO RSE,tr F7	R	89%	45.7	54.16908	Ref	0.25	-0.23	-0.32	0.077	0.036	0.026	0.16	683	695	540	568	824	700	726	791	841.1	2520.4	3	0.0089	3.533

Heterogeneous nuclear ribonucleoprotein A1 OS=Pan troglodytes GN=HNRNPA1 PE=2 SV=1	4 ROA1_PANTR,sp P04256 ROA1_RA T,sp P09651 ROA1_HUMAN,sp P09867 ROA1_BOVIN,sp P49312 ROA1_MOUSE,tr D4ACJ7 D4ACJ7_RA T,tr E1BKB5 E1BKB5_BOVIN, tr E2QYP1 E2QYP1_CANFA, tr F1PP96 F1PP96_C ANFA, tr F6Y244 F6YZ44_HO RSE, tr F7R	nQG GYG GSSS SSSY GSG	95%	58.6	47.94007	Ref	-0.024	0.037	-0.17	-0.083	0.13	-0.09	0.36	1100	1010	1140	1110	1300	1320	1180	1600	999.9	1997.9	2	0.0132	6.581
	Heterogeneous nuclear ribonucleoprotein A1 OS=Pan troglodytes GN=HNRNPA1 PE=2 SV=1	4 ROA1_PANTR,sp P04256 ROA1_RA T,sp P09651 ROA1_HUMAN,sp P09867 ROA1_BOVIN,sp P49312 ROA1_MOUSE, tr D4ACJ7 D4ACJ7_RA T, tr E1BKB5 E1BKB5_BOVIN, tr E2QYP1 E2QYP1_CANFA, tr F1PP96 F1PP96_C ANFA, tr F6Y244 F6YZ44_HO RSE, tr F7R	nQG GYG GSSS SSSY GSG	95%	81	46.82741	Ref	-0.081	0.17	-0.42	0.018	0.34	-0.43	0.34	3430	2890	3730	2790	4160	4550	2790	4700	1000	1998.9	2	0.014

Heterogeneous nuclear ribonucleoprotein A1 OS=Pan troglodytes GN=HNRNPA1 PE=2 SV=1	4 ROA1_PANTR,sp P04256 ROA1_RA T,sp P09651 ROA1_HUMAN,sp P09867 ROA1_BOVIN,sp P49312 ROA1_MOUSE,transcript D4ACJ7 D4ACJ7_RA T,transcript E1BKB5 E1BKB5_BOVIN,transcript E2QYP1 E2QYP1_CANFA,transcript F1PP96 F1PP96_C ANFA,transcript F6Y244 F6YZ44_HO RSE,transcript F7	sSGP YGG GGQ YFAK	PR	95%	56.2	54.38783	Ref	-0.16	0.12	-0.26	-0.049	0.31	-0.29	0.31	17200	13400	17600	15200	19400	21600	15000	22500	746.4	2236.2	3	0.0214	9.547
	Heterogeneous nuclear ribonucleoprotein A1 OS=Pan troglodytes GN=HNRNPA1 PE=2 SV=1	4 ROA1_PANTR,sp P04256 ROA1_RA T,sp P09651 ROA1_HUMAN,sp P09867 ROA1_BOVIN,sp P49312 ROA1_MOUSE,transcript D4ACJ7 D4ACJ7_RA T,transcript E1BKB5 E1BKB5_BOVIN,transcript E2QYP1 E2QYP1_CANFA,transcript F1PP96 F1PP96_C ANFA,transcript F6Y244 F6YZ44_HO RSE,transcript F7	sSGP YGG GGQ YFAK	PR	87%	44	54.40601	Ref	0.039	-0.09	-0.15	0.037	0.17	-0.29	0.33	32700	29600	29300	31600	39600	38000	28900	44100	746.4	2236.2	3	0.0179

Heterogeneous nuclear ribonucleoprotein A1 OS=Pan troglodytes GN=HNRNPA1 PE=2 SV=1	4 ROA1_PANTR,sp P04256 ROA1_RA T,sp P09651 ROA1_HUMAN,sp P09867 ROA1_BOVIN,sp P49312 ROA1_MOUSE,transcript D4ACJ7 D4ACJ7_RA T,transcript E1BKB5 E1BKB5_BOVIN,transcript E2QYP1 E2QYP1_CANFA,transcript F1PP96 F1PP96_C ANFA,transcript F6Y244 F6YZ44_HO RSE,transcript F7	sSGP YGG GGQ YFAK	PR	94%	52	54.41016	Ref	-0.022	-0.01	-0.15	-0.22	0.28	-0.29	0.38	15700	13300	14500	14800	15500	19200	13500	21300	746.4	2236.2	3	0.0206	9.212
	Heterogeneous nuclear ribonucleoprotein A1 OS=Pan troglodytes GN=HNRNPA1 PE=2 SV=1	4 ROA1_PANTR,sp P04256 ROA1_RA T,sp P09651 ROA1_HUMAN,sp P09867 ROA1_BOVIN,sp P49312 ROA1_MOUSE,transcript D4ACJ7 D4ACJ7_RA T,transcript E1BKB5 E1BKB5_BOVIN,transcript E2QYP1 E2QYP1_CANFA,transcript F1PP96 F1PP96_C ANFA,transcript F6Y244 F6YZ44_HO RSE,transcript F7	sSGP YGG GGQ YFAK	PR	95%	59	54.42312	Ref	-0.081	-0.03	-0.21	-0.1	0.12	-0.25	0.44	1600	1210	1360	1350	1600	1640	1330	2110	746.4	2236.2	3	0.0197

Nucleosome assembly protein 1-like 1 OS=Bos taurus GN=NAP1L1 PE=2 SV=1	7 NP1L1_BOVIN,sp P28656 NP1L1_MOUSE,sp P55209 NP1L1_HUMAN,sp Q5R4D4 NP1L1_PONAB,sp Q9Z2G8 NP1L1_RAT, tr B3KNT8 B3KNT8_HUMAN, tr B7Z2V4 B7Z2V4_HUMAN, tr B7Z9C2 B7Z9C2_HUMAN, tr E1BH W2 E1BH W2_BOVIN, tr E9P W66 E9P	fYEE VHD LER	93%	46.5	51.21937	Ref	-0.091	-0.51	0.28	0.091	-0.04	-0.36	0.026	36200	29200	23600	45900	44400	35500	29600	38400	547.6	1639.8	3	0.0145	8.812
Nucleosome assembly protein 1-like 1 OS=Bos taurus GN=NAP1L1 PE=2 SV=1	7 NP1L1_BOVIN,sp P28656 NP1L1_MOUSE,sp P55209 NP1L1_HUMAN,sp Q5R4D4 NP1L1_PONAB,sp Q9Z2G8 NP1L1_RAT, tr B3KNT8 B3KNT8_HUMAN, tr B7Z2V4 B7Z2V4_HUMAN, tr B7Z9C2 B7Z9C2_HUMAN, tr E1BH W2 E1BH W2_BOVIN, tr E9P W66 E9P	fYEE VHD LER	95%	52.6	51.29084	Ref	-0.045	-0.2	0.12	-0.089	-0.01	-0.23	-0.02	6760	5740	5600	7840	7470	6910	6190	7110	820.9	1639.8	2	0.0127	7.718

<p>Nucleosome assembly protein 1-like 1 OS=Bos taurus GN=NAP1L1 PE=2 SV=1</p>	<p>7 NP1L1_BOVIN,sp P28656 NP1L1_MOUSE,sp P55209 NP1L1_HUMAN,sp Q5R4D4 NP1L1_PONAB,sp Q9Z2G8 NP1L1_RAT, tr B3KNT8 B3KNT8_HUMAN, tr B7Z2V4 B7Z2V4_HUMAN, tr B7Z9C2 B7Z9C2_HUMAN, tr E1BW2 E1BW2_BOVIN, tr E9PW66 E9P</p>	<p>gIPE FWL TVFK</p>	<p>83%</p>	<p>39.6</p>	<p>52.22865</p>	<p>Ref</p>	<p>-0.43</p>	<p>0.026</p>	<p>0.29</p>	<p>0.062</p>	<p>-0.14</p>	<p>-0.08</p>	<p>-0.17</p>	<p>241</p>	<p>166</p>	<p>247</p>	<p>333</p>	<p>314</p>	<p>239</p>	<p>259</p>	<p>242</p>	<p>649</p>	<p>1944.1</p>	<p>3</p>	<p>0.0082</p>	<p>4.234</p>
<p>Nucleosome assembly protein 1-like 1 OS=Bos taurus GN=NAP1L1 PE=2 SV=1</p>	<p>7 NP1L1_BOVIN,sp P28656 NP1L1_MOUSE,sp P55209 NP1L1_HUMAN,sp Q5R4D4 NP1L1_PONAB,sp Q9Z2G8 NP1L1_RAT, tr B3KNT8 B3KNT8_HUMAN, tr B7Z2V4 B7Z2V4_HUMAN, tr B7Z9C2 B7Z9C2_HUMAN, tr E1BW2 E1BW2_BOVIN, tr E9PW66 E9P</p>	<p>gIPE FWL TVFK</p>	<p>70%</p>	<p>35.7</p>	<p>52.43901</p>	<p>Ref</p>	<p>-0.059</p>	<p>-0.01</p>	<p>-0.23</p>	<p>0.043</p>	<p>-0.04</p>	<p>-0.47</p>	<p>-0.09</p>	<p>531</p>	<p>358</p>	<p>402</p>	<p>388</p>	<p>516</p>	<p>425</p>	<p>329</p>	<p>426</p>	<p>649</p>	<p>1944.1</p>	<p>3</p>	<p>0.0156</p>	<p>7.997</p>

Nucleosome assembly protein 1-like 1 OS=Bos taurus GN=NAP1L1 PE=2 SV=1	7 NP1L1_BOVIN,sp P28656 NP1L1_MOUSE,sp P55209 NP1L1_HUMAN,sp Q5R4D4 NP1L1_PONAB,sp Q9Z2G8 NP1L1_RAT,tr B3KNT8 B3KNT8_HUMAN,tr B7Z2V4 B7Z2V4_HUMAN,tr B7Z9C2 B7Z9C2_HUMAN,tr E1BH W2 E1BH W2_BOVIN,tr E9P W66 E9P	g PEFWLTVFK	78%	37.5	51.95833	Ref	-0.071	0.02	0.012	-0.014	-0.25	-0.23	-0.45	186	117	135	150	163	120	128	109	649.1	1944.1	3	0.0053	2.722
	7 NP1L1_BOVIN,sp P28656 NP1L1_MOUSE,sp P55209 NP1L1_HUMAN,sp Q5R4D4 NP1L1_PONAB,sp Q9Z2G8 NP1L1_RAT,tr B3KNT8 B3KNT8_HUMAN,tr B7Z2V4 B7Z2V4_HUMAN,tr B7Z9C2 B7Z9C2_HUMAN,tr E1BH W2 E1BH W2_BOVIN,tr E9P W66 E9P	KYAVLYQPLFDK	84%	39.4	51.16272	Ref	-0.16	-0.33	0.21	-0.036	-0.08	-0.17	-0.23	1630	1060	1020	1660	1550	1310	1290	1220	799.8	2396.4	3	0.0186	7.76

Nucleosome assembly protein 1-like 1 OS=Bos taurus GN=NAP1L1 PE=2 SV=1	7 NP1L1_BOVIN,sp P28656 NP1L1_MOUSE,sp P55209 NP1L1_HUMAN,sp Q5R4D4 NP1L1_PONAB,sp Q9Z2G8 NP1L1_RAT, tr B3KN T8 B3KNT8_HUMAN, tr B7Z2V4 B7Z2V4_HUMAN, tr B7Z9C2 B7Z9C2_HUMAN, tr E1BH W2 E1BH W2_BOVIN, tr E9P W66 E9P	KYAVLYQPLFDK	56%	29	50.57609	Ref	0.038	-0.2	0.006	-0.12	-0.05	-0.17	0.095	1790	1680	1550	2000	2020	1850	1780	2120	600.1	2396.4	4	0.0089	3.721
Nucleosome assembly protein 1-like 1 OS=Bos taurus GN=NAP1L1 PE=2 SV=1	7 NP1L1_BOVIN,sp P28656 NP1L1_MOUSE,sp P55209 NP1L1_HUMAN,sp Q5R4D4 NP1L1_PONAB,sp Q9Z2G8 NP1L1_RAT, tr B3KN T8 B3KNT8_HUMAN, tr B7Z2V4 B7Z2V4_HUMAN, tr B7Z9C2 B7Z9C2_HUMAN, tr E1BH W2 E1BH W2_BOVIN, tr E9P W66 E9P	KYAVLYQPLFDK	59%	30.2	51.16966	Ref	-0.061	-0.29	0.059	-0.11	-0.1	0.024	0.011	4220	3510	3250	4650	4560	4000	4560	4490	600.1	2396.4	4	0.0187	7.792

Nucleosome assembly protein 1-like 1 OS=Bos taurus GN=NAP1L1 PE=2 SV=1	7 NP1L1_BOVIN,sp P28656 NP1L1_MOUSE,sp P55209 NP1L1_HUMAN,sp Q5R4D4 NP1L1_PONAB,sp Q9Z2G8 NP1L1_RAT, tr B3KNT8 B3KNT8_HUMAN, tr B7Z2V4 B7Z2V4_HUMAN, tr B7Z9C2 B7Z9C2_HUMAN, tr E1BH W2 E1BH W2_BOVIN, tr E9P W66 E9P	KYAV LYQP LFDK	79%	36.3	50.43169	Ref	0.003	-0.3	0.073	-0.048	-0.1	-0.24	-0.04	1460	1140	1010	1460	1480	1250	1190	1350	799.8	2396.4	3	0.0071	2.942
Nucleosome assembly protein 1-like 1 OS=Bos taurus GN=NAP1L1 PE=2 SV=1	7 NP1L1_BOVIN,sp P28656 NP1L1_MOUSE,sp P55209 NP1L1_HUMAN,sp Q5R4D4 NP1L1_PONAB,sp Q9Z2G8 NP1L1_RAT, tr B3KNT8 B3KNT8_HUMAN, tr B7Z2V4 B7Z2V4_HUMAN, tr B7Z9C2 B7Z9C2_HUMAN, tr E1BH W2 E1BH W2_BOVIN, tr E9P W66 E9P	KYAV LYQP LFDK	94%	44.3	49.72384	Ref	-0.28	-0.41	0.26	0.008	0.03	-0.19	0.18	10600	8510	8410	15100	13900	12400	11100	14300	639.1	2552.5	4	0.0126	4.932

Nucleosome assembly protein 1-like 1 OS=Bos taurus GN=NAP1L1 PE=2 SV=1	7 NP1L1_BOVIN,sp P28656 NP1L1_MOUSE,sp P55209 NP1L1_HUMAN,sp Q5R4D4 NP1L1_PONAB,sp Q9Z2G8 NP1L1_RAT, tr B3KNT8 B3KNT8_HUMAN, tr B7Z2V4 B7Z2V4_HUMAN, tr B7Z9C2 B7Z9C2_HUMAN, tr E1BHW2 E1BHW2_BOVIN, tr E9PW66 E9P	KYAV LYQP LFDK R	80%	34.1	49.85355	Ref	-0.083	-0.38	0.3	-0.005	0.054	-0.19	0.084	3450	3610	3190	5740	5120	4660	4110	4930	639.1	2552.5	4	0.0136	5.308
Uncharacterized protein (Fragment) OS=Monodelphis domestica GN=LOC100028564 PE=4 SV=1	tr F7AJW2 F7AJW2_MONDELPHIS_DOMESTICA	iVEM STSk	78%	36.8	52.19521	Ref	0.1	-0.13	0.14	-0.18	0.043	-0.26	-0.18	41700	38700	35700	48400	42700	43600	36900	38800	751.9	1501.8	2	0.0191	12.74
Uncharacterized protein (Fragment) OS=Monodelphis domestica GN=LOC100028564 PE=4 SV=1	tr F7AJW2 F7AJW2_MONDELPHIS_DOMESTICA	iVEM STSk	67%	34.5	52.026	Ref	-0.066	-0.25	0.37	-0.19	0.047	-0.41	0.074	89200	80300	76500	132000	98800	1E+05	77400	108000	501.6	1501.9	3	0.0134	8.893

Uncharacterized protein (Fragment) OS=Monodelphis domestica GN=LOC100028564 PE=4 SV=1	tr F7AJW2 F7AJW2_MONDO	iVEM STSk	89%	41.2	52.05591	Ref	0.034	-0.2	0.044	0.006	0.12	-0.19	-0.24	16000	14400	13300	17700	19000	17900	15100	14500	751.9	1501.9	2	0.0068	4.531
Uncharacterized protein (Fragment) OS=Monodelphis domestica GN=LOC100028564 PE=4 SV=1	tr F7AJW2 F7AJW2_MONDO	vHLV GlnIF TGk	81%	36.6	49.9029	Ref	0.068	-0.37	0.12	-0.11	-0.28	0.09	0.045	17300	16300	13100	20600	19400	15000	20300	19500	636.4	1906.2	3	0.0016	0.814
Uncharacterized protein (Fragment) OS=Monodelphis domestica GN=LOC100028564 PE=4 SV=1	tr F7AJW2 F7AJW2_MONDO	vHLV GlnIF TGk	95%	63.9	50.61106	Ref	0.037	-0.48	-0.06	-0.1	0.12	-0.17	0.016	35700	28800	21900	32800	35200	35800	30500	34500	636.4	1906.1	3	0.0087	4.566
Uncharacterized protein (Fragment) OS=Monodelphis domestica GN=LOC100028564 PE=4 SV=1	tr F7AJW2 F7AJW2_MONDO	vHLV GlnIF TGk	95%	57.9	50.39497	Ref	0.08	-0.23	0.016	-0.05	0.1	-0.32	-0.06	2130	1960	1720	2280	2400	2330	1810	2160	954.1	1906.1	2	0.0063	3.32

Uncharacterized protein (Fragment) OS=Monodelphis domestica GN=LOC100028564 PE=4 SV=1	tr F7AJW2 F7AJW2_MONDO	vHLV GlnIF TGk	95%	59.7	50.76181	Ref	-7E-04	-0.37	0.01	-0.17	0.19	-0.23	0.035	1050	885	745	1090	1060	1190	927	1100	954.1	1906.1	2	0.0118	6.194
Uncharacterized protein (Fragment) OS=Monodelphis domestica GN=LOC100028564 PE=4 SV=1	tr F7AJW2 F7AJW2_MONDO	vHLV GlnIF TGk	94%	47.6	50.65135	Ref	-0.011	-0.08	-0.08	0.15	-0.06	-0.14	-0.19	1040	916	951	1070	1380	1040	1030	981	636.4	1906.1	3	0.0098	5.148
Uncharacterized protein (Fragment) OS=Monodelphis domestica GN=LOC100028564 PE=4 SV=1	tr F7AJW2 F7AJW2_MONDO	vHLV GlnIF TGk	95%	55.9	50.44006	Ref	0.062	-0.24	0.077	-0.1	-0.05	-0.28	-0.04	1220	1030	905	1270	1230	1120	996	1170	636.4	1906.1	3	0.0056	2.946
Uncharacterized protein (Fragment) OS=Monodelphis domestica GN=LOC100028564 PE=4 SV=1	tr F7AJW2 F7AJW2_MONDO	vHLV GlnIF TGk	70%	33.9	50.62003	Ref	0.1	-0.37	-0.23	0.018	-0.32	-0.12	0.1	388	299	234	289	378	261	313	363	636.4	1906.1	3	0.0095	4.959

Uncharacterized protein (Fragment) OS=Monodelphis domestica GN=LOC100028564 PE=4 SV=1	tr F7AJW2 F7AJW2_MONDO	vHLV GlnIF TGk	89%	41.1	50.19722	Ref	0.23	-0.02	-0.05	0.008	0.15	-0.43	0.026	194	275	252	276	317	306	214	291	636.4	1906.1	3	0.0023	1.216
Uncharacterized protein (Fragment) OS=Equus caballus GN=Eca.8560 PE=4 SV=1	tr F6ZN26 F6ZN26_HORSE	aGDL LEDS Pk	95%	51.7	52.79347	Ref	-0.43	-0.16	-0.14	-0.034	0.34	-0.52	0.096	8570	6120	8020	9110	10800	12200	7050	10700	827	1651.9	2	0.0182	10.99
Uncharacterized protein (Fragment) OS=Equus caballus GN=Eca.8560 PE=4 SV=1	tr F6ZN26 F6ZN26_HORSE	aSGY QSS Qk	73%	36.3	52.85598	Ref	-0.45	-0.04	-0.22	-0.027	0.45	-0.5	-0.05	6770	4940	7120	7080	8920	10800	5880	7970	782.4	1562.8	2	0.0259	16.54
Uncharacterized protein (Fragment) OS=Equus caballus GN=Eca.8560 PE=4 SV=1	tr F6ZN26 F6ZN26_HORSE	eAE DPE GEEK	95%	46.6	51.73574	Ref	-0.41	0.14	-0.14	-0.21	0.31	-0.47	-0.29	17600	11000	17400	16200	16900	21200	12900	14500	870.9	1739.9	2	0.0129	7.42

Uncharacterized protein (Fragment) OS=Equus caballus GN=Eca.8560 PE=4 SV=1	tr F6ZN26_1 F6ZN26_1 HORSE	gPP QEEE EEEE EEEE AKED AEA PGIR	95%	55.3	52.83186	Ref	-0.6	-0.14	-0.27	-0.016	0.2	-0.3	-0.07	5290	2630	3940	4040	5300	5390	3970	4630	877.2	3504.6	4	0.0326	9.301
Uncharacterized protein (Fragment) OS=Equus caballus GN=Eca.8560 PE=4 SV=1	tr F6ZN26_1 F6ZN26_1 HORSE	gPP QEEE EEEE EEEE AKED AEA PGIR	92%	45.3	53.05712	Ref	-0.33	0.085	0.052	-0.39	0.36	-0.99	-0	4720	3250	4690	5140	4160	6130	2520	4950	877.2	3504.6	4	0.0255	7.281
Uncharacterized protein (Fragment) OS=Equus caballus GN=Eca.8560 PE=4 SV=1	tr F6ZN26_1 F6ZN26_1 HORSE	iDE MPE AAV k	89%	42.7	53.00034	Ref	-0.4	-0.1	-0.12	-0.18	0.38	-0.56	-0.02	46400	30700	41000	45500	48300	61900	33700	48800	856	1709.9	2	0.0184	10.76
Uncharacterized protein (Fragment) OS=Equus caballus GN=Eca.8560 PE=4 SV=1	tr F6ZN26_1 F6ZN26_1 HORSE	iDE MPE AAV k	86%	42.3	53.02517	Ref	-0.5	-0.07	-0.17	0.051	0.33	-0.29	-0.08	1E+05	72300	1E+05	111000	142000	2E+05	1E+05	117000	571	1709.9	3	0.0153	8.939
Uncharacterized protein (Fragment) OS=Equus caballus GN=Eca.8560 PE=4 SV=1	tr F6ZN26_1 F6ZN26_1 HORSE	kGFS EGL WEIE NNP TVk	92%	48.9	54.28964	Ref	-0.36	-0.18	-0.01	-0.2	0.33	-0.3	-0.09	1540	1130	1380	1750	1690	2130	1440	1660	954.2	2859.6	3	0.0134	4.672

Uncharacterized protein (Fragment) OS=Equus caballus GN=Eca.8560 PE=4 SV=1	tr F6ZN26_1 F6ZN26_1_HORSE	kGFS EGL WEIE NNP TVK	67%	37.1	54.57895	Ref	-0.49	-0.26	-0.28	-0.081	0.25	-0.14	-0.16	701	383	485	539	680	749	596	585	954.2	2859.6	3	0.0231	8.059
Uncharacterized protein (Fragment) OS=Equus caballus GN=Eca.8560 PE=4 SV=1	tr F6ZN26_2 F6ZN26_2_HORSE	sSVE EPEP EPEA TEG DGD kk	65%	37.5	55.45374	Ref	-0.62	-0.02	-0.1	-0.15	0.42	-0.46	-0.32	9640	4890	8080	8540	9110	11800	6680	7340	1015	3041.5	3	0.015	4.936
Uncharacterized protein OS=Bos taurus GN=ZYG PE=2 SV=1	tr Q08DQ6_1 Q08DQ6_1_BOVIN	aISV SAPV FYAP Qk	95%	64.5	52.61501	Ref	-0.097	0.31	0.12	-0.062	0.12	0.12	0.2	22700	18300	26300	25900	25100	24900	26000	27400	696.1	2085.2	3	0.0106	5.087
Uncharacterized protein OS=Bos taurus GN=ZYG PE=2 SV=1	tr Q08DQ6_2 Q08DQ6_2_BOVIN	aISV SAPV FYAP Qk	95%	66.1	52.88612	Ref	-0.025	0.36	0.15	-0.2	0.15	-0.05	0.31	10300	8880	12600	12200	10600	11700	10700	13600	696.1	2085.2	3	0.0168	8.063
Uncharacterized protein OS=Bos taurus GN=ZYG PE=2 SV=1	tr Q08DQ6_3 Q08DQ6_3_BOVIN	aISV SAPV FYAP Qkk	92%	44.7	50.11689	Ref	-0.28	0.099	-0.03	0.1	0.51	-0.06	0.31	2880	2090	2940	3020	3650	4220	2970	3820	840.2	2517.5	3	0.0183	7.26
Uncharacterized protein OS=Bos taurus GN=ZYG PE=2 SV=1	tr Q08DQ6_4 Q08DQ6_4_BOVIN	aISV SAPV FYAP Qkk	65%	30.4	50.19482	Ref	-0.32	-0.06	0.035	0.29	0.23	0.22	0.31	5650	4060	5260	6300	8270	6940	7190	7600	630.4	2517.5	4	0.0194	7.703

Uncharacterized protein OS=Bos taurus GN=ZYG PE=2 SV=1	tr Q08DQ6 Q08DQ6_BOVIN	a SV SAPV FYAP Qkk	95%	64.5	49.49493	Ref	-0.096	0.073	0.11	0.074	0.48	0.074	0.18	2190	2080	2530	2910	3140	3640	2860	3050	840.2	2517.5	3	0.0088	3.484
Uncharacterized protein OS=Bos taurus GN=ZYG PE=2 SV=1	tr Q08DQ6 Q08DQ6_BOVIN	e VEE LEQL TQk	75%	38.3	53.73927	Ref	0.089	-0.06	0.024	0.17	0.24	0.16	-0.08	13900	11200	11000	13100	16000	14600	14500	12100	652	1953.1	3	0.0123	6.276
Uncharacterized protein OS=Bos taurus GN=ZYG PE=2 SV=1	tr Q08DQ6 Q08DQ6_BOVIN	f SPG APG GPG SQP HQk	92%	48.3	54.1898	Ref	0.23	-0.34	0.3	-0.16	0.49	-0.4	0.5	9720	11100	8180	14300	11400	15700	8820	16300	719.7	2156.1	3	0.0147	6.808
Uncharacterized protein OS=Bos taurus GN=ZYG PE=2 SV=1	tr Q08DQ6 Q08DQ6_BOVIN	g PLA PSPA Pk	84%	36.7	49.72883	Ref	0.064	0.26	-0.67	0.23	0.48	0.07	-0.54	14900	9760	12100	7130	14700	15300	12000	7820	772	1541.9	2	0.0097	6.308
Uncharacterized protein OS=Bos taurus GN=ZYG PE=2 SV=1	tr Q08DQ6 Q08DQ6_BOVIN	k FAP VVA PkPk	91%	30.4	37.11976	Ref	-0.037	-0.04	-0.05	0.17	0.53	-0.2	0.092	6480	4830	5210	5820	7470	8390	5280	6410	800.2	2397.6	3	0.0015	0.618
Uncharacterized protein OS=Bos taurus GN=ZYG PE=2 SV=1	tr Q08DQ6 Q08DQ6_BOVIN	v VAL Dk	65%	30.5	48.4988	Ref	-0.002	-0	0.043	0.13	0.21	-0.05	0.12	54100	38200	41400	48000	56100	52000	45300	50500	418.3	1251.8	3	0.0054	4.308

Uncharacterized protein OS=Bos taurus GN=Bt.77209 PE=4 SV=1	tr F1MYS7 F1MYS7_BOVIN, tr Q3MH P6 Q3MH P6_BOVIN	aRPA ADSF DDY PPR	74%	36.3	52.20189	Ref	0.32	0.15	-0.08	-0.12	0.019	-0.33	0.091	10100	11600	11200	10700	11400	11000	9020	12000	628	1880.9	3	0.0126	6.709
Uncharacterized protein OS=Bos taurus GN=Bt.77209 PE=4 SV=1	tr F1MYS7 F1MYS7_BOVIN, tr Q3MH P6 Q3MH P6_BOVIN	eDD SSAS TSQS SR	78%	31.2	46.42316	Ref	-0.17	-0.25	0.17	-0.25	0.43	-0.43	0.11	1430	931	957	1440	1190	1660	951	1370	830.9	1659.7	2	0.0168	10.13
Uncharacterized protein OS=Bos taurus GN=Bt.77209 PE=4 SV=1	tr F1MYS7 F1MYS7_BOVIN, tr Q3MH P6 Q3MH P6_BOVIN	eREV EER	76%	35.3	50.5327	Ref	-0.62	0.15	0.28	-0.17	0.47	-0.45	0.16	32300	19400	36000	44000	35600	48600	26800	40600	417.6	1249.6	3	0.0099	7.884
Uncharacterized protein OS=Bos taurus GN=Bt.77209 PE=4 SV=1	tr F1MYS7 F1MYS7_BOVIN, tr Q3MH P6 Q3MH P6_BOVIN	eRSR TGSE SSQT GTS ATS GR	89%	42.1	52.90278	Ref	Value Missing (-1.0683267)	0.36	0.092	-0.34	0.26	-0.11	0.36	139	Value Missing (-1.0683267)	166	154	126	167	135	185	587.3	2345.1	4	0.0145	6.188
Uncharacterized protein OS=Bos taurus GN=Bt.77209 PE=4 SV=1	tr F1MYS7 F1MYS7_BOVIN, tr Q3MH P6 Q3MH P6_BOVIN	sQSS DTE QQS PTSG GKG	95%	53.1	53.06948	Ref	-0.47	-0.28	0.24	-0.099	0.55	-0.81	0.28	2380	1300	1610	2590	2260	3090	1260	2650	1145	2288.1	2	0.0195	8.519
Uncharacterized protein OS=Bos taurus GN=Bt.77209 PE=4 SV=1	tr F1MYS7 F1MYS7_BOVIN, tr Q3MH P6 Q3MH P6_BOVIN	sQSS DTE QQS PTSG GKG	95%	62.1	53.09193	Ref	-0.29	-0.25	-0.08	-0.024	0.73	-0.62	0.1	4140	2740	3060	3870	4430	6530	2670	4370	763.7	2288.1	3	0.0192	8.369

Uncharacterized protein OS=Bos taurus GN=Bt.77209 PE=4 SV=1	tr F1MYS7 F1MYS7_BOVIN, tr Q3MH P6 Q3MH P6_BOVIN	sQSS DTEq QSPT SGG Gk	95%	57.4	52.5486	Ref	-0.22	0.12	0.073	-0.18	0.27	-0.47	0.32	1350	1030	1410	1530	1420	1690	1060	1820	764	2289.1	3	0.0211	9.221
Uncharacterized protein OS=Bos taurus GN=Bt.77209 PE=4 SV=1	tr F1MYS7 F1MYS7_BOVIN, tr Q3MH P6 Q3MH P6_BOVIN	sTPk EDD SSAS TSQS SR	89%	45.1	53.54172	Ref	-0.39	-0.29	0.008	0.13	0.67	-0.72	0.4	6550	5160	5990	8250	9910	12500	5000	10800	793.4	2377.2	3	0.0162	6.801
Uncharacterized protein OS=Bos taurus GN=Bt.77209 PE=4 SV=1	tr F1MYS7 F1MYS7_BOVIN, tr Q3MH P6 Q3MH P6_BOVIN	sTPk EDD SSAS TSQS SR	83%	40.7	53.40141	Ref	-0.71	-0.37	0.23	0.15	0.64	-0.48	0.33	3510	2240	3070	5220	5440	6640	3210	5590	793.4	2377.2	3	0.0229	9.64
Uncharacterized protein OS=Bos taurus GN=Bt.77209 PE=4 SV=1	tr F1MYS7 F1MYS7_BOVIN, tr Q3MH P6 Q3MH P6_BOVIN	tGSE SSQT GTS ATS GR	95%	60.4	50.574	Ref	-0.058	-0.4	0.014	-0.03	0.43	-0.47	0.091	1030	717	612	918	981	1180	659	966	909.4	1816.9	2	0.0101	5.561
Reticulocalbin-3 OS=Bos taurus GN=RCN3 PE=2 SV=1	sp Q2KJ39 RCN3_BOVIN	dIVI AETL EDLD R	95%	53.6	53.27625	Ref	-0.41	0.68	-0.14	0.13	0.025	0.25	-0.19	4350	2700	6240	3970	5250	4270	5230	3820	903.5	1805	2	0.0194	10.73
Reticulocalbin-3 OS=Bos taurus GN=RCN3 PE=2 SV=1	sp Q2KJ39 RCN3_BOVIN	dIVI AETL EDLD R	95%	51.9	53.32859	Ref	-0.54	0.8	-0.13	0.031	-0.08	0.23	-0.02	991	572	1570	928	1150	928	1200	1000	903.5	1805	2	0.0127	7.011
Reticulocalbin-3 OS=Bos taurus GN=RCN3 PE=2 SV=1	sp Q2KJ39 RCN3_BOVIN	dSVS AAW NTY DTD RDG R	82%	37.1	50.04343	Ref	-0.31	0.62	-0.34	0.26	0.008	0.39	-0.12	26500	19900	41100	23700	39500	29000	39500	27600	745	2232	3	0.016	7.186

Reticulocalbin-3 OS=Bos taurus GN=RCN3 PE=2 SV=1	sp Q2KJ3 9 RCN3_ BOVIN	eELT AFLH PEEF PHM R	90%	46	53.62143	Ref	0.0068	0.41	-0.25	0.22	-0.12	0.11	0.26	1150	1040	1490	1060	1620	1110	1370	1500	763.1	2286.1	3	0.0074	3.224
Reticulocalbin-3 OS=Bos taurus GN=RCN3 PE=2 SV=1	sp Q2KJ3 9 RCN3_ BOVIN	eELT AFLH PEEF PHM R	91%	46.6	53.44447	Ref	0.13	0.31	-0.01	-0.033	-0.08	0.32	0.057	798	794	978	874	950	802	1110	916	763	2286.1	3	0.0158	6.91
Reticulocalbin-3 OS=Bos taurus GN=RCN3 PE=2 SV=1	sp Q2KJ3 9 RCN3_ BOVIN	eELT AFLH PEEF PHm R	79%	37.2	53.15706	Ref	0.43	0.51	-0.09	-0.18	-0.04	-0.03	0.005	5110	6310	7230	5350	5540	5340	5620	5700	576.5	2302.1	4	0.0177	7.677
Reticulocalbin-3 OS=Bos taurus GN=RCN3 PE=2 SV=1	sp Q2KJ3 9 RCN3_ BOVIN	eFD QLTP EESQ AR	92%	43.1	51.48827	Ref	-0.42	0.67	-0.33	0.089	-0	0.22	-0.14	16300	8670	20100	11300	16600	13600	16600	12800	927.5	1852.9	2	0.014	7.56
Reticulocalbin-3 OS=Bos taurus GN=RCN3 PE=2 SV=1	sp Q2KJ3 9 RCN3_ BOVIN	eVAk EFD QLTP EESQ AR	52%	34.6	54.95316	Ref	-0.34	0.46	-0.06	0.26	0.16	0.13	0.095	2800	2130	4040	3160	4350	3540	3610	3510	862.5	2584.3	3	0.0278	10.76
Reticulocalbin-3 OS=Bos taurus GN=RCN3 PE=2 SV=1	sp Q2KJ3 9 RCN3_ BOVIN	vAD QDG DSM ATR	94%	42.5	48.53692	Ref	-0.55	0.76	-0.3	0.2	-0.11	0.35	-0.19	62300	33900	91300	49200	76500	54100	77500	53000	785.4	1568.7	2	0.0123	7.841
Reticulocalbin-3 OS=Bos taurus GN=RCN3 PE=2 SV=1	sp Q2KJ3 9 RCN3_ BOVIN	vAD QDG DSm ATR	73%	31.2	47.7805	Ref	-0.55	0.81	-0.11	0.12	-0.07	0.2	-0.22	8170	4450	12400	7330	9470	7280	9140	6800	793.4	1584.7	2	0.0113	7.14

Nuclear migration protein nudC OS=Bos taurus GN=NUDC PE=2 SV=1	sp Q17QG2 NUDC_BOVIN,tri E2QTG9 E2QTG9_CANFA,tri F1STR6 F1STR6_PIG	fMD QHP EMD FSk	75%	36.8	52.17968	Ref	-0.064	-0.42	0.005	-0.078	0.092	-0.18	-0.03	14000	12700	10800	16200	16900	16600	14300	15800	707.3	2119	3	0.0124	5.872
Nuclear migration protein nudC OS=Bos taurus GN=NUDC PE=2 SV=1	sp Q17QG2 NUDC_BOVIN,tri E2QTG9 E2QTG9_CANFA,tri F1STR6 F1STR6_PIG	kTDF FVG GEE GMA Ek	89%	46.3	55.14136	Ref	-0.11	-0.36	0.025	-0.11	0.12	-0.34	-0.01	4840	3980	3650	5350	5380	5490	4180	5200	853.1	2556.3	3	0.0335	13.09
Nuclear migration protein nudC OS=Bos taurus GN=NUDC PE=2 SV=1	sp Q17QG2 NUDC_BOVIN,tri E2QTG9 E2QTG9_CANFA,tri F1STR6 F1STR6_PIG	lITQT FNH HNQ LAQk	58%	33	54.24297	Ref	0.0033	-0.25	-0.05	-0.26	-0.12	-0.03	0.086	10400	10100	9170	11800	11300	10900	12100	13000	601.1	2400.3	4	0.0282	11.75
Nuclear migration protein nudC OS=Bos taurus GN=NUDC PE=2 SV=1	sp Q17QG2 NUDC_BOVIN,tri E2QTG9 E2QTG9_CANFA,tri F1STR6 F1STR6_PIG	lITQT FNH HNQ LAQk	87%	43.3	53.56099	Ref	0.12	-0.4	-0.03	-0.13	-0.03	-0.32	-0.05	1750	1640	1240	1790	1840	1720	1470	1770	801.1	2400.3	3	0.0031	1.29
Nuclear migration protein nudC OS=Bos taurus GN=NUDC PE=2 SV=1	sp Q17QG2 NUDC_BOVIN,tri E2QTG9 E2QTG9_CANFA,tri F1STR6 F1STR6_PIG	lITQT FnH HNQ LAQk	87%	44.3	54.26675	Ref	0.056	-0.19	0.11	-0.2	-0.12	-0.22	-0.07	3270	3310	3030	4180	3730	3430	3350	3680	801.4	2401.3	3	0.0131	5.438
Nuclear migration protein nudC OS=Bos taurus GN=NUDC PE=2 SV=1	sp Q17QG2 NUDC_BOVIN,tri E2QTG9 E2QTG9_CANFA,tri F1STR6 F1STR6_PIG	lVSS DPEI NTk	60%	34.3	53.59655	Ref	-0.048	-0.43	0.17	-0.2	0.2	-0.61	-0.09	19200	15500	13000	22100	18800	21600	12900	18400	906	1810	2	0.0155	8.542

Nuclear migration protein nudC OS=Bos taurus GN=NUDC PE=2 SV=1	sp Q17QG2 NUDC_BOVIN,tri E2QTG9 E2QTG9_CANFA,tri F1STR6 F1STR6_PIG	sETS GPQIk	84%	39.3	52.65919	Ref	-0.18	-0.28	0.12	-0.17	0.27	-0.58	-0.07	26700	20800	21100	31200	28100	33200	19300	27300	777.9	1553.9	2	0.0232	14.9
Nuclear migration protein nudC OS=Bos taurus GN=NUDC PE=2 SV=1	sp Q17QG2 NUDC_BOVIN,tri E2QTG9 E2QTG9_CANFA,tri F1STR6 F1STR6_PIG	sETS GPQIk	94%	45.6	52.3373	Ref	-0.076	-0.33	0.093	-0.13	0.1	-0.68	-0.03	4830	3640	3320	4980	4690	4840	2940	4560	777.9	1553.9	2	0.0091	5.875
Nuclear migration protein nudC OS=Bos taurus GN=NUDC PE=2 SV=1	sp Q17QG2 NUDC_BOVIN,tri E2QTG9 E2QTG9_CANFA,tri F1STR6 F1STR6_PIG	tDFF VGG EEG MAEk	95%	55.2	52.9985	Ref	-0.13	-0.09	0.017	-0.26	-0.03	-0.43	-0.03	8160	5980	6680	8050	7300	7490	5940	7790	709	2124	3	0.0204	9.618
Nuclear migration protein nudC OS=Bos taurus GN=NUDC PE=2 SV=1	sp Q17QG2 NUDC_BOVIN,tri E2QTG9 E2QTG9_CANFA,tri F1STR6 F1STR6_PIG	tDFF VGG EEG MAEk	87%	43.3	53.3236	Ref	-0.07	-0.14	-0.06	-0.28	0.04	-0.34	-0.05	6800	5280	5450	6480	6120	6670	5360	6520	709	2124.1	3	0.0091	4.267

Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2	5 SRSF1_ HUMAN,s p Q0VCY 7 SRSF1_ BOVIN,sp Q3YLA6 SRSF1_PI G,sp Q5R 7H2 SRSF 1_PONAB, sp Q6PD M2 SRSF 1_MOUSE ,tr D4A9L 2 D4A9L2 _RAT,tr E 2RIL3 E2 RIL3_CAN FA,tr F6R 520 F6R5 20_MAC MU,tr F6 YHN4 F6Y HN4_HOR SE,tr F7J0 L2 F7JOL2 _CRIGR	DAE DAV YGR	66%	30.9	49.11232	Ref	0.038	-0.07	-0.17	-0.26	-0.01	-0.19	-0.13	1E+05	123000	1E+05	129000	133000	1E+05	1E+05	133000	650.3	1298.6	2	0.0105	8.06
	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2	5 SRSF1_ HUMAN,s p Q0VCY 7 SRSF1_ BOVIN,sp Q3YLA6 SRSF1_PI G,sp Q5R 7H2 SRSF 1_PONAB, sp Q6PD M2 SRSF 1_MOUSE ,tr D4A9L 2 D4A9L2 _RAT,tr E 2RIL3 E2 RIL3_CAN FA,tr F6R 520 F6R5 20_MAC MU,tr F6 YHN4 F6Y HN4_HOR SE,tr F7J0 L2 F7JOL2 _CRIGR	dGY DYD GYR	59%	26.1	45.49677	Ref	-0.15	0.009	-0.07	-0.28	0.17	-0.37	0.066	28500	24400	29500	31500	29800	35600	25600	34400	714.3	1426.6	2	0.0088

Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2	5 SRSF1_HUMAN,sp Q0VCY7 SRSF1_BOVIN,sp Q3YLA6 SRSF1_PI G,sp Q5R7H2 SRSF1_PONAB,sp Q6PD M2 SRSF1_MOUSE, tr D4A9L2 D4A9L2_RAT, tr E2RIL3 E2RIL3_CAN FA, tr F6R520 F6R520_MAC MU, tr F6YHN4 F6YHN4_HOR SE, tr F7J0L2 F7J0L2_CRIGR	dGY DYD GYR	82%	31	45.14933	Ref	-0.23	-0.07	-0.08	-0.18	0.18	-0.43	0.16	11300	9080	11000	12300	12600	14100	9680	14400	714.3	1426.6	2	0.0119	8.366
	5 SRSF1_HUMAN,sp Q0VCY7 SRSF1_BOVIN,sp Q3YLA6 SRSF1_PI G,sp Q5R7H2 SRSF1_PONAB,sp Q6PD M2 SRSF1_MOUSE, tr D4A9L2 D4A9L2_RAT, tr E2RIL3 E2RIL3_CAN FA, tr F6R520 F6R520_MAC MU, tr F6YHN4 F6YHN4_HOR SE, tr F7J0L2 F7J0L2_CRIGR	eAG DVcY ADV YR	94%	41.5	47.18876	Ref	-0.032	-0.14	-0.23	-0.45	0.18	-0.3	0.28	15800	14800	14900	15700	14900	20000	15100	22400	855.9	1709.8	2	0.0122	7.117

Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2	5 SRSF1_HUMAN,sp Q0VCY7 SRSF1_BOVIN,sp Q3YLA6 SRSF1_PI G,sp Q5R7H2 SRSF1_PONAB,sp Q6PD M2 SRSF1_MOUSE, tr D4A9L2 D4A9L2_RAT, tr E2RIL3 E2RIL3_CAN FA, tr F6R520 F6R520_MAC MU, tr F6YHN4 F6YHN4_HOR SE, tr F7J0L2 F7J0L2_CRIGR	eAG DVCY ADV YR	56%	27.7	47.37463	Ref	-0.46	-0	-0.24	-0.46	-0.07	0.12	0.56	11800	10200	15300	14600	13800	15700	18700	25300	570.9	1709.8	3	0.0099	5.764
Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2	5 SRSF1_HUMAN,sp Q0VCY7 SRSF1_BOVIN,sp Q3YLA6 SRSF1_PI G,sp Q5R7H2 SRSF1_PONAB,sp Q6PD M2 SRSF1_MOUSE, tr D4A9L2 D4A9L2_RAT, tr E2RIL3 E2RIL3_CAN FA, tr F6R520 F6R520_MAC MU, tr F6YHN4 F6YHN4_HOR SE, tr F7J0L2 F7J0L2_CRIGR	gPA GNN DcR	90%	34.7	44.3183	Ref	-0.14	-0.15	-0.25	-0.35	0.2	-0.45	0.13	28700	20100	21700	22700	23200	29700	19900	29400	627.3	1252.5	2	0.0134	10.68

Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2	5 SRSF1_ HUMAN,s p Q0VCY 7 SRSF1_ BOVIN,sp Q3YLA6 SRSF1_PI G,sp Q5R 7H2 SRSF 1_PONAB, sp Q6PD M2 SRSF 1_MOUSE ,tr D4A9L 2 D4A9L2 _RAT,tr E 2RIL3 E2 RIL3_CAN FA,tr F6R 520 F6R5 20_MAC MU,tr F6 YHN4 F6Y HN4_HOR SE,tr F7J0 L2 F7JOL2 _CRIGR	gPA GnN DcR	95%	41.5	43.00422	Ref	-0.24	-0.11	-0.14	-0.24	0.29	-0.69	0.091	43100	28800	34300	37600	38500	48700	25800	44000	627.8	1253.5	2	0.0108	8.643
	5 SRSF1_ HUMAN,s p Q0VCY 7 SRSF1_ BOVIN,sp Q3YLA6 SRSF1_PI G,sp Q5R 7H2 SRSF 1_PONAB, sp Q6PD M2 SRSF 1_MOUSE ,tr D4A9L 2 D4A9L2 _RAT,tr E 2RIL3 E2 RIL3_CAN FA,tr F6R 520 F6R5 20_MAC MU,tr F6 YHN4 F6Y HN4_HOR SE,tr F7J0 L2 F7JOL2 _CRIGR	iYVG NLPP DIR	87%	40.5	52.09652	Ref	-0.12	-0.1	-0.23	-0.32	0.2	-0.43	0.13	13200	10100	11000	11300	11800	14700	9950	14500	780.9	1559.9	2	0.0139	8.901

Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2	5 SRSF1_ HUMAN,s p Q0VCY 7 SRSF1_ BOVIN,sp Q3YLA6 SRSF1_PI G,sp Q5R 7H2 SRSF 1_PONAB, sp Q6PD M2 SRSF 1_MOUSE ,tr D4A9L 2 D4A9L2 _RAT,tr E 2RIL3 E2 RIL3_CAN FA,tr F6R 520 F6R5 20_MAC MU,tr F6 YHN4 F6Y HN4_HOR SE,tr F7J0 L2 F7JOL2 _CRIGR	iYVG NLPP DIR	85%	40	52.65323	Ref	-0.14	-0.13	-0.2	-0.28	0.2	-0.51	0.18	18900	14300	15700	16800	17400	21300	13600	21700	781	1559.9	2	0.0056	3.583
Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2	5 SRSF1_ HUMAN,s p Q0VCY 7 SRSF1_ BOVIN,sp Q3YLA6 SRSF1_PI G,sp Q5R 7H2 SRSF 1_PONAB, sp Q6PD M2 SRSF 1_MOUSE ,tr D4A9L 2 D4A9L2 _RAT,tr E 2RIL3 E2 RIL3_CAN FA,tr F6R 520 F6R5 20_MAC MU,tr F6 YHN4 F6Y HN4_HOR SE,tr F7J0 L2 F7JOL2 _CRIGR	sHEG ETAY IR	71%	34.3	50.94338	Ref	-0.11	-0.03	-0.17	-0.25	0.13	-0.36	0.11	18100	15200	17400	17700	18400	20900	15700	21400	489.6	1465.7	3	0.0141	9.602

Phosphatidylethanolamine-binding protein 1 OS=Bos taurus GN=PEBP1 PE=1 SV=2	sp P13696 PEBP1_BOVIN	gNNI SSGT VLSD YVGS GPPk	93%	51.1	54.98214	Ref	0.47	-0.45	0.31	0.13	-0.22	-0.21	-0.53	7330	9610	5520	10500	10200	7030	7370	5870	853.1	2556.3	3	0.0187	7.321
Phosphatidylethanolamine-binding protein 1 OS=Bos taurus GN=PEBP1 PE=1 SV=2	sp P13696 PEBP1_BOVIN	gnNI SSGT VLSD YVGS GPPk	95%	69	55.04147	Ref	0.09	-0.15	0.084	-0.078	-0.14	0.18	-0.1	2530	2790	2560	3380	3330	2780	3630	2980	853.5	2557.3	3	0.0192	7.51
Phosphatidylethanolamine-binding protein 1 OS=Bos taurus GN=PEBP1 PE=1 SV=2	sp P13696 PEBP1_BOVIN	gnNI SSGT VLSD YVGS GPPk	95%	81.4	55.09567	Ref	0.3	-0.27	0.024	-0.072	0.053	-0.55	0.011	4030	4210	3080	4230	4370	4160	2860	4180	853.5	2557.3	3	0.0165	6.443
Phosphatidylethanolamine-binding protein 1 OS=Bos taurus GN=PEBP1 PE=1 SV=2	sp P13696 PEBP1_BOVIN	gNNI SSGT VLSD YVGS GPPk	88%	43.3	54.63316	Ref	0.16	-0.26	0.1	-0.056	-0.17	-0.06	-0.08	4400	4260	3450	4980	4920	3980	4480	4380	716.1	2860.6	4	0.0104	3.622
Phosphatidylethanolamine-binding protein 1 OS=Bos taurus GN=PEBP1 PE=1 SV=2	sp P13696 PEBP1_BOVIN	IYTL VLTD PDA PSR	85%	40.5	53.51168	Ref	0.17	-0.12	0.1	-0.22	-0.05	-0.3	-0.07	4310	3920	3480	4570	4010	3950	3460	4040	933	1864	2	0.0146	7.844

Phosphatidylethanolamine-binding protein 1 OS=Bos taurus GN=PEBP1 PE=1 SV=2	sp P13696 PEBP1_BOVIN	vLTP TQV k	76%	31.9	47.90194	Ref	0.16	-0.4	0.23	-0.16	0.16	-0.56	0.009	30800	28700	21200	36700	30900	33700	21400	31500	747.5	1492.9	2	0.0071	4.72
Phosphatidylethanolamine-binding protein 1 OS=Bos taurus GN=PEBP1 PE=1 SV=2	sp P13696 PEBP1_BOVIN	vLTP TQV k	79%	33.4	47.41774	Ref	0.11	-0.41	0.16	-0.12	0.13	-0.5	0.027	22500	19200	14600	24200	21900	22800	15400	22000	498.7	1492.9	3	0.0033	2.227
Phosphatidylethanolamine-binding protein 1 OS=Bos taurus GN=PEBP1 PE=1 SV=2	sp P13696 PEBP1_BOVIN	wSG PLSL QEV DER PQH PLQ Vk	88%	42.8	54.61261	Ref	0.018	-0.25	0.27	-0.13	0.26	-0.61	-0.01	5900	5380	4860	7780	6520	7440	4250	6400	763.7	3050.7	4	0.004	1.314
Phosphatidylethanolamine-binding protein 1 OS=Bos taurus GN=PEBP1 PE=1 SV=2	sp P13696 PEBP1_BOVIN	yGG AEV DELG k	68%	35.9	53.15012	Ref	0.084	-0.14	0.1	-0.054	0.038	-0.31	-0.01	19500	18800	17500	23200	23000	21400	17600	21500	582.7	1744.9	3	0.0149	8.523
Phosphatidylethanolamine-binding protein 1 OS=Bos taurus GN=PEBP1 PE=1 SV=2	sp P13696 PEBP1_BOVIN	yVW LVYE QEG PLk	88%	44.9	54.07692	Ref	0.3	-0.34	0.23	-0.1	0.17	-0.59	-0.2	3810	4080	2830	4750	4140	4380	2700	3510	744.7	2231.2	3	0.02	8.94

Serpin A3-1 OS=Bos taurus GN=SERPINA3-1 PE=1 SV=3	sp Q9TTE1 SPA31_BOVIN, tr Q28921 Q28921_BOVIN	dTQSIIFLGK	60%	32.5	51.49558	Ref	0.73	0.43	0.19	0.14	0.51	0.49	0.2	4490	4510	3990	3790	4040	4550	4690	3810	577.3	1729	3	0.0067	3.845
Serpin A3-1 OS=Bos taurus GN=SERPINA3-1 PE=1 SV=3	sp Q9TTE1 SPA31_BOVIN, tr Q28921 Q28921_BOVIN	iHEL YLPK	77%	35.2	49.95872	Ref	0.88	0.11	0.55	0.43	-0.08	0.97	0.11	9440	16100	10200	15600	15800	9660	20900	11400	541	1620	3	0.0135	8.312
Serpin A3-1 OS=Bos taurus GN=SERPINA3-1 PE=1 SV=3	sp Q9TTE1 SPA31_BOVIN, tr Q28921 Q28921_BOVIN	iHEL YLPK	86%	38.7	49.77531	Ref	0.96	0.1	0.44	0.33	-0.02	0.97	0.2	10300	18500	11100	15800	16100	11100	22900	13300	541	1620	3	0.0082	5.036
Serpin A3-1 OS=Bos taurus GN=SERPINA3-1 PE=1 SV=3	sp Q9TTE1 SPA31_BOVIN, tr Q28921 Q28921_BOVIN	sLIN DYVvk	91%	43.2	52.15624	Ref	1	-0.07	0.69	0.43	0.012	0.79	0.035	14600	26300	13600	25800	23800	15500	27700	16300	780.5	1558.9	2	0.0085	5.457
Serpin A3-1 OS=Bos taurus GN=SERPINA3-1 PE=1 SV=3	sp Q9TTE1 SPA31_BOVIN, tr Q28921 Q28921_BOVIN	sNYE LNDI LSQL GIR	95%	58.1	53.93882	Ref	0.63	0.15	0.42	0.46	0.097	0.81	-0.01	354	325	253	342	388	263	449	253	680.4	2038.1	3	0.0043	2.089
Serpin A3-1 OS=Bos taurus GN=SERPINA3-1 PE=1 SV=3	sp Q9TTE1 SPA31_BOVIN, tr Q28921 Q28921_BOVIN	sNYE LNDI LSQL GIR	95%	69.2	54.00881	Ref	0.51	0.27	0.39	0.29	0.25	0.95	0.51	253	331	304	369	379	323	548	401	680.4	2038.1	3	0.009	4.428

Serpin A3-1 OS=Bos taurus GN=SERPINA3-1 PE=1 SV=3	sp Q9TTE1 SPA31_BOVIN, tr Q28921 Q28921_BOVIN	sNYE LNDI LSQL GIR	84%	42.2	53.93264	Ref	0.95	-0.11	0.57	0.48	0.24	0.17	0.21	210	242	125	225	234	173	172	176	680.4	2038.1	3	0.0026	1.28
Serpin A3-1 OS=Bos taurus GN=SERPINA3-1 PE=1 SV=3	sp Q9TTE1 SPA31_BOVIN, tr Q28921 Q28921_BOVIN	tELV LVNY IYFK	88%	42.7	52.26182	Ref	0.73	0.015	0.6	0.32	-0.4	1.1	0.38	993	1390	918	1550	1400	745	2190	1320	704.1	2109.2	3	0.0123	5.842
Serpin A3-1 OS=Bos taurus GN=SERPINA3-1 PE=1 SV=3	sp Q9TTE1 SPA31_BOVIN, tr Q28921 Q28921_BOVIN	tELV LVNY IYFK	88%	43.3	52.45969	Ref	1	0.07	0.83	0.37	-0.23	0.88	0.021	272	602	337	643	512	295	665	365	704.1	2109.2	3	0.0172	8.174
Serpin A3-1 OS=Bos taurus GN=SERPINA3-1 PE=1 SV=3	sp Q9TTE1 SPA31_BOVIN, tr Q28921 Q28921_BOVIN	vNRP FLIAI VLk	70%	23.5	42.28913	Ref	1	0.45	0.58	0.21	-0.13	0.45	-0.13	1310	1640	1190	1460	1250	862	1340	893	498.6	1990.3	4	0.0012	0.605
Thioltransferase OS=Ovis aries PE=4 SV=1	tr B2ZA84 B2ZA84_SHEEP	aQA FVNS k	95%	55.1	51.18255	Ref	1.7	0.027	-0.31	-0.86	-0.16	-0.71	0.53	1190	4150	1400	1250	937	1330	950	2230	605.8	1209.7	2	0.0104	8.555
Thioltransferase OS=Ovis aries PE=4 SV=1	tr B2ZA84 B2ZA84_SHEEP	kTQE LLSQ LPFk	54%	28.4	48.4005	Ref	0.2	-0.3	0.68	0.095	0.73	-0.52	0.52	1020	1010	780	1720	1260	1710	752	1540	782.1	2343.4	3	0.0108	4.604
Thioltransferase OS=Ovis aries PE=4 SV=1	tr B2ZA84 B2ZA84_SHEEP	kTQE LLSQ LPFk	92%	40	48.09654	Ref	0.24	-0.18	0.57	-0.024	0.79	-0.4	0.48	3190	3280	2660	5040	3670	5640	2580	4700	586.9	2343.4	4	0.0055	2.346

Thioltransferase OS=Ovis aries PE=4 SV=1	tr B2ZA8 4 B2ZA84 _SHEEP	kTQE LLSQ LPFK	94%	45.5	48.45284	Ref	0.31	-0.24	0.56	0.043	0.78	-0.41	0.54	816	976	722	1410	1090	1580	725	1390	782.1	2343.4	3	0.0128	5.461
Thioltransferase OS=Ovis aries PE=4 SV=1	tr B2ZA8 4 B2ZA84 _SHEEP	qIGA LQ	91%	37.9	46.86886	Ref	1.2	0.96	-0.15	-0.63	0.23	-0.62	0.074	433	1220	1100	572	453	715	417	667	467.3	932.56	2	0.0034	3.641
Thioltransferase OS=Ovis aries PE=4 SV=1	tr B2ZA8 4 B2ZA84 _SHEEP	qIGA LQ	55%	26.8	46.86368	Ref	1.2	1.1	-0.18	-0.41	0.12	-0.86	0.2	368	1170	1140	544	512	645	342	706	467.3	932.56	2	0.0028	3.041
Thioltransferase OS=Ovis aries PE=4 SV=1	tr B2ZA8 4 B2ZA84 _SHEEP	qIGA LQ	86%	34.7	46.96156	Ref	0.88	0.46	-0.06	-0.11	0.14	-0.07	0.34	2090	3310	2680	2100	2230	2320	2100	2770	467.3	932.55	2	0.0055	5.934
Thioltransferase OS=Ovis aries PE=4 SV=1	tr B2ZA8 4 B2ZA84 _SHEEP	qIGA LQ	82%	32.9	46.96496	Ref	1	0.69	-0.22	-0.19	0.055	-0.02	-0.02	1520	2580	2240	1330	1500	1550	1540	1520	467.3	932.55	2	0.0052	5.527
Thioltransferase OS=Ovis aries PE=4 SV=1	tr B2ZA8 4 B2ZA84 _SHEEP	vVVF Ik	84%	25.4	37.478	Ref	-0.03	-0.04	0.25	0.27	0.5	-0.2	0.75	2100	1620	1750	2400	2690	2750	1770	3390	438.3	1311.9	3	0.0038	2.901
Thioltransferase OS=Ovis aries PE=4 SV=1	tr B2ZA8 4 B2ZA84 _SHEEP	vVVF Ik	56%	19.7	39.27576	Ref	-0.17	0.032	0.47	0.082	0.39	-0.13	0.87	2960	2260	2810	4280	3600	3890	2840	5620	438.3	1311.9	3	0.0028	2.126
Endothelin converting enzyme (Fragment) OS=Ovis aries GN=ECE PE=2 SV=1	tr Q9GM C4 Q9GM C4_SHEEP	fME VMY GTK	77%	37.2	52.83102	Ref	0.13	-0.43	0.058	0.018	0.21	-0.5	0.004	3400	2970	2190	3440	3690	3680	2340	3300	857.5	1712.9	2	0.0195	11.38

Endothelin converting enzyme (Fragment) OS=Ovis aries GN=ECE PE=2 SV=1	tr Q9GM C4 Q9GM C4_SHEEP	fQD Adek	82%	37.8	51.63656	Ref	0.29	-0.63	0.14	-0.076	0.4	-0.94	0.1	47100	49200	28200	54000	51300	62300	25600	52500	730.9	1459.8	2	0.006	4.08
Endothelin converting enzyme (Fragment) OS=Ovis aries GN=ECE PE=2 SV=1	tr Q9GM C4 Q9GM C4_SHEEP	niAG EIIIEI k	95%	49.4	49.50063	Ref	0.26	-0.46	-0.01	-0.19	0.32	-0.57	0.12	3700	3670	2420	3720	3600	4490	2540	4060	607.7	1820.1	3	0.0123	6.761
Endothelin converting enzyme (Fragment) OS=Ovis aries GN=ECE PE=2 SV=1	tr Q9GM C4 Q9GM C4_SHEEP	niAG EIIIEI k	88%	39.7	49.16286	Ref	0.24	-0.79	0.22	-0.083	0.38	-0.9	0.22	1330	1380	736	1670	1480	1780	766	1650	607.7	1820.1	3	0.0083	4.554
Endothelin converting enzyme (Fragment) OS=Ovis aries GN=ECE PE=2 SV=1	tr Q9GM C4 Q9GM C4_SHEEP	niAG EIIIEI k	95%	49	48.80693	Ref	0.25	-0.72	0.09	-0.096	0.39	-0.64	0.047	3180	3090	1710	3360	3250	3980	2030	3250	607.7	1820.1	3	0.0045	2.445

Endothelin converting enzyme (Fragment) OS=Ovis aries GN=ECE PE=2 SV=1	tr Q9GM C4 Q9GM C4_SHEEP	niAG EIIIEI k	95%	51.9	48.8015	Ref	0.33	-0.74	0.23	-0.043	0.21	-0.64	0.097	2450	2760	1420	3130	2850	2970	1720	2840	607.7	1820.1	3	0.0041	2.231
Endothelin converting enzyme (Fragment) OS=Ovis aries GN=ECE PE=2 SV=1	tr Q9GM C4 Q9GM C4_SHEEP	niAG EIIIEI k	86%	38.6	49.16864	Ref	0.093	-0.43	0.27	-0.038	0.12	-0.24	0.079	1840	1970	1490	2710	2410	2360	1920	2370	607.7	1820.1	3	0.0079	4.356
Endothelin converting enzyme (Fragment) OS=Ovis aries GN=ECE PE=2 SV=1	tr Q9GM C4 Q9GM C4_SHEEP	niAG EIIIEI k	90%	41.1	48.6318	Ref	-0.007	-0.26	0.19	0.079	0.06	-0.08	-0.11	695	663	605	925	945	814	770	750	607.7	1820.1	3	0.0025	1.377
Endothelin converting enzyme (Fragment) OS=Ovis aries GN=ECE PE=2 SV=1	tr Q9GM C4 Q9GM C4_SHEEP	niAG EIIIEI kk	76%	26.5	43.54607	Ref	-0.13	-0.56	0.15	0.12	0.31	-0.62	0.33	2590	2250	1810	3320	3600	3570	1950	3770	564.1	2252.4	4	0.0021	0.921

Endothelin converting enzyme (Fragment) OS=Ovis aries GN=ECE PE=2 SV=1	tr Q9GM C4 Q9GM C4_SHEEP	wM DED TR	87%	33.9	45.83912	Ref	0.24	-0.37	-0	0.075	0.29	-1.1	0.03	18400	16900	12000	17400	20200	20400	8420	17700	628.8	1255.6	2	0.0096	7.655
Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5	6 IF4H_H UMAN,sp Q5RBR8 IF4H_PO NAB,sp Q 5X172 IF4 H_RAT,sp Q9WUK2 IF4H_M OUSE,tr E 2RQG8 E 2RQG8_C ANFA,tr F 7HNN0 F 7HNN0_ MACMU,t r F7HNN2 F7HNN2 _MACMU, tr F8WG1 4 F8WG1 4_RAT,tr Q3TG58 Q3TG58_ MOUSE,tr Q3V244 Q3V244_	eALT YDG ALLG DR	95%	57.3	52.69527	Ref	-0.084	-0.27	-0.09	-0.26	0.1	-0.44	-0.12	17700	12600	12000	15300	15000	16800	12100	14900	849.4	1696.9	2	0.0141	8.32

Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5	6 IF4H_HUMAN,sp Q5RBR8 IF4H_PONAB,sp Q5XI72 IF4H_RAT,sp Q9WUK2 IF4H_MOUSE,tr E2RQG8 E2RQG8_CANFA,tr F7HNN0 F7HNN0_MACMU,tr F7HNN2 F7HNN2_MACMU,tr F8WG14 F8WG14_RAT,tr Q3TG58 Q3TG58_MOUSE,tr Q3V244 Q3V244_DR	eALTYDGLLGD	95%	49.4	52.71158	Ref	-0.022	-0.26	-0.03	-0.074	0.24	-0.86	-0.19	9940	7940	7320	9630	10300	11200	5420	8590	849.4	1696.9	2	0.0116	6.812
Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5	6 IF4H_HUMAN,sp Q5RBR8 IF4H_PONAB,sp Q5XI72 IF4H_RAT,sp Q9WUK2 IF4H_MOUSE,tr E2RQG8 E2RQG8_CANFA,tr F7HNN0 F7HNN0_MACMU,tr F7HNN2 F7HNN2_MACMU,tr F8WG14 F8WG14_RAT,tr Q3TG58 Q3TG58_MOUSE,tr Q3V244 Q3V244_DR	eALTYDGLLGD	94%	46.8	52.71082	Ref	0.011	-0.26	-0.09	-0.27	0.2	-0.59	-0.22	6080	4610	4140	5230	5080	6180	3720	4770	849.4	1696.9	2	0.0113	6.671

Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5	6 IF4H_H UMAN,sp Q5RBR8 IF4H_PO NAB,sp Q 5XI72 IF4 H_RAT,sp Q9WUK2 IF4H_M OUSE,tr E 2RQG8 E 2RQG8_C ANFA,tr F 7HNN0 F 7HNN0_ MACMU,t r F7HNN2 F7HNN2 _MACMU, tr F8WG1 4 F8WG1 4_RAT,tr Q3TG58 Q3TG58_ MOUSE,tr Q3V244 Q3V244_ EEER	gSN MDF REPT EEER	83%	36.7	48.9679	Ref	-0.16	-0.38	0.046	-0.24	0.27	-0.57	0.071	67500	54400	50600	76600	69300	86200	50100	77700	667.6	1999.9	3	0.0145	7.259
Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5	6 IF4H_H UMAN,sp Q5RBR8 IF4H_PO NAB,sp Q 5XI72 IF4 H_RAT,sp Q9WUK2 IF4H_M OUSE,tr E 2RQG8 E 2RQG8_C ANFA,tr F 7HNN0 F 7HNN0_ MACMU,t r F7HNN2 F7HNN2 _MACMU, tr F8WG1 4 F8WG1 4_RAT,tr Q3TG58 Q3TG58_ MOUSE,tr Q3V244 Q3V244_ EEER	gSN MDF REPT EEER	83%	35.3	48.90924	Ref	-0.38	-0.53	0.052	-0.008	0.071	-0.38	0.2	1250	850	831	1400	1480	1360	1040	1540	1001	1999.9	2	0.0161	8.041

Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5	6 IF4H_H UMAN,sp Q5RBR8 IF4H_PO NAB,sp Q 5XI72 IF4 H_RAT,sp Q9WUK2 IF4H_M OUSE,tr E 2RQG8 E 2RQG8_C ANFA,tr F 7HNN0 F 7HNN0_ MACMU,t r F7HNN2 F7HNN2 _MACMU, tr F8WG1 4 F8WG1 4_RAT,tr Q3TG58 Q3TG58_ MOUSE,tr Q3V244 Q3V244_ EEER	gSN MDF REPT	68%	31.7	48.91231	Ref	-0.22	-0.34	0.058	-0.13	0.3	-0.67	-0.12	28300	20100	20100	29700	28800	33800	18100	26200	667.6	1999.9	3	0.016	7.979
Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5	6 IF4H_H UMAN,sp Q5RBR8 IF4H_PO NAB,sp Q 5XI72 IF4 H_RAT,sp Q9WUK2 IF4H_M OUSE,tr E 2RQG8 E 2RQG8_C ANFA,tr F 7HNN0 F 7HNN0_ MACMU,t r F7HNN2 F7HNN2 _MACMU, tr F8WG1 4 F8WG1 4_RAT,tr Q3TG58 Q3TG58_ MOUSE,tr Q3V244 Q3V244_ RPR	tVAT PLN QVA NPN SAIF GGA	82%	42.2	54.91729	Ref	-0.033	-0.57	0.008	-0.087	0.044	-0.39	0.029	2700	2240	1680	2810	2900	2770	2150	2850	885.8	2654.4	3	0.0212	7.993

Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5	6 IF4H_H UMAN,sp Q5RBR8 IF4H_PO NAB,sp Q 5XI72 IF4 H_RAT,sp Q9WUK2 IF4H_M OUSE,tr E 2RQG8 E 2RQG8_C ANFA,tr F 7HNN0 F 7HNN0_ MACMU,t r F7HNN2 F7HNN2 _MACMU, tr F8WG1 4 F8WG1 4_RAT,tr Q3TG58 Q3TG58_ MOUSE,tr Q3V244 Q3V244_ RPR	tVAT PLN QVA NPN SAIF GGA	77%	40.2	54.92755	Ref	-0.56	-0.6	0.017	-0.1	0.22	-0.23	0.23	2200	1360	1440	2470	2510	2750	2100	2860	885.8	2654.4	3	0.0223	8.411
Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5	6 IF4H_H UMAN,sp Q5RBR8 IF4H_PO NAB,sp Q 5XI72 IF4 H_RAT,sp Q9WUK2 IF4H_M OUSE,tr E 2RQG8 E 2RQG8_C ANFA,tr F 7HNN0 F 7HNN0_ MACMU,t r F7HNN2 F7HNN2 _MACMU, tr F8WG1 4 F8WG1 4_RAT,tr Q3TG58 Q3TG58_ MOUSE,tr Q3V244 Q3V244_ PR	tVAT PLN QVA NPnS AIFG GAR	84%	43.2	55.05125	Ref	-0.55	-0.19	-0.09	-0.012	0.3	-0.43	0.085	3200	2090	2920	3490	4070	4400	2770	3940	886.1	2655.4	3	0.0195	7.326

<p>Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5</p>	<p>6 IF4H_HUMAN,sp Q5RBR8 IF4H_PONAB,sp Q5XI72 IF4H_RAT,sp Q9WUK2 IF4H_MOUSE,tr E2RQG8 E2RQG8_CANFA,tr F7HNN0 F7HNN0_MACMU,tr F8WG14 F8WG14_RAT,tr Q3TG58 Q3TG58_MOUSE,tr Q3V244 Q3V244_PR</p>	<p>tVAT PLN QVA NPnS AIFG GAR</p>	<p>89%</p>	<p>46.5</p>	<p>54.95908</p>	<p>Ref</p>	<p>-0.33</p>	<p>-0.41</p>	<p>0.039</p>	<p>-0.11</p>	<p>0.22</p>	<p>-0.16</p>	<p>0.094</p>	<p>352</p>	<p>302</p>	<p>309</p>	<p>474</p>	<p>472</p>	<p>516</p>	<p>414</p>	<p>491</p>	<p>886.2</p>	<p>2655.4</p>	<p>3</p>	<p>0.0103</p>	<p>3.882</p>
<p>60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1</p>	<p>9 RL31_HUMAN,sp P62900 RL31_MOUSE,sp P62901 RL31_PIG,sp P62902 RL31_RAT,sp Q1KSC7 RL31_ARMOS,sp Q56JX3 RL31_BOVIN,tr B2R4C1 B2R4C1_HUMAN,tr D3ZU04 D3ZU04_RAT,tr D3ZX87 D3ZX87_RAT,tr D4ABZ9 D4ABZ9_RAT,tr E2R8G3 E2R8G3_NIHK</p>	<p>eYTI NIHK</p>	<p>58%</p>	<p>33</p>	<p>52.2253</p>	<p>Ref</p>	<p>0.29</p>	<p>-0.05</p>	<p>0.42</p>	<p>-0.018</p>	<p>0.31</p>	<p>0.004</p>	<p>0.23</p>	<p>33700</p>	<p>40100</p>	<p>34500</p>	<p>53300</p>	<p>43500</p>	<p>47800</p>	<p>40300</p>	<p>46900</p>	<p>542.7</p>	<p>1624.9</p>	<p>3</p>	<p>0.0109</p>	<p>6.71</p>

60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	9 RL31_H UMAN,sp P62900 RL31_MO USE,sp P6 2901 RL3 1_PIG,sp P62902 R L31_RAT,s p Q1KSC7 RL31_M ARMO,sp Q56JX3 RL31_BO VIN,tr B2 R4C1 B2R 4C1_HUM AN,tr D3Z U04 D3Z U04_RAT, tr D3ZX8 7 D3ZX87 _RAT,tr D 4ABZ9 D4 ABZ9_RAT ,tr E2R8G 3 E2R8G3	iHGV GfK	63%	28.9	49.01845	Ref	0.26	-0.16	0.53	-0.26	0.72	-0.28	0.37	12000	18100	14800	26600	17000	29400	15300	23800	342.2	1364.8	4	0.0176	12.86
60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	9 RL31_H UMAN,sp P62900 RL31_MO USE,sp P6 2901 RL3 1_PIG,sp P62902 R L31_RAT,s p Q1KSC7 RL31_M ARMO,sp Q56JX3 RL31_BO VIN,tr B2 R4C1 B2R 4C1_HUM AN,tr D3Z U04 D3Z U04_RAT, tr D3ZX8 7 D3ZX87 _RAT,tr D 4ABZ9 D4 ABZ9_RAT ,tr E2R8G 3 E2R8G3	iHGV GfK	53%	27.8	47.92665	Ref	0.25	0.068	0.55	-0.05	0.29	-0.16	0.21	36900	43400	41400	64800	47200	52100	40000	51200	456	1364.8	3	0.0023	1.713

60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	9 RL31_H UMAN,sp P62900 RL31_MO USE,sp P6 2901 RL3 1_PIG,sp P62902 R L31_RAT,s p Q1KSC7 RL31_M ARMO,sp Q56JX3 RL31_BO VIN,tr B2 R4C1 B2R 4C1_HUM AN,tr D3Z U04 D3Z U04_RAT, tr D3ZX8 7 D3ZX87 _RAT,tr D 4ABZ9 D4 ABZ9_RAT ,tr E2R8G 3 E2R8G3	iHGV GfK	62%	27.5	47.87347	Ref	0.068	-0.23	0.59	-0.23	0.8	-0.34	0.34	5040	6020	5310	10500	6580	11700	5560	8830	342.2	1364.8	4	0.002	1.439
60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	9 RL31_H UMAN,sp P62900 RL31_MO USE,sp P6 2901 RL3 1_PIG,sp P62902 R L31_RAT,s p Q1KSC7 RL31_M ARMO,sp Q56JX3 RL31_BO VIN,tr B2 R4C1 B2R 4C1_HUM AN,tr D3Z U04 D3Z U04_RAT, tr D3ZX8 7 D3ZX87 _RAT,tr D 4ABZ9 D4 ABZ9_RAT ,tr E2R8G 3 E2R8G3	lyTLV TYVP VTTF k	55%	27.5	49.25735	Ref	0.25	-0.19	0.34	0.23	-0.02	0.045	0.16	487	426	340	554	564	414	452	487	640.1	2556.5	4	0.0101	3.966

60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	9 RL31_H UMAN,sp P62900 RL31_MO USE,sp P6 2901 RL3 1_PIG,sp P62902 R L31_RAT,s p Q1KSC7 RL31_M ARMO,sp Q56JX3 RL31_BO VIN,tr B2 R4C1 B2R 4C1_HUM AN,tr D3Z U04 D3Z U04_RAT, tr D3ZX8 7 D3ZX87 _RAT,tr D 4ABZ9 D4 ABZ9_RAT ,tr E2R8G 3 E2R8G3	nEDE DSP Nk	68%	33.3	51.11124	Ref	0.18	0.23	0.5	-0.13	0.31	-0.23	0.12	7080	7000	7850	10600	7560	8960	6450	8110	828.4	1654.8	2	0.0152	9.2
60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	9 RL31_H UMAN,sp P62900 RL31_MO USE,sp P6 2901 RL3 1_PIG,sp P62902 R L31_RAT,s p Q1KSC7 RL31_M ARMO,sp Q56JX3 RL31_BO VIN,tr B2 R4C1 B2R 4C1_HUM AN,tr D3Z U04 D3Z U04_RAT, tr D3ZX8 7 D3ZX87 _RAT,tr D 4ABZ9 D4 ABZ9_RAT ,tr E2R8G 3 E2R8G3	nLQT VNV DEN	95%	48.3	50.82645	Ref	No Values (0.3656 0732)	No Value s (0.24 79140 5)	No Value s (0.081 0.0591 3191)	No Values (- 0.0591 6005)	No Value s (0.136 71237)	No Value s (0.073 94574)	No Values (0.084 81974)	No Values (0.163 21754)	No Values (0.365607 32)	No Value s (0.24 79140 5)	No Values (0.0813 191)	No Values (- 0.059160 05)	No Value s (0.13 67123 7)	No Values (0.073 94574 74)	No Values (0.084819 74)	725.4	1448.7	2	0.0058	4.026

60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	9 RL31_H UMAN,sp P62900 RL31_MO USE,sp P6 2901 RL3 1_PIG,sp P62902 R L31_RAT,s p Q1KSC7 RL31_M ARMO,sp Q56JX3 RL31_BO VIN,tr B2 R4C1 B2R 4C1_HUM AN,tr D3Z U04 D3Z U04_RAT, tr D3ZX8 7 D3ZX87 _RAT,tr D 4ABZ9 D4 ABZ9_RAT ,tr E2R8G 3 E2R8G3	nLQT VNV DEN	91%	41.5	50.67844	Ref	0.028	0.48	-0.05	0.013	-0.29	0.013	0.037	554	309	458	357	411	290	374	378	725.4	1448.7	2	0.0128	8.827
60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	9 RL31_H UMAN,sp P62900 RL31_MO USE,sp P6 2901 RL3 1_PIG,sp P62902 R L31_RAT,s p Q1KSC7 RL31_M ARMO,sp Q56JX3 RL31_BO VIN,tr B2 R4C1 B2R 4C1_HUM AN,tr D3Z U04 D3Z U04_RAT, tr D3ZX8 7 D3ZX87 _RAT,tr D 4ABZ9 D4 ABZ9_RAT ,tr E2R8G 3 E2R8G3	nLQT VNV DEN	95%	70.8	50.68498	Ref	0.58	-0.02	0.55	-0.028	-0.15	-0.37	0.047	795	863	616	1030	759	608	545	724	725.4	1448.7	2	0.0123	8.482

60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	9 RL31_HUMAN,sp P62900 RL31_MOUSE,sp P62901 RL31_PIG,sp P62902 RL31_RAT,sp Q1KSC7 RL31_MARMO,sp Q56JX3 RL31_BOVIN,tr B2R4C1 B2R4C1_HUMAN,tr D3ZU04 D3ZU04_RAT,tr D3ZX87 D3ZX87_RAT,tr D44ABZ9 D4ABZ9_RAT,tr E2R8G3 E2R8G3	nLQTVNVV	95%	50.7	50.65356	Ref	0.66	-0.36	0.33	-0.07	-0.07	-0.3	0.022	831	775	416	750	627	549	488	605	725.4	1448.7	2	0.0118	8.151
Calpastatin isoform II OS=Ovis aries GN=CAST PE=2 SV=1	tr C3V6M4 C3V6M4_SHEEP	cGEDEETVPSEYR	95%	45.4	44.78394	Ref	-0.41	-0.35	0.034	0.07	0.45	-0.43	0.24	14000	8880	10100	14700	16600	18800	10700	17000	932.4	1862.8	2	0.0113	6.074
Calpastatin isoform II OS=Ovis aries GN=CAST PE=2 SV=1	tr C3V6M4 C3V6M4_SHEEP	dFTVPSDTSSPQFEDAK	81%	39.1	53.52225	Ref	-0.52	-0.51	0.21	0.29	0.76	-1.3	0.24	780	554	603	1120	1300	1570	406	1140	1240	2478.2	2	0.0315	12.7
Calpastatin isoform II OS=Ovis aries GN=CAST PE=2 SV=1	tr C3V6M4 C3V6M4_SHEEP	ePLPPLSEDFLLDALSK	95%	58.8	53.98809	Ref	-0.14	-0.3	-0.03	-0.034	0.38	-0.51	0.35	1560	1260	1220	1650	1810	2110	1190	2140	831.5	2491.4	3	0.0191	7.663

Calpastatin isoform II OS=Ovis aries GN=CAST PE=2 SV=1	tr C3V6M 4 C3V6M 4_SHEEP	kcGE DEET VPSE YR	58%	32.2	51.45927	Ref	-0.22	-0.13	-0.02	0.035	0.35	-0.55	0.22	5420	3980	4610	5570	6370	6930	3880	6560	766	2295.1	3	0.019	8.258
Calpastatin isoform II OS=Ovis aries GN=CAST PE=2 SV=1	tr C3V6M 4 C3V6M 4_SHEEP	sQD EISG GGk	95%	50.1	52.25351	Ref	-0.45	-0.4	0.18	0.08	0.62	-0.9	0.14	7370	4360	4870	8170	8420	10700	3890	7930	793.4	1584.8	2	0.027	17
Calpastatin isoform II OS=Ovis aries GN=CAST PE=2 SV=1	tr C3V6M 4 C3V6M 4_SHEEP	sSS MNP TEAK	73%	36.5	52.60055	Ref	-0.17	-0.33	-0.07	-0.11	0.73	-0.56	0.06	31000	23900	23200	31200	33500	52300	22400	34200	554	1658.9	3	0.0076	4.587
Calpastatin isoform II OS=Ovis aries GN=CAST PE=2 SV=1	tr C3V6M 4 C3V6M 4_SHEEP	tEAS PAA APV PVAE DVP R	89%	45.6	54.05328	Ref	0.23	0.65	-0.37	-0.36	-0.57	0.35	-0.23	629	763	1110	614	683	515	1020	677	694.4	2080.1	3	0.0156	7.496
Calpastatin isoform II OS=Ovis aries GN=CAST PE=2 SV=1	tr C3V6M 4 C3V6M 4_SHEEP	tEAS PAA APV PVAE DVP R	95%	109	54.07374	Ref	-0.38	-0.29	0.23	-0.034	0.51	-0.69	0.43	3640	3020	3470	5620	5150	6560	2970	6420	1041	2080.1	2	0.0139	6.671
Calpastatin isoform II OS=Ovis aries GN=CAST PE=2 SV=1	tr C3V6M 4 C3V6M 4_SHEEP	VTTS SASA Sk	95%	64.8	52.34419	Ref	-0.32	-0.52	0.005	-0.004	0.66	-0.65	0.14	5310	3330	3160	5080	5570	7680	3250	5590	773.9	1545.9	2	0.0143	9.222

Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3	sp Q96AE4 FUBP1_HUMAN, tr B4DT31 B4DT31_HUMAN, tr F1MX51 F1MX51_BOVIN, tr F1S9S9 F1S9S9_PIG, tr F6X888 F6X888_CALJA, tr F6ZHP9 F6ZHP9_CALJA, tr F6ZYU6 F6ZYU6_HORSE, tr F7HB82 F7HB82_MALCMU	cQHA AEIITDL LR	59%	33.9	53.01201	Ref	Value Missing (-0.551455)	Value Missing (-0.36)	0.07	Value Missing (-0.7803505)	Value Missing (-0.35433)	Value Missing (-0.1535)	Value Missing (-0.1134367)	Value Missing (-0.1153505)	Value Missing (-0.1273)	Value Missing (-0.6117)	Value Missing (-0.18319)	3	0.0098	5.362					
Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3	sp Q96AE4 FUBP1_HUMAN, tr B4DT31 B4DT31_HUMAN, tr F1MX51 F1MX51_BOVIN, tr F1S9S9 F1S9S9_PIG, tr F6X888 F6X888_CALJA, tr F6ZHP9 F6ZHP9_CALJA, tr F6ZYU6 F6ZYU6_HORSE, tr F7HB82 F7HB82_MALCMU	cQHA AEIITDL LR	94%	49.9	53.05846	Ref	Value Missing (-0.032)	Value Missing (-0.30811998)	-0.12	-0.093	0.044	-0.27	-0.1	501	390	427	480	460	387	432	611.7	1832	3	0.0072	3.954

<p>Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3</p>	<p>sp Q96AE4 FUBP1_HUMAN,transcript B4DT31 B4DT31_HUMAN,transcript F1MX51 F1MX51_BOVIN,transcript F1S9S9 F1S9S9_PIG,transcript F6X888 F6X888_CALJA,transcript F6ZHP9 F6ZHP9_CALJA,transcript F6ZYU6 F6ZYU6_HORSE,transcript F7HB82 F7HB82_MAITDL</p>	<p>cQH AAEI ITDL LR</p>	<p>89%</p>	<p>44.3</p>	<p>53.06455</p>	<p>Ref</p>	<p>-0.15</p>	<p>-0.26</p>	<p>-0.19</p>	<p>-0.042</p>	<p>0.28</p>	<p>-0.05</p>	<p>0.15</p>	<p>171</p>	<p>178</p>	<p>179</p>	<p>212</p>	<p>258</p>	<p>283</p>	<p>234</p>	<p>268</p>	<p>611.7</p>	<p>1832</p>	<p>3</p>	<p>0.0082</p>	<p>4.462</p>
<p>Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3</p>	<p>sp Q96AE4 FUBP1_HUMAN,transcript B4DT31 B4DT31_HUMAN,transcript F1MX51 F1MX51_BOVIN,transcript F1S9S9 F1S9S9_PIG,transcript F6X888 F6X888_CALJA,transcript F6ZHP9 F6ZHP9_CALJA,transcript F6ZYU6 F6ZYU6_HORSE,transcript F7HB82 F7HB82_MAITDPQ QIDY</p>	<p>gTPQ QIDY AR</p>	<p>74%</p>	<p>35.5</p>	<p>51.77643</p>	<p>Ref</p>	<p>-0.066</p>	<p>-0.27</p>	<p>-0.15</p>	<p>-0.13</p>	<p>0.38</p>	<p>-0.52</p>	<p>0.13</p>	<p>86600</p>	<p>76700</p>	<p>72100</p>	<p>88100</p>	<p>98400</p>	<p>1E+05</p>	<p>68500</p>	<p>107000</p>	<p>726.9</p>	<p>1451.8</p>	<p>2</p>	<p>0.0107</p>	<p>7.382</p>

Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3	sp Q96AE4 FUBP1_HUMAN,transcript B4DT31 B4DT31_HUMAN,transcript F1MX51 F1MX51_BOVIN,transcript F1S9S9 F1S9S9_PIG,transcript F6X888 F6X888_CALJA,transcript F6ZHP9 F6ZHP9_CALJA,transcript F6ZYU6 F6ZYU6_HORSE,transcript F7HB82 F7HB82_MALCMU	iGGD AGT SLNS nDY GYG GQk	95%	60.8	53.71275	Ref	-0.12	-0.19	0.039	-0.38	0.22	-0.34	-0.03	5170	3780	3900	5130	4230	5600	3960	4890	861.8	2582.3	3	0.0161	6.213
Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3	sp Q96AE4 FUBP1_HUMAN,transcript B4DT31 B4DT31_HUMAN,transcript F1MX51 F1MX51_BOVIN,transcript F1S9S9 F1S9S9_PIG,transcript F6X888 F6X888_CALJA,transcript F6ZHP9 F6ZHP9_CALJA,transcript F6ZYU6 F6ZYU6_HORSE,transcript F7HB82 F7HB82_MALCMU	iGGN EGID VPIP R	95%	53.9	52.73966	Ref	-0.12	-0.47	-0.13	-0.14	0.35	-0.6	0.2	11600	8610	7330	10400	11400	14000	7520	13100	821	1639.9	2	0.0124	7.576

Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3	sp Q96AE4 FUBP1_HUMAN, tr B4DT31 B4DT31_HUMAN, tr F1MX51 F1MX51_BOVIN, tr F1S9S9 F1S9S9_PIG, tr F6X88 F6X88_CALJA, tr F6ZHP9 F6ZHP9_CALJA, tr F6ZYU6 F6ZYU6_HORSE, tr F7HB82 F7HB82_MA	qQA AYYA QTSP QG MPQ HPP APQ GQ	87%	43.6	53.47976	Ref	-0.13	0.73	-0.32	-0.12	-0.13	-0.44	-0.22	929	894	1760	958	1210	1050	887	1020	962.5	2884.4	3	0.0179	6.189
Uncharacterized protein OS=Sus scrofa GN=Ssc.53948 PE=3 SV=1	tr F2Z5C1 F2Z5C1_PIG, tr F7CL15 F7CL15_HORSE	gAG TDD HTLI R	95%	54.6	51.51823	Ref	-0.3	-0.32	-0.04	-0.14	-0.41	-0.32	-0.76	78600	58000	61900	84400	86400	63000	69700	51100	487.3	1458.8	3	0.013	8.885
Uncharacterized protein OS=Sus scrofa GN=Ssc.53948 PE=3 SV=1	tr F2Z5C1 F2Z5C1_PIG, tr F7CL15 F7CL15_HORSE	gAG TDD HTLI R	76%	35.8	51.73798	Ref	-0.28	-0.2	-0.33	-0.22	-0.45	-0.33	-0.48	12500	8930	10300	10500	12500	9260	10500	9460	730.4	1458.8	2	0.0112	7.675
Uncharacterized protein OS=Sus scrofa GN=Ssc.53948 PE=3 SV=1	tr F2Z5C1 F2Z5C1_PIG, tr F7CL15 F7CL15_HORSE	gAG TDEK	53%	31	51.10866	Ref	-0.54	-0.19	-0.22	-0.14	-0.42	-0.23	-0.78	23000	12600	17400	19200	22400	16100	19200	13000	429.2	1284.7	3	0.0016	1.27

Uncharacterized protein OS=Sus scrofa GN=Ssc.53948 PE=3 SV=1	tr F2Z5C1 F2Z5C1_PIG,tr F7CL15 F7CL15_HORSE	gLGT DEES ILTLL TSR	95%	91.3	53.74013	Ref	-0.45	-0.41	-0.07	-0.09	-0.4	-0.24	-0.44	3060	2210	2460	3490	3800	2690	3130	2690	1005	2008.1	2	0.0091	4.547
Uncharacterized protein OS=Sus scrofa GN=Ssc.53948 PE=3 SV=1	tr F2Z5C1 F2Z5C1_PIG,tr F7CL15 F7CL15_HORSE	gTVT DFP GFD ER	90%	40.4	50.71632	Ref	-0.55	-0.31	0.009	-0.11	-0.47	-0.4	-0.53	13000	7730	9950	13900	14100	9590	10500	9530	822.9	1643.8	2	0.0118	7.187
Uncharacterized protein OS=Sus scrofa GN=Ssc.53948 PE=3 SV=1	tr F2Z5C1 F2Z5C1_PIG,tr F7CL15 F7CL15_HORSE	IIVAL MkP SR	91%	39.7	46.96278	Ref	0.015	-0.09	-0.78	-0.27	-0.45	-0.32	-1.2	6460	4510	4560	3170	4980	3820	4370	2390	579.4	1735.1	3	0.0078	4.495
Uncharacterized protein OS=Sus scrofa GN=Ssc.53948 PE=3 SV=1	tr F2Z5C1 F2Z5C1_PIG,tr F7CL15 F7CL15_HORSE	qEIA VAFk	81%	37.2	50.33231	Ref	-0.19	-0.32	-0.21	-0.25	-0.41	-0.14	-0.49	9230	8350	8310	10100	10700	8430	10600	8230	505.3	1512.9	3	0.0037	2.474
Uncharacterized protein OS=Sus scrofa GN=Ssc.53948 PE=3 SV=1	tr F2Z5C1 F2Z5C1_PIG,tr F7CL15 F7CL15_HORSE	sIPA YLAE TLYY AMK	94%	52.2	54.53184	Ref	0.12	-0.11	-0.64	-0.17	-0.74	-0.14	-0.64	232	241	222	174	264	155	247	173	781.4	2341.3	3	0.0144	6.144
Uncharacterized protein OS=Sus scrofa GN=Ssc.53948 PE=3 SV=1	tr F2Z5C1 F2Z5C1_PIG,tr F7CL15 F7CL15_HORSE	sIPA YLAE TLYY Amk	94%	51.1	54.52113	Ref	-0.4	-0.31	0.093	-0.22	-0.55	-0.26	-0.81	527	342	393	585	520	361	459	312	786.8	2357.3	3	0.0148	6.286

ATP synthase subunit beta, mitochondrial OS=Bos taurus GN=ATP5B PE=1 SV=2	sp P00829 ATPB_BOVIN, tr F1SLA0 F1SLA0_PIG	aDKL AEE HS	55%	32.6	52.65596	Ref	0.16	-0.24	0.31	-0.48	-0.09	-0.07	-0.17	3630	3770	3080	5090	3240	3710	3920	3640	804.4	1606.9	2	0.0195	12.13
ATP synthase subunit beta, mitochondrial OS=Bos taurus GN=ATP5B PE=1 SV=2	sp P00829 ATPB_BOVIN, tr F1SLA0 F1SLA0_PIG	iGLF GGA GVG k	94%	47.8	49.84955	Ref	0.22	-0.32	-0.13	-0.41	-0.13	0.056	-0.02	10500	9850	7320	9410	8550	9040	10800	10100	528.7	1583	3	0.0045	2.847
ATP synthase subunit beta, mitochondrial OS=Bos taurus GN=ATP5B PE=1 SV=2	sp P00829 ATPB_BOVIN, tr F1SLA0 F1SLA0_PIG	iMD PNIV GSE HYD VAR	86%	42.2	53.25817	Ref	0.2	0.081	-0.07	-0.22	-0.12	-0.01	-0.13	5240	6500	6470	6550	6480	6060	6840	6240	707.4	2119.1	3	0.0092	4.338
ATP synthase subunit beta, mitochondrial OS=Bos taurus GN=ATP5B PE=1 SV=2	sp P00829 ATPB_BOVIN, tr F1SLA0 F1SLA0_PIG	iMN VIGE PIDE R	86%	40.5	52.79665	Ref	0.49	-0.14	0.097	-0.4	-0.31	-0.07	-0.42	8960	11000	7730	10200	8000	7430	9130	7110	845.5	1688.9	2	0.0055	3.241
ATP synthase subunit beta, mitochondrial OS=Bos taurus GN=ATP5B PE=1 SV=2	sp P00829 ATPB_BOVIN, tr F1SLA0 F1SLA0_PIG	iVLE VAQ HLGE STVR	95%	61.3	52.95903	Ref	0.26	-0.19	0.009	-0.22	-0.27	-0.07	-0.18	896	899	710	918	864	727	871	805	652.4	1954.1	3	0.0078	3.984

ATP synthase subunit beta, mitochondrial OS=Bos taurus GN=ATP5B PE=1 SV=2	sp P00829 ATPB_B OVIN,tr F1 1SLA0 F1 SLA0_PIG	IVLE VAQ HLGE STVR	82%	40.2	52.94601	Ref	0.22	-0.18	-0.07	0.069	0.01	-0.04	-0.42	252	294	242	293	355	297	299	229	652.4	1954.1	3	0.0076	3.892
ATP synthase subunit beta, mitochondrial OS=Bos taurus GN=ATP5B PE=1 SV=2	sp P00829 ATPB_B OVIN,tr F1 1SLA0 F1 SLA0_PIG	tVLI MELI NNV AK	88%	41.3	50.81729	Ref	-0.068	-0.23	0.2	0.11	-0.81	0.13	-0.43	234	161	157	237	245	113	226	152	689.4	2065.2	3	0.0163	7.881
ATP synthase subunit beta, mitochondrial OS=Bos taurus GN=ATP5B PE=1 SV=2	sp P00829 ATPB_B OVIN,tr F1 1SLA0 F1 SLA0_PIG	tVLI MELI NNV AK	65%	31.9	49.75395	Ref	0.29	-0.32	0.2	-0.44	-0.47	0.21	-0.28	253	262	186	300	212	181	303	214	689.4	2065.2	3	#####	0.346
ATP synthase subunit beta, mitochondrial OS=Bos taurus GN=ATP5B PE=1 SV=2	sp P00829 ATPB_B OVIN,tr F1 1SLA0 F1 SLA0_PIG	vALV YGQ MNE PPG AR	69%	36	53.43728	Ref	0.31	-0.23	0.25	-0.35	-0.18	-0.17	-0.3	3680	3960	2960	4630	3360	3300	3470	3150	953.5	1905	2	0.008	4.212

14-3-3 protein beta/alpha OS=Pongo abelii GN=YWHAB PE=3 SV=1	9 1433B_PONAB,sp P31946 1433B_HUMAN,sp P35213 1433B_RAT,sp P68250 1433B_BOVIN,sp P68251 1433B_SHEEP,sp Q4R572 1433B_MAFCA,tr B5BU24 B5BU24_HUMAN,tr D2H6L9 D2H6L9_AILME,tr F1MNP5 F1MNP5_BOVIN,tr F1PKW7 F1PKW7_CA	aVTE QGH ELSN EER	95%	61.2	51.77721	Ref	0.34	-0.02	0.11	-0.013	0.4	-0.28	0.32	33600	37200	31400	38500	39100	45400	29600	44700	635	1901.9	3	0.0143	7.524
14-3-3 protein beta/alpha OS=Pongo abelii GN=YWHAB PE=3 SV=1	9 1433B_PONAB,sp P31946 1433B_HUMAN,sp P35213 1433B_RAT,sp P68250 1433B_BOVIN,sp P68251 1433B_SHEEP,sp Q4R572 1433B_MAFCA,tr B5BU24 B5BU24_HUMAN,tr D2H6L9 D2H6L9_AILME,tr F1MNP5 F1MNP5_BOVIN,tr F1PKW7 F1PKW7_CA	aVTE QGH ELSN EER	95%	53	51.80719	Ref	0.45	-0.44	0.25	0.017	0.58	-0.5	0.21	2970	3420	2000	3620	3390	4380	2170	3500	952	1901.9	2	0.0132	6.917

14-3-3 protein beta/alpha OS=Pongo abelii GN=YWHAB PE=3 SV=1	9 1433B_PONAB,sp P31946 1433B_HUMAN,sp P35213 1433B_RAT,sp P68250 1433B_BOVIN,sp P68251 1433B_SHEEP,sp Q4R572 1433B_MAFCA,tr B5BU24 B5BU24_HUMAN,tr D2H6L9 D2H6L9_AILME,tr F1MNP5 F1MNP5_BOVIN,tr F1PKW7 F1PKW7_CA	aVTE QGH ELSn EER	86%	40.2	50.95776	Ref	0.81	-0.13	-0.08	-0.1	0.4	-0.08	0.13	20400	38800	21900	25500	27600	34000	25700	29300	635.3	1902.9	3	0.0153	8.014
14-3-3 protein beta/alpha OS=Pongo abelii GN=YWHAB PE=3 SV=1	9 1433B_PONAB,sp P31946 1433B_HUMAN,sp P35213 1433B_RAT,sp P68250 1433B_BOVIN,sp P68251 1433B_SHEEP,sp Q4R572 1433B_MAFCA,tr B5BU24 B5BU24_HUMAN,tr D2H6L9 D2H6L9_AILME,tr F1MNP5 F1MNP5_BOVIN,tr F1PKW7 F1PKW7_CA	aVTE QGH ELSn EER	75%	35.8	51.10782	Ref	0.81	-0.14	-0.12	-0.076	0.41	-0.07	-0.05	22500	37100	20800	23700	26900	32800	24600	24700	635.3	1902.9	3	0.0123	6.469

14-3-3 protein beta/alpha OS=Pongo abelii GN=YWHAB PE=3 SV=1	9 1433B_PONAB,sp P31946 1433B_HUMAN,sp P35213 1433B_RA T,sp P68250 1433B_BOVIN,sp P68251 1433B_SHEEP,sp Q4R572 1433B_MA CFA,tr B5BU24 B5BU24_HUMAN,tr D2H6L9 D2H6L9_AILME,tr F1MNP5 F1MNP5_BOVIN,tr F1PKW7 F1PKW7_CA	qTTV SNS QQA YQE AFEI	Sk	93%	51.7	55.22601	Ref	0.55	-0.2	0.11	0.04	0.29	-0.18	0.096	2600	3040	1970	2730	2870	2980	2240	2700	923.1	2766.4	3	0.021	7.58
14-3-3 protein beta/alpha OS=Pongo abelii GN=YWHAB PE=3 SV=1	9 1433B_PONAB,sp P31946 1433B_HUMAN,sp P35213 1433B_RA T,sp P68250 1433B_BOVIN,sp P68251 1433B_SHEEP,sp Q4R572 1433B_MA CFA,tr B5BU24 B5BU24_HUMAN,tr D2H6L9 D2H6L9_AILME,tr F1MNP5 F1MNP5_BOVIN,tr F1PKW7 F1PKW7_CA	vSSI	EQK	86%	38.5	50.65972	Ref	0.53	-0.27	0.27	0.11	0.31	-0.32	0.11	26200	31900	20000	32500	32100	32200	21700	29000	756.5	1510.9	2	0.0046	3.051

14-3-3 protein beta/alpha OS=Pongo abelii GN=YWHAB PE=3 SV=1	9 1433B_ PONAB,sp P31946 1433B_H UMAN,sp P35213 1433B_RA T,sp P682 50 1433B _BOVIN,s p P68251 1433B_S HEEP,sp Q4R572 1 433B_MA CFA,tr B5 BU24 B5 BU24_HU MAN,tr D 2H6L9 D2 H6L9_AIL ME,tr F1 MNP5 F1 MNP5_BO VIN,tr F1 PKW7 F1 PKW7_CA	YLSE VAS GDN k	95%	61.7	53.50502	Ref	0.38	-0.17	0.37	0.094	0.29	-0.26	0.14	8030	9090	6750	11100	10000	10100	7150	9390	896	1790	2	0.0155	8.647
60S ribosomal protein L12 OS=Canis familiaris GN=RPL12 PE=1 SV=1	8 RL12_C ANFA,sp P30050 R L12_HUM AN,sp P3 5979 RL1 2_MOUSE ,sp P6128 4 RL12_B OVIN,tr D 2H3Y2 D2 H3Y2_AIL ME,tr F1 RS17 F1R S17_PIG,t r F2X246 F2X246_ AILME,tr F6RXN0 F 6RXN0_C ALJA,tr F 6T1A4 F6 T1A4_HO RSE,tr F7 G7L4 F7G 7L4_MAC MU,tr F7	cTG GEV GAT SALA Pk	90%	45.6	53.79005	Ref	0.36	0.072	0.24	0.039	0.006	0.26	0.21	17600	18500	16400	20800	19800	16900	21100	20300	672.7	2015	3	0.0223	11.07

60S ribosomal protein L12 OS=Canis familiaris GN=RPL12 PE=1 SV=1	8 RL12_C ANFA,sp P30050 R L12_HUM AN,sp P3 5979 RL1 2_MOUSE ,sp P6128 4 RL12_B OVIN,tr D 2H3Y2 D2 H3Y2_AIL ME,tr F1 RS17 F1R S17_PIG,t r F2X246 F2X246_ AILME,tr F6RXNO F 6RXNO_C ALJA,tr F 6T1A4 F6 T1A4_HO RSE,tr F7 G7L4 F7G 7L4_MAC NVD MU,tr F7 GR	eILG TAQ SVGc NVD	95%	60.6	51.99547	Ref	0.46	-0.05	0.43	-0.015	0.23	-0.1	0.31	5280	6690	5070	7960	6450	6690	5560	7290	985	1968	2	0.014	7.119
60S ribosomal protein L12 OS=Canis familiaris GN=RPL12 PE=1 SV=1	8 RL12_C ANFA,sp P30050 R L12_HUM AN,sp P3 5979 RL1 2_MOUSE ,sp P6128 4 RL12_B OVIN,tr D 2H3Y2 D2 H3Y2_AIL ME,tr F1 RS17 F1R S17_PIG,t r F2X246 F2X246_ AILME,tr F6RXNO F 6RXNO_C ALJA,tr F 6T1A4 F6 T1A4_HO RSE,tr F7 G7L4 F7G 7L4_MAC DEIV MU,tr F7 NIAR	hSG NITF DEIV	86%	42.6	53.68021	Ref	0.28	0.036	0.12	0.035	0.25	0.041	0.32	3960	3620	3320	3940	4110	4170	3760	4540	664	1989	3	0.0118	5.941

60S ribosomal protein L12 OS=Canis familiaris GN=RPL12 PE=1 SV=1	8 RL12_C ANFA,sp P30050 R L12_HUM AN,sp P3 5979 RL1 2_MOUSE ,sp P6128 4 RL12_B OVIN,tr D 2H3Y2 D2 H3Y2_AIL ME,tr F1 RS17 F1R S17_PIG,t r F2X246 F2X246_ AILME,tr F6RXNO F 6RXNO_C ALJA,tr F 6T1A4 F6 T1A4_HO RSE,tr F7 G7L4 F7G 7L4_MAC MU,tr F7	hSG NITF DEIV NIAR	90%	44	53.70335	Ref	0.18	-0	0.51	-0.006	0.19	0.05	0.24	525	483	462	742	571	572	542	611	498.3	1989	4	0.0124	6.256
60S ribosomal protein L12 OS=Canis familiaris GN=RPL12 PE=1 SV=1	8 RL12_C ANFA,sp P30050 R L12_HUM AN,sp P3 5979 RL1 2_MOUSE ,sp P6128 4 RL12_B OVIN,tr D 2H3Y2 D2 H3Y2_AIL ME,tr F1 RS17 F1R S17_PIG,t r F2X246 F2X246_ AILME,tr F6RXNO F 6RXNO_C ALJA,tr F 6T1A4 F6 T1A4_HO RSE,tr F7 G7L4 F7G 7L4_MAC MU,tr F7	hSG NITF DEIV NIAR	95%	56.9	53.90456	Ref	0.46	0.15	0.27	-0.063	0.21	-0.02	0.49	1990	3070	2680	3270	2860	3020	2690	3810	664	1989.1	3	0.0103	5.184

60S ribosomal protein L12 OS=Canis familiaris GN=RPL12 PE=1 SV=1	8 RL12_C ANFA,sp P30050 R L12_HUM AN,sp P3 5979 RL1 2_MOUSE ,sp P6128 4 RL12_B OVIN,tr D 2H3Y2 D2 H3Y2_AIL ME,tr F1 RS17 F1R S17_PIG,t r F2X246 F2X246_ AILME,tr F6RXNO F 6RXNO_C ALJA,tr F 6T1A4 F6 T1A4_HO RSE,tr F7 G7L4 F7G 7L4_MAC MU,tr F7	hSG NITF DEIV NIAR	93%	49	53.68226	Ref	0.51	-0.17	0.28	0.31	-0.03	0.23	0.13	207	265	180	276	312	214	268	249	664	1989	3	0.0107	5.399
60S ribosomal protein L12 OS=Canis familiaris GN=RPL12 PE=1 SV=1	8 RL12_C ANFA,sp P30050 R L12_HUM AN,sp P3 5979 RL1 2_MOUSE ,sp P6128 4 RL12_B OVIN,tr D 2H3Y2 D2 H3Y2_AIL ME,tr F1 RS17 F1R S17_PIG,t r F2X246 F2X246_ AILME,tr F6RXNO F 6RXNO_C ALJA,tr F 6T1A4 F6 T1A4_HO RSE,tr F7 G7L4 F7G 7L4_MAC MU,tr F7	iGPL GLSP k	86%	35.4	46.22856	Ref	0.39	0.001	0.31	0.045	0.29	-0.02	0.24	13300	15200	12600	17500	16000	16600	14000	16600	497.3	1488.9	3	0.0043	2.87

60S ribosomal protein L12 OS=Canis familiaris GN=RPL12 PE=1 SV=1	8 RL12_C ANFA,sp P30050 R L12_HUM AN,sp P3 5979 RL1 2_MOUSE ,sp P6128 4 RL12_B OVIN,tr D 2H3Y2 D2 H3Y2_AIL ME,tr F1 RS17 F1R S17_PIG,t r F2X246 F2X246_ AILME,tr F6RXNO F 6RXNO_C ALJA,tr F 6T1A4 F6 T1A4_HO RSE,tr F7 G7L4 F7G 7L4_MAC MU,tr F7	qAQI EVVP SASA Llik	62%	29.6	50.09238	Ref	-0.24	-0.14	0.24	0.18	0.15	-0.07	0.52	3030	1590	1850	2700	2860	2450	2190	3280	569.6	2274.4	4	0.0206	9.059
60S ribosomal protein L12 OS=Canis familiaris GN=RPL12 PE=1 SV=1	8 RL12_C ANFA,sp P30050 R L12_HUM AN,sp P3 5979 RL1 2_MOUSE ,sp P6128 4 RL12_B OVIN,tr D 2H3Y2 D2 H3Y2_AIL ME,tr F1 RS17 F1R S17_PIG,t r F2X246 F2X246_ AILME,tr F6RXNO F 6RXNO_C ALJA,tr F 6T1A4 F6 T1A4_HO RSE,tr F7 G7L4 F7G 7L4_MAC MU,tr F7	qAQI EVVP SASA Llik	92%	44.3	49.75804	Ref	0.35	-0.09	0.22	0.11	0.21	0.16	0.33	9320	10600	8490	11800	12100	11300	11400	12700	759.1	2274.4	3	0.0158	6.965

Heat shock 70kD protein binding protein OS=Bos taurus GN=ST13 PE=2 SV=1	tr A7E3S8 A7E3S8_BOVIN	alDL FTDA Ik	91%	45.2	51.96033	Ref	0.018	-0.51	-0.01	-0.14	0.24	-0.48	0.19	6630	4830	3630	5770	5820	6580	4180	6630	572.3	1714	3	0.0181	10.56
Heat shock 70kD protein binding protein OS=Bos taurus GN=ST13 PE=2 SV=1	tr A7E3S8 A7E3S8_BOVIN	alEIN PDS AQP Yk	95%	50.7	53.92761	Ref	0.19	-0.48	0.21	0.053	0.26	-0.76	0.027	7340	7290	4980	8990	8890	8970	4610	7900	1028	2053.1	2	0.0156	7.594
Heat shock 70kD protein binding protein OS=Bos taurus GN=ST13 PE=2 SV=1	tr A7E3S8 A7E3S8_BOVIN	iPPA AHk	66%	32.4	50.18726	Ref	-0.071	-0.34	-0.05	-0.18	0.11	0.077	0.26	23400	20600	18600	25500	25700	27400	28000	31500	447.9	1340.8	3	0.0244	18.18
Heat shock 70kD protein binding protein OS=Bos taurus GN=ST13 PE=2 SV=1	tr A7E3S8 A7E3S8_BOVIN	iPPA AHk	76%	33.7	48.79326	Ref	0.11	-0.22	0.043	-0.061	0.23	-0.33	-0.04	45800	42800	37100	49900	51200	54700	38600	47000	448	1340.8	3	0.0055	4.068
Heat shock 70kD protein binding protein OS=Bos taurus GN=ST13 PE=2 SV=1	tr A7E3S8 A7E3S8_BOVIN	iAILY Ak	55%	24.3	44.31911	Ref	0.17	-0.55	0.21	-0.005	0.33	-0.45	-0.04	11200	11700	7660	14600	13900	15300	9260	12200	700.5	1398.9	2	0.0014	0.979

Heat shock 70kD protein binding protein OS=Bos taurus GN=ST13 PE=2 SV=1	tr A7E3S8 A7E3S8_BOVIN	IDYD EDAS AML k	95%	59.4	53.09852	Ref	0.13	-0.45	0.085	-0.064	0.18	-0.54	0.078	23100	19200	13900	22700	22600	23400	14800	22500	660.3	1978	3	0.0165	8.314
Heat shock 70kD protein binding protein OS=Bos taurus GN=ST13 PE=2 SV=1	tr A7E3S8 A7E3S8_BOVIN	IDYD EDAS AML k	82%	40.4	53.26069	Ref	0.2	-0.08	0.088	-0.13	0.11	-0.39	-0.13	8640	8360	7440	9400	8920	9160	6800	8070	660.3	1978	3	0.0123	6.192
Heat shock 70kD protein binding protein OS=Bos taurus GN=ST13 PE=2 SV=1	tr A7E3S8 A7E3S8_BOVIN	vAAI DAL NDG ELQk	88%	44.1	53.54222	Ref	-0.012	-0.09	0.058	-0.066	-0.06	0.006	0.19	7590	7870	8080	10100	10200	8920	9750	11000	689.1	2064.1	3	0.0184	8.889
Heat shock 70kD protein binding protein OS=Bos taurus GN=ST13 PE=2 SV=1	tr A7E3S8 A7E3S8_BOVIN	vAAI DAL NDG ELQk	63%	35.1	53.45709	Ref	0.014	-0.2	0.19	-0.18	-0	-0.07	0.25	5380	5740	5370	7880	6710	6650	6650	8190	689.1	2064.2	3	0.0163	7.915
Microtubule-associated protein 4 OS=Bos taurus GN=MAP4 PE=1 SV=1	sp P36225 MAP4_BOVIN, tr F1MAZ1 F1MAZ1_BOVIN, tr F1MAZ3 F1MAZ3_BOVIN	dVES SIES DMA LVk	81%	41	54.10178	Ref	-0.14	-0.22	-0.27	-0.32	-0.3	-0.4	-0.4	4670	3940	4050	4390	4650	4130	4020	4000	711	2130.1	3	0.0193	9.076

Microtubule-associated protein 4 OS=Bos taurus GN=MAP4 PE=1 SV=1	sp P36225 MAP4_BOVIN, tr F1MAZ1 F1MAZ1_BOVIN, tr F1MAZ3 F1MAZ3_BOVIN	dVES SIES DMA LVk	53%	34.1	54.20454	Ref	-0.22	-0.31	-0.37	-0.36	-0.25	-0.52	-0.43	3740	2400	2440	2630	2920	2760	2370	2520	711.1	2130.1	3	0.0058	2.714
Microtubule-associated protein 4 OS=Bos taurus GN=MAP4 PE=1 SV=1	sp P36225 MAP4_BOVIN, tr F1MAZ1 F1MAZ1_BOVIN, tr F1MAZ3 F1MAZ3_BOVIN	dVVL PVQ TEET AVk	85%	41.3	52.97507	Ref	-0.6	0.09	-0.29	-0.3	-0.22	-0.42	-0.43	12200	7260	12700	10900	12000	11100	10100	9920	712.7	2135.2	3	0.0173	8.085
Microtubule-associated protein 4 OS=Bos taurus GN=MAP4 PE=1 SV=1	sp P36225 MAP4_BOVIN, tr F1MAZ1 F1MAZ1_BOVIN, tr F1MAZ3 F1MAZ3_BOVIN	hSLP TDE DSVL ELEE Qk	89%	46.7	54.9865	Ref	-0.49	0.074	-0.41	-0.49	-0.19	-0.36	-0.14	2320	1640	2630	2110	2210	2370	2200	2530	859.8	2576.3	3	0.015	5.817
Microtubule-associated protein 4 OS=Bos taurus GN=MAP4 PE=1 SV=1	sp P36225 MAP4_BOVIN, tr F1MAZ1 F1MAZ1_BOVIN, tr F1MAZ3 F1MAZ3_BOVIN	sTTT SSVk	79%	36.6	51.70696	Ref	-0.73	-0.13	-0.44	-0.26	-0.07	-0.47	-0.19	11300	5720	9430	8550	10600	10600	8410	10100	709.9	1417.8	2	0.0023	1.617
Microtubule-associated protein 4 OS=Bos taurus GN=MAP4 PE=1 SV=1	sp P36225 MAP4_BOVIN, tr F1MAZ1 F1MAZ1_BOVIN, tr F1MAZ3 F1MAZ3_BOVIN	sTTT SSVk	87%	39.5	51.48186	Ref	-0.74	0.034	-0.39	-0.21	-0.05	-0.54	-0.44	18200	9250	17200	14400	17900	17500	13000	13900	709.9	1417.8	2	0.0045	3.168
Microtubule-associated protein 4 OS=Bos taurus GN=MAP4 PE=1 SV=1	sp P36225 MAP4_BOVIN, tr F1MAZ1 F1MAZ1_BOVIN, tr F1MAZ3 F1MAZ3_BOVIN	tDYI PLLD VDEK	83%	40.1	53.79158	Ref	-0.85	-0.11	-0.42	-0.25	-0.03	-0.48	-0.28	9190	4140	7480	6790	8430	8570	6520	7470	1015	2028.1	2	0.0165	8.108

Microtubule-associated protein 4 OS=Bos taurus GN=MAP4 PE=1 SV=1	sp P36225 MAP4_BOVIN,tr F1MAZ1 F1MAZ1_BOVIN,tr F1MAZ3 F1MAZ3_BOVIN	vGSL DNL GHL PAG GAV k	68%	35.9	53.16507	Ref	-0.56	-0.24	-0.38	-0.18	-0.04	-0.57	-0.19	22600	13800	18700	19100	24100	23200	16800	21800	733.8	2198.2	3	0.0229	10.4
Microtubule-associated protein 4 OS=Bos taurus GN=MAP4 PE=1 SV=1	sp P36225 MAP4_BOVIN,tr F1MAZ1 F1MAZ1_BOVIN,tr F1MAZ3 F1MAZ3_BOVIN	vGSL DNL GHL PAG GAV k	95%	52.3	53.16807	Ref	-0.57	-0.15	-0.28	-0.31	-0.08	-0.45	-0.35	17400	10200	14800	15200	16300	16800	13500	14400	733.8	2198.2	3	0.0234	10.65
Superoxide dismutase (Fragment) OS=Capra hircus GN=MnSOD PE=2 SV=1	tr C6KGS6 C6KGS6_CAPHI,tr C8BKD6 C8BKD6_SHEEP	gDVT AQIA LQP ALK	95%	57	51.10718	Ref	0.38	-0.66	-0.03	-0.36	-0.05	-0.89	-0.05	37400	36400	19200	33200	29200	31600	18400	32800	678.4	2032.2	3	0.0162	7.975
Superoxide dismutase (Fragment) OS=Capra hircus GN=MnSOD PE=2 SV=1	tr C6KGS6 C6KGS6_CAPHI,tr C8BKD6 C8BKD6_SHEEP	gDVT AQIA LQP ALK	95%	77.5	50.99767	Ref	0.38	-0.76	0.13	-0.16	-0.06	-1.1	0.033	4430	5020	2470	5140	4610	4340	2200	4780	1017	2032.2	2	0.0127	6.236
Superoxide dismutase (Fragment) OS=Capra hircus GN=MnSOD PE=2 SV=1	tr C6KGS6 C6KGS6_CAPHI,tr C8BKD6 C8BKD6_SHEEP	gELL EAIk	94%	47.2	49.69663	Ref	0.35	-0.57	0.18	-0.37	-0.03	-0.89	-0.23	3340	3300	1910	3570	2690	2990	1720	2700	494.3	1479.9	3	0.0045	3.054

Superoxide dismutase (Fragment) OS=Capra hircus GN=MnSOD PE=2 SV=1	tr C6KGS6 C6KGS6_CAPHI,tr C8BKD6 C8BKD6_S HEEP	gELL EAIk	94%	47.3	49.3681	Ref	0.57	-1.1	0.18	-0.42	-0.12	-0.93	-0.16	2540	2830	998	2640	1910	2060	1220	2070	494.3	1479.9	3	0.0023	1.576
Superoxide dismutase (Fragment) OS=Capra hircus GN=MnSOD PE=2 SV=1	tr C6KGS6 C6KGS6_CAPHI,tr C8BKD6 C8BKD6_S HEEP	hHA AYV NNL NVA EEK	92%	48.3	54.48165	Ref	0.029	-0.33	0.037	-0.38	0.071	-0.52	0.021	4680	4290	3620	5260	4340	5180	3590	5190	773.1	2316.2	3	0.0174	7.504
Superoxide dismutase (Fragment) OS=Capra hircus GN=MnSOD PE=2 SV=1	tr C6KGS6 C6KGS6_CAPHI,tr C8BKD6 C8BKD6_S HEEP	hHA AYVn NLN VAEE k	64%	36.5	54.63757	Ref	-0.13	0.01	-0.18	-0.21	0.024	-0.59	-0.06	3510	2720	3240	3180	3440	3530	2410	3460	773.4	2317.2	3	0.006	2.575
Superoxide dismutase (Fragment) OS=Capra hircus GN=MnSOD PE=2 SV=1	tr C6KGS6 C6KGS6_CAPHI,tr C8BKD6 C8BKD6_S HEEP	hHA AYVn NLN VAEE k	95%	50.3	54.50546	Ref	0.063	-0.36	-0.05	-0.023	-0.09	-0.45	-0.05	30400	29900	24100	33700	37700	31500	25600	33500	580.3	2317.2	4	0.0167	7.21
Superoxide dismutase (Fragment) OS=Capra hircus GN=MnSOD PE=2 SV=1	tr C6KGS6 C6KGS6_CAPHI,tr C8BKD6 C8BKD6_S HEEP	hHA AYVn NLN VAEE k	95%	75.2	54.51279	Ref	-0.065	-0.36	-0.17	-0.14	-0.01	-0.29	0.29	3850	4120	3650	4670	5250	5020	4310	6410	773.4	2317.2	3	0.0148	6.367

Superoxide dismutase (Fragment) OS=Capra hircus GN=MnSOD PE=2 SV=1	tr C6KGS6 C6KGS6_CAPHI, tr C8BKD6 C8BKD6_SHEEP	hHAAYVnNLNVAEEK	88%	43.2	54.5798	Ref	0.16	-0.22	-0.1	-0.2	-0.16	-0.1	-0.12	18400	21900	18300	22300	23000	20600	22400	21900	580.3	2317.2	4	0.0101	4.363
Ubiquilin-1 OS=Pongo abelii GN=UBQLN1 PE=2 SV=1	4 UBQL1_PONAB,sp Q9UMX0 UBQL1_HUMAN, tr B3KNI2 B3KNI2_HUMAN, tr B3KNI8 B3KNI8_HUMAN, tr C5ISB7 C5ISB7_SHEEP, tr D2H0N7 D2H0N7_AI LME, tr E2RPC0 E2RPCO_CANFA, tr F1N1A3 F1N1A3_BOVIN, tr F6VA D6 F6VA D6_ORNA N, tr F6VA E7 F6VAE	aLSNLESIPGGYNALR	88%	42.4	53.79146	Ref	-0.061	-0.36	0.037	-0.094	0.19	-0.26	0.079	3170	2990	2640	3900	3920	4170	3190	4000	990	1978.1	2	0.0067	3.378

Ubiquilin-1 OS=Pongo abelii GN=UBQLN1 PE=2 SV=1	4 UBQL1_PONAB,s p Q9UMX 0 UBQL1_HUMAN, tr B3KNI2 B3KNI2_HUMAN,t r B3KNI8 B3KNI8_HUMAN,t r C5ISB7 C5ISB7_S HEEP,tr D2H0N7 D2H0N7_AI LME,tr E2RPC0 E2RPCO_CAN FA,tr F1N1A3 F1N1A3_BOVI N,tr F6VA D6 F6VA D6_ORNA N,tr F6VA E7 F6VAE	aLSN LESIP GGy NAL R	63%	35.4	53.74754	Ref	-0.26	-0.35	0.2	-0.17	0.16	-0.53	0.073	3440	2270	2320	3820	3260	3570	2300	3480	761.8	2282.3	3	0.0151	6.628
Ubiquilin-1 OS=Pongo abelii GN=UBQLN1 PE=2 SV=1	4 UBQL1_PONAB,s p Q9UMX 0 UBQL1_HUMAN, tr B3KNI2 B3KNI2_HUMAN,t r B3KNI8 B3KNI8_HUMAN,t r C5ISB7 C5ISB7_S HEEP,tr D2H0N7 D2H0N7_AI LME,tr E2RPC0 E2RPCO_CAN FA,tr F1N1A3 F1N1A3_BOVI N,tr F6VA D6 F6VA D6_ORNA N,tr F6VA E7 F6VAE	ILGS QPS	74%	32.5	48.98917	Ref	0.068	-0.54	0.056	-0.2	0.21	-0.21	-0.07	1160	1050	750	1270	1180	1360	1070	1170	503.3	1004.6	2	0.0064	6.401

Ubiquilin-1 OS=Pongo abelii GN=UBQLN1 PE=2 SV=1	4 UBQL1 _PONAB,s p Q9UMX 0 UBQL1 _HUMAN, tr B3KNI2 B3KNI2_ HUMAN,t r B3KNI8 B3KNI8_ HUMAN,t r C5ISB7 C5ISB7_S HEEP,tr D 2H0N7 D 2H0N7_AI LME,tr E2 RPC0 E2R PCO_CAN FA,tr F1N 1A3 F1N1 A3_BOVI N,tr F6VA D6 F6VA D6_ORNA N,tr F6VA E7 F6VAE	nPEI SHM LNN PDI MR	95%	64.5	53.07597	Ref	0.1	-0.16	-0.04	-0.25	-0.03	-0.11	-0.14	13600	12300	11200	13600	13000	13200	13000	12600	695.7	2084	3	0.015	7.197
Ubiquilin-1 OS=Pongo abelii GN=UBQLN1 PE=2 SV=1	4 UBQL1 _PONAB,s p Q9UMX 0 UBQL1 _HUMAN, tr B3KNI2 B3KNI2_ HUMAN,t r B3KNI8 B3KNI8_ HUMAN,t r C5ISB7 C5ISB7_S HEEP,tr D 2H0N7 D 2H0N7_AI LME,tr E2 RPC0 E2R PCO_CAN FA,tr F1N 1A3 F1N1 A3_BOVI N,tr F6VA D6 F6VA D6_ORNA N,tr F6VA E7 F6VAE	nPEI SHM LNN PDI MR	88%	43.9	53.132	Ref	0.075	-0.17	0.055	-0.11	-0.24	0.085	-0.16	4780	4790	4370	5750	5650	4520	5900	4940	695.7	2084	3	0.0119	5.701

Ubiquilin-1 OS=Pongo abelii GN=UBQLN1 PE=2 SV=1	4 UBQL1_PONAB,s p Q9UMX0 UBQL1_HUMAN, tr B3KNI2 B3KNI2_HUMAN,t r B3KNI8 B3KNI8_HUMAN,t r C5ISB7 C5ISB7_S HEEP,tr D2H0N7 D2H0N7_AI LME,tr E2RPC0 E2RPCO_CAN FA,tr F1N1A3 F1N1A3_BOVI N,tr F6VAD6 F6VAD6_ORNA N,tr F6VAE7 F6VAE	sHTD QLVL IFAG k	69%	35.3	52.33633	Ref	0.033	-0.51	-0.03	-0.23	0.31	-0.88	0.36	3350	2970	2210	3470	3320	4210	1930	4530	679.7	2036.2	3	0.0128	6.259
Ubiquilin-1 OS=Pongo abelii GN=UBQLN1 PE=2 SV=1	4 UBQL1_PONAB,s p Q9UMX0 UBQL1_HUMAN, tr B3KNI2 B3KNI2_HUMAN,t r B3KNI8 B3KNI8_HUMAN,t r C5ISB7 C5ISB7_S HEEP,tr D2H0N7 D2H0N7_AI LME,tr E2RPC0 E2RPCO_CAN FA,tr F1N1A3 F1N1A3_BOVI N,tr F6VAD6 F6VAD6_ORNA N,tr F6VAE7 F6VAE	sHTD QLVL IFAG k	66%	34.5	52.21247	Ref	0.1	-0.35	0.11	-0.25	0.19	-0.37	0.038	2760	2860	2270	3500	3010	3550	2520	3320	679.7	2036.2	3	0.0107	5.272

Ubiquilin-1 OS=Pongo abelii GN=UBQLN1 PE=2 SV=1	4 UBQL1_PONAB,s p Q9UMX0 UBQL1_HUMAN, tr B3KNI2 B3KNI2_HUMAN,t r B3KNI8 B3KNI8_HUMAN,t r C5ISB7 C5ISB7_S HEEP,tr D2H0N7 D2H0N7_AI LME,tr E2RPC0 E2RPCO_CAN FA,tr F1N1A3 F1N1A3_BOVI N,tr F6VAD6 F6VAD6_ORNA N,tr F6VAE7 F6VAE	sHTD QLVL IFAG k	73%	36.1	52.20605	Ref	-0.13	0.003	-0.09	-0.17	0.14	-0.43	-0.06	2500	1860	2210	2330	2420	2630	1840	2360	679.7	2036.2	3	0.0095	4.639
Ubiquilin-1 OS=Pongo abelii GN=UBQLN1 PE=2 SV=1	4 UBQL1_PONAB,s p Q9UMX0 UBQL1_HUMAN, tr B3KNI2 B3KNI2_HUMAN,t r B3KNI8 B3KNI8_HUMAN,t r C5ISB7 C5ISB7_S HEEP,tr D2H0N7 D2H0N7_AI LME,tr E2RPC0 E2RPCO_CAN FA,tr F1N1A3 F1N1A3_BOVI N,tr F6VAD6 F6VAD6_ORNA N,tr F6VAE7 F6VAE	sHTD QLVL IFAG k	60%	31.5	52.22472	Ref	-0.033	-0.34	-0.27	-0.2	0.055	-0.48	0.52	2100	1840	1610	1900	2200	2300	1660	3280	510.1	2036.2	4	0.009	4.441

Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Bos taurus GN=C1QBP PE=2 SV=1	sp Q3T0B6 C1QBP_BOVIN	aEEQ EPEL TSTP NFV VEVT k	95%	67.8	55.45787	Ref	0.1	0.093	-0.08	-0.18	0.18	-0.17	-0.14	2280	2360	2550	2540	2620	2920	2390	2420	952.5	2854.5	3	0.0333	11.67
Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Bos taurus GN=C1QBP PE=2 SV=1	sp Q3T0B6 C1QBP_BOVIN	aEEQ EPEL TSTP NFV VEVT k	89%	44.7	55.46757	Ref	-0.078	-0.05	-0.12	-0.38	0.06	0.14	0.27	4920	4770	5280	5630	5200	6150	6800	7350	714.6	2854.5	4	0.0302	10.56
Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Bos taurus GN=C1QBP PE=2 SV=1	sp Q3T0B6 C1QBP_BOVIN	aEEQ EPEL TSTP NFV VEVT k	95%	58.7	55.47394	Ref	0.4	-0.32	0.25	-0.13	0.004	-0.75	0.18	2890	3910	2570	4300	3620	3480	2160	4060	952.5	2854.5	3	0.0223	7.821

Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Bos taurus GN=C1QBP PE=2 SV=1	sp Q3T0B6 C1QBP_BOVIN	aEEQ EPEL TSTP NFV VEVT k	95%	74.2	55.46278	Ref	0.056	-0.02	0.033	0.034	-0.15	-0.1	-0.16	991	895	924	1070	1180	912	981	937	952.5	2854.5	3	0.0176	6.151
Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Bos taurus GN=C1QBP PE=2 SV=1	sp Q3T0B6 C1QBP_BOVIN	mSG GWE LEVn GTE Ak	93%	49.9	53.60626	Ref	-0.026	-0.02	0.11	-0.32	0.15	-0.38	0.075	7240	6050	6590	8090	6620	8000	5790	7880	739.7	2216.1	3	0.0206	9.27
Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Bos taurus GN=C1QBP PE=2 SV=1	sp Q3T0B6 C1QBP_BOVIN	mSG GWE LEVn GTE Ak	85%	42.3	53.63432	Ref	-0.04	-0.04	0.075	-0.02	0.16	-0.29	-0.02	5970	5640	6140	7440	7670	7590	5790	6940	739.7	2216.1	3	0.0187	8.444

Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Bos taurus GN=C1QBP PE=2 SV=1	sp Q3T0B6 C1QBP_BOVIN	mSG GWE LEVn GTE Ak	95%	70	53.64902	Ref	-0.36	-0.08	0.062	-0.22	0.23	-0.36	0.085	1240	732	965	1190	1080	1290	892	1210	1109	2216.1	2	0.0176	7.918
Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Bos taurus GN=C1QBP PE=2 SV=1	sp Q3T0B6 C1QBP_BOVIN	mSG GWE LEVn GTE Ak	68%	36	53.30728	Ref	0.12	-0.02	0.04	-0.26	-0.02	-0.16	-0.02	6860	6490	6360	7460	6680	6900	6550	7120	745	2232.1	3	0.0166	7.436
Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Bos taurus GN=C1QBP PE=2 SV=1	sp Q3T0B6 C1QBP_BOVIN	mSG GWE LEVn GTE Ak	94%	51.3	53.31257	Ref	-0.084	-0.22	-0.04	-0.033	0.17	-0.23	0.093	15900	13000	12800	16300	18000	18200	14300	17800	745	2232.1	3	0.0164	7.342

DNA binding protein (Fragment) OS=Canis familiaris GN=dpbA variant PE=2 SV=1	tr Q9XSU1 Q9XSU1_CANFA	gAEA ANV TGP DGV PVE GSR	95%	67.3	53.17357	Ref	-0.41	0.27	0.34	0.012	0.54	-0.02	0.98	1030	657	1140	1350	1180	1490	1060	2080	1044	2086	2	0.0222	10.64
DNA binding protein (Fragment) OS=Canis familiaris GN=dpbA variant PE=2 SV=1	tr Q9XSU1 Q9XSU1_CANFA	gAEA ANV TGP DGV PVE GSR	95%	82.3	53.38512	Ref	-0.32	0.52	0.13	0.015	0.81	-0.18	0.8	7430	5370	10400	8940	9090	13800	7220	14200	1044	2086	2	0.0136	6.535
DNA binding protein (Fragment) OS=Canis familiaris GN=dpbA variant PE=2 SV=1	tr Q9XSU1 Q9XSU1_CANFA	sVG DGE TVqF DVV EGEK	95%	50.5	54.10469	Ref	-0.72	0.26	0.3	0.24	0.88	-0.42	0.95	2280	1280	2720	3150	3340	4520	1920	4910	1203	2403.2	2	0.0212	8.822
DNA binding protein (Fragment) OS=Canis familiaris GN=dpbA variant PE=2 SV=1	tr Q9XSU1 Q9XSU1_CANFA	sVG DGE TVqF DVV EGEK	83%	41.6	54.12408	Ref	-0.27	0.36	0.068	0.24	0.99	-0.11	0.52	5210	3800	6390	5840	7250	10600	5180	7980	802.1	2403.2	3	0.0204	8.475

DNA binding protein (Fragment) OS=Canis familiaris GN=dpbA variant PE=2 SV=1	tr Q9XSU1 Q9XSU1_CANFA	sVG DGE TVqF DVV EGEK	73%	38.2	54.12506	Ref	-0.27	0.33	0.36	0.31	0.7	-0.48	0.99	44700	43300	71000	81600	86700	99200	45900	126000	802.1	2403.2	3	0.0197	8.176
DNA binding protein (Fragment) OS=Canis familiaris GN=dpbA variant PE=2 SV=1	tr Q9XSU1 Q9XSU1_CANFA	sVG DGE TVqF DVV EGEK	91%	47.4	54.0917	Ref	-0.064	0.42	0.34	0.39	0.45	0.29	0.27	2890	2380	3620	3830	4370	3990	3710	3640	802.1	2403.2	3	0.0226	9.386
DNA binding protein (Fragment) OS=Canis familiaris GN=dpbA variant PE=2 SV=1	tr Q9XSU1 Q9XSU1_CANFA	sVG DGE TVqF DVV EGEK	81%	40.8	54.19119	Ref	0.17	0.24	-0	0.15	0.47	0.21	0.76	743	716	812	772	949	1030	902	1310	802.1	2403.2	3	0.0162	6.728
DNA binding protein (Fragment) OS=Canis familiaris GN=dpbA variant PE=2 SV=1	tr Q9XSU1 Q9XSU1_CANFA	sVG DGE TVqF DVV EGEK	76%	39.1	54.30971	Ref	-0.32	0.25	0.31	0.2	0.46	0.21	0.75	406	262	421	494	504	529	462	670	802.1	2403.2	3	0.0109	4.52

DNA binding protein (Fragment) OS=Canis familiaris GN=dpbA variant PE=2 SV=1	tr Q9XSU1 Q9XSU1_CANFA	sVG DGE TVqF DVV EGEK	95%	55.7	54.07326	Ref	No Values (-2.731676)	Reference Missing (0.52795684)	Reference Missing (1.0146731)	Reference Missing (0.905271)	Reference Missing (1.232552)	No Values (-3.0233378)	Reference Missing (0.6668909)	No Values (-2.934066)	No Values (-2.731676)	Reference Missing (0.52795684)	Reference Missing (1.0146731)	Reference Missing (0.905271)	Reference Missing (1.232552)	No Values (-3.0233378)	Reference Missing (0.6668909)	802.1	2403.2	3	0.0227	9.461
UMP-CMP kinase OS=Bos taurus GN=CMPK1 PE=2 SV=2	sp Q2KIW9 KCY_BOVIN	iVPV EITIS LLR	94%	41.3	48.02445	Ref	0.16	0.1	-0.05	0.075	0.012	0.085	-0.21	913	889	929	940	1130	942	1040	837	829	1656	2	0.0132	7.942
UMP-CMP kinase OS=Bos taurus GN=CMPK1 PE=2 SV=2	sp Q2KIW9 KCY_BOVIN	iVPV EITIS LLR	86%	35.7	47.792	Ref	0.21	0.018	-0.07	0.04	0.15	0.018	-0.1	1720	1860	1770	1860	2220	2100	1990	1820	829	1656	2	0.0097	5.878
UMP-CMP kinase OS=Bos taurus GN=CMPK1 PE=2 SV=2	sp Q2KIW9 KCY_BOVIN	iVPV EITIS LLR	89%	39.4	48.11414	Ref	0.32	-0.14	0.014	-0.051	-0.08	-0.01	-0.04	245	241	190	238	251	215	235	229	553	1656	3	0.0058	3.528
UMP-CMP kinase OS=Bos taurus GN=CMPK1 PE=2 SV=2	sp Q2KIW9 KCY_BOVIN	iVPV EITIS LLR	95%	52.7	48.21985	Ref	0.2	-0.17	0.15	0.14	-0.25	0.16	0.016	409	445	372	523	572	381	528	475	553	1656	3	0.0075	4.524
UMP-CMP kinase OS=Bos taurus GN=CMPK1 PE=2 SV=2	sp Q2KIW9 KCY_BOVIN	iVPV EITIS LLR	82%	35.3	48.18569	Ref	0.18	0.042	-0.39	-0.13	0.42	0.011	-0.23	176	157	155	129	171	217	171	144	553	1656	3	0.0068	4.089

UMP-CMP kinase OS=Bos taurus GN=CMPK1 PE=2 SV=2	sp Q2KIW9 KCY_BOVIN	IVPV EITIS LLR	94%	46	48.21985	Ref	Value Missing (- 1.5247 099)	0.61	0.73	-0.13	0.008	Value Missi ng (- 1.816 3713)	0.18	129	Value Missing (- 1.524709 9)	144	177	107	Value Missin g (- 1.8163 713)	103	121	553	1656	3	0.0075	4.524
UMP-CMP kinase OS=Bos taurus GN=CMPK1 PE=2 SV=2	sp Q2KIW9 KCY_BOVIN	mkP QVV FVLG GPG AGk	93%	45.9	50.47645	Ref	-0.024	-0.01	0.088	0.15	0.11	-0.04	-0.3	1640	1240	1360	1630	1880	1590	1510	1250	833.2	2496.5	3	0.0214	8.574
UMP-CMP kinase OS=Bos taurus GN=CMPK1 PE=2 SV=2	sp Q2KIW9 KCY_BOVIN	mkP QVV FVLG GPG AGk	89%	39.1	50.1468	Ref	0.11	0.044	-0	0.1	0.19	-0.11	-0.19	7280	6850	7070	7700	9130	8480	7200	6760	625.1	2496.5	4	0.0155	6.202
UMP-CMP kinase OS=Bos taurus GN=CMPK1 PE=2 SV=2	sp Q2KIW9 KCY_BOVIN	mkP QVV FVLG GPG AGk	90%	39.9	49.84041	Ref	0.02	0.052	5E-04	0.091	0.063	0.099	-0.12	8780	7860	8720	9440	11100	9490	10200	8680	625.1	2496.5	4	0.0101	4.056
Profilin-1 OS=Bos taurus GN=PFN1 PE=1 SV=2	sp P02584 PROF1_BOVIN	cYE MAS HLR	86%	36.5	47.33518	Ref	0.64	-0.19	0.13	-0.15	-0.08	0.042	0.013	8310	11500	6960	9770	8870	8120	9250	8990	487.2	1458.7	3	0.0113	7.73
Profilin-1 OS=Bos taurus GN=PFN1 PE=1 SV=2	sp P02584 PROF1_BOVIN	cYE MAS HLR	95%	53.8	47.6505	Ref	0.34	-0.26	-0.04	0.07	-0.06	0.23	0.013	11200	10900	7810	10200	12200	9680	12400	10600	487.2	1458.7	3	0.0067	4.585
Profilin-1 OS=Bos taurus GN=PFN1 PE=1 SV=2	sp P02584 PROF1_BOVIN	dSLL QDG EFT MDL R	84%	38.8	52.05889	Ref	0.56	-0.26	0.068	0.07	0.087	0.061	0.084	2690	4220	2600	3650	4030	3560	3650	3680	972.5	1943	2	0.01	5.14

Profilin-1 OS=Bos taurus GN=PFN1 PE=1 SV=2	sp P02584 PROF1_BOVIN	sSFF VnGL TLG GQk	94%	50.2	53.72363	Ref	0.4	-0.34	0.12	0.11	0.037	0.18	-0.08	8600	9700	6290	9720	10700	8840	10200	8460	688.7	2063.1	3	0.013	6.297
Profilin-1 OS=Bos taurus GN=PFN1 PE=1 SV=2	sp P02584 PROF1_BOVIN	sSFF VnGL TLG GQk	72%	37.4	53.74847	Ref	0.27	0.019	0.06	0.006	-0.03	-0.07	0.22	2850	2890	2630	3040	3220	2750	2780	3380	688.7	2063.1	3	0.0167	8.07
Profilin-1 OS=Bos taurus GN=PFN1 PE=1 SV=2	sp P02584 PROF1_BOVIN	sTGG APTF NITV TMT Ak	94%	52.6	54.37925	Ref	0.22	-0.2	0.21	0.081	0.22	0.058	0.03	1430	1570	1270	1890	1910	1830	1710	1670	769.1	2304.3	3	0.0086	3.729
Profilin-1 OS=Bos taurus GN=PFN1 PE=1 SV=2	sp P02584 PROF1_BOVIN	tFVN ITPA EVGI LVGk	95%	60.4	50.63896	Ref	0.46	-0.22	0.25	-0.023	-0.06	-0.07	0.14	1250	1530	1030	1620	1470	1250	1290	1490	756.1	2265.3	3	0.0124	5.457
Profilin-1 OS=Bos taurus GN=PFN1 PE=1 SV=2	sp P02584 PROF1_BOVIN	tLVLL MGk	85%	36.7	48.0058	Ref	0.6	-0.73	0.52	-0.042	-0.14	-0.03	-0.09	6110	7620	3280	8760	6550	5330	6010	5720	495	1481.9	3	0.0093	6.268
FBLN1 protein OS=Bos taurus GN=FBLN1 PE=2 SV=1	tr A5D7S8 A5D7S8_BOVIN, tr F1MYN5 F1MYN5_BOVIN	aiTP AyPA NHA DIIF DITD GNL R	87%	43.3	55.32806	Ref	-0.056	0.23	-0.07	0.14	0.11	0.3	0.081	791	754	1000	907	1160	988	1180	1010	777.4	3105.7	4	0.0094	3.025
FBLN1 protein OS=Bos taurus GN=FBLN1 PE=2 SV=1	tr A5D7S8 A5D7S8_BOVIN, tr F1MYN5 F1MYN5_BOVIN	cLAF EcPE NYR	61%	25.8	44.48026	Ref	0.36	0.017	-0.17	-0.075	-0.24	0.14	0.2	950	886	758	747	880	686	930	965	580.9	1739.7	3	0.0099	5.681
FBLN1 protein OS=Bos taurus GN=FBLN1 PE=2 SV=1	tr A5D7S8 A5D7S8_BOVIN, tr F1MYN5 F1MYN5_BOVIN	gQET ADF APG DGG DLQ ETAK	72%	37.6	53.92461	Ref	-0.64	0.31	0.065	-0.032	0.19	0.15	0.44	14200	8580	18000	17000	17600	17900	18200	22000	872.4	2614.3	3	0.0198	7.577

FBLN1 protein OS=Bos taurus GN=FBLN1 PE=2 SV=1	tr A5D7S8 A5D7S8_BOVIN, tr F1MYN5 F1MYN5_BOVIN	gYHL NEE GTR	53%	29.8	50.27121	Ref	-0.23	0.25	-0.08	0.11	0.21	0.16	0.2	5060	4000	6040	5420	6820	6340	6420	6550	740.4	1478.7	2	0.0127	8.562
FBLN1 protein OS=Bos taurus GN=FBLN1 PE=2 SV=1	tr A5D7S8 A5D7S8_BOVIN, tr F1MYN5 F1MYN5_BOVIN	IEM NVV VGG VVS HR	87%	43.7	53.67447	Ref	0.26	0.012	0.06	-0.015	0.11	0.047	0.099	2210	2260	2070	2400	2510	2380	2390	2460	622	1863	3	0.0025	1.332
FBLN1 protein OS=Bos taurus GN=FBLN1 PE=2 SV=1	tr A5D7S8 A5D7S8_BOVIN, tr F1MYN5 F1MYN5_BOVIN	qVRP IVGP FHA VLk	67%	33	50.51017	Ref	0.37	0.37	-0.09	0.004	0.042	-0.1	-0.07	2450	2800	3030	2480	2920	2610	2480	2510	616.7	1847.1	3	0.0084	4.549
FBLN1 protein OS=Bos taurus GN=FBLN1 PE=2 SV=1	tr A5D7S8 A5D7S8_BOVIN, tr F1MYN5 F1MYN5_BOVIN	tcVD INeC R	85%	30.9	43.85106	Ref	-0.25	0.2	0.032	0.18	0.026	0.27	0.068	81900	59100	87300	87300	106000	83600	1E+05	89300	724.8	1447.6	2	0.0091	6.309
FBLN1 protein OS=Bos taurus GN=FBLN1 PE=2 SV=1	tr A5D7S8 A5D7S8_BOVIN, tr F1MYN5 F1MYN5_BOVIN	vSEIE EEQE DPYL NDR	85%	38.1	50.95375	Ref	-0.39	0.28	-0.2	0.1	0.19	0.23	0.18	1640	1020	1760	1420	1930	1790	1920	1840	1135	2268.1	2	0.0178	7.841

RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1	7 FUS_H UMAN,sp P56959 FUS_MOU SE,sp Q2 8009 FUS _BOVIN,tr A8K4H1 A8K4H1_ HUMAN,t r B4DR70 B4DR70_ HUMAN,t r E7EUX0 E7EUX0_ HUMAN,t r F1N198 F1N198_ BOVIN,tr F1PBJ4 F 1PBJ4_CA NFA,tr F6 T5U5 F6T 5U5_MAC MU,tr F7 D056 F7D 056_MAC	aPkp DGP GGG PGG SHM GGN YGD DR	95%	53.2	52.74825	Ref	-0.08	0.046	-0.26	-0.37	0.079	-0.47	-0.11	10800	10300	12200	11100	11300	13500	9620	12200	573.1	2860.3	5	0.0333	11.63
RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1	7 FUS_H UMAN,sp P56959 FUS_MOU SE,sp Q2 8009 FUS _BOVIN,tr A8K4H1 A8K4H1_ HUMAN,t r B4DR70 B4DR70_ HUMAN,t r E7EUX0 E7EUX0_ HUMAN,t r F1N198 F1N198_ BOVIN,tr F1PBJ4 F 1PBJ4_CA NFA,tr F6 T5U5 F6T 5U5_MAC MU,tr F7 D056 F7D 056_MAC	aPkp DGP GGG PGG SHM GGN YGD DR	95%	58.7	53.04807	Ref	-0.52	-0.29	-0.1	-0.27	0.27	-0.62	0.089	12500	7910	10000	12800	12700	16000	9020	14600	716.1	2860.4	4	0.0248	8.661

RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1	7 FUS_H UMAN,sp P56959 FUS_MOU SE,sp Q2 8009 FUS _BOVIN,tr A8K4H1 A8K4H1_ HUMAN,t r B4DR70 B4DR70_ HUMAN,t r E7EUX0 E7EUX0_ HUMAN,t r F1N198 F1N198_ BOVIN,tr F1PBJ4 F 1PBJ4_CA NFA,tr F6 T5U5 F6T 5U5_MAC MU,tr F7 D056 F7D 056_MAC	aPkP DGP GGG PGG SHM GGN yGD DR	77%	34.8	55.14443	Ref	-0.45	-0.37	-0.09	-0.12	0.18	-0.69	0.015	13800	8600	9850	13400	14500	15600	8860	14400	633.9	3164.6	5	0.0183	5.784
RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1	7 FUS_H UMAN,sp P56959 FUS_MOU SE,sp Q2 8009 FUS _BOVIN,tr A8K4H1 A8K4H1_ HUMAN,t r B4DR70 B4DR70_ HUMAN,t r E7EUX0 E7EUX0_ HUMAN,t r F1N198 F1N198_ BOVIN,tr F1PBJ4 F 1PBJ4_CA NFA,tr F6 T5U5 F6T 5U5_MAC MU,tr F7 D056 F7D 056_MAC	eFSG NPIK	62%	33.2	52.07734	Ref	-0.31	-0.45	-0.14	-0.32	0.34	-0.75	-0.04	98200	64200	63300	87900	85500	1E+05	58100	94100	750.4	1498.8	2	0.0169	11.29

RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1	7 FUS_H UMAN,sp P56959 FUS_MOU SE,sp Q2 8009 FUS _BOVIN,tr A8K4H1 A8K4H1_ HUMAN,t r B4DR70 B4DR70_ HUMAN,t r E7EUX0 E7EUX0_ HUMAN,t r F1N198 F1N198_ BOVIN,tr F1PBJ4 F 1PBJ4_CA NFA,tr F6 T5U5 F6T 5U5_MAC MU,tr F7 D056 F7D 056_MAC	eFSG NPIK	76%	36.2	51.99978	Ref	-0.21	-0.44	-0.12	-0.25	0.2	-0.83	-0.07	36100	24200	22400	31300	31400	37500	19100	32300	750.4	1498.9	2	0.0074	4.945
RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1	7 FUS_H UMAN,sp P56959 FUS_MOU SE,sp Q2 8009 FUS _BOVIN,tr A8K4H1 A8K4H1_ HUMAN,t r B4DR70 B4DR70_ HUMAN,t r E7EUX0 E7EUX0_ HUMAN,t r F1N198 F1N198_ BOVIN,tr F1PBJ4 F 1PBJ4_CA NFA,tr F6 T5U5 F6T 5U5_MAC MU,tr F7 D056 F7D 056_MAC	eEAT VSFD DPPS Ak	95%	55.5	53.83309	Ref	-0.27	-0.12	-0.17	-0.23	0.19	-1.1	0.1	7480	5400	6500	7060	7460	8700	3690	8500	1015	2028	2	0.0133	6.548

RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1	7 FUS_H UMAN,sp P56959 FUS_MOU SE,sp Q2 8009 FUS _BOVIN,tr A8K4H1 A8K4H1_ HUMAN,t r B4DR70 B4DR70_ HUMAN,t r E7EUX0 E7EUX0_ HUMAN,t r F1N198 F1N198_ BOVIN,tr F1PBJ4 F 1PBJ4_CA NFA,tr F6 T5U5 F6T 5U5_MAC MU,tr F7 D056 F7D 056_MAC	qIGII k	55%	22.8	42.6321	Ref	-0.24	-0.31	-0.15	-0.23	0.26	-0.65	0.019	10800	8810	9100	11500	12000	14600	8110	12800	427.3	1278.8	3	0.0046	3.604
RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1	7 FUS_H UMAN,sp P56959 FUS_MOU SE,sp Q2 8009 FUS _BOVIN,tr A8K4H1 A8K4H1_ HUMAN,t r B4DR70 B4DR70_ HUMAN,t r E7EUX0 E7EUX0_ HUMAN,t r F1N198 F1N198_ BOVIN,tr F1PBJ4 F 1PBJ4_CA NFA,tr F6 T5U5 F6T 5U5_MAC MU,tr F7 D056 F7D 056_MAC	tGQP MIN LYTD R	89%	41.8	52.67313	Ref	-0.46	-0.32	-0.2	-0.39	0.34	-0.56	0.051	13500	8500	10200	12500	12000	17400	9730	14800	856.9	1711.9	2	0.0111	6.475

Histone H2A.x OS=Homo sapiens GN=H2AFX PE=1 SV=2	sp P16104 H2AX_HUMAN, tr E2RNBO E2RNBO_CANFA, tr F7FGT7 F7FGT7_MACMU, tr Q17QG8 Q17QG8_BOVIN	aGL QFP VGR	94%	48.1	51.62299	Ref	-0.38	0.32	-0.64	-0.16	-0.07	-0.05	0.64	3470	2260	3970	2290	3520	3270	3470	5570	416.9	1247.7	3	0.0111	8.889
Histone H2A.x OS=Homo sapiens GN=H2AFX PE=1 SV=2	sp P16104 H2AX_HUMAN, tr E2RNBO E2RNBO_CANFA, tr F7FGT7 F7FGT7_MACMU, tr Q17QG8 Q17QG8_BOVIN	aGL QFP VGR	95%	52.6	51.84703	Ref	Value Missing (-0.3170157)	0.46	Value Missing (-0.60130364)	0.18	0.3	-0	-0.14	4710	Value Missing (-0.3170157)	6440	Value Missing (-0.60130364)	6560	6210	5270	4740	416.9	1247.7	3	0.0057	4.565
Histone H2A.x OS=Homo sapiens GN=H2AFX PE=1 SV=2	sp P16104 H2AX_HUMAN, tr E2RNBO E2RNBO_CANFA, tr F7FGT7 F7FGT7_MACMU, tr Q17QG8 Q17QG8_BOVIN	aGL QFP VGR	95%	55.5	51.82312	Ref	No Values (-0.21019465)	Reference Missing (0.39134824)	No Values (-0.49448282)	Reference Missing (0.23583135)	Reference Missing (0.18505676)	Reference Missing (0.30252373)	Reference Missing (0.1744924)	No Values (-0.4125847)	No Values (-0.21019465)	Reference Missing (0.39134824)	No Values (-0.49448282)	Reference Missing (0.23583135)	Reference Missing (0.18505676)	Reference Missing (0.30252373)	Reference Missing (0.17449234)	416.9	1247.7	3	0.0094	7.496
Histone H2A.x OS=Homo sapiens GN=H2AFX PE=1 SV=2	sp P16104 H2AX_HUMAN, tr E2RNBO E2RNBO_CANFA, tr F7FGT7 F7FGT7_MACMU, tr Q17QG8 Q17QG8_BOVIN	aTQ ASQ EY	57%	28.2	47.86027	Ref	1.4	0.6	-1	-0.97	-0.94	-0.95	-0.95	5000	8710	5400	1990	2250	2010	2080	2060	601.3	1200.6	2	0.0133	11.05

Histone H2A.x OS=Homo sapiens GN=H2AFX PE=1 SV=2	sp P16104 H2AX_HUMAN, tr E2RNBO E2RNBO_CANFA, tr F7FGT7 F7FGT7_MACMU, tr Q17QG8 Q17QG8_BOVIN	aTQASQ EY	95%	50	48.19136	Ref	0.62	0.29	-1.2	-0.73	-0.42	-0.74	-0.43	6590	4020	3480	1380	2130	2300	1920	2370	601.3	1200.6	2	0.0118	9.836
Histone H2A.x OS=Homo sapiens GN=H2AFX PE=1 SV=2	sp P16104 H2AX_HUMAN, tr E2RNBO E2RNBO_CANFA, tr F7FGT7 F7FGT7_MACMU, tr Q17QG8 Q17QG8_BOVIN	kATQAS QEY	67%	34.7	52.59377	Ref	-0.61	0.32	-1.2	0.16	0.36	-0	0.43	2500	1460	3010	1180	3350	3360	2720	3650	817.4	1632.9	2	0.0242	14.78
Histone H2A.x OS=Homo sapiens GN=H2AFX PE=1 SV=2	sp P16104 H2AX_HUMAN, tr E2RNBO E2RNBO_CANFA, tr F7FGT7 F7FGT7_MACMU, tr Q17QG8 Q17QG8_BOVIN	nDEE LNK	81%	38.4	52.58726	Ref	-0.54	0.4	-1.6	0.2	0.18	0.22	0.45	3E+05	193000	4E+05	116000	434000	4E+05	4E+05	468000	735.4	1468.8	2	0.0171	11.61

Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2	4 CAPR1_HUMAN,sp Q1LZB6 CAPR1_BOVIN,sp Q5M9G3 CAPR1_RAT,sp Q60865 CAPR1_MOUSE,transcript E2RKU8 E2RKU8_CANFA,transcript E9PLA9 E9PLA9_HUMAN,transcript F1MPH9 F1MPH9_BOVIN,transcript F1NH0 F1NH0_BOVIN,transcript F1SGS6 F1SGS6_PIG,transcript Q3UFZ6 Q3UFZ6_AVSK	INQD QLD AVSk	92%	47.1	52.9722	Ref	-0.061	-0.17	0.053	-0.24	0.008	-0.39	0.083	24600	20700	20800	27300	24400	25400	20100	27800	613.7	1838	3	0.0121	6.558
Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2	4 CAPR1_HUMAN,sp Q1LZB6 CAPR1_BOVIN,sp Q5M9G3 CAPR1_RAT,sp Q60865 CAPR1_MOUSE,transcript E2RKU8 E2RKU8_CANFA,transcript E9PLA9 E9PLA9_HUMAN,transcript F1MPH9 F1MPH9_BOVIN,transcript F1NH0 F1NH0_BOVIN,transcript F1SGS6 F1SGS6_PIG,transcript Q3UFZ6 Q3UFZ6_AVSK	INQD QLD AVSk	95%	66.4	52.92872	Ref	-0.37	-0.26	0.17	-0.16	0.22	-0.68	0.23	20900	14700	17200	26000	22800	25800	14400	27000	920	1838	2	0.0107	5.826

Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2	4 CAPR1_HUMAN,sp Q1LZB6 CAPR1_BOVIN,sp Q5M9G3 CAPR1_RAT,sp Q60865 CAPR1_MOUSE,transcript E2RKU8 E2RKU8_CANFA,transcript E9PLA9 E9PLA9_HUMAN,transcript F1MPH9 F1MPH9_BOVIN,transcript F1NH0 F1NH0_BOVIN,transcript F1SGS6 F1SGS6_PIG,transcript Q3UFZ6 Q3UFZ6_	qILG VIDK	79%	34.4	48.47887	Ref	-0.1	-0.27	-0.05	-0.34	0.18	-0.39	0.13	2410	1880	1810	2370	2140	2680	1890	2670	498.6	1492.9	3	0.0236	15.78
Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2	4 CAPR1_HUMAN,sp Q1LZB6 CAPR1_BOVIN,sp Q5M9G3 CAPR1_RAT,sp Q60865 CAPR1_MOUSE,transcript E2RKU8 E2RKU8_CANFA,transcript E9PLA9 E9PLA9_HUMAN,transcript F1MPH9 F1MPH9_BOVIN,transcript F1NH0 F1NH0_BOVIN,transcript F1SGS6 F1SGS6_PIG,transcript Q3UFZ6 Q3UFZ6_	qILG VIDK	67%	30.3	47.77137	Ref	-0.27	-0.03	0.058	-0.16	0.086	-0.47	-0.05	29900	20500	26300	31300	29600	30700	21900	29000	498.7	1492.9	3	0.0049	3.273

Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2	4 CAPR1_HUMAN,sp Q1LZB6 CAPR1_BOVIN,sp Q5M9G3 CAPR1_RAT,sp Q60865 CAPR1_MOUSE,transcript E2RKU8 E2RKU8_CANFA,transcript E9PLA9 E9PLA9_HUMAN,transcript F1MPH9 F1MPH9_BOVIN,transcript F1NH0 F1NH0_BOVIN,transcript F1SGS6 F1SGS6_PIG,transcript Q3UFZ6 Q3UFZ6_LDK	tVLE LQYV LDK	89%	43.1	51.47024	Ref	-0.087	-0.22	0.089	-0.25	-0.01	-0.3	-0.01	4290	3360	3320	4630	4030	4150	3550	4320	643.7	1928.1	3	0.0151	7.843
Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2	4 CAPR1_HUMAN,sp Q1LZB6 CAPR1_BOVIN,sp Q5M9G3 CAPR1_RAT,sp Q60865 CAPR1_MOUSE,transcript E2RKU8 E2RKU8_CANFA,transcript E9PLA9 E9PLA9_HUMAN,transcript F1MPH9 F1MPH9_BOVIN,transcript F1NH0 F1NH0_BOVIN,transcript F1SGS6 F1SGS6_PIG,transcript Q3UFZ6 Q3UFZ6_LDK	tVLE LQYV LDK	87%	41	51.47144	Ref	0.041	-0.32	0.058	-0.19	-0.08	-0.4	0.12	524	465	392	572	532	502	420	595	643.7	1928.1	3	0.0157	8.123

Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2	4 CAPR1_HUMAN,sp Q1LZB6 CAPR1_BOVIN,sp Q5M9G3 CAPR1_RAT,sp Q60865 CAPR1_MOUSE,transcript E2RKU8 E2RKU8_CANFA,transcript E9PLA9 E9PLA9_HUMAN,transcript F1MPH9 F1MPH9_BOVIN,transcript F1NH0 F1NH0_BOVIN,transcript F1SGS6 F1SGS6_PIG,transcript Q3UFZ6 Q3UFZ6_AK	yQEVTN NLEF	67%	37	54.52232	Ref	-0.14	-0.39	-0	-0.057	-0	-0.17	0.069	2310	1830	1680	2460	2610	2370	2200	2580	790.1	2367.3	3	0.0327	13.81
Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2	4 CAPR1_HUMAN,sp Q1LZB6 CAPR1_BOVIN,sp Q5M9G3 CAPR1_RAT,sp Q60865 CAPR1_MOUSE,transcript E2RKU8 E2RKU8_CANFA,transcript E9PLA9 E9PLA9_HUMAN,transcript F1MPH9 F1MPH9_BOVIN,transcript F1NH0 F1NH0_BOVIN,transcript F1SGS6 F1SGS6_PIG,transcript Q3UFZ6 Q3UFZ6_AK	yQEVTN NLEF	95%	64.7	54.10514	Ref	-0.2	-0.29	0.057	-0.2	0.26	-0.66	0.18	6310	4890	4970	7090	6550	7850	4330	7700	1033	2064.1	2	#####	0.125

Fibronectin OS=Bos taurus GN=FN1 PE=1 SV=4	sp P07589 FINC_BOVIN, tr B8Y9S9 B8Y9S9_BOVIN, tr B8Y9T0 B8Y9T0_BOVIN	cDP HEA TcYD DGk	57%	24.7	44.26121	Ref	-0.078	0.45	-0.37	0.05	0.16	0.21	0.084	28600	23100	36100	23000	33900	32100	34700	31500	718.6	2152.9	3	0.0191	8.867
Fibronectin OS=Bos taurus GN=FN1 PE=1 SV=4	sp P07589 FINC_BOVIN, tr B8Y9S9 B8Y9S9_BOVIN, tr B8Y9T0 B8Y9T0_BOVIN	cTcV GnG R	78%	24.8	40.17326	Ref	0.011	0.54	-0.12	-0.18	-0.03	0.29	0.007	10500	9070	14200	10100	10700	10300	13500	11000	603.8	1205.5	2	0.0106	8.778
Fibronectin OS=Bos taurus GN=FN1 PE=1 SV=4	sp P07589 FINC_BOVIN, tr B8Y9S9 B8Y9S9_BOVIN, tr B8Y9T0 B8Y9T0_BOVIN	eSkP LTAQ QAT k	79%	38.2	52.39507	Ref	0.033	0.47	-0.35	0.075	-0.23	0.59	-0.31	8640	7230	10600	6770	10000	7090	13000	6930	738.8	2213.3	3	0.0407	18.38
Fibronectin OS=Bos taurus GN=FN1 PE=1 SV=4	sp P07589 FINC_BOVIN, tr B8Y9S9 B8Y9S9_BOVIN, tr B8Y9T0 B8Y9T0_BOVIN	fTNV GPD TMR	82%	36.7	50.80431	Ref	0.044	0.84	-0.54	-0.09	-0.32	0.61	-0.3	37900	38300	72300	31100	46900	35000	69400	36600	721.4	1440.7	2	0.0115	7.942
Fibronectin OS=Bos taurus GN=FN1 PE=1 SV=4	sp P07589 FINC_BOVIN, tr B8Y9S9 B8Y9S9_BOVIN, tr B8Y9T0 B8Y9T0_BOVIN	gATY NIIV EAVK	76%	36.3	51.44886	Ref	-0.15	0.64	-0.23	-0.076	-0.19	0.49	-0.12	7830	6150	11600	7070	8670	6990	11700	7630	629.4	1885.1	3	0.0085	4.492
Fibronectin OS=Bos taurus GN=FN1 PE=1 SV=4	sp P07589 FINC_BOVIN, tr B8Y9S9 B8Y9S9_BOVIN, tr B8Y9T0 B8Y9T0_BOVIN	sTTP DITG YR	53%	30.7	51.06548	Ref	-0.11	0.75	-0.78	-0.084	-0.33	0.81	-0.3	50900	41900	82700	32200	57300	42200	97100	44600	707.9	1413.7	2	0.0127	8.953

Fibronectin OS=Bos taurus GN=FN1 PE=1 SV=4	sp P07589 FINC_BOVIN,tr B8Y9S9 B8Y9S9_BOVIN,tr B8Y9T0 B8Y9T0_BOVIN	ySfc TDH TVLV	QTR	50%	33.6	54.18939	Ref	-0.081	0.48	-0.19	0.047	-0.07	0.39	0.071	3450	3090	4940	3490	4540	3660	5240	4180	775.4	2323.2	3	0.0151	6.487
40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1	7 RS28_HUMAN,sp P62858 RS28_MOUSE,sp P62859 RS28_RAT,sp Q56JX6 RS28_BOVIN,sp Q6QAT1 RS28_PIG,tr B2R4R9 B2R4R9_HUMAN,tr D2HZS4 D2HZS4_AILME,tr E2RNL7 E2RNL7_CANFA,tr F6WVD1 F6WVD1_HUMAN,sp F6WXM1 F6WXM1_CALIA,tr	eGD VLTL LESE	R	95%	50.4	52.95072	Ref	-0.22	0.022	0.29	0.18	0.4	-0.09	0.42	13600	10200	13100	17600	18100	18400	13600	19200	832.9	1663.9	2	0.0144	8.638

40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1	7 RS28_H UMAN,sp P62858 RS28_MO USE,sp P6 2859 RS2 8_RAT,sp Q56JX6 RS28_BO VIN,sp Q 6QAT1 RS 28_PIG,tr B2R4R9 B2R4R9_ HUMAN,t r D2HZS4 D2HZS4_ AILME,tr E2RNL7 E 2RNL7_CA NFA,tr F6 WVD1 F6 WVD1_H ORSE,tr F 6WXM1 F 6WXM1_ CALJA,tr	eGD VLT LESE R	95%	51.4	52.98377	Ref	-0.084	0.015	0.31	0.089	0.39	-0.14	0.46	15200	12800	14900	20500	19400	20900	15000	22600	833	1663.9	2	0.0063	3.796
40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1	7 RS28_H UMAN,sp P62858 RS28_MO USE,sp P6 2859 RS2 8_RAT,sp Q56JX6 RS28_BO VIN,sp Q 6QAT1 RS 28_PIG,tr B2R4R9 B2R4R9_ HUMAN,t r D2HZS4 D2HZS4_ AILME,tr E2RNL7 E 2RNL7_CA NFA,tr F6 WVD1 F6 WVD1_H ORSE,tr F 6WXM1 F 6WXM1_ CALJA,tr	eGD VLT LESE R	95%	52	52.95783	Ref	-0.21	0.081	0.32	0.14	0.36	0.056	0.34	1950	1510	2000	2660	2580	2620	2220	2680	832.9	1663.9	2	0.0116	6.956

<p>40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1</p>	<p>7 RS28_H UMAN,sp P62858 RS28_MO USE,sp P6 2859 RS2 8_RAT,sp Q56JX6 RS28_BO VIN,sp Q 6QAT1 RS 28_PIG,tr B2R4R9 B2R4R9_ HUMAN,t r D2HZS4 D2HZS4_ AILME,tr E2RNL7 E 2RNL7_CA NFA,tr F6 WVD1 F6 WVD1_H ORSE,tr F 6WXM1 F 6WXM1_ CALJA,tr </p>	<p>tGSQ GQc TQV R</p>	<p>79%</p>	<p>34.3</p>	<p>49.15368</p>	<p>Ref</p>	<p>-0.14</p>	<p>0.017</p>	<p>0.27</p>	<p>0.22</p>	<p>0.2</p>	<p>0.13</p>	<p>0.18</p>	<p>11800</p>	<p>8000</p>	<p>9680</p>	<p>13000</p>	<p>13800</p>	<p>11900</p>	<p>11900</p>	<p>12100</p>	<p>757.9</p>	<p>1513.7</p>	<p>2</p>	<p>0.0135</p>	<p>8.925</p>
<p>40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1</p>	<p>7 RS28_H UMAN,sp P62858 RS28_MO USE,sp P6 2859 RS2 8_RAT,sp Q56JX6 RS28_BO VIN,sp Q 6QAT1 RS 28_PIG,tr B2R4R9 B2R4R9_ HUMAN,t r D2HZS4 D2HZS4_ AILME,tr E2RNL7 E 2RNL7_CA NFA,tr F6 WVD1 F6 WVD1_H ORSE,tr F 6WXM1 F 6WXM1_ CALJA,tr </p>	<p>tGSQ GQc TQV R</p>	<p>88%</p>	<p>38.3</p>	<p>49.27334</p>	<p>Ref</p>	<p>0.048</p>	<p>-0.03</p>	<p>0.39</p>	<p>-0.071</p>	<p>0.22</p>	<p>0.12</p>	<p>0.27</p>	<p>4730</p>	<p>3890</p>	<p>3990</p>	<p>6000</p>	<p>4810</p>	<p>5140</p>	<p>5010</p>	<p>5530</p>	<p>757.9</p>	<p>1513.7</p>	<p>2</p>	<p>0.0124</p>	<p>8.199</p>

40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1	7 RS28_HUMAN,sp P62858 RS28_MOUSE,sp P62859 RS28_RAT,sp Q56JX6 RS28_BOVIN,sp Q6QAT1 RS28_PIG,tri B2R4R9 B2R4R9_HUMAN,tri D2HZS4 D2HZS4_AILME,tri E2RNL7 E2RNL7_CANFA,tri F6WVD1 F6WVD1_HORSE,tri F6WXM1 F6WXM1_CALJA,tri	tGSq GqcT	67%	30.6	48.59415	Ref	Reference Missing (1.3465909)	No Values (-0.4251612)	No Values (-0.59175605)	Reference Missing (1.1094838)	No Values (-0.5363265)	No Values (-0.599555)	No Values (-0.5098578)	Reference Missing (1.3465909)	No Values (-0.4251612)	No Values (-0.59175605)	Reference Missing (1.1094838)	No Values (-0.5363265)	No Values (-0.599555)	No Values (-0.588255)	758.9	1515.7	2	0.0158	10.39	
40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1	7 RS28_HUMAN,sp P62858 RS28_MOUSE,sp P62859 RS28_RAT,sp Q56JX6 RS28_BOVIN,sp Q6QAT1 RS28_PIG,tri B2R4R9 B2R4R9_HUMAN,tri D2HZS4 D2HZS4_AILME,tri E2RNL7 E2RNL7_CANFA,tri F6WVD1 F6WVD1_HORSE,tri F6WXM1 F6WXM1_CALJA,tri	VEF MDD TSR	87%	36.3	48.35545	Ref	-0.09	0.17	0.32	0.042	0.38	-0.07	0.3	81600	66400	86400	107000	97700	1E+05	82200	106000	702.3	1402.7	2	0.0117	8.333

40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1	7 RS28_HUMAN,sp P62858 RS28_MOUSE,sp P62859 RS28_RAT,sp Q56JX6 RS28_BOVIN,sp Q6QAT1 RS28_PIG,tr B2R4R9 B2R4R9_HUMAN,tr D2HZS4 D2HZS4_AILME,tr E2RNL7 E2RNL7_CANFA,tr F6WVD1 F6WVD1_HORSE,tr F6WXM1 F6WXM1_CAJLA,tr	VEF MDD TSR	86%	36.3	48.3988	Ref	0.037	0.058	0.21	0.094	0.42	-0.09	0.37	37500	34600	38100	47400	48300	52800	38900	52900	702.3	1402.7	2	0.0108	7.72
Transthyretin OS=Bos taurus GN=TTR PE=1 SV=1	sp O46375 TTHY_BOVIN,sp P12303 TTHY_SHEEP	aAD ETW EPFA SGk	55%	33.8	53.51158	Ref	0.49	0.33	0.53	0.4	0.47	0.44	0.29	18700	21000	20400	26200	26500	24200	24900	22300	673	2016	3	0.0219	10.86
Transthyretin OS=Bos taurus GN=TTR PE=1 SV=1	sp O46375 TTHY_BOVIN,sp P12303 TTHY_SHEEP	aAD ETW EPFA SGk	94%	50.9	53.51611	Ref	0.32	0.33	0.73	0.35	0.075	1	-0.08	27000	28700	31400	46600	39600	28500	57200	26500	673	2016	3	0.019	9.406
Transthyretin OS=Bos taurus GN=TTR PE=1 SV=1	sp O46375 TTHY_BOVIN,sp P12303 TTHY_SHEEP	aAD ETW EPFA SGk	95%	49.4	53.56477	Ref	0.29	0.27	0.56	0.53	0.065	0.86	0.23	5870	5750	6160	8430	9090	5760	10500	6710	1009	2016	2	0.0182	9.006

Transthyretin OS=Bos taurus GN=TTR PE=1 SV=1	sp O46375 TTHY_BOVIN,sp P12303 TTHY_SHEEP	aAD ETW EPFA SGk	95%	52.3	53.59282	Ref	0.38	0.35	0.62	0.49	0.12	0.96	-0.01	11000	13200	14100	19100	19200	13000	24300	12300	1009	2016	2	0.0179	8.887
Transthyretin OS=Bos taurus GN=TTR PE=1 SV=1	sp O46375 TTHY_BOVIN,sp P12303 TTHY_SHEEP	gSPA ANV GVk	87%	39.1	51.04105	Ref	0.42	0.4	0.52	0.56	0.03	0.8	0.11	26700	29000	30900	37900	42900	25900	46100	28500	754.4	1506.9	2	0.0209	13.83
Transthyretin OS=Bos taurus GN=TTR PE=1 SV=1	sp O46375 TTHY_BOVIN,sp P12303 TTHY_SHEEP	gSPA ANV GVk	95%	46.9	51.13121	Ref	0.25	0.55	0.44	0.56	0.26	0.79	0.15	7240	7930	10600	11000	13200	9360	14100	8990	754.4	1506.9	2	0.025	16.57
Transthyretin OS=Bos taurus GN=TTR PE=1 SV=1	sp O46375 TTHY_BOVIN,sp P12303 TTHY_SHEEP	gSPA ANV GVk	84%	38.9	50.85929	Ref	0.25	0.36	0.66	0.63	-0.08	0.93	0.077	1E+05	143000	2E+05	232000	249000	1E+05	3E+05	154000	503.3	1506.9	3	0.0145	9.602
Transthyretin OS=Bos taurus GN=TTR PE=1 SV=1	sp O46375 TTHY_BOVIN,sp P12303 TTHY_SHEEP	kAA DET WEP FASG k	67%	37.2	54.67127	Ref	0.46	0.043	0.74	0.5	0.13	0.88	0.093	7230	8790	7160	13000	12200	8240	14400	8290	817.1	2448.3	3	0.0149	6.078
Collagen alpha-2(I) chain OS=Bos taurus GN=COL1A2 PE=1 SV=2	sp P02465 CO1A2_BOVIN	dGN PGN DGP PGR	95%	55.3	48.91822	Ref	-1.4	1.5	-1.8	0.15	-1.4	1.2	-2	7490	2190	17500	2020	8540	2550	16000	1760	728.9	1455.7	2	0.0122	8.358
Collagen alpha-2(I) chain OS=Bos taurus GN=COL1A2 PE=1 SV=2	sp P02465 CO1A2_BOVIN	dYEV DATL k	88%	41.6	52.87331	Ref	-1.3	1.3	-1.5	0.16	-1.3	1.3	-1.7	17700	5710	38100	6300	21300	6710	43200	5400	831.5	1660.9	2	0.0182	10.92

Collagen alpha-2(I) chain OS=Bos taurus GN=COL1A2 PE=1 SV=2	sp P02465 CO1A2_BOVIN	gDG GPP GAT GFP GAA GR	93%	44.9	51.95883	Ref	-1.9	1.6	-2.7	0.15	-1.9	1.4	-2.5	6950	1570	20300	1150	9040	1870	19300	1290	873.4	1744.9	2	0.0127	7.259
Collagen alpha-2(I) chain OS=Bos taurus GN=COL1A2 PE=1 SV=2	sp P02465 CO1A2_BOVIN	gEA GPA GPA GPA GPR	69%	34.6	52.14685	Ref	-1	1.2	-0.78	0.13	-0.56	0.65	-0.22	10100	3910	19200	5570	11600	6250	15100	8200	783.4	1564.8	2	0.0146	9.34
Collagen alpha-2(I) chain OS=Bos taurus GN=COL1A2 PE=1 SV=2	sp P02465 CO1A2_BOVIN	gHn GLQ GLP GLA GHH GDQ GAP GAV GPA GPR	79%	39.6	55.61838	Ref	0.26	0.15	-0.07	0.078	-0.15	0.47	0.17	4030	4550	4570	4430	5400	4020	6440	5210	765.1	3056.5	4	0.0204	6.67
Collagen alpha-2(I) chain OS=Bos taurus GN=COL1A2 PE=1 SV=2	sp P02465 CO1A2_BOVIN	gIPG PVG AAG ATG AR	92%	44.3	52.42616	Ref	-0.79	1.3	-1.1	-0.048	-0.79	0.99	-0.94	13800	6900	32800	7000	15500	8100	29200	7560	778.4	1554.9	2	0.0132	8.462
Collagen alpha-2(I) chain OS=Bos taurus GN=COL1A2 PE=1 SV=2	sp P02465 CO1A2_BOVIN	gSTG EIGP AGP PGP PGLR	93%	46.5	53.75504	Ref	-1.3	1.4	-1.7	0.22	-1.4	1.2	-1.5	4850	1790	12600	1620	6740	1860	12500	1850	961	1920	2	0.0145	7.549

Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1	sp O35814 STIP1_RAT,sp P31948 STIP1_HUMAN,sp Q60864 STIP1_MOUSE,tra A8K690 A8K690_HUMAN,tra B4DM70 B4DM70_HUMAN,tra F5H0T1 F5H0T1_HUMAN,tra F6SR Y5 F6SR Y5_CALJA,tra Q3THQ5_MOUSE	aLDL DSSc k	92%	42.9	51.47612	Ref	-0.054	-0.34	-0.02	-0.13	0.049	-0.48	-0.1	22800	19100	17000	23800	24300	24000	17300	22400	803.4	1604.8	2	0.0258	16.1
	sp O35814 STIP1_RAT,sp P31948 STIP1_HUMAN,sp Q60864 STIP1_MOUSE,tra A8K690 A8K690_HUMAN,tra B4DM70 B4DM70_HUMAN,tra F5H0T1 F5H0T1_HUMAN,tra F6SR Y5 F6SR Y5_CALJA,tra Q3THQ5_MOUSE	IIIEQ MQk	80%	37.1	51.72507	Ref	0.1	-0.31	-0.09	-0.26	0.12	-0.39	-0.4	7870	6820	5540	7250	7100	8090	5930	5850	806	1610	2	0.0095	5.893

Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1	sp O35814 STIP1_RAT,sp P31948 STIP1_HUMAN,sp Q60864 STIP1_MOUSE,tr A8K690 A8K690_HUMAN,tr B4DM70 B4DM70_HUMAN,tr F5H0T1 F5H0T1_HUMAN,tr F6SR Y5 F6SRY5_CALJA, tr Q3THQ5 Q3THQ5_MOUSE	ILEF QLAL k	93%	42	46.88909	Ref	0.15	-0.43	-0.08	-0.27	-0.24	-0.21	0.079	3570	3650	2660	3810	3680	3280	3490	4230	561.7	1682.1	3	0.0057	3.408
Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1	sp O35814 STIP1_RAT,sp P31948 STIP1_HUMAN,sp Q60864 STIP1_MOUSE,tr A8K690 A8K690_HUMAN,tr B4DM70 B4DM70_HUMAN,tr F5H0T1 F5H0T1_HUMAN,tr F6SR Y5 F6SRY5_CALJA, tr Q3THQ5 Q3THQ5_MOUSE	IMD VGLI AIR	95%	72.3	50.83012	Ref	0.008	-0.24	0.023	-0.19	0.07	-0.58	-0.05	2940	2800	2560	3450	3270	3430	2280	3270	469	1403.8	3	0.0071	5.019

Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1	sp O35814 STIP1_RAT,sp P31948 STIP1_HUMAN,sp Q60864 STIP1_MOUSE,tr A8K690 A8K690_HUMAN,tr B4DM70 B4DM70_HUMAN,tr F5H0T1 F5H0T1_HUMAN,tr F6SR Y5 F6SRY5_CALJA, tr Q3THQ5 Q3THQ5_MOUSE	mEQ VNEL k	79%	35.9	50.8888	Ref	0.26	-0.65	-0.31	-0.014	-0.02	-0.62	-0.14	518	463	268	380	515	449	309	428	668.9	1335.7	2	0.0116	8.66
Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1	sp O35814 STIP1_RAT,sp P31948 STIP1_HUMAN,sp Q60864 STIP1_MOUSE,tr A8K690 A8K690_HUMAN,tr B4DM70 B4DM70_HUMAN,tr F5H0T1 F5H0T1_HUMAN,tr F6SR Y5 F6SRY5_CALJA, tr Q3THQ5 Q3THQ5_MOUSE	mEQ VNEL k	75%	34.8	50.89347	Ref	0.19	-0.4	-0.29	-0.35	-0.22	-0.39	0.26	985	959	694	838	885	849	788	1220	668.9	1335.7	2	0.013	9.752

Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1	sp O35814 STIP1_RAT,sp P31948 STIP1_HUMAN,sp Q60864 STIP1_MOUSE,tr A8K690 A8K690_HUMAN,tr B4DM70 B4DM70_HUMAN,tr F5H0T1 F5H0T1_HUMAN,tr F6SR Y5 F6SR Y5_CALJA, tr Q3THQ5 Q3THQ5_MOUSE	sAAY Ak	60%	30.9	50.07236	Ref	-0.079	-0.26	-0.21	-0.082	0.16	-0.34	-0.22	16900	14100	13500	15700	18900	19500	14500	15600	609.9	1217.7	2	0.0051	4.187
60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	0 RL7A_MOUSE,sp P62424 RL7A_HUMAN,sp P62425 RL7A_RAT,sp Q2TBQ5 RL7A_BOVIN,sp Q4R5C2 RL7A_MACFA, tr BOK021 BOK021_RAT, tr D3YVE6 D3YVE6_MOUSE, tr D3YXT4 D3YXT4_MOUSE, tr D3Z3R0 D3Z3R0_MOUSE, tr D3ZPL5 D3ZPL5_RAT, tr D3Z	kVAP APA VVk	67%	28.1	45.7179	Ref	0.014	-0.01	0.18	0.043	0.4	-0.21	0.31	14100	12100	12900	16500	16500	18500	12700	18100	631.4	1891.2	3	0.037	19.57

60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	0 RL7A_MOUSE,sp P62424 RL7A_HUMAN,sp P62425 RL7A_RAT,sp Q2TBQ5 RL7A_BOVIN,sp Q4R5C2 RL7A_MAFCA,tr BOK021 BOK021_RAT,tr D3YVE6 D3YVE6_MOUSE,tr D3YXT4 D3YXT4_MOUSE,tr D3Z3R0 D3Z3R0_MOUSE,tr D3ZPL5 D3ZPL5_RAT,tr D3Z	kVAP APA Vvk	82%	32.2	44.99357	Ref	0.039	0.038	0.26	0.069	0.42	-0.18	0.2	14900	14000	15200	19900	19200	21400	14700	19100	631.4	1891.2	3	0.0354	18.7
60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	0 RL7A_MOUSE,sp P62424 RL7A_HUMAN,sp P62425 RL7A_RAT,sp Q2TBQ5 RL7A_BOVIN,sp Q4R5C2 RL7A_MAFCA,tr BOK021 BOK021_RAT,tr D3YVE6 D3YVE6_MOUSE,tr D3YXT4 D3YXT4_MOUSE,tr D3Z3R0 D3Z3R0_MOUSE,tr D3ZPL5 D3ZPL5_RAT,tr D3Z	IkVP PAIN QFT QAL DR	93%	47.6	51.80656	Ref	0.25	-0.23	0.38	0.1	0.35	-0.06	0.36	2500	3750	2930	5020	4560	4730	3710	4920	807.1	2418.4	3	0.0118	4.86

60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	0 RL7A_MOUSE,sp P62424 RL7A_HUMAN,sp P62425 RL7A_RAT,sp Q2TBQ5 RL7A_BOVIN,sp Q4R5C2 RL7A_MAFCA,tr BOK021 BOK021_RAT,trans D3YVE6 D3YVE6_MOUSE,trans D3YXT4 D3YXT4_MOUSE,trans D3Z3R0 D3Z3R0_MOUSE,trans D3ZPL5 D3ZPL5_RAT,trans D3Z	nFGI GQD IQPK	95%	58.3	53.11195	Ref	0.23	-0.33	0.34	-0.073	0.41	-0.2	0.27	24600	24500	17900	32100	26600	32500	22200	30600	913	1824	2	0.0161	8.815
60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	0 RL7A_MOUSE,sp P62424 RL7A_HUMAN,sp P62425 RL7A_RAT,sp Q2TBQ5 RL7A_BOVIN,sp Q4R5C2 RL7A_MAFCA,tr BOK021 BOK021_RAT,trans D3YVE6 D3YVE6_MOUSE,trans D3YXT4 D3YXT4_MOUSE,trans D3Z3R0 D3Z3R0_MOUSE,trans D3ZPL5 D3ZPL5_RAT,trans D3Z	vAPA PAV Vk	95%	47.5	46.02939	Ref	0.055	-0.06	0.2	-0.14	0.55	-0.37	0.4	59900	53900	53800	72400	63300	89200	49100	83300	487.3	1458.9	3	0.0136	9.319

60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	0 RL7A_MOUSE,sp P62424 RL7A_HUMAN,sp P62425 RL7A_RAT,sp Q2TBQ5 RL7A_BOVIN,sp Q4R5C2 RL7A_MAFCA,tr BOK021 BOK021_RAT,trans D3YVE6 D3YVE6_MOUSE,trans D3YXT4 D3YXT4_MOUSE,trans D3Z3R0 D3Z3R0_MOUSE,trans D3ZPL5 D3ZPL5_RAT,trans D3ZAT,trans D3Z	VAPA PAV Vk	61%	28.3	47.43478	Ref	0.1	-0.01	0.24	0.002	0.46	-0.18	0.16	10800	10200	10200	13600	12700	15300	10200	12800	730.5	1458.9	2	0.0274	18.79
60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	0 RL7A_MOUSE,sp P62424 RL7A_HUMAN,sp P62425 RL7A_RAT,sp Q2TBQ5 RL7A_BOVIN,sp Q4R5C2 RL7A_MAFCA,tr BOK021 BOK021_RAT,trans D3YVE6 D3YVE6_MOUSE,trans D3YXT4 D3YXT4_MOUSE,trans D3Z3R0 D3Z3R0_MOUSE,trans D3ZPL5 D3ZPL5_RAT,trans D3ZAT,trans D3Z	VAPA PAV Vk	82%	34.6	47.35471	Ref	0.033	-0.18	-0	-0.16	0.4	-0.22	0.71	15100	13400	12500	15900	15700	20300	13800	26000	487.3	1458.9	3	0.0256	17.54

Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	sp P24534 EF1B_HUMAN,sp P34826 EF1B_RABIT,sp Q5E983 EF1B_BOVIN,tron D2HEP4 D2HEP4_AILME,tron E2ROV2 E2ROV2_CANFA,tron F1SHD6 F1SHD6_PIG,tron F6QN95 F6QN95_MACMU,tron F7GY27 F7GY27_CALJAVR	IEEc	77%	34	48.70573	Ref	-0.29	-0.3	0.22	-0.43	0.43	-0.75	-0.23	3500	2830	3060	4910	3450	5490	2520	3600	366.9	1097.5	3	0.004	3.617
Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	sp P24534 EF1B_HUMAN,sp P34826 EF1B_RABIT,sp Q5E983 EF1B_BOVIN,tron D2HEP4 D2HEP4_AILME,tron E2ROV2 E2ROV2_CANFA,tron F1SHD6 F1SHD6_PIG,tron F6QN95 F6QN95_MACMU,tron F7GY27 F7GY27_CALJAVK	IVPV GYI	90%	38.1	48.27757	Ref	-0.57	-0.29	-0.01	-0.1	0.12	-0.53	-0.04	43400	24700	32500	44300	45700	46600	31000	43400	777.5	1553	2	0.0128	8.231

Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	sp P24534 EF1B_HUMAN,sp P34826 EF1B_RABIT,sp Q5E983 EF1B_BOVIN,tron D2HEP4 D2HEP4_AILME,tron E2ROV2 E2ROV2_CANFA,tron F1SHD6 F1SHD6_PIG,tron F6QN95 F6QN95_MACM U,tron F7GY27 F7GY27_CALIA	SIQA DGL VWG SSk	93%	49.5	53.67641	Ref	-0.49	-0.26	3E-04	-0.04	0.1	-0.53	0.008	43800	29400	37500	50400	54000	52000	35100	50500	652.7	1955.1	3	0.0206	10.52
Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	sp P24534 EF1B_HUMAN,sp P34826 EF1B_RABIT,sp Q5E983 EF1B_BOVIN,tron D2HEP4 D2HEP4_AILME,tron E2ROV2 E2ROV2_CANFA,tron F1SHD6 F1SHD6_PIG,tron F6QN95 F6QN95_MACM U,tron F7GY27 F7GY27_CALIA	SIQA DGL VWG SSk	95%	55.3	53.64356	Ref	-0.29	-0.24	-0.05	-0.25	0.12	-0.45	-0.21	9720	6570	7340	9450	9030	10200	7200	8430	978.5	1955.1	2	0.0176	8.974

Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	sp P24534 EF1B_HUMAN,sp P34826 EF1B_RABIT,sp Q5E983 EF1B_BOVIN,tron D2HEP4 D2HEP4_AILME,tron E2ROV2 E2ROV2_CANFA,tron F1SHD6 F1SHD6_PIG,tron F6QN95 F6QN95_MACM U,tron F7GY27 F7GY27_CALIA	sPAG LQVL NDYL ADK	91%	47.8	54.20083	Ref	-0.37	-0.21	-0.16	-0.13	0.033	-0.59	0.1	33100	22200	26900	31400	35400	34500	23400	37500	738.1	2211.2	3	0.0366	16.55
Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	sp P24534 EF1B_HUMAN,sp P34826 EF1B_RABIT,sp Q5E983 EF1B_BOVIN,tron D2HEP4 D2HEP4_AILME,tron E2ROV2 E2ROV2_CANFA,tron F1SHD6 F1SHD6_PIG,tron F6QN95 F6QN95_MACM U,tron F7GY27 F7GY27_CALIA	sPAG LQVL NDYL ADK	67%	36.4	53.8055	Ref	0.046	-0.36	-0.31	-0.35	0.029	-0.23	0.031	461	457	375	436	467	529	462	549	738.1	2211.2	3	0.0066	2.976

Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	sp P24534 EF1B_HUMAN,sp P34826 EF1B_RABIT,sp Q5E983 EF1B_BOVIN,tri D2HEP4 D2HEP4_AILME,tri E2ROV2 E2ROV2_CANFA,tri F1SHD6 F1SHD6_PIG,tri F6QN95 F6QN95_MACM U,tri F7GY27 F7GY27_CALIA	sPAG LQVL nDYL	ADK	87%	43.8	54.33444	Ref	-0.095	-0.36	-0.11	-0.24	0.008	-0.32	-0.13	8120	6610	5970	7940	8020	8310	6910	7830	738.4	2212.2	3	0.0261	11.8
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_016835 PE=3 SV=1	tr D2HWI4 D2HWI4_AILME	aTGP PVSE LITK	LITK	89%	43.2	51.60775	Ref	-0.84	0.37	-1.3	-0.42	-0.72	-0.16	-0.8	19700	9700	24300	8700	17400	12300	19000	12100	607.7	1820.1	3	0.0235	12.93
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_016835 PE=3 SV=1	tr D2HWI4 D2HWI4_AILME	aTGP PVSE LITK	LITK	95%	50.1	51.36445	Ref	-1.2	0.46	-1.9	-0.23	-0.66	-0.21	-0.79	63900	24200	80600	18000	61500	39900	57100	37800	607.7	1820.1	3	0.0173	9.52

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_016835 PE=3 SV=1	tr D2HWI 4 D2HWI 4_AILME	kATG PPVS ELITk	94%	47.6	49.49073	Ref	-1.2	0.22	-1.5	-0.11	-0.59	-0.14	-0.46	18900	8020	23600	8170	23300	14600	20800	16500	751.8	2252.4	3	0.0352	15.63
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_016835 PE=3 SV=1	tr D2HWI 4 D2HWI 4_AILME	kATG PPVS ELITk	72%	31.1	49.37939	Ref	-0.92	0.098	-1.1	-0.28	-0.74	-0.15	-0.59	15900	7290	16100	8070	15300	9730	15200	11200	564.1	2252.4	4	0.0336	14.91
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_016835 PE=3 SV=1	tr D2HWI 4 D2HWI 4_AILME	kATG PPVS ELITk	68%	29.7	46.86189	Ref	-1.1	0.25	-1.2	-0.4	-0.6	-0.23	-0.22	10300	5160	13900	5860	11000	8370	11300	11300	751.8	2252.4	3	0.0032	1.442

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_016835 PE=3 SV=1	tr D2HWI4 D2HWI4_AILME	nGLS LAAL k	90%	43.6	51.02986	Ref	-1.4	0.51	-1.8	-0.48	-0.69	-0.19	-0.72	18100	5260	21300	4930	13300	10000	14800	10100	499.3	1494.9	3	0.0236	15.78
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_016835 PE=3 SV=1	tr D2HWI4 D2HWI4_AILME	sETA PAET AAP APVE k	61%	34.1	53.16061	Ref	-0.77	0.22	Value Missing (-2.5630846)	-0.24	-0.7	-0.04	-0.59	259	127	274	Value Missing (-2.5630846)	246	156	258	175	958	1914	2	0.0152	7.956
Clusterin OS=Bos taurus GN=CLU PE=1 SV=1	sp P17697 CLUS_BOVIN	aSSI MDE LFQ DR	95%	49.3	51.57596	Ref	0.17	0.47	0.12	0.31	-0.04	0.51	0.25	876	974	1300	1140	1440	985	1510	1250	858.4	1714.8	2	0.0111	6.461
Clusterin OS=Bos taurus GN=CLU PE=1 SV=1	sp P17697 CLUS_BOVIN	kLLLS SLEE Ak	76%	31.5	48.52327	Ref	0.035	0.44	0.2	0.32	0.087	0.45	0.09	2620	2260	3250	3090	3690	2740	3690	2850	536.6	2142.3	4	0.0326	15.22
Clusterin OS=Bos taurus GN=CLU PE=1 SV=1	sp P17697 CLUS_BOVIN	kLLLS SLEE Ak	93%	42.7	46.44586	Ref	0.045	0.41	0.25	0.23	0.077	0.55	0.15	2670	2490	3470	3490	3800	2980	4330	3260	715.1	2142.3	3	0.0082	3.833
Clusterin OS=Bos taurus GN=CLU PE=1 SV=1	sp P17697 CLUS_BOVIN	kLLLS SLEE Ak	93%	44.1	48.45923	Ref	0.28	0.19	0.14	0.28	0.21	0.47	0.17	1580	1720	1750	1910	2310	1920	2400	1940	715.1	2142.3	3	0.0307	14.34

Clusterin OS=Bos taurus GN=CLU PE=1 SV=1	sp P17697 CLUS_BOVIN	rPQD TQYY SPFS SFPR	63%	34.7	53.09272	Ref	0.38	0.29	0.079	0.21	0.2	0.21	0.34	3380	3820	3890	3780	4560	3960	4160	4510	760.7	2279.1	3	0.0149	6.55
Clusterin OS=Bos taurus GN=CLU PE=1 SV=1	sp P17697 CLUS_BOVIN	rPQD TQYY SPFS SFPR	63%	34.7	53.12523	Ref	0.23	0.5	0.11	0.22	0.16	0.25	0.22	2010	2010	2630	2250	2680	2250	2490	2420	760.7	2279.1	3	0.014	6.156
Clusterin OS=Bos taurus GN=CLU PE=1 SV=1	sp P17697 CLUS_BOVIN	tPyH FPT MEF TEnN DR	74%	34.9	52.63875	Ref	0.16	0.25	0.2	0.15	0.15	0.35	0.41	3430	3180	3680	3990	4250	3720	4460	4610	652.8	2607.2	4	0.0255	9.776
Interferon-induced GTP-binding protein Mx1 OS=Ovis aries GN=MX1 PE=2 SV=1	sp P33237 MX1_SHEEP, tr A0SVJ0_SHEEP	ITNE LIMH Lck	75%	38.2	53.7353	Ref	-0.49	-1.1	0.15	-0.048	-0.45	-0.88	0.089	940	582	403	1100	1060	701	544	1060	657	1968.1	3	0.0032	1.606
Interferon-induced GTP-binding protein Mx1 OS=Ovis aries GN=MX1 PE=2 SV=1	sp P33237 MX1_SHEEP, tr A0SVJ0_SHEEP	sSVL EALS GVA LPR	52%	31.4	52.00837	Ref	-0.72	-1.2	0.12	-0.15	0.2	-1.1	0.092	2950	1770	1390	3870	3550	3930	1640	3790	852	1702	2	0.007	4.139
Interferon-induced GTP-binding protein Mx1 OS=Ovis aries GN=MX1 PE=2 SV=1	sp P33237 MX1_SHEEP, tr A0SVJ0_SHEEP	sSVL EALS GVA LPR	95%	57.7	52.16469	Ref	-0.26	-0.31	-0.23	-0.22	-0.39	-0.3	-0.29	953	827	864	1030	1140	887	987	982	568.3	1702	3	0.01	5.874

Interferon-induced GTP-binding protein Mx1 OS=Ovis aries GN=MX1 PE=2 SV=1	sp P33237 MX1_S HEEP,tr A OSVJO A0 SVJO_SHE EP	VRPc IDLI DSLRL	95%	56	53.41124	Ref	-1.1	-1.3	0.38	-0.28	0.27	Value Missing (- 3.466 4001)	0.08	753	254	231	841	587	Value Missing (- 3.4664 001)	755	684	584	1749	3	0.0039	2.256
Interferon-induced GTP-binding protein Mx1 OS=Ovis aries GN=MX1 PE=2 SV=1	sp P33237 MX1_S HEEP,tr A OSVJO A0 SVJO_SHE EP	VRPc IDLI DSLRL	76%	38.2	53.35233	Ref	-1	-1.5	0.089	-0.16	-0.02	-0.8	0.009	592	204	162	548	509	489	297	517	584	1749	3	#####	0.267
Interferon-induced GTP-binding protein Mx1 OS=Ovis aries GN=MX1 PE=2 SV=1	sp P33237 MX1_S HEEP,tr A OSVJO A0 SVJO_SHE EP	VRPc IDLI DSLRL	54%	33.5	53.44331	Ref	-0.72	-0.86	-0.14	-0.23	0.009	-0.99	-0.05	856	381	373	692	717	739	385	736	584	1749	3	0.0085	4.879
Interferon-induced GTP-binding protein Mx1 OS=Ovis aries GN=MX1 PE=2 SV=1	sp P33237 MX1_S HEEP,tr A OSVJO A0 SVJO_SHE EP	VRPc IDLI DSLRL	95%	54.9	53.41124	Ref	-1.2	-0.77	0.21	-0.13	0.19	-1.5	0.092	751	324	460	1020	885	964	315	933	584	1749	3	0.0039	2.256

Calnexin OS=Canis familiaris GN=CANX PE=1 SV=3	sp P24643 CALX_CANFA,tr D2HGC1 D2HGC1_AILME,tr F1S441 F1S441_PIG	aPVP TGE VYFA DSF DR	58%	33.3	52.55627	Ref	0.38	-0.02	0.01	-0.13	-0	-0.35	0.078	6630	8010	6610	7570	7590	7230	5940	7910	692.3	2074	3	0.0157	7.578
Calnexin OS=Canis familiaris GN=CANX PE=1 SV=3	sp P24643 CALX_CANFA,tr D2HGC1 D2HGC1_AILME,tr F1S441 F1S441_PIG	aPVP TGE VYFA DSF DR	95%	74.5	52.60081	Ref	0.1	-0.11	0.055	-0.094	0.37	-0.61	0.007	9020	7970	7480	9390	9330	11300	5950	9060	1038	2074	2	0.0144	6.929
Calnexin OS=Canis familiaris GN=CANX PE=1 SV=3	sp P24643 CALX_CANFA,tr D2HGC1 D2HGC1_AILME,tr F1S441 F1S441_PIG	aPVP TGE VYFA DSF DR	95%	66	52.60946	Ref	0.084	0.044	0.15	-0.13	0.23	-0.39	0.08	3830	4030	4260	5160	4670	5230	3560	4890	1038	2074	2	0.0132	6.341
Calnexin OS=Canis familiaris GN=CANX PE=1 SV=3	sp P24643 CALX_CANFA,tr D2HGC1 D2HGC1_AILME,tr F1S441 F1S441_PIG	aPVP TGE VYFA DSF DR	68%	35.4	52.70262	Ref	0.16	-0	0.021	-0.12	0.048	-0.03	-0.11	5580	5410	5260	5990	5980	5870	5800	5470	692.3	2074	3	0.0113	5.467
Calnexin OS=Canis familiaris GN=CANX PE=1 SV=3	sp P24643 CALX_CANFA,tr D2HGC1 D2HGC1_AILME,tr F1S441 F1S441_PIG	gTLS GWI Lsk	92%	46.6	51.73058	Ref	-0.082	-0.19	0.13	-0.11	0.22	0.02	0.041	9620	8370	8420	11800	11000	12100	11000	11100	557.3	1669	3	0.0289	17.31
Calnexin OS=Canis familiaris GN=CANX PE=1 SV=3	sp P24643 CALX_CANFA,tr D2HGC1 D2HGC1_AILME,tr F1S441 F1S441_PIG	gTLS GWI Lsk	95%	53.6	51.21373	Ref	-0.13	-0.19	0.28	-0.19	0.33	-0.48	0.13	4120	3160	3310	5150	4070	5120	3050	4610	835.5	1669	2	0.0168	10.08

Calnexin OS=Canis familiaris GN=CANX PE=1 SV=3	sp P24643 CALX_CANFA,tr D2HGC1 D2HGC1_AILME,tr F1S441 F1S441_PIG	kIPN PDFF EDLE PFk	74%	36.7	54.28645	Ref	-0.007	-0.25	0.098	-0.13	0.12	-0.2	0.25	4070	3470	3190	4540	4280	4450	3720	5020	687.9	2747.5	4	0.0128	4.662
Translationally-controlled tumor protein OS=Bos taurus GN=TPT1 PE=2 SV=1	sp Q5E984 TCTP_BOVIN,tr A5JST3 A5JST3_CAPHI	dLIS HDE MFS DIYk	74%	38.5	54.30207	Ref	-0.035	-0.23	0.24	-0.012	0.22	-0.38	0.14	16900	13800	13000	20300	18800	19200	13300	18900	774.4	2320.2	3	0.0124	5.327
Translationally-controlled tumor protein OS=Bos taurus GN=TPT1 PE=2 SV=1	sp Q5E984 TCTP_BOVIN,tr A5JST3 A5JST3_CAPHI	eVA DGLc LEVE Gk	95%	63.8	53.79395	Ref	0.03	-0.21	0.25	-0.024	0.14	-0.46	0.24	7020	6140	5630	8720	7940	7760	5370	8620	1009	2015	2	0.0128	6.35
Translationally-controlled tumor protein OS=Bos taurus GN=TPT1 PE=2 SV=1	sp Q5E984 TCTP_BOVIN,tr A5JST3 A5JST3_CAPHI	eVA DGLc LEVE Gk	93%	50.3	53.8183	Ref	0.16	-0.2	0.3	-0.22	0.19	-0.36	0.13	30800	30600	25900	41100	31500	36700	26100	36400	672.7	2015	3	0.0041	2.048
Translationally-controlled tumor protein OS=Bos taurus GN=TPT1 PE=2 SV=1	sp Q5E984 TCTP_BOVIN,tr A5JST3 A5JST3_CAPHI	eVA DGLc LEVE Gk	87%	43.7	53.88978	Ref	0.046	-0.09	0.3	-0.045	0.042	-0.12	-0.07	2170	1940	1920	2820	2440	2270	2120	2170	672.7	2015	3	0.0038	1.869

Translationally-controlled tumor protein OS=Bos taurus GN=TPT1 PE=2 SV=1	sp Q5E984 TCTP_BOVIN, tr A5JST3 A5JST3_CAPHI	eVADGLcLEVEGk	91%	46.8	53.69145	Ref	0.16	-0.1	0.12	-0.008	0.11	-0.16	0.006	2660	2650	2400	3140	3170	2990	2600	2890	672.7	2015	3	0.016	7.955
Translationally-controlled tumor protein OS=Bos taurus GN=TPT1 PE=2 SV=1	sp Q5E984 TCTP_BOVIN, tr A5JST3 A5JST3_CAPHI	eVADGLcLEVEGk	72%	37.6	53.80915	Ref	0.31	0.053	0.063	-0.19	0.084	-0.1	-0.13	365	404	367	415	385	405	372	363	672.7	2015	3	0.0089	4.414
Translationally-controlled tumor protein OS=Bos taurus GN=TPT1 PE=2 SV=1	sp Q5E984 TCTP_BOVIN, tr A5JST3 A5JST3_CAPHI	hILANFk	53%	29	49.15247	Ref	0.18	-0.16	0.058	-0.19	0.23	-0.15	0.097	10300	10100	8670	11300	10500	12300	9830	11600	484.3	1449.9	3	0.0013	0.892

40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	1 RS25_H UMAN,sp P62852 RS25_MO USE,sp P6 2853 RS2 5_RAT,sp Q56JX5 RS25_BO VIN,sp Q 6Q311 RS 25_SHEEP ,tr BOVXX 0 BOVXK0 _CALJA,tr C6ZIA4 C6ZIA4_AI LME,tr D 2I334 D2I 334_AILM E,tr D3Z WX8 D3Z WX8_RAT ,tr E2RS4 9 E2RS49 _CANFA,tr F1M6F4	aALQ ELLS k	67%	33.3	50.70337	Ref	-0.45	-0.02	0.1	-0.094	0.24	-0.05	0.35	4230	2110	3080	3760	3630	3990	3400	4460	527.7	1580	3	0.0225	14.23
40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	1 RS25_H UMAN,sp P62852 RS25_MO USE,sp P6 2853 RS2 5_RAT,sp Q56JX5 RS25_BO VIN,sp Q 6Q311 RS 25_SHEEP ,tr BOVXX 0 BOVXK0 _CALJA,tr C6ZIA4 C6ZIA4_AI LME,tr D 2I334 D2I 334_AILM E,tr D3Z WX8 D3Z WX8_RAT ,tr E2RS4 9 E2RS49 _CANFA,tr F1M6F4	aALQ ELLS k	95%	50	49.9456	Ref	-0.63	0.16	-0.05	0.22	0.35	0.039	0.57	3550	2750	5160	4990	6660	6360	5340	7680	791	1580	2	0.0078	4.931

40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	1 RS25_HUMAN,sp P62852 RS25_MOUSE,sp P62853 RS25_RAT,sp Q56JX5 RS25_BOVIN,sp Q6Q311 RS25_SHEEP,tr BOVXK0 BOVXK0_CALJA,tr C6ZIA4 C6ZIA4_AILME,tr D2I334 D2I334_AILME,tr D3ZWX8 D3ZWX8_RAT,tr E2RS49 E2RS49_CANFA,tr F1M6F4	gGD APA AGE DA	64%	27.9	46.39357	Ref	No Values (0.29704753)	No Values (0.17935394)	No Values (0.0127759045)	No Values (0.06815258)	No Values (0.0053857183)	No Values (0.016259793)	No Values (0.094657353)	No Values (0.17935394)	No Values (0.01275904594)	No Values (0.1277198)	No Values (0.06815258)	No Values (0.0053857183)	No Values (0.016259793)	617.8	1233.6	2	0.0152	12.34
40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	1 RS25_HUMAN,sp P62852 RS25_MOUSE,sp P62853 RS25_RAT,sp Q56JX5 RS25_BOVIN,sp Q6Q311 RS25_SHEEP,tr BOVXK0 BOVXK0_CALJA,tr C6ZIA4 C6ZIA4_AILME,tr D2I334 D2I334_AILME,tr D3ZWX8 D3ZWX8_RAT,tr E2RS49 E2RS49_CANFA,tr F1M6F4	gGD APA AGE DA	67%	28.6	46.48224	Ref	No Values (0.29704753)	No Values (0.17935409)	No Values (0.0127759556)	No Values (0.06815274)	No Values (0.0053858897)	No Values (0.01625995)	No Values (0.0946576253)	No Values (0.17935409)	No Values (0.01275955676)	No Values (0.12771976)	No Values (0.06815274)	No Values (0.0053858897)	No Values (0.016259965)	617.8	1233.6	2	0.0135	10.96

40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	1 RS25_HUMAN,sp P62852 RS25_MOUSE,sp P62853 RS25_RAT,sp Q56JX5 RS25_BOVIN,sp Q6Q311 RS25_SHEEP, tr BOVXK0 BOVXK0_CALJA, tr C6ZIA4 C6ZIA4_AILME, tr D2I334 D2I334_AILME, tr D3ZWX8 D3ZWX8_RAT, tr E2RS49 E2RS49_CANFA, tr F1M6F4	gGD APA AGE DA	84%	33.2	46.57123	Ref	No Values (0.093217015)	No Values (-0.024476482)	No Values (-0.19107126)	No Values (-0.3315048)	Reference Missing (1.013444687635)	No Values (-0.198444687069)	No Values (-0.10917317)	No Values (0.093217015)	No Values (-0.024476482)	No Values (-0.19107126)	No Values (-0.3315048)	Reference Missing (1.013444687635)	No Values (-0.198444687069)	No Values (-0.18757069)	617.8	1233.6	2	0.0112	9.079
40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	1 RS25_HUMAN,sp P62852 RS25_MOUSE,sp P62853 RS25_RAT,sp Q56JX5 RS25_BOVIN,sp Q6Q311 RS25_SHEEP, tr BOVXK0 BOVXK0_CALJA, tr C6ZIA4 C6ZIA4_AILME, tr D2I334 D2I334_AILME, tr D3ZWX8 D3ZWX8_RAT, tr E2RS49 E2RS49_CANFA, tr F1M6F4	gGD APA AGE DA	64%	28	46.51637	Ref	No Values (-0.06509833)	No Values (-0.18279158)	No Values (-0.34938657)	No Values (-0.4898657)	No Values (-0.2939931)	No Values (-0.3567598)	Reference Missing (1.40882928836)	No Values (-0.06509833)	No Values (-0.18279158)	No Values (-0.34938657)	No Values (-0.4898657)	No Values (-0.2939931)	No Values (-0.3567598)	Reference Missing (1.4088292)	617.8	1233.6	2	0.0139	11.25

<p>40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1</p>	<p>1 RS25_HUMAN,sp P62852 RS25_MOUSE,sp P62853 RS25_RAT,sp Q56JX5 RS25_BOVIN,sp Q6Q311 RS25_SHEEP,tr BOVXK0 BOVXK0_CALJA,tr C6ZIA4 C6ZIA4_ALME,tr D2I334 D2I334_AILME,tr D3ZWX8 D3ZWX8_RAT,tr E2RS49 E2RS49_CANFA,tr F1M6F4 </p>	<p>gGDA</p>	<p>58%</p>	<p>27</p>	<p>46.57123</p>	<p>Ref</p>	<p>4753</p>	<p>93540</p>	<p>75921</p>	<p>0.1277</p>	<p>15258</p>	<p>38588</p>	<p>25979</p>	<p>(0.094</p>	<p>(0.297047</p>	<p>93540</p>	<p>(0.0127</p>	<p>0.127719</p>	<p>81525</p>	<p>38588</p>	<p>(0.016259</p>	<p>793)</p>	<p>617.8</p>	<p>1233.6</p>	<p>2</p>	<p>0.0108</p>	<p>8.788</p>
<p>60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1</p>	<p>8 RLA0_HUMAN,sp P14869 RLA0_MOUSE,sp P19945 RLA0_RAT,sp Q29214 RLA0_PIG,sp Q95140 RLA0_BOVIN,tr A7E336 A7E336_BOVIN,tr A8K424 A8K424_HUMAN,tr D2I459 D2I459_AILME,tr F1M2B8 F1M2B8_RAT,tr F1MDN4 F1MDN4_BOVIN,tr F1P720 </p>	<p>gTIEI LSDV QLIK</p>	<p>91%</p>	<p>43</p>	<p>49.4998</p>	<p>Ref</p>	<p>0.31</p>	<p>-0.04</p>	<p>0.007</p>	<p>-0.11</p>	<p>-0.39</p>	<p>0.032</p>	<p>-0.32</p>	<p>1360</p>	<p>1480</p>	<p>1270</p>	<p>1470</p>	<p>1500</p>	<p>1080</p>	<p>1500</p>	<p>1170</p>	<p>679.8</p>	<p>2036.2</p>	<p>3</p>	<p>0.0042</p>	<p>2.065</p>	

60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	8 RLA0_HUMAN,sp P14869 RLA0_MOUSE,sp P19945 RLA0_RAT,sp Q29214 RLA0_PIG,sp Q95140 RLA0_BOVIN,tr A7E336 A7E336_BOVIN,tr A8K424 HUMAN,tr D2I459 D2I459_AILME, tr F1M2B8 F1M2B8_RAT, tr F1MDN4 F1MDN4_BOVIN, tr F1P720	gTIEI LSDV QLIK	88%	39.9	49.49805	Ref	0.14	-0.16	0.22	-0.19	-0.22	-0	-0.43	702	623	548	803	664	570	692	511	679.8	2036.2	3	0.0033	1.609
60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	8 RLA0_HUMAN,sp P14869 RLA0_MOUSE,sp P19945 RLA0_RAT,sp Q29214 RLA0_PIG,sp Q95140 RLA0_BOVIN,tr A7E336 A7E336_BOVIN,tr A8K424 HUMAN,tr D2I459 D2I459_AILME, tr F1M2B8 F1M2B8_RAT, tr F1MDN4 F1MDN4_BOVIN, tr F1P720	gTIEI LSDV QLIK	81%	36.6	49.83604	Ref	0.092	-0.34	0.002	-0.12	-0.13	0.12	-0.04	378	362	292	414	421	364	452	401	679.7	2036.2	3	0.0099	4.848

60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	8 RLA0_HUMAN,sp P14869 RLA0_MOUSE,sp P19945 RLA0_RAT,sp Q29214 RLA0_PIG,sp Q95140 RLA0_BOVIN,tr A7E336 A7E336_BOVIN,tr A8K424 HUMAN,tr D2I459 D2I459_AILME,tr F1M2B8 F1M2B8_RAT,tr F1MDN4 F1MDN4_BOVIN,tr F1P720	ILPHI R	83%	31.7	44.23803	Ref	0.56	-0.26	0.042	-0.38	0.044	-0.19	-0.44	4590	6070	3720	5150	4230	4970	4420	3670	351.6	1051.7	3	0.0041	3.855
60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	8 RLA0_HUMAN,sp P14869 RLA0_MOUSE,sp P19945 RLA0_RAT,sp Q29214 RLA0_PIG,sp Q95140 RLA0_BOVIN,tr A7E336 A7E336_BOVIN,tr A8K424 HUMAN,tr D2I459 D2I459_AILME,tr F1M2B8 F1M2B8_RAT,tr F1MDN4 F1MDN4_BOVIN,tr F1P720	ILPHI R	87%	34.3	44.23803	Ref	0.51	-0.32	0.073	-0.35	0.013	-0.14	-0.44	3240	4020	2450	3610	2980	3330	3130	2520	351.6	1051.7	3	0.0028	2.63

60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	8 RLA0_HUMAN,sp P14869 RLA0_MOUSE,sp P19945 RLA0_RAT,sp Q29214 RLA0_PIG,sp Q95140 RLA0_BOVIN,tr A7E336 A7E336_BOVIN,tr A8K424 A8K424_HUMAN,tr D2I459 D2I459_AILME, tr F1M2B8 F1M2B8_RAT, tr F1MDN4 F1MDN4_BOVIN, tr F1P720	ILPHI R	88%	35	44.23803	Ref	0.52	-0.48	0.22	-0.38	-0.11	-0.18	-0.43	6000	6940	3760	6850	5000	5260	5240	4360	351.6	1051.7	3	0.0032	3.057
60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	8 RLA0_HUMAN,sp P14869 RLA0_MOUSE,sp P19945 RLA0_RAT,sp Q29214 RLA0_PIG,sp Q95140 RLA0_BOVIN,tr A7E336 A7E336_BOVIN,tr A8K424 A8K424_HUMAN,tr D2I459 D2I459_AILME, tr F1M2B8 F1M2B8_RAT, tr F1MDN4 F1MDN4_BOVIN, tr F1P720	ILPHI R	78%	29.9	44.23803	Ref	0.58	-0.27	0.11	-0.45	-0.15	-0.17	-0.46	6410	7750	4680	6840	5110	5470	5630	4570	351.6	1051.7	3	0.0018	1.746

Calmodulin-like protein 3 OS=Rattus norvegicus GN=Calml3 PE=2 SV=1	sp Q5U206 CALL3_RAT	anQL TEEQ IAEF k	87%	40.8	52.55747	Ref	Value Missing (-1.9495907)	0.44	0.089	1.2	0.93	0.11	0.49	526	Value Missing (-1.9495907)	672	592	1390	1020	605	779	934.5	1866.9	2	0.0194	10.38
Calmodulin-like protein 3 OS=Rattus norvegicus GN=Calml3 PE=2 SV=1	sp Q5U206 CALL3_RAT	anQL TEEQ IAEF k	95%	59.5	52.58778	Ref	Value Missing (-1.9361292)	0.36	0.36	0.57	0.99	0.51	0.66	194	Value Missing (-1.9361292)	230	257	328	382	288	316	934.5	1866.9	2	0.0177	9.458
Calmodulin-like protein 3 OS=Rattus norvegicus GN=Calml3 PE=2 SV=1	sp Q5U206 CALL3_RAT	anQL TEEQ IAEF k	82%	38.5	52.65453	Ref	Value Missing (-1.8655157)	-0.05	0.51	0.96	0.9	0.23	0.8	324	Value Missing (-1.8655157)	315	521	786	654	430	636	934.5	1866.9	2	0.0162	8.676
Calmodulin-like protein 3 OS=Rattus norvegicus GN=Calml3 PE=2 SV=1	sp Q5U206 CALL3_RAT	anQL TEEQ IAEF k	95%	60.1	52.7264	Ref	Value Missing (-1.613563)	0.71	0.28	0.58	0.9	0.23	0.85	436	Value Missing (-1.613563)	824	690	936	1020	668	1020	934.5	1866.9	2	0.0143	7.637
Calmodulin-like protein 3 OS=Rattus norvegicus GN=Calml3 PE=2 SV=1	sp Q5U206 CALL3_RAT	anQL TEEQ IAEF k	69%	35.3	52.7937	Ref	Value Missing (-1.7709587)	0.76	0.1	0.38	1	0.39	0.45	361	Value Missing (-1.7709587)	463	329	440	598	402	418	934.5	1866.9	2	0.0128	6.845

Calmodulin-like protein 3 OS=Rattus norvegicus GN=Calml3 PE=2 SV=1	sp Q5U206 CALL3_6 RAT	aNqL TEEQ IAEFK	95%	70.3	52.67719	Ref	Value Missing (-1.6260425)	0.64	0.25	0.57	1.2	-0.14	0.79	233	Value Missing (-1.6260425)	406	349	480	646	267	507	934.5	1866.9	2	0.0161	8.612
Calmodulin-like protein 3 OS=Rattus norvegicus GN=Calml3 PE=2 SV=1	sp Q5U206 CALL3_6 RAT	aNqL TEEQ IAEFK	95%	56.1	52.66805	Ref	Value Missing (-1.6687646)	0.53	0.37	0.89	1.1	-0.16	0.4	188	Value Missing (-1.6687646)	257	258	406	426	180	263	934.5	1866.9	2	0.015	8.023
RCN1 protein OS=Bos taurus GN=RCN1 PE=2 SV=1	tr A4IF88 A4IF88_BOVIN	aADL DSD QTA TR	89%	40	50.68909	Ref	-0.62	0.097	0.005	-0.28	4E-04	-0.65	0.27	9080	5130	9180	9660	8720	9270	6180	11600	784.4	1566.8	2	0.0121	7.693
RCN1 protein OS=Bos taurus GN=RCN1 PE=2 SV=1	tr A4IF88 A4IF88_BOVIN	eEFT AFLH PEEF EHM k	83%	40	54.39238	Ref	-0.24	0.057	-0.09	-0.23	-0.1	-0.42	0.046	3930	2880	3850	3900	3900	3720	3110	4280	658.1	2628.3	4	0.0121	4.59
RCN1 protein OS=Bos taurus GN=RCN1 PE=2 SV=1	tr A4IF88 A4IF88_BOVIN	eEFT AFLH PEEF EHM k	81%	39.1	54.33213	Ref	-0.18	-0.04	-0.16	-0.21	-0.1	-0.2	0.05	2050	1680	2010	2070	2200	2090	2030	2400	658.1	2628.3	4	0.0148	5.625
RCN1 protein OS=Bos taurus GN=RCN1 PE=2 SV=1	tr A4IF88 A4IF88_BOVIN	iDSD GDG FVTT EELK	95%	61.7	54.08484	Ref	-0.59	-0.08	0.008	-0.34	-0.07	-0.76	0.21	36500	16600	25700	30600	26500	27900	18100	35200	745.4	2233.1	3	0.0189	8.466
RCN1 protein OS=Bos taurus GN=RCN1 PE=2 SV=1	tr A4IF88 A4IF88_BOVIN	tFDQ LTSE ESK	95%	64.8	53.60445	Ref	-0.34	0.12	-0.09	-0.32	0.16	-0.66	-0.24	27500	16000	23900	23100	21800	26400	15700	20800	947	1892	2	0.0145	7.663

RCN1 protein OS=Bos taurus GN=RCN1 PE=2 SV=1	tr A4IF88 A4IF88_ BOVIN	yIYD NVA k	94%	46.6	52.77298	Ref	-0.44	0.024	-0.07	-0.099	0.2	-0.51	-0.05	11700	8120	12100	12800	13800	14900	9460	12900	797.4	1592.9	2	0.0185	11.62
Calumenin OS=Bos taurus GN=CALU PE=2 SV=1	sp Q3T0K 1 CALU_B OVIN	dIVV qEP MED IDk	52%	33.8	54.18586	Ref	0.025	0.042	-0.28	-0.3	-0.14	-0.11	-0.29	7320	5510	6050	5450	5890	5780	6130	5380	714.1	2139.1	3	0.0121	5.653
Calumenin OS=Bos taurus GN=CALU PE=2 SV=1	sp Q3T0K 1 CALU_B OVIN	hLVY ESD QnK	91%	47.1	53.5498	Ref	-0.29	0.039	-0.06	-0.28	0.12	-0.35	0.009	19000	13400	18300	19200	18200	21000	15800	20100	614.3	1840	3	0.0176	9.581
Calumenin OS=Bos taurus GN=CALU PE=2 SV=1	sp Q3T0K 1 CALU_B OVIN	mDk EETK DWI LPSD YDH AEAE AR	95%	65	55.70377	Ref	-0.66	0.18	-0.02	-0.14	0.039	-0.22	0.093	2120	1290	2500	2440	2480	2450	2140	2640	916.2	3660.8	4	0.0282	7.699
Calumenin OS=Bos taurus GN=CALU PE=2 SV=1	sp Q3T0K 1 CALU_B OVIN	tFDQ LTPE ESk	95%	55	53.38156	Ref	-0.44	0.32	0.039	-0.35	0.088	-0.24	-0.31	11100	7100	13100	12100	10200	12000	10000	9450	952	1902	2	0.022	11.54
Calumenin OS=Bos taurus GN=CALU PE=2 SV=1	sp Q3T0K 1 CALU_B OVIN	tFDQ LTPE ESKE R	72%	37.5	54.3602	Ref	-0.75	0.23	-0.22	-0.087	0.47	-0.29	0.048	2660	1940	4150	3420	4130	5300	3280	4100	1095	2187.2	2	0.0122	5.564
Calumenin OS=Bos taurus GN=CALU PE=2 SV=1	sp Q3T0K 1 CALU_B OVIN	vHH EPQL Sdk	61%	34.3	53.33699	Ref	-0.54	0.32	-0.1	-0.27	0.15	-0.21	-0.27	7960	4760	9400	7860	7720	9020	7310	6970	899.5	1797	2	0.0097	5.415

Endoplasmic reticulum resident protein 29 OS=Bos taurus GN=ERP29 PE=1 SV=2	sp P81623 ERP29_BOVIN, tr B2LYK8 B2LYK8_SH_EEP	gALP LDTI TFYK	84%	39.6	52.91357	Ref	0.21	0.069	0.083	0.015	-0.03	-0.02	-0.02	4730	4580	4500	5100	5370	4560	4780	4760	974.1	1946.1	2	0.026	13.34
Endoplasmic reticulum resident protein 29 OS=Bos taurus GN=ERP29 PE=1 SV=2	sp P81623 ERP29_BOVIN, tr B2LYK8 B2LYK8_SH_EEP	iLDQ GED FPAS EMT R	95%	51.9	51.50034	Ref	-0.042	0.091	0.3	0.014	0.11	-0.06	-0.01	1910	1670	1990	2580	2340	2190	2030	2080	1007	2012	2	0.0148	7.329
Endoplasmic reticulum resident protein 29 OS=Bos taurus GN=ERP29 PE=1 SV=2	sp P81623 ERP29_BOVIN, tr B2LYK8 B2LYK8_SH_EEP	qGQ DNL ASVk	94%	46.4	52.73973	Ref	-0.14	0.15	0.14	-0.067	0.13	0.017	0.047	17500	12900	17100	19000	18200	18200	17600	17900	834.5	1666.9	2	0.0185	11.11
Endoplasmic reticulum resident protein 29 OS=Bos taurus GN=ERP29 PE=1 SV=2	sp P81623 ERP29_BOVIN, tr B2LYK8 B2LYK8_SH_EEP	sLNIL TAF Qk	95%	64.3	50.86392	Ref	-0.13	0.08	0.14	-0.092	0.21	-0.02	0.038	3310	2420	3030	3540	3330	3570	3200	3290	872	1742	2	0.0168	9.65

Endoplasmic reticulum resident protein 29 OS=Bos taurus GN=ERP29 PE=1 SV=2	sp P81623 ERP29_BOVIN, tr B2LYK8 B2LYK8_SH_EEP	sLNIL TAF Qk	94%	46.9	50.34653	Ref	-0.11	0.13	0.14	-0.081	0.12	0.13	0.28	17100	16800	21400	24300	23000	23000	24200	26700	581.7	1742	3	0.0098	5.626
Endoplasmic reticulum resident protein 29 OS=Bos taurus GN=ERP29 PE=1 SV=2	sp P81623 ERP29_BOVIN, tr B2LYK8 B2LYK8_SH_EEP	sLNIL TAF Qk	89%	41.4	50.24252	Ref	-0.044	0.003	0.06	-0.023	-0.03	0.11	0.34	2060	1820	2040	2380	2480	2160	2470	2880	581.7	1742.1	3	0.0051	2.906
SFRS4 protein OS=Bos taurus GN=SFRS4 PE=2 SV=1	tr A7MB38 A7MB38_BOVIN	eGR GEG EDA GAN QET R	91%	43.1	49.96117	Ref	-0.38	-0.16	-0.01	-0.29	0.4	-0.73	0.014	1360	1190	1490	1870	1690	2390	1140	1890	660.6	1978.9	3	0.0095	4.775
SFRS4 protein OS=Bos taurus GN=SFRS4 PE=2 SV=1	tr A7MB38 A7MB38_BOVIN	gEGE DAG ANQ ETR	95%	67.2	48.49432	Ref	-0.051	-0.18	-0.04	-0.45	0.032	-0.63	-0.1	3100	2520	2500	3090	2570	3130	2060	2960	546.6	1636.8	3	0.0076	4.649
SFRS4 protein OS=Bos taurus GN=SFRS4 PE=2 SV=1	tr A7MB38 A7MB38_BOVIN	gEGE DAG ANQ ETR	95%	64.5	48.49855	Ref	-0.004	-0.23	-0.21	-0.47	0.21	-0.73	-0.11	4560	3700	3440	3920	3590	5030	2740	4170	819.4	1636.8	2	0.0067	4.083
SFRS4 protein OS=Bos taurus GN=SFRS4 PE=2 SV=1	tr A7MB38 A7MB38_BOVIN	qAG EVTY ADA HK	93%	43.1	50.27219	Ref	-0.12	-0.17	-0.22	-0.29	0.006	-0.23	-0.23	18600	15200	15900	17200	18100	19400	17200	17100	788.9	1575.8	2	0.0144	9.116

SFRS4 protein OS=Bos taurus GN=SFRS4 PE=2 SV=1	tr A7MB3 8 A7MB3 8_BOVIN	qAG EVTY ADA HK	95%	58.1	53.49507	Ref	0.0051	-0.38	-0.01	-0.34	0.032	-0.48	-0.19	32100	27500	22900	33100	29000	32900	24200	29200	633.3	1897	3	0.0184	9.706
SFRS4 protein OS=Bos taurus GN=SFRS4 PE=2 SV=1	tr A7MB3 8 A7MB3 8_BOVIN	vIVE HAR	86%	41.8	52.64374	Ref	0.13	-0.2	-0.06	-0.55	0.17	-0.48	-0.3	14100	14700	12600	15600	12200	17600	11700	13200	376.6	1126.7	3	0.0104	9.25
UV excision repair protein RAD23 homolog B OS=Bos taurus GN=RAD23B PE=2 SV=1	sp Q29RK 4 RD23B_ BOVIN	aVEY LLM GIPG DR	92%	44.4	52.98945	Ref	0.083	-0.26	0.061	-0.16	0.14	-0.57	-0.03	2870	2610	2230	3140	2960	3190	2040	2940	869.5	1736.9	2	0.0044	2.517
UV excision repair protein RAD23 homolog B OS=Bos taurus GN=RAD23B PE=2 SV=1	sp Q29RK 4 RD23B_ BOVIN	aVEY LLM GIPG DR	95%	53.8	53.06387	Ref	0.051	-0.34	0.032	-0.081	0.081	-0.65	0.004	541	438	361	527	537	524	331	515	869.5	1736.9	2	0.0094	5.394
UV excision repair protein RAD23 homolog B OS=Bos taurus GN=RAD23B PE=2 SV=1	sp Q29RK 4 RD23B_ BOVIN	iDID PDET VR	89%	40.7	51.60427	Ref	0.0002	-0.32	0.037	-0.22	0.26	-0.37	0.004	49800	45600	39600	57000	52500	64000	43200	55600	738.9	1475.8	2	0.0111	7.499

UV excision repair protein RAD23 homolog B OS=Bos taurus GN=RAD23B PE=2 SV=1	sp Q29RK4 RD23B_BOVIN	iLND DTAL k	64%	33.7	51.75854	Ref	-0.21	-0.23	0.11	-0.12	0.031	-0.22	-0.06	16800	12100	13000	18500	17400	16800	14800	16400	537.7	1609.9	3	0.0052	3.213
UV excision repair protein RAD23 homolog B OS=Bos taurus GN=RAD23B PE=2 SV=1	sp Q29RK4 RD23B_BOVIN	qEkP AERP VETP VATT PTST DSTS GDS SR	81%	40.3	55.78911	Ref	-0.27	-0.2	0.21	-0.036	0.023	-0.7	0.2	2010	1470	1670	2490	2310	2110	1330	2470	910.7	3638.8	4	0.0284	7.816
UV excision repair protein RAD23 homolog B OS=Bos taurus GN=RAD23B PE=2 SV=1	sp Q29RK4 RD23B_BOVIN	tLQQ QTFK	86%	39.2	51.59444	Ref	-0.11	-0.3	0.13	-0.17	0.25	-0.54	0.066	7160	5980	5670	8590	7700	8970	5410	8200	801.5	1600.9	2	0.0067	4.173
Annexin A1 OS=Bos taurus GN=ANXA1 PE=2 SV=2	sp P46193 ANXA1_BOVIN, tr F1N650 F1N650_BOVIN	aLLS LAK	64%	27.5	45.65199	Ref	-0.065	-0.37	-0.35	0.008	-0.01	0.042	-0.6	8680	7280	6410	7280	10300	8860	9600	6090	442	1322.9	3	0.0017	1.251
Annexin A1 OS=Bos taurus GN=ANXA1 PE=2 SV=2	sp P46193 ANXA1_BOVIN, tr F1N650 F1N650_BOVIN	aLLS LAK	51%	27.9	48.43861	Ref	0.083	0.014	-0.57	-0.016	0.11	-0.11	-0.65	11100	12500	13000	9730	15700	14900	13400	9190	442	1322.9	3	0.0212	15.98
Annexin A1 OS=Bos taurus GN=ANXA1 PE=2 SV=2	sp P46193 ANXA1_BOVIN, tr F1N650 F1N650_BOVIN	amV SEFL k	95%	54.9	50.80663	Ref	0.34	0.026	-0.84	-0.3	0.033	-0.25	-0.67	1810	1900	1660	1020	1630	1800	1550	1150	643.8	1285.7	2	0.0075	5.858

Annexin A1 OS=Bos taurus GN=ANXA1 PE=2 SV=2	sp P46193 ANXA1_BOVIN, tr F1N650 F1N650_BOVIN	gDRS EELA VND DLA DSD AR	87%	41.2	51.63033	Ref	-0.15	-0.33	-0.02	-0.11	-0.14	-0.21	0.01	7530	7320	7040	9740	10200	8640	8620	9950	784.7	2351.1	3	0.0142	6.038
Annexin A1 OS=Bos taurus GN=ANXA1 PE=2 SV=2	sp P46193 ANXA1_BOVIN, tr F1N650 F1N650_BOVIN	gGP GSA VSPY PTFN PSSD VEAL HK	56%	36	55.61161	Ref	-0.46	-0.05	-0.66	0.27	0.13	-0.03	-0.78	1240	776	1110	823	1720	1360	1270	756	1008	3021.5	3	0.0235	7.771
Annexin A1 OS=Bos taurus GN=ANXA1 PE=2 SV=2	sp P46193 ANXA1_BOVIN, tr F1N650 F1N650_BOVIN	gVDE ATIIE ILTK	91%	45.1	51.96616	Ref	-0.083	-0.47	-0.27	0.038	-0.12	-0.06	-0.72	1910	1320	1100	1410	1930	1500	1640	1030	670.7	2009.2	3	0.0168	8.38
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MKC1 F1MKC1_BOVIN	eAEE TOS GLQ AEcD QYR	64%	28.9	47.02129	Ref	0.22	-0.38	-0.18	0.07	0.11	-0	-0.05	10700	10600	7570	9770	12800	11400	11100	10700	769.7	2306	3	0.0142	6.153
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MKC1 F1MKC1_BOVIN	IEAE LEK	85%	38.3	51.2608	Ref	-0.15	-0.09	-0.09	-0.003	0.055	-0.05	-0.06	23200	15300	17200	19400	22700	20600	20100	19700	720.4	1438.8	2	#####	0.324
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MKC1 F1MKC1_BOVIN	SILAE TEA MLK	95%	54.2	52.37089	Ref	-0.11	0.16	-0.12	0.024	-0.11	0.079	-0.26	7210	5130	6720	6190	7540	5980	7140	5610	605.4	1813	3	0.0069	3.796

Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MKC 1 F1MKC 1_BOVIN	sVEE EEQ VWK	88%	43.7	53.48383	Ref	-0.14	0.17	0.18	-0.026	-0.01	-0.17	-0.08	7780	6460	8690	9820	9360	8290	7700	8180	624.3	1870	3	0.0176	9.421
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MKC 1 F1MKC 1_BOVIN	sVEE EEQ VWK	90%	45.6	53.46824	Ref	0.051	-0.2	0.061	0.093	-0.03	-0	-0.05	8600	7950	7230	9760	11000	8840	9380	9030	624.3	1870	3	0.0153	8.154
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MKC 1 F1MKC 1_BOVIN	vSAA EEEL QES R	60%	32	51.22881	Ref	1.2	-0.79	-1	-0.85	1.3	-0.91	-0.82	4860	16600	4680	4410	5580	21300	4860	5150	826.4	1650.8	2	0.0174	10.55
Lupus La protein homolog OS=Bos taurus GN=SSB PE=2 SV=2	sp P1088 1 LA_BO VIN	aAQ AGS Ak	54%	31.6	51.81807	Ref	-0.23	-0.31	0.024	-0.067	0.22	-0.58	-0.08	23400	17300	17900	25200	26100	27700	16600	23500	656.4	1310.8	2	0.0041	3.139
Lupus La protein homolog OS=Bos taurus GN=SSB PE=2 SV=2	sp P1088 1 LA_BO VIN	gSIF AVF DSIE SAk	95%	56.7	53.93006	Ref	0.11	-0.42	-0.37	-0.14	-0.1	-0.37	0.25	767	721	539	625	811	730	632	960	693.7	2078.1	3	0.0205	9.883
Lupus La protein homolog OS=Bos taurus GN=SSB PE=2 SV=2	sp P1088 1 LA_BO VIN	gSIF AVF DSIE SAk	57%	34.3	53.79516	Ref	0.47	-0.85	-0.02	-0.27	-0.15	-0.31	-0.28	312	333	145	289	268	254	239	242	693.7	2078.1	3	0.0035	1.702

Lupus La protein homolog OS=Bos taurus GN=SSB PE=2 SV=2	sp P10881 LA_BOVIN	IIEDQQE SLNK	71%	37.2	53.60205	Ref	0.023	-0.25	-0.1	-0.005	0.12	-0.72	-0.16	30700	26400	23800	29500	34800	33100	19400	28300	642.4	1924.1	3	0.011	5.726
Lupus La protein homolog OS=Bos taurus GN=SSB PE=2 SV=2	sp P10881 LA_BOVIN	kFVE TPG QK	63%	31.6	49.95429	Ref	0.046	-0.31	0.083	-0.16	-0.02	-0.2	-0.24	13700	13400	11300	16700	15600	15000	13800	13300	649.4	1945.2	3	0.0062	3.193
Lupus La protein homolog OS=Bos taurus GN=SSB PE=2 SV=2	sp P10881 LA_BOVIN	ITTD FNVI VEAL Sk	95%	56.6	52.6611	Ref	0.22	-0.93	0.019	-0.4	0.12	-0.12	0.01	328	356	175	378	311	391	346	375	720.1	2157.2	3	0.008	3.722
Kininogen-1 OS=Bos taurus GN=KNG1 PE=1 SV=1	sp P01044 KNG1_BOVIN,sp P01045 KNG2_BOVIN	IHGL GLG Hk	61%	29.6	50.10368	Ref	0.19	0.19	0.5	0.12	0.17	0.76	0.052	30200	27000	29300	40800	34500	31300	49200	29800	385.7	1538.9	4	0.0056	3.65
Kininogen-1 OS=Bos taurus GN=KNG1 PE=1 SV=1	sp P01044 KNG1_BOVIN,sp P01045 KNG2_BOVIN	IHGL GLG Hk	72%	31.9	50.0356	Ref	0.27	0.21	0.42	0.19	0.15	0.76	0.15	5090	5300	5530	7160	6740	5710	9140	5960	385.7	1538.9	4	0.0048	3.105
Kininogen-1 OS=Bos taurus GN=KNG1 PE=1 SV=1	sp P01044 KNG1_BOVIN,sp P01045 KNG2_BOVIN	mDN PDTF YSLk	93%	49.1	53.10334	Ref	0.62	0.26	0.21	0.21	-0.13	0.58	0.37	10800	14400	12300	13300	14600	10100	17200	14800	647	1938	3	0.0173	8.898
Kininogen-1 OS=Bos taurus GN=KNG1 PE=1 SV=1	sp P01044 KNG1_BOVIN,sp P01045 KNG2_BOVIN	mDN PDTF YSLk	84%	41.4	53.1391	Ref	0.4	0.1	0.39	0.27	-0.1	0.81	0.4	7640	10500	9270	12700	12900	8710	17000	12700	647	1938	3	0.016	8.248

Kininogen-1 OS=Bos taurus GN=KNG1 PE=1 SV=1	sp P01044 KNG1_BOVIN,sp P01045 KNG2_BOVIN	qHG LGH GHK	83%	40	52.40591	Ref	0.31	0.47	0.19	0.23	0.061	0.64	0.17	16600	16300	19700	18300	20800	16100	25000	18100	527	1577.9	3	0.0213	13.48
Kininogen-1 OS=Bos taurus GN=KNG1 PE=1 SV=1	sp P01044 KNG1_BOVIN,sp P01045 KNG2_BOVIN	sLSS GDT GEcT Dk	95%	75.1	50.29887	Ref	0.48	0.11	0.35	0.33	-0.25	0.93	0.22	6660	9700	8120	10800	11700	6810	16100	9790	977.5	1952.9	2	0.0127	6.483
Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	7 SRC8_HUMAN,sp Q60598 SRC8_MOUSE,trans D3ZGE6 D3ZGE6_RAT,trans D3ZRB0 D3ZRB0_RAT,trans E2RIQ2 E2RIQ2_CANFA,trans F1RY84 F1RY84_PIG,trans F6WKM3 F6WKM3_HORSE,trans F6X4S0 F6X4S0_HORSE,trans O70419 O70419_RAT,trans O70420 O70420_RAT,trans Q1RMR3	sAV GFY QGk	50%	32.4	53.02108	Ref	-0.2	-0.41	-0.51	-0.36	-0.18	-0.66	-0.05	44100	32800	30800	32100	39400	38900	29100	44100	565.3	1692.9	3	0.0145	8.563

Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	7 SRC8_H UMAN,sp Q60598 SRC8_MO USE,tr D3 ZGE6 D3Z GE6_RAT, tr D3ZRB 0 D3ZRB0 _RAT,tr E 2RIQ2 E2 RIQ2_CA NFA,tr F1 RY84 F1R Y84_PIG,t r F6WKM 3 F6WKM 3_HORSE, tr F6X4S0 F6X4S0_ HORSE,tr O70419 O70419_R AT,tr O70 420 O704 20_RAT,tr Q1RMR3	SAV GFEY QGk	95%	54.9	53.07669	Ref	-0.49	-0.36	-0.54	-0.18	0.11	-0.88	-0.16	16600	10000	11900	11800	16600	17800	9350	15300	847.5	1692.9	2	0.014	8.27
Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	7 SRC8_H UMAN,sp Q60598 SRC8_MO USE,tr D3 ZGE6 D3Z GE6_RAT, tr D3ZRB 0 D3ZRB0 _RAT,tr E 2RIQ2 E2 RIQ2_CA NFA,tr F1 RY84 F1R Y84_PIG,t r F6WKM 3 F6WKM 3_HORSE, tr F6X4S0 F6X4S0_ HORSE,tr O70419 O70419_R AT,tr O70 420 O704 20_RAT,tr Q1RMR3	vDQ SAV GFEY QGk	95%	51.2	53.77927	Ref	-0.58	-0.41	-0.62	-0.098	0.13	-0.68	-0.23	9400	5310	6490	6270	9940	10100	6070	8190	1019	2035.1	2	0.0174	8.557

Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	7 SRC8_H UMAN,sp Q60598 SRC8_MO USE,tr D3 ZGE6 D3Z GE6_RAT, tr D3ZRB 0 D3ZRB0 _RAT,tr E 2RIQ2 E2 RIQ2_CA NFA,tr F1 RY84 F1R Y84_PIG,t r F6WKM 3 F6WKM 3_HORSE, tr F6X4S0 F6X4S0_ HORSE,tr O70419 O70419_R AT,tr O70 420 O704 20_RAT,tr Q1RMR3	vDQ SAV GFEY QGK	95%	54.8	53.77863	Ref	-0.47	-0.42	-0.54	-0.29	0.029	-0.7	0.12	63500	43900	49500	51200	67100	72900	45800	80400	679.4	2035.1	3	0.0171	8.422
Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	7 SRC8_H UMAN,sp Q60598 SRC8_MO USE,tr D3 ZGE6 D3Z GE6_RAT, tr D3ZRB 0 D3ZRB0 _RAT,tr E 2RIQ2 E2 RIQ2_CA NFA,tr F1 RY84 F1R Y84_PIG,t r F6WKM 3 F6WKM 3_HORSE, tr F6X4S0 F6X4S0_ HORSE,tr O70419 O70419_R AT,tr O70 420 O704 20_RAT,tr Q1RMR3	vDQ SAV GFEY QGK	95%	54	53.74594	Ref	-0.48	-0.44	-0.57	-0.35	0.093	-0.71	0.13	54400	37000	41000	42200	54400	64300	38500	68300	679.4	2035.1	3	0.0149	7.332

Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	7 SRC8_HUMAN,sp Q60598 SRC8_MOUSE,triD3ZGE6 D3ZGE6_RAT,triD3ZRB0 D3ZRB0_RAT,triE2RIQ2 E2RIQ2_CAF1RIFA,triF1RY84 F1RY84_PIG,triF6WK3 F6WK3_HORSE,triF6X4S0 F6X4S0_HORSE,triO70419 O70419_RAT,triO70420 O70420_RAT,triQ1RMR3	YGLFPANRYVEL	92%	44.5	53.16801	Ref	-0.46	-0.29	-0.5	-0.32	0.097	-0.69	-0.18	2870	1840	2260	2190	2730	3190	1920	2720	873.5	1744.9	2	0.0149	8.51
Alpha-1B-glycoprotein OS=Bos taurus GN=A1BG PE=1 SV=1	sp Q2KJF1 A1BG_BOVIN	gAEEQLVPR	73%	34.4	50.99249	Ref	0.74	0.28	0.46	0.39	-0.04	0.73	0.2	15100	21900	17300	22000	23100	15000	26700	18300	651.9	1301.7	2	0.0105	8.04
Alpha-1B-glycoprotein OS=Bos taurus GN=A1BG PE=1 SV=1	sp Q2KJF1 A1BG_BOVIN	gVTFLLR	60%	30.3	49.48002	Ref	0.86	0.064	0.64	0.32	-0.26	0.92	0.11	27900	49100	30800	51500	45400	26500	62800	35600	555.3	1108.7	2	0.0089	8.008
Alpha-1B-glycoprotein OS=Bos taurus GN=A1BG PE=1 SV=1	sp Q2KJF1 A1BG_BOVIN	IEGEDQFLEVAEPAEATQATFPVHR	95%	106	55.28553	Ref	Reference Missing (0.58562493)	Reference Missing (0.6225689)	Reference Missing (0.34078515)	Reference Missing (0.53490085)	Reference Missing (0.31190085)	Reference Missing (0.7516165)	No Values (-0.29224774)	No Values (-0.21385014)	Reference Missing (0.58562493)	Reference Missing (0.6225689)	Reference Missing (0.34078515)	Reference Missing (0.5343475)	Reference Missing (0.31190085)	Reference Missing (0.7516165)	No Values (-0.29224774)	1030	3087.5	3	0.0131	4.249

Alpha-1B-glycoprotein OS=Bos taurus GN=A1BG PE=1 SV=1	sp Q2KJF1 A1BG_BOVIN	vLSP AGP EAQ FELR	82%	40.5	53.33223	Ref	1.2	-0.07	4E-04	0.43	0.069	0.24	0.089	2430	3070	1420	1680	2490	1690	2000	1780	606.7	1817	3	0.0152	8.352
Alpha-1B-glycoprotein OS=Bos taurus GN=A1BG PE=1 SV=1	sp Q2KJF1 A1BG_BOVIN	vLSP AGP EAQ FELR	94%	50.8	53.37273	Ref	0.29	0.35	0.73	0.12	-0.1	0.45	0.23	2440	1570	1790	2600	1880	1410	2160	1830	606.7	1817	3	0.0134	7.345
Alpha-1B-glycoprotein OS=Bos taurus GN=A1BG PE=1 SV=1	sp Q2KJF1 A1BG_BOVIN	vLSP AGP EAQ FELR	88%	42	53.34323	Ref	0.76	-0.02	0.44	0.48	-0.1	0.89	0.26	2710	4210	2660	4110	4670	2720	5660	3630	909.5	1817	2	0.0053	2.941
14-3-3 protein eta OS=Bos taurus GN=YWHAH PE=1 SV=2	sp P68509 1433F_BOVIN,sp P68510 1433F_MOUSE,sp P68511 1433F_RAT,tr B2KIH1 B2KIH1_RHIFE,tr B7NZM8 B7NZM8_RABIT,tr C3PSX4 C3PSX4_DASNO,tr F2Z4Y1 F2Z4Y1_PIG,tr F6WA79 F6WA79_MOND_O	avTE LNEP LSNE DR	95%	51.5	52.63963	Ref	0.13	-0.26	0.21	-0.065	0.26	-0.48	0.089	9450	9000	7460	11600	10500	11600	7220	10600	946	1890	2	0.0134	7.091

14-3-3 protein eta OS=Bos taurus GN=YWHAH PE=1 SV=2	sp P68509 1433F_BOVIN,sp P68510 1433F_MOUSE,sp P68511 1433F_RAT, tr B2KIH1 B2KIH1_RHIFE, tr B7NZM8 B7NZM8_RABIT, tr C3PSX4 C3PSX4_DASNO, tr F2Z4Y1 F2Z4Y1_PIG, tr F6WA79 F6WA79_MONDO	eHM QPT HPIR	95%	68.5	51.97815	Ref	0.22	-0.18	0.25	-0.21	0.16	-0.08	0.014	38600	45600	37700	56800	45600	51500	45500	48200	388.2	1548.8	4	0.0122	7.884
14-3-3 protein eta OS=Bos taurus GN=YWHAH PE=1 SV=2	sp P68509 1433F_BOVIN,sp P68510 1433F_MOUSE,sp P68511 1433F_RAT, tr B2KIH1 B2KIH1_RHIFE, tr B7NZM8 B7NZM8_RABIT, tr C3PSX4 C3PSX4_DASNO, tr F2Z4Y1 F2Z4Y1_PIG, tr F6WA79 F6WA79_MONDO	eHM QPT HPIR	81%	38.8	52.16185	Ref	0.036	-0.01	-0.23	-0.24	0.38	0.12	-0.08	13800	12600	13200	12800	13900	18800	16300	14100	517.3	1548.8	3	0.0105	6.757

14-3-3 protein eta OS=Bos taurus GN=YWHAH PE=1 SV=2	sp P68509 1433F_BOVIN,sp P68510 1433F_MOUSE,sp P68511 1433F_RAT, tr B2KIH1 B2KIH1_RHIFE, tr B7NZM8 B7NZM8_RABIT, tr C3PSX4 C3PSX4_DASNO, tr F2Z4Y1 F2Z4Y1_PIG, tr F6WA79 F6WA79_MOND	eHm QPT HPIR	67%	32.4	51.79268	Ref	0.29	-0.07	0.13	-0.35	0.24	-0.44	-0.03	14900	14700	12400	16000	12700	16700	10900	14300	392.2	1564.8	4	0.0116	7.416
14-3-3 protein eta OS=Bos taurus GN=NUCB1 PE=1 SV=2	sp P68509 1433F_BOVIN,sp P68510 1433F_MOUSE,sp P68511 1433F_RAT, tr B2KIH1 B2KIH1_RHIFE, tr B7NZM8 B7NZM8_RABIT, tr C3PSX4 C3PSX4_DASNO, tr F2Z4Y1 F2Z4Y1_PIG, tr F6WA79 F6WA79_MOND	eHm QPT HPIR	81%	38.4	51.91973	Ref	0.2	-0.09	-0.02	-0.24	0.17	-0.09	-0.05	8930	8290	7400	8670	8220	9520	8330	8520	522.6	1564.8	3	0.0113	7.195
Nucleobindin-1 OS=Bos taurus GN=NUCB1 PE=2 SV=1	sp Q0P569 NUCB1_BOVIN	IVTL EEFL AST QR	95%	55	53.72894	Ref	Value Missing (-1.670629)	0.25	-0.05	0.54	0.068	0.088	0.002	165	Value Missing (-1.670629)	138	126	210	132	139	130	604.3	1810	3	0.0091	5.011

Nucleobindin-1 OS=Bos taurus GN=NUCB1 PE=2 SV=1	sp Q0P56 9 NUCB1 _BOVIN	IVTL EEFL AST QR	58%	34.4	53.73317	Ref	0.042	0.18	0.1	0.2	-0.31	-0.11	0.27	229	195	232	247	292	179	214	277	604.3	1810	3	0.0098	5.425
Nucleobindin-1 OS=Bos taurus GN=NUCB1 PE=2 SV=1	sp Q0P56 9 NUCB1 _BOVIN	mDA QQE PNIQ LDHL NLLK	88%	43.7	55.14481	Ref	-0.097	-0.15	0.24	-0.094	0.41	0.013	0.095	5290	4240	4420	6530	5690	7050	5600	5880	682.9	2727.5	4	0.0238	8.718
Nucleobindin-1 OS=Bos taurus GN=NUCB1 PE=2 SV=1	sp Q0P56 9 NUCB1 _BOVIN	mDA QQE PNIQ LDHL NLLK	95%	63.4	55.09045	Ref	-0.008	-0.04	0.1	0.038	0.36	-0.16	0.19	1570	1380	1470	1820	1920	2100	1530	1930	910.2	2727.5	3	0.0199	7.286
Nucleobindin-1 OS=Bos taurus GN=NUCB1 PE=2 SV=1	sp Q0P56 9 NUCB1 _BOVIN	rFEE ELAA R	58%	32.6	51.92587	Ref	0.47	0.45	0.15	-0.26	0.039	-0.17	-0.16	2950	4100	4370	3980	3300	3550	3200	3200	475.6	1423.8	3	0.0135	9.477
Nucleobindin-1 OS=Bos taurus GN=NUCB1 PE=2 SV=1	sp Q0P56 9 NUCB1 _BOVIN	rFEE ELAA R	80%	38	51.8531	Ref	0.2	0.31	0.14	-0.17	0.18	-0.28	0.21	8960	10200	11900	11900	10600	11800	8910	12400	475.6	1423.8	3	0.011	7.751
PEST proteolytic signal-containing nuclear protein OS=Bos taurus GN=PCNP PE=2 SV=1	sp Q32PF 3 PCNP_B OVIN	fGFA IGSQ TTk	88%	43.6	53.12492	Ref	-0.051	-0.04	0.14	0.24	0.25	0.12	0.23	5990	5810	6340	8100	9520	8380	8030	8610	589	1764	3	0.0274	15.55

PEST proteolytic signal-containing nuclear protein OS=Bos taurus GN=PCNP PE=2 SV=1	sp Q32PF3 PCNP_BOVIN	sAED ETA DLPT kPTK	90%	46.6	54.43554	Ref	-0.53	-0.11	0.24	0.083	0.65	-0.38	0.35	13800	7790	11400	16200	16000	20700	10600	17500	839.1	2514.4	3	0.0197	7.838
PEST proteolytic signal-containing nuclear protein OS=Bos taurus GN=PCNP PE=2 SV=1	sp Q32PF3 PCNP_BOVIN	sAED ETA DLPT kPTK	70%	37.8	54.58952	Ref	-0.36	-0.18	0.24	0.068	0.58	-0.33	0.51	4890	3530	4340	6490	6370	7910	4400	7830	839.1	2514.4	3	0.0303	12.06
PEST proteolytic signal-containing nuclear protein OS=Bos taurus GN=PCNP PE=2 SV=1	sp Q32PF3 PCNP_BOVIN	tVSS SnG GEnS SR	80%	32.8	47.52364	Ref	-0.24	0.047	0.42	-0.039	0.3	-0.41	0.35	441	299	397	577	463	511	326	550	794.4	1586.7	2	0.0161	10.13
PEST proteolytic signal-containing nuclear protein OS=Bos taurus GN=PCNP PE=2 SV=1	sp Q32PF3 PCNP_BOVIN	tVSS SnG GEnS SR	87%	35.7	47.58238	Ref	-0.35	-0.1	0.31	-0.32	0.36	-0.18	0.42	440	236	304	452	323	450	325	489	794.4	1586.7	2	0.0141	8.897

PEST proteolytic signal-containing nuclear protein OS=Bos taurus GN=PCNP PE=2 SV=1	sp Q32PF3 PCNP_BOVIN	tVSS SnG GEnS SR	93%	40.3	47.7172	Ref	-0.43	-0.08	0.54	0.047	0.45	-0.37	0.37	1360	942	1310	2240	1760	2030	1200	1990	794.4	1586.7	2	0.0132	8.292	
Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	0 PABP1_HUMAN,sp P29341 PABP1_MOUSE,sp P61286 PABP1_BOVIN,sp Q5R8F7 PABP1_PONAB,sp Q9EPH8 PABP1_RAT,sp Q9H361 PABP3_HUMAN,tr B3KT93 B3KT93_HUMAN,tr B4DQX0 B4DQX0_HUMAN, B4DZW4 B4DZW4_HUMAN, D2GY	aVNS ATG VPTV	95%	56.7	51.20705	Ref	No Values (0.30067667)	No Values (0.18298334)	No Values (0.01638869)	No Values (-0.124090575)	No Values (0.07178198)	Reference Missing (0.010438468)	No Values (0.019889135)	No Values (0.0982867567)	No Values (0.300676298334)	No Values (0.18298334)	No Values (0.01638869)	No Values (-0.124090575)	No Values (0.07178198)	Reference Missing (0.010438468)	No Values (0.019889135)	No Values (0.019889135)	660.4	1318.7	2	0.0073	5.525

Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	0 PABP1_ HUMAN,s p P29341 PABP1_ MOUSE,s p P61286 PABP1_B OVIN,sp Q5R8F7 P ABP1_PO NAB,sp Q 9EPH8 PA BP1_RAT, sp Q9H36 1 PABP3_ HUMAN,t r B3KT93 B3KT93_ HUMAN,t r B4DQX0 B4DQX0 _HUMAN, tr B4DZW 4 B4DZW 4_HUMA N,tr D2G Y31 D2GY	nFGE DMD DER	59%	23.7	43.10226	Ref	0.42	-0.1	0.27	-0.098	0.04	-0.12	-0.02	22500	24000	18200	26400	22500	21600	20200	21500	766.3	1530.6	2	0.0146	9.544
Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	0 PABP1_ HUMAN,s p P29341 PABP1_ MOUSE,s p P61286 PABP1_B OVIN,sp Q5R8F7 P ABP1_PO NAB,sp Q 9EPH8 PA BP1_RAT, sp Q9H36 1 PABP3_ HUMAN,t r B3KT93 B3KT93_ HUMAN,t r B4DQX0 B4DQX0 _HUMAN, tr B4DZW 4 B4DZW 4_HUMA N,tr D2G Y31 D2GY	skVD EAV AVL QAH QAK	90%	44.7	52.09585	Ref	-0.099	-0.13	0.22	0.082	0.37	0.024	0.16	1440	1240	1310	1880	1880	2010	1650	1800	869.5	2605.5	3	0.0308	11.82

Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	0 PABP1_ HUMAN,s p P29341 PABP1_ MOUSE,s p P61286 PABP1_B OVIN,sp Q5R8F7 P ABP1_PO NAB,sp Q 9EPH8 PA BP1_RAT, sp Q9H36 1 PABP3_ HUMAN,t r B3KT93 B3KT93_ HUMAN,t r B4DQX0 B4DQX0 _HUMAN, tr B4DZW 4 B4DZW 4_HUMA N,tr D2G Y31 D2GY	skVD	EAV	AVL	QAH	QAK	82%	32.8	51.17636	Ref	-0.25	-0.11	0.11	0.038	0.46	0.023	0.24	3740	2730	3260	4270	4480	5230	4040	4660	522.1	2605.5	5	0.0133	5.116
Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	0 PABP1_ HUMAN,s p P29341 PABP1_ MOUSE,s p P61286 PABP1_B OVIN,sp Q5R8F7 P ABP1_PO NAB,sp Q 9EPH8 PA BP1_RAT, sp Q9H36 1 PABP3_ HUMAN,t r B3KT93 B3KT93_ HUMAN,t r B4DQX0 B4DQX0 _HUMAN, tr B4DZW 4 B4DZW 4_HUMA N,tr D2G Y31 D2GY	skVD	EAV	AVL	QAH	QAK	94%	43.6	51.59763	Ref	-0.054	-0.04	0.21	-0.017	0.13	0.071	0.27	5470	4540	4970	6670	6260	6040	6070	6890	522.1	2605.5	5	0.0209	8.032

<p>Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2</p>	<p>0 PABP1_HUMAN,sp P29341 PABP1_MOUSE,sp P61286 PABP1_BOVIN,sp Q5R8F7 PABP1_PONAB,sp Q9EPH8 PABP1_RAT,sp Q9H361 PABP3_HUMAN,tr B3KT93 B3KT93_HUMAN,tr B4DQX0 B4DQX0_HUMAN,tr B4DZW4 B4DZW4_HUMAN,N,tr D2GY31 D2GY</p>	<p>skVD EAV AVL QAH</p>	<p>91%</p>	<p>41.7</p>	<p>51.06847</p>	<p>Ref</p>	<p>0.015</p>	<p>-0.06</p>	<p>0.16</p>	<p>0.051</p>	<p>0.34</p>	<p>-0.12</p>	<p>0.19</p>	<p>7750</p>	<p>6960</p>	<p>7180</p>	<p>9400</p>	<p>9570</p>	<p>10200</p>	<p>7740</p>	<p>9560</p>	<p>652.4</p>	<p>2605.5</p>	<p>4</p>	<p>0.0111</p>	<p>4.266</p>
<p>Vinculin OS=Sus crofa GN=VCL PE=1 SV=4</p>	<p>sp P26234 VINC_PIG,sp P85972 VINC_RAT,sp Q64727 VINC_MOUSE,tr D2HEE4 D2HEE4_AILME,tr F1N789 F1N789_BOVIN,tr F1PKR3 F1PKR3_CANFA,tr F1SU37 F1SU37_PIG,tr F6ZS25 F6ZS25_HORSE,tr F6ZT22 F6ZT22_HORSE,tr F6ZT60 F6ZT60_HORSE</p>	<p>gLVA EGH R</p>	<p>51%</p>	<p>30</p>	<p>50.57833</p>	<p>Ref</p>	<p>-0.032</p>	<p>0.28</p>	<p>-0.37</p>	<p>-0.3</p>	<p>-0.48</p>	<p>0.11</p>	<p>-0.29</p>	<p>5800</p>	<p>4710</p>	<p>6320</p>	<p>4520</p>	<p>5240</p>	<p>4050</p>	<p>6360</p>	<p>4770</p>	<p>381.6</p>	<p>1141.6</p>	<p>3</p>	<p>0.0079</p>	<p>6.941</p>

Vinculin OS=Sus scrofa GN=VCL PE=1 SV=4	sp P26234 VINC_PIG,sp P85972 VINC_RAT,sp Q64727 VINC_MOUSE,tr D2HEE4 D2HEE4_AILME,tr F1N789 F1N789_BOVIN,tr F1PKR3 F1PKR3_CANFA,tr F1SU37 F1SU37_PIG,tr F6ZS25 F6ZS25_HORSE,tr F6ZT22 F6ZT22_HORSE,tr F6ZT60 F6ZT60_HORSE	gQG ASPV AMQ k	72%	36.8	53.11048	Ref	-0.41	0.46	-0.34	-0.2	-0.51	0.23	-0.23	15800	11300	22400	14500	17500	12400	21500	15600	561.3	1680.9	3	0.0245	14.59
Vinculin OS=Sus scrofa GN=VCL PE=1 SV=4	sp P26234 VINC_PIG,sp P85972 VINC_RAT,sp Q64727 VINC_MOUSE,tr D2HEE4 D2HEE4_AILME,tr F1N789 F1N789_BOVIN,tr F1PKR3 F1PKR3_CANFA,tr F1SU37 F1SU37_PIG,tr F6ZS25 F6ZS25_HORSE,tr F6ZT22 F6ZT22_HORSE,tr F6ZT60 F6ZT60_HORSE	iLLV Ak	76%	24.3	39.509	Ref	-0.7	0.54	-0.62	-0.16	-1	0.82	-0.95	2360	1210	3110	1560	2370	1150	4250	1240	422.3	1263.9	3	0.0209	16.49

Vinculin OS=Sus scrofa GN=VCL PE=1 SV=4	sp P26234 VINC_PIG,sp P85972 VINC_RAT,sp Q64727 VINC_MOUSE,tr D2HEE4 D2HEE4_AILME,tr F1N789 F1N789_BOVIN,tr F1PKR3 F1PKR3_CANFA,tr F1SU37 F1SU37_PIG,tr F6ZS25 F6ZS25_HORSE,tr F6ZT22 F6ZT22_HORSE,tr F6ZT60 F6ZT60_HORSE	iLLV AK	89%	27	35.41829	Ref	-0.64	0.54	-0.63	-0.077	-0.68	0.67	-0.88	3820	2170	5330	2660	4310	2470	6610	2240	422.3	1263.9	3	0.0097	7.663
Vinculin OS=Sus scrofa GN=VCL PE=1 SV=4	sp P26234 VINC_PIG,sp P85972 VINC_RAT,sp Q64727 VINC_MOUSE,tr D2HEE4 D2HEE4_AILME,tr F1N789 F1N789_BOVIN,tr F1PKR3 F1PKR3_CANFA,tr F1SU37 F1SU37_PIG,tr F6ZS25 F6ZS25_HORSE,tr F6ZT22 F6ZT22_HORSE,tr F6ZT60 F6ZT60_HORSE	qQEL THQ EHR	90%	43.6	51.67696	Ref	-0.42	0.1	-0.13	-0.25	-0.11	0.091	-0.12	12100	8330	13000	12400	12500	12100	14500	12400	537.3	1608.8	3	0.0174	10.81

Vinculin OS=Sus scrofa GN=VCL PE=1 SV=4	sp P26234 VINC_PIG,sp P85972 VINC_RAT,sp Q64727 VINC_MOUSE,tr D2HEE4 D2HEE4_AILME,tr F1N789 F1N789_BOVIN,tr F1PKR3 F1PKR3_CANFA,tr F1SU37 F1SU37_PIG,tr F6ZS25 F6ZS25_HORSE,tr F6ZT22 F6ZT22_HORSE,tr F6ZT60 F6ZT60_HO	qQEL THQ EHR	91%	42.4	51.85825	Ref	-0.79	0.56	-0.88	-0.084	-0.71	0.78	-0.88	2390	1180	3250	1340	2570	1450	4280	1340	805.4	1608.8	2	0.0132	8.174
40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	6 RS23_HUMAN,sp P62267 RS23_MOUSE,sp P62268 RS23_RAT,sp P62298 RS23_CHILA,sp Q3T199 RS23_BOVIN,sp Q6SA96 RS23_PIG,tr A8K517 A8K517_HUMAN,tr D2H3P7 D2H3P7_AILME,tr D3YXF9 D3YXF9_MOUSE,tr E1B8G4 E1B8G4_BOVIN,tr E1BAM7	aNPF GGA SHAK	89%	44.3	52.98546	Ref	0.18	-0.24	0.23	-0.11	0.27	-0.27	0.26	31600	29600	24100	37400	32600	36900	26600	38200	555.6	1663.9	3	0.018	10.84

40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	6 RS23_H UMAN,sp P62267 RS23_MO USE,sp P6 2268 RS2 3_RAT,sp P62298 RS23_CHI LA,sp Q3 T199 RS2 3_BOVIN, sp Q6SA9 6 RS23_P IG,tr A8K 517 A8K5 17_HUMA N,tr D2H 3P7 D2H3 P7_AILME ,tr D3YXF 9 D3YXF9 _MOUSE,t r E1B8G4 E1B8G4_ BOVIN,tr E1BAM7	aNPF GGA SHAk	91%	43.5	52.97973	Ref	0.15	-0.38	0.37	-0.038	0.24	-0.21	0.21	3890	3760	2810	5340	4420	4700	3580	4770	833	1663.9	2	0.0172	10.32
40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	6 RS23_H UMAN,sp P62267 RS23_MO USE,sp P6 2268 RS2 3_RAT,sp P62298 RS23_CHI LA,sp Q3 T199 RS2 3_BOVIN, sp Q6SA9 6 RS23_P IG,tr A8K 517 A8K5 17_HUMA N,tr D2H 3P7 D2H3 P7_AILME ,tr D3YXF 9 D3YXF9 _MOUSE,t r E1B8G4 E1B8G4_ BOVIN,tr E1BAM7	g VL Ek	62%	30.1	48.69683	Ref	0.14	-0.41	0.39	-0.13	0.35	-0.37	0.3	7820	7460	5530	10800	8310	10100	6420	10200	422.9	1265.8	3	0.0204	16.14

40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	6 RS23_H UMAN,sp P62267 RS23_MO USE,sp P6 2268 RS2 3_RAT,sp P62298 RS23_CHI LA,sp Q3 T199 RS2 3_BOVIN, sp Q6SA9 6 RS23_P IG,tr A8K 517 A8K5 17_HUMA N,tr D2H 3P7 D2H3 P7_AILME ,tr D3YXF 9 D3YXF9 _MOUSE,t r E1B8G4 E1B8G4_ BOVIN,tr E1BAM7	gIVL Ek	55%	28.1	48.21343	Ref	0.2	-0.3	0.23	-0.13	0.23	-0.09	0.25	13600	13500	10400	16900	14400	16200	13600	17000	633.9	1265.8	2	0.0035	2.777
40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	6 RS23_H UMAN,sp P62267 RS23_MO USE,sp P6 2268 RS2 3_RAT,sp P62298 RS23_CHI LA,sp Q3 T199 RS2 3_BOVIN, sp Q6SA9 6 RS23_P IG,tr A8K 517 A8K5 17_HUMA N,tr D2H 3P7 D2H3 P7_AILME ,tr D3YXF 9 D3YXF9 _MOUSE,t r E1B8G4 E1B8G4_ BOVIN,tr E1BAM7	VAN VSLL ALYK	95%	54.7	48.58501	Ref	0.5	-0.52	0.38	-0.18	0.025	-0.09	0.22	4810	6330	3400	7100	5310	5340	5150	6320	600.4	1798.1	3	0.0153	8.502

40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	6 RS23_H UMAN,sp P62267 RS23_MO USE,sp P6 2268 RS2 3_RAT,sp P62298 RS23_CHI LA,sp Q3 T199 RS2 3_BOVIN, sp Q6SA9 6 RS23_P IG,tr A8K 517 A8K5 17_HUMA N,tr D2H 3P7 D2H3 P7_AILME ,tr D3YXF 9 D3YXF9 _MOUSE,t r E1B8G4 E1B8G4_ VAN BOVIN,tr VSL E1BAM7 ALYK	95%	51.4	48.5561	Ref	0.36	-0.39	0.39	-0.17	0.2	-0.12	0.25	8230	10700	6940	13300	9950	11300	9390	12100	600.4	1798.1	3	0.0148	8.202
LDLR chaperone MESD OS=Bos taurus GN=MESDC2 PE=2 SV=1	sp Q3T0U 1 MESD_ BOVIN,tr cAD F1RIE0 F1 VTLE RIE0_PIG GQV YPGk	95%	52.5	53.73171	Ref	0.19	-0.07	0.15	-0.068	0.025	0.23	0.1	5250	5130	4640	6090	5760	5360	6470	5870	712	2133.1	3	0.0226	10.6
LDLR chaperone MESD OS=Bos taurus GN=MESDC2 PE=2 SV=1	sp Q3T0U 1 MESD_ BOVIN,tr cAD F1RIE0 F1 VTLE RIE0_PIG GQV YPGk	55%	33.9	53.81357	Ref	0.45	0.051	-0.03	-0.033	-0.04	-0	-0.01	7760	8230	6780	7210	7910	6900	7370	7270	712	2133.1	3	0.019	8.885
LDLR chaperone MESD OS=Bos taurus GN=MESDC2 PE=2 SV=1	sp Q3T0U 1 MESD_ BOVIN,tr dYN F1RIE0 F1 DAD RIE0_PIG MAR	85%	32.2	44.96418	Ref	0.014	0.081	0.16	-0.057	0.28	-0.07	0.32	30100	30000	34200	40400	38400	42300	34800	45200	687.8	1373.6	2	0.0119	8.686

LDLR chaperone MESD OS=Bos taurus GN=MESDC2 PE=2 SV=1	sp Q3T0U1 MESD_BOVIN, tr F1RIE0 F1RIE0_PIG	dYNDADmAR	85%	31.6	44.27145	Ref	0.11	0.17	-0.1	-0.018	0.34	-0.16	0.34	6720	7030	7980	7430	8660	9710	7150	10000	695.8	1389.6	2	0.0128	9.2
LDLR chaperone MESD OS=Bos taurus GN=MESDC2 PE=2 SV=1	sp Q3T0U1 MESD_BOVIN, tr F1RIE0 F1RIE0_PIG	rPSA PIDF SQID PGkP ESILk	75%	34.6	52.0594	Ref	-0.083	0.068	0.32	0.028	0.29	-0.11	0.073	2360	1970	2370	3160	2850	2980	2360	2660	802.7	3206.8	4	0.0218	6.809
LDLR chaperone MESD OS=Bos taurus GN=MESDC2 PE=2 SV=1	sp Q3T0U1 MESD_BOVIN, tr F1RIE0 F1RIE0_PIG	rPSA PIDF SQID PGkP ESILk	64%	28.9	52.44492	Ref	0.14	-0.1	0.052	-0.024	0.028	0.043	0.37	1670	1530	1400	1750	1830	1650	1750	2170	642.4	3206.8	5	0.0306	9.542
Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Bos taurus GN=FKBP1A PE=1 SV=2	sp P18203 FKB1A_BOVIN, sp P26883 FKB1A_MOUSE, sp P62942 FKB1A_HUMAN, sp P62943 FKB1A_RABIT, tr A2AT05 A2AT05_MOUSE, tr F7GBW1 F7GBW1_MACMU, tr Q2VTP6 Q2VTP6_PIG, tr Q3ULN5 Q3ULN5_MOUSE	gVQ VETI SPG DGR	95%	67.9	52.39512	Ref	-0.11	-0.23	-0.05	-0.011	0.35	-0.62	0.014	54200	43100	43000	54600	62000	69500	36900	57100	809.9	1617.9	2	0.0124	7.673

Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Bos taurus GN=FKBP1A PE=1 SV=2	sp P18203 FKB1A_BOVIN,sp P26883 FKB1A_MOUSE,sp P62942 FKB1A_HUMAN,sp P62943 FKB1A_RABIT, tr A2AT05 A2AT05_MOUSE, tr F7GBW1 F7GBW1_MACMU, tr Q2VTP6 Q2VTP6_PIG, tr Q3ULN5 Q3ULN5_MOUSE	gVQVETISPGDGR	63%	33.6	52.39512	Ref	-0.26	-0.1	0.067	0.095	0.33	-0.56	-0.04	32100	26100	31800	40000	44900	46000	26100	37000	809.9	1617.9	2	0.0124	7.673
Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Bos taurus GN=FKBP1A PE=1 SV=2	sp P18203 FKB1A_BOVIN,sp P26883 FKB1A_MOUSE,sp P62942 FKB1A_HUMAN,sp P62943 FKB1A_RABIT, tr A2AT05 A2AT05_MOUSE, tr F7GBW1 F7GBW1_MACMU, tr Q2VTP6 Q2VTP6_PIG, tr Q3ULN5 Q3ULN5_MOUSE	gVQVETISPGDGR	91%	45.3	52.40619	Ref	-0.18	4E-04	-0.23	0.11	0.055	-0.15	0.034	42700	36100	44500	42500	59300	49900	45300	51000	540.3	1617.9	3	0.0103	6.336

Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Bos taurus GN=FKBP1A PE=1 SV=2	sp P18203 FKB1A_BOVIN,sp P26883 FKB1A_MOUSE,sp P62942 FKB1A_HUMAN,sp P62943 FKB1A_RABIT, tr A2AT05 A2AT05_MOUSE, tr F7GBW1 F7GBW1_MACMU, tr Q2VTP6 Q2VTP6_PIG, tr Q3ULN5 Q3ULN5_MOUSE	gWE EGV AQM SVG QR	95%	51.5	51.62445	Ref	0.024	-0.18	-0.04	0.005	0.37	-0.74	-0.14	15200	13300	12600	15400	17600	19800	9600	14400	919.5	1836.9	2	0.0146	7.96
Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Bos taurus GN=FKBP1A PE=1 SV=2	sp P18203 FKB1A_BOVIN,sp P26883 FKB1A_MOUSE,sp P62942 FKB1A_HUMAN,sp P62943 FKB1A_RABIT, tr A2AT05 A2AT05_MOUSE, tr F7GBW1 F7GBW1_MACMU, tr Q2VTP6 Q2VTP6_PIG, tr Q3ULN5 Q3ULN5_MOUSE	gWE EGV AQM SVG QR	94%	46.2	51.67303	Ref	0.17	-0.19	0.13	-0.19	-0.02	-0.53	-0.05	18600	17000	14400	20200	17800	17600	12800	17800	919.5	1836.9	2	0.0135	7.362

Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Bos taurus GN=FKBP1A PE=1 SV=2	sp P18203 FKB1A_BOVIN,sp P26883 FKB1A_MOUSE,sp P62942 FKB1A_HUMAN,sp P62943 FKB1A_RABIT, tr A2AT05 A2AT05_MOUSE, tr F7GBW1 F7GBW1_MACMU, tr Q2VTP6 Q2VTP6_PIG, tr Q3ULN5 Q3ULN5_MOUSE	gWE EGV AQM SVG QR	92%	42.6	51.26222	Ref	-0.15	-0.1	0.077	-0.04	0.083	-0.23	-0.12	2380	1880	2110	2680	2720	2590	2180	2330	919.5	1836.9	2	0.0211	11.47
60S ribosomal protein L4 OS=Canis familiaris GN=RPL4 PE=1 SV=2	sp Q28346 RL4_CANFA,sp Q58DW0 R L4_BOVIN, tr E2R546 E2R546_CANFA, tr F1PD88 F1PD88_CANFA, tr F1PVZ2 F1PVZ2_CANFA, tr F6VX41 F6VX41_HORSE	aAA ALEA k	90%	42.3	49.87764	Ref	Value Missing (-0.12980463)	0.15	-0.02	0.009	0.1	-0.07	-0.06	1E+05	63	1E+05	105000	119000	1E+05	1E+05	102000	451.6	1351.8	3	0.0034	2.498

60S ribosomal protein L4 OS=Canis familiaris GN=RPL4 PE=1 SV=2	sp Q28346 RL4_CANFA,sp Q58DW0 RL4_BOVIN, tr E2R546 E2R546_CANFA, tr F1PD88 F1PD88_CANFA, tr F1PVZ2 F1PVZ2_CANFA, tr F6VX41 F6VX41_HORSE	aAA ALEA k	90%	42.4	49.87764	Ref	0.035	-0.14	0.21	-0.084	0.1	0.087	0.082	69000	73600	70900	101000	91000	90400	93400	92400	451.6	1351.8	3	0.0034	2.498
60S ribosomal protein L4 OS=Canis familiaris GN=RPL4 PE=1 SV=2	sp Q28346 RL4_CANFA,sp Q58DW0 RL4_BOVIN, tr E2R546 E2R546_CANFA, tr F1PD88 F1PD88_CANFA, tr F1PVZ2 F1PVZ2_CANFA, tr F6VX41 F6VX41_HORSE	nVTL PAVF k	74%	34.2	49.97496	Ref	0.09	-0.03	0.049	-0.15	0.054	-0.11	0.17	4280	3980	3970	4710	4510	4550	4250	5100	533	1596	3	0.0099	6.182
60S ribosomal protein L4 OS=Canis familiaris GN=RPL4 PE=1 SV=2	sp Q28346 RL4_CANFA,sp Q58DW0 RL4_BOVIN, tr E2R546 E2R546_CANFA, tr F1PD88 F1PD88_CANFA, tr F1PVZ2 F1PVZ2_CANFA, tr F6VX41 F6VX41_HORSE	nVTL PAVF k	75%	34	50.10533	Ref	0.025	-0.02	0.17	-0.092	0.001	-0.05	-0	7680	6580	6900	8860	8140	7580	7660	7830	799	1596	2	0.0114	7.167

60S ribosomal protein L4 OS=Canis familiaris GN=RPL4 PE=1 SV=2	sp Q28346 RL4_CANFA,sp Q58DW0 RL4_BOVIN,tr E2R546 E2R546_CANFA,tr F1PD88 F1PD88_CANFA,tr F1PVZ2 F1PVZ2_CANFA,tr F6VX41 F6VX41_HORSE	nVTL PAVFK	82%	37.3	49.96201	Ref	0.028	-0.1	0.19	0.03	0.076	-0.14	-0.03	4340	3830	3800	5210	5140	4630	4160	4480	533	1596	3	0.0033	2.049
60S ribosomal protein L4 OS=Canis familiaris GN=RPL4 PE=1 SV=2	sp Q28346 RL4_CANFA,sp Q58DW0 RL4_BOVIN,tr E2R546 E2R546_CANFA,tr F1PD88 F1PD88_CANFA,tr F1PVZ2 F1PVZ2_CANFA,tr F6VX41 F6VX41_HORSE	sNYN LPM HK	62%	34.3	52.96731	Ref	0.11	-0.21	0.18	-0.11	0.18	-0.14	0.17	39700	41200	36000	52900	47700	50800	42500	52300	571.3	1710.9	3	0.0057	3.343

26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psm7 PE=1 SV=2	6 PSD7_MOUSE,s p P51665 PSD7_H UMAN,sp Q3ZBD0 PSD7_B OVIN,tr A 1L3B8 A1 L3B8_MO USE,tr A1 L5B1 A1L 5B1_BOVI N,tr B2R D27 B2R D27_HU MAN,tr D 4AEH3 D 4AEH3_R AT,tr E2R BA7 E2RB A7_CANF A,tr F6TS 39 F6TS3 9_MACM U,tr F7E7 72 F7E77	ITNQ VHG Lk	71%	33.9	50.39224	Ref	0.15	-0.08	0.073	-0.083	0.074	-0.09	0.027	23400	22400	20700	25900	25600	24900	23200	25000	540	1617	3	0.0109	6.75
26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psm7 PE=1 SV=2	6 PSD7_MOUSE,s p P51665 PSD7_H UMAN,sp Q3ZBD0 PSD7_B OVIN,tr A 1L3B8 A1 L3B8_MO USE,tr A1 L5B1 A1L 5B1_BOVI N,tr B2R D27 B2R D27_HU MAN,tr D 4AEH3 D 4AEH3_R AT,tr E2R BA7 E2RB A7_CANF A,tr F6TS 39 F6TS3 9_MACM U,tr F7E7 72 F7E77	vVV HPLV LLSV VDH FNR	94%	46.9	51.64329	Ref	0.44	-0.28	-0.06	0.14	-0.15	-0.11	-0.1	555	617	409	532	677	482	518	519	562.6	2246.3	4	0.0131	5.808

26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psm7 PE=1 SV=2	6 PSD7_MOUSE,s p P51665 PSD7_H UMAN,sp Q3ZBD0 PSD7_B OVIN,tr A 1L3B8 A1 L3B8_MO USE,tr A1 L5B1 A1L 5B1_BOVI N,tr B2R D27 B2R D27_HU MAN,tr D 4AEH3 D 4AEH3_R AT,tr E2R BA7 E2RB A7_CANF A,tr F6TS 39 F6TS3 9_MACM U,tr F7E7 72 F7E77	vVV HPLV LLSV VDH FNR	78%	34.8	51.36479	Ref	0.41	-0.29	-0.01	0.16	-0.07	-0.08	-0.13	377	438	292	398	493	369	383	366	562.6	2246.3	4	0.0084	3.743
26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psm7 PE=1 SV=2	6 PSD7_MOUSE,s p P51665 PSD7_H UMAN,sp Q3ZBD0 PSD7_B OVIN,tr A 1L3B8 A1 L3B8_MO USE,tr A1 L5B1 A1L 5B1_BOVI N,tr B2R D27 B2R D27_HU MAN,tr D 4AEH3 D 4AEH3_R AT,tr E2R BA7 E2RB A7_CANF A,tr F6TS 39 F6TS3 9_MACM U,tr F7E7 72 F7E77	vVV HPLV LLSV VDH FNR	66%	31.7	51.15767	Ref	0.19	-0.23	0.1	-0.11	0.31	-0.08	-0.22	201	191	155	219	209	244	194	175	562.6	2246.3	4	0.0035	1.572

40S ribosomal protein S17 OS=Bos taurus GN=RPS17 PE=2 SV=1	3 RS17_BOVIN,sp P04644 RS17_RAT,sp P08708 RS17_HUMAN,sp POCW22 RS17L_HUMAN,sp P63273 RS17_CANFA,sp P63274 RS17_CRIGR,sp P63275 RS17_FELCA,sp P63276 RS17_MOUSE,sp Q6QAP7 RS17_PIG,tr A4D1Q6 A4D1Q6_HUMAN,tr D2HD06	iAGY VTHL Mk	63%	33.7	52.07667	Ref	0.15	-0.04	0.54	0.2	0.45	0.24	0.37	6600	6280	5980	10000	8750	9030	8210	8890	581	1740	3	0.0088	5.038
40S ribosomal protein S17 OS=Bos taurus GN=RPS17 PE=2 SV=1	3 RS17_BOVIN,sp P04644 RS17_RAT,sp P08708 RS17_HUMAN,sp POCW22 RS17L_HUMAN,sp P63273 RS17_CANFA,sp P63274 RS17_CRIGR,sp P63275 RS17_FELCA,sp P63276 RS17_MOUSE,sp Q6QAP7 RS17_PIG,tr A4D1Q6 A4D1Q6_HUMAN,tr D2HD06	iAGY VTHL Mk	95%	49.9	52.26474	Ref	0.15	0.002	0.51	0.17	0.5	0.14	0.43	1540	1460	1430	2280	1980	2170	1770	2150	871	1740	2	0.0169	9.727

40S ribosomal protein S17 OS=Bos taurus GN=RPS17 PE=2 SV=1	3 RS17_BOVIN,sp P04644 RS17_RAT,sp P08708 RS17_HUMAN,sp POCW22 RS17L_HUMAN,sp P63273 RS17_CANFA,sp P63274 RS17_CRIGR,sp P63275 RS17_FELCA,sp P63276 RS17_MOUSE,sp Q6QAP7 RS17_PIG,tr A4D1Q6 A4D1Q6_HUMAN,tr D2HD06	iAGY VTHL Mk	70%	35.3	52.00974	Ref	0.13	0.016	0.54	0.26	0.45	0.14	0.36	48400	44900	44900	72500	65800	65400	55200	64000	581	1740	3	0.0064	3.676
40S ribosomal protein S17 OS=Bos taurus GN=RPS17 PE=2 SV=1	3 RS17_BOVIN,sp P04644 RS17_RAT,sp P08708 RS17_HUMAN,sp POCW22 RS17L_HUMAN,sp P63273 RS17_CANFA,sp P63274 RS17_CRIGR,sp P63275 RS17_FELCA,sp P63276 RS17_MOUSE,sp Q6QAP7 RS17_PIG,tr A4D1Q6 A4D1Q6_HUMAN,tr D2HD06	iAGY VTHL Mk	58%	33.2	52.40137	Ref	0.13	0.099	0.47	0.31	0.39	0.25	0.34	2690	2600	2760	4010	3940	3640	3440	3650	581	1740	3	0.0183	10.52

40S ribosomal protein S17 OS=Bos taurus GN=RPS17 PE=2 SV=1	3 RS17_BOVIN,sp P04644 RS17_RAT,sp P08708 RS17_HUMAN,sp POCW22 RS17L_HUMAN,sp P63273 RS17_CANFA,sp P63274 RS17_CRIGR,sp P63275 RS17_FELCA,sp P63276 RS17_MOUSE,sp Q6QAP7 RS17_PIG,tr A4D1Q6 A4D1Q6_HUMAN,tr D2HD06	iAGY VTHL Mk	60%	33.2	52.06143	Ref	0.19	-0.05	0.58	0.26	0.44	0.17	0.35	495	499	457	794	701	695	603	674	581	1740	3	0.0108	6.192
40S ribosomal protein S17 OS=Bos taurus GN=RPS17 PE=2 SV=1	3 RS17_BOVIN,sp P04644 RS17_RAT,sp P08708 RS17_HUMAN,sp POCW22 RS17L_HUMAN,sp P63273 RS17_CANFA,sp P63274 RS17_CRIGR,sp P63275 RS17_FELCA,sp P63276 RS17_MOUSE,sp Q6QAP7 RS17_PIG,tr A4D1Q6 A4D1Q6_HUMAN,tr D2HD06	iAGY VTHL mk	52%	32.3	52.67866	Ref	0.29	0.03	0.42	0.2	0.38	0.34	0.4	12700	14800	13400	19600	18600	18400	18600	19400	586.3	1756	3	0.0229	13.06

40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1	7 RS24_H UMAN,sp P62848 RS24_ME SAU,sp P 62849 RS 24_MOUS E,sp P628 50 RS24_ RAT,sp Q 4R5H5 RS 24_MACF A,sp Q56J U9 RS24_ BOVIN,sp Q5RAQ8 RS24_PO NAB,tr C7 SZ45 C7S Z45_AILM E,tr D2H9 88 D2H98 8_AILME,t r D212K9 D212K9_A ILME,tr D 3ZFZ8 D3	tTPD VIFV FGFR	95%	48.9	52.99571	Ref	-0.092	-0.46	0.23	-0.098	0.22	-0.46	0.33	1240	1360	1150	2070	1820	1990	1290	2220	852	1701.9	2	0.0099	5.791
40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1	7 RS24_H UMAN,sp P62848 RS24_ME SAU,sp P 62849 RS 24_MOUS E,sp P628 50 RS24_ RAT,sp Q 4R5H5 RS 24_MACF A,sp Q56J U9 RS24_ BOVIN,sp Q5RAQ8 RS24_PO NAB,tr C7 SZ45 C7S Z45_AILM E,tr D2H9 88 D2H98 8_AILME,t r D212K9 D212K9_A ILME,tr D 3ZFZ8 D3	tTPD VIFV FGFR	90%	45.3	52.87949	Ref	-0.19	-0.12	-0.12	-0.33	-0.22	-0.38	0.36	1070	659	752	845	803	757	709	1170	568.3	1701.9	3	0.0074	4.373

40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1	7 RS24_H UMAN,sp P62848 RS24_ME SAU,sp P 62849 RS 24_MOUS E,sp P628 50 RS24_ RAT,sp Q 4R5H5 RS 24_MACF A,sp Q56J U9 RS24_ BOVIN,sp Q5RAQ8 RS24_PO NAB,tr C7 SZ45 C7S Z45_AILM E,tr D2H9 88 D2H98 8_AILME,t r D212K9 D212K9_A ILME,tr D 3ZFZ8 D3	tTPD VIFV FGFR	60%	34	52.92661	Ref	0.11	0.31	-0.17	-0.27	-0.34	-0.27	-0.06	361	318	396	319	328	272	299	343	568.3	1701.9	3	0.008	4.69
40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1	7 RS24_H UMAN,sp P62848 RS24_ME SAU,sp P 62849 RS 24_MOUS E,sp P628 50 RS24_ RAT,sp Q 4R5H5 RS 24_MACF A,sp Q56J U9 RS24_ BOVIN,sp Q5RAQ8 RS24_PO NAB,tr C7 SZ45 C7S Z45_AILM E,tr D2H9 88 D2H98 8_AILME,t r D212K9 D212K9_A ILME,tr D 3ZFZ8 D3	tTPD VIFV FGFR	55%	33.1	52.92661	Ref	0.037	-0.15	-0.05	-0.11	-0.3	0.27	-0.15	532	507	482	583	614	470	728	542	568.3	1701.9	3	0.008	4.69

40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1	7 RS24_H UMAN,sp P62848 RS24_ME SAU,sp P 62849 RS 24_MOUS E,sp P628 50 RS24_ RAT,sp Q 4R5H5 RS 24_MACF A,sp Q56J U9 RS24_ BOVIN,sp Q5RAQ8 RS24_PO NAB,tr C7 SZ45 C7S Z45_AILM E,tr D2H9 88 D2H98 8_AILME,t r D212K9 D212K9_A ILME,tr D 3ZFZ8 D3	tTPD VIFV FGFR	70%	36.2	52.94685	Ref	-0.13	-0.06	0.068	-0.24	-0.28	-0.34	0.099	482	315	360	441	393	332	334	449	568.3	1701.9	3	0.0109	6.417
40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1	7 RS24_H UMAN,sp P62848 RS24_ME SAU,sp P 62849 RS 24_MOUS E,sp P628 50 RS24_ RAT,sp Q 4R5H5 RS 24_MACF A,sp Q56J U9 RS24_ BOVIN,sp Q5RAQ8 RS24_PO NAB,tr C7 SZ45 C7S Z45_AILM E,tr D2H9 88 D2H98 8_AILME,t r D212K9 D212K9_A ILME,tr D 3ZFZ8 D3	tTPD VIFV FGFR	70%	36.1	52.9743	Ref	0.12	0.1	0.17	-0.35	-0.29	0.12	-0.12	171	207	222	261	201	182	253	212	568.3	1701.9	3	0.0309	18.13

Stathmin OS=Rattus norvegicus GN=Stmn1 PE=1 SV=2	8 STMN1_RAT,sp P16949 STMN1_HUMAN,sp P54227 STMN1_MOUSE,sp Q3T0C7 STMN1_BOVIN,sp Q4R712 STMN1_MACFA,sp Q6DUB7 STMN1_PIG,tr B5BU83 B5BU83_HUMAN,tr D2GWF5 D2GWF5_AILME,tr D3Z5N2 D3Z5N2_MOUSE,tr E2R2D9 E2R	aiEENnN	Fsk	95%	58	52.78966	Ref	-1	0.73	0.88	0.95	1.4	0.32	1.6	6160	3000	11000	13700	15800	18700	9330	21800	888	1773.9	2	0.0189	10.64
Stathmin OS=Rattus norvegicus GN=Stmn1 PE=1 SV=2	8 STMN1_RAT,sp P16949 STMN1_HUMAN,sp P54227 STMN1_MOUSE,sp Q3T0C7 STMN1_BOVIN,sp Q4R712 STMN1_MACFA,sp Q6DUB7 STMN1_PIG,tr B5BU83 B5BU83_HUMAN,tr D2GWF5 D2GWF5_AILME,tr D3Z5N2 D3Z5N2_MOUSE,tr E2R2D9 E2R	aSGQAFELILS	PR	95%	53.6	52.8331	Ref	-0.02	0.72	0.74	0.93	1.2	0.58	1.4	2500	1970	3570	4040	5090	5230	3640	6280	847	1691.9	2	0.0127	7.489

Stathmin OS=Rattus norvegicus GN=Stmn1 PE=1 SV=2	8 STMN1 _RAT,sp P16949 S TMN1_H UMAN,sp P54227 STMN1_ MOUSE,s p Q3T0C7 STMN1_ BOVIN,sp Q4R712 STMN1_ MACFA,sp Q6DUB7 STMN1_ PIG,tr B5 BU83 B5 BU83_HU MAN,tr D 2GWF5 D 2GWF5_A ILME,tr D 3Z5N2 D3 Z5N2_MO USE,tr E2 R2D9 E2R	dLSL EEIQ	k	95%	53.5	52.72144	Ref	-0.68	0.66	0.85	1.1	1.3	0.31	1.4	8220	4470	12300	15700	20500	21200	10800	23600	842	1682	2	0.0183	10.86
Stathmin OS=Rattus norvegicus GN=Stmn1 PE=1 SV=2	8 STMN1 _RAT,sp P16949 S TMN1_H UMAN,sp P54227 STMN1_ MOUSE,s p Q3T0C7 STMN1_ BOVIN,sp Q4R712 STMN1_ MACFA,sp Q6DUB7 STMN1_ PIG,tr B5 BU83 B5 BU83_HU MAN,tr D 2GWF5 D 2GWF5_A ILME,tr D 3Z5N2 D3 Z5N2_MO USE,tr E2 R2D9 E2R	eAQ MAA	k	56%	31.7	51.64555	Ref	-0.19	0.75	0.72	0.91	1.3	0.64	1.3	25500	18700	38900	42800	53600	60400	40600	65500	678.9	1355.7	2	0.0243	17.89

Stathmin OS=Rattus norvegicus GN=Stmn1 PE=1 SV=2	8 STMN1_RAT,sp P16949 STMN1_HUMAN,sp P54227 STMN1_MOUSE,sp Q3TOC7 STMN1_BOVIN,sp Q4R712 STMN1_MACFA,sp Q6DUB7 STMN1_PIG,tr B5BU83 B5BU83_HUMAN,tr D2GWF5 D2GWF5_AILME,tr D3Z5N2 D3Z5N2_MOUSE,tr E2R2D9 E2R	sHEA EVLK	90%	42.5	52.73214	Ref	-0.17	0.75	0.66	0.92	1.3	0.54	1.4	2390	2040	4170	4400	5830	6800	4070	7490	760.9	1519.9	2	0.0227	14.91
Uncharacterized protein OS=Bos taurus GN=Bt.30397 PE=3 SV=1	tr F1MQ21 F1MQ21_BOVIN	aPW AGA PLHL GQG QFLK	95%	55	53.28573	Ref	-0.32	0.12	-0.51	-0.28	-0.07	-0.43	-0.04	1230	918	1360	981	1270	1280	1040	1350	800.5	2398.4	3	0.016	6.66
Uncharacterized protein OS=Bos taurus GN=Bt.30397 PE=3 SV=1	tr F1MQ21 F1MQ21_BOVIN	aPW AGA PLHL GQG QFLK	63%	33	53.16627	Ref	-0.33	-0.15	-0.39	-0.14	-0.24	-0.19	-0.06	2660	1910	2360	2240	2930	2390	2590	2820	600.6	2398.4	4	0.0143	5.95
Uncharacterized protein OS=Bos taurus GN=Bt.30397 PE=3 SV=1	tr F1MQ21 F1MQ21_BOVIN	dNLA EEVE GVA SR	93%	44.2	52.01946	Ref	-0.18	-0.28	-0.38	-0.16	-0.42	-0.1	-0.11	2110	1560	1580	1650	2120	1540	2030	1990	846.9	1691.9	2	0.0091	5.39

Uncharacterized protein OS=Bos taurus GN=Bt.30397 PE=3 SV=1	tr F1MQ21 F1MQ21_BOVIN	sLEE ENLE TLk	95%	52.5	53.51396	Ref	-0.38	-0.09	-0.48	-0.19	-0.28	-0.1	-0.15	5740	3660	4850	4150	5610	4600	5440	5200	957	1912.1	2	0.0105	5.472
Uncharacterized protein OS=Bos taurus GN=Bt.30397 PE=3 SV=1	tr F1MQ21 F1MQ21_BOVIN	sLEK ETLE LLkPI Gk	77%	19.7	40.19656	Ref	-0.32	-0.04	-0.46	-0.15	-0.38	-0.06	-0.18	2750	1910	2520	2110	2900	2150	2800	2560	583.8	2913.8	5	0.0031	1.066
Uncharacterized protein OS=Monodelphis domestica GN=TUBB6 PE=3 SV=1	tr F7CB79 F7CB79_MONDO	eIVH IQAG QcG NQI GtK	86%	43.9	54.77201	Ref	0.14	-0.57	0.3	-0.051	0.25	-0.06	0.15	2080	2160	1430	2940	2540	2740	2310	2630	817.4	2449.3	3	0.0161	6.572
Uncharacterized protein OS=Monodelphis domestica GN=TUBB6 PE=3 SV=1	tr F7CB79 F7CB79_MONDO	eVD EQM LAIQ Nk	93%	49.3	53.78156	Ref	0.062	-0.06	-0	0.18	-0.01	-0.12	-0.22	20200	14600	14500	16900	21200	16200	15700	14500	676	2025.1	3	0.0127	6.264
Uncharacterized protein OS=Monodelphis domestica GN=TUBB6 PE=3 SV=1	tr F7CB79 F7CB79_MONDO	ISEQ FSA MFR	87%	39.3	51.32794	Ref	0.31	-0.21	0.27	-0.085	-0.15	-0.2	-0.14	5970	5250	3960	6220	5360	4460	4510	4680	760.4	1518.8	2	0.0106	6.977

Uncharacterized protein OS=Monodelphis domestica GN=TUBB6 PE=3 SV=1	tr F7CB79 F7CB79_MONDO	IHFF MPG FAPL TAR	79%	39.4	53.65411	Ref	0.093	-0.48	0.038	-0.018	0.004	-0.04	0.56	378	385	281	451	479	424	429	647	637	1908	3	0.0075	3.927
Uncharacterized protein OS=Monodelphis domestica GN=TUBB6 PE=3 SV=1	tr F7CB79 F7CB79_MONDO	IHFF mPG FAPL TAR	95%	59.1	53.62923	Ref	0.23	-0.07	0.014	-0.14	-0.11	-0.22	0.42	1560	1580	1400	1660	1650	1470	1420	2200	642.3	1924	3	0.0104	5.414
Cadherin-5 OS=Bos taurus GN=CDH5 PE=2 SV=1	sp Q6URK6 CADH5_BOVIN	kPLI GSVL AK	86%	24.3	37.41546	Ref	-0.3	-0.92	0.36	-0.001	0.32	-1.4	0.22	24500	15000	10600	28800	24800	27100	8430	26200	485.3	1937.3	4	0.0026	1.329
Cadherin-5 OS=Bos taurus GN=CDH5 PE=2 SV=1	sp Q6URK6 CADH5_BOVIN	kPLI GSVL AK	95%	43.7	37.27623	Ref	-0.1	-0.55	0.16	-0.091	0.09	-0.41	0.15	12100	10200	8120	14900	13800	13700	10100	14800	646.8	1937.3	3	0.002	1.026
Cadherin-5 OS=Bos taurus GN=CDH5 PE=2 SV=1	sp Q6URK6 CADH5_BOVIN	IVVQ ISAT DkDI TPR	95%	65.1	52.06543	Ref	0.0071	-0.91	0.57	-0.76	0.35	-0.9	0.76	2780	5540	3180	9950	4370	8250	3620	11300	755.4	2263.3	3	0.017	7.517
Cadherin-5 OS=Bos taurus GN=CDH5 PE=2 SV=1	sp Q6URK6 CADH5_BOVIN	nLES PSSF TIK	94%	46.5	53.15868	Ref	-0.2	-0.81	0.26	-0.17	0.09	-0.84	0.38	11600	7970	5670	13400	11000	11400	6280	14500	916	1830	2	0.0097	5.316
Cadherin-5 OS=Bos taurus GN=CDH5 PE=2 SV=1	sp Q6URK6 CADH5_BOVIN	yTFS VPE DIR	57%	32.1	51.90615	Ref	-0.13	-0.61	0.2	-0.2	0.22	-0.83	0.32	11400	9040	7030	13800	11500	13500	6810	15000	765.9	1529.8	2	0.0146	9.555

Transitional endoplasmic reticulum ATPase OS=Sus scrofa GN=VCP PE=1 SV=5	sp P03974 TERA_PIG,sp P46462 TERA_RAT,sp P55072 TERA_HUMAN,sp Q01853 TERA_MOUSE,sp Q3ZBT1 TERA_BOVIN,trans E2RLQ9 E2RLQ9_CANFA,trans F6WT88 F6WT88_MACMU,trans F7A525 F7A525_CALJA,trans F7BWW6 F7BWW6_HORSE	gDDL STAI Lk	95%	63.8	52.05166	Ref	-0.24	-0.29	-0.01	-0.096	-0.09	-0.42	-0.33	9910	6300	6580	8970	9330	8200	6820	7190	821	1640	2	0.008	4.899
Transitional endoplasmic reticulum ATPase OS=Sus scrofa GN=VCP PE=1 SV=5	sp P03974 TERA_PIG,sp P46462 TERA_RAT,sp P55072 TERA_HUMAN,sp Q01853 TERA_MOUSE,sp Q3ZBT1 TERA_BOVIN,trans E2RLQ9 E2RLQ9_CANFA,trans F6WT88 F6WT88_MACMU,trans F7A525 F7A525_CALJA,trans F7BWW6 F7BWW6_HORSE	gGNI GDG GGA ADR	95%	65.1	49.42231	Ref	-0.052	-0.24	-0.02	-0.07	-0.28	-0.17	-0.41	8190	6700	6390	8340	8880	6690	7550	6330	710.9	1419.7	2	0.0111	7.796

Transitional endoplasmic reticulum ATPase OS=Sus scrofa GN=VCP PE=1 SV=5	sp P03974 TERA_PIG,sp P46462 TERA_RAT,sp P55072 TERA_HUMAN,sp Q01853 TERA_MOUSE,sp Q3ZBT1 TERA_BOVIN,trans E2RLQ9 E2RLQ9_CANFA,trans F6WT88 F6WT88_MACMU,trans F7A525 F7A525_CALJA,trans F7BWW6 F7BWW6_HORSE	KYEMFAMFAQTLQQSR	85%	43.2	54.7159	Ref	0.0005	-0.14	-0.15	-0.16	-0.32	-0.19	-0.17	6060	5420	5340	5930	6490	5100	5810	5840	746.7	2237.2	3	0.0149	6.644
Transitional endoplasmic reticulum ATPase OS=Sus scrofa GN=VCP PE=1 SV=5	sp P03974 TERA_PIG,sp P46462 TERA_RAT,sp P55072 TERA_HUMAN,sp Q01853 TERA_MOUSE,sp Q3ZBT1 TERA_BOVIN,trans E2RLQ9 E2RLQ9_CANFA,trans F6WT88 F6WT88_MACMU,trans F7A525 F7A525_CALJA,trans F7BWW6 F7BWW6_HORSE	KYEMFAMFAQTLQQSR	63%	36.4	54.71214	Ref	0.073	-0.32	-0.21	-0.14	-0.16	-0.07	-0.13	4110	4400	3630	4410	5090	4380	4880	4630	746.7	2237.2	3	0.013	5.826

Transitional endoplasmic reticulum ATPase OS=Sus scrofa GN=VCP PE=1 SV=5	sp P03974 TERA_PIG,sp P46462 TERA_RAT,sp P55072 TERA_HUMAN,sp Q01853 TERA_MOUSE,sp Q3ZBT1 TERA_BOVIN,tr E2RLQ9 E2RLQ9_CANFA,tr F6WT88 F6WT88_MACMU,tr F7A525 F7A525_CALJA,tr F7BWW6 F7BWW6_HORSE	IHLQ IHTK	80%	35.5	49.07524	Ref	-0.056	-0.22	-0.16	-0.18	-0.31	0.004	-0.26	4660	3890	3760	4420	4800	3820	4970	4100	568.4	1702.1	3	0.0088	5.152
Uncharacterized protein OS=Sus scrofa GN=Ssc.1952 PE=4 SV=1	tr F1S880 F1S880_PIG,tr F1S884 F1S884_PIG	dLIH DQD EDEE EEEE QR	95%	79.2	47.03068	Ref	0.11	-0.22	0.16	0.071	0.18	-0.33	-0.18	5800	4380	3790	5510	5720	5400	3960	4360	797.4	2389	3	0.0153	6.383
Uncharacterized protein OS=Sus scrofa GN=Ssc.1952 PE=4 SV=1	tr F1S880 F1S880_PIG,tr F1S884 F1S884_PIG	eHG AVA VER	74%	35.1	50.89806	Ref	0.092	0.23	0.18	-0.16	0.19	-0.4	0.016	10700	9890	11800	12800	11100	12400	8600	11400	424.6	1270.7	3	0.008	6.262
Uncharacterized protein OS=Sus scrofa GN=Ssc.1952 PE=4 SV=1	tr F1S880 F1S880_PIG,tr F1S884 F1S884_PIG	IGAA PEEE SAYV AGE R	95%	49.2	52.40896	Ref	0.044	-0.43	0.22	0.14	0.27	-0.62	0.31	11700	10200	7990	14000	14600	14000	7880	14900	977	1952	2	0.0135	6.93

Uncharacterized protein OS=Sus scrofa GN=Sc.1952 PE=4 SV=1	tr F1S880 F1S880_PIG, tr F1S884 F1S84_PIG	IGAA PEEE SAYV AGE R	85%	41.2	52.40868	Ref	-0.08	-0.02	0.28	0.21	-0.1	-0.05	-0.05	13000	10800	12100	16900	17600	12400	13400	13400	651.7	1952	3	0.0133	6.805
Uncharacterized protein OS=Sus scrofa GN=Sc.1952 PE=4 SV=1	tr F1S880 F1S880_PIG, tr F1S884 F1S84_PIG	IGST APQ VLNT SSPA QQA ENE AK	84%	43.3	55.51626	Ref	-0.021	0.31	0.31	0.08	0.062	-0.9	0.2	1950	1820	2480	2790	2620	2260	1210	2570	983.9	2948.5	3	0.0195	6.62
Alpha-actinin-1 OS=Macaca fascicularis GN=ACTN1 PE=2 SV=1	sp Q2PFV7 ACTN1_MACFA, sp Q3B7N2 ACTN1_BOVIN, tr A4ZZF8 A4ZZF8_BOVIN, tr E2QY07 E2QY07_CA_NFA, tr E2QY08 E2QY08_CA_NFA, tr F1MNY7 F1MNY7_BOVIN, tr F1PGU0 F1PGU0_CA_NFA, tr F1SA20 F1SA20_PIG	dGL GFcA LIHR	95%	53.9	52.09461	Ref	-0.23	-0.41	-0.23	-0.45	-0.71	-0.26	-0.65	2470	1480	1420	1810	1710	1250	1780	1350	517.9	1550.8	3	0.0045	2.915

Alpha-actinin-1 OS=Macaca fascicularis GN=ACTN1 PE=2 SV=1	sp Q2PFV7 ACTN1_MACFA,sp Q3B7N2 ACTN1_BOVIN,tr A4ZZF8 A4ZZF8_BOVIN,tr E2QY07 E2QY07_CANFA,tr E2QY08 E2QY08_CANFA,tr F1MNY7 F1MNY7_BOVIN,tr F1PGU0 F1PGU0_CANFA,tr F1SA20 F1SA20_PIG	eTADTDQVMASFK	81%	39.9	53.16938	Ref	-0.34	-0.26	-0.6	-0.006	-0.13	-0.49	-0.55	6980	5300	6110	5400	8980	7210	5870	5570	780.1	2337.1	3	0.019	8.143
Alpha-actinin-1 OS=Macaca fascicularis GN=ACTN1 PE=2 SV=1	sp Q2PFV7 ACTN1_MACFA,sp Q3B7N2 ACTN1_BOVIN,tr A4ZZF8 A4ZZF8_BOVIN,tr E2QY07 E2QY07_CANFA,tr E2QY08 E2QY08_CANFA,tr F1MNY7 F1MNY7_BOVIN,tr F1PGU0 F1PGU0_CANFA,tr F1SA20 F1SA20_PIG	IAILG IHNE Vsk	75%	32.4	49.71906	Ref	-0.42	-0.36	-0.52	-0.33	-0.34	-0.06	-0.45	2320	1500	1700	1710	2150	1860	2360	1790	476.3	1901.1	4	0.0078	4.112

Alpha-actinin-1 OS=Macaca fascicularis GN=ACTN1 PE=2 SV=1	sp Q2PFV7 ACTN1_MACFA,sp Q3B7N2 ACTN1_BOVIN,tr A4ZZF8 A4ZZF8_BOVIN,tr E2QY07 E2QY07_CANFA,tr E2QY08 E2QY08_CANFA,tr F1MNY7 F1MNY7_BOVIN,tr F1PGU0 F1PGU0_CANFA,tr F1SA20 F1SA20_PIG	nYIT VDEL R	56%	32.1	52.07333	Ref	-0.2	-0.28	-0.24	-0.4	-0.64	-0.34	-0.56	33400	23100	23700	27500	27100	20100	25800	22000	713.9	1425.8	2	0.0111	7.768
Alpha-actinin-1 OS=Macaca fascicularis GN=ACTN1 PE=2 SV=1	sp Q2PFV7 ACTN1_MACFA,sp Q3B7N2 ACTN1_BOVIN,tr A4ZZF8 A4ZZF8_BOVIN,tr E2QY07 E2QY07_CANFA,tr E2QY08 E2QY08_CANFA,tr F1MNY7 F1MNY7_BOVIN,tr F1PGU0 F1PGU0_CANFA,tr F1SA20 F1SA20_PIG	rDQ ALTE EHA R	88%	41.1	52.92965	Ref	-0.3	-0.11	-0.23	-0.41	-0.33	-0.32	-0.47	22100	18600	23100	23800	23200	21300	22400	20100	408.2	1628.8	4	0.0122	7.495

Macrophage-capping protein OS=Bos taurus GN=CAPG PE=2 SV=1	sp Q865V6 CAPG_BOVIN	aHVE IVTD GEEP ADM IQVL GPKP Slk	84%	36.7	54.30378	Ref	-0.32	0.25	-0.7	-0.12	-0.24	0.23	-0.86	3250	2110	3400	1970	3250	2610	3770	1770	738	3685	5	0.032	8.675
Macrophage-capping protein OS=Bos taurus GN=CAPG PE=2 SV=1	sp Q865V6 CAPG_BOVIN	aHVE IVTD GEEP ADM IQVL GPKP Slk	88%	42.6	54.1905	Ref	-0.15	-0.01	-0.32	0.11	-0.27	-0.08	-0.82	1090	811	967	874	1300	872	1040	617	922.3	3685	4	0.028	7.585
Macrophage-capping protein OS=Bos taurus GN=CAPG PE=2 SV=1	sp Q865V6 CAPG_BOVIN	eGN PEED LTAD R	95%	51.3	49.42494	Ref	-0.24	0.19	-0.47	-0.004	-0.26	0.037	-0.71	9360	6970	10200	7230	11000	8060	10400	6120	825.4	1648.8	2	0.016	9.682
Macrophage-capping protein OS=Bos taurus GN=CAPG PE=2 SV=1	sp Q865V6 CAPG_BOVIN	IPGL HIW R	54%	29.8	49.74899	Ref	-0.28	0.068	-0.31	-0.091	-0.1	0.045	-0.79	4030	2880	3980	3440	4410	3840	4420	2460	432.6	1294.8	3	0.0028	2.159
Macrophage-capping protein OS=Bos taurus GN=CAPG PE=2 SV=1	sp Q865V6 CAPG_BOVIN	yAP NTQ VEIL PQG R	95%	62.4	53.54604	Ref	-0.5	0.23	-0.6	0.16	-0.19	0.06	-0.64	10200	6630	11900	7540	14100	9610	12000	7320	945.5	1889	2	0.013	6.898

Cysteine and glycine rich protein 1 OS=Rattus norvegicus GN=Csrp1 PE=2 SV=2	sp P47875 CSR1_1_RAT,sp Q3MHY1 CSR1_BOVIN, tr E2R707 E2R707_CANF	gFGF GQG AGA LVHS	E	95%	63.7	51.80347	Ref	0.17	0.13	0.074	-0.097	0.16	-0.09	-0.07	6580	6500	6850	7390	7230	7530	6630	6660	869.4	1736.9	2	0.019	10.94
Cysteine and glycine rich protein 1 OS=Rattus norvegicus GN=Csrp1 PE=2 SV=2	sp P47875 CSR1_1_RAT,sp Q3MHY1 CSR1_BOVIN, tr E2R707 E2R707_CANF	gFGF GQG AGA LVHS	E	95%	70	52.15002	Ref	-0.007	0.043	-0.06	-0.065	0.26	-0.07	0.15	6450	5580	6270	6560	7190	7900	6550	7540	869.4	1736.9	2	0.0072	4.126
Cysteine and glycine rich protein 1 OS=Rattus norvegicus GN=Csrp1 PE=2 SV=2	sp P47875 CSR1_1_RAT,sp Q3MHY1 CSR1_BOVIN, tr E2R707 E2R707_CANF	gLES TTLA DkD GEIY	ck	93%	50.9	55.33733	Ref	0.19	0.09	0.17	-0.12	0.19	-0.08	-0.2	4390	4390	4440	5280	4760	5130	4450	4050	934.5	2800.4	3	0.0283	10.1
Cysteine and glycine rich protein 1 OS=Rattus norvegicus GN=Csrp1 PE=2 SV=2	sp P47875 CSR1_1_RAT,sp Q3MHY1 CSR1_BOVIN, tr E2R707 E2R707_CANF	gYGY GQG AGTL SMD	k	95%	68	53.18835	Ref	0.43	0.13	0.081	-0.15	-0.03	-0.05	-0.27	18400	20900	18500	20000	18900	17900	18400	15700	705	2112.1	3	0.0238	11.28

Cysteine and glycine rich protein 1 OS=Rattus norvegicus GN=Csrp1 PE=2 SV=2	sp P47875 CSR1_RAT,sp Q3MHY1 CSR1_BOVIN, tr E2R707 E2R707_CANF	gYGY GQG AGTL SMD	k	95%	68.2	53.35191	Ref	0.5	0.04	0.047	-0.077	0.044	-0.13	-0.27	20400	24800	19600	22100	22400	21200	19700	17800	705	2112.1	3	0.0158	7.478
Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2	2 RANG_MOUSE,sp P43487 RANG_HUMAN,sp Q3T0M7 RANG_BOVIN, tr D4A2G9 D4A2G9_RAT, tr E2RHK9 E2RHK9_CANFA, tr F1RHM8 F1RHM8_PIG, tr F6SRX1 F6SRX1_MONDO, tr F7C2T0 F7C2T0_ORNAN, tr F7C2T7 F7C2T7_ORNAN, tr F7CN40 F7CN40_C	fLNA ENA Qk	Qk	95%	50.9	52.68259	Ref	-0.25	0.47	0.8	0.6	0.96	0.41	1	5550	3950	7050	9970	9520	10700	7610	11400	822	1641.9	2	0.0216	13.13

Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2	2 RANG_MOUSE,s p P43487 RANG_HUMAN,sp Q3T0M7 RANG_BOVIN,tr D4A2G9 D4A2G9_RAT,tr E2RHK9 E2RHK9_CANFA,tr F1RHM8 F1RHM8_PIG,tr F6SRX1 F6SRX1_MONDO,tr F7C2T0 F7C2T0_ORNAN,tr F7C2T7 F7C2T7_ORNAN,tr F7CN40 F7CN40_C	tLEE DEEE LFk	95%	67.9	53.45438	Ref	-0.2	0.62	0.73	0.64	0.97	0.39	1	1750	1560	2990	3610	3750	4110	2860	4440	995.5	1989	2	0.0157	7.905
Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2	2 RANG_MOUSE,s p P43487 RANG_HUMAN,sp Q3T0M7 RANG_BOVIN,tr D4A2G9 D4A2G9_RAT,tr E2RHK9 E2RHK9_CANFA,tr F1RHM8 F1RHM8_PIG,tr F6SRX1 F6SRX1_MONDO,tr F7C2T0 F7C2T0_ORNAN,tr F7C2T7 F7C2T7_ORNAN,tr F7CN40 F7CN40_C	tLEE DEEE LFk	88%	44.3	53.47917	Ref	-0.38	0.54	0.76	0.7	0.96	0.29	1.1	10600	7150	14700	19200	20300	21200	13900	23500	664	1989	3	0.013	6.526

60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	sp P05387 RLA2_HUMAN,sp P42899 RLA2_BOVIN,tr F7CGS1 F7C	iLDS VGIE ADD DRL Nk	79%	38.3	54.44513	Ref	-0.76	0.48	0.12	0.32	0.48	0.4	0.94	10200	5540	14200	12300	15600	15200	15100	21800	596.1	2380.3	4	0.0079	3.329
60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	sp P05387 RLA2_HUMAN,sp P42899 RLA2_BOVIN,tr F7CGS1 F7C	nIED VIAQ GIGk	95%	71.7	52.19453	Ref	-0.51	0.65	0.24	0.39	0.5	0.39	0.49	4300	2620	6380	5400	6590	6200	5980	6390	933	1864.1	2	0.019	10.2
60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	sp P05387 RLA2_HUMAN,sp P42899 RLA2_BOVIN,tr F7CGS1 F7C	yVAS YLLA ALG GNS SPSA k	95%	87.7	54.45084	Ref	-0.53	0.3	0.25	0.34	0.61	0.61	0.71	357	256	494	536	631	665	695	735	826.5	2476.4	3	0.0194	7.828
60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	sp P05387 RLA2_HUMAN,sp P42899 RLA2_BOVIN,tr F7CGS1 F7C	yVAS YLLA ALG GNS SPSA k	95%	66.8	54.32204	Ref	-0.043	0.38	0.45	0.31	0.31	0.23	0.49	171	121	176	207	206	181	179	212	826.5	2476.4	3	0.0148	5.987

60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	sp P05387 RLA2_HUMAN,sp P42899 RLA2_BOVIN,tr F7CGS1 F7CGS1_MAC MU,tr Q6FG96 Q6FG96_HUMAN	yVAS YLLA ALG GNS SPSA k	86%	40.7	53.37489	Ref	0.11	0.33	0.2	0.17	0.29	0.53	0.62	696	608	765	784	850	805	992	1050	696.1	2780.6	4	0.0184	6.629
Probable ATP-dependent RNA helicase DDX5 OS=Pan troglodytes GN=DDX5 PE=2 SV=1	2 DDX5_PANTR,sp P17844 DDX5_HUMAN,sp Q4R6M5 DDX5_MACFA,sp Q5R4I9 DDX5_PONAB,sp Q61656 DDX5_MOUSE,tr A1L333 A1L333_MOUSE,tr B4DLW8 B4DLW8_HUMAN,tr B4DN41 B4DN41_HUMAN, N, tr B4DNG2 B4DNG2_HUMAN, tr B5BUE6 B5	aPILI ATD VAS R	82%	37.2	51.3477	Ref	0.11	-0.25	-0.1	-0.18	-0.25	-0.13	-0.08	5090	4780	4040	5040	5230	4360	4930	5070	766	1529.9	2	0.0112	7.323

<p>Probable ATP-dependent RNA helicase DDX5 OS=Pan troglodytes GN=DDX5 PE=2 SV=1</p>	<p>2 DDX5_PANTR,sp P17844 DDX5_HUMAN,sp Q4R6M5 DDX5_MA CFA,sp Q5R4I9 DDX5_PONAB,sp Q61656 DDX5_MOUSE,transcript A1L333 A1L333_MOUSE,transcript B4DLW8 B4DLW8_HUMAN,transcript B4DN41 B4DN41_HUMAN,transcript B4DNG2 B4DNG2_HUMAN,transcript B5BUE6 B5</p>	<p>aPILI ATD VAS R</p>	<p>82%</p>	<p>37.1</p>	<p>50.97868</p>	<p>Ref</p>	<p>0.14</p>	<p>-0.42</p>	<p>-0.02</p>	<p>-0.042</p>	<p>-0.07</p>	<p>-0.28</p>	<p>-0.1</p>	<p>8260</p>	<p>8630</p>	<p>6330</p>	<p>9400</p>	<p>10200</p>	<p>8720</p>	<p>7870</p>	<p>8880</p>	<p>766</p>	<p>1529.9</p>	<p>2</p>	<p>0.0019</p>	<p>1.261</p>
<p>Probable ATP-dependent RNA helicase DDX5 OS=Pan troglodytes GN=DDX5 PE=2 SV=1</p>	<p>2 DDX5_PANTR,sp P17844 DDX5_HUMAN,sp Q4R6M5 DDX5_MA CFA,sp Q5R4I9 DDX5_PONAB,sp Q61656 DDX5_MOUSE,transcript A1L333 A1L333_MOUSE,transcript B4DLW8 B4DLW8_HUMAN,transcript B4DN41 B4DN41_HUMAN,transcript B4DNG2 B4DNG2_HUMAN,transcript B5BUE6 B5</p>	<p>gLDV EDV</p>	<p>83%</p>	<p>38.4</p>	<p>51.94581</p>	<p>Ref</p>	<p>0.12</p>	<p>-0.22</p>	<p>-0.11</p>	<p>-0.16</p>	<p>-0.09</p>	<p>-0.28</p>	<p>-0.19</p>	<p>25100</p>	<p>23200</p>	<p>19900</p>	<p>24100</p>	<p>25700</p>	<p>23500</p>	<p>21500</p>	<p>22700</p>	<p>741.9</p>	<p>1481.9</p>	<p>2</p>	<p>0.0052</p>	<p>3.526</p>

Probable ATP-dependent RNA helicase DDX5 OS=Pan troglodytes GN=DDX5 PE=2 SV=1	2 DDX5_PANTR,sp P17844 DDX5_HUMAN,sp Q4R6M5 DDX5_MA CFA,sp Q5R4I9 DDX5_PONAB,sp Q61656 DDX5_MOUSE,transcript A1L333 A1L333_MOUSE,transcript B4DLW8 B4DLW8_HUMAN,transcript B4DN41 B4DN41_HUMAN,transcript B4DNG2 B4DNG2_HUMAN,transcript B5BUE6 B5R	ILQLVED	54%	31	51.19583	Ref	0.17	-0.32	0.094	-0.27	-0.19	-0.31	-0.03	6640	6800	5260	7860	6710	6230	5970	7200	645.4	1288.7	2	0.0161	12.48
	2 DDX5_PANTR,sp P17844 DDX5_HUMAN,sp Q4R6M5 DDX5_MA CFA,sp Q5R4I9 DDX5_PONAB,sp Q61656 DDX5_MOUSE,transcript A1L333 A1L333_MOUSE,transcript B4DLW8 B4DLW8_HUMAN,transcript B4DN41 B4DN41_HUMAN,transcript B4DNG2 B4DNG2_HUMAN,transcript B5BUE6 B5ADR	tTYLVLDE	95%	65.5	52.33565	Ref	0.26	-0.3	0.033	-0.41	-0.3	-0.15	-0.16	12200	12200	8940	12700	10300	9710	11300	11000	800.4	1598.8	2	0.0096	6.008

14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	8 1433E_ HUMAN,s p P62259 1433E_ MOUSE,s p P62260 1433E_R AT,sp P62 261 1433 E_BOVIN, sp P6226 2 1433E_ SHEEP,tr E2QWD6 E2QWD6_ CANFA,tr F6XA04 F 6XA04_H ORSE,tr F 7FT92 F7 FT92_OR NAN,tr F7 GZ27 F7G Z27_CALJ A,tr F7HJ T3 F7HJT 3_CALJA,t	aASD IAM TELP PTHP IR	95%	55.3	54.24495	Ref	0.24	-0.02	-0.03	-0.099	0.11	-0.03	-0.01	7320	7490	6810	7590	7970	8020	7660	7660	708.7	2123.1	3	0.0174	8.179
14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	8 1433E_ HUMAN,s p P62259 1433E_ MOUSE,s p P62260 1433E_R AT,sp P62 261 1433 E_BOVIN, sp P6226 2 1433E_ SHEEP,tr E2QWD6 E2QWD6_ CANFA,tr F6XA04 F 6XA04_H ORSE,tr F 7FT92 F7 FT92_OR NAN,tr F7 GZ27 F7G Z27_CALJ A,tr F7HJ T3 F7HJT 3_CALJA,t	aASD IAM TELP PTHP IR	95%	73.8	54.23148	Ref	0.32	0.013	0.093	-0.23	-0.1	0.079	-0.06	7120	7720	6770	8030	7060	6770	7990	7230	708.7	2123.1	3	0.0092	4.309

14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	8 1433E_ HUMAN,s p P62259 1433E_ MOUSE,s p P62260 1433E_R AT,sp P62 261 1433 E_BOVIN, sp P6226 2 1433E_ SHEEP,tr E2QWD6 E2QWD6_ CANFA,tr F6XA04 F 6XA04_H ORSE,tr F 7FT92 F7 FT92_OR NAN,tr F7 GZ27 F7G Z27_CALJ A,tr F7HJ T3 F7HJT 3_CALJA,t	eAAE nSLV AYk	70%	36.5	53.39974	Ref	-0.07	-0.13	0.18	-0.033	0.2	-0.13	0.15	11300	9630	10100	14000	13300	13600	11300	13700	602	1803	3	0.0126	6.999
14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	8 1433E_ HUMAN,s p P62259 1433E_ MOUSE,s p P62260 1433E_R AT,sp P62 261 1433 E_BOVIN, sp P6226 2 1433E_ SHEEP,tr E2QWD6 E2QWD6_ CANFA,tr F6XA04 F 6XA04_H ORSE,tr F 7FT92 F7 FT92_OR NAN,tr F7 GZ27 F7G Z27_CALJ A,tr F7HJ T3 F7HJT 3_CALJA,t	VAG MDV ELTV EER	95%	49.6	52.7187	Ref	0.21	-0.29	0.18	-0.14	0.2	-0.42	0.13	5860	5250	4040	6260	5560	6130	4170	6050	876.5	1750.9	2	0.0127	7.227

14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	8 1433E_ HUMAN,s p P62259 1433E_ MOUSE,s p P62260 1433E_R AT,sp P62 261 1433 E_BOVIN, sp P6226 2 1433E_ SHEEP,tr E2QWD6 E2QWD6_ CANFA,tr F6XA04 F 6XA04_H ORSE,tr F 7FT92 F7 FT92_OR NAN,tr F7 GZ27 F7G Z27_CALJ A,tr F7HJ T3 F7HJT 3_CALJA,t	vAG MDV ELTV EER	82%	38.7	52.74334	Ref	0.2	-0.19	0.096	-0.084	0.27	-0.23	0.057	3070	3090	2560	3500	3400	3790	2800	3390	876.5	1750.9	2	0.0105	5.983
Peptidyl-prolyl cis- trans isomerase FKBP3 OS=Bos taurus GN=FKBP3 PE=1 SV=2	sp P2688 4 FKBP3_ BOVIN,tr D2I0W1 D2I0W1_ AILME,tr F6SLA3 F 6SLA3_H ORSE	ILGN Ik	70%	28.3	45.07694	Ref	-0.38	-0.42	-0.12	-0.24	0.34	-0.58	0.096	20800	14700	15500	21400	21700	28400	15700	24800	422.6	1264.8	3	0.0029	2.256
Peptidyl-prolyl cis- trans isomerase FKBP3 OS=Bos taurus GN=FKBP3 PE=1 SV=2	sp P2688 4 FKBP3_ BOVIN,tr D2I0W1 D2I0W1_ AILME,tr F6SLA3 F 6SLA3_H ORSE	ILGN Ik	63%	26.8	45.07694	Ref	-0.25	-0.38	-0.14	-0.29	0.22	-0.58	0.15	2530	1940	1930	2560	2530	3160	1900	3120	422.6	1264.8	3	0.0016	1.237

Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Bos taurus GN=FKBP3 PE=1 SV=2	sp P26884 FKBP3_BOVIN,tr D2I0W1 D2I0W1_AILME,tr F6SLA3 F6SLA3_HORSE	sEET LDEG PPk	95%	63.5	53.35466	Ref	-0.27	-0.14	-0.01	-0.19	0.24	-0.59	-0.41	53500	37400	44300	54700	53200	62700	36600	41400	604	1808.9	3	0.0166	9.174
Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Bos taurus GN=FKBP3 PE=1 SV=2	sp P26884 FKBP3_BOVIN,tr D2I0W1 D2I0W1_AILME,tr F6SLA3 F6SLA3_HORSE	sEET LDEG PPk	91%	44.6	53.37351	Ref	-0.095	-0.41	-0.16	-0.19	0.29	-0.9	-0.17	18300	13200	11600	15400	16700	20300	9290	15300	905.5	1808.9	2	0.015	8.286
Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Bos taurus GN=FKBP3 PE=1 SV=2	sp P26884 FKBP3_BOVIN,tr D2I0W1 D2I0W1_AILME,tr F6SLA3 F6SLA3_HORSE	vGIG KVIR	94%	41.9	43.85696	Ref	-0.07	-0.31	-0.1	-0.46	0.23	-0.33	-0.25	6400	5300	4860	6330	5420	7650	5420	5690	382.6	1144.8	3	0.0063	5.524

Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	1 DEST_H UMAN,sp P60982 DEST_PIG, sp Q5E9D 5 DEST_B OVIN,tr B 4DYA6 B4 DYA6_HU MAN,tr B 7Z9M9 B 7Z9M9_H UMAN,tr D2HRE4 D2HRE4_ AILME,tr F2Z4P7 F 2Z4P7_CA NFA,tr F2 Z5I9 F2Z5 I9_PIG,tr F6TEG7 F 6TEG7_M ACMU,tr F7CL80 F 7CL80_HO RSE,tr F7	hEcQ AnG PEDL NR	92%	41.1	46.42494	Ref	-0.07	-0.37	-0.24	-0.64	-0.52	-0.31	-0.68	16800	14500	12800	15700	13200	12500	15000	11600	611.9	1832.8	3	0.0131	7.148
Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	1 DEST_H UMAN,sp P60982 DEST_PIG, sp Q5E9D 5 DEST_B OVIN,tr B 4DYA6 B4 DYA6_HU MAN,tr B 7Z9M9 B 7Z9M9_H UMAN,tr D2HRE4 D2HRE4_ AILME,tr F2Z4P7 F 2Z4P7_CA NFA,tr F2 Z5I9 F2Z5 I9_PIG,tr F6TEG7 F 6TEG7_M ACMU,tr F7CL80 F 7CL80_HO RSE,tr F7	IGGS LIVA FEGC PV	95%	49.6	52.72596	Ref	Value Missing (- 0.2434 3146)	Value Missi ng (- 0.361 12487)	Value Missi ng (- 0.527 0.527 7197)	Value Missin g (- 0.6681 0.6681 989)	Value Missin g (- 0.4723 0.4723 265)	Value Missi ng (- 0.535 0.535 09325)	Value Missin g (- 0.5242 0.5242 191)	Value Missi ng (- 0.243431 0.243431)	Value Missi ng (- 0.361 12487 197)	Value Missi ng (- 0.5277 0.5277 9)	Value Missi ng (- 0.668198 0.668198 3265)	Value Missi ng (- 0.472 0.472 9325)	Value Missin g (- 0.5350 0.5350 1)	Value Missing (- 0.524219 0.524219 1)	856.4	1710.9	2	0.0184	10.76	

Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	1 DEST_H UMAN,sp P60982 DEST_PIG, sp Q5E9D 5 DEST_B OVIN,tr B 4DYA6 B4 DYA6_HU MAN,tr B 7Z9M9 B 7Z9M9_H UMAN,tr D2HRE4 D2HRE4_ AILME,tr F2Z4P7 F 2Z4P7_CA NFA,tr F2 Z5I9 F2Z5 I9_PIG,tr F6TEG7 F 6TEG7_M ACMU,tr F7CL80 F 7CL80_HO RSE,tr F7	IGGS LIVA FEGc PV	75%	36.7	52.87634	Ref	No Values (- 0.1211 4624)	No Value s (- 0.238 8396)	No Value s (- 0.405 4346)	No Values (- 0.5459 1376)	No Values (- 0.3500 413)	No Value s (- 0.412 8079)	No Values (- 0.4019 3376)	No Values (- 0.3235 3625)	No Values (- 0.121146 24)	No Value s (- 0.238 8396)	No Values (- 0.4054 346)	No Values (- 0.545913 76)	No Value s (- 0.350 0413)	No Values (- 0.4128 079)	No Values (- 0.401933 76)	856.5	1710.9	2	0.0095	5.547
Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	1 DEST_H UMAN,sp P60982 DEST_PIG, sp Q5E9D 5 DEST_B OVIN,tr B 4DYA6 B4 DYA6_HU MAN,tr B 7Z9M9 B 7Z9M9_H UMAN,tr D2HRE4 D2HRE4_ AILME,tr F2Z4P7 F 2Z4P7_CA NFA,tr F2 Z5I9 F2Z5 I9_PIG,tr F6TEG7 F 6TEG7_M ACMU,tr F7CL80 F 7CL80_HO RSE,tr F7	yALY DASF ETK	71%	37	53.46781	Ref	-0.18	-0.86	-0.59	-0.34	-0.41	-0.47	-0.17	5050	3730	2510	3420	4490	3730	3730	4550	639.3	1915	3	0.0177	9.237

Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	1 DEST_H UMAN,sp P60982 DEST_PIG, sp Q5E9D 5 DEST_B OVIN,tr B 4DYA6 B4 DYA6_HU MAN,tr B 7Z9M9 B 7Z9M9_H UMAN,tr D2HRE4 D2HRE4_ AILME,tr F2Z4P7 F 2Z4P7_CA NFA,tr F2 Z5I9 F2Z5 I9_PIG,tr F6TEG7 F 6TEG7_M ACMU,tr F7CL80 F 7CL80_HO RSE,tr F7	yALY DASF ETk	71%	37	53.48155	Ref	-0.12	-0.56	-0.21	-0.32	-0.4	-0.38	-0.45	4780	4920	3940	5620	5750	4750	5020	4750	639.3	1915	3	0.0124	6.466
Nucleoside diphosphate kinase OS=Bos taurus GN=NME1-NME2 PE=3 SV=1	tr F1MPL 4 F1MPL4 BOVIN	fLQA SEEL Lk	85%	40.2	51.80516	Ref	0.13	-0.43	-0.29	-0.4	-0.39	-0.37	-0.73	2780	2010	1470	1820	1860	1630	1730	1340	596	1785	3	0.0104	5.797
Nucleoside diphosphate kinase OS=Bos taurus GN=NME1-NME2 PE=3 SV=1	tr F1MPL 4 F1MPL4 BOVIN	gLM GEIk	54%	30.5	50.51017	Ref	0.047	-0.45	-0.23	-0.36	-0.32	-0.05	-0.2	1670	1790	1380	1800	1820	1620	2050	1830	490.3	1467.9	3	0.0026	1.752

Nucleoside diphosphate kinase OS=Bos taurus GN=NME1-NME2 PE=3 SV=1	tr F1MPL4 F1MPL4_BOVIN	gLM GEIk	65%	32.7	50.60104	Ref	-0.061	-0.54	-0.23	-0.32	-0	-0.27	-0.29	19100	17100	13300	18500	19200	20900	18100	17800	490.3	1467.9	3	0.004	2.691
Nucleoside diphosphate kinase OS=Bos taurus GN=NME1-NME2 PE=3 SV=1	tr F1MPL4 F1MPL4_BOVIN	tFIAI kPD GVQ R	90%	41.8	51.50081	Ref	-0.23	-0.44	-0.09	-0.17	-0.16	-0.43	-0.29	1630	1200	1130	1620	1680	1480	1280	1410	977.1	1952.2	2	0.0168	8.61
Nucleoside diphosphate kinase OS=Bos taurus GN=NME1-NME2 PE=3 SV=1	tr F1MPL4 F1MPL4_BOVIN	vmL GET NPA DskP GTIR	67%	37.2	54.6198	Ref	-0.11	-0.41	-0.21	-0.082	-0.43	-0.23	-0.34	13800	11100	9730	12600	15200	10400	12500	11500	804.1	2409.3	3	0.0162	6.734

Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2	1 ROA3_HUMAN,sp Q6URK4 ROA3_RAT,sp Q8BG05 ROA3_MOUSE,trl A2AL12 A2AL12_MOUSE,trl B2R XM2 B2R XM2_MOUSE,trl B4DDB6 B4DDB6_HUMAN,trl B4E3E6 B4E3E6_HUMAN,trl D3ZJF4_RAT,trl D4ACQ0 D4ACQ0_RAT,trl E1BEG2 E1BEG2_B	sSGS PYG GGY GSG GGS GGY GSR	95%	52.2	47.66576	Ref	0.056	-0.08	-0.18	-0.071	0.12	0.009	0.05	3900	3700	3670	3830	4550	4550	4390	4480	739	2214	3	0.0158	7.127
Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2	1 ROA3_HUMAN,sp Q6URK4 ROA3_RAT,sp Q8BG05 ROA3_MOUSE,trl A2AL12 A2AL12_MOUSE,trl B2R XM2 B2R XM2_MOUSE,trl B4DDB6 B4DDB6_HUMAN,trl B4E3E6 B4E3E6_HUMAN,trl D3ZJF4_RAT,trl D4ACQ0 D4ACQ0_RAT,trl E1BEG2 E1BEG2_B	sSGS PyG GGY GSG GGS GGY GSR	64%	33.7	51.97873	Ref	-0.15	0.12	-0.32	-0.13	0.13	-0.3	0.38	1980	1550	2020	1670	2100	2210	1700	2710	840.4	2518.2	3	0.0142	5.618

<p>Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2</p>	<p>1 ROA3_HUMAN,sp Q6URK4 ROA3_RAT,sp Q8BG05 ROA3_MOUSE,transcript A2AL12 A2AL12_MOUSE,transcript B2R XM2 B2R XM2_MOUSE,transcript B4DDB6 B4DDB6_HUMAN,transcript B4E3E6 B4E3E6_HUMAN,transcript D3ZJF4 D3ZJF4_RAT,transcript D4ACQ0 D4ACQ0_RAT,transcript E1BEG2 E1BEG2_B</p>	<p>yHTInGH NCEV</p>	<p>60%</p>	<p>33.8</p>	<p>52.62994</p>	<p>Ref</p>	<p>0.18</p>	<p>0.072</p>	<p>-0.29</p>	<p>-0.095</p>	<p>0.026</p>	<p>-0.07</p>	<p>0.036</p>	<p>10400</p>	<p>10600</p>	<p>10600</p>	<p>9240</p>	<p>11700</p>	<p>11100</p>	<p>10900</p>	<p>11600</p>	<p>690.7</p>	<p>2069</p>	<p>3</p>	<p>0.0205</p>	<p>9.908</p>
<p>Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1</p>	<p>6 CTND1_HUMAN,transcript C9JZR2 C9JZR2_HUMAN,transcript D2HK71 D2HK71_AILME,transcript E1BQ11 E1BQ11_BOVIN,transcript E2R434 E2R434_CANFA,transcript E9PIE5 E9PIE5_HUMAN,transcript F1SJY6 F1SJY6_PIG,transcript F6QHE6 F6QHE6_MCMU,transcript F6QHF6 F6QHF6_MCMU,transcript F6QHH2 F6QHH2_</p>	<p>aLSA IADL LTNE HER</p>	<p>95%</p>	<p>75.1</p>	<p>53.77472</p>	<p>Ref</p>	<p>0.3</p>	<p>-0.58</p>	<p>0.2</p>	<p>-0.2</p>	<p>-0.01</p>	<p>-0.32</p>	<p>0.17</p>	<p>315</p>	<p>305</p>	<p>180</p>	<p>347</p>	<p>291</p>	<p>289</p>	<p>244</p>	<p>339</p>	<p>653</p>	<p>1956</p>	<p>3</p>	<p>0.0092</p>	<p>4.706</p>

Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1	6 CTND1_HUMAN, tr C9JZR2 C9JZR2_HUMAN, tr D2HK71 D2HK71_AILME, tr E1BQ11 E1BQ11_BOVIN, tr E2R434 E2R434_CANFA, tr E9PIE5 E9PIE5_HUMAN, tr F1SY6 F1SY6_PIG, tr F6QHE6 F6QHE6_MACMU, tr F6QHF6 F6QHF6_MACMU, tr F6QHH2 F6QHH2_HER	aLSA IADL LTNE HER	95%	60.2	53.84113	Ref	0.46	Value Missing (-1.8965379)	0.72	0.54	0.45	Value Missing (-2.070506)	Value Missing (-2.0596323)	181	Value Missing (-1.8965379)	233	226	186	Value Missing (-2.070506)	Value Missing (-2.0596323)	653	1956.1	3	#####	0.49	
Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1	6 CTND1_HUMAN, tr C9JZR2 C9JZR2_HUMAN, tr D2HK71 D2HK71_AILME, tr E1BQ11 E1BQ11_BOVIN, tr E2R434 E2R434_CANFA, tr E9PIE5 E9PIE5_HUMAN, tr F1SY6 F1SY6_PIG, tr F6QHE6 F6QHE6_MACMU, tr F6QHF6 F6QHF6_MACMU, tr F6QHH2 F6QHH2_HER	aLSA IADL LTNE HER	95%	66.1	53.77423	Ref	0.61	0.52	-0.44	-0.18	-0.2	-0.2	-0.39	267	410	419	242	319	274	287	250	653	1956	3	0.0152	7.787

<p>Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1</p>	<p>6 CTND1_HUMAN, tr C9JZR2 C9JZR2_HUMAN, tr D2HK71 D2HK71_AILME, tr E1BQ11 E1BQ11_BOVIN, tr E2R434 E2R434_CANFA, tr E9PIE5 E9PIE5_HUMAN, tr F1SY6 F1SY6_PIG, tr F6QHE6 F6QHE6_MACMU, tr F6QHF6 F6QHF6_MACMU, tr F6QHH2 F6QHH2_R</p>	<p>knGn GGP GPY VGQ AGT ATLP R</p>	<p>90%</p>	<p>47</p>	<p>55.05709</p>	<p>Ref</p>	<p>0.12</p>	<p>-0.37</p>	<p>0.039</p>	<p>-0.21</p>	<p>0.28</p>	<p>-0.49</p>	<p>0.35</p>	<p>5270</p>	<p>4980</p>	<p>3840</p>	<p>5730</p>	<p>5310</p>	<p>6530</p>	<p>3990</p>	<p>7090</p>	<p>874.8</p>	<p>2621.4</p>	<p>3</p>	<p>0.0168</p>	<p>6.421</p>
<p>Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1</p>	<p>6 CTND1_HUMAN, tr C9JZR2 C9JZR2_HUMAN, tr D2HK71 D2HK71_AILME, tr E1BQ11 E1BQ11_BOVIN, tr E2R434 E2R434_CANFA, tr E9PIE5 E9PIE5_HUMAN, tr F1SY6 F1SY6_PIG, tr F6QHE6 F6QHE6_MACMU, tr F6QHF6 F6QHF6_MACMU, tr F6QHH2 F6QHH2_R</p>	<p>nLAV DAR</p>	<p>57%</p>	<p>29.7</p>	<p>49.40512</p>	<p>Ref</p>	<p>0.26</p>	<p>-0.09</p>	<p>0.27</p>	<p>-0.16</p>	<p>-0.08</p>	<p>-0.51</p>	<p>0.096</p>	<p>19900</p>	<p>20800</p>	<p>17700</p>	<p>25400</p>	<p>20700</p>	<p>19200</p>	<p>14800</p>	<p>22500</p>	<p>531.8</p>	<p>1061.6</p>	<p>2</p>	<p>0.0089</p>	<p>8.366</p>

40S ribosomal protein S20 OS=Sus scrofa GN=RPS20 PE=3 SV=1	U9 RS20_PIG,sp P60866 RS20_HUMAN,sp P60867 RS20_MOUSE,sp P60868 RS20_RAT,sp Q3ZBH8 RS20_BOVIN,sp Q4R5D0 RS20_MACFA,sp Q5R924 RS20_PONAB,tr B4DW28 B4DW28_HUMAN,tr D2H950 D2H950_AILME,tr D3ZZK1 D3ZZK1_RAT,tr E2RB	IIDLH SPSE IVk	69%	33.5	52.56843	Ref	0.29	-0.22	0.36	0.12	0.019	-0.25	0.036	17300	17600	13400	22400	21100	17100	14800	17900	490.5	1958.2	4	0.0162	8.287
40S ribosomal protein S20 OS=Sus scrofa GN=RPS20 PE=3 SV=1	U9 RS20_PIG,sp P60866 RS20_HUMAN,sp P60867 RS20_MOUSE,sp P60868 RS20_RAT,sp Q3ZBH8 RS20_BOVIN,sp Q4R5D0 RS20_MACFA,sp Q5R924 RS20_PONAB,tr B4DW28 B4DW28_HUMAN,tr D2H950 D2H950_AILME,tr D3ZZK1 D3ZZK1_RAT,tr E2RB	IIDLH SPSE IVk	70%	35.8	52.56634	Ref	0.39	0.028	0.31	-0.25	0.09	-0.12	0.009	11500	13400	11300	15400	11500	12800	11500	12500	653.7	1958.2	3	0.0153	7.789

40S ribosomal protein S20 OS=Sus scrofa GN=RPS20 PE=3 SV=1	U9 RS20_PIG,sp P60866 RS20_HUMAN,sp P60867 RS20_MOUSE,sp P60868 RS20_RAT,sp Q3ZBH8 RS20_BOVIN,sp Q4R5D0 RS20_MACFA,sp Q5R924 RS20_PONAB,tr B4DW28 B4DW28_HUMAN,tr D2H950 D2H950_AILME,tr D3ZZK1 D3ZZK1_RAT,tr E2RB	IIDLH SPSE IVk	95%	49.7	51.55931	Ref	0.088	-0.08	0.34	0.044	0.13	-0.12	0.068	2270	2090	2020	3030	2720	2530	2210	2500	980.1	1958.2	2	0.0121	6.158
40S ribosomal protein S20 OS=Sus scrofa GN=RPS20 PE=3 SV=1	U9 RS20_PIG,sp P60866 RS20_HUMAN,sp P60867 RS20_MOUSE,sp P60868 RS20_RAT,sp Q3ZBH8 RS20_BOVIN,sp Q4R5D0 RS20_MACFA,sp Q5R924 RS20_PONAB,tr B4DW28 B4DW28_HUMAN,tr D2H950 D2H950_AILME,tr D3ZZK1 D3ZZK1_RAT,tr E2RB	IIDLH SPSE IVk	63%	34.2	52.53578	Ref	0.31	-0.14	0.17	-0.024	0.083	0.048	0.16	3290	3880	3090	4300	4150	3900	3970	4270	653.7	1958.2	3	0.0141	7.222

40S ribosomal protein S20 OS=Sus scrofa GN=RPS20 PE=3 SV=1	U9 RS20_PIG,sp P60866 RS20_HUMAN,sp P60867 RS20_MOUSE,sp P60868 RS20_RAT,sp Q3ZBH8 RS20_BOVIN,sp Q4R5D0 RS20_MACFA,sp Q5R924 RS20_PONAB,tr B4DW28 B4DW28_HUMAN,tr D2H950 D2H950_AILME,tr D3ZZK1 D3ZZK1_RAT,tr E2RB	tPVE PEVA IHR	95%	51.7	52.22743	Ref	0.28	0.061	0.2	-0.099	0.004	0.19	-0.17	29100	30700	28600	35300	31700	29700	35400	27200	518	1550.9	3	0.0112	7.226
Histone H2A.Z OS=Bos taurus GN=H2AFZ PE=1 SV=2	4 H2AZ_BOVIN,sp P0C0S5 H2AZ_HUMAN,sp P0C0S6 H2AZ_MOUSE,sp P0C0S7 H2AZ_RAT,sp Q32LA7 H2AV_BOVIN,sp Q3THW5 H2AV_MOUSE,sp Q5RC42 H2AZ_PONAB,sp Q6YNC8 H2AZ_SHEEP,sp Q71UI9 H2AV_HUMAN,tr B1PEY3 B1PEY3_PIG,tr B2RVP5	tTIA GGG VIPH IHK	95%	54.5	50.89655	Ref	-0.28	0.23	-0.45	0.15	0.16	0.11	0.22	21700	15900	24500	17300	28800	25300	25500	27300	660.4	1978.2	3	0.0164	8.29

Histone H2A.Z OS=Bos taurus GN=H2AFZ PE=1 SV=2	4 H2AZ_B OVIN,sp P0C0S5 H 2AZ_HUM AN,sp P0 C0S6 H2A Z_MOUSE ,sp P0C0S 7 H2AZ_R AT,sp Q3 2LA7 H2A V_BOVIN, sp Q3TH W5 H2AV _MOUSE, sp Q5RC4 2 H2AZ_P ONAB,sp Q6YNC8 H2AZ_SH EEP,sp Q 71UI9 H2 AV_HUM AN,tr B1P EY3 B1PE Y3_PIG,tr B2RVP5	aTIA GGG VIPH IHK	62%	30.5	50.89531	Ref	-0.35	0.43	-0.87	0.22	0.11	0.11	0.22	34500	23600	43800	19900	46800	37800	39500	42400	495.6	1978.2	4	0.0162	8.197
Histone H2A.Z OS=Bos taurus GN=H2AFZ PE=1 SV=2	4 H2AZ_B OVIN,sp P0C0S5 H 2AZ_HUM AN,sp P0 C0S6 H2A Z_MOUSE ,sp P0C0S 7 H2AZ_R AT,sp Q3 2LA7 H2A V_BOVIN, sp Q3TH W5 H2AV _MOUSE, sp Q5RC4 2 H2AZ_P ONAB,sp Q6YNC8 H2AZ_SH EEP,sp Q 71UI9 H2 AV_HUM AN,tr B1P EY3 B1PE Y3_PIG,tr B2RVP5	aTIA GGG VIPH IHK	66%	30.9	50.48624	Ref	0.077	0.018	-0.03	0.004	0.081	0.059	0.065	8370	7950	8290	9010	10200	9350	9620	9580	495.6	1978.2	4	0.0082	4.135

Histone H2A.Z OS=Bos taurus GN=H2AFZ PE=1 SV=2	4 H2AZ_B OVIN,sp P0C0S5 H 2AZ_HUM AN,sp P0 C0S6 H2A Z_MOUSE ,sp P0C0S 7 H2AZ_R AT,sp Q3 2LA7 H2A V_BOVIN, sp Q3TH W5 H2AV _MOUSE, sp Q5RC4 2 H2AZ_P ONAB,sp Q6YNC8 H2AZ_SH EEP,sp Q 71UI9 H2 AV_HUM AN,tr B1P EY3 B1PE Y3_PIG,tr B2RVP5	gDEE LDL	95%	61.4	53.3649	Ref	-0.18	0.44	-0.85	0.32	0.085	-0.06	-0.06	35000	23400	39100	17900	44600	33000	31100	31000	864	1725.9	2	0.0163	9.453
	Histone H2A.Z OS=Bos taurus GN=H2AFZ PE=1 SV=2	4 H2AZ_B OVIN,sp P0C0S5 H 2AZ_HUM AN,sp P0 C0S6 H2A Z_MOUSE ,sp P0C0S 7 H2AZ_R AT,sp Q3 2LA7 H2A V_BOVIN, sp Q3TH W5 H2AV _MOUSE, sp Q5RC4 2 H2AZ_P ONAB,sp Q6YNC8 H2AZ_SH EEP,sp Q 71UI9 H2 AV_HUM AN,tr B1P EY3 B1PE Y3_PIG,tr B2RVP5	gDEE LDL	89%	44.5	53.31036	Ref	-0.53	0.33	-1.1	0.35	0.12	0.1	0.24	94300	50800	99900	42100	125000	93300	96000	105000	576.3	1725.9	3	0.0152

Basigin OS=Bos taurus GN=BSG PE=2 SV=1	tr Q3ZBX 0 Q3ZBX0 _BOVIN	sGQ YScIF LPEH AGR	95%	60.6	51.3492	Ref	-0.074	-0.01	-0.23	0.18	-0.06	0.061	0.64	1020	997	1130	1090	1600	1180	1340	1980	672.3	2014	3	0.0124	6.147
Basigin OS=Bos taurus GN=BSG PE=2 SV=1	tr Q3ZBX 0 Q3ZBX0 _BOVIN	sGQ YScIF LPEH AGR	95%	61.9	51.42083	Ref	0.33	0.047	0.008	0.047	-0.19	-0	0.24	2020	2320	2070	2260	2560	1890	2260	2650	672.3	2014	3	0.0109	5.417
Basigin OS=Bos taurus GN=BSG PE=2 SV=1	tr Q3ZBX 0 Q3ZBX0 _BOVIN	sGQ YScIF LPEH AGR	95%	56.2	51.56737	Ref	0.2	-0.08	-0.02	0.067	-0.12	0.14	0.23	1260	1260	1130	1320	1540	1190	1480	1560	672.3	2014	3	0.0069	3.422
Basigin OS=Bos taurus GN=BSG PE=2 SV=1	tr Q3ZBX 0 Q3ZBX0 _BOVIN	sGQ YScIF LPEH AGR	55%	31.6	51.47045	Ref	0.17	-0	0.032	0.17	0.29	-0.17	-0.18	1080	995	960	1100	1340	1270	964	950	672.3	2014	3	0.0098	4.866
Basigin OS=Bos taurus GN=BSG PE=2 SV=1	tr Q3ZBX 0 Q3ZBX0 _BOVIN	tEYE VDSE DR	95%	52.5	47.17928	Ref	-0.055	0.18	-0.1	-0.03	-0.06	0.26	0.082	20300	15400	19700	18200	21000	18000	23400	20600	773.9	1545.7	2	0.0111	7.169

Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	9 CLIC1_HUMAN,sp Q5E9B7 CLIC1_BOVIN,sp Q6MG61 CLIC1_RAT,sp Q95MF9 CLIC1_RABIT,sp Q9Z1Q5 CLIC1_MOUSE,trans D2I497 D2I497_AILME,trans F1PBH0 F1PBH0_CANFA,trans F1PKI4 F1PKI4_CANFA,trans F1PTB9 F1PTB9_CANFA,trans F1Q097 F1Q097_CANFA,trans F	IFmV LWL k	72%	34	50.38171	Ref	-0.18	-0.45	-0.19	-0.12	-0.06	-0.28	-0.24	412	305	274	370	426	388	348	357	558.7	1673	3	0.0038	2.258
	9 CLIC1_HUMAN,sp Q5E9B7 CLIC1_BOVIN,sp Q6MG61 CLIC1_RAT,sp Q95MF9 CLIC1_RABIT,sp Q9Z1Q5 CLIC1_MOUSE,trans D2I497 D2I497_AILME,trans F1PBH0 F1PBH0_CANFA,trans F1PKI4 F1PKI4_CANFA,trans F1PTB9 F1PTB9_CANFA,trans F1Q097 F1Q097_CANFA,trans F	IFmV LWL k	69%	33.4	50.40638	Ref	0.24	-0.3	-0.29	-0.17	-0.45	-0.31	-0.49	502	461	345	391	466	336	386	339	558.7	1673	3	0.0014	0.824

40S ribosomal protein S3a OS=Rattus norvegicus GN=Rps3a PE=1 SV=2	2 RS3A_RAT,sp P61246 RS3A_FELCA,sp P61247 RS3A_HUMAN,sp P97351 RS3A_MOUSE,sp Q4R4Z6 RS3A_MACFA,sp Q56JV9 RS3A_BOVIN,tr A8K4W0 A8K4W0_HUMAN,tr D2GXR5 D2GXR5_AILME,tr D3Z6C3 D3Z6C3_MOUSE,tr D3Z7W7 D3Z7W7_MOUSE,tr	acQS IYPL HDV FVR	65%	35.3	53.33173	Ref	0.13	-0.27	0.21	-0.055	-0.1	0.37	0.01	746	819	673	1050	969	820	1180	917	666.7	1997	3	0.0035	1.731
40S ribosomal protein S3a OS=Rattus norvegicus GN=Rps3a PE=1 SV=2	2 RS3A_RAT,sp P61246 RS3A_FELCA,sp P61247 RS3A_HUMAN,sp P97351 RS3A_MOUSE,sp Q4R4Z6 RS3A_MACFA,sp Q56JV9 RS3A_BOVIN,tr A8K4W0 A8K4W0_HUMAN,tr D2GXR5 D2GXR5_AILME,tr D3Z6C3 D3Z6C3_MOUSE,tr D3Z7W7 D3Z7W7_MOUSE,tr	eVQ TNDL k	84%	39	52.31477	Ref	0.3	-0.03	0.29	-0.26	0.081	-0.24	-0.29	17800	16700	14300	20100	15100	16800	14100	13500	777.9	1553.9	2	0.0046	2.968

40S ribosomal protein S3a OS=Rattus norvegicus GN=Rps3a PE=1 SV=2	2 RS3A_R AT,sp P61246 RS3A_FELCA,sp P61247 RS3A_HUMAN,sp P97351 RS3A_MOUSE,sp Q4R4Z6 RS3A_MACFA,sp Q56JV9 RS3A_BOVIN,tr A8K4W0 A8K4W0_HUMAN,tr D2GXR5 D2GXR5_AILME,tr D3Z6C3 D3Z6C3_MOUSE,tr kTSY AQH QQV	75%	36.3	53.60137	Ref	0.17	-0.06	-0.03	-0.076	0.21	-0.12	0.12	8290	8540	7890	9030	9660	10300	8530	10000	489.3	1953.1	4	0.0127	6.489
40S ribosomal protein S3a OS=Rattus norvegicus GN=Rps3a PE=1 SV=2	2 RS3A_R AT,sp P61246 RS3A_FELCA,sp P61247 RS3A_HUMAN,sp P97351 RS3A_MOUSE,sp Q4R4Z6 RS3A_MACFA,sp Q56JV9 RS3A_BOVIN,tr A8K4W0 A8K4W0_HUMAN,tr D2GXR5 D2GXR5_AILME,tr D3Z6C3 D3Z6C3_MOUSE,tr IIPDS IGK	55%	28.8	48.56088	Ref	0.38	-0.17	0.21	-0.16	-0.05	-0.21	-0.17	44900	43100	32000	46600	39800	37500	35000	35800	484.3	1449.9	3	0.0035	2.395

Cation-dependent mannose-6- phosphate receptor OS=Bos taurus GN=M6PR PE=1 SV=1	sp P11456 MPRD_BOVIN,sp P20645 MPRD_HUMAN,tr E2QTJ1 E2QTJ1_CA_NFA,tr F1SLX0 F1SLX0_PIG,tr F7DKQ6 F7DKQ6_MACMU,tr F7I5Z9 F7I5Z9_CALJA,tr Q53GY9 Q53GY9_HUMAN,tr Q6I9U3 Q6I9U3_HUMAN	hTLA DNF NPV SEER	87%	42.1	52.23833	Ref	-0.068	-0.59	0.036	-0.52	0.32	-0.49	0.41	5310	5190	3920	6790	5080	7950	4740	8770	645	1931.9	3	0.0146	7.571
	sp P11456 MPRD_BOVIN,sp P20645 MPRD_HUMAN,tr E2QTJ1 E2QTJ1_CA_NFA,tr F1SLX0 F1SLX0_PIG,tr F7DKQ6 F7DKQ6_MACMU,tr F7I5Z9 F7I5Z9_CALJA,tr Q53GY9 Q53GY9_HUMAN,tr Q6I9U3 Q6I9U3_HUMAN	hTLA DNF NPV SEER	95%	73.8	52.23833	Ref	-0.11	-0.47	0.11	-0.18	0.31	-0.47	-0.2	16300	12700	10700	17900	16200	19900	12100	14400	645	1931.9	3	0.0146	7.571

Cation-dependent mannose-6- phosphate receptor OS=Bos taurus GN=M6PR PE=1 SV=1	sp P11456 MPRD_BOVIN,sp P20645 MPRD_HUMAN,tri E2QTJ1 E2QTJ1_CA_NFA,tri F1SLX0 F1SLX0_PIG,tri F7DKQ6 F7DKQ6_MACMU,tri F7I5Z9 F7I5Z9_CALJA,tri Q53GY9 Q53GY9_HUMAN,tri Q6I9U3 Q6I9U3_HUMAN	hTLA DNF NPV SEER	90%	42.2	52.26112	Ref	-0.57	-0.42	0.25	-0.21	0.21	-0.86	0.38	3000	1750	2110	3780	3020	3530	1760	4110	967	1932	2	0.0129	6.684
Cation-dependent mannose-6- phosphate receptor OS=Bos taurus GN=M6PR PE=1 SV=1	sp P11456 MPRD_BOVIN,sp P20645 MPRD_HUMAN,tri E2QTJ1 E2QTJ1_CA_NFA,tri F1SLX0 F1SLX0_PIG,tri F7DKQ6 F7DKQ6_MACMU,tri F7I5Z9 F7I5Z9_CALJA,tri Q53GY9 Q53GY9_HUMAN,tri Q6I9U3 Q6I9U3_HUMAN	hTLA DNF NPV SEER	95%	59.5	52.22891	Ref	0.017	-0.11	-0.18	-0.2	-0.07	-0.05	0.059	6070	6490	6440	6900	7510	7160	7610	8120	645	1932	3	0.0135	6.997

<p>Cation-dependent mannose-6- phosphate receptor OS=Bos taurus GN=M6PR PE=1 SV=1</p>	<p>sp P11456 MPRD_BOVIN,sp P20645 MPRD_HUMAN,tr E2QTJ1 E2QTJ1_CA_NFA,tr F1SLX0 F1SLX0_PIG,tr F7DKQ6 F7DKQ6_MACMU, tr F715Z9 F715Z9_CALJA,tr Q53GY9 Q53GY9_HUMAN,tr Q6I9U3 Q6I9U3_HUMAN</p>	<p>tcDL VGEK</p>	<p>90%</p>	<p>41.9</p>	<p>51.89563</p>	<p>Ref</p>	<p>-0.12</p>	<p>-0.56</p>	<p>0.12</p>	<p>-0.25</p>	<p>0.27</p>	<p>-0.66</p>	<p>0.12</p>	<p>43700</p>	<p>34100</p>	<p>27200</p>	<p>49200</p>	<p>41700</p>	<p>52500</p>	<p>28700</p>	<p>49100</p>	<p>759.9</p>	<p>1517.8</p>	<p>2</p>	<p>0.0118</p>	<p>7.774</p>
<p>Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3</p>	<p>4 PGRC1_HUMAN,sp O55022 PGRC1_MOUSE,sp Q17QC0 PGRC1_BOVIN,sp Q5RED0 PGRC1_PONAB,sp Q95250 PGRC1_PIG,tr D2H3C2 D2H3C2_AILME, tr E2RJW8 E2RJW8_CANFA, tr F6WPT4 F6WPT4_HORSE, tr F7BA07 F7BA07_MACMU, tr Q3TFP8 Q3TFP8_R</p>	<p>fDGV QDP</p>	<p>95%</p>	<p>45.4</p>	<p>50.26917</p>	<p>Ref</p>	<p>0.039</p>	<p>0.2</p>	<p>0.035</p>	<p>-0.074</p>	<p>0.13</p>	<p>-0.19</p>	<p>0.1</p>	<p>27200</p>	<p>21700</p>	<p>26300</p>	<p>26300</p>	<p>26900</p>	<p>27000</p>	<p>22600</p>	<p>27500</p>	<p>619.3</p>	<p>1236.6</p>	<p>2</p>	<p>0.0099</p>	<p>7.974</p>

Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3	4 PGRC1_HUMAN,sp O55022 PGRC1_MOUSE,sp Q17QC0 PGRC1_BOVIN,sp Q5REDO PGRC1_PONAB,sp Q95250 PGRC1_PIG,tr D2H3C2 D2H3C2_AILME,tr E2RJW8 E2RJW8_CANFA,tr F6WPT4 F6WPT4_HORSE,tr F7BA07 F7BA07_MACMU,tr Q3TFP8 Q3TFP8_	iLMA InGk	56%	31.7	51.37167	Ref	-0.32	0.04	0.2	0.16	0.34	-0.09	0.014	6980	4810	6730	8420	9060	8940	6930	7390	490.3	1467.9	3	0.0219	14.88
Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3	4 PGRC1_HUMAN,sp O55022 PGRC1_MOUSE,sp Q17QC0 PGRC1_BOVIN,sp Q5REDO PGRC1_PONAB,sp Q95250 PGRC1_PIG,tr D2H3C2 D2H3C2_AILME,tr E2RJW8 E2RJW8_CANFA,tr F6WPT4 F6WPT4_HORSE,tr F7BA07 F7BA07_MACMU,tr Q3TFP8 Q3TFP8_	iLMA InGk	62%	32.7	51.26453	Ref	-0.008	0.091	0.12	0.009	0.088	0.16	0.029	2110	1900	2200	2520	2570	2370	2610	2360	490.3	1467.9	3	0.0183	12.45

Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3	4 PGRC1_HUMAN,sp O55022 PGRC1_MOUSE,sp Q17QC0 PGRC1_BOVIN,sp Q5REDO PGRC1_PONAB,sp Q95250 PGRC1_PIG,tr D2H3C2 D2H3C2_AILME,tr E2RJW8 E2RJW8_CANFA,tr F6WPT4 F6WPT4_HORSE,tr F7BA07 F7BA07_MACMU,tr Q3TFP8 Q3TFP8_	iLMA InGk	55%	31	51.07461	Ref	-0.18	0.034	0.079	0.043	0.35	-0.09	0.15	14200	10900	13700	15900	17100	18400	14200	16700	734.9	1467.9	2	0.0122	8.289
Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3	4 PGRC1_HUMAN,sp O55022 PGRC1_MOUSE,sp Q17QC0 PGRC1_BOVIN,sp Q5REDO PGRC1_PONAB,sp Q95250 PGRC1_PIG,tr D2H3C2 D2H3C2_AILME,tr E2RJW8 E2RJW8_CANFA,tr F6WPT4 F6WPT4_HORSE,tr F7BA07 F7BA07_MACMU,tr Q3TFP8 Q3TFP8_	rDFT PAEL R	68%	34.9	52.0499	Ref	0.013	0.2	0.18	-0.093	0.15	-0.1	0.23	4700	4770	5900	6520	5950	6150	5390	6740	470.3	1407.8	3	0.0132	9.405

60S ribosomal protein L10 OS=Ovis aries GN=RPL10 PE=2 SV=1	1 RL10_S HEEP,sp A9CB60 R L10_PAPA N,sp P27 635 RL10 _HUMAN, sp P8604 8 RL10_ MOUSE,s p Q29195 RL10_PI G,sp Q2T BW8 RL1 0L_BOVIN ,sp Q4R4 D3 RL10L _MACFA,s p Q4R7Y2 RL10_M ACFA,sp Q5R931 RL10_PO NAB,sp Q 6PDV7 RL 10_RAT,s p Q6ZWW	IHPF HVIR	88%	38.7	50.00382	Ref	0.8	-0.1	0.91	0.027	1	-0.07	0.18	7360	13400	7730	17500	10500	18000	8910	10600	331.5	1321.8	4	0.0068	5.155
60S ribosomal protein L10 OS=Ovis aries GN=RPL10 PE=2 SV=1	1 RL10_S HEEP,sp A9CB60 R L10_PAPA N,sp P27 635 RL10 _HUMAN, sp P8604 8 RL10_ MOUSE,s p Q29195 RL10_PI G,sp Q2T BW8 RL1 0L_BOVIN ,sp Q4R4 D3 RL10L _MACFA,s p Q4R7Y2 RL10_M ACFA,sp Q5R931 RL10_PO NAB,sp Q 6PDV7 RL 10_RAT,s p Q6ZWW	IHPF HVIR	89%	38.6	49.83951	Ref	0.77	0.006	0.92	0.055	0.95	-0.05	0.1	4120	6890	4420	9350	5650	9190	4780	5280	331.5	1321.8	4	0.0031	2.312

<p>60S ribosomal protein L10 OS=Ovis aries GN=RPL10 PE=2 SV=1</p>	<p>1 RL10_SHEEP,sp A9CB60 RL10_PAPAN,sp P27635 RL10_HUMAN,sp P86048 RL10_MOUSE,sp Q29195 RL10_PIG,sp Q2TBW8 RL10L_BOVIN,sp Q4R4D3 RL10L_MACFA,sp Q4R7Y2 RL10_MACFA,sp Q5R931 RL10_PONAB,sp Q6PDV7 RL10_RAT,sp Q6ZWV</p>	<p>IHPF</p>	<p>78%</p>	<p>35.4</p>	<p>49.83946</p>	<p>Ref</p>	<p>0.71</p>	<p>0.16</p>	<p>0.75</p>	<p>0.14</p>	<p>0.51</p>	<p>0.31</p>	<p>0.36</p>	<p>5040</p>	<p>7140</p>	<p>5320</p>	<p>8970</p>	<p>6500</p>	<p>7340</p>	<p>6650</p>	<p>6840</p>	<p>441.6</p>	<p>1321.8</p>	<p>3</p>	<p>0.0027</p>	<p>2.028</p>
<p>60S ribosomal protein L10 OS=Ovis aries GN=RPL10 PE=2 SV=1</p>	<p>1 RL10_SHEEP,sp A9CB60 RL10_PAPAN,sp P27635 RL10_HUMAN,sp P86048 RL10_MOUSE,sp Q29195 RL10_PIG,sp Q2TBW8 RL10L_BOVIN,sp Q4R4D3 RL10L_MACFA,sp Q4R7Y2 RL10_MACFA,sp Q5R931 RL10_PONAB,sp Q6PDV7 RL10_RAT,sp Q6ZWV</p>	<p>VHIG QVI</p>	<p>61%</p>	<p>32.4</p>	<p>51.51483</p>	<p>Ref</p>	<p>0.75</p>	<p>0.34</p>	<p>0.53</p>	<p>0.32</p>	<p>0.28</p>	<p>0.36</p>	<p>0.39</p>	<p>1150</p>	<p>1600</p>	<p>1300</p>	<p>1680</p>	<p>1600</p>	<p>1350</p>	<p>1500</p>	<p>1510</p>	<p>779</p>	<p>1555.9</p>	<p>2</p>	<p>0.013</p>	<p>8.38</p>

60S ribosomal protein L10 OS=Ovis aries GN=RPL10 PE=2 SV=1	1 RL10_SHEEP,sp A9CB60 RL10_PAPAN,sp P27635 RL10_HUMAN,sp P86048 RL10_MOUSE,sp Q29195 RL10_PIG,sp Q2TBW8 RL10L_BOVIN,sp Q4R4D3 RL10L_MACFA,sp Q4R7Y2 RL10_MACFA,sp Q5R931 RL10_PONAB,sp Q6PDV7 RL10_RAT,sp Q6ZVWV	VHIGQVI	MSIR	91%	44.5	51.10812	Ref	0.85	0.06	0.82	0.13	0.52	0.13	0.21	3870	5490	3450	6590	4490	5140	4080	4280	519.6	1555.9	3	0.0056	3.566
Protein kinase C delta-binding protein OS=Bos taurus GN=PRKCDBP PE=2 SV=1	sp A4FV37 PRDBP_BOVIN	kGH AAP TPTP VkPP	R	78%	35.2	49.67787	Ref	-0.43	-0.35	1.4	-1.5	0.77	-0.52	1.2	174	432	494	1840	275	1170	495	1640	822.8	2465.5	3	0.0333	13.51
Protein kinase C delta-binding protein OS=Bos taurus GN=PRKCDBP PE=2 SV=1	sp A4FV37 PRDBP_BOVIN	kGH AAP TPTP VkPP	R	91%	41	49.60827	Ref	-0.33	0.027	1	-0.64	0.49	-0.34	1.1	1860	2210	3070	6900	2390	4560	2690	7400	617.4	2465.5	4	0.0311	12.62

Protein kinase C delta-binding protein OS=Bos taurus GN=PRKCDBP PE=2 SV=1	sp A4FV37 PRDBP_BOVIN	IEAN HGLL VAR	52%	31.7	51.92693	Ref	0.3	0.02	0.57	0.089	0.52	-0.26	0.48	42000	44900	40100	66100	52100	61300	37400	61900	499.6	1495.9	3	0.0106	7.086
Protein kinase C delta-binding protein OS=Bos taurus GN=PRKCDBP PE=2 SV=1	sp A4FV37 PRDBP_BOVIN	IHVL LFK	60%	23.8	42.65384	Ref	0.37	0.1	0.37	0.024	0.37	-0.18	0.38	1100	937	848	1150	993	1100	784	1150	493.3	1477	3	0.0019	1.297
Protein kinase C delta-binding protein OS=Bos taurus GN=PRKCDBP PE=2 SV=1	sp A4FV37 PRDBP_BOVIN	IHVL LFK	50%	22.1	42.76646	Ref	0.3	-0.08	0.62	-0.017	0.5	-0.1	0.28	1950	1730	1450	2620	1860	2320	1610	2080	493.3	1477	3	0.001	0.692
Superoxide dismutase [Cu-Zn] OS=Ovis aries GN=SOD1 PE=1 SV=2	sp P09670 SODC_SHEEP,tr B9VGZ6 B9VGZ6_SH_EEP	gDG PVQ GTIR	53%	30.8	51.18836	Ref	-0.23	-0.42	-0.22	-0.072	0.22	-0.65	-0.22	2E+05	110000	1E+05	135000	164000	2E+05	1E+05	134000	652.4	1302.7	2	0.0119	9.156
Superoxide dismutase [Cu-Zn] OS=Ovis aries GN=SOD1 PE=1 SV=2	sp P09670 SODC_SHEEP,tr B9VGZ6 B9VGZ6_SH_EEP	gGN EEST k	90%	41.8	51.5752	Ref	-0.31	-0.41	-0.17	-0.034	0.26	-0.66	-0.2	24600	17300	17400	23100	28000	30000	16600	22600	715.4	1428.8	2	0.0104	7.24

Superoxide dismutase [Cu-Zn] OS=Ovis aries GN=SOD1 PE=1 SV=2	sp P09670 SODC_SHEEP, tr B9VGZ6 B9VGZ6_SH_EEP	gGN EESTk	80%	37.7	51.60202	Ref	-0.28	-0.18	-0.02	-0.12	0.13	-0.6	-0.27	12900	10000	11700	14600	15100	15600	9810	12200	477.3	1428.8	3	0.0096	6.748
Superoxide dismutase [Cu-Zn] OS=Ovis aries GN=SOD1 PE=1 SV=2	sp P09670 SODC_SHEEP, tr B9VGZ6 B9VGZ6_SH_EEP	gGnE ESTK	70%	34	51.25221	Ref	-0.19	-0.33	-0.24	-0.066	0.17	-0.79	-0.26	17900	12300	12100	14500	18000	18500	9930	14200	715.9	1429.7	2	0.0108	7.577
Superoxide dismutase [Cu-Zn] OS=Ovis aries GN=SOD1 PE=1 SV=2	sp P09670 SODC_SHEEP, tr B9VGZ6 B9VGZ6_SH_EEP	hVGD LG NVk	55%	32.2	52.24396	Ref	-0.25	-0.3	-0.15	-0.18	0.25	-0.5	-0.24	6100	4690	4930	6130	6630	7780	4820	5730	773.9	1545.9	2	0.0259	16.72
Platelet-activating factor acetylhydrolase IB subunit beta OS=Rattus norvegicus GN=Pafah1b2 PE=1 SV=1	4 PA1B2_RAT, sp P68401 PA1B2_BOVIN, sp P68402 PA1B2_HUMAN, sp Q5R4G2 PA1B2_PONAB, sp Q61206 PA1B2_MOUSE, tr B0KWR3 B0KWR3_CALJAT, tr B2KIG1 B2KIG1_RHIFE, tr B3RF71 B3RF71_SORAR, tr B5SNQ5 B5SNQ5_OTOGA, tr D2HC75 D2HC75_LLPR	iIVLG LLPR	95%	37.9	35.59188	Ref	-0.16	-0.29	-0.39	-0.33	-0.05	-0.18	-0.37	330	205	202	212	243	258	246	214	433.3	1296.9	3	0.0024	1.862

Barrier-to-autointegration factor OS=Mus musculus GN=Banf1 PE=1 SV=1	2 BAF_M OUSE,sp O75531 B AF_HUM AN,sp P6 1283 BAF _BOVIN,s p Q5RBU 9 BAF_P ONAB,sp Q9R1T1 B AF_RAT,tr B2R4V4 B2R4V4_ HUMAN,t r D2H4N2 D2H4N2 _AILME,tr E2RGE0 E2RGE0_C ANFA,tr F 1RU33 F1 RU33_PIG ,tr F6QR2 3 F6QR23 _MONDO, tr F6T830	k	95%	51.6	48.58182	Ref	-0.37	0.021	-0.23	-0.13	0.14	-0.01	-0.46	1110	703	1000	946	1120	1180	1110	806	653.4	1957.2	3	0.013	6.637
Barrier-to-autointegration factor OS=Mus musculus GN=Banf1 PE=1 SV=1	2 BAF_M OUSE,sp O75531 B AF_HUM AN,sp P6 1283 BAF _BOVIN,s p Q5RBU 9 BAF_P ONAB,sp Q9R1T1 B AF_RAT,tr B2R4V4 B2R4V4_ HUMAN,t r D2H4N2 D2H4N2 _AILME,tr E2RGE0 E2RGE0_C ANFA,tr F 1RU33 F1 RU33_PIG ,tr F6QR2 3 F6QR23 _MONDO, tr F6T830	k	95%	55.2	47.87383	Ref	-0.37	-0.14	-0.05	-0.091	0.08	-0.23	-0.04	581	403	513	613	656	645	542	616	653.4	1957.2	3	0.0042	2.148

Barrier-to-autointegration factor OS=Mus musculus GN=Banf1 PE=1 SV=1	2 BAF_MOUSE,sp O75531 BAF_HUMAN,sp P61283 BAF_BOVIN,sp Q5RBU9 BAF_PONAB,sp Q9R1T1 BAF_RAT,transcript B2R4V4 B2R4V4_HUMAN,transcript D2H4N2 D2H4N2_AILME,transcript E2RGE0 E2RGE0_CANFA,transcript F1RU33 F1RU33_PIG,transcript F6QR23 F6QR23_MONDO,transcript F6T830	k	94%	46.2	49.15294	Ref	0.043	0.02	-0.13	-0.41	-0.06	-0.26	-0.1	323	289	309	313	284	315	288	319	653.4	1957.2	3	0.0216	11.03
Barrier-to-autointegration factor OS=Mus musculus GN=Banf1 PE=1 SV=1	2 BAF_MOUSE,sp O75531 BAF_HUMAN,sp P61283 BAF_BOVIN,sp Q5RBU9 BAF_PONAB,sp Q9R1T1 BAF_RAT,transcript B2R4V4 B2R4V4_HUMAN,transcript D2H4N2 D2H4N2_AILME,transcript E2RGE0 E2RGE0_CANFA,transcript F1RU33 F1RU33_PIG,transcript F6QR23 F6QR23_MONDO,transcript F6T830	Lk	57%	28.6	48.07	Ref	0.31	0.024	0.045	-0.3	Value Missing (-2.907764)	-0.19	0.29	128	124	110	126	109	Value Missing (-2.907764)	107	148	653.4	1957.2	3	0.0093	4.768

Barrier-to-autointegration factor OS=Mus musculus GN=Banf1 PE=1 SV=1	2 BAF_M OUSE,sp O75531 B AF_HUM AN,sp P6 1283 BAF _BOVIN,s p Q5RBU 9 BAF_P ONAB,sp Q9R1T1 B AF_RAT,tr B2R4V4 B2R4V4_ HUMAN,t r D2H4N2 D2H4N2 _AILME,tr E2RGE0 E2RGE0_C ANFA,tr F 1RU33 F1 RU33_PIG ,tr F6QR2 3 F6QR23 _MONDO, tr F6T830	ayVV LGQ FLVL k	53%	22.3	44.2695	Ref	-0.36	-0.07	-0.02	-0.19	-0.18	-0.05	0.11	940	696	925	1070	1050	925	1050	1170	566.4	2261.4	4	0.003	1.341
Prothymosin alpha OS=Bos taurus GN=PTMA PE=1 SV=2	2 PTMA_ BOVIN,sp P06454 PTMA_HU MAN,sp Q5R790 P TMA_PO NAB,tr B8 ZZQ6 B8Z ZQ6_HU MAN,tr C 3VVV8 C3 VVV8_PIG ,tr E7CYG 5 E7CYG5 _AILME,tr F7GZS2 F7GZS2_ MACMU,t r Q15202 Q15202_ HUMAN,t r Q15204 Q15204_ HUMAN,t r Q29286 Q29286_	aAE DDE DDD VDTk	95%	54.8	49.71378	Ref	-0.29	0.3	-0.04	0.074	0.67	-0.19	0.69	9580	7170	11700	10400	12400	16400	9420	17300	682.7	2044.9	3	0.0213	10.43

Prothymosin alpha OS=Bos taurus GN=PTMA PE=1 SV=2	2 PTMA_ BOVIN,sp P06454 PTMA_HU MAN,sp Q5R790 P TMA_PO NAB,tr B8 ZZQ6 B8Z ZQ6_HU MAN,tr C 3VVV8 C3 VVV8_PIG ,tr E7CYG 5 E7CYG5 _AILME,tr F7GZS2 F7GZS2_ MACMU,t r Q15202 Q15202_ HUMAN,t r Q15204 Q15204_ HUMAN,t r Q29286 Q29286_	aAE DDE DDD VDTk	91%	44.3	53.93819	Ref	-0.88	-0	0.092	0.19	0.98	-0.45	0.77	75500	37400	74500	89300	105000	2E+05	61700	143000	620.3	2477.2	4	0.0296	11.96
Prothymosin alpha OS=Bos taurus GN=PTMA PE=1 SV=2	2 PTMA_ BOVIN,sp P06454 PTMA_HU MAN,sp Q5R790 P TMA_PO NAB,tr B8 ZZQ6 B8Z ZQ6_HU MAN,tr C 3VVV8 C3 VVV8_PIG ,tr E7CYG 5 E7CYG5 _AILME,tr F7GZS2 F7GZS2_ MACMU,t r Q15202 Q15202_ HUMAN,t r Q15204 Q15204_ HUMAN,t r Q29286 Q29286_	eVVE EAEn GR	90%	40	49.70714	Ref	-0.002	0.23	0.18	0.048	0.54	0.024	0.34	21500	17800	22600	24600	24800	30300	22200	27500	718.9	1435.7	2	0.0132	9.16

Prothymosin alpha OS=Bos taurus GN=PTMA PE=1 SV=2	2 PTMA_ BOVIN,sp P06454 PTMA_HUMAN,sp Q5R790 PTMA_PO NAB,tr B8ZZQ6 B8Z ZQ6_HUMAN,tr C3V VV8 C3V VV8_PIG ,tr E7CYG5 E7CYG5 _ALME,tr F7GZS2 F7GZS2_ MACMU,t r Q15202 Q15202_ HUMAN,t r Q15204 Q15204_ HUMAN,t r Q29286 Q29286_ sDA AVD TSSEI TTK	95%	61.8	51.95812	Ref	-0.26	0.19	0.18	0.18	0.45	-0.33	0.52	454	257	382	424	467	494	299	535	885.9	1769.9	2	0.0028	1.577
Synaptosomal-associated protein OS=Bos taurus GN=SNAP23 PE=3 SV=1	tr F1MZ54 F1MZ54_BOVIN, tr Q2T9M8 Q2T9M8_BOVIN, aNQ VTDE SLES TR	95%	54	51.9752	Ref	-0.47	-0.39	-0.03	-0.28	0.31	-0.77	0.13	15400	8950	10200	14800	13700	18000	8870	16500	877.4	1752.9	2	0.0112	6.387
Synaptosomal-associated protein OS=Bos taurus GN=SNAP23 PE=3 SV=1	tr F1MZ54 F1MZ54_BOVIN, tr Q2T9M8 Q2T9M8_BOVIN, aTW GDG GDN SPSN IVSk	95%	75.4	54.03801	Ref	-0.29	-0.15	-0.21	-0.19	0.26	-0.67	-0	14700	10400	12400	13400	14900	17800	9730	15400	771.7	2312.2	3	0.0185	7.985
Synaptosomal-associated protein OS=Bos taurus GN=SNAP23 PE=3 SV=1	tr F1MZ54 F1MZ54_BOVIN, tr Q2T9M8 Q2T9M8_BOVIN, tITM LDE QGE QlKR	52%	33.7	54.10725	Ref	-0.34	-0.41	0.041	-0.13	0.18	-0.66	0.072	15100	10400	10700	16500	16200	17500	10200	16800	757.4	2269.2	3	0.0152	6.69

Synaptosomal-associated protein OS=Bos taurus GN=SNAP23 PE=3 SV=1	tr F1MZ54 F1MZ54_BOVIN, tr Q2T9M8 Q2T9M8_BOVIN	vTnG QPQ QAT AGA ASG GYIK	95%	80.1	55.07625	Ref	-0.32	0.49	-0.02	-0.38	-0.02	-1.1	0.061	914	763	1450	1150	979	1100	537	1210	843.5	2527.3	3	0.0168	6.655
Putative RNA-binding protein Luc7-like 2 OS=Mus musculus GN=Luc7l2 PE=1 SV=1	4 LC7L2_MOUSE,s p Q9Y383 LC7L2_HUMAN, tr B2RYP6 B2RYP6_RA T, tr B3KR R1 B3KRR1_HUMAN, tr B3KSL5 B3KSL5_HUMAN, tr B7Z4Q3 B7Z4Q3_HUMAN, tr B7Z500 B7Z500_HUMAN, tr D2GYM7 D2GYM7_AILME, tr E2QTS3 E2QTS3_CA NFA, tr E2QTS4 E2	aDYE IASK	86%	40.2	52.36157	Ref	-0.027	-0.24	-0.09	-0.21	0.082	-0.44	-0.03	22800	19800	18500	23100	23400	25000	18200	24100	752.9	1503.8	2	0.025	16.61

Putative RNA-binding protein Luc7-like 2 OS=Mus musculus GN=Luc7l2 PE=1 SV=1	4 LC7L2_MOUSE,s p Q9Y383 LC7L2_HUMAN,tr B2RYP6 B2RYP6_RA T,tr B3KRR1 B3KRR1_HUMAN, tr B3KSL5_HUMAN, tr B7Z4Q3 B7Z4Q3_HUMAN, tr B7Z500 B7Z500_HUMAN, tr D2GYM7 D2GYM7_AIL ME,tr E2QTS3 E2QTS3_CA NFA,tr E2QTS4 E2	VEQL GAE GNV EESQ	82%	41.2	54.29125	Ref	0.062	-0.27	-0.08	-0.27	0.1	-0.4	0.04	24300	24900	21500	27500	26400	30000	22100	29700	742.4	2224.2	3	0.0251	11.3
Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=1 SV=1	9 SRSF7_HUMAN,s p Q3T106 SRSF7_BOVIN,sp Q8BL97 SRSF7_MOUSE,tr A6 NNE8 A6NNE8_HUMAN, tr A6YLN1 A6YLN1_CER EL,tr B4DEK2 B4DEK2_HUMAN, tr C9JAB2 C9JAB2_HUMAN, tr D2HNQ2 D2HNQ2_AIL ME,tr D3Z964 D3Z964_RAT, tr D4A720 D4A720	gHYA YDcH R	95%	43	44.8484	Ref	0.2	-0.11	0.058	-0.37	0.33	Value Missing (-1.641423)	0.054	21800	21700	18900	23900	19700	27800	Value Missing (-1.641423)	23800	368.7	1470.6	4	0.0139	9.47

<p>Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=1 SV=1</p>	<p>9 SRSF7_ HUMAN,sp Q3T106 SRSF7_BOVIN,sp Q8BL97 SRSF7_MOUSE,trans A6NNE8 A6NNE8_HUMAN,trans A6YLN1 A6YLN1_CEREL,trans B4DEK2 B4DEK2_HUMAN,trans C9JAB2 C9JAB2_HUMAN,trans D2HNQ2 D2HNQ2_AILME,trans D3Z964 D3Z964_RAT,trans D4A720 D4A720</p>	<p>vYVG NLG TGA Gk</p>	<p>90%</p>	<p>45.5</p>	<p>52.96573</p>	<p>Ref</p>	<p>-0.01</p>	<p>-0.09</p>	<p>-0.06</p>	<p>-0.31</p>	<p>0.1</p>	<p>-0.38</p>	<p>-0</p>	<p>44900</p>	<p>40000</p>	<p>41000</p>	<p>47200</p>	<p>43500</p>	<p>50700</p>	<p>37800</p>	<p>48800</p>	<p>582</p>	<p>1743</p>	<p>3</p>	<p>0.0178</p>	<p>10.18</p>
<p>ATP synthase subunit alpha, mitochondrial OS=Bos taurus GN=ATP5A1 PE=1 SV=1</p>	<p>sp P19483 ATPA_BOVIN,trans B2ZF46 B2ZF46_PIG,trans E2RNG2 E2RNG2_CANFA,trans F1MLB8 F1MLB8_BOVIN,trans F1RPS8 F1RPS8_PIG,trans F1T2M2 F1T2M2_ME SAU,trans F6V9Q4 F6V9Q4_OR NAN</p>	<p>iLGA DTSV DLEE TGR</p>	<p>95%</p>	<p>65.6</p>	<p>53.31348</p>	<p>Ref</p>	<p>-0.021</p>	<p>-0.09</p>	<p>-0.01</p>	<p>-0.1</p>	<p>0.24</p>	<p>-0.18</p>	<p>0.13</p>	<p>3120</p>	<p>3060</p>	<p>3170</p>	<p>3770</p>	<p>3890</p>	<p>4290</p>	<p>3360</p>	<p>4140</p>	<p>940.5</p>	<p>1879</p>	<p>2</p>	<p>0.0141</p>	<p>7.521</p>

ATP synthase subunit alpha, mitochondrial OS=Bos taurus GN=ATP5A1 PE=1 SV=1	sp P19483 ATPA_BOVIN, tr B2ZF46 B2ZF46_PIG, tr E2RNG2 E2RNG2_CANFA, tr F1MLB8 F1MLB8_BOVIN, tr F1RPS8 F1RPS8_PIG, tr F1T2M2 F1T2M2_ME SAU, tr F6V9Q4 F6V9Q4_OR NAN	nVQ AEE MVE FSSG Lk	87%	44.1	54.43932	Ref	-0.25	-0.15	-0.11	-9E-04	-0	0.045	0.015	6520	4030	4710	5420	6440	5610	6060	5900	759.4	2275.2	3	0.0206	9.032
ATP synthase subunit alpha, mitochondrial OS=Bos taurus GN=ATP5A1 PE=1 SV=1	sp P19483 ATPA_BOVIN, tr B2ZF46 B2ZF46_PIG, tr E2RNG2 E2RNG2_CANFA, tr F1MLB8 F1MLB8_BOVIN, tr F1RPS8 F1RPS8_PIG, tr F1T2M2 F1T2M2_ME SAU, tr F6V9Q4 F6V9Q4_OR NAN	tGTA EVSS ILEE R	89%	42.3	52.95264	Ref	0.024	0.023	0.13	-0.32	0.13	-0.24	-0.07	10300	8500	9210	11200	8960	10700	8650	9680	848.5	1694.9	2	0.0113	6.684

ATP synthase subunit alpha, mitochondrial OS=Bos taurus GN=ATP5A1 PE=1 SV=1	sp P19483 ATPA_BOVIN, tr B2ZF46 B2ZF46_PIG, tr E2RNG2 E2RNG2_CANFA, tr F1MLB8 F1MLB8_BOVIN, tr F1RPS8 F1RPS8_PIG, tr F1T2M2 F1T2M2_ME SAU, tr F6V9Q4 F6V9Q4_OR NAN	VLSI GDGI AR	57%	31.6	51.33913	Ref	-0.28	0.13	0.032	-0.3	0.24	-0.14	0.16	15700	12100	17400	18200	16000	20200	16300	19800	652.9	1303.8	2	0.0134	10.27
Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Homo sapiens GN=FKBP10 PE=1 SV=1	sp Q96AY3 FKB10_HUMAN, tr D2HIR8 D2HIR8_AILME, tr E2QZA8 E2QZA8_C ANFA, tr F5H1P8 F5H1P8_HUMAN, tr F7H5Q0 F7H5Q0_M ACMU, tr Q658U4 Q658U4_HUMAN, tr Q6ZME7 Q6ZME7_HUMAN	GGT yDTY VGS GWL lk	91%	47.7	54.48196	Ref	0.14	0.098	-0.03	-0.018	-0.02	0.14	0.059	3500	3200	3380	3470	3860	3360	3910	3680	742.4	2224.2	3	0.0229	10.29

Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Homo sapiens GN=FKBP10 PE=1 SV=1	sp Q96AY3 FKB10_HUMAN, tr D2HIR8 D2HIR8_AILME, tr E2QZA8 E2QZA8_CANFA, tr F5H1P8 F5H1P8_HUMAN, tr F7H5Q0 F7H5Q0_MACMU, tr Q658U4 Q658U4_HUMAN, tr Q6ZME7 Q6ZME7_HUMAN	gLM GMc VNE R	53%	26.9	47.33936	Ref	0.073	0.16	0.087	0.022	-0.19	0.19	0.15	7350	7140	8230	8780	9250	6970	9450	9180	730.3	1458.7	2	0.0141	9.678
Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Homo sapiens GN=FKBP10 PE=1 SV=1	sp Q96AY3 FKB10_HUMAN, tr D2HIR8 D2HIR8_AILME, tr E2QZA8 E2QZA8_CANFA, tr F5H1P8 F5H1P8_HUMAN, tr F7H5Q0 F7H5Q0_MACMU, tr Q658U4 Q658U4_HUMAN, tr Q6ZME7 Q6ZME7_HUMAN	gVP GSA VLLF EVEL VSR	95%	57.3	53.02619	Ref	0.41	0.37	0.2	0.24	Value Missing (-1.4948)	-0.14	0.028	145	154	162	161	183	Value Missing (-1.4948)	128	143	692.7	2075.2	3	0.0116	5.577

Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Homo sapiens GN=FKBP10 PE=1 SV=1	sp Q96AY3 FKB10_HUMAN, tr D2HIR8 D2HIR8_AILME, tr E2QZA8 E2QZA8_CANFA, tr F5H1P8 F5H1P8_HUMAN, tr F7H5Q0 F7H5Q0_MACMU, tr Q658U4 Q658U4_HUMAN, tr Q6ZME7 Q6ZME7_HUMAN	iiIPP FLAY GK	83%	38.9	51.27911	Ref	0.058	0.042	0.048	0.066	-0.12	0.16	0.23	5800	5500	5910	6660	7430	5700	7250	7510	657.1	1968.2	3	0.0298	15.11
Calponin-3 OS=Bos taurus GN=CNN3 PE=2 SV=1	sp Q32L92 CNN3_BOVIN, tr F1S543 F1S543_PIG, tr F7DC H4 F7DC H4_HORSE	dYQY GDQ GIDY	94%	39.2	45.84535	Ref	0.055	-0.31	-0.12	-0.061	-0.26	0.065	-0.18	175	175	148	190	217	166	216	181	820.9	1639.7	2	0.019	11.59
Calponin-3 OS=Bos taurus GN=CNN3 PE=2 SV=1	sp Q32L92 CNN3_BOVIN, tr F1S543 F1S543_PIG, tr F7DC H4 F7DC H4_HORSE	dYQY GDQ GIDY	95%	64.4	46.01702	Ref	Reference Missing (0.364029)	Missing (0.14424513)	Reference Missing (0.05807696)	Reference Missing (0.0939032)	Reference Missing (0.448569)	No Values (-1.810455)	Reference Missing (0.10453317)	No Values (-1.7207737)	Reference Missing (0.3640029)	Reference Missing (0.14424513)	Reference Missing (0.058076967)	Reference Missing (0.09399032)	Reference Missing (0.4448569455)	No Values (-1.810455)	Reference Missing (0.10453317)	820.9	1639.7	2	0.0165	10.03
Calponin-3 OS=Bos taurus GN=CNN3 PE=2 SV=1	sp Q32L92 CNN3_BOVIN, tr F1S543 F1S543_PIG, tr F7DC H4 F7DC H4_HORSE	gAS QAG MLA PGT R	85%	39.3	52.18231	Ref	-0.053	-0.16	-0.05	-0.25	-0.06	-0.2	-0.15	10500	8800	8880	10700	10300	10200	9710	10000	760.9	1519.8	2	0.0107	7.046

Calponin-3 OS=Bos taurus GN=CNN3 PE=2 SV=1	sp Q32L92 CNN3_BOVIN, tr F1S543 F1S543_PI G, tr F7DC H4 F7DC H4_HORS E	gPSY GLSA EVK	95%	52.5	52.82668	Ref	-0.1	0.076	-0.21	-0.31	-0.17	-0.06	-0.18	5050	4060	4980	4590	4720	4540	5100	4670	858.5	1715	2	0.0166	9.663
Uncharacterized protein OS=Bos taurus GN=GLG1 PE=4 SV=1	tr E1BDY3 E1BDY3_BOVIN	cAV GVT HFQ LVQ Mk	92%	48.3	54.36297	Ref	0.28	-0.41	0.27	-0.096	0.1	-0.12	0.081	1830	1870	1260	2260	1940	1940	1740	1980	739.1	2214.2	3	0.0101	4.543
Uncharacterized protein OS=Bos taurus GN=GLG1 PE=4 SV=1	tr E1BDY3 E1BDY3_BOVIN	hHcA AITP GR	83%	37.9	50.51777	Ref	0.13	-0.07	0.16	-0.045	0.29	-0.24	0.11	18300	19200	18100	23800	22800	25100	18200	23000	471.6	1411.7	3	0.0102	7.195
Uncharacterized protein OS=Bos taurus GN=GLG1 PE=4 SV=1	tr E1BDY3 E1BDY3_BOVIN	I LEL QYFI SR	77%	36.3	52.03427	Ref	0.36	-0.27	0.15	-0.17	0.12	-0.29	0.13	1230	1260	887	1340	1180	1260	986	1310	793.5	1584.9	2	0.0145	9.141
Uncharacterized protein OS=Bos taurus GN=GLG1 PE=4 SV=1	tr E1BDY3 E1BDY3_BOVIN	ISSD cED QIR	86%	35.8	48.04242	Ref	0.37	-0.35	0.084	-0.11	0.22	-0.25	0.19	29600	34300	22500	34200	33100	36100	27300	36900	758.4	1514.7	2	0.0138	9.09

Prefoldin subunit 2 OS=Bos taurus GN=PFDN2 PE=2 SV=1	sp A1A4P5 PFD2_BOVIN,sp Q9UHV9 PFD2_HUMAN,tr B1AQP2 B1AQP2_HUMAN,tr F1S192 F1S192_PIG,tr F6V169 F6V169_MACMU,tr F6W739 F6W739_HORSE,tr F7F6X9 F7F6X9_CALJIA,tr Q862M6 Q862M6_BOVIN	enSE GAG Ak	62%	33	51.51667	Ref	-0.071	0.22	0.092	0.056	0.26	-0.08	0.24	18600	14300	19100	19600	21000	21200	17400	21700	491.3	1470.8	3	0.0237	16.13
Prefoldin subunit 2 OS=Bos taurus GN=PFDN2 PE=2 SV=1	sp A1A4P5 PFD2_BOVIN,sp Q9UHV9 PFD2_HUMAN,tr B1AQP2 B1AQP2_HUMAN,tr F1S192 F1S192_PIG,tr F6V169 F6V169_MACMU,tr F6W739 F6W739_HORSE,tr F7F6X9 F7F6X9_CALJIA,tr Q862M6 Q862M6_BOVIN	enSE GAG Ak	79%	37	52.06877	Ref	-0.29	0.29	0.26	0.17	0.38	-0.24	0.054	8980	5930	9610	10600	11000	11000	7500	9140	736.4	1470.8	2	0.0024	1.637

<p>Prefoldin subunit 2 OS=Bos taurus GN=PFDN2 PE=2 SV=1</p>	<p>sp A1A4P5 PFD2_BOVIN,sp Q9UHV9 PFD2_HUMAN,tr B1AQP2 B1AQP2_HUMAN,tr F1S192 F1S192_PIG,tr F6V169 F6V169_MACMU,tr F6W739 F6W739_HORSE,tr F7F6X9 F7F6X9_CALJIA, tr Q862M6 Q862M6_BOVIN</p>	<p>gAVS AEQ VIAG FNR</p>	95%	58.4	53.05859	Ref	-0.078	0.23	0.17	0.19	0.37	-0.1	0.13	2980	2680	3610	3870	4320	4290	3240	3770	862	1721.9	2	0.0111	6.436
<p>Prefoldin subunit 2 OS=Bos taurus GN=PFDN2 PE=2 SV=1</p>	<p>sp A1A4P5 PFD2_BOVIN,sp Q9UHV9 PFD2_HUMAN,tr B1AQP2 B1AQP2_HUMAN,tr F1S192 F1S192_PIG,tr F6V169 F6V169_MACMU,tr F6W739 F6W739_HORSE,tr F7F6X9 F7F6X9_CALJIA, tr Q862M6 Q862M6_BOVIN</p>	<p>IIETL TQQ LQAK</p>	95%	56.1	50.45053	Ref	0.059	0.16	0.14	-0.045	0.27	0.1	0.26	521	509	591	656	636	693	642	710	665.4	1993.2	3	0.011	5.527

F-actin-capping protein subunit alpha-1 OS=Pongo abelii GN=CAPZA1 PE=2 SV=3	sp Q5NV M0 CAZA1_PONAB, tr F6QI70 F6QI70_CALJA, tr F6QUE9 F6QUE9_CALJA, tr F6R5F1 F6R5F1_MA CMU, tr F6WWW7 F6WWW7_HORSE	eAS DPQ PEEV DGG Lk	91%	46.9	53.93305	Ref	-0.14	0.67	-0.19	-0.034	0.06	-0.11	0.009	16700	12000	22800	14100	17400	16200	15000	16200	727	2178.1	3	0.0173	7.952
F-actin-capping protein subunit alpha-1 OS=Pongo abelii GN=CAPZA1 PE=2 SV=3	sp Q5NV M0 CAZA1_PONAB, tr F6QI70 F6QI70_CALJA, tr F6QUE9 F6QUE9_CALJA, tr F6R5F1 F6R5F1_MA CMU, tr F6WWW7 F6WWW7_HORSE	fITH APP GEF NEVF NDV R	92%	48.9	54.15613	Ref	0.24	0.1	0.068	0.16	0.099	3E-04	0.16	1200	1500	1480	1630	1910	1600	1560	1720	798.4	2392.2	3	0.0145	6.069
F-actin-capping protein subunit alpha-1 OS=Pongo abelii GN=CAPZA1 PE=2 SV=3	sp Q5NV M0 CAZA1_PONAB, tr F6QI70 F6QI70_CALJA, tr F6QUE9 F6QUE9_CALJA, tr F6R5F1 F6R5F1_MA CMU, tr F6WWW7 F6WWW7_HORSE	fTITP PTA QVV GVlk	87%	39.5	49.66733	Ref	0.35	-0.08	0.16	0.001	-0.1	0.15	-0.04	8060	8480	6850	9060	8940	7300	9060	7890	727.1	2178.3	3	0.0108	4.958

F-actin-capping protein subunit alpha-1 OS=Pongo abelii GN=CAPZA1 PE=2 SV=3	sp Q5NV M0 CAZA1_PONAB, tr F6Q170 F6Q170_CALJA, tr F6QUE9 F6QUE9_CALJA, tr F6R5F1 F6R5F1_MA CMU, tr F6WWW7 F6WWW7_HORSE	fTITP PTA QVV GVLk	92%	44.3	49.80971	Ref	0.48	-0.02	0.18	0.024	-0.1	0.057	-0.06	2160	2770	2130	2740	2710	2180	2530	2310	727.1	2178.3	3	0.0122	5.619
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_018794 PE=4 SV=1	tr D2I0Q2 D2I0Q2_AILME, tr F1MQB4 F1MQB4_BOVIN, tr F1N770 F1N770_BOVIN, tr F1S93 F1S93_PIG, tr Q0VCQ9 Q0VCQ9_BOVIN	eALL GGQ EEVD EYVk	95%	71.6	54.52263	Ref	-0.083	0.34	0.053	-0.35	0.43	-0.64	0.29	16300	12700	18400	16900	14100	21200	10500	20000	763.1	2286.2	3	0.0187	8.155
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_018794 PE=4 SV=1	tr D2I0Q2 D2I0Q2_AILME, tr F1MQB4 F1MQB4_BOVIN, tr F1N770 F1N770_BOVIN, tr F1S93 F1S93_PIG, tr Q0VCQ9 Q0VCQ9_BOVIN	hYA MQE AK	62%	33.8	52.3689	Ref	0.0072	0.16	0.039	-0.19	0.24	-0.25	0.32	27100	23500	28300	29200	27500	32400	24100	35400	529.3	1584.8	3	0.0139	8.776

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_018794 PE=4 SV=1	tr D2IQ2 D2IQ2_AILME,tr F1MQB4 F1MQB4_BOVIN,tr F1N770 F1N770_BOVIN,tr F1S93 F1S93_PIG,tr Q0VCQ9 Q0VCQ9_BOVIN	hYA mQE Ak	79%	37.7	52.00626	Ref	0.096	-0.13	0.11	-0.096	0.4	-0.35	0.28	22300	20900	19400	25800	24600	30200	18800	28800	534.6	1600.8	3	0.0262	16.34
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_018794 PE=4 SV=1	tr D2IQ2 D2IQ2_AILME,tr F1MQB4 F1MQB4_BOVIN,tr F1N770 F1N770_BOVIN,tr F1S93 F1S93_PIG,tr Q0VCQ9 Q0VCQ9_BOVIN	qLH DEYF YHD EL	93%	42.2	49.57579	Ref	0.16	-0.23	0.03	-0.18	0.51	-0.41	0.51	1150	1350	1110	1490	1430	2000	1110	2080	956.9	1911.9	2	0.0145	7.579
PGRMC2 protein OS=Bos taurus GN=PGRMC2 PE=2 SV=1	tr A5PJQ6 A5PJQ6_BOVIN,tr A9LM01 A9LM01_PIG,tr D2HSJ7 D2HSJ7_AILME,tr F7GWG6 F7GWG6_CALJA	fYGP AGP YGIF AGR	92%	47.4	52.67197	Ref	-0.02	-0.24	-0.04	-0.22	-0.28	-0.39	0.057	1870	1490	1380	1790	1740	1460	1420	1910	593	1775.9	3	0.0115	6.493

PGRMC2 protein OS=Bos taurus GN=PGRMC2 PE=2 SV=1	tr A5PQ6 A5PQ6_BOVIN, tr A9LM01 A9LM01_PIG, tr D2HSJ7 D2HSJ7_AIL ME, tr F7GWG6 F7GWG6_C ALJA	gLAT FcLD k	72%	36.3	52.58738	Ref	-0.31	-0.18	-0.11	-0.14	0.065	-0.37	0.012	5600	3870	4610	5440	5850	5890	4550	5880	541.3	1620.9	3	0.0255	15.73
PGRMC2 protein OS=Bos taurus GN=PGRMC2 PE=2 SV=1	tr A5PQ6 A5PQ6_BOVIN, tr A9LM01 A9LM01_PIG, tr D2HSJ7 D2HSJ7_AIL ME, tr F7GWG6 F7GWG6_C ALJA	iLLA VnG k	55%	26.5	46.50424	Ref	-0.27	-0.29	0.064	-0.07	-0.1	-0.37	0.041	20400	14900	16000	22800	22900	19600	17000	22400	719	1435.9	2	0.0022	1.508
PGRMC2 protein OS=Bos taurus GN=PGRMC2 PE=2 SV=1	tr A5PQ6 A5PQ6_BOVIN, tr A9LM01 A9LM01_PIG, tr D2HSJ7 D2HSJ7_AIL ME, tr F7GWG6 F7GWG6_C ALJA	rGLG AGA GAG EESP AASL PR	92%	47.9	54.11148	Ref	-0.1	-0.2	-0.06	-0.11	0.071	-0.26	-0.08	6170	5830	5900	7310	7780	7710	6400	7190	710	2127.1	3	0.0149	7.017
Transcription factor BTF3 OS=Mus musculus GN=Btf3 PE=2 SV=3	sp Q64152 BTF3_MOUSE	kLQF SLK	59%	25	44.43325	Ref	-0.063	-0.26	0.25	-0.039	0.31	-0.44	0.21	5820	4830	4550	7290	6590	7330	4540	7080	888.6	1775.1	2	0.006	3.357

Transcription factor BTF3 OS=Mus musculus GN=Btf3 PE=2 SV=3	sp Q6415 2 BTF3_ MOUSE	tATA DDk	73%	34.8	51.40404	Ref	-0.15	-0.14	0.26	-0.066	0.37	-0.53	0.2	51100	40400	44200	65500	57500	68000	38100	62500	665.4	1328.7	2	0.0251	18.9
Transcription factor BTF3 OS=Mus musculus GN=Btf3 PE=2 SV=3	sp Q6415 2 BTF3_ MOUSE	tGAP TQA DSR	80%	36.5	51.1388	Ref	-0.01	-0.1	0.22	-0.17	0.33	-0.43	0.12	4440	3710	3770	5280	4440	5490	3400	4930	654.3	1306.7	2	0.0067	5.116
Transcription factor BTF3 OS=Mus musculus GN=Btf3 PE=2 SV=3	sp Q6415 2 BTF3_ MOUSE	vQA SLAA NTFT ITGH AETk	95%	86.9	54.58831	Ref	-0.25	-0.32	0.4	-0.01	0.18	-0.37	0.31	3050	2240	2310	4270	3550	3530	2510	4000	856.8	2567.4	3	0.0164	6.382

Heterogeneous nuclear ribonucleoprotein Q2 OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	6 HNRPQ_HUMAN,sp Q7TMK9 HNRPQ_MOUSE,trans A7E355 A7E355_BOVIN,trans B2R8Z8 B2R8Z8_HUMAN,trans B7Z645 B7Z645_HUMAN,trans D2HLE8 D2HLE8_AILME,trans D3ZF34 D3ZF34_RAT,trans D3ZME6 D3ZME6_RAT,trans E2QVD2 E2QVD2_CANFA,trans E2QVD3 E2QVD3	dLFE DELV PLFE k	92%	48.6	54.2565	Ref	0.19	-0.16	-0.09	-0.39	-0.25	-0.05	0.23	616	608	516	610	544	524	629	756	734.7	2201.2	3	0.0177	8.029
	Heterogeneous nuclear ribonucleoprotein Q2 OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	6 HNRPQ_HUMAN,sp Q7TMK9 HNRPQ_MOUSE,trans A7E355 A7E355_BOVIN,trans B2R8Z8 B2R8Z8_HUMAN,trans B7Z645 B7Z645_HUMAN,trans D2HLE8 D2HLE8_AILME,trans D3ZF34 D3ZF34_RAT,trans D3ZME6 D3ZME6_RAT,trans E2QVD2 E2QVD2_CANFA,trans E2QVD3 E2QVD3	gYAF VTfc Tk	50%	32.4	52.95525	Ref	0.31	-0.3	-0.09	-0.29	-0.13	-0.15	0.17	2230	2420	1720	2240	2140	2090	2150	2670	597.6	1789.9	3	0.0108

Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	6 HNRPQ_HUMAN,sp Q7TMK9 HNRPQ_MOUSE,trans A7E355 A7E355_BOVIN,trans B2R8Z8 B2R8Z8_HUMAN,trans B7Z645 B7Z645_HUMAN,trans D2HLE8 D2HLE8_AILME,trans D3ZF34 D3ZF34_RAT,trans D3ZME6 D3ZME6_RAT,trans E2QVD2 E2QVD2_CANFA,trans E2QVD3 E2QVD3	lkDYAFIH	85%	40.7	54.23929	Ref	0.11	-0.26	0.088	-0.14	-0.07	-0.04	0.049	3060	3220	2700	3870	3640	3340	3560	3750	541.3	2161.2	4	0.0094	4.347
	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	6 HNRPQ_HUMAN,sp Q7TMK9 HNRPQ_MOUSE,trans A7E355 A7E355_BOVIN,trans B2R8Z8 B2R8Z8_HUMAN,trans B7Z645 B7Z645_HUMAN,trans D2HLE8 D2HLE8_AILME,trans D3ZF34 D3ZF34_RAT,trans D3ZME6 D3ZME6_RAT,trans E2QVD2 E2QVD2_CANFA,trans E2QVD3 E2QVD3	tGYTLDVTTGQR	79%	37.4	52.29823	Ref	0.096	-0.16	0.093	-0.096	-0	-0.24	-0.14	23900	21800	19900	26500	25700	23900	21200	22500	808.4	1614.8	2	0.0152

Uncharacterized protein OS=Ornithorhynchus anatinus GN=AHNAK PE=4 SV=1	tr F7FUG3 F7FUG3_ORNAN	aDID VSG Pk	93%	44.2	51.98503	Ref	-0.59	-0.28	-0.11	0.096	0.053	-0.71	-0.26	2E+05	82600	1E+05	141000	178000	2E+05	92800	126000	755.4	1508.9	2	0.0151	10.01
Uncharacterized protein OS=Ornithorhynchus anatinus GN=AHNAK PE=4 SV=1	tr F7FUG3 F7FUG3_ORNAN	gDID ISGP k	95%	54.2	51.8443	Ref	-0.74	-0.14	-0.12	-0.014	0.12	-0.45	-0.38	63600	30700	50200	57400	68000	65100	45800	47900	504	1508.9	3	0.0139	9.207
Uncharacterized protein OS=Ornithorhynchus anatinus GN=AHNAK PE=4 SV=1	tr F7FUG3 F7FUG3_ORNAN	iSMP DIDL NLkG Pk	66%	31.4	50.98433	Ref	-0.75	-0.31	-0.11	0.13	0.054	-0.37	-0.1	13800	7750	11400	14800	19100	15900	12300	14800	614.1	2452.4	4	0.0072	2.934
Uncharacterized protein OS=Ornithorhynchus anatinus GN=AHNAK PE=4 SV=1	tr F7FUG3 F7FUG3_ORNAN	iSMP DIDL nLkG Pk	55%	30.5	52.07734	Ref	-0.48	-0.42	-0.3	-0.011	0.17	-0.21	-0.07	3520	2540	2870	3490	4700	4670	3740	4090	614.4	2453.4	4	0.0167	6.816
CD93 OS=Ovis aries GN=CD93 PE=2 SV=1	tr C5ISB5 C5ISB5_SHEEP	kQQ PQS AAD SYA WVP ER	90%	47	55.00445	Ref	-0.023	-0.61	0.6	0.2	0.37	-0.66	0.6	3890	3140	2260	5910	4920	4820	2470	5860	857.1	2568.3	3	0.0236	9.17
CD93 OS=Ovis aries GN=CD93 PE=2 SV=1	tr C5ISB5 C5ISB5_SHEEP	ILDD LVSc ASR	95%	48.5	51.78873	Ref	-0.092	-1.1	0.59	0.17	0.55	-1.5	0.88	1960	1430	754	2800	2300	2620	669	3410	771.4	1540.8	2	0.0082	5.29

CD93 OS=Ovis aries GN=CD93 PE=2 SV=1	tr C5ISB5 C5ISB5_ SHEEP	rPSL PAR	61%	29.7	48.48663	Ref	0.23	0.3	0.42	-0.068	0.47	-0.8	0.36	10100	12000	13600	16600	13000	16500	7170	15800	367.6	1099.7	3	0.0156	14.15
CD93 OS=Ovis aries GN=CD93 PE=2 SV=1	tr C5ISB5 C5ISB5_ SHEEP	rPSL PAR	74%	31.7	47.2863	Ref	0.1	-0.16	0.63	0.028	0.43	-0.81	0.5	58000	57700	52000	101000	73500	84500	37500	92500	367.6	1099.7	3	0.0078	7.086
Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	1 TBB2C_ HUMAN,s p P68372 TBB2C_ MOUSE,s p Q3MH M5 TBB2 C_BOVIN, sp Q6P9T 8 TBB2C_ RAT,tr E2 QWZ6 E2 QWZ6_CA NFA,tr F2 Z571 F2Z 571_PIG,t r F6WYK8 F6WYK8 _MONDO, tr F7GW5 7 F7GW5 7_MACM U,tr Q604 55 Q6045 5_CRIGR,t r Q8IWP6 Q8IWP6	aLTV PELT QQ MFD Ak	89%	45.3	54.16206	Ref	0.18	-0.42	-0.07	-0.23	-0.17	-0.1	-0.15	1740	1640	1170	1670	1660	1500	1650	1580	767.4	2299.3	3	0.0143	6.202

Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	1 TBB2C_ HUMAN,s p P68372 TBB2C_ MOUSE,s p Q3MH M5 TBB2 C_BOVIN, sp Q6P9T 8 TBB2C_ RAT,tr E2 QWZ6 E2 QWZ6_CA NFA,tr F2 Z571 F2Z 571_PIG,t r F6WYK8 F6WYK8 _MONDO, tr F7GW5 7 F7GW5 7_MACM U,tr Q604 55 Q6045 5_CRIGR,t r Q8IWP6 Q8IWP6	aVLV DLEP GTM DSV R	89%	42.8	53.53655	Ref	0.16	-0.42	0.006	-0.11	0.023	-0.51	-0.11	3660	3500	2530	3820	3890	3720	2690	3510	953.5	1905	2	0.0115	6.012
Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	1 TBB2C_ HUMAN,s p P68372 TBB2C_ MOUSE,s p Q3MH M5 TBB2 C_BOVIN, sp Q6P9T 8 TBB2C_ RAT,tr E2 QWZ6 E2 QWZ6_CA NFA,tr F2 Z571 F2Z 571_PIG,t r F6WYK8 F6WYK8 _MONDO, tr F7GW5 7 F7GW5 7_MACM U,tr Q604 55 Q6045 5_CRIGR,t r Q8IWP6 Q8IWP6	aVLV DLEP GTM DSV R	88%	42.2	53.56204	Ref	0.19	-0.4	-0.07	-0.043	-0.02	-0.55	0.021	3320	3450	2480	3520	3940	3500	2530	3730	953.5	1905	2	0.0041	2.161

Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	1 TBB2C_HUMAN,sp P68372 TBB2C_MOUSE,sp Q3MHM5 TBB2C_BOVIN,sp Q6P9T8 TBB2C_RAT,tr E2QWZ6 E2QWZ6_CANFA,tr F2Z571 F2Z571_PIG,tr F6WYK8 F6WYK8_MONDO,tr F7GW57 F7GW57_MACMU,tr Q60455 Q60455_CRIGR,tr Q8IWP6 Q8IWP6	iINVY YNE ATG Gk	87%	43.6	53.78109	Ref	-0.2	-0.3	0.018	-0.1	0.15	-0.39	-0.04	14800	11400	11600	16100	16300	16900	12200	15500	646.4	1936	3	0.0101	5.226
Uncharacterized protein OS=Bos taurus GN=Bt.45504 PE=4 SV=1	tr E1B7W1 E1B7W1_BOVIN	eEST TGF Dk	88%	41	52.11905	Ref	-0.14	0.019	-0.26	-0.39	-0.22	-0.37	-0.14	17900	13400	16300	15100	15200	14800	14000	16300	811.4	1620.8	2	0.0136	8.415
Uncharacterized protein OS=Bos taurus GN=Bt.45504 PE=4 SV=1	tr E1B7W1 E1B7W1_BOVIN	eSEF DDE Pk	57%	31.1	50.90353	Ref	-0.18	-0.02	-0.5	-0.33	0.11	-0.65	0.19	12100	10500	12700	10300	12700	15000	9280	16400	852.4	1702.8	2	0.0239	14.03
Uncharacterized protein OS=Bos taurus GN=Bt.45504 PE=4 SV=1	tr E1B7W1 E1B7W1_BOVIN	gSEQ EAAK	79%	37.1	52.20247	Ref	-0.027	-0.15	-0.34	-0.43	-0.03	-0.52	-0.08	10800	8600	8590	8440	8740	10100	7450	10100	714.4	1426.8	2	0.0132	9.22

Uncharacterized protein OS=Bos taurus GN=Bt.45504 PE=4 SV=1	tr E1B7W1 E1B7W1_BOVIN	kTEE LEEE SFSE R	79%	39.7	53.74013	Ref	-0.044	-0.35	-0.46	-0.43	0.056	-0.35	0.15	24200	21500	18900	19500	22100	27000	21300	29900	741	2220.1	3	0.0207	9.314
Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	sp P23246 SFPQ_HUMAN, tr E1BQ37 E1BQ37_BOVIN, tr Q86VG2 Q86VG2_HUMAN, tr Q9BSV4 Q9BSV4_HUMAN	fATH AAA LSVR	70%	35.2	52.06886	Ref	-0.01	-0.07	-0.14	-0.26	-0.11	-0.15	-0.09	11100	10600	11100	11800	12000	11700	11800	12200	483.3	1446.8	3	0.0084	5.787
Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	sp P23246 SFPQ_HUMAN, tr E1BQ37 E1BQ37_BOVIN, tr Q86VG2 Q86VG2_HUMAN, tr Q9BSV4 Q9BSV4_HUMAN	mGG GGA MN MGD PYGS GGQ k	80%	38	51.56419	Ref	-0.01	-0.08	-0.46	-0.37	0.029	-0.36	0.071	5220	4250	4390	3790	4460	5110	4070	5460	794	2379.1	3	0.0211	8.845
Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	sp P23246 SFPQ_HUMAN, tr E1BQ37 E1BQ37_BOVIN, tr Q86VG2 Q86VG2_HUMAN, tr Q9BSV4 Q9BSV4_HUMAN	qGP GPG GPK	79%	37.5	51.58398	Ref	-0.17	0.11	-0.55	-0.25	-0.02	-0.29	0.075	24400	18900	24900	17600	23900	24600	21300	27200	468.3	1401.8	3	0.0234	16.66

Actin-like protein (Fragment) OS=Homo sapiens GN=ACT PE=2 SV=1	tr Q562M 3 Q562M 3_HUMA N	vAPE EHP VLLT QAP LNPk	63%	35	53.29711	Ref	0.24	-0.05	-0.1	0.13	0.013	-0.04	-0.05	15200	17400	15400	16700	21600	17400	17600	17300	854.5	2560.4	3	0.0349	13.62
Actin-like protein (Fragment) OS=Homo sapiens GN=ACT PE=2 SV=1	tr Q562M 3 Q562M 3_HUMA N	vAPE EHP VLLT qAPL NPK	72%	36.4	52.74303	Ref	0.025	-0.06	-0.06	-0.047	-0.09	0.22	-0.43	29200	20300	20800	23200	25900	21900	28300	18000	854.8	2561.5	3	0.005	1.946
Actin-like protein (Fragment) OS=Homo sapiens GN=ACT PE=2 SV=1	tr Q562M 3 Q562M 3_HUMA N	vAPE EHP VLLT qAPL NPK	95%	70.1	53.32305	Ref	-0.012	0.032	-0.02	0.051	-0.05	0.22	-0.28	2420	2020	2260	2450	2830	2310	2900	2030	1282	2561.4	2	0.0197	7.704
Actin-like protein (Fragment) OS=Homo sapiens GN=ACT PE=2 SV=1	tr Q562M 3 Q562M 3_HUMA N	vAPE EHP VLLT qAPL NPK ANR	95%	53.2	54.19093	Ref	0.24	-0.19	-0.06	0.068	-0.15	0.19	-0.09	5450	5800	4670	5730	6900	5170	6860	5600	650.6	2598.4	4	0.0162	6.241

40S ribosomal protein S5 OS=Rattus norvegicus GN=Rps5 PE=2 SV=3	0 RS5_RA T,sp P46782 RS5_HUMAN,sp P97461 RS5_MOUSE,sp Q5E988 RS5_BOVIN,tr B0BN81 B0BN81_RAT,tr D2HWG8 D2HWG8_AILME,tr E2RIQ8 E2RIQ8_CAF6R6P5 F6R6P5_ORNAN,tr F6T2T8 F	gSSn SYAI	84%	39.3	52.69487	Ref	-0.2	0.018	0.086	-0.046	0.17	-0.16	-0.14	11800	8580	10800	12700	12800	13000	10800	10900	768.4	1534.8	2	0.0138	8.97
40S ribosomal protein S5 OS=Rattus norvegicus GN=Rps5 PE=2 SV=3	0 RS5_RA T,sp P46782 RS5_HUMAN,sp P97461 RS5_MOUSE,sp Q5E988 RS5_BOVIN,tr B0BN81 B0BN81_RAT,tr D2HWG8 D2HWG8_AILME,tr E2RIQ8 E2RIQ8_CAF6R6P5 F6R6P5_ORNAN,tr F6T2T8 F	rVN QAI WLLc TGA R	73%	37.8	53.81844	Ref	-0.026	-0.05	-0.04	-0.025	-0.08	-0	0.1	370	331	353	398	444	375	411	439	651	1950.1	3	0.0067	3.411

40S ribosomal protein S5 OS=Rattus norvegicus GN=Rps5 PE=2 SV=3	0 RS5_RA T,sp P46782 RS5_HUMAN,sp P97461 RS5_MOUSE,sp Q5E988 RS5_BOVIN,tr B0BN81 B0BN81_RAT,tr D2HWG8 D2HWG8_AILME,tr E2RIQ8 E2RIQ8_CAFNA,tr F2X205 F2X205_AILME,tr F2Z5E6 F2Z5E6_PIG,tr F6R6P5 F6R6P5_ORNAN,tr F6T2T8 F	vNQ AIWL LcTG AR	94%	47	53.27723	Ref	-0.18	-0.14	0.081	-0.017	-0.05	-0.1	0.12	779	570	634	830	855	730	736	850	898	1794	2	0.0082	4.548
40S ribosomal protein S5 OS=Rattus norvegicus GN=Rps5 PE=2 SV=3	0 RS5_RA T,sp P46782 RS5_HUMAN,sp P97461 RS5_MOUSE,sp Q5E988 RS5_BOVIN,tr B0BN81 B0BN81_RAT,tr D2HWG8 D2HWG8_AILME,tr E2RIQ8 E2RIQ8_CAFNA,tr F2X205 F2X205_AILME,tr F2Z5E6 F2Z5E6_PIG,tr F6R6P5 F6R6P5_ORNAN,tr F6T2T8 F	vNQ AIWL LcTG AR	69%	35.6	53.20821	Ref	-0.19	-0.24	0.11	-0.11	0.073	0.082	0.1	481	379	398	568	540	534	561	565	898	1793.9	2	0.0101	5.629

Plasminogen activator inhibitor 1 OS=Bos taurus GN=SERPINE1 PE=1 SV=1	sp P13909 PAI1_BOVIN, tr D4N532 D4N532_SHEP	ILVLPk	94%	26.1	28.77371	Ref	0.3	-0.11	0.59	-0.38	-0.35	-0.39	0.18	1460	2070	1690	3080	1730	1550	1570	2320	431	1289.9	3	0.0029	2.268
Plasminogen activator inhibitor 1 OS=Bos taurus GN=SERPINE1 PE=1 SV=1	sp P13909 PAI1_BOVIN, tr D4N532 D4N532_SHEP	ILVLPk	85%	17.6	28.77371	Ref	0.5	-0.06	0.56	-0.5	-0.37	Value Missing (-2.1243453)	0.13	2750	2780	2050	3540	1870	1790	Value Missing (-2.1243453)	2620	431	1289.9	3	0.0036	2.756
Plasminogen activator inhibitor 1 OS=Bos taurus GN=SERPINE1 PE=1 SV=1	sp P13909 PAI1_BOVIN, tr D4N532 D4N532_SHEP	qQIQEAMQFk	95%	51.8	51.39892	Ref	0.43	-0.3	0.18	-0.38	-0.16	-0.3	0.096	578	663	433	676	508	514	488	638	769.4	1536.8	2	0.0144	9.355
Plasminogen activator inhibitor 1 OS=Bos taurus GN=SERPINE1 PE=1 SV=1	sp P13909 PAI1_BOVIN, tr D4N532 D4N532_SHEP	qQIQEAMQFk	59%	34.4	53.53605	Ref	0.2	-0.18	0.32	-0.29	-0.05	-0.23	-0.04	6450	6590	5510	8700	6320	6480	5990	6770	620.3	1858	3	0.0105	5.64
Uncharacterized protein OS=Sus scrofa GN=PDLM5 PE=4 SV=1	tr F1RW4 F1RWW4_PIG	gQPQPSnEDTLVQR	95%	54.7	52.54768	Ref	-0.38	0.29	-0.71	-0.057	-0.86	0.22	-0.7	13900	10300	17800	10000	17300	8650	19200	10100	937.5	1872.9	2	0.0115	6.111

Uncharacterized protein OS=Sus scrofa GN=PDLIM5 PE=4 SV=1	tr F1RW W4 F1R WW4_PIG	iLAQI TGTE HLK	91%	43.8	50.73454	Ref	-0.38	0.1	-0.55	-0.087	-0.6	-0.03	-0.54	6340	4230	6420	4560	6950	4260	6610	4590	644.7	1931.2	3	0.015	7.762
Uncharacterized protein OS=Sus scrofa GN=PDLIM5 PE=4 SV=1	tr F1RW W4 F1R WW4_PIG	iLAQI TGTE HLK	77%	35.9	50.74663	Ref	-0.51	0.06	-0.46	-0.12	-0.56	0.077	-0.63	3720	2210	3560	2780	3870	2500	4060	2470	644.7	1931.2	3	0.0137	7.095
Uncharacterized protein OS=Sus scrofa GN=PDLIM5 PE=4 SV=1	tr F1RW W4 F1R WW4_PIG	iLAQI TGTE HLK	94%	44.6	50.16369	Ref	-0.37	0.09	-0.59	-0.17	-0.47	-0.06	-0.44	1800	1210	1810	1270	1870	1330	1840	1410	483.8	1931.2	4	0.0055	2.838
Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Bos taurus GN=ANP32A PE=1 SV=2	sp P5112 2 AN32A _BOVIN,s p Q8HY6 7 AN32A _CANFA,tr F1PQ43 F1PQ43_C ANFA,tr F 1SIU2 F1 SIU2_PIG, tr F7BTD 7 F7BTD7 _MONDO	eLVL DNc R	71%	32.9	50.01448	Ref	-0.28	0.16	0.14	0.11	0.41	-0.05	0.2	33400	25200	37100	40900	44400	47600	36100	42700	656.3	1310.7	2	0.0106	8.072

Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Bos taurus GN=ANP32A PE=1 SV=2	sp P51122 AN32A_BOVIN,sp Q8HY67 AN32A_CANFA,tr F1PQ43 F1PQ43_CANFA,tr F1SIU2 F1SIU2_PIG, tr F7BTD7 F7BTD7_MONDO	iSGG LEVL AEk	91%	43.7	51.02029	Ref	-0.049	0.27	0.01	0.23	0.23	0.056	-0.03	4950	4240	5740	5370	6880	6020	5580	5220	575.3	1723	3	0.0085	4.953
Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Bos taurus GN=ANP32A PE=1 SV=2	sp P51122 AN32A_BOVIN,sp Q8HY67 AN32A_CANFA,tr F1PQ43 F1PQ43_CANFA,tr F1SIU2 F1SIU2_PIG, tr F7BTD7 F7BTD7_MONDO	rIHLE LR	85%	38.5	52.02235	Ref	0.24	0.8)	-0.073	0.54	-0.55	-0.02	5020	5050	8110	Value Missing (-0.95963204)	5470	7280	3570	5120	310.9	1239.8	4	0.0116	9.338
Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Bos taurus GN=ANP32A PE=1 SV=2	sp P51122 AN32A_BOVIN,sp Q8HY67 AN32A_CANFA,tr F1PQ43 F1PQ43_CANFA,tr F1SIU2 F1SIU2_PIG, tr F7BTD7 F7BTD7_MONDO	rIHLE LR	85%	38.3	51.95163	Ref	0.17	0.91	Value Missing (-0.7684114)	-0.16	0.41	-0.5	-0.05	6730	6410	11600	Value Missing (-0.7684114)	6840	8870	4910	6680	310.9	1239.8	4	0.0091	7.372

60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=1 SV=3	6 RL10A_MOUSE,s p P62906 RL10A_H UMAN,sp P62907 RL10A_RA T,sp Q4R 5P3 RL10 A_MACFA ,sp Q5E9 E6 RL10A _BOVIN,tr A1XQU2 A1XQU2 _PIG,tr D 2GYW8 D 2GYW8_A ILME,tr E 2R9V0 E2 R9V0_CA NFA,tr F1 M8D2 F1 M8D2_RA T,tr F1RY Z5 F1RYZ 5_PIG,tr	aVDI PHM DIEA Lk	73%	37.7	53.81878	Ref	0.33	-0.15	-0.08	-0.47	-0.29	-0.28	-0.39	4820	6110	4730	5610	4710	4650	4900	4490	687.4	2059.1	3	0.0167	8.107
60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=1 SV=3	6 RL10A_MOUSE,s p P62906 RL10A_H UMAN,sp P62907 RL10A_RA T,sp Q4R 5P3 RL10 A_MACFA ,sp Q5E9 E6 RL10A _BOVIN,tr A1XQU2 A1XQU2 _PIG,tr D 2GYW8 D 2GYW8_A ILME,tr E 2R9V0 E2 R9V0_CA NFA,tr F1 M8D2 F1 M8D2_RA T,tr F1RY Z5 F1RYZ 5_PIG,tr	iLGP GLNk	65%	27	44.97192	Ref	0.22	-0.59	0.18	-0.33	-0.28	-0.37	-0.36	13200	13800	8580	16300	12700	11400	11200	11200	474	1418.9	3	0.0046	3.223

60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=1 SV=3	6 RL10A_MOUSE,s p P62906 RL10A_HUMAN,sp P62907 RL10A_RA T,sp Q4R5P3 RL10A_MACFA, sp Q5E9E6 RL10A_BOVIN,tr A1XQU2 A1XQU2_PIG,tr D 2GYW8 D 2GYW8_A ILME,tr E 2R9V0 E2 R9V0_CA NFA,tr F1 M8D2 F1 M8D2_RA T,tr F1RYZ5 F1RYZ5_PIG,tr	Vk	92%	43.2	50.66456	Ref	0.14	-0.37	-0.05	-0.52	-0.23	-0.29	-0.38	2100	1800	1370	1920	1530	1640	1630	1530	466.5	1862.1	4	0.003	1.628
60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=1 SV=3	6 RL10A_MOUSE,s p P62906 RL10A_HUMAN,sp P62907 RL10A_RA T,sp Q4R5P3 RL10A_MACFA, sp Q5E9E6 RL10A_BOVIN,tr A1XQU2 A1XQU2_PIG,tr D 2GYW8 D 2GYW8_A ILME,tr E 2R9V0 E2 R9V0_CA NFA,tr F1 M8D2 F1 M8D2_RA T,tr F1RYZ5 F1RYZ5_PIG,tr	Vk	95%	60.8	51.1916	Ref	-0.063	-0.73	0.015	-0.15	-0.33	-0.03	-0.3	756	610	418	784	770	596	765	629	621.7	1862.1	3	0.018	9.654

60S ribosomal protein L6 OS=Bos taurus GN=RPL6 PE=2 SV=3	sp Q58DQ3 RL6_BOVIN, tr B0LRM7 B0LRM7_SHEEP	aSITPGTI LIILTGR	57%	29.4	49.07476	Ref	0.91	-0.69	0.54	-0.26	0.54	-0.44	0.47	383	571	204	538	340	518	273	510	915.6	1829.1	2	0.0049	2.656
60S ribosomal protein L6 OS=Bos taurus GN=RPL6 PE=2 SV=3	sp Q58DQ3 RL6_BOVIN, tr B0LRM7 B0LRM7_SHEEP	fVIA TSTK	77%	35.6	50.39383	Ref	0.46	-0.21	0.68	0.17	0.35	0.17	0.32	7620	10600	7220	15000	11600	11500	10600	11700	492.3	1473.9	3	0.0047	3.187
60S ribosomal protein L6 OS=Bos taurus GN=RPL6 PE=2 SV=3	sp Q58DQ3 RL6_BOVIN, tr B0LRM7 B0LRM7_SHEEP	hQE GEIF DTER	84%	37.5	50.47949	Ref	0.75	-0.33	0.53	0.011	0.46	-0.11	0.35	4640	6980	3570	7280	5610	6700	4710	6420	832.9	1663.8	2	0.0126	7.543
60S ribosomal protein L6 OS=Bos taurus GN=RPL6 PE=2 SV=3	sp Q58DQ3 RL6_BOVIN, tr B0LRM7 B0LRM7_SHEEP	hQE GEIF DTER	95%	49.1	50.49687	Ref	0.64	-0.03	0.44	-0.068	0.4	-0.14	0.46	35800	47000	32000	50100	38700	46700	33600	50700	555.6	1663.8	3	0.012	7.222

40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=1 SV=2	1 RS15_H UMAN,sp P62842 RS15_ME SAU,sp P 62843 RS 15_MOUS E,sp P628 44 RS15_ PIG,sp P6 2845 RS1 5_RAT,sp Q56K10 RS15_BO VIN,sp Q 5RDI7 RS 15_PONA B,tr B5KK L3 B5KKL 3_AILME,t r F6UJC4 F6UJC4_ ORNAN,tr F6VFF5 F6VFF5_ MACMU,t r F7AS95	aEVE Qk	67%	31.3	49.31636	Ref	Value Missing (- 1.8860 887)	0.27	0.47	0.095	0.26	-0.01	0.22	2680	Value Missing (- 1.886088 7)	3040	3910	3320	3260	2820	3280	525.3	1048.6	2	0.0078	7.415
40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=1 SV=2	1 RS15_H UMAN,sp P62842 RS15_ME SAU,sp P 62843 RS 15_MOUS E,sp P628 44 RS15_ PIG,sp P6 2845 RS1 5_RAT,sp Q56K10 RS15_BO VIN,sp Q 5RDI7 RS 15_PONA B,tr B5KK L3 B5KKL 3_AILME,t r F6UJC4 F6UJC4_ ORNAN,tr F6VFF5 F6VFF5_ MACMU,t r F7AS95	aEVE Qk	91%	40.2	49.27113	Ref	Value Missing (- 1.9034 969)	0.23	0.35	0.027	0.43	-0.02	0.19	2840	Value Missing (- 1.903496 9)	2890	3520	3110	3600	2750	3160	525.3	1048.6	2	0.0089	8.463

40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=1 SV=2	1 RS15_H UMAN,sp P62842 RS15_ME SAU,sp P 62843 RS 15_MOUS E,sp P628 44 RS15_ PIG,sp P6 2845 RS1 5_RAT,sp Q56K10 RS15_BO VIN,sp Q 5RDI7 RS 15_PONA B,tr B5KK L3 B5KKL 3_AILME,t r F6UJC4 F6UJC4_ ORNAN,tr F6VFF5 F6VFF5_ MACMU,t r F7AS95	aEVE Qk	68%	31.5	49.31595	Ref	Value Missing (- 1.9985 136)	0.11	0.46	-0.009	0.6	0.009	0.15	3430	Value Missing (- 1.998513 6)	3630	5200	4130	5490	3820	4190	525.3	1048.6	2	0.0079	7.529
40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=1 SV=2	1 RS15_H UMAN,sp P62842 RS15_ME SAU,sp P 62843 RS 15_MOUS E,sp P628 44 RS15_ PIG,sp P6 2845 RS1 5_RAT,sp Q56K10 RS15_BO VIN,sp Q 5RDI7 RS 15_PONA B,tr B5KK L3 B5KKL 3_AILME,t r F6UJC4 F6UJC4_ ORNAN,tr F6VFF5 F6VFF5_ MACMU,t r F7AS95	dMII LPE MVG SMV GVY nGk	93%	50.5	55.36173	Ref	0.17	0.053	0.19	-0.043	0.13	-0.27	0.14	1700	1660	1670	2070	1930	1900	1510	1990	888.1	2661.4	3	0.0127	4.784

ATP synthase subunit delta, mitochondrial OS=Bos taurus GN=ATP5D PE=1 SV=2	sp P05630 ATPD_BOVIN	aQSE LLGA ADE ATR	95%	64	52.48187	Ref	0.044	0.066	0.27	-0.17	0.36	-0.37	0.35	57300	52100	57400	74100	60300	76100	47900	78200	868.4	1734.9	2	0.0208	12.01
ATP synthase subunit delta, mitochondrial OS=Bos taurus GN=ATP5D PE=1 SV=2	sp P05630 ATPD_BOVIN	aQSE LLGA ADE ATR	95%	65	52.68074	Ref	0.088	0.062	0.17	-0.14	0.43	-0.28	0.21	75700	68800	73400	89000	79000	1E+05	65400	91000	868.5	1734.9	2	0.013	7.513
ATP synthase subunit delta, mitochondrial OS=Bos taurus GN=ATP5D PE=1 SV=2	sp P05630 ATPD_BOVIN	aQSE LLGA ADE ATR	95%	60.3	52.79247	Ref	0.6	0.31	0.057	-0.24	0.093	-0.23	-0.3	26100	30900	27400	25800	23200	25400	21200	20000	579.3	1734.9	3	0.0112	6.427
ATP synthase subunit delta, mitochondrial OS=Bos taurus GN=ATP5D PE=1 SV=2	sp P05630 ATPD_BOVIN	iEAN EALV k	86%	40.5	51.27801	Ref	-0.21	0.019	0.29	-0.069	0.5	-0.27	0.33	1E+05	105000	1E+05	181000	156000	2E+05	1E+05	186000	532.3	1593.9	3	0.0159	9.949

60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	8 RL22_H UMAN,sp P67984 RL22_MO USE,sp P6 7985 RL2 2_PIG,sp Q4R5I3 R L22_MAC FA,tr D2H N89 D2H N89_AIL ME,tr D3 YC70 D3Y C70_BOS GF,tr D3Z SC4 D3ZS C4_RAT,tr E2RMG4 E2RMG4 _CANFA,tr F1M3S4 F1M3S4_ RAT,tr F1 N301 F1N 301_BOVI N,tr F1P	aGN LGG GVV TIER	92%	44.2	52.36197	Ref	0.38	-0.08	0.41	-0.098	0.17	-0.14	0.13	18200	19900	15700	24700	19200	20200	17000	20300	773.9	1545.9	2	0.0128	8.275
60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	8 RL22_H UMAN,sp P67984 RL22_MO USE,sp P6 7985 RL2 2_PIG,sp Q4R5I3 R L22_MAC FA,tr D2H N89 D2H N89_AIL ME,tr D3 YC70 D3Y C70_BOS GF,tr D3Z SC4 D3ZS C4_RAT,tr E2RMG4 E2RMG4 _CANFA,tr F1M3S4 F1M3S4_ RAT,tr F1 N301 F1N 301_BOVI N,tr F1P	iTVT SEVP FSK	67%	34.9	52.442	Ref	0.53	-0.38	0.41	0.018	0.43	-0.3	-0.02	18600	23700	13700	26800	22400	26000	16400	19700	606	1815	3	0.015	8.261

60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	8 RL22_H UMAN,sp P67984 RL22_MO USE,sp P6 7985 RL2 2_PIG,sp Q4R5I3 R L22_MAC FA,tr D2H N89 D2H N89_AIL ME,tr D3 YC70 D3Y C70_BOS GF,tr D3Z SC4 D3ZS C4_RAT,tr E2RMG4 E2RMG4 _CANFA,tr F1M3S4 F1M3S4_ RAT,tr F1 N301 F1N 301_BOVI N,tr F1P	ITVT SEVP FSk	88%	42.8	52.30168	Ref	0.42	-0.05	0.23	0.029	0.27	-0.07	-0.01	16100	18400	14300	19600	18800	19400	16000	16600	606	1815	3	0.0108	5.948
60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	8 RL22_H UMAN,sp P67984 RL22_MO USE,sp P6 7985 RL2 2_PIG,sp Q4R5I3 R L22_MAC FA,tr D2H N89 D2H N89_AIL ME,tr D3 YC70 D3Y C70_BOS GF,tr D3Z SC4 D3ZS C4_RAT,tr E2RMG4 E2RMG4 _CANFA,tr F1M3S4 F1M3S4_ RAT,tr F1 N301 F1N 301_BOVI N,tr F1P	ITVT SEVP FSK	91%	42.7	52.21341	Ref	0.37	-0.71	0.13	-0.21	-0.04	1.2	-0.36	5970	8040	4120	8320	7210	7090	17000	5880	908.5	1815.1	2	0.0102	5.631

Uncharacterized protein OS=Bos taurus GN=Bt.22969 PE=3 SV=1	tr E1BMJ0 E1BMJ0_BOVIN, tr F1MMJ0 F1MMJ0_BOVIN	hHL QDL EQAL STAV Fk	84%	40.2	54.12968	Ref	0.41	0.34	0.45	0.3	-0.03	0.93	0.5	906	1060	1100	1330	1320	917	1870	1370	612.1	2444.3	4	0.0157	6.439
Uncharacterized protein OS=Bos taurus GN=Bt.22969 PE=3 SV=1	tr E1BMJ0 E1BMJ0_BOVIN, tr F1MMJ0 F1MMJ0_BOVIN	hQA TLEL TESG VEAT AAS VVS VAR	77%	40.6	55.29186	Ref	Reference Missing (0.80654085)	No Value (-1.8152733)	Reference Missing (0.9853438)	Reference Missing (0.6750396)	Reference Missing (0.6850735)	Reference Missing (0.39460883)	Reference Missing (0.7540491)	No Values (-1.8999699)	Reference Missing (0.80654085)	No Value (-1.8152733)	Reference Missing (0.9853438)	Reference Missing (0.6750396)	Reference Missing (0.6850735)	Reference Missing (0.39460883)	Reference Missing (0.7540491)	910.8	2729.4	3	0.0172	6.298
Uncharacterized protein OS=Bos taurus GN=Bt.22969 PE=3 SV=1	tr E1BMJ0 E1BMJ0_BOVIN, tr F1MMJ0 F1MMJ0_BOVIN	hQA TLEL TESG VEAT AAS VVS VAR	95%	104	55.29186	Ref	0.44	0.32	0.23	0.5	0.034	0.61	0.8	287	339	337	355	474	299	467	527	910.8	2729.4	3	0.0172	6.298
Uncharacterized protein OS=Bos taurus GN=Bt.22969 PE=3 SV=1	tr E1BMJ0 E1BMJ0_BOVIN, tr F1MMJ0 F1MMJ0_BOVIN	hQA TLEL TESG VEAT AAS VVS VAR	95%	75.7	55.29586	Ref	0.67	0.42	0.36	0.37	0.29	0.59	0.15	905	1100	1000	1080	1200	988	1280	934	683.4	2729.4	4	0.016	5.864
Glucose-6-phosphate isomerase OS=Sus scrofa GN=GPI PE=1 SV=3	sp P08059 G6PI_PIG, sp Q3ZBD7 G6PI_BOVIN, tr F1RNU9 F1RNU9_PIG	aALT QNP QFk	95%	58.2	52.6041	Ref	-0.2	-0.16	0.25	-0.19	0.14	0.5	0.13	684	460	514	766	622	686	916	705	732.4	1462.8	2	0.0152	10.41
Glucose-6-phosphate isomerase OS=Sus scrofa GN=GPI PE=1 SV=3	sp P08059 G6PI_PIG, sp Q3ZBD7 G6PI_BOVIN, tr F1RNU9 F1RNU9_PIG	aVLH VALR	73%	35.4	51.46423	Ref	0.19	0.32	0.21	-0.018	0.064	0.16	-0.22	3900	3810	4520	4690	4430	4090	4550	3480	394.9	1181.7	3	0.01	8.459

Glucose-6-phosphate isomerase OS=Sus scrofa GN=GPI PE=1 SV=3	sp P08059 G6PI_PIG,sp Q3ZBD7 G6PI_BOVIN, tr F1RNU9 F1RNU9_PIG	aVLH VALR	77%	36.6	51.46488	Ref	0.16	0.062	0.29	0.005	0.07	0.17	0.006	7100	7020	7100	9360	8450	7710	8650	7650	394.9	1181.7	3	0.0073	6.201
Glucose-6-phosphate isomerase OS=Sus scrofa GN=GPI PE=1 SV=3	sp P08059 G6PI_PIG,sp Q3ZBD7 G6PI_BOVIN, tr F1RNU9 F1RNU9_PIG	aVLH VALR	77%	36.2	51.09514	Ref	0.18	0.14	0.28	-0.019	0.059	0.25	-0.11	3460	3510	3720	4590	4120	3790	4520	3490	394.9	1181.7	3	0.011	9.296
Glucosidase 2 subunit beta OS=Bos taurus GN=PRKCSH PE=2 SV=1	sp Q28034 GLU2B_BOVIN	eTLQ QMA EVTR	89%	41.8	52.23509	Ref	0.015	-0.13	-0	-0.11	0.14	-0.37	9E-05	58500	50700	49800	60900	62500	64500	47600	60900	805.4	1608.8	2	0.0172	10.68
Glucosidase 2 subunit beta OS=Bos taurus GN=PRKCSH PE=2 SV=1	sp Q28034 GLU2B_BOVIN	eTVV TSTT EPSR	70%	35	52.3433	Ref	-0.044	-0.13	0.05	-0.18	0.24	-0.51	0.09	24800	21200	21600	27600	25900	30400	18800	28300	805.9	1609.8	2	0.0125	7.786
Glucosidase 2 subunit beta OS=Bos taurus GN=PRKCSH PE=2 SV=1	sp Q28034 GLU2B_BOVIN	sLED QVE VLR	62%	34.2	52.76158	Ref	0.17	-0.09	-0.11	-0.16	-0.05	-0.39	-0.03	4110	3490	3170	3500	3740	3520	2890	3680	497.9	1490.8	3	0.0108	7.217

Glucosidase 2 subunit beta OS=Bos taurus GN=PRKCSH PE=2 SV=1	sp Q28034 GLU2B_BOVIN	sLED QVE VLR	51%	32	52.65773	Ref	0.095	-0.03	0.035	-0.21	0.14	-0.4	-0.02	61700	59700	59200	69800	64700	72200	52000	66800	746.4	1490.8	2	0.0094	6.282
Thioredoxin domain containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1	sp O95881 TXD12_HUMAN,sp Q5E936 TXD12_BOVIN,tr E2QSY3 E2QSY3_CANFA,tr F1S6G4 F1S6G4_PIG,tr F6R0F4 F6R0F4_MONDO,tr F6XFL5 F6XFL5_HORSE,tr F7FG46 F7FG46_MACMU,tr F710E2 F710E2_CALJ	eAA ASGL PLM VIIHk	95%	55.2	52.19878	Ref	-0.26	0.35	0.15	0.3	0.37	0.25	0.23	5720	4190	6940	6760	8260	7590	7300	7130	720.1	2157.3	3	0.0267	12.35

Thioredoxin domain containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1	sp O9588 1 TXD12_ HUMAN,s p Q5E936 TXD12_B OVIN,tr E 2QSY3 E2 QSY3_CA NFA,tr F1 S6G4 F1S 6G4_PIG,t r F6R0F4 F6R0F4_ MONDO,t r F6XFL5 F6XFL5_H ORSE,tr F 7FG46 F7 FG46_MA CMU,tr F 7I0E2 F7I 0E2_CALJ A	eAA ASGL PLM VIIHk	95%	47.3	51.82375	Ref	-0.059	0.33	0.19	0.27	0.13	0.35	0.23	1480	1220	1730	1770	2060	1630	1990	1810	540.3	2157.3	4	0.0172	7.976
Thioredoxin domain containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1	sp O9588 1 TXD12_ HUMAN,s p Q5E936 TXD12_B OVIN,tr E 2QSY3 E2 QSY3_CA NFA,tr F1 S6G4 F1S 6G4_PIG,t r F6R0F4 F6R0F4_ MONDO,t r F6XFL5 F6XFL5_H ORSE,tr F 7FG46 F7 FG46_MA CMU,tr F 7I0E2 F7I 0E2_CALJ A	eAA ASGL PLM VIIHk	95%	57.1	51.73029	Ref	-0.23	0.19	0.23	0.24	0.46	0.17	0.27	2210	1560	2260	2600	2900	2940	2520	2670	720.1	2157.3	3	0.0166	7.681

Thioredoxin domain-containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1	sp O95881 TXD12_HUMAN,sp Q5E936 TXD12_BOVIN,tr E2QSY3 E2QSY3_CA_NFA,tr F1S6G4 F1S6G4_PIG,tr F6R0F4 F6R0F4_MONDO,tr F6XFL5 F6XFL5_HORSE,tr F7FG46 F7FG46_MA_CMU,tr F7I0E2 F7I0E2_CALI	hLED EL	67%	30.8	48.80351	Ref	-0.21	0.34	0.17	0.38	0.45	0.054	0.27	23500	18900	30200	30100	38400	35200	27900	32000	530.3	1058.5	2	0.0089	8.381
Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1	sp P26447 S10A4_HUMAN,sp Q9TV56 S10A4_CANFA,tr D2HJR5 D2HJR5_ALME,tr F1SFV7 F1SFV7_PIG,tr F6UF75 F6UF75_HORSE,tr F6XCP7 F6XCP7_CALJA,tr F7GDB8 F7GDB8_M	aLDV MVS TFHK	86%	42.4	53.21698	Ref	0.39	0.54	0.65	0.84	1.2	0.45	0.92	10300	14000	17000	20400	25800	28900	17900	24600	619.4	1855	3	0.017	9.162

Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1	sp P26447 S10A4_HUMAN,sp Q9TV56 S10A4_CANFA,triD2HJR5 D2HJR5_AILME,triF1SFV7 F1SFV7_PIG,triF6UF75 F6UF75_HORSE,triF6XCP7 F6XCP7_CAJA,triF7GDB8 F7GDB8_MACMU	aLDV MVS TFHK	90%	45.6	53.12264	Ref	0.22	0.59	0.69	0.82	1.1	0.6	0.93	2090	2180	3030	3650	4400	4560	3460	4310	619.4	1855	3	0.0141	7.595
Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1	sp P26447 S10A4_HUMAN,sp Q9TV56 S10A4_CANFA,triD2HJR5 D2HJR5_AILME,triF1SFV7 F1SFV7_PIG,triF6UF75 F6UF75_HORSE,triF6XCP7 F6XCP7_CAJA,triF7GDB8 F7GDB8_MACMU	aLDV MVS TFHK	87%	43.1	53.123	Ref	0.32	0.5	0.62	0.84	0.92	0.65	0.93	2450	2270	2790	3400	4380	4050	3500	4230	619.4	1855	3	0.0139	7.498

Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1	sp P26447 S10A4_HUMAN,sp Q9TV56 S10A4_CANFA,tr D2HJR5 D2HJR5_ALME,tr F1SFV7 F1SFV7_PIG, tr F6UF75 F6UF75_HORSE,tr F6XCP7 F6XCP7_CAJA,tr F7GDB8 F7GDB8_MACMU	tDEAFQk	81%	37.9	52.1235	Ref	0.19	0.8	0.62	0.91	1.2	0.33	0.77	16700	16200	26900	26500	35700	37400	21900	29400	759.4	1516.8	2	0.0248	16.31
Serine/arginine-rich splicing factor 2 OS=Homo sapiens GN=SRSF2 PE=1 SV=4	Q SRSF2_HUMAN,sp Q06A98 SRSF2_PIG,sp Q3MHR5 SRSF2_BOVIN,sp Q5R1W5 SRSF2_PANTR,sp Q62093 SRSF2_MOUSE,sp Q6PDU1 SRSF2_RAT,tr A2AA29 AA29_MOUSE,tr B3KUF7 B3KUF7_HUMAN,tr B3KVY2 B3KVY2_HUMAN,tr B3KX15 B3KX15_HUMA	gFAFVR	52%	29.3	49.51527	Ref	-0.12	-0.12	Value Missing (-0.6556876)	-0.38	0.98	Value Missing (-0.6630611)	0.82	3410	2850	3110	Value Missing (-0.6556876)	3200	7190	Value Missing (-0.6630611)	6660	334.2	999.57	3	0.0133	13.32

Serine/arginine-rich splicing factor 2 OS=Homo sapiens GN=SRSF2 PE=1 SV=4	0 SRSF2_ HUMAN,s p Q06A9 8 SRSF2_ PIG,sp Q3 MHR5 SR SF2_BOVI N,sp Q5R 1W5 SRS F2_PANT R,sp Q62 093 SRSF 2_MOUSE ,sp Q6PD U1 SRSF2 _RAT,tr A 2AA29 A2 AA29_MO USE,tr B3 KUF7 B3K UF7_HUM AN,tr B3K VY2 B3KV Y2_HUMA N,tr B3KX 15 B3KX1 5_HUMA	SYGR PPP DVE GmT SLk	59%	34	53.10474	Ref	-0.055	0.17	0.098	-0.005	0.26	0.22	0.062	19600	16300	20700	22100	22700	23900	24100	21500	699.4	2095	3	0.015	7.159
Serine/arginine-rich splicing factor 2 OS=Homo sapiens GN=SRSF2 PE=1 SV=4	0 SRSF2_ HUMAN,s p Q06A9 8 SRSF2_ PIG,sp Q3 MHR5 SR SF2_BOVI N,sp Q5R 1W5 SRS F2_PANT R,sp Q62 093 SRSF 2_MOUSE ,sp Q6PD U1 SRSF2 _RAT,tr A 2AA29 A2 AA29_MO USE,tr B3 KUF7 B3K UF7_HUM AN,tr B3K VY2 B3KV Y2_HUMA N,tr B3KX 15 B3KX1 5_HUMA	VGD VYIP R	91%	43.8	51.05514	Ref	0.12	0.093	0.19	-0.12	0.56	-0.53	0.24	12700	12100	12800	15400	13700	19200	9360	15900	408.2	1221.7	3	0.0074	6.013

<p>Serine/arginine-rich splicing factor 2 OS=Homo sapiens GN=SRSF2 PE=1 SV=4</p>	<p>0 SRSF2_HUMAN,sp Q06A98 SRSF2_PIG,sp Q3MHR5 SRSF2_BOVIN,sp Q5R1W5 SRSF2_PANTR,sp Q62093 SRSF2_MOUSE,sp Q6PDU1 SRSF2_RAT,transcript AA29 AA29_MOUSE,transcript B3KUF7 B3KUF7_HUMAN,transcript B3KVY2 B3KVY2_HUMAN,transcript B3KX15 B3KX15_HUMAN</p>	<p>VGD VYIP R</p>	<p>84%</p>	<p>37.9</p>	<p>51.14711</p>	<p>Ref</p>	<p>-0.03</p>	<p>0.15</p>	<p>0.087</p>	<p>-0.026</p>	<p>0.58</p>	<p>-0.55</p>	<p>0.23</p>	<p>18900</p>	<p>14900</p>	<p>18400</p>	<p>19700</p>	<p>20100</p>	<p>26800</p>	<p>12700</p>	<p>21700</p>	<p>611.9</p>	<p>1221.7</p>	<p>2</p>	<p>0.0104</p>	<p>8.47</p>
<p>Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4</p>	<p>sp P21333 FLNA_HUMAN,transcript A9CB59 A9CB59_PAN,transcript E9KL45 E9KL45_HUMAN,transcript F6YST5 F6YST5_MACMU,transcript F7GCM2 F7GCM2_MACMU,transcript F7GCM8 F7GCM8_MACMU,transcript Q5HY54 Q5HY54_HUMAN,transcript Q60FE5 Q60FE5_HUMAN,transcript Q60FE6 Q60FE6_HUMAN</p>	<p>eTGE HLV HVk</p>	<p>50%</p>	<p>30.3</p>	<p>52.72376</p>	<p>Ref</p>	<p>-0.12</p>	<p>-0.13</p>	<p>-0.17</p>	<p>-0.18</p>	<p>-0.08</p>	<p>-0.16</p>	<p>-0.33</p>	<p>30500</p>	<p>25100</p>	<p>27100</p>	<p>29500</p>	<p>32300</p>	<p>30200</p>	<p>29900</p>	<p>26300</p>	<p>440</p>	<p>1756</p>	<p>4</p>	<p>0.0243</p>	<p>13.83</p>

Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	sp P21333 FLNA_HUMAN, tr A9CB59 A9CB59_PAN, tr E9KL45 E9KL45_HUMAN, tr F6YST5 F6YST5_MACMU, tr F7GCM2 F7GCM2_MACMU, tr F7GCM2 F7GCM2_MACMU, tr Q5HY54 Q5HY54_HUMAN, tr Q60FE5 Q60FE5_HUMAN, tr Q60FE6 Q60FE6_HUMAN	eTGEHLVHvk	73%	36.2	52.70455	Ref	-0.3	-0.08	-0.31	-0.044	-0.24	-0.06	-0.23	3360	2320	2940	2810	3720	2840	3360	2960	879	1756	2	0.0144	8.185
Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	sp P21333 FLNA_HUMAN, tr A9CB59 A9CB59_PAN, tr E9KL45 E9KL45_HUMAN, tr F6YST5 F6YST5_MACMU, tr F7GCM2 F7GCM2_MACMU, tr F7GCM2 F7GCM2_MACMU, tr Q5HY54 Q5HY54_HUMAN, tr Q60FE5 Q60FE5_HUMAN, tr Q60FE6 Q60FE6_HUMAN	tGVAVNkPAEFTVD	78%	38.3	52.89475	Ref	-0.33	0.012	-0.2	-0.004	-0.19	-0.17	-0.38	14600	9910	13700	13200	16700	12900	13600	11700	853.8	2558.5	3	0.0272	10.63

Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	sp P21333 FLNA_HUMAN, tr A9CB59 A9CB59_PAN, tr E9KL45 E9KL45_HUMAN, tr F6YST5 F6YST5_MACMU, tr F7GCM2 F7GCM2_MACMU, tr F7GCM2 F7GCM2_MACMU, tr Q5HY54 Q5HY54_HUMAN, tr Q60FE5 Q60FE5_HUMAN, tr Q60FE6 Q60FE6_HUMAN	tGVA VNK PAEF TVD AK	92%	47	53.10145	Ref	-0.28	-0.08	-0.12	-0.28	-0.11	-0.02	-0.31	3840	2790	3470	3800	3740	3670	4100	3320	853.8	2558.5	3	0.0334	13.06
Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=2	6 CDC42_MOUSE, sp P60952 CDC42_CANFA, sp P60953 CDC42_HUMAN, sp Q007T2 CDC42_PIG, sp Q2KJ93 CDC42_BOVIN, sp Q4R4R6 CDC42_MACFA, sp Q8CFN2 CDC42_RAT, tr B4E1U9 B4E1U9_HUMAN, tr B6VAP7 B6VAP7_BOVIN, tr D2HCB2 D2HCB2_AILM	cVVV GDG AVG k	89%	42	52.92938	Ref	0.15	-0.11	0.042	-0.14	-0.17	-0.01	-0.22	11800	11100	10000	12500	12200	10400	12100	10400	829.5	1656.9	2	0.0136	8.232

Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=2	6 CDC42_MOUSE,sp P60952 CDC42_CANFA,sp P60953 CDC42_HUMAN,sp Q007T2 CDC42_PIG,sp Q2KJ93 CDC42_BOVIN,sp Q4R4R6 CDC42_MACFA,sp Q8CFN2 CDC42_RAT,tr B4E1U9 B4E1U9_HUMAN,tr B6VAP7 B6VAP7_BOVIN,tr D2HCB2 D2HCB2_AILM	cVVVGDGAVGk	72%	36.6	52.87497	Ref	0.14	-0.19	-0.13	-0.11	-0.2	0.1	-0.3	16200	13500	11600	13600	15200	12500	16000	12100	553.3	1656.9	3	0.0105	6.323
Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=2	6 CDC42_MOUSE,sp P60952 CDC42_CANFA,sp P60953 CDC42_HUMAN,sp Q007T2 CDC42_PIG,sp Q2KJ93 CDC42_BOVIN,sp Q4R4R6 CDC42_MACFA,sp Q8CFN2 CDC42_RAT,tr B4E1U9 B4E1U9_HUMAN,tr B6VAP7 B6VAP7_BOVIN,tr D2HCB2 D2HCB2_AILM	cVVVGDGAVGk	87%	42.8	52.87497	Ref	0.11	-0.2	-0.04	-0.04	-0.04	0.014	-0.17	25800	24900	21800	27400	30100	26300	28500	24900	553.3	1656.9	3	0.0105	6.323

Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=2	6 CDC42_MOUSE,sp P60952 CDC42_CANFA,sp P60953 CDC42_HUMAN,sp Q007T2 CDC42_PIG,sp Q2KJ93 CDC42_BOVIN,sp Q4R4R6 CDC42_MACFA,sp Q8CFN2 CDC42_RAT,tr B4E1U9 B4E1U9_HUMAN,tr B6VAP7 B6VAP7_BOVIN,tr D2HCB2 D2HCB2_AILM	nVF DEAI LAAL EPPE Pk	78%	39.7	54.15332	Ref	0.0041	-0.17	-0	-0.1	0.018	-0.02	-0.01	1750	1660	1600	2010	2070	1960	1990	2000	821.1	2460.4	3	0.0126	5.104
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MQ37 F1MQ37_BOVIN	aDTE HK	51%	31.5	51.95424	Ref	-0.55	0.39	-0.74	-0.39	-0.56	-0.14	-0.53	26000	14500	30200	15500	21800	16800	23600	17900	436.9	1307.7	3	0.0046	3.532
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MQ37 F1MQ37_BOVIN	dVLL QVD DER R	62%	34.3	52.82989	Ref	-0.15	0.076	-0.59	-0.28	-0.46	-0.37	-0.27	9180	7720	9780	6930	9430	7280	8120	8600	554.6	1660.9	3	0.0128	7.71
Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MQ37 F1MQ37_BOVIN	qSVS NLEK	78%	36.5	51.78799	Ref	-0.66	0.44	-0.83	-0.33	-0.61	-0.04	-0.46	17400	9610	22300	10400	16200	11700	18100	13400	756.9	1511.9	2	0.0074	4.901

Uncharacterized protein (Fragment) OS=Bos taurus PE=4 SV=1	tr F1MQ37 F1MQ37_BOVIN	qSVS nLEk	53%	31.7	52.19645	Ref	-0.56	0.27	-0.79	-0.25	-0.62	-0.07	-0.32	14100	8320	16000	8630	13800	9330	14200	11900	757.4	1512.8	2	0.0269	17.8
Collagen alpha-2(V) chain OS=Homo sapiens GN=COL5A2 PE=1 SV=3	7 CO5A2_HUMAN,sp Q3U962 CO5A2_MOUSE,tr B4DNJ0 B4DNJ0_HUMAN,tr D2HA12 D2HA12_AILME,tr F1LQ00 F1LQ00_RAT,tr F1N2Y2_BOVIN,tr F1PG08 F1PG08_CANFA,tr F6V0F2 F6V0F2_MACMU,tr F6V6S9 F6V6S9_MACMU,tr F7BH47 F7BH47_PGLk	gFPG APGL PGLk	52%	31.6	51.98335	Ref	-0.056	0.72	-0.42	0.016	-0.27	0.5	-0.21	2720	2140	3960	2020	3010	2150	3850	2330	573.7	1718	3	0.023	13.39

Collagen alpha-2(V) chain OS=Homo sapiens GN=COL5A2 PE=1 SV=3	7 CO5A2_HUMAN, sp Q3U962 CO5A2_MOUSE,t r B4DNJ0 B4DNJ0_HUMAN,t r D2HA12 D2HA12_AILME,tr F1LQ00 F1LQ00_R AT,tr F1N2Y2 F1N2Y2_BOVIN ,tr F1PG08 F1PG08_CANFA,tr F6V0F2 F6V0F2_MACMU,t r F6V6S9 F6V6S9_MACMU,t r F7BH47 F7BH47_GPR	gRP GPA GPP GSQ GPR	63%	34.6	52.91296	Ref	-0.26	1	-0.74	-0.21	-0.3	0.74	-0.33	5930	4860	13000	4240	6740	5550	11900	5630	564.6	1690.9	3	0.0172	10.19
Collagen alpha-2(V) chain OS=Homo sapiens GN=COL5A2 PE=1 SV=3	7 CO5A2_HUMAN, sp Q3U962 CO5A2_MOUSE,t r B4DNJ0 B4DNJ0_HUMAN,t r D2HA12 D2HA12_AILME,tr F1LQ00 F1LQ00_R AT,tr F1N2Y2 F1N2Y2_BOVIN ,tr F1PG08 F1PG08_CANFA,tr F6V0F2 F6V0F2_MACMU,t r F6V6S9 F6V6S9_MACMU,t r F7BH47 F7BH47_GPR	gRP GPA GPP GSQ GPR	68%	35.6	52.90035	Ref	-0.4	1.1	-1.1	-0.28	-0.54	0.96	-0.52	13800	9320	29100	7140	13600	9930	29500	10500	564.6	1690.9	3	0.0163	9.661

Collagen alpha-2(V) chain OS=Homo sapiens GN=COL5A2 PE=1 SV=3	7 CO5A2 _HUMAN, sp Q3U96 2 CO5A2 _MOUSE,t r B4DNJ0 B4DNJ0_ HUMAN,t r D2HA12 D2HA12 _A1LME,tr F1LQ00 F1LQ00_R AT,tr F1N 2Y2 F1N2 Y2_BOVIN ,tr F1PG0 8 F1PG08 _CANFA,tr F6V0F2 F6V0F2_ MACMU,t r F6V6S9 F6V6S9_ MACMU,t r F7BH47 F7BH47_	gRP GPA GPP GSQ	79%	38.6	52.89565	Ref	-0.31	0.93	-0.52	-0.09	-0.16	0.57	-0.37	11000	7500	19300	7920	11700	9770	16900	8730	564.6	1690.9	3	0.0152	9.005
Histone H2A type 2- C OS=Bos taurus GN=HIST2H2AC PE=2 SV=1	1 H2A2C_ BOVIN,sp A9UMV8 H2AJ_RA T,sp P022 62 H2A1_ RAT,sp P 04908 H2 A1B_HU MAN,sp P 0C0S8 H2 A1_HUM AN,sp P0 C0S9 H2A 1_BOVIN, sp P0C16 9 H2A1C_ RAT,sp P 0C170 H2 A1E_RAT, sp P0CC0 9 H2A2A _RAT,sp P20671 H 2A1D_HU MAN,sp P 22752 H2	VTIA QGG VLPN IQAV LLPk	95%	94.1	43.16955	Ref	-0.81	0.52	-1.5	0.28	0.28	0.19	0.56	4320	2600	7130	1940	7490	6530	6400	8220	1270	2538.6	2	0.0134	5.295

Histone H2A type 2-C OS=Bos taurus GN=HIST2H2AC PE=2 SV=1	1 H2A2C_BOVIN,sp A9UMV8 H2AJ_RAT,sp P02262 H2A1_RAT,sp P04908 H2A1B_HUMAN,sp P0C0S8 H2A1_HUMAN,sp P0C0S9 H2A1_BOVIN,sp P0C169 H2A1C_RAT,sp P0C170 H2A1E_RAT,sp P0CC09 H2A2A_RAT,sp P20671 H2A1D_HUMAN,sp P22752 H2	VTIA QGG VLPN IQAV LLPk	95%	50.1	46.58002	Ref	-0.61	0.52	-0.94	0.13	-0.08	0.29	0.46	1190	692	1640	668	1550	1170	1580	1770	847.2	2538.5	3	0.0238	9.387
Histone H2A type 2-C OS=Bos taurus GN=HIST2H2AC PE=2 SV=1	1 H2A2C_BOVIN,sp A9UMV8 H2AJ_RAT,sp P02262 H2A1_RAT,sp P04908 H2A1B_HUMAN,sp P0C0S8 H2A1_HUMAN,sp P0C0S9 H2A1_BOVIN,sp P0C169 H2A1C_RAT,sp P0C170 H2A1E_RAT,sp P0CC09 H2A2A_RAT,sp P20671 H2A1D_HUMAN,sp P22752 H2	VTIA QGG VLPN IQAV LLPk	80%	30.8	46.44566	Ref	-0.43	0.42	-0.97	0.11	0.21	0.035	0.24	756	408	799	341	797	745	690	791	635.6	2538.6	4	0.0216	8.508

Histone H2A type 2-C	1 H2A2C_BOVIN,sp A9UMV8 H2AJ_RAT,sp P02262 H2A1_RAT,sp P04908 H2A1B_HUMAN,sp P0C0S8 H2A1_HUMAN,sp P0C0S9 H2A1_BOVIN,sp P0C169 H2A1C_RAT,sp P0C170 H2A1E_RAT,sp P0CC09 H2A2A_RAT,sp P20671 H2A1D_HUMAN,sp P22752 H2	VLIA QGG VLPN IQAV LLPK	82%	32.9	45.96179	Ref	Value Missing (-1.150699)	0.58	0.9881	0.46	0.6	-0.25	0.2	119	9	165	187	180	104	142	847.2	2538.6	3	0.0167	6.576	
60S ribosomal protein L35	8 RL35_RAT,sp P42766 RL35_HUMAN,sp Q29361 RL35_PIG,sp Q3MHM7 RL35_BOVIN,sp Q6ZVV7 RL35_MOUSE,tr D2H3W2 D2H3W2_AILME,tr D3Z942 D3Z942_RAT,tr D3ZN79 D3ZN79_RAT,tr E2RPE5 E2RPE5_CANFA,tr F1MDW8 F1MDW8_BOVIN,tr F	VLTV INQT QK	88%	40.6	50.12635	Ref	0.2	0.56	0.73	0.25	0.5	0.34	0.64	10500	9890	13800	17400	13700	14300	13300	16200	584.7	1751.1	3	0.019	10.86

60S ribosomal protein L35 OS=Rattus norvegicus GN=Rpl35 PE=1 SV=3	8 RL35_RAT,sp P42766 RL35_HUMAN,sp Q29361 RL35_PIG,sp Q3MHM7 R_L35_BOVIN,sp Q6ZVV7 RL35_MOUSE,tri D2H3W2 D2H3W2_AILME,tri D3Z942 D3Z942_RAT,tri D3Z942 D3Z942_RAT,tri E2RPE5 E2RPE5_CANFA,tri F1MDW8_BOVIN,tri FQk	vLTV INQT	95%	50.3	50.00235	Ref	0.2	0.54	0.71	0.42	0.64	0.48	0.56	4260	5470	7540	9530	8590	8680	8140	8550	876.5	1751.1	2	0.0175	10.01
60S ribosomal protein L35 OS=Rattus norvegicus GN=Rpl35 PE=1 SV=3	8 RL35_RAT,sp P42766 RL35_HUMAN,sp Q29361 RL35_PIG,sp Q3MHM7 R_L35_BOVIN,sp Q6ZVV7 RL35_MOUSE,tri D2H3W2 D2H3W2_AILME,tri D3Z942 D3Z942_RAT,tri E2RPE5 E2RPE5_CANFA,tri F1MDW8_BOVIN,tri FQk	vLTV INQT	90%	42.3	50.14705	Ref	0.43	0.59	0.56	0.29	0.5	0.33	0.63	7690	8800	10700	11700	10700	10800	10100	12300	584.7	1751.1	3	0.0179	10.24

60S ribosomal protein L35 OS=Rattus norvegicus GN=Rpl35 PE=1 SV=3	8 RL35_RAT,sp P42766 RL35_HUMAN,sp Q29361 RL35_PIG,sp Q3MHM7 RL35_BOVIN,sp Q62WV7 RL35_MOUSE, tr D2H3W2 D2H3W2_AILME, tr D3Z942 D3Z942_RAT, tr D3ZN79 D3ZN79_RAT, tr E2RPE5 E2RPE5_CANFA, tr F1MDW8_BOVIN, tr F	vLTV INQT Qk	94%	43.9	50.00456	Ref	0.26	0.57	0.62	0.31	0.57	0.45	0.58	3520	3730	5030	5860	5210	5440	5230	5670	876.5	1751.1	2	0.0163	9.317
Uncharacterized protein (Fragment) OS=Canis familiaris PE=3 SV=1	tr F1PZK2 F1PZK2_CANFA	kIED NNT LVFI VNV k	75%	33.9	51.33753	Ref	0.3	0.48	0.34	0.54	0.83	0.11	0.96	1860	1970	2420	2460	3120	3340	2120	3770	665.4	2657.5	4	0.0428	16.11
Uncharacterized protein (Fragment) OS=Canis familiaris PE=3 SV=1	tr F1PZK2 F1PZK2_CANFA	kIED NNT LVFI VNV k	64%	32.1	50.17008	Ref	-0.086	0.47	0.72	0.34	0.86	0.25	0.9	476	372	592	794	672	840	573	895	886.9	2657.6	3	0.0228	8.579
Uncharacterized protein (Fragment) OS=Canis familiaris PE=3 SV=1	tr F1PZK2 F1PZK2_CANFA	kIED NNT LVFI VnVk	95%	54.2	50.85951	Ref	-0.16	0.36	0.75	0.42	1	0.089	1	1900	1770	2760	4050	3560	4700	2580	4950	887.2	2658.6	3	0.0171	6.426

Uncharacterized protein (Fragment) OS=Canis familiaris PE=3 SV=1	tr F1PZK2 F1PZK2_ CANFA	kIED nNTL VFIV nVk	95%	48	52.12914	Ref	0.053	0.36	0.6	0.38	0.72	0.28	1.1	585	532	716	950	899	993	761	1340	665.9	2659.5	4	0.0258	9.687
Uncharacterized protein (Fragment) OS=Ornithorhynchus anatinus GN=TUSC3 PE=4 SV=1	tr F6WYB 4 F6WYB 4_ORNAN ,tr F6WYT 4 F6WYT 4_ORNAN ,tr F6WY U3 F6WY U3_ORNA N,tr F6W YV3 F6W YV3_ORN AN	nLLA Ek	71%	32.7	49.69961	Ref	0.44	Value Missi ng (- 1.689 2284)	0.009	-0.079	-0.07	0.68	0.18	493	558	Value Missi ng (- 1.689 2284)	505	523	459	809	566	517.8	1033.6	2	0.0111	10.76
Uncharacterized protein (Fragment) OS=Ornithorhynchus anatinus GN=TUSC3 PE=4 SV=1	tr F6WYB 4 F6WYB 4_ORNAN ,tr F6WYT 4 F6WYT 4_ORNAN ,tr F6WY U3 F6WY U3_ORNA N,tr F6W YV3 F6W YV3_ORN AN	nLLA Ek	92%	41.5	50.02287	Ref	0.088	Value Missi ng (- 1.093 7086)	0.37	0.066	-0.06	0.55	0.12	1630	1570	Value Missi ng (- 1.093 7086)	2320	2070	1660	2650	1950	517.8	1033.6	2	0.0014	1.376
Uncharacterized protein (Fragment) OS=Ornithorhynchus anatinus GN=TUSC3 PE=4 SV=1	tr F6WYB 4 F6WYB 4_ORNAN ,tr F6WYT 4 F6WYT 4_ORNAN ,tr F6WY U3 F6WY U3_ORNA N,tr F6W YV3 F6W YV3_ORN AN	nLLA Ek	92%	41.5	49.98093	Ref	-0.012	Value Missi ng (- 1.079 4264)	0.3	0.26	-0.23	0.79	0.085	2250	2380	Value Missi ng (- 1.079 4264)	3580	3850	2390	5070	3090	517.8	1033.6	2	0.0033	3.154

Uncharacterized protein (Fragment) OS=Ornithorhynchus anatinus GN=TUSC3 PE=4 SV=1	tr F6WYB4 F6WYB4_ORNAN, tr F6WYT4 F6WYT4_ORNAN, tr F6WYU3 F6WYU3_ORNAN, tr F6WYV3 F6WYV3_ORNAN	nLLA Ek	69%	32.5	50.01379	Ref	0.56	Value Missing (-1.7287935)	-0.14	-0.45	-0.11	0.91	0.03	865	999	Value Missing (-1.7287935)	748	669	736	1560	842	517.8	1033.6	2	0.0044	4.218
40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	7 RS13_HUMAN,sp P62278 RS13_RAT,sp P62279 RS13_PIG,sp P62301 RS13_MOUSE,sp Q56JX8 RS13_BOVIN,sp Q9WVH0 RS13_CRI, tr D2HRK8 D2HRK8_AILME, tr E1BGR6 E1BGR6_BOVIN, tr E2QTJ2 E2QTJ2_CANFA, tr E7D091 E7D091_AILME, tr F6Q5P0	kGLT PSQI GVIL R	70%	30.5	47.35248	Ref	0.44	0.16	0.41	0.18	0.43	-0.04	0.28	11900	13300	11900	15900	14900	15500	11700	14600	664.1	1989.2	3	0.0207	10.38

40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	7 RS13_H UMAN,sp P62278 RS13_RAT ,sp P6227 9 RS13_P IG,sp P62 301 RS13 _MOUSE, sp Q56JX 8 RS13_B OVIN,sp Q9WVH0 RS13_CRI GR,tr D2 HRK8 D2 HRK8_AIL ME,tr E1 BGR6 E1 BGR6_BO VIN,tr E2 QTJ2 E2Q TJ2_CANF A,tr E7D0 91 E7D09 1_AILME,t r F6Q5PO	kGLT PSQI GVIL R	52%	26.4	46.71941	Ref	0.39	-0.02	0.48	0.13	0.57	-0.06	0.33	15200	17000	13900	21900	19000	22500	15200	19800	664.1	1989.2	3	0.0146	7.354
40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	7 RS13_H UMAN,sp P62278 RS13_RAT ,sp P6227 9 RS13_P IG,sp P62 301 RS13 _MOUSE, sp Q56JX 8 RS13_B OVIN,sp Q9WVH0 RS13_CRI GR,tr D2 HRK8 D2 HRK8_AIL ME,tr E1 BGR6 E1 BGR6_BO VIN,tr E2 QTJ2 E2Q TJ2_CANF A,tr E7D0 91 E7D09 1_AILME,t r F6Q5PO	kGLT PSQI GVIL R	90%	36.8	46.47755	Ref	0.48	0.18	0.53	0.13	0.29	0.16	0.3	2230	3080	2700	3880	3220	3140	3000	3300	498.3	1989.2	4	0.0108	5.407

<p>40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2</p>	<p>7 RS13_H UMAN,sp P62278 RS13_RAT ,sp P6227 9 RS13_P IG,sp P62 301 RS13 _MOUSE, sp Q56JX 8 RS13_B OVIN,sp Q9WVH0 RS13_CRI GR,tr D2 HRK8 D2 HRK8_AIL ME,tr E1 BGR6 E1 BGR6_BO VIN,tr E2 QTJ2 E2Q TJ2_CANF A,tr E7D0 91 E7D09 1_AILME,t r F6Q5PO</p>	<p>kGLT PSQI GVIL R</p>	<p>91%</p>	<p>36.9</p>	<p>46.1574</p>	<p>Ref</p>	<p>0.45</p>	<p>0.19</p>	<p>0.4</p>	<p>0.01</p>	<p>0.25</p>	<p>0.25</p>	<p>0.4</p>	<p>2590</p>	<p>3130</p>	<p>2830</p>	<p>3680</p>	<p>3090</p>	<p>3200</p>	<p>3330</p>	<p>3660</p>	<p>498.3</p>	<p>1989.2</p>	<p>4</p>	<p>0.0073</p>	<p>3.679</p>
<p>40S ribosomal protein SA OS=Ovis aries GN=RPSA PE=2 SV=1</p>	<p>8 RSSA_S HEEP,sp P08865 R SSA_HUM AN,sp P1 4206 RSS A_MOUSE ,sp P2645 2 RSSA_B OVIN,sp P38982 R SSA_CRIG R,sp P389 83 RSSA_ RAT,sp Q 2L9X0 RS SA_CHLAE ,sp Q4G WZ2 RSS A_PIG,tr B0L419 B 0L419_RA BIT,tr B2 CY77 B2C Y77_MOU SE,tr B8K 1X7 B8K1</p>	<p>aIVal ENP ADV SVIS SR</p>	<p>95%</p>	<p>66.9</p>	<p>53.44995</p>	<p>Ref</p>	<p>0.26</p>	<p>-0.31</p>	<p>0.027</p>	<p>-0.16</p>	<p>-0.2</p>	<p>-0.11</p>	<p>-0.14</p>	<p>1920</p>	<p>1850</p>	<p>1360</p>	<p>1920</p>	<p>1860</p>	<p>1580</p>	<p>1770</p>	<p>1710</p>	<p>1023</p>	<p>2044.1</p>	<p>2</p>	<p>0.0051</p>	<p>2.493</p>

40S ribosomal protein SA OS=Ovis aries GN=RPSA PE=2 SV=1	8 RSSA_S HEEP,sp P08865 R SSA_HUMAN,sp P14206 R SSA_MOUSE,sp P26452 R SSA_BOVIN,sp P38982 R SSA_CRIGR,sp P38983 R SSA_RAT,sp Q2L9X0 SSA_CHLAE,sp Q4GWZ2 SSA_PIG,tr B0L419 B0L419_RA BIT,tr B2CY77 B2CY77 MOU SE,tr B8K1X7	R	95%	58.4	53.70635	Ref	0.33	-0.3	0.1	-0.4	-0.26	-0.1	0.045	1890	2060	1450	2150	1670	1600	1870	2060	1002	2002	2	0.0111	5.535
40S ribosomal protein SA OS=Ovis aries GN=RPSA PE=2 SV=1	8 RSSA_S HEEP,sp P08865 R SSA_HUMAN,sp P14206 R SSA_MOUSE,sp P26452 R SSA_BOVIN,sp P38982 R SSA_CRIGR,sp P38983 R SSA_RAT,sp Q2L9X0 SSA_CHLAE,sp Q4GWZ2 SSA_PIG,tr B0L419 B0L419_RA BIT,tr B2CY77 B2CY77 MOU SE,tr B8K1X7	R	85%	36.8	49.35517	Ref	0.34	-0.18	0.021	-0.074	-0.18	-0.15	-0.18	7290	8810	6630	8580	8850	7200	7650	7450	608.9	1215.7	2	0.0097	8.001

T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2 PE=1 SV=4	4 TCPB_MOUSE,sp Q3ZBH0 TCPB_BOVIN,sp Q5XIM9 TCPB_RAT, tr B6V9S9 B6V9S9_RABIT, tr DOG0C8 DOG0C8_PIG, tr D2HIW0 D2HIW0_AILME, tr E2QSH7 E2QSH7_CANFA, tr F6TK05 F6TK05_HORS E, tr F7CWM9 F7CWM9_CA	hGIN cFIN R	82%	37.8	50.51897	Ref	-0.1	0.047	-0.06	-0.4	-0.21	-0.16	-0.11	7690	6230	7490	7800	6780	6760	7330	7520	475.2	1422.7	3	0.0063	4.449
T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2 PE=1 SV=4	4 TCPB_MOUSE,sp Q3ZBH0 TCPB_BOVIN,sp Q5XIM9 TCPB_RAT, tr B6V9S9 B6V9S9_RABIT, tr DOG0C8 DOG0C8_PIG, tr D2HIW0 D2HIW0_AILME, tr E2QSH7 E2QSH7_CANFA, tr F6TK05 F6TK05_HORS E, tr F7CWM9 F7CWM9_CA	ISSFI GAIA IGDL Vk	95%	57.6	49.55135	Ref	-0.2	-0.21	-0.01	-0.16	-0.27	-0.46	0.072	618	410	443	570	567	457	419	603	704.8	2111.3	3	0.0088	4.161

T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2 PE=1 SV=4	4 TCPB_MOUSE,sp Q3ZBH0 TCPB_BOVIN,sp Q5XIM9 TCPB_RAT, tr B6V9S9 B6V9S9_RABIT, tr DOG0C8 DOG0C8_PIG, tr D2HIW0 D2HIW0_AILME, tr E2QSH7 E2QSH7_CANFA, tr F1PGK7 F1PGK7_CANFA, tr F6TK05 F6TK05_HORSE, tr F7CWM9 F7CWM9_CA	nIGV DNP AAk	95%	55.6	51.72833	Ref	-0.23	-0.22	0.078	-0.22	0.095	-0.23	-0.28	17000	12600	13800	19100	17100	18600	15500	14900	804	1605.9	2	0.0064	4.006
Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3	9 TCP4_HUMAN,sp Q4R947 TCP4_MACFA,sp Q5R6D0 TCP4_PONAB, tr D2HD87 D2HD87_AILME, tr E2R6X3 E2R6X3_CANFA, tr F2Z5D3 F2Z5D3_PIG, tr F6QR51 F6QR51_HORSE, tr F7AF44 F7AF44_MACMU, tr F7I1C7 F7I1C7_CALJA, tr Q59G24 Q59G24_HU	dDN MFQ IGk	95%	51.5	52.29633	Ref	-0.56	0.39	-0.24	0.31	0.007	0.27	-0.25	8730	5290	11100	8030	13000	9170	11500	7980	838.4	1674.9	2	0.0209	12.44

Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3	9 TCP4_HUMAN,sp Q4R947 TCP4_MA CFA,sp Q5R6D0 TCP4_PONA B,tr D2H D87 D2H D87_AIL ME,tr E2 R6X3 E2R 6X3_CAN FA,tr F2Z 5D3 F2Z5 D3_PIG,tr F6QR51 F6QR51_HORSE,tr F7AF44 F7AF44_MACMU,tr F711C7 F711C7_CALJ A,tr Q59 G24 Q59 G24_HU	eQIS DIDD AVR	94%	46	51.50634	Ref	-0.87	0.4	-0.3	0.3	0.19	0.11	-0.14	43100	19100	49900	34500	57900	46500	46100	38400	782.9	1563.8	2	0.0161	10.28
Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3	9 TCP4_HUMAN,sp Q4R947 TCP4_MA CFA,sp Q5R6D0 TCP4_PONA B,tr D2H D87 D2H D87_AIL ME,tr E2 R6X3 E2R 6X3_CAN FA,tr F2Z 5D3 F2Z5 D3_PIG,tr F6QR51 F6QR51_HORSE,tr F7AF44 F7AF44_MACMU,tr F711C7 F711C7_CALJ A,tr Q59 G24 Q59 G24_HU	eYW MDP EGE MkP GR	75%	37.3	52.74424	Ref	-0.48	0.18	-0.25	0.26	0.078	0.22	-0.02	8570	5350	9170	7640	12000	9210	10600	8930	778.4	2332.1	3	0.0218	9.334

26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1	6 PSMD4_HUMAN, tr A7UHZ2 A7UHZ2_SHEEP, tr A9X198 A9X198_PAPAN, tr B0KWB9 B0KWB9_CALJA, tr B1MTG0 B1MTG0_CALMO, tr F1SSZ6 F1SSZ6_PI G, tr F1SSZ7 F1SSZ7_PIG, tr F7CW85 F7CW85_MACMU, tr F7HNP3 F7HNP3_MACMU, tr Q32YV9 Q32YV9_k	aAA ASA AEA GIAT TGTE DSD DALL	95%	119	55.49559	Ref	-0.06	0.12	-0.07	0.018	0.062	-0.05	-0.05	920	815	1000	985	1150	1040	1000	996	976.8	2927.5	3	0.0096	3.288
26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1	6 PSMD4_HUMAN, tr A7UHZ2 A7UHZ2_SHEEP, tr A9X198 A9X198_PAPAN, tr B0KWB9 B0KWB9_CALJA, tr B1MTG0 B1MTG0_CALMO, tr F1SSZ6 F1SSZ6_PI G, tr F1SSZ7 F1SSZ7_PIG, tr F7CW85 F7CW85_MACMU, tr F7HNP3 F7HNP3_MACMU, tr Q32YV9 Q32YV9_cHSK	IQAQ QDA VNIV cHSK	95%	62.7	54.49883	Ref	0.16	-0.25	0.076	-0.036	0.11	-0.16	-0.06	1360	1310	1070	1510	1540	1480	1280	1370	770.1	2307.2	3	0.0163	7.076

26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1	6 PSMD4_HUMAN, tr A7UHZ2 A7UHZ2_SHEEP, tr A9X198 A9X198_PAPAN, tr B0KWB9 B0KWB9_CALJA, tr B1MTG0 B1MTG0_CALMO, tr F1SSZ6 F1SSZ6_PI G, tr F1SSZ7 F1SSZ7_PIG, tr F7CW85 F7CW85_MACMU, tr F7HNP3 F7HNP3_MACMU, tr Q32YV9 Q32YV9	mTIS QQE FGR	70%	33.9	51.30482	Ref	0.11	-0.22	0.027	-0.024	0.14	-0.25	0.062	30500	28700	24700	32900	35000	34300	27200	33600	750.9	1499.8	2	0.0113	7.543
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1N1S2 F1N1S2_BOVIN	aVLD ALLE Gk	65%	32	49.92739	Ref	-0.13	-0.11	0.089	0.005	-0.4	-0.51	-0.13	3690	4230	4660	6000	6240	4120	3980	5160	546.3	1636	3	0.0018	1.11
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1N1S2 F1N1S2_BOVIN	kTD DVE DMS SQA GLTL DER	95%	62.8	54.59319	Ref	-0.85	-0.28	-0.03	0.06	-0.32	-0.34	-0.03	3090	1490	2400	3200	3760	2520	2610	3210	906.8	2717.3	3	0.0186	6.849
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr F1N1S2 F1N1S2_BOVIN	tAEA AAA ALGT VAA AAA VAG LATT GPA k	95%	88.2	52.84293	Ref	Value Missing (-0.96048534)	Value Missing (-1.0781786)	0.24	0.23	Value Missing (-1.1893802)	Value Missing (-1.2521471)	0.31	137	Value Missing (-0.96048534)	Value Missing (-1.0781786)	111	122	Value Missing (-1.1893802)	Value Missing (-1.2521471)	116	992.6	2974.7	3	0.0055	1.847

Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr E1BBH3 E1BBH3_BOVIN	hELT EIST VDV ETQP Gk	77%	40.2	54.92956	Ref	-0.17	-0.08	-0.4	-0.075	0.15	-0.19	-0.16	4600	2990	3430	3090	4280	4360	3590	3660	831.1	2490.3	3	0.0203	8.151
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr E1BBH3 E1BBH3_BOVIN	iSM QDV DLSL GSSK	91%	47.9	54.1668	Ref	-0.2	-0.1	-0.03	-0.024	0.032	-0.21	-0.07	21400	16300	18900	22300	24600	22300	19700	21500	696.7	2087.1	3	0.0186	8.914
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr E1BBH3 E1BBH3_BOVIN	vGSP GVS VnAk	95%	49.9	51.80467	Ref	-0.37	-0.07	-0.06	0.15	0.18	-0.36	-0.11	11200	7660	10200	11500	14700	13100	9390	11100	812.5	1622.9	2	0.0094	5.773
Proteasome subunit alpha type-1 OS=Rattus norvegicus GN=Psm1 PE=1 SV=2	0 PSA1_RAT,sp P25786 PSA1_HUMAN,sp Q3T0X5 PSA1_BOVIN,sp Q4R3H2 PSA1_MACFA,sp Q5REN2 PSA1_PONAB,sp Q9R1P4 PSA1_MOUSE,tr E2R767 E2R767_CANFA,tr E9Q3B7 E9Q3B7_MOUSE,tr F1P8D6 F1P8D6_CANFA,tr F2Z5L7 F2Z5L7_PIG,tr F6WZWR	aDEP MEH	95%	55.2	44.88903	Ref	0.24	-0.43	-0.06	-0.34	0.12	-0.56	-0.21	17600	17400	11900	17200	15600	18700	12200	15500	566.8	1131.5	2	0.0094	8.281

Proteasome subunit alpha type-1 OS=Rattus norvegicus GN=Psm1 PE=1 SV=2	0 PSA1_R AT,sp P25786 PSA1_HUMAN,sp Q3T0X5 PSA1_BOVIN,sp Q4R3H2 PSA1_MACFA,sp Q5REN2 PSA1_PONAB,sp Q9R1P4 PSA1_MOUSE, tr E2R767 E2R767_CANFA, tr E9Q3B7 E9Q3B7_MOUSE, tr F1P8D6 F1P8D6_CANFA, tr F2Z5L7 F2Z5L7_PIG, tr F6WZWK	eTLP AEQ DLTT	61%	35	53.73182	Ref	0.3	-0.25	-0.09	-0.4	-0.19	-0.26	-0.23	9920	10600	7850	9890	8780	8880	8830	8920	652	1953.1	3	0.0133	6.799
Proteasome subunit alpha type-1 OS=Rattus norvegicus GN=Psm1 PE=1 SV=2	0 PSA1_R AT,sp P25786 PSA1_HUMAN,sp Q3T0X5 PSA1_BOVIN,sp Q4R3H2 PSA1_MACFA,sp Q5REN2 PSA1_PONAB,sp Q9R1P4 PSA1_MOUSE, tr E2R767 E2R767_CANFA, tr E9Q3B7 E9Q3B7_MOUSE, tr F1P8D6 F1P8D6_CANFA, tr F2Z5L7 F2Z5L7_PIG, tr F6WZWK	iHQI EYA MEA Vk	95%	54.6	53.70855	Ref	0.21	-0.35	-0	-0.26	-0.04	-0.26	-0.14	1390	1650	1210	1730	1600	1620	1460	1570	680.7	2039.1	3	0.0074	3.649

Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2	5 SF3B2_HUMAN, tr A4FV01 A4FV01_BOVIN, tr D2H4M9 D2H4M9_AILME, tr D3ZJX7 D3ZJX7_RA T, tr D3Z MS1 D3Z MS1_RAT, tr E1BBQ7 E1BBQ7_BOVIN, tr E2RL65 E2RL65_C ANFA, tr E9PPJO E9PPJO_HUMAN, tr F1MC31 F1MC31_BOVIN, tr F1RU38 F1RU38_PIG	gPPP PPG DEN R	95%	60.5	50.71672	Ref	-0.17	-0.06	-0.19	-0.42	-0.18	-0.57	-0.29	9760	6560	7640	7850	7390	7620	6060	7300	718.9	1435.7	2	0.0137	9.504
Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2	5 SF3B2_HUMAN, tr A4FV01 A4FV01_BOVIN, tr D2H4M9 D2H4M9_AILME, tr D3ZJX7 D3ZJX7_RA T, tr D3Z MS1 D3Z MS1_RAT, tr E1BBQ7 E1BBQ7_BOVIN, tr E2RL65 E2RL65_C ANFA, tr E9PPJO E9PPJO_HUMAN, tr F1MC31 F1MC31_BOVIN, tr F1RU38 F1RU38_PIG	IAQQ QAA LLM QQE ER	95%	52.9	54.16181	Ref	0.16	-0.29	-0.4	-0.23	-0.34	-0.1	-0.32	1960	2070	1640	1710	2110	1710	2110	1800	687.7	2060.1	3	0.0125	6.066

Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2	5 SF3B2_HUMAN, tr A4FV01 A4FV01_BOVIN, tr D2H4M9 D2H4M9_AILME, tr D3ZJX7 D3ZJX7_RA T, tr D3ZMS1 D3ZMS1_RAT, tr E1BBQ7 E1BBQ7_BOVIN, tr E2RL65 E2RL65_CANFA, tr E9PPJO E9PPJO_HUMAN, tr F1MC31 F1MC31_BOVIN, tr F1RU38 F1RU38_PIG	ILVH Lk	61%	20.8	39.42703	Ref	-0.28	-0.2	-0.37	-0.28	-0.1	-0.41	0.024	35100	25100	28900	28900	33800	33400	28100	37700	444.3	1329.9	3	0.0034	2.556
Deoxyuridine triphosphatase OS=Bos taurus GN=DUT PE=2 SV=1	tr Q2NKU1 Q2NKU1_BOVIN	aTEA GDM R	56%	27.7	47.66264	Ref	0.41	-1.3	0.27	0.1	0.55	-1.6	0.23	3140	3150	1010	3480	3410	4060	963	3380	585.8	1169.6	2	0.0055	4.674
Deoxyuridine triphosphatase OS=Bos taurus GN=DUT PE=2 SV=1	tr Q2NKU1 Q2NKU1_BOVIN	gNV GVV LFNF Gk	95%	55.8	52.06081	Ref	0.16	-0.53	0.4	-0.048	0.26	-0.52	0.18	4460	4340	2910	6210	5030	5440	3300	5310	620.4	1858.1	3	0.0115	6.192
Deoxyuridine triphosphatase OS=Bos taurus GN=DUT PE=2 SV=1	tr Q2NKU1 Q2NKU1_BOVIN	hFID VGA GVID EDYR	95%	59.4	52.85404	Ref	0.21	-0.38	0.12	-0.072	0.17	-0.1	0.37	6820	8440	6110	9680	9340	9610	8360	11500	670.7	2009	3	0.0132	6.55

Phosphoserine phosphatase OS=Bos taurus GN=PSPH PE=2 SV=1	sp Q2KH U0 SERB_ BOVIN, tr D0G7E3 D0G7E3_ PIG, tr F1 RIU1 F1RI U1_PIG	fcGV EDA VSE MTR	95%	47.8	47.17513	Ref	-0.21	-0.52	-0.35	-0.19	-0.37	-0.41	-0.3	2960	2470	2170	2730	3360	2600	2640	2830	897.4	1792.8	2	0.0165	9.177
Phosphoserine phosphatase OS=Bos taurus GN=PSPH PE=2 SV=1	sp Q2KH U0 SERB_ BOVIN, tr D0G7E3 D0G7E3_ PIG, tr F1 RIU1 F1RI U1_PIG	fYFn GEY AGF DET QPT AES GGk	86%	41.9	52.69256	Ref	-0.1	-0.39	-0.5	-0.31	-0.17	-0.6	-0.5	1330	1070	956	990	1240	1200	931	989	1009	3023.4	3	0.0182	6.031
Phosphoserine phosphatase OS=Bos taurus GN=PSPH PE=2 SV=1	sp Q2KH U0 SERB_ BOVIN, tr D0G7E3 D0G7E3_ PIG, tr F1 RIU1 F1RI U1_PIG	nVQ VFLI SGG FR	84%	39.3	52.54151	Ref	-0.34	-0.38	-0.3	-0.36	-0.56	-0.31	-0.61	5360	3130	3290	3910	4120	3150	3900	3140	821	1639.9	2	0.0105	6.378
Annexin A3 OS=Bos taurus GN=ANXA3 PE=2 SV=3	sp Q3SW X7 ANXA 3_BOVIN, tr F1MJW 6 F1MJW 6_BOVIN, tr F1MW Q2 F1M WQ2_BO VIN	aLLIL AnG RR	90%	40.4	48.37317	Ref	0.4	-0.08	0.28	-0.018	0.16	-0.35	0.049	4590	5260	4090	5910	5290	5210	3830	5020	468	1400.9	3	0.0066	4.74
Annexin A3 OS=Bos taurus GN=ANXA3 PE=2 SV=3	sp Q3SW X7 ANXA 3_BOVIN, tr F1MJW 6 F1MJW 6_BOVIN, tr F1MW Q2 F1M WQ2_BO VIN	sEID LLDI R	77%	36.7	52.23626	Ref	0.56	-0.41	0.31	-0.11	0.22	-0.31	0.12	8070	11100	6090	11300	9320	10200	7400	9860	689.4	1376.8	2	0.0133	9.643

Annexin A3 OS=Bos taurus GN=ANXA3 PE=2 SV=3	sp Q3SWX7 ANXA3_BOVIN, tr F1MJW6 F1MJW6_BOVIN, tr F1MWQ2 F1MWQ2_BOVIN	sLGD EISSE TSG DFR	95%	48.2	50.69494	Ref	0.53	-0.69	0.46	-0.032	0.19	-0.9	0.15	7920	8310	3900	9690	7580	7710	3800	7800	952.5	1902.9	2	0.0111	5.821
Thrombospondin-1 OS=Bos taurus GN=THBS1 PE=2 SV=2	sp Q28178 TSP1_BOVIN, tr F1N3A1 F1N3A1_BOVIN	aQG YSGL SVk	95%	61.5	52.59113	Ref	-0.72	0.28	-0.19	0.12	-0.66	0.79	-0.07	5220	2680	5790	4690	6410	3260	9340	5080	809.5	1616.9	2	0.0238	14.7
Thrombospondin-1 OS=Bos taurus GN=THBS1 PE=2 SV=2	sp Q28178 TSP1_BOVIN, tr F1N3A1 F1N3A1_BOVIN	dNc QYV YNV DQk	87%	40.9	51.38132	Ref	-0.081	0.35	-0.13	-0.019	-0.2	0.23	-0.05	7970	6550	9610	7700	9170	7050	9930	8110	715	2142	3	0.025	11.65
Thrombospondin-1 OS=Bos taurus GN=THBS1 PE=2 SV=2	sp Q28178 TSP1_BOVIN, tr F1N3A1 F1N3A1_BOVIN	gFLL LASL R	72%	31.1	47.97538	Ref	-0.47	0.27	-0.02	-0.13	-0.99	1	-0.43	1640	1030	1870	1720	1750	842	3570	1290	647.4	1292.8	2	0.0094	7.251
Protein CASC3 OS=Bos taurus GN=CASC3 PE=2 SV=1	sp A5D7H5 CASC3_BOVIN, tr E2R5K5 E2R5K5_CAFNA	aGAL HLR	89%	39.5	48.47498	Ref	-0.088	-0.01	0.32	-0.25	0.6	-0.42	-0.29	3540	2900	3320	4670	3470	5450	2820	3050	347.9	1040.6	3	0.0129	12.37
Protein CASC3 OS=Bos taurus GN=CASC3 PE=2 SV=1	sp A5D7H5 CASC3_BOVIN, tr E2R5K5 E2R5K5_CAFNA	gLFF EHDL R	83%	39.4	51.9656	Ref	-0.2	0.037	0.063	-0.56	-0.01	-0.53	0.57	2960	1710	2190	2500	1790	2300	1670	3540	479.9	1436.8	3	0.0115	7.993
Protein CASC3 OS=Bos taurus GN=CASC3 PE=2 SV=1	sp A5D7H5 CASC3_BOVIN, tr E2R5K5 E2R5K5_CAFNA	kGLF FEH DLR	90%	42.7	53.03989	Ref	-0.078	-0.01	-0.05	-0.25	0.38	-0.65	0.55	6520	5640	6410	6990	6710	9060	4640	10600	468.3	1869	4	0.0231	12.34

26S proteasome non-ATPase regulatory subunit 9 OS=Bos taurus GN=PSMD9 PE=1 SV=1	sp Q3SZ19 PSMD9_BOVIN,transcript C3V9V8 C3V9V8_BOVIN	dQS QGL SPA QAF Ak	95%	55.3	54.15256	Ref	-0.35	-0.38	-0.04	-0.073	0.24	-0.59	0.051	23600	15300	16200	23100	24800	26900	15900	24500	686	2055.1	3	0.0222	10.77
26S proteasome non-ATPase regulatory subunit 9 OS=Bos taurus GN=PSMD9 PE=1 SV=1	sp Q3SZ19 PSMD9_BOVIN,transcript C3V9V8 C3V9V8_BOVIN	hNIV cLQN Dhk	70%	36.8	53.55827	Ref	-0.039	-0.29	-0.09	-0.25	0.12	-0.46	0.029	11900	10100	9150	11800	11700	13200	9190	12800	659	1974	3	0.0215	10.88
26S proteasome non-ATPase regulatory subunit 9 OS=Bos taurus GN=PSMD9 PE=1 SV=1	sp Q3SZ19 PSMD9_BOVIN,transcript C3V9V8 C3V9V8_BOVIN	qVE DAL HQL HAR	86%	40.6	53.45184	Ref	-0.029	-0.38	0.1	-0.29	0.2	-0.13	-0.09	6370	7070	6000	9450	7950	9700	8060	8240	431	1719.9	4	0.0082	4.758
EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=2	sp Q9Y6C2 EMIL1_HUMAN,transcript D3Z9E1 D3Z9E1_RAT,transcript E1BLS8 E1BLS8_BOVIN,transcript E2RCF2 E2RCF2_CANFA,transcript F1SDQ5 F1SDQ5_PIG,transcript F6SMZ4 F6SMZ4_HO RSE,transcript F7GPS2 F7GPS2_MACMU	rLDV VAG SVTV LSGR	95%	52.9	51.80622	Ref	0.28	0.35	0.056	-0.01	-0.11	0.27	0.052	4090	4310	4910	4500	4740	3850	5260	4480	611.7	1832.1	3	0.0118	6.45

SAFB protein OS=Bos taurus GN=SAFB PE=2 SV=1	tr A5PJP2 A5PJP2_ BOVIN,tr E1B9I2 E 1B9I2_BO VIN,tr E1 BDE7 E1B DE7_BOVI N,tr E1BG 66 E1BG6 6_BOVIN	eSSA SEG ADQ k	95%	50	52.05071	Ref	-0.45	-0.32	-0.93	-0.38	-0.31	-0.49	-0.16	14000	9130	10800	7980	12900	11800	10900	13600	858.9	1715.9	2	0.0177	10.29
SAFB protein OS=Bos taurus GN=SAFB PE=2 SV=1	tr A5PJP2 A5PJP2_ BOVIN,tr E1B9I2 E 1B9I2_BO VIN,tr E1 BDE7 E1B DE7_BOVI N,tr E1BG 66 E1BG6 6_BOVIN	rEPV EQT GDD ER	95%	47	50.69142	Ref	-0.19	0.091	-1.2	-0.52	-0.38	-0.41	-0.76	735	550	726	345	588	565	578	450	867.9	1733.8	2	0.0123	7.09
SAFB protein OS=Bos taurus GN=SAFB PE=2 SV=1	tr A5PJP2 A5PJP2_ BOVIN,tr E1B9I2 E 1B9I2_BO VIN,tr E1 BDE7 E1B DE7_BOVI N,tr E1BG 66 E1BG6 6_BOVIN	rEPV EQT GDD ER	89%	39.8	50.6592	Ref	0.14	0.41	Value Missi ng (- 1.425 7195)	-0.94	-0.95	-0.83	-0.3	709	680	888	Value Missing (- 1.4257 195)	430	373	424	606	867.9	1733.8	2	0.0135	7.794
Uncharacterized protein OS=Bos taurus GN=Bt.64790 PE=3 SV=1	tr F1N4M 7 F1N4M 7_BOVIN, tr Q32P14 Q32P14_ BOVIN	gFQL GAL DTH R	95%	51.8	52.11353	Ref	0.43	0.27	-0.09	0.1	-0.08	0.31	0.22	5830	7470	7220	6330	7960	6150	8400	7810	506.9	1517.8	3	0.0103	6.785
Uncharacterized protein OS=Bos taurus GN=Bt.64790 PE=3 SV=1	tr F1N4M 7 F1N4M 7_BOVIN, tr Q32P14 Q32P14_ BOVIN	gFQL GAL DTH R	79%	37.9	52.07209	Ref	0.15	-0.12	0.2	0.18	-0.05	0.2	0.48	3670	3460	3120	4360	4730	3530	4380	5290	506.9	1517.8	3	0.0134	8.839

Uncharacterized protein OS=Bos taurus GN=Bt.64790 PE=3 SV=1	tr F1N4M7 F1N4M7_BOVIN, tr Q32P14 Q32P14_BOVIN	rDPD PNS AEcL HVR	95%	54.1	51.01383	Ref	0.083	0.47	0.021	0.11	-0.03	0.39	0.029	10100	9320	13200	10900	12700	10100	14100	10900	490.5	1957.9	4	0.0132	6.722
Putative uncharacterized protein OS=Mus musculus GN=Actb PE=2 SV=1	tr Q3U804 Q3U804_MOUSE, tr Q3U939 Q3U939_MOUSE	vAPE EHP VLLT EAPL NPK	72%	36.4	52.74303	Ref	-0.18	-0.26	-0.27	-0.25	-0.3	0.009	-0.63	29200	20300	20800	23200	25900	21900	28300	18000	854.8	2561.5	3	0.005	1.946
Putative uncharacterized protein OS=Mus musculus GN=Actb PE=2 SV=1	tr Q3U804 Q3U804_MOUSE, tr Q3U939 Q3U939_MOUSE	vAPE EHP VLLT EAPL NPK	95%	70.1	53.32305	Ref	-0.22	-0.17	-0.22	-0.16	-0.26	0.012	-0.49	2420	2020	2260	2450	2830	2310	2900	2030	1282	2561.4	2	0.0197	7.704
Uncharacterized protein OS=Bos taurus GN=Bt.43863 PE=4 SV=1	tr E1BME9 E1BME9_BOVIN	gGSP VAE ASR	81%	36.1	50.27158	Ref	-0.33	-0.11	-0.1	-0.38	0.075	-0.62	-0.16	16000	11100	14100	15900	14500	17300	11100	15200	617.8	1233.7	2	0.0085	6.894
Uncharacterized protein OS=Bos taurus GN=Bt.43863 PE=4 SV=1	tr E1BME9 E1BME9_BOVIN	gQQ LAPP TAD AVSk	71%	36.5	53.56749	Ref	-0.43	-0.21	-0.05	-0.55	0.31	-0.78	-0.11	5500	3550	4500	5630	4400	6950	3410	5390	996.1	1990.1	2	0.0197	9.917
Uncharacterized protein OS=Bos taurus GN=Bt.43863 PE=4 SV=1	tr E1BME9 E1BME9_BOVIN	qGS DSEA AQW GR	95%	56.3	49.32514	Ref	-0.42	-0.27	-0.07	-0.3	0.06	-1	0.12	13200	8230	9920	12900	12000	13500	6730	14600	798.4	1594.8	2	0.0114	7.173

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.6409 PE=4 SV=1	tr F1MM F4 F1MM F4_BOVIN	rPED ESPP AAA ATS GAA PAR	69%	36.7	53.75507	Ref	-0.17	-0.4	-0.27	-0.13	-0.1	-0.36	-0.16	10700	8240	7620	9400	11400	10200	8820	10100	742.7	2225.1	3	0.0129	5.803
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.6409 PE=4 SV=1	tr F1MM F4 F1MM F4_BOVIN	rPED ESPP AAA ATS GAA PAR	94%	51.8	53.66236	Ref	0.048	0.043	-0.58	-0.21	-0.24	-0.35	-0.34	2330	2150	2320	1690	2410	2060	1990	1990	742.7	2225.1	3	0.0171	7.703
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.6409 PE=4 SV=1	tr F1MM F4 F1MM F4_BOVIN	sTTT ASEE DVSS R	95%	54.4	50.05086	Ref	-0.36	-0.4	-0.24	-0.22	0.21	-1	0.052	11200	7020	7430	9290	10400	12200	5370	11400	837.4	1672.8	2	0.0115	6.841
Uncharacterized protein OS=Bos taurus GN=ATXN2L PE=4 SV=1	tr E1BJ59 E1BJ59_ BOVIN	aDGL QVG QDA R	85%	38.4	51.10499	Ref	-0.34	-0.02	-0.21	-0.15	0.33	-0.46	0.084	17000	11700	15800	15500	17900	21800	13200	19000	717.4	1432.7	2	0.0133	9.26
Uncharacterized protein OS=Bos taurus GN=ATXN2L PE=4 SV=1	tr E1BJ59 E1BJ59_ BOVIN	eFNP TkPL LSVN k	61%	29.9	50.5942	Ref	-0.18	-0.18	-0.08	-0.16	0.2	-0.38	0.06	9060	6860	7460	8980	9340	10500	7310	9850	600.6	2398.4	4	0.0192	7.985
Uncharacterized protein OS=Bos taurus GN=ATXN2L PE=4 SV=1	tr E1BJ59 E1BJ59_ BOVIN	fELA VDA VHR	95%	67.3	52.09633	Ref	0.039	0.19	0.046	-0.23	-0.15	-0.4	-0.12	3050	2860	3440	3500	3190	2940	2580	3120	487.6	1459.8	3	0.0098	6.688

Zinc finger CCCH domain-containing protein 15 OS=Bos taurus GN=ZC3H15 PE=2 SV=1	M1 ZC3HF_BOVIN, sp Q3TIV5 ZC3HF_MOUSE, sp Q6U6G5 ZC3HF_RAT, sp Q8WU90 ZC3HF_HUMAN, tr B1B079 B1B079_MOUSE, tr B7Z592 B7Z592_HUMAN, tr D211X0 D211X0_AILME, tr F1PEL5 F1PEL5_CANFA, tr F1RYJ5 F1RYJ5_PI, tr F5H0F5 F5H0F5_HUMA	aVTH QVk	52%	28.4	48.85587	Ref	-0.27	-0.36	-0.16	-0.27	0.21	-0.89	-0.06	12600	9410	9580	12400	12600	15400	7480	13200	695.9	1389.9	2	0.0044	3.142
Zinc finger CCCH domain-containing protein 15 OS=Bos taurus GN=ZC3H15 PE=2 SV=1	M1 ZC3HF_BOVIN, sp Q3TIV5 ZC3HF_MOUSE, sp Q6U6G5 ZC3HF_RAT, sp Q8WU90 ZC3HF_HUMAN, tr B1B079 B1B079_MOUSE, tr B7Z592 B7Z592_HUMAN, tr D211X0 D211X0_AILME, tr F1PEL5 F1PEL5_CANFA, tr F1RYJ5 F1RYJ5_PI, tr F5H0F5 F5H0F5_HUMA	ITLES FLA WK	87%	41.4	51.62499	Ref	-0.086	-0.45	-0.35	-0.34	-0.27	-0.29	-0.17	793	560	474	568	630	577	595	642	606	1815.1	3	0.0092	5.067

Zinc finger CCCH domain-containing protein 15 OS=Bos taurus GN=ZC3H15 PE=2 SV=1	M1 ZC3HF_BOVIN, sp Q3TIV5 ZC3HF_MOUSE, sp Q6U6G5 ZC3HF_RAT, sp Q8WU90 ZC3HF_HUMAN, tr B1B079 B1B079_MOUSE, tr B7Z592 B7Z592_HUMAN, tr D211X0 D211X0_AILME, tr F1PEL5 F1PEL5_CANFA, tr F1RYJ5 F1RYJ5_PI1R1YJ5 F1RYJ5 F5H0G, tr F5H0F5 F5H0F5_HUMA	qVAQSEAEk	95%	51.7	52.99425	Ref	-0.19	-0.37	-0.03	-0.16	-0	-0.9	-0.19	5260	4000	3840	5470	5490	5350	3010	4870	799.4	1596.9	2	0.0121	7.543
Elongation factor 2 OS=Bos taurus GN=EEF2 PE=2 SV=3	sp Q3SYU2 EF2_BOVIN	eTVSEESNVLcLSk	95%	70.6	53.9423	Ref	0.0085	-0.03	0.003	0.046	-0	-0.11	0.02	2810	2080	2190	2520	2860	2410	2340	2540	731.4	2191.1	3	0.0194	8.845
Elongation factor 2 OS=Bos taurus GN=EEF2 PE=2 SV=3	sp Q3SYU2 EF2_BOVIN	eTVSEESNVLcLSk	95%	62.5	54.0815	Ref	0.034	-0.18	0.19	-0.016	-0.18	0.23	0.061	2930	2610	2440	3550	3380	2630	3650	3230	731.4	2191.1	3	0.0121	5.505
Elongation factor 2 OS=Bos taurus GN=EEF2 PE=2 SV=3	sp Q3SYU2 EF2_BOVIN	gHVF EETQVAGTPM FVVK	94%	51.6	55.02846	Ref	0.21	0.041	0.2	-0.067	-0.17	0.11	-0.13	577	605	582	732	668	543	689	578	862.1	2583.4	3	0.0174	6.746

Peptidyl-prolyl cis-trans isomerase D OS=Bos taurus GN=PPID PE=1 SV=6	sp P26882 PPID_BOVIN	aAAEDADGAK	95%	66.3	52.66352	Ref	0.58	-0.47	-0.09	0.25	0.28	-0.54	-0.36	8450	8830	4620	6740	9420	8390	4980	5570	763.9	1525.8	2	0.0072	4.695
Peptidyl-prolyl cis-trans isomerase D OS=Bos taurus GN=PPID PE=1 SV=6	sp P26882 PPID_BOVIN	hVVF GQVIk	93%	44.3	48.80156	Ref	0.34	-0.02	0.1	-0.07	-0.02	0.12	0.044	21100	26200	22100	27100	26400	24000	27600	25900	545.7	1634	3	0.0073	4.477
Peptidyl-prolyl cis-trans isomerase D OS=Bos taurus GN=PPID PE=1 SV=6	sp P26882 PPID_BOVIN	hVVF GQVIk	91%	41.2	48.11233	Ref	0.26	-0.04	0.052	-0.055	-0	0.01	0.14	5840	6080	5350	6400	6560	5930	6250	6810	545.7	1634	3	#####	#####

THO complex subunit 4 OS=Mus musculus GN=Thoc4 PE=1 SV=3	3 THOC4 _MOUSE, sp Q3T0I 4 THOC4 _BOVIN,s p Q86V81 THOC4_ HUMAN,t r D2GVF2 D2GVF2 _AILME,tr D3ZXH5 D3ZXH5_ RAT,tr D3 ZXH7 D3Z XH7_RAT, tr E9PB61 E9PB61_ HUMAN,t r F1PL92 F1PL92_C ANFA,tr F 6Q1W2 F 6Q1W2_ MONDO,t r F6S9B3 F6S9B3_ R	aAV HYD	90%	42.5	50.37725	Ref	-0.35	0.34	-0.05	-0.14	0.35	-0.24	0.51	63100	41400	72500	62000	64200	78600	54500	91300	379.2	1134.6	3	0.01	8.827
THO complex subunit 4 OS=Mus musculus GN=Thoc4 PE=1 SV=3	3 THOC4 _MOUSE, sp Q3T0I 4 THOC4 _BOVIN,s p Q86V81 THOC4_ HUMAN,t r D2GVF2 D2GVF2 _AILME,tr D3ZXH5 D3ZXH5_ RAT,tr D3 ZXH7 D3Z XH7_RAT, tr E9PB61 E9PB61_ HUMAN,t r F1PL92 F1PL92_C ANFA,tr F 6Q1W2 F 6Q1W2_ MONDO,t r F6S9B3 F6S9B3_ R	kAA VHY DR	78%	35.8	52.21414	Ref	-0.17	0.23	0.029	0.002	0.34	-0.13	0.38	45900	38000	54500	53100	57400	63400	47900	67300	392.7	1566.9	4	0.0242	15.41

THO complex subunit 4 OS=Mus musculus GN=Thoc4 PE=1 SV=3	3 THOC4_MOUSE,sp Q3T014 THOC4_BOVIN,sp Q86V81 THOC4_HUMAN, tr D2GVF2 D2GVF2_AILME, tr D3ZXH5 D3ZXH5_RAT, tr D3ZXH7 D3ZXH7_RAT, tr E9PB61 E9PB61_HUMAN, tr F1PL92 F1PL92_CANFA, tr F6Q1W2 F6Q1W2_MONDO, tr F6S9B3 F6S9B3_HFER	SLGT ADV	83%	39.5	51.87309	Ref	0.096	0.3	-0.16	-0.016	0.35	-0.28	0.29	3380	3140	3930	3200	3900	4380	2950	4340	512.6	1534.8	3	0.012	7.818
Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnp1 PE=1 SV=3	7 HNRH1_MOUSE,sp P31943 HNRH1_HUMAN, tr B4DP51 B4DP51_HUMAN, tr D2HGC3 D2HGC3_AILME, tr D3ZSG5 D3ZSG5_RAT, tr D3ZYW2 D3ZYW2_RAT, tr E1BF20 E1BF20_BOVIN, tr E2R8D4 E2R8D4_CANFA, tr E2R8D6 E2R8D6_CANFA, tr E2R8G1 E2R8G1_CA	VHIEI GPD GR	92%	46.7	51.97382	Ref	0.26	0.22	0.081	-0.16	-0.2	-0.04	-0.31	21000	21900	23100	23500	21900	18700	21800	17900	466.3	1395.8	3	0.0115	8.199

Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnp1 PE=1 SV=3	7 HNRH1_MOUSE,sp P31943 HNRH1_HUMAN, tr B4DP51 B4DP51_HUMAN, tr D2HGC3 D2HGC3_AILME, tr D3ZSG5 D3ZSG5_RAT, tr D3ZYW2 D3ZYW2_RA T, tr E1BF20 E1BF20_BOVIN, tr E2R8D4 E2R8D4_CANFA, tr E2R8D6 E2R8D6_C ANFA, tr E2R8G1 E2R8G1_CA	VHIEI GPD	76%	36.8	51.97413	Ref	0.24	0.083	0.018	-0.077	0.055	-0.24	-0.14	9460	9850	9610	10300	10600	10200	8650	9210	466.3	1395.8	3	0.0118	8.414
	7 HNRH1_MOUSE,sp P31943 HNRH1_HUMAN, tr B4DP51 B4DP51_HUMAN, tr D2HGC3 D2HGC3_AILME, tr D3ZSG5 D3ZSG5_RAT, tr D3ZYW2 D3ZYW2_RA T, tr E1BF20 E1BF20_BOVIN, tr E2R8D4 E2R8D4_CANFA, tr E2R8D6 E2R8D6_C ANFA, tr E2R8G1 E2R8G1_CA	VTGE ADV EFAT HED AVA AMS k	95%	53	54.91559	Ref	0.21	-0.08	-0.52	-0.083	0.069	-0.02	0.073	11900	10500	9330	7710	11500	11100	11000	11600	697.4	2785.4	4	0.0123	4.426

SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SARNP PE=1 SV=3	sp P82979 SARNP_HUMAN,sp Q498U4 SARNP_RAT,sp Q5R4V4 SARNP_PONAB,tr Q2TBX1 Q2TBX1_BOVIN	aTETVELHk	84%	38.1	51.4288	Ref	-0.27	-0.22	-0.58	-0.54	-0.25	-0.12	-0.29	42400	22600	25300	22200	25200	26800	30600	27000	687.4	1372.7	2	0.0108	7.885
SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SARNP PE=1 SV=3	sp P82979 SARNP_HUMAN,sp Q498U4 SARNP_RAT,sp Q5R4V4 SARNP_PONAB,tr Q2TBX1 Q2TBX1_BOVIN	fGIVTSSAGTGTTEDTEAK	95%	67.2	54.92599	Ref	-0.25	-0.35	-0.56	-0.15	0.009	-0.5	0.084	9030	6590	6710	6490	9480	9260	6810	10100	827.4	2479.3	3	0.0195	7.869
SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SARNP PE=1 SV=3	sp P82979 SARNP_HUMAN,sp Q498U4 SARNP_RAT,sp Q5R4V4 SARNP_PONAB,tr Q2TBX1 Q2TBX1_BOVIN	fGLNVSSISR	51%	31.1	51.73586	Ref	-0.43	-0.05	-0.46	-0.23	-0.08	-0.29	0.16	13800	11000	15500	13200	16900	16500	14800	20100	692.4	1382.8	2	0.0115	8.276
Uncharacterized protein OS=Bos taurus GN=VTN PE=2 SV=1	tr Q3ZBS7 Q3ZBS7_BOVIN	fQDGVLEPDFP	83%	38.8	52.38894	Ref	-0.09	0.72	-0.04	0.19	-0.08	0.72	0.14	9440	7710	14700	9730	12600	9110	16600	11000	862.4	1722.9	2	0.0146	8.489
Uncharacterized protein OS=Bos taurus GN=VTN PE=2 SV=1	tr Q3ZBS7 Q3ZBS7_BOVIN	gLYcYELDEk	89%	42.8	51.86009	Ref	0.14	0.51	-0.01	0.097	-0.07	0.91	0.077	3260	3370	4720	3710	4400	3410	7060	3930	629.6	1885.9	3	0.0195	10.35

Uncharacterized protein OS=Bos taurus GN=VTN PE=2 SV=1	tr Q3ZBS7 Q3ZBS7_BOVIN	rVDA VIPP YPR	73%	35.9	51.87794	Ref	0.48	0.41	0.16	0.074	0.071	0.45	0.075	8770	10300	10700	10100	10500	9110	12400	9460	529.6	1585.9	3	0.014	8.831
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_007210 PE=4 SV=1	tr D2HA11 D2HA11_AILME	gGA GPP GPE GGk	95%	47.9	52.53163	Ref	-1.7	1.5	-2.2	0.046	-1.5	1.3	-2.5	4030	1060	10400	946	4850	1430	10400	776	794.9	1587.9	2	0.0244	15.35
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_007210 PE=4 SV=1	tr D2HA11 D2HA11_AILME	gGA GPP GPE GGk	77%	37.5	52.45291	Ref	-0.36	0.67	-0.67	-0.045	-0.38	0.72	-0.26	16900	10900	24200	10800	18200	12600	28300	14200	530.3	1587.9	3	0.0219	13.79
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_007210 PE=4 SV=1	tr D2HA11 D2HA11_AILME	nGD RGET GPA GPS GAP GPA GSR	90%	44.3	52.40032	Ref	-0.88	1.1	-0.76	-0.017	-0.54	0.87	-0.67	9000	4660	19300	6160	11400	6910	19200	6550	757.4	2269.1	3	0.0192	8.438

Phosphoglycerate kinase 1 OS=Pan troglodytes GN=PGK1 PE=2 SV=1	4 PGK1_P ANTR,sp P00558 PGK1_HUMAN,sp P00559 PGK1_HORSE,sp Q3T0P6 PGK1_BOVIN,sp Q5NVB5 PGK1_PONAB,sp Q60HD8 PGK1_MAFCA,sp Q7SIB7 PGK1_PIG,trans A8K4W6 A8K4W6_HUMAN,trans B7TJ13 B7TJ13_SHEEP,trans B7Z7A9 B7Z7A9_HUMAN,trans VK	aLM DEV	94%	45.2	51.68831	Ref	-0.16	-0.14	-0.1	-0.24	-0.12	-0.36	23500	18300	20100	23200	23100	20200	23000	19300	756.9	1511.9	2	0.0068	4.509	
Phosphoglycerate kinase 1 OS=Pan troglodytes GN=PGK1 PE=2 SV=1	4 PGK1_P ANTR,sp P00558 PGK1_HUMAN,sp P00559 PGK1_HORSE,sp Q3T0P6 PGK1_BOVIN,sp Q5NVB5 PGK1_PONAB,sp Q60HD8 PGK1_MAFCA,sp Q7SIB7 PGK1_PIG,trans A8K4W6 A8K4W6_HUMAN,trans B7TJ13 B7TJ13_SHEEP,trans B7Z7A9 B7Z7A9_HUMAN,trans k	dcVG PEVE	53%	32.6	52.68353	Ref	-0.19	-0.24	-0.08	-0.26	-0.25	0.042	-0.44	21000	15700	16500	20600	20100	17600	22500	16000	544	1628.8	3	0.0079	4.869

Phosphoglycerate kinase 1 OS=Pan troglodytes GN=PGK1 PE=2 SV=1	4 PGK1_P ANTR,sp P00558 PGK1_HUMAN,sp P00559 PGK1_HORSE,sp Q3T0P6 PGK1_BOVIN,sp Q5NVB5 PGK1_PONAB,sp Q60HD8 PGK1_MA CFA,sp Q7SIB7 PGK1_PIG,tra8K4W6 A8K4W6_HUMAN,traB7TJ13 B7TJ13_SHEEP,traB7Z7A9 B7Z7A9_HUMAN,traHR	IGDV YVN DAF GTA	77%	38.3	52.96281	Ref	-0.24	-0.43	-0.1	-0.31	-0.13	-0.08	0.24	22300	21600	20500	29100	27600	27400	29700	36700	647	1938	3	0.0134	6.923
Chloride intracellular channel protein 4 OS=Mus musculus GN=Clic4 PE=1 SV=3	B1 CLIC4_MOUSE,sp Q9XSA7 CLIC4_BOVIN,sp Q9Y696 CLIC4_HUMAN,sp Q9Z0W7 CLIC4_RAT,traB4DWC4 B4DWC4_HUMAN,traE2RGI4 E2RGI4_CANFA,traF5H1F8 F5H1F8_HUMAN,traF6PP70 F6PP70_MACM U,traF7EXF2 F7EXF2_CALJA,traF7H766 F7H766	aGS DGE SIGN cPFS QR	86%	37.2	47.89687	Ref	0.4	0.008	-0	-0.2	-0.28	-0.12	-0.16	5350	6130	5080	5670	5430	4510	5250	5070	659	1973.9	3	0.0111	5.645

Chloride intracellular channel protein 4 OS=Mus musculus GN=Clic4 PE=1 SV=3	B1 CLIC4_MOUSE,sp Q9XSA7 CLIC4_BOVIN,sp Q9Y696 CLIC4_HUMAN,sp Q9Z0W7 CLIC4_RAT,tr B4DWC4 B4DWC4_HUMAN,tr E2RGI4 E2RGI4_CANFA,tr F5H1F8 F5H1F8_HUMAN,tr F6PP70 F6PP70_MACMU,tr F7EXF2 F7EXF2_CALJAr F7H766 F7H766	gVVF SVTT VDLK	92%	46.5	51.5982	Ref	0.2	-0.03	0.037	-0.076	-0.2	0.081	-0.15	1690	1870	1730	2030	2070	1660	2110	1790	625	1872.1	3	0.011	5.859
Chloride intracellular channel protein 4 OS=Mus musculus GN=Clic4 PE=1 SV=3	B1 CLIC4_MOUSE,sp Q9XSA7 CLIC4_BOVIN,sp Q9Y696 CLIC4_HUMAN,sp Q9Z0W7 CLIC4_RAT,tr B4DWC4 B4DWC4_HUMAN,tr E2RGI4 E2RGI4_CANFA,tr F5H1F8 F5H1F8_HUMAN,tr F6PP70 F6PP70_MACMU,tr F7EXF2 F7EXF2_CALJAr F7H766 F7H766	gVVF SVTT VDLK	95%	51.5	51.56467	Ref	0.3	-0.1	0.11	-0.22	-0.08	-0.11	-0.26	709	736	606	786	692	666	680	609	625	1872.1	3	0.0086	4.593

Uncharacterized protein OS=Bos taurus GN=Bt.56566 PE=4 SV=1	tr E1BEM3 E1BEM3_BOVIN	eDPS DNW EEG GGG GGG VEK	95%	55.8	51.33091	Ref	-0.15	0.52	0.35	0.59	0.71	0.41	0.7	10700	5330	9170	9160	12000	11300	9620	11700	828.7	2483.1	3	0.0202	8.149
Uncharacterized protein OS=Bos taurus GN=Bt.56566 PE=4 SV=1	tr E1BEM3 E1BEM3_BOVIN	eVD YSGL R	60%	31.4	50.58339	Ref	-0.65	0.25	0.62	0.57	1	0.09	1.2	39400	21800	44100	64100	68100	81100	44600	98100	621.8	1241.6	2	0.0101	8.134
Uncharacterized protein OS=Bos taurus GN=Bt.56566 PE=4 SV=1	tr E1BEM3 E1BEM3_BOVIN	kAP QGP PEIY SDT QFPS LQST AK	63%	35.1	55.3016	Ref	-0.3	0.28	0.54	0.6	0.98	0.34	1.2	1320	1150	1860	2500	2870	3280	2190	3870	851.5	3401.8	4	0.0348	10.23
Uncharacterized protein OS=Bos taurus GN=UBAP2 PE=4 SV=1	tr E1BA82 E1BA82_BOVIN	aAPL MTS Gk	52%	32	52.39047	Ref	0.17	0.043	0.038	-0.13	0.054	-0.12	-0	9550	9780	9730	10900	10700	10600	9800	10600	495.3	1482.8	3	0.0287	19.33
Uncharacterized protein OS=Bos taurus GN=UBAP2 PE=4 SV=1	tr E1BA82 E1BA82_BOVIN	dGSL TNN PYSG DVTK	64%	35.9	54.11411	Ref	0.025	-0.18	0.055	-0.1	0.18	-0.35	0.29	14400	12800	12000	15900	15700	16600	12000	18600	726	2175.1	3	0.0181	8.324
Uncharacterized protein OS=Bos taurus GN=UBAP2 PE=4 SV=1	tr E1BA82 E1BA82_BOVIN	ekPQ ISAT QAT QLQ k	95%	58.2	52.45041	Ref	-0.46	-0.11	0.074	-0.06	0.49	-0.48	0.2	2220	1320	1810	2320	2330	2970	1590	2520	861.8	2582.5	3	0.037	14.31

Myosin regulatory light polypeptide 9 OS=Homo sapiens GN=MYL9 PE=1 SV=4	4 MYL9_HUMAN,sp P29269 MYL9_PI G,sp Q5RBA4 MYL9_PONAB,sp Q64122 MYL9_RAT,sp Q9CQ19 MYL9_MOUSE,SE,tr A1L5B0 A1L5B0_BOVIN,tr A2AVY6 A2AVY6_MOUSE,tr B0BMS8 B0BMS8_RAT,tr D2H464 D2H464_AILME,tr F1MLA6 F1MLA6_BOVIN,tr	fTDE EVDE	MYR	62%	28.4	47.27517	Ref	-1.3	1.2	-0.86	-0.019	-0.48	0.39	-0.6	7990	2910	17300	4640	9190	5850	11200	5570	869.4	1736.8	2	0.0126	7.224
Myosin regulatory light polypeptide 9 OS=Homo sapiens GN=MYL9 PE=1 SV=4	4 MYL9_HUMAN,sp P29269 MYL9_PI G,sp Q5RBA4 MYL9_PONAB,sp Q64122 MYL9_RAT,sp Q9CQ19 MYL9_MOUSE,SE,tr A1L5B0 A1L5B0_BOVIN,tr A2AVY6 A2AVY6_MOUSE,tr B0BMS8 B0BMS8_RAT,tr D2H464 D2H464_AILME,tr F1MLA6 F1MLA6_BOVIN,tr	fTDE EVDE	MYR	95%	47.2	47.47715	Ref	-0.79	1.1	-0.95	-0.065	-0.53	0.41	-0.64	19400	9070	36500	9850	20100	12700	25500	12200	869.4	1736.8	2	0.0097	5.601

Myosin regulatory light polypeptide 9 OS=Homo sapiens GN=MYL9 PE=1 SV=4	4 MYL9_HUMAN,sp P29269 MYL9_PI G,sp Q5RBA4 MYL9_PONAB,sp Q64122 MYL9_RAT,sp Q9CQ19 MYL9_MOUSE,SE,tr A1L5B0 A1L5B0_BOVIN, tr A2AVY6 A2AVY6_MOUSE, tr B0BMS8 B0BMS8_RAT, tr D2H464 D2H464_AILME, tr F1MLA6 F1MLA6_BOVIN, tr	gNFn YVEF TR	80%	35.4	50.23956	Ref	-0.46	0.69	-0.65	0.088	-0.14	0.29	-0.35	9630	6140	14700	6560	12000	8930	12600	8010	776.4	1550.8	2	0.0143	9.186
Antithrombin-III OS=Bos taurus GN=SERPINC1 PE=1 SV=2	sp P41361 ANT3_BOVIN, tr F1MSZ6 F1MSZ6_BOVIN	aTEG QGS EQk	92%	44.6	52.66243	Ref	0.43	0.26	0.39	0.19	-0.35	0.95	-0.17	1910	2230	2160	2650	2540	1530	3910	1790	821.9	1641.9	2	0.0139	8.45
Antithrombin-III OS=Bos taurus GN=SERPINC1 PE=1 SV=2	sp P41361 ANT3_BOVIN, tr F1MSZ6 F1MSZ6_BOVIN	dIPV NPM clyR	67%	36.2	53.60722	Ref	0.47	0.15	0.29	0.27	-0.09	0.73	0.043	2570	2950	2570	3170	3430	2340	4330	2660	659	1974	3	0.0171	8.671
Antithrombin-III OS=Bos taurus GN=SERPINC1 PE=1 SV=2	sp P41361 ANT3_BOVIN, tr F1MSZ6 F1MSZ6_BOVIN	kATE GQG SEQk	59%	34.3	53.44196	Ref	0.38	0.26	0.3	0.29	-0.16	0.93	-0.19	7020	8100	8090	9320	10200	6520	14500	6610	692.4	2074.2	3	0.006	2.911

L-lactate dehydrogenase B chain OS=Bos taurus GN=LDHB PE=2 SV=4	sp Q5E9B1 LDHB_BOVIN, tr A0FH34 A0FH34_BO SMU, tr A0FH35 A0FH35_BO SMU, tr B0JYN3 B0JYN3_BOVIN, tr F1MRW3 F1MRW3_BOVIN	iHPV STM Vlk	77%	36	51.53824	Ref	-0.071	-0.24	-0.09	-0.19	-0.16	-0.17	-0.17	7350	6080	5890	7330	7500	6680	6970	6890	810.5	1618.9	2	0.0209	12.88
L-lactate dehydrogenase B chain OS=Bos taurus GN=LDHB PE=2 SV=4	sp Q5E9B1 LDHB_BOVIN, tr A0FH34 A0FH34_BO SMU, tr A0FH35 A0FH35_BO SMU, tr B0JYN3 B0JYN3_BOVIN, tr F1MRW3 F1MRW3_BOVIN	sADT LWG IQk	95%	56.3	52.80917	Ref	-0.23	-0.15	-0.15	0.01	-0.23	-0.05	-0.27	15100	11300	13000	14600	18000	13300	15800	13400	864	1726	2	0.0176	10.16
L-lactate dehydrogenase B chain OS=Bos taurus GN=LDHB PE=2 SV=4	sp Q5E9B1 LDHB_BOVIN, tr A0FH34 A0FH34_BO SMU, tr A0FH35 A0FH35_BO SMU, tr B0JYN3 B0JYN3_BOVIN, tr F1MRW3 F1MRW3_BOVIN	sADT LWG IQk	83%	40.5	52.78267	Ref	-0.37	-0.23	-0.14	-8E-04	-0.11	-0.09	-0.25	66100	42300	50700	60300	73400	59500	63000	56100	576.3	1726	3	0.0165	9.542

Uncharacterized protein OS=Bos taurus GN=Bt.101217 PE=4 SV=1	tr E1B997 E1B997_BOVIN	TLLES QAQ Wk	51%	32.9	53.45629	Ref	0.47	0.045	0.21	-0.014	0.11	-0.26	0.057	4650	5380	4340	5450	5150	4890	3960	4900	604.7	1811	3	0.0129	7.093
Uncharacterized protein OS=Bos taurus GN=Bt.101217 PE=4 SV=1	tr E1B997 E1B997_BOVIN	TLLES QAQ Wk	76%	38.3	53.61239	Ref	0.52	-0.11	0.19	-0.17	0.27	-0.32	0.29	11600	15400	10800	14900	12800	15200	10600	15900	604.7	1811	3	0.0233	12.85
Uncharacterized protein OS=Bos taurus GN=Bt.101217 PE=4 SV=1	tr E1B997 E1B997_BOVIN	vPAV APLE GLTV TLR	95%	48.4	48.5915	Ref	0.6	-0.12	0.3	-0.3	0.39	-0.54	0.12	479	631	417	623	454	638	352	549	651.7	1952.2	3	0.0018	0.93
Charged multivesicular body protein 4b OS=Mus musculus GN=Chmp4b PE=2 SV=2	sp Q9D8B3 CHM4B_MOUSE, sp Q9H444 CHM4B_HUMAN, tr F7H0S7 F7H0S7_MACMU, tr Q08E32 Q08E32_BOVIN	aALQ ALK	87%	35.7	45.57772	Ref	-0.25	-0.23	0.09	-0.16	0.38	-0.63	0.059	14800	10400	11500	16100	14900	18900	9800	15700	441.6	1321.9	3	#####	0.165
Charged multivesicular body protein 4b OS=Mus musculus GN=Chmp4b PE=2 SV=2	sp Q9D8B3 CHM4B_MOUSE, sp Q9H444 CHM4B_HUMAN, tr F7H0S7 F7H0S7_MACMU, tr Q08E32 Q08E32_BOVIN	kIEQ ELTA Ak	73%	33	48.91102	Ref	-0.071	-0.23	-0	7E-05	0.066	0.014	0.01	9470	9700	9450	12400	13700	12500	12600	12500	681.8	2042.2	3	0.0021	1.017

Charged multivesicular body protein 4b OS=Mus musculus GN=Chmp4b PE=2 SV=2	sp Q9D8B3 CHM4B_MOUSE, sp Q9H444 CHM4B_HUMAN, tr F7H0S7 F7H0S7_MACMU, tr Q08E32 Q08E32_BOVIN	IFGA GGG k	62%	31.1	49.60247	Ref	-0.37	Value Missing (-2.7189023)	0.13	-0.021	0.55	-0.47	0.57	13800	9320	Value Missing (-2.7189023)	15900	15900	20600	10600	21600	438.9	1313.8	3	0.0035	2.676
Small inducible cytokine subfamily E, member 1 (Endothelial monocyte-activating) OS=Bos taurus GN=SCYE1 PE=2 SV=2	tr Q3ZBX5 Q3ZBX5_BOVIN	aEIQ nGV k	79%	36.2	51.3313	Ref	0.071	-0.22	0.062	-0.035	0.2	-0.3	0.061	25000	23500	20800	28400	29300	30000	22300	28300	734.4	1466.9	2	0.0038	2.557
Small inducible cytokine subfamily E, member 1 (Endothelial monocyte-activating) OS=Bos taurus GN=SCYE1 PE=2 SV=2	tr Q3ZBX5 Q3ZBX5_BOVIN	mVV LLcN LkPA k	82%	36.1	48.964	Ref	0.084	-0.4	0.2	-0.062	0.029	-0.23	0.14	1210	1120	867	1480	1360	1260	1100	1410	763.1	2286.4	3	0.0022	0.963

Small inducible cytokine subfamily E, member 1 (Endothelial monocyte-activating) OS=Bos taurus GN=SCYE1 PE=2 SV=2	tr Q3ZBX5 Q3ZBX5_BOVIN	qQP VAG SADS kPVD VSR	67%	37	54.46916	Ref	0.035	-0.37	0.23	-0.16	0.27	-0.32	-0.09	4170	3440	2820	4790	4050	4750	3300	3840	783.8	2348.3	3	0.0151	6.438
Huntingtin-interacting protein K (Predicted) OS=Sorex araneus GN=HYPK PE=4 SV=1	tr B3RF13 B3RF13_SORAR, tr B5SNJ9 B5SNJ9_OT OGA, tr B7NZF4 B7NZF4_RA BIT	aTEG DVEL ELET ETSG PERP PEKPR	72%	38.9	55.09746	Ref	No Values (0.20238991)	No Values (0.084696814)	No Values (0.08189808)	No Values (-0.22237726)	No Values (-0.026504943)	No Values (0.08927164)	No Values (-0.07839756)	No Values (0.0)	No Values (0.20238991)	No Values (0.084696814)	No Values (-0.0818980826)	No Values (-0.2223773)	No Values (0.026504943)	No Values (-0.0892716456)	No Values (-0.07839756)	1038	3111.5	3	0.0192	6.177
Huntingtin-interacting protein K (Predicted) OS=Sorex araneus GN=HYPK PE=4 SV=1	tr B3RF13 B3RF13_SORAR, tr B5SNJ9 B5SNJ9_OT OGA, tr B7NZF4 B7NZF4_RA BIT	eHM GNV VEAL IALT N	95%	55.2	53.5776	Ref	No Values (0.20238991)	No Values (0.08469649)	No Values (0.08189826)	No Values (-0.2223773)	No Values (-0.02650503)	No Values (0.08927173)	No Values (-0.078397736)	No Values (0.0)	No Values (0.20238991)	No Values (0.08469649)	No Values (-0.0818982636)	No Values (-0.2223773)	No Values (0.02650503)	No Values (-0.08927173736)	No Values (-0.078397736)	958	1914	2	0.0093	4.837

Cellular nucleic acid binding protein OS=Mus musculus GN=Cnbp PE=2 SV=2	6 CNBP_MOUSE,sp P62633 CNBP_HUMAN,sp P62634 CNBP_RA_T,sp Q3T0Q6 CNBP_BOVIN,sp Q5R5R5 CNBP_PONAB,tr A8K7V4 A8K7V4_HUMAN,tr A9XHW5 A9XHW5_CRIGR,tr B4DP17 B4DP17_HUMAN,tr D0G6R9 D0G6R9_PIG,tr D2H7C8 D2H7C8_AIL	ecTIE ATA	84%	32.7	45.82881	Ref	Value Missing (-1.0797033)	-0.46	0.15	-0.17	0.4	1.3	2.5	478	Value Missing (-1.0797033)	489	836	738	957	1840	4290	594.3	1186.5	2	0.0123	10.36
Cellular nucleic acid binding protein OS=Mus musculus GN=Cnbp PE=2 SV=2	6 CNBP_MOUSE,sp P62633 CNBP_HUMAN,sp P62634 CNBP_RA_T,sp Q3T0Q6 CNBP_BOVIN,sp Q5R5R5 CNBP_PONAB,tr A8K7V4 A8K7V4_HUMAN,tr A9XHW5 A9XHW5_CRIGR,tr B4DP17 B4DP17_HUMAN,tr D0G6R9 D0G6R9_PIG,tr D2H7C8 D2H7C8_AIL	ecTIE ATA	80%	31.2	45.89458	Ref	Value Missing (-1.276297)	-0.12	-0.35	-0.82	0.59	1.6	2.3	846	Value Missing (-1.276297)	731	702	559	1300	2760	4520	594.3	1186.5	2	0.0107	9.027

<p>Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3</p>	<p>sp Q15691 MARE1_HUMAN, sp Q5R7Z5 MARE1_PONAB, tr B4DM33 B4DM33_HUMAN, tr D2H827 D2H8Z7_AILME, tr E2QYH4 E2QYH4_CANFA, tr F6SAB2 F6SAB2_HORSE, tr F7A401 F7A401_CALJA, tr F7GS88 F7GS88_MACMU, tr Q2XVP5 Q2XVP5_PIG</p>	<p>ITVE DLEK</p>	<p>68%</p>	<p>34.5</p>	<p>52.1301</p>	<p>Ref</p>	<p>0.2</p>	<p>0.12</p>	<p>0.39</p>	<p>0.094</p>	<p>0.28</p>	<p>-0.15</p>	<p>0.11</p>	<p>13200</p>	<p>9770</p>	<p>10100</p>	<p>13600</p>	<p>12200</p>	<p>12200</p>	<p>9410</p>	<p>11200</p>	<p>778</p>	<p>1553.9</p>	<p>2</p>	<p>0.0083</p>	<p>5.327</p>
<p>Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3</p>	<p>sp Q15691 MARE1_HUMAN, sp Q5R7Z5 MARE1_PONAB, tr B4DM33 B4DM33_HUMAN, tr D2H827 D2H8Z7_AILME, tr E2QYH4 E2QYH4_CANFA, tr F6SAB2 F6SAB2_HORSE, tr F7A401 F7A401_CALJA, tr F7GS88 F7GS88_MACMU, tr Q2XVP5 Q2XVP5_PIG</p>	<p>qGQ ETAV APSL VAP ALNK Pk</p>	<p>76%</p>	<p>33.4</p>	<p>50.51118</p>	<p>Ref</p>	<p>0.32</p>	<p>0.14</p>	<p>0.22</p>	<p>0.075</p>	<p>0.21</p>	<p>0.26</p>	<p>0.29</p>	<p>2850</p>	<p>3100</p>	<p>2970</p>	<p>3530</p>	<p>3510</p>	<p>3370</p>	<p>3640</p>	<p>3690</p>	<p>733.7</p>	<p>2930.7</p>	<p>4</p>	<p>0.0282</p>	<p>9.617</p>

<p>Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3</p>	<p>sp Q15691 MARE1_HUMAN, sp Q5R7Z5 MARE1_PONAB, tr B4DM33 B4DM33_HUMAN, tr D2H8Z7 D2H8Z7_AILME, tr E2QYH4 E2QYH4_CANFA, tr F6SAB2 F6SAB2_HORSE, tr F7A401 F7A401_CALJA, tr F7GS88 F7GS88_MACMU, tr Q2XVP5 Q2XVP5_PIG</p>	<p>qGQ ETAV APSL VAP ALNk Pk</p>	<p>95%</p>	<p>54.7</p>	<p>50.20046</p>	<p>Ref</p>	<p>0.12</p>	<p>0.073</p>	<p>0.49</p>	<p>0.008</p>	<p>0.52</p>	<p>0.012</p>	<p>0.28</p>	<p>864</p>	<p>855</p>	<p>899</p>	<p>1350</p>	<p>1060</p>	<p>1330</p>	<p>973</p>	<p>1160</p>	<p>977.9</p>	<p>2930.7</p>	<p>3</p>	<p>0.0229</p>	<p>7.803</p>
<p>Clathrin light chain A OS=Mus musculus GN=Clta PE=1 SV=1</p>	<p>5 CLCA_MOUSE, sp P04973 CLCA_BOVIN, sp P08081 CLCA_RAT, sp P09496 CLCA_HUMAN, tr B1AWD8 B1AWD8_MOUSE, tr B1AWD9 B1AWD9_MOUSE, tr B1AWE0 B1AWE0_MOUSE, tr B1AWE1 B1AWE1_MOUSE, tr B4DIN1 B4DIN1_HUMAN, tr B5ATG0 B5AT</p>	<p>IEAL DAn SR</p>	<p>95%</p>	<p>51.1</p>	<p>52.2626</p>	<p>Ref</p>	<p>-0.22</p>	<p>-0.12</p>	<p>-0.26</p>	<p>-0.048</p>	<p>0.088</p>	<p>-0.65</p>	<p>-0.15</p>	<p>34000</p>	<p>25400</p>	<p>29600</p>	<p>30100</p>	<p>38400</p>	<p>36800</p>	<p>23100</p>	<p>32400</p>	<p>647.3</p>	<p>1292.7</p>	<p>2</p>	<p>0.0119</p>	<p>9.222</p>

Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr E1B8S4 E1B8S4_BOVIN, tr E1BLH2 E1BLH2_BOVIN, tr F1MEQ6 F1MEQ6_BOVIN, tr F1MRV2 F1MRV2_BOVIN	g IPH LVTH DAR	84%	38.7	52.40619	Ref	0.032	-0.04	0.039	-0.33	0.19	-0.21	-0.23	16800	14900	15400	18300	15600	19500	15500	15100	380.7	1518.8	4	0.0098	6.42
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr E1B8S4 E1B8S4_BOVIN, tr E1BLH2 E1BLH2_BOVIN, tr F1MEQ6 F1MEQ6_BOVIN, tr F1MRV2 F1MRV2_BOVIN	g IPH LVTH DAR	87%	40.1	52.51823	Ref	0.29	0.047	-0.14	-0.42	-0.02	-0.18	-0.38	10100	9610	8810	8700	7910	9110	8480	7340	380.7	1518.8	4	0.008	5.289
Uncharacterized protein OS=Bos taurus PE=4 SV=1	tr E1B8S4 E1B8S4_BOVIN, tr E1BLH2 E1BLH2_BOVIN, tr F1MEQ6 F1MEQ6_BOVIN, tr F1MRV2 F1MRV2_BOVIN	v ND TIQI DLET GK	88%	44	53.82523	Ref	0.32	-0.19	0.064	-0.22	-0.11	-0.15	-0.11	5090	6170	4720	6310	5710	5400	5460	5580	685.4	2053.1	3	0.0151	7.334

Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2	6 UCHL1_HUMAN,sp P23356 UCHL1_BOVIN,sp Q60HC8 UCHL1_MACFA,sp Q6SEG5 UCHL1_PIG,sp Q9GM50 UCHL1_HORSE,tr A6NLJ7 A6NLJ7_HUMAN,tr B2RD14 B2RD14_HUMAN,tr D6R956 D6R956_HUMAN,tr D6R974 D6R974_HUMAN,tr D6RBT8 D6RBT8	nEAI QAA HDA VAQ EGQ cR	95%	77.6	50.81117	Ref	-0.35	-0.19	-0.45	-0.084	-0.52	0.027	-0.38	6900	4720	5720	5340	7600	4890	7480	5590	754.4	2260	3	0.0174	7.71
Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2	6 UCHL1_HUMAN,sp P23356 UCHL1_BOVIN,sp Q60HC8 UCHL1_MACFA,sp Q6SEG5 UCHL1_PIG,sp Q9GM50 UCHL1_HORSE,tr A6NLJ7 A6NLJ7_HUMAN,tr B2RD14 B2RD14_HUMAN,tr D6R956 D6R956_HUMAN,tr D6R974 D6R974_HUMAN,tr D6RBT8 D6RBT8	nEAI QAA HDA VAQ EGQ cR	95%	76.9	50.86563	Ref	-0.28	-0.05	-0.55	-0.14	-0.4	-0.04	-0.45	7190	5210	6660	5260	7740	5620	7530	5630	754.4	2260	3	0.016	7.073

Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2	6 UCHL1_HUMAN,sp P23356 UCHL1_BOVIN,sp Q60HC8 UCHL1_MACFA,sp Q6SEG5 UCHL1_PIG,sp Q9GM50 UCHL1_HORSE,tr A6NLJ7 A6NLJ7_HUMAN, tr B2RD14 B2RD14_HUMAN, tr D6R956 D6R956_HUMAN, tr D6R974 D6R974_HUMAN, tr D6RBT8 D6RBT8	qFLS ETEK	62%	31	50.00629	Ref	-0.35	-0.12	-0.57	-0.12	-0.79	0.27	-0.6	670	422	537	443	667	366	798	431	634.8	1267.6	2	0.0176	13.84
Actin-like protein (Fragment) OS=Homo sapiens GN=ACT PE=2 SV=1	tr Q562Z4 Q562Z4_HUMAN	tTGI VMD SGD GVT HTV PIYK GYAL PHAIR	61%	35.3	55.93386	Ref	0.12	-0.59	-0.11	-0.071	Value Missing (-1.5767647)	0.42	-0.11	164	155	103	161	183	Value Missing (-1.5767647)	235	161	872.5	3485.8	4	0.0797	22.87
Actin-like protein (Fragment) OS=Homo sapiens GN=ACT PE=2 SV=1	tr Q562Z4 Q562Z4_HUMAN	vAPE EHP VLLT EAPL NPK	72%	36.4	52.74303	Ref	-0.12	-0.21	-0.21	-0.2	-0.24	0.067	-0.58	29200	20300	20800	23200	25900	21900	28300	18000	854.8	2561.5	3	0.005	1.946

Actin-like protein (Fragment) OS=Homo sapiens GN=ACT PE=2 SV=1	tr Q562Z4 Q562Z4_HUMAN	vAPE EHP VLLT EAPL NPK	95%	70.1	53.32305	Ref	-0.16	-0.12	-0.17	-0.098	-0.2	0.069	-0.43	2420	2020	2260	2450	2830	2310	2900	2030	1282	2561.4	2	0.0197	7.704
Prolyl 4-hydroxylase subunit alpha-1 OS=Bos taurus GN=P4HA1 PE=1 SV=1	sp Q1RMU3 P4HA1_BOVIN, tr A6QL77 A6QL77_BOVIN	gAA VDYL PER	60%	32.8	51.97215	Ref	-0.015	0.51	-0.15	0.027	-0.49	0.58	-0.49	18600	16800	26300	18700	23200	14100	31000	14700	697.9	1393.7	2	0.0118	8.474
Prolyl 4-hydroxylase subunit alpha-1 OS=Bos taurus GN=P4HA1 PE=1 SV=1	sp Q1RMU3 P4HA1_BOVIN, tr A6QL77 A6QL77_BOVIN	sSSD DQS DQk	72%	34.6	51.04705	Ref	-0.18	0.87	-0.48	-0.14	-0.74	0.84	-1	7280	5570	12500	5520	7700	4430	13900	3770	569	1703.8	3	0.0128	7.512
Prolyl 4-hydroxylase subunit alpha-1 OS=Bos taurus GN=P4HA1 PE=1 SV=1	sp Q1RMU3 P4HA1_BOVIN, tr A6QL77 A6QL77_BOVIN	sSSD DQS DQk	95%	46.3	51.04705	Ref	-0.27	0.85	-0.63	0.021	-0.64	0.78	-0.94	2450	1700	4000	1620	2800	1540	4330	1300	852.9	1703.8	2	0.0128	7.503
Uncharacterized protein OS=Equus caballus GN=Eca.4103 PE=4 SV=1	tr F7D6B3 F7D6B3_HORSE	qLLL ESQS QLD AAk	78%	38.3	52.91806	Ref	-0.065	-0.17	-0.23	-0.22	-0.21	-0.26	-0.16	5570	5090	5120	5520	6120	5380	5430	5790	718.1	2151.2	3	0.0091	4.244

Uncharacterized protein OS=Equus caballus GN=Eca.4103 PE=4 SV=1	tr F7D6B3 F7D6B3_HORSE	qNA ELAK	55%	31	50.99802	Ref	-0.27	-0.19	-0.25	-0.21	-0.14	-0.21	-0.21	9370	6740	7730	8340	9480	8670	8630	8570	691.4	1380.8	2	0.0215	15.54
Uncharacterized protein OS=Equus caballus GN=Eca.4103 PE=4 SV=1	tr F7D6B3 F7D6B3_HORSE	sEGT PNQ Gk	80%	37.9	52.69782	Ref	-0.43	-0.06	-0.16	-0.22	0.029	-0.48	-0.26	10700	6720	9440	9860	10400	10800	7930	9200	763.4	1524.8	2	0.0051	3.342
Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Bos taurus GN=NUCKS1 PE=2 SV=1	sp Q29S11 NUCKS1_BOVIN	aTVT PSPV k	61%	30.1	49.2139	Ref	-0.31	-0.01	-0.07	0.037	0.19	-0.18	-0.11	16700	12700	17000	18300	21800	21000	17100	17700	754.5	1506.9	2	0.0057	3.793
Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Bos taurus GN=NUCKS1 PE=2 SV=1	sp Q29S11 NUCKS1_BOVIN	aTVT PSPV k	91%	43.3	50.27639	Ref	-0.028	-0.1	-0.15	-0.007	-0.01	-0.19	-0.06	21500	18300	18900	20400	24900	21700	20000	21800	503.3	1506.9	3	0.0235	15.59

Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Bos taurus GN=NUCKS1 PE=2 SV=1	sp Q29S11 NUCKS_BOVIN	ekTP SPkE EDEE PESP LEK	74%	37.6	55.41645	Ref	-0.74	-0.36	0.13	-0.003	0.48	-0.66	0.17	4440	2280	3200	5050	5080	6190	2940	5170	854.5	3413.8	4	0.0211	6.19
40S ribosomal protein S9 OS=Bos taurus GN=RPS9 PE=2 SV=1	5 RS9_BOVIN,sp A9L913 RS9_PAPAN,sp P29314 RS9_RAT,sp P46781 RS9_HUMAN,sp Q6ZWN5 RS9_MOUSE,tr A9C4C1 A9C4C1_HUMAN,tr B0VXI8 B0VXI8_CALJA,tr B2KIM3 B2KIM3_RHIFE,tr B3RFF7 B3RFF7_SO RAR,tr B5FWB6 B5FWB6_OT OGA,tr B7NZS8 B7	kGQ GGA GAG DDE EED	95%	63.8	50.28067	Ref	-0.028	0.16	0.25	0.12	0.33	-0.17	0.18	7250	6190	7620	9110	9210	9310	6870	8700	681.7	2041.9	3	0.0178	8.694

40S ribosomal protein S9 OS=Bos taurus GN=RPS9 PE=2 SV=1	5 RS9_BOVIN,sp A9L913 RS9_PAPAN,sp P29314 RS9_RAT,sp P46781 RS9_HUMAN,sp Q6ZWN5 RS9_MOUSE,trans A9C4C1 A9C4C1_HUMAN,trans B0VXI8 CALJA,trans B2KIM3 B2KIM3_RHIFE,trans B3RFF7 B3RFF7_SO RAR,trans B5FWB6 B5FWB6_OTOGA,trans B7N2S8 B7	kGQ GGA GAG DDE EED	95%	47.3	50.3527	Ref	-0.21	0.16	0.53	0.094	0.3	-0.39	0.065	4580	3070	4290	6220	5070	5090	3310	4500	1022	2041.9	2	0.016	7.82
40S ribosomal protein S9 OS=Bos taurus GN=RPS9 PE=2 SV=1	5 RS9_BOVIN,sp A9L913 RS9_PAPAN,sp P29314 RS9_RAT,sp P46781 RS9_HUMAN,sp Q6ZWN5 RS9_MOUSE,trans A9C4C1 A9C4C1_HUMAN,trans B0VXI8 CALJA,trans B2KIM3 B2KIM3_RHIFE,trans B3RFF7 B3RFF7_SO RAR,trans B5FWB6 B5FWB6_OTOGA,trans B7N2S8 B7	kQV VNIP SFIV R	52%	27.7	48.07075	Ref	0.42	-0.27	0.39	-0.011	0.053	0.061	0.16	4850	5670	3810	6750	5650	5150	5410	5740	670.1	2007.2	3	0.0102	5.075

Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	6 VDAC1_HUMAN,sp P45879 VDAC1_BOVIN,sp Q60932 VDAC1_MOUSE,sp Q9M216 VDAC1_PIG,sp Q9TT15 VDAC1_RABIT,sp Q9Z2L0 VDAC1_RAT,trans B2LYK9 B2LYK9_SH EEP,trans B3KTS5 B3KTS5_HUMAN,trans B4DEI3 B4DEI3_HUMAN,trans E7ER14 E7ER14_HUMAN	gYGF GLJK	51%	29.9	50.62093	Ref	0.88	0.34	0.32	-0.13	0.096	-0.09	-0.01	10200	16300	12100	13400	10800	11100	10200	10600	731.9	1461.9	2	0.0046	3.158
Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	6 VDAC1_HUMAN,sp P45879 VDAC1_BOVIN,sp Q60932 VDAC1_MOUSE,sp Q9M216 VDAC1_PIG,sp Q9TT15 VDAC1_RABIT,sp Q9Z2L0 VDAC1_RAT,trans B2LYK9 B2LYK9_SH EEP,trans B3KTS5 B3KTS5_HUMAN,trans B4DEI3 B4DEI3_HUMAN,trans E7ER14 E7ER14_HUMAN	vNN SSLI GLG YTQT LkPG ik	95%	47.8	48.83707	Ref	0.62	0.12	0.31	0.019	0.011	0.26	0.13	1310	1570	1210	1550	1400	1210	1510	1370	754.7	3014.8	4	0.0111	3.678

Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	6 VDAC1_HUMAN,sp P45879 VDAC1_BOVIN,sp Q60932 VDAC1_MOUSE,sp Q9MZ16 VDAC1_PIG,sp Q9TT15 VDAC1_RABIT,sp Q9Z2LO VDAC1_RAT,tr B2LYK9 B2LYK9_SH EEP,tr B3KTS5 B3KTS5_HUMAN,tr B4DEI3 B4DEI3_HUMAN,tr E7ER14_HUMAN	vnNS SLIG LGYT QTLk	PGIK	86%	37.9	50.83062	Ref	0.7	-0.01	0.35	-0.14	0.27	0.3	0.21	3680	5870	3900	5590	4400	5100	5440	5100	754.9	3015.7	4	0.0279	9.262
Uncharacterized protein (Fragment) OS=Equus caballus GN=TOR1AIP2 PE=4 SV=1	tr F6U4U7 F6U4U7_HORSE	aAV	VHR	91%	42.1	48.39918	Ref	0.25	0.046	0.48	-0.25	0.63	-0.52	-0.26	3800	3570	3370	5120	3390	5450	2570	3060	319.5	955.58	3	0.0036	3.735
Uncharacterized protein (Fragment) OS=Equus caballus GN=TOR1AIP2 PE=4 SV=1	tr F6U4U7 F6U4U7_HORSE	aAV	VHR	89%	39.7	48.35062	Ref	0.34	-0.15	0.65	-0.59	0.75	-0.46	-0.17	4600	5410	4170	8160	3810	8390	3800	4620	319.5	955.59	3	0.0017	1.791

Uncharacterized protein (Fragment) OS=Equus caballus GN=TOR1AIP2 PE=4 SV=1	tr F6U4U7 F6U4U7_HORSE	iSHL VLPV QPV R	66%	30.4	48.04705	Ref	0.26	0.2	0.098	-0.038	0.16	0.078	0.1	3030	3150	3280	3430	3440	3450	3400	3430	554.7	1661	3	0.0065	3.923
Prolyl 4-hydroxylase subunit alpha-2 OS=Mus musculus GN=P4ha2 PE=2 SV=1	6 P4HA2_MOUSE, tr B5FW61 B5FW61_OTOGA, tr C3PT80 C3PT80_DASNO, tr D2GVH1 D2GVH1_AILME, tr F1MJQ4 F1MJQ4_BOVIN, tr F6PQC1 F6PQC1_HORSE, tr F6PQW4 F6PQW4_HORSE, tr Q3SYY3 Q3SYY3_BOVIN, tr Q5SX74 Q5SX74_MOUSE, tr Q5SX75 Q5SX75_QSLK	dLV	59%	32.2	51.58378	Ref	-0.18	0.27	-0.25	-0.24	-0.63	0.064	-0.5	22800	16500	24500	19200	21300	14200	24000	16100	705.9	1409.8	2	0.0232	16.42

Serine/threonine-protein kinase PAK2 OS=Rattus norvegicus GN=Pak2 PE=1 SV=1	sp Q64303 PAK2_RAT, tr F1S2QW0 F1S2QW0_PIG	iISIFS STEK	71%	34.8	51.40024	Ref	0.13	-0.2	0.3	-0.24	-0.16	-0.15	0.26	3710	4080	3510	5590	4240	3900	4120	5410	578.3	1732	3	0.0027	1.548
Serine/threonine-protein kinase PAK2 OS=Rattus norvegicus GN=Pak2 PE=1 SV=1	sp Q64303 PAK2_RAT, tr F1S2QW0 F1S2QW0_PIG	iISIFS STEK	85%	40.3	51.94733	Ref	-0.21	-0.2	0.1	-0.11	0.066	-0.26	0.28	2420	1690	1840	2550	2420	2390	1990	2870	578.3	1732	3	0.0138	7.988
Serine/threonine-protein kinase PAK2 OS=Rattus norvegicus GN=Pak2 PE=1 SV=1	sp Q64303 PAK2_RAT, tr F1S2QW0 F1S2QW0_PIG	KNP QAV LDVL k	78%	33.2	47.53124	Ref	-0.048	0.015	-0.03	-0.047	0.057	-0.05	-0.05	5420	4560	5170	5640	6130	5750	5570	5510	713.1	2136.3	3	0.0265	12.38
SRA stem-loop-interacting RNA-binding protein OS=Ovis aries GN=SLIRP PE=4 SV=1	tr B9VGZ7 B9VGZ7_SHEEP	eHF AQF GHV R	75%	35.6	51.71589	Ref	-0.12	0.15	0.23	0.15	0.4	-0.07	0.41	6470	4420	5760	6840	7180	7450	5610	7760	766.4	1530.8	2	0.0116	7.552

SRA stem-loop-interacting RNA-binding protein OS=Ovis aries GN=SLIRP PE=4 SV=1	tr B9VGZ7 B9VGZ7_SHEEP	eHF AQF GHV R	88%	40.5	51.7302	Ref	-0.006	0.022	0.44	-0.14	0.53	-0.57	0.77	10200	8870	9820	14700	10800	15100	7340	18500	383.7	1530.8	4	0.0103	6.698
SRA stem-loop-interacting RNA-binding protein OS=Ovis aries GN=SLIRP PE=4 SV=1	tr B9VGZ7 B9VGZ7_SHEEP	kIPW TAAS GELR	71%	35.6	52.14592	Ref	0.2	0.095	0.28	0.16	0.41	0.018	0.26	6970	6950	7020	8940	9060	9440	7510	8820	646.4	1936.1	3	0.0111	5.73
60S ribosomal protein L26 OS=Rattus norvegicus GN=Rpl26 PE=1 SV=1	9 RL26_RAT,sp P61254 RL26_HUMAN,sp P61255 RL26_MOUSE,sp P61256 RL26_MACFA,sp P61257 RL26_BOVIN,sp A6NE05 A6NE05_HUMAN,sp B1AR_A3 B1AR_A3_MOUSE,sp B1AR_A5 B1AR_A5_MOUSE,sp D4A12 D4A12_RAT,sp E2QUE7 E2QUE7_CAN,sp F	hFN APS HIR	86%	38.9	51.86386	Ref	0.39	0.083	0.94	0.09	1.2	0.084	0.9	5150	6030	5280	10700	6570	12100	5960	10400	346.4	1381.7	4	0.0113	8.137

60S ribosomal protein L26 OS=Rattus norvegicus GN=Rpl26 PE=1 SV=1	9 RL26_R AT,sp P61254 RL26_HUMAN,sp P61255 RL26_MOUSE,sp P61256 RL26_MACFA,sp P61257 RL26_BOVIN,tr A6NE05 A6NE05_HUMAN,tr B1AR A3 B1AR A3_MOUSE, E,tr B1AR A5 B1AR A5_MOUSE, E,tr D4A1Z2 D4A1Z2_RAT,tr E2QUE7 E2QUE7_C ANFA,tr F	hFN APS HIR	89%	41.2	51.90475	Ref	0.48	0.11	0.95	0.16	1.1	-0.1	0.91	1850	2240	1880	3770	2410	4050	1840	3680	346.4	1381.7	4	0.0077	5.562
60S ribosomal protein L26 OS=Rattus norvegicus GN=Rpl26 PE=1 SV=1	9 RL26_R AT,sp P61254 RL26_HUMAN,sp P61255 RL26_MOUSE,sp P61256 RL26_MACFA,sp P61257 RL26_BOVIN,tr A6NE05 A6NE05_HUMAN,tr B1AR A3 B1AR A3_MOUSE, E,tr B1AR A5 B1AR A5_MOUSE, E,tr D4A1Z2 D4A1Z2_RAT,tr E2QUE7 E2QUE7_C ANFA,tr F	kIMS SPLS	62%	32.2	50.73014	Ref	0.37	0.43	0.68	0.5	0.67	0.54	0.79	11600	12300	13900	18500	18000	17700	17000	20100	635.1	1902.1	3	0.0345	18.12

60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1 SV=4	3 RL13A_MOUSE,sp P40429 RL13A_HUMAN,sp Q3SZ90 RL13A_BOVIN,sp Q4R8Z2 RL13A_MAL13A_MA_CFA,sp Q5RA38 RL13A_PONAB,sp Q95307 RL13A_PIG,sp Q9XSU0 RL13A_CANFA,tr D2H7V7 D2H7V7_AILME,tr E2RLF4 E2RLF4_CANFA,tr E9Q5A0 E9Q5A0_MOUSE	gHLL GR	74%	32.7	48.52327	Ref	0.3	0.35	0.78	-0.16	0.69	-0.04	0.18	9880	10600	11900	18000	10300	16200	10200	11800	319.5	955.57	3	0.0124	12.99
60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1 SV=4	3 RL13A_MOUSE,sp P40429 RL13A_HUMAN,sp Q3SZ90 RL13A_BOVIN,sp Q4R8Z2 RL13A_MAL13A_MA_CFA,sp Q5RA38 RL13A_PONAB,sp Q95307 RL13A_PIG,sp Q9XSU0 RL13A_CANFA,tr D2H7V7 D2H7V7_AILME,tr E2RLF4 E2RLF4_CANFA,tr E9Q5A0 E9Q5A0_MOUSE	gHLL GR	81%	34.9	48.35062	Ref	0.43	0.28	0.83	-0.11	0.59	-0.04	0.18	5320	6550	6380	10500	6060	8530	5780	6700	319.5	955.59	3	0.0018	1.888

60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1 SV=4	3 RL13A_MOUSE,sp P40429 RL13A_HUMAN,sp Q35Z90 RL13A_BOVIN,sp Q4R8Z2 RL13A_MALCFA,sp Q5RA38 RL13A_PONAB,sp Q95307 RL13A_PIG,sp Q9XSU0 RL13A_CANFNA,tr D2H7V7 D2H7V7_AILME,tr E2RLF4 E2RLF4_CANFA,tr E9Q5A0 E9Q5A0_MOUSE	mVV PAAL k	75%	33.2	48.54743	Ref	0.32	0.099	0.51	0.2	0.37	0.26	0.33	6940	6290	5850	8700	7770	7640	7370	7700	479.6	1435.9	3	0.0247	17.16
MCG124046 OS=Mus musculus GN=Prss1 PE=2 SV=1	tr Q9Z1R9 Q9Z1R9_MOUSE	IGEH NinV LEG NEQ FIDA Ak	88%	43.7	55.27145	Ref	-0.031	-0.33	0.024	-0.05	0.075	-0	0.48	65900	56100	49600	71000	74300	70800	70100	97300	705.9	2819.5	4	0.0045	1.601
MCG124046 OS=Mus musculus GN=Prss1 PE=2 SV=1	tr Q9Z1R9 Q9Z1R9_MOUSE	IGEH NinV LEG NEQ FIDA Ak	78%	38.8	55.33054	Ref	0.077	-0.13	-0.04	-0.028	0.095	-0.22	0.41	10000	8960	8430	10100	11200	10600	8900	13800	705.9	2819.5	4	0.0196	6.962
MCG124046 OS=Mus musculus GN=Prss1 PE=2 SV=1	tr Q9Z1R9 Q9Z1R9_MOUSE	tLnN DIML ik	59%	33.2	52.27625	Ref	0.88	-0.18	-0.04	-0.26	-0.1	-0.06	-0.18	2590	4570	2380	2950	2800	2730	2910	2660	595.3	1783	3	0.013	7.308

40S ribosomal protein S7 OS=Bos taurus GN=RPS7 PE=2 SV=1	9 RS7_BOVIN,sp P62081 RS7_HUMAN,sp P62082 RS7_MOUSE,sp P62083 RS7_RAT,sp Q5RT64 RS7_FELCA,tr B5DEL9 B5DEL9_RAT,tr B5MCP9 B5MCP9_HUMAN,tr D2I2A9 D2I2A9_AILME,tr E2R8A8 E2R8A8_CANFA,tr F66SVV1 F6SVV1_MOUSE,tr F6Y6J2 F6Y6	hVVF	71%	34	50.4093	Ref	0.45	-0.09	0.6	-0.028	0.025	0.14	0.39	7880	9980	7460	13500	9630	8720	9870	11600	425.3	1272.8	3	0.0083	6.527
40S ribosomal protein S7 OS=Bos taurus GN=RPS7 PE=2 SV=1	9 RS7_BOVIN,sp P62081 RS7_HUMAN,sp P62082 RS7_MOUSE,sp P62083 RS7_RAT,sp Q5RT64 RS7_FELCA,tr B5DEL9 B5DEL9_RAT,tr B5MCP9 B5MCP9_HUMAN,tr D2I2A9 D2I2A9_AILME,tr E2R8A8 E2R8A8_CANFA,tr F66SVV1 F6SVV1_MOUSE,tr F6Y6J2 F6Y6	hVVF	74%	34.6	50.21731	Ref	0.71	-0.24	0.52	-0.032	0.086	0.11	0.18	12100	17100	9600	18300	13800	13000	13900	14500	425.3	1272.8	3	0.008	6.315

40S ribosomal protein S7 OS=Bos taurus GN=RPS7 PE=2 SV=1	9 RS7_BOVIN,sp P62081 RS7_HUMAN,sp P62082 RS7_MOUSE,sp P62083 RS7_RAT,sp Q5RT64 RS7_FELCA,tr B5DEL9 B5DEL9_RAT,tr B5MCP9 B5MCP9_HUMAN,tr D2I2A9 D2I2A9_AILME,tr E2R8A8 E2R8A8_CANFA,tr F6SVV1 F6SVV1_MOUSE, tr F6Y6I2 F6Y6	kAIII FVPV PQLK	79%	23.2	39.08646	Ref	0.28	0.46	0.27	-0.058	-0.08	0.29	0.3	665	690	847	834	733	631	849	851	595.4	2377.5	4	0.0353	14.83
Heterogeneous nuclear ribonucleoprotein G OS=Pan troglodytes GN=RBMX PE=2 SV=1	M3 HNRPG_PANTR,sp P38159 HNRPG_HUMAN, tr A2AFI3 A2AFI3_MOUSE, tr C0SSX0 C0SSX0_9MURI, tr D2HD91 D2HD91_AILME, tr D3JUI8 D3JUI8_BOVIN, tr F1RQ90 F1RQ90_PIG, tr F6XJB9 F6XJB9_HORSE, tr F7EC60 F7EC60_CALJA, tr F7HGT3 F7HGT3_CALJ	iVEV LLMk	77%	33.6	48.37134	Ref	0.29	0.17	-0.52	-0.51	-0.48	-0.02	-0.07	774	819	823	571	634	564	814	780	518.3	1552	3	0.0102	6.564

Heterogeneous nuclear ribonucleoprotein G OS=Pan troglodytes GN=RBMX PE=2 SV=1	M3 HNRPG_PANTR,sp P38159 HNRPG_HUMAN, tr A2AFI3 A2AFI3_MOUSE, tr COSSX0 COSSX0_9MURI, tr D2HD91 D2HD91_AILME, tr D3JUI8 D3JUI8_BOVIN, tr F1RQ90 F1RQ90_PIG, tr F6XJB9 F6XJB9_HORSE, tr F7EC60 F7EC60_CALJA, tr F7HGT3 F7HGT3_CALJ	iVEV	88%	37.6	47.36604	Ref	-0.13	-0.13	-0.21	-0.27	-0.53	-0.18	0.18	1010	681	742	787	828	606	804	1030	518.3	1552	3	#####	0.073
	M3 HNRPG_PANTR,sp P38159 HNRPG_HUMAN, tr A2AFI3 A2AFI3_MOUSE, tr COSSX0 COSSX0_9MURI, tr D2HD91 D2HD91_AILME, tr D3JUI8 D3JUI8_BOVIN, tr F1RQ90 F1RQ90_PIG, tr F6XJB9 F6XJB9_HORSE, tr F7EC60 F7EC60_CALJA, tr F7HGT3 F7HGT3_CALJ	rEPL PSR	52%	29.2	49.56903	Ref	-0.17	0.32	-0.09	-0.32	-0	-0.47	-0.11	28900	25500	38800	32800	30900	33500	25400	32200	386.9	1157.7	3	0.013	11.22

Intercellular adhesion molecule-1 OS=Ovis aries GN=ICAM-1 PE=2 SV=1	tr O97692 O97692_SHEEP	kLQT YVLP STDP HLEA PPV VEV GSR	75%	36.7	53.96074	Ref	-0.28	-1.4	0.059	-0.42	-0.37	-1.4	0.23	3590	2960	1440	4560	3610	3250	1720	5140	836	3339.8	4	0.0201	6.027
Intercellular adhesion molecule-1 OS=Ovis aries GN=ICAM-1 PE=2 SV=1	tr O97692 O97692_SHEEP	kLQT YVLP STDP HLEA PPV VEV GSR	75%	36.6	53.99857	Ref	-0.46	-1.2	-0.19	-0.35	-0.16	-1.1	-0.01	736	466	303	685	674	670	372	774	836	3339.8	4	0.0216	6.47
Intercellular adhesion molecule-1 OS=Ovis aries GN=ICAM-1 PE=2 SV=1	tr O97692 O97692_SHEEP	qPV GKEE PAEV TFM VQP R	73%	39	55.10313	Ref	-0.71	-0.82	0.041	-0.31	-0.69	-1.2	-0.07	5030	2280	2300	4670	4050	2700	1970	4330	884.1	2649.4	3	0.0242	9.116

Elongation factor 1- gamma OS=Equus caballus GN=EEF1G PE=2 SV=1	7 EF1G_H ORSE,sp P29694 E F1G_RABI T,sp Q3SZ V3 EF1G_ BOVIN,sp Q4R7H5 EF1G_M ACFA,tr D 2HS91 D2 HS91_AIL ME,tr F1 MG05 F1 MG05_BO VIN,tr F7 HML3 F7 HML3_M ACMU,tr F7IIA5 F7 IIA5_CALJ A,tr F7IIA 9 F7IIA9_ CALJA,tr Q1JPA2 Q1JPA2_B OVIN,tr Q	aVLG Evk	66%	31.4	49.06782	Ref	0.017	-0.35	-0.22	-0.26	-0.33	0.12	-0.21	9600	8640	7260	8920	9550	7940	11300	8970	442	1322.8	3	0.0044	3.299
Elongation factor 1- gamma OS=Equus caballus GN=EEF1G PE=2 SV=1	7 EF1G_H ORSE,sp P29694 E F1G_RABI T,sp Q3SZ V3 EF1G_ BOVIN,sp Q4R7H5 EF1G_M ACFA,tr D 2HS91 D2 HS91_AIL ME,tr F1 MG05 F1 MG05_BO VIN,tr F7 HML3 F7 HML3_M ACMU,tr F7IIA5 F7 IIA5_CALJ A,tr F7IIA 9 F7IIA9_ CALJA,tr Q1JPA2 Q1JPA2_B OVIN,tr Q	iLGLL DAH Lk	80%	33.1	46.90763	Ref	0.3	-0.54	-0.2	-0.18	-0.47	0.032	-0.34	3730	4000	2420	3450	3850	2740	4060	3110	567.7	1700.1	3	#####	0.169

Elongation factor 1-gamma OS=Equus caballus GN=EEF1G PE=2 SV=1	7 EF1G_H ORSE,sp P29694 E F1G_RABI T,sp Q3SZ V3 EF1G_ BOVIN,sp Q4R7H5 EF1G_M ACFA,tr D 2HS91 D2 HS91_AIL ME,tr F1 MG05 F1 MG05_BO VIN,tr F7 HML3 F7 HML3_M ACMU,tr F7IIA5 F7 IIA5_CALJ A,tr F7IIA 9 F7IIA9_ CALJA,tr Q1JPA2 Q1JPA2_B OVIN,tr Q	iLGLL DAH	Lk	70%	30.8	47.68082	Ref	0.1	-0.31	-0.09	-0.3	-0.36	0.052	-0.41	832	771	629	819	784	655	912	657	567.7	1700.1	3	0.0107	6.306
Eukaryotic translation initiation factor 2 subunit 2 OS=Oryctolagus cuniculus GN=EIF2S2 PE=1 SV=1	sp P4103 5 IF2B_R ABIT,sp Q 5E9D0 IF 2B_BOVIN ,tr D2H43 1 D2H431 _AILME,tr F1P247 F1P247_C ANFA,tr F 1S4Y8 F1 S4Y8_PIG, tr F7DE88 F7DE88_ HORSE	dYTY EELL	NR	69%	33.6	51.16611	Ref	0.26	-0.11	0.4	0.21	0.45	-0.22	0.48	5560	5930	4960	7960	7690	7920	5180	8380	810.4	1618.8	2	0.0133	8.198

Eukaryotic translation initiation factor 2 subunit 2 OS=Oryctolagus cuniculus GN=EIF2S2 PE=1 SV=1	sp P41035 IF2B_RABIT,sp Q5E9D0 IF2B_BOVIN, tr D2H431 D2H431_AILME, tr F1PZ47 F1PZ47_C ANFA, tr F1S4Y8 F1S4Y8_PIG, tr F7DE88 F7DE88_HORSE	dYTYEELLNR	55%	31.2	51.26271	Ref	0.38	-0.34	0.21	0.3	0.4	0.14	0.37	4820	5460	3580	5920	6950	6470	5650	6600	810.4	1618.8	2	0.0122	7.519
Eukaryotic translation initiation factor 2 subunit 2 OS=Oryctolagus cuniculus GN=EIF2S2 PE=1 SV=1	sp P41035 IF2B_RABIT,sp Q5E9D0 IF2B_BOVIN, tr D2H431 D2H431_AILME, tr F1PZ47 F1PZ47_C ANFA, tr F1S4Y8 F1S4Y8_PIG, tr F7DE88 F7DE88_HORSE	eVEPEPTEDKDVEADEEDSR	73%	36.5	52.39727	Ref	0.14	0.08	0.28	0.12	0.49	-0.33	0.35	9570	7290	7570	9760	9610	10900	6410	10200	976.1	2925.4	3	0.0257	8.78
Uncharacterized protein OS=Monodelphis domestica GN=PDIA4 PE=3 SV=1	tr F6SNH9 F6SNH9_MONDO	fDVTGYPTLk	78%	38.4	52.92885	Ref	-0.019	0.037	-0.1	-0.12	-0.2	0.21	-0.18	5310	4560	5140	5240	5700	4720	6540	4960	583.7	1748	3	0.0072	4.117

Uncharacterized protein OS=Monodelphis domestica GN=PDIA4 PE=3 SV=1	tr F6SNH9 F6SNH9_MONDO	nLVI Ak	57%	25.3	45.07694	Ref	-0.065	-0.05	0.03	-0.099	-0.03	-0.19	0.027	19800	16100	17700	20900	21100	19400	18000	20800	633.4	1264.8	2	0.0028	2.202
Uncharacterized protein OS=Monodelphis domestica GN=PDIA4 PE=3 SV=1	tr F6SNH9 F6SNH9_MONDO	nLVI Ak	62%	26.6	45.07694	Ref	0.32	-0.08	-0.2	-0.45	0.061	-0.01	-0.07	5880	6470	5300	5500	5080	6330	6300	6000	422.6	1264.8	3	0.0026	2.088
Cytochrome c OS=Equus caballus GN=CYCS PE=1 SV=2	4 CYC_HORSE,sp P00007 CYC_HIPAM,sp P00008 CYC_RABBIT,sp P00011 CYC_CANFA,sp P00012 CYC_MIRLE,sp P00013 CYC_MINSC,sp P62894 CYC_BOVIN,sp P62895 CYC_PIG,sp P62896 CYC_SHEEP,sp P62897 CYC_MOUSE,sp P62898 CYC_RAT,sp P6809	mIFA Gik	59%	30.6	49.70375	Ref	-0.21	0.33	0.25	0.38	0.74	0.092	0.87	6260	4620	7300	7750	9350	10500	6990	11900	463.3	1386.9	3	0.0018	1.289

Cytochrome c OS=Equus caballus GN=CYCS PE=1 SV=2	4 CYC_H ORSE,sp P00007 C YC_HIPA M,sp P00 008 CYC_ RABIT,sp P00011 C YC_CANF A,sp P000 12 CYC_ MIRLE,sp P00013 C YC_MINS C,sp P628 94 CYC_B OVIN,sp P62895 C YC_PIG,sp P62896 CYC_SHEE P,sp P628 97 CYC_ MOUSE,s p P62898 CYC_RAT ,sp P6809	mIFA Glik	56%	31.4	51.09511	Ref	-0.56	0.41	0.29	0.53	0.86	0.029	0.94	9460	7280	15400	15900	20700	22800	13400	24900	463.3	1386.8	3	0.0233	16.79
Cytochrome c OS=Equus caballus GN=CYCS PE=1 SV=2	4 CYC_H ORSE,sp P00007 C YC_HIPA M,sp P00 008 CYC_ RABIT,sp P00011 C YC_CANF A,sp P000 12 CYC_ MIRLE,sp P00013 C YC_MINS C,sp P628 94 CYC_B OVIN,sp P62895 C YC_PIG,sp P62896 CYC_SHEE P,sp P628 97 CYC_ MOUSE,s p P62898 CYC_RAT ,sp P6809	tGPN LHGL FGR	54%	32	52.01706	Ref	-0.26	0.39	0.34	0.28	0.7	0.26	0.8	6770	4930	8390	9100	9590	11200	8630	12400	491.6	1471.8	3	0.0049	3.342

Eukaryotic translation initiation factor 3 subunit F OS=Pan troglodytes GN=EIF3F PE=2 SV=1	3 EIF3F_P ANTR,sp O00303 E IF3F_HUMAN,sp Q4R5B8 E IF3F_MACFA,sp Q9DCH4 EIF3F_MOUSE, tr B3KSH1 B3KSH1_HUMAN, tr B4DMT5 B4DMT5_HUMAN, tr D2H3J4 D2H3J4_AILME, tr D4AC36 D4AC36_RAT, tr E1BLZ8 E1BLZ8_BOVIN, tr E9PQV8 E9PQV8	IHPV ILASI VDSY ER	72%	37.2	53.34174	Ref	0.14	0.24	-0.22	0.11	0.23	0.25	0.13	312	313	363	297	410	391	413	378	672.7	2015.1	3	0.0099	4.932
Peroxisomal membrane protein PEX14 OS=Homo sapiens GN=PEX14 PE=1 SV=1	1 PEX14_HUMAN,sp Q642G4 PEX14_RAT, tr B7Z4Z4_HUMAN, tr E1BFW8 E1BFW8_BOVIN, tr F1RHS6 F1RHS6_PIG, tr F5H4J2 F5H4J2_HUMAN, tr F6SDL5 F6SDL5_HORSE, tr F6SJ43 F6SJ43_CALJA, tr F6XV44 F6XV44_CALJA, tr F7BHA3 F7BHA3_CALJA, tr	rPEG ASN ESER D	95%	52.7	49.707	Ref	-0.44	0.57	0.37	-0.2	0.46	-0.49	0.33	921	590	1290	1260	936	1290	698	1230	550.9	1649.8	3	0.0108	6.541

Peroxisomal membrane protein PEX14 OS=Homo sapiens GN=PEX14 PE=1 SV=1	1 PEX14_HUMAN,sp Q642G4 PEX14_RAT, tr B7Z4Z4 B7Z4Z4_HUMAN, tr E1BFW8 E1BFW8_BOVIN, tr F1RHS6 F1RHS6_PIG, tr F5H4J2 F5H4J2_HUMAN, tr F6SDL5 F6SDL5_HORSE, tr F6SJ43 F6SJ43_CALJA, tr F6XV44 F6XV44_CALJA, tr F7BHA3 F7BHA3_CALJA, tr	rPEG ASN ESER D	89%	41	49.70849	Ref	-0.024	0.27	0.062	-0.15	0.44	-0.21	0.31	669	501	666	647	615	809	537	768	550.9	1649.8	3	0.01	6.087
Peroxisomal membrane protein PEX14 OS=Homo sapiens GN=PEX14 PE=1 SV=1	1 PEX14_HUMAN,sp Q642G4 PEX14_RAT, tr B7Z4Z4 B7Z4Z4_HUMAN, tr E1BFW8 E1BFW8_BOVIN, tr F1RHS6 F1RHS6_PIG, tr F5H4J2 F5H4J2_HUMAN, tr F6SDL5 F6SDL5_HORSE, tr F6SJ43 F6SJ43_CALJA, tr F6XV44 F6XV44_CALJA, tr F7BHA3 F7BHA3_CALJA, tr	rPEG ASnE SERD	93%	44.7	48.95644	Ref	-0.12	0.44	0.22	-0.12	0.38	-0.43	0.45	1340	1110	1770	1710	1500	1840	1100	2000	551.3	1650.8	3	0.0069	4.199

60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	6 RLA1_H UMAN,sp P19944 RLA1_RAT ,sp Q56K 14 RLA1_ BOVIN,tr A9XSS6 A 9XSS6_AIL ME,tr D2 HF22 D2 HF22_AIL ME,tr E1 BCL5 E1B CL5_BOVI N,tr E2RP 70 E2RP7 O_CANFA, tr F1RJ90 F1RJ90_ PIG,tr F1 RN65 F1R N65_PIG,t r F1SIT7 F1SIT7_PI G,tr F6TQ 53 F6TQS	aAG VNV EPF WPG LFAK	95%	64.4	53.80658	Ref	0.29	0.32	0.24	0.27	0.36	0.46	0.52	4710	4080	4520	4780	5400	5000	5610	5810	771.1	2310.3	3	0.0138	5.968
60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	6 RLA1_H UMAN,sp P19944 RLA1_RAT ,sp Q56K 14 RLA1_ BOVIN,tr A9XSS6 A 9XSS6_AIL ME,tr D2 HF22 D2 HF22_AIL ME,tr E1 BCL5 E1B CL5_BOVI N,tr E2RP 70 E2RP7 O_CANFA, tr F1RJ90 F1RJ90_ PIG,tr F1 RN65 F1R N65_PIG,t r F1SIT7 F1SIT7_PI G,tr F6TQ 53 F6TQS	aAG VNV EPF WPG LFAK	95%	54.6	53.95277	Ref	1.8	-0.27	-0.68	0.31	-0.3	-0.19	0.75	1240	6820	1730	1460	3190	1830	2070	3930	578.6	2310.3	4	0.0236	10.19

60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	6 RLA1_HUMAN,sp P19944 RLA1_RAT,sp Q56K14 RLA1_BOVIN,tr A9XSS6 A9XSS6_AILME,tr D2HF22 D2HF22_AILME,tr E1BCL5 E1BCL5_BOVIN,tr E2RP70 E2RP70_CANFA, tr F1RJ90 F1RJ90_PIG, tr F1RN65 F1RN65_PIG, tr F1SIT7 F1SIT7_PIG, tr F6TQ53 F6TQ53 FAK	aAG VNV EPF WPG LFAK	95%	55	53.84416	Ref	-0.67	0.4	0.26	0.31	0.54	0.67	0.8	1140	622	1420	1450	1650	1690	1930	2090	771.1	2310.3	3	0.0152	6.591
Protein disulfide-isomerase A3 (Fragments) OS=Papio hamadryas GN=PDIA3 PE=1 SV=1	sp P81246 PDIA3_PAPHA	sDVL ELTD DNF ESR	95%	80.2	51.18017	Ref	-0.17	-0.2	0.12	-0.08	0.33	-0.56	0.22	26500	20400	21600	30300	29000	33600	19000	32200	972.5	1942.9	2	0.0143	7.332
Protein disulfide-isomerase A3 (Fragments) OS=Papio hamadryas GN=PDIA3 PE=1 SV=1	sp P81246 PDIA3_PAPHA	sDVL ELTD DNF ESR	93%	46.7	51.2009	Ref	-0.17	-0.01	0.16	-0.009	0.04	-0.06	0.097	12800	11500	14000	17600	17300	15700	15300	16900	648.7	1942.9	3	0.0131	6.749

Protein disulfide-isomerase A3 (Fragments) OS=Papio hamadryas GN=PDIA3 PE=1 SV=1	sp P81246 PDIA3_PAPHA	sDVL ELTD DNF ESR	95%	79.6	51.35212	Ref	-0.044	-0.11	0.13	-0.085	0.24	-0.54	0.14	6490	5470	5670	7530	7140	7790	4760	7540	972.5	1942.9	2	0.0115	5.892
Selenoprotein M OS=Sus scrofa GN=Selm PE=2 SV=1	tr C4PK53 C4PK53_PIG, tr E1BKK9 E1BKK9_BOVI N, tr F6V9B1 F6V9B1_HORSE	hLPG ADP ELVL LGH R	95%	59.4	52.91462	Ref	-0.21	0.34	0.088	0.082	0.37	-0.19	0.34	3250	2490	3960	3720	4090	4360	3090	4420	482.8	1927.1	4	0.0051	2.668
Selenoprotein M OS=Sus scrofa GN=Selm PE=2 SV=1	tr C4PK53 C4PK53_PIG, tr E1BKK9 E1BKK9_BOVI N, tr F6V9B1 F6V9B1_HORSE	hLPG ADP ELVL LGH R	95%	55.5	53.00589	Ref	0.062	0.096	0.21	0.05	0.23	0.15	0.092	3360	3000	3340	4060	4000	3940	3910	3720	643.4	1927.1	3	0.0099	5.118
Selenoprotein M OS=Sus scrofa GN=Selm PE=2 SV=1	tr C4PK53 C4PK53_PIG, tr E1BKK9 E1BKK9_BOVI N, tr F6V9B1 F6V9B1_HORSE	hLPG ADP ELVL LGH R	93%	46.6	53.00589	Ref	-0.2	0.006	0.28	0.078	0.62	-0.24	0.19	3730	2830	3530	4800	4590	5840	3360	4480	482.8	1927.1	4	0.0098	5.075

U2 small nuclear ribonucleoprotein B" OS=Homo sapiens GN=SNRPB2 PE=1 SV=1	9 RU2B_HUMAN,sp P09012 SNRPA_HUMAN,sp Q06AA4 SNRPA_PIG,sp Q2KIR1 SNRPA_BOVIN,sp Q62189 SNRPA_MOUSE,sp Q9CQI7 RU2B_MOUSE,tr A2BGM2 A2BGM2_MOUSE,tr A2CES4 A2CES4_MOUSE,tr A8QKB2 A8QKB2_MUSSP,tr B2LYL4 B2LYL4_S	gQAFVIF	89%	41.2	50.25961	Ref	0.024	-0.16	-0.05	-0.29	0.005	-0.18	0.57	4440	4170	3980	4840	4490	4820	4420	7380	506.6	1516.9	3	#####	0.277
U2 small nuclear ribonucleoprotein B" OS=Homo sapiens GN=SNRPB2 PE=1 SV=1	9 RU2B_HUMAN,sp P09012 SNRPA_HUMAN,sp Q06AA4 SNRPA_PIG,sp Q2KIR1 SNRPA_BOVIN,sp Q62189 SNRPA_MOUSE,sp Q9CQI7 RU2B_MOUSE,tr A2BGM2 A2BGM2_MOUSE,tr A2CES4 A2CES4_MOUSE,tr A8QKB2 A8QKB2_MUSSP,tr B2LYL4 B2LYL4_S	gQAFVIF	89%	41.9	50.90921	Ref	-0.24	-0.17	0.068	-0.27	0.036	-0.24	0.53	21800	15000	17000	22600	19700	21300	18400	31000	506.6	1516.9	3	0.0128	8.419

U2 small nuclear ribonucleoprotein B" OS=Homo sapiens GN=SNRPB2 PE=1 SV=1	9 RU2B_HUMAN,sp P09012 SNRPA_HUMAN,sp Q06AA4 SNRPA_PIG,sp Q2KIR1 SNRPA_BOVIN,sp Q62189 SNRPA_MOUSE,sp Q9CQI7 RU2B_MOUSE,transcript A2BGM2 A2BGM2_MOUSE,transcript A2CES4 A2CES4_MOUSE,transcript A8QKB2 A8QKB2_MUSSP,transcript B2LYL4 B2LYL4_S	gQA FVIF	67%	32.6	50.18975	Ref	0.028	-0.17	0.018	-0.12	-0.06	-0.11	0.35	1920	1700	1600	2060	2060	1880	1890	2580	506.6	1516.9	3	0.0015	0.988
Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1	2 SRSF9_HUMAN,sp Q5PPI1 SRSF9_RAT,sp Q9D0B0 SRSF9_MOUSE,transcript A4FUC6 A4FUC6_BOVIN,transcript A8K3M9 A8K3M9_HUMAN,transcript B4DFT9 B4DFT9_HUMAN,transcript D2I5D9 D2I5D9_AILME,transcript E2RK20 E2RK20_CANFA,transcript F1MWF4 F1MWF4_BOVIN,transcript F1RJ0 F1RJ0_PIG,transcript	hGLV PFAF VR	85%	40	51.62743	Ref	-0.17	-0.11	-0.2	-0.38	-0.15	-0.27	-0.03	2070	1530	1740	1830	1780	1820	1740	2050	483	1445.8	3	0.009	6.186

Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1	2 SRSF9_HUMAN,sp Q5PPI1 SRSF9_RAT,sp Q9D0B0 SRSF9_MOUSE,trans A4FUC6_BOVIN,trans A8K3M9 A8K3M9_HUMAN,trans B4DFT9 B4DFT9_HUMAN,trans D2I5D9 D2I5D9_AILME,trans E2RK20 E2RK20_CANFA,trans F1MWF4 F1MWF4_BOVIN,trans F1RJ0 F1RJ0_PIG,trans	hGLV PFAF VR	73%	35.5	51.62949	Ref	-0.16	-0.16	-0.15	-0.34	-0.15	-0.18	0.003	2630	2190	2360	2670	2590	2580	2630	2970	483	1445.8	3	0.009	6.248
Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1	2 SRSF9_HUMAN,sp Q5PPI1 SRSF9_RAT,sp Q9D0B0 SRSF9_MOUSE,trans A4FUC6_BOVIN,trans A8K3M9 A8K3M9_HUMAN,trans B4DFT9 B4DFT9_HUMAN,trans D2I5D9 D2I5D9_AILME,trans E2RK20 E2RK20_CANFA,trans F1MWF4 F1MWF4_BOVIN,trans F1RJ0 F1RJ0_PIG,trans	hGLV PFAF VR	77%	36.7	51.50812	Ref	-0.14	-0.14	-0.1	-0.35	-0.13	-0.28	-0.08	1260	999	1080	1250	1160	1180	1100	1260	483	1445.8	3	0.0051	3.532

Tax_Id=10090 Gene_Symbol=Krt2 3 Keratin, type I cytoskeletal 23	PI001214 62.1 SWI SS- PROT:Q99 PS0,REV_t r B0VXC2 B0VXC2_ CALJA,RE V_tr F1M QV2 F1M QV2_BOV IN,REV_tr F1Q463 F1Q463_C ANFA,REV _tr F6V3Z 0 F6V3Z0 _HORSE,R EV_tr F6V MW7 F6 VMW7_M ONDO,RE V_tr F6VZ M1 F6VZ M1_HORS E,REV_tr F7E356 F	vLLG ik	65%	20.9	38.85926	Ref	-0.28	-0.03	-0.34	-0.23	-0.25	-0.08	-0.52	3170	2220	2870	2590	3070	2640	3120	2280	417.6	1249.9	3	0.002	1.598
Tax_Id=10090 Gene_Symbol=Krt2 3 Keratin, type I cytoskeletal 23	PI001214 62.1 SWI SS- PROT:Q99 PS0,REV_t r B0VXC2 B0VXC2_ CALJA,RE V_tr F1M QV2 F1M QV2_BOV IN,REV_tr F1Q463 F1Q463_C ANFA,REV _tr F6V3Z 0 F6V3Z0 _HORSE,R EV_tr F6V MW7 F6 VMW7_M ONDO,RE V_tr F6VZ M1 F6VZ M1_HORS E,REV_tr F7E356 F	vLLG ik	64%	21.8	40.24937	Ref	-0.44	0.06	-0.42	-0.043	-0.33	-0.02	-0.55	11400	7260	11200	8970	12900	9220	11900	8180	625.9	1249.8	2	0.0241	19.3

PI001214 62.1 SWI SS- PROT:Q99 PS0,REV_t r B0VXC2 B0VXC2_ CALJA,RE V_tr F1M QV2 F1M QV2_BOV IN,REV_tr F1Q463 F1Q463_C ANFA,REV _tr F6V3Z 0 F6V3Z0 _HORSE,R EV_tr F6V MW7 F6 VMW7_M ONDO,RE V_tr F6VZ M1 F6VZ M1_HORS E,REV_tr F7E356 F	VLLG lk	78%	25.8	40.24937	Ref	-0.36	0.22	-0.75	0.14	-0.37	-0.07	-0.76	3720	2530	4110	2360	4800	2940	3780	2320	417.6	1249.8	3	0.0219	17.55	
Vasodilator- stimulated phosphoprotein OS=Bos taurus GN=VASP PE=2 SV=3	sp Q2TA4 9 VASP_B OVIN	dESA NQE ESDA R	95%	48	46.63041	Ref	-0.83	-0.06	-0.91	-0.23	-0.49	-0.6	-0.78	3180	1440	2680	1660	2930	2140	2070	1810	827.9	1653.7	2	0.0078	4.706
Vasodilator- stimulated phosphoprotein OS=Bos taurus GN=VASP PE=2 SV=3	sp Q2TA4 9 VASP_B OVIN	qEEA SAG PVA Pk	95%	67.7	53.4505	Ref	-0.32	-0.88	-0.36	-0.42	-0.02	-1.1	-0.57	7350	5520	4060	6530	6910	7960	4050	5650	896.5	1791	2	0.0147	8.227

Apolipoprotein E OS=Bos taurus GN=APOE PE=2 SV=1	sp Q03247 APOE_BOVIN, tr A7YWR0 A7YWR0_BOVIN, tr Q0ZCB4 Q0ZCB4_BOVIN	aYkE ELEG QLG PMA QET QAR	95%	54.3	55.46203	Ref	-0.064	0.23	0.14	0.33	0.31	0.38	0.43	1570	1330	1760	1860	2350	2010	2210	2260	953.2	2856.5	3	0.0212	7.424
Apolipoprotein E OS=Bos taurus GN=APOE PE=2 SV=1	sp Q03247 APOE_BOVIN, tr A7YWR0 A7YWR0_BOVIN, tr Q0ZCB4 Q0ZCB4_BOVIN	sEVQ AML GQS TEEL R	95%	59.2	53.29036	Ref	-0.34	0.43	0.045	0.33	0.2	0.5	0.43	1490	1010	1860	1600	2140	1710	2210	2080	991.5	1981	2	0.0012	0.624
S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2	8 SKP1_HUMAN, sp P63209 SKP1_CAVPO, sp Q3ZCF3 SKP1_BOVIN, sp Q4R5B9 SKP1_MACFA, sp Q5R512 SKP1_PO NAB, sp Q6PEC4 SKP1_RAT, sp Q9WTX5 SKP1_MOUSE, tr B8QGA5 B8QGA5_SHEEP, tr E5RJR5 E5RJR5_HUMAN, tr F6S4R4 F6S4R4_HORSE, tr F	IQSS DGEI FEVD VEIA k	94%	51.8	54.85185	Ref	0.36	0.28	-0.11	0.49	0.21	0.47	0.47	170	176	181	155	258	186	066	232	829.8	2486.3	3	0.0183	7.357

<p>S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2</p>	<p>8 SKP1_H UMAN,sp P63209 SKP1_CAV PO,sp Q3 ZCF3 SKP 1_BOVIN, sp Q4R5B 9 SKP1_ MACFA,sp Q5R512 SKP1_PO NAB,sp Q 6PEC4 SK P1_RAT,s p Q9WTX 5 SKP1_ MOUSE,tr B8QGA5 B8QGA5 _SHEEP,tr E5RJR5 E5RJR5_H UMAN,tr F6S4R4 F 6S4R4_H ORSE,tr F</p>	<p>nDFT EEEE AQV R</p>	<p>95%</p>	<p>46.9</p>	<p>49.47953</p>	<p>Ref</p>	<p>-0.1</p>	<p>-0.05</p>	<p>0.19</p>	<p>0.17</p>	<p>0.45</p>	<p>-0.22</p>	<p>0.47</p>	<p>11400</p>	<p>10000</p>	<p>11300</p>	<p>15000</p>	<p>16200</p>	<p>17200</p>	<p>11300</p>	<p>18100</p>	<p>885.9</p>	<p>1769.8</p>	<p>2</p>	<p>0.0123</p>	<p>6.949</p>
<p>Cysteine and glycine rich protein 2 OS=Mus musculus GN=Csrp2 PE=1 SV=3</p>	<p>4 CSR2_ MOUSE,s p Q16527 CSR2_H UMAN,sp Q32LE9 CSR2_B OVIN,sp Q62908 C SRP2_RAT ,tr D2HF3 3 D2HF33 _AILME,tr F1RYJ8 F 1RYJ8_PI G,tr F6TZ P6 F6TZP 6_HORSE, tr F6WW F1 F6WW F1_ORNA N,tr F6XV E3 F6XVE 3_MOND O,tr F7DZ IO F7DZIO _MACMU, AQ</p>	<p>gFGY GQG AGA LVH AQ</p>	<p>95%</p>	<p>98.3</p>	<p>52.55499</p>	<p>Ref</p>	<p>-0.45</p>	<p>0.55</p>	<p>-0.95</p>	<p>-0.046</p>	<p>-0.66</p>	<p>0.3</p>	<p>-0.79</p>	<p>7270</p>	<p>4620</p>	<p>10000</p>	<p>3980</p>	<p>8200</p>	<p>4680</p>	<p>9510</p>	<p>4420</p>	<p>868.9</p>	<p>1735.9</p>	<p>2</p>	<p>0.0111</p>	<p>6.38</p>

<p>Cysteine and glycine rich protein 2 OS=Mus musculus GN=Csrp2 PE=1 SV=3</p>	<p>4 CSRP2_ MOUSE,s p Q16527 CSRP2_H UMAN,sp Q32LE9 CSRP2_B OVIN,sp Q62908 C SRP2_RAT ,tr D2HF3 3 D2HF33 _ALIME,tr F1RYJ8 F 1RYJ8_ PI G,tr F6TZ P6 F6TZP 6_HORSE, tr F6WW F1 F6WW F1_ORNA N,tr F6XV E3 F6XVE 3_MOND tVYH O,tr F7DZ AEEV IO F7DZIO QcD _MACMU, GR</p>	<p>91%</p>	<p>41.9</p>	<p>48.57254</p>	<p>Ref</p>	<p>-0.16</p>	<p>0.11</p>	<p>-0.56</p>	<p>-0.15</p>	<p>-0.16</p>	<p>-0.04</p>	<p>-0.49</p>	<p>12600</p>	<p>9860</p>	<p>12800</p>	<p>9090</p>	<p>13300</p>	<p>11500</p>	<p>13100</p>	<p>9500</p>	<p>619.6</p>	<p>1855.8</p>	<p>3</p>	<p>0.0148</p>	<p>7.979</p>
<p>Actin-related protein 2 OS=Bos taurus GN=ACTR2 PE=1 SV=1</p>	<p>62 ARP2_ BOVIN,sp P61160 ARP2_HU MAN,sp P 61161 AR P2_MOUS E,sp Q5M 7U6 ARP 2_RAT,sp Q5R4K0 ARP2_PO NAB,tr B5 APU3 B5 APU3_PIG ,tr D3ZEA 6 D3ZEA6 _RAT,tr E 2QXY7 E2 QXY7_CA NFA,tr F6 ZPQ4 F6Z PQ4_MO NDO,tr F dLM 7BAD3 F7 VGD BAD3_MA EASE CMU,tr F LR</p>	<p>94%</p>	<p>46</p>	<p>51.74905</p>	<p>Ref</p>	<p>-0.23</p>	<p>-0.09</p>	<p>-0.07</p>	<p>-0.26</p>	<p>0.081</p>	<p>-0.5</p>	<p>-0.37</p>	<p>23700</p>	<p>17300</p>	<p>20600</p>	<p>23500</p>	<p>22700</p>	<p>25100</p>	<p>17500</p>	<p>18900</p>	<p>819.9</p>	<p>1637.8</p>	<p>2</p>	<p>0.003</p>	<p>1.853</p>

Actin-related protein 2 OS=Bos taurus GN=ACTR2 PE=1 SV=1	62 ARP2_BOVIN,sp P61160 ARP2_HUMAN,sp P61161 ARP2_MOUSE,sp Q5M7U6 ARP2_RAT,sp Q5R4K0 ARP2_PONAB,tr B5APU3 B5APU3_PIG,tr D3ZEA6 D3ZEA6_RAT,tr E2QXY7 E2QXY7_CANFA,tr F6ZPQ4 F6ZPQ4_MOUSE,tr F7BAD3 F7BAD3_MAMCU,tr F	kVVV cDn GTG FVk	92%	48	54.09113	Ref	-0.16	-0.21	-0.25	-0.11	-0.1	-0.34	-0.15	11000	8770	9200	10000	12200	10700	9470	10700	775.8	2324.3	3	0.0197	8.493
Eukaryotic translation initiation factor 1b OS=Homo sapiens GN=EIF1B PE=1 SV=2	9 EIF1B_HUMAN,sp P41567 EIF1_HUMAN,sp P48024 EIF1_MOUSE,sp P61220 EIF1B_PIG,sp Q4R4X9 EIF1B_MACFA,sp Q5E938 EIF1_BOVIN,sp Q5RFF4 EIF1_PONAB,sp Q9CXU9 EIF1B_MOUSE,tr B0K008 B0K008_RAT,tr B2KI38 B2KI38_RHIFE,tr B5DFN1 B5DF	tLTT VQGI ADD YDK	95%	54.2	54.24635	Ref	0.25	0.17	0.25	0.3	0.14	0.27	0.32	3770	3620	3720	4420	5050	3950	4510	4640	716.7	2147.1	3	0.0228	10.6

<p>Eukaryotic translation initiation factor 1b OS=Homo sapiens GN=EIF1B PE=1 SV=2</p>	<p>9 EIF1B_HUMAN,sp P41567 EIF1_HUMAN,sp P48024 EIF1_MOUSE,sp P61220 EIF1B_PIG,sp Q4R4X9 EIF1B_MACFA,sp Q5E938 EIF1_BOVIN,sp Q5RFF4 EIF1_PONAB,sp Q9CXU9 EIF1B_MOUSE,tr B0K008 B0K008_RAT,tr B2KI38 B2KI38_RHIFN1 B5DF</p>	<p>tLTT VQGI ADD YDkk</p>	<p>90%</p>	<p>45.8</p>	<p>53.58998</p>	<p>Ref</p>	<p>-0.28</p>	<p>0.11</p>	<p>0.32</p>	<p>0.4</p>	<p>0.49</p>	<p>0.34</p>	<p>0.37</p>	<p>3560</p>	<p>2770</p>	<p>3910</p>	<p>5080</p>	<p>5940</p>	<p>5520</p>	<p>5180</p>	<p>5260</p>	<p>860.8</p>	<p>2579.4</p>	<p>3</p>	<p>0.0085</p>	<p>3.284</p>
<p>Cold-inducible RNA-binding protein OS=Mus musculus GN=Cirbp PE=1 SV=1</p>	<p>4 CIRBP_MOUSE,sp P60825 CIRBP_RAT,sp P60826 CIRBP_P_CRIGR,sp Q14011 CIRBP_HUMAN,sp Q5RF83 CIRBP_PONAB,tr A5XDT6 A5XDT6_CRI GR,tr E1BJQ6 E1BJQ6_BOVIN,tr E2R6G2 E2R6G2_CANFA,tr F1S6R1 F1S6R1_PIG,tr F5BHI1 F5BHI1_PIG,tr F7AB</p>	<p>dSYD SYAT HNE</p>	<p>87%</p>	<p>32.3</p>	<p>43.91323</p>	<p>Ref</p>	<p>0.054</p>	<p>-0.09</p>	<p>0.18</p>	<p>0.006</p>	<p>0.4</p>	<p>0.087</p>	<p>0.39</p>	<p>7440</p>	<p>6640</p>	<p>6550</p>	<p>8830</p>	<p>8630</p>	<p>9910</p>	<p>8320</p>	<p>10200</p>	<p>803.3</p>	<p>1604.7</p>	<p>2</p>	<p>0.0129</p>	<p>8.047</p>

<p>Cold-inducible RNA-binding protein OS=Mus musculus GN=Cirbp PE=1 SV=1</p>	<p>4 CIRBP_ MOUSE,s p P60825 CIRBP_R AT,sp P60 826 CIRB P_CRIGR,s p Q14011 CIRBP_H UMAN,sp Q5RF83 CIRBP_PO NAB,tr A 5XDT6 A5 XDT6_CRI GR,tr E1B JQ6 E1BJ Q6_BOVI N,tr E2R6 G2 E2R6 G2_CANF A,tr F1S6 R1 F1S6R 1_PIG,tr F5BH1 F 5BH1_PI G,tr F7AB</p>	<p>yGQI SEVV Vvk</p>	<p>95%</p>	<p>51.4</p>	<p>51.52866</p>	<p>Ref</p>	<p>0.51</p>	<p>0.33</p>	<p>-0.03</p>	<p>0.13</p>	<p>-0.02</p>	<p>-0.08</p>	<p>0.2</p>	<p>4240</p>	<p>5310</p>	<p>5080</p>	<p>4440</p>	<p>5480</p>	<p>4320</p>	<p>4310</p>	<p>5220</p>	<p>610.4</p>	<p>1828.1</p>	<p>3</p>	<p>0.0196</p>	<p>10.7</p>
<p>60S ribosomal protein L21 OS=Capra hircus GN=RPL21 PE=2 SV=1</p>	<p> RL21_CA PHI,sp O0 9167 RL2 1_MOUSE ,sp P2028 0 RL21_R AT,tr D3Y VN8 D3Y VN8_MO USE,tr D3 YWP4 D3 YWP4_M OUSE,tr D3Z1Q1 D3Z1Q1_ MOUSE,tr D3Z422 D3Z422_ MOUSE,tr D3Z9G3 D3Z9G3_ RAT,tr D3 ZEP1 D3Z EP1_RAT,t r D3ZF08 D3ZF08_ RAT,tr D3</p>	<p>hGV VPLA TYM R</p>	<p>94%</p>	<p>49.5</p>	<p>52.85515</p>	<p>Ref</p>	<p>0.77</p>	<p>0.025</p>	<p>0.57</p>	<p>0.27</p>	<p>0.51</p>	<p>0.2</p>	<p>0.71</p>	<p>5050</p>	<p>7380</p>	<p>4760</p>	<p>7790</p>	<p>6960</p>	<p>7180</p>	<p>6060</p>	<p>8550</p>	<p>618</p>	<p>1851</p>	<p>3</p>	<p>0.0203</p>	<p>10.96</p>

<p>60S ribosomal protein L21 OS=Capra hircus GN=RPL21 PE=2 SV=1</p>	<p> RL21_CA PHI,sp O0 9167 RL2 1_MOUSE ,sp P2028 0 RL21_R AT,tr D3Y VN8 D3Y VN8_MO USE,tr D3 YWP4 D3 YWP4_M OUSE,tr D3Z1Q1 D3Z1Q1_ MOUSE,tr D3Z422 D3Z422_ MOUSE,tr D3Z9G3 D3Z9G3_ RAT,tr D3 ZEP1 D3Z EP1_RAT,t r D3ZF08 D3ZF08_ RAT,tr D3</p>	<p>VYNV TQH AVGI IVNK</p>	<p>88%</p>	<p>42.6</p>	<p>51.9953</p>	<p>Ref</p>	<p>0.36</p>	<p>0.2</p>	<p>0.24</p>	<p>0.48</p>	<p>0.7</p>	<p>0.26</p>	<p>0.87</p>	<p>1980</p>	<p>2250</p>	<p>2190</p>	<p>2520</p>	<p>3280</p>	<p>3340</p>	<p>2570</p>	<p>3890</p>	<p>755.1</p>	<p>2262.3</p>	<p>3</p>	<p>0.0121</p>	<p>5.355</p>
<p>Malate dehydrogenase, mitochondrial OS=Sus scrofa GN=MDH2 PE=1 SV=2</p>	<p>6 MDHM _PIG,sp P 04636 M DHM_RAT ,sp P0824 9 MDHM _MOUSE, sp P4092 6 MDHM _HUMAN, sp Q32LG 3 MDHM _BOVIN,s p Q4R568 MDHM_ MACFA,sp Q5NVR2 MDHM_ PONAB,tr B4DE44 B4DE44_ HUMAN,t r D4QGC 3 D4QGC 3_BUBBU, tr E9PDB 2 E9PDB2</p>	<p>tIIPLI SQcT Pk</p>	<p>83%</p>	<p>39.8</p>	<p>52.38187</p>	<p>Ref</p>	<p>0.59</p>	<p>-0.05</p>	<p>-0.05</p>	<p>-0.17</p>	<p>-0.3</p>	<p>-0.21</p>	<p>-0.54</p>	<p>1230</p>	<p>1760</p>	<p>1230</p>	<p>1370</p>	<p>1390</p>	<p>1110</p>	<p>1230</p>	<p>977</p>	<p>656.7</p>	<p>1967.1</p>	<p>3</p>	<p>0.0099</p>	<p>5.022</p>

Malate dehydrogenase, mitochondrial OS=Sus scrofa GN=MDH2 PE=1 SV=2	6 MDHM_PIG,sp P04636 M DHM_RAT,sp P08249 MDHM_MOUSE,sp P40926 MDHM_HUMAN,sp Q32LG3 MDHM_BOVIN,sp Q4R568 MDHM_MACFA,sp Q5NVR2 MDHM_PONAB,transcript B4DE44 B4DE44_HUMAN,transcript D4QGC3 D4QGC3_BUBBU,transcript E9PDB2 E9PDB2	vAVL GAS GGI GQP LSLLL	95%	69.5	46.46208	Ref	0.47	-0.44	0.22	-0.064	-0.83	-0.12	-0.32	281	313	180	320	290	149	256	221	801.2	2400.5	3	0.0166	6.931
BAG3 protein OS=Bos taurus GN=BAG3 PE=2 SV=1	tr A2VE51 A2VE51_BOVIN,transcript F1MIU2 F1MIU2_BOVIN,transcript Q156J1 Q156J1_RA T,transcript Q5U2U8 Q5U2U8_RAT	eLLA LDSV DPE GR	85%	40	52.84618	Ref	0.75	0.61	0.85	0.76	0.96	0.43	0.91	2320	2780	2730	3620	3760	3760	2720	3770	859.5	1716.9	2	0.0082	4.745
BAG3 protein OS=Bos taurus GN=BAG3 PE=2 SV=1	tr A2VE51 A2VE51_BOVIN,transcript F1MIU2 F1MIU2_BOVIN,transcript Q156J1 Q156J1_RA T,transcript Q5U2U8 Q5U2U8_RAT	eTAS SAn GPS R	94%	43.7	49.67773	Ref	-0.091	0.77	0.92	0.82	1.4	0.025	1.2	628	655	1290	1610	1660	2200	870	1940	691.3	1380.7	2	0.0066	4.759

Thioredoxin domain-containing protein 17 OS=Mus musculus GN=Txndc17 PE=1 SV=1	sp Q9CQM5 TXD17_MOUSE, tr CSIWT7 CSIWT7_SHEEP, tr F1MHF7 F1MHF7_BOVIN, tr F1RGM3 F1RGM3_PIG, tr Q95M40 Q95M40_BOVIN	iTAVPTLLk	81%	31.3	44.67904	Ref	0.32	-0.08	0.22	0.13	-0.01	-0.35	-0.11	8520	9800	8070	11200	11500	9160	7550	8830	522	1563	3	0.0048	3.041
Thioredoxin domain-containing protein 17 OS=Mus musculus GN=Txndc17 PE=1 SV=1	sp Q9CQM5 TXD17_MOUSE, tr CSIWT7 CSIWT7_SHEEP, tr F1MHF7 F1MHF7_BOVIN, tr F1RGM3 F1RGM3_PIG, tr Q95M40 Q95M40_BOVIN	tIFAYFSGSk	95%	49.3	52.98218	Ref	0.16	-0.24	0.15	-0.094	0.15	-0.08	-0.03	1290	1180	971	1430	1330	1370	1220	1260	865	1728	2	0.0183	10.58
Tryptophanyl-tRNA synthetase, cytoplasmic OS=Bos taurus GN=WARS PE=1 SV=3	sp P17248 SYWC_BOVIN	eLIEVLQPLIAEHQAR	80%	39.4	53.12016	Ref	0.018	-0.28	-0.07	-0.03	-0.24	-0.02	0.066	256	278	244	318	360	271	330	349	721.7	2162.2	3	0.0094	4.362

Tryptophanyl-tRNA synthetase, cytoplasmic OS=Bos taurus GN=WARS PE=1 SV=3	sp P17248 SYWC_BOVIN	eVT DEIVk	95%	49.3	52.07069	Ref	-0.1	-1.1	0.22	-0.16	0.44	-1.1	-0.05	19200	13100	7250	20000	17000	22500	8090	16500	771	1539.9	2	0.0078	5.06
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Bos taurus GN=DDAH1 PE=1 SV=3	sp P56965 DDAH1_BOVIN, tr F1N2V6 F1N2V6_BOVIN	aTHV VVR	92%	44.2	50.17818	Ref	0.51	-0.07	0.51	-0.49	-0.08	-0.52	-0.07	69400	92600	67400	113000	62400	72300	55800	75300	362.6	1084.7	3	0.0068	6.267
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Bos taurus GN=DDAH1 PE=1 SV=3	sp P56965 DDAH1_BOVIN, tr F1N2V6 F1N2V6_BOVIN	gAEI LADT Fk	87%	42.2	52.1573	Ref	0.57	-0.34	0.17	-0.2	-0.05	-0.18	-0.26	4600	5520	3190	5100	4350	4210	4040	3770	558.3	1672	3	0.005	2.977
Peroxiredoxin-6 OS=Bos taurus GN=PRDX6 PE=1 SV=3	sp O77834 PRDX6_BOVIN	IPFPI IDDK NR	90%	43.6	51.83022	Ref	0.24	-0.03	0.42	0.13	0.008	0.13	0.46	17300	18900	17000	26000	23400	18800	21400	26800	646	1935.1	3	0.0139	7.181
Peroxiredoxin-6 OS=Bos taurus GN=PRDX6 PE=1 SV=3	sp O77834 PRDX6_BOVIN	VIISL QLTA Ek	89%	40.3	48.84614	Ref	0.16	-0.06	0.36	0.002	0.007	0.6	0.079	606	556	518	779	668	586	924	638	608.4	1822.1	3	0.0169	9.263

Coactosin-like protein OS=Bos taurus GN=COTL1 PE=2 SV=3	sp Q2HJ57 COTL1_BOVIN	aGG ANY DAQ TE	95%	73.5	47.08285	Ref	0.43	-0.31	0.14	0.48	0.23	0.071	-0.44	369	444	289	444	618	455	425	295	700.8	1399.6	2	0.013	9.314
Coactosin-like protein OS=Bos taurus GN=COTL1 PE=2 SV=3	sp Q2HJ57 COTL1_BOVIN	dDSS AVI WVT Fk	76%	38.5	53.75153	Ref	0.4	-0.14	0.043	0.15	0.17	0.16	-0.08	578	645	481	612	725	643	666	561	659.4	1975.1	3	0.0056	2.837
Splicing factor 3A subunit 1 OS=Bos taurus GN=SF3A1 PE=2 SV=1	sp A2VDN6 SF3A1_BOVIN, tr F7DA32 F7DA32_MONDO	tQQ AAQ ANIT LQE QIEA IHK	95%	51.1	54.61707	Ref	-0.06	-0.55	-0.19	-0.34	-0.43	-0.17	-0.28	8970	9440	7310	10500	10400	8550	10700	9850	711.6	2842.6	4	0.0238	8.367
Splicing factor 3A subunit 1 OS=Bos taurus GN=SF3A1 PE=2 SV=1	sp A2VDN6 SF3A1_BOVIN, tr F7DA32 F7DA32_MONDO	vMQ QQQ QAS QQQ LPQk	73%	38.9	54.95485	Ref	-0.23	-0.61	-0.47	-0.58	-0.4	-0.37	-0.13	4790	2930	2450	3040	3100	3070	3250	3820	836.1	2505.3	3	0.0231	9.2

Small acidic protein OS=Homo sapiens GN=SMAP PE=1 SV=1	3 SMAP_ HUMAN,s p Q3MHL 8 SMAP_ BOVIN,sp Q5RD18 SMAP_P ONAB,sp Q9R0P4 S MAP_MO USE,tr D2 HRK6 D2 HRK6_AIL ME,tr D3 YVR9 D3Y VR9_MO USE,tr E3 W975 E3 W975_HU MAN,tr E 9PM92 E 9PM92_H UMAN,tr E9PRZ9 E 9PRZ9_H UMAN,tr F15994 F	iNEE LESQ YQQ SMD	Sk	95%	52.9	53.68848	Ref	-0.017	0.16	0.11	0.15	0.38	0.011	0.36	3180	2600	3200	3450	3930	4010	3250	4090	846.4	2536.2	3	0.021	8.289
Small acidic protein OS=Homo sapiens GN=SMAP PE=1 SV=1	3 SMAP_ HUMAN,s p Q3MHL 8 SMAP_ BOVIN,sp Q5RD18 SMAP_P ONAB,sp Q9R0P4 S MAP_MO USE,tr D2 HRK6 D2 HRK6_AIL ME,tr D3 YVR9 D3Y VR9_MO USE,tr E3 W975 E3 W975_HU MAN,tr E 9PM92 E 9PM92_H UMAN,tr E9PRZ9 E 9PRZ9_H UMAN,tr F15994 F	iVIG	DHk	73%	34.6	50.64727	Ref	-0.46	0.19	0.24	0.23	0.71	-0.27	0.37	45200	30100	51300	59400	65300	79200	42000	65100	464	1388.8	3	0.0233	16.77

Coiled-coil domain-containing protein 50 OS=Homo sapiens GN=CCDC50 PE=1 SV=1	sp Q8IVM0 CCD50_HUMAN, tr D2HKJ3 D2HKJ3_AILME, tr E2RNH5 E2RNH5_CANFA, tr F1MZZ9 F1MZZ9_BOVIN, tr F6SPZ0 F6SPZ0_MACMU, tr F6SQ01 F6SQ01_MACMU, tr F7HK81 F7HK81_CALJA, tr F7HK83 F7HK83_CALJA, tr F7IR51 F7IR51_CALJA	aAQ VAQ DEEI AR	92%	43.9	52.17873	Ref	-0.37	-0.04	-0.14	-0.098	0.27	-0.41	0.083	17100	11400	15600	16200	18500	20700	13500	18900	802.9	1603.8	2	0.0129	8.047
Coiled-coil domain-containing protein 50 OS=Homo sapiens GN=CCDC50 PE=1 SV=1	sp Q8IVM0 CCD50_HUMAN, tr D2HKJ3 D2HKJ3_AILME, tr E2RNH5 E2RNH5_CANFA, tr F1MZZ9 F1MZZ9_BOVIN, tr F6SPZ0 F6SPZ0_MACMU, tr F6SQ01 F6SQ01_MACMU, tr F7HK81 F7HK81_CALJA, tr F7HK83 F7HK83_CALJA, tr F7IR51 F7IR51_CALJA	kLQE EELL ATQ VDM R	82%	41.8	54.56347	Ref	-0.27	-0.04	-0.03	-0.14	0.27	-0.3	-0.14	3430	2490	3170	3590	3670	4260	2990	3320	804.4	2410.3	3	0.0232	9.615

Crk-like protein OS=Homo sapiens GN=CRKL PE=1 SV=1	9 CRKL_H UMAN,sp P47941 CRKL_MO USE,sp Q 5U2U2 C RKL_RAT,t r A2RS58 A2RS58_ MOUSE,tr D2HUK7 D2HUK7 _AILME,tr E2RF98 E2RF98_C ANFA,tr F 1RKX9 F1 RKX9_PIG ,tr F6QM U5 F6QM U5_HORS E,tr F6VK 11 F6VK1 1_MACM U,tr F6Z4 K4 F6Z4K 4_MOND	gLFP FTHV k	72%	34	52.25312	Ref	-0.13	-0.52	0.021	-0.11	0.27	-0.68	0.57	2950	2290	1900	3090	3110	3530	1910	4520	414.2	1653	4	0.02	12.11
Crk-like protein OS=Homo sapiens GN=CRKL PE=1 SV=1	9 CRKL_H UMAN,sp P47941 CRKL_MO USE,sp Q 5U2U2 C RKL_RAT,t r A2RS58 A2RS58_ MOUSE,tr D2HUK7 D2HUK7 _AILME,tr E2RF98 E2RF98_C ANFA,tr F 1RKX9 F1 RKX9_PIG ,tr F6QM U5 F6QM U5_HORS E,tr F6VK 11 F6VK1 1_MACM U,tr F6Z4 K4 F6Z4K 4_MOND	iHYL DTTT LIEP APR	95%	57	53.82656	Ref	0.24	0.009	0.049	-0.13	-0.06	-0.11	-0.15	3080	3250	3000	3470	3380	3090	3120	3010	682	2043.1	3	0.0154	7.515

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.40073 PE=4 SV=1	tr F1MNT 4 F1MNT 4_BOVIN	eTV DSVE k	72%	35.5	52.43301	Ref	0.077	-0.53	-0.31	-0.33	-0.03	-0.67	-0.29	15200	15100	10700	14000	15200	16400	11000	14200	757.9	1513.8	2	0.0072	4.735
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.40073 PE=4 SV=1	tr F1MNT 4 F1MNT 4_BOVIN	tLDN ELDE k	95%	51.5	52.94706	Ref	-0.028	-0.61	-0.24	-0.31	0.055	-1.1	-0.29	10300	8180	5940	8590	9000	10200	4890	8300	843	1683.9	2	0.0129	7.661
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.12746 PE=4 SV=1	tr F1MXK 2 F1MXK 2_BOVIN, tr F1N4E3 F1N4E3_ BOVIN	hAL QQH QETP k	71%	37	53.65406	Ref	-0.64	0.008	-0.06	-0.19	0.13	-0.39	-0.09	28900	15900	27000	29000	29100	31700	23100	28300	642.4	1924.1	3	0.0199	10.34
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.12746 PE=4 SV=1	tr F1MXK 2 F1MXK 2_BOVIN, tr F1N4E3 F1N4E3_ BOVIN	sLGS EEAT NPIS R	95%	56.6	52.51363	Ref	-0.41	-0.13	-0.14	-0.35	0.11	-0.64	0.3	13800	9210	12100	13500	12800	15500	9620	18300	832.9	1663.9	2	0.0141	8.488

WW domain-binding protein 11 OS=Rattus norvegicus GN=Wbp11 PE=2 SV=1	Q2 WBP11_RAT,sp Q923D5 WBP11_MOUSE,sp Q9Y2W2 WBP11_HUMAN, tr B4DM D3 B4DM D3_HUMAN, tr B4DY34 B4DY34_HUMAN, tr D2HZU4 D2HZU4_AI LME, tr E2RER0 E2RERO_CAN FA, tr F5H721 F5H721_HUMAN, tr F6S9X4 F6S9X4_MACM U, tr F6SF	aVSI LPLL GHG VPR	95%	55.8	48.98922	Ref	0.075	-0.09	-0.07	-0.27	0.11	-0.1	0.077	3100	2760	2670	3050	2930	3320	2990	3360	578.4	1732.1	3	0.0076	4.398
WW domain-binding protein 11 OS=Rattus norvegicus GN=Wbp11 PE=2 SV=1	Q2 WBP11_RAT,sp Q923D5 WBP11_MOUSE,sp Q9Y2W2 WBP11_HUMAN, tr B4DM D3 B4DM D3_HUMAN, tr B4DY34 B4DY34_HUMAN, tr D2HZU4 D2HZU4_AI LME, tr E2RER0 E2RERO_CAN FA, tr F5H721 F5H721_HUMAN, tr F6S9X4 F6S9X4_MACM U, tr F6SF	kATA TISA kPQI TNPk	70%	27.7	46.36337	Ref	-0.31	-0.08	-0.02	-0.063	0.3	-0.21	0.15	8090	5830	7450	8660	9290	10400	7670	9720	722.2	2884.7	4	0.0345	11.97

Splicing factor 1 OS=Homo sapiens GN=SF1 PE=1 SV=4	7 SF01_H UMAN,sp Q64213 SF01_MO USE,tr A2 VDM7 A2 VDM7_B OVIN,tr B OCM65 B OCM65_P APAN,tr B0KWK3 B0KWK3_ CALJA,tr B1MTL4 B1MTL4_ CALMO,tr B2KIB5 B2KIB5_R HIFE,tr B 3RF39 B3 RF39_SOR AR,tr B4D JU4 B4DJ U4_HUM AN,tr B5S NK8 B5S	qGIE TPED QND LR	93%	44.8	51.7316	Ref	0.036	-0.16	-0.21	-0.33	0.33	-0.51	0.16	8910	7320	6930	7530	7600	10500	6150	9680	910	1817.9	2	0.0162	8.916
Splicing factor 1 OS=Homo sapiens GN=SF1 PE=1 SV=4	7 SF01_H UMAN,sp Q64213 SF01_MO USE,tr A2 VDM7 A2 VDM7_B OVIN,tr B OCM65 B OCM65_P APAN,tr B0KWK3 B0KWK3_ CALJA,tr B1MTL4 B1MTL4_ CALMO,tr B2KIB5 B2KIB5_R HIFE,tr B 3RF39 B3 RF39_SOR AR,tr B4D JU4 B4DJ U4_HUM AN,tr B5S NK8 B5S	tVIP GMP TVIP PGLT R	75%	35.9	51.90228	Ref	-0.046	-0.15	0.091	-0.23	0.11	-0.19	0.11	2600	2390	2410	3210	2820	3130	2660	3240	977.1	1952.1	2	0.0044	2.234

Uncharacterized protein OS=Bos taurus GN=Bt.76525 PE=4 SV=1	tr E1BHQ9 E1BHQ9_BOVIN	eVTVPVFYPAER	79%	38	53.01117	Ref	-0.055	-0.91	-0.32	-0.22	0.09	-1	-0.28	7700	6080	3650	6160	7300	7880	3800	6310	856	1709.9	2	0.0122	7.123
Uncharacterized protein OS=Bos taurus GN=Bt.76525 PE=4 SV=1	tr E1BHQ9 E1BHQ9_BOVIN	sVLQAQVSk	92%	44.7	50.32369	Ref	0.022	-0.65	-0.25	-0.24	-0.04	-0.76	-0.43	22000	20700	14100	20900	23200	23300	14800	18400	523.3	1566.9	3	0.0062	3.925
Uncharacterized protein OS=Bos taurus GN=Bt.102053 PE=3 SV=1	tr F1MXV8 F1MXV8_BOVIN, tr Q3SZQ8 Q3SZQ8_BOVIN, tr Q5J801 Q5J801_BOVIN	kIFTS DAD FSGI TDD HK	91%	45.9	55.36209	Ref	1	0.27	0.87	0.69	0.33	0.93	0.64	11800	20400	13000	22100	21500	14600	23100	18700	703.1	2808.5	4	0.0267	9.512
Uncharacterized protein OS=Bos taurus GN=Bt.102053 PE=3 SV=1	tr F1MXV8 F1MXV8_BOVIN, tr Q3SZQ8 Q3SZQ8_BOVIN, tr Q5J801 Q5J801_BOVIN	IAVS HVIH k	82%	34.2	48.27583	Ref	1.1	0.19	0.94	0.55	0.38	0.98	0.59	2600	5100	2900	5480	4590	3570	5640	4270	806.5	1611	2	0.0102	6.34
Macrophage migration inhibitory factor OS=Bos taurus GN=MIF PE=1 SV=6	sp P80177 MIF_BOVIN,sp Q1ZZU7 MIF_SHEEP	ILcGL LTER	95%	52.8	51.82589	Ref	-0.081	0.31	0.4	-0.15	-0.23	0.31	0.075	919	868	1240	1470	1110	914	1390	1180	456.6	1366.8	3	0.0087	6.342

Macrophage migration inhibitory factor OS=Bos taurus GN=MIF PE=1 SV=6	sp P80177 MIF_BOVIN,sp Q1ZZU7 MIF_SHEEP	pMFVNV TNV PR	66%	34.5	52.68309	Ref	0.034	0.025	0.2	-0.1	-0.14	0.39	-0.08	15500	12200	13100	16600	14900	12700	19100	13700	789.4	1576.9	2	0.013	8.265
MARCKS-related protein OS=Bos taurus GN=MARCKSL1 PE=2 SV=1	sp Q0VBZ9 MRP_BOVIN	aAAT PESQ EPQ Ak	71%	37.2	53.80116	Ref	-0.45	0.43	0.006	0.025	0.13	-0.2	0.18	8570	5960	11900	9960	11100	10400	8670	11200	646	1935	3	0.0166	8.593
MARCKS-related protein OS=Bos taurus GN=MARCKSL1 PE=2 SV=1	sp Q0VBZ9 MRP_BOVIN	gAEA SAA Ak	94%	45.9	51.96306	Ref	-0.75	-0.01	0.035	0.096	0.28	-0.28	0.4	9600	4560	8280	9590	11000	10900	7730	12300	692.4	1382.8	2	0.0294	21.24
Uncharacterized protein OS=Equus caballus GN=Eca.12978 PE=4 SV=1	tr F6QD89 F6QD89_HORSE	iTVD PTTD GPTk	94%	47.2	53.39346	Ref	-0.37	0.25	-0.02	-0.03	-0.26	-0.1	0.3	7080	4510	7500	6980	7630	5680	6640	8660	927	1852	2	0.0226	12.17
Uncharacterized protein OS=Equus caballus GN=Eca.12978 PE=4 SV=1	tr F6QD89 F6QD89_HORSE	IkDE GVEL FAV Gik	71%	32.2	50.63082	Ref	0.12	0.45	0.004	-0.13	-0.76	0.037	0.092	2930	2940	4030	3310	3320	1870	3400	3510	608.4	2429.4	4	0.035	14.42

Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Mus musculus GN=Anp32e PE=1 SV=2	2 AN32E_MOUSE,s p Q5XIE0 AN32E_RAT,sp Q9BTT0 AN32E_HUMAN,tr B4E0D5 B4E0D5_HUMAN,tr D2HBV1 D2HBV1_AILME,tr D3Z9Y8 D3Z9Y8_RAT, tr E2QV22 E2QV22_CANFA,tr E9PLC4 E9PLC4_HUMAN,tr E9PZF5 E9PZF5_MOUSE,tr E9Q5H2 E9Q5H2_M	cPNL TYLN LSGN k	78%	39.5	54.07723	Ref	-0.19	-0.51	-0.31	-0.37	-0.06	0.81	-0.3	5660	5030	4370	5620	5950	6430	12300	5650	697.7	2090.1	3	0.0154	7.383
Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Mus musculus GN=Anp32e PE=1 SV=2	2 AN32E_MOUSE,s p Q5XIE0 AN32E_RAT,sp Q9BTT0 AN32E_HUMAN,tr B4E0D5 B4E0D5_HUMAN,tr D2HBV1 D2HBV1_AILME,tr D3Z9Y8 D3Z9Y8_RAT, tr E2QV22 E2QV22_CANFA,tr E9PLC4 E9PLC4_HUMAN,tr E9PZF5 E9PZF5_MOUSE,tr E9Q5H2 E9Q5H2_M	kLEL SDNI ISGG LEVL AEk	92%	42.9	51.26196	Ref	-0.074	-0.32	-0.06	-0.22	0.22	-0.35	-0.15	1100	794	726	973	965	1140	799	913	735.9	2939.7	4	0.0299	10.17

Actin-related protein 2/3 complex subunit 5-like protein OS=Rattus norvegicus GN=Arpc5l PE=1 SV=2	8 ARP5L_RAT,sp Q5E963 ARP5L_BOVIN,sp Q5R4M1 ARP5L_PONAB,sp Q9BPX5 ARP5L_HUMAN,sp Q9D898 ARP5L_MOUSE, tr A3KQ6 A3KQ6_MOUSE, tr B5APV1 B5APV1_PIG, E2RPG0 E2RPG0_CANFA, tr F1SKQ9 F1SKQ9_PIG, tr F6WNGN=Arpc5l PE=1 SV=2	aFHAALR	60%	30	48.91007	Ref	-0.39	0.071	0.32	-0.21	0.27	-0.62	0.32	25700	18300	27300	36500	27900	33900	19100	36400	363.9	1088.6	3	0.009	8.24
Actin-related protein 2/3 complex subunit 5-like protein OS=Rattus norvegicus GN=Arpc5l PE=1 SV=2	8 ARP5L_RAT,sp Q5E963 ARP5L_BOVIN,sp Q5R4M1 ARP5L_PONAB,sp Q9BPX5 ARP5L_HUMAN,sp Q9D898 ARP5L_MOUSE, tr A3KQ6 A3KQ6_MOUSE, tr B5APV1 B5APV1_PIG, E2RPG0 E2RPG0_CANFA, tr F1SKQ9 F1SKQ9_PIG, tr F6WNGN=Arpc5l PE=1 SV=2	aLAVGGLGSII	95%	67.6	49.9393	Ref	0.043	0.08	-0.07	-0.12	0.034	-0.16	0.027	2060	1720	1920	1940	2060	2010	1840	2070	477.6	1429.9	3	0.0138	9.663

60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	9 RL23_H UMAN,sp P62830 RL23_MO USE,sp P6 2831 RL2 3_PIG,sp P62832 R L23_RAT,s p Q3T057 RL23_BO VIN,sp Q 5REU2 RL 23_PONA B,tr A1XE D4 A1XE D4_BOVI N,tr A2A6 F9 A2A6F 9_MOUSE ,tr D2H53 7 D2H537 _AILME,tr F2X264 F2X264_A ILME,tr F 2Z4P3 F2	gSAI TGP VAk	90%	40.2	49.78993	Ref	0.11	0.01	0.4	0.16	0.28	0.088	0.29	5940	5390	5450	8020	7470	7120	6490	7410	755	1507.9	2	0.0061	4.03
60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	9 RL23_H UMAN,sp P62830 RL23_MO USE,sp P6 2831 RL2 3_PIG,sp P62832 R L23_RAT,s p Q3T057 RL23_BO VIN,sp Q 5REU2 RL 23_PONA B,tr A1XE D4 A1XE D4_BOVI N,tr A2A6 F9 A2A6F 9_MOUSE ,tr D2H53 7 D2H537 _AILME,tr F2X264 F2X264_A ILME,tr F 2Z4P3 F2	VHP AVVI R	78%	32.8	47.17862	Ref	0.41	0.069	0.52	0.081	0.2	0.054	0.053	39200	47100	40200	61800	50100	47600	44900	44500	398.9	1193.7	3	0.0057	4.758

Uncharacterized protein OS=Bos taurus GN=Bt.41853 PE=4 SV=1	tr E1BC59 E1BC59_BOVIN	sGSY SYSE ER	56%	27.9	47.89066	Ref	-0.091	-0.05	-0.11	-0.15	0.2	-0.44	0.067	9280	8170	9100	9830	10500	11700	7840	11100	734.8	1467.7	2	0.0122	8.298
Uncharacterized protein OS=Bos taurus GN=Bt.41853 PE=4 SV=1	tr E1BC59 E1BC59_BOVIN	sTQ GVTL TDL QEA Ek	95%	55.6	54.51785	Ref	-0.18	-0.33	0.13	-0.018	0.19	-0.56	-0.08	25800	18500	18000	27800	27700	27900	17400	24000	743.4	2227.2	3	0.0171	7.692
LOC535277 protein OS=Bos taurus GN=LOC535277 PE=2 SV=1	tr A6QR15 A6QR15_BOVIN, tr D2GUY3 D2GUY3_AILME	mEAl k	67%	33.3	51.26128	Ref	0.73	0.16	-0.77	-0.45	0.73	-1.4	-0.01	820	1370	999	589	809	1610	396	997	469.3	936.51	2	0.0171	18.2
LOC535277 protein OS=Bos taurus GN=LOC535277 PE=2 SV=1	tr A6QR15 A6QR15_BOVIN, tr D2GUY3 D2GUY3_AILME	qVEE ELTH LQk	93%	45.4	52.52884	Ref	0.014	-0.41	-0.01	0.029	0.48	-0.77	0.14	11100	8550	6940	10300	11600	13900	6090	11400	820.9	1639.9	2	0.0122	7.424
Tyrosyl-tRNA synthetase, cytoplasmic OS=Bos taurus GN=YARS PE=2 SV=4	sp Q29465 SYYC_BOVIN, tr F1MHM5 F1MHM5_BOVIN, tr F6SK64 F6SK64_MONDO, tr F6VBB2 F6VBB2_MONDO, tr F6VBB9 F6VBB9_MONDO, tr Q0III5 Q0III5_BOVIN	hVLF PLk	87%	37.3	47.7628	Ref	0.28	-0	-0.06	-0.18	-0.18	0.08	-0.28	13800	13200	11800	12700	12900	11300	14100	10900	488	1460.9	3	0.0246	16.83

Tyrosyl-tRNA synthetase, cytoplasmic OS=Bos taurus GN=YARS PE=2 SV=4	sp Q29465 SYYC_BOVIN, tr F1MHM5 F1MHM5_BOVIN, tr F6SK64 F6SK64_MONDO, tr F6VBB2 F6VBB2_MONDO, tr F6VBB9 F6VBB9_MONDO, tr Q0III5 Q0III5_BOVIN	iHLM NPM VPGL TGsk	82%	40.6	53.36556	Ref	0.31	0.024	-0.01	-0.096	-0.12	-0.01	-0.12	1060	1270	1130	1240	1290	1100	1250	1150	735.1	2202.2	3	0.0083	3.761
Uncharacterized protein OS=Bos taurus GN=Bt.2096 PE=4 SV=1	tr E1BJV0 E1BJV0_BOVIN	sISII DSP GILS GEK	95%	53.6	52.88994	Ref	-0.062	-0.21	-0.06	-0.2	-0.06	-0.29	0.14	5090	4000	3930	4880	4880	4690	4170	5580	708.7	2123.2	3	0.0214	10.05
Uncharacterized protein OS=Bos taurus GN=Bt.2096 PE=4 SV=1	tr E1BJV0 E1BJV0_BOVIN	vHAY IISFL k	52%	28.7	49.1096	Ref	0.13	-0.33	-0.03	-0.026	-0.16	0.007	-0.15	843	850	672	932	1030	816	959	855	600.4	1798.1	3	0.0035	1.966

U2 small nuclear ribonucleoprotein A' OS=Homo sapiens GN=SNRPA1 PE=1 SV=2	1 RU2A_HUMAN,sp P57784 RU2A_MOUSE,sp Q4R8Y8 RU2A_MACFA,tr A6H788 A6H788_BOVIN,tr B2LU27 B2LU27_SHEEP,tr D2I7R5 D2I7R5_AILME,tr D3ZZR5 D3ZZR5_RAT,tr E2QWU2 E2QWU2_CANFA,tr F1RWS8 F1RWS8_PIG,tr F6T1N4 F6T1N4_ORNAN,tr	gLLQSGQI	86%	39.1	51.28997	Ref	-0.11	-0.11	-0.28	-0.25	-0.15	-0.13	-0.06	16800	14500	15800	15800	17700	16600	17500	18200	715.4	1428.8	2	0.0128	8.95
U2 small nuclear ribonucleoprotein A' OS=Homo sapiens GN=SNRPA1 PE=1 SV=2	1 RU2A_HUMAN,sp P57784 RU2A_MOUSE,sp Q4R8Y8 RU2A_MACFA,tr A6H788 A6H788_BOVIN,tr B2LU27 B2LU27_SHEEP,tr D2I7R5 D2I7R5_AILME,tr D3ZZR5 D3ZZR5_RAT,tr E2QWU2 E2QWU2_CANFA,tr F1RWS8 F1RWS8_PIG,tr F6T1N4 F6T1N4_ORNAN,tr	nAIA NAS TLAE VER	82%	39.5	53.33085	Ref	-0.21	-0.23	-0.12	-0.22	-0.24	-0.25	-0.04	7730	5440	5840	7030	7250	6250	6470	7430	882	1761.9	2	0.0125	7.113

Sorting nexin-1 OS=Bos taurus GN=SNX1 PE=2 SV=1	2 SNX1_B OVIN,sp Q13596 S NX1_HU MAN,sp Q4R503 S NX1_MAC FA,sp Q5 RFP8 SNX 1_PONAB, sp Q99N2 7 SNX1_R AT,sp Q9 WV80 SN X1_MOUS E,tr A5YB M3 A5YB M3_HORS E,tr A6NK H4 A6NK H4_HUM AN,tr D2 GYR2 D2 GYR2_AIL ME,tr D3 Z8Y0 D3Z 8Y0_RAT,t	KLHA VVET LVN HR	82%	34.7	49.8205	Ref	0.13	-0.17	0.035	-0.005	-0	-0.06	0.055	1050	1110	980	1270	1360	1190	1190	1280	531.8	2123.3	4	0.005	2.365
Sorting nexin-1 OS=Bos taurus GN=SNX1 PE=2 SV=1	2 SNX1_B OVIN,sp Q13596 S NX1_HU MAN,sp Q4R503 S NX1_MAC FA,sp Q5 RFP8 SNX 1_PONAB, sp Q99N2 7 SNX1_R AT,sp Q9 WV80 SN X1_MOUS E,tr A5YB M3 A5YB M3_HORS E,tr A6NK H4 A6NK H4_HUM AN,tr D2 GYR2 D2 GYR2_AIL ME,tr D3 Z8Y0 D3Z 8Y0_RAT,t	LAIV R	87%	26.6	38.49665	Ref	0.24	-0.33	0.17	-0.059	-0.02	-0.35	-0.07	9520	8860	6450	10300	9640	8630	7200	8680	494.8	987.66	2	0.0127	12.81

Prefoldin subunit 3 OS=Homo sapiens GN=VBP1 PE=1 SV=3	8 PFD3_H UMAN,sp P61759 PFD3_MO USE,sp Q 2TBX2 PF D3_BOVI N,sp Q5R CG9 PFD 3_PONAB, tr A3KGB 1 A3KGB 1_MOUSE ,tr A3KMJ 8 A3KMJ 8_MOUSE ,tr B0KW U9 B0KW U9_CALJA ,tr B4DW R3 B4DW R3_HUM AN,tr B7 NZR7 B7 NZR7_RA BIT,tr D3 DWY7 D3	dQFT TTEV NMA R	84%	38.2	51.57112	Ref	0.44	0.18	-0.07	-0.029	0.37	-0.15	0.01	11000	13500	12200	11500	13100	15000	11000	12200	858.9	1715.8	2	0.0123	7.167
Prefoldin subunit 3 OS=Homo sapiens GN=VBP1 PE=1 SV=3	8 PFD3_H UMAN,sp P61759 PFD3_MO USE,sp Q 2TBX2 PF D3_BOVI N,sp Q5R CG9 PFD 3_PONAB, tr A3KGB 1 A3KGB 1_MOUSE ,tr A3KMJ 8 A3KMJ 8_MOUSE ,tr B0KW U9 B0KW U9_CALJA ,tr B4DW R3 B4DW R3_HUM AN,tr B7 NZR7 B7 NZR7_RA BIT,tr D3 DWY7 D3	fMEL NLA QK	83%	40.2	52.71233	Ref	0.43	0.1	0.1	-0.01	0.11	0.01	-0.03	5580	6320	5450	6120	6240	5930	5770	5570	568	1701	3	0.0099	5.845

60S ribosomal protein L14 OS=Sus scrofa GN=RPL14 PE=2 SV=1	sp A1XQU3 RL14_PIG,sp Q3T0U2 RL14_BOVIN, tr F1SJQ6 F1SJQ6_PIG	aAPP Pk	64%	28.4	46.88944	Ref	0.24	0.035	0.44	-0.052	0.44	-0.28	0.21	21500	21600	20400	30300	23700	29000	18500	25800	594.9	1187.7	2	0.003	2.543
60S ribosomal protein L14 OS=Sus scrofa GN=RPL14 PE=2 SV=1	sp A1XQU3 RL14_PIG,sp Q3T0U2 RL14_BOVIN, tr F1SJQ6 F1SJQ6_PIG	IVAI VDVI DQNR	92%	43.4	51.95916	Ref	0.63	-0.29	0.42	-0.055	0.14	-0.03	0.19	2780	3830	2190	4020	3190	3200	2960	3430	830	1658	2	0.0034	2.04
Probable rRNA-processing protein EBP2 OS=Homo sapiens GN=EBNA1BP2 PE=1 SV=2	sp Q99848 EBP2_HUMAN, tr D2HSR8 D2HSR8_AILME, tr E2QVV3 E2QVV3_CANFA, tr F1MUZ0 F1MUZ0_BOVIN, tr F1S312 F1S312_PIG, tr F7H747 F7H747_MACM U, tr Q3T0K6 Q3T0K6_BOVIN, tr Q6IB29 Q6IB29_HUMAN	eSYD DVSS FR	82%	34.2	48.24054	Ref	-0.06	0.39	-0.4	-0.12	-0.25	-0.05	-0.08	12800	10500	15600	10200	13600	10900	13000	12600	754.9	1507.7	2	0.011	7.264

<p>Probable rRNA-processing protein EBP2 OS=Homo sapiens GN=EBNA1BP2 PE=1 SV=2</p>	<p>sp Q99848 EBP2_HUMAN, tr D2HSR8 D2HSR8_AILME, tr E2QVV3 E2QVV3_CANFA, tr F1MUZ0 F1MUZ0_BOVIN, tr F1S312 F1S312_PI G, tr F7H747 F7H747_MACM U, tr Q3T0K6 Q3T0K6_BOVIN, tr Q6IB29 Q6IB29_HUMAN</p>	<p>gLLk PGL NVV LEGP k</p>	<p>83%</p>	<p>33.5</p>	<p>45.973</p>	<p>Ref</p>	<p>-0.13</p>	<p>0.47</p>	<p>-0.77</p>	<p>-0.002</p>	<p>-0.35</p>	<p>-0.01</p>	<p>0.11</p>	<p>1070</p>	<p>859</p>	<p>1420</p>	<p>674</p>	<p>1260</p>	<p>864</p>	<p>1140</p>	<p>1230</p>	<p>816.2</p>	<p>2445.5</p>	<p>3</p>	<p>0.0336</p>	<p>13.71</p>
<p>Nucleobindin-2 OS=Homo sapiens GN=NUCB2 PE=1 SV=2</p>	<p>sp P80303 NUCB2_HUMAN, tr D3DQX5 D3DQX5_HUMAN, tr E9PKG6 E9PKG6_HUMAN, tr F1S9A4 F1S9A4_PIG, tr F6TKU8 F6TKU8_MACMU, tr F6Y426 F6Y426_HORSE, tr F6YXD8 F6YXD8_HORSE, tr F7IH71 F7IH71_CALJA</p>	<p>aDIE Eik</p>	<p>84%</p>	<p>38.5</p>	<p>51.81381</p>	<p>Ref</p>	<p>-0.17</p>	<p>0.14</p>	<p>0.068</p>	<p>-0.035</p>	<p>0.25</p>	<p>-0.13</p>	<p>-0</p>	<p>16600</p>	<p>13000</p>	<p>17500</p>	<p>18700</p>	<p>19200</p>	<p>20400</p>	<p>16400</p>	<p>17700</p>	<p>713.4</p>	<p>1424.8</p>	<p>2</p>	<p>0.0227</p>	<p>15.91</p>

<p>Nucleobindin-2 OS=Homo sapiens GN=NUCB2 PE=1 SV=2</p>	<p>sp P80303 NUCB2_HUMAN, tr D3DQX5 D3DQX5_HUMAN, tr E9PKG6 E9PKG6_HUMAN, tr F1S9A4 F1S9A4_PIG, tr F6TKU8 F6TKU8_MACMU, tr F6Y426 F6Y426_HORSE, tr F6YXD8 F6YXD8_HORSE, tr F71H71 F71H71_CALJAK</p>	<p>IVTL EEFLK</p>	<p>81%</p>	<p>36.1</p>	<p>49.50783</p>	<p>Ref</p>	<p>-0.26</p>	<p>0.18</p>	<p>-0.15</p>	<p>-9E-04</p>	<p>0.3</p>	<p>0.039</p>	<p>-0.05</p>	<p>445</p>	<p>318</p>	<p>467</p>	<p>417</p>	<p>511</p>	<p>550</p>	<p>479</p>	<p>448</p>	<p>567.4</p>	<p>1699</p>	<p>3</p>	<p>0.0043</p>	<p>2.54</p>
<p>Caveolin-1 OS=Papio anubis GN=CAV1 PE=3 SV=1</p>	<p>R6 CAV1_PAPAN, sp A0M8S7 CAV1_FE LCA, sp P33724 CAV1_CANFA, sp P41350 CAV1_RAT, sp P49817 CAV1_MOUSE, sp P79132 CAV1_BOVIN, sp Q03135 CAV1_HUMAN, sp Q07DV9 CAV1_AOTNA, sp Q07DY2 CAV1_NOMLE, sp Q07DZ2 CAV1_COLGU, sp Q07E2</p>	<p>qVY DAH TK</p>	<p>82%</p>	<p>39.8</p>	<p>52.58014</p>	<p>Ref</p>	<p>-0.2</p>	<p>-0.26</p>	<p>0.2</p>	<p>-0.37</p>	<p>0.097</p>	<p>-0.68</p>	<p>0.16</p>	<p>38400</p>	<p>29100</p>	<p>30200</p>	<p>46700</p>	<p>34600</p>	<p>41800</p>	<p>25600</p>	<p>45400</p>	<p>524</p>	<p>1568.9</p>	<p>3</p>	<p>0.0071</p>	<p>4.54</p>

Uncharacterized protein OS=Bos taurus GN=Bt.103427 PE=4 SV=1	tr F1MCA8 F1MCA8_BOVIN, tr F1MSQ9 F1MSQ9_BOVIN	hAA PILPI TEFS DIPR	91%	46.5	53.64772	Ref	-0.024	-0.17	0.063	0.094	-0.11	0.1	-0.08	1260	1250	1220	1620	1820	1380	1670	1460	694.4	2080.2	3	0.0124	5.971
Uncharacterized protein OS=Bos taurus GN=Bt.103427 PE=4 SV=1	tr F1MCA8 F1MCA8_BOVIN, tr F1MSQ9 F1MSQ9_BOVIN	nRPP LATS	65%	34.9	52.84336	Ref	-0.019	-0.23	-0.02	-0.15	0.061	-0.51	0.24	17900	13500	12600	16500	16600	16700	11700	19600	622	1863.1	3	0.0254	13.61
Annexin A8 OS=Pan troglodytes GN=ANXA8 PE=2 SV=1	sp A5A6L7 ANXA8_PANTR,s p P13928 ANXA8_HUMAN,s p Q5T2P8 AXA81_HUMAN,s p Q5VT79 AXA82_HUMAN,t r B2R939 B2R939_HUMAN,t r B4DQE1 B4DQE1_HUMAN, tr B4DTF2 B4DTF2_HUMAN, tr F6YNN1 F6YNN1_MACMU	gIGT NEQ AIID VLTK	87%	42.4	52.72925	Ref	0.068	0.001	-0.1	0.17	0.2	0.21	-0.24	6770	5650	5860	6130	8140	7260	7620	5550	727.4	2179.2	3	0.0196	9.007

Annexin A8 OS=Pan troglodytes GN=ANXA8 PE=2 SV=1	sp A5A6L7 ANXA8_PANTR,s p P13928 ANXA8_HUMAN,s p Q5T2P8 AXA81_HUMAN,s p Q5VT79 AXA82_HUMAN,t r B2R939 B2R939_HUMAN,t r B4DQE1 B4DQE1_HUMAN, tr B4DTF2 B4DTF2_HUMAN, tr F6YNN1 F6YNN1_MACMU	sATH LLR	75%	33.3	48.66925	Ref	0.28	-0.02	0.25	-0.25	0.52	-0.01	-0.35	6470	7490	6630	8930	6980	10400	7510	5910	367.9	1100.6	3	0.0116	10.49
Vitamin D-binding protein OS=Bos taurus GN=GC PE=2 SV=1	sp Q3MHN5 VTDB_BOVIN, tr F1N5M2 F1N5M2_BOVIN	dVcD EGN Tk	85%	36.5	49.28396	Ref	-0.019	0.68	0.74	0.81	0.7	1.5	0.71	13900	9630	17000	19800	22900	18600	32700	19500	817.9	1633.8	2	0.0226	13.8
Vitamin D-binding protein OS=Bos taurus GN=GC PE=2 SV=1	sp Q3MHN5 VTDB_BOVIN, tr F1N5M2 F1N5M2_BOVIN	vLDQ YIFEL SR	77%	37.5	53.06708	Ref	0.046	0.61	0.67	0.83	0.077	1.9	0.86	544	638	1020	1200	1470	764	2790	1360	844	1685.9	2	0.0119	7.072

40S ribosomal protein S21 OS=Rattus norvegicus GN=Rps21 PE=1 SV=1	5 RS21_R AT,sp P63220 RS21_HUMAN,sp P63221 RS21_PIG,sp Q32PB8 RS21_BOVIN,sp Q9CQR2 RS21_MOUSE,tra A2ABW8 A2ABW8_MOUSE,tra D2HT80 D2HT80_AILME,tra D3ZSE0 D3ZSE0_RAT,tra E2RCL4 E2RCL4_CANFA,tra F2X220 F2X220_AILME,tra F6VAR7 F6VAR7 F	mGESDD	54%	29	49.29904	Ref	-0.075	0.4	0.34	0.07	0.45	-0	0.27	42500	34600	52200	56100	51300	58100	44500	53300	721.9	1441.7	2	0.0114	7.93
40S ribosomal protein S21 OS=Rattus norvegicus GN=Rps21 PE=1 SV=1	5 RS21_R AT,sp P63220 RS21_HUMAN,sp P63221 RS21_PIG,sp Q32PB8 RS21_BOVIN,sp Q9CQR2 RS21_MOUSE,tra A2ABW8 A2ABW8_MOUSE,tra D2HT80 D2HT80_AILME,tra D3ZSE0 D3ZSE0_RAT,tra E2RCL4 E2RCL4_CANFA,tra F2X220 F2X220_AILME,tra F6VAR7 F6VAR7 F	rMGESD DSILR	92%	45.9	51.58263	Ref	0.091	0.37	0.41	0.11	0.29	-0.1	0.35	21400	20100	26400	30500	27300	27000	21600	29200	528.3	1581.8	3	0.0115	7.283

cDNA FLJ52535, highly similar to Homo sapiens lysosomal- associated membrane protein 2 (LAMP2), transcript variant LAMP2B, mRNA OS=Homo sapiens PE=2 SV=1	9 B4DF49 _HUMAN, tr B4E2S7 B4E2S7_ HUMAN,t r D2HJT7 D2HJT7_ AILME,tr E7EVR5 E 7EVR5_H UMAN,tr F1PLJ7 F1 PLJ7_CAN FA,tr F6Z 9A8 F6Z9 A8_HORS E,tr F7AK N2 F7AK N2_CALJA ,tr F7AKS 6 F7AKS6 _CALJA,tr F7BCK9 F7BCK9_ MACMU,t r Q3SZJ7 Q3SZJ7_B	sYAG	88%	38.1	49.21754	Ref	-0.29	-0.14	-0.28	-0.44	0.28	-0.28	0.082	833	696	835	851	840	1210	855	1090	603.8	1205.6	2	0.0149	12.33
	cDNA FLJ52535, highly similar to Homo sapiens lysosomal- associated membrane protein 2 (LAMP2), transcript variant LAMP2B, mRNA OS=Homo sapiens PE=2 SV=1	9 B4DF49 _HUMAN, tr B4E2S7 B4E2S7_ HUMAN,t r D2HJT7 D2HJT7_ AILME,tr E7EVR5 E 7EVR5_H UMAN,tr F1PLJ7 F1 PLJ7_CAN FA,tr F6Z 9A8 F6Z9 A8_HORS E,tr F7AK N2 F7AK N2_CALJA ,tr F7AKS 6 F7AKS6 _CALJA,tr F7BCK9 F7BCK9_ MACMU,t r Q3SZJ7 Q3SZJ7_B	yLDF VFA Vk	64%	34.2	52.45417	Ref	-0.27	-0.35	0.017	-0.42	-0.32	-0.16	0.01	666	418	428	621	506	473	552	617	570.7	1709	3	0.019

Uncharacterized protein OS=Bos taurus GN=Bt.43120 PE=4 SV=1	tr E1BMD6 E1BMD6_BOVIN	eQG YTPS GPG NQN PAG MYP VAG Pk	90%	47.2	55.17916	Ref	0.6	-0.33	-0.29	0.22	-0.29	-0.1	-0.33	1570	2270	1290	1500	2340	1430	1720	1450	1009	3024.5	3	0.0173	5.706
Uncharacterized protein OS=Bos taurus GN=Bt.43120 PE=4 SV=1	tr E1BMD6 E1BMD6_BOVIN	mVIP NQP PLTA Tk	52%	32.2	52.54016	Ref	0.003	-0.18	-0.16	-0.048	0.18	-0.25	-0.06	9140	7330	7000	7950	9500	9680	7530	8540	678.7	2033.2	3	0.0146	7.194
Uncharacterized protein OS=Bos taurus GN=Bt.22353 PE=4 SV=1	tr F1MI03 F1MI03_BOVIN	gQSP TSPD SR	51%	29	49.74143	Ref	-0.082	-0.38	0.27	0.05	0.56	-0.6	0.61	1220	832	732	1290	1220	1520	712	1640	668.3	1334.7	2	0.0088	6.561
Uncharacterized protein OS=Bos taurus GN=Bt.22353 PE=4 SV=1	tr F1MI03 F1MI03_BOVIN	sQSD SFSY PAID Sk	90%	45.5	53.59462	Ref	1	0.6	-0.19	-0.32	-0.07	-0.22	-0.08	7510	16800	13500	8680	8770	9090	8560	9370	714	2139.1	3	0.0144	6.72

Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	8 PSA7_H UMAN,sp Q3ZBG0 PSA7_B OVIN,sp Q9Z2U0 PSA7_MO USE,tr A7 E3D5 A7E 3D5_BOVI N,tr F1PU B5 F1PUB 5_CANFA, tr F6WS8 9 F6WS8 9_MOND O,tr F6ZQ X6 F6ZQX 6_HORSE, tr F7DLV7 F7DLV7_ MONDO,t r F7H5U7 F7H5U7_ MACMU,t r F7IGD2 F7IGD2_ k	aLLE VVQ SGG	86%	40	50.93436	Ref	-0.077	-0.54	-0.14	-0.11	-0.22	-0.42	-0.39	16300	13000	10200	15200	17000	13800	12600	12700	570.4	1708	3	0.0054	3.175
Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	8 PSA7_H UMAN,sp Q3ZBG0 PSA7_B OVIN,sp Q9Z2U0 PSA7_MO USE,tr A7 E3D5 A7E 3D5_BOVI N,tr F1PU B5 F1PUB 5_CANFA, tr F6WS8 9 F6WS8 9_MOND O,tr F6ZQ X6 F6ZQX 6_HORSE, tr F7DLV7 F7DLV7_ MONDO,t r F7H5U7 F7H5U7_ MACMU,t r F7IGD2 F7IGD2_ iLNPEEIEK	iLNPEEIEK	60%	32.7	52.03376	Ref	-0.046	-0.52	-0.06	-0.26	0.011	-0.58	-0.39	15600	13600	10600	16400	15800	16600	11500	13000	847	1692	2	0.0146	8.64

Cytosol aminopeptidase OS=Bos taurus GN=LAP3 PE=1 SV=3	sp P00727 AMPL_BOVIN,sp P28838 AMPL_HUMAN, tr F6TQJ2 F6TQJ2_MA CMU, tr F7IIB5 F7IIB5_CALJAK	gLV GIYS	88%	39.7	49.40746	Ref	-0.11	-0.43	-0.03	0.041	0.27	-0.28	0.006	6140	5090	4440	6570	7590	7790	5560	6710	520	1556.9	3	0.0253	16.25
Cytosol aminopeptidase OS=Bos taurus GN=LAP3 PE=1 SV=3	sp P00727 AMPL_BOVIN,sp P28838 AMPL_HUMAN, tr F6TQJ2 F6TQJ2_MA CMU, tr F7IIB5 F7IIB5_CALJAK	sAG AcTA AAFL	52%	33	53.22637	Ref	0.044	-0.2	-0.01	-0.21	0.009	-0.47	0.23	6110	5310	4870	6220	5960	6070	4560	7340	589	1763.9	3	0.0253	14.31
Peroxiredoxin 2 OS=Ovis aries GN=PRDX2 PE=2 SV=1	tr C8BKC5 C8BKC5_SHEEP	gLFV IDGK	85%	36.7	49.39479	Ref	0.2	-0.2	0.067	-0.069	0.015	-0.08	-0.25	16200	16200	13300	18000	18000	16700	16400	14400	729	1455.9	2	0.003	2.072
Peroxiredoxin 2 OS=Ovis aries GN=PRDX2 PE=2 SV=1	tr C8BKC5 C8BKC5_SHEEP	qVTV NDL PVG R	58%	32.4	51.95213	Ref	0.17	-0.17	-0	-0.062	-0.06	-0.01	-0.14	32700	32000	27400	34500	36600	31900	34500	31300	751.4	1500.8	2	0.0151	10.06

60S ribosomal protein L15 OS=Canis familiaris GN=RPL15 PE=1 SV=1	3 RL15_C ANFA,sp P61313 R L15_HUM AN,sp P6 1314 RL1 5_RAT,sp Q4R5B2 RL15_MA CFA,sp Q 5EAD6 RL 15_BOVIN ,sp Q5NV E0 RL15_ PONAB,sp Q9CZM2 RL15_M OUSE,tr B 4DLP4 B4 DLP4_HU MAN,tr D 2HKU3 D 2HKU3_AI LME,tr D 3ZU80 D3 ZU80_RAT ,tr D3ZXA	nTLQ LHR	80%	36.5	50.11295	Ref	0.36	0.18	0.35	-0.16	0.42	-0.19	0.14	45300	49600	47600	59900	46400	60600	41500	51800	395.9	1184.7	3	0.0088	7.453
60S ribosomal protein L15 OS=Canis familiaris GN=RPL15 PE=1 SV=1	3 RL15_C ANFA,sp P61313 R L15_HUM AN,sp P6 1314 RL1 5_RAT,sp Q4R5B2 RL15_MA CFA,sp Q 5EAD6 RL 15_BOVIN ,sp Q5NV E0 RL15_ PONAB,sp Q9CZM2 RL15_M OUSE,tr B 4DLP4 B4 DLP4_HU MAN,tr D 2HKU3 D 2HKU3_AI LME,tr D 3ZU80 D3 ZU80_RAT ,tr D3ZXA	sLQS VAEE R	67%	33.5	51.50342	Ref	0.64	-0.08	0.34	-0.004	0.2	0.035	0.011	42200	58200	38200	57400	50000	50200	46800	45700	661.9	1321.7	2	0.0113	8.558

<p>Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Bos taurus GN=COX41 PE=1 SV=1</p>	<p>sp P00423 COX41_BOVIN,sp P10888 COX41_RAT,sp Q9TTT8 COX41_RABIT, tr D7PDS5 D7PDS5_MINFU, tr D7PDS6 D7PDS6_CYN,sp, tr D7PDS7 D7PDS7_ROULE</p>	<p>dYPL PDV AHV k</p>	<p>82%</p>	<p>40.5</p>	<p>53.32337</p>	<p>Ref</p>	<p>0.24</p>	<p>0.18</p>	<p>0.42</p>	<p>-0.021</p>	<p>0.32</p>	<p>0.024</p>	<p>0.32</p>	<p>14800</p>	<p>14500</p>	<p>15000</p>	<p>19900</p>	<p>16200</p>	<p>17900</p>	<p>15300</p>	<p>18600</p>	<p>621.4</p>	<p>1861</p>	<p>3</p>	<p>0.0178</p>	<p>9.538</p>
<p>Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Bos taurus GN=COX41 PE=1 SV=1</p>	<p>sp P00423 COX41_BOVIN,sp P10888 COX41_RAT,sp Q9TTT8 COX41_RABIT, tr D7PDS5 D7PDS5_MINFU, tr D7PDS6 D7PDS6_CYN,sp, tr D7PDS7 D7PDS7_ROULE</p>	<p>sEDY ALPS YVD R</p>	<p>63%</p>	<p>32.1</p>	<p>50.88317</p>	<p>Ref</p>	<p>0.39</p>	<p>0.19</p>	<p>0.4</p>	<p>-0.013</p>	<p>0.48</p>	<p>-0.35</p>	<p>0.37</p>	<p>7930</p>	<p>9500</p>	<p>8940</p>	<p>11600</p>	<p>9620</p>	<p>11800</p>	<p>6950</p>	<p>11400</p>	<p>859.9</p>	<p>1717.8</p>	<p>2</p>	<p>0.0141</p>	<p>8.227</p>

<p>Endothelin-converting enzyme 1 OS=Bos taurus GN=ECE1 PE=1 SV=2</p>	<p>sp P42891 ECE1_BOVIN,sp P42893 ECE1_RAT,sp P97739 ECE1_CAVPO,tr D2HCA3 D2HCA3_AILME,tr F1M824 F1M824_RAT,tr F1SU04 F1SU04_PIG,tr F6YGG8 F6YGG8_HORSE,tr Q28010 Q28010_BOVIN,tr Q28868 Q28868_BOVIN,tr Q6IN10 Q6IN10_RAT</p>	<p>aNP VPD GHS R</p>	<p>54%</p>	<p>30.8</p>	<p>51.09703</p>	<p>Ref</p>	<p>0.31</p>	<p>-0.32</p>	<p>0.18</p>	<p>0.15</p>	<p>0.55</p>	<p>-0.91</p>	<p>0.28</p>	<p>3610</p>	<p>3480</p>	<p>2450</p>	<p>3870</p>	<p>4180</p>	<p>4830</p>	<p>1830</p>	<p>4140</p>	<p>677.4</p>	<p>1352.7</p>	<p>2</p>	<p>0.0082</p>	<p>6.021</p>
<p>Endothelin-converting enzyme 1 OS=Bos taurus GN=ECE1 PE=1 SV=2</p>	<p>sp P42891 ECE1_BOVIN,sp P42893 ECE1_RAT,sp P97739 ECE1_CAVPO,tr D2HCA3 D2HCA3_AILME,tr F1M824 F1M824_RAT,tr F1SU04 F1SU04_PIG,tr F6YGG8 F6YGG8_HORSE,tr Q28010 Q28010_BOVIN,tr Q28868 Q28868_BOVIN,tr Q6IN10 Q6IN10_RAT</p>	<p>hTLG ENIA DnG GLk</p>	<p>85%</p>	<p>42.6</p>	<p>53.98319</p>	<p>Ref</p>	<p>0.15</p>	<p>-0.28</p>	<p>0.4</p>	<p>0.071</p>	<p>0.12</p>	<p>0.2</p>	<p>0.23</p>	<p>28000</p>	<p>30500</p>	<p>24500</p>	<p>44300</p>	<p>38800</p>	<p>35100</p>	<p>38700</p>	<p>39300</p>	<p>683.4</p>	<p>2047.1</p>	<p>3</p>	<p>0.0152</p>	<p>7.411</p>

Pyruvate kinase isozyme M1 OS=Felis catus GN=PKM2 PE=1 SV=2	9 KPYM_ FELCA,tr A5D984 A5D984_ BOVIN,tr B3IVM0 B3IVM0_ HORSE,tr B3IVM1 B3IVM1_ HORSE,tr F1MIZ0 F 1MIZ0_B OVIN,tr F 1PHR2 F1 PHR2_CA NFA,tr F1 SHL7 F1S HL7_PIG,t r F1SHL8 F1SHL8_ PIG,tr F6 Q907 F6 Q907_CAL JA,tr F6W IDID 3M5 F6W SPPI 3M5_HOR TAR	81%	37.7	51.91652	Ref	-0.002	0.077	-0.11	-0.016	-0.12	0.27	-0.35	41600	35500	40700	40100	47200	38500	52500	34000	751.4	1500.8	2	0.0116	7.702
Pyruvate kinase isozyme M1 OS=Felis catus GN=PKM2 PE=1 SV=2	9 KPYM_ FELCA,tr A5D984 A5D984_ BOVIN,tr B3IVM0 B3IVM0_ HORSE,tr B3IVM1 B3IVM1_ HORSE,tr F1MIZ0 F 1MIZ0_B OVIN,tr F 1PHR2 F1 PHR2_CA NFA,tr F1 SHL7 F1S HL7_PIG,t r F1SHL8 F1SHL8_ PIG,tr F6 Q907 F6 Q907_CAL JA,tr F6W VNLA 3M5 F6W MNV 3M5_HOR GK	62%	33.3	51.82974	Ref	0.32	0.22	-0.12	-0.3	-0.18	-0.01	-0.15	5760	6350	6430	5700	5570	5270	6180	5570	518.6	1552.9	3	0.0226	14.53

Metadherin OS=Bos taurus GN=MTDHP E=2 SV=1	tr Q24JZ4 Q24JZ4_BOVIN	tIEV AEEE VVR	50%	31.8	52.60727	Ref	-0.14	-0.21	-0.18	-0.25	-0.02	-0.17	-0.22	14300	12000	12400	14200	14900	15300	14400	13800	789.4	1576.9	2	0.0105	6.638
Metadherin OS=Bos taurus GN=MTDHP E=2 SV=1	tr Q24JZ4 Q24JZ4_BOVIN	tLPP AIST EPSV ILSk	86%	39.9	50.93873	Ref	-0.44	-0.32	-0.2	-0.25	0.14	-0.2	-0.17	6210	3760	4420	5410	5770	6590	5430	5490	754.5	2260.3	3	0.0193	8.551
28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=1 SV=1	2 HAP28_HUMAN,s p Q3UHX 2 HAP28_MOUSE,s p Q62785 HAP28_RAT,tr B2RTB0 B2RTB0_MOUSE,tr D2HP72 D2HP72_AILME,tr F1MNS8 F1MNS8_BOVIN,tr F1PU14 F1PU14_CANFA,tr F1REX6 F1REX6_PIG,tr F1RNS8 F1RNS8_PIG,tr F6QSX1 F6QSX1_ORNAN,tr	aDLA R	54%	28.8	49.00012	Ref	0.029	1.2	1.1	1.1	1.4	0.89	1.7	18600	17200	42600	45600	49200	51000	38200	65900	425.3	848.49	2	0.0119	14.06

<p>28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=1 SV=1</p>	<p>2 HAP28_HUMAN,sp Q3UHX2 HAP28_MOUSE,sp Q62785 HAP28_RAT,tr B2RTB0 B2RTB0_MOUSE,tr D2HP72 D2HP72_AILME,tr F1MNS8 F1MNS8_BOVIN,tr F1PU14 F1PU14_CANFA,tr F1REX6 F1REX6_PIG,tr F1RNS8 F1RNS8_PIG,tr F6QXS1 F6QXS1_ORNAN,tr</p>	<p>KGVE GLID IENP NR</p>	<p>83%</p>	<p>40.9</p>	<p>53.47102</p>	<p>Ref</p>	<p>-0.068</p>	<p>0.93</p>	<p>1</p>	<p>1.2</p>	<p>1.5</p>	<p>0.8</p>	<p>1.8</p>	<p>15700</p>	<p>12500</p>	<p>27000</p>	<p>32600</p>	<p>41100</p>	<p>43900</p>	<p>27800</p>	<p>53900</p>	<p>721.4</p>	<p>2161.2</p>	<p>3</p>	<p>0.0202</p>	<p>9.342</p>
<p>T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1</p>	<p>3 TCPE_HUMAN,sp P80316 TCPE_MOUSE,sp Q4R6V2 TCPE_MACFA,sp Q5RF02 TCPE_PONAB,sp Q68FQ0 TCPE_RAT,tr A8K2X8 A8K2X8_HUMAN,tr B2KI54 B2KI54_RHIFE,tr B4DXI1 B4DXI1_HUMAN,tr B4DYC8 B4DYC8_HUMAN,tr B4DZT5 B4DZT5_HUMAN,tr</p>	<p>g HPI R</p>	<p>69%</p>	<p>30.3</p>	<p>47.24685</p>	<p>Ref</p>	<p>-0.074</p>	<p>0.23</p>	<p>0.28</p>	<p>-0.32</p>	<p>0.38</p>	<p>-0.23</p>	<p>-0.22</p>	<p>5020</p>	<p>4900</p>	<p>6560</p>	<p>7610</p>	<p>5530</p>	<p>7840</p>	<p>5370</p>	<p>5360</p>	<p>332.9</p>	<p>995.61</p>	<p>3</p>	<p>0.0044</p>	<p>4.462</p>

T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1	3 TCPE_H UMAN,sp P80316 TCPE_MO USE,sp Q 4R6V2 TC PE_MACF A,sp Q5R F02 TCPE _PONAB,s p Q68FQ 0 TCPE_R AT,tr A8K 2X8 A8K2 X8_HUMA N,tr B2KI 54 B2KI5 4_RHIFE,t r B4DXI1 B4DXI1_H UMAN,tr B4DYC8 B 4DYC8_H UMAN,tr B4DZT5 B 4DZT5_H UMAN,tr	IMGL EALK	71%	33.9	50.51299	Ref	0.15	-0.19	0.07	-0.13	0.062	-0.35	0.079	2050	1710	1470	1970	1890	1890	1480	1980	495	1481.9	3	0.0023	1.542
Uncharacterized protein OS=Canis familiaris GN=TMOD3 PE=4 SV=1	tr E2QWL 1 E2QWL 1_CANFA, tr F6PZY1 F6PZY1_ HORSE	fGYQ FTQ QGP R	64%	33.3	51.8771	Ref	-0.11	-0.47	-0.25	-0.19	0.063	-0.18	-0.04	5690	4590	3860	5060	5800	6060	5330	5850	816.9	1631.8	2	0.0135	8.285
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_018456 PE=4 SV=1	tr D2I019 D2I019_ AILME,tr E2RI84 E 2RI84_CA NFA	eNSS EDQ GSk	66%	34.3	52.02129	Ref	-0.3	-0.24	-0.16	-0.19	0.18	-0.63	0.007	5450	3850	4350	5160	5560	6280	3740	5780	563.6	1687.8	3	0.0104	6.171

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_018456 PE=4 SV=1	tr D2I019 D2I019_AILME, tr E2R184 E2R184_CA_NFA	qQSELSAAVER	69%	34.6	52.04633	Ref	-0.44	-0.22	-0.04	-0.21	0.11	-0.44	-0.05	22800	14700	18500	23500	23100	25100	17900	23400	761.4	1520.8	2	0.0132	8.649
cDNA FLJ51794, highly similar to Annexin A4 OS=Homo sapiens PE=2 SV=1	tr B4DDZ4 B4DDZ4_HUMAN, tr F7GDF3 F7GDF3_MONDO	gLGT Dn TLIR	57%	32.4	52.1187	Ref	0.23	-0.4	-0.08	-0.22	-0.33	-0.22	-0.56	25100	27800	19500	27400	27400	22200	25000	19700	740.4	1478.8	2	0.0119	8.067
cDNA FLJ51794, highly similar to Annexin A4 OS=Homo sapiens PE=2 SV=1	tr B4DDZ4 B4DDZ4_HUMAN, tr F7GDF3 F7GDF3_MONDO	nHLL HVF DEYR	76%	35.5	52.70889	Ref	-0.15	-0.38	-0.2	-0.42	0.073	-0.63	-0.15	1190	861	793	1020	959	1180	757	1050	437.5	1745.9	4	0.0081	4.616
Alpha-2-antiplasmin OS=Bos taurus GN=SERPINF2 PE=1 SV=2	sp P28800 A2AP_BOVIN	lcQD LGP GAF R	54%	31	51.27607	Ref	0.82	0.24	0.75	0.58	0.11	0.96	0.5	2380	3460	2510	4020	3930	2480	4670	3370	763.9	1525.8	2	0.011	7.182

Alpha-2-antiplasmin OS=Bos taurus GN=SERPINF2 PE=1 SV=2	sp P2880 0 A2AP_B OVIN	IPPLS LLk	77%	28.5	43.30414	Ref	0.64	0.36	0.89	0.77	-0.04	1.1	0.22	7180	10300	9200	14900	15100	7520	17100	9360	497	1488	3	0.0119	7.968
Dihydrolipoyllysine- residue succinyltransferase component of 2- oxoglutarate dehydrogenase complex, mitochondrial OS=Bos taurus GN=DLST PE=1 SV=2	sp P1117 9 ODO2_ BOVIN,sp Q9N0F1 ODO2_PI G,tr E1BA P2 E1BAP 2_BOVIN, tr E2R0H 0 E2R0H0 _CANFA,tr F1MEQ3 F1MEQ3 _BOVIN,tr F7E1R7 F7E1R7_ MONDO	aAVE DPR	75%	32.6	48.83991	Ref	0.0076	-0.2	-0.32	-0.34	-0.32	-0.39	-0.2	20500	17200	16200	16700	18200	16100	16000	18100	531.3	1060.6	2	#####	0.314
Dihydrolipoyllysine- residue succinyltransferase component of 2- oxoglutarate dehydrogenase complex, mitochondrial OS=Bos taurus GN=DLST PE=1 SV=2	sp P1117 9 ODO2_ BOVIN,sp Q9N0F1 ODO2_PI G,tr E1BA P2 E1BAP 2_BOVIN, tr E2R0H 0 E2R0H0 _CANFA,tr F1MEQ3 F1MEQ3 _BOVIN,tr F7E1R7 F7E1R7_ MONDO	dDVI TVk	57%	31.2	50.87135	Ref	-0.11	-0.35	-0.06	-0.36	-0.1	-0.56	-0.13	25300	21200	19500	26600	24000	25000	19000	25400	699.4	1396.8	2	#####	0.507

Prefoldin subunit 4 OS=Bos taurus GN=PFDN4 PE=2 SV=1	sp Q2TBR6 PFD4_BOVIN,sp Q9NQP4 PFD4_HUMAN,tr A5GHK3 A5GHK3_PIG,tr E9PQY2 E9PQY2_HUMAN,tr F1MYY3 F1MYY3_BOVIN,tr F7BMN8 F7BMN8_CALJA,tr F7HSD0 F7HSD0_MACMU	KNL QEEI DALE SR	77%	39.3	54.11435	Ref	-0.032	-0.02	0.086	0.13	0.28	-0.16	0.11	4140	3530	3860	4670	5300	5160	3960	4730	718.4	2152.2	3	0.0151	7.003
Prefoldin subunit 4 OS=Bos taurus GN=PFDN4 PE=2 SV=1	sp Q2TBR6 PFD4_BOVIN,sp Q9NQP4 PFD4_HUMAN,tr A5GHK3 A5GHK3_PIG,tr E9PQY2 E9PQY2_HUMAN,tr F1MYY3 F1MYY3_BOVIN,tr F7BMN8 F7BMN8_CALJA,tr F7HSD0 F7HSD0_MACMU	VLAD Lk	51%	27.5	48.01493	Ref	-0.37	-0.18	0.17	0.062	0.57	-0.34	0.27	6880	4620	5710	8160	8360	10400	5790	8710	422.9	1265.8	3	0.0027	2.144
Myosin-10 OS=Bos taurus GN=MYH10 PE=2 SV=2	sp Q27991 MYH10_BOVIN,tr F1SSA6 F1SSA6_PIG	eLDD ATEA NEG LSR	74%	34.4	50.75079	Ref	-1	0.34	-1.6	-0.19	-1.4	0.023	-1.7	7490	3040	8470	2550	7220	2790	7650	2280	912.4	1822.9	2	0.0149	8.157

Myosin-10 OS=Bos taurus GN=MYH10 PE=2 SV=2	sp Q27991 MYH10_BOVIN, tr F1SSA6 F1SSA6_PIG	qLEE AEEE ATR	55%	30.5	50.54579	Ref	-1	0.28	-1.7	-0.09	-1.2	-0.03	-1.3	8170	3750	9950	2910	9510	3830	9070	3800	804.9	1607.8	2	0.0125	7.794
Protein DJ-1 OS=Bos taurus GN=PARK7 PE=2 SV=1	sp Q5E946 PARK7_BOVIN	IVEV LVGK	50%	27.2	47.76498	Ref	0.69	-0.02	0.21	-0.15	0.078	0.12	-0.08	2990	4360	2880	3810	3260	3340	3580	3110	489	1463.9	3	0.0245	16.75
Protein DJ-1 OS=Bos taurus GN=PARK7 PE=2 SV=1	sp Q5E946 PARK7_BOVIN	VTTT PLAK	75%	33.1	49.22061	Ref	0.34	0.045	0.099	0.018	0.28	-0.01	0.11	8420	8960	7900	9210	9600	10000	8610	9280	738	1473.9	2	0.0044	2.961
Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2	7 SRSF6_HUMAN, sp Q3B7L6 SRSF6_BOVIN, tr A8K588 A8K588_HUMAN, tr F1MX9 F1MX9_BOVIN, tr F1PTE0 F1PTE0_CAF6 F6PIF7 F6PIF7_MONDO, tr F6TV78 F6TV78_CALJA, tr F7GJ43 F7GJ43_MONDO, tr Q06AA0 Q06AA0_PIG, tr Q3TWW8 Q3TWW8	qAG EVTY ADA HKER	62%	33.9	54.27601	Ref	0.19	0.3	0.012	-0.016	0.27	0.022	0.56	7150	7770	9070	8340	9020	9620	8440	12200	546.5	2182.1	4	0.0192	8.774

<p>Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2</p>	<p>7 SRSF6_HUMAN,sp Q3B7L6 SRSF6_BOVIN,tr A8K588 A8K588_HUMAN,tr F1MXY9 F1MXY9_BOVIN,tr F1PTE0 F1PTE0_CANFA,tr F6PIF7 F6PIF7_MONDO,tr F6TV78 F6TV78_CALJATR F7GJ43 F7GJ43_MONDO,tr Q06AA0 Q06AA0_PIG,tr Q3TWW8 Q3TWW8</p>	<p>tNEG VIEF R</p>	<p>61%</p>	<p>32.6</p>	<p>51.71475</p>	<p>Ref</p>	<p>0.2</p>	<p>0.27</p>	<p>0.33</p>	<p>-0.084</p>	<p>0.28</p>	<p>-0.1</p>	<p>0.26</p>	<p>21300</p>	<p>19600</p>	<p>22200</p>	<p>26100</p>	<p>21600</p>	<p>24200</p>	<p>19500</p>	<p>24700</p>	<p>684.9</p>	<p>1367.7</p>	<p>2</p>	<p>0.008</p>	<p>5.868</p>
<p>EH domain-containing protein 2 OS=Rattus norvegicus GN=Ehd2 PE=1 SV=1</p>	<p>sp Q4V8H8 EHD2_RAT,sp Q8BH64 EHD2_MOUSE,tr D2H814 D2H814_AILME,tr F1PNP7 F1PNP7_CANFA,tr Q2KJ47 Q2KJ47_BOVIN,tr Q8R2X0 Q8R2X0_MOUSE</p>	<p>kLNP FGN TFLN R</p>	<p>68%</p>	<p>35.4</p>	<p>52.68852</p>	<p>Ref</p>	<p>-0.028</p>	<p>-0.41</p>	<p>8E-04</p>	<p>-0.27</p>	<p>-0.24</p>	<p>-0.23</p>	<p>-0.22</p>	<p>1660</p>	<p>1360</p>	<p>1130</p>	<p>1690</p>	<p>1540</p>	<p>1370</p>	<p>1450</p>	<p>1450</p>	<p>677.1</p>	<p>2028.2</p>	<p>3</p>	<p>0.0156</p>	<p>7.699</p>

EH domain-containing protein 2 OS=Rattus norvegicus GN=Ehd2 PE=1 SV=1	sp Q4V8H8 EHD2_RAT,sp Q8BH64 EHD2_MOUSE,tr D2H814 D2H814_AILME,tr F1PNP7 F1PNP7_CANFA,tr Q2KJ47 Q2KJ47_BOVIN,tr Q8R2X0 Q8R2X0_MOUSE	IEGH GLPT NLPR	53%	32.3	52.53646	Ref	-0.27	-0.34	-0.02	-0.22	-0.09	-0.21	-0.07	8850	6640	6890	9640	9240	8830	8480	9270	536.6	1606.9	3	0.012	7.439
Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	1 H31_HUMAN,sp P68432 H31_BOVIN,sp P68433 H31_MOUSE,sp P84227 H32_BOVIN,sp P84228 H32_MOUSE,sp Q16695 H31T_HUMAN,sp Q64400 H32_CRILLO,sp Q6LBE8 H32_MUSPA,sp Q6LBF0 H31_MUSPA,sp Q6LED0 H31_RAT,sp Q71DI3 H32_HUMA	kSAP ATG GVK	55%	28.4	48.29536	Ref	0.23	0.23	-0.55	0.1	0.2	0.15	0.31	16700	18400	19900	13100	22600	21000	21300	23600	610.1	1827.1	3	0.004	2.201

Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	1 H31_H UMAN,sp P68432 H31_BOVI N,sp P68 433 H31_ MOUSE,s p P84227 H32_BO VIN,sp P8 4228 H32 _MOUSE, sp Q1669 5 H31T_H UMAN,sp Q64400 H32_CRIL O,sp Q6L BE8 H32_ MUSPA,sp Q6LBF0 H31_MUS PA,sp Q6 LED0 H31 _RAT,sp Q71D13 H 32_HUMA	sAPA TGG Vk	64%	31.9	50.42524	Ref	0.37	0.47	-0.71	0.11	0.037	0.092	-0.02	6400	6700	7800	3860	7490	6220	6750	6190	698.4	1394.8	2	0.0058	4.18
Tax1-binding protein 3 OS=Homo sapiens GN=TAX1BP3 PE=1 SV=2	7 TX1B3_ HUMAN,s p Q9DBG 9 TX1B3_ MOUSE,tr A2SZV5 A2SZV5_P IG,tr B2K GB7 B2K GB7_MO USE,tr D4 ADL4 D4 ADL4_RA T,tr E2R9J 0 E2R9J0 _CANFA,tr F2Z516 F2Z516_PI G,tr F6WI C5 F6WIC 5_HORSE, tr F6XW7 6 F6XW7 6_CALJA,t r F7E319 F7E319_M ACMU,tr	vSEG GPA EIAG LQIG DK	95%	58	54.13866	Ref	0.44	-0.16	0.37	0.22	0.15	-0.15	-0.16	4200	5170	3710	6000	5960	4940	4200	4130	750.4	2248.2	3	0.0183	8.138

<p>Tax1-binding protein 3 OS=Homo sapiens GN=TAX1BP3 PE=1 SV=2</p>	<p>7 TX1B3_ HUMAN,s p Q9DBG 9 TX1B3_ MOUSE,tr A2SZV5 A2SZV5_P IG,tr B2K GB7 B2K GB7_MO USE,tr D4 ADL4 D4 ADL4_RA T,tr E2R9J 0 E2R9J0 _CANFA,tr F2Z516 F2Z516_PI G,tr F6WI C5 F6WIC 5_HORSE, tr F6XW7 6 F6XW7 6_CALJA,t r F7E3I9 F7E3I9_M ACMU,tr </p>	<p>vSEG GPA EIAG LQIG</p>	<p>Dk</p>	<p>89%</p>	<p>44.8</p>	<p>53.80866</p>	<p>Ref</p>	<p>0.095</p>	<p>0.083</p>	<p>0.015</p>	<p>0.45</p>	<p>-0.22</p>	<p>0.24</p>	<p>-0.01</p>	<p>6290</p>	<p>5610</p>	<p>6040</p>	<p>6460</p>	<p>9620</p>	<p>5280</p>	<p>7600</p>	<p>6330</p>	<p>750.4</p>	<p>2248.3</p>	<p>3</p>	<p>#####</p>	<p>0.403</p>
<p>Dystrglycan OS=Bos taurus GN=DAG1 PE=1 SV=1</p>	<p>sp O1873 8 DAG1_ BOVIN,sp Q14118 DAG1_HU MAN,tr F 1N7D7 F1 N7D7_BO VIN,tr F6 RU72 F6R U72_MAC MU,tr F6 TRX4 F6T RX4_CALJ A,tr F6X9 U4 F6X9U 4_HORSE</p>	<p>gGLS AVD AFEI HVH</p>	<p>R</p>	<p>62%</p>	<p>35.2</p>	<p>53.75609</p>	<p>Ref</p>	<p>0.072</p>	<p>0.12</p>	<p>-0.12</p>	<p>-0.11</p>	<p>0.003</p>	<p>-0.12</p>	<p>-0.01</p>	<p>3740</p>	<p>3860</p>	<p>4320</p>	<p>4120</p>	<p>4570</p>	<p>4310</p>	<p>4120</p>	<p>4450</p>	<p>638</p>	<p>1911</p>	<p>3</p>	<p>0.0108</p>	<p>5.637</p>

Dystrglycan OS=Bos taurus GN=DAG1 PE=1 SV=1	sp O18738 DAG1_BOVIN,sp Q14118 DAG1_HUMAN,tr F1N7D7 F1N7D7_BOVIN,tr F6RU72 F6RU72_MACMU,tr F6TRX4 F6TRX4_CALA,tr F6X9U4 F6X9U4_HORSE	gGLS AVD AFEI HVH R	95%	55.1	53.7289	Ref	-0.13	-0.18	-0.1	-0.2	-0.03	-0.1	0.22	2780	1980	2070	2450	2520	2480	2470	3060	478.8	1911	4	0.0089	4.662
Aspartate aminotransferase, mitochondrial OS=Bos taurus GN=GOT2 PE=1 SV=2	sp P12344 AATM_BOVIN	iSVA GVTS GNV AYLA HAIH QVT k	95%	57.5	53.30811	Ref	0.067	-0.1	-0.09	-0.18	0.038	0.001	-0.04	603	588	567	643	663	675	687	662	736.9	2943.7	4	0.0211	7.17
Aspartate aminotransferase, mitochondrial OS=Bos taurus GN=GOT2 PE=1 SV=2	sp P12344 AATM_BOVIN	iSVA GVTS GNV AYLA HAIH QVT k	95%	64.9	52.92905	Ref	0.084	-0.16	0.022	-0.13	-0.22	0.18	-0.34	1110	955	877	1110	1100	907	1250	868	736.9	2943.7	4	0.0109	3.692

Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	6 PSA5_H UMAN,sp Q5E987 PSA5_BO VIN,sp Q 9Z2U1 PS A5_MOUS E,tr D3YX 79 D3YX7 9_MOUSE ,tr E2R4H 4 E2R4H4 _CANFA,tr F2Z5K2 F2Z5K2_PI G,tr F6Q W93 F6Q W93_MO NDO,tr F 6UT72 F6 UT72_OR NAN,tr F6 VEA3 F6V EA3_HOR SE,tr F6V LE9 F6VL E9_MAC	IFQV EYAI EAIK	95%	55.1	52.17102	Ref	0.5	-0.28	0.22	-0.23	-0.12	-0.25	-0.32	1370	1450	919	1450	1170	1110	1060	1000	678.1	2031.2	3	0.0132	6.488
Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	6 PSA5_H UMAN,sp Q5E987 PSA5_BO VIN,sp Q 9Z2U1 PS A5_MOUS E,tr D3YX 79 D3YX7 9_MOUSE ,tr E2R4H 4 E2R4H4 _CANFA,tr F2Z5K2 F2Z5K2_PI G,tr F6Q W93 F6Q W93_MO NDO,tr F 6UT72 F6 UT72_OR NAN,tr F6 VEA3 F6V EA3_HOR SE,tr F6V LE9 F6VL E9_MAC	IFQV EYAI EAIK	75%	36.5	52.07365	Ref	0.22	-0.59	0.37	0.019	-0.16	0.31	-0.2	362	436	269	589	509	393	568	395	678.1	2031.2	3	0.0099	4.864

Hematopoietic progenitor cell antigen CD34 OS=Homo sapiens GN=CD34 PE=1 SV=2	6 CD34_HUMAN,sp Q64314 CD34_MOUSE,tra A8KAG5 A8KAG5_HUMAN,tra B1PLB1 B1PLB1_RAT,tra B4DG27 B4DG27_HUMAN,tra B4DUX4 B4DUX4_HUMAN,tra D2HUI0 D2HUI0_AILME,tra F1MN25 F1MN25_BOVIN,tra F1PE59 F1PE59_CANFA,tra F1SF32 F1SF3	gAQ EnGT GQA TSR	95%	45	50.01418	Ref	-0.5	-0.93	0.53	-0.18	0.67	-1.6	0.64	1820	1100	885	2720	1840	2900	623	2930	791.4	1580.8	2	0.0091	5.778
	6 CD34_HUMAN,sp Q64314 CD34_MOUSE,tra A8KAG5 A8KAG5_HUMAN,tra B1PLB1 B1PLB1_RAT,tra B4DG27 B4DG27_HUMAN,tra B4DUX4 B4DUX4_HUMAN,tra D2HUI0 D2HUI0_AILME,tra F1MN25 F1MN25_BOVIN,tra F1PE59 F1PE59_CANFA,tra F1SF32 F1SF3	gAQ EnGT GQA TSR	95%	53.7	49.98412	Ref	-0.59	-0.91	0.67	-0.17	0.48	-1.8	0.79	1350	798	696	2340	1440	1960	427	2520	791.4	1580.8	2	0.0079	5.007

Small ubiquitin-related modifier 3 OS=Homo sapiens GN=SUMO3 PE=1 SV=2	4 SUMO3_HUMAN,sp P61955 SUMO2_BOVIN,sp P61956 SUMO2_HUMAN,sp P61957 SUMO2_MOUSE,sp P61958 SUMO2_PIG,sp P61959 SUMO2_RAT,sp Q17QV3 SUMO3_BOVIN,sp Q2PFW2 SUMO2_MACFA,sp Q5XF4 SUMO3_RAT,sp Q6EEV6 SUMO4_QFk	VAG QDG SVV QFk	95%	66.4	53.33343	Ref	-0.61	-0.01	-0	0.16	0.5	-0.2	0.36	36800	23700	39200	44100	54300	60400	38700	56700	922	1842	2	0.0173	9.39
Small ubiquitin-related modifier 3 OS=Homo sapiens GN=SUMO3 PE=1 SV=2	4 SUMO3_HUMAN,sp P61955 SUMO2_BOVIN,sp P61956 SUMO2_HUMAN,sp P61957 SUMO2_MOUSE,sp P61958 SUMO2_PIG,sp P61959 SUMO2_RAT,sp Q17QV3 SUMO3_BOVIN,sp Q2PFW2 SUMO2_MACFA,sp Q5XF4 SUMO3_RAT,sp Q6EEV6 SUMO4_QFk	VAG QDG SVV QFk	95%	51.8	53.23504	Ref	-0.04	0.011	0.016	0.061	0.083	-0.05	0.042	14500	10900	12300	13800	15700	13900	13300	14000	615	1842	3	0.0166	9.003

Calponin-2 OS=Mus musculus GN=Cnn2 PE=2 SV=1	3 CNN2_MOUSE,sp Q3SYU6 CNN2_BOVIN,sp Q5RFN6 CNN2_PONAB,sp Q99439 CNN2_HUMAN,transcript B4DDF4 B4DDF4_HUMAN,transcript B4DHU5 B4DHU5_HUMAN,transcript B4DUT8 B4DUT8_HUMAN,transcript E2R5Q1 E2R5Q1_CANFA,transcript E7ENR3 E7ENR3_HUMAN,transcript F7BIZ6 F7	gLQSGVDI	95%	51.6	52.26456	Ref	0.016	0.027	-0.24	-0.2	-0.19	0.13	-0.22	89800	80300	87800	82200	92700	81600	1E+05	82600	561	1680	3	0.0159	9.438
Calponin-2 OS=Mus musculus GN=Cnn2 PE=2 SV=1	3 CNN2_MOUSE,sp Q3SYU6 CNN2_BOVIN,sp Q5RFN6 CNN2_PONAB,sp Q99439 CNN2_HUMAN,transcript B4DDF4 B4DDF4_HUMAN,transcript B4DHU5 B4DHU5_HUMAN,transcript B4DUT8 B4DUT8_HUMAN,transcript E2R5Q1 E2R5Q1_CANFA,transcript E7ENR3 E7ENR3_HUMAN,transcript F7BIZ6 F7	gLQSGVDI	95%	57.5	52.10083	Ref	0.076	0.21	-0.19	-0.23	-0.24	-0.16	-0.22	21100	19000	22600	19300	20600	18000	19800	18900	841	1680	2	0.0108	6.448

Cysteine-rich protein 2 OS=Bos taurus GN=CRIP2 PE=2 SV=1	sp Q0VFX8 CRIP2_BOVIN	gVNT GAV GSYI YDk DPE Gk	92%	49.1	55.22315	Ref	0.025	0.17	0.11	0.31	0.69	-0.21	0.1	3420	3030	3630	3930	4960	5610	3140	3880	961.5	2881.5	3	0.0226	7.831
Cysteine-rich protein 2 OS=Bos taurus GN=CRIP2 PE=2 SV=1	sp Q0VFX8 CRIP2_BOVIN	gVNT GAV GSYI YDk DPE Gk	95%	52.4	55.15524	Ref	0.24	7E-04	0.21	0.12	0.55	-0.12	0.26	11700	12000	11000	14400	14900	17400	11500	14800	721.4	2881.5	4	0.0165	5.723
Astrocytic phosphoprotein PEA-15 OS=Homo sapiens GN=PEA15 PE=1 SV=2	1 PEA15_HUMAN,sp Q5R529 PEA15_PONAB,sp Q5U318 PEA15_RAT,sp Q62048 PEA15_MOUSE,sp Q9Z297 PEA15_CRIGR, B1AKZ3 B1AKZ3_HUMAN,t B1AKZ4 B1AKZ4_HUMAN,t B1AKZ5 B1AKZ5_HUMAN,t D2I016 D2I016_ALME, D3Z375 D3Z375_MO	rPDL LTM VVD YR	95%	55.3	53.45491	Ref	Value Missing (-0.0011906972)	0.89	0.59	0.55	0.46	0.46	0.46	5540	6972	10100	9290	9950	8150	8510	8430	594.7	1781	3	0.0204	11.43

Astrocytic phosphoprotein PEA-15 OS=Homo sapiens GN=PEA15 PE=1 SV=2	1 PEA15_HUMAN,sp Q5R529 PEA15_PONAB,sp Q5U318 PEA15_RA T,sp Q62048 PEA15_MOUSE,sp Q9Z297 PEA15_CRIGR,tr B1AKZ3 B1AKZ3_HUMAN,tr B1AKZ4 B1AKZ4_HUMAN,tr B1AKZ5 B1AKZ5_HUMAN,tr D2I016 D2I016_ALME,tr D3Z375 D3Z375_MO	rPDL LTM VVD YR	95%	61	53.33951	Ref	-0.065	0.86	0.45	0.54	0.66	0.42	0.41	1580	1250	2590	2170	2560	2420	2150	2110	594.7	1781	3	0.0101	5.675
Alpha-1-acid glycoprotein OS=Bos taurus GN=ORM1 PE=2 SV=1	sp Q3SZR3 A1AG_BOVIN,tr E1BEB5 E1BEB5_BOVIN,tr E1UYU1 E1UYU1_RU PRU,tr F1ME86 F1ME86_BOVIN,tr Q5GN72 Q5GN72_BOVIN	alQA AFFY LEPR	85%	41.4	53.02796	Ref	-0.35	-0.1	-0.4	-0.61	-0.73	0.15	0.005	637	520	671	613	587	470	901	811	577.3	1728.9	3	0.011	6.336

Alpha-1-acid glycoprotein OS=Bos taurus GN=ORM1 PE=2 SV=1	sp Q3SZR3 A1AG_BOVIN, tr E1BEB5 E1BEB5_BOVIN, tr E1UYU1 E1UYU1_RU PRU, tr F1ME86 F1ME86_BOVIN, tr Q5GN72 Q5GN72_BOVIN	alQA AFFY LEPR	95%	59.3	53.08878	Ref	-0.066	-0.39	-0.35	-0.42	-0.62	-0.29	-0.35	462	329	286	328	344	262	344	329	577.3	1728.9	3	0.0102	5.92
Costars family protein C6orf115 homolog OS=Bos taurus PE=3 SV=1	sp Q3ZBN0 CF115_BOVIN	ILVE EIHR	95%	51.6	51.3527	Ref	0.066	-0.59	0.69	0.088	0.67	-0.38	0.4	6680	6470	4460	12100	8810	11600	5800	9890	438.3	1311.8	3	0.0097	7.38
Costars family protein C6orf115 homolog OS=Bos taurus PE=3 SV=1	sp Q3ZBN0 CF115_BOVIN	ILVE EIHR	89%	42.8	51.51808	Ref	0.25	-0.1	0.48	0.009	0.48	-0.12	0.15	3310	3220	2740	4610	3660	4430	3040	3640	438.3	1311.8	3	0.0057	4.318

Calcium-regulated heat stable protein 1 OS=Mus musculus GN=Carhsp1 PE=1 SV=1	6 CHSP1_MOUSE,s p Q9WU49 CHSP1_RAT,sp Q9Y2V2 CHSP1_HUMAN,tr D2HCQ6 D2HCQ6_AILME,tr E2QZZ6 E2QZZ6_CANFA,tr F1RKY9 F1RKY9_PIG,tr F6VUJ6 F6VUJ6_HORSE,tr F7F6H6 F7F6H6_MACMU,tr F71981 F71981_CALA,tr F71P66 CALJA,tr	IQAV EVVI THLA PGTk	95%	59.3	50.28034	Ref	-0.37	-0.22	-0.45	-0.17	0.25	-0.29	-0.38	965	591	713	682	908	1060	765	713	571.8	2283.4	4	0.0189	8.292
Calcium-regulated heat stable protein 1 OS=Mus musculus GN=Carhsp1 PE=1 SV=1	6 CHSP1_MOUSE,s p Q9WU49 CHSP1_RAT,sp Q9Y2V2 CHSP1_HUMAN,tr D2HCQ6 D2HCQ6_AILME,tr E2QZZ6 E2QZZ6_CANFA,tr F1RKY9 F1RKY9_PIG,tr F6VUJ6 F6VUJ6_HORSE,tr F7F6H6 F7F6H6_MACMU,tr F71981 F71981_CALA,tr F71P66 CALJA,tr	IQAV EVVI THLA PGTk	82%	37.9	50.62913	Ref	-0.34	-0.07	-0.25	0.024	0.12	-0.53	-0.23	274	209	273	271	360	336	224	273	762.1	2283.4	3	0.0255	11.17

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_010443 PE=4 SV=1	tr D2HH84 D2HH84_AILME,t r E2QS21 E2QS21_CANFA,tr E2QXN0 E2QXN0_CANFA,tr F1MH61 F1MH61_BOVIN,tr F1SS16 F1SS16_PI G,tr F6VV66 F6VV66_HORSE, tr F7CK98 F7CK98_MONDO	TTITL AHLL AAR	95%	50.7	49.98839	Ref	-0.34	-0.94	-0.72	-1.2	-0.97	-0.83	-0.81	2740	1450	1040	1360	1090	1100	1270	1270	529	1584	3	0.0078	4.924
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_010443 PE=4 SV=1	tr D2HH84 D2HH84_AILME,t r E2QS21 E2QS21_CANFA,tr E2QXN0 E2QXN0_CANFA,tr F1MH61 F1MH61_BOVIN,tr F1SS16 F1SS16_PI G,tr F6VV66 F6VV66_HORSE, tr F7CK98 F7CK98_MONDO	TTITL AHLL AAR	95%	71	50.11744	Ref	-0.28	-0.72	-0.38	-0.74	-0.77	-0.84	-0.64	1920	1940	1550	2200	1880	1620	1610	1830	529	1584	3	0.0085	5.378
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.14715 PE=3 SV=1	tr F1MZN6 F1MZN6_BOVIN, tr Q3SZH5 Q3SZH5_BOVIN	kVEA LTFQ HNFL TR	95%	52.7	53.04512	Ref	0.9	0.17	0.5	0.4	0.12	0.96	0.52	1450	2150	1400	1990	2040	1470	2740	2000	771.4	2311.3	3	0.0116	5.004

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.14715 PE=3 SV=1	tr F1MZN6 F1MZN6_BOVIN, tr Q3SZH5 Q3SZH5_BOVIN	kVEA LTFQ HNFL TR	95%	61.5	52.81735	Ref	0.83	0.2	0.67	0.45	0.18	1.2	0.2	526	898	632	982	931	673	1380	706	771.4	2311.3	3	0.0061	2.63
Uncharacterized protein OS=Sus scrofa GN=CD44 PE=4 SV=1	tr F1SGT4 F1SGT4_PIG, tr F6PQF3 F6PQF3_ORN AN, tr F6PQG1 F6PQG1_ORN AN	yGFI DGH VVIP R	95%	59.9	53.00008	Ref	-0.76	0.24	-0.83	-0.064	-0.39	0.13	-0.68	8240	4470	9700	5210	9740	6790	10200	5740	559.6	1675.9	3	0.0125	7.426
Uncharacterized protein OS=Sus scrofa GN=CD44 PE=4 SV=1	tr F1SGT4 F1SGT4_PIG, tr F6PQF3 F6PQF3_ORN AN, tr F6PQG1 F6PQG1_ORN AN	yGFI DGH VVIP R	95%	52.7	52.8667	Ref	-0.62	-0.01	-0.75	-0.089	-0.38	0.079	-0.62	11700	6270	10400	6950	12100	8670	12400	7580	496	1980.1	4	0.0129	6.523
MHC class I antigen (Fragment) OS=Ovis aries PE=4 SV=1	tr Q30825 Q30825_SHEEP	eYIA LNED LR	95%	51.9	52.31745	Ref	0.12	-0.18	2.6	-0.17	-0.09	0.076	2.6	4310	5180	4540	35300	5680	5230	6130	35400	770.4	1538.8	2	0.0126	8.151
MHC class I antigen (Fragment) OS=Ovis aries PE=4 SV=1	tr Q30825 Q30825_SHEEP	eYIA LNED LR	92%	44.3	52.34963	Ref	0.13	-0.12	2.5	0.031	-0.01	-0.07	2.6	5260	4130	3780	26400	5180	4400	4390	27300	770.4	1538.8	2	0.0117	7.592

60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	9 RL9_HUMAN,sp P51410 RL9_MOUSE,sp Q3SYR7 RL9_BOVIN,sp Q5IFJ7 RL9_MACFA,sp Q5R9Q7 RL9_PONAB,tr D2HRN7 D2HRN7_AILME,tr D3YYQ0 D3YYQ0_MOUSE,tr D9ZLV7 D9ZLV7_AILME,tr E1BCK0 E1BCK0_BOVIN,tr E2R149 E2R149_CANFA,tr F1M	gTV QQA DE	94%	42.7	48.47788	Ref	0.23	-0.04	0.02	-0.36	0.085	-0.61	-0.04	158	164	147	173	146	174	112	165	576.3	1150.6	2	0.0106	9.202
60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	9 RL9_HUMAN,sp P51410 RL9_MOUSE,sp Q3SYR7 RL9_BOVIN,sp Q5IFJ7 RL9_MACFA,sp Q5R9Q7 RL9_PONAB,tr D2HRN7 D2HRN7_AILME,tr D3YYQ0 D3YYQ0_MOUSE,tr D9ZLV7 D9ZLV7_AILME,tr E1BCK0 E1BCK0_BOVIN,tr E2R149 E2R149_CANFA,tr F1M	gTV QQA DE	81%	34.5	48.64636	Ref	0.31	Value Missing (-1.409)	Value Missing (-1.575)	0.1	0.37	0.018	0.32	112	118	Value Missing (-1.409)	Value Missing (-1.575)	137	145	118	144	576.3	1150.6	2	0.009	7.83

COL18A1 protein OS=Bos taurus GN=COL18A1 PE=2 SV=1	tr A4FV05 A4FV05_BOVIN, tr A8E654 A8E654_BOVIN, tr E1B744 E1B744_BOVIN, tr E1B935 E1B935_BOVIN, tr F1N6W9 F1N6W9_BOVIN	tAAS FELP ALD GR	94%	47.1	52.89756	Ref	0.042	-0.23	-0.34	-0.3	0.14	-0.34	-0.02	2610	2360	2120	2200	2500	2960	2210	2760	826.4	1650.9	2	0.0127	7.671
COL18A1 protein OS=Bos taurus GN=COL18A1 PE=2 SV=1	tr A4FV05 A4FV05_BOVIN, tr A8E654 A8E654_BOVIN, tr E1B744 E1B744_BOVIN, tr E1B935 E1B935_BOVIN, tr F1N6W9 F1N6W9_BOVIN	tAAS FELP ALD GR	92%	45	52.89473	Ref	0.14	-0.1	-0.37	-0.37	0.04	-0.35	-0.09	3260	3090	2840	2630	2910	3380	2700	3200	826.4	1650.9	2	0.0111	6.715

Protein CYR61 OS=Pan troglodytes GN=CYR61 PE=2 SV=1	1 CYR61_PANTR,sp O00622 CYR61_HUMAN,tr B4DI61 B4DI61_HUMAN,tr F6RUJ8 F6RUJ8_HORSE,tr F6XGF4 F6XGF4_MACMU,tr F6XHD7 F6XHD7_MACMU,tr F7I1R4 F7I1R4_CALJA,tr F7I427 F7I427_CALJA,tr F8W9U7 F8W9U7_HUMAN,tr Q307G9 Q307G9_EPR	rLPV FGM	84%	40.2	52.33993	Ref	0.01	0.28	0.65	0.058	0.25	0.3	0.83	5980	5160	6770	9770	7160	7130	7710	11100	502.6	1504.8	3	0.011	7.319
Protein CYR61 OS=Pan troglodytes GN=CYR61 PE=2 SV=1	1 CYR61_PANTR,sp O00622 CYR61_HUMAN,tr B4DI61 B4DI61_HUMAN,tr F6RUJ8 F6RUJ8_HORSE,tr F6XGF4 F6XGF4_MACMU,tr F6XHD7 F6XHD7_MACMU,tr F7I1R4 F7I1R4_CALJA,tr F7I427 F7I427_CALJA,tr F8W9U7 F8W9U7_HUMAN,tr Q307G9 Q307G9_EPR	rLPV FGM	92%	47.2	52.49986	Ref	0.19	0.2	0.74	-0.13	0.53	-0.45	1	6470	6490	7120	11600	6980	9660	5100	14000	502.6	1504.8	3	0.0094	6.243

Protein S100-A11 OS=Oryctolagus cuniculus GN=S100A11 PE=1 SV=2	0 S10AB_ RABIT,sp P31949 S10AB_HUMAN,sp P50543 S10AB_MOUSE,sp Q6B345 S10AB_RAT, tr D2I3J1 D2I3J1_ AILME, tr E2QXH6 E2QXH6_ CANFA, tr F1MX83 F1MX83_ BOVIN, tr F1PFF2 F1PFF2_ CANFA, tr F6 UGT9 F6 UGT9_MA CMU, tr F7 DD73 F7 DD73_CA	Qk	91%	47.1	53.41765	Ref	-0.81	0.047	-0.03	0.24	0.12	0.43	0.77	211	100	197	210	278	224	290	365	635.7	1904.1	3	0.013	6.845
Protein S100-A11 OS=Oryctolagus cuniculus GN=S100A11 PE=1 SV=2	0 S10AB_ RABIT,sp P31949 S10AB_HUMAN,sp P50543 S10AB_MOUSE,sp Q6B345 S10AB_RAT, tr D2I3J1 D2I3J1_ AILME, tr E2QXH6 E2QXH6_ CANFA, tr F1MX83 F1MX83_ BOVIN, tr F1PFF2 F1PFF2_ CANFA, tr F6 UGT9 F6 UGT9_MA CMU, tr F7 DD73 F7 DD73_CA	Qk	83%	40.9	53.3854	Ref	-0.45	0.41	0.12	0.021	0.1	0.45	0.48	202	135	264	242	250	231	306	311	635.7	1904.1	3	0.0116	6.089

Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4	sp P40124 CAP1_MOUSE,s p Q08163 CAP1_RAT,sp Q3SYV4 CAP1_BOVIN, tr A6QLB7 A6QLB7_BOVIN, tr F1SMCO F1SMCO_PIG, tr Q3TC53 Q3TC53_MOUSE, tr Q3U0U5 Q3U0U5_MOUSE, tr Q3UNQ0 Q3UNQ0_MOUSE, tr Q3UVJ2 Q3UVJ2_MOUSE	KEPALLELEGk	82%	33.6	48.6169	Ref	0.15	-0.29	-0.12	-0.13	-0.23	0.01	-0.25	19300	17500	13900	17600	19300	15800	19400	16100	535.6	2138.3	4	0.006	2.805
Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4	sp P40124 CAP1_MOUSE,s p Q08163 CAP1_RAT,sp Q3SYV4 CAP1_BOVIN, tr A6QLB7 A6QLB7_BOVIN, tr F1SMCO F1SMCO_PIG, tr Q3TC53 Q3TC53_MOUSE, tr Q3U0U5 Q3U0U5_MOUSE, tr Q3UNQ0 Q3UNQ0_MOUSE, tr Q3UVJ2 Q3UVJ2_MOUSE	KEPALLELEGk	91%	41.6	48.23076	Ref	-0.18	-0.23	0.054	-0.054	-0.04	-0.04	-0.13	5760	4720	4940	6770	6920	6090	6370	5950	713.8	2138.3	3	0.0013	0.587

Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2	Z4 LRRF1_HUMAN, sp Q3UZ39 LRRF1_MOUSE, sp Q66HF9 LRRF1_RAT, tr A6H5U5 A6H5U5_MOUSE, tr A6QP40 A6QP40_BOVIN, tr B4DPC0 B4DPC0_HUMAN, tr D3ZQT9 D3ZQT9_RAT, tr D4A480 D4A480_RAT, tr D4A4R0 D4A4R0_RAT, tr E2RTD8 E2RTD8_CAN	hAH SILQ FQF AEVk	91%	44.6	54.15322	Ref	0.069	-0.21	0.048	-0.18	0.33	-0.33	0.73	2620	2330	2080	2800	2640	3280	2170	4480	566.6	2262.3	4	0.0204	9.002
	Z4 LRRF1_HUMAN, sp Q3UZ39 LRRF1_MOUSE, sp Q66HF9 LRRF1_RAT, tr A6H5U5 A6H5U5_MOUSE, tr A6QP40 A6QP40_BOVIN, tr B4DPC0 B4DPC0_HUMAN, tr D3ZQT9 D3ZQT9_RAT, tr D4A480 D4A480_RAT, tr D4A4R0 D4A4R0_RAT, tr E2RTD8 E2RTD8_CAN	hAH SILQ FQF AEVk	91%	47.1	54.16908	Ref	0.081	-0.19	0.28	-0.059	0.56	-0.27	0.24	715	674	607	940	820	1100	647	916	755.1	2262.3	3	0.0135	5.986

Prostacyclin synthase OS=Mus musculus GN=Ptgis PE=2 SV=1	4 PTGIS_MOUSE,s p Q29626 PTGIS_BOVIN,sp Q62969 P TGIS_RAT, tr A2A5T 5 A2A5T5_MOUSE,t r D2GVP2 D2GVP2 _AILME,tr F1MZ09 F1MZ09_ BOVIN,tr F1PD41 F 1PD41_C ANFA,tr F 1PZ83 F1 PZ83_CA NFA,tr F1 SBE5 F1S BE5_PIG,t r F6YMG 4 F6YMG 4_HORSE,	hGDI FTVL VGG R	91%	45.1	52.34414	Ref	-0.14	-0.64	0.021	-0.44	-0.27	-0.7	-0.47	1930	1380	1060	1880	1510	1480	1150	1330	525.6	1573.9	3	0.0062	3.954
Prostacyclin synthase OS=Mus musculus GN=Ptgis PE=2 SV=1	4 PTGIS_MOUSE,s p Q29626 PTGIS_BOVIN,sp Q62969 P TGIS_RAT, tr A2A5T 5 A2A5T5_MOUSE,t r D2GVP2 D2GVP2 _AILME,tr F1MZ09 F1MZ09_ BOVIN,tr F1PD41 F 1PD41_C ANFA,tr F 1PZ83 F1 PZ83_CA NFA,tr F1 SBE5 F1S BE5_PIG,t r F6YMG 4 F6YMG 4_HORSE,	hGDI FTVL VGG R	67%	34.8	52.34026	Ref	0.013	-0.63	-0.12	-0.46	-0.3	-0.5	-0.26	1370	1330	926	1490	1290	1260	1140	1350	525.6	1573.9	3	0.0057	3.592

Uncharacterized protein (Fragment) OS=Bos taurus GN=CYB5B PE=4 SV=1	tr F2Z4J9 F2Z4J9_BOVIN, tr F6RNJ3 F6RNJ3_MONDO, tr Q0P5F6 Q0P5F6_BOVIN	diWLR	90%	44.8	52.16153	Ref	0.15	-0.1	0.31	-0.11	0.35	-0.18	0.067	1920	1840	1670	2500	2060	2480	1790	2110	471.6	1411.8	3	0.0096	6.802
Uncharacterized protein (Fragment) OS=Bos taurus GN=CYB5B PE=4 SV=1	tr F2Z4J9 F2Z4J9_BOVIN, tr F6RNJ3 F6RNJ3_MONDO, tr Q0P5F6 Q0P5F6_BOVIN	diWLR	91%	44.8	52.06627	Ref	0.067	0.1	0.56	-0.021	-0.07	-0.01	-0.13	3120	2870	3190	4910	3620	3050	3330	3040	471.6	1411.8	3	0.0067	4.722
Importin subunit beta-1 OS=Rattus norvegicus GN=Kpnb1 PE=1 SV=1	6 IMB1_RAT, sp P70168 IMB1_MOUSE, sp Q14974 IMB1_HUMAN, tr B2RBR9 B2RBR9_HUMAN, tr E1BFV0 E1BFV0_BOVIN, tr E2R2I0 E2R2I0_CANFA, tr F1RWJ5 F1RWJ5_PIG, tr F2Z3Q8 F2Z3Q8_RAT, tr F6Q111 F6Q111_MONDO, tr F7I7IN96 F7I7IN96_CAJA, tr Q3TF	mELITILEK	90%	42	51.84086	Ref	-0.4	-0.28	0.011	-0.13	-0.37	-0.29	-0.23	1310	855	1000	1380	1380	1020	1130	1160	718.4	1434.8	2	0.0018	1.254

Importin subunit beta-1 OS=Rattus norvegicus GN=Kpnb1 PE=1 SV=1	6 IMB1_R AT,sp P70 168 IMB1 _MOUSE, sp Q1497 4 IMB1_ HUMAN,t r B2RBR9 B2RBR9_ HUMAN,t r E1BFV0 E1BFV0_ BOVIN,tr E2R2I0 E 2R2I0_CA NFA,tr F1 RWJ5 F1 RWJ5_PIG ,tr F2Z3Q 8 F2Z3Q8 _RAT,tr F 6Q1I1 F6 Q1I1_MO NDO,tr F 7IN96 F7I N96_CALJ A,tr Q3TF	mELI TILEK	74%	35.6	52.00924	Ref	-0.52	-0.24	-0.19	-0.48	-0.17	0.21	-0.33	179	110	145	169	152	164	224	153	718.4	1434.8	2	0.0075	5.252
Adapter molecule crk OS=Homo sapiens GN=CRK PE=1 SV=2	8 CRK_H UMAN,sp Q63768 CRK_RAT, sp Q6401 0 CRK_M OUSE,tr D2H8D0 D2H8D0_ AILME,tr E1BQ32 E 1BQ32_B OVIN,tr E 2QWD3 E 2QWD3_C ANFA,tr F 7BME5 F 7BME5_H ORSE,tr F 7DCK2 F7 DCK2_CAL JA,tr F7D T53 F7DT 53_CALJA, tr Q5ND5 1 Q5ND5 1_MOUSE	gHFP FTHV R	89%	40.9	51.568	Ref	0.34	-0.12	0.31	-0.38	0.47	-0.36	0.21	2670	2880	2280	3440	2350	3700	2180	3190	351.2	1400.8	4	0.011	7.832

Adapter molecule crk OS=Homo sapiens GN=CRK PE=1 SV=2	8 CRK_H UMAN,sp Q63768 CRK_RAT, sp Q6401 0 CRK_M OUSE,tr D2H8D0 D2H8D0_ AILME,tr E1BQ32 E 1BQ32_B OVIN,tr E 2QWD3 E 2QWD3_C ANFA,tr F 7BME5 F 7BME5_H ORSE,tr F 7DCK2 F7 DCK2_CAL JA,tr F7D T53 F7DT 53_CALJA, tr Q5ND5 1 Q5ND5 1_MOUSE	gHFP FTHV R	85%	38.4	51.59456	Ref	0.2	-0.08	0.35	-0.31	0.43	-0.33	0.31	1840	1870	1680	2540	1760	2590	1590	2470	351.2	1400.8	4	0.0044	3.124
Peptidyl-prolyl cis- trans isomerase FKBP11 OS=Bos taurus GN=FKBP11 PE=2 SV=1	sp Q2YDL 5 FKB11_ BOVIN,tr F1MT51 F1MT51_ BOVIN,tr F1SPN1 F 1SPN1_PI G,tr F7BS X0 F7BSX 0_HORSE	viIPS HLAY Gk	89%	41.2	50.30284	Ref	0.11	-0.11	0.15	-0.077	0.064	-0.22	0.034	21600	20100	18700	25200	23700	22800	19600	23200	602.7	1805.1	3	0.0185	10.26
Peptidyl-prolyl cis- trans isomerase FKBP11 OS=Bos taurus GN=FKBP11 PE=2 SV=1	sp Q2YDL 5 FKB11_ BOVIN,tr F1MT51 F1MT51_ BOVIN,tr F1SPN1 F 1SPN1_PI G,tr F7BS X0 F7BSX 0_HORSE	viIPS HLAY Gk	55%	30.2	50.05502	Ref	0.16	-0.32	0.16	-0.11	0.066	-0.24	0.2	24700	24200	18800	29500	27000	26600	22400	30200	602.7	1805.1	3	0.0145	8.033

Putative RNA-binding protein 3 OS=Mus musculus GN=Rbm3 PE=1 SV=1	6 RBM3_MOUSE,s p P98179 RBM3_H UMAN,sp Q925G0 RBM3_R AT,tr D2H 7N9 D2H 7N9_AIL ME,tr D5 FGC9 D5F GC9_CRIG R,tr E2R7 71 E2R77 1_CANFA, tr E2R8T5 E2R8T5_ CANFA,tr F1SRZ8 F 1SRZ8_PI G,tr F6YE U3 F6YEU 3_HORSE, tr Q545K 5 Q545K5 _MOUSE,t	aMn GESL DGR	83%	34.7	48.20891	Ref	-0.32	0.098	-0.33	-0.25	0.003	-0.5	0.15	1E+05	85900	1E+05	104000	121000	1E+05	93200	144000	677.8	1353.6	2	0.0116	8.541
Putative RNA-binding protein 3 OS=Mus musculus GN=Rbm3 PE=1 SV=1	6 RBM3_MOUSE,s p P98179 RBM3_H UMAN,sp Q925G0 RBM3_R AT,tr D2H 7N9 D2H 7N9_AIL ME,tr D5 FGC9 D5F GC9_CRIG R,tr E2R7 71 E2R77 1_CANFA, tr E2R8T5 E2R8T5_ CANFA,tr F1SRZ8 F 1SRZ8_PI G,tr F6YE U3 F6YEU 3_HORSE, tr Q545K 5 Q545K5 _MOUSE,t	aMn GESL DGR	88%	37.2	48.23585	Ref	-0.26	-0.13	-0.2	-0.34	0.058	-0.59	0.41	44100	33900	40300	43000	43100	49600	33100	65400	677.8	1353.6	2	0.0107	7.906

Ras-interacting protein 1 OS=Mus musculus GN=Rasip1 PE=1 SV=3	6 RAIN_MOUSE,sp Q5U651 RAIN_HUMAN,trap A0JNY4 A0JNY4_MOUSE,trap B9EK92 B9EK92_MOUSE,trap E1BDB1 E1BDB1_BOVIN,trap E2RRM5 E2RRM5_CANFA,trap E9Q3D5 E9Q3D5_MOUSE,trap F1LN01 F1LN01_RAT,trap F6UC01 F6UC01_HORSE,trap F6Y5H3 F6Y5H3_O	IHLP VGL WIN SPR	87%	41.6	51.59732	Ref	0.22	-0.2	0.08	-0.1	0.11	-0.15	0.16	914	935	758	1030	1000	1010	887	1090	602.7	1805.1	3	0.0075	4.148
Ras-interacting protein 1 OS=Mus musculus GN=Rasip1 PE=1 SV=3	6 RAIN_MOUSE,sp Q5U651 RAIN_HUMAN,trap A0JNY4 A0JNY4_MOUSE,trap B9EK92 B9EK92_MOUSE,trap E1BDB1 E1BDB1_BOVIN,trap E2RRM5 E2RRM5_CANFA,trap E9Q3D5 E9Q3D5_MOUSE,trap F1LN01 F1LN01_RAT,trap F6UC01 F6UC01_HORSE,trap F6Y5H3 F6Y5H3_O	IHLP VGL WIN SPR	87%	41.3	51.45342	Ref	0.2	-0.37	0.071	-0.046	0.35	-0.34	0.14	853	841	619	939	955	1100	712	981	602.7	1805.1	3	0.0049	2.736

60S ribosomal protein L29 OS=Bos taurus GN=RPL29 PE=2 SV=3	sp Q58DW3 RL29_BOVIN	akPP AAA APA Ak	80%	35.6	49.23265	Ref	0.083	0.79	0.81	0.65	1.3	0.47	1.4	6010	5380	9550	10900	10700	14300	8590	16700	659.4	1975.2	3	0.0341	17.26
60S ribosomal protein L29 OS=Bos taurus GN=RPL29 PE=2 SV=3	sp Q58DW3 RL29_BOVIN	akPP AAA APA Ak	87%	39.2	49.23265	Ref	0.04	0.73	0.89	0.61	1.2	0.63	1.5	12800	11700	20600	25800	23400	30300	21600	38500	659.4	1975.2	3	0.0341	17.26
Uncharacterized protein OS=Bos taurus GN=Bt.62844 PE=4 SV=1	tr E1B968 E1B968_BOVIN, tr E2RHZ7 E2RHZ7_CANFA, tr E2RI01 E2RI01_CANFA, tr E2RI12 E2RI12_CANFA, tr F6PTA3 F6PTA3_CALJA, tr F6QFQ7 F6QFQ7_CALJA, tr F6WP00 F6WP00_HORSE, tr F6WVX4 F6WVX4_HORSE	nLSL PFIF HEK	87%	42.4	52.76875	Ref	0.99	-0.07	0.64	-0.14	0.61	-0.19	0.68	2090	3780	1980	3620	2330	3420	2050	3700	651.7	1952.1	3	0.0183	9.365

<p>Uncharacterized protein OS=Bos taurus GN=Bt.62844 PE=4 SV=1</p>	<p>tr E1B968 E1B968_BOVIN, tr E2RHZ7 E2RHZ7_CANFA, tr E2RI01 E2RI01_CANFA, tr E2RI12 E2RI12_CANFA, tr F6PTA3 F6PTA3_CALJA, tr F6QFQ7 F6QFQ7_CALJA, tr F6WP00 F6WP00_HORSE, tr F6WVX4 F6WVX4_HORSE</p>	<p>nLSL PFIF HEK</p>	<p>51%</p>	<p>32.1</p>	<p>52.52401</p>	<p>Ref</p>	<p>0.67</p>	<p>-0.04</p>	<p>0.66</p>	<p>0.074</p>	<p>0.59</p>	<p>0.011</p>	<p>0.67</p>	<p>2750</p>	<p>3640</p>	<p>2400</p>	<p>4380</p>	<p>3220</p>	<p>4030</p>	<p>2810</p>	<p>4410</p>	<p>651.7</p>	<p>1952.1</p>	<p>3</p>	<p>0.011</p>	<p>5.617</p>
<p>Calpain small subunit 1 OS=Mus musculus GN=Capns1 PE=2 SV=1</p>	<p>6 CPNS1_MOUSE, sp P04574 CPNS1_PIG, sp P04632 CPNS1_HUMAN, sp P06813 CPNS1_RABBIT, sp P13135 CPNS1_BOVIN, sp Q64537 CPNS1_RAT, tr D3YW48 D3YW48_MOUSE, tr F1M6Z5 F1M6Z5_RAT, tr F6RLT8 F6RLT8_HORSE, tr F6X8A9 F6X8A9_MACMUT</p>	<p>mFL VNSF Lk</p>	<p>50%</p>	<p>31.3</p>	<p>52.09244</p>	<p>Ref</p>	<p>0.08</p>	<p>-0.34</p>	<p>0.022</p>	<p>-0.074</p>	<p>0.23</p>	<p>-0.43</p>	<p>0.57</p>	<p>1470</p>	<p>1450</p>	<p>1170</p>	<p>1690</p>	<p>1740</p>	<p>1880</p>	<p>1240</p>	<p>2460</p>	<p>722.9</p>	<p>1443.8</p>	<p>2</p>	<p>0.0094</p>	<p>6.495</p>

Calpain small subunit 1 OS=Mus musculus GN=Capns1 PE=2 SV=1	6 CPNS1_MOUSE,s p P04574 CPNS1_P IG,sp P04632 CPNS1_HUMAN,sp P06813 CPNS1_RABIT,s p P13135 CPNS1_BOVIN,sp Q64537 CPNS1_RAT,tr D3YW48 D3YW48_MOUSE, tr F1M6Z5 F1M6Z5_RAT, tr F6RLT8 F6RLT8_HORSE, tr F6X8A9 F6X8A9_MACMU, t	mFL VNSF Lk	87%	40.1	52.08245	Ref	0.027	-0.27	0.14	-0.059	0.31	-0.39	0.22	510	425	375	560	537	607	388	588	722.9	1443.8	2	0.0123	8.516
Reticulon-4 OS=Mus musculus GN=Rtn4 PE=1 SV=2	2 RTN4_MOUSE,s p Q9NQC3 RTN4_HUMAN, tr A5A6K0 A5A6K0_PANTR, tr A6XGP7 A6XGP7_HUMAN, tr A7YVI6 A7YVI6_BOVIN, tr B9VGZ5 B9VGZ5_SH EEP, tr D6W5C2 D6W5C2_HUMAN, tr E2R925 E2R925_CANFA, tr F1N405 F1N405_BOVIN, tr F1SQK2 F1SQK	hQA QID HYLK LANK	85%	42.7	54.19134	Ref	-0.13	-0.09	0.008	0.14	0.017	0.033	-0.22	9030	7440	8330	9990	12100	9680	10200	8530	739.4	2215.2	3	0.0191	8.619

Reticulon-4 OS=Mus musculus GN=Rtn4 PE=1 SV=2	2 RTN4_ MOUSE,s p Q9NQC 3 RTN4_ HUMAN,t r A5A6K0 A5A6K0_ PANTR,tr A6XGP7 A6XGP7_ HUMAN,t r A7YVI6 A7YVI6_ B OVIN,tr B 9VGZ5 B9 VGZ5_SH EEP,tr D6 W5C2 D6 W5C2_ HU MAN,tr E 2R925 E2 R925_CA NFA,tr F1 N405 F1N hQA 405_BOVI QID N,tr F1SQ HYLG K2 F1SQK LANK	68%	36.9	54.14166	Ref	-0.087	-0.21	-0.12	0.16	-0.01	0.014	-0.1	4920	3880	3870	4630	6170	4800	5090	4660	739.4	2215.2	3	0.0175	7.875
Acid ceramidase OS=Bos taurus GN=ASAH1 PE=2 SV=3	sp Q17Q ITVY B3 ASAH TVLI 1_BOVIN DVTk	80%	36.9	50.5959	Ref	0.19	-0.47	-0.32	-0.38	-0.67	-0.3	-0.79	502	440	303	376	397	284	383	271	658.4	1972.2	3	0.0229	11.62
Acid ceramidase OS=Bos taurus GN=ASAH1 PE=2 SV=3	sp Q17Q ITVY B3 ASAH TVLI 1_BOVIN DVTk	85%	38.3	49.85687	Ref	0.13	-0.52	0.03	-0.57	-0.09	-0.48	-0.84	212	232	160	263	192	234	186	144	658.4	1972.2	3	0.0116	5.875

Cartilage-associated protein OS=Homo sapiens GN=CRTAP PE=1 SV=1	8 CRTAP_HUMAN, tr B3KME2 B3KME2_HUMAN, tr B3KQR7 B3KQR7_HUMAN, tr B3KS71 B3KS71_HUMAN, tr B3KUPO B3KUP0_HUMAN, tr B3KX16 B3KX16_HUMAN, tr C9JP16 C9JP16_HUMAN, tr D2HB00 D2HB00_AILM E, tr E1BJ75 E1BJ75_BOVIN, tr E2RCK3	aIAA AHTF LLk	84%	37.2	49.32504	Ref	0.041	0.013	-0.13	-0.12	-0.25	0.18	-0.24	5500	4660	4960	5050	5580	4460	6270	4670	588.7	1763.1	3	0.0196	11.13
Cartilage-associated protein OS=Homo sapiens GN=CRTAP PE=1 SV=1	8 CRTAP_HUMAN, tr B3KME2 B3KME2_HUMAN, tr B3KQR7 B3KQR7_HUMAN, tr B3KS71 B3KS71_HUMAN, tr B3KUPO B3KUP0_HUMAN, tr B3KX16 B3KX16_HUMAN, tr C9JP16 C9JP16_HUMAN, tr D2HB00 D2HB00_AILM E, tr E1BJ75 E1BJ75_BOVIN, tr E2RCK3	aIAA AHTF LLk	80%	31.9	47.7002	Ref	0.2	-0.11	-0.31	-0.11	0.049	0.18	-0.27	1270	1340	1180	1150	1460	1420	1620	1180	441.8	1763.1	4	0.0043	2.418

Gamma-soluble NSF attachment protein OS=Bos taurus GN=NAPG PE=1 SV=3	7 SNAG_BOVIN,sp Q99747 SNAG_HUMAN,sp Q9CWZ7 SNAG_MOUSE,trans B4DFC9 B4DFC9_HUMAN,trans D2HHS6 D2HHS6_ALME,trans D3Z4B2 D3Z4B2_MOUSE,trans D3ZU08 D3ZU08_RAT,trans D4A0E2 D4A0E2_RAT,trans E2R561 E2R561_CAF6Z0B6 F6Z0B6_MACR	tIAQ VLV HLH R	81%	36	49.28703	Ref	0.11	-0.22	-0.2	-0.34	0.031	-0.02	-0.21	809	837	721	822	820	926	931	814	531	1590	3	0.006	3.8
Gamma-soluble NSF attachment protein OS=Bos taurus GN=NAPG PE=1 SV=3	7 SNAG_BOVIN,sp Q99747 SNAG_HUMAN,sp Q9CWZ7 SNAG_MOUSE,trans B4DFC9 B4DFC9_HUMAN,trans D2HHS6 D2HHS6_ALME,trans D3Z4B2 D3Z4B2_MOUSE,trans D3ZU08 D3ZU08_RAT,trans D4A0E2 D4A0E2_RAT,trans E2R561 E2R561_CAF6Z0B6 F6Z0B6_MACR	tIAQ VLV HLH R	74%	31.7	49.34463	Ref	0.032	-0.53	-0.12	-0.35	-0.23	-0	0.033	319	260	191	284	268	253	310	316	398.5	1590	4	0.0068	4.287

Histidine triad nucleotide-binding protein 1 OS=Bos taurus GN=HINT1 PE=1 SV=2	8 HINT1_BOVIN,sp P62959 HINT1_RA T,sp P70349 HINT1_MOUSE,sp P80912 HINT1_RABIT,tr A1XEA3 A1XEA3_BOVIN,tr A1XEC3 A1XEC3_BOVIN,tr A1XEC4 A1XEC4_BOVIN,tr B1AZK3 B1AZK3_MOUSE,tr D2HVN8 D2HVN8_AILME,tr D4A269 D4A269_RAT,trl	CAA DLGL	77%	36.5	52.06178	Ref	-0.12	-0.42	-0.14	-0.36	-0.12	-0.57	-0.18	19200	15400	13600	18500	17500	18100	13800	17900	722.9	1443.8	2	0.0036	2.52
Histidine triad nucleotide-binding protein 1 OS=Bos taurus GN=HINT1 PE=1 SV=2	8 HINT1_BOVIN,sp P62959 HINT1_RA T,sp P70349 HINT1_MOUSE,sp P80912 HINT1_RABIT,tr A1XEA3 A1XEA3_BOVIN,tr A1XEC3 A1XEC3_BOVIN,tr A1XEC4 A1XEC4_BOVIN,tr B1AZK3 B1AZK3_MOUSE,tr D2HVN8 D2HVN8_AILME,tr D4A269 D4A269_RAT,trl	CAA DLGL	81%	38.8	52.09687	Ref	-0.23	-0.33	-0.12	-0.24	-0.21	-0.62	-0.17	26400	19500	19700	25500	25800	23200	18200	24600	482.3	1443.8	3	0.0028	1.964

Casein kinase II subunit beta OS=Bos taurus GN=CSNK2B PE=1 SV=1	8 CSK2B_BOVIN,sp P67870 CSK2B_HUMAN,sp P67871 CSK2B_MOUSE,sp P67872 CSK2B_PIG,sp P67873 CSK2B_RABBIT,sp P67874 CSK2B_RAT, tr BOUXA9 BOUXA9_HUMAN, tr B7U170 B7U170_SHEEP, tr B9TSQ8 B9TSQ8_PIG, tr D2I4A3 D2I4A3_AILME, tr E2RP7	rPAN QFV PR	79%	37.6	51.63647	Ref	0.27	0.52	-0.04	-0.073	0.11	0.13	-0.03	16700	17400	22400	17200	18400	18200	19300	17100	463.6	1387.8	3	0.0107	7.713
Casein kinase II subunit beta OS=Bos taurus GN=CSNK2B PE=1 SV=1	8 CSK2B_BOVIN,sp P67870 CSK2B_HUMAN,sp P67871 CSK2B_MOUSE,sp P67872 CSK2B_PIG,sp P67873 CSK2B_RABBIT,sp P67874 CSK2B_RAT, tr BOUXA9 BOUXA9_HUMAN, tr B7U170 B7U170_SHEEP, tr B9TSQ8 B9TSQ8_PIG, tr D2I4A3 D2I4A3_AILME, tr E2RP7	rPAN QFV PR	77%	37	51.63113	Ref	0.37	0.42	0.089	-0.11	0.046	0.1	-0.02	23000	25900	29100	26000	25000	24300	26400	24100	463.6	1387.8	3	0.01	7.173

ATPase inhibitor, mitochondrial OS=Bos taurus GN=ATPIF1 PE=1 SV=2	sp P01096 ATIF1_BOVIN,sp Q29307 ATIF1_PIG	dAG GAF Gk	78%	35.9	51.20182	Ref	-0.51	0.8	0.48	0.65	1.2	0.26	1	30500	19000	50800	45600	56700	71200	39600	65700	665.9	1329.7	2	0.0216	16.22
ATPase inhibitor, mitochondrial OS=Bos taurus GN=ATPIF1 PE=1 SV=2	sp P01096 ATIF1_BOVIN,sp Q29307 ATIF1_PIG	dAG GAF Gk	51%	30.8	51.21668	Ref	0.26	0.8	0.51	0.82	0.9	0.29	0.68	5090	5230	8240	7560	10300	9500	6530	8460	444.3	1329.7	3	0.0197	14.79
ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2	4 ARF3_HUMAN,sp P61205 ARF3_MOUSE,sp P61206 ARF3_RAT,sp P84077 ARF1_HUMAN,sp P84078 ARF1_MOUSE,sp P84079 ARF1_RAT,sp P84080 ARF1_BOVIN,sp P84081 ARF2_BOVIN,sp P84082 ARF2_RAT,sp Q4R5P2 ARF1_MACFA,sp Q5E916 ARF3_BO	IGLH SLR	75%	34.9	50.29246	Ref	0.17	-0.24	0.37	-0.27	0.27	-0.44	-0.41	6180	6230	5070	8710	6160	7830	4980	5070	367.2	1098.7	3	0.0035	3.201

<p>ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2</p>	<p>4 ARF3_HUMAN,sp P61205 ARF3_MOUSE,sp P61206 ARF3_RAT,sp P84077 ARF1_HUMAN,sp P84078 ARF1_MOUSE,sp P84079 ARF1_RAT,sp P84080 ARF1_BOVIN,sp P84081 ARF2_BOVIN,sp P84082 ARF2_RAT,sp Q4R5P2 ARF1_MACACA,sp Q5E9I6 ARF3_BO</p>	<p>IGLH SLR</p>	<p>66%</p>	<p>33.3</p>	<p>50.96722</p>	<p>Ref</p>	<p>-0.026</p>	<p>-0.27</p>	<p>0.32</p>	<p>-0.38</p>	<p>0.3</p>	<p>-0.32</p>	<p>-0.21</p>	<p>32000</p>	<p>26500</p>	<p>24200</p>	<p>41000</p>	<p>27800</p>	<p>38800</p>	<p>26500</p>	<p>28300</p>	<p>367.2</p>	<p>1098.7</p>	<p>3</p>	<p>0.0066</p>	<p>5.957</p>
<p>ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3</p>	<p>1 DDX3X_HUMAN,sp O15523 DDX3Y_HUMAN,sp P16381 DDX3L_MOUSE,sp Q5RF43 DDX3Y_PONAB,sp Q62095 DDX3Y_MOUSE,sp Q62167 DDX3X_MOUSE,sp Q6GVM6 DDX3Y_PANTR,tr B4DK29 B4DK29_HUMAN,tr B4DLU5 B4DLU5_HUMAN,tr B4DXX7 B4</p>	<p>hAIPI Ik</p>	<p>70%</p>	<p>28.9</p>	<p>45.76986</p>	<p>Ref</p>	<p>-0.12</p>	<p>-0.1</p>	<p>-0.12</p>	<p>-0.29</p>	<p>-0.3</p>	<p>-0.29</p>	<p>-0.27</p>	<p>23800</p>	<p>18600</p>	<p>20600</p>	<p>22800</p>	<p>22300</p>	<p>19300</p>	<p>20300</p>	<p>20500</p>	<p>467.3</p>	<p>1398.9</p>	<p>3</p>	<p>0.0231</p>	<p>16.49</p>

ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	1 DDX3X_HUMAN,sp O15523 DDX3Y_HUMAN,sp P16381 DDX3L_MOUSE,sp Q5RF43 DDX3Y_PONAB,sp Q62095 DDX3Y_MOUSE,sp Q62167 DDX3X_MOUSE,sp Q6GVM6 DDX3Y_PANTR,tr B4DK29 B4DK29_HUMAN,tr B4DLU5 B4DLU5_HUMAN,tr B4DXX7 B4	hAIP1	75%	28.5	43.90263	Ref	-0.013	-0.24	-0.24	-0.18	-0.17	-0.18	-0.39	24100	21200	19600	22000	25300	22300	23100	19800	467.3	1398.9	3	0.0045	3.228
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform OS=Homo sapiens GN=PPP2R5C PE=1 SV=3	2 2A5G_HUMAN,sp Q14738 2A5D_HUMAN,sp Q28651 2A5G_RABIT,sp Q28653 2A5D_RABIT,sp Q60996 2A5G_MOUSE,tr A4FV55 A4FV55_BOVIN,tr A5GFQ9 A5GFQ9_PIG,tr A8K6Y2 A8K6Y2_HUMAN,tr B4DSD7 B4DSD7_HUMAN,tr B4DYJ8 B4DYJ8_HUMAN,t	vLLP LHK	74%	24.8	40.43166	Ref	-0.066	-0.05	-0.39	-0.45	-0.49	-0.2	-0.73	3390	3100	3410	3000	3200	2700	3450	2380	476.7	1426.9	3	0.0032	2.261

<p>Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform OS=Homo sapiens GN=PPP2R5C PE=1 SV=3</p>	<p>2 2A5G_HUMAN,sp Q14738 2A5D_HUMAN,sp Q28651 2A5G_RA BIT,sp Q28653 2A5D_RABIT,sp Q60996 2A5G_MOUSE,transcript A4FV55 A4FV55_BOVIN,transcript A5GFQ9 A5GFQ9_PIG,transcript A8K6Y2 A8K6Y2_HUMAN,transcript B4DSD7 B4DSD7_HUMAN,transcript B4DYJ8 B4DYJ8_HUMAN,t</p>	<p>VLLP LHK</p>	<p>51%</p>	<p>20</p>	<p>40.43166</p>	<p>Ref</p>	<p>-0.41</p>	<p>-0.12</p>	<p>-0.53</p>	<p>-0.22</p>	<p>-0.6</p>	<p>-0.29</p>	<p>-0.49</p>	<p>4860</p>	<p>2910</p>	<p>3870</p>	<p>3260</p>	<p>4440</p>	<p>2990</p>	<p>3870</p>	<p>3360</p>	<p>476.7</p>	<p>1426.9</p>	<p>3</p>	<p>0.0037</p>	<p>2.576</p>
<p>60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2</p>	<p>6 RL27A_HUMAN,sp Q4R723 RL27A_MACFA,sp Q56K03 RL27A_BOVIN,sp Q5R1X0 RL27A_PANTR,sp Q5REY2 RL27A_PONAB,transcript D2GX71 D2GX71_AILME,transcript D2H317 D2H317_AILME,transcript D2HDG8 D2HDG8_AILME,transcript D3YZN6 D3YZN6_MOUSE,transcript D3ZG03 D3ZG03_VRR</p>	<p>tGAA PIIID VVR</p>	<p>57%</p>	<p>31</p>	<p>50.77081</p>	<p>Ref</p>	<p>0.086</p>	<p>-0.17</p>	<p>0.2</p>	<p>-0.24</p>	<p>0.056</p>	<p>-0.18</p>	<p>0.14</p>	<p>11100</p>	<p>11600</p>	<p>10600</p>	<p>15300</p>	<p>12500</p>	<p>13300</p>	<p>11800</p>	<p>14600</p>	<p>708.4</p>	<p>1414.8</p>	<p>2</p>	<p>0.0156</p>	<p>11.02</p>

60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2	6 RL27A_HUMAN,sp Q4R723 RL27A_MACFA,sp Q56K03 RL27A_BOVIN,sp Q5R1X0 RL27A_PANTR,sp Q5REY2 RL27A_PONAB,tr D2GX71 D2GX71_AILME,tr D2H317 D2H317_AILME,tr D2HDG8 D2HDG8_AILME,tr D3YZN6 D3YZN6_MOUN6,SE,tr D3ZG03 D3ZVVR	tGAA PIID	73%	34.5	50.3585	Ref	0.3	0.005	0.098	-0.23	-0.21	-0.23	-0.21	2850	2730	2420	2890	2540	2250	2320	2320	472.6	1414.8	3	0.0095	6.698
Uncharacterized protein C1orf226 OS=Homo sapiens GN=C1orf226 PE=1 SV=1	1L170 CA226_HUMAN,REV,sp A4IFJ0 CA226_BOVIN,REV,sp Q5REP3 LYSM4_PONAB,REV,sp Q5XG99 LYSM4_HUMAN,REV,sp Q8CC84 LYSM4_MOUSE,REV,sp Q9JJ26 MEFV_MOUSE,REV,tr A2VDV4 A2VDV4_BOVIN,REV,tr C9JB9 C9JB9_HUMAN,REV,tr nK	eLFD	71%	32.9	49.95007	Ref	-0.024	0.31	0.029	-0.067	-0.09	0.25	-0.6	2E+05	171000	2E+05	216000	223000	2E+05	3E+05	140000	535.8	1069.6	2	0.0034	3.215

Uncharacterized protein C1orf226 OS=Homo sapiens GN=C1orf226 PE=1 SV=1	1L170 CA226_HUMAN,REV_sp A4IFJ0 CA226_BOVIN,REV_sp Q5REP3 LYSM4_PONAB,REV_sp Q5XG99 LYSM4_HUMAN,REV_sp Q8CC84 LYSM4_MOUSE,REV_sp Q9JJ26 MEFV_MOUSE,REV_tr A2VDV4 A2VDV4_BOVIN,REV_tr C9J1B9 C9J1B9_HUMAN,REV_tr	eLFD nK	58%	30.3	49.88091	Ref	-0.034	0.25	-0.04	0.04	-0.04	0.055	-0.18	19800	17500	23100	21200	24700	20400	22700	19100	535.8	1069.6	2	0.002	1.851
Uncharacterized protein OS=Bos taurus GN=Bt.45180 PE=4 SV=1	BC49 E1BC49_BOVIN,REV_tr F7BJ67 F7BJ67_ORNAN,sp O14561 ACPM_HUMAN,sp P52505 ACPM_BOVIN,sp Q0MQC1 ACPM_PONPY,sp Q0MQC2 ACPM_GORG,sp Q0MQC3 ACPM_PANTR,sp Q9CR21 ACPM_MOUSE,rev_tr A4UCS3 A4UCS3_HUMAN,rev_tr DOG	vLYV ik	64%	25.8	43.85731	Ref	-0.25	0.59	0.69	0.41	0.92	0.36	0.94	4160	3020	5860	7030	6390	7940	5650	8350	448.3	1341.9	3	0.0217	16.13

Uncharacterized protein OS=Bos taurus GN=Bt.45180 PE=4 SV=1	BC49 E1B C49_BOVIN,REV_tr F7BJ67 F7BJ67_OR NAN,sp O14561 ACPM_HUMAN,sp P52505 ACPM_BOVIN,sp Q0MQC1 ACPM_PONPY,sp Q0MQC2 ACPM_GORG O,sp Q0MQC3 ACPM_PANT R,sp Q9CR21 ACPM_MOUSE,sp A4UCS3 A4UCS3_HUMAN,sp D0G	vLYVik	71%	26	42.51833	Ref	-0.38	0.62	0.74	0.48	1	0.32	0.82	6500	4360	9510	11600	10600	13400	8690	12200	448.3	1341.9	3	0.0092	6.859
Uncharacterized protein OS=Ornithorhynchus anatinus GN=ABCB11 PE=3 SV=1	WP30 F6 WP30_OR NAN,REV_tr F7F2T7 F7F2T7_MONDO,sp Q8VDM6 HNRL1_MOUSE,sp Q9BUJ2 HNRL1_HUMAN,sp A4FUC2 A4FUC2_BOVIN,sp A8K3W4 A8K3W4_HUMAN,sp A8K5K0 A8K5K0_HUMAN,sp A8K6U7 A8K6U7_HUMAN,sp B3KM6 B3KM6_HUMAN,sp D0G	TnEEGk	60%	27.5	46.8302	Ref	-0.51	0.003	-0.13	-0.21	0.24	-0.58	0.16	821	454	701	719	748	895	527	875	491.7	981.48	2	0.0098	9.986

Uncharacterized protein OS=Ornithorhynchus anatinus GN=ABC11 PE=3 SV=1	WP30 F6 WP30_OR NAN,REV_ tr F7F2T7 F7F2T7_ MONDO,s p Q8VDM 6 HNRL1_ MOUSE,s p Q9BUJ2 HNRL1_ HUMAN,t r A4FUC2 A4FUC2_ BOVIN,tr A8K3W4 A8K3W4_ HUMAN,t r A8K5K0 A8K5K0_ HUMAN,t r A8K6U7 A8K6U7_ HUMAN,t r B3KM6 B3KM6 0_HUMA	TnEE Gk	71%	29.9	47.03936	Ref	-0.38	0.019	-0.07	-0.18	0.28	-0.51	0.19	794	593	849	895	914	1100	665	1070	491.7	981.48	2	0.0079	8.052
Ubiquitin thioesterase OTUB1 OS=Rattus norvegicus GN=Otub1 PE=1 SV=1	6 OTUB1 _RAT,sp Q7TQI3 O TUB1_MO USE,sp Q 96FW1 O TUB1_HU MAN,tr B 3KUV5 B 3KUV5_H UMAN,tr B4DPD5 B4DPD5_ HUMAN,t r B4E053 B4E053_ HUMAN,t r C5H0C6 C5H0C6_ PIG,tr D2 H4U8 D2 H4U8_AIL ME,tr D3 YWF6 D3 YWF6_M OUSE,tr F 1PIA2 F1	fFEH FIEG GR	71%	34.9	51.54406	Ref	0.053	-0.28	0.14	-0.39	-0.51	-0.41	-0.11	1280	1150	991	1490	1130	912	1020	1250	514.9	1541.8	3	0.0092	5.934

Ubiquitin thioesterase OTUB1 OS=Rattus norvegicus GN=Otub1 PE=1 SV=1	6 OTUB1 _RAT,sp Q7TQI3 O TUB1_MO USE,sp Q 96FW1 O TUB1_HU MAN,tr B 3KUV5 B 3KUV5_H UMAN,tr B4DPD5 B4DPD5_ HUMAN,t r B4E053 B4E053_ HUMAN,t r C5H0C6 C5H0C6_ PIG,tr D2 H4U8 D2 H4U8_AIL ME,tr D3 YWF6 D3 YWF6_M OUSE,tr F 1PIA2 F1	fFEH FIEG GR	62%	32.9	51.55901	Ref	0.026	-0.18	-0.09	-0.56	-0.35	-0.38	0.033	1830	1610	1520	1810	1440	1460	1490	1970	514.9	1541.8	3	0.0079	5.098
Uncharacterized protein OS=Equus caballus GN=CCDC15 PE=4 SV=1	REV_tr F6 YK38 F6Y K38_HOR SE	APqI Aqk	67%	31.8	49.72175	Ref	0.61	0.74	0.44	0.65	0.68	1.3	0.7	1160	1420	1690	1530	1960	1740	2850	1840	531.3	1060.6	2	0.0124	11.7
Uncharacterized protein OS=Equus caballus GN=CCDC15 PE=4 SV=1	REV_tr F6 YK38 F6Y K38_HOR SE	APqI Aqk	68%	31.7	49.47914	Ref	0.62	0.71	0.6	0.55	0.53	1.6	0.43	1820	2660	3070	3190	3400	2920	6520	2840	531.3	1060.6	2	0.0096	9.063

<p>Serine/arginine-rich splicing factor 11 OS=Homo sapiens GN=SRSF11 PE=1 SV=1</p>	<p>9 SRS11_HUMAN, tr B4DTC1 B4DTC1_HUMAN, tr B4DWT1 B4DWT1_HUMAN, tr D2HTF1 D2HTF1_AILME, tr D3Z4B0 D3Z4B0_MOUSE, tr D3ZBT0 D3ZBT0_RAT, tr D3ZN26 D3ZN26_RAT, tr D4A4E2 D4A4E2_RAT, tr D6RE22 D6RE22_MOUSE, tr E9Q6E5 E9Q6E5_MOUSE</p>	<p>tLFG FLGK</p>	<p>58%</p>	<p>30.3</p>	<p>49.51585</p>	<p>Ref</p>	<p>-0.31</p>	<p>-0.28</p>	<p>0.27</p>	<p>-0.24</p>	<p>0.27</p>	<p>-0.57</p>	<p>0.5</p>	<p>4630</p>	<p>3270</p>	<p>3640</p>	<p>5950</p>	<p>4620</p>	<p>5760</p>	<p>3350</p>	<p>6970</p>	<p>497.6</p>	<p>1489.9</p>	<p>3</p>	<p>0.0039</p>	<p>2.633</p>
<p>Serine/arginine-rich splicing factor 11 OS=Homo sapiens GN=SRSF11 PE=1 SV=1</p>	<p>9 SRS11_HUMAN, tr B4DTC1 B4DTC1_HUMAN, tr B4DWT1 B4DWT1_HUMAN, tr D2HTF1 D2HTF1_AILME, tr D3Z4B0 D3Z4B0_MOUSE, tr D3ZBT0 D3ZBT0_RAT, tr D3ZN26 D3ZN26_RAT, tr D4A4E2 D4A4E2_RAT, tr D6RE22 D6RE22_MOUSE, tr E9Q6E5 E9Q6E5_MOUSE</p>	<p>tLFG FLGK</p>	<p>66%</p>	<p>31</p>	<p>49.16722</p>	<p>Ref</p>	<p>0.22</p>	<p>-0.17</p>	<p>0.049</p>	<p>-0.11</p>	<p>0.21</p>	<p>-0.4</p>	<p>0.025</p>	<p>7060</p>	<p>7090</p>	<p>5870</p>	<p>7650</p>	<p>7570</p>	<p>8230</p>	<p>5640</p>	<p>7510</p>	<p>746</p>	<p>1489.9</p>	<p>2</p>	<p>#####</p>	<p>0.021</p>

Cholecystokinin OS=Sus scrofa GN=CCK PE=1 SV=1	6 CCKN_P IG,sp P06 307 CCKN _HUMAN, sp P2336 2 CCKN_ MACFA,sp Q9TS44 CCKN_CA NFA,tr B7 Z6Q9 B7Z 6Q9_HU MAN,tr D 2HN41 D 2HN41_AI LME,tr F6 QGZ9 F6 QGZ9_CA LJA,tr F6 QMJ5 F6 QMJ5_M ACMU,tr F7BAG1 F 7BAG1_H ORSE,tr F 7GS85 F7 GS85_CAL	aHLG ALLA R	62%	33.1	51.61814	Ref	0.16	0.16	0.37	-0.041	0.086	0.18	0.33	8670	9040	9800	12700	10500	10000	11200	12400	409.3	1224.8	3	0.0076	6.222
Cholecystokinin OS=Sus scrofa GN=CCK PE=1 SV=1	6 CCKN_P IG,sp P06 307 CCKN _HUMAN, sp P2336 2 CCKN_ MACFA,sp Q9TS44 CCKN_CA NFA,tr B7 Z6Q9 B7Z 6Q9_HU MAN,tr D 2HN41 D 2HN41_AI LME,tr F6 QGZ9 F6 QGZ9_CA LJA,tr F6 QMJ5 F6 QMJ5_M ACMU,tr F7BAG1 F 7BAG1_H ORSE,tr F 7GS85 F7 GS85_CAL	aHLG ALLA R	64%	33.5	51.61392	Ref	0.052	0.063	0.34	-0.1	0.062	0.1	0.51	25600	21600	23600	32200	26100	25500	27400	36200	409.3	1224.8	3	0.0096	7.861

Ras suppressor protein 1 OS=Mus musculus GN=Rsu1 PE=2 SV=3	0 RSU1_MOUSE,sp Q15404 RSU1_HUMAN,sp Q5E9C0 RSU1_BOVIN, tr A2AUR7 A2AUR7_MOUSE, tr A88KA46 A8KA46_HUMAN, tr B0YJ73 B0YJ73_HUMAN, tr C77BDX2 C7BDX2_SHEEP, tr D2H9Y0 D2H9Y0_AILME, tr D3ZCX0 D3ZCX0_RAT, tr D4A8F2 D4A8F2	eIGE LTQL k	55%	31.3	51.22439	Ref	-0.45	-0.17	-0.26	-0.23	-0.34	-0.18	-0.46	6650	4540	5950	6270	7080	5740	6700	5470	547	1638	3	0.0039	2.37
Ras suppressor protein 1 OS=Mus musculus GN=Rsu1 PE=2 SV=3	0 RSU1_MOUSE,sp Q15404 RSU1_HUMAN,sp Q5E9C0 RSU1_BOVIN, tr A2AUR7 A2AUR7_MOUSE, tr A88KA46 A8KA46_HUMAN, tr B0YJ73 B0YJ73_HUMAN, tr C77BDX2 C7BDX2_SHEEP, tr D2H9Y0 D2H9Y0_AILME, tr D3ZCX0 D3ZCX0_RAT, tr D4A8F2 D4A8F2	eIGE LTQL k	63%	32.8	51.2394	Ref	-0.2	-0.33	-0.45	-0.37	-0.27	-0.29	-0.4	5350	3800	3770	3900	4530	4250	4380	4010	547	1638	3	0.0033	2.041

Tax_Id=9606 Gene_Symbol=KRT9 Keratin, type I cytoskeletal 9	IPI:CON_0 0019359. 3 SWISS- PROT:P35 527,sp P3 5527 K1C 9_HUMA N	sGG GGG GGL GSG GSIR	95%	59.9	51.46922	Ref	-0.45	0.31	0.12	-1.2	-0.54	0.42	-0.45	4480	2850	5230	5160	2280	3150	6390	3470	768.9	1535.8	2	0.014	9.114
Ataxin 3 variant ref (Fragment) OS=Homo sapiens GN=ATXN3 PE=2 SV=1	REV_tr D 3VVF6 D3 VVF6_HU MAN,REV _tr D3VV M1 D3VV M1_HUM AN,REV_t r D3VVP0 D3VVP0 _HUMAN, REV_tr D 3VVS5 D3 VVS5_HU MAN,tr E 1BGH0 E 1BGH0_B OVIN	qQQ QQQ QQQ QQQ Qk	95%	56.7	54.92362	Ref	Refer ence Missing (3.4620 218)	Refer ence Missin g (2.79 39718)	Refer ence Missin g (2.980 702)	Refer ence Missin g (0.744 6217)	Refer ence Missin g (4.295 423)	Refer ence Missin g (2.622 807)	Refer ence Missin g (3.270 3993)	No Values (0.0)	Refer ence Missing (3.462021 8)	Refer ence Missin g (2.79 39718)	Refer ence Missin g (2.9807 02)	Refer ence Missing (0.744621 7)	Refer ence Missin g (4.29 5423)	Refer ence Missin g (2.622 807)	Refer ence Missing (3.270399 3)	807.8	2420.2	3	0.0163	6.725
Phosphatidate cytidyltransferase 2 OS=Bos taurus GN=CDS2 PE=1 SV=1	sp A0JNC 1 CDS2_B OVIN	aDG ETAS DSES R	95%	63.5	47.03661	Ref	-0.63	-0.44	-0.18	-0.28	-0.06	-1	-0.14	1740	979	1210	1630	1680	1700	903	1670	764.9	1527.7	2	0.0078	5.09

Eukaryotic translation initiation factor 3 subunit J OS=Rattus norvegicus GN=Eif3j PE=2 SV=1	9 EIF3J_RAT,sp O75822 EIF3J_HUMAN,sp Q0VCU8 EIF3J_BOVIN,sp Q5R8D1 EIF3J_PONAB,sp Q66JS6 EIF3J_MOUSE,tr B4DUI3 B4DUI3_HUMAN,tr D2GW38 D2GW38_AILME,tr F1SN05 F1SN05_PIG,tr F1SN07 F1SN07_PIG,tr F5H425 F5H425_HUMAN,tr F6W	VLTP EEQL ADK	95%	48.5	52.77779	Ref	-0.23	-0.19	-0.08	-0.11	0.2	-0.52	-0.05	8790	6500	7270	8810	9490	10300	6500	8980	926	1850	2	0.0139	7.51
Eukaryotic initiation factor 4A-I OS=Pan troglodytes GN=EIF4A1 PE=2 SV=1	4 IF4A1_PANTR,sp P29562 IF4A1_RABIT,sp P60842 IF4A1_HUMAN,sp P60843 IF4A1_MOUSE,sp Q3SZ54 IF4A1_BOVIN,sp Q4R8K5 IF4A1_MACFA,sp Q5R5F5 IF4A1_PONAB,tr A6M928 A6M928_PIG,tr A8K088 A8K088_HUMAN,tr A8K7F6 A8K7F6_HUMAN	IQM EAP HIIV GTP GR	95%	60.4	53.49027	Ref	0.11	-0.11	-0	-0.26	-0.31	0.24	-0.21	3940	3680	3450	4150	3850	3230	4940	3580	641.7	1922.1	3	0.0111	5.775

Splicing factor 3A subunit 2 OS=Bos taurus GN=SF3A2 PE=2 SV=1	8 SF3A2_BOVIN,sp Q15428 SF3A2_HUMAN,sp Q62203 SF3A2_MOUSE,sp Q6AXT8 SF3A2_RAT, tr D2HTL8 D2HTL8_AILME, tr D3YW09 D3YW09_MOUSE, tr D3Z5A6 D3Z5A6_MOUSE, tr E2QXZ1 E2QXZ1_CANFA, tr F1S818 F1S818_PIG, tr F6U6H6 F6U6H6_MONDO, t	tGSG GVA SSSE	SNR	95%	69.9	50.22873	Ref	0.028	-0.12	0.15	-0.18	-0.04	-0.24	0.017	2680	2380	2330	3150	2750	2660	2410	2860	800.4	1598.8	2	0.0067	4.185
Double-stranded RNA-binding protein Staufenhomolog 1 OS=Ailuropoda melanoleuca GN=STAU1 PE=3 SV=1	7 STAU1_AILME,sp O95793 STAU1_HUMAN,sp Q9Z108 STAU1_MOUSE, tr A2A5R8 A2A5R8_MOUSE, tr A2A5S2 A2A5S2_MOUSE, tr A2A5S3 A2A5S3_MOUSE, tr A6QNY4 A6QNY4_BOVIN, tr A8K622 A8K622_HUMAN, tr B3KRE0 B3KRE0_HUMAN, tr B4DPJ9 B4DPJ9	eLLY GGT SPTA ETILK	ETILK	95%	57.7	53.44461	Ref	-0.061	-0.34	-0.05	2E-04	-0.16	-0.3	-0.13	3210	2680	2390	3280	3750	2920	2770	3100	767.8	2300.3	3	0.0141	6.145

40S ribosomal protein S3 OS=Canis familiaris GN=RPS3 PE=1 SV=1	7 RS3_CA NFA,sp P 23396 RS 3_HUMA N,sp P62 908 RS3_ MOUSE,s p P62909 RS3_RAT ,sp Q0Z8 U2 RS3_P IG,sp Q3T 169 RS3_ BOVIN,sp Q5R465 RS3_PON AB,tr B2K I51 B2KI5 1_RHIFE,t r D2H1D2 D2H1D2 _AILME,tr D3YV43 D3YV43_ MOUSE,tr E9PJH4 E9PJH4_H	eLAE DGY SGVE VR	95%	48.5	51.5567	Ref	0.57	-0.27	0.44	0.12	-0.03	0.26	0.14	6830	8790	5330	9830	8660	6810	8710	7940	864.4	1726.9	2	0.0174	10.09
NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=Homo sapiens GN=NDUFS4 PE=1 SV=1	1 NDUS4 _HUMAN, sp POCB9 5 NDUS4 _PONAB,s p POCB96 NDUS4_ PONPY,sp Q02375 NDUS4_B OVIN,sp Q0MQH0 NDUS4_ GORG0,s p Q0MQ H1 NDUS 4_PANTR, sp Q9CXZ 1 NDUS4 _MOUSE,t r D7NYH8 D7NYH8 _MINSC,tr D7NYH9 D7NYH9 _CYNSP,tr D7NYI0	IDITT LTGV PEEH ik	95%	57	53.4109	Ref	-0.24	-0.06	-0.12	-0.42	0.1	-0.46	-0.1	8200	6040	7420	8000	7130	8980	6330	8080	758.8	2273.3	3	0.0211	9.256

Density-regulated protein OS=Homo sapiens GN=DENR PE=1 SV=2	sp O43583 DENR_HUMAN,sp Q2HJ47 DENR_BOVIN,sp Q5RFP5 DENR_PONAB,tr E1BIK7 E1BIK7_BOVIN,tr E2R300 E2R300_CANFA,tr F6X4Y8 F6X4Y8_HORSE,tr F7GK79 F7GK79_MAEMU,tr F8VVL1 F8VVL1_HUMAN,tr Q4R604 Q4R604_MAIFA	qEA GISE GQG TAG EEEE k	95%	64	53.07308	Ref	-0.11	0.068	0.087	-0.32	0.39	-0.65	0.016	2740	2200	2700	3070	2560	3640	1860	2920	819.7	2456.2	3	0.0295	11.99
Zinc finger protein 207 OS=Homo sapiens GN=ZNF207 PE=1 SV=1	0 ZNF207_HUMAN,sp Q5R8K4 ZNF207_PONAB,tr A8MTG3 A8MTG3_HUMAN, tr B4DQT7 B4DQT7_HUMAN, tr D2GU63 D2GU63_AILME, tr D3ZEK1 D3ZEK1_RAT, tr D3ZHE8 D3ZHE8_RAT, tr E1P660 E1P660_HUMAN, tr E2RI63 E2RI63_CANIFA, tr E2RI65 E2RI65_CANIFA	IIHP DEDI SLEE R	95%	56.1	53.29412	Ref	0.41	0.51	0.049	-0.086	0.51	-0.18	0.36	6580	7620	8820	7200	7230	9570	6190	8890	624	1869	3	0.0154	8.247

40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=2 SV=4	1 RS16_MOUSE,s p P62249 RS16_H UMAN,sp P62250 RS16_RAT ,sp Q292 01 RS16_ PIG,sp Q3 TOX6 RS1 6_BOVIN, tr A4FUS 1 A4FUS1 _MOUSE,t r B0K038 B0K038_ RAT,tr B6 V8C7 B6V 8C7_PIG,t r C0JKE5 C0JKE5_C AVPO,tr E 1BAT6 E1 BAT6_BO VIN,tr F0 UY67 FOU	ILEP VLLL Gk	95%	48.7	40.43362	Ref	0.52	-0.41	0.7	0.056	0.48	0.02	0.58	2430	3040	1720	4180	2950	3450	2620	3830	568.4	1702.1	3	0.0073	4.285
N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3	6 GNS_H UMAN,sp P50426 GNS_CAP HI,sp Q1L ZH9 GNS _BOVIN,s p Q8BFR4 GNS_MO USE,tr A8 K6V6 A8K 6V6_HUM AN,tr B4 DTT0 B4D TTO_HUM AN,tr B4 DYH8 B4 DYH8_HU MAN,tr B 4E284 B4 E284_HU MAN,tr D 2HDL0 D 2HDL0_AI LME,tr E1 B8S8 E1B 8S8_BOVI	sDVL VEY QGE GR	95%	53.9	51.84623	Ref	0.6	-0.45	0.22	-0.18	0.68	-0.59	0.3	10800	14200	7480	13400	11100	17700	7650	14000	828.4	1654.8	2	0.0124	7.505

Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	sp P16401 H15_HUMAN, tr F7BRW5 F7BRW5_MACMU	aLAA GGY DVEk	95%	54.9	53.05166	Ref	-1.3	0.43	-1.7	-0.35	-0.78	-0.32	-0.7	30700	10800	38900	10100	28000	18200	26200	19900	851.5	1700.9	2	0.018	10.6
Transcription factor jun-B OS=Homo sapiens GN=JUNB PE=1 SV=1	sp P17275 JUNB_HUMAN, sp Q0VBZ5 JUNB_BOVIN, tr E2RQI9 E2RQI9_CA_NFA, tr F6U5C5 F6U5C5_MA CMU, tr F6Y5A4 F6Y5A4_HO RSE, tr Q53HP8 Q53HP8_HUMAN, tr Q5U079 Q5U079_HUMAN	gGG SGG GAG GAG GGV TEEQ EGF ADG FVk	95%	91.5	54.22214	Ref	-0.22	-0.07	-0.19	-0.31	0.035	-0.78	-0.17	3380	2520	3040	3140	3180	3530	2100	3160	1007	3019.5	3	0.0177	5.861
NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Bos taurus GN=NDUFS6 PE=1 SV=2	sp P23934 NDUS6_BOVIN, tr A8YXY4 A8YXY4_BOVIN, tr F1S031 F1S031_PIG, tr F6XVS1 F6XVS1_HORSE	vISc DGG GGA LGH PR	95%	58.3	51.35314	Ref	0.23	0.38	-0.1	-0.086	0.077	0.22	0.11	8530	8680	10500	8450	9380	9160	10600	9750	582.6	1744.8	3	0.0189	10.8

60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	3 RL13_HUMAN,sp P41123 RL13_RAT,sp P47963 RL13_MOUSE,sp Q56JZ1 RL13_BOVIN,sp Q9Z313 RL13_CRIGR,tr A8K4C8 A8K4C8_HUMAN, tr B4DLX3 B4DLX3_HUMAN, tr D2HVV4 D2HVV4_AILME, tr D3YX54 D3YX54_MOUSE, tr D3Z9H4 D3Z9H4_RAT, tr D3	eAAE QDV Ek	95%	48.8	52.61945	Ref	0.29	-0.17	0.39	-0.19	0.59	-0.32	0.46	5330	5690	4470	7390	5470	8180	4540	7770	813.9	1625.9	2	0.0075	4.632
14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	8 1433T_HUMAN,sp P68254 1433T_MOUSE,sp P68255 1433T_RAT,sp Q3SZI4 1433T_BOVIN,sp Q5RFJ2 1433T_PONAB,sp Q6Q6X0 1433T_RABIT, tr A3KML3 A3KML3_MOUSE, tr B0JYM5 B0JYM5_BOVIN, tr D2HLL8 D2HLL8_AILME, tr D3ZM53 D3ZM53_RAT,	avTE QGA ELSN EER	95%	53.6	51.93598	Ref	0.15	-0.4	0.24	-0.049	0.098	-0.53	-0.09	18500	17800	13200	23100	20800	20100	13700	18300	919	1835.9	2	0.0132	7.16

Lysosome membrane protein 2 OS=Rattus norvegicus GN=Scarb2 PE=1 SV=2	sp P27615 SCRB2_RAT, tr A6QQP4 A6QQP4_BOVIN, tr F1N1Q4 F1N1Q4_BOVIN	gQGSTDEGTA	95%	43.5	47.82902	Ref	0.37	-0.74	0.37	-0.38	0.33	-1.4	0.11	848	953	479	1160	760	1090	349	967	813.9	1625.7	2	0.0066	4.032
Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3	sp P27816 MAP4_HUMAN, tr B9ZVR1 B9ZVR1_HUMAN, tr C6ZLB4 C6ZLB4_FELCA, tr E7EVA0 E7EVA0_HUMAN, tr F1SLI3 F1SLI3_PIG	eAQTLDSQIQE	95%	77.2	52.5994	Ref	No Values (0.20238991)	Reference Missing (2.2384343)	No Values (-1.852022237726)	Reference Missing (1.6908888)	Reference Missing (1.6914568)	Reference Missing (2.0147984)	No Values (0.0)	No Values (0.20238991)	Reference Missing (2.2384343)	Reference Missing (1.852045)	No Values (-0.22237726)	Reference Missing (1.6908888)	Reference Missing (1.6914568)	Reference Missing (2.0147984)		934	1865.9	2	0.0176	9.406

<p>Guanine nucleotide-binding protein-like 1 OS=Homo sapiens GN=GNL1 PE=1 SV=2</p>	<p>5 GNL1_HUMAN,sp P36916 GNL1_MOUSE,sp Q4R8D2 GNL1_MA CFA,sp Q5RA07 GNL1_PON AB,sp Q5TM59 GNL1_MAC MU,sp Q6MG06 GNL1_RAT,sp Q7YR35 GNL1_P ANTR,tr A2VDH5 A2VDH5_MOUSE,tr A5PJR9 A5PJR9_BOVIN,tr A8MPZO A8MPZO_HUM</p>	<p>iPVQ ALLH LR</p>	<p>95%</p>	<p>52.8</p>	<p>47.43996</p>	<p>Ref</p>	<p>0.057</p>	<p>-0.06</p>	<p>-0.22</p>	<p>-0.32</p>	<p>-0.24</p>	<p>-0.06</p>	<p>-0.42</p>	<p>1530</p>	<p>1380</p>	<p>1380</p>	<p>1400</p>	<p>1430</p>	<p>1320</p>	<p>1570</p>	<p>1210</p>	<p>488.6</p>	<p>1462.9</p>	<p>3</p>	<p>0.0108</p>	<p>7.39</p>
<p>Thyroxine-binding globulin OS=Ovis aries GN=SERPINA7 PE=2 SV=1</p>	<p>sp P50450 THBG_SHEEP,sp Q9TT35 THBG_PIG,sp Q9TT36 THBG_BOVIN,tr F1PB85 F1PB85_CANFA,tr F1RXM6 F1RXM6_PIG,tr F6ZRF6 F6ZRF6_HORSE,tr Q3SYR0 Q3SYR0_BOVIN</p>	<p>sFLLL ILEk</p>	<p>95%</p>	<p>45.2</p>	<p>44.48598</p>	<p>Ref</p>	<p>1.2</p>	<p>0.078</p>	<p>0.52</p>	<p>0.12</p>	<p>-0.35</p>	<p>0.67</p>	<p>0.39</p>	<p>505</p>	<p>1000</p>	<p>503</p>	<p>767</p>	<p>640</p>	<p>403</p>	<p>855</p>	<p>701</p>	<p>562</p>	<p>1683.1</p>	<p>3</p>	<p>0.0068</p>	<p>4.009</p>

<p>Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3</p>	<p>2 HNRPM_HUMAN,sp Q62826 HNRPM_RAT,sp Q9D0E1 HNRPM_MOUSE,tri B8JK30 B8JK30_MOUSE,tri B8JK32 B8JK32_MOUSE,tri B8JK33 B8JK33_MOUSE,tri D2HZS9 D2HZS9_AILME,tri E2RMR3 E2RMR3_CANFA,tri E9Q0P7 E9Q0P7_MOUSE,tri F1L1V13 F1R</p>	<p>mGP LGLD HMA SSIE</p>	<p>95%</p>	<p>57.6</p>	<p>53.04102</p>	<p>Ref</p>	<p>0.38</p>	<p>0.13</p>	<p>-0.07</p>	<p>-0.1</p>	<p>0.018</p>	<p>0.1</p>	<p>0.087</p>	<p>4800</p>	<p>5420</p>	<p>4970</p>	<p>4840</p>	<p>5210</p>	<p>4950</p>	<p>5470</p>	<p>5390</p>	<p>640</p>	<p>1917</p>	<p>3</p>	<p>0.0027</p>	<p>1.427</p>
<p>39S ribosomal protein L12, mitochondrial OS=Homo sapiens GN=MRPL12 PE=1 SV=2</p>	<p>5 RM12_HUMAN,sp P52827 RM12_CRICR,sp Q7YR75 R M12_BOVIN,sp Q9DB15 RM12_MOUSE,tri D2GVF9 D2GVF9_AILME,tri D3ZXF9 D3ZXF9_RAT,tri E2QVI3 E2QVI3_CANFA,tri F6XA D7 F6XA D7_HORSE,tri F7H0R4 F7H0R4_MACM U,tri F7HX83 F7HX83_CALJA,t</p>	<p>aALE AVG GTV VLE</p>	<p>95%</p>	<p>67.4</p>	<p>52.4701</p>	<p>Ref</p>	<p>0.0062</p>	<p>0.12</p>	<p>-0.04</p>	<p>0.22</p>	<p>0.56</p>	<p>0.34</p>	<p>0.64</p>	<p>273</p>	<p>238</p>	<p>280</p>	<p>280</p>	<p>371</p>	<p>409</p>	<p>368</p>	<p>448</p>	<p>766.9</p>	<p>1531.9</p>	<p>2</p>	<p>0.0164</p>	<p>10.73</p>

Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	8 UBE2N_HUMAN,sp P61089 UBE2N_MOUSE,sp Q0P5K3 UBE2N_BOVIN,sp Q4R411 UBE2N_MACFA,sp Q5JXB2 UE2NL_HUMAN,sp Q5R7J6 UBE2N_PONAB,tra A2RTT4 A2RTT4_MOUSE,tra A5D987 A5D987_BOVIN,tra C5IS99 C5IS99_SHEEP,tra E1BHR2 E1BHR2	TNEAQAIE	95%	51.2	52.3472	Ref	0.14	0.016	0.21	0.042	0.052	-0.1	-0	12200	11700	11600	14900	14600	12900	12100	12800	754.4	1506.8	2	0.0116	7.678
40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	4 RS15A_HUMAN,sp P62245 RS15A_MOUSE,sp P62246 RS15A_RAT,sp Q5R938 RS15A_PONAB,sp Q76I82 RS15A_BOVIN,tra A8K7H3 A8K7H3_HUMAN,tra B2R4W8 B2R4W8_HUMAN,tra D2GX76 D2GX76_AILME,tra D2HEL7 D2HEL7_AILME,tra D3YBZ8 D3YBZ8	qFGFIVLTTSA GIM DHE EAR	95%	79.5	54.50625	Ref	0.45	-0.09	-0.09	-0.18	-0.57	0.26	-0.01	182	216	161	182	188	125	232	191	842.8	2525.3	3	0.018	7.128

Small nuclear ribonucleoprotein F OS=Homo sapiens GN=SNRPF PE=1 SV=1	6 RUXF_HUMAN,sp P62307 RUXF_MOUSE,sp Q3T028 RUXF_BOVIN,trans D4A39 RAT,trans D4AAT4 RAT,trans F1Q0L5 F1Q0L5_CANFA,trans F1SQR4 F1SQR4_PIG,trans F6Q5W2 F6Q5W2_ORNAN,trans F6UZL4 F6UZL4_CAJA,trans F7CC29 F7CC29_HORSE,trans F	gVEE EEED GEM RE	95%	45.3	45.19447	Ref	0.3	0.38	0.44	0.27	0.46	0.26	0.65	11500	12300	14200	16600	16200	16100	14600	19100	921.4	1840.8	2	0.0123	6.684
RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1	4 EWS_HUMAN,sp Q61545 EWS_MOUSE,trans B0QYK0 B0QYK0_HUMAN,trans B0QYK1 B0QYK1_HUMAN,trans B1WC50 B1WC50_RAT,trans C9JGE3 C9JGE3_HUMAN,trans D2H238 D2H238_AILME,trans D4A458 RAT,trans E2RA07 E2RA07_CANFA,trans E2RA46 E2RA46_CAN	gDAT VSYE DPPT Ak	95%	65.4	53.90587	Ref	-0.44	-0.34	-0.14	-0.4	0.22	-1.1	-0.08	8610	5520	6390	8250	7630	10200	4250	8600	1030	2058.1	2	0.0114	5.559

CDGSH iron-sulfur domain-containing protein 2 OS=Bos taurus GN=CISD2 PE=2 SV=1	sp Q05B71 CISD2_BOVIN,sp Q8N5K1 CISD2_HUMAN,tr E2R702 E2R702_CAFNA,tr F1MH13 F1MH13_BOVIN,tr F6URX4 F6URX4_MACMU,tr F6Z4H8 F6Z4H8_CALJA,tr F7E5W3 F7E5W3_MONDO	rLPV PESI TGF AR	95%	53.9	52.69188	Ref	0.34	0.21	0.29	0.13	0.28	0.16	0.17	5580	6150	6080	7220	7120	6880	6630	6650	583	1746	3	0.0087	4.986
Filamin-binding LIM protein 1 OS=Bos taurus GN=FBLIM1 PE=2 SV=1	sp Q1JQB5 FBLI1_BOVIN	rDEA VVEE VR	95%	69.7	52.39485	Ref	0.65	0.31	0.31	0.13	0.22	-0.24	0.22	17200	23500	20000	22500	21900	20300	15500	21100	502.6	1504.8	3	0.0103	6.857

RNA-binding protein 8A OS=Rattus norvegicus GN=Rbm8a PE=2 SV=1	01 RBM8A_RAT,sp Q3ZCE8 RBM8A_BOVIN,sp Q9CWXZ3 RBM8A_MOUSE,sp Q9Y559 RBM8A_HUMAN,tra D2HQ50 D2HQ50_AILME,tra E2QV85 E2QV85_CANFA,tra F2Z5K7 F2Z5K7_PIG,tra F6XEW8 F6XEW8_HORSE,tra F7DRZ4 F7DRZ4_CALIA,tra F7EF23 F7EF23_R	mRE DYE SVE QDG DEP GPQ	95%	67.9	48.19004	Ref	-0.12	-0.06	-0.41	0.34	0.023	-0.19	-0.07	12000	9560	10800	9530	17700	12400	11200	12000	843	2526.1	3	0.0181	7.146
Protein FAM114A2 OS=Bos taurus GN=FAM114A1 PE=2 SV=1	1 F1142_BOVIN,sp Q9NRY5 F1142_HUMAN,tra B3KTE4 B3KTE4_HUMAN,tra B4DQT0 B4DQT0_HUMAN,tra B4E1J2 B4E1J2_HUMAN,tra E7ESJ7 E7ESJ7_HUMAN,tra F1N189 F1N189_BOVIN,tra F6TP08 F6TP08_HORSE,tra F7H224 F7H224_MACMU,tra F7HTQ6 F7	tAAL VLH GR	95%	55.8	50.64821	Ref	0.065	-0.13	-0	-0.3	0.064	-0.13	-0.12	9810	8920	8460	10400	9290	10500	9530	9540	414.6	1240.8	3	0.0047	3.76

GTP-binding protein SAR1a OS=Bos taurus GN=SAR1A PE=2 SV=1	7 SAR1A_BOVIN,sp Q52NJ3 SAR1A_PIG,sp Q5R548 SAR1A_PONAB,sp Q9NR31 SAR1A_HUMAN, tr B2R679 B2R679_HUMAN, tr B4DQ19 B4DQ19_HUMAN, tr D2GXH1 D2GXH1_AILME, tr E2RQR5 E2RQR5_CANFA, tr E9PBN0 E9PBN0_HUMAN, tr F1SUD3 F1	elFG LYG QTT Gk	95%	52.9	53.41227	Ref	0.16	-0.23	-0.18	-0.14	-0.25	-0.19	-0.21	2820	2740	2260	2630	2990	2410	2620	2580	641.4	1921.1	3	0.013	6.789
Follistatin-related protein 1 OS=Bos taurus GN=FSTL1 PE=2 SV=1	sp Q58D84 FSTL1_BOVIN	gAQ TQA EEE MTR	95%	57.5	50.48438	Ref	-0.45	-0.02	0.11	0.085	0.61	-0.29	0.83	8970	5700	8350	10300	11100	13900	7780	16800	827.9	1653.8	2	0.0125	7.58

<p>Tumor protein D54 OS=Pongo abelii GN=TPD52L2 PE=2 SV=1</p>	<p>1 TPD54_PONAB,sp Q6PCT3 TPD54_R AT,sp Q9 CY22 TPD 54_MOUS E,tr A2AU D5 A2AU D5_MOU SE,tr A2A UD6 A2A UD6_MO USE,tr A2 AUE0 A2 AUE0_MO USE,tr D3 ZJ46 D3ZJ 46_RAT,tr D3ZRQ2 D3ZRQ2 _RAT,tr D 3ZW65 D 3ZW65_R AT,tr F6V Q81 F6V Q81_MO</p>	<p>tSAA LST MGS AISR</p>	<p>95%</p>	<p>48.6</p>	<p>53.21099</p>	<p>Ref</p>	<p>-0.17</p>	<p>-0.14</p>	<p>0.026</p>	<p>0.011</p>	<p>0.34</p>	<p>-0.29</p>	<p>0.089</p>	<p>9500</p>	<p>7330</p>	<p>8140</p>	<p>10200</p>	<p>11200</p>	<p>12300</p>	<p>8280</p>	<p>10700</p>	<p>828.9</p>	<p>1655.9</p>	<p>2</p>	<p>0.0127</p>	<p>7.653</p>
<p>Zinc finger protein 787 OS=Homo sapiens GN=ZNF787 PE=1 SV=2</p>	<p>sp Q6DD 87 ZN787 _HUMAN, sp Q8BIF 9 ZN787_ MOUSE,tr D3ZDN6 D3ZDN6 _RAT,tr E 1BGX5 E1 BGX5_BO VIN,tr F1 PSY3 F1P SY3_CANF A,tr F6ZIP 9 F6ZIP9_ MACMU</p>	<p>gFG HGA GLLA HQR</p>	<p>95%</p>	<p>54.8</p>	<p>52.78264</p>	<p>Ref</p>	<p>0.041</p>	<p>0.026</p>	<p>0.35</p>	<p>-0.12</p>	<p>0.39</p>	<p>-0.11</p>	<p>0.22</p>	<p>3670</p>	<p>3280</p>	<p>3520</p>	<p>4960</p>	<p>3920</p>	<p>4890</p>	<p>3620</p>	<p>4510</p>	<p>407</p>	<p>1623.9</p>	<p>4</p>	<p>0.0056</p>	<p>3.466</p>

Plexin domain-containing protein 2 OS=Homo sapiens GN=PLXDC2 PE=1 SV=1	1 PXDC2_HUMAN,sp Q9DC11 PXDC2_MOUSE,tra A0JN47 A0JN47_BOVIN,tra B1AY84 B1AY84_MOUSE,tra B1AY85 B1AY85_MOUSE,tra B1AY86 B1AY86_MOUSE,tra B4E367 B4E367_HUMAN,tra B5DEZ8 B5DEZ8_RAT,tra B7WP84 B7WP84_HUMAN,tra C0SQ70 C0SQ70	vGLS DAF VVV HR	95%	77.5	52.16602	Ref	0.67	0.11	0.53	-0.002	0.35	-0.07	0.85	2450	3370	2480	3730	2850	3170	2470	4650	535	1601.9	3	0.005	3.117
Alpha-2-macroglobulin OS=Bos taurus GN=A2M PE=1 SV=2	sp Q7SIH1 A2MG_BOVIN,tra E1BJW0 E1BJW0_BOVIN	sPTS QEV MFL TIQV k	95%	53.9	53.78344	Ref	0.3	-0.03	-0.04	0.2	-0.19	0.73	-0.2	372	399	343	382	500	332	657	341	772.8	2315.3	3	0.0085	3.683

SH3 domain-containing kinase-binding protein 1 OS=Mus musculus GN=Sh3kbp1 PE=1 SV=1	0 SH3K1_ MOUSE,s p Q925Q 9 SH3K1_ RAT,sp Q 96B97 SH 3K1_HUM AN,tr A2 AG61 A2 AG61_M OUSE,tr A 4IF79 A4I F79_BOVI N,tr B1AV E8 B1AVE 8_MOUSE ,tr B1AZ8 5 B1AZ85 _MOUSE,t r D2GXZ2 D2GXZ2_ AILME,tr D3ZBP1 D3ZBP1_R AT,tr E2R JD8 E2RJ D8_CANF	k	eTTG	SESD	GGD	SSST	95%	72.9	50.86096	Ref	-0.62	-0.61	-0.17	-0.24	0.46	-1.1	0.11	2730	1550	1690	2570	2700	3840	1330	3110	718.3	2152	3	0.0206	9.549
Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1	2 H1X_H UMAN,tr D2H7C5 D2H7C5_ AILME,tr D3ZIX4 D 3ZIX4_RA T,tr E2RQ 07 E2RQ0 7_CANFA, tr F1MM U4 F1M MU4_BO VIN,tr F1 MP74 F1 MP74_BO VIN,tr F1 MV98 F1 MV98_BO VIN,tr F1 SPG1 F1S PG1_PIG,t r F6U5J8 F6U5J8_O RNAN,tr F6Z1X9 F 6Z1X9_M	aLVQ NDTL LQVvk					95%	60.4	50.82688	Ref	-0.05	0.29	-0.2	-0.082	-0.04	0.19	0.17	5870	4930	6780	5420	6470	5830	7140	6990	650.7	1949.2	3	0.0132	6.782

Golgi reassembly-stacking protein 2 OS=Mus musculus GN=Gorasp2 PE=1 SV=3	3 GORS2_MOUSE,sp Q9H8Y8 GORS2_HUMAN,sp Q9R064 GORS2_RAT, tr A2ATI6 A2ATI6_MOUSE, tr A2ATI7 A2ATI7_MOUSE, tr A2ATI8 A2ATI8_MOUSE, tr A2ATI9 A2ATI9_MOUSE, tr B4DEI4 B4DEI4_HUMAN, tr B4DKT0 B4DKT0_HUMAN, tr B4DNR1 B4DNR1_MOUSE, tr	YVYNTDNTDNcR	95%	44.3	47.39414	Ref	0.29	0.11	-0.01	5E-04	0.056	-0.04	-0.15	5670	6030	5770	5960	6620	6010	5870	5420	913.9	1825.8	2	0.0205	11.22
Protein canopy homolog 2 OS=Mus musculus GN=Cnpy2 PE=2 SV=1	0 CNPY2_MOUSE,sp Q9Y2B0 CNPY2_HUMAN, tr A0JN30 A0JN30_RAT, tr D2H353 D2H353_AILME, tr E2QVC3 E2QVC3_CANFA, tr F1MSP1 F1MSP1_BOVIN, tr F1SLY7 F1SLY7_PIG, tr F6Z678 F6Z678_MACMU, tr F7DEN7 F7DEN7_HORSE, tr F7H125 F7H125_C	INPDGSSQSVVEVPYAR	95%	56.8	54.20216	Ref	-0.39	0.27	-0.1	-0.09	0.43	-0.33	0.023	9390	6210	10700	9240	10300	12900	7920	10100	1018	2034.1	2	0.0143	7.003

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_015716 PE=3 SV=1	tr D2HU05 D2HU05_AILME, tr E2RHL0 E2RHL0_CANFA, tr F1MKD7 F1MKD7_BOVIN, tr F1MU66 F1MU66_BOVIN, tr F1MUU7 F1MUU7_BOVIN, tr F6QA35 F6QA35_HORSE	aVAF QNP QAH VLEN LHA AAY R	95%	55.6	55.16222	Ref	0.24	0.087	0.11	0.13	0.27	-0.19	0.15	927	951	929	1060	1190	1140	863	1080	656.9	2623.4	4	#####	0.133
Bone marrow stromal cell antigen 2B OS=Ovis aries GN=Bst-2B PE=2 SV=1	tr D5JZS8 D5JZS8_SHEEP	qLN QPQ EVLH Ek	95%	56.3	53.73585	Ref	-0.42	-0.39	0.19	-0.056	0.07	-0.88	0.27	8820	5710	6360	10700	9890	9420	5100	11200	691.1	2070.1	3	0.0252	12.17
Uncharacterized protein OS=Bos taurus GN=SYNPO PE=4 SV=1	tr E1BA93 E1BA93_BOVIN	rPLG NFTP PPTY AETL STAP LTSG VR	95%	75.1	55.43708	Ref	Reference Missing (1.5899063)	No Value s (0.0846968)	No Value s (-0.08189826)	No Values (-0.22237736)	Reference Missing (1.2231872)	Reference Missing (1.2701883)	Reference Missing (1.2875856)	No Value s (0.0)	Reference Missing (1.5899063)	No Value s (0.0814)	No Values (-0.0819826)	No Values (-0.22237736)	Reference Missing (1.2231872)	Reference Missing (1.2701883)	Reference Missing (1.2875856)	1017	3046.6	3	0.0123	4.045
Uncharacterized protein OS=Bos taurus GN=NEXN PE=4 SV=1	tr E1BDF0 E1BDF0_BOVIN, tr F1S9S8 F1S9S8_PIG	qMV NEEE ENQ DTE NIFK	95%	55.7	52.87237	Ref	-0.94	0.27	-1.5	-0.36	-1.2	-0.37	-1.6	4880	2220	5550	1890	4420	2130	4020	1690	902.4	2704.3	3	0.0308	11.37

Golgi phosphoprotein 3 (Coat-protein) OS=Bos taurus GN=GOLPH3 PE=2 SV=1	tr Q1RMW9 Q1RMW9_BOVIN	aAG GGG GND EDD AQS R	95%	76.2	47.16471	Ref	-0.34	0.3	-0.13	-0.15	0.15	-0.11	-0.02	479	330	557	464	504	543	474	500	594.3	1779.8	3	0.0071	3.963
Deoxyhypusine hydroxylase OS=Bos taurus GN=DOHH PE=1 SV=1	sp Q0VC53 DOHH_BOVIN	aiPV LLDV LR	95%	45.5	46.83155	Ref	0.66	0.21	0.65	-0.22	-0.43	-0.01	-0.31	157	216	171	260	157	119	165	133	471.6	1411.9	3	0.0103	7.307
YTH domain family protein 2 OS=Bos taurus GN=YTHDF2 PE=2 SV=1	3 YTHD2_BOVIN,sp Q4R5D9 YTHD2_MACFA,sp Q9Y5A9 YTHD2_HUMAN, tr B5BU99 B5BU99_HUMAN, tr D2GWL2 D2GWL2_AILME, tr E2QWK6 E2QWK6_CANFA, tr F1PCG5 F1PCG5_CANFA, tr F5H817 F5H817_HUMAN, tr F6SGT3 F6SGT3_CAJA, tr F6T950 F6T9	IGST EVAS NVP k	95%	51	52.48356	Ref	0.069	-0.09	0.097	-0.19	0.25	-0.26	0.23	14500	13200	12800	16400	14800	17600	12800	17900	604	1809	3	0.0108	5.964

Beta-2-microglobulin OS=Bos taurus GN=B2M PE=1 SV=2	8 B2MG_BOVIN,sp Q6QAT4 B2MG_SHEEP,tr A4ZVY6 A4ZVY6_SHEEP,tr A4ZVY7 A4ZVY7_SHEEP,tr A4ZVY8_SHEEP,tr A4ZVY9 A4ZVY9_SHEEP,tr F1N5H5 F1N5H5_BOVIN,tr Q1HI14 Q1HI14_CEREL,tr Q6VUQ8 Q6VUQ8_BOVIN,tr Q862Q3 Q862Q3_BOVI	sEQS DLSF Sk	94%	47.5	53.02619	Ref	-1.4	-0.24	0.022	0.44	0.34	-0.38	0.2	16800	5460	13400	18000	26500	21700	13700	20400	868.5	1734.9	2	0.0083	4.764
Protein CWC15 homolog OS=Bos taurus GN=CWC15 PE=2 SV=1	3 CWC15_BOVIN,sp Q5BJP2 CWC15_RAT,sp Q5RE65 CWC15_POONAB,sp Q9JHS9 CWC15_MOUSE,sp Q9P013 CWC15_HUMAN,tr D2HT52 D2HT52_AILME,tr E2RQA3 E2RQA3_CAF1NFA,tr F1STJ3 F1STJ3_PIG,tr F6PQC3 F6PQC3_CALJA,tr F66XA31 F66XA31_MO	gTTQ DAP EEVR	94%	45.3	50.96117	Ref	0.048	0.9	0.3	0.37	1	0.28	1.1	1880	1690	3310	2460	2840	3830	2430	4260	789.4	1576.8	2	0.0138	8.729

Transcription factor 4 OS=Canis familiaris GN=TCF4 PE=2 SV=2	1 ITF2_C ANFA,sp P15884 IT F2_HUMA N,tr A6Q PK5 A6Q PK5_BOVI N,tr B3KT 62 B3KT6 2_HUMA N,tr B3KU C0 B3KU C0_HUM AN,tr B3K VA4 B3K VA4_HU MAN,tr B 4DUG3 B 4DUG3_H UMAN,tr B7Z5M6 B7Z5M6_ HUMAN,t r B7Z6Y1 B7Z6Y1_ HUMAN,t r D2GZT6	GSGA AGSS QTG DAL Gk	94%	51.5	53.78821	Ref	0.19	-0.27	0.011	-0.18	0.15	-0.54	-0.01	7760	7680	6080	8280	7990	8760	5670	8140	658	1971	3	0.0167	8.479
Protein Red OS=Homo sapiens GN=IK PE=1 SV=3	3 RED_H UMAN,sp Q5NVI3 RED_PON AB,sp Q6 6HG8 RE D_RAT,sp Q9Z1M8 RED_MO USE,tr A4 FUY8 A4F UY8_BOVI N,tr B2R5 Y4 B2R5Y 4_HUMA N,tr D2G UN7 D2G UN7_AIL ME,tr D6 RAY9 D6 RAY9_HU MAN,tr D 6RCQ4 D 6RCQ4_H UMAN,tr D6REL4 D 6REL4_HU	eYNE DED PAA R	94%	40.4	46.67219	Ref	-0.065	-0.16	-0.33	-0.17	-0.2	-0.25	0.003	3220	2680	2720	2710	3330	2860	2870	3410	806.9	1611.7	2	0.0135	8.382

MAP7 domain-containing protein 1 OS=Mus musculus GN=Map7d1 PE=1 SV=1	MA7D1_MOUSE,sp Q3KQU3 MA7D1_HUMAN, tr A2AJH9 A2AJH9_MOUSE, tr A2AJI1 A2AJI1_MOUSE, tr A8Y5P4 A8Y5P4_MOUSE, tr B5MDZ6 B5MDZ6_HUMAN, tr D3DPS3 D3DPS3_HUMAN, tr D3ZAY9 D3ZAY9_RAT, tr D3ZU44 D3ZU44_RAT, tr D4A644 D4A644_RAT	aQA EQEE QER	94%	43	49.5639	Ref	-0.36	-0.07	-0.2	-0.21	0.21	-0.7	0.089	7040	4770	6330	6500	7130	8320	4620	7910	761.4	1520.7	2	0.0118	7.76
Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	F2A_HUMAN,sp P68101 F2A_RAT,sp P68102 F2A_BOVIN,sp Q5R493 F2A_PONAB,sp Q6ZWX6 F2A_MOUSE, tr D2HRG8 D2HRG8_AILME, tr E2QVA3 E2QVA3_CANFA, tr F2Z5J8 F2Z5J8_PIG, tr F6Q1N2 F6Q1N2_ORF6RU41 F6RU41_MOUSE, tr F6NDO, tr F6	WVTD TDET ELAR	94%	45.6	52.18107	Ref	0.14	-0.1	0.091	-0.049	0.27	-0.22	0.077	8250	7890	7240	9300	9300	10100	7550	9180	826.9	1651.8	2	0.0151	9.138

Meiotic recombination protein SPO11 OS=Mus musculus GN=Spo11 PE=2 SV=2	K8 SPO11_MOUSE,sp Q9Y5K1 SPO11_HUMAN,ter A2ASD0 A2ASD0_MOUSE,ter A2ASD1 A2ASD1_MOUSE,ter A2ASD2 A2ASD2_MOUSE,ter A5GFN4 A5GFN4_PIG,ter A5GFN5 A5GFN5_PIG,ter A6NLT8 HUMAN,ter D2H1Z1 ALME,ter D3Z8A8 D3Z8A8	gLIA GnLR	94%	43.8	50.45288	Ref	-0.46	-0.43	-0.39	-0.28	-0.08	-1	-0.58	16400	10400	11400	13200	15800	15800	8490	11600	559.8	1117.7	2	0.0057	5.107
	9 VAPB_BOVIN,sp A5GFS8 VAPB_PIG,sp O95292 VAPB_HUMAN,sp Q9QY76 VAPB_MOUSE,sp Q9Z269 VAPB_RAT,ter E2RRB7 E2RRB7_CANF,A,ter E5RK64 E5RK64_HUMAN,ter F7ATW4 F7ATW4_MACMU,ter F7E7N1 F7E7N1_MOB OS=Bos taurus GN=VAPB PE=2 SV=1	VEQ VLSL EPQ HELK	93%	49.1	53.26831	Ref	-0.35	-0.01	-0.08	-0.1	-0.02	-0.26	-0.1	7270	4950	6790	7260	7910	7330	6450	7180	753.1	2256.3	3	0.015	6.647

Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3	9 COPE_ HUMAN,s p Q28104 COPE_B OVIN,sp Q5RFR8 COPE_PO NAB,tr A 1XEC5 A1 XEC5_BO VIN,tr A6 MK98 A6 MK98_CA LJA,tr A6 NE29 A6 NE29_HU MAN,tr A 6NKA3 A 6NKA3_H UMAN,tr D2GV44 D2GV44_ AILME,tr E2RAT6 E 2RAT6_C ANFA,tr F 1RXG7 F1	VLQ, YAPS A	93%	44.2	51.55907	Ref	0.098	-0.27	-0.01	-0.27	0.098	0.3	-0.02	583	542	457	612	565	635	766	605	633.4	1264.7			2	0.0158	12.52
V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3	8 VATG1 _HUMAN, sp Q9CR5 1 VATG1 _MOUSE,t r B2GUV5 B2GUV5 _RAT,tr D 2H210 D2 H210_AIL ME,tr D7 NY50 D7 NY50_SC OKU,tr D 7NY51 D7 NY51_MI NSC,tr D7 NY52 D7 NY52_CY NSP,tr D7 NY53 D7 NY53_RO ULE,tr F1 PWU9 F1 PWU9_CA NFA,tr F1 SMJ7 F1S	eEA QAEI EQY R	93%	43.2	50.82409	Ref	0.12	0.37	0.42	0.59	0.83	0.34	0.86	5770	5460	7040	8200	10100	10500	7790	11100	835.4	1668.8			2	0.0167	9.999

Ubiquitin-like modifier-activating enzyme 1 OS=Bos taurus GN=UBA1 PE=2 SV=1	V5 UBA1 _BOVIN,s p P22314 UBA1_H UMAN,sp P31255 UBE1Y_M ACRU,sp Q02053 UBA1_M OUSE,sp Q29504 UBA1_RA BIT,sp Q5 U300 UB A1_RAT,tr A7LAC4 A7LAC4_R AT,tr B4D DE4 B4D DE4_HUM AN,tr B4 DL67 B4D L67_HUM AN,tr B9E HN0 B9E HN0_MO	nFPN AIEH TLQ WAR	92%	48.7	53.81216	Ref	0.39	-0.1	-0.06	0.26	0.016	0.47	0.28	926	1060	814	939	1290	954	1360	1190	667.7	2000	3	0.0079	3.956
LFA-3(Delta D2) OS=Ovis sp. PE=2 SV=1	tr Q2875 2 Q28752 _9CETA,tr Q28753 Q28753_9 CETA,tr Q 28754 Q2 8754_9CE TA	IDED VYEI ESPS Vk	92%	49.2	54.31348	Ref	-1	-1.2	-0.88	-0.8	-0.63	-1.2	-0.85	12300	5200	4950	7070	8240	8110	5750	7190	744.4	2230.2	3	0.0154	6.882

<p>26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1</p>	<p>8 PSMD6_HUMAN,sp Q3T0B2 PSMD6_BOVIN,sp Q99J14 PSMD6_MOUSE,tr C9IZE4 C9IZE4_HUMAN,tr C9J7B7 C9J7B7_HUMAN,tr D2H1Q0 D2H1Q0_AILME,tr F1MXE4 F1MXE4_BOVIN,tr F1SGF1 F1SGF1_PIG,tr F6PLG4 F6PLG4_MONDO,tr F7BGG5 F7BGG5</p>	<p>fLLSL PEH R</p>	<p>92%</p>	<p>46.3</p>	<p>51.51557</p>	<p>Ref</p>	<p>-0.2</p>	<p>-0.51</p>	<p>-0.07</p>	<p>-0.38</p>	<p>-0.08</p>	<p>-0.44</p>	<p>-0.03</p>	<p>3260</p>	<p>2470</p>	<p>2160</p>	<p>3290</p>	<p>2910</p>	<p>3150</p>	<p>2550</p>	<p>3380</p>	<p>472.6</p>	<p>1414.8</p>	<p>3</p>	<p>0.0166</p>	<p>11.7</p>
<p>GLO1 protein OS=Bos taurus GN=GLO1 PE=2 SV=1</p>	<p>tr A4FUZ1 A4FUZ1_BOVIN,tr D2HVT9 D2HVT9_AILME,tr F1MUW8 F1MUW8_BOVIN,tr F1RVR3 F1RVR3_PIG</p>	<p>gFG HIGI AVP DVH GAck</p>	<p>92%</p>	<p>49.4</p>	<p>54.67661</p>	<p>Ref</p>	<p>0.28</p>	<p>-0.22</p>	<p>-0.06</p>	<p>-0.081</p>	<p>-0</p>	<p>-0.01</p>	<p>-0.16</p>	<p>1140</p>	<p>1200</p>	<p>921</p>	<p>1150</p>	<p>1260</p>	<p>1160</p>	<p>1200</p>	<p>1080</p>	<p>778.1</p>	<p>2331.2</p>	<p>3</p>	<p>0.0043</p>	<p>1.829</p>

40S ribosomal protein S14 OS=Rattus norvegicus GN=Rps14 PE=2 SV=3	1 RS14_RAT,sp P62263 RS14_HUMAN,sp P62264 RS14_MOUSE,sp P62265 RS14_CRIGR,tr A4D1M5 A4D1M5_HUMAN,tr D2H8L8 D2H8L8_AILME,tr D3YVF4 D3YVF4_MOUSE,tr D3Z711 D3Z711_MOUSE,tr D4A290 D4A290_RAT,tr D9ZLV2 D9ZLV2_AILM	eLGI TALH Ik	92%	43.7	49.02612	Ref	0.21	-0.19	0.3	-0.018	-0.05	-0.03	-0.01	8690	8710	7200	11300	10000	8580	9060	9110	568.4	1702.1	3	0.0068	3.972
Galectin-3-binding protein OS=Bos taurus GN=LGALS3BP PE=1 SV=1	sp A7E3W2 LG3B_P_BOVIN	IADG GSA NqG R	92%	41.9	50.26566	Ref	-0.63	-0.41	-0.24	0.002	0.001	-0.63	-0.12	10900	6100	7710	9740	12700	11100	7480	10500	675.8	1349.7	2	0.0106	7.841
LOC100138545 protein (Fragment) OS=Bos taurus GN=LOC100138545 PE=2 SV=1	tr A6QQE3 A6QQE3_BOVIN, tr E5L8L8 E5L8L8_BOVIN	eVV AHV LEQE R	92%	46.5	52.7206	Ref	0.18	-0.1	-0.1	-0.054	-0.28	-0.13	0.049	8420	8300	7410	8320	9460	7080	8190	9200	538.3	1611.9	3	0.0112	6.927

<p>Craniofacial development protein 2 OS=Bos taurus GN=CFDP2 PE=1 SV=2</p>	<p>sp O02751 CFDP2_BOVIN, tr B6F238 B6F238_CA PHI, tr F1MS40 F1MS40_BOVIN, tr Q4ADK3 Q4ADK3_MU NRE, tr Q7YRU5 Q7YRU5_GIR CA, tr Q8S Q39 Q8S Q39_CER NI</p>	<p>IIEFc HHN R</p>	<p>91%</p>	<p>43.6</p>	<p>50.3356</p>	<p>Ref</p>	<p>0.37</p>	<p>-0.19</p>	<p>0.081</p>	<p>-0.23</p>	<p>0.029</p>	<p>-0.13</p>	<p>0.2</p>	<p>1670</p>	<p>1870</p>	<p>1380</p>	<p>1870</p>	<p>1660</p>	<p>1730</p>	<p>1620</p>	<p>2030</p>	<p>506.9</p>	<p>1517.7</p>	<p>3</p>	<p>0.0093</p>	<p>6.139</p>
<p>Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1</p>	<p>5 SGTA_HUMAN, sp Q32LM2 SGTA_BOVIN, tr B4DEA6 B4DEA6_HUMAN, tr D2HMF6 D2HMF6_A ILME, tr E2R2T8 R2T8_CAFNA, tr E7EMJ6 E7EMJ6_HUMAN, tr F1S8G6 F1S8G6_PIG, tr F7FGF5 F7FGF5_MACMU, tr F7H688 F7H688_CALJA, tr F7H696 F7H696_C</p>	<p>VENF EAA VHFY Gk</p>	<p>91%</p>	<p>47.2</p>	<p>54.10004</p>	<p>Ref</p>	<p>-0.15</p>	<p>-0.23</p>	<p>0.097</p>	<p>-0.14</p>	<p>0.11</p>	<p>-0.41</p>	<p>-0.04</p>	<p>2210</p>	<p>1730</p>	<p>1780</p>	<p>2500</p>	<p>2340</p>	<p>2440</p>	<p>1770</p>	<p>2270</p>	<p>707</p>	<p>2118.1</p>	<p>3</p>	<p>0.011</p>	<p>5.178</p>

<p>Integrin-linked protein kinase OS=Mus musculus GN=Ilk PE=1 SV=2</p>	<p>2 ILK_MO USE,sp P5 7044 ILK_ CAVPO,sp Q13418 ILK_HUM AN,sp Q3 SWY2 ILK _BOVIN,s p Q5R5V 4 ILK_PO NAB,sp Q 99J82 ILK _RAT,tr B 7Z1I0 B7Z 1I0_HUM AN,tr B7Z 418 B7Z4 18_HUMA N,tr COSS X9 COSSX 9_CRIGR,t r D2HR59 D2HR59 _AILME,tr E2R5H4 E2R5H4_C</p>	<p>gMA FLHT LEPLI PR</p>	<p>91%</p>	<p>46.2</p>	<p>53.11548</p>	<p>Ref</p>	<p>-0.23</p>	<p>-0.46</p>	<p>-0.4</p>	<p>-0.19</p>	<p>-0.71</p>	<p>-0.23</p>	<p>-0.5</p>	<p>418</p>	<p>310</p>	<p>286</p>	<p>334</p>	<p>427</p>	<p>261</p>	<p>379</p>	<p>311</p>	<p>633.7</p>	<p>1898.1</p>	<p>3</p>	<p>0.0082</p>	<p>4.304</p>
<p>T-complex protein 1 subunit eta OS=Bos taurus GN=CCT7 PE=1 SV=1</p>	<p>sp Q2NKZ 1 TCPH_B OVIN,tr F 1MWR8 F1MWR8 _BOVIN</p>	<p>sTVD ASPA AGR</p>	<p>91%</p>	<p>41.7</p>	<p>51.00308</p>	<p>Ref</p>	<p>-0.27</p>	<p>-0.11</p>	<p>-0.07</p>	<p>-0.081</p>	<p>0.085</p>	<p>0.004</p>	<p>0.047</p>	<p>10800</p>	<p>7770</p>	<p>9400</p>	<p>10900</p>	<p>11900</p>	<p>11600</p>	<p>11500</p>	<p>11700</p>	<p>668.4</p>	<p>1334.7</p>	<p>2</p>	<p>0.01</p>	<p>7.471</p>

Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1	2 PA1B3_HUMAN,sp Q29460 PA1B3_BOVIN,sp Q5R6X1 PA1B3_PO NAB,tr D2H2H2 D2H2H2_AI LME,tr E2RLA8 E2RLA8_CANFA,tr F1RGI2 F1RGI2_PIG,tr F6TCP3 F6TCP3_MA CMU,tr F7DB59 F7DB59_HO RSE,tr F7GVZ1 F7GVZ1_MA CMU,tr F7H805 F7H805_CAL	aALAGHP	91%	43.4	50.33344	Ref	-0.032	-0.05	-0.19	-0.31	-0.05	-0.41	-0.25	13700	11700	12600	12800	13000	13500	11000	12200	366.2	1095.6	3	0.011	10.01
Secretory phospholipase A2 receptor OS=Homo sapiens GN=PLA2R1 PE=1 SV=2	sp Q13018 PLA2R_HUMAN,sp Q5R880 PLA2R_PONAB,tr B7ZML4 B7ZML4_HUMAN,tr F6Y1A5 F6Y1A5_HORSE	ILEWqDK	91%	41.6	51.09953	Ref	-0.48	-0.03	-1.3	-0.37	-0.97	-0.24	-0.94	6E+05	350000	5E+05	248000	509000	3E+05	5E+05	309000	618.8	1235.7	2	0.0143	11.53
Glutathione S-transferase P OS=Bos taurus GN=GSTP1 PE=1 SV=2	sp P28801 GSTP1_BOVIN,tr Q9TRF8 Q9TRF8_RABIT,tr Q9TRQ0 Q9TRQ0_BOVIN	pPYTIVYFPVQGR	91%	44	53.484	Ref	0.3	-0.43	-0.02	-0.15	0.066	-0.3	-0.18	9470	10200	6610	9910	9990	10100	8190	8830	921	1840	2	0.0129	7.011

Ubiquitin-conjugating enzyme E2 J1 OS=Homo sapiens GN=UBE2J1 PE=1 SV=2	5 UB2J1_HUMAN, tr B4DUF8 B4DUF8_HUMAN, tr D2HK27 D2HK27_AILME, tr E2R4Q6 E2R4Q6_CANFA, tr F1MBQ2 F1MBQ2_BOVIN, tr F5GWD1 F5GWD1_HUMAN, tr F6Q7G1 F6Q7G1_HORSE, tr F6WK78 F6WK78_CALJA, tr F6WK86 F6WK86_CALJA, tr F7F155 F	sGSD SSQ ADQ EAK	91%	44.9	52.21758	Ref	-0.32	-0.5	-0.58	-0.44	-0.24	-0.63	-0.63	6360	4420	4250	4520	5480	5500	4390	4340	640	1916.9	3	0.0135	7.052
Sodium/potassium-transporting ATPase subunit alpha-1 OS=Ovis aries GN=ATP1A1 PE=1 SV=1	4 AT1A1_SHEEP, sp P05023 AT1A1_HUMAN, sp P05024 AT1A1_PIG, sp P06685 AT1A1_RAT, sp P50997 AT1A1_CANFA, sp Q08DA1 AT1A1_BOVIN, sp Q5RDR3 AT1A1_PONAB, sp Q8VDN2 AT1A1_MOUSE, sp Q9NOZ6 AT1A1_RABBIT, tr B3SIO6 B3SIO6_CALJA, tr B3VPO, tr B3	ISLD ELHR	90%	43.6	50.90833	Ref	-0.28	-0.15	0.17	-0.27	0.11	-0.28	-0.22	12000	8610	10300	14300	11600	13200	10500	10900	429.6	1285.7	3	0.0077	6.012

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.26029 PE=4 SV=1	tr F1MTK0 F1MTK0_BOVIN, tr F6WM07 F6WM07_ORNA_N	gSEE ELTD Ik	90%	45.2	53.00948	Ref	-0.3	-0.76	-0.5	-0.55	-0.24	-0.89	-0.73	22700	16000	12700	16900	18000	19500	13000	14400	577	1727.9	3	0.0079	4.586
Glycylpeptide N-tetradecanoyltransferase 1 OS=Homo sapiens GN=NMT1 PE=1 SV=2	9 NMT1_HUMAN,sp P31717 NMT1_BOVIN,sp Q5RAF3 NMT1_PONAB, tr B7Z8J4 B7Z8J4_HUMAN, tr F1MZK0 F1MZK0_BOVIN, tr F7A039 F7A039_HORSE, tr Q32LK5 Q32LK5_BOVIN, tr Q5NVB6 Q5NVB6_PONAB, tr Q96HI4 Q96HI4_HUMAN, tr Q9Y465 Q9Y465	gSET DSA QDQ PVK	90%	45.3	53.26627	Ref	-0.022	-0.36	-0.02	0.016	0.12	-0.2	-0.11	11600	9920	8520	12100	13700	12900	10800	11300	657.3	1969	3	0.0244	12.39
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_018506 PE=4 SV=1	tr D2I059 D2I059_AILME, tr E2QZ19 E2QZ19_CANFA, tr E2R4E7 E2R4E7_CAFIFA, tr F1RUM1 F1RUM1_PIG	rNPF VFAP TLLT VAA R	90%	43.9	52.03498	Ref	0.4	0.17	0.46	0.18	0.36	0.54	0.77	1160	1330	1230	1690	1530	1520	1800	2100	693.1	2076.2	3	0.0081	3.908

Drebrin-like protein OS=Bos taurus GN=DBNL PE=2 SV=1	2 DBNL_ BOVIN,sp Q9UJU6 DBNL_HUMAN,tr B4DDD6 B4DDD6_HUMAN,tr B4DDP6 B4DDP6_HUMAN,t r B4DDU5 B4DDU5_HUMAN,tr B4DEM2 B4DEM2_HUMAN,tr B4DKZ4 B4DKZ4_HUMAN,tr B4DUF9 B4DUF9_HUMAN,tr B4DXL9 B4DXL9_HUMAN,tr	aMS TTSIS SPQ PGk	89%	45.4	53.90648	Ref	0.26	0.58	0.09	0.085	0.35	4E-04	0.34	3880	4050	5460	4380	4810	5050	4130	5200	667.4	1999.1	3	0.0132	6.623
Proteasomal ubiquitin receptor ADRM1 OS=Bos taurus GN=ADRM1 PE=2 SV=1	6 ADRM1_BOVIN,sp Q16186 ADRM1_HUMAN,t r A6MK32 A6MK32_CALJA,t r D2HT81 D2HT81_AILME,tr E2RDP4 E2RDP4_CANFA,tr E9PEC0 E9PEC0_HUMAN,tr F7F015 F7F015_MACMU,tr F7FSU5 F7FSU5_MACMU,tr F71NM3 F71NM3_CALJA,tr F71TA	sQSA AVTP SSTT SSTR	89%	42.2	52.72591	Ref	0.085	-0.47	0.12	-0.31	0.31	-0.83	0.037	2120	1950	1440	2440	2000	2670	1270	2300	936.5	1870.9	2	0.0149	7.938

Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.28075 PE=4 SV=1	tr F1N7Q7_BOVIN	sISIG YLLV k	89%	39.9	48.49254	Ref	0.31	-0.15	-0.09	-0.19	-0.04	-0.04	-0.08	2960	3200	2510	2940	3030	2940	3070	2960	567.7	1700.1	3	0.0098	5.769
Hypoxanthine-guanine phosphoribosyltransferase OS=Mus musculus GN=Hprt1 PE=1 SV=3	3 HPRT_MOUSE,sp P00494 HPRT_CRIGR,sp P27605 HPRT_RAT,sp Q45FY6 HPRT_PIG,sp Q64531 HPRT_MUSSP,sp Q6WIT9 HPRT_CANFA,tr A7X8X3_RABIT,tr A8D004 A8D004_FELCA,tr BOLXK8 BOLXK8_PIG,tr B1B0W8 B1B0W8_MOUSE,tr D2HA99	tMQ TLLS LVk	89%	40.8	49.48994	Ref	0.1	-0.63	-0.29	-0.62	-0.54	-0.65	-0.68	1770	1650	1080	1530	1340	1240	1200	1160	581.4	1741.1	3	0.0013	0.738

Leucine-rich repeat flightless-interacting protein 2 OS=Homo sapiens GN=LRRFIP2 PE=1 SV=1	8 LRRF2_ HUMAN, tr C9JSU1 C9JSU1_ HUMAN, tr E1BBW0 E1BBW0_BOVIN, tr E2RHP4 E2RHP4_CANFA, tr F6PZ86 F6PZ86_ORNAN, tr F6Q1Z8 F6Q1Z8_HORSE, tr F6YA06 F6YA06_MACMU, tr F7EW06 F7EW06_CALJA, tr F7GJ79 F7GJ79_MO NDO, tr F7IDP2 F7I	dQIQDVEGR	89%	39.7	50.39383	Ref	-0.76	-0.02	-0.68	-0.38	-0.54	-0.37	-0.67	29100	14900	27100	19200	26100	20400	24000	19200	682.4	1362.7	2	0.0122	8.929
Ornithine aminotransferase, mitochondrial OS=Bos taurus GN=OAT PE=2 SV=1	sp Q3ZCF5 OAT_BOVIN, tr B0LY44 B0LY44_PIG, tr F1MYG0 F1MYG0_BOVIN, tr F7C9Y5 F7C9Y5_HORSE, tr F7HX55 F7HX55_CALJA, tr Q29591 Q29591_PIG	tVQGPPS SDYI FER	89%	41.9	52.66859	Ref	0.15	-0.16	0.3	-0.061	0.3	-0.35	0.017	6970	6740	5870	9080	7790	8710	5800	7440	950.5	1899	2	0.0177	9.307

Inter-alpha-trypsin inhibitor heavy chain H2 OS=Suscrofa GN=ITIH2 PE=2 SV=1	8 ITIH2_PIG,sp P19823 ITIH2_HUMAN,sp P97279 ITIH2_MESAU,sp Q61703 ITIH2_MOUSE,tr A2RTY6 A2RTY6_HUMAN,tr A5D7R6 A5D7R6_BOVIN,tr B4DM79 B4DM79_HUMAN,tr D2I3D3 D2I3D3_AILME,tr D3DRR6 D3DRR6_HUMAN,tr D3ZFHS D3ZFHS_RAT	kFYNQVSTPLL	88%	42.9	52.1755	Ref	0.81	0.38	0.32	0.27	0.011	0.91	0.32	3930	5990	4810	5200	5540	4030	7830	5180	692.1	2073.2	3	0.0164	7.884
Uncharacterized protein OS=Bos taurus GN=Bt.37218 PE=4 SV=1	tr F1MZD9 F1MZD9_BOVIN, tr Q32L21 Q32L21_BOVIN	IQPE SPFL FHV Nk	88%	44	53.42711	Ref	0.21	0.014	0.027	-0.25	0.013	-0.1	0.12	2530	2540	2410	2730	2470	2600	2500	2900	722.1	2163.2	3	0.0168	7.779
Uncharacterized protein OS=Monodelphis domestica GN=ENSMODG000025454 PE=4 SV=1	tr F6RKA3 F6RKA3_MONDO, tr F7HAP3 F7HAP3_CALJA	rLQq VIR	88%	40.4	50.00833	Ref	0.45	0.23	0.28	-0.04	0.42	-0.01	0.12	4920	5840	5430	6310	5590	6720	5190	5650	406.6	1216.7	3	0.0102	8.343

Phosphoglucomutase-1 OS=Bos taurus GN=PGM1 PE=2 SV=1	sp Q08DP0 PGM1_BOVIN, tr A6QPB5 A6QPB5_BOVIN, tr D2H7H6 D2H7H6_AILME, tr F1MJS4 F1MJS4_BOVIN, tr F1N1X7 F1N1X7_BOVIN, tr F1PUL4 F1PUL4_CANFA, tr F1S814 F1S814_PIG, tr F6X8Q2 F6X8Q2_HORSE	tGEH DFG AAF DGD GDR	87%	36.2	46.1764	Ref	-0.36	-0.05	-0.74	-0.098	-0.33	-0.02	-0.32	14600	9900	13300	9210	15900	11800	15300	12300	657.6	1969.9	3	0.0208	10.53
Palmitoyl-protein thioesterase 1 OS=Bos taurus GN=PPT1 PE=1 SV=1	sp P45478 PPT1_BOVIN, tr F1MSA1 F1MSA1_BOVIN	kIPGI HVLS LEIG	87%	33.3	45.55082	Ref	0.17	-0.3	-0.07	-0.19	-0.04	-0.32	-0.17	1340	1310	1030	1350	1370	1320	1140	1250	604.9	2415.5	4	0.038	15.71

Lamin-B1 OS=Mus musculus GN=Lmb1 PE=1 SV=3	3 LMNB1_MOUSE,sp P20700 LMNB1_HUMAN,sp P70615 LMNB1_RAT, tr A7YY47 A7YY47_BOVIN, tr B4DZT3 B4DZT3_HUMAN, tr D2H8G0 D2H8G0_AILME, tr E1B8N6 E1B8N6_BOVIN, tr E1BCJ4 E1BCJ4_BOVIN, tr E9PBF6 E9PBF6_HUMAN, tr F1MG04 F1MG04_MR	IAQALHE	87%	41.2	51.51685	Ref	-0.16	-0.21	-0.32	-0.33	-0.39	-0.22	-0.29	4450	3460	3610	3770	4140	3460	4070	3840	458.3	1371.8	3	0.0085	6.177
ATP synthase subunit g, mitochondrial OS=Bos taurus GN=ATP5L PE=1 SV=3	sp Q28852 ATP5L_BOVIN, tr D2GWW0 D2GWW0_AILME, tr D2HYH1 D2HYH1_AILME, tr E1BCK5 E1BCK5_BOVIN, tr F7BYD1 F7BYD1_HO_RSE	aPALVNA AVTY	86%	40.9	51.46885	Ref	0.44	0.24	0.35	0.16	0.32	0.33	0.3	3240	3820	3590	4380	4210	4110	4330	4210	722.8	2165.3	3	0.0095	4.388

<p>Tubulin-specific chaperone A OS=Homo sapiens GN=TBCA PE=1 SV=3</p>	<p>7 TBCA_HUMAN,sp P48427 TBCA_BOVIN,sp P48428 TBCA_MOUSE,sp P80584 TBCA_RABBIT,sp Q6PEC1 TBCA_RAT,transcript B4DT30 B4DT30_HUMAN,transcript E5RIW3 E5RIW3_HUMAN,transcript E5RJD8 E5RJD8_HUMAN,transcript F1M825 F1M825_RAT,transcript F1S2G3 F1S2G3_PIG,transcript </p>	<p>qAEI LQES</p>	<p>R</p>	<p>86%</p>	<p>39.6</p>	<p>52.0831</p>	<p>Ref</p>	<p>-0.23</p>	<p>0.24</p>	<p>0.31</p>	<p>0.43</p>	<p>0.7</p>	<p>-0.11</p>	<p>0.53</p>	<p>69000</p>	<p>51000</p>	<p>76900</p>	<p>90400</p>	<p>109000</p>	<p>1E+05</p>	<p>68200</p>	<p>105000</p>	<p>689.4</p>	<p>1376.7</p>	<p>2</p>	<p>0.0089</p>	<p>6.457</p>
<p>Poly(rC)-binding protein 1 OS=Oryctolagus cuniculus GN=PCBP1 PE=2 SV=1</p>	<p>8 PCBP1_RABBIT,sp P60335 PCBP1_MOUSE,sp Q15365 PCBP1_HUMAN,sp Q5E9A3 PCBP1_BOVIN,transcript D2H0E6 D2H0E6_AILME,transcript D3ZS68 D3ZS68_RAT,transcript E2QT85 E2QT85_CANFA,transcript F6S7P4 F6S7P4_CALJAr F6V8I5 F6V8I5_HORSE,transcript F7DX65 F7DX65_CALJAr Q29</p>	<p>iITLT GPT NAIF</p>	<p>k</p>	<p>86%</p>	<p>38.6</p>	<p>49.67188</p>	<p>Ref</p>	<p>0.23</p>	<p>-0.89</p>	<p>-0.57</p>	<p>-0.82</p>	<p>-0.73</p>	<p>-0.89</p>	<p>-1</p>	<p>4910</p>	<p>5020</p>	<p>2510</p>	<p>3500</p>	<p>3240</p>	<p>3000</p>	<p>2820</p>	<p>2570</p>	<p>666.4</p>	<p>1996.2</p>	<p>3</p>	<p>0.0124</p>	<p>6.2</p>

WW domain-containing transcription regulator protein 1 OS=Mus musculus GN=Wwtr1 PE=1 SV=2	5 WWTR1_MOUSE,sp Q9GZV5 WWT R1_HUMAN, tr C9J038 C9J038_HUMAN, tr C9JQ58 C9JQ8_HUMAN, tr C9JR84 C9JR84_HUMAN, tr E1BP N1 E1BP N1_BOVIN, tr E2R3R3 E2R3R3_CANFA, tr F1SJN7 F1SJN7_PIG, tr F1SJP0 F1SJP0_PIG, tr F6XXC8 F6XXC8_M	IAGG AQH VR	85%	40	51.2739	Ref	0.17	-0.12	0.51	0.016	0.6	-0.36	0.37	1E+05	113000	1E+05	175000	137000	2E+05	95800	158000	404.9	1211.7	3	0.0086	7.118
Centrosomal protein of 170 kDa OS=Homo sapiens GN=CEP170 PE=1 SV=1	79 CE170_HUMAN, sp Q6A065 CE170_MOUSE, tr B1ARM6 B1ARM6_HUMAN, tr B4DL23 B4DL23_HUMAN, tr B4DS35 B4DS35_HUMAN, tr D21453 D21453_ALME, tr D3ZET9 D3ZET9_RAT, tr E1BGI2 E1BGI2_BOVIN, tr E2R695 E2R695_CANFA, tr E7ES90 E7ES90_HU	gGH GVP HGK	85%	38.2	51.5911	Ref	0.3	0.28	0.33	-0.11	0.43	-0.21	0.23	10000	10700	11400	13300	10800	13700	9190	12400	364.2	1452.8	4	0.0039	2.698

Proteasome subunit beta type-2 OS=Rattus norvegicus GN=Psmb2 PE=1 SV=1	7 PSB2_R AT,sp P49 721 PSB2 _HUMAN, sp Q5E9K 0 PSB2_B OVIN,sp Q9R1P3 P SB2_MOU SE,tr A2A 882 A2A8 82_MOUS E,tr B7Z4 78 B7Z47 8_HUMA N,tr E2Q W34 E2Q W34_CAN FA,tr F1P CR8 F1PC R8_CANF A,tr F6XJL 9 F6XJL9_ MACMU,t r F7CSY1 F7CSY1_O RNASN,tr	fiLNL PTFS VR	85%	39.1	51.87893	Ref	0.62	-0.79	-0.12	-0.5	-0.14	-0.95	-0.21	513	683	281	499	422	474	282	469	806	1609.9	2	0.0083	5.135
Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	9 PSA4_H UMAN,sp Q3ZCK9 PSA4_BO VIN,sp Q 4R932 PS A4_MACF A,tr B2RD G0 B2RD G0_HUM AN,tr D2 HL18 D2 HL18_AIL ME,tr E2 RDF5 E2R DF5_CAN FA,tr F1P JW0 F1PJ W0_CANF A,tr F2Z5 28 F2Z52 8_PIG,tr F6QQJ2 F 6QQJ2_C ALJA,tr F 6Z688 F6 Z688_HO	sALA LAik	85%	35.9	47.36381	Ref	0.51	-0.15	0.009	-0.32	-0.15	-0.45	-0.36	5270	6500	4490	5610	4940	4830	4110	4340	465.6	1393.9	3	0.0057	4.103

<p>Microtubule-associated tumor suppressor candidate 2 homolog OS=Mus musculus GN=Mtus2 PE=2 SV=1</p>	<p>sp Q3UH D3 MTUS 2_MOUSE ,sp Q5JR5 9 MTUS2 _HUMAN, tr D3Z9L7 D3Z9L7_ RAT,tr D3 ZTQ0 D3Z TQ0_RAT, tr F1PPX5 F1PPX5_ CANFA,tr F1RSU2 F 1RSU2_PI G,tr F7FP R1 F7FPR 1_CALJA,t r F7GDB7 F7GDB7_ ORNAN</p>	<p>rSLLP APk</p>	<p>85%</p>	<p>32.2</p>	<p>43.84927</p>	<p>Ref</p>	<p>-0.56</p>	<p>0.23</p>	<p>-0.37</p>	<p>0.16</p>	<p>0.17</p>	<p>0.31</p>	<p>0.35</p>	<p>6370</p>	<p>3760</p>	<p>7030</p>	<p>5200</p>	<p>8280</p>	<p>7290</p>	<p>8400</p>	<p>8590</p>	<p>497.3</p>	<p>1489</p>	<p>3</p>	<p>0.0047</p>	<p>3.185</p>
<p>Prostaglandin E synthase 3 OS=Rattus norvegicus GN=Ptges3 PE=1 SV=2</p>	<p>8 TEBP_R AT,sp Q1 5185 TEB P_HUMA N,sp Q3Z BF7 TEBP _BOVIN,s p Q5NVM 4 TEBP_P ONAB,sp Q6PWL5 TEBP_MA CFA,sp Q 9ROQ7 TE BP_MOUS E,tr B2GV 92 B2GV9 2_RAT,tr B3KUY2 B 3KUY2_H UMAN,tr B4DHP2 B4DHP2_ HUMAN,t r B4DP11 B4DP11_ HUMAN,t</p>	<p>ITFSc LGGs DNF</p>	<p>84%</p>	<p>41.5</p>	<p>53.25382</p>	<p>Ref</p>	<p>-0.056</p>	<p>-0.31</p>	<p>-0.03</p>	<p>-0.18</p>	<p>0.15</p>	<p>-0.56</p>	<p>0.064</p>	<p>5450</p>	<p>4560</p>	<p>4150</p>	<p>5670</p>	<p>5620</p>	<p>6140</p>	<p>3920</p>	<p>6020</p>	<p>681.7</p>	<p>2042</p>	<p>3</p>	<p>0.0169</p>	<p>8.294</p>

40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	3 RS6_HUMAN,sp P62754 RS6_MOUSE,sp P62755 RS6_RAT,sp Q4R4K6 RS6_MACFAS,sp Q5E995 RS6_BOVIN,tr A1XQU8 A1XQU8_PIG,tr A2A3R5 A2A3R5_HUMAN,tr A2A3R6 A2A3R6_HUMAN,tr A5JSR8 A5JSR8_CAPHI,tr C3PT39 C3PT39_DASNO,tr D1M	qGVL THG R	84%	38.6	50.47532	Ref	0.3	0.24	0.17	-0.18	0.25	-0.28	0.14	26800	28700	29800	31800	27600	32400	23500	31100	391.2	1170.7	3	0.0056	4.815
Uncharacterized protein OS=Bos taurus GN=Bt.58604 PE=4 SV=1	tr F1MYX9 F1MYX9_BOVIN, tr F6ZDJ2 F6ZDJ2_HORSE, tr F7BSA8 F7BSA8_HORSE	nLQ QEA DELS R	84%	38.6	51.72177	Ref	-0.34	-0.45	-0.06	-0.19	0.41	-0.76	0.08	18700	12900	13000	19000	19100	25300	11700	20900	803.9	1605.8	2	0.0128	7.967
Transmembrane protein 109 OS=Bos taurus GN=TMEM109 PE=2 SV=1	tr A7E3R8 A7E3R8_BOVIN, tr Q29RH9 Q29RH9_BOVIN	dFVT PGQ QK	84%	39.6	52.83007	Ref	-0.25	-0.28	0.42	-0.2	0.73	-0.48	0.32	13300	9670	10300	18800	13500	22400	10100	17600	814.5	1626.9	2	0.0159	9.738

Uncharacterized protein OS=Bos taurus GN=Bt.86622 PE=4 SV=1	tr E1BDB0 E1BDB0_BOVIN	gDAE ETA QR	84%	36.3	49.53745	Ref	-0.13	0.13	-0.03	-0.1	0.055	-0.28	0.045	1820	1440	1880	1890	1970	1920	1590	1980	640.8	1279.6	2	0.0088	6.846
Coiled-coil domain-containing protein 47 OS=Macaca fascicularis GN=CCDC47 PE=2 SV=1	4 CCD47_MACFA,sp Q3ZC50 CCD47_BOVIN,sp Q5RCL4 CCD47_PO NAB,sp Q5U2X6 CCD47_RAT,sp Q96A33 CCD47_HUMAN,sp Q9D024 CC47_MOUSE,tr E2RBH4 E2RBH4_CANFA,tr F1MG07 F1MG07_BOVIN,tr F6R7Z7 F6R7Z7_MONDO,tr F6S804 F6S804_OR	rLEE AALR	84%	38.8	50.86239	Ref	0.29	0.53	0.16	-0.034	0.2	-0.13	0.11	6930	7360	9420	8170	7900	8120	6720	7870	421.3	1260.7	3	0.0118	9.38

RNA-binding motif, single-stranded-interacting protein 1 OS=Homo sapiens GN=RBMS1 PE=1 SV=3	8 RBMS1_HUMAN,sp Q3ZBP3 RBMS1_BOVIN,sp Q5PQP1 RBMS1_RAT,sp Q5RBD3 RBMS3_PONAB,sp Q6XE24 RBMS3_HUMAN,sp Q8BWL5 RBMS3_MOUSE,sp Q91W59 RBMS1_MOUSE,trans A8K9S4 A8K9S4_HUMAN,trans B4DN88 B4DN88_HUMAN,trans B4E2S3	gYGFVDFDSPAAAQk	84%	42.1	54.16176	Ref	-0.1	-0.42	-0.07	-0.032	0.054	-0.34	-0.14	3350	2710	2350	3370	3820	3540	2820	3200	727.7	2180.1	3	0.0179	8.195
UPF0587 protein C1orf123 homolog OS=Bos taurus PE=2 SV=1	6 CA123_BOVIN,sp Q498R7 CA123_RAT,sp Q8BHG2 CA123_MOUSE,sp Q9NWV4 CA123_HUMAN,trans A2A8E1 A2A8E1_MOUSE,trans A2A8E2 A2A8E2_MOUSE,trans A2A8E4 A2A8E4_MOUSE,trans B7ZC71 B7ZC71_MOUSE,trans B7ZC72 B7ZC72_MOUSE,trans D2H2F1 D2H2F1_	IMDSVALk	84%	38.6	50.74425	Ref	0.22	-0.08	-0.18	-0.11	-0.04	-0.19	-0.4	4630	4690	4130	4320	5010	4590	4310	3720	495.6	1483.9	3	0.0056	3.74

Uncharacterized protein (Fragment) OS=Callithrix jacchus GN=AHNAK2 PE=4 SV=1	tr F7GZ18 F7GZ18_CALJA,tr F7H4K7 F7H4K7_CALJA	mPS FGVS APSk	84%	40.8	52.92502	Ref	-0.17	-0.76	-0.34	-0.28	-0.14	-0.76	-0.23	22400	17300	12400	18700	21500	20600	14100	20200	572.7	1715	3	0.003	1.775
Uncharacterized protein OS=Bos taurus GN=ENG PE=4 SV=1	tr E1BG97 E1BG97_BOVIN,tr E1BJ42 E1BJ42_BOVIN,tr F6W046 F6W046_HORSE,tr Q1RMV1 Q1RMV1_BOVIN,tr Q5R771 Q5R771_PO_NAB	IEGV AGH k	84%	38.4	50.56608	Ref	0.73	0.026	-0.04	-0.12	0.23	0.083	0.23	6660	9600	6400	6860	7160	7960	7510	8260	473.6	1417.8	3	0.004	2.834
Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	6 GELS_HUMAN,sp P20305 GELS_PIG,sp Q28372 GELS_HORSE,sp Q3SX14 GELS_BOVIN,tr A2A418 A2A418_HUMAN,tr B3KS49 B3KS49_HUMAN,tr B72X4 B72X4_HUMAN,tr B72373 B72373_HUMAN,tr B724U6 B724U6_HUMAN,tr B7Z5V1 B7Z5V1_HUM	eGG QTA PAST R	83%	37.6	51.00619	Ref	0.53	0.19	0.26	0.028	0.048	0.45	-0.28	2720	3400	2930	3430	3230	2860	3950	2360	689.9	1377.7	2	0.0083	6.006

Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Homo sapiens GN=FKBP9 PE=1 SV=2	2 FKBP9_HUMAN,sp Q2KJC8 FKBP9_BOVIN,sp Q66H94 FKBP9_RAT,sp Q9Z247 FKBP9_MOUSE,trans A1L517 A1L517_BOVIN,trans B3KQQ0 B3KQQ0_HUMAN,trans B7Z230 B7Z230_HUMAN,trans B7Z6H3 B7Z6H3_HUMAN,trans D2HI36 D2HI36_AILME,trans F1Q1F5 F1Q1F5_C	gLLG McV Gek	83%	40.5	52.7622	Ref	0.15	0.22	-0.36	-0.24	-0.38	0.26	-0.5	4550	4390	5000	3770	4510	3560	5790	3390	554.3	1659.9	3	0.0041	2.462
Palmdelphin OS=Sus scrofa GN=PALMD PE=2 SV=1	V9 PALMD_PIG,sp Q3MHH7 PALMD_BOVIN,sp Q9NP74 PALMD_HUMAN,trans D2HFF2 D2HFF2_AILME,trans F1MZD8 F1MZD8_BOVIN,trans F1PAP4 F1PAP4_CANFA,trans F1S554 F1S554_PIG,trans F6QXT0 F6QXT0_CALJA,trans F6TV06 F6TV06_HORSE,trans F7GRL6 F7GRL6_MA	qNQ QDQ HQI QVLE QSIL R	83%	42.7	54.90896	Ref	0.062	-0.64	-0.11	-0.45	0.16	-0.65	-0.01	2320	2100	1400	2270	1980	2640	1570	2430	837.1	2508.3	3	0.0193	7.707

<p>Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1</p>	<p>1 CTNA1_ MOUSE,s p P35221 CTNA1_ HUMAN,s p Q3MH M6 CTNA 1_BOVIN, sp Q59I7 2 CTNA1_ RABBIT,tr B3KSR8 B 3KSR8_H UMAN,tr B4DKT9 B 4DKT9_H UMAN,tr B4DU00 B4DU00_ HUMAN,t r B4E2G8 B4E2G8_ HUMAN,t r E2R9S7 E2R9S7_ CANFA,tr E5RGY7 E</p>	<p>kHV NPV QALS EFk</p>	<p>83%</p>	<p>39.4</p>	<p>51.72197</p>	<p>Ref</p>	<p>0.046</p>	<p>-0.28</p>	<p>0.31</p>	<p>0.18</p>	<p>0.35</p>	<p>-0.56</p>	<p>0.3</p>	<p>488</p>	<p>438</p>	<p>380</p>	<p>642</p>	<p>643</p>	<p>633</p>	<p>353</p>	<p>636</p>	<p>803.8</p>	<p>2408.4</p>	<p>3</p>	<p>0.031</p>	<p>12.86</p>
<p>Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_014444 PE=3 SV=1</p>	<p>tr D2HR5 6 D2HR5 6_AILME,t r F1RMQ 4 F1RMQ 4_PIG,tr F6R4H9 F 6R4H9_H ORSE,tr Q 0II53 Q0II 53_BOVIN</p>	<p>rDSN LTL NQLL QGL R</p>	<p>83%</p>	<p>39.8</p>	<p>52.22587</p>	<p>Ref</p>	<p>0.37</p>	<p>0.39</p>	<p>0.47</p>	<p>0.086</p>	<p>0.22</p>	<p>0.2</p>	<p>0.2</p>	<p>254</p>	<p>285</p>	<p>313</p>	<p>373</p>	<p>314</p>	<p>302</p>	<p>310</p>	<p>307</p>	<p>720.1</p>	<p>2157.3</p>	<p>3</p>	<p>#####</p>	<p>0.188</p>

Peptidyl-prolyl cis-trans isomerase FKBP7 OS=Pongoabelii GN=FKBP7 PE=2 SV=1	2 FKBP7_PONAB,sp Q9Y680 FKBP7_HUMAN, tr A6QPJ6 A6QPJ6_BOVIN, tr B2CR55 B2CR55_PIG, tr B4DRE2 B4DRE2_HUMAN, tr D2HAF2 D2HAF2_AILME, tr D3DPF8 D3DPF8_HUMAN, tr F1P8W6 F1P8W6_CANFA, tr F1PQ96 F1PQ96_CANFA, tr F1PQ98 F1PQ98_CA	wFVL GVG QVIK	83%	37	49.45729	Ref	-0.29	0.17	-0.52	-0.037	-0.34	0.29	-0.66	1630	1160	1730	1200	1850	1310	2110	1090	618.7	1853.1	3	0.0124	6.702
DNA-binding protein RFX5 OS=Homo sapiens GN=RFX5 PE=1 SV=1	2 RFX5_HUMAN, tr A2A3Q3 A2A3Q3_HUMAN, tr A2A3Q4 A2A3Q4_HUMAN, tr A9X1A1 A9X1A1_PAPAN, tr B0KWC2 B0KWC2_CALJA, tr B1MTG8 B1MTG8_CALMO, tr B2KI65 B2KI65_RHIFE, tr B2R5R9 B2R5R9_HUMAN, tr B3EX62 B3EX62_SO RAR, tr B4UT10 B4	fLLQ QHLI SAR	83%	38.3	50.82512	Ref	0.3	-0.06	0.13	-0.16	-0.01	-0.1	0.21	1590	1700	1430	1850	1670	1610	1580	1950	544	1629	3	0.0013	0.778

<p>26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1</p>	<p>3 PRS10_ HUMAN,s p P62334 PRS10_ MOUSE,s p P62335 PRS10_S PETR,sp Q2KIW6 PRS10_B OVIN,tr A 6MK92 A 6MK92_C ALJA,tr D 2I273 D2I 273_AILM E,tr F1ML V1 F1ML V1_BOVI N,tr F1PG 58 F1PG5 8_CANFA, tr F1SFE6 F1SFE6_ PIG,tr F6 RR88 F6R R88_ORN</p>	<p>iHAG PITk</p>	<p>82%</p>	<p>36.5</p>	<p>49.2508</p>	<p>Ref</p>	<p>0.16</p>	<p>-0.01</p>	<p>-0.08</p>	<p>-0.23</p>	<p>-0.05</p>	<p>-0.21</p>	<p>-0.09</p>	<p>20600</p>	<p>20000</p>	<p>19300</p>	<p>20600</p>	<p>20600</p>	<p>20300</p>	<p>18900</p>	<p>20500</p>	<p>482.3</p>	<p>1443.9</p>	<p>3</p>	<p>0.0022</p>	<p>1.539</p>
<p>High mobility group protein B1 OS=Papio anubis GN=HMGB1 PE=3 SV=1</p>	<p>4 HMGB1 _PAPAN,s p B0CM9 9 HMGB1 _CALJA,sp B1MTB0 HMGB1_ CALMO,sp P09429 HMGB1_ HUMAN,s p P10103 HMGB1_ BOVIN,sp P12682 HMGB1_P IG,sp P63 158 HMG B1_MOUS E,sp P631 59 HMGB 1_RAT,sp Q08IE6 HMGB1_ HORSE,sp Q4R844 HMGB1_</p>	<p>kHP DAS VNFS EFSK</p>	<p>82%</p>	<p>40</p>	<p>54.78978</p>	<p>Ref</p>	<p>0.14</p>	<p>0.11</p>	<p>0.31</p>	<p>0.037</p>	<p>0.41</p>	<p>0.44</p>	<p>0.63</p>	<p>20000</p>	<p>19200</p>	<p>20400</p>	<p>26200</p>	<p>23900</p>	<p>27000</p>	<p>28800</p>	<p>32600</p>	<p>627.1</p>	<p>2504.4</p>	<p>4</p>	<p>0.0289</p>	<p>11.55</p>

Protein LZIC OS=Homo sapiens GN=LZIC PE=1 SV=1	sp Q8WZ A0 LZIC_ HUMAN,t r B4E2N0 B4E2N0_ HUMAN,t r E2QV57 E2QV57_ CANFA,tr F1MFP9 F1MFP9_ BOVIN,tr F6UHP6 F 6UHP6_M ONDO,tr F7BV86 F 7BV86_C ALJA,tr Q 3S296 Q3 S296_BOV IN	vSTD LGSG Dk	82%	38.6	52.48201	Ref	-0.3	-0.31	0.01	-0.034	0.35	-0.68	0.17	14600	10300	11100	15600	16700	19000	9710	17400	793.9	1585.9	2	0.0105	6.595
Chromobox protein homolog 3 OS=Mus musculus GN=Cbx3 PE=1 SV=2	8 CBX3_ MOUSE,s p Q13185 CBX3_H UMAN,sp Q5R6X7 CBX3_PO NAB,tr A 4D177 A4 D177_HU MAN,tr A 6H7C4 A6 H7C4_BO VIN,tr D2 GVC6 D2 GVC6_AIL ME,tr D2 H3E9 D2 H3E9_AIL ME,tr D3 YV86 D3Y V86_MOU SE,tr D3Z RS6 D3ZR S6_RAT,tr E2QXC6 E2QXC6_	ITW HScP EDE AQ	82%	32.3	46.27356	Ref	0.12	-0.09	-0.02	0.038	0.24	-0.21	-0.05	6020	5670	5330	6280	7210	7260	5530	6130	883.4	1764.8	2	0.0116	6.556

<p>Transforming growth factor beta-1-induced transcript 1 protein OS=Homo sapiens GN=TGFB111 PE=1 SV=2</p>	<p>4 TGF1_HUMAN,sp Q3MHZ4 TGF1_BOVIN,sp Q62219 TGF1_MOUSE,sp Q99PD6 TGF1_RAT, tr D3ZDW8 D3ZDW8_RAT, tr D3ZIW6 D3ZIW6_RAT, tr D3ZWZ2 D3ZWZ2_RAT, tr D3ZWZ3 D3ZWZ3_RAT, tr E2RTE0 E2RTE0_CANFA, tr E9PYQ1 E9PYQ1_MOUSE, tr E</p>	<p>rDFL QLFA PR</p>	<p>82%</p>	<p>38.9</p>	<p>51.89631</p>	<p>Ref</p>	<p>-0.38</p>	<p>-0.34</p>	<p>-0.5</p>	<p>-0.61</p>	<p>-0.65</p>	<p>-0.42</p>	<p>-0.66</p>	<p>1090</p>	<p>729</p>	<p>814</p>	<p>816</p>	<p>833</p>	<p>710</p>	<p>869</p>	<p>728</p>	<p>523</p>	<p>1565.9</p>	<p>3</p>	<p>0.0074</p>	<p>4.742</p>
<p>Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCC6IP PE=1 SV=1</p>	<p>M4 PDC6I_HUMAN,sp Q9QZA2 PDC6I_RAT,sp Q9WU78 PDC6I_MOUSE, tr B4DHD2 B4DHD2_HUMAN, tr B7Z5C1 B7Z5C1_HUMAN, tr B8JL8 B8JL8_MOUSE, tr D2HB07 D2HB07_AILME, tr E1BKM4 E1BKM4_BOVIN, tr E9PFU1 E9PFU1_HUMAN, tr F7AFS1 F7AFS</p>	<p>niQV SHQ EFSK</p>	<p>82%</p>	<p>40.7</p>	<p>53.71529</p>	<p>Ref</p>	<p>0.046</p>	<p>-0.05</p>	<p>-0.2</p>	<p>-0.12</p>	<p>0.05</p>	<p>-0.15</p>	<p>0.068</p>	<p>4690</p>	<p>4210</p>	<p>4260</p>	<p>4320</p>	<p>5040</p>	<p>4950</p>	<p>4510</p>	<p>5190</p>	<p>642.4</p>	<p>1924.1</p>	<p>3</p>	<p>0.0111</p>	<p>5.763</p>

Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=3	ACINU_MOUSE,s p Q9UKV3 ACINU_HUMAN, tr A4FUB9 A4FUB9_BOVIN, tr A7Z082 A7Z082_BOVIN, tr B2RTT4 B2RTT4_HUMAN, tr B4DQZ7 B4DQZ7_HUMAN, tr B8JJ88 B8JJ88_MOUSE, tr B8JJ90 B8JJ90_MOUSE, tr B8JJ91 B8JJ91_MOUSE, tr B8JJ92 B8JJ92_MOUSE	kPSISITTE	Slk	82%	35	48.01569	Ref	0.013	-0.07	-0.23	-0.066	-0.06	-0.07	0.025	5260	4610	4730	4740	5860	5140	5320	5650	739.5	2215.4	3	0.0056	2.523
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3	PCKGM_HUMAN, tr B2RYG2 B2RYG2_RAT, tr B4DW73 B4DW73_HUMAN, tr C5I4T6 C5I4T6_PIG, tr D2HG60 D2HG60_AILME, tr F1LQJ7 F1LQJ7_RAT, tr F1MDS3 F1MDS3_BOVIN, tr F6QQ15 F6QQ15_C	eTPI	GLVP	82%	36.8	50.87792	Ref	-0.18	-0.02	-0.29	-0.18	-0.14	-0.36	-0.35	5390	4140	5020	4660	5540	4980	4460	4460	781.5	1560.9	2	0.0239	15.3

Uncharacterized protein OS=Sus scrofa GN=DCTPP1 PE=4 SV=1	tr F1RG62 F1RG62_PIG, tr F6R4W4 F6R4W4_H ORSE, tr F7BMM4 F7BMM4_CALJA, tr F7GUH8 F7GUH8_CALJA	vDLP QAV LSk	82%	36.9	49.94832	Ref	0.47	1.1	0.28	0.35	0.11	-0.04	0.23	5940	7180	12100	7630	8860	6530	6170	7340	560	1677	3	0.0251	14.99
Uncharacterized protein OS=Rattus norvegicus GN=ll6 PE=4 SV=1	LPT5 F1LPT5_RAT, sp Q29503 UB2R2_RABIT, sp Q6ZWZ2 UB2R2_MOUSE, sp Q712K3 UB2R2_HUMAN, tr B2RZ96 B2RZ96_RAT, tr D2HUA0 D2HUA0_AILME, tr D3ZNR7 D3ZNR7_RAT, tr E9PSL9 E9PSL9_RAT, tr F7E9R9 F7E9R9_CALJA, tr F7FAJ7 F7FAJ7_MONDO	aLM LqIk	82%	36.4	49.49892	Ref	-0.19	-0.18	0.18	-0.036	0.23	-0.46	0.18	2200	1670	1830	2640	2510	2630	1700	2640	476	1424.9	3	0.0031	2.189
Uncharacterized protein (Fragment) OS=Bos taurus GN=Bt.77725 PE=4 SV=1	tr F1MM14 F1MM14_BOVIN, tr F1PUU5 F1PUU5_CANFA, tr F7AX25 F7AX25_HORSE	sVDL DSFT VR	82%	37.7	51.85276	Ref	0.1	-0.25	0.075	-0.13	0.18	-0.77	0.071	13200	12300	10500	14800	14100	15300	8260	14700	721.9	1441.8	2	0.0115	7.941

40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	1 RS8_HUMAN,sp P62242 RS8_MOUSE,sp P62243 RS8_RAT,sp Q4R6P8 RS8_MACFA,sp Q5E958 RS8_BOVIN,tr B2R9R8 B2R9R8_RAT,tr D2HUN9 D2HUN9_AILME,tr D3ZIE1 D3ZIE1_RAT,tr E2RFR0 E2RFR0_CANFA,tr F2X209 F2X209_AILME,tr F2Z5F5 F2Z5F5	qWY ESHY ALPL GR	81%	40.1	53.23879	Ref	0.45	-0.05	0.44	0.11	0.23	0.068	0.29	4870	5780	4430	6980	6150	5830	5440	6290	642	1923	3	0.0087	4.536
Uncharacterized protein OS=Bos taurus GN=Bt.7899 PE=4 SV=1	tr E1BNQ9 E1BNQ9_BOVIN	aAEE ATAE SGG VNG GEEq GTG kGEE DEPER	81%	36	51.23959	Ref	-0.56	-0.66	-0.63	-0.23	-0.3	-0.67	-0.3	812	479	483	554	811	672	545	695	932.9	3727.7	4	0.0245	6.583

<p>Osteoclast-stimulating factor 1 OS=Mus musculus GN=Ostf1 PE=1 SV=2</p>	<p>2 OSTF1_MOUSE,s p Q6P686 OSTF1_RAT,sp Q8MJ49 OSTF1_PIG,s p Q8MJ50 OSTF1_BOVIN,sp Q92882 OSTF1_HUMAN,tr A6YLN0 A6YLN0_CEREL,tr A8K646 A8K646_HUMAN,tr D215R0 D215R0_AILME,tr F1MWK2 F1MWK2_BOVIN,tr F1P8W3 F1P8W3_CANF</p>	<p>IGDT ALH AAA Wk</p>	81%	39.5	52.80797	Ref	-0.12	-0.3	-0.15	-0.11	-0.07	-0.11	-0.19	8870	7100	6820	8480	9580	8600	8760	8190	621.4	1861.1	3	0.011	5.919
<p>Protein HEXIM1 OS=Homo sapiens GN=HEXIM1 PE=1 SV=1</p>	<p>2 HEX11_HUMAN,s p Q0X0C4 HEX11_BOVIN,sp Q8R409 HEX11_MOUSE,tr B3KN49 B3KN49_HUMAN,tr D2HCX4 D2HCX4_AILME,tr F1PRR3 F1PRR3_CANFA,tr F1RR19 F1RR19_PIG,tr F7BGX2 F7BGX2_MACMU,tr F7DSW2 F7DSW2_HORSE,tr F7F2K3 F7F2K3</p>	<p>aENL QLLT ENEL HR</p>	80%	40.4	53.96042	Ref	2	1.7	0.035	-0.16	0.25	0.062	0.23	7370	25300	22800	7990	7710	8930	8190	9100	662	1983.1	3	0.0138	6.972

Ribosomal L1 domain-containing protein 1 OS=Bos taurus GN=RSL1D1 PE=2 SV=1	sp A4FV97 RL1D1_BOVIN, tr Q58DV6 Q58DV6_BOVIN	ISLP HGIR	80%	36.7	50.32474	Ref	0.13	-0.08	-0.52	-0.53	-0.39	0.044	-0.18	4850	4620	4320	3590	3920	3780	5320	4520	399.6	1195.7	3	0.0081	6.783
Angiogenic factor with G patch and FHA domains 1 OS=Mus musculus GN=Aggf1 PE=2 SV=1	sp Q7TN31 AGGF1_MOUSE	dLSS EDqK	80%	34.2	48.8513	Ref	-0.18	-0.21	-0.17	-0.002	0.041	-0.48	-0.18	18000	13800	14700	16900	21000	18900	13800	16800	613.8	1225.6	2	#####	0.026
Paraspeckle component 1 OS=Bos taurus GN=PSPC1 PE=2 SV=1	9 PSPC1_BOVIN, sp Q4KLH4 PSPC1_RA_T, sp Q8R326 PSPC1_MOUSE, sp Q8WXF1 PSPC1_HUMAN, tr B4DWI8 B4DWI8_HUMAN, tr D2HT12 D2HT12_AILME, tr E2QXH2 E2QXH2_CANFA, tr F1RN28 F1RN28_PIG, tr F5H656 F5H656_HUMAN, tr F6UAH8 F6UAH8_C	gFVE FAAk PPA R	80%	38.8	52.46848	Ref	0.33	-0	-0.01	-0.059	0.12	0.062	0.26	16200	17600	15200	17000	18100	17900	18000	20500	633.4	1897.1	3	0.0138	7.268

Protocadherin-1 OS=Homo sapiens GN=PCDH1 PE=1 SV=2	4 PCDH1_HUMAN, tr A4IFK1 A4IFK1_BOVIN, tr A8K0E7 A8K0E7_HUMAN, tr B3KQM8 B3KQM8_HUMAN, tr B4DUA8 B4DUA8_HUMAN, tr B4E2D8 B4E2D8_HUMAN, tr C4MH74 C4MH74_MUSPF, tr D2GUL7 D2GUL7_AILME, tr E2QX92 E2QX92_CANFA, tr E2QX93 E	qASE TGS DSK	80%	38.3	52.1731	Ref	-0.027	-0.23	0.096	-0.12	-0.15	-0.86	0.17	5720	4880	4620	6480	6160	5260	3370	6800	540	1616.8	3	0.007	4.326
Obg-like ATPase 1 OS=Rattus norvegicus GN=Ola1 PE=2 SV=1	OLA1_RAT, sp Q2HJ33 OLA1_BOVIN, sp Q5R821 OLA1_PONAB, sp Q9CZ30 OLA1_MOUSE, sp Q9NTK5 OLA1_HUMAN, tr B1AYJ9 B1AYJ9_MOUSE, tr B4DK14 B4DK14_HUMAN, tr C9JK6 C9JK6_HUMAN, tr D2HE13 D2HE13_AILME, tr D3ZG25 D3ZG25_RAT, tr D	iPAF LNV VDIA GLVK	80%	34.6	48.50481	Ref	-1.1	-1.3	-1.2	-1.1	-1.3	-1.6	-1.5	499	207	196	230	272	200	173	188	726.5	2176.3	3	0.014	6.408

Discs, large (Drosophila) homolog-associated protein 4 OS=Bos taurus GN=DLGAP4 PE=2 SV=1	tr A0JNK4 A0JNK4_BOVIN, tr F1N5I2 F1N5I2_BOVIN	kAPP PVPk	79%	28.4	42.61929	Ref	-0.023	0.087	0.058	0.004	0.19	-0.04	0.21	17100	14600	17100	18900	20000	19900	17800	20900	582.7	1745.1	3	#####	0.55
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	3 2AAA_HUMAN, sp P54612 2AAA_PIG, sp Q32PI5 2AAA_BOVIN, sp Q76MZ3 2AAA_MOUSE, tr A5D973 A5D973_BOVIN, tr A8K3H8 A8K3H8_HUMAN, tr A8K7B7 A8K7B7_HUMAN, tr B3KQV6 B3KQV6_HUMAN, tr B4DDF7 B4DDF7_HUMAN, tr B4DE69 B4DE69	hML PTVL R	79%	37.2	51.47781	Ref	0.01	0.059	0.22	-0.17	0.001	-0.11	0.009	9190	8050	9030	11300	9550	9370	9060	9770	424.3	1269.7	3	0.0104	8.19
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_015269 PE=4 SV=1	tr D2HT27 D2HT27_AILME	vLAG HK	78%	32.2	47.53069	Ref	0.3	-0.28	0.41	0.044	0.43	-0.19	0.47	35800	38300	27900	50500	43100	49300	33500	52200	616.9	1231.8	2	0.0022	1.767

Sec61 beta subunit OS=Bos taurus GN=SEC61B PE=4 SV=1	tr Q2NKT 5 Q2NKT 5_BOVIN	pGP APS GTN VGSS GR	78%	36.8	52.16789	Ref	-0.22	-0.12	0.093	-0.097	0.083	0.15	0.055	5600	4180	4870	6320	6110	6040	6630	6140	822.9	1643.8	2	0.0129	7.853
Vesicle-associated membrane protein- associated protein A OS=Bos taurus GN=VAPA PE=2 SV=1	sp Q0VCY 1 VAPA_ BOVIN,sp Q5R601 VAPA_PO NAB,sp Q 9POL0 VA PA_HUM AN,tr A8K A83 A8K A83_HUM AN,tr D2 HHS4 D2 HHS4_AIL ME,tr E2 R580 E2R 580_CANF A,tr F7BT 84 F7BT8 4_MOND O	hEQI LVLD PPTD Lk	78%	36.5	53.01193	Ref	0.21	0.27	0.022	0.028	0.11	-0.02	0.12	4410	4430	5000	4740	5240	4860	4620	5050	557.3	2225.3	4	0.0194	8.726
Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial OS=Sus scrofa GN=SUCLG1 PE=1 SV=2	sp O1906 9 SUCA_P IG,sp Q58 DR8 SUC A_BOVIN, tr E2R0Y5 E2R0Y5_ CANFA,tr F1MZ38 F 1MZ38_B OVIN,tr F 1SNZ6 F1 SNZ6_PIG, tr F1SNZ7 F1SNZ7_ PIG,tr F6 QTC9 F6 QTC9_HO RSE,tr F6 WVM3 F 6WVM3_ MONDO	tHLG LPVF NTVk	78%	36.1	50.73348	Ref	0.4	-0.02	0.27	0.017	-0.01	0.16	0.12	4130	4750	3850	5280	4880	4180	4910	4740	645.4	1933.1	3	0.0139	7.188

<p>DnaJ homolog subfamily B member 4 OS=Bos taurus GN=DNAJB4 PE=2 SV=1</p>	<p>sp Q2KIT4 DNJB4_BOVIN,sp Q5R8J8 DNJB4_PONAB,sp Q9UDY4 DNJB4_HUMAN,tr C9JUL4 C9JUL4_HUMAN,tr D2HJ67 D2HJ67_AILME,tr F6W2E8 F6W2E8_CAJA</p>	<p>gkDY YcIL GIEk</p>	<p>78%</p>	<p>38.2</p>	<p>54.74375</p>	<p>Ref</p>	<p>-0.026</p>	<p>-0.21</p>	<p>-0.18</p>	<p>-0.061</p>	<p>-0.22</p>	<p>-0.29</p>	<p>-0.34</p>	<p>1900</p>	<p>1620</p>	<p>1550</p>	<p>1770</p>	<p>2130</p>	<p>1660</p>	<p>1650</p>	<p>1580</p>	<p>590.8</p>	<p>2359.3</p>	<p>4</p>	<p>0.0348</p>	<p>14.74</p>
<p>Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1</p>	<p>0 NTF2_HUMAN,sp P61971 NTF2_MOUSE,sp P61972 NTF2_RAT,sp Q32KP9 NTF2_BOVIN,sp Q5R8G4 NTF2_PONAB,tr D2H9F9 D2H9F9_AILME,tr E2RKL9 E2RKL9_CANFA,tr F1S2K3 F1S2K3_PIG,tr F1SH55 F1SH55_PIG,tr F6XJB0 F6XJB0_HORSE,tr F7IRG6</p>	<p>aDE DPI MGF HQM FLLk</p>	<p>77%</p>	<p>40.2</p>	<p>54.84424</p>	<p>Ref</p>	<p>0.38</p>	<p>-0.42</p>	<p>-0.03</p>	<p>-0.25</p>	<p>-0.19</p>	<p>-0.36</p>	<p>-0.6</p>	<p>907</p>	<p>1030</p>	<p>639</p>	<p>942</p>	<p>889</p>	<p>813</p>	<p>751</p>	<p>633</p>	<p>834.1</p>	<p>2499.3</p>	<p>3</p>	<p>0.0147</p>	<p>5.882</p>

Mediator of RNA polymerase II transcription subunit 24 OS=Homo sapiens GN=MED24 PE=1 SV=1	75448 M ED24_HU MAN,REV _sp Q4V8 B3 MED2 4_RAT,RE V_sp Q99 K74 MED 24_MOUS E,REV_tr A6PW47 A6PW47_ MOUSE,R EV_tr B4 DDR8 B4 DDR8_HU MAN,REV _tr B4DS Q6 B4DS Q6_HUM AN,REV_t r B4E1A5 B4E1A5_ HUMAN,R EV_tr B9T X63 B9TX 63_HUMA	IAIHL LR	77%	35.6	50.23623	Ref	-0.13	-0.21	-0.59	-0.48	-0.34	-0.3	-0.42	1050	831	852	736	874	841	905	828	380.6	1138.7	3	0.0073	6.369
Uncharacterized protein C1orf50 homolog OS=Mus musculus PE=2 SV=1	sp Q5EBG 8 CA050_ MOUSE,s p Q9BV1 9 CA050_ HUMAN,t r A2A7Q3 A2A7Q3 _MOUSE,t r F1MZT6 F1MZT6 _BOVIN,tr F7GIR8 F7GIR8_ MACMU,t r F7IGR7 F7IGR7_C ALIA	ITVIA EQIq HLQ EQA R	77%	39.4	54.05145	Ref	-0.36	-0.49	-0.48	-0.53	-0.28	-0.36	-0.2	400	271	269	303	323	335	332	367	728.1	2181.2	3	0.0024	1.079

<p>PDZ and LIM domain protein 7 OS=Bos taurus GN=PDLIM7 PE=2 SV=1</p>	<p>0 PDL17_ BOVIN,sp Q3TJD7 PDL17_M OUSE,sp Q9NR12 PDL17_HU MAN,sp Q9Z1Z9 P DLI7_RAT, tr A1L5A7 A1L5A7_ BOVIN,tr B4DHD7 B4DHD7_ HUMAN,t r B8JJB1 B8JJB1_M OUSE,tr B8 JJB2 B8J JB2_MOU SE,tr B8J B3 B8JJB 3_MOUSE ,tr B8JJB5 B8JJB5_ MOUSE,tr</p>	<p>mDS Fk</p>	77%	32.3	47.83718	Ref	-0.42	-0.51	-1.1	-0.93	-0.9	-0.78	-0.87	1490	963	985	728	910	809	920	859	487.2	972.48	2	0.0107	10.95
<p>ATP synthase subunit gamma, mitochondrial OS=Bos taurus GN=ATP5C1 PE=1 SV=3</p>	<p>sp P05631 ATPG_ BOVIN</p>	<p>sEAA NLA AAG k</p>	77%	37.6	52.35347	Ref	0.34	0.076	0.24	-0.19	0.093	0.22	-0.03	9440	10400	9390	11800	9670	10300	11700	9780	537.6	1609.9	3	0.0029	1.772

<p>Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5</p>	<p>sp Q9NR30 DDX21_HUMAN, tr A4FV23 A4FV23_BOVIN, tr D2GX14 D2GX14_AILME, tr E2QTL6 E2QTL6_CANFA, tr F1SUG7 F1SUG7_PIG, tr F6SQN9 F6SQN9_MACMU, tr F6SQP8 F6SQP8_MACMU, tr F6ZZU6 F6ZZU6_HORSE, tr F7D5Y8 F7D5Y8_CALIA</p>	<p>gVTF LFPI QAK</p>	<p>77%</p>	<p>36</p>	<p>50.81218</p>	<p>Ref</p>	<p>0.12</p>	<p>0.25</p>	<p>-0.11</p>	<p>0.082</p>	<p>-0.16</p>	<p>0.43</p>	<p>0.26</p>	<p>3030</p>	<p>2860</p>	<p>3410</p>	<p>2970</p>	<p>3750</p>	<p>2770</p>	<p>4350</p>	<p>3840</p>	<p>610.4</p>	<p>1828.1</p>	<p>3</p>	<p>0.0128</p>	<p>7.003</p>
<p>Ubiquitin domain-containing protein UBF1 OS=Homo sapiens GN=UBFD1 PE=1 SV=2</p>	<p>2 UBFD1_HUMAN, sp Q78JW9 UBFD1_MOUSE, tr A6QQL4 A6QQL4_BOVIN, tr B3KW52 B3KW52_HUMAN, tr E2QVE4 E2QVE4_CANFA, tr E9QB07 E9QB07_MOUSE, tr F1PHN9 F1PHN9_CANFA, tr F1SAB5 F1SAB5_PIG, tr F6SMI8 F6SMI8_HORSE, tr F7AF69 F7</p>	<p>dAA QQD Ak</p>	<p>77%</p>	<p>36.4</p>	<p>52.01187</p>	<p>Ref</p>	<p>-0.016</p>	<p>-0.2</p>	<p>-0.01</p>	<p>-0.2</p>	<p>0.21</p>	<p>-0.38</p>	<p>-0.06</p>	<p>13400</p>	<p>11500</p>	<p>11000</p>	<p>14100</p>	<p>13600</p>	<p>15700</p>	<p>10900</p>	<p>13600</p>	<p>727.9</p>	<p>1453.8</p>	<p>2</p>	<p>0.0055</p>	<p>3.76</p>

Liprin-beta-1 OS=Homo sapiens GN=PPFIBP1 PE=1 SV=2	92 LIPB1_ HUMAN,s p Q8C8U 0 LIPB1_ MOUSE,tr D2H5Z0 D2H5Z0_ AILME,tr D3ZJW3 D3ZJW3_ RAT,tr D3 ZSQ9 D3Z SQ9_RAT, tr F1MQ Q8 F1MQ Q8_BOVI N,tr F5GY 63 F5GY6 3_HUMA N,tr F5H0 E0 F5H0E 0_HUMA N,tr F5H1 A9 F5H1A 9_HUMA N,tr F5H4 95 F5H49	aLHL VEDL R	76%	37.4	52.37443	Ref	0.26	0.24	0.4	-0.15	0.22	0.055	-0.03	3240	3380	3610	4520	3400	3840	3580	3360	457.3	1368.8	3	0.0121	8.85
DnaJ homolog subfamily B member 11 OS=Canis familiaris GN=DNAJB11 PE=1 SV=2	9 DJB11_ CANFA,sp Q3ZBA6 DJB11_BO VIN,sp Q 5RAJ6 DJ B11_PON AB,sp Q6 TUG0 DJB 11_RAT,s p Q99KV 1 DJB11_ MOUSE,s p Q9UBS 4 DJB11_ HUMAN,t r B3KW6 3 B3KW6 3_HUMA N,tr D2H 076 D2H0 76_AILME ,tr F1PXX 5 F1PXX5 _CANFA,tr F1SFJ8 F 1SFJ8_PIG	tLEV EIEP GVR	76%	36.3	52.09375	Ref	0.29	-0.22	0.046	-0.18	-0.19	-0.02	0.065	12900	13800	10400	14100	13300	11500	13600	14300	773.4	1544.9	2	0.0111	7.173

ISG15 protein OS=Ovis aries GN=ISG15 PE=4 SV=1	tr D5FS21 D5FS21_ SHEEP,tr F2X355 F 2X355_CA PHI,tr Q9 GKP4 Q9 GKP4_SH EEP	eVLQ EGV PLVH QGL k	76%	34.3	51.4349	Ref	0.071	-0.29	-0.11	-0.21	-0.24	-0.17	-0.24	4900	4470	3790	4820	4940	4240	4650	4390	564.3	2253.3	4	0.0077	3.419
SF4 protein OS=Bos taurus GN=SF4 PE=2 SV=1	tr A4FV6 4 A4FV64 _BOVIN,tr E1BMW 4 E1BM W4_BOVI N	rPPLI SSPL GQV k	75%	33.3	48.64938	Ref	0.32	0.17	0.27	0.15	0.37	0.23	0.31	7490	8120	7960	9520	9670	9860	9360	9790	667.4	1999.2	3	0.0152	7.623
60S ribosomal protein L28 OS=Mus musculus GN=Rpl28 PE=1 SV=2	5 RL28_ MOUSE,s p P46779 RL28_HU MAN,sp Q3T0L7 R L28_BOVI N,tr B4DE P9 B4DEP 9_HUMA N,tr C9JB 50 C9JB5 0_HUMA N,tr D2H UW2 D2 HUW2_AI LME,tr D 3ZEIO D3 ZEIO_RAT, tr D3ZJD3 D3ZJD3_ RAT,tr E2 ROA6 E2R 0A6_CAN FA,tr E9P B24 E9PB 24_HUMA	tVGV EPA ADG k	75%	37.3	52.63134	Ref	0.22	-0.23	0.21	-0.13	0.23	-0.18	0.17	22100	22300	17700	27000	23500	26300	20700	26200	551.3	1650.9	3	0.0108	6.53

Transcription elongation factor A protein 1 OS=Mus musculus GN=Tcea1 PE=1 SV=2	1 TCEA1_MOUSE,s p P23193 TCEA1_HUMAN,sp Q29RL9 TCEA1_BOVIN,sp Q4KLL0 T CEA1_RAT ,tr B7Z4 W0 B7Z4 WO_HUMAN,tr D2I 302 D2I3 02_AILME ,tr E2QV N6 E2QV N6_CANFA, tr E2RH4 3 E2RH4 3_CANFA, tr E2RH4 5 E2RH45 _CANFA,tr E9PYD5 E9PYD5_	dTYV SSFP R	75%	34.8	50.906	Ref	0.14	-0.23	0.061	-0.17	0.093	-0.28	0.019	15000	14300	12000	16600	15600	16300	13200	16100	688.4	1374.7	2	0.0111	8.054
Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5	REV_sp P 01266 TH YG_HUMAN,REV_t r B2RU26 B2RU26_ HUMAN	LAPT LDqk	75%	34.2	50.328	Ref	0.34	-0.25	0.18	0.062	-0.28	0.28	-0.01	27100	29900	21600	32500	33000	22800	35000	28500	595.8	1189.7	2	0.0073	6.134
Cyclin-dependent kinase 12 OS=Bos taurus GN=CDK12 PE=3 SV=1	sp E1BB5 0 CDK12_BOVIN,tr F1RWL3 F1RWL3_ PIG,tr F8S 1I2 F8S11 2_PIG	sNEE nDD HGk	75%	34.4	49.86517	Ref	-0.28	-0.26	-0.27	-0.48	-0.05	-0.65	-0.04	1450	1040	1140	1270	1210	1430	982	1490	585.3	1752.8	3	0.0138	7.861

Malate dehydrogenase, cytoplasmic OS=Sus scrofa GN=MDH1 PE=1 SV=4	8 MDHC_PIG,sp P40925 MDHC_HUMAN,sp Q3T145 MDHC_BOVIN,sp Q7YRU4 MDHC_FELCA,tr B4DUN2 B4DUN2_HUMAN,AN,tr B7Z317 B7Z317_HUMAN,AN,tr B8ZZ51 B8ZZ51_HUMAN,AN,tr B9A041 B9A041_HUMAN,AN,tr D2HHZ6 D2HHZ6_AILME,AN,tr E2QV08 E2QV08	alcD	75%	33.3	48.77498	Ref	0.19	-0.54	0.19	-0.32	0.081	-0.24	-0.31	6190	6130	4000	7480	5770	6670	5570	5260	388.5	1162.6	3	0.0072	6.149
Sulfotransferase family cytosolic 1B member 1 OS=Bos taurus GN=SULT1B1 PE=2 SV=1	sp Q3T0Y3 ST1B1_BOVIN	eMSETELQFR	75%	34.3	50.5222	Ref	-0.4	-0.59	-0.16	-0.17	-0.38	-0.7	-0.21	7640	5040	4780	7220	7940	5970	5010	7000	787.4	1572.8	2	0.0072	4.565

Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2	7 CYB5_H UMAN,sp P00169 CYB5_RA BIT,sp P0 0170 CYB 5_HORSE, sp P0017 1 CYB5_B OVIN,sp P00172 C YB5_PIG,t r A5HEW 3 A5HEW 3_CAPHI,t r C9E8M7 C9E8M7 _SHEEP,tr D9ILX1 D9ILX1_C ANFA,tr E 2R119 E2 R119_CA NFA,tr P7 0116 P70 116_MES AU,tr Q5	tFIIG ELHP DDR	75%	37.3	52.78591	Ref	0.028	0.11	-0.14	-0.052	-0.25	6E-04	-0.11	6190	5480	6310	5950	6970	5290	6590	6050	573	1715.9	3	0.0143	8.353
Oxidized low- density lipoprotein receptor 1 OS=Bos taurus GN=OLR1 PE=1 SV=1	sp P7939 1 OLR1_B OVIN,tr A 1L4Z7 A1 L4Z7_BOV IN	qNL NLQ EVLK	74%	35.5	51.27338	Ref	-0.8	-0.83	-0.72	-0.94	-0.88	-1.2	-0.27	17000	8450	9010	10900	10300	9350	8010	14800	603	1806.1	3	0.0195	10.77
Uncharacterized protein (Fragment) OS=Canis familiaris GN=FAIM3 PE=4 SV=1	tr F1PYL6 F1PYL6_ CANFA	aSSV AASK	73%	32.7	49.25163	Ref	0.12	-0.06	0.057	-0.39	-0.25	-0.14	-0.31	22400	21200	20300	24700	20000	19200	21600	19000	512.8	1023.6	2	0.0098	9.553

<p>Cytochrome c oxidase subunit 5A, mitochondrial OS=Nycticebus coucang GN=COX5A PE=2 SV=1</p>	<p>2 COX5A_NYCCO,sp B0VYY3 COX5A_OTOCR,sp B0VYY4 COX5A_EULFU,sp B0VYY5 COX5A_MA_CPM,sp P00426 COX5A_BOVIN,sp P11240 COX5A_RAT,sp P12787 COX5A_MOUSE,trans D2HKX8 D2HKX8_AILME,trans D7NY67 D7NY67_SgMN COKU,trans D7NY68 D7NY68_PEPK</p>	<p>73%</p>	<p>38.4</p>	<p>54.33107</p>	<p>Ref</p>	<p>0.37</p>	<p>0.42</p>	<p>0.76</p>	<p>0.3</p>	<p>0.63</p>	<p>0.49</p>	<p>0.8</p>	<p>6160</p>	<p>6950</p>	<p>7780</p>	<p>11000</p>	<p>8870</p>	<p>9710</p>	<p>9180</p>	<p>11400</p>	<p>747.7</p>	<p>2240.2</p>	<p>3</p>	<p>0.0148</p>	<p>6.584</p>
<p>Translin-associated protein X OS=Macaca fascicularis GN=TSNAX PE=2 SV=1</p>	<p>9 TSNAX_MACFA,sp Q5RC21 TSNAX_PONAB,sp Q99598 TSNAX_HUMAN,sp Q9JHB5 TSNAX_RAT,sp Q9QZE7 TSNAX_MOUSE,trans A3RLZ2 A3RLZ2_BOVIN,trans A3RLZ3 A3RLZ3_BOSMU,trans B1APC6 B1APC6_HUMAN,trans C4P0D4 C4P0D4_HUMAN,trans C4P0D6 C4P0D6_HUMAN</p>	<p>73%</p>	<p>33.7</p>	<p>49.68931</p>	<p>Ref</p>	<p>0.42</p>	<p>0.43</p>	<p>0.19</p>	<p>-0.33</p>	<p>0.23</p>	<p>-0.26</p>	<p>-0.04</p>	<p>1440</p>	<p>1680</p>	<p>1830</p>	<p>1740</p>	<p>1340</p>	<p>1720</p>	<p>1280</p>	<p>1480</p>	<p>401.9</p>	<p>1202.7</p>	<p>3</p>	<p>0.0021</p>	<p>1.73</p>

Calpain II small subunit (Fragment) OS=Ovis aries PE=2 SV=1	tr Q1PCR9 Q1PCR9_SHEEP, tr Q9GL70 Q9GL70_SHEEP	tDGF GVD TcR	73%	29.8	46.51016	Ref	0.045	-0.33	-0	-0.33	-0.17	-0.26	-0.21	31300	28100	23600	33200	29100	28500	27800	28600	710.8	1419.6	2	0.0106	7.455
UPF0552 protein C15orf38 homolog OS=Bos taurus PE=2 SV=1	U3 CO038_BOVIN, sp Q726K5 CO038_HUMAN, sp Q9D0A3 CO038_MOUSE, tr D2I419 D2I419_AI LME, tr E2QRD5 E2QRD5_HUMAN, tr E2RT25 E2RT25_CA NFA, tr F1SK02 F1SK02_PIG, tr F6THE8 F6THE8_CALJA, tr F6W2Q3 F6W2Q3_HORSE, tr F6YHY1 F6YHY1_CAYk	kVNT GFL MSS	73%	35.6	53.6377	Ref	0.11	-0.21	0.063	-0.1	0.1	-0.28	0.16	7280	6840	5930	8040	7900	7970	6390	8610	572.6	2286.3	4	0.0343	15

Endophilin-A1 OS=Rattus norvegicus GN=Sh3gl2 PE=1 SV=2	9 SH3G2_ RAT,sp O35964 SH3G1_RAT,sp Q2KJA1 SH3G1_BOVIN,sp Q62419 SH3G1_MOUSE,sp Q62420 SH3G2_MOUSE,sp Q99961 SH3G1_HUMAN,sp Q99962 SH3G2_HUMAN,tr A2ALV1 A2ALV1_MOUSE,tr A2ALV3 A2ALV3_MOUSE,tr B7Z1K6 B7Z1K6_HUMA	tIEYL QPN	PASR	73%	36.2	52.8867	Ref	-0.17	-0.03	-0.09	-0.045	0.069	-0.06	-0.08	12000	9260	11100	11900	13500	12800	12200	12000	847	1691.9	2	0.0118	6.983
Aminoacyl tRNA synthase complex- interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	sp Q12904 AIMP1_HUMAN,t r F6RYT0 F6RYT0_ MACMU,t r Q5R6N9 Q5R6N9_PONAB	kHP DAD SLYV EEVD VGEI	APR	72%	37.3	55.39598	Ref	0.2	0.14	0.41	0.081	0.13	0.14	0.52	2770	2760	2870	3880	3410	3080	3250	4180	737.6	2946.5	4	0.035	11.88

Uncharacterized protein (Fragment) OS=Bos taurus GN=DCHS2 PE=4 SV=1	MQP6 F1 MQP6_B OVIN,sp P97372 P SME2_M OUSE,sp QSE9G3 PSME2_B OVIN,sp Q63798 P SME2_RA T,sp Q86 3Z0 PSM E2_PIG,sp Q924A2 CIC_MOU SE,sp Q9 6RK0 CIC _HUMAN, sp Q9UL4 6 PSME2 _HUMAN, tr A7XAK 3 A7XAK3 _HUMAN, tr A8M27 6 A8M27	aLVH ER	72%	33	49.30307	Ref	0.16	-0.58	0.42	-0.56	0.41	-0.81	-0.4	7300	7070	4600	10300	5780	9880	4410	5850	343.5	1027.6	3	0.0041	3.939
Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	3 SF3B1_HUMAN,sp Q99NB9 SF3B1_MOUSE,trans A0JLN0 A0JLN0_MOUSE,trans A0JLT9 A0JLT9_HUMAN,trans A0PJH5 A0PJH5_HUMAN,trans D2HDI4 D2HDI4_AILME,trans F1MX61 F1MX61_BOVIN,trans F1PKF6 F1PKF6_CANFA,trans F1SMZ9 F1SMZ9_PIG,trans F6R058 F6R058	iWD PTPS HTP AGA ATP GR	72%	37.4	53.78743	Ref	-0.12	-0.06	-0.08	-0.24	-0.05	-0.03	-0.05	6510	5200	5900	6520	6440	6430	6770	6670	712.7	2135.1	3	0.0255	11.94

Transcriptional activator protein Pur-beta OS=Mus musculus GN=Purb PE=1 SV=3	sp O35295 PURB_MOUSE,sp Q68A21 PURB_RAT,sp Q96QR8 PURB_HUMAN,tr F1LSL1 F1LSL1_RAT,tr F6PGI5 F6PGI5_CALJA,tr F7G9V3 F7G9V3_MOUSE,NDONDO	iAEV GAG Gsk	71%	35.3	51.83073	Ref	0.1	-0.17	-0.01	-0.037	0.14	0.1	-0.02	14500	13500	12200	15300	16500	16300	16600	15100	499.6	1495.9	3	#####	0.482
UPF0568 protein C14orf166 homolog OS=Pongo abelii PE=2 SV=1	2 CN166_PONAB,sp Q9CQE8 CN166_MOUSE,sp Q9Y224 CN166_HUMAN,tr D2HV44 D2HV44_AILME,tr D3ZBL9 D3ZBL9_RAT,tr E2RFC7 E2RFC7_CANFA,tr F1SFF4 F1SFF4_PIG,tr F6SGY9 F6SGY9_HORSE,tr F6TL07 F6TL07_CALJA,tr F7E9I3 F7E9I3_MACM	ITQD AVA k	71%	34	51.06466	Ref	-0.2	-0.34	-0.23	-0.44	-0.06	-0.57	-0.28	41200	31100	30700	37300	35500	40300	29600	35800	727.4	1452.9	2	0.0073	5.024
Tetratricopeptide repeat protein 1 OS=Bos taurus GN=TTC1 PE=2 SV=1	sp Q3ZBR5 TTC1_BOVIN,tr F1RR38 F1RR38_PIG,tr F7E2T3 F7E2T3_HORSE	eMA ISDc Sk	71%	33.7	50.22028	Ref	-0.042	-0.1	-0.18	-0.16	-0.02	-0.27	-0.09	14400	12200	12700	13400	15100	14500	12800	14300	546.6	1636.8	3	0.0239	14.57

Uncharacterized protein (Fragment) OS=Monodelphis domestica GN=AFAP1L1 PE=4 SV=1	REV_tr F6 XZ22 F6X Z22_MON DO,REV_t r Q862G1 Q862G1 _BOVIN	PnAS EVK	71%	32.2	49.33938	Ref	0.67	0.047	0.51	0.18	0.22	0.017	0.59	4180	5790	4080	6330	5530	4950	4500	6660	525.3	1048.6	2	0.0106	10.1
CDGSH iron-sulfur domain-containing protein 1 OS=Rattus norvegicus GN=Cisd1 PE=3 SV=1	0 CISD1_ RAT,sp Q 3ZBU2 CI SD1_BOVI N,sp Q91 WS0 CISD 1_MOUSE ,sp Q9NZ 45 CISD1 _HUMAN, tr D2I216 D2I216_ AILME,tr F1PNJ5 F 1PNJ5_CA NFA,tr F1 SD10 F1S D10_PIG,t r F6QXV3 F6QXV3_ HORSE,tr F6SHE0 F 6SHE0_CA LJA,tr F7 DRZ5 F7D RZ5_MON DO,tr F7F	hNEE TGD NVG PLIHK	71%	37.9	54.5016	Ref	0.13	0.13	-0.06	0.066	0.26	0.23	0.22	5890	5610	6070	5990	7190	7200	7330	7220	748.7	2243.2	3	0.0184	8.179

Protein kinase C and casein kinase substrate in neurons 2 protein OS=Rattus norvegicus GN=Pacsin2 PE=1 SV=2	7 PACN2_RAT,sp Q9UNF0 PACN2_HUMAN,sp Q9WVVE8 PACN2_MOUSE,tr F1PUE2 F1PUE2_CANFA,tr F1SJR5 F1SJR5_PIG, tr F6RH78 F6RH78_CALJA, tr F6XXK2 F6XXK2_MACMU, tr F7B6B8 F7B6B8_ORNAN, tr F7B6C6 F7B6C6_O RNAN, tr F7B9Q9 F7B9Q9_H	Fk	70%	37.3	54.01483	Ref	-0.17	-0.07	-0.16	-0.13	0.2	-0.47	0.005	4570	3520	4110	4330	4880	5330	3510	4840	851.4	2551.2	3	0.0204	8.011
Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	0 VDAC2_HUMAN, sp P68002 VDAC2_BOVIN, sp P68003 VDAC2_RABIT, sp P81155 VDAC2_RAT, sp Q60930 VDAC2_MOUSE, sp Q9MZ15 VDAC2_PIG, tr B4DKM5 B4DKM5_HUMAN, tr D4AD77 D4AD77_RAT, tr E2R948 E2R948_CANFA, tr E2RDZ1 E2RDZ1_CAN	YQLD PTAS ISAK	70%	36.6	53.33221	Ref	0.33	0.007	0.021	-0.12	-0.13	0.15	-0.05	12200	13300	11500	13100	13100	11300	14400	12500	634.7	1901.1	3	0.0157	8.239

Ubiquitin carboxyl-terminal hydrolase 49 OS=Homo sapiens GN=USP49 PE=2 SV=1	sp Q70CQ1 UBP49_HUMAN, tr Q5T3E1 Q5T3E1_HUMAN	VPA ATLK	70%	30.9	48.15067	Ref	0.038	0.13	0.092	-0.047	-0.01	0.21	-0.08	8530	7610	8780	9620	9630	8600	10500	8520	502.3	1002.6	2	0.0107	10.69
Biglycan OS=Ovis aries GN=BGN PE=2 SV=1	0 PGS1_SHEEP,sp O46403 PGS1_HORSE,sp P21809 PGS1_BOVIN,sp P21810 PGS1_HUMAN,sp P28653 PGS1_MOUSE,sp P47853 PGS1_RAT,sp Q9GKQ6 PGS1_PIG, tr A6NLG9 A6NLG9_HUMAN, tr A8K7E0 A8K7E0_HUMAN, tr B3KS75 B3KS75_HUMAN, tr B4D	gLQ HLVA LVLV NNK	70%	33.7	50.36832	Ref	0.1	0.48	0.13	-0.011	-0.03	0.75	-0.06	1000	935	1320	1160	1160	998	1800	1020	730.8	2189.3	3	0.013	5.925

B-cell receptor-associated protein 31-like protein (Fragment) OS=Callithrix jacchus PE=2 SV=1	tr A6MKK9 A6MKK9_CALJA, tr D2I1N6 D2I1N6_AILME, tr F1S2A8 F1S2A8_PI G, tr F6RP01 F6RP01_ORNAN, tr F6RP12 F6RP12_ORNAN, tr F7DHC3 F7DHC3_CALJA, tr F7FTW2 F7FTW2_MONDO, tr F7FTX3 F7FTX3_MONDO, tr Q5E9F1 Q5E9F1_BOVIN	aENq ALA MR	70%	33.6	50.91153	Ref	-0.15	-0.33	0.013	-0.24	0.053	-0.48	-0.2	14400	11200	10800	15300	14200	15200	10900	13200	654.8	1307.7	2	0.0094	7.161
Uncharacterized protein (Fragment) OS=Ornithorhynchus anatinus GN=MLC1 PE=4 SV=1	tr F7AG62 F7AG62_ORNAN	SNEE cFk	70%	26.5	43.93435	Ref	0.13	0.008	0.25	0.084	0.81	-0.23	0.48	2800	2660	2650	3510	3460	4980	2540	4110	603.8	1205.5	2	0.0117	9.696

Procollagen galactosyltransferase 1 OS=Bos taurus GN=GLT25D1 PE=2 SV=1	sp A5PK45 GT251_BOVIN,sp Q8K297 GT251_MOUSE,sp Q8NBJ5 GT251_HUMAN,tr B1H282 B1H282_RAT,tr F1S940 F1S940_PIG,tr F6W8D5 F6W8D5_MONDO,tr F7CE53 F7CE53_CALIA	VLIALLAR	69%	17	34.53318	Ref	-0.081	-0.27	-0.09	-0.49	-0.4	-0.19	-0.6	5580	4590	4360	5540	4640	4300	5210	3890	586.9	1171.8	2	0.0055	4.658
Uncharacterized protein (Fragment) OS=Equus caballus GN=Eca.5196 PE=3 SV=1	tr F7D038 F7D038_HORSE	kTEG YSG ADIS VIVR	69%	36.7	53.79969	Ref	0.28	0.053	0.11	0.072	0.1	0.25	0.1	9300	9830	9100	10700	11400	10200	11800	10500	735.1	2202.2	3	0.0256	11.62
DnaJ homolog subfamily B member 1 OS=Bos taurus GN=DNAJB1 PE=2 SV=3	sp Q3MI00 DNJB1_BOVIN,tr D2HFZ7 D2HFZ7_AILME,tr E2R9D7 E2R9D7_CANFA,tr F1SCF5 F1SCF5_PIG	SRPA QEPT R	69%	34.2	51.28098	Ref	0.0038	0.11	0.28	-0.082	0.22	-0.41	-0.02	2750	2390	2800	3530	3030	3260	2190	2850	449.2	1344.7	3	0.0138	10.24

Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2	sp Q15050 RRS1_HUMAN,sp Q2KIH4 RRS1_BOVIN,tr D2H419 D2H419_AILME,tr F1MPT7 F1MPT7_BOVIN,tr F1PRD1 F1PRD1_CANFA,tr F6PSSO F6PSO_HORSE,tr F7HZW9 F7HZW9_CALJAW	VEEAIVAR	69%	32.3	49.89837	Ref	-0.12	0.27	-1	-0.24	-0.49	-0.17	-0.09	28700	23000	32700	14700	28300	20700	27200	28400	595.9	1189.7	2	0.0106	8.894
Collagen alpha-1(V) chain OS=Homo sapiens GN=COL5A1 PE=1 SV=3	8 CO5A1_HUMAN,tr B2ZZ86 B2ZZ86_HUMAN,tr D2HF79 D2HF79_AILME,tr F1PHX8 F1PHX8_CANFA,tr F1S019 F1S019_PIG,tr F1S022 F1S022_PIG,tr F6PLH0 F6PLH0_HORSE,tr F6Q357 F6Q357_HORSE,tr F6SUU9 F6SUU9_HORSE,tr F6ZCA5 F6ZCA5_ORNANTk	VLDFHNL PDGI	68%	36.3	53.41755	Ref	0.023	0.71	-0.15	0.24	-0.26	1	-0.32	4120	3630	6340	3930	5660	3500	8850	3490	693.1	2076.2	3	0.019	9.135

Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1	4 RHOC_HUMAN,sp P24406 RHOA_CANFA,sp P61585 RHOA_BOVIN,sp P61586 RHOA_HUMAN,sp P61589 RHOA_RAT,sp P62745 RHOBRHOB_HUMAN,sp P62746 RHOB_MOUSE,sp P62747 RHOBRAT,sp Q1RMJ6 RHOC_BOVIN,sp Q3ZBW5 RHOBRHOB_BOVIN,sp Q	tcLLI VFSK	68%	34	51.20011	Ref	-0.15	-0.46	-0.16	-0.31	-0.4	-0.11	-0.25	3060	2400	2090	2910	2880	2370	3010	2720	560	1677	3	0.0024	1.409
Nucleolar protein 16 OS=Bos taurus GN=NOP16 PE=2 SV=1	sp Q5E996 NOP16_BOVIN,transcript F1LVIO F1LVIO_RAT,transcript F1S17 F1S17_PIG,transcript F6SK9 F6SK9_CALJA,transcript F6VNP7 F6VNP7_CALJA,transcript F6XJR9 F6XJR9_CALJA	aVPL Lk	68%	19.7	36.90816	Ref	0.23	0.5	0.34	0.19	0.57	0.087	0.51	2560	2600	3410	3430	3410	3880	2890	3840	417	1247.8	3	0.0024	1.947

<p>Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1</p>	<p>sp Q29RF7 PDS5A_HUMAN,ter B3KMN2 B3KMN2_HUMAN,triE1BK G4 E1BK G4_BOVIN,triF6UEY4 F6UEY4_MACMU,triF7EZH0 F7EZH0_MACMU,triQ96DB6 Q96DB6_HUMAN</p>	<p>tVTA AGA ENIQ QK</p>	<p>68%</p>	<p>36.1</p>	<p>53.31781</p>	<p>Ref</p>	<p>0.34</p>	<p>-0.2</p>	<p>-0.21</p>	<p>-0.29</p>	<p>0.028</p>	<p>-0.36</p>	<p>-0.06</p>	<p>15600</p>	<p>17100</p>	<p>12800</p>	<p>14200</p>	<p>14900</p>	<p>16200</p>	<p>12900</p>	<p>15800</p>	<p>647</p>	<p>1938.1</p>	<p>3</p>	<p>0.0177</p>	<p>9.117</p>
<p>CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2</p>	<p>2 CD63_HUMAN,sp P28648 CD63_RAT,sp P41731 CD63_MOUSE,sp Q28709 CD63_RABIT,sp Q76B49 CD63_FELCA,sp Q9XSK2 CD63_BOVIN,triB0JYM4 B0JYM4_BOVIN,triC9JV86 C9JV86_HUMAN,triD2I560 D2I560_AILME,triF1LPA7 F1LPA7_RAT,triF1PIT4 F1PI</p>	<p>sGYE Vm</p>	<p>68%</p>	<p>28.5</p>	<p>46.28726</p>	<p>Ref</p>	<p>-0.48</p>	<p>-0.4</p>	<p>-0.57</p>	<p>-0.59</p>	<p>-0.6</p>	<p>-0.49</p>	<p>-0.39</p>	<p>1800</p>	<p>1120</p>	<p>1290</p>	<p>1290</p>	<p>1390</p>	<p>1210</p>	<p>1370</p>	<p>1450</p>	<p>503.2</p>	<p>1004.5</p>	<p>2</p>	<p>0.015</p>	<p>14.97</p>

<p>WD repeat-containing protein 78 OS=Rattus norvegicus GN=Wdr78 PE=2 SV=1</p>	<p>4V8G4 WDR78_RA T,REV_sp Q5VTH9 WDR78_HUMAN,REV_tr A0AVI9 A0AVI9_HUMAN,REV_tr D2HIA8 D2HIA8_AILME,REV_tr D4A7V5 D4A7V5_RAT,REV_tr D4A7W4 D4A7W4_RAT,REV_tr E1B9S6 E1B9S6_BOVIN,REV_tr E2RML5 E2RML5_CANFA,REV_tr E2R</p>	<p>qSILAEk</p>	<p>67%</p>	<p>31.2</p>	<p>49.08743</p>	<p>Ref</p>	<p>0.73</p>	<p>0.37</p>	<p>0.51</p>	<p>0.56</p>	<p>0.2</p>	<p>0.91</p>	<p>0.49</p>	<p>1320</p>	<p>1900</p>	<p>1600</p>	<p>1990</p>	<p>2270</p>	<p>1540</p>	<p>2630</p>	<p>1950</p>	<p>538.8</p>	<p>1075.6</p>	<p>2</p>	<p>0.0028</p>	<p>2.624</p>
<p>Chromobox protein homolog 5 OS=Homo sapiens GN=CBX5 PE=1 SV=1</p>	<p>3 CBX5_HUMAN,sp Q61686 CBX5_MOUSE,tr B2RYU7 B2RYU7_RA T,tr C8BKD4 C8BKD4_SHEEP,tr D2HM50 D2HM50_AILME,tr D3Z0U2 D3Z0U2_MOUSE,tr E2QYK6 E2QYK6_CANFA,tr F1MXF8 F1MXF8_BOVIN,tr F2Z4J7 F2Z4J7_BOVIN,tr F2Z5T3 F2Z5T3_PIG,tr </p>	<p>gQV EYLLk</p>	<p>67%</p>	<p>32.7</p>	<p>50.13115</p>	<p>Ref</p>	<p>-0.31</p>	<p>-0.28</p>	<p>-0.19</p>	<p>-0.14</p>	<p>-0.15</p>	<p>-0.09</p>	<p>0.007</p>	<p>7650</p>	<p>5370</p>	<p>5930</p>	<p>7080</p>	<p>8120</p>	<p>7030</p>	<p>7660</p>	<p>8120</p>	<p>520</p>	<p>1556.9</p>	<p>3</p>	<p>0.0043</p>	<p>2.781</p>

Uncharacterized protein (Fragment) OS=Callithrix jacchus GN=LOC100391287 PE=4 SV=1	REV_tr F7 GQB0 F7 GQB0_CA LJA	aGE QLAk	67%	32.9	50.78693	Ref	0.2	0.042	0.36	0.098	0.19	0.1	0.24	22100	22100	21500	30100	27600	25600	25300	27600	662.9	1323.8	2	0.0221	16.66
Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus GN=Hnrnpu PE=1 SV=1	3 HNRPU_MOUSE,t r B4DLR3 B4DLR3_ HUMAN,t r F1MMU 2 F1MM U2_BOVI N,tr F7G WA9 F7G WA9_MA CMU,tr O 88568 O8 8568_MO USE,tr Q3 TGN5 Q3 TGN5_M OUSE,tr Q3TS50 Q3TS50_ MOUSE,tr Q3TVV6 Q3TVV6_ MOUSE,tr Q3TWN5 Q3TWN5 _MOUSE,t	qGQ QQA GGD Gk	67%	35.6	53.06217	Ref	0.013	0.028	-0.35	-0.49	-0.24	-0.51	-0.13	5350	4690	5140	4430	4460	4620	4010	5160	561.3	1680.9	3	0.0135	8.049
Bucentaur-2 OS=Bos taurus GN=p97bcnt2 PE=2 SV=1	tr A0JBZ9 A0JBZ9_ BOVIN	vFDI AGEk	67%	34.4	51.83031	Ref	0.013	-0.17	-0.08	-0.24	0.055	-0.3	-0.02	11200	9850	9420	11300	11100	11900	9690	11700	496.3	1485.8	3	0.0236	15.84

<p>WD repeat-containing protein 44 OS=Homo sapiens GN=WDR44 PE=1 SV=1</p>	<p>3 WDR44_HUMAN,sp Q6NV E8 WDR44_MOUSE,sp Q9XC3 WDR44_BOVIN, tr A5PK07 A5PK07_BOVIN, tr B1AXB8 B1AXB8_MOUSE, tr B4DSE9 B4DSE9_HUMAN, tr B7Z947 B7Z947_HUMAN, tr D2H3B6 D2H3B6_AILME, tr E2RPX4 E2RPX4_CANFA, tr E9PCI7 E9</p>	<p>IPTGI NPLT LHIM R</p>	<p>67%</p>	<p>34.6</p>	<p>52.09416</p>	<p>Ref</p>	<p>0.33</p>	<p>0.25</p>	<p>1.8</p>	<p>1.4</p>	<p>0.51</p>	<p>2.5</p>	<p>2.2</p>	<p>1340</p>	<p>1460</p>	<p>1500</p>	<p>5040</p>	<p>4040</p>	<p>1950</p>	<p>8050</p>	<p>6320</p>	<p>627.4</p>	<p>1879.1</p>	<p>3</p>	<p>0.0104</p>	<p>5.508</p>
<p>Growth arrest-specific protein 8 OS=Rattus norvegicus GN=Gas8 PE=2 SV=1</p>	<p>sp Q499U4 GAS8_RAT,sp Q60779 GAS8_MOUSE, tr A1X3U7 A1X3U7_MOUSE, tr F1LMQ8 F1LMQ8_RAT, tr Q49MD7 Q49MD7_MOUSE</p>	<p>kDm RVLk</p>	<p>66%</p>	<p>30.3</p>	<p>48.42871</p>	<p>Ref</p>	<p>-0.097</p>	<p>-0.28</p>	<p>0.14</p>	<p>-0.038</p>	<p>0.14</p>	<p>-0.24</p>	<p>-0.07</p>	<p>8420</p>	<p>6840</p>	<p>6520</p>	<p>9830</p>	<p>9570</p>	<p>9470</p>	<p>7590</p>	<p>8500</p>	<p>909.6</p>	<p>1817.1</p>	<p>2</p>	<p>0.0138</p>	<p>7.575</p>

T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	8 TCPG_HUMAN,sp P80318 TCPG_MOUSE,sp Q29068 TCPG_PIG,sp Q3T0K2 TCPG_BOVIN,sp Q4R963 TCPG_MACFA,sp Q5NVF9 TCPG_PONAB,sp Q6P502 TCPG_RAT,tr B3KX11 B3KX11_HUMAN,tr B4DUR8 B4DUR8_HUMAN,tr D2HW70 D2HW70_AILME,tr E	eIQV QHP	AAk	66%	34.2	51.90875	Ref	0.077	-0.15	-0.07	-0.2	-0.17	-0.26	-0.12	15500	14200	13200	15600	15800	14000	13800	15000	577	1728	3	0.0118	6.804
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_013925 PE=4 SV=1	tr D2HQ01 D2HQ01_AILME	eHE GQY YcTA	SNR	66%	27.2	44.89438	Ref	0.41	0.34	0.27	0.33	0.51	0.13	0.43	6180	7150	7390	7890	9030	8970	7200	8810	636.6	1906.8	3	0.0156	8.151

<p>Cyclin-dependent kinase 11B OS=Homo sapiens GN=CDK11B PE=1 SV=3</p>	<p>7 CD11B_HUMAN,sp P24788 CDK11_MOUSE,sp P46892 CDK11_RAT,sp Q9UQ88 CD11A_HUMAN,tran A2A9P5 A2A9P5_MOUSE,tran A2A9P6 A2A9P6_MOUSE,tran A4VC15 A4VC15_HUMAN,tran B4E3D9 B4E3D9_HUMAN,tran B7ZVY7 B7ZVY7_HUMAN,tran D2HN D2Hk</p>	<p>aPELLGA</p>	<p>66%</p>	<p>28.7</p>	<p>46.49598</p>	<p>Ref</p>	<p>0.4</p>	<p>3E-04</p>	<p>0.091</p>	<p>-0.1</p>	<p>0.057</p>	<p>-0.14</p>	<p>-0.05</p>	<p>2010</p>	<p>2300</p>	<p>1890</p>	<p>2260</p>	<p>2180</p>	<p>2130</p>	<p>1940</p>	<p>2040</p>	<p>507.3</p>	<p>1519</p>	<p>3</p>	<p>0.0068</p>	<p>4.49</p>
<p>F-box only protein 24 OS=Homo sapiens GN=FBXO24 PE=2 SV=2</p>	<p>75426 FBX24_HUMAN,REV_sp Q4R327 FBX24_MACFA,REV_tr A4D2D3 A4D2D3_HUMAN,sp O75525 KHDR3_HUMAN,sp P18052 PTPRA_MOUSE,sp P18433 PTPRA_HUMAN,sp Q03348 PTPRA_RAT,sp Q07666 KHDR1_HUMAN,sp Q5VWX1 KHDR2_HUMAN,tran Vk</p>	<p>vLLP</p>	<p>66%</p>	<p>19.6</p>	<p>37.40678</p>	<p>Ref</p>	<p>-0.34</p>	<p>-0.43</p>	<p>-0.08</p>	<p>-0.53</p>	<p>-0.18</p>	<p>-0.43</p>	<p>-0.38</p>	<p>3370</p>	<p>2320</p>	<p>2360</p>	<p>3370</p>	<p>2730</p>	<p>3020</p>	<p>2660</p>	<p>2730</p>	<p>426.3</p>	<p>1275.9</p>	<p>3</p>	<p>0.0215</p>	<p>16.85</p>

SWI/SNF complex subunit SMARCC1 OS=Mus musculus GN=Smarcc1 PE=1 SV=2	6 SMRC1_MOUSE,sp Q6PDG5 SMRC2_MOUSE,sp Q8TAQ2 SMRC2_HUMAN,sp Q92922 SMRC1_HUMAN,transcript B4DF22 B4DF22_HUMAN,transcript B4DYF9 B4DYF9_HUMAN,transcript B4DYQ1 B4DYQ1_HUMAN,transcript D2GVA3 D2GVA3_ALME,transcript D2H346 D2H346_AILME,transcript D3	tQDEcILHFLR	66%	34.2	51.99986	Ref	0.0039	0.064	-0.59	-0.26	-0.43	0.042	-0.38	1490	1300	1470	1050	1460	1130	1640	1210	575.6	1723.9	3	0.0082	4.762
Dynamin-2 OS=Bos taurus GN=DNM2 PE=2 SV=1	6H715 DYN2_BOVIN,REV_sp P39052 DYN2_RAT,REV_sp P39054 DYN2_MOUSE,REV_sp P50570 DYN2_HUMAN,REV_transcript A8K1B6 A8K1B6_HUMAN,REV_transcript B3KUU8 B3KUU8_HUMAN,REV_transcript B4DJ53 B4DJ53_HUMAN,REV_transcript D2HGX7 D2HGX7_AILME,transcript D	iLNDLPLMKK	65%	32.3	50.58714	Ref	-0.21	-0.86	-0.23	-0.59	-0.26	-0.59	-0.41	1230	919	636	1110	948	1040	869	976	745	1487.9	2	0.0108	7.28

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_007126 PE=4 SV=1	REV_tr D2H9U4 D2H9U4_AILME,REV_tr F1PRF9 F1PRF9_CANFA	EPFV NNT k	65%	32.5	50.76251	Ref	0.51	0.47	0.72	0.51	0.4	0.85	0.48	44300	55000	57900	77200	73600	59400	84700	65400	626.9	1251.7	2	0.017	13.56
Uncharacterized protein OS=Bos taurus GN=Bt.36741 PE=4 SV=1	tr E1B7F5 E1B7F5_BOVIN	vVDE SQET ENQ EEK	65%	35.3	53.32186	Ref	-0.027	-0.09	-0.04	-0.057	0.42	-0.22	0.052	6500	5550	5740	6680	7290	8840	5940	7110	758	2271.1	3	0.0148	6.524
60S ribosomal protein L19 OS=Canis familiaris GN=RPL19 PE=1 SV=1	Q5 RL19_CANFA,sp P84098 RL19_HUMAN,sp P84099 RL19_MOUSE,sp P84100 RL19_RAT,sp Q3TOW9 RL19_BOVIN,sp Q5RB99 RL19_PONAB,sp Q8HXN9 RL19_MACFA,sp A2A547 A2A547_MOUSE,sp D2H531 D2H531_AILME,sp F1M5A9 F1M5A9_RAT,sp F1	ILAD QAE AR	64%	32.8	51.33418	Ref	0.31	0.11	0.4	0.078	0.55	-0.06	0.47	46100	49500	46800	64500	56700	68500	47100	67300	645.9	1289.7	2	0.0108	8.393

<p>26S proteasome non-ATPase regulatory subunit 13 OS=Bos taurus GN=PSMD13 PE=2 SV=1</p>	<p>4 PSD13_BOVIN,sp Q9UNM6 PSD13_HUMAN,ter A6MKV9 A6MKV9_CALJA,ter B2RBM7 B2RBM7_HUMAN,tri B4DJ66 B4DJ66_HUMAN,tri D2I616 D2I616_AILME,ter E2QV21 E2QV21_CANFA,tri E2R5N5 E2R5N5_CANFA,tri F1RGC9 F1RGC9_PIG,tri F6X6G5 F6X6G5</p>	<p>sME MLV EHQ AHDI LT</p>	<p>64%</p>	<p>34.5</p>	<p>52.59988</p>	<p>Ref</p>	<p>0.2</p>	<p>-0.12</p>	<p>0.2</p>	<p>-0.038</p>	<p>-0.06</p>	<p>-0.14</p>	<p>-0.15</p>	<p>2080</p>	<p>2090</p>	<p>1810</p>	<p>2540</p>	<p>2370</p>	<p>2040</p>	<p>2010</p>	<p>1990</p>	<p>686.7</p>	<p>2057</p>	<p>3</p>	<p>0.0124</p>	<p>6.015</p>
<p>TMEM119 protein OS=Bos taurus GN=TMEM119 PE=2 SV=1</p>	<p>tr A2VE84 A2VE84_BOVIN,tri F1N070 F1N070_BOVIN</p>	<p>aAPS SGDL AR</p>	<p>64%</p>	<p>32.2</p>	<p>50.72754</p>	<p>Ref</p>	<p>-0.34</p>	<p>1.9</p>	<p>-0.83</p>	<p>0.054</p>	<p>-0.62</p>	<p>1.7</p>	<p>-0.89</p>	<p>12100</p>	<p>8300</p>	<p>43600</p>	<p>7170</p>	<p>14600</p>	<p>7980</p>	<p>41300</p>	<p>6850</p>	<p>624.8</p>	<p>1247.7</p>	<p>2</p>	<p>0.0127</p>	<p>10.15</p>

CTP synthase 1 OS=Homo sapiens GN=CTPS PE=1 SV=2	2 PYRG1_ HUMAN,s p P70698 PYRG1_ MOUSE,tr A0JNE9 A0JNE9_B BOVIN,tr B 1AS53 B1 AS53_MO USE,tr B1 WC02 B1 WC02_RA T,tr B4DR 64 B4DR6 4_HUMA N,tr B4E1 E0 B4E1E 0_HUMA N,tr F6W FF7 F6WF F7_MON DO,tr F7A SP8 F7AS P8_CALJA, tr F7CKK2 F7CKK2_	fVG QDV EGER	64%	32.1	50.71363	Ref	-0.042	-0.24	-0.1	-0.13	0.055	-0.41	-0.17	12600	10700	10100	12500	13500	13400	10100	11800	720.4	1438.7		2	0.0145	10.08
Serine/arginine-rich splicing factor 5 OS=Mus musculus GN=Srsf5 PE=1 SV=1	6 SRSF5_ MOUSE,s p Q09167 SRSF5_R AT,sp Q1 3243 SRS F5_HUMA N,tr A6H7 B7 A6H7 B7_BOVIN ,tr B4DJK 0 B4DJK0 _HUMAN, tr B4DUA 4 B4DUA 4_HUMA N,tr B5B UD8 B5B UD8_HU MAN,tr D 2H5R1 D 2H5R1_AI LME,tr E2 R8E5 E2R 8E5_CANF A,tr E9QK W3 E9QK	vTIE HAR	64%	31.6	49.78322	Ref	0.038	0.042	0.5	-0.006	0.39	-0.11	0.11	20700	18400	20100	30900	24000	27500	20300	23500	377.2	1128.6		3	0.0102	8.995

Neudesin OS=Bos taurus GN=NENF PE=2 SV=1	sp Q1JQA5 NENF_BOVIN,sp Q6IUR5 NENF_RAT,sp Q9CQ45 NENF_MOUSE,sp Q9UMX5 NENF_HUMAN, tr F1PUL1 F1PUL1_CANFA, tr F1S2V9 F1S2V9_PIG, tr F6Q4X8 F6Q4X8_MONDO, tr F6UN10 F6UN10_MACMU, tr F6XKX8 F6XKX8_OR_NAN	gVVF DVTS Gk	63%	34.1	52.48422	Ref	-0.05	-0	0.064	0.062	0.43	-0.1	0.11	9410	7900	8860	10400	11500	12900	9350	10700	539.6	1615.9	3	0.0239	14.8
BH3 interacting domain death agonist transcript variant 2 OS=Bos taurus GN=BID2 PE=2 SV=1	tr Q05KI5 Q05KI5_BOVIN, tr Q05KI6 Q05KI6_BOVIN, tr Q17QH5 Q17QH5_BOVIN	tQLL LTM LLak	62%	28	46.4874	Ref	-1.5	-1.3	-1.4	-1.2	-1.5	-1.9	-1.7	475	145	183	192	242	175	132	155	618.4	1852.2	3	0.0081	4.379

Cyclic AMP-dependent transcription factor ATF-1 OS=Homo sapiens GN=ATF1 PE=1 SV=2	6 ATF1_HUMAN,sp P81269 ATF1_MOUSE,sp Q08DA8 ATF1_BOVIN,tr B2R8K4 B2R8K4_HUMAN,tr D2HF5 D2HF5_AILME,tr E9PWM8 E9PWM8_MOUSE,tr E9PZ49 E9PZ49_MOUSE,tr E9Q356 E9Q356_MOUSE,tr F6YIC3 F6YIC3_HORSE,tr F7BRQ2 F7BRQ2 Z02_CANFA,sp Q9Z0U1 Z02_MOUSE,tr A6QF3 A6QF3_BOVIN,tr D2GZ5 D2GZ5_AILME,tr D3ZUD2 D3ZUD2_RAT,tr E9PT08 E9PT08_RAT,tr E9PTS1 E9PTS1_RAT,tr F1MBN2 F1MBN2_BOVIN,tr F1MTP9 F1MTP9_BOVIN,tr F1PEE3 F1PEE3_CANFA,tr F1	mED	SHk	62%	27.1	46.10745	Ref	0.08	0.096	0.24	0.015	0.5	-0.69	0.29	486	447	490	609	573	700	320	629	554.8	1107.5	2	0.0053	4.815
Tight junction protein ZO-2 OS=Canis familiaris GN=TJP2 PE=1 SV=1	8 Z02_CANFA,sp Q9Z0U1 Z02_MOUSE,tr A6QF3 A6QF3_BOVIN,tr D2GZ5 D2GZ5_AILME,tr D3ZUD2 D3ZUD2_RAT,tr E9PT08 E9PT08_RAT,tr E9PTS1 E9PTS1_RAT,tr F1MBN2 F1MBN2_BOVIN,tr F1MTP9 F1MTP9_BOVIN,tr F1PEE3 F1PEE3_CANFA,tr F1	iAAI	VVk	61%	20.1	38.78177	Ref	0.75	-0.29	0.67	1.3	1.3	1.1	0.34	2460	3590	1900	4160	7090	6000	5550	3280	441.3	1320.9	3	0.0029	2.16

Alanyl-tRNA editing protein Aarsd1 OS=Bos taurus GN=AARSD1 PE=2 SV=1	1 AASD1_ BOVIN,sp Q3THG9 AASD1_ MOUSE,s p Q5XI97 AASD1_ RAT,sp Q 9BTE6 AA SD1_HUM AN,tr A2 A4P3 A2 A4P3_MO USE,tr A2 A4P4 A2 A4P4_MO USE,tr A2 AI35 A2A I35_MOU SE,tr B3K SP9 B3KS P9_HUMA N,tr B4DI 73 B4DI7 3_HUMA N,tr C9J5 N1 C9J5N GPIR	gLPD DHA	61%	33.6	52.20791	Ref	-4E-04	-0.12	-0.01	-0.12	-0.16	-0.52	-0.1	12100	10500	10500	12700	13000	11000	8910	11900	484.6	1450.8	3	0.009	6.228
Lactase-phlorizin hydrolase OS=Oryctolagus cuniculus GN=LCT PE=1 SV=1	09849 LP H_RABIT, REV_tr Q 29518 Q2 9518_RAB IT,REV_tr Q29519 Q29519_R ABIT,sp P 61289 PS ME3_HU MAN,sp P 61290 PS ME3_MO USE,sp P6 1291 PS ME3_PIG, sp Q4R4V 3 PSME3 _MACFA,s p Q5RFD 3 PSME3 _PONAB,s p Q9H4K 7 GTPB5_ HUMAN,s p Q9NRA	vDQ qVq	61%	32.2	51.1956	Ref	0.025	-0.12	0.052	-0.032	-0.09	-0.17	-0.24	30200	26800	26300	33200	34500	28900	28600	27000	663.4	1324.8	2	0.0028	2.092

Uncharacterized protein OS=Bos taurus GN=Bt.94420 PE=4 SV=1	tr E1BM82 E1BM82_BOVIN, tr F1N1T3 F1N1T3_BOVIN	rAnG HPPE QPR	61%	33.5	52.17313	Ref	-0.51	-0.08	-0.09	-0.11	0.02	-0.01	0.27	2150	1320	1930	2140	2330	2230	2280	2740	521.9	1562.8	3	0.0104	6.626
Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_016730 PE=4 SV=1	tr D2HW A0 D2HW A0_AILME, tr E2RLN2 E2RLN2_CANFA, tr F7DUR1 F7DUR1_HORSE	eGS VLD VLk	61%	32.7	51.55761	Ref	-0.36	-0.02	-0.48	-0.22	-0.07	-0.49	-0.05	3900	2640	3630	2960	3900	3780	2960	3970	523.3	1566.9	3	0.0183	11.67
Uncharacterized protein OS=Sus scrofa GN=LRG1 PE=4 SV=1	tr F1S7K2 F1S7K2_PIG, tr Q2KIF2 Q2KIF2_BOVIN	fLLP VPPQ Lk	61%	26.9	45.73939	Ref	-0.018	1.1	0.18	0.16	-0.15	0.53	0.011	1840	1580	3720	2200	2400	1690	2830	1960	555	1662.1	3	0.0097	5.831
Complement C3 OS=Bos taurus GN=C3 PE=1 SV=2	sp Q2UVX4 CO3_BOVIN, tr O97941 O97941_BOVIN	tSQG LETQ QR	60%	32.7	51.90701	Ref	0.41	0.16	0.28	0.12	-0.14	0.54	0.31	4970	5760	5250	6390	6300	4610	7710	6510	726.4	1450.8	2	0.0107	7.38

<p>Cadherin-13 OS=Homo sapiens GN=CDH13 PE=1 SV=1</p>	<p>0 CAD13_ HUMAN,s p Q3B7N 0 CAD13_ BOVIN,sp Q5R5W6 CAD13_P ONAB,sp Q9WTR5 CAD13_M OUSE,tr A 8D737 A8 D737_PIG ,tr B7Z59 0 B7Z590 _HUMAN, tr B7Z9B1 B7Z9B1_ HUMAN,t r C9JRI6 C9JRI6_H UMAN,tr D2H7K1 D2H7K1_ AILME,tr F1M7X3 F1M7X3_</p>	<p>iNEN TGSV SVTR</p>	<p>60%</p>	<p>33.4</p>	<p>52.6172</p>	<p>Ref</p>	<p>-0.26</p>	<p>-0.28</p>	<p>-0.47</p>	<p>-0.54</p>	<p>0.19</p>	<p>-1.3</p>	<p>-0.29</p>	<p>13500</p>	<p>9780</p>	<p>10500</p>	<p>10300</p>	<p>10800</p>	<p>15600</p>	<p>5930</p>	<p>11600</p>	<p>790.9</p>	<p>1579.8</p>	<p>2</p>	<p>0.0095</p>	<p>6.004</p>
<p>Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3</p>	<p>7 LAMC1_ HUMAN, tr D2HN9 4 D2HN9 4_AILME,t r F1MD7 7 F1MD7 7_BOVIN, tr F1PHK 9 F1PHK9 _CANFA,tr F1S663 F1S663_Pi G,tr F6R W10 F6R W10_MO NDO,tr F 6WNY2 F 6WNY2_O RNAN,tr F6WVB2 F6WVB2_ MACMU,t r F6XUE1 F6XUE1_ MONDO,t r F7CQA4</p>	<p>gKTE QQT ADQ LLAR</p>	<p>60%</p>	<p>34.8</p>	<p>53.75746</p>	<p>Ref</p>	<p>-0.034</p>	<p>-0.81</p>	<p>0.016</p>	<p>-0.3</p>	<p>0.44</p>	<p>-1</p>	<p>0.12</p>	<p>41900</p>	<p>35600</p>	<p>22600</p>	<p>44900</p>	<p>39900</p>	<p>58000</p>	<p>21600</p>	<p>48000</p>	<p>723.1</p>	<p>2166.2</p>	<p>3</p>	<p>0.0153</p>	<p>7.066</p>

Uncharacterized protein (Fragment) OS=Ornithorhynchus anatinus GN=100081713 PE=4 SV=1	REV_tr F7ET84 F7ET84_ORNAN	IVFLLASK	60%	25.1	44.37988	Ref	0.063	-0.31	-0.59	-0.51	-0.18	-0.45	-0.19	56300	51100	42700	39500	46200	50600	43900	52200	597.9	1193.8	2	0.0227	19.03
T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	1 TCPD_HUMAN,sp P80315 TCPD_MOUSE,sp Q2T9X2 TCPD_BOVIN,sp Q5R637 TCPD_PONAB,sp Q7TPB1 TCPD_RAT,sp A8K3C3 A8K3C3_HUMAN,sp B7Z2Z8 B7Z2Z8_HUMAN,sp B7Z9L0 B7Z9L0_HUMAN,sp F1N0E5 F1N0E5_BOVIN,sp F1Q331 F1Q331_CANFA,sp F1Q331_CANFA,sp	qMQVLHP	60%	33.1	52.08775	Ref	-0.25	0.1	-0.15	-0.37	-0.12	-0.34	0.21	37300	27300	37800	35600	33700	34800	31300	45400	485.6	1453.8	3	0.0095	6.558
Pentraxin-related protein PTX3 OS=Homo sapiens GN=PTX3 PE=1 SV=3	sp P26022 PTX3_HUMAN	mEGAEAqR	59%	27.3	46.6928	Ref	0.056	-0.16	-0.21	-0.5	-0.15	-0.13	0.12	408	369	344	374	337	375	396	469	606.8	1211.6	2	0.0061	5.007

Hemopexin OS=Bos taurus GN=HPX PE=2 SV=1	sp Q3SZV7 HEMO_BOVIN	dAPS PVD AAF R	59%	32	51.31747	Ref	0.35	0.21	0.066	0.11	-0.23	0.74	0.29	18900	20900	20700	21000	23900	16400	33600	24500	725.4	1448.7	2	0.0089	6.136
Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens GN=PPA2 PE=1 SV=2	U2 IPYR2_HUMAN, tr A8KOP2 A8KOP2_HUMAN, tr D7NYK1 D7NYK1_SCOKU, tr D7NYK2 D7NYK2_D7NYK2_MINSC, tr D7NYK3 D7NYK3_CYNBP, tr E2QRM6 E2QRM6_HUMAN, tr F6PMS8 F6PMS8_MACMU, tr F6PMT8 F6PMT8_MACMU, tr F6PN84 F6PN84_MACMU, tr F6PN	aFAL EVIK	59%	30	49.16048	Ref	0.16	-0.2	0.007	-0.26	-0.15	-0.33	-0.16	3340	3240	2750	3550	3260	3060	2830	3160	500.3	1497.9	3	0.0214	14.26

Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3	1 ARPC5_HUMAN,sp Q3SYX9 ARPC5_BOVIN,sp Q4KLF8 ARPC5_RAT,sp Q5R516 ARPC5_PONAB,sp Q9CPW4 ARPC5_MOUSE,tr B5APV0 B5APV0_PIG,tr D3ZUQ6 D3ZUQ6_RA T,tr D4A366 D4A366_RAT,tr E2RD65 E2RD65_C ANFA,tr F1S658 F1S658_PIG, tr F6VU8R	aLAA GGV GSIV R	59%	31	50.45534	Ref	0.1	0.12	0.17	0.31	0.43	0.23	0.14	43600	40600	44800	52100	63000	59900	54600	50800	687.9	1373.8	2	0.011	7.969
Enhancer of rudimentary homolog OS=Mus musculus GN=Erh1_MACM PE=1 SV=1	9 ERH_MOUSE,sp P84090 ERH_HUMAN,sp Q3SZC0 ERH_BOVIN,tr B2RYQ5 B2RYQ5_RAT,tr E1BKC7 E1BKC7_BOVIN,tr E2RKE8 E2RKE8_CANFA, tr F2Z5J5 F2Z5J5_PIG,tr F7AUD4 F7AUD4_HORSE,tr F7E9A4 F7E9A4_CALI A,tr F7EDC1 F7EDC1_MACM U,tr Q4FZ	sHTI LLVQ PTK	59%	32.6	52.06737	Ref	0.29	0.11	0.056	-0.028	0.25	0.1	0.22	5010	5320	5100	5520	5730	6070	5730	6150	792	1581.9	2	0.0128	8.076

<p>N-alpha-acetyltransferase 38, NatC auxiliary subunit OS=Homo sapiens GN=NAA38 PE=1 SV=3</p>	<p>7 NAA38_HUMAN, sp Q3ZCE0 NAA38_BOVIN, sp Q5RCP3 NAA38_PONAB, sp Q6ZW M4 NAA38_MOUSE, tr A4D0 W0 A4D0 W0_HUMAN, tr B2RZ B6 B2RZ B6_RAT, tr E2R3V2 E2R3V2_C ANFA, tr F2Z2Y6 F2Z2Y6_HUMAN, tr F2Z5P9 F2Z5P9_PIG, tr F6Z555 F6Z555_</p>	<p>tVAV ITSD GR</p>	<p>58%</p>	<p>32.5</p>	<p>51.98924</p>	<p>Ref</p>	<p>0.21</p>	<p>-0.1</p>	<p>0.083</p>	<p>-0.078</p>	<p>0.27</p>	<p>-0.17</p>	<p>0.11</p>	<p>23900</p>	<p>23900</p>	<p>21000</p>	<p>26800</p>	<p>26400</p>	<p>29300</p>	<p>22500</p>	<p>27200</p>	<p>661.9</p>	<p>1321.7</p>	<p>2</p>	<p>0.0112</p>	<p>8.466</p>
<p>Uncharacterized protein (Fragment) OS=Equus caballus GN=LOC100055297 PE=3 SV=1</p>	<p>tr F6T323 F6T323_HORSE, tr F6W0J7 F6W0J7_C ALIA</p>	<p>LGEY NIEV VEG NEQ FINA Ak</p>	<p>58%</p>	<p>35.7</p>	<p>54.94922</p>	<p>Ref</p>	<p>0.28</p>	<p>0.53</p>	<p>0.65</p>	<p>0.48</p>	<p>0.74</p>	<p>0.11</p>	<p>0.83</p>	<p>11700</p>	<p>12400</p>	<p>16000</p>	<p>19500</p>	<p>19100</p>	<p>19900</p>	<p>13500</p>	<p>22000</p>	<p>847.8</p>	<p>2540.3</p>	<p>3</p>	<p>0.0044</p>	<p>1.724</p>

<p>Ubiquitin-fold modifier 1 OS=Homo sapiens GN=UFM1 PE=1 SV=1</p>	<p>0 UFM1_ HUMAN,s p P61961 UFM1_ MOUSE,s p Q2KJG2 UFM1_B OVIN,sp Q4R4I2 U FM1_MA CFA,sp Q 5BJP3 UF M1_RAT,s p Q5R4N 5 UFM1_ PONAB,tr D2HYE6 D2HYE6_ AILME,tr D3YW97 D3YW97_ MOUSE,tr F1Q2H2 F1Q2H2_ CANFA,tr F6U588 F 6U588_C</p>	<p>iTLTS DPR</p>	<p>58%</p>	<p>32.3</p>	<p>51.8816</p>	<p>Ref</p>	<p>-0.29</p>	<p>0.43</p>	<p>-0.33</p>	<p>0.01</p>	<p>-0.12</p>	<p>0.11</p>	<p>-0.43</p>	<p>24000</p>	<p>17000</p>	<p>30400</p>	<p>20300</p>	<p>28200</p>	<p>22600</p>	<p>27500</p>	<p>18900</p>	<p>603.8</p>	<p>1205.7</p>	<p>2</p>	<p>0.0105</p>	<p>8.674</p>
<p>40S ribosomal protein S2 OS=Bos taurus GN=RPS2 PE=2 SV=2</p>	<p>9 RS2_BO VIN,sp P1 5880 RS2_ HUMAN, sp P2544 4 RS2_M OUSE,sp P27952 R S2_RAT,s p P46791 RS2_CRI GR,tr D2 HE04 D2 HE04_AIL ME,tr D3 YVC1 D3Y VC1_MO USE,tr D3 YWA0 D3 YWA0_M OUSE,tr D3YWJ3 D3YWJ3_ MOUSE,tr D3Z659 D3Z659_ MOUSE,tr</p>	<p>gcTA TLG NFAk</p>	<p>58%</p>	<p>33.8</p>	<p>53.10519</p>	<p>Ref</p>	<p>0.49</p>	<p>-0.19</p>	<p>0.16</p>	<p>-0.13</p>	<p>-0.04</p>	<p>-0.01</p>	<p>0.1</p>	<p>16800</p>	<p>20600</p>	<p>13900</p>	<p>19900</p>	<p>17900</p>	<p>16700</p>	<p>17800</p>	<p>19100</p>	<p>579.6</p>	<p>1735.9</p>	<p>3</p>	<p>0.0082</p>	<p>4.699</p>

40S ribosomal protein S11 OS=Macaca fascicularis GN=RPS11 PE=2 SV=3	0 RS11_ MACFA,sp P62280 RS11_HUMAN,sp P62281 RS11_MOUSE,sp P62282 RS11_RAT,sp Q3TOV4 RS11_BOVIN,sp Q9XSU4 RS11_CANFA,trl D2H7V6 D2H7V6_AILME,trl D3YC01 D3YC01_AILME,trl D3Z3M6 D3Z3M6_MOUSE,trl D3ZE37 D3ZE37_RAT,trl E9PX	VLLG ETGk	57%	30.6	49.95947	Ref	0.44	-0.24	0.076	-0.25	0.019	-0.32	-0.32	11900	14100	9520	13300	11700	12300	10200	10100	475.6	1423.9	3	0.0031	2.153
Transmembrane emp24 domain-containing protein 7 OS=Homo sapiens GN=TMED7 PE=1 SV=2	3 TMED7_HUMAN,trl A4IFT6 A4IFT6_BOVIN,trl B4E2C1 B4E2C1_HUMAN,trl D2HGS6 D2HGS6_AILME,trl D3YZZ5 D3YZZ5_MOUSE,trl D3ZTX0 D3ZTX0_RAT,trl E2R3T9 E2R3T9_CANFA,trl E9Q7G1 E9Q7G1_MOUSE,trl F1RLE5 F1RLE5_PIG,trl F6QDX4 F6QDX4_HFR	sVID YQT HFR	57%	32.7	52.15254	Ref	0.57	0.17	0.19	0.14	0.25	0.34	0.22	8850	11400	9380	10700	11400	10800	11900	10900	523.9	1568.8	3	0.012	7.649

SPARC OS=Mus musculus GN=Sparc PE=1 SV=1	4 SPRC_MOUSE,s p P09486 SPRC_HUMAN,sp P13213 SPRC_BOVIN,sp P16975 SPRC_RAT,sp P20112 SPRC_PIG,sp P36233 SPRC_RABIT,sp Q5R767 SPRC_PONAB,tr A4H2R5 A4H2R5_PIG,tr A9LLG1 A9LLG1_CAPI, tr B2RDL6 B2RDL6_HUMAN, tr B4DRV4 B	IHLD YIGP	57%	34.5	53.97469	Ref	-0.059	0.36	-0.02	0.025	0.032	0.4	-0.09	4390	3670	5320	4580	5220	4580	6180	4350	605	1812	3	0.0084	4.645
Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	4 THRB_HUMAN,s p P00735 THRB_BOVIN,sp P18292 THRB_RAT,sp Q19AZ8 THRB_PIG,sp Q5R537 THRB_PONAB,tr A0N064 A0N064_MACMU, tr B3STX9 B3STX9_PIG, tr B4DDT3 B4DDT3_HUMAN, tr C8BKD1 C8BKD1_SHHEP, tr D2HHJ1 D2HHJ1_AILME, tr E2	iYIHP R	57%	30.1	49.54373	Ref	0.35	0.46	0.48	0.13	0.35	0.99	-0.08	13100	14600	17000	19300	16700	17000	27600	13100	368.2	1101.7	3	0.0054	4.876

26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	1 PSD11_HUMAN,sp Q2K142 PSD11_BOVIN,sp Q8BG32 PSD11_MOUSE,transcript A1L5A1 A1L5A1_BOVIN,transcript B4DTS5 B4DTS5_HUMAN,transcript B5DEP6 B5DEP6_RAT,transcript D2GU64 D2GU64_AILME,transcript D3Z950 D3Z950_RAT,transcript E2RJ26 E2RJ26_CANFA,transcript F1LMZ8 F1LMZ8_RAK	tGQAAELGGLL	57%	31.6	51.05926	Ref	0.11	0.006	0.023	-0.038	-0.07	0.2	-0.05	13500	12700	12800	14500	15300	13100	16400	13800	589.4	1765	3	0.0093	5.25
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC PE=1 SV=1	3 PP1G_HUMAN,sp P61287 PP1G_BOVIN,sp P61292 PP1B_PIG,sp P62136 PP1A_HUMAN,sp P62137 PP1A_MOUSE,sp P62138 PP1A_RAT,sp P62139 PP1A_RABIT,sp P62140 PP1B_HUMAN,sp P62141 PP1B_MOUSE,sp P62142 PP1B_RAT,sp P62143 PP1B	aHQVVE DGYEFFA	57%	34.5	54.05357	Ref	0.27	0.052	-0.02	-0.13	0.001	-0.12	0.11	2470	2580	2410	2580	2620	2510	2410	2810	750.1	2247.1	3	0.0303	13.46

<p>Hematological and neurological expressed 1 protein OS=Bos taurus GN=HN1 PE=2 SV=3</p>	<p>5 HN1_BOVIN,sp Q6AXU6 HN1_RAT,sp Q9UK76 HN1_HUMAN,tr B8ZZT7 B8ZZT7_HUMAN,tr D3ZYK6 D3ZYK6_RAT,tr F1RVX2 F1RVX2_PIG,tr F6W184 F6W184_MACMU,tr F6W1B9 F6W1B9_MACMU,tr F7A978 F7A978_HORSE,tr F7I951 F7I951_CAU</p>	<p>vLRP PGG GSN FSLG FDEP TEQP</p>	<p>VR</p>	<p>57%</p>	<p>35.8</p>	<p>55.31387</p>	<p>Ref</p>	<p>-0.49</p>	<p>-0.33</p>	<p>-0.15</p>	<p>0.028</p>	<p>0.32</p>	<p>-0.24</p>	<p>0.17</p>	<p>874</p>	<p>539</p>	<p>655</p>	<p>831</p>	<p>1040</p>	<p>1110</p>	<p>786</p>	<p>1040</p>	<p>954.2</p>	<p>2859.5</p>	<p>3</p>	<p>0.0233</p>	<p>8.146</p>
<p>Uncharacterized protein OS=Canis familiaris GN=DSG4 PE=3 SV=1</p>	<p>REV_tr E2RKX2 E2RKX2_CANFA,REV_tr F6YF31 F6YF31_MACMU,REV_tr F6YF38 F6YF38_MACMU,REV_tr F7G259 F7G259_MACMU,s Q8K078 SO4A1_MOUSE,s Q99N01 SO4A1_RAT,tr A2ACT3 A2ACT3_MOUSE,tr Q4V8N6 Q4V8N6_RAT</p>	<p>gEID Lk</p>	<p>56%</p>	<p>31.5</p>	<p>51.07793</p>	<p>Ref</p>	<p>-0.36</p>	<p>-0.66</p>	<p>-0.3</p>	<p>-0.68</p>	<p>-0.35</p>	<p>-0.65</p>	<p>-0.77</p>	<p>2570</p>	<p>1740</p>	<p>1540</p>	<p>2200</p>	<p>1870</p>	<p>2050</p>	<p>1740</p>	<p>1590</p>	<p>428.3</p>	<p>1281.8</p>	<p>3</p>	<p>0.013</p>	<p>10.14</p>	

SH3 domain-binding glutamic acid-rich-like protein OS=Bos taurus GN=SH3BGRL PE=3 SV=1	sp Q58DU7 SH3L1_BOVIN, tr B5DFD8 B5DFD8_RAT, tr F1MBW7 F1MBW7_BOVIN, tr F6RMM1 F6RMM1_HORSE, tr F6SVIO F6SVIO_MACMU, tr Q5T3H5 Q5T3H5_HUMAN	eAEA QAK	56%	31.8	51.65363	Ref	0.021	-0.12	0.1	0.042	0.52	-0.4	0.12	17400	15300	15100	19800	20900	25400	14100	19900	677.9	1353.8	2	0.0029	2.145
tRNA-splicing ligase RtcB homolog OS=Papio anubis PE=3 SV=1	2 RTCB_PAPAN, sp Q19PY3 RTCB_PIG, sp Q4R6X4 RTCB_MACFA, sp Q5E9T9 RTCB_BOVIN, sp Q6AYT3 RTCB_RAT, sp Q99LF4 RTCB_MOUSE, sp Q9Y3I0 RTCB_HUMAN, tr B0KWT0 B0KWT0_CALJA, tr B1MTS3 B1MTS3_CALMO, tr B2KIH7 B2KIH7_RHIFE, tr B3RF81 B3	tLLV HR	56%	29.1	48.77291	Ref	0.17	-0.15	-0.18	-0.51	-0.1	-0.02	-0.62	4600	4500	3900	4290	3770	4360	4820	3170	348.2	1041.7	3	0.0038	3.602

Wiskott-Aldrich syndrome protein family member 2 OS=Bos taurus GN=WASF2 PE=2 SV=1	sp A2VDK6 WASF2_BOVIN,transcript F1ME13 F1ME13_BOVIN,transcript F1STN6 F1STN6_PIG	sSTV QDQ	56%	31.9	51.87035	Ref	0.15	-0.19	0.057	0.047	0.3	0.004	0.43	5500	5290	4530	6060	6630	6910	5870	7830	750.9	1499.8	2	0.0067	4.463
Src kinase-associated phosphoprotein 1 OS=Mus musculus GN=Skap1 PE=1 SV=1	3UUV5 SKAP1_MOUSE,REV_transcript Q4V7G1 SKAP1_RAT,REV_transcript Q86WV1 SKAP1_HUMAN,REV_transcript Q9WUQ1 ATS1_RAT,REV_transcript A2A881 A2A881_MOUSE,REV_transcript A8K453 A8K453_HUMAN,REV_transcript A8Y5F0 A8Y5F0_MOUSE,REV_transcript A8Y5F1 A8Y5F1_MOUSE,REV_transcript	gLIH R	55%	27.7	47.51349	Ref	0.15	-0.22	Value Missing (-2.381706)	-0.26	Value Missing (-2.3263128)	-0.29	-0.74	3140	3030	2550	Value Missing (-2.381706)	3050	Value Missing (-2.3263128)	2730	1980	300.5	898.56	3	0.0035	3.904
Craniofacial development protein 2 OS=Tragulus javanicus GN=CFDP2 PE=2 SV=1	sp Q588U8 CFDP2_TRAJA,sp Q8HXY9 CFDP1_BOVIN,transcript B6F237 B6F237_CAPHI	gVES EDA R	55%	29.2	49.25317	Ref	-0.31	-0.33	-0.25	-0.28	0.17	-0.7	-0.16	8240	5760	6170	7350	7940	9450	5410	7810	583.8	1165.6	2	0.0088	7.508

Putative uncharacterized protein (Fragment) OS=Ailuropoda melanoleuca GN=PANDA_015251 PE=4 SV=1	2HT16 D2 HT16_AIL ME,REV_tr D2HWC9 D2HWC9_AILME,REV_tr E2 QWJ0 E2 QWJ0_CANFA,REV_tr E2RMC1 E2RMC1_CANFA,REV_tr F1 PMD5 F1 PMD5_CANFA,REV_tr F7FN86 F7FN86_MONDO,sp P51587 BRCA2_HUMAN,sp Q8C863 ITCH_MOUSE,sp Q96J02 IT	elDn qK	55%	28.8	48.90974	Ref	-0.51	0.35	-0.63	-0.33	-0.55	-0.14	-0.48	2E+05	93100	2E+05	104000	142000	1E+05	1E+05	115000	526.8	1051.5	2	0.0011	1.063
Endothelial protein C receptor OS=Bos taurus GN=PROCR PE=2 SV=1	sp Q28105 EPCR_BOVIN	gVTF PLIIR	54%	29	49.30322	Ref	-0.33	-0.88	-0.09	0.34	0.66	-0.74	0.032	7530	5220	3870	7490	11100	12100	4800	8130	660.4	1318.8	2	0.0072	5.445

Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1	6 PIN1_H UMAN,sp Q4R383 PIN1_MA CFA,sp Q 5BIN5 PI N1_BOVI N,tr B3KU M4 B3KU M4_HUM AN,tr D2 HGV6 D2 HGV6_AIL ME,tr E7E QR5 E7E QR5_HU MAN,tr F 1P6C1 F1 P6C1_CA NFA,tr F1 S3G5 F1S 3G5_PIG,t r F7BLZ7 F7BLZ7_H ORSE,tr F 7HDX7 F7 HDX7_MA	tkEE ALELI nGYI Qk	54%	32.6	52.59907	Ref	-0.21	-0.35	0.019	0.064	0.042	-0.22	0.038	2050	1540	1520	2200	2500	2150	1880	2230	888.2	2661.5	3	0.0182	6.828
Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1	9 DEK_H UMAN,sp Q6AXS3 DEK_RAT, sp Q7TN V0 DEK_ MOUSE,tr A5PJQ1 A5PJQ1_B OVIN,tr B 4DFG0 B 4DFG0_H UMAN,tr B4DN37 B4DN37_ HUMAN,t r D2HIB3 D2HIB3_ AILME,tr D3YVJ6 D 3YVJ6_M OUSE,tr D6RDA2 D6RDA2_ HUMAN,t r E3VX55 E3VX55_	iLNFL MHP k	54%	30.4	50.42202	Ref	-0.096	-0.66	-0.32	-0.75	-0.32	-0.83	-0.3	2000	1620	1190	1690	1390	1630	1190	1720	574.4	1720	3	0.0038	2.186

Fumarate hydratase, mitochondrial OS=Sus scrofa GN=FH PE=1 SV=1	3 FUMH_PIG,sp P14408 FUMH_RAT,trans C5IWV1 C5IWV1_SHEEP,trans D2H9H6 D2H9H6_AILME,trans E2RGR9 E2RGR9_CANFA,trans F6U5R1 F6U5R1_HORSE,trans F6XCG4 F6XCG4_MONDO,trans Q148D3 Q148D3_BOVIN,trans Q4PNY4 Q4PNY4_CRIGR,trans Q5M964 Q5M964_RA	mPIP VLk	53%	25.7	45.74506	Ref	-0.13	-0.26	-0.11	-0.27	-0.51	-0.27	-0.6	8170	6480	6440	8030	7920	5870	7200	5700	469.3	1404.9	3	0.003	2.138
RING finger protein 113A OS=Bos taurus GN=RNF113A PE=2 SV=1	sp Q67ER4 R113A_BOVIN	aVH NPM IQk	53%	32.3	52.38563	Ref	-0.005	-0.02	-0.08	-0.072	0.23	-0.11	0.09	24500	21200	22700	24600	27200	29200	24200	27500	549.3	1645	3	0.0084	5.075

60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3	1 RL17_HUMAN,sp P24049 RL17_RAT,sp Q3T025 RL17_BOVIN,sp Q5XTY7 RL17_FELCA,sp Q9CPR4 RL17_MOUSE,tr B4E3C2 B4E3C2_HUMAN,tr B7NZF8 B7NZF8_RABIT,tr D3Z3R2 D3Z3R2_MOUSE,tr D3Z9G9 D3Z9G9_RAT,tr D3ZP66 D3ZP66_RAT,tr D3ZXH6	nAES nAEL	53%	33	53.30172	Ref	0.23	0.15	0.46	0.009	0.46	0.06	0.3	10200	10400	10700	14800	12000	14300	11300	13200	792.9	1583.9	2	0.0104	6.534
Semaphorin-3C OS=Bos taurus GN=SEMA3C PE=2 SV=1	7MB70 SEM3C_BOVIN,REV_sp O70418 RN112_RAT,REV_sp P05708 HXX1_RAT,REV_sp P17710 HXX1_MOUSE,REV_sp P19367 HXX1_HUMAN,REV_sp P27595 HXX1_BOVIN,REV_sp P56560 AOFB_BOVIN,REV_sp Q2TB90 HKDC1_HUMAN,REV_sp Q4R6N4 CPXC	IVILR	53%	17.9	38.36324	Ref	0.33	0.25	0.31	-0.18	0.11	0.23	0.094	5260	5740	5900	6890	5420	5780	6540	5920	459.3	916.63	2	0.0121	13.14

Endoplasmic reticulum resident protein 44 OS=Bos taurus GN=ERP44 PE=2 SV=1	2 ERP44_BOVIN,sp Q9BS26 ERP44_HUMAN,sp Q9D1Q6 ERP44_MOUSE,tr A6ML26 A6ML26_CALJA,tr B1AY76 B1AY76_MOUSE,tr B6CVD6 B6CVD6_PIG,tr D2H0F7 D2H0F7_AILME,tr F1M396 F1M396_RA_T,tr F1PQG3 F1PQG3_CANF_A,tr F1SSD2 F1SSD	qFVFDLHSGk	53%	32.9	53.13125	Ref	-0.31	-0.58	-0.5	-0.26	-0.86	-0.45	-0.82	12900	9000	8140	9650	12500	7220	10000	7710	596	1785	3	0.0088	4.922
Pseudopodium-enriched atypical kinase 1 OS=Mus musculus GN=Peak1 PE=1 SV=4	69Z38 PEAK1_MOUSE,REV_sp Q9H792 PEAK1_HUMAN,REV_tr D2I0Q5 D2I0Q5_AILME,REV_tr D4A563 D4A563_RAT,REV_tr E1B8H0 E1B8H0_BOVIN,REV_tr E2QUM4 E2QUM4_CANFA,REV_tr F1SJ90 F1SJ90_PIG,REV_tr F6QWL8 F6QWL8_CALJA,REV_tr F6	ILALVk	52%	19.2	39.509	Ref	-0.26	-0.72	-0.24	-0.61	-0.04	-0.95	-0.14	2310	1680	1320	2080	1770	2300	1280	2220	422.3	1263.9	3	0.0206	16.27

Uncharacterized protein OS=Callithrix jacchus GN=MLIP PE=4 SV=1	REV_tr F7 ETD9 F7E TD9_CALJ A	vLSA LnSS AK	52%	30.2	50.71617	Ref	-0.038	-0.21	-0.37	-0.19	-0.36	-0.47	-0.25	1490	1260	1210	1220	1530	1190	1150	1320	647.9	1293.8	2	0.0104	8.04
Calpain-2 catalytic subunit OS=Bos taurus GN=CAPN2 PE=2 SV=2	sp Q27971 CAN2_BOVIN, tr A81F71 A81F71_SH_EEP	rPTEI cDnP QFIT GGA TR	52%	32.3	52.63781	Ref	-0.3	0.6	0.11	-0.022	0.15	-0.35	-0.09	2520	1780	3600	2890	2900	2860	2110	2500	776.4	2326.1	3	0.0163	6.999
Synaptonemal complex protein SC65 (Fragment) OS=Rattus norvegicus GN=Leprel4 PE=2 SV=2	sp Q64375 SC65_RAT, sp Q8K2B0 SC65_MOUSE, tr D4ABF0 D4ABF0_RAT, tr F6W113 MOUSE, tr Q8C112 Q8C112_MOUSE	IFGH VLER	52%	31.3	51.67143	Ref	-0.076	-0.18	0.006	-0.28	0.008	0.004	-0.14	3840	3170	3190	4080	3700	3930	4090	3670	425.6	1273.7	3	0.0022	1.73
Uncharacterized protein OS=Sus scrofa GN=PNP PE=4 SV=1	tr F1S8H8 F1S8H8_PIG	wLLS HTk	51%	29.2	49.66269	Ref	0.47	-0.19	0.46	0.011	0.15	-0.29	0.29	17200	20700	14300	25100	20300	19500	15000	22200	498.3	1491.9	3	0.002	1.369

