Supplemental Table S1B: Imputed dataset of 2353 total proteins with 175 differential proteins (p<0.

Gene names	Significant	Difference	- Log p value	Log2(LFQ Col8-/-_1)	Log2(LFQ Col8-/-_2)
Fech	+	3.382236958	1.509117644	25.05540085	24.68351364
Osgep	+	2.571752071	4.198728173	22.97807693	23.28404427
Acot11	+	2.105901241	1.477232221	22.80023575	23.47691917
Plod3	+	2.065131187	1.320346218	22.24388504	22.87096405
Aga	+	1.916537285	1.952750923	23.07559776	23.04953003
N/A	+	1.894077301	1.627378591	23.97893333	23.95863342
Tprg1l	+	1.859460831	1.459186143	21.97018051	22.67443657
Pdk1	+	1.718135357	1.364022477	21.80510712	23.23567009
Napg	+	1.707140446	1.575229482	23.01886177	22.83447266
Apeh	+	1.483808041	1.350586667	22.50811577	23.10737991
Prrc1	+	1.472318172	1.480287455	21.9770813	22.06312561
Fam3c	+	1.170875072	1.596592242	22.62377167	23.00008392
Myl6	+	0.963307381	1.932907005	26.58634758	26.26184082
S100a10	+	0.923115253	1.527461865	28.97645378	28.7265358
Hsd17b4	+	0.883117676	1.448991828	22.89554214	22.33606339
Ag2	+	0.825303078	1.404460446	22.41933823	22.58756065
Pdss2	+	0.804397106	1.629235851	27.95775986	27.64251328
Palld	+	0.784472942	1.376404508	25.50139427	25.6823082
Col14a1	+	0.780597687	2.956347157	30.35657501	30.3982563
Des	+	0.684178352	2.150121794	26.64801025	26.81445694
Zmpste24	+	0.58784771	1.454550102	23.2572422	23.38824272
Rnase4	+	0.578791618	1.907243873	23.26899338	23.64899826
Sparc	+	0.458203793	1.497319792	25.92899704	25.61734009
Ppic	+	0.449406147	1.484907598	24.42451096	24.67195702
Septin6	+	0.446534157	1.441540276	24.66893005	24.68715096
Pcolce	+	0.446055889	1.766074634	25.24847412	25.23979759
Ano6	+	0.441217899	1.517635831	25.0868721	24.85243416
Eif5b	+	0.430675507	1.323926204	24.34921837	24.57253647
Pdlim5	+	0.422596931	3.713346636	27.666008	27.62477684
Inpp4a	+	0.422566414	1.322632322	23.68346024	23.72504807
Cacna2d1	+	0.417637825	2.153721852	27.2155838	27.2382679
Dysf	+	0.402622223	1.754338759	25.6613121	25.82536697
Gng5	+	0.401665688	1.596523616	25.11481667	24.92043495
Mapre3	+	0.400437832	1.463449141	23.35420609	23.43974304
Tubb6	+	0.398900986	1.467921769	25.66218185	25.76309204
Map7d1	+	0.379518986	1.336743609	23.73624229	23.79004669
Xirp1	+	0.378246784	1.815044061	25.26935196	25.60133171

Pef1	+	0.374653339	1.992174377	25.33391571	25.26874352
Atp1a2	+	0.373134613	1.685453985	25.29435349	25.5515976
Col6a6	+	0.368633747	2.880480138	30.15665627	30.15966606
Postn	+	0.363574028	2.618942746	32.7892952	32.76885986
Gls	+	0.357828617	1.949762298	25.11310768	25.42604828
Mavs	+	0.351365566	1.357410679	25.08557701	25.03477287
Dpt	+	0.349676609	2.057678821	29.64504051	29.3788166
Col15a1	+	0.332344055	3.853583172	29.97404861	30.0622673
Septin9	+	0.320576668	1.632315337	26.97956467	27.09275055
Ikbip	+	0.313050747	2.174552403	22.8907814	23.1792984
Cnn3	+	0.312690735	2.428891312	28.44490051	28.6069603
Lox	+	0.312326431	1.788710765	27.57758713	27.66295624
Bcat2	+	0.311786652	1.91010126	26.36456108	26.27806473
Ckap4	+	0.306010723	1.496717889	27.17996979	26.87220573
Synpo2	+	0.300588608	1.741957695	28.75560379	29.05602646
Smtn	+	0.300449848	1.427133861	29.67586517	29.5233345
Mapre1	+	0.297382832	2.844330519	25.44243622	25.44132805
Add1	+	0.296934605	1.638212174	26.0907135	26.25571251
Fkbp1a	+	0.295899391	1.698164618	26.39373589	26.20318031
Aebp1	+	0.295713902	2.888858796	28.49598503	28.47278214
Cnn1	+	0.290062428	1.6707636	31.95202827	32.14099121
Capza1	+	0.289375305	2.661441709	25.19276047	25.44874954
Gng12	+	0.289208889	1.474308694	25.15278816	25.18733406
Eln	+	0.285712719	1.705780039	30.99435616	31.04472542
Gpc6	+	0.280003548	1.854856518	26.24495888	26.43868065
Serpinh1	+	0.279938698	1.750765154	30.54250145	30.46187782
Flnc	+	0.278014183	1.879247947	28.74413109	28.87844467
Atp5j2	+	0.2706213	1.377106951	26.44771004	26.58534431
Col6a2	+	0.266316414	1.812660516	32.48450089	32.27957916
Bgn	+	0.248378277	1.601781521	32.01498032	32.00871658
Col6a1	+	0.228528023	2.414907347	32.67900467	32.58075714
Tagln2	+	0.225367546	2.073449461	33.17859268	33.20180511
Ilk	+	0.222169399	1.932825727	29.49604225	29.63167953
Stxbp1	+	0.216610432	1.658707579	24.85252953	24.94172096
Pdlim7	+	0.214846611	1.783134215	29.42053413	29.64218521
Col4a3	+	0.210779667	1.649142227	24.85486031	24.91556549
Emilin1	+	0.197975159	2.735112584	29.54646301	29.62808418
Mcam	+	0.186146736	1.968394678	28.60629082	28.49712753
Ace	+	0.186111927	1.447291351	29.13359451	29.1193409
Esyt2	+	0.184381485	1.658399485	26.52329254	26.66979599
Actn1	+	0.183374882	1.651234385	32.13332367	32.07530212

Dpysl3	+	0.176403046	2.149529908	29.88419342	29.89678955
Cdh13	+	0.169661045	1.840471833	28.44122505	28.52361488
Eml1	+	0.165255547	1.475157482	26.51246834	26.60272026
Anxa2	+	0.155399799	1.348407701	32.11759186	32.07399368
Cspg4	+	0.153440475	2.079168947	28.77476692	28.73110962
Col18a1	+	0.145747185	1.601072611	30.99280548	30.96781158
Psmc1	+	0.144684315	1.556294436	24.96172714	24.89587402
Ptrf	+	0.144393921	1.664753772	30.86097527	30.71013832
Trip6	+	0.140184402	1.941335083	25.72179413	25.67559433
Acta2	+	0.130793571	1.438138306	32.22934341	32.31051254
Septin2	+	0.122727871	1.354165961	27.87788963	27.83611298
Pfn1	+	0.117507935	1.482114928	29.87654495	29.9797821
Fermt2	+	0.061072826	1.635816459	29.42310143	29.48123741
Dnpep	+	-0.133137226	1.39825063	26.12143326	26.27330589
Anxa4	+	-0.14982748	2.052195908	27.44695282	27.4587326
Hspe1	+	-0.151346207	1.389927566	27.82765961	27.81323242
Gstm1	+	-0.156620026	1.473395469	31.84067345	32.02604294
Vps35	+	-0.184728146	1.337457155	26.74162674	26.87114716
Anxa5	+	-0.185384274	2.256435074	30.84849358	30.90073967
Mgll	+	-0.190984726	1.555665639	25.43338966	25.39640045
Ran	+	-0.200575829	1.761454627	27.03023148	26.87829971
Erh	+	-0.201847076	1.391264905	24.4596405	24.6105423
Sdpr	+	-0.202011585	2.200247205	27.32937241	27.186409
Thsd4	+	-0.20222187	1.391342274	26.76217842	26.61610603
Cbr2	+	-0.206911564	2.381958636	29.34229469	29.47514153
Ero1l	+	-0.207582951	1.821528878	23.4199543	23.57922935
Cbr1	+	-0.208376884	2.52535862	26.10243416	26.19392586
Anxa1	+	-0.21546936	1.754064215	29.50958252	29.37254143
Kpnb1	+	-0.224582672	1.632023766	27.99728012	28.14472198
Gstt3	+	-0.245191097	1.551442179	25.95493507	25.9819622
Txndc17	+	-0.253442287	1.326701901	25.05374336	25.22423935
Prpf8	+	-0.254412174	1.319518303	24.73943901	25.0110321
Psmc4	+	-0.260583401	2.085046181	26.32656288	26.27396393
Ecm29	+	-0.266244888	2.099504176	24.11925697	24.18978691
Snrpb	+	-0.269165039	1.75161097	24.45255661	24.52903938
Rpl29	+	-0.269359589	1.403472826	23.76070786	23.5308857
Psmd2	+	-0.273206711	1.392006362	26.53712273	26.95271492
Efhd2	+	-0.274438858	1.435783514	22.44657516	22.49267387
Bag6	+	-0.274927139	2.410392586	23.58817863	23.48099136
Aldh9a1	+	-0.292712688	1.504561653	25.39597511	25.80891991
Ica	+	-0.304176807	2.234487269	23.69370461	23.6307869

Sqrdl	+	-0.309355736	2.55796225	25.21778488	25.17983818
Samhd1	+	-0.321038246	1.32920908	25.98522377	26.24149132
Snx1	+	-0.333074093	1.398544911	24.80538177	24.23622513
Cct6a	+	-0.335685253	2.400818155	26.52881622	26.73013687
Psme2	+	-0.340397358	1.333763087	26.83857918	26.9755249
Chd4	+	-0.361102581	1.769169824	24.02799988	24.05142212
Hsd17b11	+	-0.369546413	1.533005111	25.31772423	25.30396271
Fuom	+	-0.369997501	3.408404696	23.40846825	23.32841301
Srsf3	+	-0.38270092	1.575580588	25.28439713	25.4262085
Ptpn12	+	-0.386180401	1.743130884	20.49648285	20.76287842
Ttr	+	-0.38838768	1.43735993	27.87050056	27.41554642
C4b	+	-0.390030384	1.850333428	27.21595383	27.0348568
Psip1	+	-0.411422729	1.714939472	24.31347466	24.29123116
Usp9x	+	-0.41556263	1.377910081	26.13269234	26.2021904
Xdh	+	-0.445792675	1.633279591	24.03775024	24.51989365
Got1	+	-0.448171616	1.437077909	24.29284477	23.76971436
Gda	+	-0.451441765	2.726573966	23.38837433	23.33142281
Abhd14b	+	-0.459507942	2.182724107	25.36432838	25.25821304
Ftl1	+	-0.46950388	1.347296887	27.421175	27.68912506
Bphl	+	-0.522892475	1.330260568	24.98220062	25.24959564
Psma4	+	-0.551069736	1.659442713	25.50908852	25.41037941
Rhot1	+	-0.554106712	1.642700766	23.58394051	23.86145401
Hectd1	+	-0.585552692	1.707000578	20.15783119	20.0256691
Skiv2l2	+	-0.591099739	1.731264979	22.95064735	23.29963875
Glrx3	+	-0.6247859	3.014130406	24.44354248	24.4126091
Dnajc19	+	-0.714222908	1.405937349	19.41191673	20.41131592
Eif3l	+	-0.729324818	1.440879694	23.41531944	23.36946297
Ddx46	+	-0.798279762	1.342070807	21.94724846	21.52759743
Ugdh	+	-0.808923721	1.855664876	24.7023983	24.58588982
Hrg	+	-0.854629517	1.98443226	24.21304512	23.97342491
Pla2g16	+	-0.862401009	2.583043286	19.66872025	19.71246719
Adh1	+	-0.883069038	2.884839784	24.91218758	24.99429512
Srpr	+	-0.937836647	1.408000733	20.55384254	21.50280762
Pon2	+	-0.94248867	1.319213301	21.09674072	22.08440018
App	+	-0.950093746	1.305315927	23.54274178	23.05569839
Rpa2	+	-0.969217777	2.807017235	20.87597656	20.61522102
Serpina3m	+	-0.969385147	1.639047947	28.06522369	28.71364975
Itm2b	+	-0.978942871	1.697472672	20.41253853	20.86045074
Tomm5	+	-0.991278648	1.794444913	20.15368843	21.06058693
Tmem256	+	-1.0166049	1.454500478	22.73479652	21.37952042
Ighm	+	-1.062169075	2.044592935	26.5625267	26.13090706

Lgals3bp	+	-1.125296593	1.487051636	20.7720356	21.08783531
Dcxr	+	-1.183615685	2.20030632	19.19366455	19.84251595
Notch3	+	-1.268364429	1.81593516	20.03216934	20.96126938
Bzrap1	+	-1.346906185	1.803504606	23.50263786	22.55980492
Pik3r1	+	-1.353751183	1.796219196	20.53821373	21.62627029
Epn3	+	-1.823766232	1.992903155	20.84386253	19.96886826
Dapk3	+	-2.171921253	1.908911262	22.5104351	20.32747078
Krt85	+	-2.224033356	1.79078334	20.43018913	19.5817585
Dsp	+	-2.268306255	1.345420326	22.99941444	23.49350548
Mup9	+	-2.306945324	2.670881061	20.2466774	19.43536568
Kdm1b	+	-2.740858555	3.921611003	21.24747467	20.75329208
Krt33a	+	-3.085149288	1.58439243	21.08062172	20.51421928
S100a3	+	-3.496547222	1.568638597	19.87410164	20.41849327
Krtap8-1	+	-3.615775585	1.529090935	19.91387367	21.44516563
Krtap19-3	+	-4.09680891	1.667719358	20.70944977	20.24485016
A2m		-0.257859707	0.82480271	30.17521858	29.5590477
Aars		-0.058942318	0.141175184	24.89541245	24.87722397
Aarsd1		-1.070933819	0.894965128	21.46166229	19.40851974
Abat		-0.219346046	0.524549879	24.17287445	24.69789886
Abca8b		-0.777572632	0.453511016	19.55714989	21.60860252
Abcc9		-0.060088158	0.05773205	22.91816139	22.71969032
Abcd3		-0.201580524	0.604377113	23.12746811	23.70767212
Abce1		-0.092211723	0.280394132	23.20457649	22.82444572
Abcf1		-0.093919277	0.18306465	21.19291878	21.84406471
Abhd11		-0.037024498	0.151922086	23.93183899	24.26011848
Abhd12		-0.096956253	0.198577009	24.21334076	24.1710434
Abhd16a		-0.073053837	0.183821242	24.4432888	24.5961647
Abhd5		-0.31103611	0.364919406	24.09240723	23.69168282
Abi1		-0.334907532	0.146061145	21.28374481	21.79219055
Ablim1		0.51310873	0.265707933	19.74240875	22.59325027
Abracl		-0.031710625	0.123387318	25.2886982	25.41876602
Acaa1a		0.031332016	0.083328364	25.72712708	25.97688103
Acaa2		-0.116802692	0.089604216	29.89387131	30.24762344
Acaca		-0.21006918	0.251331609	25.16614723	25.62745094
Acad10		0.657740593	0.480120991	22.42943573	22.29605675
Acad9		0.172578812	0.37772703	23.97167206	24.12447357
Acadl		-0.214492321	0.194506296	29.18222237	29.28299332
Acadm		-0.002643585	0.002230688	29.15812492	29.44239235
Acads		-0.065029621	0.079402514	27.63297844	27.74233246
Acadsb		-0.073194504	0.149805874	25.86046028	25.75159454
Acadvl		-0.113926888	0.108281319	28.78892708	28.9890728

Acan	0.460333824	0.749294844	27.49754715	27.31553268
Acat1	-0.088744164	0.216152677	29.2882843	29.24238586
Acat2	-0.239433289	1.027706342	25.15695953	25.27856064
Acin1	-0.299306393	0.304611808	23.11543655	23.150877
Acly	0.009790897	0.021806671	27.89342308	28.54896164
Aco1	0.021155357	0.069438156	26.72728348	26.83508873
Aco2	-0.051834106	0.043836967	30.53917694	30.7950573
Acot13	-0.242779732	0.310901548	23.93283081	24.53593636
Acot2	0.118498325	0.272678354	25.23786736	25.61217499
Acot7	0.066975594	0.047876708	22.5036087	22.43221855
Acot9	0.039908886	0.118627102	26.34423065	26.65389824
Acp1	-0.116752625	0.342497501	25.14755821	25.12245941
Acsf2	-0.790815353	0.545031648	21.97645187	22.75641823
Acsf3	-0.090058804	0.047589474	21.13076591	20.77988625
Acsl1	-0.141486645	0.240790373	28.70091057	28.77548981
Acsl5	-0.390666962	0.66476597	20.67115784	20.82601738
Actb	0.51196909	1.203114736	28.12346649	27.27967644
Actc1	0.087364197	0.548376259	35.3516922	35.40505219
Actg1	0.092303276	0.92967418	33.47157669	33.55167389
Actl6a	-0.052636147	0.058887608	22.00764847	23.21775436
Actn4	0.262200356	1.229807547	29.34280396	29.12072563
Actr10	-0.28963089	0.382301948	22.67441559	23.24627876
Actr1a	-0.125317574	0.425214026	24.65731049	24.79530907
Actr1b	-0.160355568	0.64470743	27.12907982	27.00859833
Actr2	-0.000394821	0.000938406	28.03070641	28.27825928
Actr3	0.066427708	0.429475951	29.46460533	29.48218155
Acyp1	-0.065456867	0.127155044	24.03456306	24.13241768
Adam10	0.332565308	0.326167714	20.99085426	20.83198166
Adamtsl4	0.6644063	0.496843906	23.0403614	23.41969872
Adck3	0.023924351	0.021959397	24.78161812	24.84119797
Adcy5	-0.020297527	0.061002244	25.11513519	25.31544495
Adcy7	0.43220377	0.52798435	21.83124733	21.77217293
Add3	0.436903954	0.698268126	23.55438232	23.11577034
Adh5	-0.10977459	0.522810013	26.74931908	26.97650909
Adh7	0.714199066	0.252378378	23.28277206	24.02326775
Adipoq	0.113071918	0.361772418	24.76111412	25.17165375
Adk	-0.210632801	0.215257321	25.9557991	25.96710396
Adpgk	0.106284142	0.326855579	21.53026772	21.65298462
Adrbk2	0.045748711	0.038590639	21.85753059	21.97000504
Adrm1	-0.301197052	0.139164038	21.29832458	21.23274612
Adsl	0.088407516	0.325499938	25.54450989	25.60305977

Adssl1	0.491183281	0.618077668	22.55065346	22.16545677
Afg3l2	0.232080936	0.555565873	22.59850693	22.52090073
Afm	-0.085717678	0.119126619	20.93488312	20.59841537
Agk	-0.630475521	0.315984277	23.6568737	23.58989525
Ago2	-1.092789173	0.603086644	23.2254982	23.15901756
Agpat2	0.363395214	0.467959697	22.54667854	22.640131
Agrn	-0.068068504	0.209886347	25.42684746	25.0267334
Ahcy	-0.073794365	0.117317173	26.09703827	26.51288986
Ahcyl1	-0.210496426	0.409620885	23.42572784	23.86693382
Ahsa1	-0.178017616	0.392435222	23.47506523	24.24554062
Ahsg	0.009993076	0.015772415	29.90382957	29.34161758
Aifm1	0.255277634	0.459756559	24.84340477	25.00919533
Aifm2	1.188244343	0.997895552	20.45792007	22.72100639
Aimp1	-0.034053802	0.058007135	24.65075111	24.93093681
Aimp2	0.007547855	0.015016048	23.5370636	24.22655678
Aip	-0.131065369	0.071521017	21.05938339	22.95569229
Ak1	-0.213637829	0.912690524	27.2541275	27.49251366
Ak2	-0.287996292	0.973631808	26.91524696	27.11783218
Ak3	0.131917953	0.962317311	27.22765923	27.12642479
Akap12	0.255045414	0.7548176	25.66367531	25.7654705
Akr1a1	-0.125985146	0.746193675	26.9854393	26.93741798
Akr1b1	-0.028944969	0.152588557	27.83888054	27.85346985
Akr1b7	0.057573318	0.10730141	23.74755287	24.04393578
Akr1b8	0.233963966	0.50696079	25.61742401	25.77122498
Akr7a2	-0.047966003	0.126639063	24.71109009	24.93359566
Akt1s1	0.030324459	0.047608279	21.58458328	22.00411987
Alad	0.319130898	0.173808443	23.31534195	22.60885048
Alb	-0.23001194	0.592210343	34.44047928	33.877285
Alcam	-0.330226898	0.497158073	24.2493782	24.79188538
Aldh16a1	-0.255509853	0.209946802	19.96691132	20.49306488
Aldh18a1	0.513132095	0.440766856	21.66409874	20.68159103
Aldh1a1	0.235945225	0.244785063	24.00581741	23.24090576
Aldh1l2	-0.333593845	0.24240565	21.12155724	23.00537109
Aldh2	0.044559479	1.18986637	30.65897942	30.65855217
Aldh3a2	0.008934498	0.026574162	25.66065979	25.92098045
Aldh4a1	-0.047771454	0.056798336	24.63848495	24.50911903
Aldh5a1	0.661359787	0.5175275	21.93340683	22.21273232
Aldh6a1	0.039993286	0.094692586	28.08050346	28.25065422
Aldh7a1	0.00402689	0.017237415	26.66410828	26.76217842
Aldoa	-0.218126297	0.610396885	29.39601135	29.57818031
Alg2	-0.187947273	0.298392684	21.73343086	22.26533508

Alox5ap	0.037076473	0.039374863	20.78148842	20.56318474
Alyref	0.752319813	0.443860219	24.11195564	24.0839138
Anapc1	0.771293163	0.632321351	21.95532036	23.28714943
Ank1	0.340174675	0.861983503	27.57455826	26.89793015
Ank2	-0.357489586	0.976344746	23.24981308	23.07238007
Ankfy1	-0.774113655	0.640871402	22.20815468	20.85597229
Ano10	0.41706562	0.96145605	24.94122887	24.11569023
Anp32a	-0.148119926	0.326945073	25.22725487	25.20445061
Anp32b	0.086294174	0.320474159	24.73505402	24.95593262
Anp32e	-0.152810574	0.298757732	24.95215988	25.25860977
Anpep	-0.089501858	0.183296525	28.3731842	28.45748138
Anxa11	-0.150018215	1.115954354	27.63394928	27.71992874
Anxa3	-0.165409088	1.227886192	28.42358208	28.35665894
Anxa6	0.014432907	0.138142665	31.24081802	31.28432846
Anxa7	-0.046670437	0.3810673	27.56398201	27.53274536
Aoc3	0.000328541	0.002122875	31.61802483	31.73335838
Aox1	-0.128930092	0.747405324	23.14497757	23.42828751
Ap1b1	-0.064511299	0.133170879	24.6373806	24.5937748
Ap1g1	-0.109521389	0.190094654	22.55655861	23.04010963
Ap2a1	0.070261955	0.366269828	26.93280792	27.07255173
Ap2a2	-0.014687538	0.053404758	27.81775284	28.06321907
Ap2b1	-0.041480541	0.181031655	27.76774597	27.89966011
Ap2m1	-0.059380531	0.831282786	26.57214546	26.70977783
Ap2s1	-0.021205425	0.036350181	24.50524521	24.88781166
Ap3b1	0.065863132	0.112903743	23.62287903	24.02614212
Ap3d1	0.01295948	0.068853784	22.692173	22.80124283
Apex1	-0.261209965	0.2992716	23.69349289	23.76779556
Api5	-0.192539692	0.626805755	24.2110405	24.16015625
Apmap	0.136705399	0.051920487	22.69608498	23.56465149
Apoa1	-0.094760895	0.101390327	29.34625435	28.27364349
Apoa1bp	-0.153061867	0.811305931	26.82832527	26.91410637
Apoa2	0.038075924	0.030704192	26.22284126	25.34877968
Apoa4	-0.251269341	0.588977682	27.57823563	27.03296661
Apoc1	1.056295872	0.464777819	25.28439713	24.19865417
Apoc2	-0.980708599	0.608212011	24.24067116	23.89171028
Apoe	0.086492538	0.180131104	25.59565353	24.96172714
Apoh	0.063871384	0.199355054	27.23544121	26.99604225
Apoo	-0.067653179	0.098897625	22.88940811	23.02211761
Apool	0.002538681	0.003721995	24.01111794	24.67330551
Appl1	0.16797781	1.173834564	24.36205482	24.22567558
Aprt	-0.207539558	0.681859941	24.8818512	24.99524498

Aqp1	0.216496468	0.217317434	25.17896461	26.17369461
Arcn1	-0.241546631	0.664831411	24.84474564	24.84426689
Arf1	-0.192079067	1.24775557	27.34324837	27.47946548
Arf2	-0.121993542	0.391181785	21.33598137	21.51306534
Arf4	0.171702385	0.167787721	25.90046501	26.56579971
Arf5	0.85008812	0.725374987	23.09453583	23.02725601
Arf6	0.456562996	0.473975968	22.20651627	22.90538216
Arfgef2	-0.606719494	0.482643627	20.72492409	20.58279228
Arhgap1	-0.025662899	0.102751356	26.32225418	26.42321396
Arhgap17	0.263404846	0.219062455	22.85881996	23.69115067
Arhgap32	-1.554393291	0.474394531	21.71430779	27.56674194
Arhgdia	-0.002401352	0.010837246	28.43650627	28.24603844
Arhgdib	-0.156968117	0.569653869	23.63832092	23.55754089
Arhgef2	0.809628487	0.426378549	23.43313599	23.694767
Arhgef7	-1.317762852	0.725560751	21.0735836	20.20353508
Arl1	-0.089370251	0.188923858	23.73913002	23.86750031
Arl3	-0.128546715	0.536308134	24.88753319	25.13825035
Arl6ip1	-0.508405685	1.244009374	21.77023888	22.52432442
Arl6ip5	0.084452629	0.537280049	25.83593178	25.69943428
Arl8b	0.397414684	0.799619138	24.93678856	25.13371277
Armc1	0.096776009	0.197812541	23.6738987	23.9910965
Arpc1b	0.063853264	0.170270462	28.16384506	28.63865089
Arpc2	0.00421381	0.013310211	27.53934288	27.52372742
Arpc3	0.095059872	0.87811448	27.68919182	27.6502037
Arpc4	4.15E-05	0.000216111	28.17807198	28.3225975
Arpc5	-0.067485809	0.327295623	25.44085312	25.31392479
Arpc5l	-0.118808746	0.421147572	24.45192719	24.60240936
Asah1	-0.193537712	0.40665817	24.92619324	25.051754
Asl	-0.278310776	0.609331539	23.71952248	23.49960136
Asna1	-0.264382839	0.391015889	22.88743973	23.98919296
Asph	0.133377075	0.660737828	25.84239769	25.94176674
Aspn	0.066062927	0.433445358	31.60337448	31.42787361
Asrgl1	-0.731586933	0.446349482	19.58349991	21.95734215
Atad3	0.257356167	0.520075912	22.00058365	22.37464523
Atg5	0.398751259	0.832835922	23.14476013	23.06633186
Atg7	0.010608196	0.012711132	22.05337906	22.61573601
Atic	-0.166256428	1.180544755	27.32036018	27.3572464
Atl2	-1.15511179	0.561320977	19.47372627	19.84638023
Atl3	0.069384098	0.390954227	27.89550591	27.99356079
Atox1	-0.04338789	0.086387744	26.085495	25.79307747
Atp1a1	0.028580666	0.137411321	27.31613731	27.41086388

Atp1b1	0.091607571	0.107997595	25.05763245	24.86116982
Atp1b3	-0.248932838	0.548724783	24.93463135	25.00066948
Atp2a2	-0.052320957	0.217719651	27.44490051	27.55325508
Atp2a3	0.071470261	0.162493349	23.40522575	23.59160805
Atp2b1	0.693659306	0.655169889	21.58998489	22.25824928
Atp2b4	0.031209946	0.162699943	26.21830177	26.34197807
Atp5a1	-0.036808014	0.961185392	30.5963707	30.62679672
Atp5b	-0.077164173	0.900629935	31.40735245	31.53027344
Atp5c1	-0.021743774	0.191104774	27.08588028	27.04374695
Atp5f1	-0.15955162	0.613914937	27.68210793	27.70285988
Atp5h	0.011185169	0.07307611	27.30947304	27.33321571
Atp5i	0.18934679	0.607304855	24.65681839	24.96194839
Atp5j	-0.120993614	0.031587927	23.50106049	23.06324005
Atp5l	-0.141303539	0.490209447	26.01692963	26.09277153
Atp5o	-0.052155018	0.173786946	28.70744133	28.90535164
Atp6v0a1	0.001414299	0.000605284	18.8936348	21.44440269
Atp6v0d1	1.036431313	0.65852961	23.29656029	24.01639748
Atp6v1a	-0.139462948	0.382834216	24.77735901	25.34506035
Atp6v1b2	-0.113855839	0.09059524	19.9057312	21.06769371
Atp6v1e1	-0.419242859	0.517298047	22.2246151	23.36892891
Atxn10	-0.401813507	0.239751431	22.57798386	19.90834427
Auh	-0.898886204	0.539441227	22.98269653	22.97715187
Axl	-0.33712101	0.553862852	22.35231972	23.12186813
B2m	-0.227510452	0.711176641	24.60229492	24.34143448
B4galt2	-0.252451897	0.082305815	20.26031303	22.5577507
Bag3	0.158191681	0.448454834	24.90187073	24.92202377
Bag5	0.086276531	0.20396481	21.71162605	21.89167213
Banf1	0.107152462	0.851290232	27.87097168	28.00029373
Bax	-0.028315544	0.113768609	22.85540199	22.80195236
Bcam	0.077244759	0.528768464	28.42049408	28.24008942
Bcar1	0.431628704	0.444852841	20.97840881	21.04006004
Bcas3	0.110262394	0.456170022	21.16527176	21.29260635
Bckdha	0.027868748	0.054768697	23.8314209	24.21237564
Bckdhb	-0.094271183	0.065499356	25.13922691	24.08237267
Bckdk	-0.594061375	1.095650165	21.84467888	22.07985115
Blmh	0.013599396	0.034523859	24.93039513	25.12970924
Blvra	0.39931345	0.644931518	24.58915138	25.00710106
Blvrb	-0.075775623	0.214288171	25.4616394	25.36599731
Bpgm	0.937111855	1.185011118	21.79427719	20.59221268
Bpnt1	-0.353139877	0.923699168	23.97219849	24.14180183
Bre	-0.02106142	0.011175558	20.7305088	21.16949463

Brox	0.11485815	0.301664718	22.52152443	22.5745697
Btf3	0.689844608	0.763396386	20.748209	21.51955795
Btk	-0.695064545	0.90999618	19.40955734	20.3400631
C1qbp	-0.040477753	0.059678333	24.81753349	24.25983047
C3	0.057627678	0.219112333	28.11132813	27.73744202
C4bpa	0.201809883	0.436454184	25.92942619	25.3335743
C5	-0.337580681	0.806689366	22.8450222	22.1429863
C9	-0.029914856	0.062122725	21.88498306	21.24655533
Ca1	1.001214504	0.918759226	24.58880806	23.49277306
Ca2	-0.114824295	0.10628737	28.33146667	26.93831635
Ca3	-0.489739895	0.537500356	29.85412407	29.46374893
Cab39	-0.020797729	0.202156694	25.27820587	25.42540741
Cacybp	0.052295685	0.033832468	22.23172188	21.69178963
Cad	-0.213037014	0.364493481	21.824543	22.69829178
Calm3	-0.0023036	0.004222214	27.421175	26.79253197
Calr	0.070388317	0.190590296	27.64753151	27.48600388
Calu	-0.602280617	1.047637335	24.04418564	24.19204521
Camk1	-0.12471056	0.49198561	23.06956291	23.30646896
Camk2d	0.022273064	0.08958573	27.36360931	27.53489876
Camk2g	0.23003912	0.804717561	26.01180077	26.25459671
Camlg	-0.591819286	0.919517236	21.32108116	22.0586071
Cand1	-0.124158382	0.943567517	28.12307167	28.33415413
Canx	0.137093067	0.4315203	28.20899582	28.30247307
Cap1	-0.130134583	0.508922556	30.30736923	30.45522881
Cap2	-0.048529625	0.163172454	26.66166496	26.86064911
Capg	0.176898479	0.531534427	25.33643723	25.55452728
Capn1	0.00391674	0.005998625	24.03355408	24.51839256
Capn2	-0.017270088	0.035330008	28.45928001	28.63996315
Capns1	-0.039508343	0.09122921	28.28202248	28.63068962
Caprin1	-0.156851292	0.371160618	21.81354713	21.90418816
Capza2	-0.015239716	0.059368111	27.53860283	27.63899612
Capzb	-0.071054935	0.480536326	27.35110664	27.18034935
Carhsp1	1.298843384	0.710817759	24.48499107	24.33626747
Carkd	0.118932724	0.591731838	25.53647041	25.68386269
Carkd	-0.059309006	0.098940642	21.93052292	21.7424221
Carm1	0.56560564	0.551686024	21.61328697	21.6714592
Cars	-0.311420918	0.186342894	20.52257729	18.92737007
Casp8	0.457921982	0.350648365	21.17675972	21.40301704
Casq1	-0.114733696	0.08663952	27.33048248	28.20853043
Cast	0.21156311	0.883358837	24.46276283	24.235569
Cat	-0.12440443	0.26473115	24.94650459	24.77525139

Cav1	0.095373154	0.669125612	29.26865578	29.27417755
Cav2	0.105098248	0.372318573	25.93613815	25.72327805
Cbr3	-0.405020714	0.954713442	23.42687988	23.99645233
Ccar1	0.363002777	0.418651873	21.82325935	21.6887207
Ccar2	-0.590852261	0.337612811	22.01621056	22.25675392
Ccbl2	0.771899223	0.501791734	22.6835041	22.6566124
Ccdc127	-0.415537834	0.464739736	20.92702675	21.97337151
Ccdc47	0.344362736	0.536014479	24.30785942	24.74452972
Ccdc80	0.213381767	0.398251795	24.00213051	24.4889183
Ccdc90b	0.290511608	0.240524759	24.98758888	25.49393272
Ccny	0.70490551	0.555694323	21.22922897	22.14693642
Cct2	-0.049694538	0.183209285	27.78954887	28.00533485
Cct3	0.010333538	0.032032764	27.3176899	27.52753448
Cct4	-0.123590469	0.432734309	26.59562492	26.92558289
Cct5	-0.167820454	0.862667473	27.44482231	27.57953072
Cct7	-0.112504482	0.503602681	26.90127182	27.0519619
Cct8	-0.131860733	0.541865095	26.61988831	26.56685829
Cd109	0.23738718	0.427203094	26.39870071	26.47294426
Cd151	0.076759815	0.056098176	23.99800301	23.71670151
Cd163	-0.147076607	0.260355716	22.48096657	22.29980659
Cd200	0.195149422	0.491493958	25.54324341	25.55458641
Cd2ap	-0.011860847	0.019439366	23.89522743	23.18790054
Cd34	-0.194326878	0.619476994	24.95438004	24.39486313
Cd36	-0.076335907	0.147156037	27.28735924	26.96510124
Cd44	0.194512844	0.095255095	22.37023354	22.60571289
Cd47	-0.0709548	0.236335757	24.27042007	24.20635223
Cd81	0.21285677	1.272987144	27.90873337	28.18399811
Cd9	-0.149211407	0.174359826	26.12537956	26.2784729
Cd97	0.00530386	0.019361564	24.56569672	24.58554649
Cd99	-0.302051544	0.363004819	20.17645454	19.79634666
Cdc37	0.01881218	0.055538242	24.38284492	24.68805885
Cdc42	-0.059426308	0.281525726	27.08212852	27.31285286
Cdc42bpb	-0.056244373	0.103571757	23.58806419	24.30584335
Cdh6	-0.031506062	0.052904709	21.06657791	21.41338348
Cdipt	-0.988401413	0.765938798	20.21430969	21.7654705
Cdk13	-0.21476984	0.096827207	19.19792557	21.75389099
Cdk5	0.614443302	0.49408204	21.59545898	21.84176445
Cds2	-1.020140648	0.549986081	20.63287735	24.26284409
Celf2	-0.447123051	0.335696382	21.27861023	23.37225533
Cenpv	0.001819611	0.003197251	24.77097321	24.70112801
Ces1c	-0.154058933	0.458346371	27.93134308	27.3352623

Ces1d	-0.331356049	0.516028978	29.28096008	29.27072906
Cfb	-0.373797894	0.619486998	24.39558411	23.94190025
Cfd	0.233580589	0.080354483	24.10653496	23.25939941
Cfh	-0.029550076	0.107785963	27.8228054	27.75398064
Cfi	0.530840874	1.134066229	23.88939095	23.14056969
Cfl1	0.025596142	0.55581373	29.41691399	29.39754295
Cfl2	-0.075022221	0.26556109	25.27696419	25.14312553
Chchd3	-0.146456718	0.051355935	23.68624306	21.11737633
Chchd6	-0.164325714	0.220890167	23.63433647	24.09248924
Chmp3	0.724585056	0.288898619	22.93975067	19.45580101
Chmp4b	0.906894684	0.569020572	23.00935936	23.51725197
Chst12	0.283240318	0.395586643	21.33984566	21.4772892
Chtop	0.650859833	0.463028914	23.1517601	22.90697861
Cisd1	-0.291673183	0.846359063	24.63372803	25.01992226
Ckb	0.090852261	0.668969102	30.63451958	30.63538551
Ckm	-0.974234104	0.421992126	26.04082489	26.48937607
Clasp1	-0.235426903	0.350820128	23.60512543	23.62789536
Clcc1	-0.891243935	0.45459546	20.34891129	22.82098389
Clec10a	-0.514551163	0.233791129	22.35914803	21.64930534
Clec3b	0.330034256	0.740842203	25.16422844	24.65594673
Clic1	-0.077071667	0.314516284	26.5544548	26.74829674
Clic4	0.080552578	0.362476391	27.84906006	28.05522537
Clint1	-0.181238174	0.176177508	20.18422699	21.04733467
Clptm1l	0.364793301	0.241760595	21.79451561	21.92954826
Cltb	0.073387146	0.037871026	23.06215286	22.79251099
Cltc	0.015411377	0.088769184	30.65983009	30.75126839
Clu	-0.168105125	0.485946965	26.89942932	26.53259659
Clybl	-0.028868198	0.041621859	25.34173965	25.8680172
Cma1	0.196232319	0.316257322	27.7983532	27.66091728
Cmpk1	-0.274219513	0.774428673	24.79887199	24.79496193
Cnbp	0.214896679	0.729433838	23.94904518	24.38844109
Cndp2	-0.053713799	0.129932622	25.82868767	25.61414146
Cnn2	0.308525562	1.079341723	28.30234337	28.69488144
Cnp	1.226006985	0.576175433	23.625	23.60873795
Cnpy2	0.280058861	0.639882447	22.26106453	22.15505219
Cnpy4	0.243174553	0.138491263	22.83547401	22.45191574
Coa3	0.351763725	0.185673788	22.67493248	22.32802963
Coasy	0.41616106	0.649239506	22.62468719	23.31368256
Col12a1	1.396833897	0.913237451	22.86107635	22.08987236
Col1a1	0.167331696	1.065834766	33.8180275	33.66902542
Col1a2	0.088726044	0.160805733	33.18681717	32.897892

Col2a1	0.142735481	0.318845877	31.08391762	30.69760132
Col3a1	-0.549921036	1.131730433	26.8411026	26.62547302
Col4a1	0.031013012	0.195882743	30.81818008	30.84565544
Col4a2	0.043800354	0.266752065	30.55270386	30.43489838
Col4a4	-0.510688305	0.166981162	23.25341034	20.10921288
Col5a1	0.189917088	0.646718526	28.28797722	28.08217812
Col5a2	0.092316628	0.709440543	27.8226223	27.70424652
Col6a5	0.183423042	0.911865125	25.87011337	26.27676964
Colgalt1	0.582501888	0.664241798	23.31132889	23.46886444
Commd3	-0.110738754	0.327015778	22.59902954	22.8869381
Commd4	-0.156558514	0.195456568	21.17318916	20.91012955
Commd9	-0.121246338	0.191712577	23.15778351	23.47654915
Comt	-0.105543613	0.278164126	24.29094887	24.69774055
Comtd1	0.867017269	0.54436049	22.37552071	22.34770584
Copa	0.073307514	0.173834344	26.55092239	26.93786621
Copb1	-0.181018353	0.881658384	26.05515289	26.1404171
Copb2	-0.06163311	0.147223864	23.81685066	24.44550133
Cope	-0.046069622	0.377284291	24.96230125	24.96000481
Copg1	-0.11427021	0.389947338	26.30270958	26.48205376
Copg2	-0.989785194	0.559504999	21.66738892	19.83529282
Cops2	-0.046397209	0.136695813	25.91090775	26.1863327
Cops3	-0.032067299	0.113140418	24.99455452	24.98541832
Cops4	-0.137800217	0.266340842	23.77565193	24.35137749
Cops5	-0.06323576	0.15859346	23.83325577	23.82104301
Cops6	1.233935356	0.976278053	21.76263428	20.47058868
Cops7a	-0.23268795	0.731881194	23.57299805	23.52372742
Copz1	0.033593178	0.054614523	22.71820641	23.08056831
Coq10b	0.148429871	0.124078551	21.61481667	21.77076149
Coq6	-0.717856884	0.844272737	22.33076668	23.70081139
Coq9	-0.264202595	0.427443933	24.11402321	24.63311768
Coro1a	0.027542591	0.068564951	22.63458061	22.49025345
Coro1b	0.065253735	0.199227505	25.75468063	25.80579948
Coro1c	0.092270851	0.777202061	28.01674843	28.05785942
Cotl1	-0.656263828	0.899723063	20.95155525	21.58109283
Cox4i1	0.052263737	0.05396117	27.2703495	27.45489502
Cox5a	-0.083042145	0.104411562	28.78572083	28.83092499
Cox5b	0.143768311	0.155356191	26.03151512	26.51504326
Cox6a1	-0.351594925	0.559301897	27.92382622	28.62044907
Cox6b1	0.056001186	0.053900691	27.68163872	27.81451797
Cox6c	0.062657833	0.071446287	26.10902786	26.27794075
Cox7a1	-0.234397888	0.121427897	26.1822834	26.47995949

Cox7a2	-0.035969734	0.051087348	25.12340736	25.17714119
Cox7c	-0.128566265	0.164179679	24.51255798	24.49777412
Cp	0.003232956	0.00813729	25.68805885	25.67959976
Cpa3	0.076701641	0.117299914	28.01393127	27.79965019
Cpe	-0.115323067	0.536565636	23.6718483	23.80901909
Cpne1	-0.047725201	0.239691181	26.32003403	26.4998436
Cpne2	0.014857292	0.028353625	22.56755447	22.40267754
Cpne3	-0.251984119	0.654692855	26.21737671	26.36108398
Cpox	0.769266129	1.029433135	21.29888344	21.37363625
Cpped1	0.130086899	0.064292588	22.75745583	22.24971199
Cpq	-0.122635365	0.275229897	24.27391052	24.36892891
Cpsf6	-0.067979813	0.107236887	25.01363182	25.77484894
Cpsf7	-0.342238426	0.934694418	23.48861122	23.86325073
Cpt1a	0.095938683	0.187232676	24.33626747	24.57276726
Cpt1b	-0.049588203	0.030639104	25.18955994	25.28210068
Cpt2	-0.214389324	0.167882517	26.80291939	26.72090721
Cr1l	0.848997116	0.272951562	19.46365547	23.58554649
Crat	-0.068255901	0.115229516	25.10848999	25.26029778
Creld1	0.336287975	0.570060162	21.07711601	21.1196537
Crip1	0.229366302	0.834227398	30.02762413	29.87926483
Crip2	-0.023108006	0.087295157	29.75995827	29.51793861
Crk	0.061703682	0.154013305	24.96119881	25.15019417
Crkl	-0.703371048	0.473768012	22.80573654	20.44957733
Cryab	0.069995403	0.141554005	25.22567558	25.29516029
Cryl1	-0.116388321	0.18187806	24.64735222	24.9092598
Cryz	0.115751743	0.161737396	23.64746284	23.57172585
Cs	-0.072940826	0.108505817	29.95240974	30.18316841
Csad	-0.055038929	0.423403792	25.60102081	25.71235085
Cse1l	-0.172746658	0.499778376	27.08304214	27.69875908
Csk	-0.373658657	0.094679073	24.07871246	23.29501915
Csnk1a1	-0.526488304	0.417176593	22.69104385	22.37994003
Csnk2a1	-0.042280674	0.123500522	24.77006721	24.69285393
Csnk2b	0.103713036	0.163577718	23.57819176	23.97788429
Csrp1	0.148897171	0.370839499	30.09785652	29.67230988
Csrp2	0.279573917	1.081923915	29.66510963	29.42145729
Cst3	-0.430748463	0.093118253	20.24684143	24.26334572
Cstb	-0.067324638	0.148133737	25.49838448	25.90841293
Cstf2	0.285981178	0.472368939	23.2401619	23.59046555
Ctbp1	-0.116924763	0.338382459	24.85357666	25.20780373
Ctcf	-1.094777107	0.526880493	20.36894798	19.58022308
Ctnna1	0.208731174	0.867740003	26.28705978	26.59348869

Ctnna2	-0.00507021	0.009042345	22.51835823	23.03316879
Ctnna3	-0.226282597	0.114475808	22.51523209	23.18522453
Ctnnal1	0.042337894	0.060630537	23.78974915	23.70482635
Ctnnb1	0.025350571	0.034530502	25.95681953	26.1867485
Ctnnbl1	-0.754252434	1.118898021	20.9833889	19.86314583
Ctnnd1	0.069756985	0.162586788	24.61194992	24.72769928
Ctsb	-0.09815836	0.244325537	25.8439064	25.64135551
Ctsd	-0.176429749	0.730778191	27.48792076	27.85934639
Ctsh	-0.050832272	0.148808404	24.27141953	24.13029861
Cttn	0.066232681	0.096135982	24.59622192	24.73923302
Cttnbp2nl	1.162543774	0.696318842	21.97449303	22.9908371
Cul1	-0.217363834	0.204614172	22.64967728	21.68050194
Cul3	-0.120494366	0.261103492	22.68395233	23.10098076
Cul4a	0.107190132	0.403648113	22.38255501	22.2994709
Cul5	-0.437201977	0.295447478	21.6438427	22.87408257
Cuta	0.003725052	0.010333384	25.72145462	25.85043144
Cutc	-0.164737225	0.105260464	19.91231537	22.5797348
Cxcl12	0.075733185	0.034282865	20.885746	22.73322296
Cyb5a	-0.506489277	1.115722446	24.30500793	25.37109184
Cyb5b	0.310202599	0.75379391	23.82880974	23.35460854
Cyb5r1	0.455872536	0.609233125	23.98468018	24.38093185
Cyb5r3	0.134104729	1.163521182	30.09005165	29.99050713
Cybc1	-0.330804348	0.542533664	23.08516312	23.18213654
Cyc1	-0.065135956	0.092228197	27.15682411	27.40754509
Cycs	0.155739307	0.229096441	27.36118507	27.50256348
Cyfip1	-0.033795357	0.094769597	25.92725754	25.98428917
Cygb	-0.421719551	0.820417519	24.69853401	24.70408821
Cyp20a1	-0.276651859	0.593185756	23.11122322	23.58726311
Cyp2f2	0.22888279	0.125585396	21.67202187	21.75308609
Cyp4b1	0.023000717	0.048325588	21.20329285	20.74648857
D10Jhu81e	-0.024106026	0.049428022	27.49220657	27.99561119
Daam1	0.137265205	0.053865924	22.23864746	22.42601013
Dab2	-0.107289791	0.75801393	22.65510559	22.60118484
Dag1	0.224229813	0.910053174	26.58777809	26.26264763
Dars	0.066120625	0.404607632	26.40304947	26.52454948
Dazap1	1.386911869	0.991333882	22.18252945	21.55739975
Dbi	0.25147438	0.512944864	27.30860519	27.51758194
Dbnl	0.303606033	0.894095746	25.13606071	25.09083366
Dbt	-0.084015369	0.217132869	26.13586617	26.28489113
Dcn	0.099228859	0.507567645	32.52710724	32.5931015
Dcps	-0.784836292	1.218805311	23.24295616	23.4832077

Dctn1	0.115978241	0.337463411	25.72777748	25.84804535
Dctn2	0.051029205	0.135628481	26.50737953	26.4243679
Dctn3	0.978607178	0.769952311	22.32794762	21.92860794
Dctn5	0.11336422	0.088411626	21.60900879	21.23742294
Ddah2	0.218298912	0.983448186	26.62030792	26.64828491
Ddb1	0.048857212	0.205743598	25.13402557	25.25569534
Ddhd2	0.117966652	0.10234521	21.84473228	20.69445229
Ddost	0.179980755	0.966915402	27.06579018	27.17083359
Ddrgk1	-0.154101372	0.321270283	23.71208954	24.13547516
Ddt	-0.097459793	0.521333601	26.93966103	27.16920853
Ddx1	-0.02880621	0.085533299	26.75697327	26.88681221
Ddx17	-0.719148636	1.225128448	23.3013134	23.88836861
Ddx21	0.659347057	0.507861524	22.2870369	22.6842308
Ddx25	0.097173691	0.140251416	21.46238899	22.01998138
Ddx39b	-0.161455631	1.140970881	27.16930389	27.19516563
Ddx3x	-0.008786678	0.034508151	27.16374969	27.3944397
Ddx3y	-0.230748653	0.439435139	23.46749687	24.30619049
Ddx42	0.164587975	0.034454989	20.52866554	24.57721329
Ddx5	-0.064747334	0.200048095	26.80402756	27.01169395
Ddx50	3.056016922	0.719881258	26.3973465	27.21141052
Ddx6	0.010370255	0.021792734	22.44866753	22.81464195
Decr1	-0.002551079	0.004502291	28.3224678	28.56481743
Dek	-0.601313114	1.256628667	24.2437973	24.60540771
Derl1	0.629016876	0.783430492	23.60229492	23.66242599
Dhdh	-0.079171658	0.234075309	24.41538429	24.6746521
Dhrs1	-0.144222736	0.560488413	24.04268265	24.13719559
Dhrs7b	-0.625470638	0.401267733	19.52606773	22.32501221
Dhx15	-0.221403122	0.555030785	23.142519	23.80882263
Dhx29	-0.165678978	0.24103485	20.42506981	19.83699608
Dhx9	-0.173043728	0.5646067	26.51899338	26.89700699
Diaph1	-0.667241573	0.731527647	20.60094261	21.65913963
Dkc1	0.18623209	0.428656602	22.83209801	22.44164467
Dlat	-0.097628117	0.157344301	28.62072754	28.81711197
Dld	-0.036375999	0.05476581	28.07331848	28.4271431
Dlst	0.030176163	0.036973732	27.74746323	27.96691704
Dmd	0.032982826	0.159054111	29.73439217	29.87158775
Dmpk	0.456612587	0.673364109	23.11521339	23.98858643
Dnaja1	-0.079546452	0.072726577	23.89938354	24.39982605
Dnaja2	0.140731335	0.347324196	24.52772903	24.54827881
Dnaja3	-1.326421738	0.6266212	23.11013985	23.79094124
Dnajb4	0.14665699	0.374385333	25.75103188	25.8843441

Dnajc10	-0.21524477	0.301767758	23.00207901	22.24249077
Dnajc11	0.134235382	0.229034262	22.95221329	23.31299019
Dnajc3	-0.056228161	0.097203304	23.33742523	23.42111206
Dnm1	0.632845879	0.643636237	21.49492264	21.78735924
Dnm1l	-0.078848362	0.384921072	26.69245529	26.84505653
Dnm2	-0.037050247	0.126670144	26.13700104	26.43313599
Dock7	-0.084240913	0.12382067	23.45287132	23.43987083
Dpep1	0.018333435	0.045287818	28.62184525	28.20503807
Dpp3	0.034862041	0.050763418	23.75246239	23.84143829
Dpp7	0.03042078	0.053978567	21.68965912	21.95418549
Dpy30	-0.318422794	0.853310933	26.27326965	26.48861122
Dpysl2	0.087738037	0.552639476	29.60376358	29.6468792
Drap1	0.419731617	0.189920476	19.79514313	21.49511719
Dst	0.005829811	0.003117317	21.23701477	21.92585945
Dstn	0.053282261	0.157791745	31.12083626	31.21575737
Dtd2	0.64063406	1.144578664	22.39715195	21.93437958
Dtna	0.324570656	0.855473442	26.57758713	26.81164169
Dusp19	0.111412525	0.330695412	28.26628876	28.52790833
Dusp3	-0.001640797	0.009097687	25.79911995	25.92406464
Dync1h1	-0.006140232	0.026962863	29.64607239	29.72487831
Dync1i2	0.129072666	0.141307779	23.40093422	24.02495956
Dync1li1	0.171361446	0.898278787	25.25385666	25.54698563
Dynll1	0.033114433	0.171490119	27.49220657	27.84146118
Dynlrb1	0.706539154	0.488721321	24.4800663	25.00667381
Dynlt1	0.147241592	0.292696328	21.53919411	22.16582489
Dynlt3	0.905399323	0.61916846	23.16643715	23.45575714
Ech1	0.067955017	0.083978115	25.86540031	26.31357956
Echdc2	0.135474682	0.274980816	20.05271721	20.25845146
Echs1	-0.096655369	0.183631368	27.93982887	28.17845154
Eci1	0.033265114	0.035305912	28.24399757	28.42686462
Eci2	0.081393242	0.168509626	23.97709846	24.68239021
Ecm1	-0.014993191	0.034400277	25.43249893	25.19812965
Ecsit	-0.271515846	0.559787177	21.524683	21.67934227
Eef1a1	0.087480545	0.481849927	31.19929123	31.37331963
Eef1b	0.119135857	0.526047393	26.88378525	26.52483177
Eef1d	0.210659027	0.442323484	26.40509605	25.88439178
Eef1e1	0.142960548	0.350554344	21.84640121	21.53431129
Eef1g	-0.122993946	0.408383695	27.33756065	27.61750793
Eef2	-0.05855608	0.317871056	29.67185593	29.83694077
Efemp1	-0.15218401	0.466276665	27.91245079	28.06507111
Efemp2	-0.044258118	0.187186395	26.99085808	27.15701675

Efhd1	0.040663242	0.097667066	24.16061783	24.01920128
Efr3a	-0.162278652	0.260115286	22.28571129	22.89287758
Eftud2	-0.240797043	0.71522585	24.41441727	24.25385666
Egfr	-0.050537109	0.056024357	24.13688278	23.62889671
Ehbp1l1	0.067277431	0.155273297	22.82801437	23.30033684
Ehd1	0.1646595	0.595695898	27.69119072	27.5547924
Ehd2	0.005164146	0.022012234	31.8134861	31.92340851
Ehd3	0.356059551	0.641295048	22.04056168	22.5114727
Ehd4	-0.041295052	0.245157235	28.39059067	28.3972168
Eif2s1	0.322244644	1.027171281	24.76531982	24.51080894
Eif2s3x	0.018317223	0.039434179	24.33101273	24.61874199
Eif3a	-0.05309391	0.195480597	26.13412285	26.46906662
Eif3b	-0.21690321	0.51853654	23.83797836	23.6799221
Eif3c	-0.23903513	0.596408148	24.62561226	24.71847916
Eif3d	-0.08041048	0.143124843	23.71973228	24.3192749
Eif3e	-0.166686058	0.257191033	23.70049477	23.88212967
Eif3f	-0.412025452	1.258559575	26.0377903	26.14518738
Eif3g	1.063074589	0.738478339	23.27810097	23.15835381
Eif3h	-0.297520638	0.071505027	23.31561852	19.46909523
Eif3j1	-0.028189659	0.050689574	23.56208992	23.21787262
Eif3k	-0.219656944	0.643811109	23.40691376	23.57207298
Eif3m	-0.028717041	0.063637051	24.11052132	24.39342499
Eif4a1	-0.061619282	0.267319903	27.45002556	27.71482849
Eif4a2	-0.006748199	0.015594619	24.31118965	24.10381699
Eif4a3	-0.239799023	0.506080168	24.98246193	25.23194885
Eif4b	-0.128510952	0.091521934	25.87055969	25.8475666
Eif4e	0.323359013	0.876408181	23.01343727	23.50227356
Eif4g1	-0.303627014	0.522019708	24.01962471	24.41073418
Eif4g2	0.428677559	0.902351477	24.12186813	24.26449203
Eif4h	-0.129153252	0.683849538	25.43698311	25.37560654
Eif5	0.212378502	0.745842818	24.6105423	24.4274559
Eif5a	0.069833279	0.349736258	27.46839905	27.44963074
Elavl1	0.660917759	0.640720741	24.82624054	25.10573578
Elovl1	0.145040512	0.22700213	24.67071533	25.3036499
Emc1	0.26346159	0.748754315	23.9706192	23.64339447
Emc8	0.078438759	0.063671119	22.83439445	21.60259056
Emd	0.043158054	0.049528925	25.6537075	26.49414635
Eml2	0.069220543	0.307407774	26.65239334	26.93303299
Enah	0.140511513	0.424990134	27.30452156	27.54067421
Endod1	0.103750706	0.34739706	26.72780228	26.96884155
Eno1	-0.017283916	0.052846447	29.91342163	29.89125252

Eno2	0.221944332	0.10175653	19.89756966	21.04526901
Eno3	-1.348907471	0.517143831	23.3066082	24.28862762
Enpep	1.387796402	0.650406929	23.13381386	22.1692543
Enpp1	0.099663734	0.199723312	23.76304054	24.06529617
Enpp3	-0.125246048	0.399530727	24.68383598	24.79971123
Enpp4	0.065306664	0.116042658	21.44778633	21.4480381
Entpd1	-0.016931534	0.077758268	27.05682755	27.1399498
Entpd2	0.08845377	0.547057062	29.26010895	29.27675247
Epb41	1.088612556	0.796401136	23.67012024	23.49679947
Epb41l2	0.116186619	0.227911151	25.281147	25.49838448
Ephx1	-0.026206493	0.110388955	28.53534317	28.81130409
Ephx2	-0.505263805	0.870489981	24.76915932	25.27223778
Epn1	0.179525375	0.343178071	22.22125626	22.2835083
Epn2	-0.038054466	0.034695942	22.62609291	22.91239738
Eppk1	1.090432644	0.774062089	22.69850349	22.89737129
Eprs	-0.03626585	0.271712711	26.4360466	26.42017937
Eps15	-1.180955887	0.863199052	21.87150955	21.16870308
Eps8l2	0.792981148	0.612143271	19.89300728	21.74722672
Erap1	-0.134144783	0.099672359	21.16559601	23.29516029
Erbb2ip	-0.127054214	0.11020091	20.83182716	21.2455101
Ergic1	0.092006207	0.194276459	25.30326653	25.13430023
Erp29	0.014099121	0.035218169	24.64834023	24.45676041
Erp44	0.109712124	0.454607101	25.48271561	25.67521858
Esd	0.083991528	0.956142594	28.00785065	28.09642601
Esyt1	0.055150986	0.181645858	28.59665489	28.92119026
Etf1	-0.151554108	0.058063675	22.97601509	24.0077858
Etfa	-0.110780239	0.132874983	30.06303978	30.21847343
Etfb	0.012453079	0.015524232	28.51194	28.43678474
Etfdh	-0.154636383	0.292973773	26.4772892	26.45843506
Ethe1	0.151788712	0.186163908	25.09099579	25.57678032
Exoc2	0.546858788	0.442929987	20.42481422	21.94395828
Exoc6b	-0.266280651	0.682954314	22.93992996	23.36999512
F13a1	-0.08232832	0.600305671	27.10419655	26.98119926
F2	0.062363148	0.219748714	25.9862442	25.48443794
Fabp3	-0.032030106	0.026889771	25.14289284	25.06853867
Fabp4	-0.105353355	0.137264616	28.57967377	28.66661644
Faf2	-0.219882965	0.851185893	22.47516251	22.43086624
Fah	-0.094665527	0.233352012	25.79803085	25.97037697
Fam114a1	0.215253353	0.561663876	23.87408257	24.02106667
FAM120A	1.063603401	0.414245224	21.61295509	22.99986076
Fam129a	0.123778343	0.646813882	27.57123566	27.53267097

Fam129b	0.014713764	0.031967659	24.5182724	24.66476059
Fam162a	0.038000107	0.217317585	23.99152946	24.14156723
Fam175b	-0.669087887	0.855625962	19.5257473	20.77015686
Fam213a	-0.064660549	0.095759277	22.80291939	22.94922256
Fam50b	0.034074783	0.087050057	26.0277462	25.90736008
Fam98a	-0.228487968	0.298494195	21.07894135	21.79249191
Fam98b	-1.641573906	0.91339272	22.67178345	20.3831234
Farsa	0.074122906	0.177696925	25.07030106	25.30058098
Farsb	0.0545578	0.119616503	24.32182312	24.44088364
Fasn	-0.265231133	0.326220602	29.91127968	30.80624199
Fau	-0.260846138	0.886597871	25.35319519	25.7816925
Fbl	-0.104809284	0.13316847	24.95118141	24.99321556
Fblim1	0.109244823	0.559946954	30.0187664	30.24081802
Fbln1	0.014970303	0.020082177	23.97989273	23.24656868
Fbln1	-0.733127117	0.274755123	23.97438812	19.31196785
Fbln2	0.146187305	0.480727379	26.5435524	26.40194321
Fbln5	0.057639122	0.448602199	32.55593109	32.58300018
Fbn1	-0.065778732	0.400934354	33.15394211	32.99797821
Fbn2	-0.057299137	0.100223767	24.56656837	24.61532021
Fbxo2	0.389374256	0.623449167	22.10648537	22.71751595
Fbxo30	0.938150406	1.086845519	22.15295029	22.64193916
Fbxo6	-0.663291931	0.427200567	20.9642334	22.66826057
Fcgrt	0.13815403	0.052941013	23.71743202	23.89393234
Fcho2	-0.474270344	0.384042798	20.03705978	21.97868729
Fdps	-0.06191349	0.110124923	21.67297173	21.79594231
Fermt3	-0.378377438	0.24106613	23.80222893	24.03883743
Fetub	0.340463161	0.627021632	22.88171959	22.1434536
Fga	0.504131794	0.717084258	30.34064102	29.36026382
Fgb	0.572722912	0.858643665	31.24496269	30.20244789
Fgf1	0.220460892	0.144863143	21.99227333	22.55426407
Fgg	0.410741806	0.59070137	31.30644417	30.44726753
Fgl2	-1.060919285	1.01794191	20.41739845	20.4780159
Fh	0.051974297	0.073035742	28.57697487	28.87238121
Fhl1	0.011892796	0.081771101	29.86444855	29.86680794
Fhl3	0.299580097	0.691984954	24.44063187	24.17378998
Filip1l	-0.168264866	0.331525612	25.04701805	25.64449501
Fis1	-0.028856754	0.165566525	26.35863876	26.44314766
Fkbp10	0.283065796	0.810883835	24.07577896	23.71397781
Fkbp2	-0.332186222	0.859194468	23.94913483	23.84373856
Fkbp3	-0.779573917	0.335329455	22.89044762	20.56496048
Fkbp4	0.132615566	0.226779965	24.59588051	24.46973419

Fkbp9	-0.136005402	0.188874401	23.52133179	23.85528755
Flii	0.007236481	0.016150174	26.57773209	27.02062225
Flna	0.092729568	1.039025526	34.92362213	34.82373047
Flnb	0.130073547	0.487769355	27.54973412	27.65253067
Flot1	0.204302788	0.974187079	24.98489761	25.18812561
Flot2	0.188123703	0.717680256	25.36916161	25.47144127
Fmnl3	0.558428288	0.264964114	20.21497536	22.53300285
Fmo1	-0.081962109	0.486970584	26.91353607	27.01797104
Fmo2	-0.041926384	0.231287357	30.26595306	30.39335442
Fmo3	-1.139480591	0.949758802	23.65162849	23.37012672
Fmod	0.275642872	0.667940983	26.80353546	26.88331985
Fmr1	-0.110060215	0.240297	20.56308746	21.09410095
Fn1	0.260981083	1.175488573	31.98182487	31.69946289
Fnta	-1.321856022	0.727470133	20.33201218	23.26728058
Folh1	0.151384354	0.05080718	22.6528759	22.12133026
Fry	-0.226841927	0.037600632	25.40295029	26.10045052
Fstl1	0.073712826	0.160173015	23.28107452	23.04463577
Fth1	-0.157977104	0.7793167	26.77793694	26.87443542
Fundc2	-1.576900482	0.886647096	23.21870041	20.08012772
Fus	0.001475334	0.001815754	25.00573158	24.70709419
Fxr1	0.172223091	0.336388672	23.52205086	23.72640038
G3bp1	-0.236632347	0.730011536	24.85133743	25.28181839
G3bp2	1.692518234	1.144241984	23.3198967	23.12831688
G6pdx	-0.024579525	0.074330991	26.23432541	26.55838776
Gaa	0.334541798	0.428896963	22.00672531	22.55048752
Gabarap	-0.028036118	0.014315004	20.33839417	21.67793846
Gak	0.064891815	0.077468694	21.13433075	21.26504898
Galk1	0.12311697	0.204530061	25.07206154	25.5908947
Galm	-0.106181145	0.215829611	22.52995682	22.82683182
Gamt	0.200746059	0.461940956	23.59331894	23.49081612
Ganab	-0.166163445	0.924447958	27.5382328	27.72838783
Gapdh	-0.060293198	0.267313009	32.00068283	32.27844238
Gars	1.853736877	1.094794739	23.94216919	23.04708481
Gart	-0.238458633	0.489065814	23.97709846	24.03296661
Gbas	-0.148548126	0.395858713	23.94100571	24.26327324
Gbe1	-0.145986557	0.283184221	22.87274933	23.49594688
Gbp2	-0.43089962	0.740592682	23.69678497	23.99765778
Gc	-0.21313858	0.787185338	28.31012344	27.95598793
Gcat	-0.251189232	0.642590566	21.59441185	21.66405487
Gcdh	0.182087898	0.069179943	23.10828972	22.6117363
Gcn1	0.004926205	0.010315889	24.42104721	24.48775291

Gdi1	-0.048883438	0.26603617	27.06332207	27.2674942
Gdi2	0.049740314	0.263334301	29.15759468	29.33898544
Ggcx	-0.033967972	0.026101456	21.12237358	21.26109314
Gid8	0.475729465	0.917563875	23.09863663	23.18682671
Gimap4	0.546303749	0.297518813	22.41441727	20.31601715
Git1	-0.230033398	0.833568091	22.82902145	23.27526093
Git2	1.053547382	0.525417332	20.95965576	23.34095955
Glg1	0.157552719	0.875086392	25.58571815	25.71887016
Glo1	0.081397533	0.750373164	27.70536804	27.77152824
Glod4	0.034009933	0.074295702	25.26895905	25.61624718
Glrx	-0.080267906	0.124141437	24.85362434	25.81264496
Gltp	-0.169753551	0.390128383	23.30424118	23.40236664
Glud1	0.077620029	0.577843603	28.80654907	28.67475319
Glul	-0.432672024	0.607673326	25.38830948	25.59801292
Glyr1	-0.138494968	0.23528611	23.26785278	23.83855629
Gmfb	-0.0309062	0.012646357	21.02239227	23.61750793
Gmppa	0.124222755	0.372912512	23.161726	23.53504562
Gmppb	0.008634567	0.01846576	24.4667511	24.53070831
Gmps	0.813362598	0.539254723	23.05316353	22.92565918
Gna11	0.016092777	0.070568929	26.02123642	25.8901329
Gna13	-0.140210152	0.430496417	23.19096184	22.76805878
Gnai1	0.188326359	0.524031741	23.62811852	23.24703407
Gnai2	-0.01351881	0.073325965	27.96620178	27.93550873
Gnao1	0.401932716	1.290463818	25.81604385	25.74314308
Gnao1	0.345319748	0.976858027	23.21102524	23.11985779
Gnaq	0.145722389	1.127468855	26.01620674	26.07855034
Gnas	-0.132884026	0.800020957	25.85248184	25.94534302
Gnb1	-0.070222855	0.333594128	26.30455589	26.18046379
Gnb2	0.116326332	0.534481373	27.81451797	27.70681763
Gnb2l1	-0.05505085	0.217438457	26.88261986	27.03149414
Gnb4	1.555021286	0.714660016	20.75059128	23.76273727
Gnpda2	-0.51416254	0.378426779	20.29561806	22.35329056
Gnpnat1	-0.216300011	0.210204209	20.27584839	21.76453972
Golga2	0.278148174	0.143352962	21.09448814	22.07372093
Gorasp2	0.286891937	1.052763167	23.56488419	23.54179573
Gosr2	-0.262347221	0.160197351	21.14432526	20.77571297
Got2	-0.082381725	0.378087581	28.74957466	28.94815445
Gp5	0.200482368	0.102954631	23.06899071	22.23321533
Gpc4	-1.700539589	1.196346569	20.27596474	19.53022575
Gpd1	-0.362633228	0.295192175	27.55691147	28.15272141
Gpd1l	-0.095249653	0.222451379	26.3537674	26.58849335

Gpd2	-0.079981804	0.09594453	28.31324196	28.72789955
Gpi	0.009307861	0.046671926	29.93297768	30.14673805
Gpnmb	-1.839092255	0.904303441	20.51623917	20.71952248
Gps1	0.449738026	0.325274112	22.08173752	22.25361252
Gpx1	0.106138229	0.540535051	28.54414177	28.69368553
Gpx3	-0.16533947	0.905113078	28.88273621	29.01573944
Gpx4	-0.148204327	0.355296516	23.84823608	24.03305054
Gpx7	0.19753027	0.552507572	23.24580193	23.48885536
Grb2	-0.025794506	0.026794003	24.31215858	23.31699944
Grhpr	-0.131929398	0.331291335	26.54176712	27.09264946
Grn	0.18861866	0.345723033	25.34177399	24.9718914
Grpel1	0.044831276	0.017384471	22.15579414	22.51665115
Gsk3a	0.115463257	0.054557864	21.8644619	22.17105865
Gsk3b	-0.01213932	0.057762353	22.88624954	22.79008675
Gsn	0.228021622	1.204809427	30.50417328	30.35142326
Gsn	0.047690392	0.088810556	23.76779556	24.3997612
Gsr	-0.019433975	0.037503278	24.81220436	25.12750626
Gss	-1.692577839	0.896160227	20.67372894	23.688591
Gsta3	-0.302276134	0.197917196	22.42272949	20.96564293
Gstk1	-0.14204216	0.864643896	25.47246361	25.55177307
Gstm2	-0.051552773	0.243669041	29.23233223	29.31291771
Gstm5	0.028856277	0.077040417	24.5133419	24.39630127
Gstm7	-0.243318558	0.576157797	23.26913643	23.26298714
Gsto1	0.068773746	0.268120662	23.48197746	23.86315727
Gstp1	-0.010990143	0.028948321	30.44608498	30.4841423
Gstt1	-0.234376431	0.853838137	27.34916878	27.67714119
Gstt2	-0.057165623	0.075066923	23.57276726	23.55414772
Gstz1	-0.393967628	1.072298914	25.02136421	24.93530655
Gtf2i	0.436861038	0.130165338	23.63300705	23.42560005
Gucy1a3	-0.156480789	1.007126987	27.29245949	27.36919594
Gucy1b3	-0.021048546	0.036628821	25.4789257	26.09043121
Gulp1	0.274913311	0.831008364	24.67276573	24.19670486
Gyg1	1.108811855	0.628399588	23.43224335	23.29628181
Gys1	-0.410912991	0.461078287	21.9842968	22.35589981
H1f0	0.102053165	0.37437955	29.04374695	28.76771355
H2-Aa	-0.76551342	0.775820775	20.35422516	20.34022713
H2-D1	-0.176886082	0.406712102	25.43669701	25.02301407
H2-K1	-1.509066582	0.964634243	19.46066284	22.62348175
H2-Q10	-0.433310509	0.764865821	24.19151878	23.27326965
H2afv	-0.192457199	0.718141754	27.6274929	27.02981186
H2afy	-0.20872736	0.895704033	28.25042725	28.38179016

H2afy2	0.090472221	0.234140241	24.04159737	24.24959564
H3f3a	-0.244657993	0.648286038	31.88928795	32.35969162
H6pd	0.091081619	0.139595235	23.9616394	23.63212013
Hadh	-0.21903801	0.311831827	29.63834	29.74979973
Hadha	-0.156888485	0.234272248	30.5229969	30.93417168
Hadhb	-0.080850124	0.090639789	29.69052505	29.99374962
Hagh	-0.189793587	0.524937957	22.66888809	22.64972115
Hamp	0.31038475	0.801303612	22.85944557	22.82302666
Hapln1	-0.703884125	0.296798158	20.05722237	23.92913246
Hars	1.521865845	0.800170824	24.64476967	24.5693531
Hax1	-0.269219875	0.462438302	21.01181602	21.09145546
Hba	-0.08118248	0.152551441	34.79105377	33.992939
Hbb-b1	-0.147515297	0.258541819	34.88212585	33.99175644
Hbb-b2	0.227172852	0.154041313	26.76875496	25.25104141
Hbb-bh1	1.052812576	1.118670565	22.95077324	22.52552032
Hcfc1	-0.034957886	0.066022023	23.72348595	24.1070137
Hdac2	-0.343112946	0.463907141	22.50460434	23.31271362
Hdgf	1.00143671	0.386805598	24.42751884	24.59821129
Hdgfrp3	0.259008408	0.363407341	25.13175201	25.56241035
Hdhd2	0.936766148	0.582580411	24.50379181	24.68511963
Hdlbp	0.156442165	0.71907329	25.46257591	25.47472382
Hexa	0.06298399	0.346844894	23.20164871	23.37411308
Hexb	0.505712509	0.545478899	21.26272011	21.99144363
Hgs	0.133899689	0.306714255	21.90642738	21.56113434
Hibadh	-0.005980492	0.018339778	26.67559433	27.01818275
Hibch	0.117986679	0.173222013	25.73166656	25.98361397
Higd1a	-0.099011898	0.167857824	21.36035347	21.85923767
Hint1	-0.084648609	0.755400379	27.80168724	27.70806694
Hint2	-0.00412035	0.011482461	24.94480705	24.99679565
Hip1	-0.336651325	0.460539171	24.51092911	24.63173103
Hist1h1a	-1.660927773	1.274505034	24.24510384	24.56801987
Hist1h1b	-0.524837971	1.275537185	25.58657646	25.91230202
Hist1h1c	-0.306052685	0.754364594	29.15583611	29.41354942
Hist1h1d	-1.43915987	0.566176073	23.61099243	21.41476822
Hist1h1e	-0.056037903	0.099230337	29.04739189	28.7107296
Hist1h2ah	-0.525030136	0.223343404	24.05291557	25.41199493
Hist1h2bp	-0.217025757	0.462815145	32.81657791	32.50308609
Hist1h3a	-0.036213875	0.063869456	29.88497925	30.05115891
Hist1h3b	-0.170877457	0.397061286	32.094841	32.07562256
Hist1h4a	-0.174758911	0.536921274	32.51789093	32.69235229
Hist2h2ab	0.037199497	0.065283538	23.79946518	23.55098152

Hist2h2ac	-0.332463264	0.858110433	32.71616364	32.60939789
Hk1	0.030592918	0.122888597	27.74464417	28.06486511
Hk2	0.031122208	0.032202668	25.55045319	25.88012314
Hmbs	-0.236418247	1.079241466	22.52566338	22.79697227
Hmgb1	-0.284488201	1.110984218	29.41687393	29.28252983
Hmgb2	-2.304348469	0.744024055	21.11600494	19.45676804
Hmgcl	0.033202171	0.055519855	23.48000526	23.89670563
Hmgcs2	-0.245805264	0.13519108	20.82036209	22.70617676
Hmgn2	0.044405937	0.129424764	22.8589344	22.75242233
Hmgn5	0.868988514	0.749843146	23.49838448	23.68709755
Hmox2	0.494164467	0.211193921	23.82648277	23.0506916
Hnrnpa0	0.471336842	0.32686004	21.95748329	21.63900566
Hnrnpa1	-0.135269642	0.435303733	24.92442703	25.18021774
Hnrnpa2b1	-0.031232357	0.07656081	28.15213966	27.80931282
Hnrnpa3	0.084713936	0.222918071	28.39823723	28.15995407
Hnrnpab	-0.006546021	0.027701238	26.56891823	26.51401901
Hnrnpc	-0.047374249	0.104509762	24.81811905	24.73334885
Hnrnpd	-0.042480946	0.123259256	27.07785797	27.19413376
Hnrnpdl	0.195519447	0.533884601	22.7858429	23.15568542
Hnrnpf	-0.285405159	0.712803463	24.93413544	25.23052025
Hnrnph1	-0.083388329	0.214327698	26.76407814	26.44197655
Hnrnph2	0.224895954	0.427902508	24.02233696	24.24713516
Hnrnpk	-0.132106304	0.459972664	28.56015968	28.85424232
Hnrnpl	-0.004099369	0.008685732	27.52991867	27.63478088
Hnrnpll	0.21228075	0.320945541	23.45838928	23.7091465
Hnrnpm	-0.113491058	0.542672966	26.93842697	27.21752548
Hnrnpu	-0.067111015	0.346231876	28.68849182	28.79398918
Hnrnpul1	0.696953297	0.167892773	23.9900589	20.52280998
Hnrnpul2	-0.087050438	0.406195518	24.71816444	24.95615387
Hook3	1.484453201	0.93089006	22.00370789	22.20732117
Hoxd8	-0.637834072	0.602628583	20.70288086	20.86423492
Hp	-0.745884895	0.307461548	22.42580414	20.24088097
Hp1bp3	-0.007847786	0.024108781	27.74970245	27.92677116
Hpcal1	-0.038732052	0.042489347	23.1678772	23.85176659
Hprt1	-0.351793289	0.511488665	23.25738716	24.42258835
Hpx	-0.167945385	0.421933949	28.22595978	27.79754829
Hsbp1	-0.04545784	0.009727636	20.09339142	24.48019028
Hsd11b1	-0.237752914	0.09185042	21.80369759	21.99992943
Hsd17b10	-0.012997627	0.035739029	28.12435532	28.20713425
Hsd17b12	-0.11417675	0.546028521	25.67583656	25.93559837
Hsdl2	1.72359705	0.994454746	23.70967293	24.19618034

Hsp90aa1	-0.097835541	0.578936572	28.01350403	28.24163628
Hsp90ab1	-0.123443127	0.64789416	29.78509712	29.84719467
Hsp90b1	0.048792362	0.164013032	29.52518463	29.5117321
Hspa12a	0.396568775	0.645563204	24.10477638	24.31492805
Hspa12b	-0.023220539	0.060453198	25.77210808	25.80626678
Hspa1a	0.031219959	0.169952287	29.11284447	29.17159653
Hspa1b	-0.716973305	0.411680471	24.65419769	21.88005638
Hspa2	-0.181988716	0.556987135	26.98315811	27.21039009
Hspa4	-0.026486874	0.125831183	27.6224041	27.67532539
Hspa4l	0.217271805	0.450859462	23.79302788	24.1231308
Hspa5	-0.014383316	0.036091809	29.61433411	29.52232361
Hspa8	-0.007498264	0.049639832	30.95601654	30.9856987
Hspa9	-0.000939369	0.001657128	27.9596405	27.89486885
Hspb1	0.03622961	0.158353892	29.94823837	29.88337708
Hspb6	0.149028778	0.450838905	26.63394928	27.02083397
Hspb7	0.307779312	0.940128366	25.40272331	25.22872353
Hspb8	-0.039201736	0.089994161	24.03414345	24.38686371
Hspd1	-0.115259171	0.43700781	29.71256828	29.86823654
Hspg2	0.083109856	1.004842789	33.60774612	33.56422424
Hsph1	-0.037275791	0.106481424	24.69131088	24.80267334
Htra1	0.206830978	0.564925892	27.38977051	27.27746201
Huwe1	-0.291837215	0.610481651	23.30883026	23.98693848
Hyou1	-0.126718044	1.013772941	26.40512848	26.47716713
Iah1	-0.17766571	0.531982568	22.2980175	22.55595016
Iars	0.891998768	0.825099883	22.80764389	22.42370415
Iars2	-0.11136961	0.322525546	26.2824192	26.52351761
Icam1	1.418144226	0.729151903	21.89418983	22.62620354
Icam2	0.6755867	0.405363041	20.86488342	22.93653679
Ide	0.202030659	0.23052903	22.84781647	22.78374672
Idh1	0.008660316	0.025247479	27.35816956	27.7358284
Idh2	-0.138422012	0.483414034	29.33515549	29.50546265
Idh3a	-0.00012064	0.000129579	29.46524811	29.67123032
Idh3g	-0.072813034	0.074236193	27.12612915	27.37856865
Ifi35	0.10705328	0.105140253	22.00061798	21.74139404
Igbp1	0.315267563	0.968897073	22.15690613	22.76670456
Igfals	-0.239654541	0.297682406	21.09526062	20.88223648
Igfbp6	-0.277768135	0.592514072	23.98320198	23.84018898
Igfbp7	0.276018143	1.024477783	28.01361084	28.10454559
Igh-3	-0.70055294	0.836471359	25.79647255	24.7710247
Ighg1	0.820037842	0.500670119	23.05080795	21.09921646
Igkc	-0.548035622	1.077417529	26.0720005	25.35927582

Ikbip	0.026838303	0.096583512	21.92317581	21.62506676
Ikbkb	-0.40597105	0.558903984	20.67115784	21.55140495
Ilf2	-0.067592621	0.186214385	23.93093681	24.41589928
Ilf3	-0.379234791	0.211992552	23.07349205	20.70246696
Ilvbl	-0.230368137	0.112557955	21.23975372	21.28229141
Immt	0.099254608	0.283434527	28.00372696	28.03862953
Impa1	-0.089402676	0.309736142	25.12155151	25.22044373
Inf2	-0.031744957	0.087298677	23.42803001	23.99222183
Inmt	-0.147054195	0.259674231	26.67532539	26.37466049
Inpp1	-0.122152805	0.457384612	24.28100395	24.56674194
Ints3	-0.021615982	0.011771903	20.33374214	21.10162163
Ipo4	-0.130344868	0.087313407	21.68478775	21.87886047
Ipo5	0.268226147	0.922290255	25.84491348	26.07449341
Ipo7	0.004541874	0.005867087	24.21556473	24.64019775
Ipo9	-0.093484402	0.049655843	20.84390831	23.02076149
Iqgap1	0.08523941	0.999362345	29.18595886	29.30317116
Irf2bpl	0.118895054	0.664823251	27.00785065	27.09164238
Isg15	-0.889184475	0.665600792	20.4726429	22.8999176
Islr	0.175852299	0.259533567	27.18120384	27.75136375
Isoc1	-0.866475105	0.681441916	21.78680038	20.29142761
Isoc2a	-0.04929781	0.162776895	27.1662426	27.30817223
Isyna1	0.059637547	0.043501817	22.32064056	23.01605797
Itch	1.101051807	0.738662718	21.92542458	22.22608566
Itga1	0.188559532	0.323032435	23.31160545	23.35366631
Itga2b	0.53132534	0.3186259	25.12364388	24.27675247
Itga3	0.082457542	0.289679705	26.03206253	26.20890236
Itga5	0.002038956	0.009567023	25.87780762	25.8275013
Itga6	0.530888557	0.196843893	19.27454185	22.12053871
Itga8	-0.018790245	0.064011694	30.22871399	30.25157928
Itga9	0.223595142	0.731251933	25.79634857	25.92583084
Itgav	-0.06551075	0.340803136	27.44537544	27.36352539
Itgb1	0.147577286	0.913432461	30.67261505	30.75198746
Itgb3	0.180078506	1.192598921	25.33128738	25.26298714
Itgb5	0.039982796	0.074659869	26.16999245	25.79191017
Itgb6	-0.076819897	0.281853267	26.52445984	26.80217934
Itih1	-0.271115303	0.625864912	25.97079468	25.80862617
Itih2	-0.337211609	0.437841645	24.84689903	24.42258835
Itih4	-0.223635674	0.735029684	25.31979179	24.8601284
Itpa	0.108469009	0.173012979	24.73324394	24.88460159
Itpr1	-0.024681091	0.055221002	26.35670853	26.75468063
Itpr3	-0.094249725	0.334246089	23.10782814	22.85365295

Ivd	-0.337821484	0.831673693	26.81213188	26.8836689
Jak1	-0.244308949	0.498305974	22.62471008	23.10234261
Jph2	0.073901176	0.125940573	23.6118927	24.3773613
Jup	-0.977134705	0.897340914	22.5522728	22.47640038
Kank2	0.0120368	0.064663155	27.28224182	27.49990463
Kars	-0.051843643	0.127179147	24.61599541	24.88697433
Katnal2	-0.060902596	0.157282107	24.78830528	25.21852303
Kcmf1	1.000825882	0.453967348	23.20356178	23.39532089
Kcnk4	-1.43139267	0.380601871	20.03161049	26.50087738
Kdelc2	0.131997585	0.384992427	24.96022606	25.23976135
Kdsr	0.016089439	0.007032476	22.68555832	21.16329002
Khdrbs1	-0.244519234	0.823620629	23.54321289	24.05531693
Khsrp	0.059247971	0.158092808	25.64044571	25.3415699
Kiaa0196	1.050205708	0.71690172	22.26040459	22.73291397
Kif13a	-0.125630856	0.208918063	22.69725227	23.11691093
Kif3a	-0.624766827	0.741620091	21.69629669	21.86476326
Kif5a	-0.110375404	0.113841967	23.85214806	23.90472031
Kif5b	-0.241363049	0.952145699	24.69407654	24.96380234
Klc1	-0.195312023	0.418440288	23.95278168	24.32251167
Klk1b27	-2.36823988	0.688268695	20.13703918	19.40500069
Kmt2a	-1.322288036	0.821006037	22.80388451	23.12254715
Kng1	-0.086666107	0.19734234	27.26901245	26.62226486
Kpna4	-0.167156696	0.444002745	24.89003944	25.16564751
Kpna6	-0.556573391	0.657185988	23.83903694	24.74750328
Kras	-0.08105135	0.235961066	24.41628647	23.96842384
Krt81	-5.238294601	1.129873852	24.12407875	20.9010334
Krt83	-3.170921803	1.026907289	23.24179268	21.49882126
Krtap14	-4.075039864	1.283253467	19.62823105	21.4608078
Krtap15-1	-3.451173306	1.193364088	20.68249893	20.63568115
Krtap19-5	-3.064190388	1.27250087	21.606884	19.24315834
Krtap3-1	-1.821218014	0.884989952	21.22794342	18.93153191
Krtap7-1	-4.039756298	0.68775221	25.0694828	20.55758476
Ktn1	-1.575419903	0.986237763	19.75471497	18.62550545
L3hypdh	-1.052731037	0.653710983	20.60993195	19.94429779
Lactb2	-0.829219818	0.420335446	23.09274673	22.11279869
Lama2	0.275167465	0.555498381	26.13899231	26.12026596
Lama4	0.045531273	0.174139525	28.52798271	28.38759422
Lama5	-0.018876553	0.092768693	29.83558655	29.85508919
Lamb1	0.279755116	0.323390729	25.03178978	24.99403572
Lamb2	0.00147438	0.005797338	30.77439117	30.61868095
Lamc1	-0.010967731	0.029406212	29.86067963	29.61487961

Lamp1	0.611097336	0.332642355	23.2424469	22.92940331
Lamp2	0.014429569	0.044268062	24.65233994	24.75287056
Lamtor1	-0.008638859	0.005444454	23.47171974	23.17316437
Lamtor5	-0.807964325	0.578188234	22.22337723	23.64030838
Lancl2	-0.488975048	0.305206588	20.59902573	23.27710724
Lap3	0.079027653	0.345665837	25.27895164	25.39715195
Lars	0.579282761	0.700649865	21.01923561	21.05675697
Lasp1	0.022983551	0.045865661	24.30674744	24.48246956
Lcp1	-0.457569122	1.143089635	24.46830559	24.81264496
Ldb3	0.047653675	0.142720133	27.85578728	27.87061882
Ldha	-0.113595963	0.42133966	29.42119598	29.65440941
Ldhb	-0.145787716	0.525641332	27.14753914	27.50271416
Lect1	1.745850563	1.093913755	24.04909706	24.54150009
Lemd2	0.367120743	0.929596936	24.63212013	24.32930374
Leprel2	0.164515972	0.415284447	21.38690186	21.56299973
Letm1	0.096612453	0.207237427	25.97116852	26.26712036
Letmd1	0.110895157	0.047197176	23.60523796	25.39845657
Lgals1	0.176759243	1.061855564	31.9256382	31.81367683
Lgals3	0.818135262	1.132743953	25.70255661	25.77140236
Lgmn	-0.317374229	0.401228267	23.32978249	22.20922661
Lifr	-0.13017416	0.232558839	27.18678665	26.35566711
Limch1	-0.223662853	0.451262078	23.61560249	24.10309601
Lims1	0.038398266	0.255719169	27.2123394	27.37575531
Lims2	0.064538479	0.247030958	26.45221138	26.67532539
Lipa	-0.437417507	0.655177122	21.5985527	22.69822693
Lipe	-0.550319672	0.694747835	26.16878891	26.23198509
Lman1	0.262961388	0.650574716	25.76984024	25.70223999
Lman2	0.245860577	0.459689756	24.16469002	24.35897446
Lmcd1	-0.037926197	0.186479361	28.79293442	28.67999649
Lmf2	1.252511024	0.53817942	23.97035599	23.60206985
Lmna	0.122790337	0.463292702	31.52840996	31.34408569
Lmnb1	-0.243190765	0.960589384	27.70563126	27.87355423
Lmnb2	0.031430244	0.197643192	25.86076736	25.73347664
Lmod1	0.066597462	0.295180072	28.304739	28.46041298
Lnpep	-0.179834366	0.550388866	24.40723801	24.66041374
Lonp1	-0.175330639	0.611198107	25.31468582	25.54939651
Loxl1	-0.025512218	0.147437348	30.18978119	29.99334526
Loxl3	0.210427284	0.386378223	23.05284882	22.89141273
Lpl	0.41982317	0.217041932	21.41364288	20.06941605
Lpp	0.189660549	1.104615419	31.05484962	31.24246597
Lrp1	0.03401947	0.252832196	28.13349724	28.19408607

Lrpap1	0.280653	0.900854118	24.69381142	25.00414658
Lrpprc	-0.041917324	0.185855994	26.36367607	26.40948868
Lrrc17	-0.05227232	0.073590163	28.02178764	28.40867996
Lrrc39	0.49332428	1.117618913	22.76579475	22.88890839
Lrrc40	-1.270496368	0.642853951	24.31236649	24.36746407
Lrrc4c	2.375864983	0.757559948	25.08172226	20.12498093
Lrrc59	-0.072156429	0.22229782	26.32890892	26.32784843
Lrrfip1	-0.011092663	0.020409429	25.33469963	25.13382912
Lsm3	0.494785309	0.367846452	22.59882545	22.45480347
Lsm5	-0.413800716	0.261011121	21.89148712	19.87336349
Lsm7	1.147771358	0.655568301	24.62572479	24.2228775
Lta4h	-0.078971386	0.451536042	27.19751167	27.37085915
Ltbp1	-0.183403492	1.191388783	28.53363609	28.51216698
Ltbp2	-1.506007671	0.737074371	20.41333199	19.64944267
Ltbp3	-0.021269321	0.0370323	23.83999634	24.15475845
Ltbp4	-0.12997961	0.723473776	30.74703217	30.63918686
Luc7l2	-0.581267357	0.253340933	22.0293808	22.22107887
Luc7l3	-0.051635265	0.065885549	23.06307602	23.14086533
Lum	0.128063202	0.768348889	32.60831833	32.67629623
Lxn	0.095737934	0.229482072	25.83612442	25.44404793
Ly6a	-0.259973526	0.681553897	23.35555077	23.16320038
Ly6c1	0.097661495	0.181522227	24.36372566	24.58657646
Lypla1	-0.043151855	0.066585363	26.35129356	26.66234398
Lypla2	0.011380672	0.017096223	24.85362434	24.87890816
Lyrm5	-0.086666107	0.097061623	20.66327286	21.37962341
M6pr	0.717637062	0.89989619	24.30145454	24.93822479
Macf1	-0.430117607	0.698649369	24.20314407	24.72291374
Macrod1	-0.128229618	0.363748007	25.58325195	25.9623909
Man2c1	-0.446096897	1.106659514	22.95530319	23.778162
Manf	0.154394627	0.297551369	25.1764946	25.03204155
Maoa	-0.140217781	0.152045034	23.30507851	24.11179543
Maob	-0.141768456	0.901110493	26.55956841	26.7888031
Map1a	0.523739815	0.462735549	25.05490303	25.83646202
Map1b	0.240746975	0.888387974	27.94044495	28.05982018
Map1lc3a	0.354236126	1.224413256	24.06587219	24.34204483
Map1lc3b	0.297087193	0.774890301	24.85424232	24.82943916
Map1s	0.017912388	0.020551489	22.33510971	23.29221344
Map2k1	-0.096850395	0.589120337	24.96767616	24.92075348
Map2k3	0.358457565	0.323548325	21.83922768	22.18549728
Map2k4	1.597585678	0.825593826	22.96185112	22.76775551
Map3k19	0.845505714	0.410460714	23.8834362	23.64614296

Map4	0.06970787	0.178538543	26.4855442	26.44833946
Map6	1.397093296	0.744960866	19.62213707	23.27398109
Mapk1	0.138703823	0.227573665	26.18604851	26.09315491
Mapk14	-0.566809177	0.484390374	22.07107162	21.78640175
Mapk3	0.284298897	0.600016304	24.40282059	24.75087929
Mapre2	0.253111362	0.785015359	24.35083771	24.2854557
Mars	0.965010643	0.41876881	20.78492928	22.86977959
Marveld1	-0.148269653	0.059956837	22.49850464	19.41157532
Mat2a	0.181400776	0.14585433	22.61652184	22.27571487
Matr3	-0.05585289	0.137984287	26.62226486	27.06116104
Mb	-0.445954323	0.292569513	23.66242599	24.83740044
Mbd2	0.500824928	0.359966373	21.88464737	22.06305885
Mbl1	-0.094364166	0.235818509	24.03590584	23.68901825
Mbl2	-0.422938347	0.28246702	21.62533379	21.13295174
Mbnl1	-0.067630291	0.144299242	24.99722672	24.9269619
Mboat7	0.258487701	0.853808792	22.0290451	22.06825256
Mbp	3.443705559	0.474648158	19.17723465	15.48871899
Mccc1	-0.151192188	0.436572333	25.34102821	25.39463425
Mccc2	-0.349367142	1.108508361	24.85195732	25.44887543
Mcee	-0.702640533	0.378163997	22.89454269	23.15804672
Mcfd2	0.428349018	0.162178197	22.4201088	23.14507103
Mcpt3	0.142730713	0.199980831	22.63049889	22.2681942
Mcpt4	0.308060169	0.426685675	27.96911621	27.62561226
Mcu	-0.917449951	0.493229324	20.42300987	23.60433388
Mdh1	-0.052687645	0.15067249	28.58652687	28.61006355
Mdh2	-0.134683609	0.34033638	29.93058205	30.06046486
Mdp1	0.511753559	0.461851816	23.34055138	23.48946953
Me1	-0.10766077	0.399022233	27.23516655	27.57751465
Mecp2	-0.207092762	0.60011674	24.90237617	25.4650383
Mecr	-0.02098465	0.020910454	25.62078476	25.96121979
Megf6	-0.243921757	0.101792758	22.74777985	20.666605
Memo1	0.107573986	0.287847929	22.7440052	22.5797348
Metap2	-0.435365677	0.158178953	20.60490608	22.27403831
Mfap2	0.011942387	0.020903924	25.84529495	25.51171494
Mfap4	-0.087651253	0.154011228	31.01038742	31.2536087
Mfap5	0.015072346	0.020724053	26.99150848	26.64168549
Mfge8	0.084208012	0.361669616	29.60121536	29.56699562
Mfn2	-0.696813583	0.337492301	22.88222313	22.56148529
Mgp	0.008347988	0.018350181	24.27824211	24.28411484
Mgst1	-0.467947006	0.576421139	24.79907036	24.87539673
Mgst3	-0.061410904	0.053719818	22.13144493	22.65208817

Mical1	-0.009108067	0.012215787	23.74816895	24.36472893
Mical2	0.288770199	0.078617417	23.89217377	24.30820656
Micall1	1.018857479	0.637990829	22.45671082	22.30215073
Mif	-0.027348518	0.127634649	27.85453987	28.02786255
Minos1	0.285999298	0.614283019	24.74611855	25.22221375
Mlec	-0.54598856	0.439886548	20.75232697	22.44440269
Mmaa	0.319930553	0.404539695	21.48044968	21.52171516
Mmgt1	0.488736629	0.685115775	20.40520859	20.99313164
Mms19	-0.015387535	0.016547477	21.16263199	22.28990936
Mns1	1.530734062	0.534584825	26.19730568	23.8451767
Mogs	-0.271672726	0.961889079	22.44685173	22.46587944
Mp68	0.032416821	0.090450149	24.68346024	25.01077652
Mpc1	-0.325597286	0.555499748	24.95690727	25.37970924
Mpc2	-0.135727406	0.302792576	26.18391228	26.43809509
Mpp1	0.058352947	0.068155373	24.43765068	23.38863754
Mpst	-0.01870966	0.036670751	22.90789604	22.1918354
Mpz	2.557182312	0.816513741	26.03720474	23.52276993
Mrc1	0.161303997	0.500513907	26.28439713	25.91077042
Mrc2	-0.182098389	0.702134258	22.66953659	22.87549019
Mrgprf	-0.331064224	0.275393703	23.20396423	23.53005219
Mri1	-0.127463341	0.04847976	23.91433334	24.16675949
Mrpl12	-0.433162689	1.065457582	22.43374634	21.58218575
Mrps36	-0.195793152	0.25028697	25.19411469	24.99886322
Mrvi1	-0.194560528	0.360438687	23.55297661	23.91870689
Msn	0.121212006	0.677627986	30.4152832	30.25518608
Msra	-0.417756557	0.149004429	23.72317505	19.64627457
Msrb3	-0.189730644	0.39581075	25.13684464	25.00384521
Mtap	0.020746231	0.073977428	26.11894035	26.28429222
Mtarc2	0.01585865	0.039696485	24.96807098	24.84598923
Mtatp8	0.016730785	0.062747754	25.89272881	26.12760544
Mtch2	-0.072988987	0.23917923	27.15585899	27.60900688
Mtco2	0.108239174	0.133246858	28.97070694	29.38333702
Mtfr1l	-0.600682735	0.366775766	23.50190926	23.49643517
Mthfd1	0.033802032	0.088038784	25.49786568	25.12518311
Mthfd1l	-0.271491051	0.195519142	21.97046089	23.44897079
Mtnd4	-0.567676544	0.381721243	22.46918678	19.8863678
Mtnd5	-0.23272562	0.228603506	22.4169693	22.73723221
Mtor	0.497853279	0.811629408	22.22293663	22.04393578
Mtpn	-0.059993744	0.272487743	27.04019737	27.19159508
Mtx1	-0.266900063	0.111621387	22.76395226	23.01969337
Mtx2	0.03480196	0.065111165	24.71103859	24.80607033

Mug1	-0.231517792	0.781494824	28.75792694	28.19394493
Mut	-0.081791878	0.122557645	23.96859932	23.89818382
Mvp	-0.003957748	0.01976361	26.89052773	27.00966644
Myadm	0.2443223	0.802091401	24.72234154	24.53801155
Mybbp1a	-0.289583683	0.768937685	24.94445038	24.98058891
Mycbp	0.241936684	0.599849459	22.19838524	22.49228287
Myd88	-0.045521259	0.076780431	20.93128014	21.0633564
Myg1	0.191912651	0.146461772	21.868536	22.34751701
Myh10	0.001768589	0.010392259	30.03642845	30.10337067
Myh11	0.139996529	0.635192074	34.66172028	34.42160416
Myh11	-0.006118774	0.008397252	23.36546326	23.00324631
Myh14	0.156035423	0.262497861	26.9871769	26.59448624
Myh4	-2.018617153	0.366229019	22.79778481	24.0952282
Myh9	0.055650234	0.332902641	29.14011955	28.97533417
Myl1	-0.472912788	0.240669194	26.70028305	26.58448601
Myl12b	0.156806946	0.697625142	27.19281769	27.33756065
Myl6	0.046937943	0.24173997	31.93029976	31.89439201
Myl9	0.208859444	1.240568788	30.86326599	30.64022064
Mylk	0.100126743	1.268739888	30.3348999	30.41336823
Myo18a	1.109720707	0.468092091	20.31375504	23.07706642
Myo1a	-0.096738815	0.037275167	21.21936798	23.30410194
Myo1c	0.110252857	0.951634683	30.19519043	30.2720871
Myo1d	-0.022123337	0.038153145	25.15657425	25.44663811
Myo9b	0.345799446	0.563773203	21.81686974	21.71703529
Myof	0.102907181	0.483886787	27.34214783	27.44387436
N/A	0.291443348	0.756373344	23.12995338	23.48983574
N/A	0.017683506	0.020434674	20.9619751	20.4247036
N/A	-0.234057426	0.73395729	24.12888336	24.48031425
N/A	-0.288837433	0.569367832	28.14535332	27.82444572
N/A	-0.407013893	0.469372586	24.12888336	23.93048668
N/A	-0.442372322	0.307218305	24.91757011	24.24154472
N/A	-0.506009579	0.612778432	22.95843887	22.99439812
N6amt1	0.461749077	0.258606004	20.81169128	22.72429848
Naa15	-0.727341652	0.636570049	20.50381088	21.65800667
Naalad2	0.279420853	1.020606164	24.91861725	25.20250893
Naca	0.074637413	0.103896212	23.99740028	25.11433983
Nae1	0.432528496	0.284701601	21.03965759	22.76585579
Naga	-0.259925842	0.46836236	23.97543716	24.45557022
Nampt	0.081120014	0.205341964	25.04000854	25.1188221
Nap1l1	0.061984062	0.329559984	25.60223961	25.74980545
Nap1l4	-0.062837124	0.297063736	24.85462189	25.10868835

Napa	0.221674442	0.743922727	24.7490387	24.66215324
Naprt	-0.260052681	0.396427666	23.13062859	23.17144012
Nars	0.078588486	0.160109298	23.46625328	24.05415916
Ncald	0.854136467	0.663766605	22.30838776	22.03553581
Ncam1	0.212423801	0.538177077	25.89020157	25.90536308
Nceh1	-0.491277695	0.148681886	19.66902351	23.90407753
Nckap1	0.121566772	0.422705049	24.87829971	25.1240387
Ncl	-0.136611938	0.640614266	27.01563263	27.15112495
Ncln	0.204990864	0.266355354	22.9117775	22.74038696
Ndrg1	0.365174294	0.805079046	25.30966377	25.8528862
Ndrg2	-0.071869373	0.176256663	26.88005257	27.24318123
Ndufa1	-0.159780502	0.106817297	21.86143494	22.47758675
Ndufa10	-0.035879612	0.072492864	26.85233879	27.049263
Ndufa11	-0.723229885	0.798748775	21.537323	23.10856056
Ndufa12	-0.081252575	0.105452249	24.89008713	25.40051079
Ndufa13	-0.005791664	0.010224132	24.75123596	25.11187553
Ndufa2	0.227889538	0.29926334	22.65368462	23.44139099
Ndufa3	0.457859516	1.032911491	24.4998436	24.8773632
Ndufa4	-0.079559326	0.096852212	26.57873917	26.82432365
Ndufa5	0.842504025	0.386610138	22.93560219	23.67766571
Ndufa6	-0.134500504	0.285182551	25.0277462	25.2437973
Ndufa8	0.153457165	0.175408938	26.39886475	26.43346977
Ndufa9	-0.110751629	0.341598021	26.13541603	26.41104126
Ndufaf4	0.653853416	0.565432512	21.79534912	21.94438744
Ndufaf7	-0.285532475	0.510818917	19.99658394	20.73360825
Ndufb1	-0.018470287	0.030483538	25.56497002	25.88208389
Ndufb10	0.067773819	0.083756938	25.51123238	25.5182724
Ndufb3	-0.013975143	0.018242993	23.98979759	24.25673866
Ndufb4	-0.839618206	0.340001441	25.12218285	25.2457943
Ndufb5	-0.345545292	0.322720555	23.11230469	23.46787071
Ndufb6	0.868642807	0.673553001	22.97354698	23.3303299
Ndufb7	0.059812546	0.021651853	23.69029808	23.97727394
Ndufb9	-0.081052303	0.105727522	24.63405991	25.19099236
Ndufc2	-0.000195503	0.000297623	24.9586792	25.29631615
Ndufs1	-0.071464062	0.101886649	27.26579666	27.63630295
Ndufs2	0.006774902	0.012864895	26.76862907	26.76673508
Ndufs3	-0.113228798	0.161857146	25.88553238	26.0739212
Ndufs4	0.786414623	0.474320704	24.46575546	25.0091114
Ndufs5	1.268167496	0.442770824	25.07806015	25.39486313
Ndufs6	0.926928043	0.229325477	23.91031265	23.85861206
Ndufs7	0.26959753	0.537652145	24.92723465	25.42761612

Ndufs8	0.185089588	0.357488591	25.54942513	25.91586113
Ndufv1	0.12008667	0.17284467	26.95160484	27.22811699
Ndufv2	0.100402355	0.142854479	25.01154327	24.87417603
Ndufv3	0.032056332	0.044249645	21.49267387	21.02052498
Nebl	0.151679993	0.037487561	19.6319561	23.86655617
Nedd4	0.06519556	0.32508884	26.86053085	26.84744835
Nedd8	-0.809409618	0.946438283	23.76405334	24.52850342
Nefm	2.341698647	0.643909903	21.06552696	20.01495171
Nelfcd	0.10026741	0.121467738	27.51050758	26.8766613
Nes	-0.160932064	0.383110096	23.34204483	23.2609787
Nexn	-0.013329506	0.036350882	22.96858215	22.8894825
Nfib	0.040197372	0.022659248	22.49472618	21.29754066
Nfic	0.273478985	1.26388358	22.75759888	22.43852615
Nfix	0.299719334	0.748453715	24.23950768	24.2540741
Nfu1	0.200421333	0.35904353	22.37260056	23.23407745
Ngef	0.042678356	0.079252868	23.05319786	23.41969872
Nhp2l1	-0.130513668	0.184951434	24.23432541	24.09095573
Nid1	0.217837811	0.815020018	28.72546387	28.5209198
Nid2	0.050275803	0.134245688	26.45639992	26.26277161
Nif3l1	-0.353191376	0.839179504	21.81819725	22.6170826
Ninj1	0.238433361	0.594675942	24.25089836	24.04218292
Nit1	-0.049796581	0.183087243	24.74149704	24.68029785
Nit2	-0.145010948	0.332498613	30.60310936	30.70981026
Nlrx1	1.087310314	0.578005808	23.1593399	21.28506851
Nme1	0.089560032	0.510515835	25.01869202	24.82444572
Nme2	0.057051182	0.20548182	28.77542686	28.57416153
Nme3	0.210373402	0.164669105	21.58224106	21.8669529
Nmral1	0.179624081	0.07663794	22.15514565	22.53442955
Nmt1	0.133278847	0.249770888	24.51851273	25.0953083
Nnt	0.01969862	0.07478349	26.92897415	27.08405685
Nono	-0.383267403	0.593731601	25.46522522	25.55499649
Nop58	-0.000440598	0.001019444	23.43478966	23.6686058
Nov	0.125854492	0.302007633	25.26967239	25.00658798
Npepl1	-0.844683647	0.241497332	23.86976051	23.73510551
Npepps	0.01970911	0.088777497	25.97338104	26.22565651
Npm1	0.278305054	0.928872992	26.28816986	26.4522419
Npnt	-0.148953438	0.820897548	29.40423965	29.3118782
Npnt	-0.265904903	0.445073589	24.53391838	23.88241005
Nptn	0.118142128	0.848410376	25.59753036	25.52668381
Nqo1	0.06477499	0.47428991	24.79694366	24.83855629
Nqo2	-0.252167702	0.81591782	23.9557991	23.70281982

Nsf	-0.377810955	0.686783074	23.99938011	24.60229492
Nsfl1c	0.019639492	0.033897745	24.63189697	23.95064735
Nt5c	-0.141360283	0.396172999	25.26072884	25.50727463
Nt5e	-0.659063339	0.320989861	21.25734138	23.86221123
Ntn1	-0.10215044	0.464290697	25.92849922	25.91729736
Nucb1	-0.05567646	0.161750925	25.09571075	24.80301857
Nucb2	0.042910576	0.086450066	22.83171082	22.66405487
Nudc	-0.04365778	0.24933042	24.62739563	24.7470932
Nudt11	-0.534310341	0.429016279	22.22042847	22.58820152
Nudt16	0.920001507	0.464247369	22.53772736	22.95884705
Nudt18	-0.111361504	0.28085707	20.59103584	20.96662903
Nudt21	-0.179591656	0.517263312	24.76319313	24.77459717
Nudt6	-0.222826004	0.526254018	23.79530907	24.41422272
Nudt7	-0.095087051	0.102389504	20.25626373	21.55744743
Numa1	-0.462292671	0.735047878	23.58083916	22.8772316
Nup133	-0.246746063	0.503176179	22.88684464	22.83120918
Nup155	0.176154137	0.184236313	21.68675613	21.71695137
Nup160	-0.117238045	0.101272918	22.49645805	22.06361961
Nup93	0.336549759	0.329046375	22.28212166	21.47516251
Nutf2	0.207271576	0.919873427	26.87208748	27.00891876
Nynrin	-0.232080936	0.530430182	25.32896042	25.48062134
Oat	0.074504852	0.382760468	27.95299339	28.25691986
Ociad1	-0.000459671	0.000121727	18.49855995	23.24331856
Ogdh	-0.019624233	0.022536647	29.85456848	30.18435287
Ogn	0.093150139	0.579844778	32.49961853	32.36304092
Ola1	0.031775951	0.121762997	26.04545593	26.36304092
Omd	0.424599648	0.86141183	25.48225403	26.20841789
Opa1	0.034185886	0.077778559	25.56427383	25.82128525
Orm1	-0.193552494	0.51104724	24.4497261	24.01563263
Osbp	0.347324371	0.850952442	23.74693871	24.1479454
Osbpl11	-0.879416466	0.835642301	22.20164871	20.19979858
Osbpl3	-0.237632751	0.15900848	23.05458832	23.30730247
Osbpl9	0.047013283	0.108132724	22.33068466	22.58865929
Ostc	-0.047912121	0.139519268	24.48068237	24.18888092
Ostf1	0.047071934	0.087387614	25.31053162	25.53510666
Otub1	-0.03831768	0.142649025	26.20342445	26.19584274
Oxct1	0.094892502	0.408160632	28.3740139	28.58050156
Oxsr1	0.125287533	0.964321459	23.71156311	23.70514297
P4hb	0.051568985	0.310014895	28.84322929	28.86782455
Pa2g4	-0.186274052	0.451626312	24.5973587	24.57525253
Pabpc1	-0.017221451	0.053070339	26.54683685	26.7551899

Pabpn1	0.778682232	0.238536271	23.25896835	22.61117172
Pacsin2	0.090332508	0.337006815	25.58020592	25.49283409
Pafah1b1	-0.136503696	0.105470431	23.86806488	23.50385284
Pafah1b2	-0.258474827	0.916656998	25.82517433	26.03632545
Paics	-0.032139301	0.061415768	24.36619759	24.83069611
Pak2	0.205796719	0.199860025	24.3566246	24.82133484
Palm	0.03800869	0.104290291	23.08577919	22.99095917
Paox	0.43469286	0.29391205	20.66980743	23.10299873
Papln	0.632527828	0.469235855	23.46774673	23.43834877
Papss2	-0.276792526	0.770526588	23.64844894	23.81528664
Park7	-0.157483101	0.869660683	28.69885826	28.83656502
Parp12	0.61542654	0.697306949	20.27172661	20.243536
Parp3	-0.297847748	0.515267218	24.39159012	25.42040443
Parva	0.050222397	0.236668839	27.88896179	28.00088501
Parvb	0.050300598	0.026994742	21.41534615	20.67020607
Pawr	0.137163162	0.956442529	25.891222	26.0580864
Pbrm1	-0.194644928	0.673627098	20.51267815	20.16001129
Pbxip1	0.084103107	0.289321366	26.32678604	26.20263863
Pc	-0.126300812	0.359572264	27.90793228	28.14967155
Pcbp1	-0.07122612	0.233632671	27.63671684	27.6189785
Pcbp2	-0.244129181	0.801527056	26.08281898	25.98947334
Pcca	0.030013084	0.042345645	25.16188622	25.00872612
Pccb	-0.127656937	0.324010559	25.74082947	25.85704613
Pck2	-0.090819836	0.600716251	25.11259079	25.22652054
Pcmt1	0.168166637	0.76390447	25.8806839	26.10585594
Pcyox1	0.112610817	0.320202484	23.6399765	24.34495926
Pcyox1l	0.155683994	0.702989992	22.55421829	22.89506149
Pcyt1a	-0.277259827	0.17381898	22.2110405	21.13952446
Pdcd10	1.424868107	0.399651664	23.86258888	24.73138046
Pdcd5	-0.027614594	0.073827263	24.87323761	24.67831039
Pdcd6	0.12767458	0.597697126	26.70872498	26.55013084
Pdcd6ip	0.02046442	0.090242804	27.53304291	27.60547829
Pddc1	-0.772409916	0.343678697	22.41959572	19.65229034
Pde3a	0.067774296	0.186607789	25.31496239	25.71526146
Pde5a	-0.328614712	0.427511012	22.49159813	22.66932106
Pdgfrb	0.264741898	0.607697314	24.22228813	24.17827988
Pdha1	-0.075728893	0.103685822	27.41602898	27.65594673
Pdhb	-0.009065151	0.010952331	27.96790695	28.4814682
Pdhx	0.973659515	0.459792099	22.98837662	23.61661148
Pdia3	0.020380974	0.110793662	30.09030533	30.07393074
Pdia4	0.101449966	0.441384014	26.88425064	26.61343956

Pdia5	0.512764454	0.550960104	22.78426743	22.48005486
Pdia6	-0.068639755	0.675389002	27.0507164	27.15884781
Pdk2	-1.059381962	0.655226795	22.09622574	22.25110054
Pdk3	-0.038624763	0.057174583	24.10221481	24.52390671
Pdlim1	0.095106602	0.512566921	29.02011871	29.07615089
Pdlim3	0.061995983	0.391602041	28.2444973	28.09893608
Pdlim4	0.047411919	0.176208793	26.60724258	26.85661888
Pdp1	0.088434219	0.145004963	21.43969345	21.77177048
Pds5a	0.003192902	0.002159115	20.85686111	21.42224121
Pds5b	0.178643703	0.649586335	24.30445099	24.1300621
Pdxdc1	0.50185442	0.878955322	22.12193108	22.37063408
Pdxk	-0.072168827	0.305056704	25.34468842	25.45622826
Pea15	0.259934902	1.252840948	25.48591232	25.41118813
Pebp1	-0.046563148	0.191588335	29.21479607	29.26490211
Pecam1	-0.117699146	0.355990292	23.98667717	24.44682693
Pepd	-0.852768898	0.636495452	19.86849022	22.11974716
Pex19	0.603070736	0.667705892	21.17590714	21.19868469
Pex5	-0.024426937	0.029680826	19.7758255	19.81932831
Pf4	0.084619045	0.139247936	25.99946594	25.43151093
Pfdn2	-0.052258015	0.092957987	23.85528755	23.87427139
Pfdn5	0.109199524	0.307436633	23.57865334	23.76415443
Pfdn6	-0.707824707	0.368377245	22.71751595	23.43275261
Pfkl	-0.016974449	0.041150006	25.4464798	25.89696121
Pfkm	0.086946964	0.12851241	25.66147423	26.06383705
Pfkp	0.090168953	0.441065006	27.38549805	27.65649223
Pgam1	0.120462418	1.076400202	28.47587585	28.65570641
Pgd	-0.169696808	0.614372696	26.84445763	27.1193161
Pgk1	-0.059468746	0.378632543	28.76461601	28.86523056
Pgls	-0.101901531	0.442646377	27.78923798	28.12701416
Pgm1	-0.125063896	0.523988508	27.96157265	27.98375702
Pgm2	0.279842854	0.57850508	21.71586227	21.93642998
Pgm3	-1.140089989	1.084537692	20.38819885	22.56064606
Pgm5	0.054956913	0.36664824	30.5508709	30.77273941
Pgp	-0.269067287	0.983406302	24.16307831	24.57577133
Pgrmc1	-0.079629421	0.332161412	26.20120049	26.2647419
Pgrmc2	0.112338066	0.045683189	23.58416939	24.22611618
Phb	0.164865017	0.619537415	27.97010422	28.062397
Phb2	-0.042022705	0.113574408	26.76483727	26.77856255
Phgdh	-0.343536854	0.634171261	22.12801743	21.65368462
Phyhd1	0.254216671	0.293805684	20.9122448	20.86817551
Pi15	0.332234859	0.886756922	25.91513252	26.31106758

Pi4ka	0.026453495	0.034448629	23.54557228	23.79897118
Picalm	0.032754898	0.088974306	27.07826424	27.30791092
Pigs	-0.04866457	0.015430968	19.35215759	22.48214912
Pin1	-0.170759678	0.304401582	23.26627922	23.43987083
Pip4k2a	-0.008842945	0.005112847	20.94820786	20.34080505
Pir	0.011144161	0.017579752	20.7803669	21.35035133
Pitpna	0.061398029	0.155940133	25.08768272	25.25266647
Pitpnb	0.123758316	0.2454509	22.40509605	23.09261703
Pitrm1	0.028150082	0.058846701	24.58290672	24.59360313
Pkm	-0.005401134	0.029391781	31.18718719	31.33330154
Pkm	-0.43968153	1.277321007	27.38401604	27.78649902
Pkn1	-0.315158367	0.818953863	21.26476288	22.01041794
Pla2g4a	0.185898304	0.249568896	24.09868622	24.23819542
Plcb1	-0.162642956	0.071866693	22.63333893	21.93252373
Plcb3	-0.041264057	0.083408527	23.50470161	24.05548286
Plcd1	-0.074910641	0.344742065	27.45269775	27.56478119
Plec	0.250845909	1.295287289	29.06802177	29.08929443
Plg	-0.015329361	0.05310436	27.09285164	26.7113533
Plin1	-0.190173626	0.241152749	28.62613487	28.58437729
Plin3	0.024189949	0.068205745	26.1680603	26.45838928
Plin4	-0.009443283	0.124955757	28.21868134	28.23703766
Plp2	0.24102354	0.743835956	23.8752079	24.51953316
Pls3	-0.023848057	0.183711487	30.00343323	30.15267181
Plscr3	0.675777912	0.595184108	22.42108536	22.83246422
Plxdc2	0.262118816	0.36584407	22.72065163	22.29698181
Plxnb2	-0.130447865	0.248740471	23.73210526	23.30257034
Pml	0.541294575	0.652121256	21.5534687	21.88788605
Pmpca	-0.288850784	0.613722556	24.61037254	25.06258202
Pnn	-0.14851284	0.064748682	19.72033501	22.00247383
Pnp	-0.247362137	1.036467341	25.74832153	26.03263092
Podn	1.376428604	0.482730592	24.98398399	25.27013588
Pofut2	0.542508125	1.06869469	22.3073864	23.03326988
Poglut1	0.240800381	0.814834161	22.45274544	22.7907238
Polr2h	-0.325835705	0.407158799	22.14914131	22.46109009
Pon1	-1.012909412	0.785522789	22.92357635	20.34993553
Pon3	-0.242507935	1.093185036	26.35220337	26.42913246
Por	-0.1572299	0.698304822	26.51453018	26.8595829
Postn	0.760054588	0.298199502	24.55537605	24.09876633
Ppa1	0.206244946	0.879948827	25.96587181	25.66345787
Ppa2	0.143684864	0.315633656	24.81738663	25.22236061
Ppia	0.038095474	0.230938233	31.36416245	31.35384369

Ppib	0.047586441	0.192036953	27.80814743	27.72279739
Ppid	-0.135253906	0.484356065	24.4086628	24.54780769
Ppl	-0.122098923	0.311969831	23.12384224	23.50591278
Ppm1b	0.227903366	0.610713785	22.20553207	21.62956429
Ppme1	-0.117491722	0.162034822	23.26255798	23.58657646
Ppp1ca	-0.065059185	0.108169828	24.37404823	24.29242516
Ppp1cb	0.008270264	0.044205206	28.66840935	28.69474792
Ppp1cc	-0.234242916	0.307749767	21.55576324	21.9770813
Ppp1r12a	0.058156967	0.350426503	28.08547592	28.25858307
Ppp1r12b	-0.110131741	0.315486541	24.16859627	23.59991455
Ppp1r12c	0.866800308	0.49953699	23.30493927	23.59889221
Ppp1r14a	-0.147548199	0.337778005	26.65061569	26.61694717
Ppp1r7	-0.080361843	0.469274591	25.33493805	25.49591637
Ppp2ca	0.00229311	0.009760332	26.10757256	26.07432938
Ppp2r1a	-0.023220539	0.134925861	28.51239204	28.63882446
Ppp2r2a	-0.02105999	0.071001772	24.7056694	24.86112213
Ppp2r4	-0.093636513	0.857249518	25.90209961	26.11741447
Ppp2r5a	0.962063789	0.959295933	22.50496674	22.91011238
Ppp2r5c	0.464705944	0.392218227	22.86913872	23.46961021
Ppp6c	0.009315968	0.028140331	21.98140335	22.27750397
Ppp6r3	-0.162840366	0.315675244	20.13833618	20.73686028
Ppt1	0.326597214	0.711265032	24.84842682	24.69715691
Praf2	-0.061084747	0.189521299	23.1310997	23.5639534
Prdx1	0.026266098	0.171693305	29.43105507	29.61519432
Prdx2	-0.023663998	0.063478191	28.60084343	28.18219948
Prdx3	0.167610168	0.372601902	26.68204117	26.59818268
Prdx4	0.009584427	0.068436228	26.74842453	26.89377022
Prdx5	-0.06347084	0.7753106	28.44994545	28.46193504
Prdx6	-0.122124672	1.289626142	28.4336834	28.58745766
Prelp	0.230492592	1.047987169	31.77956581	31.92121124
Prep	-0.00668478	0.010043103	23.56604576	23.6654644
Prkaa1	0.174044609	0.556634225	24.06332207	24.00264549
Prkaca	0.000892162	0.001475142	24.4954586	24.45129967
Prkag1	-0.215206623	0.933177356	24.54951286	24.72020149
Prkar1a	0.138710499	0.433275554	25.37845421	25.46329308
Prkar2a	0.084947109	0.206756789	23.91679573	23.93508148
Prkar2b	0.423299789	0.552793189	24.68901825	24.5903511
Prkca	0.282485485	0.599085823	21.98638153	22.73721123
Prkcd	0.108380795	0.034283074	24.08699417	20.25527573
Prkcdbp	0.112717628	0.718589734	28.86085701	28.94002533
Prkcsh	1.070489883	0.474152396	24.33333588	24.26119423

Prkg1	0.167239189	1.128412667	25.54347801	25.7091465
Prkra	0.086604595	0.040478507	21.67719269	20.0256691
Proc	0.009448528	0.00615019	21.38911057	21.15715218
Procr	-0.223341942	0.719622699	23.41338348	23.33019257
Prosc	-0.029397488	0.069291165	24.48240852	24.6724968
Prpf19	0.141516685	0.191127752	23.72463226	24.17835617
Prph	0.997899055	0.339428452	24.85775757	24.15946388
Prps1	-0.281809807	0.493822576	23.71376801	24.77695847
Prpsap1	3.67E-05	4.32E-05	23.52288818	23.99714088
Psap	-0.190981865	0.769020084	26.70279312	26.26468849
Psma1	-0.012994289	0.03979894	26.84385872	26.97760201
Psma2	-0.065008163	0.375547901	26.27426529	26.38460922
Psma3	0.178674698	0.200100252	25.27557945	25.35625648
Psma5	0.039572239	0.152140094	26.31321526	26.1018734
Psma6	-0.150496006	0.723412186	26.06070709	25.97097015
Psma7	0.079950809	0.221442024	26.18729591	26.17871666
Psmb1	-0.202271461	0.801948114	26.89942932	27.14802361
Psmb2	-0.087762356	0.256774776	26.15986824	26.33834267
Psmb3	-0.061714172	0.124014634	24.89240456	25.0507164
Psmb4	-0.104557991	0.268279197	23.79887199	24.23381424
Psmb5	-0.661294937	0.33143239	23.21918869	20.11299896
Psmb6	0.045309544	0.089865044	24.44436455	24.76612854
Psmb7	0.087243557	0.200691604	23.74868011	24.16584015
Psmc2	0.133191109	0.518957334	25.29487991	25.51629066
Psmc3	0.040229321	0.107337079	26.1246891	26.15303993
Psmc5	-0.213349819	0.768465922	24.94360161	25.04597664
Psmc6	0.053749561	0.141103554	25.80279541	26.04980278
Psmd1	-0.21703434	0.51047817	25.60209656	26.19302368
Psmd11	-0.214276791	0.796298924	25.96441841	26.49867249
Psmd12	0.272715569	0.860389624	24.91524696	25.25133133
Psmd13	-0.710547447	1.21119882	23.48234558	24.36573029
Psmd14	0.233007431	0.57920488	25.51668167	25.72265244
Psmd3	-0.08641386	0.314293639	24.00966644	24.19257355
Psmd4	-0.117525101	0.136206868	23.28841591	23.61503983
Psmd5	-0.10474062	0.264568503	25.09260941	25.14623833
Psmd6	0.121938705	0.252347372	23.48037529	23.39165497
Psmd7	-0.345146656	1.016226709	25.59767151	25.84625244
Psmd8	-0.224086285	0.250369983	23.90967178	24.08804703
Psmd9	-0.195538521	0.606735351	23.87041855	23.68784523
Psme1	-0.043861389	0.213130407	27.3358593	27.48761559
Psmg1	0.278205395	0.320819272	21.32734299	21.42798042

Ptbp1	-0.097963333	0.333423595	27.88127899	28.1234169
Ptbp2	-0.562803745	0.255065406	19.97107315	22.16103363
Ptcd3	-0.390862942	0.177022866	19.76180077	22.58694267
Pter	0.691034317	0.526756714	22.69104385	22.99477768
Ptges2	1.01339674	0.586001661	25.1378994	24.16798401
Ptges3	-0.083045006	0.268692233	25.86251831	26.05856133
Ptgfrn	-0.34069252	0.821590116	21.70184708	21.74554443
Ptgis	0.046309948	0.145154932	30.10287094	30.35310745
Ptgr1	0.15866518	0.517787294	23.30298805	23.55367851
Ptgr2	0.571092129	0.509881653	23.94252777	23.85566902
Ptgs1	-0.081809521	0.274076646	25.55888367	25.4564476
Ptms	-0.042605877	0.058787363	24.36138535	23.40600395
Ptp4a2	-0.179782391	0.519892988	22.87438393	23.14237785
Ptpn11	-0.17539978	0.39492008	24.21326637	24.11195564
Ptpn23	0.255795479	0.220636649	21.62760735	21.90142822
Ptprc	-1.186885357	1.101896401	20.21652222	19.74691772
Ptrh2	-0.372835159	0.449158172	23.72296524	23.78496552
Puf60	1.028447151	0.667779525	22.79920769	23.21654129
Pura	0.208666325	1.286874888	25.21419334	25.30838013
Pxdn	-0.142689228	0.364810886	23.24026489	22.92219734
Pxn	0.011556625	0.020993923	25.19940376	25.66470528
Pygb	-0.043135643	0.191251948	28.14593697	28.35384369
Pygl	0.247104645	0.605728949	24.68228149	24.91529274
Pygm	-0.390717506	0.440863509	28.2417717	28.43507576
Qars1	0.091554165	0.237898588	25.96452904	26.43934822
Qdpr	-0.025873661	0.123993272	26.07177544	26.15003967
Qil1	0.128818035	0.332643888	24.64696693	24.81572723
Qki	0.165293217	0.223213532	21.77916527	22.36671638
Rab10	-0.028997421	0.103260226	25.77723503	25.62697792
Rab11b	0.119086266	0.290200734	25.87398911	25.82975197
Rab12	0.464749813	0.312362223	21.12949753	21.93008995
Rab14	0.098796844	0.336251792	26.18201828	26.48509789
Rab18	0.303142548	1.027833395	23.90738297	23.94163132
Rab1A	0.148743153	0.741944411	26.65102577	26.65253067
Rab1b	0.043751717	0.149719989	24.23381424	24.52360725
Rab21	-0.17781353	0.595544983	25.25053596	24.93701363
Rab27b	-0.171857834	0.244615561	21.22081375	21.24881554
Rab2a	0.190159321	0.305279944	24.76405334	24.28679657
Rab34	-0.262886047	0.840985287	22.46988297	22.75156403
Rab35	-0.067196846	0.079835485	24.37185669	24.46213913
Rab5a	-0.02308321	0.009001663	24.22618866	23.42700768

Rab5b	0.02129221	0.126928035	26.43790436	26.34177399
Rab5c	0.107824802	0.733360149	25.21193123	25.19121742
Rab6b	0.036092758	0.088893772	24.48572731	24.39649773
Rab7a	-0.029636383	0.102472696	26.12180901	26.21821022
Rab8a	-0.833353519	0.60236577	23.48222351	23.24971199
Rab8b	0.653046131	0.795520017	22.27829933	22.38492775
Rac1	-0.019871712	0.169786874	28.35144424	28.46964073
Rad23b	0.182869434	0.449299221	24.625	25.09188461
Rala	0.191687584	0.390917504	24.34340096	25.17394257
Raly	0.423199177	0.191146207	22.89461708	22.82394028
Ranbp1	0.233981133	0.787834765	25.49115181	25.67597198
Ranbp2	-0.36177969	0.771421139	22.90479469	23.30980301
Rangap1	-0.607573509	0.482139835	20.75319672	19.41313553
Rap1a	0.12289381	0.383358379	25.45051193	25.63621902
Rap1b	-0.030347347	0.198788847	28.4499855	28.21784973
Rap2c	0.288210392	0.390711741	19.8657074	20.90448189
Rarres2	0.080789089	0.113994687	23.83759308	23.9273243
Rars	-0.09769392	0.524586001	26.36862946	26.68872452
Raver1	0.017243862	0.011399802	20.46380424	22.12189865
Rbbp4	-0.191856384	1.064342386	24.52784729	24.56749725
Rbbp7	1.072342396	0.512911141	23.10375214	22.87766266
Rbbp9	0.115822792	0.557622185	27.30869293	27.64223671
Rbm14	0.621326923	0.866445718	22.068964	21.70303154
Rbm19	-0.607652664	0.383610609	21.19872475	23.90591431
Rbm25	-0.757311344	0.655565427	23.48971367	23.92623901
Rbm3	-0.0105443	0.019402603	25.72640038	26.18188667
Rbm39	0.204586506	0.237704713	23.52073288	23.05410957
Rbmxl1	0.06872654	0.166294472	22.90831757	23.29333687
Rbp1	-0.024802685	0.165510278	28.0102005	28.0775013
Rbp4	-0.070727348	0.180628933	23.22144699	23.29221344
Rbpms	0.065032482	0.18008058	26.18194199	26.45011902
Rbpms2	1.197909832	0.657413357	21.01601982	22.91367722
Rcc1	-0.979747295	1.094149256	20.54747009	22.03264618
Rcn2	0.2332654	0.78945757	22.59176636	22.80487061
Rcn3	0.254718781	0.577777954	25.28460884	26.07940483
Rdh11	-0.901132584	0.389371292	20.70147705	23.11391068
Rdh14	-0.198983669	0.359178884	21.64204979	21.71941948
Rdx	-0.108765602	0.260364201	23.43185997	23.53931236
Reep5	0.064603329	0.111955184	24.44588089	24.64212799
Rexo2	-0.058875084	0.079470326	22.61587143	21.53445244
Rgs18	0.579203129	0.49687878	23.97254944	24.49381065

Rhoa	-0.005956173	0.017276488	28.36076546	28.39619637
Rhob	-0.303122044	0.506840942	23.09040642	22.87732697
Rhoc	0.022580624	0.059439892	24.7164917	24.54427528
Rhoq	-0.590908527	1.072608866	20.03858757	20.453825
Rilpl1	-0.007641792	0.007283547	22.5460434	23.40171432
Rmdn1	-0.609412193	0.318024711	23.17881203	23.59297562
Rmdn3	-0.124567032	0.156159216	23.37703133	23.77595329
Rnh1	0.040047646	0.191903461	27.47514153	27.70193481
Rnpep	-0.152561665	0.446037952	25.07748985	25.55584526
Rock1	0.142386436	0.715472243	26.48692513	26.51115608
Rock2	-0.184947014	0.715361173	23.93192863	24.05109024
Rpe	-0.042203903	0.300766588	22.61865234	22.57408524
Rpl10	0.030964375	0.064060986	26.49614525	26.58649063
Rpl10a	0.122014523	0.477962289	26.69643974	26.47645569
Rpl11	-0.382401943	0.515323721	24.36158562	24.35709572
Rpl12	-0.050619602	0.121805746	26.53023148	26.12488747
Rpl13	0.042719364	0.10826817	26.75276947	27.14850807
Rpl13a	-0.252561092	0.572631287	24.6516819	24.99511528
Rpl14	-0.127293587	0.479371622	26.10765266	26.28961372
Rpl15	0.033385277	0.071058067	26.46741867	26.54515839
Rpl17	0.087658405	0.237632328	26.91661263	26.98706818
Rpl18	-0.164745331	0.239554861	24.57207298	25.3755722
Rpl18a	0.336297989	0.545359418	24.03573799	24.33244705
Rpl19	-0.052975178	0.074465862	24.17561913	23.68773842
Rpl21	-0.212451935	0.48485701	24.70160484	24.91747856
Rpl22	-0.041488171	0.073185355	24.94494057	24.55713081
Rpl23	-0.220473289	1.039338188	26.14734459	26.32777977
Rpl23a	-0.119134426	0.15241244	24.80365944	24.89693642
Rpl24	0.009761333	0.029634136	26.70120811	26.5903511
Rpl26	-0.048163414	0.13426305	24.97513199	24.9711895
Rpl27	-0.059208393	0.284900142	24.74437523	24.70429802
Rpl27a	0.017274857	0.072756873	26.22552681	26.45057487
Rpl28	0.748671055	0.438702982	24.98294067	25.01367569
Rpl3	-0.177086353	1.064908252	26.72520447	26.74085426
Rpl30	-0.121501446	0.345442917	24.41183281	24.22699738
Rpl31	-0.032973289	0.06671889	26.10529518	26.60470009
Rpl32	-0.027044296	0.058040715	25.44871902	25.67268562
Rpl34	-0.211116314	0.661911831	24.46026421	24.49771309
Rpl35	-0.404290676	1.048584011	23.91469955	23.96322823
Rpl35a	0.470489025	0.172662197	23.87979507	22.57588577
Rpl36	-0.297890186	0.531911345	24.68736458	24.20672417

Rpl37a	-0.032270908	0.108497572	23.77926445	23.90205383
Rpl38	0.010000229	0.025923359	23.82026291	23.84038162
Rpl39	0.016385555	0.034181879	24.65769196	25.27625465
Rpl4	-0.082959652	0.495696561	28.46668816	28.47490883
Rpl5	0.008746147	0.025520091	26.50964737	26.61104774
Rpl6	-0.070726871	0.180344396	26.40335846	26.61245537
Rpl7	0.018950462	0.085992216	26.72351265	26.80415154
Rpl7a	-0.097984791	0.411952663	26.80193329	26.88809013
Rpl8	0.06492424	0.349349825	26.48647881	26.3175869
Rpl9	-0.184434891	0.622284869	24.93341637	24.76915932
Rplp0	0.100195408	0.585399203	27.25268555	27.29166985
Rplp1	0.050721645	0.207237301	27.94737434	28.12336731
Rplp2	-0.011410713	0.050661133	27.24626541	27.16796494
Rpn1	0.076024532	0.31814663	27.60780716	27.70971107
Rpn2	0.092065334	0.354127602	27.61210442	27.73195076
Rps10	-0.296375751	1.251403726	25.63356018	25.52513123
Rps11	0.022392273	0.044041904	25.30643463	25.0716114
Rps12	-0.04950428	0.226320448	25.61571312	25.80678368
Rps13	-0.037015438	0.090745575	27.32018852	27.5587368
Rps14	-0.098327637	0.18560217	24.7399025	24.71633339
Rps15	-0.318683624	0.75916902	25.69935608	26.20487976
Rps15a	0.070083618	0.292434122	26.14012527	26.14604378
Rps16	0.013156891	0.011825947	22.61124039	22.94519234
Rps17	-0.059662342	0.162478466	26.23684692	26.28665543
Rps18	-0.022591591	0.066051014	26.88541603	26.88890266
Rps19	-0.207912922	0.543149543	26.48763084	26.79538345
Rps2	-0.106030464	0.511800111	26.38633728	26.0730629
Rps20	-0.299014568	0.965752764	24.84570313	24.8554306
Rps21	1.091411114	0.490424982	23.39204979	23.22934723
Rps23	0.121173859	0.338425529	24.58577538	24.29691124
Rps24	0.207537651	0.793516349	25.03657532	25.03216743
Rps25	-0.049501896	0.109778555	24.93364143	25.40927887
Rps26	-0.165701866	0.48574434	25.00088501	24.81044006
Rps27a	-0.187564373	0.402282897	28.22807121	27.6288147
Rps27l	0.006402016	0.006408548	27.14462471	26.15342712
Rps28	-0.166125298	0.140133289	23.92741394	23.13693047
Rps29	0.712216854	0.369990962	24.14546013	24.26406097
Rps3	0.020480633	0.07002761	26.29217911	26.25441551
Rps3a	-0.037218571	0.092047459	27.26364899	27.47429085
Rps4x	-0.027787209	0.080839291	27.23278999	27.36352539
Rps5	0.130575657	0.660641733	26.10671425	26.30499077

Rps6	-0.461790085	0.088614934	24.99079323	26.12151146
Rps6ka3	0.182404041	0.653546071	21.97819901	22.02766228
Rps7	-0.143507004	1.064734624	26.12888336	26.24695396
Rps8	-0.027210712	0.126898222	27.16739082	26.98261452
Rps9	0.023240089	0.079231577	26.77919006	26.91581535
Rpsa	0.033908844	0.224319308	28.15802956	28.1834774
Rptor	-0.505429745	0.655883145	20.31694412	20.58627892
Rrad	-0.918512344	0.471891445	21.31447029	19.93259048
Rras	-0.010815144	0.043767293	27.65649223	27.65574074
Rrbp1	0.20619154	0.924582161	27.04531097	27.14170456
Rsu1	0.009796143	0.041234181	29.8022728	29.98304939
RtcA	0.527514458	0.322176324	22.48150826	22.45274544
Rtcb	0.110713482	0.424507165	25.13120079	25.48855019
Rtn1	0.25515604	0.422207901	23.57911301	22.88580132
Rtn2	-0.745333195	0.457683124	20.29218292	22.36956787
Rtn3	0.168363094	0.37142062	25.72811508	25.58247757
Rtn4	0.101045609	0.039828135	20.06549835	22.97503471
Rtn4	0.032740116	0.116814042	26.90196228	26.91706848
RTRAF	-0.016629219	0.081102776	24.91159439	25.10421562
Rufy1	0.763233662	0.40384226	21.46550369	22.70311546
Ruvbl1	-0.040445328	0.101717132	24.24742508	24.32505417
Ryr1	0.803823471	0.190461756	24.7988224	23.74847603
S100a1	-0.532903671	0.268898978	22.2112484	21.91754341
S100a11	0.154359818	0.656521033	29.41846466	29.28550911
S100a13	-0.554104805	0.364508749	23.69667816	22.5602951
S100a4	0.053864002	0.118727983	31.98063469	31.89785767
S100a5	-1.672556877	0.772749596	24.45331001	20.80788422
S100a6	-0.419755459	0.514914356	26.45871735	26.69285393
Saal1	-0.719312668	0.872078783	21.8839016	20.27192116
Sacm1l	-0.14926815	0.590332043	23.76809883	23.88966942
Sae1	-0.194126129	0.423249412	24.72254944	25.11060143
Safb2	-1.570515633	0.762851478	23.83740044	20.60450554
Samm50	0.006547451	0.01423719	25.15263367	25.03115845
Sar1a	-0.173773289	0.387851726	24.87717628	25.11886215
Sar1b	-0.398108959	0.215936417	23.15924835	20.20671463
Sars	0.07885313	0.409786574	25.23220444	25.31900024
Scamp1	-0.148257732	0.053226475	22.00333214	22.707798
Scara5	0.120751381	0.338610021	23.8579483	23.96066856
Scarb2	0.31441164	0.902580582	23.82182121	23.80262375
Sccpdh	0.152388573	0.147038295	23.07497787	23.15696716
Scfd1	-0.102920532	0.307173729	24.76668358	24.57247925

Scoc	-0.124166965	0.242726981	22.14687347	22.70583916
Scp2	-0.019952774	0.033283562	24.87215805	24.69789886
Scpep1	-0.064442635	0.176137787	22.71496201	22.73886108
Scrn1	-0.013203621	0.046615331	23.76536942	23.89087486
Scrn2	0.273170471	0.180785444	22.46687508	22.96011925
Scube3	-0.386241913	1.093562034	24.84622955	25.14456558
Sdha	0.187491417	0.258709844	28.21484184	28.60254288
Sdhb	0.279432774	0.438561221	26.64058304	26.70964622
Sdhc	-0.092556	0.110942766	25.00148582	24.94944572
Sdhd	0.144310951	0.255930444	23.38508606	24.10948563
Sec11a	0.045603275	0.07489683	22.99534798	22.93739891
Sec13	-0.164041996	0.317464524	24.34129906	24.34448624
Sec22b	-0.059791565	0.164386387	25.04180717	25.27568626
Sec23a	0.118249416	0.575412086	26.45013428	26.4731617
Sec23b	-0.890009403	0.460427719	21.4283886	21.91506386
Sec23ip	0.697387218	0.341727689	23.29586029	23.54933739
Sec31a	0.10093832	0.517017815	27.09224701	27.35925865
Sec31b	-0.088737011	0.132581475	25.90205383	25.67919731
Sec61a1	0.596955299	0.539865544	24.62667084	24.9504261
Selenbp1	-0.213356495	1.296646448	27.89758301	28.21923447
Selm	0.42234087	0.180721904	22.89258003	21.13019753
Selo	-0.084340096	0.027463504	23.09606552	23.39113045
Selt	0.394695759	0.32330278	20.86928368	20.60955048
Sephs1	-0.057322502	0.016323016	22.62952042	22.76534843
Sepp1	-0.698421001	0.580937197	22.30254173	19.93211555
Septin11	-1.075703621	0.929273493	20.85205841	21.50121498
Septin5	0.096476555	0.243158148	25.27611351	25.47849464
Septin7	-0.085668087	0.2775008	27.32740211	27.67485428
Septin8	0.362842083	1.074896901	25.52243996	25.5182724
Serbp1	-0.136796474	0.366238643	23.44252968	23.45412636
Serpina1a	0.245903015	0.138114038	25.19084167	25.10992432
Serpina1b	-0.528722286	1.289313205	27.73976135	27.33108139
Serpina1c	-0.410489559	1.04818658	30.85556412	30.26114082
Serpina1d	-0.018184662	0.032083294	27.64072227	27.39811325
Serpina1e	-0.185549259	0.285388723	27.55530357	26.96708298
Serpina3k	-0.287694454	0.410881129	28.8944931	28.20643616
Serpina3n	-0.05499506	0.236389717	23.4299469	23.53848457
Serpina6	0.493467331	0.506108762	21.82357025	21.47654915
Serpinb1a	-0.765209675	0.412568766	22.78178787	22.54366112
Serpinb6	-0.211849213	0.916655681	28.14681053	28.28594971
Serpinc1	-0.062935352	0.17838998	29.45079231	29.20650482

Serpind1	-0.070579529	0.227216762	25.27376747	25.00487518
Serpine2	-0.074191093	0.309103939	27.77259827	27.69875908
Serpinf1	0.168096066	0.541254264	26.87373161	27.00699425
Serpinf2	-0.828990459	0.403316945	22.86268425	19.16977501
Serping1	-0.049945831	0.149336077	24.97714233	24.45217896
Set	0.030669689	0.04204095	23.79590416	24.49771309
Setd7	-0.166803837	0.128065894	20.52189064	21.83634186
Sf1	0.018974781	0.027453248	23.92949295	24.70930481
Sf3a1	-1.231553078	0.481065444	22.25473595	18.80006027
Sf3a2	0.240467072	0.581117134	22.55370331	22.56064606
Sf3b1	-0.328889847	0.497509297	23.25055122	24.19940376
Sf3b3	-0.278897762	0.524004757	23.1304245	23.14907837
Sf3b4	-0.134062767	0.435867105	22.89306259	23.06531334
Sfn	0.006356239	0.007243774	25.44272041	24.99709702
Sfpq	0.033821106	0.099715749	26.01369667	25.94237137
Sfrp1	-0.142652035	0.246124814	24.84952545	25.30778885
Sfxn1	-0.240067959	0.368294811	24.06357002	24.66698265
Sfxn3	0.051419735	0.184446344	28.20041466	28.35518837
Sgca	0.121933937	0.170199044	24.72489166	24.7536869
Sgcb	0.042546749	0.115310837	25.07581902	25.3558197
Sgcd	-0.087021828	0.235295773	26.0257206	25.87820625
Sgce	0.069933414	0.211224075	26.88168716	26.80943489
Sgcg	-0.988099575	0.373643817	23.5892086	23.51219559
Sgpl1	-0.287356853	0.165898694	20.37794876	21.5831604
Sgta	-1.807784557	0.407501996	19.08303833	27.13955879
Sh3bgrl	0.110185146	0.390773893	28.01329231	27.81799698
Sh3bgrl3	0.163613796	0.138320618	24.73505402	24.739748
Sh3d21	-0.216135979	0.67597716	29.3224678	29.13672638
Sh3gl1	1.26820612	1.070004099	22.89905167	22.93572807
Sh3glb1	-0.244222164	0.777028499	23.84957314	23.74765587
Sh3glb2	0.287713528	0.670690608	24.75113487	24.32505417
Sh3pxd2a	-0.763731003	0.608921828	21.71971893	23.38692856
Shmt2	0.08945322	0.204148649	23.48099136	23.69381142
Sim2	1.018695831	0.426912071	23.7774601	23.69381142
Sirt2	-0.305059433	0.52146273	20.76707077	21.96895027
Skp1	-0.167254448	0.15178791	24.66665649	25.04893112
Slc12a6	0.065382481	0.12436998	21.57800865	22.41586113
Slc1a5	-0.173362732	0.118026532	22.82774353	22.49575233
Slc25a1	0.022566319	0.040406825	25.84405136	26.16570663
Slc25a10	-0.074984074	0.073300736	23.51292038	23.56975746
Slc25a11	-0.083045006	0.383784092	25.89751434	25.80141449

Slc25a12	-0.081445694	0.186954982	26.39211464	26.72754288
Slc25a20	-0.897358894	0.440843597	25.20650101	25.66448975
Slc25a24	-0.0910182	0.325830423	24.58674812	24.9474411
Slc25a3	-0.036548615	0.129867994	27.34358788	27.41231918
Slc25a4	0.093384266	0.791438089	30.30671692	30.50474167
Slc25a42	0.002917767	0.001775574	23.10627937	23.50433731
Slc25a5	0.064994335	0.188579063	28.05620766	27.93089294
Slc25a51	0.534737587	0.413097112	22.88115883	23.29431915
Slc27a1	-0.000334263	0.000848083	21.56448746	22.00552559
Slc29a1	-0.283090115	0.444418891	20.53801155	21.10495186
Slc2a1	0.409774303	0.24743733	22.14014816	20.42912674
Slc3a2	-1.002087593	0.738402476	23.18458939	22.66353416
Slc44a2	-0.328035355	0.921926738	24.51020622	24.30952454
Slc4a1	0.411620617	0.891717606	29.24424744	28.28819656
Slc4a7	0.604344368	0.669132117	23.84737587	22.43458557
Slit3	-0.002596855	0.003980901	23.74427223	24.00889778
Slmap	0.111719608	0.547770271	27.94770813	28.01030731
Smarca2	1.074334145	0.526824814	23.60048103	20.84671783
Smarca5	0.036178589	0.058808892	23.30089569	23.94708443
Smarcc2	0.189890862	0.795548622	23.16914749	23.6382103
Smc1a	-0.278752327	0.880211709	22.58279228	22.90420532
Smc3	0.157338142	0.16172287	20.37060738	21.44080925
Smdt1	-0.264459133	0.298822582	20.85285187	21.55041885
Smoc1	-0.165799141	0.574423541	26.10940742	26.30108833
Smpd4	0.243121624	0.394615453	22.67828941	22.07139778
Smpdl3a	0.027938843	0.018088715	21.58623314	21.67266846
Smpdl3b	0.251164436	0.626765182	21.93786621	21.73892403
Smu1	-0.128509521	0.200649031	23.10599136	23.83691978
Sncg	0.254972458	0.457346614	25.09876633	25.25165558
Snd1	-0.113245964	0.353773204	26.60851288	26.42604828
Snrnp200	-0.098091602	0.259781734	24.69407654	25.08460426
Snrnp70	-0.304590702	0.587694595	24.14071083	24.32759094
Snrpa	0.712269783	0.371697356	23.41351318	24.11886215
Snrpb2	-0.028805733	0.048171799	23.35595322	24.10325623
Snrpd1	-0.152678967	0.421754532	25.45820045	25.8191185
Snrpd3	-0.130204678	0.490957362	23.8493824	23.86429214
Snrpe	0.023798943	0.036046228	24.51875305	25.05208588
Snrpf	-0.14570713	0.331571465	23.48271561	23.34313011
Snrpg	-0.905431271	0.988350499	21.587286	23.44897079
Snta1	-0.154611588	0.80412601	25.08094978	25.22964096
Sntb1	0.006205082	0.029712018	26.6563549	26.68364716

Sntb2	0.044921875	0.347380547	26.54791069	26.69192314
Snx12	-0.013353825	0.029424973	23.39375114	23.15875435
Snx17	-0.163555622	0.064193075	22.67710686	22.79944611
Snx18	-0.05810976	0.185811947	26.10063171	26.24163628
Snx2	0.756165028	0.392021536	23.04057884	23.3249855
Snx3	0.16835022	0.543524053	24.20806503	24.44132805
Snx4	-0.550672054	0.47642463	21.14532089	21.05688858
Snx5	0.203516483	0.120047578	23.16642189	23.15860176
Snx6	0.067465305	0.085275559	22.07215118	22.56548882
Snx9	0.01566124	0.093814078	24.50893784	24.52007294
Sod1	0.020870209	0.036316101	29.08332062	28.66979599
Sod2	-0.112183094	0.242958005	27.49243546	27.46396255
Sod3	-0.104145527	0.546472099	30.35100174	30.10049057
Sorbs1	0.065758705	0.208449515	27.09928703	27.45356178
Sorbs2	0.612679958	1.289356746	27.24653625	27.26257515
Sorbs3	0.203764915	0.503832861	25.44789886	25.79111671
Sord	-0.116295338	0.351085411	23.83296585	23.93552971
Sost	-0.305438042	1.209749026	27.19657326	27.09838486
Spag9	0.561740398	0.554936288	21.18072891	22.33472633
Sparcl1	0.892180443	0.308605314	20.67547989	22.89844131
Spcs2	0.889445305	0.530050913	23.78196716	23.11762619
Spon1	0.104704857	0.260445587	24.7490387	24.17539024
Spr	-0.040131569	0.124719853	26.84852219	27.19966698
Spta1	0.332357883	0.697566618	27.6317997	26.66505814
Sptan1	0.096543312	0.44040803	29.99833107	29.86553955
Sptb	0.379864693	0.662950092	27.41062164	26.29302025
Sptbn1	0.130572319	0.744165532	30.02234268	29.92804146
Sri	-0.137924194	0.364880868	26.30975151	26.32627106
Srm	0.096249104	0.144823529	24.36419487	24.03640747
Srp14	0.097708702	0.076120366	22.04773331	22.01886177
Srp54	-0.087777615	0.33103389	22.61058617	22.96909142
Srpx	0.335148811	1.041420348	24.94319916	24.96022606
Srrm1	0.152528286	0.233351828	22.78072739	23.43389893
Srrt	0.023706436	0.005827343	21.42479897	24.02165985
Srsf1	-0.260943413	0.852086018	23.29305649	23.69168282
Srsf10	-0.054176331	0.170063661	23.51328087	23.55496788
Srsf2	-0.1171422	0.238181858	24.31589508	24.29998779
Srsf6	-0.176950932	0.274630139	24.12392044	23.95633125
Srsf7	-0.229584217	0.749530462	23.42624092	23.51953316
Ssb	-0.134290695	0.716463659	25.62452507	25.61371994
Ssbp1	-0.094903946	0.030042819	21.3326683	23.89022636

Sspn	-0.230048656	0.093087989	19.65472603	22.0975132
Ssr1	0.867743015	0.473743591	24.38093185	24.62148285
Ssr4	0.052351475	0.142797623	23.11224174	23.00020409
St13	-0.087386131	0.300750339	25.78728485	26.22271156
St3gal5	0.448764324	0.471768508	22.49955177	22.79865456
Stat3	-0.09431839	0.351548171	24.70809364	25.09884644
Steap3	0.209948063	0.3188422	24.06890869	24.51219559
Stim1	0.055395126	0.247738572	23.3308773	23.39270401
Stip1	0.000146866	0.000456824	27.1286869	27.10189438
Stk24	0.176236153	0.762910928	25.41180229	25.55449867
Stk39	-0.626968861	0.319898877	20.69765282	22.5544529
Stom	-0.025576591	0.087467607	26.53265572	26.5109005
Stoml2	-0.086045265	0.295263748	24.38502121	24.40833855
Ston1	-0.753548145	0.554874933	20.04406929	19.59588814
Strap	-0.80606842	0.362195537	20.91870117	22.95374107
Sts	0.177853584	0.325441604	23.02413177	23.57669449
Stt3a	0.124604225	0.180971819	22.26241302	22.27909279
Stt3b	0.281696796	1.090539293	22.37018013	22.85984421
Stx12	0.22582674	0.961034619	24.66090393	24.34319878
Stx16	-0.047251701	0.087371924	22.9693718	22.78907204
Stx7	0.983214378	0.56270259	22.94336891	23.01186752
Stxbp3	0.065393448	0.300708408	25.37620163	25.71910477
Sucla2	-0.093882561	0.112376309	26.89434814	27.15005875
Suclg1	-0.316310883	0.432149792	27.76938629	28.22269249
Suclg2	-0.006540775	0.016483276	25.60303116	25.43885612
Sugt1	-0.045405865	0.015437096	23.13448715	23.17689705
Sulf1	0.102065563	0.035345833	22.72442436	22.65996742
Sun1	0.164820194	0.568241131	24.16974449	24.11481667
Sun2	-0.032384872	0.077777493	26.51701164	26.67060661
Suox	-0.360158443	0.533408629	21.25790787	22.45773697
Surf4	0.009432793	0.020811515	23.81567764	23.47370338
Susd2	0.089206219	0.256734536	26.05243874	26.07889557
Svil	0.451628685	0.971799584	24.51111031	24.97180367
Sync	1.127851963	1.095191788	20.78833771	21.82578468
Syncrip	0.136822224	0.455240462	25.74023628	25.85198021
Syne1	0.214656353	0.429621627	24.80597305	24.81743622
Syne2	0.58447361	0.443321655	23.19700623	23.66622353
Synm	0.533454895	0.426206074	23.04321671	22.85079384
Synpo	0.175765991	1.03150368	25.59536934	25.76585007
Tagln	0.172629356	1.144251424	33.37075043	33.42779922
Tagln3	0.320820808	0.92621294	26.27969551	25.72129822

Taldo1	-0.114872932	0.532076823	26.51257324	26.82796097
Tapbp	-0.271061897	0.323141415	24.48726273	24.96433067
Tardbp	0.100439072	0.490455694	26.25907707	26.06968689
Tars	0.064744949	0.145769935	24.41982651	24.55092239
Tbc1d1	-1.129895687	1.147688419	19.73096466	20.80088806
Tbcd	0.258430958	0.433709443	21.44909668	22.05609512
Tcea1	-0.222082615	0.437824324	22.3118	22.96490288
Tceb1	-0.196125507	0.253882813	23.67454529	23.89068985
Tceb2	-0.260139465	0.826977346	24.79392052	25.30344009
Tcn2	-0.571621418	1.184364778	20.80937958	21.26218414
Tcp1	-0.165502548	1.039755789	27.11525345	27.22563744
Tes	0.19700861	0.909810475	27.07581902	27.30478096
Tf	-0.122513771	0.350215888	30.88961411	30.42672348
Tgfb1i1	0.031270981	0.122937312	30.48769188	30.77548981
Tgfbi	0.199584007	0.807906878	28.86688042	29.11078072
Tgm2	0.02022028	0.163630035	30.08372688	30.08042717
Th	-0.354032516	0.130215823	22.20386124	22.15526962
Thbs1	0.176159382	0.245612728	26.86903	26.007658
Thumpd1	-0.219446182	0.19653346	21.8652916	22.71320152
Thy1	-0.292264938	0.418476661	25.38142776	25.56246948
Timm13	0.74641037	0.646317705	24.23161888	25.74365616
Timm44	-0.366450787	0.303103687	20.37342072	22.51953316
Timm50	-0.302840233	0.784779794	21.13081741	21.66257858
Timp3	-0.133297443	0.218861267	23.24803352	23.15517616
Tinagl1	-0.122456074	0.691248779	29.79730225	29.86039734
Tjp1	-0.279983044	0.450923382	23.67206383	23.42534447
Tkt	-0.048878193	0.16665468	29.93466568	30.1450367
Tln1	0.082698822	0.943934973	33.09641266	33.1918869
Tln2	-0.010284424	0.017663357	24.25053596	24.52384567
Tmco1	-0.165453434	0.075911614	20.40072632	22.49770164
Tmed10	-0.057714939	0.368015874	25.62636566	25.85982132
Tmed2	0.014499664	0.019474181	24.72192383	24.76080894
Tmed9	-0.78034544	0.342439127	23.45913887	23.46861649
Tmem14c	2.229607105	0.707689269	24.53842545	24.27937508
Tmem167a	-0.092648506	0.123962476	20.91889	21.38884735
Tmem43	0.124567986	0.603581245	27.67915726	27.83171082
Tmod1	-0.827119827	0.73451689	22.399786	20.21521759
Tmod3	0.246756554	0.261854845	25.17321777	25.49987411
Tmpo	0.027092457	0.18434603	27.37500954	27.4247036
Tmpo	-0.236915112	0.892910523	23.40769005	23.41570663
Tmsb10	-0.059326172	0.063264076	22.7549305	22.46836662

Tmsb4x	0.16977787	0.259018083	27.53215027	26.73789215
Tmtc3	0.046685219	0.114759803	22.41379738	22.32909775
Tmx1	0.075701714	0.09137356	24.08610344	23.95766068
Tmx2	-0.270761013	0.44894181	20.85452843	20.72675323
Tmx4	-0.04861021	0.085047493	22.07198715	22.11511803
Tnc	1.656639576	0.817946665	21.9107132	23.00216484
Tnfaip8	-0.309360504	0.345950719	20.6457634	21.97858429
Tnpo1	-0.004243374	0.01739006	24.93192863	25.15753746
Tnpo2	0.633282661	0.48217006	22.54295349	22.89774132
Tnpo3	-0.339925289	0.547320836	23.3334713	24.58198929
Tns2	0.050353527	0.141126015	26.92150307	27.09908676
Tom1	0.361064911	1.278554055	22.96201134	22.44468117
Tom1l2	-0.16173172	0.244904532	24.08480644	24.34435081
Tomm22	0.242465019	0.440870822	23.17788506	23.03818512
Tomm34	-0.853889942	0.518578478	23.1900425	20.33805847
Tomm70a	-0.040040493	0.052119545	23.31146622	24.24401665
Top2a	0.102632523	0.161844173	27.15663147	26.3432827
Top2b	-0.236506939	0.360885171	23.57761574	24.31492805
Tor1aip1	0.465477943	0.172477878	23.09566307	23.1896801
Tor1aip2	-0.542536736	0.303976179	20.412714	20.23093796
Tor1b	0.25190115	0.463260753	23.19819069	23.38389969
Tor3a	-0.236032963	0.391202238	21.86525536	22.08271217
Tpd52	-1.379724503	1.221049424	21.2291317	20.95065308
Tpd52l2	-0.1229496	0.282825787	25.4373951	25.28704262
Tpi1	-0.062595367	0.515939594	29.48958778	29.51337242
Tpm1	0.157471657	0.452518302	29.81053925	29.67801476
Tpm3	0.030799866	0.063303803	28.98576546	28.54144859
Tpm4	0.114137173	0.409819449	26.75276947	26.44029808
Tpp1	-0.167324543	0.448040732	24.94574547	25.02863121
Tppp	0.336646557	0.800124346	21.16594696	21.24469757
Tppp3	0.126515388	0.45297491	28.13985252	27.95038033
Tpr	-0.293371677	0.311573257	22.6399765	22.78210831
Tprkb	-0.310792446	0.233893777	20.4673233	21.4998436
Tpt1	-0.053723335	0.08242434	26.81102943	26.47903442
Trap1	0.167760372	0.091936796	22.7874794	23.12363625
Trappc2	0.101322174	0.100428829	20.75955009	20.71313858
Trappc3	0.087371826	0.172746316	22.81060791	23.11516571
Trappc6b	-0.116393566	0.324477569	23.33156013	23.58646202
Trim23	-1.304745674	1.232205097	20.85741615	19.53733444
Trim28	-0.098539352	0.339026086	25.22574806	25.45979691
Trim47	0.088251114	0.278236281	24.59423065	24.75831985

Trio	0.515956402	0.772759786	22.49353027	22.47154617
Trip10	0.065036297	0.212181591	27.36068153	27.32765961
Trmt112	-0.169864655	0.152198387	22.17733765	23.13323402
Trnt1	-0.399352074	0.403287156	22.41879845	22.51515961
Tsn	0.708450794	0.356097066	24.19302368	23.55940819
Tsnax	-0.218497276	0.42182392	24.36165237	24.31381989
Tspan4	0.266926765	0.595729435	23.83759308	23.88446045
Tspan9	1.002959728	1.08981302	22.79643822	23.30410194
Tspo	0.304261684	0.439975325	25.35588646	26.28646088
Tst	0.176353931	0.553993586	24.45726204	24.26026154
Ttc28	0.333123684	0.417540682	21.33957291	21.50857353
Ttc38	-0.066304684	0.130942971	23.71628189	24.26406097
Ttll12	0.488135815	0.25246326	22.42436981	22.66758919
Ttn	-1.233510494	0.25173538	27.59747314	22.12009621
Tuba1a	-0.401970863	0.428558481	25.2026577	25.85364723
Tuba1b	0.064917088	0.332705904	31.65689278	31.72602463
Tuba1c	0.260387421	0.912886618	27.66749763	27.7980442
Tuba4a	0.167237759	0.039042466	24.12360573	23.58221817
Tubb2b	0.309022903	0.783508706	27.47026253	27.52723694
Tubb3	0.39286375	0.335575916	25.91307831	26.13586617
Tubb4a	0.392973423	0.597594299	24.0679245	23.68228149
Tubb4b	0.143409729	0.842682265	32.15161514	32.22937393
Tubb5	0.201173782	0.977579129	29.1826725	28.84508705
Tufm	-0.014064312	0.034556248	26.62631035	26.75187492
Twf1	-0.153306961	0.242188321	23.7869606	24.13265419
Twf2	-0.073271275	0.161922897	23.07336044	23.04873085
Txn	0.111138344	0.416180201	27.95338058	28.00988007
Txn2	0.510151386	0.961244698	23.55835724	23.45901489
Txndc5	0.098078251	0.305425097	26.29036903	26.48879433
Txnl1	-0.051270485	0.155111855	24.43904686	24.71560097
Txnrd1	-0.003939629	0.010648509	24.76395226	25.14941978
U2af1	0.180516243	0.325851043	23.51159286	23.72296524
U2af2	-0.244616508	0.682074994	24.55543518	24.97478104
Uap1l1	-0.117137909	0.605827937	24.07936287	24.42406273
Uba1	-0.045884132	0.306281973	29.47330475	29.56844711
Uba2	0.073765755	0.234962498	23.4966774	23.47258759
Uba3	0.164494038	0.186970917	22.40810585	22.16760254
Uba5	0.439878464	0.093414484	24.57813454	24.50911903
Ubap2l	0.85119009	0.885596963	22.1378994	21.98780441
Ube2d2	-0.165067673	0.397453651	24.74570847	25.40077019
Ube2i	-0.098370552	0.301970878	22.73811913	23.08422279

Ube2k	-0.798068523	0.427742756	23.10448837	23.23965263
Ube2l3	0.122257233	0.404774657	26.71292877	27.2473526
Ube2n	0.027359962	0.189412344	27.25304604	27.36009598
Ube2v2	0.050595284	0.104442317	24.8894825	25.18808937
Ube3c	-0.399784565	0.980758373	28.98011017	28.89680481
Ube4a	-0.787062645	0.847319396	20.5993042	21.52008629
Ube4b	-0.575336456	0.665216144	21.9642334	20.82873154
Ubl5	-0.066843987	0.06956069	20.16888809	20.26956558
Ubqln1	0.072437763	0.127025215	23.65031433	23.75195122
Ubqln2	-0.459320545	0.253213481	19.77482796	22.39490318
Ubr4	0.195713043	0.552062513	23.57773209	24.02757645
Ubxn1	0.011302471	0.009785728	23.43249893	23.43173409
Ubxn6	1.231986523	0.567539829	21.28209877	23.11187553
Uchl1	0.284908295	0.776143507	27.3411293	27.41296387
Uchl3	-1.372788429	0.522328671	20.23054123	21.16144371
Ucp1	-0.360180378	0.187505251	27.83424568	28.74765587
Ufc1	0.080644131	0.203098334	24.8137722	25.37878418
Ufd1l	-0.150527	0.313169885	24.05722046	24.65398026
Ufm1	0.030353546	0.115950224	25.01239586	25.0998497
Uggt1	-0.192722797	0.432190257	26.68819237	26.69604301
Ugp2	-0.187726974	0.861278847	25.2053833	25.44843483
Ugt1a9	0.315675259	0.577113471	21.21282196	21.53578186
Umps	-0.226836205	0.436170162	20.27491951	20.3565979
Unc45a	-0.002278328	0.006839437	26.48446846	26.7522583
Upf1	-0.123719215	0.226824766	24.5903511	24.9501133
Uqcr10	-0.226063728	0.339661979	25.62530708	25.85279083
Uqcr11	-0.005918026	0.007327277	24.14328194	24.6894989
Uqcrb	-0.102604389	0.161273674	26.57484818	26.72208023
Uqcrc1	0.014473438	0.018216029	28.4464016	28.52555656
Uqcrc2	-0.050413132	0.071754606	29.00587082	29.26939201
Uqcrfs1	-0.169576645	0.242077409	27.18262482	27.35034943
Uqcrh	-0.085243225	0.104697263	25.0214901	24.74365616
Uqcrq	-0.183642387	0.341296136	26.67114639	27.12366486
Urod	0.032152176	0.055844412	22.52054024	22.51511192
Usmg5	-0.092226028	0.059802582	21.73797607	22.27665329
Uso1	-0.17871666	0.381588836	23.92786598	24.2146759
Usp14	-0.075181007	0.136285434	24.35521317	24.76597595
Usp15	0.813306332	0.467965221	20.77072144	20.46886826
Usp20	0.136258125	0.233759852	25.77329063	25.91360474
Usp4	-1.152683258	0.543376955	23.24254799	23.64954567
Usp5	0.033867359	0.13002756	26.55236053	26.92614746

Usp7	-0.427376747	0.745926448	22.97805977	22.44775963
Vac14	-0.448499203	1.088098732	20.6120739	20.50978279
Vapa	0.063502789	0.212735172	25.22563744	25.42863846
Vapb	0.081908226	0.130039369	24.8345108	24.16851997
Vars	-0.206067562	0.533305936	25.78651237	25.67314339
Vasn	0.241764069	0.117861982	22.90906906	22.89254379
Vasp	0.130157471	0.935558443	26.76585007	26.91410637
Vat1	0.064907551	0.304145523	28.16365433	28.26807594
Vat1l	0.140511036	0.076003603	20.22678185	22.23621941
Vbp1	0.170424938	0.478201714	22.70678711	22.87370682
Vcan	0.123871326	1.026092121	28.54499054	28.51968384
Vcl	0.076272011	0.570641405	32.76440048	32.75128937
Vcp	0.023126602	0.21514357	29.40340614	29.38806725
Vdac1	-0.048779488	0.257153743	28.45701027	28.39034462
Vdac2	0.045696259	0.158825224	27.23772049	27.43642807
Vdac3	0.088506699	0.133842784	24.64932632	25.21319199
Vim	0.154067039	0.997822706	34.3678894	34.35717773
Vkorc1	0.926190853	0.518014549	23.13902473	22.89962196
Vkorc1l1	-0.063521862	0.129307499	21.38863754	21.70108604
Vps25	0.045212269	0.076538238	23.57542419	24.3089695
Vps26b	0.02892971	0.070090018	22.4925518	22.71401978
Vps28	0.478134632	0.598033291	22.28951454	22.68249702
Vps29	0.106229782	0.200580853	25.05693054	25.44455338
Vps35l	-0.476117134	0.951565987	20.47496605	21.07776833
Vps36	0.805992126	0.436702424	22.79999924	22.71944046
Vps45	0.601074696	0.487613943	21.75482941	21.90870285
Vps4a	-0.309014797	0.144325642	21.73826408	21.86298752
Vps4b	-0.006831646	0.016627059	24.96666527	25.22409248
Vta1	-0.216374397	0.521234192	21.87335014	21.91495514
Vtn	0.112242699	0.287536832	26.03384781	25.75320244
Vwa1	0.301814556	0.431785686	26.03582191	25.64416504
Vwa5a	0.226636887	0.741534511	25.59849548	25.85069466
Vwa5b2	0.449192524	1.001933257	26.93494606	27.07704163
Vwa8	0.325985909	0.669658176	22.78010559	22.92974663
Vwf	0.188414097	0.713502787	27.3960743	27.2473526
Wars	0.039242744	0.058585213	24.72004509	24.75266647
Wbp2	0.375724792	0.500637777	22.27483368	22.81252861
Wdr1	0.062448025	0.759045804	29.2280941	29.31613731
Wdr47	-1.182292461	0.765754982	23.20229149	22.5664711
Wdr61	-0.0373106	0.055863158	23.85271835	23.84153366
Wfs1	0.167385578	0.567080203	27.40932655	27.46138954

Wisp2	-0.023259163	0.063621002	26.40534019	26.64196205
Xpnpep1	0.00156498	0.001654634	23.51135254	24.03170586
Xpo1	0.063468456	0.272719997	25.71599388	25.86008072
Xxylt1	0.26612854	0.095672994	19.64884186	22.08108902
Yars	0.455374241	0.94744643	24.54480553	24.39145851
Ybx1	-0.482237339	0.56690477	22.25439072	20.78012657
Yes1	-0.429020882	0.603804239	21.43818283	22.65778923
Ykt6	0.623011589	0.239818079	21.19441223	23.62734032
Ywhab	-0.10967207	0.269386403	27.65621948	27.45528793
Ywhae	-0.079799175	0.198848045	28.42981911	27.97426796
Ywhag	-0.114621162	0.268966839	28.27244186	28.22637367
Ywhah	-0.099891663	0.255412068	26.16399956	25.81736183
Ywhaq	-0.184412479	1.069745726	28.70411491	28.86779404
Ywhaz	0.004002094	0.018886745	30.28372192	30.0787735
Zak	-0.02218008	0.026419189	24.83662987	24.71455383
Zc3h4	0.36246109	0.439679703	20.45108414	21.66994095
Zfp36l1	-0.676576614	0.427023088	21.0664444	19.47165489
Zfp58	0.250787735	0.555434374	22.85374832	22.89884758
Zw10	0.573152065	0.433135159	22.69017029	22.0981884
Zyx	0.18540287	0.455487388	29.55076218	30.01810265

05) highlighted in red (increased abundance) or green (decreased abundance). LFQ repre

Log2(LFQ Col8-/-_3)	Log2(LFQ Col8-/-_4)	Log2(LFQ Col8+/+_1)	Log2(LFQ Col8+/+_2)
19.92785645	24.36566353	20.28250313	19.84260178
22.38434792	23.09500313	19.93694115	20.24948502
22.88706779	23.13658524	20.62635422	19.41751862
23.17377472	22.44970131	22.20689201	20.08994293
21.10994339	23.02259064	20.18641663	21.15053368
23.45312119	24.37417984	23.14878464	22.1770649
22.26103592	22.41348839	19.50150299	19.36481476
21.99951744	21.9642334	21.17842293	21.23794746
22.43484116	23.37623596	20.16857719	20.57624435
22.12779808	21.16097069	19.51774025	20.87441063
21.93084717	22.9192524	22.1727066	20.2921524
22.74092102	22.56188011	22.22511482	20.80402756
27.29368782	26.75887871	25.76976395	25.35685921
29.21011162	28.91911697	27.6689167	27.62554359
23.2528038	22.81182289	21.20606041	22.04526901
22.7015934	22.74396324	22.04606819	21.83151817
28.13315392	27.6069603	27.03956985	26.54523277
25.80410194	26.34830666	24.70049477	25.27604294
30.21315002	30.58557701	29.84753799	29.73747444
27.18357086	27.32637405	26.47049522	26.20050812
23.70598602	23.36826324	22.93043137	22.28861427
23.13830566	23.40924644	22.8807106	22.99296379
25.60566139	25.50787926	25.38965607	25.48876381
24.19557953	24.47060394	23.80842972	24.37636757
24.94873238	25.05936623	24.18608665	24.79069328
25.42547226	25.47676468	25.02487564	24.82880974
24.97425652	25.22482872	24.30952454	24.63084221
24.73044777	24.71612549	24.35110664	23.7470417
27.83406448	27.73737717	27.34274101	27.23004341
23.80005836	23.77283669	22.83031845	23.55847549
27.43324661	27.39247513	26.75136375	26.82917213
25.66801071	25.41189766	25.2112999	25.00727272
24.97013664	24.98041534	24.62911987	24.38284492
23.28220749	23.24474144	23.17206573	23.17259979
25.89441872	25.75704956	25.468647	25.70543289
24.06192207	24.18442345	23.68388939	23.52790833
25.69181633	25.56952667	25.03640747	25.29970741

25.04481125	25.29841614	24.80607033	25.02165985
25.58276367	25.58760643	25.32484818	24.86414909
30.31386757	30.20874023	29.98413658	29.86385727
32.82962036	32.96282196	32.5949707	32.51516724
25.53127289	25.52832413	25.03783226	25.02360725
25.33353996	25.02955818	24.90752029	24.92795753
29.58713531	29.33202171	29.0980835	29.07510567
30.02273941	30.01025391	29.64161682	29.78606224
27.17654991	27.42742348	26.96433067	26.86336899
22.93634033	23.08901596	22.64599037	22.6766777
28.39513397	28.41872597	28.24008942	28.01812935
27.42374229	27.4856205	27.40381241	27.28038597
26.46866226	26.21567535	26.08300209	26.10525513
27.23626137	27.21252441	26.82310867	26.99830437
29.10301971	29.16937637	28.6999855	28.70780373
29.95449066	29.7781086	29.42722321	29.30458641
25.49865723	25.44205666	25.26852989	25.22368813
26.28167725	26.45989037	25.90784073	26.12212372
26.25448799	26.54281425	26.10603523	26.13131905
28.38599205	28.3563652	28.1671524	28.15802956
31.96986961	32.15990448	31.90712929	31.7040062
25.26004601	25.28520966	24.99765778	25.01529312
25.27976608	25.45214844	25.1513958	24.77750969
31.08910561	31.17104721	30.57145119	30.87650108
26.41913605	26.5780201	26.17795753	26.22495651
30.55700302	30.77995682	30.42051315	30.37098312
28.89351082	29.07387924	28.68655586	28.61009789
26.66302299	26.64787292	26.22105217	26.19584274
32.40438461	32.1750679	32.1015892	31.95286179
32.16901779	32.33314133	31.85110283	31.92234612
32.59934616	32.64407349	32.4700737	32.44532013
33.31945038	33.19423676	32.96452713	32.96225357
29.53569603	29.73869705	29.44980812	29.38195419
25.10181427	25.14406013	24.77444649	24.77369308
29.63223457	29.69877625	29.42015266	29.38123322
25.01618576	25.0888958	24.82546425	24.68971252
29.49973297	29.54203987	29.35747719	29.42836189
28.67774773	28.5362339	28.33325958	28.34460449
28.96215248	28.97560692	28.98888397	28.86964798
26.58992195	26.77026749	26.50618553	26.40260887
32.2613945	32.17610931	31.9552536	31.85945702

30.00155449	29.99765778	29.81554031	29.81622696
28.52121925	28.60102081	28.28184509	28.45705032
26.56328392	26.68885803	26.49286461	26.46651649
32.16662598	32.19078064	31.95466423	31.85326004
28.85706329	28.86458015	28.66475296	28.70011711
30.93557739	30.90533829	30.78534508	30.83447075
25.09988976	24.92451859	24.85119438	24.76395226
30.79110336	30.74943161	30.70190239	30.54738235
25.65744591	25.60390854	25.55809593	25.51086998
32.3540535	32.39721298	32.25008392	32.10948563
28.01659012	27.93702507	27.83177185	27.77611732
30.00985336	30.00222588	29.92578125	29.83090973
29.40778732	29.46497536	29.40490913	29.36181259
26.22978783	26.2207756	26.31276512	26.25349617
27.37964439	27.49258995	27.54229736	27.54951286
27.74733543	27.70140648	27.98891068	27.79643631
31.97968102	32.10577774	32.16374969	32.14488602
26.75722694	26.95914268	26.92512894	27.15846252
30.92648697	31.02472115	31.12810898	31.11830139
25.40733528	25.37315178	25.78076744	25.48000526
26.83845901	26.91444778	27.10259438	27.12927628
24.56377792	24.32615089	24.73106956	24.6102047
27.12504387	27.15807724	27.42510414	27.3537178
26.91159439	26.76660919	27.07152939	26.91775131
29.3886013	29.54811668	29.64636421	29.63091469
23.42611313	23.53587723	23.64118958	23.80124283
26.15085411	26.09168243	26.28794098	26.42527962
29.59958458	29.57161522	29.69794846	29.63129807
28.09536934	28.29784775	28.25300026	28.44177818
25.71329498	26.09301376	26.23075867	26.19102859
25.11715698	25.33302879	25.44335365	25.30772018
24.91026688	24.9955883	25.14254189	25.15880966
26.24869156	26.15129852	26.39331055	26.58161545
23.9519825	24.16553307	24.36766434	24.26391792
24.4785862	24.77243423	24.84038162	24.84421921
23.68613625	23.94779778	23.93669891	24.02664948
26.72754288	26.91010666	26.99819565	27.13819313
22.322649	22.50879288	22.90743637	22.81425095
23.5716114	23.73562241	23.89226532	23.86881828
25.46391678	25.67449188	25.84309196	25.96591568
23.74745178	23.54663086	24.02225304	23.89633751

25.30528641	25.35528183	25.59721756	25.42908478
26.11316872	26.37635231	26.38469124	26.30898666
24.58623314	24.47920418	24.72171593	24.89110756
26.79141426	26.84685135	27.00827789	27.06352806
26.46908188	26.95704079	26.97125626	27.3033886
23.87764359	24.32717896	24.6063118	24.388834
25.40054321	25.67238808	25.89384079	25.95178223
23.25508308	23.39910889	23.81137276	23.70419312
25.61815262	25.53061867	25.71670151	25.73987579
20.47070313	20.94692421	21.11897659	21.12218285
27.63484955	27.73827934	27.97781944	28.36181259
27.4368248	27.35321236	27.8511467	27.63879013
24.22854042	24.71931458	24.65867233	24.86976051
26.31848335	26.8175087	26.72637367	26.89133835
24.05424118	24.18744659	24.70888329	24.59360313
24.46506882	24.3467865	24.72181892	24.6866703
23.1223259	23.32306099	23.69498062	23.9013176
25.23344803	25.69657326	25.92759514	25.89131546
27.8176918	27.13965607	27.99663544	27.8272953
24.46594238	25.37165642	25.60673523	25.42136765
24.92782211	25.44638443	25.73324394	25.7564373
23.12549782	23.26899338	24.12549782	24.04393578
20.46622849	20.64930534	20.80962753	21.21773911
22.9197979	23.39832687	24.01758766	23.91752434
24.52276993	24.57928658	25.24901772	25.11680031
19.44439125	19.74071884	20.33854103	20.38469124
23.24270821	23.65436172	24.45801353	24.60710144
21.66114235	20.86885452	21.99527931	22.86325073
25.14926529	24.14546013	25.33258438	25.47416687
23.94046783	24.08836937	25.25418091	24.2920742
19.68317032	19.78094292	21.06937599	20.51806831
24.65790939	24.50688171	25.6315918	25.81090736
21.12003326	20.31137276	21.31792068	22.37710953
21.63280678	22.56776428	22.27775955	23.17957115
24.27426529	23.79590416	23.95881081	24.84230042
20.88434982	20.13596916	21.63458061	21.60385895
28.64794159	28.21904945	28.88553238	29.95032501
19.85429573	21.07038307	21.45843887	21.74131203
20.95232582	21.26516342	22.00034332	22.09580803
21.97519302	22.97882843	23.35649109	23.49460411
27.11277008	27.04635239	27.556036	27.4873848

21.2585659	20.46716499	21.98731995	21.02113533
19.18548584	19.81465721	21.35241699	20.49091339
20.72733498	21.12496185	22.07221603	22.18721962
23.52504158	23.97044373	24.20500946	25.47840118
20.03159904	19.81428719	21.79986	22.01226044
19.84213257	20.41487312	22.38426971	22.96448135
23.109869	21.63553619	24.11569023	24.19760513
21.1754818	22.1207943	21.91139793	23.42342186
20.31993675	20.11826897	24.19219589	24.36546326
19.73628616	20.30764771	22.26244164	22.70994568
19.94264412	21.23308182	23.54933739	23.65436172
21.77090073	20.70841599	21.13449097	25.51102066
21.46056747	21.22204018	20.91109657	24.56430244
21.36730385	19.07199287	20.66487312	25.2524147
19.33287239	19.45710373	20.24070168	25.52420425
29.93480492	29.60475349	30.17080879	30.16026688
25.22210312	25.39411163	24.88105774	25.18940926
20.44216919	21.35496902	21.07025146	22.46533203
24.10341644	24.62382889	24.53700447	24.90246773
22.16750908	23.06357002	22.36855698	22.81043053
22.90107918	23.05107498	23.13213539	23.64063835
23.52013397	23.25508308	23.75103188	23.7645607
23.43364525	23.0575676	23.14870644	23.31465149
21.30607986	21.83757401	21.41281509	21.725214
23.91159439	23.91679573	23.99489975	24.11933708
24.57137871	24.90260696	24.38363647	24.49673843
24.86263657	24.87591171	24.50312424	24.65463638
23.85100365	22.50105476	23.96675301	24.01256752
22.79550743	23.15573311	23.38824272	23.17024803
22.35107994	22.5766716	20.60582733	22.35463524
25.43793488	25.66568184	25.45067024	25.56045914
25.61748123	26.17075729	25.75427246	25.78419113
29.15032578	28.68659019	30.44351959	28.99822235
25.13018036	24.34306335	25.19636726	24.98198318
22.32289696	22.39157677	23.02855492	20.06343842
23.48456001	23.72140121	23.42700768	23.42483139
28.45222664	27.74778366	29.54231644	28.36669731
28.4932003	27.98381042	29.33063316	28.29039574
26.92592239	27.06424904	27.99614906	26.97683716
25.29775047	25.1315937	25.54965973	25.4192791
28.00303078	27.76053047	29.18579483	28.03102112

27.36753082	27.6376152	27.03925705	27.13045502
29.07913017	28.73773193	29.44132423	28.92016792
25.03510857	25.27969551	25.38353729	25.3415699
22.86270332	21.52936935	22.87556458	23.37967682
28.1572094	27.93348312	28.0922966	28.19638634
26.60583115	26.78069305	26.89214897	26.80143929
29.93550873	29.35909081	30.90045166	29.70318985
23.43033028	23.88818359	24.74960136	24.03607368
25.17298889	25.46653366	25.5412941	24.86717033
23.55543518	22.86308098	21.5865078	23.38758659
26.58060837	26.8289299	26.75021553	26.4056797
24.5552597	24.95646477	24.91597557	25.14522743
22.52025414	20.17154121	23.62075615	22.26461983
19.83329391	20.2676239	18.98584557	21.56018257
28.18011284	27.8699131	28.80906677	28.33530426
21.36635971	21.22464561	21.200243	22.09343719
28.01105309	27.48069954	26.96587181	27.16489983
35.50341034	35.64361191	35.49124527	35.39487076
33.60355377	33.69695663	33.52705765	33.44862366
23.11368942	22.8817749	22.47231483	22.73913002
29.44638062	29.3832531	28.86384201	28.97440529
24.13703918	23.43834877	24.00752831	23.38047028
24.62756157	24.69184303	24.70619774	25.18876839
26.74547768	27.28700829	27.17436218	27.28100395
28.20643616	28.56623459	28.42334175	28.38451004
29.44320297	29.68685722	29.54629707	29.35691071
23.53516579	23.75755692	23.80508614	23.98215675
21.78144836	20.15222168	20.54990196	19.84856415
22.8805809	23.09180069	23.02961731	22.84710884
24.01563263	24.38462448	25.21826553	23.75317764
25.06620026	25.29610634	25.1741333	25.28905106
21.3995266	21.57722473	21.84617043	21.66487885
23.64306259	23.78066635	22.50198364	22.76854324
26.76673508	26.63256264	26.81237602	27.03601074
22.70632362	22.6083107	23.76263428	20.65671349
25.322752	25.24437904	24.95024681	24.99394989
25.09932709	25.42460823	24.86990166	26.35989571
21.9473877	21.49877357	21.29125786	21.61436653
20.65711403	22.60061836	21.68286133	21.91327477
19.36998749	21.34261513	21.57334518	21.98039818
25.39407921	25.84182167	25.68819237	25.50297165

22.4975071	22.09972954	22.30215073	20.79932022
22.48249435	22.74868011	22.46694946	22.44293594
20.46891403	20.68676376	21.06065369	21.25072479
20.53552818	24.23257065	23.51219559	23.9201622
24.09980965	20.50147057	23.26327324	24.61728477
22.3283577	22.39254761	22.54238701	21.18259811
25.53670692	25.1602726	25.35474396	25.30525208
26.75378799	26.40078735	26.37237167	26.41598129
23.70324326	23.34638023	23.52205086	23.43504524
24.16138649	24.3467865	24.29354668	24.20015335
29.88707352	29.34053421	29.18874359	29.68106842
24.37046051	24.62488747	24.83151817	23.91743279
22.50377846	23.14647102	21.25764465	20.88464546
24.69805717	25.31858635	24.95051384	24.54020119
23.62377167	24.07920074	23.87361336	23.86069679
23.08354187	23.73034477	23.12579727	22.01226425
27.3902626	27.5610714	27.91170883	27.44332123
26.55020332	26.56331253	27.08537483	27.10679436
27.20303154	27.0940609	27.02580452	26.85531235
25.97591972	26.30197716	25.54789734	25.86211586
27.16758347	27.17359924	27.19121742	27.03443718
27.8289299	27.90276718	27.73169136	27.95947456
23.70419312	23.85490799	23.62778473	23.63489151
25.07524681	25.49133492	25.43923569	25.44578552
24.40833855	24.75338173	24.8094101	24.54356766
22.19871521	22.00747681	22.02550125	21.5124855
22.59087753	23.38666534	20.62261391	23.42751884
34.38181305	33.74324417	34.27960587	34.37651825
24.36879539	24.89370155	25.22457123	25.26259232
20.48679543	20.54961967	19.44496536	20.57614708
22.07172585	22.45986557	21.68007278	20.89136314
24.86145401	23.8080368	23.42879677	24.11577034
22.22001648	23.22212601	23.18975639	22.92388344
30.64838791	30.6428051	30.5650177	30.59885788
26.02681732	26.01915932	25.81863022	26.00684357
24.64069366	23.66090393	24.17873573	24.09039116
22.48502731	21.91345787	22.35458183	21.90994644
27.74085426	28.19798088	28.3001194	27.80119324
26.69736862	26.83508873	26.7894249	26.64993095
29.59028053	29.32485199	30.15713692	29.54250145
21.70328522	21.59841537	22.26123238	21.60394859

20.95297813	21.50610542	21.3020668	20.22773552
24.34570503	23.9057312	24.10773087	21.11341095
22.0025425	22.48040009	20.18956184	22.27994347
26.88285255	27.25907707	26.66302299	27.13565063
23.42560005	23.28079224	23.91360474	23.88334274
20.18978691	20.39926529	22.29182053	21.27116203
24.13414383	24.4127388	23.95730591	24.25053596
24.88595009	25.30851936	25.39090157	24.94131851
24.92025375	24.86169052	25.04514313	24.60444641
25.030653	25.05833435	25.56447601	24.6776123
28.52297783	28.65887642	28.35451698	28.39591026
27.63436508	27.77511215	27.91096497	27.93421555
28.34057808	28.56608963	28.62299728	28.70763969
31.37725639	31.36968422	31.3622303	31.27269745
27.70701408	27.62044907	27.6092186	27.76426888
31.62082481	31.80850792	31.72167206	31.7445488
23.16842842	23.43491745	23.46326256	23.4719677
24.49740982	24.36365891	24.07259178	24.73871803
22.5598526	23.21621513	22.74980545	22.70252419
26.91467667	27.19779205	26.99884224	27.08172226
27.87660217	28.21877289	27.98261452	28.10394669
27.83394432	28.15388107	27.96900558	27.98152542
26.61498451	26.57344627	26.63478088	26.69869423
24.05978012	24.85424232	24.42962837	24.66362
23.71868706	24.33912468	24.14063263	23.568367
22.63946915	22.65501785	22.74225807	22.81432915
22.32465553	23.73221016	23.64262199	23.60161591
23.99972343	24.44050407	24.16698837	24.25060844
23.40119362	21.4009552	23.44088364	23.79312706
29.1357975	27.93590164	28.69072533	28.64873123
27.0590992	26.84481621	27.09968948	26.99075127
25.48572731	25.02483368	25.95847893	25.67720985
27.16221428	26.6408596	27.22775078	27.41796112
24.44632149	24.12778282	24.36666298	24.35366631
23.9982605	21.02541924	24.02174377	24.30089569
25.50491333	25.23355865	25.16111755	24.92976379
27.21447182	27.41771889	26.90644264	27.23662758
22.39869118	21.9840889	22.6210022	22.58276939
23.95588875	24.6352787	24.62343788	24.04276657
24.24778748	24.06972694	24.01503754	24.09595299
24.79877281	25.27156067	25.09393883	25.45729256

26.12931633	25.43755531	24.60110474	25.71156311
25.36332512	25.00260162	25.18952179	25.07838631
27.22775078	27.32423019	27.58691978	27.62142754
21.81882095	21.83402824	21.63608551	21.76951218
25.8137722	26.12474823	24.87384796	26.38534927
23.14053917	23.39949989	20.65918732	22.81743622
21.95850945	21.67620277	20.86811638	21.80774117
20.72334099	20.88472176	20.79296875	20.60068512
26.34440041	26.51444054	26.53261185	26.5625267
23.48468399	23.54533577	23.53730011	24.00204468
27.64388847	27.73963165	27.7498951	27.74271774
28.50544357	28.26369476	28.33321571	28.27364349
23.82861519	23.84115028	23.74550438	23.75154305
23.64118958	23.41428757	23.65829086	23.47852516
20.52056503	23.6506424	23.32553291	21.45729065
23.88864708	23.79332542	23.46288681	23.87932777
25.0868721	25.34972572	25.14662552	25.26728058
22.76706886	22.47278595	22.83589935	22.97168922
25.84615707	25.63522339	25.78431702	25.55651665
25.01286507	25.04247475	24.73753166	25.13938332
23.88557816	24.10181427	23.97666168	23.82366753
28.16763115	28.64151382	28.41477966	28.38706017
27.24435997	27.29998779	27.36836433	27.57924271
27.74759293	27.70266151	27.54561615	27.57967377
28.27590942	28.3631916	28.30264854	28.33577347
25.41670609	25.63931465	25.37441254	25.51023483
24.39754295	24.80798721	24.85813713	24.79143906
25.2550106	25.53557968	25.32896042	25.18759727
23.51376343	22.82927322	23.66849899	23.47766113
23.51002502	24.17934418	24.04685211	23.72327805
26.25373077	26.13516045	25.93968391	25.92506218
31.67366791	31.72635078	31.53894424	31.5570488
21.25406265	22.30162048	22.44576645	22.40241814
21.90657425	21.84597969	21.88550377	21.24894333
22.97669601	23.25580406	22.63023186	22.2991066
21.88341713	23.04633522	22.21889305	22.51693916
27.3558197	27.54965973	27.52005768	27.6685791
22.96407509	22.88756943	21.99672699	22.44255638
27.92750549	28.12470055	28.01701355	28.00865173
26.25292015	25.74939728	25.67882156	26.01192856
27.65492249	27.44797707	27.34832382	27.45458221

26.11275101	25.04606056	25.01150131	25.56830978
25.61689186	25.55332756	25.63342285	25.58917999
27.58813667	27.69849586	27.81695938	27.62763214
23.74980545	23.85861206	23.50857353	23.42675209
21.88937187	22.36121178	20.68705368	22.0313015
26.22480965	26.42334175	26.2477684	26.42507172
30.62339973	30.6553154	30.63927269	30.67547798
31.45238304	31.49342918	31.57673073	31.51559067
26.93898773	26.92524338	27.05030251	27.00774193
27.79977417	27.57441521	27.64051437	28.0799427
27.34680367	27.25772858	27.32817268	27.15460396
24.76622963	24.86443329	24.96481514	24.54037857
23.84613228	19.3735199	23.13354683	20.15570831
25.70661926	25.9403553	26.09029007	26.11441994
29.01916313	29.16753578	29.07640457	29.01916313
21.96564293	21.89500618	20.54518509	21.41333199
25.13653183	24.08107185	23.90416908	21.14152718
25.48357582	25.2669239	25.41586876	25.43749046
21.56676483	21.06946564	21.01420212	20.24423409
23.26785278	23.71313858	23.62800789	23.68367577
21.82489204	22.68504524	22.30580139	22.67603111
22.34648895	19.80333328	23.29445839	22.56411552
23.32827568	23.16752625	23.1368351	22.94754791
24.51568985	24.7810173	24.99425125	24.87290955
19.66628838	22.77182961	22.41002274	19.24309731
25.48508263	24.95304871	24.82570648	24.90687752
21.81130219	22.33581734	21.63871384	21.90675926
27.86230659	28.10973549	27.79680634	27.83803749
22.90747452	22.89502335	22.73770714	23.12434578
28.47626305	28.37761879	28.27599716	28.27781677
20.55964279	20.88814545	20.19503784	21.10399246
21.33745193	21.48973846	21.42141533	21.26619339
23.7165966	23.43936348	23.96393394	23.65839958
22.96017265	23.70345497	24.71497345	23.57357597
21.39105225	21.83491516	21.75401306	22.9392128
24.89439583	25.04159737	24.63245201	24.99157333
24.53913498	25.27721405	24.65102577	25.03279877
25.53376961	25.20288277	25.1091671	25.64507103
21.15933418	22.3364315	20.32685089	20.7525444
24.11949539	24.7358284	24.39937019	24.85167122
21.58421516	22.61112785	22.06985855	22.0435009

22.05599594	22.33815956	22.01000786	22.17648697
21.32865906	21.67495346	19.86559105	20.06594086
19.3846283	19.47611237	19.64963913	20.08550453
25.16683578	24.48173141	24.91456223	24.36719704
27.86141968	27.67134857	27.86230659	27.82735634
25.41419029	25.95584297	25.37125778	25.1862011
22.45938873	22.63154221	22.80140114	23.09534073
21.82869339	21.56991959	21.45281982	21.6306324
24.32216835	23.23594856	23.33497238	21.64513206
28.10639381	26.83677483	27.74848747	27.80488968
29.31583405	28.04301643	29.86929512	29.74534988
25.41151047	25.36135101	25.40590668	25.44922256
22.28824806	22.22764397	20.54746056	22.67009926
22.39223289	22.87708282	22.66270828	22.94754791
27.21243286	26.68083382	27.06074905	26.93629456
27.86336899	27.42582321	27.41045952	27.39451981
23.34638023	24.03548622	24.72312164	24.78910255
23.00799179	23.18904686	23.41789627	23.33115005
27.50241089	27.65539932	27.53096008	27.36869621
26.21525002	26.43273735	26.26731682	25.90664864
21.14388847	22.15360069	22.20654488	22.83172989
28.07280731	28.13114357	28.24054527	28.33955956
28.43300819	28.13486671	28.05708504	27.86797142
30.32967186	30.52477264	30.54489708	30.78316116
26.79315186	26.86702919	27.0131855	27.03275681
25.74624634	25.88469315	25.31489182	25.48578835
24.45029259	24.91679573	24.64196205	24.30424118
28.28674316	28.8877697	28.65188026	28.86502266
28.25615501	28.8006382	28.64023781	28.68291092
22.02276039	21.93581772	21.76263428	22.58566093
27.87660217	27.68598938	27.63733864	27.62449837
27.2652607	27.13721466	27.21261787	27.23242378
24.29424858	24.67745209	20.61432457	23.37238884
25.76258469	25.5970459	25.51177406	25.74855232
22.27255821	22.67104912	22.21903992	22.34350967
21.33352661	22.21118927	19.92749977	21.15616417
20.37634087	20.51281738	21.43501854	21.0283699
20.39881897	21.19604492	20.47196388	21.18020248
27.96455193	28.07091522	29.26657867	27.85869408
24.63931465	24.55713081	24.45863914	24.26763725
25.34884644	24.81406403	25.29582596	24.67481422

29.44687462	29.15126991	29.20669174	29.25169182
25.77429581	25.74031448	25.87415314	25.41882896
23.3089695	23.99394989	24.20888329	23.89901352
22.10632706	22.50457954	22.40960884	21.30628395
19.33066559	22.44288445	21.98314857	22.23829651
22.6465168	22.35579109	22.95397186	21.86170006
20.5561657	22.18289375	21.92763138	21.98426247
24.18601227	25.1064949	24.32793427	23.82405663
24.37112617	24.6320076	23.75185013	24.29705048
24.84009361	25.52061272	25.43408966	23.55952644
20.98294067	22.60988808	21.9372921	19.81743622
27.95221519	28.2408638	28.11431122	27.93162537
27.13398552	27.42350197	27.40446281	27.228302
26.48265457	26.97366524	26.90184784	26.86561394
27.40811157	27.7723465	27.74477196	27.63982391
26.82335281	27.23068428	27.24825668	27.01722717
26.76597595	26.67060661	26.72832298	26.77994156
26.25943565	26.58734894	26.06056213	26.65703773
25.77622986	24.81728935	24.14709091	24.72998238
22.45078278	22.13210487	22.84900093	21.8631382
26.27701759	25.58960915	25.5723629	25.48812103
23.51641083	23.502882	23.40574455	23.94922256
24.81122589	24.57392311	24.7957058	24.69805717
26.82723427	26.83303833	27.16230965	26.67060661
19.66143608	22.26728058	21.88241005	20.93733978
24.3471241	24.63566589	24.3924427	24.64982033
28.17126274	28.31678391	27.9020195	27.97421265
26.23357773	26.83821869	26.90104103	26.72090721
24.70160484	24.8560009	24.73551941	24.75938797
19.85044289	20.30084038	19.65219688	20.67839813
24.64135551	24.83209801	24.60918999	24.52312851
27.41981125	27.38393402	27.23361397	27.42630386
23.92533302	24.34251976	23.94225883	24.20925522
21.34277725	21.35412407	20.98356628	21.6462326
19.76639175	20.13156319	21.07672501	22.52250671
21.48772812	21.67081261	19.65918922	21.65394783
21.84521484	22.37872505	22.18131256	20.84009552
23.52516174	24.13210487	24.47704315	24.23987198
23.47741318	23.53824806	23.09445572	23.51496696
24.85405159	24.53777313	24.56569672	24.4639473
27.66756439	27.38615608	27.76357269	27.86307526

28.59693909	28.19835472	29.3358593	28.88631821
24.26870918	24.43720627	24.38225174	25.41564178
24.62772942	20.25868416	22.65569496	21.84643936
27.75015068	27.80384254	27.93769836	27.64766693
23.5716114	23.52193069	22.72165298	23.15377045
29.47645569	29.42271996	29.43987846	29.39040565
25.32416153	25.33582497	25.52345657	25.40304947
23.88352966	23.49753189	20.93762779	23.57865334
23.06188965	23.02086258	23.40652466	24.06035614
22.46288681	22.71985817	21.8392868	19.91030312
23.31257439	23.4913044	23.75276947	22.94899178
21.60014153	22.6808033	21.60154724	21.32141113
23.30270958	21.87680244	22.1558876	20.76772308
24.85761452	24.69322586	25.39528847	24.81156921
30.81604385	30.80585861	30.72183609	30.64658737
27.77052116	25.2621994	29.89074516	26.0720005
23.40730286	23.9731617	23.94529915	24.61026001
19.92753029	21.49462128	22.80616951	22.50642014
19.51797676	22.07077599	20.23880577	21.96273613
25.71897507	25.12506485	24.83605194	24.78111839
26.62449837	26.94022179	26.68899155	26.9392128
27.98527718	28.15243149	28.06937981	27.99830437
20.47842598	21.40877914	20.71716118	21.49760437
21.52716827	22.39848328	22.11955833	22.38292503
23.50227356	21.25653076	23.21448326	23.2731266
30.66237831	30.82744598	30.65761566	30.74069405
26.95482445	26.43745995	26.97901917	26.93202019
25.0875206	25.09277153	25.79540825	25.04531097
28.29395103	28.29048347	27.60886574	27.64691353
24.36859703	25.11119843	25.12734985	25.185709
24.20254517	24.60755348	24.08342743	24.03111649
26.09208488	25.87741089	25.67317009	25.73000717
28.38067627	28.88588142	28.42278099	28.26552963
26.29205513	22.65447235	22.34285927	23.97744751
22.93136978	22.05225182	22.00343513	21.99624443
20.60839462	22.62354851	20.66417503	22.54587746
22.2907238	22.13216782	22.46109009	22.7580452
22.75857544	22.59684753	22.96280479	21.7477169
22.76439857	24.02445221	20.53953552	23.49374962
33.99201202	33.73034286	33.66670227	33.5112381
33.55750656	32.61324692	32.8741188	32.86494446

31.33410072	30.87957001	30.67227745	30.61131287
27.10819054	26.12980652	26.87806511	27.38944244
30.88939667	31.00142097	30.73303413	30.86452103
30.69062424	30.57650566	30.4682045	30.51512146
21.25093269	24.78461647	23.43783951	21.20578575
28.27377701	28.31272125	27.88878632	27.77762222
27.92133141	27.89827538	27.73666763	27.63754654
26.13709831	26.03370094	25.82245255	25.79503632
24.83788109	23.27611351	23.35124207	22.72847748
23.00269699	22.64577103	22.94483376	23.0180645
21.06486893	21.28883934	21.69011497	21.81331062
23.62433052	24.17561913	23.48234558	23.60195541
24.2657795	24.72614098	24.66752434	24.33039856
21.91444397	22.33112335	19.18474197	22.10671043
26.72468376	27.05569077	26.78069305	26.91570282
25.9023304	26.18124199	26.47407341	26.24927139
24.12699509	23.9392128	24.29949951	23.96208191
24.87121773	24.99191856	25.07618523	24.97324944
26.1654377	26.74149704	26.61371994	26.47504807
20.48677254	20.95723724	19.54231834	22.58772087
25.94091606	25.82422638	25.85098076	25.97471619
25.16015625	25.40288544	25.15379333	25.24445152
23.91415215	24.10940742	23.66579056	24.29508972
23.93292046	24.28982353	23.96947861	24.34543419
22.64337158	20.740242	20.28617287	18.96962929
23.25767517	23.7470417	23.81880188	23.99118423
23.15807724	23.1516037	22.62823105	22.7059021
21.34564972	21.55215454	21.92784882	21.84314537
22.62003899	23.45713615	24.2315464	23.06284523
23.65643692	23.82551384	24.83610153	24.10101318
22.69176865	22.40979004	22.23327255	22.69108582
25.41193008	25.53011322	25.54754448	25.56278992
28.06460762	28.07030106	28.04280853	28.05305099
20.93329811	21.08569717	20.91269112	21.94845772
26.84864235	26.26036835	27.52050781	26.52348709
28.38018036	28.17636108	29.33108139	28.21247864
26.32051659	25.32988548	26.44863892	25.32381821
27.66722679	27.71338654	28.84311104	27.96002769
27.39050865	26.74342537	27.97180367	26.68431664
26.1315155	25.28520966	26.46734238	25.4086628
24.97026825	24.00358772	26.83062363	24.81782532

25.29852104	24.34719276	25.23019028	24.70065308
23.62900925	23.74960136	24.77243423	23.99049187
26.19754982	26.03797913	25.82050705	25.8752327
28.38484001	28.16916084	27.7972393	27.77730942
23.62800789	23.68217468	23.60116196	24.03942299
26.49629784	26.65594673	26.54730797	26.65253067
22.69095802	22.81983376	22.33172417	23.05495262
25.95568848	26.47226143	26.20362854	26.85982132
20.93890762	21.16894913	20.70859528	20.31395531
20.1331501	22.48895454	22.23937607	22.12151909
23.86994934	24.5912075	24.24459648	24.45901489
25.09317398	25.51111031	25.13907051	25.18040657
23.69444847	23.81019592	23.57519341	24.12226295
24.31195259	24.50039101	23.93840599	24.85095596
23.82900238	23.60048103	25.50263786	24.28841591
25.36208725	25.23538589	26.80550385	25.86580276
22.94229507	23.14066315	23.88734627	21.38968849
24.65719986	24.54986572	25.3492527	24.80301857
20.7519722	21.32201576	20.19048119	21.06879997
29.97514343	30.23043251	29.88537216	29.458498
29.78721619	29.52837372	29.55771637	29.56734085
24.99899292	25.20213509	25.14678192	25.16917038
23.18808174	23.23444366	23.20715714	23.28742981
25.97830009	25.57842255	25.66158295	25.46538162
24.52981377	25.04938889	24.78201866	25.26895905
23.35769844	23.52671432	23.31492805	22.75952911
29.56136322	29.52950859	30.39703369	29.5480442
25.54657364	25.48686409	25.63969994	25.73301125
27.28938484	27.60059547	27.57629013	27.69072533
18.94221497	23.10181427	23.58439827	20.17101479
22.28087807	20.39894485	21.98287201	22.86921501
25.16989708	25.0641861	25.02144814	24.88049698
23.08224106	23.91643143	23.72650337	23.26356125
30.09521866	29.52872658	29.65592957	29.52067566
29.73670006	29.25505066	29.22458076	29.09743118
19.01150513	24.2896843	23.67594528	22.31254768
25.15460396	25.55520058	25.52172089	25.50102997
22.7917366	23.47938919	22.49814034	22.94583511
24.87211037	25.35140991	24.98776245	25.33340454
22.46129036	20.39266586	22.20505524	19.66051674
26.49417686	26.74560547	26.15977097	26.31554985

22.32865906	22.84350967	22.8281498	22.81381989
20.26045799	22.62604713	23.15290451	22.15697289
23.39047623	24.0543232	24.15784645	23.87773705
26.05372429	26.51550865	25.5339489	26.34996033
20.19823837	21.29759789	21.08420563	21.2170887
25.10904884	25.06459808	24.6753521	24.68463898
25.80999947	25.23917961	25.62505531	25.64336586
27.48423767	27.70497131	28.02157593	27.66621017
24.52085304	24.46369934	24.46294975	24.27859688
24.80774117	23.93102837	24.45387459	24.09393883
22.9061718	23.07918549	21.81604958	23.08687973
22.31409836	22.20794678	22.34602928	23.41325569
22.44611931	22.72415352	22.67022896	23.10181427
22.32726288	22.70821953	22.23771477	22.5212841
21.80754471	23.8314209	22.73516846	22.15903282
25.78469086	26.15137672	25.95805931	26.00966644
21.26802254	21.40945244	21.08660507	21.67232323
23.01115227	23.25522614	23.35164642	22.04069519
25.05063438	24.69906425	25.50993347	25.39191818
23.98754501	23.49032593	23.1720047	23.08938789
23.76121521	24.39466858	23.82473755	22.87314415
30.17925835	30.10299492	29.93915749	29.87522697
22.34529877	23.60715866	23.1965847	23.36332512
26.88820648	26.71881866	27.72299194	26.92263603
26.77140236	26.64044571	27.37534142	26.54554176
25.98048019	26.46766853	26.10824966	26.21267319
24.56523132	24.50445747	24.28785324	25.26441956
23.2637043	23.73541641	23.38337326	23.84469795
20.51758957	20.63307381	20.64912987	21.02177811
21.45568275	21.33226967	21.25660896	21.22564507
27.36594582	27.69584274	27.84625244	27.39100075
21.87023163	21.7474308	21.79594231	23.58221817
22.45010376	22.48042488	22.67588043	22.51862144
26.52747536	26.44833946	26.21648979	25.9982605
26.39247513	26.61610603	26.28556252	26.42660904
21.9349575	22.31370926	22.20967293	20.94915771
27.49708939	26.97607231	26.79352379	26.80833054
25.73383904	25.14262009	24.89536667	24.9086647
26.2405262	25.95951843	26.61876869	25.97554779
32.75258636	32.90655518	32.56787491	32.59428024
22.63949013	24.19392586	24.1791172	24.36833

26.18029404	26.0474968	25.61487198	25.72119331
26.89295959	26.3788166	26.33703423	26.49800301
22.11047363	22.3066349	19.48988724	21.05130196
19.91127205	21.09892654	21.41335487	21.20012283
26.68525314	26.99183273	26.65608215	26.5101757
25.23979759	25.41931152	25.14417648	25.11632538
20.32259941	20.14757919	20.16570282	20.89141273
26.96807098	27.30094719	26.89388657	26.95249367
23.2123909	23.8630619	24.00718689	23.74663162
27.1340847	26.91809273	27.15112495	26.99269676
26.49845886	26.83328056	26.5610714	26.9082756
24.37012672	24.35178185	24.66242599	24.70033455
22.38041687	23.12842751	22.47951126	20.2995739
22.30563354	22.50268745	22.14080429	22.24617767
27.0413475	27.24209023	27.34036446	27.28674316
27.0377903	27.31613731	27.13447571	27.24018097
23.52921867	24.14623833	24.23139954	24.0907135
24.88943672	25.33640289	25.14623833	24.7136097
26.85638046	27.24572182	27.04364395	26.94391441
26.58132744	27.26981544	19.8731823	20.78365707
22.53205299	23.14510155	22.6770649	22.64394379
28.08542442	28.160532	28.70493889	27.94898987
23.54380226	24.57213211	24.95171547	24.69067192
23.04438591	23.0836544	23.13417435	23.13243294
24.73799515	24.30375481	24.80818367	24.60574722
24.00573158	24.39754295	24.19527817	24.53267097
21.65442848	21.91411591	22.40384865	21.61222267
23.60648155	23.97578812	23.94681549	23.90223885
20.24376869	20.28624725	20.41028214	19.64713669
26.58233261	26.75110817	26.93100548	26.72871208
22.31581116	22.05311394	22.55189705	22.88351059
22.14416885	22.72737694	22.59907532	22.28059387
28.31471062	28.04588318	29.03154755	28.27475357
27.8294754	27.8993721	28.62592697	27.88430977
27.44939613	27.1498661	28.17702675	27.15624619
29.75903893	29.91213608	29.89203453	29.87252808
23.08432007	24.04759979	23.24058533	23.57392311
23.49179459	23.67981529	23.15800095	23.72806168
23.84823608	24.1791172	23.98172188	24.15019417
19.3044014	22.81794357	23.66698265	23.53076744
25.63286781	26.34997749	25.75824356	25.80407715

23.22169876	22.53131485	22.58845329	23.02813339
22.95102119	23.87549019	23.18780899	23.35997963
22.52056503	23.17032433	23.04901505	23.24301338
22.09690094	21.61764336	21.2924633	22.30888748
26.69935608	26.90011978	26.90701485	26.99042702
26.3803215	26.65799141	26.4472847	26.49955559
22.90370941	23.89328384	23.21403885	23.94190025
28.52028275	28.78125572	28.69849586	28.54318428
24.37185669	24.48726273	24.11052132	24.31354332
21.69102287	22.27534676	22.20350266	21.52109146
25.97156143	26.70292664	26.67613411	26.73995399
29.69701958	29.44886398	29.37343407	29.58709908
20.65883636	21.45322227	21.78008652	20.0307579
21.24237442	21.62359428	19.70240974	22.04360199
30.98739243	31.31202888	31.39053917	31.16392899
21.81499481	22.18156052	21.39712524	21.11821556
26.78593826	26.89214897	26.85281372	26.48779869
28.59565926	28.37898254	28.30125237	28.34781647
25.79153824	25.67895508	25.82267189	25.84194183
29.71925926	29.94307518	29.70219994	29.86231995
23.59240532	24.24590302	24.0845623	24.22390938
25.29403877	25.46877098	25.29645538	25.35144424
27.69032478	27.62651825	27.65006638	27.58548927
25.47128487	25.13606071	24.78516579	25.00135612
21.90873909	22.20904732	22.22013474	21.62479973
23.67281914	23.18330193	20.47445488	23.43987083
25.33395004	25.43033028	26.18465042	25.28947258
20.17267609	20.60928726	19.69312096	20.08336067
27.53400803	27.58125496	28.19605827	27.59889221
27.66580391	27.06054306	28.05470657	27.55566978
24.20291901	24.06972694	24.21393394	23.90168571
25.00573158	25.26860237	24.95743942	25.40973091
21.28957176	20.66535759	21.44500923	21.59750748
31.27358818	31.39079475	31.20472336	31.14363861
26.62895393	26.56706238	26.54754448	26.35169792
26.60342789	25.92727852	25.78643608	25.86431503
21.83995819	21.92694473	21.60842323	22.06463814
27.47560501	27.57463074	27.59789848	27.54863167
29.62528229	29.92478943	29.82012939	29.91399193
27.68772507	28.2556591	28.01126671	28.32392883
27.01073265	27.23480225	27.15180206	27.1964798

23.84095764	24.03431129	23.93615913	23.59809875
22.72665024	23.31686211	22.8556881	22.97701073
23.93526077	24.31955147	24.17554283	24.5217514
24.79738808	23.84239769	24.11290932	24.66519356
23.03543472	23.23796272	23.01447487	23.39767265
28.0376339	27.84463692	27.48169899	27.50967789
31.78433228	32.13332367	31.940382	31.90795326
22.56153107	21.90884781	21.28417969	22.20323372
28.42977905	28.18881416	28.35812759	28.30513
24.49252892	24.77660751	24.66876793	24.22780609
24.26241302	24.8385067	24.50379181	24.72806168
26.359375	26.55632782	26.49908447	26.37856865
24.16530418	24.08358955	23.93364143	23.97997856
24.30813599	24.96252251	25.03136826	24.71481514
24.08115387	24.1964798	24.36899567	24.08432007
23.90793228	24.03279877	24.67459869	23.86834717
25.42940521	26.14108086	26.27399826	26.3571949
23.22745323	23.13824272	23.13978958	20.06222534
21.50884438	22.92869759	22.59634781	22.77253532
23.13238716	23.67594528	23.39401436	23.57991982
23.08687973	23.71983719	23.53136253	23.52516174
24.43096733	24.58204651	24.10573578	24.49124336
27.68985748	27.57780266	27.72195053	27.53615952
24.49167252	24.29775047	23.95916557	24.35823631
24.86207008	25.61397362	25.72093201	25.45588303
24.58743477	24.28086281	24.42713547	25.45851326
23.38679695	23.51965332	22.74396324	23.27241516
23.49850464	24.59097862	24.18729591	24.72665977
24.15668869	24.28855705	24.12384224	23.07747459
25.43914032	25.75758362	25.62226486	25.66587257
24.72192383	24.92700768	24.57409668	24.51586914
27.32276917	27.24590302	27.25178337	27.39149284
25.04992867	25.39718437	23.91378593	24.70777702
24.64938164	25.67422104	25.0043602	24.99036217
23.57922935	24.16054153	23.71334839	23.27838326
22.71531868	22.59361458	21.36003304	22.76783562
25.57669449	26.30467796	25.5114727	26.48502159
26.67101097	26.51442528	26.66938972	26.62825775
27.21752548	27.35296059	27.56201744	27.17769241
26.98043633	27.0964756	26.85982132	26.82699203
29.86008644	29.43916512	29.84507179	29.75460052

23.37105942	22.77812195	21.81426048	21.49785042
25.070261	20.90295792	27.08324432	23.67098427
23.71408272	23.92043495	23.2014389	21.34878349
23.66123009	23.42111206	23.99817467	23.29473877
25.03464699	24.87295723	24.81112671	25.31084251
20.91334724	21.65796471	21.16815376	21.70927238
27.1572094	27.15913582	27.09093475	26.9613533
29.2728653	29.54602051	29.18959236	29.31287384
24.08082771	23.74960136	23.46973419	23.44543839
25.82648277	25.20646477	25.24466896	25.07361412
28.70365143	28.82914162	28.78923798	28.76667213
23.99593353	24.45255661	25.36128426	24.98093796
22.52573395	22.62571335	22.05453873	21.96321106
21.30826569	22.80029488	22.55292892	22.4506073
22.91571999	22.1515274	22.90600586	20.51412201
26.29747009	26.45062256	26.32806969	26.49806404
19.48567963	22.57694817	22.98356628	22.45447731
21.91561127	21.84766388	21.67697716	20.10771179
23.01263618	22.98459244	22.90864754	22.6205101
20.67831039	20.97987366	21.99316025	21.13144493
25.11810875	25.52942657	25.16157913	25.54197311
24.91879845	24.86693382	24.68634987	24.93611526
25.66158295	25.64141083	25.37404823	25.47676468
28.08090973	28.20862389	28.05945969	28.00704765
28.73911667	29.08029938	28.80042267	28.92167282
23.43122292	21.09537506	21.0250473	23.75552177
29.45142174	29.13030815	30.27041626	29.41369057
28.14676094	27.68378258	28.70150566	27.74931908
26.18292809	25.80587387	26.78394127	26.03393364
25.69808388	25.48588181	25.45935822	25.49670792
20.78148842	21.80262375	21.22103691	19.48893929
22.85760689	23.41183281	23.22231674	23.57588577
26.87161827	26.90873337	27.06855965	27.07081223
25.77766037	25.6905117	25.61812592	25.57265282
25.60209656	24.03850365	25.53433418	24.36693001
28.04369545	27.43380356	28.32658768	28.18758774
22.55365562	22.91511917	22.70777702	22.85256767
25.96210289	26.51083946	26.04528999	26.29498482
23.94252777	23.69402313	23.99550247	23.28390312
22.35129547	22.87166023	19.17520523	23.18930244
27.56361771	27.80790138	27.50892258	27.66492271

24.40301704	24.5637207	24.6223774	24.80523491
24.10517502	24.2347641	24.0743084	24.1906147
21.08206367	19.72555542	20.76821899	20.87530327
23.28813553	22.23526192	22.59641457	22.90600586
26.20052719	25.79810524	25.93597984	26.17771149
20.70910454	21.200243	21.01062965	22.06236839
19.79225349	19.83535957	23.18805122	20.51297379
24.65025902	25.33251572	25.09723854	25.04013443
24.54433441	24.86665154	24.25284767	24.83504105
29.89569283	29.21660042	30.19389915	30.27119637
25.19279861	25.63433647	25.656847	25.93901062
24.56150818	25.36158562	25.16384506	24.93710327
30.12989044	30.37916756	30.15520859	30.12398529
23.61930084	23.22865677	22.99814034	23.75144196
23.59194946	23.50554848	23.23915672	23.31782722
26.81164169	26.33379555	26.14139175	26.49472618
32.48529434	32.74131775	32.56354141	32.57025146
33.2871933	33.14068604	33.26024246	33.09033585
24.03002167	24.94663811	24.81919098	24.58319473
23.07143021	23.12576675	22.30056	22.38540268
22.16692734	23.05928421	22.39322853	20.54687309
21.24341583	19.4525795	22.03173637	21.52363014
23.85148048	20.66059875	23.30730247	22.75080681
22.13705444	22.23233604	22.26816559	22.11597633
22.4930172	22.39139366	22.17529869	22.16665268
23.20188904	21.25363159	23.45425224	23.26083565
22.12420464	22.42188263	21.98541069	21.83174896
29.40764618	29.32984161	28.69912338	29.54117203
30.22008896	30.23386574	29.44353867	30.28967094
23.27639771	23.22801208	22.52824211	23.64152145
30.45356178	30.46684456	29.84438324	30.77784157
21.08769035	21.01114845	22.39649773	22.31774521
28.17059326	28.26914597	28.9626503	28.02733421
29.86373901	29.83567619	29.96389008	29.77319527
24.83171082	24.18298531	24.28164101	23.69996452
25.6885643	25.9819622	25.64438438	25.56305122
26.56929398	26.62797928	26.4659729	26.55980301
24.49429893	24.0871563	23.8038063	23.6227684
23.92116165	23.9842453	24.11346626	23.87117195
22.78426743	20.25644302	23.52456284	20.41371918
24.86448097	24.55631256	24.31513405	24.24814796

23.63765717	23.16948318	23.47654915	24.20120049
26.8646698	27.21261787	26.77793694	27.1096859
35.02461624	34.908535	34.82012177	34.79764175
27.71757698	28.03107452	27.52499771	27.49029541
25.062994	25.39643288	25.08990479	24.93620491
25.78049278	25.77140236	25.4376812	25.23374176
23.07744217	22.70782089	20.36300659	22.46856689
26.83677483	27.11941528	27.02411461	27.12543869
30.32806587	30.47933006	30.51258087	30.48481369
21.35584641	24.00795746	24.17004967	24.66231728
26.74624634	27.46138954	26.93887711	26.83364296
21.27099037	20.88653946	20.90903091	21.27980042
31.93287086	32.03829575	31.56760406	31.67850304
20.43245888	23.59194946	23.2187748	23.50130272
23.10245514	21.98475266	23.47827721	19.27838707
19.29154205	27.27692986	25.00358772	26.26970863
23.6408596	23.50567055	23.45538139	23.2166748
27.0163765	27.07500267	27.20759964	26.91433334
20.66966629	20.43635941	21.08166885	22.93441582
24.68971252	24.24575806	24.79188538	24.24219894
23.32058525	24.12478828	23.13728905	23.53635216
25.0845623	25.5705986	25.49384117	25.5112915
23.23656082	23.39675903	19.88481712	20.7010498
26.21487999	26.58663368	26.38365364	26.58075333
22.86581993	22.96084404	21.66205597	22.24388504
20.35250854	19.59352875	19.04683113	21.21210861
20.41833496	21.10929489	20.32058525	21.19044876
25.12194633	25.88187408	24.89661407	25.32254601
22.41789627	22.91451645	22.65737534	23.22798157
24.01384544	23.24250412	23.51665115	23.37491035
27.63830566	27.85144424	27.9472065	27.92002678
32.01561356	32.09461975	32.3167305	32.03606796
22.6620121	23.12472534	22.23683167	19.35831261
23.47184372	24.23994446	24.14289284	24.49381065
24.35346603	24.125103	24.72826958	24.24045372
23.38416481	23.6300087	23.78785706	23.65752792
24.00573158	24.62772942	24.1734848	25.05419922
28.40125084	27.97792816	28.18806076	28.34032249
21.49950409	21.94367218	21.55238914	21.77056122
20.61793518	22.79590416	19.851614	22.79382133
23.96895027	24.68869781	24.30570412	24.2896843

27.13104439	27.2380867	27.10299492	27.38080025
29.15356636	29.36189651	29.2132206	29.18749428
19.61882782	21.45372391	20.48607826	20.93200111
22.80011749	23.00278282	22.67219353	22.80626678
22.35347939	22.04156494	21.02297401	22.18007278
23.37451172	23.31534195	23.34800339	23.31091309
23.54238701	22.43104362	20.79157257	21.12791443
25.56040001	25.68546677	25.3972168	25.46101379
27.80402756	27.86058998	27.69816399	27.68177223
25.57383728	25.93309975	25.7634964	25.45676041
25.32601357	25.85633278	25.53922462	25.69734192
23.39047623	24.00940895	23.64262199	23.98554802
28.76132202	28.78300476	28.66451645	28.67236137
24.79406929	24.19992828	25.70809364	25.48499107
23.63123131	24.14941978	23.50772858	24.222435
23.39440536	24.06735039	23.25115776	21.73172569
22.94191933	23.33579063	23.18703842	23.28107452
24.67938614	24.41351318	24.32003403	24.9444046
22.91152	22.61658859	23.35474396	21.85316086
25.98654747	26.05653763	25.93037415	26.12693596
23.27469254	22.79253197	23.07326317	23.01646614
23.74529839	23.74724579	23.24869919	23.38363647
28.1725502	28.17697906	28.0412941	28.08947182
26.03462601	25.65951538	25.25720596	25.15147209
22.82524109	23.65774536	22.93651962	22.70153046
26.13848495	26.31591225	25.97991371	25.97443199
26.07832527	25.91447067	25.94366837	26.25794411
26.39966393	26.11141777	26.40005493	26.20856857
27.86655617	27.60448837	27.53526878	27.66499138
26.95582199	27.08547592	27.07867241	26.90127182
23.43758583	23.23185349	21.2732563	20.51054573
20.98572159	21.97340775	21.21544838	21.40358925
21.63962364	21.94059372	21.89840508	21.71933556
22.03560257	21.95567513	19.81025887	20.92433739
23.77001572	23.92352104	23.44430161	23.14239311
19.76157951	21.88072968	21.63092041	21.37268066
28.64388847	29.00372696	28.99191284	28.9842186
20.21231842	21.37533379	21.05589676	22.51857376
20.11005592	22.64884377	22.64165306	21.58001518
27.11475754	25.92066193	28.12519264	27.26642227
26.25069809	26.97059631	26.5909214	26.78867912

28.00587082	27.71554947	28.89758301	27.92874718
29.9878006	30.19295883	30.08777809	30.09307861
18.93858147	23.57623291	23.02238846	22.96082687
22.28976822	22.2510128	22.08825684	21.7897892
28.59793472	28.8052578	28.68648911	28.65710449
29.08840942	29.12314606	29.35541916	29.0731144
23.53278923	23.57253647	24.12628555	24.07496262
23.56045914	23.48787498	23.13749313	22.92116165
24.31118965	24.03473091	23.35944366	24.17432404
27.31553268	27.09224701	27.22038841	27.04541397
25.83277321	25.02656555	24.8854847	24.90104103
22.31724739	19.49758148	20.44172096	22.21611214
22.42239571	20.07632828	21.43705368	22.30304337
22.80053139	23.00063515	22.84045792	22.98506165
30.6129837	30.41709518	30.24547195	30.01025391
23.97596359	23.68013763	24.03707886	23.69029808
24.82914734	25.08448219	25.23768425	24.625
23.19675064	19.78970146	23.49801826	23.35137749
23.54450989	23.02179527	22.12905693	23.18572426
25.6224041	25.62438583	25.78291702	25.66142082
29.25460052	29.31533813	29.4424324	29.38683319
24.69290733	24.52151108	24.81245041	24.50142479
22.85709381	23.40600395	23.51074791	23.78875351
23.71502495	23.8877182	23.63942528	23.72327805
30.78892708	30.55444336	30.4900856	30.35247612
27.20685577	27.70450974	27.85715294	27.78643608
23.79857635	23.37822151	23.14631462	23.49826241
24.67943954	24.30973244	24.94225883	25.23381424
23.53433418	19.6835556	20.53162766	20.92331123
27.42438316	27.46334076	27.63996315	27.64320183
26.0275135	26.08338737	26.15555	26.17761612
24.00461769	24.24691772	23.96587181	24.25421715
23.96137428	23.79491234	23.72202873	22.64107895
20.9221344	22.56302261	22.84137917	22.29574966
28.96543121	28.81470108	28.63187027	28.65259933
20.91135979	19.84950066	21.75816727	20.05843735
25.58917999	25.34343529	25.50230408	25.1331234
21.09823036	22.92688942	23.08668709	23.00139046
23.66557312	22.99391556	24.22721863	23.84162903
27.47080421	27.28603745	27.58046532	27.50111961
28.4562664	28.62756157	28.49781227	28.5533638

24.63544464	24.21992683	24.39675903	24.12817574
31.57194901	31.85786438	32.09851456	32.38923264
23.83084106	24.52384567	23.72213173	23.91342163
28.86664581	28.89023781	30.01158714	29.19861221
30.18387985	30.05426788	31.08790398	30.21974182
29.13097191	28.95490646	30.11557579	29.1198597
22.68088913	23.25738716	23.17465782	22.82636642
23.23959351	22.7924118	22.26770973	22.44108772
23.24510384	24.37583733	23.75235939	24.04618454
23.43834877	24.72421646	21.20688057	24.07062912
20.12586021	20.81682968	20.61468124	21.12742043
34.58082581	34.07829666	34.56881714	34.4935112
34.77342606	34.18334579	34.75483704	34.60366058
26.79686928	24.88557816	25.63123131	25.32079124
23.08869362	21.82294846	22.38113022	20.45226669
23.67927742	24.06324005	24.13758659	23.82327843
22.51612282	23.28841591	23.79114151	23.34475708
24.105896	25.00577354	20.23781395	25.11354637
25.34590721	26.0011425	25.4418335	25.56598854
24.38541603	24.63311768	24.6431179	24.17759705
25.23052025	25.15247917	25.29031563	24.9858532
23.09783363	23.04102898	23.14088249	23.0616436
21.92940331	21.87567711	20.34770775	20.84494781
21.90341568	22.20821381	22.13689804	21.59404755
26.80538177	26.9690609	27.09908676	26.8052578
25.21460152	25.04414368	25.66497803	24.9666214
20.91320229	21.15090752	21.43344116	21.42167664
27.74573517	27.81053925	27.81488419	27.72884178
24.60506821	24.8080864	25.08885574	24.80134201
24.2359333	24.96358109	24.87661362	25.70472145
23.02845383	25.75597954	26.97803688	25.16710472
25.54306602	25.86230659	26.45726204	25.76202583
29.78512764	29.28056145	29.67347336	29.40098572
23.69879913	19.8177433	23.7613163	21.46171379
29.14727211	28.7380867	28.84717941	28.6092186
24.033638	24.86971283	24.59582329	27.64223671
32.75475693	32.31170654	32.81705475	32.45539856
29.76867676	30.01504707	29.83629417	29.63356781
32.0889473	32.05924225	32.06515884	32.02085495
32.48392487	32.91557693	32.97468185	32.67652893
23.98215675	24.2004528	23.68324661	23.54780769

32.90322113	33.24147034	33.03837585	33.48279572
28.02654266	28.13030815	27.98739243	28.00260162
24.98693848	25.01580238	25.95269203	24.78775787
22.48392105	22.61540031	23.02457047	22.93730927
29.33475113	29.40074158	29.56920815	29.38687515
23.8263855	21.9645462	25.39407921	24.65937996
23.1047287	23.64449501	23.71303368	23.16988182
23.95783806	23.32759094	22.75778198	23.16161728
22.59948349	22.35493088	22.54380226	22.61596107
22.85635185	23.23461914	22.16951752	21.17423248
23.16147995	22.24694633	23.43695068	19.96637344
21.89145088	22.22110748	22.05301476	21.92059898
24.71894836	24.98346329	25.17771149	24.7983284
28.0131855	27.88901901	28.03033829	27.78768349
28.31423569	28.19699669	28.19947815	27.89988899
26.56494141	26.63505745	26.50864983	26.4573555
25.23319244	24.524683	24.70044136	24.82919693
27.08009529	27.33108139	27.06424904	27.0877018
23.25623512	23.18460464	22.71473122	22.7835083
25.05672455	25.60583115	25.77658272	25.24445152
26.64855957	26.56674194	26.64182472	26.3898201
23.89448738	24.72108841	23.91897964	24.02453613
28.6048069	28.96567917	28.85370636	28.78322411
27.10759163	27.74310303	27.64395714	27.37525749
22.8244648	22.79651642	23.08526039	23.39728165
27.10199356	27.32611656	27.20936775	27.24490547
28.7206459	28.8967762	28.69288635	28.81897163
24.17234039	24.83262825	24.81386948	21.3384819
24.89407158	24.99114037	25.06755447	25.03825188
22.77880478	23.40652466	19.48445511	20.23734474
21.83313942	19.4183197	21.38120842	21.20323372
21.57163811	20.83161736	23.51761246	22.15597916
27.75919724	28.13525963	27.95726204	27.79240799
23.55754089	23.84249306	24.45913887	23.2903862
23.44417381	24.08828926	24.30966377	24.46749687
28.32984161	27.62512589	28.28542137	28.20736694
20.07179832	20.06565857	19.25709534	19.87299347
19.63223076	22.22320175	22.1866169	19.50886726
27.75200272	28.00683403	28.2423172	27.99991608
25.85676193	25.82267189	26.01971054	25.81926537
22.89670563	22.63083076	23.26913643	19.60027885

28.11802864	28.1763134	28.16062737	28.16451645
30.04231262	29.90913391	29.96154594	30.00931931
29.6123333	29.59537506	29.44367599	29.29410362
25.10693359	24.44436455	23.60218239	24.5114727
25.97495651	25.65744591	25.8182888	25.59753036
29.20144272	29.41621017	29.16367722	29.26847649
24.78586388	25.27891541	24.75000954	24.84713745
27.2380867	27.41409492	27.34883118	27.21900368
27.6408596	27.88174438	27.6205883	27.78069305
24.10197449	24.38811111	23.85946465	23.69285393
29.79217529	29.53599167	29.56793976	29.41288376
31.04335594	31.07546234	31.0012188	30.98148537
27.82559776	27.35707855	28.03543282	27.44545364
29.99213028	30.16086769	29.95532227	29.98168945
27.11137772	27.27124023	26.91832161	26.96080017
25.18135452	25.82284164	25.07255173	24.9595623
24.2186718	24.71774673	24.48640251	24.42579269
29.52960205	29.50568962	29.91669846	29.53688049
33.608078	33.68070602	33.56774139	33.55316162
24.91492653	25.14148903	25.00633049	25.08411789
27.24399757	27.67418098	26.97891045	27.43388367
23.57577133	24.16261673	23.95358086	24.38060188
26.45792007	26.32685471	26.4648819	26.46463394
22.23227882	22.28886795	22.87704468	22.59224701
22.70406723	22.56583595	21.9642334	20.17825508
25.90788651	26.37769318	26.46940804	26.47159576
22.99201393	23.20791626	19.80871582	19.58839226
22.72033691	22.33530045	20.70336723	20.4711113
22.57258224	22.91356659	23.44139099	21.7598877
27.30825806	27.55844498	27.51818275	27.62016869
29.1683712	29.32960701	29.77398109	29.38849831
29.14632416	28.67505646	29.82201576	28.75620842
26.45425224	26.43647575	27.61722755	26.44129562
21.67413521	22.2061882	21.68110275	20.88844299
22.41835976	22.26616478	22.10993195	22.26690865
20.33325005	21.68028831	21.59755325	21.40660095
23.23088646	24.01631355	24.19189453	24.24001694
28.1484108	28.31229019	27.89411736	27.94536591
25.72559357	24.09900665	25.52276993	25.77545166
22.67917061	23.05487061	20.57699203	20.69420242
25.89358521	25.2888031	25.72413826	26.59562492

21.65092659	21.90708923	21.91768837	21.63165283
21.00573158	21.46148872	20.78044701	21.85323334
24.19400215	24.5341568	24.38890076	24.28298569
23.76799774	23.29949951	22.74833298	22.75472641
20.50917625	22.810215	21.59996033	22.68483162
27.83905983	27.83340073	28.1791172	27.53103447
25.58158684	25.04701805	25.37497711	25.25878906
23.46313667	23.72546387	23.71554947	23.69338608
26.48810577	26.38922882	26.00577354	26.71502495
24.36579704	24.5892086	24.29670143	24.69975281
22.49590302	19.86380577	21.54372597	20.53069496
21.68431664	22.87558365	23.05513573	22.82632828
25.84357262	25.97261429	25.50597382	25.92589951
24.36419487	25.06858063	25.06500816	24.22169876
20.94152451	22.64636421	21.40753555	21.35479355
29.25817871	29.3480072	29.13687325	29.14821815
27.07183647	27.38755417	27.05455208	27.00206566
21.95500183	22.56541824	23.34177399	22.38763809
27.58670616	28.0485878	27.71115685	27.91376305
22.21513557	22.36260223	22.27067757	21.61737442
26.85424232	27.16700935	27.26767349	27.30591202
21.86400795	22.86408424	23.17497826	21.42653847
20.96685791	22.51161766	20.33418465	22.26195526
24.04117966	24.0322094	23.552742	23.08386612
22.8352623	23.98737144	23.45638466	24.29761124
26.03111649	26.44292641	26.05839729	26.28607368
25.86261368	26.10617447	25.94561195	25.83525848
23.25695419	22.87363243	20.21628571	20.55442238
30.16973495	30.39141083	30.44233322	30.43559265
26.13498497	26.09228706	25.64866829	26.10123253
27.35262299	27.60116196	27.59512711	27.60978127
31.02029037	30.79187965	30.63961792	30.58208084
25.31337166	25.45506859	25.15085411	25.30023193
25.97026825	26.42539215	25.77127647	26.41932869
26.93988419	26.62435913	26.7522583	26.97289848
25.72956657	26.3521347	26.25333405	26.49917412
24.13241768	25.37315178	24.78775787	25.4306488
25.05767441	25.24129105	25.40125847	25.49759293
24.57732773	24.17919159	24.86891365	24.10485649
26.39448738	26.80279541	26.86620331	26.66193771
22.58378029	22.96358109	22.94037819	23.08069801

26.11439896	26.2312336	26.80587387	26.76040268
22.77637672	22.84111214	22.77970505	23.10798645
24.13656998	23.99144363	23.93328094	24.34292793
22.41074753	21.86075401	21.72325706	23.89022636
27.37277031	27.51765823	27.49312401	27.40616608
24.44309998	24.4630127	24.78116798	24.89138603
24.90476608	25.28792381	25.21048164	25.06800652
23.4655056	23.67863274	23.4913044	19.47979355
26.55882454	26.67774773	26.19067192	26.6069603
25.24724388	25.66402817	25.12376213	25.20022774
23.10702896	23.28022575	22.60462761	23.35917473
23.99178886	23.88864708	24.23943329	23.83325577
25.26888657	25.63328362	25.22637367	25.29845047
22.49057007	22.83770943	22.5487957	20.37135696
22.80469322	23.15690613	22.95480537	22.94856453
20.28063583	21.88069344	21.71908379	22.39670753
23.28587914	24.60382462	24.25695419	24.23542213
24.9647274	25.07398224	25.07537079	25.46348
23.85252953	24.46045303	24.41866875	24.7206192
22.17873573	20.47343636	21.22311401	21.10922241
24.93966103	21.17958069	24.74929428	23.69242859
26.99010086	26.61988831	26.89862251	27.13065147
24.82065201	25.4299469	25.10297585	25.42572784
23.36038017	25.08646774	24.65981483	25.00478935
24.40256119	24.52390671	24.52623749	24.24408913
24.67341232	19.94020081	21.27726364	29.78732491
20.44021988	18.67921638	20.30839157	25.54760361
19.54439545	21.04450035	19.68760109	25.86440849
20.53454971	20.77140808	19.55020523	25.6430912
20.52599335	21.26520729	20.29392242	24.68179893
21.5782032	21.48963737	20.20148277	23.15918732
26.278862	19.98792648	19.94041061	29.18013573
19.2852726	22.28993607	21.855896	21.84984016
21.73231316	21.81073189	22.68470192	22.80878258
19.38146019	22.97501755	22.92983627	22.32904243
26.86950111	26.09006691	25.68845749	26.33888817
28.75423431	28.40482712	28.32834435	28.46676636
30.02088737	29.86724854	29.75531769	29.90856171
25.41053963	25.26090813	24.1914444	24.78705978
30.94300461	30.81497574	30.71816444	30.75899124
30.15773964	29.88127899	29.78701401	29.81593704

22.88840675	22.67947197	22.9099102	23.17837143
24.90283585	24.96741295	24.93296623	24.77228355
21.36834717	22.79239273	22.08219337	22.9779377
20.50366402	22.28988075	23.07362175	22.60650444
22.96310425	23.37185669	22.81606865	23.45713615
25.33568764	25.3033371	25.52802658	25.16188622
21.41002274	21.03328514	21.38216019	19.77961159
24.94104958	24.14195824	24.37072563	24.49570274
25.00902557	24.75496101	24.78496552	25.17995071
28.0131321	28.15894318	28.01887131	28.16192436
29.37722588	29.36790466	29.83955574	29.59151077
27.21382332	27.0674324	27.57101822	27.43141365
24.2303009	24.54209137	23.51014519	23.05453873
24.46880341	24.52563858	24.11083984	23.62700653
21.76109314	21.98196602	21.65324783	21.31329536
25.71541786	25.95178223	26.31836319	25.70985603
24.28164101	22.29930305	25.08594131	22.92759514
31.92060852	31.69838715	31.54669189	31.57307816
26.64636421	25.90485764	25.12439346	24.34908295
23.53409576	23.36546326	22.95281792	23.40535545
27.35649109	27.04395676	27.09928703	26.97530746
23.53812981	23.98311424	24.20411491	24.44316292
27.42478371	27.49800301	27.3358593	27.36636353
26.88774109	26.6477356	26.6159668	26.47954178
21.50013542	21.52936172	22.3857708	21.92690849
24.99127007	24.80000877	26.15015602	26.25183678
25.84143829	25.90041924	25.6340313	25.30521584
24.06324005	24.23264313	24.11830711	23.26499176
28.78447342	28.75066185	28.87458229	28.64395714
23.48283768	24.35776711	19.42170715	23.56232262
31.67568779	31.21477318	31.33148766	31.14789009
27.99172401	27.89029503	28.02051544	27.87396622
25.74834824	25.98093796	25.81870461	25.72580338
28.55369377	28.7371521	28.52850342	28.4154644
24.31001091	24.62371635	24.8759594	24.84985924
25.16349983	25.69421005	25.73551941	25.69389153
30.13699532	30.06303978	30.14770889	30.20943642
23.34732819	23.05887222	22.94470978	23.29544067
21.92723465	22.68133926	19.52043724	21.96979332
31.33351517	31.36087036	31.10268211	30.94914246
28.21502686	28.3346653	28.23562241	28.24748802

24.83711243	25.14109993	24.64146614	24.81728935
26.19524193	26.30690384	26.52547455	26.30692101
27.72338295	28.13506317	28.25164795	28.66803741
23.19618034	22.92819214	22.17392731	22.11263847
20.69736481	24.65829086	24.86069679	24.72941208
24.44493294	25.21922493	20.30049896	19.92555428
26.49562645	26.77064705	26.50554848	26.53417015
24.72759438	25.32464218	25.22221375	25.25824928
22.02722359	22.67245293	22.98431396	21.94488716
22.07825661	22.48490524	22.30955315	21.15992546
23.76688576	24.63936996	23.65031433	23.40171432
27.21539688	27.17131042	27.27319908	27.29360008
28.71066475	28.73505402	28.94890594	28.70800209
23.36666298	23.51653099	23.09474564	23.08406067
24.16599274	23.59571075	23.69561768	24.3046608
30.86828041	30.61069679	30.76706696	30.76769829
20.04835701	19.57431602	19.67969322	21.94037819
22.61580467	23.28855705	22.47550964	23.03795052
32.87189865	32.94701767	32.59085083	32.67636108
25.66158295	25.34306335	25.60543633	25.11279106
23.58187294	23.57242012	23.84718513	23.50203133
24.04451942	24.6003685	24.7204628	23.91706848
26.16031075	26.99690437	26.79921722	26.66722679
24.97219849	25.67370987	25.32824135	25.22449684
20.32805634	21.33638763	21.28872681	20.45794868
24.74478531	24.61133003	22.86470604	23.9330101
24.07169342	24.44139099	24.24249077	25.33848
25.76567268	25.32209778	25.8836689	25.8245182
23.41053963	23.70091629	23.67335892	24.10333633
24.54845619	25.58720589	24.83200073	24.99907875
24.1985054	24.30646896	23.53599548	24.7810173
26.68177223	26.88739204	26.83110619	26.98239708
25.8712883	25.58897972	23.76283836	25.92002678
28.34078979	28.38488007	27.82917213	28.16427803
24.40334129	24.35863876	24.23637199	24.05515289
25.35470963	25.36108398	24.67997551	24.99330139
23.01624489	23.31118965	23.01842117	23.48357582
24.69901085	24.75108337	24.96137428	24.8191433
20.8795166	22.22975731	21.94370842	22.00829887
22.9977951	22.51357079	20.58981133	18.77374268
23.97447586	23.69093704	23.88446045	23.70830345

26.98294067	26.58132744	26.29778671	26.58333778
23.39884758	22.7488842	20.2843647	20.75255966
25.84685135	26.03975868	25.24190903	25.99433708
19.80275345	21.87612724	22.07368851	21.89929008
24.38949203	25.24564934	24.13531876	24.57542419
24.23103333	23.89919853	23.70672417	24.27916336
22.34057999	22.26330185	22.86081123	22.43984413
22.53744125	22.51722908	21.21160889	22.1601162
21.78244781	22.94688797	22.98692131	22.73721123
26.64278793	27.20694733	27.02210426	26.91672707
25.62914848	24.10789108	26.13137817	24.15846252
22.51874161	20.80163765	21.49662971	21.71997452
23.77303886	23.824543	23.58267784	23.83422089
19.09719658	21.69046783	21.60878372	21.39435387
25.00328827	24.55596161	24.57380867	24.87464523
21.69595718	22.1160717	21.48222351	21.69926643
29.21567535	21.912323	14.83930206	20.96476555
24.89189529	24.93179321	25.43096733	25.15414047
24.87628555	24.84594154	25.22956657	25.5331459
19.89146233	23.16625404	23.160326	22.61600494
23.24247551	23.55543518	23.57450104	23.66806602
23.19871521	22.46622849	21.97840881	22.59423065
28.21062279	28.26874352	27.44434929	27.40047836
23.6866703	23.90747452	23.90967178	24.28630257
28.79977417	28.4672718	28.48623466	28.71266556
29.76995277	29.47842407	30.21904945	29.66197014
23.57068443	23.87192345	23.6307869	21.61785889
27.30443382	27.32010269	27.258358	27.56725121
25.17417145	25.5897522	25.57588577	25.39888
24.94095993	25.50008774	26.31021881	25.15379333
22.00460052	22.69574547	23.05027771	22.89372826
22.74658966	22.80463409	23.02147293	22.3155899
20.18228722	22.82382393	22.65121269	23.0145607
26.0794239	25.56758499	25.4361248	25.5769825
30.87905884	31.29690742	31.50085449	31.53110886
27.50149918	26.36666298	26.81164169	26.78992271
29.69541168	29.44813538	29.32785225	29.56641579
19.23407555	22.76678467	22.46191406	22.37174988
24.66882324	24.11553192	24.12801743	24.18381691
24.33687973	23.47506523	24.30667686	24.77851295
22.04153061	22.11260796	21.64504433	23.3566246

24.06907272	24.37802315	24.34962273	24.38811111
21.42507362	24.63776779	24.46450806	19.97456741
21.42966652	23.56975746	23.18339348	20.47201347
28.03611565	27.96680832	27.98706818	27.93106079
24.72878838	24.85433769	24.91720581	24.16200256
23.08154297	23.1181488	22.96225739	22.89358139
21.4719429	21.30763626	21.96895027	21.10354424
20.22434998	21.66851997	20.61764336	20.41142082
20.97168922	21.76890564	21.77023888	21.58407784
24.78855515	24.04109573	19.56742859	24.09900665
22.73034477	22.54224586	23.07954216	22.57253647
24.84402657	24.72108841	24.70382309	24.71392441
24.58800697	24.23059273	25.19561768	25.09643555
25.92549133	25.76761818	26.54965973	26.00320244
23.39806557	23.29600143	23.55566978	23.8303566
22.6060524	22.82956314	22.43748474	22.7585144
30.37015343	24.64883423	22.38780785	23.5892086
26.14941978	26.17981911	26.10809135	25.6135807
22.72945404	22.86727333	22.80163765	23.23505783
23.33687973	24.54763222	23.46101379	25.14160728
23.55051231	20.89993477	23.48591232	21.73413277
22.2900486	22.3631382	22.7817688	22.66092491
24.48572731	24.1532135	24.98979759	24.34671783
24.35790062	24.3653965	24.46668816	24.44688988
30.42352104	30.08334541	30.12410736	30.11545181
23.53219604	22.71596718	21.33192062	23.24942207
25.78750801	24.92338562	25.59135056	25.26008224
26.12490654	26.26447296	25.93791199	26.16098404
24.75082779	24.99804497	24.84732819	24.58468628
25.98407173	26.22177124	25.97969627	25.90350342
27.15826988	27.47869492	27.47312927	27.30190659
28.70335579	28.64533234	29.46390533	28.21192169
20.6382885	23.32526016	23.35676003	23.33319855
25.25709915	25.42322922	25.6092453	25.125103
22.21812439	22.70746231	21.84835052	23.80675888
21.6536026	22.3558197	22.82341576	22.25159073
21.9338398	22.27506256	23.14896965	23.25030518
22.33021927	22.35261726	21.57758331	22.42490768
27.22545433	27.32044601	27.40657234	27.19102859
20.47278595	20.26760292	23.04811668	20.71291924
24.34638023	24.19497871	24.61240005	24.22809982

28.49712753	28.33321571	28.80464363	28.65413666
23.32937241	23.26356125	24.05109024	23.61009216
27.0488472	27.14860535	26.93696785	27.13447571
24.68869781	24.82847023	24.50324631	24.82206345
24.72582817	25.57013512	25.24339867	25.30236053
22.62408447	22.82667732	22.02215195	22.16478157
21.22045898	21.3226223	21.30084038	21.61974907
22.07810402	22.38924217	21.98983192	21.96259308
30.22848511	30.13540649	30.062397	30.06753349
34.86502838	34.51782227	34.50267029	34.3513298
23.78526497	22.68792915	23.09035873	23.36693001
27.17035484	26.35250473	26.5780201	26.44983673
25.15429497	22.94763756	32.21396255	22.84174538
29.0493412	29.00557709	28.84950829	28.93753052
27.36419487	26.61245537	29.55588913	26.06804657
27.66146088	27.48323822	27.20536423	27.17207336
32.1846199	32.06708527	31.97674751	31.93160439
30.89200592	30.86702919	30.76263809	30.50682449
30.47769165	30.3108387	30.31397629	30.2822876
22.60546494	22.77396393	18.69830322	22.81581497
22.92208862	21.69989204	20.30311394	23.85414696
30.31764603	30.43251038	30.22216415	30.27164078
24.97543716	25.75266647	25.49963188	25.44335365
22.15875435	22.81626511	21.68221855	21.99844933
27.51908302	27.76420593	27.51314545	27.39966393
23.40210533	23.0068264	22.98233223	22.9587574
20.9151001	21.57431602	20.58159828	21.22199059
24.02445221	24.47982025	24.72103691	24.48332977
28.33836937	27.42278099	27.91461945	28.11798096
24.86046028	25.10101318	25.03489876	25.54813194
25.53783226	24.83547401	25.74077797	25.68214798
23.39034462	22.93953514	22.60360909	24.0202198
22.67256165	23.10428047	21.89537621	22.81401634
20.18336487	20.95432663	21.67740822	21.51349831
24.81675339	25.40914917	24.78046608	24.73163986
24.36165237	24.37491035	24.14250374	24.31962013
22.47271156	21.8416481	20.16448212	22.10347939
23.89226532	24.94100571	24.45356178	24.63344955
24.82972908	25.10113335	25.25753021	25.0521698
25.89356232	25.95475769	25.73670578	25.77039337
25.09018898	25.08294106	25.15826988	25.22361374

24.79872322	24.81440735	24.5266552	24.55929184
22.75983429	23.50881577	22.7702179	23.70746231
23.93957138	24.15776825	23.71690941	24.11577034
23.1725235	22.83016396	22.60526085	22.63103104
26.11320877	26.00393105	26.0175457	26.00750732
23.59832573	23.81997108	23.62811852	21.08252716
24.94167709	25.40561485	24.91488075	25.02407265
26.96455193	27.04635239	27.10858917	26.97486877
22.48797417	22.66453171	22.92529678	22.67329407
26.29538727	26.04053116	25.66356659	25.57406807
27.21271133	27.62964821	27.43404198	27.28550911
21.96426964	20.36983299	22.31002426	21.14863586
26.53192711	26.50216866	27.12317085	26.61147118
22.83551216	22.57574844	23.93309975	23.40457535
25.08845139	24.28735924	25.322752	24.56267357
24.63145256	24.85899162	25.31679344	24.59786987
22.22873116	22.60177422	23.00336647	22.08751297
24.34820557	24.15977097	24.43466377	23.68163872
26.49193192	25.79578018	27.02316284	26.06603622
22.78334808	22.83707428	24.09595299	23.38258171
24.61554527	24.71387291	25.37895012	24.78701019
26.2362442	25.68051338	26.51099014	25.19730568
25.98687363	26.13684464	26.58075333	26.27872086
22.00302315	21.31557083	20.63552094	21.83915138
20.72758484	20.03012276	20.72400665	20.21193123
25.16273308	25.44934845	25.9601593	25.31834412
24.84455299	24.77585411	25.62053299	24.62433052
23.55660439	23.47122383	24.20500946	23.33197021
24.98815155	20.94561386	25.27692986	24.50342751
22.15526962	22.63648415	24.08172226	22.3841114
22.84995461	23.64987564	23.52121162	22.69824791
22.6216507	21.40562248	23.98789215	22.92288589
24.23739243	24.40989304	25.20519638	24.41937637
24.77640533	24.63306236	25.411026	24.73871803
26.88331985	26.67344093	27.58734894	26.89029503
26.47517204	26.39278603	27.02643776	26.43801498
25.05017662	25.3973465	25.98888969	25.44079018
23.91150284	24.4225235	24.78436661	24.10453606
25.27301979	25.31108475	25.41028214	20.16012001
24.02867317	20.3453846	24.45192719	21.17658043
24.5817585	24.67287445	24.98407173	24.42021179

25.55186081	25.28887367	25.78663635	24.93517113
26.65717316	26.36564636	27.191782	26.25697327
24.76283836	24.15275002	24.89254379	24.04826546
21.36575699	20.76190567	21.6481514	20.9912014
23.66459656	24.90173149	23.92415619	23.70809364
26.92998886	27.02136421	26.99550247	26.7398243
24.48099136	25.25292015	25.30879593	26.06661034
27.36051559	20.98399544	20.28084373	20.51295853
27.68351364	26.48753738	26.80562782	26.89942932
23.41183281	23.44771004	23.7751503	23.81401634
22.54252815	23.05210304	22.85079384	22.90089417
22.61744118	20.86108398	22.69066048	21.12254715
22.53129196	22.9359436	22.45096016	22.38113022
23.72806168	24.07830429	23.67766571	24.18063545
23.11403847	23.01711273	23.03734779	22.61405182
23.08908081	23.46388626	23.44821358	23.32526016
24.38436127	24.83233833	24.86476326	24.2766819
28.98527718	28.71430397	28.26619911	28.62055397
26.75887871	26.65703773	26.21804237	26.57294083
22.01685715	22.64116859	22.66379356	22.55852127
23.67745209	24.1002903	24.19730568	23.55133438
24.5547924	25.04051208	24.83889198	24.81465149
29.94726181	30.60452461	30.75334167	30.663311
22.826231	23.62834167	20.88477135	19.97303009
25.12482834	24.98893166	24.80656242	24.92669106
28.82662964	28.59558868	28.59793472	28.51408768
20.77101707	21.72037888	21.73719215	20.03713989
22.64715385	21.29362106	23.09119797	19.71390152
24.55841637	24.83831406	24.82629013	24.53350258
27.24744225	27.19891739	27.0824337	27.25250435
25.13037682	25.6501503	25.07549286	25.80341148
23.08016014	23.59832573	23.60738373	23.37238884
25.14129448	24.81220436	25.07634926	24.82483292
18.56961632	23.94485283	23.49497032	24.08212852
26.13852501	26.21613884	26.24680901	26.16438293
26.32717896	26.55754089	26.21066856	25.73673248
29.43430138	29.12910461	29.4420166	29.38763618
24.56313896	24.13758659	24.9190712	24.24008942
25.67039108	25.50969124	25.49536705	25.33422279
24.63804436	24.688591	24.68651009	24.55987549
23.75908279	24.15383148	24.0214901	24.09514809

24.52163124	24.7426281	24.27618408	25.21874619
24.49941826	24.66280556	24.39512634	24.11251259
25.06443405	25.25364113	25.04322624	25.45466042
24.67017365	24.21845055	22.93194771	24.60512543
25.77525139	25.92472267	26.06433105	25.96853256
24.85965538	24.52097321	24.72754288	24.94543266
23.26527786	23.08556747	23.22892189	22.90098572
24.61818123	24.60303116	24.81904602	24.52037239
20.40447998	22.66648483	22.43814468	22.71034431
22.81299782	23.14175415	23.11765671	19.30661392
20.87597656	20.59076309	20.7135582	21.11623001
24.38449287	24.95282555	24.85690308	25.1866169
24.58101082	24.59097862	24.64982033	24.5192337
20.38511276	20.3959198	21.07632065	20.56746292
22.56917953	23.76182365	23.98893166	23.45651054
22.64678192	22.96299934	23.46762085	22.67342377
22.06230164	21.88222313	21.08425522	22.12063408
22.2593708	20.93529129	21.59463501	22.27454948
22.43616295	22.44753265	21.83892059	22.12606621
26.87970161	27.11604691	26.64361382	26.71554947
25.18922043	25.80064964	25.69521904	25.95024681
28.03946495	28.29438972	28.0164299	28.06779099
21.88065529	22.75474739	20.93580246	22.38561249
29.36523819	29.25898743	30.26125336	29.35041237
32.50282288	32.63998413	32.44374084	32.2988205
26.1876545	26.43050575	26.22938347	26.31215858
25.60727119	26.36273956	25.70408821	25.20936775
25.61346817	25.27177429	25.72067261	25.25576782
24.2099247	23.7940197	24.37338448	24.41138077
24.16177177	24.20776749	23.82502747	23.47283554
21.30284882	22.40717316	22.139431	22.77615547
21.09477043	23.56825066	22.84299088	23.0473671
22.87794304	22.38147354	22.36038017	22.775774
24.59536934	24.72718048	24.49704361	24.55619621
25.54223824	25.72587967	25.64421844	25.80072403
26.23908806	26.50940514	26.4029026	26.44362068
28.22416687	28.38376808	28.46310616	28.33619881
23.89189529	23.77203178	23.68346024	23.49460411
29.04676819	28.85801315	28.74999046	28.80085373
24.67298126	24.4889183	24.86651039	24.80045319
26.27810097	26.74085426	26.52951622	26.64663887

23.8472805	20.21190834	19.44192123	22.74845505
25.44534302	25.37438011	25.30410194	25.13637352
24.10813141	22.29100609	22.96229362	23.42431831
25.82982445	26.1756382	26.33522797	26.43429756
24.18055916	24.68190765	24.53676605	24.80877304
24.61666679	25.10549545	25.03174782	24.6028614
22.78596306	23.31215858	22.93039513	22.89396858
22.49996567	22.76099205	21.05239487	21.67787743
23.42930794	24.1848011	21.3666935	23.45362473
23.17406464	23.89485741	23.90756607	24.11418152
28.95210457	28.94901657	28.88393211	29.02472115
20.40551186	21.8020153	19.47470474	20.09248924
24.81494522	25.38455963	25.24383354	25.52453423
27.78930092	28.08431053	27.95986176	28.01238632
22.35661507	19.65237236	21.28838921	20.20657539
25.73861504	25.9491787	25.77381897	25.85804176
20.12174034	20.24423409	20.29793358	20.71657562
26.19021988	26.63685608	26.40850067	26.30467796
27.65690041	27.48929977	27.88075256	27.92076492
27.43475914	27.91479111	27.69358444	27.84613228
25.55297661	26.08288002	26.30311012	26.12729073
24.46668816	24.84627724	25.16207886	24.44455338
25.47837067	25.2068367	25.9338665	25.5903511
24.96035957	25.02643776	25.28351402	25.12095833
26.33362579	26.17786217	25.89434814	25.86691093
24.08488846	24.04593468	23.82395935	23.95704079
22.59898376	22.85614395	22.42049408	22.69066048
19.8001442	21.56397629	21.28528786	20.79047203
24.52838516	24.8263855	24.83629417	24.63034248
25.24612045	25.00966644	24.8496685	24.98797798
26.56405449	26.42969131	26.53778839	26.52447319
27.31345749	27.67317009	27.50892258	27.56536293
22.64550591	22.06943321	23.19380569	20.4774971
25.36419487	25.57288361	25.60238075	25.39956474
22.04576874	23.15352249	22.97860146	23.43733215
24.68789864	25.01907349	24.12471008	24.27526093
27.03873253	26.83050156	27.87003136	26.96741295
27.64897156	27.54421616	28.43065643	27.56841087
22.97819901	20.5102005	20.1890583	20.98406601
30.13197708	30.17652702	30.00209236	30.02907372
26.86230659	26.86632156	26.69099045	26.60724258

22.56362724	22.64306259	22.79384232	20.85313034
27.191782	27.18829536	27.16720009	27.20527077
21.86086655	19.17077255	23.15537643	22.32849503
24.41390038	24.83841133	24.60597229	24.91447067
29.2623291	29.10161781	28.90414619	28.92552567
28.34802818	28.36915398	28.27288628	28.16283798
26.62254524	26.93190575	26.63270187	26.82868767
21.7065773	22.32171249	21.98631287	21.87915993
20.84689903	21.71653366	20.97112846	20.22135925
23.89272881	24.46929932	23.98224449	24.0606041
22.32665825	22.75415611	22.50127792	21.88740158
25.52868271	25.60789299	25.54515839	25.74678612
25.63561058	25.5339489	25.21870804	25.36007881
29.4346199	29.51231766	29.48828506	29.38518906
24.1300621	24.44909668	24.31906891	24.42335701
22.051157	22.75523567	22.59827995	22.84115028
21.69784737	20.60982132	20.19678116	19.70653343
19.35702705	19.6673336	18.97381973	19.91425323
25.25824928	25.21881866	25.3212738	25.58548927
24.06167603	24.47667122	23.89919853	24.54645538
23.94091606	24.21400833	23.60862541	23.89356232
20.29839897	24.00453186	23.524683	23.43936348
25.39034462	25.43917274	25.6798954	25.40762711
25.7024498	25.45472336	26.24167252	25.64548492
27.59526825	27.77272415	27.57614517	27.58498764
28.61143494	28.59828949	28.56394577	28.36694717
26.83231544	27.09717941	27.31544495	27.32182312
28.91655731	28.72084045	29.02377129	28.86906052
27.83340073	28.03899574	27.90230751	28.20475769
27.73621559	27.66030502	28.18063545	27.89746857
21.45312119	21.9908886	21.33358192	21.32970047
21.87072754	22.71875	23.03333664	22.70581818
30.63027382	30.77415466	30.64915848	30.68787384
24.13233948	24.46693802	24.83016396	24.46238899
26.56412697	26.32426453	26.25598335	26.42196274
21.7704792	24.42053413	23.83277321	23.83797836
27.70898819	27.85525322	27.94976807	27.48023605
26.51762772	26.39808083	26.94525337	26.63367271
22.30047607	22.4379673	22.45123672	22.44473076
20.09662247	20.18350029	20.52602196	19.57296753
26.02783012	26.51594543	25.92730141	26.02415657

23.55648804	24.25349617	24.30883026	23.72473526
27.15605354	27.62818909	27.35825348	27.28947258
22.46238899	23.86088562	20.8956356	21.78506851
22.60025597	22.82925415	23.13172722	23.01002502
21.4453125	21.49814034	19.56252289	21.69225883
21.59868813	21.39435387	20.90065384	21.43984413
25.45572662	25.72842598	25.4124794	25.32457352
22.94037819	23.1019268	22.91719627	22.49889565
24.18472672	24.82425117	24.64526367	24.6814785
31.26147652	31.22968864	31.40405655	31.13699532
27.60625458	27.67229462	28.27954483	28.3092556
21.80703354	22.07453728	21.98666	22.25193787
23.66177368	24.18040657	23.1930542	24.08188438
20.39710617	23.0920372	20.56811905	22.79205513
23.84162903	23.92442703	23.62956429	24.19955444
27.29754066	27.62561226	27.67215919	27.65047836
29.19455528	29.4698925	28.84305	29.0351181
26.70714569	27.00163651	26.85910988	26.86997223
27.81659317	27.53170395	28.68525314	27.9301033
25.98997116	26.50908852	26.28624916	26.27181053
28.25696373	28.31440926	28.22080421	28.31479836
24.08042145	24.3347683	24.02267647	23.77826309
30.06162453	30.17795372	30.03944016	30.17557526
23.21243668	23.08102226	20.84737778	22.36196136
22.62290192	22.79376221	22.43568039	22.75631523
23.5118351	23.94172096	23.54427528	23.6959362
21.88323021	21.76190567	20.56709099	20.553545
24.20015335	24.74447823	25.20825195	24.95340347
22.06562424	22.01791	19.89793015	21.88591385
25.84615707	26.05614471	26.00703621	26.44993019
24.81470108	25.73298645	25.10461617	25.23578835
23.10019493	22.98872375	22.40673065	22.79519081
22.76983452	22.82629013	22.82510567	22.33062935
22.39333344	22.24585915	21.63878441	23.15593338
22.92506218	22.43888092	22.67994308	23.19668961
26.12317085	26.49323082	26.6807003	26.6971035
26.70120811	26.82917213	26.90345764	26.86537743
25.07103729	24.08950233	24.29523087	25.11703873
25.65132713	25.68928528	25.54507065	25.33769608
25.13754654	24.91237068	25.30549431	24.90398598
31.52023697	31.41331673	31.42026329	31.44845009

27.94782066	27.87513924	27.72526932	27.74175453
24.18351555	24.65113449	24.43109512	24.75358391
23.26011848	23.32676888	23.18812561	23.37105942
22.29389763	21.98908806	22.06529617	21.82950592
22.79756737	23.25839424	22.94132805	23.29501915
23.87314415	24.17622757	24.77329063	24.06620026
28.61452866	28.74307251	28.80396652	28.68368149
22.17456818	21.56258011	22.06641388	21.4752121
28.32547379	28.30094719	28.12238121	28.13271141
24.15784645	23.84038162	24.12234116	24.1633091
23.9117775	23.36252213	23.52085304	23.28460884
26.46065521	26.93640709	26.93021584	26.76736641
25.40636063	25.4470787	25.46513176	25.40301704
26.06819153	26.17885017	26.05746841	26.20157433
28.4622097	28.7347641	28.63540268	28.64890289
24.72987747	24.71014595	24.54456902	24.92877007
25.99748611	26.10587502	26.07553291	26.16057968
22.26350212	22.98797798	22.70685005	20.7000885
23.26313019	23.42380714	21.71019745	23.48983574
21.96155167	22.18007278	22.13580322	21.96430397
20.28883934	20.90275002	20.89932823	20.85787201
24.26927948	25.192873	24.4897747	24.29431915
23.33073997	23.15557861	23.1575985	23.32731628
29.52581787	29.58956528	29.58165169	29.59147453
28.42430305	28.13432884	28.42634392	28.27288628
26.58319473	25.96406555	26.55752563	26.06825256
26.7875576	26.82844543	26.81225395	26.7023983
28.32585907	28.38595009	28.53289413	28.4342804
28.45658112	28.58287239	28.67888832	28.62244034
32.13653564	32.28151321	31.86739731	31.78628159
23.55062866	23.60025597	23.22455597	24.21133614
24.31243706	24.19355011	24.15104675	23.60444641
23.99740028	24.74396324	24.67529869	24.54091072
24.31672287	24.59155083	24.6692009	24.99593353
25.43237114	25.79543304	25.40334129	25.06829262
23.94467354	24.38738823	24.31042671	23.84095764
24.05308151	23.85737801	24.125103	24.17371368
22.7628994	22.45540619	22.15295029	22.53404999
23.17783928	23.31174469	23.08958244	20.53897667
29.16631508	28.91698265	28.94346619	28.89038277
24.03263092	23.80459404	24.15707397	19.99446106

25.55651665	25.69742203	25.58763504	25.41180229
22.07241249	22.30783081	21.90417671	20.12063599
20.48211098	21.13545799	21.40249634	21.46109009
22.81907463	23.38968849	23.44037819	23.5685997
24.8754425	24.68008423	24.34150314	24.74304008
24.29858971	24.11290932	24.22044373	23.30785942
27.47002983	26.17165375	22.04269981	26.72429466
23.98198318	24.62209702	24.42630386	24.70260811
23.85718918	24.34150314	23.9144249	24.49862671
26.45691681	26.31499672	26.71842575	26.63020325
26.66532898	27.15981102	27.0521698	26.86750031
26.16067505	26.41659355	26.31105042	26.39949989
25.36693001	25.25003052	25.15000153	24.59462929
26.32633972	26.27627373	26.26799393	26.07991219
25.81555557	25.71017075	25.96172714	26.0375824
26.05934715	25.90129471	25.89272881	25.70988274
26.91945839	27.27141953	27.29368782	27.35262299
26.2457943	26.58749199	26.49439049	26.61484337
24.59911919	25.16353798	25.33487129	25.09635544
24.21237564	23.6216507	24.08180237	24.09418106
23.29459953	23.75735474	23.51135254	22.82793808
24.42342186	24.1380558	24.66903877	24.5349865
24.12557602	24.30709457	23.91287231	24.27284241
25.36999512	25.43907738	25.25756645	25.24445152
26.4215126	26.39507675	26.35422134	25.93584442
25.31468582	25.50821114	25.55631256	25.39476585
25.69715691	26.15460396	26.06976891	25.78740883
25.52124214	26.19334412	26.00953865	26.25970459
26.04470634	26.31414986	26.39693832	26.52170563
24.89384079	25.05920219	24.76870537	24.54521751
24.20717239	24.59985733	24.70181656	25.45098495
25.33432579	25.69821739	24.94525337	25.17930603
23.78666115	24.20560646	24.12384224	24.20284462
24.6253891	23.76364899	23.87979507	23.62287903
25.23903275	25.25555038	25.01128769	25.06968689
23.55637169	23.76638031	23.10075569	23.56581306
25.66830826	26.12921715	26.33909035	26.39711952
23.62120247	24.22066498	24.80847931	24.61784554
23.5378933	23.88725281	23.65097046	23.80891991
27.28126907	27.42989922	27.41964912	27.36544609
21.42670059	21.50925064	21.45878983	21.87594032

27.9317379	28.34735298	28.00865173	28.30373764
20.17076874	22.10312843	19.71617126	22.85692215
22.61562347	22.18259048	22.14061546	20.76607323
22.24237442	22.47447014	22.23759651	20.18553162
23.11375237	23.30033684	23.87970161	23.55964279
26.11592865	26.32885742	25.9664669	26.16905594
21.91524696	21.64996338	22.57883644	21.60552025
30.1810379	30.47595406	30.34657097	30.38699913
23.25638008	23.33415413	23.38376808	23.33633614
23.54886627	23.91688728	24.14413834	23.85186195
25.44395256	25.91298676	25.77876282	25.57259369
23.96402168	23.40431595	23.64658356	24.03355408
23.34394455	23.31146622	23.56987381	23.46811867
23.56255722	24.4642601	24.19955444	24.38712502
21.34910965	21.68470192	21.56862259	22.11648369
21.90652275	19.69385719	21.40259933	21.06039047
23.58290672	22.2615242	23.96807098	23.61481667
23.20930099	23.35178185	22.40732765	20.19664955
25.54294777	25.48566628	25.10289574	25.24633789
22.84234047	23.00108147	23.38007355	22.9841938
25.26842308	25.86485863	25.28594971	25.57016373
28.07795906	28.39030266	28.27919006	28.40141487
24.30228996	24.49941826	24.57074356	24.05225182
28.36652946	28.30856133	29.90454865	28.45497322
26.38432884	26.67128181	26.31817245	26.22007561
25.96837997	26.23613358	26.26665497	26.14689827
24.32724762	24.46979713	24.74000549	24.12147141
21.78568459	22.28999329	22.0863781	22.28858566
25.90969467	25.58909416	25.65766335	25.84675407
26.19473457	25.90460587	25.617733	25.66400146
22.12842751	21.97966576	22.25225449	21.94667435
26.4719677	26.3552475	26.22587776	26.05695152
23.81636238	23.88119698	23.44151688	24.02766228
26.76711464	26.86266136	26.70332146	26.4317646
24.70318985	24.64322853	24.42790222	24.48302269
25.32913208	25.37265396	25.4266243	25.11695862
20.91093636	21.1776123	21.54288292	21.53293228
24.88966942	24.43803024	24.22398186	24.24001694
22.82847977	23.12927628	23.19436264	22.90100479
24.11830711	24.31693077	23.64866829	24.84302139
21.45654678	24.22214127	21.67578506	23.84985924

26.37972641	26.49961662	26.30155754	26.31760406
25.14654732	25.11251259	25.03879547	25.05850029
24.53652954	24.41125107	24.04184914	24.62382889
26.14012527	26.20568085	26.12352562	26.18888092
23.44695282	20.82614708	23.41841125	23.44682693
22.51335335	22.92902374	22.37512207	20.73885918
28.5007782	28.49407768	28.46092033	28.5241375
24.94306374	24.73520851	24.58491516	24.29621124
25.03837776	25.21619415	24.75378799	24.62561226
22.86296844	20.20891571	21.05894852	20.57105064
25.78144264	25.68300629	25.58980942	25.08756065
23.59366035	23.74519539	23.98285294	23.93939209
20.91721535	19.60931969	21.12962341	19.53666115
25.48089981	25.71625519	25.7507267	25.4037323
28.4287014	28.37202263	28.33056831	28.44738579
20.85741615	21.31744194	20.67411995	20.26477432
24.338377	24.11433983	24.21785927	23.3925724
26.34438324	26.4507637	26.62114716	26.54510117
21.62346077	22.13542747	22.17575455	20.65493393
24.7536869	24.74473381	25.04847336	24.8023777
22.84130287	23.13941383	23.67540741	23.39034462
27.29105377	27.5489254	27.42606354	27.22453499
20.84337425	20.98863792	21.30069351	20.39465904
23.28206635	23.93337059	24.26363182	23.04610252
23.52552032	21.48659897	23.84861755	23.80390549
25.5532093	26.2863903	25.92804718	26.10555458
23.0364418	23.58932304	23.16692734	22.32237434
23.10444069	23.61560249	23.14766693	23.19457245
27.98901939	28.15315628	28.14467239	27.98847771
23.67658997	23.02098274	23.35890579	23.48394585
26.56843948	26.77893829	26.4652729	26.50228882
22.63827515	23.04161453	19.33586311	22.5079937
20.3383255	21.85627747	22.00367355	22.20006371
22.38168526	22.54785538	22.36027336	22.08190155
25.85737801	25.77296257	25.56124496	25.79731369
22.84465981	20.14347458	23.3877182	20.67147064
22.08527756	22.27443695	22.32066727	21.97302246
23.0245533	23.39532089	23.73117447	23.4636364
24.97583199	23.95890045	24.40749741	24.48228455
22.51732445	22.36895561	22.20681381	22.47985649
24.22545433	23.86448097	22.92028999	23.19547462

28.7440033	28.51009178	28.44363785	28.49293327
22.71946144	23.63234138	23.09943962	23.89448738
24.66063118	24.39695549	24.29298592	24.55127525
19.75027275	19.66390228	20.1293087	20.57199669
22.727211	23.13703918	22.09119797	23.31920624
21.85995865	20.22364998	23.55473328	22.91364098
22.76543045	22.99627876	23.19497871	22.94080734
27.68391609	27.86183357	27.6977005	27.64636421
25.04922295	25.39060593	25.41580391	25.68059349
26.4651165	26.74970245	26.3989296	26.61414146
23.98085022	24.22765923	24.24437904	24.52372742
22.60138893	22.55545807	22.73958206	22.62012863
26.78519058	26.7425251	26.62672806	26.24635506
26.6768055	26.72338295	26.54056931	26.43182945
23.9996376	25.0507164	25.37626839	25.13602257
26.56959915	26.32572174	26.22499466	26.29575539
27.22848511	27.32688904	27.13486671	26.85934639
25.01137352	25.35329628	25.41212463	24.81884956
26.32299232	26.40877724	26.34769821	26.39891243
26.25636101	26.71043396	26.56086731	26.71515656
26.94100571	27.10299492	26.8914547	26.68939209
25.42499161	25.38725662	25.48581886	25.44177055
24.3755722	24.43809509	24.18963432	23.83759308
23.43999672	23.45010376	23.85024071	23.56917953
25.25735092	25.45271301	24.97587585	25.37335014
25.01410103	25.05370331	24.94301987	24.53130341
26.23545837	26.2244606	26.49306297	26.37417984
25.35679245	24.55508423	24.35514641	24.98698044
26.43146133	26.72220993	26.56411362	26.40553474
25.22571182	25.30549431	24.93125343	25.09703827
24.87530327	24.71387291	24.91369438	24.90338707
26.27348328	26.33747673	26.31115532	26.20278931
24.75317764	24.86159706	24.90825272	24.67981529
26.85733032	26.58247757	26.9096489	26.77943993
23.81068611	24.32306099	24.19046402	24.46898842
26.11223412	26.72637367	26.47999001	26.55786133
25.41670609	25.4964962	25.3549118	25.2410717
24.80212975	24.56290627	24.57905579	24.77585411
23.82308578	24.37696457	24.5543232	24.79733849
24.18283272	24.50712204	20.42060471	24.08529282
24.43930054	24.37855339	24.64273262	24.19475365

23.75460434	23.43771362	23.694767	23.6449337
23.4930172	23.81342888	23.74427223	23.7923336
24.54285812	24.8868351	24.90609741	24.81548309
28.52499771	28.61484337	28.5357132	28.50074005
26.30735588	26.7167263	26.66275215	26.35036659
26.63311768	26.62505531	26.56822205	26.5207634
26.68592072	27.01137352	26.85851669	26.71607208
27.04510307	26.95471382	27.15083313	26.74906349
26.37779236	26.45831108	26.43437576	26.24573898
24.58319473	24.94859886	24.94427109	24.97736168
27.35329628	27.48485184	27.27719498	27.0694828
27.77121353	28.10254478	27.78842926	27.9320755
27.3662796	27.50203133	27.32568741	27.25349617
27.65136719	27.689991	27.42702484	27.61870003
27.80648804	28.03196716	27.57260895	27.86920738
25.32206345	25.79106522	25.82648277	25.66370201
25.13088799	24.82880974	24.9866333	24.87464523
25.92650986	25.66579056	25.92388344	25.68864441
27.5555954	27.66749763	27.66431236	27.24445152
24.93111801	24.15977097	24.61217499	24.47642517
25.55794907	26.32721329	26.26570702	26.0496788
26.29552841	26.29291534	26.04558182	26.03340721
23.49203873	23.91232491	23.03010559	23.74949837
26.05854225	26.67397881	26.32735062	26.53177834
26.74406624	26.96521187	26.79277992	26.8089447
26.6320076	27.28815269	27.09556961	27.02136421
26.3014183	26.02028275	26.29124832	26.21332169
25.29736519	25.32940483	25.3322773	25.53477859
21.18265915	23.38020515	22.98320198	20.44895744
24.71983719	24.50051308	24.35050011	24.23139954
24.9598732	24.90398598	24.70709419	25.01958275
25.60749817	25.06348801	25.23099709	25.17459106
24.92388344	24.36519623	24.95486832	24.91624832
28.10114288	27.55083466	28.01600456	27.77077293
27.60872459	26.79600143	26.89319229	26.73156166
21.81679153	22.91897964	22.96589088	23.02182961
23.41892624	23.87988853	20.80112267	23.71208954
26.34763145	26.29071999	26.47924995	26.06964493
27.58956528	27.66817284	27.50241089	27.26185799
27.20331192	27.65703773	27.45661926	27.46053123
26.27017212	26.556036	26.21269226	26.12374306

20.90836334	20.45020485	25.90035057	20.97694206
22.37153816	22.43519783	22.17648697	22.01566696
26.08510971	26.24787712	26.16223335	26.41865349
26.91330719	27.04531097	26.94257164	26.99755096
27.13555336	26.89538956	26.88483429	26.90196228
28.09471512	28.33078194	28.1509304	28.08992577
20.25199509	19.66612434	20.93409157	21.4788208
23.23257065	23.71040726	22.70322227	23.22247887
27.62797928	27.63747787	27.70450974	27.85132599
27.35144424	27.43244934	26.99798012	26.90575409
29.82846069	30.13858223	29.93466568	29.97144699
20.62203026	22.91548347	22.17127228	22.61285973
25.55637169	25.31993103	25.22648239	25.15360069
23.52456284	22.56164742	22.79076385	23.07327843
22.9281559	22.65151787	24.05631065	22.40374374
25.88329697	25.42723083	25.19876671	25.43536186
23.83248329	23.46326256	22.06690598	22.72261238
26.638237	26.93494606	26.82880974	27.01339722
24.9907074	25.13957787	25.10745239	25.09232712
22.7034111	23.11017227	22.5570488	19.47868919
24.45274544	24.70482635	24.50099945	24.66172028
20.28416252	24.40561485	25.20176125	24.22044373
21.87852478	21.60064125	22.53219604	20.48197746
29.1430912	29.52168846	29.20874023	29.3817482
22.34581184	23.74304008	22.64361382	25.17645645
31.96774292	32.46557999	32.13827896	32.13384628
24.06463814	25.36756325	25.87513924	25.69213486
26.86714554	26.79277992	26.22024155	27.84242058
21.89715004	21.97757149	22.15421867	22.36741066
24.04301643	24.22073936	24.06808853	24.30117416
24.53605461	25.29705048	25.02783012	25.41403008
24.60325813	20.98804855	23.87530327	23.78486633
24.63461304	24.97740555	25.01873398	24.71811295
24.51231766	25.29505539	25.30566978	25.25230598
22.59753036	22.56097221	23.14010239	22.90956306
25.43692017	25.50518608	25.26352501	25.18036842
22.94256401	20.1572628	19.97113609	22.14456558
24.03925705	24.13406372	24.28665543	23.6806736
23.35890579	23.866745	23.56906319	23.24250412
22.89958572	22.83622551	21.67783928	23.2429409
24.40691376	25.05241776	24.72837448	24.81665421

22.48044968	23.09756088	22.89393234	22.73134041
24.77198219	24.5026989	24.87431717	24.26198387
22.70180511	22.49604416	22.90659332	22.3389492
24.03321838	23.90426064	23.84995461	24.15776825
22.64107895	22.81025505	20.72626305	23.07337761
25.27259445	25.66755104	25.59968758	25.66486931
27.83116722	27.6444397	28.48550415	27.55325508
26.42624092	26.2437973	26.88250351	25.60791969
24.60404968	24.21185684	25.20575523	24.0914402
23.74960136	23.26484871	23.53445244	23.59514046
23.19875908	23.68410301	23.26126671	22.78470612
23.552742	24.36058235	24.12864685	24.41834641
25.5009079	25.55786133	25.32556725	25.24263573
26.51343155	26.64113426	26.24249077	26.63616371
18.58641052	22.16035652	21.8015976	21.23227882
23.57853699	21.92936707	20.33203888	22.03109932
27.10219383	27.32354164	27.0896225	27.16643333
25.04959679	25.24641037	25.92184258	25.72788048
24.53058815	24.78805542	24.39962959	22.69396019
27.88512421	28.07209206	28.21488762	28.28020859
22.17542076	21.96003151	19.11737061	22.31343269
23.49252892	20.5973587	20.35551071	23.63311768
21.88788605	21.34642029	21.34380722	21.01563263
18.72925949	22.79512978	21.69714546	20.05029869
22.02718925	22.11254311	22.26421928	22.42997169
19.91840744	20.96840668	20.49426842	21.95063019
25.38972092	25.90127182	25.52710152	25.54889679
27.69158936	27.88809013	27.8285675	27.81139755
25.61885262	25.72197533	25.06155205	24.99118423
23.80891991	23.63511276	23.59639359	23.41454506
25.27760315	24.73417473	22.86876297	25.77733421
27.27595329	27.30452156	27.50066376	28.37554741
30.79443932	30.03078461	30.89446449	30.94914246
27.74848747	26.96993828	27.2149353	27.590065
27.77410698	26.97388458	27.35422134	27.82832527
29.07469749	27.75200272	28.74784851	28.8426609
23.65948868	23.32333565	23.66795731	23.621315
21.5681591	21.22458649	19.91636848	21.92059898
22.84754753	19.57154465	22.61912155	23.30605125
27.96823692	28.36164474	28.26771736	28.59828949
29.4518528	29.66878128	29.53802872	29.68565369

25.12671852	25.40558243	25.08893585	25.48670959
27.80550385	27.90098381	27.89665985	27.88820648
26.72961998	27.203125	26.5536499	27.01605797
22.2088089	22.89727974	22.76156044	23.06946564
24.77655602	24.89328384	24.97421265	24.72093201
24.28573799	23.71219444	23.75582695	24.52957726
21.76413536	21.86578369	22.33851242	21.9372921
24.27582932	24.99834633	24.52223015	24.45957756
20.07745171	23.09609795	20.44400787	22.90851784
22.12952805	22.61681366	21.96898651	22.00703239
24.4738884	24.09876633	24.05075836	24.73163986
23.46724892	23.99248123	23.6227684	23.59126472
23.24308586	22.98495865	23.37530708	23.38363647
25.79051971	24.63178635	24.87834549	25.35006142
26.19044495	26.12648392	25.86813545	25.85725975
24.65780067	25.25922012	25.37703133	25.4541893
24.4738884	24.64025307	23.97044373	25.01137352
28.45615005	28.61544037	28.26628876	28.34040833
25.11870193	25.01656914	25.5520668	24.45004082
25.00577354	25.23790359	25.30862236	25.32512283
26.47473907	26.35383606	26.41210747	26.2206459
26.73531151	27.13016129	26.76988983	27.11515427
18.9358902	23.45274544	23.524683	23.50833321
21.51224518	21.47753716	21.0263958	20.05124664
26.45038605	26.7644577	26.83400345	27.17436218
27.83243561	27.58024979	27.62449837	27.53036499
24.73949051	24.67201042	23.23341942	24.83865166
29.43091583	28.9622364	29.39106178	29.73398781
22.84381676	22.82785988	20.66790581	22.79060364
24.12384224	24.2524147	24.51099014	24.05308151
24.37590408	24.33885384	24.32003403	24.5469265
23.50142479	21.18713951	23.31409836	23.07144737
23.66589928	24.15630341	23.79847717	23.40976334
23.9185257	24.07332802	19.69594193	24.11481667
21.37682915	20.99690056	21.58449173	21.75421715
24.51309967	24.70961952	23.74909019	25.65151787
22.01202202	22.21403885	21.79209518	22.04316711
22.84718513	21.13071251	22.52888489	21.60295296
26.08824921	25.90511131	25.68584061	26.11582947
23.33619881	23.61918831	22.8831749	23.71544456
25.64427376	25.79953957	26.03439522	25.94540977

26.63547134	27.1407299	26.6798954	26.98793602
23.82036018	21.74284363	25.65346146	24.57709694
24.70793533	25.00808525	24.98580933	24.71502495
27.35716248	27.35925865	27.3907547	27.27710724
30.32581711	30.3521595	30.38319206	30.20862389
21.85144234	22.09152031	23.72140121	22.13517761
27.6768055	27.48746109	27.69551086	27.61813927
22.23765564	22.61649895	22.36613083	20.68911552
22.02718925	22.04743385	21.76696777	21.96306992
21.33259773	21.19141388	21.52094841	21.86879921
23.00391388	21.69195938	21.25037384	22.51101494
22.28234863	20.28946304	22.75172615	23.53647041
24.70609283	25.10333633	24.8707943	24.89003944
28.77919006	28.80150223	28.08217812	28.69717026
23.1780529	22.88267136	23.05298233	22.99672699
23.19312859	24.08399582	23.63123131	23.83402824
28.0940094	28.20508385	27.97820091	28.1126709
23.38337326	23.31285286	20.64009094	21.91605377
23.71868706	23.69242859	23.71198273	23.50591278
23.3259449	23.35016251	23.17589188	23.02011681
22.88632393	23.11005974	23.39008141	22.83329391
20.92691994	21.56150818	21.387743	20.40961838
21.12053871	21.35046005	20.47238922	21.87904739
26.17996979	26.40186119	26.62324142	26.39327812
21.86721611	22.90021324	22.38110352	22.26850891
20.57380867	21.8243084	20.45513153	21.80781937
21.55599785	22.06114769	21.57427025	22.00860596
22.88650894	23.77283669	23.59149361	23.64008713
25.74213982	24.71465874	24.61526489	24.93867493
26.38977051	26.89330673	26.67626762	26.91067886
24.48357582	25.08318329	24.97640038	24.89642906
23.99886322	24.52939796	23.92079926	24.66307831
23.60320091	23.83730507	23.8839016	20.63412666
23.89633751	23.91597557	23.82493019	24.13218307
25.28104019	25.81697273	25.54760361	25.79647255
23.69890594	23.68816566	23.96305275	23.81362534
24.82653236	25.47299004	24.84632492	24.80104446
23.52061272	24.08488846	23.78026581	23.57103157
23.39375114	22.10395622	23.40314674	23.58852196
25.28068542	24.87549019	25.31627464	25.23436356
26.59063721	26.64223671	26.50089264	26.71868706

26.68244362	26.71187782	26.62603188	26.67492104
23.60002899	23.25983047	23.17622757	23.27213097
22.79512978	19.45071602	21.6439743	22.647089
25.85851669	26.39288521	26.2281723	26.30307579
23.9401989	23.51965332	23.83238792	23.38942528
24.22192001	24.66757774	24.42348671	24.00641632
19.77803612	22.18504333	21.82380486	21.89063454
22.98139191	22.86304283	23.23334694	20.97164345
23.23344803	22.92627525	22.91557503	22.51816559
24.47456932	24.59451485	24.36792946	24.6390934
29.24392891	28.56125259	28.67781448	28.83010864
27.01956177	26.91934395	27.65095711	27.10109329
30.28040695	30.29395103	30.39304733	30.25900841
27.66769981	27.53504562	27.34460449	27.40770721
27.75906944	27.72364235	26.47456932	26.57379341
25.81276894	26.15077591	25.4376812	25.84033394
24.03263092	23.47803116	23.77293777	23.97228622
26.82784081	27.21743393	27.55713081	27.43284798
21.23853111	22.47511482	21.76349449	20.36923027
23.45085907	22.7135582	20.14275932	19.34421349
23.66079521	23.16060257	20.32252121	22.85205269
24.76724052	24.87937546	24.4534359	24.52240944
27.01265335	27.10908699	27.05569077	27.34282494
27.00474548	27.26633263	26.68471909	27.10998535
30.23214912	30.0811882	29.90210533	29.85996819
26.64485168	26.86159706	26.19494057	26.81323242
30.23591995	30.09973907	29.92464828	29.86697006
26.57460213	26.37721252	26.479496	26.15052414
24.95637512	24.09956932	23.92687225	24.3064003
22.0274601	22.31221581	22.25675392	22.39160347
22.56232262	22.74568748	22.7861824	22.71137428
24.6047287	25.01818275	24.5146656	24.91333008
23.13473892	23.48787498	22.78769684	22.71000862
23.68099594	24.41125107	19.84072685	24.24030876
23.62611389	23.56104088	23.57230568	23.60104942
23.351511	23.50930023	23.46762085	23.76304054
24.10549545	23.91798019	24.00195885	24.00829887
24.84182167	24.0284214	24.4236145	24.02233696
23.74488831	23.80045319	24.03598976	23.51568985
25.48234558	25.89407158	25.72985268	25.78949928
21.18303108	23.79639816	23.51749229	20.29961014

20.31178284	21.68761063	21.48910141	22.00408554
24.51977348	24.48873329	21.15223885	24.54185486
23.17205048	22.83261871	23.00087547	22.76595688
25.91818428	26.12935448	26.20895767	26.03462601
22.62678337	22.71066093	21.02049637	22.19318962
24.78750801	25.14055443	24.94908905	25.03653336
23.45625877	24.34671783	23.70081139	23.98745918
23.16098785	23.56034279	23.42136765	23.26685143
27.4354744	27.25457764	27.13741112	27.13388824
25.41786385	25.86424446	25.47376442	25.43644333
19.67462158	22.47822762	22.3235836	22.51948547
26.42439842	26.29496765	26.73750496	26.34480667
24.03841972	24.58250618	24.54668999	24.37537384
21.01194	19.59996033	21.14939499	22.17449379
20.78949738	20.254673	23.03630829	22.9955368
23.63344955	23.92061615	23.67626762	23.50142479
22.89653969	21.6573925	22.08125114	22.10325623
22.78380775	22.60751915	22.33279037	22.57036018
24.15522194	24.36699677	24.19902992	24.06414604
22.3273716	23.17747498	22.80153847	22.82582283
22.66075134	22.99284363	22.2401619	19.53779984
25.44366837	25.68992424	25.41934395	25.52025414
26.38937569	26.20659447	27.36977768	26.43318367
27.07469749	27.25250435	28.41453743	27.50241089
25.25403786	25.4611702	25.51671219	25.10773087
20.37851524	22.78122711	23.32978249	23.0077858
19.89686775	22.73945999	22.68500137	22.50280762
23.77323914	23.82357025	23.65719986	23.6482296
26.77165413	27.13104439	27.02326775	26.75442696
22.40784645	22.51270294	22.7457695	22.50443459
23.33169746	23.8646698	23.38824272	23.621315
26.19914246	26.42958069	25.82281685	26.37757683
25.07798004	24.84182167	24.5892086	24.77182961
22.27605629	21.87526512	21.495821	19.4026413
25.82570648	25.70740891	25.47367096	25.49390221
24.68356705	25.17451477	24.86301613	25.05631065
23.29193306	23.39741325	23.69901085	21.11107445
23.14374924	23.06958008	23.04385185	20.83472252
25.94639206	25.79501152	25.48394585	25.56281853
33.49964523	33.48615646	33.38638306	33.05796814
26.19689369	25.71164322	25.64913559	25.40574455

26.47201347	26.61848831	26.72871208	26.59348869
24.25601959	24.67454529	24.84162903	24.29516029
26.09679794	26.15133667	26.22486496	25.83701515
24.32505417	24.87638092	24.58193016	24.51839256
19.4693222	21.48374939	21.22396278	21.3355999
21.50770378	22.03264618	21.02093124	21.77406502
22.87915993	22.96761513	23.19819069	23.04348373
24.16077232	23.28263092	24.54816246	24.14429283
24.92075348	25.25842857	25.13414383	25.36362648
20.76157951	21.47357941	21.72304916	22.12439346
27.12287521	27.36994553	27.41506195	27.31155396
27.19629288	27.54701424	27.21845055	27.04718399
30.88656425	30.34456253	30.70882416	30.86540604
30.65411949	30.87598801	30.757164	30.64375114
29.17085648	29.41719627	28.81243706	29.04723549
30.1740284	29.99604225	29.99698448	30.08017159
20.19186211	23.89772224	20.73615456	24.02267647
26.23668098	25.93098259	25.96543121	26.52327728
21.33832359	23.00264549	22.97200584	22.14563179
25.91026688	26.54891205	26.26054955	25.91472244
25.06274605	24.051754	23.72587967	25.18831444
22.02201462	22.21495628	22.58093071	22.2194252
21.31224251	21.72263336	22.05212021	21.89611435
23.35164642	23.86731148	23.31229782	23.83951759
29.90210533	30.03734589	30.07111931	30.03551102
24.34638023	23.32745361	24.29698181	23.89707565
29.99590683	29.65688324	29.94642639	29.89172935
33.22705078	33.2937851	33.12646484	33.12709427
24.7565918	25.09932709	24.45669746	24.83426857
21.95290565	22.80120277	20.36507988	22.76931
25.8490963	25.78179359	25.84871292	25.75839615
24.67642975	25.12269783	25.20448685	24.89518166
23.02681732	19.491045	23.03513336	23.46500778
24.6552906	24.49582481	25.2540741	18.9473896
20.97771072	21.7735424	21.62609291	21.22169876
27.57520866	27.9681263	27.64278793	27.75964165
22.223526	20.75802612	22.2930851	22.51722908
25.3213768	25.48200798	23.98875809	25.45117378
27.43714142	27.56165314	27.48523712	27.30042458
23.24115181	23.47543526	23.72577667	23.92379379
23.15744591	22.33696175	22.30641174	22.47988129

27.55362129	26.69458199	27.02305603	26.59590912
22.69981575	22.80481148	22.35995293	22.67219353
23.01205635	24.23491096	23.50809097	23.91077042
20.79994011	20.85946465	21.33570862	21.13131905
22.24057007	22.83178902	22.56841278	22.20580101
23.17423248	23.99118423	22.45530701	22.71055412
21.60819626	22.30069923	21.55102921	22.17319489
24.99727058	25.26495743	25.0507164	25.0370369
22.7842865	23.33946419	22.70737839	20.54440117
23.77525139	24.19166946	24.58657646	24.09466553
27.19760513	27.53110886	27.05672455	27.16009903
22.51333046	22.86340332	22.11524582	22.37113762
23.90361786	24.42419052	24.59212112	24.85780525
23.6839962	22.81413269	23.07814217	22.79060364
22.84571266	23.57357597	23.03236198	22.97419548
23.97901917	24.53195763	24.06101608	23.89152336
26.30045891	26.14230728	26.40340614	26.22099686
24.22081375	24.55888367	24.26799393	24.0639801
24.08082771	22.03379059	20.07050896	22.81811905
22.04786682	20.80368233	19.53922272	22.15285873
22.76514626	23.39152527	22.88957596	23.38350487
21.3104229	20.93883514	21.76034927	21.82322121
19.47408104	22.19868469	22.90600586	22.23885155
25.02373314	25.33759499	25.25745773	25.11545181
29.60930634	29.44142342	29.69511223	29.51271248
30.23683167	29.9640274	29.86505318	29.47132874
28.90970612	28.52309036	28.51190186	28.50517845
26.67922401	26.79587936	26.34482384	26.51062775
24.97836494	25.25616264	25.20284462	24.92175102
20.88427544	21.20251656	21.24132729	20.47149658
28.38960648	27.85037231	28.05491447	27.99139977
22.33153343	23.74601555	22.90139198	23.89356232
19.50835609	21.63408661	21.4643116	20.66344643
27.13829041	26.54705811	26.6563549	26.64718819
22.2147789	21.25271606	20.64423752	22.36484909
20.89903259	20.63019753	21.02072716	21.22258186
23.25037766	23.338377	22.77122498	23.36532974
23.36959457	23.69667816	23.62332535	23.87041855
19.54990768	21.78364754	21.78962898	21.96564293
25.26638794	25.49960136	25.51926422	25.4331665
24.42046928	24.57380867	24.27070618	24.55203819

22.45978928	22.73169136	22.80291939	22.29902267
27.39083672	27.73892403	27.19441605	27.48623466
21.49580002	23.18383217	22.9560833	22.74794388
22.50203133	21.25896645	21.70893097	23.11133385
24.31485748	24.29698181	23.9762249	24.31858635
23.80134201	24.48456001	24.8579483	24.33210564
23.49326134	24.12581253	23.48000526	23.79074287
23.07892418	22.57272148	21.09002304	21.22557831
25.21563911	26.0424118	25.303545	25.89562035
24.45657158	24.17027855	23.86325073	24.19655609
21.06972694	22.47047997	21.68033028	21.36099434
23.85595322	24.24357986	24.286726	23.80675888
21.05663681	21.50305176	22.23401642	20.51499176
21.89241409	22.19607544	28.65625381	24.10309601
25.97701073	26.58477211	25.84579849	27.1662426
31.91441917	31.86919975	31.63573074	31.88983154
28.11505508	28.01680183	27.33330154	27.78225517
25.29006958	19.84587288	21.27707481	21.83877563
27.99927139	27.93292046	27.10309601	27.57492065
27.59981537	26.90161705	25.50536728	26.91444778
24.97460747	24.0886116	23.37384796	23.94172096
32.48423767	32.4078331	32.1448555	32.25959778
28.90293884	29.20394135	28.69544411	28.91424751
26.52324867	26.43130302	26.8256588	26.25466919
24.08845139	24.16614723	24.79382133	24.35803413
22.68307495	23.09026146	23.06096649	23.34380722
28.17930603	28.36339951	28.01345062	27.96724701
23.11074448	22.60480881	22.44500923	22.72945404
26.49970627	26.84050179	26.49952507	26.59761429
24.72463226	24.72946358	24.72629547	24.7166481
25.13339806	25.3398056	25.05796242	25.1898613
23.65600014	23.55637169	23.1463623	22.96907425
24.61621857	24.99834633	25.16150284	25.06698036
24.31465149	24.11981201	24.35635567	24.33401871
29.48788261	29.6454525	29.54708862	29.66346359
23.53931236	23.18785477	23.32141113	23.44505882
22.29367447	22.34405136	22.4925518	22.64638519
20.80204964	24.44474411	24.59251976	24.84436226
22.31942749	22.6717186	22.17752075	20.81557274
24.97097015	25.17447662	24.98428917	25.40995789
22.95336723	23.16184807	23.01277161	22.93416214

19.9637661	23.26456261	23.52097321	23.47815514
26.78469086	26.87349701	26.93089294	26.75557327
27.32483101	27.30877876	27.37152481	27.37077522
24.59366035	25.13531876	24.839468	24.60303116
29.18366623	29.09204483	29.51694489	29.64823341
20.81291962	21.48099136	21.77112579	22.95709419
20.72616005	20.39707184	21.99137306	21.57070732
20.66220856	19.27091217	20.13257599	20.0249939
24.17302704	23.9955883	23.44139099	24.11592865
22.81499481	22.84550095	22.50246811	22.60141182
23.62086868	23.98093796	23.62911987	23.73148537
23.04656792	23.19272232	22.14314079	23.51292038
22.97270584	23.19248199	22.94799423	20.26353455
27.98413658	27.39329338	26.97169304	27.35110664
19.26282501	23.12182045	22.79378128	19.69579887
27.221035	25.71730232	28.78587532	26.97738266
25.17455292	25.26942253	24.92877007	25.03565407
24.24713516	24.47617722	24.09055138	24.56685829
24.95495605	25.12864685	24.97731781	25.10325623
26.15174294	26.93145561	27.02643776	26.96013832
25.41963387	25.30945587	25.70675087	25.39424324
21.18058968	20.7981205	20.27788544	21.25488663
20.69845581	19.9288826	20.04427719	20.60068512
26.44550133	26.78705978	26.43278503	26.7565918
23.97814751	24.61941338	24.78121758	24.82410622
25.13953972	25.09675789	26.29804802	25.3660965
23.80538177	24.30904007	24.55718994	23.79788399
26.03256798	25.8490715	26.76963806	26.3372879
27.9749794	27.82753754	28.73805428	27.737957
28.58849335	28.44915962	29.3036499	28.49151993
26.48581886	26.65703773	27.58985138	26.84565544
24.87769127	24.08058357	25.19767952	24.247715
26.62435913	26.25340652	27.25574875	26.55900002
22.16207886	22.8392868	22.85500336	22.46819305
21.60154724	20.99997711	22.60952759	22.09526062
24.13288879	24.44151688	24.74473381	24.37967682
24.328619	24.90320396	24.41383553	24.97936821
20.59577751	20.90749168	17.56340218	20.97554207
25.3475647	25.69224167	25.25810623	25.14386559
19.60431099	23.29319572	23.72930717	24.25796127
26.58132744	26.57474709	26.60300255	26.56537819

22.71129036	22.41735649	23.12265778	23.61503983
20.12098122	20.79249191	20.75238037	21.43338966
24.89360809	25.26831627	25.07398224	25.23022652
25.01239586	24.11100006	24.43154144	24.4810524
25.53611374	25.90435219	25.51065826	26.18557739
20.79082298	23.18251419	22.41586113	22.39576721
27.0142498	27.02633286	26.86903	26.8260231
28.26954651	28.46832085	28.06661034	28.19422722
22.92603874	21.43613815	22.50448799	21.47045517
23.09709549	23.22166824	22.55782127	22.91708755
28.56398201	28.65550232	28.49392509	28.2938633
32.97481918	32.87111282	32.79656601	32.66139984
29.42606354	29.49838448	29.40584183	29.31133652
28.32641792	28.32487297	28.49830818	28.36623764
27.06394005	27.18905067	27.26257515	27.08972359
25.52710152	25.47351646	25.20108795	25.18974876
34.64656448	34.51747131	34.30259705	34.21277237
23.51689148	21.30016327	20.95811272	20.36219978
21.51431656	22.02914619	21.60724831	21.7474308
24.02766228	24.35198402	24.01682281	24.02647972
22.79165649	23.16373825	22.85684586	22.69436455
22.96022606	22.16109467	21.46921158	21.60480881
25.09414101	25.90747452	25.09551048	25.34722519
20.35221481	20.33810616	20.79352379	21.57070732
21.88378143	23.33960152	19.57968712	22.63092041
21.68940163	22.39653206	21.84249306	21.97589302
19.98628426	22.22829056	22.20137978	22.35277748
24.9039402	25.44682693	25.15699768	25.26602936
22.49916267	22.50266266	22.19312859	22.44126511
25.92795753	25.99933624	26.0062027	25.9615078
26.38558006	26.30086136	25.02398682	26.21326637
25.85697556	25.6768589	25.49484825	25.42294121
27.64574623	27.16480446	26.64388847	26.32757378
22.66793442	22.15340614	22.12660027	22.77802086
26.93719292	27.08547592	26.9096489	27.15711403
24.97355652	24.92899704	24.85267067	24.66008759
22.97139168	23.65839958	22.88451767	22.16729546
29.26613235	29.22184181	29.25520897	29.23343086
20.36672211	21.42837143	23.53148079	22.26001358
23.07471657	23.6037674	23.30716324	24.01860619
27.87952614	27.85828018	27.37393188	27.5480442

26.84852219	26.90517998	26.87865067	26.73324394
23.3329258	24.06472015	23.9724617	23.80153847
25.5480442	25.6672802	25.74131775	25.6894455
21.96666527	21.83580208	22.93158722	20.85542488
24.27838326	24.88418198	23.52001381	24.47988129
21.95248032	21.03830147	22.15803909	21.5694313
22.6167469	22.27775955	22.15322876	22.72833252
22.85008812	23.824543	22.96040344	23.31838036
27.88843918	27.14024162	27.56019592	27.54855919
28.44971085	28.05940819	28.17455292	28.3862381
28.04400826	27.77467346	27.81311035	28.4438343
25.7888279	25.77705956	25.72171593	26.3173275
28.74287987	28.69839478	29.02056885	29.0350399
30.24671745	30.00410271	30.12706375	30.15870285
23.9331913	24.17447662	24.57114792	23.87389565
20.55618477	21.79499245	20.49365234	20.74657059
19.29526711	19.56874275	20.66718483	22.09351349
23.44859314	23.05417442	22.37618256	22.79159737
21.89759254	20.66702843	21.01522446	21.14419937
29.87686539	30.22377586	29.90023613	29.76602364

sents Label-free Quantification values generated by MaxQuant.

Log2(LFQ Col8+/+_3)	Log2(LFQ Col8+/+_4)	Peptides	Unique peptides	Sequence coverage [%]
20.13005829	20.24832344	2	2	7.6
20.74559402	20.52244377	1	1	5.7
20.81119537	23.02213478	2	2	7.7
18.60058594	21.58037949	2	2	3.6
20.83017159	20.42439079	1	1	3.5
20.35355377	22.50915527	3	3	6.2
20.7847538	22.23022652	1	1	6.8
20.9280777	18.78753853	1	1	5.5
22.66016388	21.43086433	3	3	10.9
21.3584938	21.2183876	3	3	7.1
20.07580185	20.46037292	2	2	7.7
22.21859741	20.99541664	2	2	12.8
25.77532578	26.14557648	11	1	78.1
27.89856339	28.94673347	4	4	72.2
22.02536583	22.48706627	4	4	7.6
22.34754372	20.92611313	2	2	4.4
26.87490463	27.66309166	1	1	8.7
24.59423065	25.62745094	10	10	22.9
29.44268799	29.40346718	46	46	39.6
26.203125	26.36157036	21	16	54.2
22.95052338	23.19877434	2	2	8.6
22.8434906	22.43321228	3	3	16.9
24.93075752	25.01788521	7	7	40.7
23.87220573	23.90802383	3	3	16.5
24.31955147	24.28171158	6	3	17.3
25.15734482	24.5952549	5	5	17.9
24.48664856	24.94650459	5	5	7
24.14452744	24.40295029	2	2	3.5
27.27559853	27.32345581	15	15	32.7
23.51581001	23.38653374	3	3	5.1
27.15769196	26.8707943	19	19	25.4
25.3012104	25.43631554	15	15	12.3
24.42040443	24.94677162	1	1	39.7
22.7152977	22.6591835	2	2	13.2
25.07496262	25.23209572	17	3	44.3
23.76324272	23.27951813	6	6	8.2
25.23187447	25.05105019	10	10	13.7

24.67125511	24.94828796	5	5	29.5
25.18959808	25.14518738	13	4	16.7
29.74927139	29.7671299	53	45	33.6
32.46630859	32.31985474	55	2	66.2
25.070261	25.03573799	10	10	25.9
24.42278099	24.81972694	5	5	21.7
29.08618355	29.284935	7	7	39.8
29.64233971	29.66991425	19	19	19.5
26.8292923	26.73698997	12	12	28
22.82148933	22.6990757	4	3	19
28.20097542	28.15576363	14	13	57
27.1848011	27.03160095	7	7	30.4
26.07795906	25.81360054	9	9	32.1
26.65962601	26.79587936	13	13	28
28.77555275	28.69832993	27	27	41.8
29.61999321	29.37819672	29	29	39.8
25.08476639	25.05796242	8	8	42.2
25.84256554	26.02772522	8	8	25.9
25.88925171	26.08401489	5	5	71.3
28.18905067	28.01403618	22	22	24.1
31.87125778	31.5801506	25	25	76.8
24.97079468	25.04551888	5	3	24.8
24.92705345	25.05924225	3	3	56.9
30.94928169	30.75914955	16	16	44.7
26.14172363	26.0161438	12	11	35.9
30.22227859	30.20780945	17	17	56.1
28.67865372	28.50260162	70	57	37
26.25279236	26.5917778	3	3	36.4
32.0824585	32.14135742	42	42	40.1
31.95265198	31.80624199	20	19	61.8
32.40509796	32.26857758	46	46	51.9
33.14176941	32.92406464	22	20	91
29.30112267	29.38055229	18	18	54.2
24.8472805	24.77826309	5	5	14.6
29.41266251	29.32029533	22	22	71.1
24.67055321	24.84665871	3	3	3.5
29.32964897	29.30893135	27	27	36.5
28.43328667	28.46166229	14	14	32.2
28.85156441	28.73615074	31	31	38.2
26.49798775	26.40896988	16	16	29.5
32.05717468	32.04074478	73	44	78.6

29.75585938	29.68695641	25	21	62.8
28.3506012	28.31893921	14	14	23.4
26.46062469	26.28630257	10	9	18.5
31.9971199	32.12234879	26	26	73.2
28.65853691	28.5903511	46	46	29.2
30.90727234	30.69145584	26	26	20.1
24.82847023	24.85965538	5	5	13.6
30.67092705	30.61386108	16	16	40.6
25.58385468	25.44518471	6	6	22.1
32.1676445	32.2407341	41	0	92
27.72214508	27.84667206	13	13	53.2
29.85660362	29.78507996	15	7	95.7
29.39674759	29.3693409	24	24	44.7
26.37414742	26.43744278	11	11	33.4
27.6776123	27.60780716	13	13	51.1
27.89186096	28.01781082	6	6	49
32.16230774	32.10771179	22	13	81.2
27.03653336	26.94793129	20	20	29.3
31.04283524	31.15273285	25	25	73.7
25.55677986	25.55666351	10	10	49.5
27.0048542	27.22701645	7	7	34.7
24.62527847	24.80094719	1	1	10.6
27.44213486	27.38599205	8	8	16.7
27.0212574	26.85483742	16	16	18
29.6585865	29.64593506	15	15	73.4
23.75052071	23.5985527	3	3	8.6
26.27602386	26.38315964	9	8	37.5
29.83540535	29.75054932	19	19	48.8
28.38964653	28.34912491	24	24	45.7
26.20560646	26.09657669	8	7	53.5
25.32892609	25.66193771	4	4	44.7
24.98819542	25.38442802	10	10	6
26.62936974	26.43855476	13	13	45
24.39159012	24.46836662	5	5	4.3
24.71816444	24.90651131	3	3	6.9
24.14476013	23.89485741	2	2	11.9
26.96035957	27.12356567	16	16	28.5
22.66773987	22.47901917	5	3	19.2
23.78815651	23.92687225	4	4	5.1
25.77301407	25.93213272	9	9	30.8
23.8292923	24.08739853	6	5	15.6

25.64088631	25.6284256	10	10	23.3
26.56072044	26.74599075	9	9	20.7
24.88743973	24.93907738	6	5	14.4
27.13025856	27.0378952	15	15	39.4
27.15595627	27.17121506	8	8	40.2
24.35568428	24.37782478	7	4	4.5
25.81426048	25.51292038	8	8	40.9
23.72826958	23.62722778	2	2	21.8
25.75842285	26.17518044	2	2	24.2
20.99886322	20.98168755	1	1	1.9
28.0175457	27.85554886	4	4	47.6
27.60498428	27.5060482	13	13	16.1
24.94565582	24.72416306	3	2	10.9
26.82189369	26.69351959	9	9	5.9
24.41209221	24.86792374	7	7	7.9
24.47889519	24.77971649	6	6	20.6
23.60433388	23.77031898	4	4	14.1
25.77152824	25.80015564	4	4	25.2
27.830019	28.29171371	9	9	50.8
25.46220207	25.67066002	4	4	19.6
26.23344803	25.77482414	6	6	39.1
24.10181427	23.7850647	5	5	7.4
20.65848732	20.95539093	1	1	0.6
23.43618965	23.56150818	2	2	2.7
25.25259399	24.83893967	6	6	30.3
20.88539314	20.25660896	1	1	16.4
24.08204651	23.45199013	6	6	14.4
22.43260002	21.90683174	1	1	1
25.24557686	25.76638031	9	9	26.8
25.2257843	24.86178589	7	7	18.7
20.43481636	20.27264404	1	1	13
25.35289192	25.80815887	6	6	21.3
21.97816467	21.56620789	1	1	4.4
23.10304832	22.59128761	1	1	4.8
25.30608559	24.3617878	11	11	16.9
21.52497101	21.62497711	1	1	8.5
29.76086235	28.92668533	6	1	19.4
21.80025482	21.11343384	1	1	3.8
21.96409225	21.33663559	1	1	23.3
23.1590786	23.1245842	1	1	24.8
27.87367249	28.18413925	10	10	28.4

22.33881187	22.73952103	1	1	3.3
20.52267265	20.40478325	1	1	7.4
22.50847816	21.15127945	1	1	0.7
24.78256798	24.4795742	1	1	1.1
21.77344894	21.8398056	2	2	4.4
22.12965393	20.88639641	1	1	1.6
23.73106956	24.22663116	3	3	8.7
23.73448563	23.13505173	16	3	33.3
23.53171921	23.91497231	8	8	4.3
22.86974144	21.11162949	1	1	8.8
23.55999184	23.37623596	1	1	1.9
25.27280807	24.49643517	17	2	53.5
25.63768387	25.84830856	2	2	34.7
25.08982468	25.25432587	2	2	13.1
25.73448563	24.63212013	2	2	48.3
30.04544067	29.92874718	35	35	36.7
25.30803299	25.24612045	5	5	8.2
21.12300491	22.29246712	1	1	2.7
24.69205475	24.34387589	4	4	12.8
22.48944473	21.8386898	2	2	1.9
23.12090302	21.93668175	4	4	3.8
23.44897079	23.45211601	3	3	6.8
23.29319572	23.13252831	3	3	11
21.53886414	21.87942123	1	1	1.2
24.09256935	23.9616394	3	3	25.4
24.80198288	24.56383705	6	6	21.6
24.92456436	24.98789215	6	5	11.3
23.55015945	23.85081291	3	3	17.9
23.47963524	20.32868004	3	3	9.5
20.84796524	21.40254784	1	1	2.2
25.58471489	25.34207916	4	4	77.8
25.82946205	25.99899292	5	5	22.9
29.73201561	29.27186394	28	28	83.1
25.02820969	25.90055847	39	36	24
22.12155151	21.59545898	3	3	3.9
24.00453186	23.75542068	2	2	5.8
28.89431953	28.71986198	21	21	45.3
28.85117722	28.61589622	14	14	43.7
27.37550735	27.27710724	12	12	47.8
25.67411423	25.69112396	6	6	18.5
28.52223015	28.25822258	38	38	74.5

27.60865402	26.19852448	20	20	11.4
29.17921066	29.16180611	15	15	55.4
25.25125885	25.73169136	7	7	29.7
22.94970512	22.65066528	3	3	8
28.06635475	28.13887596	33	33	40.1
26.44262505	26.72806168	17	17	32.3
30.26918983	29.96333885	44	44	65.4
24.34962273	23.62310219	3	3	36.4
25.19069099	25.41641617	8	4	29.4
22.79520988	23.31713676	2	2	6.5
26.48658752	26.60554886	12	12	29.6
25.07062912	25.11692047	3	3	20.3
22.15533066	22.54722023	4	4	10.1
21.44129562	20.38448143	1	1	3.4
28.4814682	28.46653366	26	25	39.9
21.07759476	21.27957344	8	7	17.9
27.36076546	27.3554821	37	1	92.3
35.33314896	35.33504486	43	0	92
33.46963501	33.50923157	37	1	92.3
23.13653946	23.08342743	2	2	6.1
29.15056801	29.25554657	68	41	75.3
23.53564072	23.73096657	2	2	9.6
24.7470417	24.63128662	13	4	45.5
27.22940254	27.1268177	13	4	45.2
28.0525322	28.22283173	15	15	51.8
29.43483734	29.47309113	16	16	63.9
23.64636421	24.28792381	3	3	28.3
20.99920654	21.02857208	1	1	1.6
20.65880203	23.23928833	2	2	2.2
24.73866653	24.21726608	8	8	17.7
25.44189835	24.96899414	6	5	6.7
20.22021103	21.12009621	2	1	3
23.47072792	23.60501099	3	3	7.7
26.75404358	26.9617939	11	10	57
20.46800995	24.87652016	6	5	20.6
24.94252777	25.16088676	3	3	13.8
26.08873367	25.97083855	7	7	28.8
21.73007584	21.56857681	2	2	8.1
21.61997223	21.68616486	2	2	2.9
19.13703918	21.75767899	1	1	3.7
25.35753059	25.48114586	11	11	33.9

22.34258842	21.90455437	2	2	7.2
22.68833542	21.82403755	3	2	4.1
20.57975769	20.14071083	1	1	6
23.38363647	23.7207756	1	1	14.5
23.19751549	24.27887917	3	2	4.7
22.01733398	22.71181488	3	3	18
25.50433731	25.25850105	16	16	11.9
26.20235825	27.06896973	12	12	37
23.98119926	24.24597549	4	4	10.8
24.23841476	24.20873451	2	2	8.6
29.74534988	29.81792068	6	6	36.2
24.73448563	24.34340096	4	4	9.6
21.22063446	20.713274	2	2	11.5
25.04735184	25.1964798	5	5	20
23.89513588	23.80695534	3	3	11.6
22.73134041	23.48382187	6	6	17.6
27.60165787	27.59583855	8	8	52.1
27.19779205	26.90861893	9	9	56.9
27.12346649	27.11892128	14	14	70
25.49810982	25.77873802	4	4	3.7
27.28091621	27.26140976	12	12	56.9
27.806427	28.04223442	12	12	46.8
23.53290939	24.32471085	2	1	5.7
25.3211689	24.81318474	4	3	18.7
24.67642975	24.96886253	3	3	12.5
21.77370262	22.36190796	1	1	4.7
23.34624481	23.22883415	2	2	10.9
34.24111557	34.46562958	49	46	77
24.14926529	24.98823929	6	6	16.5
21.70562172	20.79169655	1	1	1.6
20.36361122	21.88970566	1	1	1.5
23.36051559	24.06735039	7	5	16
22.92549706	21.86430931	3	3	5.1
30.60814285	30.65846825	27	25	68.2
25.72111511	26.04528999	7	7	17.6
24.48283768	24.88832283	6	6	17.3
19.79170418	21.84295273	2	2	5.5
27.9770546	28.03165245	19	19	50.7
26.59775734	26.9055233	11	11	37
29.5076561	29.55453491	22	22	80.8
21.69029808	22.49677658	1	1	3.9

20.81080437	21.31484413	1	1	8.1
23.89809227	24.31879234	3	3	29.4
22.0214386	22.14929581	3	3	2.4
26.77555275	26.67949295	25	24	24.1
23.19434738	23.46724892	5	3	2.3
22.29271889	20.89393234	2	2	4.4
23.71240425	24.01529312	4	4	12
25.15715218	25.72928238	4	4	21.1
24.84771156	24.63045311	2	2	11.4
25.15930939	25.50960159	4	4	13.3
28.49094582	29.12915421	28	28	37.7
27.85352898	27.66471863	15	15	32
28.48523712	28.53267097	16	16	56.7
31.27102852	31.3083992	49	49	70.9
27.61421204	27.62317276	10	10	22.9
31.65347862	31.6597023	29	29	48.4
23.4124794	23.34462166	2	2	3.2
24.79813004	24.74082947	17	5	22.5
22.99543381	23.36305809	3	3	5.6
26.86348724	26.89272881	23	16	33.3
27.9739399	27.97459602	23	16	35.7
28.00147438	27.86914825	28	16	37.2
26.70001793	26.67438316	10	10	29.9
24.69556427	24.60308838	2	2	11.3
23.66448975	24.06989098	5	5	5.2
22.59416199	22.5853157	2	2	3.3
23.41725349	23.90150261	3	3	15.8
24.49716568	24.66682053	3	3	7.7
22.94209862	20.33995438	3	3	13.7
28.81659317	28.91459084	17	17	61
26.90334129	27.26481247	9	9	46.5
25.82607079	24.46811867	2	2	32.4
27.471735	27.30190659	15	15	48.9
24.62103462	20.49060822	1	1	10.2
24.47426033	24.28199577	1	1	21.6
25.41028214	25.44871902	5	5	18.6
27.33849716	27.12662125	11	11	36.5
22.4954586	22.86568832	2	2	19.5
24.286726	24.31250572	4	4	27.9
23.95819092	24.16415215	7	7	15.7
25.25428963	24.97206688	3	3	25.6

25.99537277	25.74550438	3	3	23
25.12947273	25.62374496	9	9	22.9
27.34874535	27.58591843	9	4	68.5
21.91415215	21.67012024	5	1	47
26.36691475	26.09186363	6	3	52.8
22.58072472	23.20413017	6	2	42.8
21.67560005	22.56890106	2	2	21.7
20.92085266	23.02815056	3	3	2.5
26.40494919	26.20687294	11	11	44
21.92947578	23.05755043	3	3	8
27.75053406	27.63899612	2	2	1.4
28.41312599	28.44130325	11	11	74
23.80094719	24.19550514	2	2	23.5
20.21473122	23.59331894	5	5	7.4
22.93499184	23.00156212	3	3	7.1
23.95020294	24.35366631	2	2	13.8
25.39728165	25.16538048	4	4	35.2
22.86300659	22.89744568	1	1	4.9
25.72098541	25.61711693	6	6	28.7
23.96886253	24.69040489	5	5	30.1
24.12494659	23.34000778	3	3	27
28.19798088	28.35640717	11	10	37.9
27.42774391	27.21521187	14	14	42
27.53237343	27.75174713	9	9	53.9
28.13970566	28.3614769	9	9	66.7
25.55777359	25.63832092	3	3	29.1
24.59269142	24.49283409	2	2	16.3
25.16564751	25.86048317	5	5	19.8
23.59605217	23.9331913	5	5	19.2
23.89096832	23.96243477	5	5	17.5
25.94851112	25.82629013	11	11	19.3
31.58203697	31.48898506	19	19	54.2
20.75216484	22.4225235	1	1	3.1
22.18198395	21.78192711	2	2	4.3
23.37570572	22.54354286	1	1	6.9
22.57309151	22.24751091	2	2	4.9
27.4342804	27.62519455	18	18	48.8
22.54745483	22.80545998	2	2	4.1
27.86390114	27.77416992	15	15	46.8
26.01459122	26.34910011	5	5	58.8
27.40973091	27.50294113	20	12	23.5

25.0646801	25.06669235	3	3	12.5
25.68228149	25.19636726	8	8	39.6
27.42205811	27.62742233	19	13	28.2
23.39702034	23.98702431	7	4	11.1
20.34970474	22.25612068	4	1	4.7
26.24646378	26.16428757	12	9	14
30.63469315	30.69967079	28	28	61.7
31.47145462	31.62831879	27	27	73.5
27.05713654	26.96565247	10	10	42.6
27.66553307	28.01137352	7	7	22.7
27.32534599	27.39435768	8	8	76.4
24.33073997	24.65610886	2	2	33.8
23.24811935	23.73055267	1	1	9.3
25.81245041	26.30472946	3	3	41.7
28.81476212	29.09778214	10	10	62.4
20.61888885	21.61562347	1	1	1.2
23.72567177	23.61346817	2	2	6.6
25.30959511	25.26781654	9	9	23.8
21.15357018	21.65307236	1	1	4.3
23.02403069	23.91579247	3	3	19.5
21.96761513	21.65407181	3	3	12
22.79701233	23.04962921	3	3	9.6
23.4648819	23.76920891	3	3	4.5
24.86329842	24.42001915	3	3	40.3
22.43766212	22.17520714	1	1	2.7
24.78336716	25.11330795	9	9	26.3
21.77346039	22.0863781	1	1	2.7
27.87794876	27.90190506	5	5	62.9
22.76846313	22.94259834	1	1	6.8
28.43017769	28.22149467	17	17	46
21.0957489	19.34496307	1	1	3
21.1309433	21.02546692	1	1	1.8
23.84373856	23.62220955	3	3	12.2
23.99291229	23.98085022	3	3	18
22.45452881	22.37898827	1	1	4.1
25.12344742	25.19422722	7	7	26.4
24.12407875	24.00744438	5	5	25.8
25.58560371	25.52754974	8	8	58.3
20.16300011	20.89141273	1	1	4.6
24.51086998	24.61997223	9	9	36.7
21.9927578	20.07347488	1	1	5.7

22.52200317	22.32231903	2	2	39.8
21.5288372	21.05163193	1	1	14.2
21.10200691	20.5534687	1	1	1.7
24.65583611	24.95024681	4	4	25.5
27.67418098	27.78718376	33	33	29.7
25.77718353	25.49115181	3	3	9.2
23.06621742	22.46630287	3	3	2.9
21.88516998	21.68118858	2	2	4.2
22.94590569	23.70882988	3	3	11.9
27.3960743	27.72279739	13	13	68.1
29.19666862	29.82436943	17	17	84.6
25.35403633	25.35050011	10	8	31.1
22.26439095	22.74827003	2	2	12.7
22.46266365	22.57137871	4	4	1.6
26.95338058	27.16576385	6	6	49.7
27.48492813	27.85126686	12	12	45.4
24.69492722	23.82006836	3	3	11.7
22.99007607	23.33279037	3	3	8.6
27.6654644	27.40210533	13	9	40.2
26.07850838	25.74175453	12	5	33.3
22.14183235	21.86434746	1	1	6.8
28.22117233	28.35653305	27	27	35.8
28.13398552	28.47192955	11	11	33.5
30.54166985	30.26785278	26	25	75.9
26.63131523	26.69935608	10	9	31.3
25.29708672	25.7165432	4	4	22.7
24.72723198	24.22993279	8	8	18
28.44237137	28.38356209	21	21	40
28.49171066	28.31267929	9	9	47.2
21.93120766	22.0242157	3	3	8.3
27.67128181	27.86803055	7	5	33.9
27.38055229	27.39255714	10	10	49.3
23.94529915	24.66557312	3	3	43.2
25.3631916	25.4807148	8	1	35.8
22.30763626	21.98360252	8	1	38.9
22.00120163	21.48217392	1	1	3.1
19.07666588	20.04473495	1	1	2.9
19.17979622	21.51099014	1	1	2.9
27.67242813	27.23571396	3	3	14.3
24.27348328	24.04876518	3	3	6.8
25.19035149	25.2212925	10	10	27.7

29.20013428	29.10096741	9	9	57.9
25.58666229	25.87398911	4	4	37
23.88315582	24.35528183	5	4	18.8
22.03821754	20.91676521	2	2	3.4
21.74336815	22.44511032	1	1	1.5
19.82895088	22.6102047	2	2	6
21.62992096	21.75979424	1	1	9.8
24.02580452	24.78964996	5	5	13.8
24.63117599	23.96057892	4	4	5.7
25.198843	25.4877224	2	2	16.4
21.40835571	20.98628807	1	1	4.7
27.9949646	28.14583969	22	22	56.4
27.21335983	27.51525307	15	15	36.5
26.76040268	26.94402504	12	12	35.6
27.63381004	27.857687	15	15	53.6
27.11455917	27.07724571	17	17	39.3
26.57067108	27.07183647	14	14	24.8
26.46584892	25.58543205	11	11	13
24.69895935	24.42515182	3	3	13.4
22.54257584	22.69725227	2	2	2.7
25.61006355	25.51331139	7	7	25.5
23.53564072	23.25925636	4	4	6
24.94485283	25.07308388	2	2	8.6
26.93584442	27.44931602	12	12	33.5
21.18920517	22.11765671	1	1	3.3
24.40995789	24.29116058	1	1	4.6
27.97213173	27.88098717	3	3	27.5
26.80020523	25.65034103	2	2	11.5
24.71339989	24.47932625	5	5	11.3
19.89514542	21.10655022	2	2	27.4
24.5077877	24.82900238	4	4	13.2
27.41231918	27.36419487	8	7	57.1
24.29403877	23.941185	6	5	6.5
21.67856979	20.99451828	2	2	2.4
20.41060066	21.82150841	1	1	6.1
21.97211075	21.68418884	3	2	3.1
19.98134995	22.2006321	3	2	9.2
24.14289284	23.77374268	4	4	14.6
23.72847748	23.11711884	6	5	13.7
24.58600426	25.24099922	4	4	23.4
27.74534988	27.56456375	15	12	39.2

29.022686	29.42754364	22	19	55.9
24.4759922	24.26470566	5	5	9.3
23.2030983	23.61279297	1	1	10.1
28.02606773	27.63754654	19	19	21.4
22.65672112	23.46799469	3	3	9.8
29.37883759	29.40212631	15	13	74.1
25.42123985	25.0324192	7	5	52.4
24.05804634	24.19618034	3	3	21.6
23.59023666	23.40976334	2	2	10.6
20.26900673	22.66135979	1	1	5.4
20.32430077	22.67684937	2	2	15.6
21.43938828	21.60277176	1	1	4.1
22.27247238	23.43872833	3	3	18.3
24.86207008	25.30225563	3	3	30.6
30.63763237	30.52234268	17	16	61.7
26.25875282	27.23835945	13	12	44.4
23.56115913	23.43847466	5	5	5.2
22.58675957	20.25767326	1	1	4.5
22.2931118	23.16075706	1	1	3.3
24.88082314	24.84608459	6	6	53.5
26.70345497	26.84409904	11	11	47.7
27.91627121	27.7358284	14	14	70
20.25834656	21.37060738	1	1	2.2
19.82287979	21.86517906	1	1	3
21.29065514	22.54165459	2	2	9.5
30.6098156	30.83115196	70	70	55.5
26.97760201	26.60808945	9	9	23.2
25.38337326	25.28142929	5	5	23.1
27.5773716	28.42562485	7	7	36.8
25.0606041	24.79684448	7	7	36.2
24.16584015	24.00761414	1	1	8.8
26.0651741	26.15882874	10	10	31.8
28.1668644	28.17450523	9	8	36.1
21.29350471	23.66242599	8	8	23.2
22.01154327	22.26828003	2	2	11
22.00888062	22.32770157	1	1	4.9
22.97125053	19.82841301	1	1	9.3
22.3046875	22.61393929	3	3	9.1
20.96276665	21.15641212	10	10	8.1
33.68280029	33.67934036	15	15	11.7
33.02237701	33.13911819	21	21	20

30.96788025	31.17277718	4	3	3.9
27.53786278	27.09888649	5	2	4.3
30.96506119	30.86798477	9	9	7.5
30.64185905	30.4543457	15	15	14.8
23.66557312	23.13172722	1	1	2.1
28.191782	28.33879471	7	7	6
27.77461052	27.8283844	5	5	6.3
25.92822838	26.03827286	20	12	10.8
22.90695953	23.5775013	4	4	7.6
22.57927513	23.03521729	3	3	24.6
21.06804085	20.49179459	1	1	7.5
23.75715065	24.07781601	2	2	13.6
24.63272858	24.77213287	7	7	44.1
22.21089172	21.99838066	1	1	6.1
26.39645004	26.88308716	23	23	28.9
26.07357407	26.20629692	13	13	22.7
24.26341629	24.0500946	7	7	9.6
24.86990166	25.05038452	6	6	43.8
26.56155205	26.49845886	13	11	24.5
22.40867615	22.36711693	5	3	7.4
25.91344452	26.30883026	6	6	19.4
25.06542015	25.20761871	5	5	18
24.31236649	24.42854309	5	5	19.5
23.86353493	23.95153809	2	2	6.9
20.60932732	20.81596565	2	2	7.1
23.79302788	23.42918015	4	4	21.1
23.28305626	23.35689354	2	2	20.9
21.81092072	20.10774803	1	1	5.3
23.55180359	24.13398552	7	7	18.5
24.2004528	24.1483345	3	3	12.1
22.40418625	22.78767776	5	5	16.3
25.78563881	25.34553528	7	7	17.4
27.93814659	27.806427	14	14	37.8
21.7727375	22.54281235	1	1	11.3
26.77680779	26.80439758	5	5	36.1
28.57145119	28.39034462	7	7	54.8
25.74167824	26.10775185	7	7	51.6
28.40807152	28.12005806	4	4	61.3
27.16182899	27.58813667	8	8	70.9
25.79808044	25.87897682	4	4	59.2
25.75087929	25.17436218	1	1	16.2

24.98428917	25.17500877	3	3	56.6
24.16790771	23.97237396	1	1	14.3
25.92730141	25.96721458	10	10	14.8
27.8434391	28.64278793	12	12	31.9
23.75837135	23.85338593	4	4	10.5
26.51389885	26.44928551	8	8	20.1
22.50963783	22.52528	3	2	10.6
26.61960983	26.33128738	7	6	18.4
19.4534111	21.22735023	1	1	2.9
20.59242058	22.15560913	2	2	10.9
24.21837616	24.6725502	3	3	12.3
25.73435593	25.61085129	2	2	7.4
24.18419647	24.34380722	1	1	10.5
24.32457352	24.22368813	4	4	6.7
24.35904121	23.94940186	7	7	11.7
26.54104233	25.7665081	18	18	33.3
20.02623558	20.43290138	1	1	2.3
24.96124268	24.73536301	14	14	31.2
21.23391724	20.43240738	1	1	3.8
29.87202835	29.97910118	4	4	71.4
29.77478218	29.78607941	8	8	71.2
25.1590023	24.59075165	6	6	29.6
22.8012619	23.19547462	1	1	5
25.34624481	25.32436752	5	5	30.9
25.22177124	24.328619	6	6	26.6
23.50421524	24.06192207	2	2	10
29.93733406	29.63580132	18	18	50
25.58972359	25.60453033	9	9	29
27.39778709	27.69796562	8	8	14.3
23.3013134	23.85566902	3	3	8.9
22.27526093	22.72941208	4	4	13.2
24.86244774	25.10173416	6	6	21.5
23.79629898	23.35353279	1	1	7.9
29.65362549	29.96829224	12	12	64.8
29.45309067	29.18491936	13	13	67.4
19.60756111	23.93831635	1	1	9.3
25.53112411	25.83202553	3	3	33.7
23.52073288	22.99312019	2	2	9.1
25.30211639	25.12931633	6	6	19.1
22.29288864	23.0237751	1	1	2.4
26.29307365	26.51701164	9	7	16

22.39042282	22.71158409	2	1	3.4
22.66088295	21.52133179	3	2	6.9
23.52037239	23.21406746	2	2	5.2
26.16209793	26.56539154	9	7	17.4
21.53872108	21.51936531	2	2	3.6
24.73696327	25.13731384	9	9	14.1
25.67006683	25.98858643	6	6	25.4
27.76610374	27.78830528	11	11	37.1
24.21504593	24.63300705	2	2	11.1
24.42335701	24.83812332	6	6	11.2
19.4334507	21.96413231	1	1	3.1
22.34721947	21.61517525	4	4	5.5
23.07177544	22.59336472	3	3	4.2
22.22261238	22.30713654	2	2	3.2
23.1960144	23.81548309	3	3	5
25.85607147	25.66925621	3	3	18.6
21.20323372	21.86631203	1	1	8.1
23.15890884	21.03116417	1	1	15.7
25.22214127	25.3277626	4	4	32.1
23.45901489	23.70007133	2	2	32.2
23.58680534	24.41331863	4	4	27.9
29.92195702	30.09005165	18	18	83.5
23.29586029	23.68720436	1	1	5.3
26.98043633	26.80587387	9	9	58.6
26.84983635	26.88191986	9	5	63.8
26.07201958	26.10193443	13	13	13
25.25432587	25.35259056	5	5	37.9
23.47456932	24.10157394	2	2	7.4
19.5460434	22.4432888	2	2	3.5
20.98300934	21.18046761	2	2	5.9
27.62414932	27.78462791	8	8	53.8
22.83120918	19.52388954	3	3	4.9
22.66286087	22.75861549	2	2	5.1
26.50104523	26.21352577	12	12	17.1
26.51818275	26.44134331	8	8	19.8
20.45378494	18.8283329	3	3	14.6
27.09768105	27.59391594	2	2	39.1
24.87951469	25.2053833	6	6	22.2
26.22585869	26.13668823	12	12	26.1
32.67577362	32.54450607	19	18	53.4
23.8630619	24.28841591	5	5	20.7

26.10043144	25.90320396	10	10	13.6
26.44502831	26.71934128	11	11	35.1
22.20824432	22.00980186	1	1	8.6
20.13819885	20.65149689	1	1	5.5
26.31316376	26.59306145	9	9	43.9
25.16065598	25.43224335	7	7	8.6
20.51729965	20.96308136	1	1	3.3
26.82140732	27.11793137	8	8	30.2
23.96895027	23.81665421	1	1	5.4
27.13760567	27.26945877	9	9	95.8
26.70160484	26.9197979	9	9	16.5
24.26935196	25.15607262	12	6	22.9
22.26464844	22.79899025	3	3	3.9
21.85022163	21.66479301	1	1	3
27.18839073	27.47823143	9	9	27.8
27.31389046	27.25871658	11	3	23.1
24.23513031	23.81489563	11	3	22.2
24.78456688	20.02895164	2	2	2.7
26.91650009	27.27275467	14	8	30.1
28.29981232	26.27918053	2	2	5.3
22.77432632	22.80364799	3	3	7.5
28.28135872	28.20815849	14	14	55.2
24.9225235	24.80548096	4	4	8.7
21.6399765	22.97010994	2	2	7.6
24.37755966	24.65698242	5	5	22.8
24.19828033	24.23381424	5	5	24.6
21.38700676	22.5184288	2	2	8
23.73768616	23.83248329	3	3	4.5
20.72139168	20.67598724	2	2	2.1
26.63145256	27.15044594	11	11	10.9
21.85741615	22.00514984	5	5	5.9
22.06157684	22.45911407	2	2	6.7
28.39786911	28.48477554	20	20	37.7
28.11053276	27.75404358	11	11	31
27.43857002	27.42109489	10	10	31.5
29.78245926	29.59820175	93	93	35.7
22.72475624	22.87000465	4	4	11.9
24.13398552	24.76895714	2	2	9.3
24.20761871	24.20090103	2	2	9.2
23.3794117	23.75195122	1	1	5.4
25.57853699	25.89073563	7	7	28.5

22.74055099	23.50142479	2	2	2.4
22.93524361	23.0717411	2	2	5.5
23.09756088	23.28474998	3	3	10.3
20.60794067	20.2561512	5	0	6.2
26.90104103	26.65389824	22	22	45.4
26.42835045	26.38146019	15	10	22.4
23.44695282	23.42380714	5	5	3.6
28.36047363	28.45293427	17	17	60.7
23.63356018	24.25594711	7	7	21.3
21.82248306	21.94145393	1	1	2
26.3989296	26.89504242	3	3	45.5
29.49556541	29.58947563	27	23	65.9
18.42702866	21.48551941	2	2	10.7
22.2283783	22.03113365	5	5	0.9
30.95428276	30.91413498	18	17	81.8
22.19802475	21.05218506	1	1	13.3
26.44595909	25.98246193	11	11	27.6
28.03705788	28.63706207	1	1	5.5
25.69858742	25.83703995	5	5	38.9
29.67767906	29.81564713	106	106	30.9
23.45022964	22.98921013	1	1	5.6
25.17938232	25.0509243	7	7	22.2
27.6135807	27.6689167	3	3	27
22.44781113	25.03359604	2	2	38.5
21.78536415	21.60354042	1	1	15.9
23.28220749	22.66018486	2	2	49.1
25.6403904	25.55692673	8	8	36.1
20.41204071	20.36271095	1	1	7.2
27.75665474	28.06855965	10	10	51
27.84882164	27.80495071	14	14	59.5
24.10381699	24.38712502	5	5	16.8
25.4751873	25.12257767	7	7	17.5
21.60390282	21.59859848	1	1	3.2
31.11669159	31.42201805	25	15	65.4
26.55473328	26.67411423	4	4	30.7
26.00665283	26.32015419	6	6	33.8
21.567276	21.33543587	2	2	17.8
27.39786911	27.95288086	12	12	39.6
29.74827957	29.81069183	39	38	56.3
28.22719955	27.96724701	11	11	30
27.2795887	26.94257164	9	9	29.8

24.17012596	24.18805122	6	4	29.6
22.68579292	23.35272408	3	3	5
24.40301704	24.78596306	9	8	12.6
23.74067497	24.08893585	5	5	5.8
22.87648392	22.84400749	3	3	7.2
27.65136719	27.82687187	25	15	60.7
31.88914299	31.89641571	41	37	78.8
22.07512474	22.0356369	14	3	32.5
28.41134834	28.49697495	26	18	58.6
24.37112617	23.98858643	6	6	25.4
24.28841591	24.45713615	4	4	11
26.30391121	26.5497036	14	14	11.7
24.10389519	24.61689186	4	4	7.2
24.63123131	25.19347572	8	8	12
23.7135582	24.47140884	4	4	12.2
23.46076393	24.18638992	9	9	26.1
26.38953972	26.38083267	7	7	31.9
22.86721611	22.48062134	2	2	7.2
18.68120003	24.3622551	2	2	8
23.03415871	23.69296074	2	2	10
23.69795227	23.90985489	1	1	7.6
24.33060265	24.70424652	3	3	13.6
27.56848335	27.85239792	13	6	41.1
24.53824806	24.37577248	9	2	28.3
25.04138947	25.43144608	4	2	15.1
25.39806557	25.81675339	5	5	13.9
22.8247757	23.28757095	3	3	12.9
24.48904037	24.33135414	6	5	5
23.94145393	23.97412491	9	9	13.7
25.68616295	25.55162621	4	4	38.6
24.18343925	24.56401062	5	5	14.5
27.13467216	27.42942047	9	9	83.8
23.4667511	25.64710426	7	7	26.4
24.76688576	24.95619774	1	1	4.7
23.57496262	23.73324394	4	4	7.2
22.60494423	22.69935036	2	2	12.6
25.9759407	25.88415909	5	5	38.6
26.51831818	26.67801476	12	12	27.9
27.18224525	26.93168068	10	10	28.2
27.0856781	26.58606148	8	8	28.1
29.81549454	29.75789452	24	19	74.2

21.41178131	21.48035049	5	1	19.4
24.00127029	24.20858574	8	4	30.9
23.45010376	19.38607407	17	17	21.8
23.56267357	23.65643692	5	5	8.7
24.8241539	24.9460125	6	6	10.6
21.15690613	21.17157745	1	1	2.4
27.23662758	27.29193306	8	8	26.7
29.28740501	29.21206093	12	12	31.1
20.67930984	23.04841614	5	3	7.6
25.25774574	25.77170372	5	4	6.8
28.58437729	28.84397888	22	22	60.4
24.88301659	25.28570366	5	5	17.3
22.08355713	22.83680344	1	1	1.7
22.25807762	22.53765488	1	1	2.9
20.32285881	22.55840492	5	3	5.8
26.51092911	26.41231918	18	18	16.3
22.13980484	22.24881554	2	2	3.2
20.19470596	20.25218964	2	2	3.3
22.62408447	22.84132195	4	4	4.6
19.99726486	21.12186813	1	1	0.9
24.76577377	25.24775124	3	3	15.9
24.70751381	24.50445747	4	4	22.1
25.37779236	25.7934742	8	8	33.5
27.97623634	28.01510048	9	9	62.4
28.7183609	28.67620087	26	26	32.6
23.47506523	23.86098099	2	2	5.3
29.93438339	29.68787384	16	16	62.8
28.12750626	28.15112495	11	11	58.8
26.41021729	26.31497955	10	10	21.1
24.47171974	25.81680107	6	6	42.5
21.14139557	20.91407776	1	1	1.1
23.18136215	23.66492271	2	2	3.8
26.93528366	27.1204052	13	13	23.5
25.76496506	25.73365784	7	7	17.2
25.02381897	25.05506897	3	3	24.1
28.20256424	28.42846298	12	12	75.8
22.99076843	22.70322227	4	4	13.9
26.15309715	26.12664032	10	10	43.7
23.88222313	23.509058	6	6	9.5
19.86817169	23.34867859	5	5	7.6
27.45974922	27.34671783	27	27	40.3

24.55876732	24.10453606	9	9	19.2
24.10093307	23.95517921	2	2	12.3
20.95461082	21.18174171	2	2	5.3
22.88328743	23.14847374	2	2	11
26.03856659	25.64518166	1	1	2.7
21.41951752	21.2022171	1	1	3.3
22.74992752	22.79786301	1	1	2.8
24.90403175	25.01576042	7	7	18.9
24.40743256	24.46014023	6	6	12.6
29.93536758	30.49027634	101	101	59.3
25.66161156	25.74793816	2	2	18.6
24.49820137	25.6875782	3	3	13.5
30.11247253	29.93999672	20	20	65.6
23.49191666	23.77303886	3	2	6.4
23.15821648	23.60116196	2	1	4.4
26.53146744	26.33859825	12	12	11.9
32.48656464	32.51462936	18	18	42.2
33.22245026	33.26988602	103	99	44.1
24.60455894	24.38080025	6	2	2.2
21.94488716	22.83285141	1	1	4.7
21.90620804	21.42218971	5	5	8.7
21.27764702	22.14864349	2	2	6.8
23.84335518	21.66936302	2	2	9
21.67968559	22.21839142	2	2	4.1
22.08537483	22.17365265	2	2	12.7
23.45161438	23.64339447	3	3	7.2
22.6046505	21.78759766	2	2	11.6
29.50271416	28.6788559	22	22	49.2
30.25135422	29.62590981	32	32	68.2
22.74273109	21.25660896	2	2	15.5
30.59076118	29.81816483	21	21	57.6
20.28711128	22.23657608	1	1	4.4
28.43789673	28.25331688	17	17	57.4
29.90109825	29.74491692	23	23	69.6
24.32030869	24.12888336	7	7	35.3
25.89654541	25.93111801	8	8	12.2
26.5920639	26.49664688	4	4	27.6
23.95082474	23.86154938	2	2	5.3
24.26277161	24.7796154	1	1	8.6
22.4616642	23.214468	2	2	11.2
24.24778748	25.14487648	4	4	12

23.94368935	23.10634232	4	4	12.5
26.857687	26.90138626	17	17	18.6
34.88839722	34.80342484	162	152	74.8
27.64739418	27.7679348	41	31	24.3
24.98428917	24.80484009	7	7	24.5
25.58797836	25.38060188	6	6	23.7
20.82866287	22.63929176	2	2	3.4
26.93809128	27.12790108	10	10	28.2
30.26270866	30.37430573	24	24	60.4
23.98459244	24.12652206	7	7	16.7
26.50964737	26.50975227	7	7	29.3
20.85437584	21.21175194	1	1	3.4
31.89048386	31.47193909	87	87	51.7
23.0098362	23.18121147	4	4	15.4
23.2731266	23.22608566	3	2	3.9
26.10707283	21.59887123	3	3	1
23.51243782	22.99289513	3	3	11.4
27.03002167	27.22370529	9	9	57.7
23.24061394	23.45575714	1	1	7.3
24.38495445	25.22335625	3	3	7.9
23.5389576	23.7923336	2	2	6.5
25.32192612	25.40778732	6	5	16.3
22.52022552	23.20536804	4	3	16.3
26.28091621	26.44722176	14	14	37.7
22.15668869	22.98307991	2	2	3.1
20.75531769	21.06025696	1	1	14.5
20.78676033	21.36964798	1	1	1.8
25.42739105	25.52775764	7	7	30.4
22.50227356	22.72629547	1	1	4.7
23.0723629	23.57357597	4	4	20.8
27.67175484	27.88203621	22	22	34.3
32.05536652	32.22236633	22	22	69.1
20.62726593	23.13863373	3	3	4.5
23.77213287	24.26685143	5	5	10.5
24.13422203	24.17409515	4	4	25.3
23.26956558	23.25186539	3	3	8.8
24.62299156	24.20082664	5	5	12.9
28.47332382	28.49613762	15	15	42.9
22.14180183	22.24164772	1	1	4.3
22.78502464	22.97505379	2	2	4.8
24.49497032	24.45638466	11	11	6.5

27.17578888	27.23589706	18	15	53
29.07637978	29.33598709	24	21	66.5
21.17102814	21.00278282	2	2	3.7
21.80942917	22.8975563	1	1	10.5
22.08203125	19.6551857	1	1	9.1
23.49874878	23.55660439	2	1	2.9
23.62433052	20.51603889	2	1	3.7
25.34536552	25.7166481	12	12	12.2
27.61652756	27.81945992	9	9	54.9
25.36542892	25.67041779	6	6	25.8
25.46967125	25.46344948	3	3	23.4
23.62811852	23.52921867	2	2	12.4
28.55252075	28.82575035	23	23	55
25.12695503	25.39096832	7	7	30
23.93642998	23.77444649	3	3	9
23.36185455	23.88054276	2	2	23.9
22.96439171	23.04508591	3	3	8.8
24.4719677	24.31941414	4	4	13.6
22.83965111	20.20592499	2	2	8.1
26.04374695	25.78902626	7	2	22.8
23.22879028	23.26856613	3	3	9
23.24395752	23.73809814	9	1	27.4
28.07917976	28.09536934	16	8	54.6
25.4262085	25.81071091	9	0	28.5
22.85140419	22.94313622	8	2	30.8
26.05065536	25.96126366	9	5	31.5
26.1018734	26.01867104	9	8	30
26.45271301	26.21565628	13	7	50.9
27.47823143	27.84858322	15	7	60.9
26.90804672	27.28762436	11	11	50.5
19.71899033	23.45989037	7	3	28.5
22.31686211	22.72878838	2	2	8.8
21.20006371	21.66800117	1	1	6
22.71431351	22.59798431	2	2	2.6
23.67141724	23.39453697	2	2	11.2
21.78072739	19.82740784	2	2	18.4
28.80624199	28.89249802	21	21	60.2
21.66266441	20.85079384	3	3	11.3
22.20233727	22.94324303	3	2	8.3
27.53281975	27.27115059	24	23	66.2
26.67370987	26.49124336	6	5	25.3

28.14632416	28.10983467	28	28	53.8
30.08042717	29.96195984	22	22	50.9
21.731287	23.3924427	1	1	3.5
20.19364166	23.00549126	3	3	9.3
28.48216057	28.39071274	13	13	74.6
29.05468178	29.28817368	7	7	32.3
23.84527206	23.53290939	1	1	6.5
23.29291534	23.6413002	1	1	9.1
24.10709381	24.4373951	7	7	35.5
27.19422722	27.10988426	9	9	36.9
25.24238205	25.38962173	4	4	10.5
22.62091255	21.02920341	3	3	14.3
22.26247025	20.06982422	1	1	3.5
22.7425251	22.95801544	1	1	6.9
30.36170769	30.3561554	26	2	54.6
24.15275002	23.75276947	25	1	57
24.80454445	25.26384735	6	6	21.9
23.84498405	23.4247036	3	3	7.2
22.85460281	22.99439812	1	1	5.4
25.52641487	25.86844254	8	8	48.2
29.40954971	29.08258438	20	13	81.2
24.46724892	24.22751236	5	4	28.6
23.44796181	23.02103233	9	2	44
23.7684021	23.54167747	3	3	16.7
30.62949181	30.84550476	11	11	63.3
27.58262062	27.64897156	13	13	64.6
23.52013397	24.36766434	4	3	23.8
24.97066307	25.37497711	6	6	41.7
23.44543839	23.62867546	3	3	6.8
27.55134773	27.34078979	19	19	38.5
25.78149223	25.64979362	13	13	25.5
23.85186195	23.94940186	4	4	24.7
20.13759041	23.54886627	5	5	30.6
22.04763412	22.28424263	1	1	3.3
28.83926964	29.05964088	6	6	27.8
20.78052711	21.92023468	2	2	14.5
25.61003494	25.85440826	6	4	20.7
22.83385468	23.22359848	5	4	19
24.0230999	23.76557159	5	3	22.5
27.50854492	27.59384537	6	4	53.9
28.60713768	28.89264107	10	8	40.7

24.28982353	23.9699173	6	4	19.1
32.13705444	32.03262329	5	1	45.6
23.62008476	24.32848167	7	7	13.2
29.48218155	29.32879448	10	10	62.4
30.59601593	30.41920853	40	40	62.9
29.55793381	29.30018425	30	30	67.6
22.93394661	23.08108902	2	2	8.8
22.98217392	22.78196716	1	1	14.5
23.31865501	23.30563354	7	7	22.8
21.36650467	24.64521027	4	4	13.9
21.27815628	21.10258293	1	1	6.1
34.26974869	34.43576813	9	7	71.8
34.37211227	34.69010544	15	9	70.7
25.38534927	26.45618057	8	2	57.1
21.61503983	21.7282486	1	1	6.8
23.54674911	24.20523453	4	4	3.8
22.6093483	23.24906158	2	1	4.5
24.64521027	24.13508224	2	1	10.5
25.48034477	24.51701164	4	3	27.7
21.3771801	24.2624855	5	5	35.1
25.16522598	25.25313568	9	9	11.4
23.08138084	23.17878151	4	4	9.8
21.88877296	21.95496559	1	1	1.9
21.70133972	21.61130714	2	2	4.4
26.84385872	26.74393845	10	10	40.3
25.3894577	25.48102188	11	11	39.5
21.6746521	21.14997864	1	1	23.2
27.94787598	27.91302109	7	7	72.2
24.72842598	24.75261497	4	4	39.9
24.82191849	24.28552628	11	11	16
25.64479637	26.45133018	5	2	24.9
26.12346649	26.66084862	5	4	14.3
29.67720985	30.10761642	13	4	37.3
24.32759094	24.74832153	10	1	29.4
28.96708298	29.44415092	10	3	29.7
24.69396973	23.53635216	7	3	57.7
32.68881226	33.29296494	8	8	49.2
29.87926483	30.51559067	5	1	45.6
32.10121155	32.81493759	5	1	45.6
32.59321213	33.06435776	13	13	58.3
23.92922211	24.22398186	3	1	34.6

33.37503052	32.90390396	7	2	58.1
27.84828377	28.0057106	22	18	27.2
25.08606339	25.48231506	14	10	15.7
22.61135292	22.79439735	2	2	11.3
29.61185837	30.00490761	7	6	39.1
20.27223206	25.25540733	2	1	13.3
23.69954109	23.41066933	5	5	28.3
22.76229095	23.11349869	3	3	10.8
22.45256996	22.77581406	1	1	14.4
22.68743896	23.76931	2	2	5.7
23.26542091	23.64019775	3	3	17.8
19.65981865	22.19026756	2	2	9.2
25.11036301	25.2617321	5	5	27.2
27.8302002	28.34036446	16	16	57.8
28.06311607	28.56808472	15	15	45.1
26.54031944	26.80279541	7	7	24.6
24.90517998	25.06402206	5	5	18.2
27.1498661	27.55127525	8	7	23.7
22.80829239	23.29375839	3	2	18.3
25.6426506	25.30514717	6	4	27.2
26.65839958	27.06486511	9	3	28.3
23.66644096	24.37550735	6	1	18
28.75146103	29.1249218	11	11	35.4
27.37765884	27.63491821	9	9	30.4
22.6999855	22.75686646	3	3	8.1
27.17864227	27.40511131	13	13	25.9
28.82883835	29.02765083	21	21	35.2
24.83788109	19.73979187	4	4	7.8
24.76045418	25.04147148	9	9	15.2
22.09732056	22.63942528	4	4	5.7
21.27713585	21.50833321	1	1	2.8
22.95004272	19.42984581	2	2	8.4
27.79649734	28.05615425	14	14	29.4
23.40911674	23.41596413	2	2	10.4
24.11418152	23.72826958	4	4	18.8
28.04609108	28.11137772	16	16	49.1
24.27348328	21.48929787	1	1	25
22.16386032	22.7507267	2	2	6.5
27.86932564	28.0307579	9	9	41
25.78623772	26.12236214	5	5	20.5
22.56732368	21.1022625	6	6	19.2

28.19309998	28.42258072	24	18	36.4
29.88310051	30.22354507	33	25	46.8
29.48715401	29.82452202	33	31	41.3
23.96745682	24.30361557	7	5	10.4
25.73153687	26.15630341	10	8	18.7
29.19262886	29.15243149	25	1	49.3
24.94766426	24.92211533	25	1	49.4
27.24970436	27.75614548	24	12	42.8
27.67599869	27.84900093	24	21	37.5
23.59023666	24.39460182	5	3	9.3
29.55753326	29.98400116	29	27	49
30.95213127	31.15569115	27	17	44.1
27.66281891	27.89723778	18	18	31.8
30.10923767	29.79344559	16	16	80.4
26.87677765	26.68538666	6	6	53.1
25.3335743	25.03883743	5	5	53.8
24.4064579	24.19557953	3	3	18.9
29.79901695	29.82453728	29	29	61.8
33.57936478	33.42804718	136	136	50.6
24.92329407	24.6857605	12	10	22.2
27.42981911	26.91547394	13	13	31.7
24.03204155	23.83528137	8	8	3.6
26.54639626	26.69803047	13	13	20.3
22.28265953	22.33382607	2	2	18.5
22.21368217	22.57708549	2	2	1.2
26.19657326	26.39941788	12	12	20.1
22.99800301	22.65263557	2	2	4.3
22.16260147	22.81763077	1	1	2.5
22.46498299	22.64332771	3	3	5.8
27.31163979	27.4760685	13	12	34.1
29.47759438	29.25221062	17	16	39.8
29.2510376	29.12907982	16	16	44.8
26.99323654	26.63491821	11	11	43
22.57621002	22.04836655	2	2	11.5
21.80084801	22.16937637	1	1	3.8
20.71263504	21.23286438	1	1	3.2
24.05796242	23.69178963	1	1	6.3
28.11232376	27.52297783	9	9	42.7
25.92773056	25.96835709	4	4	15.2
22.71053314	22.62218666	1	1	3.1
26.22565651	26.26038742	4	4	53.3

21.68393135	21.76563263	3	2	16.2
21.73309898	21.94688797	1	1	2.1
24.22457123	24.44890785	3	3	13.1
23.49093819	23.36639786	4	4	6.6
20.07767868	22.40043831	2	2	9.7
27.74599075	27.86165619	23	23	37.9
25.31910324	25.37534142	6	6	18.8
23.66871452	23.65818214	3	3	4.3
26.7395668	27.05517197	7	7	51.5
24.67303467	24.62187386	3	3	8.6
20.69310951	21.11400604	1	1	1.6
21.59231377	21.17115021	2	2	2.6
25.36369324	25.86712265	15	15	20.7
24.43974304	24.54392052	8	8	11.5
22.69865036	22.36551666	2	2	4.4
29.24563026	29.22363663	46	46	39.7
26.98554802	27.0411377	2	2	3.7
22.13739967	23.58290672	2	2	11.8
26.99064255	27.24888992	7	7	20.8
22.76172256	23.47209167	1	1	4.7
27.07917976	27.04009247	6	6	54.9
22.24086189	22.98386192	5	5	14.5
19.25905991	21.37057877	1	1	1.2
23.63478088	23.71303368	4	4	5.3
24.2777462	22.06598663	11	11	18.4
26.0754509	25.96525574	11	11	15.4
25.98982048	25.89525032	11	11	14.2
22.12726212	22.50414276	3	3	3
30.15001106	30.0886631	33	33	43.8
25.8003788	25.50479126	5	5	11.8
27.45771599	27.36210442	17	17	20.1
30.7437458	30.68101883	28	28	41.6
25.21382332	24.97749138	8	8	15.1
26.03956985	25.96745682	8	8	16
26.81066132	26.66234398	1	1	1.1
26.38993454	25.80314064	10	10	20
25.35006142	24.55543518	7	7	10.7
25.45029259	25.02428436	10	10	12.2
24.21645355	24.75026512	5	5	38.9
26.49909973	26.38015556	20	15	9.8
23.00461769	22.86014748	6	2	2.2

26.99075127	26.83569145	7	7	34.4
23.63832092	22.79576492	2	2	3.6
23.93795586	23.60749817	3	3	7
23.89568901	23.69954109	4	2	7.5
27.40770721	27.3174305	16	16	30.7
24.56092453	24.38297844	8	8	18.7
24.88604355	25.27859688	1	1	2.9
23.27951813	23.48910141	2	2	10.5
26.42451096	26.27248764	1	1	10.4
25.20985031	25.04942894	6	6	16.9
20.8363533	23.37158966	2	2	9.3
24.17561913	24.20873451	4	4	8.8
25.41280365	25.70956612	8	8	13.4
20.27120209	22.92942047	2	2	2.4
22.70015526	23.67476082	3	2	2.2
22.18546677	21.92019844	1	1	2.7
24.28686714	23.30883026	4	1	4.5
25.10717392	25.01601601	9	6	13.2
24.17790031	24.05233574	6	5	16.8
21.7605648	27.57427025	7	4	46.4
24.36919594	24.52390671	3	3	1
26.79761124	27.02104568	7	7	23.8
25.05845833	25.38775063	5	5	19.6
24.70503807	24.89003944	5	2	14.6
24.49759293	24.36746407	4	4	34
29.95185471	29.57546043	26	4	55.1
25.38419724	25.303545	22	3	48.3
26.63713264	25.78895187	2	2	12.6
25.87361336	25.36192131	4	4	59.3
25.48615837	24.4361248	2	2	66.1
23.22636604	23.92515182	1	1	17.3
29.14435577	29.78797913	4	4	98.9
21.13458252	21.41679001	2	2	3.4
22.61243248	20.20228195	1	1	4.8
22.74384117	22.87618256	2	2	6.6
26.06085205	26.02995872	22	22	10.7
28.60179901	28.49560356	25	25	18.9
30.0496006	29.94083786	70	70	30.4
24.72254944	25.87719917	5	5	3.5
30.94209671	30.72590256	74	74	52.1
30.0712471	29.88425064	47	47	39.4

23.19842911	20.00862885	2	2	6.4
24.56714821	24.94534302	3	3	6.5
22.53744125	23.24260712	3	3	23.6
23.22424698	22.98471451	1	1	22
23.05210304	22.84168625	2	2	10.9
25.10809135	25.20101357	9	9	28.5
19.99973679	21.04066086	1	1	0.8
24.4932003	24.42066193	6	5	25.9
25.25932693	25.65097046	12	7	28.1
27.85120583	27.67586517	20	20	43.7
29.43430138	29.40975189	22	20	75.3
27.3533802	27.15884781	16	15	60.2
20.1571579	23.65774536	1	1	3.3
24.19550514	24.55403137	5	5	12.5
21.77019691	21.29815674	2	2	4.8
25.72496986	25.76585007	12	12	30.4
24.0789566	23.04856491	8	8	39.1
31.68745804	31.84404564	11	11	86.7
25.76615334	25.51301003	6	6	27.3
23.6905117	23.65937996	2	2	7.1
27.22333717	27.16566658	2	2	4.6
23.77575302	23.71156311	3	3	4.6
27.31665421	27.33841133	14	9	55.7
26.55543518	26.75391579	13	8	47.8
22.19499397	22.56827354	2	2	8.6
26.01620674	25.97513199	13	13	29.9
25.1906147	26.03223038	3	3	12.2
24.20806503	24.24474144	4	4	11.7
28.95828629	28.68294525	19	19	54.2
23.69943428	23.71952248	1	1	2.8
31.33718872	31.45522881	44	44	62.4
28.12080002	28.41868591	17	16	27.9
25.81452942	25.83877182	8	7	16.1
28.42205811	28.42358208	17	17	29.7
24.6673069	24.32759094	6	6	6.1
25.44565964	25.5480442	12	12	16.6
30.15073776	29.97732735	19	19	47.8
23.00492668	22.26367569	4	4	6.4
21.33821487	21.58389473	1	1	3.6
31.19771004	30.98352432	35	35	61.8
28.09592247	28.16216469	37	37	11.4

24.28637314	24.80842972	3	3	9.2
26.43133545	26.17924881	18	18	19
27.79631233	27.78200531	8	8	25.1
23.04071236	22.47850037	1	1	2.1
24.99576187	24.53160095	3	3	7.8
20.99876785	24.14258003	1	1	2.7
26.40179634	26.7701416	6	6	29.6
25.29572105	24.78895187	3	3	10.2
20.37264824	22.47231483	1	1	7.8
22.44384575	22.06989098	1	1	20.9
20.88025856	24.73148537	1	1	24.3
27.20228386	27.50188065	13	13	31.3
28.72335052	28.84487724	21	21	21.8
23.37716293	23.41403008	3	3	2
24.08869362	23.75256348	4	4	5
31.03996277	30.81038666	51	51	40.6
21.88996506	22.68816566	1	1	3.4
23.16715813	23.63422585	1	1	3.2
32.67234039	32.65172577	16	10	42.9
25.68346024	25.50017929	3	3	17.6
23.3436718	24.02005005	1	1	15.7
24.32161713	24.24539566	1	1	13.7
26.70332146	26.17369461	7	7	63.8
24.91300964	24.86717033	4	4	33.3
20.98488808	21.3224411	1	1	10.5
24.32642555	24.60110474	3	3	19.4
25.12482834	24.45381355	5	5	1.1
25.58385468	25.85429001	5	5	30.7
24.02816772	23.82444572	6	6	8.1
24.95969582	24.93584442	1	1	9.5
24.28750038	23.87820625	2	2	6.5
26.8426609	26.82844543	10	10	31.9
24.98949623	25.58431244	14	12	6.2
27.79315186	27.97634506	20	18	13.1
23.62778473	23.83364296	2	1	17.4
24.53391838	25.00393105	2	1	16.8
22.75470734	22.62640381	2	2	2.6
25.02034569	24.92506218	7	7	26.7
20.5165863	21.23157501	2	2	9.9
22.88072968	22.60634613	2	2	8.1
20.23883247	23.98137283	1	1	0.5

26.62421799	26.71397781	16	16	23.8
21.0357151	21.3828373	2	2	11.4
26.35013008	26.02462196	12	9	54.5
21.88747597	21.94313622	2	2	15.5
24.52713203	24.41377068	8	5	34.2
23.81665421	23.95153809	3	3	10.7
19.095047	20.00284576	3	3	5.1
21.27430916	22.91179466	1	1	4
21.20788574	21.96395111	2	2	6.6
26.83893967	26.97880173	10	10	21.2
24.31375122	25.41709137	6	6	52.6
19.93341255	22.11476898	1	1	5.6
24.26284409	24.0202198	4	4	16.3
21.20741081	21.02715492	1	1	4.1
25.24263573	25.06287003	4	1	11.4
21.64838409	22.04550171	1	1	4.7
20.30760765	15.90745449	8	8	41.5
25.15085411	25.42815781	8	8	16.2
25.24633789	25.41147804	9	9	19.9
23.21001434	22.93452263	2	2	27
19.69798088	23.7091465	1	1	4.8
22.48044968	22.93962479	2	2	57.1
27.42934036	28.56768608	8	8	37.4
23.59000778	23.50530624	3	3	20.4
28.50058937	28.97489738	11	11	44
29.95532227	29.94181633	17	17	63.6
23.67970848	23.29726028	3	3	36.6
27.3765831	27.66566849	18	18	59.3
25.39385033	25.59109306	7	7	19.2
25.42700768	25.21597099	12	12	56.3
23.07595825	20.07045364	1	1	1.1
22.53900528	22.5685997	4	4	20.5
22.56527901	19.39546585	1	1	3.6
25.8725338	26.07060814	3	3	20.8
31.02953529	30.72906876	8	8	50.2
26.89469528	26.94480705	5	5	30.5
29.70328903	29.37736893	24	24	55.4
22.65824699	22.73991203	2	2	6
24.49460411	24.50688171	2	2	23.1
25.00401688	25.26899338	4	4	40
22.27951813	21.90212822	2	2	24.8

24.31547928	23.54321289	9	9	12.1
24.4952755	24.17378998	3	3	4.3
20.60767365	21.41977501	3	3	8.2
27.88227081	28.19432068	5	5	71.3
24.41241455	24.91583824	1	1	42.1
22.89489555	22.82964134	1	1	5.5
21.15127945	20.27824783	3	3	9.9
20.17474937	20.1324501	1	1	16
21.30641365	21.59395599	2	2	3.4
24.36292458	24.71983719	1	1	2.4
22.62077904	22.99915504	3	3	5.8
24.61397362	25.09796333	1	1	13.8
25.36312485	24.80242729	5	5	54.1
26.15551186	26.14965248	6	6	37
23.17972374	23.72119331	5	5	17.8
22.68722534	22.72696114	2	2	8.4
23.94333267	24.42988396	7	7	24.6
25.98851967	26.16899872	10	10	10.7
22.75103188	23.08242035	4	4	3.9
23.52683258	23.8133316	2	2	9.6
24.13147736	23.68987083	1	1	7.6
22.44637299	22.51270294	1	1	6
25.37891579	24.89966011	3	3	56.9
24.1059742	23.9536705	4	4	6.1
30.20734406	30.24558449	35	24	54.9
23.49765396	23.20964241	3	3	20.7
25.30598259	25.45309067	5	5	34.4
26.36669731	26.24403381	9	9	47
24.86632156	25.20116234	6	6	26.6
26.11048317	26.16557121	1	1	14.9
27.40673447	27.5120163	10	10	44.9
28.79968071	28.79426765	7	7	44.9
23.08203125	23.5926342	3	3	15.6
25.14829445	25.28552628	9	9	14.3
23.33483696	22.44103622	5	5	6.6
21.62511063	21.93556595	1	1	4.4
22.18125725	21.71347427	2	2	5.4
21.01553345	21.94027138	4	4	2
27.32731628	27.09275055	6	6	64.4
22.28686714	21.54373169	2	2	9.5
24.75343132	24.32532883	4	4	26.6

28.7972393	28.45226669	27	17	28
23.27355385	23.85214806	5	5	9.4
26.99193954	27.0500946	13	13	25.2
24.2483654	24.22655678	4	4	13.4
25.39897919	25.43459892	10	10	10.4
22.32369423	22.66305542	1	1	19.4
21.1126709	20.68654251	1	1	6
20.7969017	23.16642189	2	2	5.3
30.1278019	30.23888397	85	57	45.3
34.52280045	34.52938843	160	4	61.3
23.13952446	23.26956558	157	1	62.3
26.37293625	27.07958794	15	2	6.3
21.95048714	26.06321907	85	18	46.8
29.02236938	29.13836288	75	50	39.9
26.63837624	26.89075851	13	13	75.5
27.32894325	27.34146881	11	4	51.2
32.08774567	31.89254761	11	1	78.1
30.48433304	30.67328835	13	6	80.2
30.23591995	30.30410767	38	11	40.9
21.57957458	21.23767471	2	2	1.9
22.48136139	22.89378357	1	1	2.4
30.14843559	30.13418198	46	45	47.1
25.4388237	25.03800011	12	12	15.9
22.02384377	21.42121506	2	2	1.4
27.34341812	27.40145493	23	23	14.6
22.58865929	23.33319855	4	4	16.3
21.28268814	20.71908379	1	1	7.7
24.24394417	24.60138893	4	4	19
28.37223053	28.4814682	4	4	12.2
24.83725548	24.2286129	2	2	14.8
26.15726852	23.72171593	7	7	40.1
24.2992897	23.38363647	1	1	16.4
20.41049576	22.34594727	2	2	13.6
20.43052292	22.58744621	1	1	1.3
24.9271431	24.79009628	8	7	15.4
24.72624397	24.36138535	3	3	19.1
21.67529869	22.44649887	2	2	3.7
24.48750687	24.72946358	4	4	14.7
24.58938026	24.86613274	6	6	20.8
25.6995945	25.74573517	5	5	14.8
25.0845623	24.92134285	6	6	24

24.17820549	24.87347221	3	3	13.6
23.27739143	23.85585785	3	3	9.9
23.60218239	23.868536	3	3	5.4
21.42892075	20.26485252	2	2	10.4
25.76988983	25.26806641	6	6	12.1
24.14918709	24.09667587	1	1	6.9
24.85714149	25.06726837	10	10	17.2
27.22140312	27.41924858	8	8	13.7
21.59618759	22.78992844	2	2	3.7
25.26838684	25.53174973	6	6	31.5
27.25907707	27.27444267	10	10	51.3
21.43862724	22.41495895	1	1	14.3
26.66790199	26.67667198	12	12	51.5
22.55229568	23.06009293	2	2	24.1
25.10984421	24.99614906	7	7	52.4
24.7200985	24.74196053	3	3	23.6
22.37105942	22.55208397	3	3	25.3
23.79431725	24.14312553	3	3	50
26.32675171	26.59306145	5	5	68.3
21.33783722	20.04730225	4	4	50.9
25.10333633	24.86966705	4	4	33.6
26.08762169	26.33934593	7	7	57
26.12393951	26.12976837	13	13	48.5
19.8824501	22.08579445	1	1	8.1
20.83174896	20.86234283	1	1	6.5
25.38301086	25.4715023	2	2	47.4
25.1898613	24.9440918	4	4	30.1
23.93202019	23.86126518	3	3	33.7
24.92374802	24.95611	4	4	38.8
23.29977798	22.98849869	3	3	16.9
20.69064713	22.41902924	3	3	32
20.76264954	23.78216743	3	3	14.6
24.38376808	24.7882061	6	6	31.3
24.75210571	24.76339531	6	6	50.8
27.12849045	27.13858223	24	24	45.9
26.54062843	26.37114143	10	10	24.8
25.90361786	25.52659416	12	12	42.6
24.21230316	21.56202888	3	3	29.7
25.10193443	25.31202126	4	4	41.5
18.68473816	24.12202454	5	5	60.3
24.42636871	24.70044136	3	3	26.8

25.29284477	25.55101013	3	3	17.9
26.55776024	26.71567917	12	12	39.7
24.71795654	24.74093246	5	5	27.4
21.12603378	20.7472496	2	2	27.9
23.28206635	20.54380417	5	4	29.3
26.70120811	26.96201515	14	11	19.5
25.35507965	24.53362083	1	1	17.3
20.54158592	18.72280693	11	9	15.1
27.04082489	27.41126823	1	1	1.7
23.47654915	23.04057884	5	5	4.1
23.020998	22.73332787	1	1	1.6
21.01249123	22.28430367	1	1	2.6
22.40085602	22.33649826	2	2	6.5
23.79986	23.44290924	2	2	12.8
22.38811111	22.89663315	2	2	9.4
23.34543419	22.73624229	5	5	12.1
24.00247383	24.92011642	4	4	50
28.49773598	28.69012451	28	27	33.3
26.58204651	26.56095505	14	13	12.9
22.65256882	22.63118744	2	2	8
23.625	23.74345016	1	1	13.2
24.72707558	24.83566666	6	6	32.4
30.45718765	30.5709095	6	6	33.3
22.91469955	22.77723885	4	4	8.6
24.83311081	25.03229332	9	4	66.4
28.53099823	28.90058136	10	5	73.7
21.38916206	21.93560219	3	3	23.1
22.12789154	22.97886276	2	2	10
24.94172096	24.17592239	3	3	11.3
26.94637108	27.09928703	23	23	28.4
26.03647041	26.41844368	7	7	25.8
23.45776176	23.34610939	4	4	12.3
25.24368858	24.58147049	4	4	20.1
24.05059242	21.87037849	1	1	6.1
25.98934364	26.07432938	12	12	23.2
26.16750526	26.39700508	5	5	29.8
29.64233971	29.40334511	21	2	41.1
24.89901352	24.12249947	20	1	41.2
25.3963356	25.60580254	4	4	17.7
24.707304	24.74934578	6	6	31
23.98085022	24.48271561	3	3	18.2

25.10393524	24.77831268	8	8	15.9
24.62393951	24.53463173	4	4	15.4
25.61832047	25.53531265	4	4	36.5
24.43961716	24.66773987	3	3	6.2
26.17767334	25.74383545	8	8	16.6
24.99718475	24.83190346	5	5	16.6
22.90760231	22.6374588	2	2	6
24.69008446	24.74082947	2	2	9
22.78823471	22.08011246	1	1	9.1
22.73727417	22.60977554	3	3	12.3
21.06657791	20.57348442	1	1	5
24.67648315	24.87347221	5	5	33.5
24.43879318	24.66497803	1	1	2.2
20.40907478	20.92223358	1	1	5.8
23.69125748	23.50154495	6	6	5.6
22.7442112	23.42956352	3	3	4.6
20.99893188	22.43979454	3	3	3.6
21.70660591	22.64790154	1	1	2.1
20.80217361	22.52762032	5	5	9.5
26.63561058	27.05289459	5	5	70.9
25.83477592	25.2475338	1	1	0.9
28.10604477	28.05548286	16	16	64.7
20.09412384	22.96358109	3	3	22.2
29.67429924	29.45567894	50	50	52.9
32.52880478	32.36149979	15	15	43
26.10395622	26.25405502	8	8	27.5
25.37954521	25.66928291	1	1	4
25.45654106	25.70107651	12	12	20
24.00393105	24.45481682	2	2	11.6
23.41157532	24.16568756	3	3	8
22.16435242	22.54919624	3	3	4.9
23.28206635	22.80301857	2	2	5.1
22.52214622	22.332407	2	2	3.1
24.42053413	24.70998764	1	1	8.1
25.49237442	24.98815155	6	6	29.3
26.13110352	26.32340431	7	7	28
28.117733	28.26584244	20	20	59
23.68880463	23.71261406	3	3	5.1
28.8723526	28.98636246	24	24	49.3
24.27255821	25.14008522	5	5	19.7
26.59690475	26.61680794	10	10	20.3

20.52433395	24.09988976	1	1	5.5
25.45845032	25.63250732	4	4	10.3
23.77253532	24.15792274	6	6	16.8
25.90419197	26.22714424	4	4	31.4
24.58089638	24.26148224	6	6	20
23.43402672	25.00829887	6	6	19.8
22.9624691	23.23599243	1	1	2.6
22.27289963	22.29182053	1	1	3.2
24.08009529	23.08967972	2	2	4.1
23.84584618	23.77223396	3	3	10.5
28.95343781	29.20438576	13	13	84.1
20.37506866	20.31882095	2	2	3.9
25.37775803	25.0567646	4	4	17.6
27.81457901	27.77574158	13	13	42.7
21.48355293	20.91481972	2	2	9.3
25.72163773	25.73495102	4	4	27
20.25810623	20.54462814	1	1	1.2
26.15443039	26.15247917	9	9	20.6
27.84983635	28.05765343	20	20	25.1
27.52738571	27.82304764	9	8	42.7
25.95480156	26.29946327	5	4	22.4
24.56307983	25.19381332	12	12	19.3
25.56923676	25.70025635	11	11	27.9
25.09353638	25.19117928	12	11	30.5
25.95571136	26.10839081	8	8	61.2
23.95491219	23.92940331	4	4	11.5
22.51296806	22.6575489	2	2	5.1
21.29636574	22.45159912	2	2	6.5
18.41363525	24.36899567	3	3	23.1
24.93853951	25.14160728	4	4	37.3
26.1877861	26.49185562	7	7	55.6
27.43849182	27.53051376	24	24	37.9
22.87880516	23.32635689	2	2	15.5
25.56470871	25.12955093	8	8	10.3
23.03771591	22.22101974	1	1	2.4
24.29628181	24.35231972	6	6	8.7
27.17902184	27.22765923	17	17	50.5
27.87314415	27.80661201	15	15	64.6
21.72920418	23.29642105	3	3	8.4
30.07533455	30.28471565	29	29	54.5
26.58677673	26.93550873	14	14	25.1

22.40314674	22.3698349	3	3	10.8
27.17016411	27.32156563	9	9	29.3
22.22450638	21.90811539	2	2	11.3
24.48406792	24.0284214	2	2	6.7
29.19706726	29.05305099	21	21	83.5
28.13804626	28.23886108	19	19	80.4
26.80415154	26.5631237	10	10	45.5
21.6687355	21.35180855	1	1	1.7
22.35764503	21.27963066	3	2	4.1
23.91314697	24.12597084	4	3	4.6
21.92911339	21.24816895	2	2	4.9
25.34698868	25.5872345	6	6	38.8
24.99589157	25.4522419	3	3	36.9
29.22673988	29.51267433	11	11	89.3
24.17516136	24.56587219	3	3	11.3
22.35428619	22.41198921	1	1	2
21.04200745	21.32465553	1	1	14.5
20.20132065	19.6278286	1	1	2.2
25.64449501	25.01831055	3	3	28.6
23.98285294	24.0484314	2	2	16.9
23.71826935	23.84047699	3	3	33.1
23.5114727	22.80897903	2	2	26.8
25.43574333	25.71759033	13	9	27.2
25.42473602	25.22280312	12	9	22.8
27.40770721	27.48046684	15	13	25.8
28.50578308	28.42278099	14	11	71.3
26.89804459	27.03674316	16	16	53.2
28.79371071	28.81857681	21	21	65.9
28.08283806	28.00635147	11	11	83.7
27.84864235	27.9153595	13	13	42
21.24858284	22.06506538	1	1	2.9
23.02115059	23.338377	3	3	7.7
30.64211655	30.52906227	27	27	63.5
24.4719677	24.64987564	4	4	18.1
26.42330933	26.57159615	7	6	41
21.58631516	24.29487991	2	1	10.6
27.82584	27.68143845	11	11	64
26.55162621	26.49664688	8	8	32.8
22.02560234	22.97272301	2	2	4.7
20.90168571	20.04300117	1	1	4.5
26.018013	25.47156525	10	10	51.9

23.30284882	23.71229935	3	3	2.5
27.29228401	27.09938812	14	14	31.3
22.60272598	23.06880951	2	2	7.9
23.07465172	23.60229492	1	1	9.1
21.73314095	21.27991486	1	1	2.2
21.37528038	21.36340523	1	1	4.1
25.39600754	25.14584923	6	4	25.1
22.61164474	23.01724815	3	1	14.8
24.52599716	24.22014809	5	5	9.2
31.23859787	31.2536087	35	4	75
28.00801086	27.61097908	34	3	73.8
22.10251999	22.07626724	2	2	2.1
24.47407341	23.68645668	5	5	10.4
22.32083321	23.02457047	2	2	3.3
23.98763275	23.67454529	5	5	7
27.47668839	27.44094849	20	20	42.3
28.91868973	29.02152252	70	68	20.1
26.95249367	26.89272881	14	14	29.1
28.22448921	28.47965813	20	20	54.9
26.30274391	26.16794586	6	6	29.5
28.26785278	28.26140976	22	22	48.3
23.92587662	24.11902046	2	2	17.8
30.16122818	30.11483192	35	29	72.1
22.33603668	23.29852104	1	1	4.4
21.50069618	22.69313049	1	1	2.3
24.22978783	23.5400238	5	5	4.1
21.77342033	22.02725601	1	1	1.5
25.03712082	24.57421303	3	3	10.9
22.30694199	22.30960846	1	1	1.5
26.06256104	26.15317535	7	7	31.8
24.96903801	19.98665047	10	10	23.6
22.13360977	21.92401123	2	2	6.8
22.33892059	22.38173676	2	2	6.9
22.71661758	23.04143143	1	1	8
23.50724411	23.30521584	4	4	16.1
26.64388847	26.34607697	7	7	39.3
26.69683838	27.06773949	12	12	27.6
24.75363541	20.60855865	55	2	67.4
25.48428345	25.77791214	5	5	26
24.49142838	24.81401634	6	6	28.5
31.21251297	31.41795158	13	13	74.4

27.65717316	28.03936195	9	9	43.5
24.66979599	24.47766113	7	7	19.7
23.84565544	23.3001976	2	2	1.1
21.66609383	21.64557266	2	2	5.1
23.14883041	23.98988533	4	4	11.9
23.87539673	24.26119423	15	3	42.7
28.51487732	28.68515205	21	8	73.1
21.85555458	22.80978394	14	1	39.6
28.32165146	28.16110802	17	17	20.1
23.92922211	23.99239349	2	2	2.4
23.56465149	20.3408165	3	3	7.3
27.15421867	26.40301704	5	5	36.7
25.43099976	25.70659256	8	8	28.3
25.91558838	26.24514008	7	7	32.7
28.59846687	28.55830002	22	16	45.5
24.94975853	24.66795731	4	4	11.9
26.15867424	26.10263443	8	8	50.8
22.33519173	21.07617378	3	3	7.8
22.18286324	23.78396606	4	3	16.4
21.9553566	22.30780411	1	1	4.3
20.57699394	20.38395309	1	1	2.8
24.197155	24.7200985	4	4	22.2
23.52444458	23.41635132	3	3	16.9
29.46433449	29.41910744	16	15	62.3
28.20134926	28.53575134	11	11	78.3
26.20674324	26.32452202	5	5	38.1
26.81213188	26.89307594	8	7	38.7
28.4228611	28.48753738	13	13	74.7
28.55994034	28.68782425	14	14	62.9
31.78359032	31.75958633	19	19	48.1
23.3240242	23.64921761	5	5	9.4
23.97342491	24.14685822	6	5	17.7
24.38857269	24.07977104	2	2	7.6
24.63228607	24.74139404	1	1	5.8
25.51842308	25.52465248	5	5	22
23.8267746	23.86599159	7	4	20.4
22.99519157	24.20262146	8	5	27.9
21.89895821	22.22599792	2	2	5.7
23.55520058	23.214571	5	5	8.5
28.77778053	28.82168007	11	11	43.1
24.09924698	23.89901352	3	3	5.8

25.53427505	25.30389404	12	12	20
21.10155678	22.61031723	1	1	6.1
21.64996338	19.61248779	1	1	1.7
23.52276993	23.31395912	1	1	7
24.93853951	24.80493927	4	4	28.1
23.72587967	24.4942379	3	3	13.1
24.15522194	25.74509239	17	12	33.4
24.57876778	24.51436615	4	4	14.5
23.91360474	23.39191818	5	5	19.9
26.41705894	26.73763466	12	12	27.8
26.90987778	26.86903	10	10	47.1
26.28737831	26.49824715	8	8	43.6
24.66736221	26.12210464	3	3	12.9
26.07979012	26.43171692	6	6	41.1
25.93692398	26.22315407	6	6	30.1
26.10137367	26.30286598	6	6	35.5
27.0083847	27.39272118	6	6	36.7
26.1230526	26.45026016	7	7	53.7
24.78011703	24.74129105	5	5	35.6
24.17576981	23.9331913	4	4	27.3
23.25079536	23.43923569	5	5	22.7
24.31534195	24.07136536	3	3	25.6
23.70070648	24.11179543	3	3	21.3
25.02926445	25.55619621	7	7	21.2
26.18446159	26.45887375	9	9	26.7
25.37573814	25.33905792	8	8	33
25.63901138	25.99317169	12	12	41.9
26.14724731	25.9613533	12	12	23.3
26.28430939	26.47610092	15	15	39.8
24.57623291	25.13860321	5	5	14
24.60608482	24.73840904	7	7	29.8
25.65891647	25.55637169	4	4	24.8
24.24822044	23.96525574	4	4	11.1
23.88269043	24.37722969	4	4	12
25.37261963	25.69879913	8	8	23.2
23.16853523	23.87192345	2	2	6.2
25.84950066	26.03632545	9	9	41.1
23.29473877	24.01486778	4	4	13.9
24.20746994	24.09820366	3	3	17.1
27.30643463	27.61855888	10	10	45.8
21.08238792	20.16133499	1	1	3.5

28.11187553	28.2513752	13	13	52.4
22.05447388	22.02965164	2	2	9.4
22.55873108	23.2449894	1	1	2.3
22.74673462	22.46866608	1	1	9.6
20.94384384	23.2831974	7	7	25
26.18584061	26.37668228	4	4	30.6
22.11308479	22.07793045	2	2	2.6
30.19260597	30.00155449	25	25	59.1
22.83778572	23.25465012	2	2	7
21.87513161	23.10844994	5	5	22.5
25.58164406	25.7665081	3	3	7.6
23.98537445	23.64063835	1	1	10.9
23.32429886	23.02901077	3	3	26.3
24.2151947	24.2517643	9	9	23.1
20.07715988	21.77739906	2	2	2
21.82151985	22.02685165	2	2	1.8
23.70070648	23.56010818	2	2	19.9
22.11171722	23.74734879	1	1	6.2
25.11830711	25.24898148	3	3	12.1
23.39884758	22.81352615	5	5	5.2
25.72382545	25.37122536	6	6	18.9
28.18518066	28.27479935	34	24	45.7
24.16890335	24.61896515	15	9	24.6
28.29692841	28.258358	40	30	53.7
26.1627121	26.3923111	14	14	25.9
26.00857735	26.10769272	7	7	39.8
24.45732498	24.4256649	3	3	50.4
22.03099823	21.15442467	2	2	10.7
25.60684776	25.90772629	4	3	19.5
25.77484894	26.27015305	7	7	37.6
19.63513374	21.47461891	1	1	3.7
26.25918388	26.55713081	7	7	47.9
23.49203873	23.37278557	4	4	22.8
26.44859314	26.75468063	7	6	38
24.42419052	24.59371758	5	4	26.9
25.46460152	25.59240532	5	5	22.1
21.67702103	20.49277306	1	1	5
24.09273148	25.06118202	6	6	37.3
23.19099236	22.94438744	2	2	6.2
24.87750435	24.16882706	1	1	9
23.87445831	24.02411461	5	3	31.6

26.4276638	26.52702713	5	3	31.6
24.89998245	25.23363113	5	3	31.5
24.35568428	24.66427231	4	4	20.2
26.002388	26.48957634	9	9	56.5
23.54969025	23.92352104	2	1	12.1
22.25902557	22.12041283	2	1	12.1
28.51307106	28.39729881	10	4	56.2
24.78046608	25.00208664	4	4	17.5
24.68319321	24.94257164	2	2	10.7
22.66940689	22.79823875	1	1	4.1
25.33487129	25.68340683	2	2	21.7
23.3731842	23.70514297	3	3	1.6
21.02992058	21.42695618	1	1	1.7
25.14553833	25.49231339	8	2	58.2
28.36381912	28.44817543	10	4	72.8
20.54578972	20.30752182	1	1	6.6
24.48043633	23.80360985	2	2	17.9
26.46922112	26.60780716	13	13	24.1
21.80309677	21.64183044	1	1	2.1
24.70835686	24.80198288	6	2	15.8
20.81956673	19.78744316	6	2	15.8
27.32928658	27.34773254	9	9	67.7
20.95296669	20.47038078	2	2	3.9
23.67497635	23.76597595	1	1	1.5
23.72234154	24.08245277	2	2	4.8
25.86542511	25.89103699	2	2	32.7
23.03103256	23.86192703	6	6	14.7
23.02489281	23.27965927	3	3	7.7
28.17045021	28.0254879	11	11	80
23.46213913	23.18915176	2	2	10
26.23493004	26.51681709	6	4	33.5
20.71503639	22.25905418	3	1	11.7
21.87026787	22.61970329	1	1	1.9
22.65289688	22.2980442	1	1	7.5
25.23344803	25.38347244	4	4	22
22.63289642	23.71596718	4	4	15.8
21.69042587	22.53300285	3	3	9.6
23.10733223	23.52396584	17	6	25.7
24.47994423	24.39460182	2	2	16.2
22.49811554	22.08731842	1	1	7.6
23.03207588	25.09164238	2	2	6.8

28.36707115	28.73123932	10	2	65.8
23.43923569	23.09886169	4	2	20.9
24.53267097	24.85109901	10	2	55.4
20.38637543	21.18254089	2	1	12.2
23.30938721	23.12278366	2	2	8.4
22.62711716	22.19755363	3	3	5.9
23.34299469	23.93418121	2	2	8.3
27.61217499	27.60639572	19	19	71.9
25.29754066	25.28947258	8	8	20.6
26.33256721	26.29771614	16	12	15.2
24.15166664	24.01154327	9	5	8.4
22.47454453	22.68414497	1	1	8.3
26.59448624	27.01892471	7	7	42.5
26.31972313	26.7929039	8	8	33.2
24.54102898	24.24532318	2	2	12.9
26.48604965	26.74611855	4	4	35.8
27.09667587	27.19488525	6	6	28.4
25.47280502	25.31793213	3	3	8.4
26.20127487	26.69032478	5	5	25.8
26.06630325	26.5035038	7	7	34.3
26.70872498	27.30747604	5	5	28.3
25.6776123	24.81367302	5	5	26.1
23.26627922	24.54315376	5	5	15.3
23.33579063	24.21014786	4	4	21.4
25.41831589	25.41141319	5	5	33.1
24.9077034	25.35380173	3	3	39.1
26.23048401	26.71920967	3	3	27.1
25.22776985	25.51911354	5	5	27.6
26.5892086	26.84732819	5	5	29.9
25.21337891	25.42851067	3	3	18.6
24.59000778	24.86759377	3	3	20.6
26.20459938	26.49941826	4	4	27.7
21.89062309	25.13801575	2	2	12.4
26.84218216	27.08294106	8	8	23.1
24.19618034	24.40295029	2	2	24.3
26.24267197	26.39997292	1	1	11.2
25.60969734	25.93710327	6	6	39.3
24.64190674	25.17066193	3	3	20.5
24.25745773	24.08602142	1	1	8.1
24.25392914	24.50385284	2	2	7.3
24.71019745	25.3558197	2	2	11.4

23.82667732	23.83634186	3	3	41.3
23.45073318	23.93975067	3	3	51.4
24.83759308	24.73892403	1	1	19.6
28.57304192	28.80378151	19	19	42.7
26.44113731	26.65553665	8	8	32.3
26.4120121	27.05589676	8	8	30.4
26.82614326	26.74842453	13	13	40.4
27.07958794	27.10229492	14	14	46.2
26.20717239	26.49318504	6	6	35.4
24.75485992	25.29561615	4	4	36.5
27.2703495	27.3646946	12	12	53.9
27.99609566	28.02501297	4	4	79.8
27.34933662	27.39966393	5	5	76.5
27.45332527	27.85572815	19	19	42.3
27.61006355	27.76236916	11	11	28.7
25.94986916	26.01726913	6	6	42.4
24.88976097	25.49713516	5	5	24.1
25.85321999	25.7470665	7	7	59.1
27.48999023	27.85132599	10	10	45
24.80282021	25.04901505	5	5	63.6
26.27744484	26.47130203	4	4	55.9
26.10004997	26.41523933	7	7	49.2
23.46637726	22.66218758	2	2	15.8
26.26679802	26.3687458	4	4	40
26.74329567	27.22894287	5	5	27.6
26.92660141	26.99129105	7	7	37.2
26.31387329	26.38677979	8	8	33.4
25.1622715	25.49463463	3	3	25.2
20.0128746	23.37358284	2	2	28.9
24.26506424	24.77137756	4	4	21.7
24.45293427	24.92284012	4	4	30
25.44859314	25.35773277	4	4	18.4
24.79461479	25.09748077	4	4	37.4
28.14549828	28.32684517	5	5	42.3
26.74650383	27.30591202	2	2	25
23.03284836	23.44404793	1	1	17.4
24.31741333	24.02884293	1	1	19.6
26.13094711	26.42318153	10	10	50.6
27.54200363	27.83827972	8	8	32.2
27.18763542	27.46302795	10	10	38.4
26.17481804	26.20435715	8	8	42.6

25.49335289	21.9473877	2	2	10.8
21.85616302	22.03466415	1	1	2.2
26.37878418	26.32318115	7	7	45.4
27.0588932	27.21845055	9	9	41.3
26.74059677	27.10559464	9	9	32.5
28.13697052	28.25354195	12	12	57.6
20.38921547	20.04093361	1	1	6.2
22.99650383	22.94188309	1	1	3.6
27.6257515	27.43936348	11	8	51.4
27.01062584	27.23178291	12	12	11.4
29.95823097	29.8488369	14	14	62.8
20.80318832	20.77438927	2	2	6.6
25.21663857	25.45647812	6	6	16.8
22.64070511	23.02575302	2	2	2.3
22.52382278	22.23888016	2	2	13.2
25.33510971	25.97842979	2	2	11
22.90886688	22.23371124	7	1	12
26.7781868	26.6408596	7	1	36.2
24.8969841	25.11584854	6	6	31.6
22.37071228	22.52281761	1	1	2.9
24.16982079	24.55929184	4	4	12.1
20.67079163	19.92878532	1	1	0.4
22.29557991	24.42981911	1	1	16
29.15433884	29.00648689	4	4	64.3
23.55625343	23.18592072	3	3	46.9
32.12241364	31.70182037	5	5	42.6
25.64652824	24.16982079	1	1	18.3
27.56165314	26.86620331	3	3	33.7
22.24199677	22.14416885	1	1	3.7
23.98502731	24.16430664	7	7	11.6
24.93039513	25.07050514	5	5	22.3
24.40717316	24.24793243	2	2	2.1
24.82318306	25.20959091	6	6	15.6
25.06968689	24.87084198	6	5	35.9
21.6243515	22.44288445	4	3	21.2
25.27252197	25.461483	10	10	28.5
23.03743172	23.25085449	1	1	6.8
23.70429802	23.83730507	2	2	13.9
23.11530876	23.66557312	3	3	10.9
23.17831039	23.2591114	2	2	13.3
24.82006836	24.84507942	7	7	22.1

22.66225243	22.63986588	1	1	22.2
24.62444115	25.16380692	5	5	40.6
22.81882095	22.84507942	2	2	5.8
23.82842255	23.81039238	2	2	7
23.20125961	22.78474617	2	2	12.7
25.772686	25.43866539	6	6	11.3
27.82323074	27.681036	17	17	44.9
26.09587288	26.31624031	8	8	31.6
24.76152039	25.07834625	3	3	17.2
23.10720444	23.69498062	2	2	20.8
23.15027237	23.43695068	2	2	6.7
24.19663048	24.5116539	3	3	18.6
25.45613289	25.59109306	3	3	18.6
26.41960144	26.3066082	17	15	30.1
22.05377769	22.562603	3	1	4.8
23.72671127	23.47370338	3	3	6.1
26.97989273	27.23753929	21	21	27.2
25.32416153	25.25832176	1	1	0.7
24.3528595	25.06147003	4	4	18.1
28.13525963	28.29710388	23	23	59.3
22.65981483	22.37824821	2	2	20
23.67087746	23.25493813	1	1	4.2
19.49630737	21.27861023	1	1	10.8
22.34651566	23.05458832	2	2	9.2
22.43928719	22.03459549	1	1	5.8
22.39725494	22.70074844	5	2	14.4
25.40918159	25.17451477	6	6	29.8
27.66972923	27.61491394	6	5	19
25.14786911	25.72956657	6	4	25.6
23.83826637	24.03866959	3	3	20
25.3960743	25.28676033	15	1	43.1
28.09108734	27.79890823	14	5	48.4
30.85786438	30.88241577	15	1	43.2
27.42213821	27.6028614	15	5	44.8
27.753088	27.07694054	12	6	32.7
28.66993141	28.81796646	13	8	34.2
23.4661274	23.41583633	7	5	17
20.86256218	21.41946602	1	1	3
22.60460472	22.27560234	4	4	11.9
28.27905655	28.46497536	16	16	55.3
29.58348083	29.22250938	18	13	42.6

25.34898186	25.16863441	8	8	21.8
28.06768799	27.62205505	16	16	49.1
26.88692856	26.68445015	6	6	24.2
22.27372551	22.34975815	1	1	1.6
24.83494377	24.76885605	6	6	23.2
23.93192863	23.95153809	3	3	19.5
21.74476433	20.63479805	1	1	4.9
24.40522575	24.45004082	4	4	13.5
22.7534008	23.04863167	3	3	4.6
22.26627922	22.65652466	1	1	3.6
24.36372566	24.19204521	6	6	7.2
23.51159286	24.12919807	4	4	5.5
22.95233727	23.01139069	1	1	5.4
25.05916023	25.54913139	3	1	10.5
26.08253479	26.32978249	11	11	25.6
25.13621712	24.67750549	7	7	34.1
24.97171593	24.8514328	7	6	38.2
28.54513741	28.26968002	13	12	60.7
24.63533401	24.48867226	5	5	17.1
24.9865036	24.88488007	6	6	26.2
26.15537643	26.29245949	5	5	18
26.69696999	26.69484711	6	6	21.3
23.17532921	23.23409271	1	1	6.5
22.43461227	22.58806419	1	1	3
26.93337059	25.72684288	2	2	7.6
27.71685791	27.93151283	6	6	71.1
25.18635178	24.97342491	3	3	57
29.41365051	29.17819023	1	1	1.6
20.43129539	22.54382706	3	3	9.2
24.27013588	24.11616707	3	3	11.5
23.70767212	24.06546021	3	3	11.3
23.44997787	23.0146122	2	2	2.2
23.8303566	23.60059547	5	5	18.6
24.03590584	23.54167747	1	1	1.1
21.48517418	21.50610542	2	2	12.3
25.06044006	25.14627647	3	3	25.8
21.94428062	22.1788578	2	2	1.6
22.46689987	23.39610672	2	2	6
25.69069862	26.42048454	7	7	33.1
23.20060158	24.53878021	2	2	11.1
25.67174149	25.8233757	8	8	34.4

26.71607208	26.83773804	12	10	26.6
24.81435776	24.97871399	8	8	43.5
24.91984367	24.99360466	6	6	21.3
27.24608421	27.70457649	11	11	34.5
30.24977303	30.27430916	20	10	58.4
22.57466316	22.11066628	2	2	12.3
27.74457932	27.8331604	20	10	55.4
22.91316605	22.92226982	1	1	6.4
21.86461258	22.05132294	2	2	2.9
20.99872589	20.91086197	1	1	2.8
20.54026794	21.32439423	2	2	3.7
23.37875175	22.76133728	3	3	9.3
25.04272461	25.137743	6	6	11.8
28.29425812	28.39304733	22	22	32.9
21.80570793	22.06989098	3	3	3.5
23.95712852	23.61829376	2	2	2.6
27.97612572	27.74323273	12	12	38.7
20.72878456	23.56115913	2	2	2.3
23.2425766	24.0539093	4	4	3.9
23.34813881	23.17975426	5	5	7
23.14153671	23.23347855	4	4	3.5
20.53944016	21.33369064	1	1	1
21.8688755	21.7117939	1	1	15.9
26.55120087	26.08780289	7	7	21
21.87571526	22.01930237	1	1	2
20.88330269	22.3990097	1	1	4.9
21.3876915	21.31871033	1	1	2.2
23.27113342	23.6135807	3	3	8.1
25.26795959	24.96543121	3	3	43.1
26.61526489	26.56841087	14	14	23.6
25.02550888	24.839468	10	10	6.6
24.86881828	24.76222992	3	3	21.7
23.37371635	24.23205757	4	3	21.6
23.49338341	23.93624878	3	2	17.8
25.6798687	25.96210289	1	1	16.8
23.66144753	24.18343925	2	2	15.1
24.86083794	25.26695824	1	1	12
23.66763306	23.99524498	1	1	24.4
23.66990471	23.49411583	1	1	9.2
25.32717896	25.20739555	6	5	18.9
26.78768349	26.54079247	12	11	33.3

26.49429893	26.65921593	11	10	24.6
23.28883934	23.72858238	4	3	22.4
21.29642677	22.78913116	1	1	4.9
26.21226501	26.08259583	6	6	15
20.25148964	23.32745361	3	2	9.4
24.11727715	24.31830978	4	3	21
21.54769135	21.10584641	2	2	5.3
23.63555527	23.5148468	6	6	16.6
22.29224205	22.80151939	2	2	4.7
24.51243782	24.5159893	8	8	21
28.77083588	29.19605827	4	4	31.8
27.28911972	27.30286598	9	9	67.6
30.54535866	30.24501801	10	10	57.4
27.43912506	27.30112267	13	13	22
27.23159981	27.26114082	20	20	46.6
25.75000954	25.35947609	6	6	10.8
24.12597084	23.87314415	2	2	7.3
27.46660995	27.10539627	5	5	26.5
21.67882729	21.17058754	3	3	2.3
23.57392311	23.10872078	2	2	3.7
23.36452866	23.62410736	1	1	8.4
24.50815201	24.66822815	5	5	8.6
26.89226532	27.03967476	6	6	32.6
26.81860542	26.62519455	37	37	23
29.90066719	30.12829399	88	88	44.9
26.47552872	26.20693016	39	36	24
29.86701393	30.10512161	77	74	46.6
26.63367271	26.87584114	7	7	44.3
24.22582245	24.61245537	4	4	22.8
20.66539955	22.70167923	1	1	12.7
22.73657227	23.00466919	4	4	12.1
24.51285934	24.2448864	6	6	20.8
23.10375214	23.62566948	1	1	1.3
24.3649292	24.99791527	3	3	2.7
23.98468018	24.05763245	3	3	25.5
23.66979599	23.24530792	2	2	15.3
24.35534859	24.74232101	2	2	10.9
24.35729599	24.85505104	2	2	4.7
23.8358593	24.02191353	3	3	26.1
25.76306534	25.86940765	7	7	24.6
23.17723083	23.58760643	1	1	9.9

19.11759186	22.06104851	1	1	4.2
24.46637726	24.37947845	2	2	8
22.84333611	23.29754066	2	2	14
25.93341637	26.23007965	4	4	12.7
22.94122124	22.68568611	2	2	4.7
25.12951279	24.99714088	6	6	16.6
23.58267784	24.27334023	4	4	11.3
23.26226997	23.27284241	2	2	3.4
27.19769859	27.4510479	18	18	33.7
25.338377	25.29487991	5	5	16.9
20.66583443	22.40392685	1	1	4.5
26.41094398	26.37197304	7	7	38.7
24.36325836	24.47314453	4	4	25.8
20.17998123	19.76218033	3	3	4.9
19.81949806	22.28954315	1	1	2.3
23.16832161	23.09746361	3	3	8
21.99962044	22.4128933	1	1	1
22.40244293	22.18897057	3	3	3.3
24.05531693	24.30452156	4	4	20.8
22.74139404	23.08354187	1	1	5.5
22.85092735	23.04708481	1	1	5.4
25.55467415	25.47305298	7	7	17.5
26.76673508	26.44621086	16	16	41.9
27.96438599	27.70318985	11	11	34.7
25.57478905	25.58402634	7	7	21.6
23.10181427	20.21336746	4	4	17
19.7831707	22.64147758	1	1	1.6
24.01580238	23.90085793	5	5	9.8
26.74201202	26.70014954	11	11	23.2
22.34656906	22.48005486	1	1	5.5
23.78825569	23.6502037	3	3	16.4
26.11123848	26.09160042	10	10	20
23.83006668	24.40509605	7	7	4.3
20.63058662	20.72498703	1	1	7.1
25.57977486	26.03069496	9	9	18.7
24.54061508	24.16292381	14	14	2.8
23.01084518	23.39375114	4	4	0.8
23.07537079	23.01957512	2	2	2.2
25.72356415	25.6292305	14	14	23.1
33.33151245	33.31797028	28	28	90.5
25.7692852	25.80208206	3	1	18.1

26.68605614	26.88227081	10	10	26.7
24.55408859	25.77552795	4	4	15.6
25.99487686	26.11838531	10	10	38.2
24.6768589	24.13602257	7	7	12.9
21.30457687	22.14036751	2	2	1.9
21.29451561	21.92230606	1	1	1.3
22.53138542	23.23874855	2	2	7.3
23.36506271	23.73562241	3	3	28.6
25.57654953	25.24278069	2	2	28
21.4904232	21.25534248	1	1	3.3
27.2556591	27.51344681	16	16	41.7
27.03632545	27.03391266	13	13	43.5
30.71906281	30.74422646	33	32	54.4
30.71669388	30.55059624	21	21	76.1
28.95229912	28.95540619	27	27	55.5
30.03577423	30.14041328	33	33	60.3
22.21723747	22.88877678	3	3	9.4
26.25760269	25.59340286	13	13	14.3
22.63931465	22.04029465	2	2	6.3
25.82201576	26.57484818	4	4	31.5
23.50166702	23.68827248	2	2	26.3
21.93488312	21.86048889	3	3	6
21.51108742	21.58031082	1	1	2.8
23.86551857	23.13802338	4	4	26.1
30.15267181	29.82767296	19	19	65
24.13014221	23.56697464	4	4	4
29.96870422	30.12114525	36	36	69.2
33.15402985	33.07075119	125	115	67.1
24.63594246	24.74452972	16	6	8.8
22.57537842	22.60458183	2	2	12.2
25.79238319	25.94844437	5	5	22.4
24.98441887	24.13977432	3	3	20.4
22.73134041	23.33551788	3	2	14.5
20.4084568	24.44056702	2	2	24.6
20.86500931	21.71678352	1	1	15
27.53830719	27.61519432	11	11	42.2
22.0160408	22.07868004	4	3	13.6
25.59200668	25.4575119	9	8	34.4
27.46123314	27.44324303	9	4	33.9
23.44720459	23.39086914	8	3	18.3
22.61456871	23.55414772	2	1	47.7

27.12208557	27.0980835	7	6	77.3
22.32583618	22.70279884	3	3	5.2
23.57114792	23.99791527	2	2	9
20.31462288	21.54207993	2	2	9.2
22.14668846	22.53300285	1	1	3.9
18.71855164	21.56732368	13	13	12.1
21.96508026	22.08138084	1	1	11.6
25.1848011	25.0961132	9	5	15.6
22.93470383	22.84483147	5	1	9.6
24.34631348	24.21452713	6	6	10.2
27.2501564	27.08090973	19	17	19.9
22.4895916	22.3631916	4	4	10.8
24.19895363	23.75501251	4	4	13.4
22.56579018	23.30980301	2	2	22.5
23.58829308	23.76809883	3	3	15.5
24.04268265	24.23139954	4	4	8.8
26.62142754	26.28631973	2	2	1.6
24.33640289	24.94989204	7	7	6.1
22.92775917	24.72166252	3	3	10.2
21.87990761	22.09335899	1	1	2.4
23.02534866	22.43272781	2	2	8.6
21.67366028	21.88412666	2	2	7.5
21.99985695	22.22673416	3	3	21.1
25.36268997	25.84196472	4	4	29.1
29.51158142	29.5846653	19	19	71.2
29.91470528	29.80843925	23	2	53.5
28.80651855	29.0132122	14	6	40.7
26.79971123	26.55645943	9	9	39.5
25.11283112	25.64077568	4	4	15.3
20.97324181	20.46478462	1	1	7.3
27.89533234	27.88250351	11	11	52.8
23.12993622	22.74822998	2	2	1.2
20.82034111	21.40468025	1	1	6.3
26.5486908	27.33807182	5	5	48.3
22.80447578	22.89400673	2	2	3.8
19.58760834	20.76571274	1	1	8.6
22.76650238	23.26198387	2	2	15
23.27298546	23.6831398	1	1	12
21.79530907	21.39670753	1	1	1.9
25.19700623	25.69625473	8	8	16.4
24.7856636	24.38541603	7	7	15.8

21.41168022	21.57910919	1	1	1
27.53058815	27.34671783	5	5	15.2
22.63486862	22.33076668	1	1	9.6
22.5472908	22.9248085	4	4	9.9
20.87916565	24.35649109	3	3	19.7
24.04942894	24.59588051	5	5	23.4
23.86636734	23.13630486	1	1	10.5
22.82115936	22.6035862	1	1	4.6
25.36952782	25.11465836	3	3	38.5
24.09152031	24.48763084	4	4	16.2
20.82065201	21.19388199	1	1	0.6
23.91916275	24.33244705	5	5	14.2
22.93479347	20.01530266	2	2	4.1
21.72754288	24.25320816	27	27	1
26.32709503	25.8868351	26	1	76.9
31.65902138	31.72228432	26	0	76.9
27.72566032	27.71463203	26	1	77.3
23.86740494	25.18955994	21	3	57.6
27.28920937	27.72637367	25	5	66.3
25.94187927	26.61722755	21	5	57.3
24.0116291	23.91433334	25	3	69.8
32.09065247	32.20431519	28	1	73.3
28.89787292	28.82238007	26	5	69.1
26.69789886	26.61076736	10	10	30.3
23.94368935	23.69189644	3	1	7.7
22.65276527	23.13097382	4	2	14.4
27.8646698	28.21604538	6	6	55.2
22.39962959	23.11822701	1	1	12.7
26.3533802	26.27653885	7	7	26.4
24.43001175	24.94087029	3	3	13.5
25.05353737	25.10097313	5	5	17.4
23.62622643	23.98320198	3	3	18.4
24.6595974	25.23516655	2	2	7.2
24.25673866	24.4593277	6	6	16.8
29.47187042	29.67620087	30	30	47.7
23.08885574	23.5460434	2	2	4.2
21.14177132	22.27474976	1	1	3.8
24.32017136	18.81748009	3	3	14.9
20.45887756	22.26011848	2	2	1.8
25.46179581	25.09615326	4	4	42.9
23.00442886	23.37967682	2	2	13.9

22.92536926	22.8402462	3	3	24.5
26.64141083	26.80156326	4	4	41.6
27.23260689	27.16240501	5	5	48
25.04205704	25.11961365	4	4	18.6
29.73222542	28.85436058	2	2	2.5
21.83460617	20.99872589	1	1	1.4
20.88651466	21.7689476	1	1	1.5
19.82559776	20.6557827	1	1	12.3
23.5909214	24.13288879	4	2	9.7
22.15158844	22.41204071	3	1	6.3
23.2734127	23.79024506	5	5	1.6
23.69816399	23.70408821	1	1	5.4
19.45850754	22.96117973	1	1	6.9
27.43173409	27.23735619	10	10	71.7
23.17817497	23.60002899	2	2	13
27.93297768	27.26472473	18	18	80.8
24.98220062	25.36733055	3	3	28.7
24.84143829	24.53777313	3	3	11.7
24.79109001	25.20277023	2	2	58.8
26.69723511	26.55451393	18	18	21.3
25.34732819	25.68549347	9	9	21.5
20.96972466	20.96211624	2	2	5.1
20.74287605	20.77836227	1	1	4.6
26.65812683	26.63089752	22	22	32.2
24.52749062	24.50008774	7	7	7.5
25.46497536	25.48953056	2	2	37.5
24.01690865	24.59889221	1	1	21.4
26.234272	26.24778748	5	5	45
28.0877533	28.15281677	22	22	55.6
28.86263084	28.85676765	19	19	60.9
27.19863701	26.71999359	8	8	46
25.03477287	24.58422661	1	1	20.2
26.80833054	26.78406715	6	6	68.3
22.45665932	22.12855339	2	2	9.5
20.3827877	21.89748192	1	1	17.2
24.41060448	23.89679909	8	8	12.2
24.40177917	24.8587532	4	4	11.2
20.57117081	20.37951851	1	1	1.6
25.8191185	25.96057892	1	1	1.3
23.23502731	23.17803764	5	5	11.2
26.58820724	26.7425251	15	15	32.8

22.40564156	23.12063408	3	3	3.5
20.76765442	20.87590218	1	1	1.4
25.0754509	25.18252945	6	6	39
24.30180168	24.58439827	3	3	17.3
25.84993172	26.17822456	8	8	13.1
23.25076675	20.74549866	2	2	6.7
26.69431686	26.81053925	10	10	27.5
28.2927227	28.35640717	15	15	44.8
21.23613739	21.05205345	1	1	3.1
22.67977142	23.06287766	2	2	22.4
28.45148087	28.54940414	9	9	20.9
32.80952454	32.78904343	74	74	72.5
29.42534447	29.48089218	33	33	53.3
28.25408173	28.57513618	14	14	58.7
27.02369118	27.36836433	9	9	39.3
24.71035576	25.40791702	5	5	15.5
34.39400864	34.36345673	65	56	88.8
22.86782074	22.96280479	1	1	8.1
21.48492813	22.04766655	2	2	11.9
23.73892403	24.30096436	5	5	29.1
22.82842255	22.66661453	1	1	3.9
22.9183445	22.18842888	3	3	19
25.22545433	25.40999031	5	5	31.9
21.01386261	20.76943016	1	1	3
22.72984695	22.57839966	2	2	4.9
19.72609138	21.8006897	2	2	4.7
22.64138794	19.85634041	3	2	10.3
24.97211075	25.17371368	4	3	12.4
22.48059654	22.54063797	1	1	4.5
25.92913246	25.36853027	6	6	15.3
26.01788521	25.90403175	7	7	35.7
25.26094246	25.89774513	14	14	25.2
26.95371437	27.10059166	1	1	4.6
22.26719475	22.05543327	6	6	4.4
27.05961418	26.78606224	25	25	13.8
24.30632973	25.39920616	5	5	16.6
22.28217888	22.88026237	3	3	13
29.10041618	29.19335747	28	28	70.6
24.06019211	22.44133949	1	1	1.1
23.52695274	23.66925621	1	1	6.6
27.40405655	27.61294746	1	1	0.8

26.71253395	26.5696125	8	8	31.1
24.16061783	22.99982643	3	3	10.3
25.42431831	25.68244362	12	12	16.2
21.71866608	18.96220589	1	1	2
24.26999283	24.00744438	6	6	15.7
21.83124733	22.3955307	2	2	9.6
22.85222435	22.97277641	2	2	5.5
19.66091537	23.06463814	2	2	11.1
27.69212151	27.77799988	12	7	47.5
28.11971283	28.55189896	15	13	55.7
28.2853775	28.23365974	12	8	50.2
26.05920219	25.84856987	12	9	41.9
28.69756699	28.99765778	10	6	36.6
30.09295273	30.21858788	20	16	60
24.59485626	24.70767212	3	3	18.3
20.91488075	20.86725426	1	1	1.3
19.77473259	19.5729847	1	1	5.3
23.13028336	22.95414925	1	1	3.3
20.48529243	22.41565514	1	1	2.1
29.8678093	29.39382553	27	27	59

Unique sequence coverage [%]	Mol. weight [kDa]	Q-value	Score	Intensity
7.6	47.13	0	7.5726	400600000
5.7	36.3	0	4.9139	135020000
7.7	67.354	0	31.722	347130000
3.6	84.921	0	5.2015	147520000
3.5	37.022	0.0035447	2.0961	63154000
6.2	35.316	0	8.6343	445040000
6.8	29.814	0	12.953	105620000
5.5	48.994	0.00043573	3.323	32204000
10.9	34.732	0.0012195	2.5349	177770000
7.1	79.964	0	10.173	183470000
7.7	46.297	0	7.4717	91331000
12.8	24.752	0	12.131	174080000
17.9	16.961	0	102.08	4221400000
72.2	11.186	0	64.184	8378300000
7.6	79.481	0	8.3432	175730000
4.4	27.072	0	8.2727	170700000
8.7	28.599	0	3.9923	5961400000
22.9	72.367	0	42.71	2701200000
39.6	191.36	0	323.31	19690000000
47.8	53.497	0	210.78	3981800000
8.6	54.734	0	6.9516	184930000
16.9	17.024	0	7.9265	239820000
40.7	34.45	0	77.193	1493800000
16.5	22.794	0	7.3941	498250000
10.5	48.763	0	39.317	730830000
17.9	50.167	0	26.88	801810000
7	106.25	0	17.007	679780000
3.5	137.61	0	34.396	525050000
32.7	63.299	0	85.369	5905700000
5.1	105.54	0	9.3355	399420000
25.4	121.96	0	92.052	4639400000
12.3	235.9	0	44.735	1105200000
39.7	7.3184	0	11.636	714590000
13.2	31.966	0	10.395	258010000
15.2	50.09	0	50.313	1054100000
8.2	89.309	0	12.444	415620000
13.7	123.43	0	64.044	1165900000

29.5	29.227	0	29.237	813480000
5.9	112.22	0	18.847	1038800000
29.4	246.32	0	323.31	20497000000
2.6	89.986	0	323.31	2.0418E+11
25.9	65.994	0	36.317	1059900000
21.7	53.398	0	34.521	773550000
39.8	23.995	0	128.43	13189000000
19.5	140.47	0	257.72	19664000000
28	64.774	0	72.02	3523600000
15	42.532	0	31.383	181080000
53.6	36.428	0	234.12	12547000000
30.4	46.7	0	108.32	6433000000
32.1	44.127	0	71.429	1984300000
28	63.691	0	58.349	3007100000
41.8	116.53	0	323.31	16928000000
39.8	100.29	0	323.31	27849000000
42.2	30.016	0	39.497	1206000000
25.9	69.886	0	106.43	1529800000
71.3	11.922	0	57	1903700000
24.1	128.36	0	245.88	9597600000
76.8	33.355	0	323.31	1.3822E+11
18.9	32.939	0	22.002	816170000
56.9	7.9972	0	17.702	801380000
44.7	71.937	0	249.95	55314000000
32.8	63.056	0	106.46	2220900000
56.1	46.533	0	278.66	32669000000
33.9	291.12	0	323.31	13526000000
36.4	10.344	0	16.801	2469500000
40.1	110.33	0	323.31	1.6492E+11
59.6	41.639	0	323.31	1.2076E+11
51.9	108.49	0	323.31	2.216E+11
79.9	22.395	0	323.31	2.4244E+11
54.2	51.373	0	205.7	20518000000
14.6	67.568	0	13.978	811090000
71.1	50.118	0	292.67	25725000000
3.5	161.72	0	13.841	678340000
36.5	107.58	0	293.9	15663000000
32.2	66.9	0	114.65	12709000000
38.2	150.92	0	226.36	10114000000
29.5	94.138	0	120.19	2751600000
57.6	103.07	0	323.31	1.5276E+11

54	61.936	0	314.51	26102000000
23.4	78.185	0	91.625	7199300000
17.5	86.41	0	57.953	2500500000
73.2	38.676	0	323.31	87976000000
29.2	252.31	0	323.31	12555000000
20.1	134.2	0	323.31	51640000000
13.6	49.184	0	26.913	837380000
40.6	43.953	0	323.31	40141000000
22.1	50.933	0	30.826	1405000000
0	42.009	0	14.074	1.2754E+11
53.2	41.525	0	198.24	6243900000
59.3	14.957	0	165.25	32217000000
44.7	77.8	0	323.31	18877000000
33.4	52.206	0	49.812	1979900000
51.1	35.915	0	242.93	4763700000
49	10.963	0	30.69	6147200000
45	25.97	0	265.2	96814000000
29.3	91.712	0	135.31	3169200000
73.7	35.752	0	262.33	51234000000
49.5	33.387	0	40.605	1367000000
34.7	24.423	0	44.216	3149100000
10.6	12.259	0	20.757	621650000
16.7	46.763	0	39.846	3535400000
18	113.24	0	49.521	3050700000
73.4	25.958	0	308.75	27009000000
8.6	54.084	0	14.332	362200000
34.7	30.641	0	43.949	1731700000
48.8	38.734	0	177.47	19782000000
45.7	97.183	0	268.63	8090300000
50.6	27.403	0	43.989	1832100000
44.7	14.015	0	26.347	886050000
6	273.61	0	34.303	924650000
45	47.408	0	98.049	2322100000
4.3	203.91	0	15.852	502260000
6.9	23.656	0	5.3473	616570000
11.9	17.587	0.0023923	2.2887	350640000
28.5	100.2	0	122.23	3316200000
10.4	26.791	0	5.2647	194490000
5.1	121.04	0	21.853	385230000
30.8	53.514	0	63.243	1496000000
14.4	76.765	0	12.988	305450000

23.3	50.282	0	38.265	933560000
20.7	74.934	0	74.305	1919900000
12.5	58.951	0	16.062	773790000
39.4	58.004	0	101.37	3175800000
40.2	27.057	0	158.7	3064100000
2.9	217.75	0	14.731	415030000
40.9	32.88	0	40.457	1158300000
21.8	13.72	0	8.9437	286690000
24.2	14.203	0	10.881	1056600000
1.9	86.525	0	7.714	44691000
47.6	15.776	0	143.17	4540400000
16.1	192.91	0	141.97	3991300000
8.5	37.425	0	12.728	524960000
5.9	290.71	0	21.036	2328900000
7.9	146.56	0	20.767	379310000
20.6	46.247	0	45.344	497970000
14.1	51.012	0	10.903	155340000
25.2	22.45	0	49.508	1269500000
50.8	20.802	0	54.342	3647100000
19.6	32.851	0	13.836	911070000
39.1	29.47	0	100.88	1498100000
7.4	72.241	0	9.533	539950000
0.6	290.08	0	4.7852	40712000
2.7	117.64	0	3.946	233740000
30.3	37.778	0	41.59	886080000
16.4	12.436	0	16.222	38977000
14.4	66.612	0	40.252	323320000
1	116.89	0.00042373	3.0101	61420000
26.8	54.831	0	23.281	649380000
18.7	59.162	0	23.157	728570000
13	17.872	0	5.7932	28413000
21.3	39.771	0	14.28	816650000
4.4	69.622	0	11.872	104280000
4.8	39.617	0	17.749	275190000
16.9	82.967	0	21.336	753160000
8.5	29.718	0.0035377	2.0748	87679000
5	47.064	0	22.699	10930000000
3.8	30.26	0.00042105	2.9386	66975000
23.3	5.1161	0.0020072	2.3784	89647000
24.8	11.655	0	12.366	224200000
28.4	49.971	0	89.586	4781100000

3.3	64.49	0	3.6421	29704000
7.4	25.746	0	18.603	72305000
0.7	244.25	0	3.8101	76978000
1.1	169.9	0.00041649	2.823	1274600000
4.4	83.516	0.0053456	1.7231	59626000
1.6	68.24	0.0020056	2.373	175080000
8.7	51.421	0	8.4826	276290000
6.9	55.759	0	4.6707	53409000
4.3	332.91	0	27.677	555910000
8.8	20.762	0.0008244	2.7303	101470000
1.9	81.182	0.0098253	1.3338	48515000
7.7	46.137	0	24.126	174230000
34.7	11.747	0	10.581	354160000
13.1	6.6973	0.0016214	2.5149	231480000
48.3	8.8225	0	26.499	307090000
36.7	165.85	0	323.31	17552000000
8.2	106.91	0	70.115	718330000
2.7	44.97	0.0087816	1.3885	45457000
12.8	50.236	0	91.958	694380000
1.9	176.16	0	8.4982	71840000
3.8	170.09	0	8.2935	203340000
6.8	75.474	0	9.26	282890000
11	67.314	0	35.318	372140000
1.2	94.944	0.00043103	3.21	80464000
25.4	33.56	0	5.5601	347770000
21.6	45.269	0	13.383	475580000
9.9	63.085	0	7.715	606330000
17.9	39.154	0	16.661	308130000
9.5	42.547	0	5.8146	144890000
2.2	62.003	0.00043879	3.4168	68982000
77.8	9.0303	0	25.861	1093700000
22.9	43.953	0	72.968	1584300000
83.1	41.829	0	323.31	25554000000
23	265.25	0	246.18	2548600000
3.9	118.98	0	7.3858	120750000
5.8	68.721	0.00041876	2.8853	190880000
45.3	47.907	0	322.03	13453000000
43.7	46.481	0	202.09	14705000000
47.8	44.889	0	73.325	5049600000
18.5	47.874	0	120.27	1369300000
74.5	70.875	0	323.31	11258000000

11.4	221.94	0	200.94	7890300000
55.4	44.816	0	321.69	16308000000
29.7	41.297	0	61.287	1131100000
8	65.356	0	6.0731	158370000
40.1	119.73	0	317.91	10992000000
32.3	98.124	0	97.255	3101800000
65.4	85.462	0	323.31	41315000000
36.4	15.183	0	30.075	660590000
19.6	49.656	0	78.74	1339300000
6.5	37.555	0.00043197	3.2323	155120000
29.6	50.56	0	55.087	2696200000
20.3	17.941	0	21.217	915020000
10.1	67.95	0	13.979	138030000
3.4	65.076	0	5.0836	31704000
38.6	77.951	0	238.92	10622000000
16.5	76.205	0	23.891	211680000
4.5	41.736	0	77.927	7413900000
0	42.019	0	323.31	1.3397E+12
4.5	41.792	0	323.31	3.6943E+11
6.1	47.447	0	5.8253	143820000
53.9	104.98	0	323.31	19968000000
9.6	46.207	0	147.06	411790000
18.4	42.613	0	48.096	930670000
18.1	42.281	0	66.664	3863900000
51.8	44.76	0	269.62	8659700000
63.9	47.357	0	145	17154000000
28.3	11.241	0	5.8262	455300000
1.6	83.967	0.0087848	1.3913	43386000
2.2	113.22	0	4.3236	103560000
17.7	71.742	0	21.354	819370000
5.4	139.12	0	33.404	962190000
1.5	122.71	0.0077548	1.4666	64142000
7.7	75.406	0	15.15	237560000
54.3	39.547	0	132.09	2964300000
17.9	39.904	0	7.1263	181970000
13.8	26.809	0	7.966	577600000
28.8	40.148	0	66.045	1525900000
8.1	53.774	0.00042535	3.0721	77677000
2.9	79.656	0	5.1777	76555000
3.7	42.06	0	3.5472	34911000
33.9	54.866	0	76.724	1327600000

7.2	50.254	0	6.0511	107060000
3.1	89.518	0	5.4691	192010000
6	49.275	0.0035322	2.0645	13872000
14.5	18.899	0	21.892	275150000
2.7	97.303	0	11.514	329720000
18	31.01	0	7.8844	193610000
11.9	198.33	0	47.847	1138300000
37	47.688	0	55.106	2295500000
10.8	58.951	0	8.1928	353570000
8.6	38.117	0	7.2044	327480000
36.2	37.325	0	158.85	15976000000
9.6	66.765	0	22.351	570350000
11.5	40.634	0	5.6663	129530000
20	33.997	0	28.86	872330000
11.6	35.377	0	15.902	412840000
17.6	37.605	0	12.032	236490000
52.1	21.539	0	138.84	5216900000
56.9	25.605	0	104	3388400000
70	25.426	0	61.923	4048300000
3.7	169.74	0	46.389	1217100000
56.9	36.586	0	132.49	3677900000
46.8	35.732	0	54.028	6631900000
3.2	35.988	0	5.2726	325260000
16.1	36.12	0	11.416	902890000
12.5	40.612	0	18.706	663090000
4.7	27.483	0.0067265	1.5497	124670000
10.9	36.023	0	18.85	266750000
74.7	68.692	0	323.31	3.5689E+11
16.5	65.091	0	15.397	518510000
1.6	84.755	0.0016168	2.477	30289000
1.5	87.052	0.00042992	3.1812	66509000
14.2	54.467	0	28.214	245350000
5.1	101.59	0	11.011	125130000
66.7	56.537	0	323.31	40297000000
17.6	53.97	0	24.167	1541400000
17.3	61.84	0	79.723	703840000
5.5	55.968	0.00041374	2.7667	88961000
50.7	57.915	0	180.08	6345000000
37	55.644	0	103.66	2918100000
80.8	39.355	0	295.16	21083000000
3.9	47.404	0	5.0584	50903000

8.1	18.136	0.0063838	1.5803	31480000
29.4	17.682	0	4.5879	419140000
2.4	215.99	0	6.3528	110680000
23.4	192.03	0	178.05	3561500000
1.7	426.26	0	7.6955	238370000
4.4	128.65	0	33.897	141760000
12	69.262	0	9.7832	361280000
21.1	28.537	0	80.802	800730000
11.4	31.078	0	9.4119	752680000
13.3	28.245	0	11.978	820600000
37.7	109.65	0	323.31	8430300000
32	54.079	0	126.84	6669000000
56.7	36.384	0	165.99	11342000000
70.9	75.884	0	323.31	73210000000
22.9	49.925	0	57.734	5135400000
48.4	84.533	0	323.31	79048000000
3.2	146.68	0	5.0626	205490000
9.2	103.93	0	21.135	671040000
5.6	91.349	0	8.0562	198290000
23.7	105.48	0	102.29	3431600000
25.9	104.02	0	178.7	5882200000
23.9	104.58	0	202.67	6565600000
29.9	49.654	0	43.826	2394900000
11.3	17.018	0.00043122	3.2121	551820000
5.2	122.74	0	15.687	401640000
3.3	135.08	0	5.0933	161930000
15.8	35.49	0	13.165	295140000
7.7	56.784	0	37.592	551020000
13.7	46.434	0	17.658	461590000
61	30.615	0	128.01	8805600000
46.5	30.972	0	59.131	3553400000
32.4	11.309	0	32.094	740480000
48.9	45.029	0	65.078	3369600000
10.2	9.6963	0.0081121	1.439	435490000
21.6	10.741	0	29.216	228390000
18.6	35.866	0	15.403	796730000
36.5	38.618	0	39.032	3683600000
19.5	18.798	0	18.082	160450000
27.9	29.26	0	30.903	591380000
15.7	79.327	0	25.957	549870000
25.6	19.724	0	15.864	919320000

23	28.793	0	80.105	2279300000
22.9	57.229	0	30.12	922780000
39.8	20.697	0	104.8	4860500000
9.9	20.746	0.00042409	3.0274	104670000
23.9	20.396	0	67.909	2463500000
13.9	20.529	0	7.779	187750000
21.7	20.082	0	4.5485	121240000
2.5	202.24	0	8.3954	52942000
44	50.41	0	78.682	2348700000
8	79.818	0	12.812	168870000
1.4	229.72	0.0057143	1.6988	4568700000
74	23.407	0	94.112	8915400000
23.5	22.851	0	15.422	290520000
7.4	108.53	0	9.5104	370720000
7.1	79.695	0	7.4201	218250000
13.8	20.411	0	49.835	391790000
35.2	20.486	0	13.894	871350000
4.9	23.437	0.00041459	2.7848	148050000
28.7	21.557	0	80.777	1668800000
30.1	21.539	0	33.235	800430000
27	31.246	0.00043802	3.4071	290410000
31.7	41.063	0	91.169	8116500000
42	34.357	0	107.78	4653200000
53.9	20.524	0	33.243	5356800000
66.7	19.667	0	125.63	8106100000
29.1	16.288	0	7.0956	1052300000
16.3	16.98	0	13.594	685420000
19.8	44.669	0	39.578	956110000
19.2	51.739	0	37.096	342540000
17.5	38.822	0	7.3528	359240000
19.3	83.041	0	74.028	1623500000
54.2	42.572	0	308.94	65270000000
3.1	33.95	0.00041442	2.7843	72788000
4.3	57.428	0	4.7269	119490000
6.9	32.402	0	4.8567	156640000
4.9	77.519	0	10.343	135880000
48.8	64.217	0	157.84	4762600000
4.1	66.223	0.00042882	3.1637	199640000
46.8	60.574	0	212.36	6599200000
58.8	7.3384	0	42.984	1783800000
14.8	112.98	0	100.17	4232600000

12.5	35.194	0	11.246	505120000
39.6	31.775	0	14.342	1219700000
18.6	109.75	0	192.37	4855800000
6.3	112.3	0	19.965	319540000
1.1	134.75	0.00041528	2.7916	60779000
10.1	122.29	0	54.812	1880100000
61.7	59.752	0	323.31	43839000000
73.5	56.3	0	323.31	82640000000
42.6	32.886	0	92.378	3902200000
22.7	28.948	0	28.853	5653400000
76.4	18.749	0	91.949	4442900000
33.8	8.2355	0	8.5163	902860000
9.3	12.496	0.00041511	2.7853	237230000
41.7	11.424	0	18.964	2098000000
62.4	23.363	0	137.93	14384000000
1.2	95.622	0.0020088	2.3841	39729000
6.6	40.301	0	6.4183	336640000
23.8	68.325	0	94.554	1232900000
4.3	56.55	0	3.9674	65807000
19.5	26.157	0	28.674	332600000
12	53.706	0	5.0238	120840000
9.6	33.395	0	4.1173	173830000
4.5	98.19	0	6.4731	221160000
40.3	13.779	0	11.851	690850000
2.7	41.909	0.0042373	1.8319	78502000
26.3	61.859	0	18.068	843580000
2.7	50.942	0	4.3363	74518000
62.9	10.102	0	30.407	6015400000
6.8	21.394	0	6.0397	193390000
46	67.669	0	169.69	9655800000
3	94.391	0	6.7535	24007000
1.8	101.02	0.00081633	2.5794	72911000
12.2	50.37	0	28.293	366370000
18	35.504	0	7.3681	432230000
4.1	46.587	0	6.2511	132130000
26.4	52.511	0	28.471	902030000
25.8	33.524	0	34.597	764750000
58.3	22.197	0	47.566	1099800000
4.6	29.978	0.0042275	1.7903	25303000
36.7	33.196	0	18.027	664170000
5.7	28.09	0.0016201	2.506	27761000

39.8	11.832	0	89.453	118560000
14.2	17.699	0	6.1045	51822000
1.7	76.437	0	4.0872	41405000
25.5	31.013	0	46.311	1103600000
29.7	186.48	0	117.61	4463800000
9.2	51.523	0.00081766	2.5987	1805700000
2.9	188.88	0	5.9504	135690000
4.2	62.002	0.00041894	2.8875	73964000
11.9	28.33	0	6.1149	303280000
68.1	29.032	0	135.15	4822100000
84.6	29.366	0	249.06	14412000000
26.7	39.842	0	56.197	1240100000
12.7	26.51	0	8.3966	127430000
1.6	235.85	0	9.5059	153500000
49.7	16.837	0	168.53	3732400000
45.4	47.994	0	99.441	5250700000
11.7	37.063	0	21.87	435350000
8.6	41.624	0	5.7082	282090000
27.2	54.113	0	110.87	4761900000
16.4	55.96	0	71.222	1998000000
6.8	32.542	0	4.9167	82662000
35.8	136.33	0	250.77	7382500000
33.5	67.277	0	116.84	7884300000
74.3	51.564	0	323.31	38732000000
29.6	52.861	0	83.638	3087900000
22.7	39.24	0	55.406	967270000
18	82.105	0	28.901	549380000
40	79.871	0	212.51	10122000000
47.2	28.463	0	209.04	11355000000
8.3	78.168	0	3.745	83205000
28	32.967	0	80.94	5045900000
49.3	30.628	0	77.176	4512300000
43.2	16.062	0	8.5806	551710000
3.1	35.217	0	59.254	1364200000
3	32.151	0.00043611	3.3341	114510000
3.1	63.459	0.0027679	2.1941	82351000
2.9	85.55	0.00043271	3.2532	9353300
2.9	55.356	0.0027756	2.2278	27222000
14.3	46.377	0	12.282	7561700000
6.8	79.694	0	17.254	485640000
27.7	59.795	0	98.574	897480000

57.9	20.538	0	80.794	13977000000
37	18.227	0	15.962	1280300000
15.9	30.953	0	9.1695	357050000
3.4	124.74	0	4.8882	108580000
1.5	103	0	6.2704	72515000
6	47.32	0	5.7362	130460000
9.8	19.152	0	5.6912	68988000
13.8	54.865	0	16.331	614280000
5.7	107.61	0	20.111	561980000
16.4	29.596	0	25.368	1045300000
4.7	36.561	0	4.8234	52427000
56.4	57.477	0	143	6642700000
36.5	60.629	0	97.761	4136800000
35.6	58.066	0	98.794	2783200000
53.6	59.623	0	206.81	4974100000
39.3	59.652	0	99.037	3441500000
24.8	59.555	0	41.912	2533500000
13	161.66	0	133.48	1400400000
13.4	28.246	0	4.5311	636800000
2.7	120.92	0	6.3005	78479000
25.5	31.256	0	24.985	1579300000
6	70.449	0	6.4296	247360000
8.6	35.262	0.001221	2.545	553350000
33.5	52.697	0	58.501	3943200000
3.3	39.998	0	3.4566	130900000
4.6	33.097	0	14.222	997230000
27.5	25.814	0	166.01	6394400000
11.5	25.258	0	107.92	4399200000
11.3	80.433	0	16.934	754380000
27.4	16.782	0	30.68	271710000
13.2	44.593	0	13.507	699770000
51.3	21.258	0	72.23	4084500000
6	194.75	0	13.561	464570000
2.4	88.354	0	3.8092	37397000
6.1	23.599	0	4.2842	34347000
2.5	158.13	0.0035101	1.9858	71309000
6.5	33.288	0	4.9745	90730000
14.6	51.313	0	32.321	337510000
11.7	55.409	0	17.835	301740000
23.4	27.541	0	14.211	606520000
33.8	61.055	0	68.782	3334000000

50.6	61.787	0	228.3	13704000000
9.3	85.004	0	20.922	430520000
10.1	27.985	0.003517	2.0109	206130000
21.4	139.14	0	87.083	4622300000
9.8	67.26	0	5.1683	204290000
63.3	18.559	0	187.86	18439000000
41.6	18.709	0	36.863	1216300000
21.6	26.334	0	12.578	420610000
10.6	29.852	0	6.6186	320790000
5.4	25.219	0.001624	2.5227	189200000
15.6	24.936	0	7.2142	250040000
4.1	49.398	0.006734	1.5515	55622000
18.3	21.978	0	5.5258	124790000
30.6	12.097	0	12.153	1008400000
59.6	42.713	0	323.31	35885000000
42.3	43.044	0	98.566	2052700000
5.2	167.94	0	13.658	380700000
4.5	60.621	0.0042324	1.7991	82092000
3.3	34.595	0.00042212	2.9791	36691000
53.5	22.257	0	46.737	795520000
47.7	27.013	0	40.686	2951500000
70	28.729	0	223.14	10051000000
2.2	51.425	0.00042194	2.9706	52558000
3	62.183	0	6.155	89487000
9.5	23.174	0	4.0927	138930000
55.5	191.55	0	323.31	41377000000
23.2	51.655	0	130.09	2914200000
23.1	37.548	0	30.911	1315200000
36.8	27.586	0	110.34	4370900000
36.2	22.165	0	24.065	1003800000
8.8	18.742	0	7.1767	485530000
31.8	52.767	0	24.025	1861500000
32.5	33.155	0	229.99	9851600000
23.2	44.654	0	47.331	296830000
11	20.767	0	9.3505	91894000
4.9	28.093	0	3.4848	70658000
9.3	11.987	0.00041477	2.785	138140000
9.1	62.022	0	7.6819	173590000
8.1	206.08	0	63.894	1210200000
11.7	138.03	0	312.54	3.1366E+11
20	129.56	0	190.18	1.58E+11

3	131.86	0	15.937	36705000000
2	138.94	0	17.752	1825800000
7.5	160.68	0	237.12	55197000000
14.8	167.32	0	260.45	42744000000
2.1	164.09	0	9.4439	248090000
6	183.77	0	254.5	5574100000
6.3	145.02	0	87.62	4745200000
7.2	289.57	0	87.26	1660800000
7.6	71.06	0	6.1355	312370000
24.6	22.037	0	12.457	150260000
7.5	21.86	0.0060583	1.6619	32267000
13.6	21.85	0	31.388	259460000
44.1	24.707	0	55.754	656340000
6.1	28.96	0	4.585	111290000
28.9	138.43	0	83.807	2786300000
22.7	107.06	0	73.83	1887700000
9.6	102.45	0	17.662	427670000
43.8	34.567	0	72.594	978920000
21.2	97.512	0	71.76	2250900000
6	97.55	0	5.0957	106020000
19.4	51.596	0	84.088	1632500000
18	47.832	0	28.101	835770000
19.5	46.284	0	24.904	466370000
6.9	37.548	0	8.9075	355790000
7.1	35.88	0.002769	2.1944	83388000
21.1	30.224	0	18.364	281780000
20.9	20.198	0	9.9118	227890000
5.3	21.693	0	3.6376	79417000
18.5	51.392	0	16.651	376970000
12.1	35.082	0	11.974	528740000
16.3	50.989	0	5.0661	109050000
17.4	53.912	0	20.237	1304500000
37.8	53.12	0	103.74	7668900000
11.3	15.944	0	5.0826	42797000
36.1	19.53	0	52.973	3848700000
54.8	16.101	0	119.92	12116000000
51.6	13.813	0	19.876	2920300000
61.3	12.352	0	71.751	11673000000
70.9	10.071	0	32.939	5606700000
59.2	8.4689	0	18.717	1912500000
16.2	8.9863	0	6.2094	1823700000

56.6	9.2908	0	13.015	1512300000
14.3	7.3325	0.0020048	2.3519	257470000
14.8	121.15	0	35.358	1138200000
31.9	48.789	0	75.685	4864000000
10.5	53.255	0	13.861	441460000
20.1	58.886	0	87.549	2242300000
8.9	61.035	0	6.1842	173460000
18.4	59.584	0	93.26	2280700000
2.9	49.714	0	3.4781	28798000
10.9	30.333	0	5.9812	75423000
12.3	51.813	0	12.661	542450000
7.4	59.152	0	54.861	1043500000
10.5	26.192	0	10.592	377080000
6.7	88.25	0	13.85	472990000
11.7	88.216	0	25.016	783720000
33.3	73.98	0	116.63	2433600000
2.3	49.074	0.0023866	2.2566	163080000
31.2	70.839	0	40.544	1047800000
3.8	45.717	0	5.5301	55255000
71.4	8.5497	0	89.598	26443000000
71.2	22.727	0	154	21204000000
29.6	33.814	0	17.308	854770000
5	33.83	0	3.5663	155910000
30.9	20.069	0	15.858	1420100000
26.6	35.208	0	19.944	737880000
10	35.268	0	4.864	292850000
50	51.736	0	323.31	30932000000
29	55.144	0	48.381	1365700000
14.3	110.45	0	55.993	4351900000
8.9	50.716	0	4.7119	320860000
13.2	37.567	0	6.3494	157920000
21.5	45.133	0	26.277	736920000
7.9	24.942	0	4.4908	300890000
64.8	20.583	0	323.31	36528000000
67.4	20.926	0	181.23	21202000000
9.3	15.531	0.00041563	2.8038	83055000
33.7	11.045	0	15.806	1087200000
9.1	61.341	0	8.7446	231550000
19.1	46.614	0	65.389	906220000
2.4	83.745	0	9.3668	30274000
13.4	100.11	0	83.916	1850600000

2	100.42	0	6.4214	144480000
5.7	99.802	0	13.036	173080000
5.2	81.462	0	14.794	261780000
15.1	85.47	0	33.819	1491300000
3.6	64.979	0.0027778	2.2308	47146000
14.1	101.74	0	25.498	816290000
25.4	37.279	0	59.279	1337400000
37.1	44.953	0	52.623	6533000000
11.1	37.17	0	16.967	354440000
11.2	61.249	0	28.215	548990000
3.1	69.84	0	5.0559	148330000
5.5	89.69	0	10.735	145210000
4.2	88.947	0	6.0782	197200000
3.2	87.752	0	8.0381	103160000
5	90.973	0	10.653	172420000
18.6	18.865	0	22.108	1691500000
8.1	29.003	0.00042034	2.9282	78093000
15.7	10.032	0	9.5733	104800000
32.1	15.241	0	12.424	747250000
32.2	16.318	0	21.984	409270000
27.9	34.134	0	25.084	397530000
83.5	31.549	0	311.38	27404000000
5.3	20.921	0	5.1883	239910000
58.6	29.497	0	118.79	4643400000
39	11.605	0	33.334	4541600000
13	144.98	0	31.57	1651700000
37.9	21.465	0	43.183	1117200000
7.4	52.149	0	14.841	321150000
3.5	55.948	0.0035143	2.0049	17082000
5.9	58.9	0	3.9006	52634000
53.8	28.09	0	91.171	5990200000
4.9	122.27	0	12.37	149770000
5.1	58.821	0	4.8016	90225000
17.1	96.904	0	64.945	2207200000
19.8	57.147	0	22.012	2305600000
14.6	43.086	0	9.1212	74977000
39.1	10	0	87.928	4022900000
22.2	48.341	0	16.872	716650000
26.1	53.246	0	41.744	2104600000
51.1	39.809	0	323.31	1.2758E+11
20.7	38.988	0	26.873	445770000

13.6	138.2	0	58.263	1614800000
35.1	44.116	0	79.04	2572900000
8.6	20.978	0	7.342	98773000
5.5	20.14	0.00042355	3.0083	30617000
43.9	29.645	0	72.344	2622000000
8.6	126.85	0	31.531	917980000
3.3	79.576	0.0035363	2.0748	18456000
30.2	49.027	0	107.46	3204100000
5.4	35.977	0	4.0751	287950000
95.8	13.077	0	65.828	3974900000
16.5	82.499	0	122.42	2766700000
12.5	72.399	0	18.735	484670000
3.9	93.55	0.00043535	3.3195	112460000
3	42.104	0	4.5608	105500000
27.8	49.035	0	60.223	3377700000
7.7	73.101	0	108.58	4026200000
6.7	73.427	0	12.75	350490000
2.7	101.96	0	4.6763	710250000
19.1	69.289	0	50.072	3039300000
5.3	82.175	0	3.8431	2009900000
7.5	54.191	0	4.8139	167630000
55.2	36.213	0	187.7	9157600000
8.7	43.158	0	7.6611	552420000
7.6	28.834	0	11.34	226500000
22.8	36.3	0	25.741	691190000
24.6	34.005	0	21.861	502820000
8	33.982	0	5.1587	97429000
4.5	91.006	0	6.9853	212060000
2.1	153.97	0	3.9336	11718000
10.9	149.47	0	61.359	2392300000
5.9	139.34	0	14.211	131920000
6.7	57.401	0	3.4735	135590000
37.7	67.941	0	178.4	11245000000
31	54.272	0	96.568	8473700000
31.5	48.994	0	64.236	5495000000
35.7	425.83	0	323.31	25368000000
11.9	46.531	0	13.114	299440000
9.3	44.868	0	48.96	519920000
9.2	45.745	0	19.507	578230000
5.4	46.847	0	13.886	178170000
28.5	37.781	0	32.978	1919700000

2.4	90.582	0.0023962	2.3032	157610000
5.5	63.232	0	13.003	243750000
10.3	57.463	0	17.13	241200000
0	96.056	0.00041408	2.77	32629000
45.4	78.01	0	132.81	3212800000
15.8	97.732	0	59.349	2215400000
3.6	241.18	0	17.045	325750000
60.7	45.722	0	318.63	11241000000
21.3	82.897	0	21.064	505020000
2	56.253	0	5.4967	74634000
45.5	11.213	0	38.474	2129700000
56.1	62.277	0	320.04	17362000000
10.7	22.278	0.00043459	3.3119	46152000
0.9	834.21	0	75.082	171230000
77.6	18.521	0	203.86	70525000000
13.3	18.05	0	5.3827	56652000
27.6	77.732	0	83.813	2516900000
5.5	24.18	0.003506	1.9738	8164200000
38.9	20.472	0	76.342	1574500000
30.9	532.04	0	323.31	23096000000
5.6	68.393	0	88.21	412850000
22.2	56.614	0	62.991	1215100000
27	10.366	0	14.854	5606500000
38.5	10.99	0	16.131	901600000
15.9	12.483	0.00043592	3.3234	61113000
49.1	12.957	0	27.907	277530000
36.1	36.118	0	134.36	1398900000
7.2	28.824	0	16.154	68011000
51	31.474	0	147.61	6572700000
59.5	32.25	0	147.96	6965100000
16.8	39.503	0	20.547	496340000
17.5	62.832	0	21.03	1228200000
3.2	49.798	0	4.0994	67244000
42.2	50.113	0	319.08	73565000000
30.7	24.693	0	34.682	2536000000
33.8	31.293	0	67.039	1858700000
17.8	19.859	0.00043403	3.2945	80603000
39.6	50.06	0	88.619	5164200000
55.1	95.313	0	323.31	22863000000
30	54.952	0	70.472	5337200000
29.8	49.425	0	157.08	3717300000

20.8	26.999	0	19.789	535040000
5	92.612	0	9.9338	187510000
11.5	109.36	0	12.3	509680000
5.8	134.85	0	19.407	304630000
7.2	83.947	0	43.626	225600000
40.6	60.602	0	99.506	5381200000
74	61.174	0	323.31	91289000000
10.7	60.82	0	22.032	214290000
46.8	61.48	0	156.64	7917600000
25.4	36.108	0	13.206	531630000
11	51.065	0	9.7172	531720000
11.7	161.93	0	35.11	1880100000
7.2	91.369	0	9.5342	398090000
12	105.53	0	23.791	805110000
12.2	63.988	0	40.942	447820000
26.1	52.22	0	23.952	463820000
31.9	37.984	0	52.338	1951100000
7.2	35.638	0	4.4639	219090000
8	39.832	0	10.558	318010000
10	29.343	0	7.592	320400000
7.6	21.307	0	4.5533	257150000
13.6	42.516	0	62.679	651050000
24.1	46.153	0	97.639	5434300000
11.3	46.402	0	25.282	574090000
9.2	46.839	0	7.4801	627410000
13.9	68.839	0	101.05	1241400000
12.9	25.053	0	5.6181	295110000
4.6	174.58	0	19.148	640710000
13.7	97.893	0	14.792	464340000
38.6	25.186	0	24.883	1024000000
14.5	48.968	0	25.615	640680000
83.8	16.832	0	123.54	5225400000
26.4	36.169	0	32.078	937620000
4.7	32.677	0	18.215	864940000
7.2	111.29	0	11.086	316110000
12.6	23.348	0	5.2773	153110000
38.6	29.435	0	36.636	1513000000
27.9	70.733	0	91.195	3018300000
28.2	56.356	0	162.2	5525600000
28.1	55.262	0	60.763	3679700000
55.3	47.14	0	323.31	30832000000

3.7	47.296	0	7.5293	48377000
15	47.024	0	12.209	312260000
21.8	107.96	0	56.515	1605800000
8.7	103.08	0	11.149	305640000
10.6	98.661	0	15.632	497000000
2.4	47.903	0.00041806	2.8713	46553000
26.7	57.205	0	175.61	4164000000
31.1	54.319	0	147.67	13583000000
5.3	89.663	0	11.205	340320000
5.8	109.94	0	23.776	871010000
60.4	52.576	0	125.73	10303000000
17.3	62.515	0	26.425	593900000
1.7	60.211	0.0016181	2.4916	113680000
2.9	62.253	0	4.1722	163260000
4.9	723.3	0	6.3	158620000
16.3	170.08	0	69.325	2182600000
3.2	98.47	0	4.8461	95222000
3.3	82.228	0.00081599	2.5739	61385000
4.6	106.6	0	7.8899	202760000
0.9	154.33	0.00082068	2.6617	20517000
15.9	32.562	0	20.676	808270000
22.1	28.823	0	8.7953	631490000
33.5	46.852	0	29.727	1369200000
62.4	31.319	0	129.71	7202800000
32.6	121.55	0	236.98	10772000000
5.3	49.03	0	3.7753	291280000
62.8	35.009	0	240.11	26576000000
58.8	27.623	0	183.48	8324700000
21.1	68.09	0	74.429	2483800000
42.5	27.738	0	52.611	1279300000
1.1	103.96	0.003882	1.9335	37140000
3.8	94.128	0	12.522	256660000
23.5	83.206	0	48.334	2687600000
17.2	70.268	0	17.618	1221000000
24.1	14.819	0	11.571	821000000
75.8	14.65	0	123.85	7878700000
13.9	52.471	0	12.488	188770000
43.7	46.175	0	36.602	1812100000
9.5	61.012	0	40.142	470660000
7.6	121.64	0	13.601	141220000
40.3	102.65	0	207.43	5168200000

19.2	84.818	0	71.61	653500000
12.3	17.725	0	5.4276	474510000
5.3	46.942	0.0004344	3.2982	77331000
11	24.394	0	5.1809	203010000
2.7	39.593	0.0063886	1.5896	1975400000
3.3	55.055	0	33.535	136360000
2.8	45.349	0	3.6279	110990000
18.9	57.598	0	27.651	782690000
12.6	65.696	0	14.323	728540000
59.3	272.43	0	323.31	46198000000
18.6	6.6478	0	4.8061	1198000000
13.5	34.306	0	17.368	779990000
65.6	41.026	0	244.12	38703000000
5	78.032	0	14.852	308980000
2.9	75.283	0	5.5982	270510000
11.9	126.5	0	73.299	3419400000
42.2	50.193	0	323.31	1.6749E+11
43.3	312.3	0	323.31	2.3922E+11
1.2	313.82	0	36.564	485300000
4.7	33.676	0.00043821	3.4085	106710000
8.7	82.687	0	23.681	199530000
6.8	34.492	0	3.6207	50779000
9	40.092	0.0098289	1.3338	128910000
4.1	88.733	0	8.2892	110150000
12.7	40.581	0	9.9006	118570000
7.2	75.634	0	30.153	401020000
11.6	42.712	0	3.6232	100020000
49.2	61.325	0	323.31	19138000000
68.2	54.752	0	323.31	33474000000
15.5	17.417	0	5.4781	192550000
57.6	49.391	0	323.31	38879000000
4.4	48.95	0	5.2515	42284000
57.4	50.052	0	207.19	10889000000
69.6	31.888	0	288.52	29411000000
35.3	31.794	0	33.973	651950000
12.2	101.85	0	63.39	1384100000
27.6	17.008	0	124.66	2420300000
5.3	64.697	0	7.462	352200000
8.6	15.344	0	4.2006	318990000
11.2	25.147	0	5.8925	116730000
12	51.572	0	14.072	683570000

12.5	62.995	0	11.744	479330000
18.6	144.8	0	94.22	3408100000
73.7	281.22	0	323.31	9.9382E+11
21.5	277.82	0	259.32	5437000000
24.5	47.513	0	33.227	901760000
23.7	41.658	0	29.172	1248100000
3.4	111.28	0	10.292	123440000
28.2	59.914	0	51.494	2872300000
60.4	60.974	0	296.97	32521000000
16.7	60.515	0	33.319	700870000
29.3	43.054	0	143.18	3711800000
3.4	47.18	0	4.2865	83026000
51.7	272.53	0	323.31	1.5461E+11
15.4	44.013	0	13.115	254450000
2.4	84.573	0.0060514	1.6473	104010000
1	339.09	0.006056	1.6612	1527700000
11.4	34.554	0	18.581	315270000
57.7	21.066	0	35.711	2532400000
7.3	16.564	0.00042337	3.0009	134850000
7.9	52.673	0	15.763	520020000
6.5	60.815	0	19.351	317680000
13.8	51.828	0	26.303	1036500000
13.6	50.784	0	4.9123	216640000
37.7	59.262	0	92.82	2082800000
3.1	106.25	0	6.5392	130610000
14.5	13.918	0.0049751	1.7295	30611000
1.8	138.34	0	26.992	74765000
30.4	42.295	0	44.478	1408500000
4.7	37.798	0	10.923	116910000
20.8	26.336	0	8.1545	275830000
34.3	106.91	0	152.82	5591500000
69.1	35.81	0	323.31	1.414E+11
4.5	81.877	0.00042937	3.1672	211590000
10.5	107.5	0	18.874	528190000
25.3	32.932	0	39.603	563520000
8.8	80.363	0	11.818	321140000
12.9	66.739	0	33.077	497700000
42.9	53.6	0	160.91	6132600000
4.3	44.93	0	6.4351	86551000
4.8	48.605	0	4.5379	160980000
6.5	293.02	0	38.1	549530000

44.7	50.521	0	106.12	4575800000
58.2	50.537	0	313.78	16988000000
3.7	87.194	0	6.9336	55113000
10.5	26.778	0	9.427	156470000
9.1	24.554	0	6.8303	57798000
1.8	85.299	0	5.8461	235370000
2.5	78.765	0	5.8592	251260000
12.2	133.73	0	36.054	1299300000
54.9	20.809	0	39.745	5555000000
25.8	32.409	0	20.701	1242000000
23.4	11.871	0	12.446	1177200000
12.4	23.689	0	13.07	312150000
55	61.336	0	226.02	11416000000
30	42.119	0	77.76	1006000000
9	59.715	0	16.165	284200000
23.9	16.723	0	8.828	260180000
8.8	46.244	0	5.8217	256160000
13.6	39.916	0	15.426	560270000
8.1	76.723	0.0038775	1.9023	158010000
8.4	42.024	0	30.181	1592200000
9	44.054	0	7.4714	207070000
4.2	40.361	0	6.7526	228120000
31.5	40.489	0	166.12	6186700000
0	40.036	0	33.117	879390000
8.8	40.084	0	8.5384	80267000
18.7	42.158	0	51.492	1647800000
27.1	44.265	0	18.722	1730400000
29.7	37.377	0	109.36	1756200000
31.8	37.331	0	145.82	4418500000
50.5	35.076	0	89.344	3459000000
14.4	37.379	0	12.655	206800000
8.8	30.913	0	4.5619	118320000
6	20.791	0.000818	2.602	87819000
2.6	110.05	0	3.9887	77137000
11.2	39.661	0	26.043	319800000
18.4	24.725	0	10.918	54861000
60.2	47.411	0	226.26	12748000000
11.3	63.467	0	62.789	192690000
5.2	62.586	0	6.2954	161760000
63	37.572	0	212.85	6910700000
21.9	34.634	0	35.446	2369100000

53.8	80.953	0	198.43	9884800000
50.9	62.766	0	323.31	38713000000
3.5	63.675	0.0094787	1.3574	42810000
9.3	53.442	0	8.2902	123310000
74.6	22.329	0	111.11	9034200000
32.3	25.424	0	41.832	11566000000
6.5	19.522	0	3.7634	328910000
9.1	21.061	0	3.8972	244400000
35.5	25.238	0	11.809	480050000
36.9	35.328	0	107.15	4078400000
10.5	63.458	0	20.423	891020000
14.3	24.307	0	7.2867	127640000
3.5	51.66	0	4.9264	100980000
6.9	46.71	0	8.0968	207250000
2.3	85.941	0	323.31	33662000000
1.2	80.762	0.00082576	2.7561	417970000
21.9	51.073	0	24.785	1007700000
7.2	52.246	0	8.9633	209520000
5.4	25.36	0.0031596	2.1598	96788000
48.2	25.704	0	31.433	1224300000
57.8	25.716	0	93.383	17334000000
24.6	26.635	0	11.54	438180000
12.8	25.709	0	5.9021	298300000
16.7	27.497	0	25.998	387250000
63.3	23.609	0	323.31	47664000000
64.6	27.374	0	94.909	4490900000
20.9	27.634	0	7.2704	334830000
41.7	24.275	0	50.524	746150000
6.8	106.05	0	12.933	182900000
38.5	77.587	0	82.066	4457300000
25.5	70.597	0	65.366	1628600000
24.7	34.47	0	26.89	442590000
30.6	37.402	0	24.597	413790000
3.3	83.926	0	3.8567	111290000
27.8	20.861	0	23.31	10305000000
14.5	28.093	0.00042845	3.1591	18642000
14.1	40.836	0	22.396	1014300000
16.3	41.301	0	6.9868	146560000
15.1	37.251	0	7.8413	291620000
46.9	13.509	0	82.267	5612700000
33.6	39.289	0	133.5	8727900000

12.1	40.092	0	6.2688	583290000
23.5	15.328	0	105.45	96672000000
13.2	88.927	0	11.14	380030000
62.4	34.463	0	302.99	19682000000
62.9	82.669	0	323.31	48147000000
67.6	51.386	0	305.17	23328000000
8.8	28.901	0	5.5203	199290000
14.5	9.352	0.00043422	3.2974	236390000
22.8	40.477	0	24.497	1015800000
13.9	57.432	0	5.0734	522820000
6.1	31.654	0	8.9603	57921000
65.5	15.085	0	270.52	4.526E+11
58.5	15.84	0	323.31	5.5827E+11
21.8	15.878	0	36.843	1140800000
6.8	16.494	0.0031571	2.1513	146040000
3.8	210.43	0	28.615	348220000
1.8	55.302	0.0004386	3.4115	219770000
7.2	26.268	0	9.4911	474020000
23.8	22.43	0	35.251	960890000
35.1	28.73	0	19.584	710560000
11.4	141.74	0	31.59	1002300000
9.8	60.612	0	10.331	181760000
1.9	61.115	0.0035006	1.9446	47237000
4.4	86.014	0	4.4582	62634000
40.3	35.44	0	156.75	3338600000
39.5	43.037	0	51.357	1546300000
23.2	10.425	0	13.3	121430000
72.2	13.777	0	97.196	6332300000
39.9	17.32	0	10.869	763670000
16	115.2	0	46.819	944900000
19.2	21.785	0	9.9724	551540000
10.3	22.576	0	7.609	1140300000
14.2	21.266	0	54.657	16895000000
7.2	22.099	0	5.2574	223300000
13.2	21.977	0	17.024	10937000000
36.2	14.135	0	41.369	821440000
49.2	13.992	0	81.232	1.7456E+11
23.5	15.404	0	72.944	25703000000
23.5	15.388	0	131.15	1.1843E+11
58.3	11.367	0	248.99	1.4573E+11
5.4	14.013	0.0023981	2.3097	334230000

14	13.988	0	240.18	1.8844E+11
24	102.3	0	173.32	6911800000
12.4	102.53	0	102.55	1684800000
11.3	37.78	0	10.3	143670000
33.5	24.893	0	96.77	14384000000
7.6	24.162	0.00042753	3.1424	333090000
28.3	34.238	0	21.358	329590000
10.8	56.822	0	7.2962	327110000
14.4	9.4226	0.00122	2.541	138190000
5.7	45.343	0	3.9694	240450000
17.8	35.738	0	11.538	186520000
9.2	30.53	0	3.8985	84518000
27.2	34.196	0	38.169	785790000
57.8	32.46	0	195.92	6186500000
45.1	37.086	0	119.2	7079900000
24.6	30.831	0	21.111	2322800000
18.2	32.223	0	10.328	709490000
20.9	30.777	0	31.905	3519600000
15.6	33.558	0.00043687	3.3584	240580000
20.7	45.729	0	39.626	1082400000
10.2	49.199	0	156.35	2636800000
3.8	49.279	0	17.85	410020000
35.4	50.976	0	202.04	12238000000
30.4	63.963	0	113.23	4188400000
8.1	64.124	0	5.1972	205050000
25.9	73.74	0	58.987	3827700000
35.2	87.917	0	210.4	10848000000
7.8	85.045	0	6.3159	524300000
15.2	84.939	0	31.299	852850000
5.7	83.217	0	15.97	122830000
2.8	31.363	0.006391	1.5938	35775000
8.4	38.752	0	8.0057	33606000
29.4	59.548	0	79.734	5989200000
10.4	22.338	0	5.8957	283480000
18.8	24.57	0	7.3663	414640000
49.1	51.317	0	87.556	5183700000
25	8.6107	0	32.211	224760000
6.5	32.364	0	3.7566	92429000
41	27.418	0	110.15	7599000000
20.5	34.741	0	20.761	1482100000
19.2	54.208	0	24.114	311710000

26.7	84.787	0	269.02	7963600000
35.1	83.28	0	323.31	26927000000
39.5	92.475	0	323.31	18264000000
8.4	74.87	0	12.396	400420000
16.8	76.118	0	56.173	1312600000
4.2	70.078	0	205.47	14381000000
4.4	70.175	0	7.6628	628000000
28	69.641	0	78.173	3461300000
32.9	94.132	0	163.73	5519400000
5.6	92.251	0	6.3583	406440000
47.3	72.421	0	279.25	21077000000
32.5	70.87	0	323.31	63657000000
31.8	73.46	0	141.51	6537500000
80.4	23.014	0	323.31	30193000000
53.1	17.521	0	95.623	2125300000
53.8	18.634	0	44.725	1064500000
18.9	21.533	0	12.954	573100000
61.8	60.955	0	318.46	26059000000
50.6	398.29	0	323.31	3.5945E+11
19.5	91.696	0	95.256	1039500000
31.7	51.213	0	60.959	6885800000
3.6	480.89	0	27.362	381600000
20.3	111.18	0	53.036	2329300000
18.5	27.974	0.00042517	3.0648	129630000
1.2	144.27	0.0008261	2.7579	105250000
20.1	112.8	0	73.8	2267800000
4.3	58.752	0	4.2861	75292000
2.5	31.39	0.000429	3.1641	103540000
5.8	117.77	0	20.483	179450000
31.9	46.674	0	81.964	4297700000
39.8	50.906	0	142.62	17063000000
44.8	39.638	0	192.45	21477000000
43	42.785	0	99.818	3796500000
11.5	31.875	0	7.4922	135610000
3.8	38.97	0	3.9435	96861000
3.2	66.959	0.0046065	1.762	47525000
6.3	25.346	0	30.495	273210000
42.7	28.969	0	112.28	10965000000
15.2	36.587	0	21.502	1088900000
3.1	35.704	0.0027767	2.2296	89933000
53.3	11.934	0	33.362	1639100000

11.9	38.476	0	6.0116	95696000
2.1	86.689	0	7.6181	97024000
13.1	43.062	0	11.292	472900000
6.6	78.092	0.0023895	2.27	214720000
9.7	42.812	0	5.7421	85970000
37.9	78.727	0	133.99	6812000000
18.8	30.436	0	15.015	1011500000
4.3	137.49	0	23.883	320710000
51.5	29.459	0	95.219	1742900000
8.6	43.346	0	22.877	612550000
1.6	117.94	0	4.909	35146000
2.6	119.27	0	7.4106	82482000
20.7	123.59	0	171.97	1753400000
11.5	119.49	0	31.059	743160000
4.4	116.05	0	9.7135	124060000
39.7	188.74	0	323.31	15468000000
3.7	80.564	0.0035239	2.04	3664100000
11.8	17.897	0	5.4986	104330000
20.8	45.614	0	16.086	4954100000
4.7	32.032	0.0064006	1.6064	69863000
54.9	22.417	0	179.91	3928300000
14.5	60.931	0	17.779	332270000
1.2	98.992	0.0035419	2.0858	21225000
5.3	130.81	0	16.981	498940000
18.4	112.68	0	93.602	925710000
15.4	116.74	0	47.077	1987900000
14.2	115.04	0	38.095	1676100000
3	119.6	0	10.71	86160000
43.8	117.55	0	323.31	34651000000
11.8	114.41	0	48.918	1523100000
20.1	115.36	0	103.92	5425400000
41.6	88.231	0	323.31	50735000000
15.1	86.738	0	18.829	1304400000
16	87.908	0	58.687	2146200000
1.1	86.041	0.0087719	1.3834	3060200000
20	101.07	0	79.156	2774000000
10.7	105.93	0	21.2	623480000
12.2	104.66	0	43.381	808270000
38.9	21.897	0	40.392	712390000
8.3	306.86	0	113.14	2755800000
1	304.27	0	5.0325	238790000

34.4	46.325	0	162.75	3156700000
3.6	133.37	0	13.917	240180000
7	74.691	0	30.964	535880000
5.1	81.8	0	23.87	154900000
30.7	90.244	0	114.92	4275500000
18.7	67.839	0	27.857	555820000
2.9	46.13	0.00043898	3.4168	690390000
10.5	32.136	0	23.277	226800000
10.4	7.5938	0.0087944	1.3966	2727200000
16.9	57.685	0	24.384	909840000
9.3	35.955	0	4.7466	139010000
8.8	48.37	0	14.235	409290000
13.4	76.775	0	39.626	1017400000
2.4	134.11	0	4.6951	157340000
1.7	195.81	0	11.664	204430000
2.7	80.169	0	11.931	93452000
0.9	117.02	0.0053558	1.7276	611600000
9.3	109.55	0	54.287	967760000
13.5	61.449	0	32.288	400010000
28.1	28.742	0	30.688	292270000
1	429.36	0.0034992	1.9438	266780000
23.8	47.898	0	98.386	2325600000
19.6	57.922	0	54.265	1060600000
7.3	59.964	0	31.681	702830000
34	21.482	0	14.658	484180000
7.3	52.862	0	323.31	5664200000
8.3	54.628	0	36.336	271730000
12.6	17.919	0	20.464	439010000
59.3	16.241	0	49.27	231480000
66.1	6.6882	0	36.816	197040000
17.3	10.271	0	5.967	82138000
98.9	9.5155	0	69.41	5016700000
3.4	143.2	0	7.1972	111420000
4.8	37.804	0	4.4849	23249000
6.6	32.754	0	3.5773	173110000
10.7	343.81	0	93.16	1383300000
18.9	201.82	0	290.61	9407500000
30.4	404.05	0	323.31	26448000000
3.5	197.09	0	12.089	804000000
52.1	196.58	0	323.31	49509000000
39.4	177.3	0	323.31	24334000000

6.4	43.865	0	8.4082	194190000
6.5	45.655	0	6.7368	702770000
23.6	17.749	0	8.5039	205800000
22	9.6418	0	11.613	96251000
10.9	50.777	0	14.356	235750000
28.5	52.75	0	81.372	1229600000
0.8	134.19	0.0053537	1.7276	52072000
22.1	29.994	0	25.606	664140000
19.5	70.148	0	28.923	583410000
43.7	70.75	0	156.04	7437800000
69	36.498	0	237.49	18124000000
56.6	36.572	0	183.59	5056900000
3.3	37.225	0.00042553	3.08	378470000
12.5	57.506	0	28.954	548150000
4.8	81.7	0	14.264	83425000
30.4	82.988	0	100.86	1893000000
39.1	31.627	0	48.487	561530000
86.7	14.866	0	288.13	94709000000
27.3	27.515	0	18.872	999750000
7.1	49.372	0	12.622	247830000
4.6	81.286	0	3.6418	4344200000
4.6	100.67	0	12.59	469380000
40.6	37.24	0	61.232	4535600000
33.4	39.031	0	48.526	2965600000
8.6	45.325	0	9.4756	124330000
29.9	83.347	0	77.319	1749000000
12.2	57.788	0	42.814	1224000000
11.7	40.429	0	9.4525	428040000
54.2	40.996	0	231.47	13155000000
2.8	79.996	0	5.0375	293510000
62.4	74.237	0	323.31	66989000000
25.9	66.785	0	223.44	5925000000
14.1	67.317	0	39.149	1641000000
29.7	66.309	0	85.106	9977100000
6.1	117.3	0	16.938	755070000
16.6	105.84	0	60.64	1283100000
47.8	66.506	0	277.22	30806000000
6.4	83.739	0	5.299	234260000
3.6	53.109	0	3.5324	63271000
61.8	65.89	0	323.31	78388000000
11.4	504.74	0	156.85	7243400000

9.2	42.215	0	12.293	685390000
19	156.61	0	79.098	2149600000
25.1	51.851	0	91.709	7338200000
2.1	39.06	0.0070475	1.4974	432270000
7.8	68.075	0	10.999	803510000
2.7	71.991	0.0027745	2.2276	273530000
29.6	34.877	0	48.694	2381500000
10.2	71.302	0	46.213	1017800000
7.8	11.845	0.005723	1.7164	112450000
20.9	9.9374	0	3.4371	92892000
24.3	11.636	0	30.182	418970000
31.3	69.05	0	148.78	4235400000
21.8	153.18	0	141.67	10944000000
2	195.83	0.00043478	3.3138	282010000
5	134.36	0	8.2802	419430000
40.6	171.3	0	323.31	45626000000
3.4	38.611	0	3.9091	34584000
3.2	51.45	0	53.25	271750000
29.9	38.265	0	319.47	1.3182E+11
17.6	25.492	0	23.982	1270500000
15.7	14.377	0	7.8344	257140000
13.7	14.192	0	4.4497	377140000
63.8	23.367	0	118.96	3038800000
33.3	24.794	0	64.718	874990000
10.5	10.391	0.00043745	3.3863	32755000
19.4	31.172	0	29.174	920270000
1.1	831.87	0	25.172	893100000
30.7	35.294	0	36.916	1429500000
8.1	115.69	0	34.374	468550000
9.5	20.373	0	6.9	746460000
6.5	59.601	0	32.635	435530000
31.9	58.557	0	78.235	2659800000
5.3	300.14	0	43.73	1569900000
12.2	270.25	0	144.08	7097600000
11.6	14.272	0	3.5532	515510000
11.2	14.617	0	5.1098	702570000
2.6	102.94	0	6.5594	182910000
26.7	43.474	0	42.102	863170000
9.9	35.836	0	5.324	84738000
8.1	44.113	0	5.1753	170280000
0.5	146.41	0.0081061	1.4339	210140000

23.8	113.65	0	63.902	2739400000
11.4	32.803	0.00082102	2.6628	199490000
41.6	41.275	0	69.159	1807200000
15.5	32.327	0.00043178	3.2317	99126000
22.1	43.066	0	25.034	570380000
10.7	36.07	0	25.529	421780000
5.1	101.43	0	3.9072	104380000
4	19.086	0.0063934	1.5943	138720000
6.6	43.688	0	5.8935	97217000
21.2	94.629	0	295.55	2929600000
52.6	17.069	0	46.722	477240000
5.6	25.45	0.00042176	2.9705	32261000
16.3	25.396	0	15.16	501200000
4.1	25.957	0.00041754	2.845	37736000
3.2	36.975	0	12.885	818600000
4.7	53.435	0	9.0025	82986000
41.5	21.502	0	76.781	954490000
16.2	79.343	0	21.758	1020100000
19.9	61.378	0	78.845	941660000
27	19.017	0	7.5184	252140000
4.8	16.168	0.0045977	1.7376	121400000
57.1	2.3277	0.0035211	2.0199	104720000
37.4	27.203	0	46.761	4650800000
20.4	23.901	0	14.571	323200000
44	36.511	0	156.46	10138000000
63.6	35.611	0	220.34	28312000000
36.6	18.582	0	27.535	347110000
59.3	63.953	0	236.53	5307400000
19.2	52.307	0	13.873	1051600000
56.3	40.342	0	101.17	1318600000
1.1	164.72	0.0063814	1.5754	67845000
20.5	33.692	0	5.2969	221190000
3.6	52.921	0	12.777	150970000
20.8	20.578	0	5.306	1033800000
50.2	28.937	0	164.71	48863000000
30.5	18.538	0	17.545	2625600000
55.4	47.169	0	272.33	25578000000
6	68.937	0	4.097	153190000
23.1	12.359	0	31.032	679190000
40	17.551	0	34.23	762150000
24.8	16.958	0	7.7037	185410000

12.1	108.69	0	40.99	545220000
4.3	110.07	0	5.4242	531490000
8.2	55.721	0	3.9843	85605000
71.3	12.504	0	77.053	7177400000
42.1	8.5669	0	47.791	820960000
5.5	32.342	0	3.5043	157700000
9.9	45.932	0.00042463	3.0467	86177000
16	14.677	0.0067365	1.562	29163000
3.4	97.458	0	10.547	97491000
2.4	60.235	0.0077634	1.4743	391490000
5.8	91.83	0	4.5659	88478000
13.8	6.6979	0.0027734	2.2205	756410000
54.1	12.454	0	177.34	1417800000
37	14.286	0	18.685	2285000000
17.8	52.227	0	20.409	348910000
8.4	33.097	0	6.7839	184820000
24.6	27.621	0	34.138	2334600000
10.7	164.98	0	48.707	1164600000
3.9	167.07	0	20.542	220740000
9.6	38.522	0	18.355	270830000
7.6	39.41	0	8.4501	281190000
6	21.708	0.0080972	1.4322	134280000
56.9	11.101	0	26.731	1042800000
6.1	93.191	0	36.735	412730000
42.6	67.766	0	323.31	33981000000
20.7	21.55	0	9.4935	253640000
34.4	26.832	0	21.607	1236100000
47	31.062	0	42.111	1946800000
26.6	38.194	0	25.14	719800000
14.9	7.7662	0	7.6851	1789000000
44.9	33.499	0	152.04	5292600000
44.9	25.976	0	125.57	16372000000
15.6	31.726	0	8.4062	247440000
14.3	101.2	0	28.847	915400000
6.6	105.73	0	17.633	216060000
4.4	51.881	0	5.0315	62643000
5.4	68.474	0	4.955	140890000
2	288.79	0	5.7765	123330000
64.4	12.861	0	60.624	4433200000
9.5	35.623	0	5.7649	75017000
26.6	29.758	0	56.191	905030000

19.7	165.3	0	212.05	7244200000
9.4	82.843	0	14.325	454600000
25.2	95.923	0	89.4	3174000000
13.4	35.284	0	37.042	579430000
10.4	152.04	0	68.577	916260000
19.4	11.97	0	5.24	166060000
6	28.683	0	5.5162	80750000
5.3	42.722	0.00042662	3.11	103360000
34.1	228.99	0	323.31	31431000000
0.6	227.03	0	323.31	7.6441E+11
0.6	223.26	0	18.994	277080000
1.3	227.76	0.00042159	2.9685	3226100000
11	222.86	0	323.31	4766000000
29.4	226.37	0	323.31	13723000000
75.5	20.594	0	127.24	3569900000
18	19.779	0	45.918	4746400000
17.9	16.93	0	320.72	1.2027E+11
47.1	19.854	0	323.31	52355000000
12.5	113.7	0	323.31	38499000000
1.9	194.04	0.00043783	3.4032	100390000
2.4	118.69	0.0031521	2.1124	87084000
46.5	121.94	0	323.31	29376000000
15.9	116.08	0	35.299	1031100000
1.4	222.44	0.0074019	1.4809	115270000
14.6	233.32	0	78.299	4024100000
16.3	33.471	0	11.015	253290000
7.7	12.374	0.0016155	2.4559	19349000
19	34.995	0	13.237	567200000
12.2	36.595	0	29.453	5712700000
14.8	36.875	0	37.416	480370000
40.1	36.228	0	12.708	867510000
16.4	11.95	0	34.215	267080000
13.6	22.983	0	5.8996	140030000
1.3	100.96	0.0004268	3.1138	58976000
13.9	82.8	0	19.371	798160000
19.1	23.384	0	23.727	634210000
3.7	60.273	0	6.1254	117930000
14.7	47.234	0	27.059	496770000
20.8	55.446	0	24.484	750800000
14.8	45.345	0	18.611	1315400000
24	42.679	0	42.475	993030000

13.6	33.189	0	13.477	555000000
9.9	58.265	0	9.839	220340000
5.4	64.279	0	18.008	389840000
10.4	22.245	0	6.5691	139890000
12.1	80.405	0	29.927	1566500000
6.9	45.739	0.0016207	2.5108	203850000
17.2	118.52	0	44.989	882860000
13.7	76.722	0	97.494	3040400000
3.7	62.907	0	9.3234	173150000
31.5	43.008	0	76.691	1787100000
51.3	39.28	0	155.07	3915500000
14.3	8.1384	0.00042772	3.1432	94808000
51.5	40.603	0	72.178	3424000000
24.1	14.982	0	4.8396	163190000
52.4	17.086	0	25.608	1069100000
23.6	16.859	0	11.055	886490000
25.3	10.916	0	7.0944	234200000
50	9.3308	0	7.2953	607400000
68.3	9.3267	0	28.156	2915200000
50.9	13.36	0	12.681	303280000
33.6	15.283	0	15.786	855870000
57	19.992	0	56.41	2344600000
48.5	42.525	0	82.792	2166200000
8.1	20.082	0	9.7874	90473000
6.5	42.524	0	3.7244	28264000
47.4	6.954	0	18.081	1407100000
30.1	21.024	0	53.093	1004800000
33.7	11.692	0	7.2229	362050000
38.8	15.081	0	30.525	803790000
16.9	21.71	0	7.9939	210470000
32	15.515	0	7.1233	238260000
14.6	16.331	0	9.7686	427680000
31.3	21.984	0	14.752	943290000
50.8	14.164	0	57.679	1129400000
45.9	79.776	0	171.34	4432900000
24.8	52.625	0	69.062	3000000000
42.6	30.149	0	65.742	1815500000
29.7	19.784	0	21.527	783270000
41.5	12.648	0	27.959	1062700000
60.3	13.02	0	26.351	493340000
26.8	24.683	0	30.707	775130000

17.9	24.038	0	27.041	1505700000
39.7	50.834	0	65.787	3118900000
27.4	27.285	0	26.196	863460000
27.9	11.813	0.0070423	1.4943	57891000
25.6	31.113	0	22.704	339550000
16.2	102.71	0	71.412	2849000000
17.3	8.9723	0	9.5619	912830000
13.7	95.915	0	71.902	268290000
1.7	66.275	0.0042487	1.8597	2600100000
4.1	201.77	0	24.355	318440000
1.6	72.107	0	4.6751	250700000
2.6	47.471	0.0035294	2.0459	68944000
6.5	47.775	0	13.191	104810000
12.8	44.637	0	21.283	295290000
9.4	28.567	0.00042608	3.1009	193220000
12.1	71.415	0	19.523	219440000
50	14.173	0	23.827	515480000
32.5	136.54	0	214.84	10405000000
12.2	153.91	0	77.896	2327700000
8	41.745	0	9.8897	157190000
13.2	16.555	0	21.747	356660000
32.4	31.886	0	25.085	732880000
33.3	30.501	0	52.336	70507000000
8.6	107.83	0	16.752	236710000
35.5	17.208	0	19.433	739640000
42.8	17.363	0	100.64	11413000000
23.1	19.099	0	5.5375	57244000
10	34.376	0	9.8887	106640000
11.3	56.888	0	18.758	632670000
28.4	113.84	0	105.42	4012400000
25.8	54.54	0	131.97	1571700000
12.3	60.342	0	16.113	251650000
20.1	38.928	0	21.44	718980000
6.1	55.939	0	27.324	375550000
23.2	103.32	0	87.712	1948200000
29.8	32.56	0	78.436	2034500000
3.4	67.061	0	198.52	18017000000
2.5	64.944	0	28.95	453550000
17.7	30.821	0	13.71	1480800000
31	30.959	0	42.262	924710000
18.2	26.248	0	11.963	422280000

15.9	82.613	0	37.691	803290000
15.4	40.709	0	26.353	459850000
36.5	23.076	0	119.43	1301600000
6.2	63.864	0	5.7513	210410000
16.6	67.81	0	24.582	1391200000
16.6	53.408	0	25.642	734550000
6	50.304	0	4.8178	162780000
9	38.358	0	11.593	636610000
9.1	18.593	0.0057186	1.7105	145150000
12.3	21.825	0	3.5897	159030000
5	35.693	0	8.9773	46732000
33.5	26.24	0	15.011	630740000
2.2	35.197	0.0053476	1.725	660610000
5.8	18.648	0.00042391	3.0135	23457000
5.6	235.63	0	8.5613	343860000
4.6	128.62	0	5.6426	190920000
3.6	155.12	0	11.187	107750000
2.1	94.529	0	4.9092	34214000
9.5	93.28	0	13.388	168480000
70.9	14.478	0	133.79	3131600000
0.9	203.07	0.0060675	1.6698	977790000
64.7	48.354	0	180.85	7200600000
22.2	20.848	0	7.4642	139020000
52.9	116.45	0	323.31	24421000000
43	34.012	0	323.31	1.3698E+11
27.5	44.729	0	45.782	2347100000
4	49.745	0.0077691	1.4775	2584500000
20	111.34	0	75.463	1502000000
11.6	23.895	0	7.6609	289420000
8	61.67	0	34.802	472040000
4.9	83.628	0.00043516	3.3181	65219000
5.1	96.965	0	18.455	309320000
3.1	71.527	0	5.6757	125070000
8.1	16.815	0	3.7166	595770000
29.3	23.782	0	22.857	1264100000
28	31.27	0	40.722	2014200000
59	55.988	0	323.31	11647000000
5.1	58.213	0	7.8291	382380000
49.3	57.058	0	255.32	12200000000
19.7	37.971	0	14.284	731850000
20.3	70.67	0	39.645	2425100000

5.5	31.044	0	7.6269	163710000
10.3	55.832	0	32.2	1300300000
16.8	46.67	0	13.267	405330000
31.4	25.581	0	54.457	1709900000
20	47.006	0	20.496	640640000
19.8	57.93	0	15.805	868510000
2.6	41.614	0.0035405	2.0819	189730000
3.2	55.446	0.0064127	1.6149	84178000
4.1	138.9	0	9.4414	257560000
10.5	70.35	0	10.901	232810000
84.1	20.021	0	228.22	14904000000
3.9	79.916	0	13.451	85397000
17.6	59.452	0	29.369	790510000
42.7	42.329	0	99.888	6954700000
9.3	41.669	0	15.949	103280000
27	30.944	0	74.527	2045100000
1.2	183.66	0.003528	2.045	28103000
20.6	81.163	0	138.92	2436800000
25.1	129.68	0	167.15	6119000000
42.7	37.497	0	110.89	5588300000
22.4	34.917	0	27.795	1746900000
19.3	79.921	0	60.624	953710000
27.9	58.408	0	55.298	1351700000
29.2	70.527	0	65.233	1173000000
61.2	24.634	0	110.01	2066200000
11.5	56.494	0	18.915	380920000
5.1	54.874	0	9.6084	151790000
6.5	41.666	0	4.6546	47956000
23.1	24.715	0	16.604	647220000
37.3	14.275	0	41.401	877840000
55.6	21.663	0	39.067	2311500000
37.9	96.023	0	171.74	5475100000
15.5	23.277	0	6.8154	110690000
10.3	124.51	0	64.268	1157200000
2.4	98.406	0	8.5355	219720000
8.7	122.8	0	14.335	599000000
50.5	43.231	0	192.57	5102400000
64.6	38.937	0	137.86	7622500000
8.4	53.998	0	7.7257	220620000
54.5	56.678	0	323.31	27091000000
25.1	71.982	0	61.893	2465000000

10.8	59.266	0	9.6797	220090000
29.3	48.1	0	107.8	3623300000
11.3	46.04	0	12.221	120140000
6.7	47.922	0	6.5476	793460000
83.5	35.774	0	323.31	21163000000
80.4	34.299	0	315.54	9836600000
45.5	35.556	0	114.1	2918800000
1.7	61.18	0.00082372	2.7182	80962000
3.2	150.33	0.00043141	3.2149	61518000
3.7	164.42	0	8.7775	401390000
4.9	78.542	0.000819	2.6129	130500000
38.8	35.015	0	38.956	1144300000
36.9	15.054	0	17.86	1028000000
89.3	20.83	0	189.7	16940000000
11.3	69.823	0	11.371	535620000
2	55.028	0.00043159	3.2235	124320000
14.5	22.774	0	8.0629	109880000
2.2	66.805	0	4.1485	32469000
28.6	11.243	0	17.785	1585800000
16.9	16.534	0	26.816	374120000
33.1	17.356	0	32.987	387740000
26.8	14.454	0.0023847	2.2503	226960000
21	85.359	0	64.785	1593300000
19.1	85.268	0	64.533	1627100000
22.2	85.454	0	221.12	4594600000
63.4	28.832	0	157.17	11830000000
53.2	53.247	0	107.51	3751800000
65.9	44.55	0	235.17	12683000000
83.7	27.254	0	173.37	7195300000
42	61.417	0	138.01	6443600000
2.9	68.747	0.00043048	3.1931	89233000
7.7	59.452	0	7.3891	154390000
63.5	62.219	0	323.31	48992000000
18.1	34.54	0	11.813	697340000
36.4	21.694	0	31.59	2166300000
6.5	23.334	0	6.277	339810000
64	29.82	0	144.81	5776000000
32.8	33.296	0	46.794	2406300000
4.7	56.585	0	5.5411	71166000
4.5	32.517	0.0070579	1.5047	51149000
51.9	29.15	0	49.877	2475600000

2.5	237.04	0	21.882	317550000
31.3	64.647	0	156.28	4082400000
7.9	61.71	0	6.9077	123110000
9.1	18.37	0	6.4238	233560000
2.2	46.151	0.0067416	1.5654	33659000
4.1	32.066	0.0023828	2.2401	51076000
18.8	31.893	0	42.574	1000100000
8.5	31.487	0	5.6513	191680000
9.2	112.84	0	14.869	566130000
9.4	57.844	0	323.31	69451000000
8.3	57.984	0	37.514	7114700000
2.1	104.41	0.00042735	3.128	85396000
10.4	85.221	0	54.811	623750000
3.3	133.33	0.00042265	2.9869	141260000
7	139.49	0	30.797	419720000
42.3	85.872	0	125.82	4715000000
18.9	533.5	0	323.31	12567000000
29.1	90.807	0	74.004	2763500000
54.9	55.595	0	271.12	8166300000
29.5	47.262	0	88.425	1930300000
48.3	139.41	0	282.98	8999300000
17.8	16.607	0.00042827	3.1526	401440000
61.3	70.741	0	323.31	30431000000
4.4	31.802	0	3.5141	170710000
2.3	59.616	0.00043917	3.4198	115410000
4.1	206.23	0	16.481	311640000
1.5	93.262	0.00043937	3.4261	90746000
10.9	58.278	0	25.934	836080000
1.5	82.435	0	4.7599	90448000
31.8	32.277	0	40.226	1302600000
23.6	68.717	0	23.464	793460000
6.8	49.429	0	5.35	137710000
6.9	46.379	0	11.802	146710000
8	17.143	0	3.6275	184740000
16.1	39.565	0	7.726	107020000
39.3	39.351	0	60.972	2323300000
27.6	77.043	0	52.977	2396400000
1.7	87.098	0.00042499	3.0598	978170000
26	32.667	0	38.081	1359200000
28.5	38.114	0	18.452	746290000
74.4	17.971	0	309.55	85419000000

43.5	23.713	0	61.234	5868300000
19.7	40.742	0	15.473	648060000
1.1	204	0	5.2147	228380000
5.1	42.888	0.00042248	2.9835	98181000
11.9	42.256	0	11.175	364130000
11.5	37.54	0	11.612	475650000
40.7	37.186	0	259.9	12795000000
4.3	36.983	0	6.3919	82346000
20.1	111.81	0	150.28	9416000000
2.4	109.05	0	11.159	488510000
7.3	84.684	0	19.555	310680000
36.7	16.649	0	59.125	4231400000
28.3	41.291	0	59.983	1174300000
32.7	35.608	0	53.639	1830500000
34.8	65.322	0	219.46	10591000000
11.9	51.691	0	35.226	717800000
50.8	36.71	0	54.082	2058500000
7.8	56.346	0	8.4112	158380000
12.6	52.817	0	18.379	382640000
4.3	35.159	0.002004	2.3458	101350000
2.8	56.752	0	4.0598	26807000
22.2	34.49	0	34.706	684690000
16.9	19.478	0	7.3057	298080000
62.3	22.176	0	126.06	20435000000
78.3	21.778	0	128.55	7452700000
38.1	28.127	0	41.218	2210800000
38.7	31.052	0	52.991	3196600000
74.7	17.015	0	135.57	9311100000
62.9	24.87	0	303.85	10994000000
48.1	43.292	0	323.31	1.0067E+11
9.4	80.751	0	19.059	347460000
14.7	63.928	0	15.152	426710000
7.6	39.802	0	9.6618	477640000
5.8	37.52	0	28.624	600340000
22	43.185	0	31.737	976600000
10.2	45.389	0	33.394	418340000
18	46.167	0	55.874	656720000
5.7	76.851	0	13.748	79315000
8.5	77.546	0	18.485	366670000
43.1	27.853	0	114.51	12795000000
5.8	58.792	0	19.846	361230000

20	77.789	0	66.347	1391600000
6.1	34.371	0	5.8702	68205000
1.7	51.818	0.0038745	1.899	21736000
7	27.189	0	8.6676	195100000
28.1	30.048	0	35.878	758910000
13.1	55.238	0	20.406	454600000
26.9	52.686	0	91.708	731740000
14.5	34.834	0	27.638	577740000
19.9	39.431	0	25.154	429220000
27.8	61.422	0	30.89	2195600000
47.1	29.546	0	99.351	3186400000
43.6	25.926	0	45.816	1967200000
12.9	28.405	0	6.8405	1078000000
41.1	26.411	0	80.64	2031100000
30.1	27.372	0	23.282	1536200000
35.5	27.855	0	30.045	1901900000
36.7	26.372	0	76.256	3271100000
53.7	22.906	0	63.027	2473500000
35.6	22.965	0	17.458	777680000
27.3	29.116	0	14.993	493570000
22.7	28.532	0	28.096	264070000
25.6	25.378	0	11.481	686120000
21.3	29.891	0	9.1907	472660000
21.2	48.647	0	18.385	1181400000
26.7	49.548	0	82.727	1915900000
33	45.626	0	57.674	1157000000
41.9	44.172	0	40.737	1350800000
23.3	105.73	0	49.369	1670200000
39.8	47.436	0	43.664	1991000000
14	52.895	0	14.579	836550000
29.8	42.809	0	35.65	791470000
24.8	34.577	0	70.878	1260500000
11.1	60.718	0	28.475	408880000
12	40.703	0	12.742	451520000
23.2	55.971	0	28.086	1129200000
6.2	45.536	0	8.2363	258150000
41.1	36.539	0	53.043	1792700000
13.9	39.93	0	12.092	519830000
17.1	24.72	0	19.058	377900000
45.8	28.673	0	92.066	4072500000
3.5	33.104	0.00043725	3.3725	36099000

52.4	56.477	0	225.62	6705500000
9.4	57.488	0.0070632	1.512	90707000
2.3	77.795	0	7.4684	75206000
9.6	28.617	0	4.5498	143960000
25	43.323	0	31.806	532450000
30.6	18.721	0	14.036	1925500000
2.6	98.72	0.0035156	2.0083	68482000
59.1	57.046	0	323.31	37593000000
7	35.56	0	8.254	175620000
22.5	34.449	0	11.426	334650000
7.6	69.042	0	10.97	952890000
10.9	11.43	0	3.4349	353580000
26.3	19.127	0	10.379	221160000
23.1	68.034	0	34.085	508300000
2	184.96	0	7.2781	82457000
1.8	130.85	0	5.4691	13312000
19.9	19.526	0	12.771	399260000
6.2	54.028	0.00041946	2.9129	244040000
12.1	34.883	0	57.301	1038100000
5.2	165.1	0	14.652	219430000
18.9	60.811	0	71.062	1421500000
32.3	96.729	0	168.53	8251600000
16.6	97.462	0	145.49	846310000
39.8	97.285	0	215.34	9313900000
25.9	87.676	0	83.115	2030700000
39.8	25.57	0	24.606	1686800000
50.4	13.373	0	22.137	827780000
10.7	35.226	0	3.4799	111530000
14	22.541	0	7.4031	1498600000
37.6	24.489	0	86.529	1493600000
3.7	27.328	0.00041597	2.8139	105080000
47.9	23.897	0	36.507	1900400000
22.8	23.035	0	11.953	388830000
32.7	22.677	0	45.53	2513500000
21.4	22.187	0	18.197	631420000
22.1	24.106	0	17.466	1113100000
5	24.56	0	3.6087	81549000
37.3	23.547	0	16.094	546620000
6.2	29.1	0.00042918	3.1654	165840000
9	23.025	0	127.86	704370000
21.9	23.598	0	14.942	321810000

21.9	23.707	0	41.825	2132100000
21.8	23.412	0	34.501	772530000
20.2	23.461	0	11.643	554410000
56.5	23.489	0	86.812	1766700000
6.8	23.668	0	9.5674	217980000
6.8	23.603	0.00043764	3.3944	112920000
21.4	21.45	0	51.781	8934600000
17.5	43.512	0	26.29	816580000
10.7	23.553	0	3.4492	678020000
4.1	31.198	0.0012235	2.5706	120160000
21.7	23.596	0	32.863	1445800000
1.6	341.12	0	17.142	263790000
1.7	63.53	0.00081967	2.6538	27378000
15.2	20.987	0	15.535	1247800000
29.9	20.825	0	198.18	8528900000
6.6	20.745	0.0023876	2.2632	22042000
17.9	18.349	0	11.506	580880000
24.1	75.673	0	43.996	2154800000
2.1	79.381	0	7.8069	64452000
10.1	47.655	0	20.175	672380000
10.1	47.789	0.0060813	1.6824	160590000
67.7	20.911	0	45.619	4785500000
3.9	69.448	0	5.1052	36243000
1.5	106.08	0.0094925	1.373	218350000
4.8	99.551	0.00043497	3.3146	316360000
32.7	16.604	0	54.923	1700100000
14.7	58.683	0	13.552	255810000
7.7	42.161	0	5.2376	205550000
80	15.846	0	107.88	8040500000
10	23.206	0	6.0923	153690000
28.4	21.816	0	52.4	2350900000
6.8	22.462	0.0042471	1.8529	179860000
1.9	44.93	0.0023904	2.2756	66662000
7.5	37.27	0	15.689	162430000
22	38.001	0	58.708	1185200000
15.8	35.147	0	6.6248	198450000
9.6	36.365	0	7.325	94860000
13.6	68.542	0	20.18	290660000
16.2	21.05	0	14.491	619720000
7.6	26.738	0	13.142	172730000
6.8	27.61	0.0067214	1.5468	451080000

18.7	21.782	0	90.048	10011000000
7.7	22.123	0.0012205	2.5426	238460000
12.4	22.006	0	3.7044	603280000
6.8	22.645	0.0063742	1.5716	11630000
8.4	47.323	0	27.713	328670000
5.9	35	0	5.5579	176040000
8.3	52.028	0	36.994	314060000
71.9	49.816	0	238.26	5247100000
20.6	72.415	0	50.559	1009500000
12	158.04	0	64.51	2562600000
5.3	160.58	0	38.843	442050000
8.3	24.945	0	10.716	161680000
42.5	24.604	0	57.628	2457500000
33.2	24.916	0	34.403	2336800000
12.9	20.252	0	14.959	505040000
35.8	17.804	0	67.3	2161700000
28.4	24.305	0	40.299	4054300000
8.4	23.464	0	3.7612	953420000
25.8	23.564	0	20.086	2125900000
34.3	24.146	0	27.33	2055300000
28.3	21.423	0	42.788	2911100000
26.1	21.644	0	16.341	978470000
15.3	20.732	0	6.3617	405920000
21.4	23.466	0	14.12	336650000
33.1	18.562	0	24.092	1049100000
39.1	14.759	0	35.447	935820000
27.1	14.865	0	13.058	1958400000
27.6	17.695	0	13.913	929870000
29.9	17.779	0	14.413	2313500000
18.6	17.258	0	4.8057	802320000
20.6	15.798	0	7.3562	681680000
27.7	16.605	0	15.655	1967000000
12.4	15.733	0	4.8082	513950000
23.1	46.109	0	46.167	2822000000
24.3	12.784	0	21.046	455030000
11.2	14.463	0	3.8687	1732000000
39.3	15.86	0	16.067	1173800000
20.5	13.293	0	3.7996	643970000
8.1	14.552	0	7.7336	429360000
7.3	12.554	0.00082474	2.731	510270000
11.4	12.215	0	4.9944	700870000

41.3	10.275	0	9.9858	296240000
51.4	8.2038	0	9.969	353410000
19.6	6.4066	0	8.0745	871390000
42.7	47.153	0	93.495	9596700000
32.3	34.4	0	28.036	1980000000
30.4	33.509	0	26.006	2460500000
40.4	31.419	0	34.89	2752600000
46.2	29.976	0	50.112	3394900000
35.4	28.024	0	55.2	2025800000
36.5	21.881	0	22.577	719730000
53.9	34.216	0	82.425	4088400000
79.8	11.475	0	145.93	5992100000
76.5	11.651	0	93.172	4188600000
42.3	68.527	0	148.9	4756000000
28.7	69.062	0	298.1	5500700000
42.4	18.916	0	23.217	1270800000
24.1	18.431	0	7.3852	830790000
59.1	14.525	0	46.167	1375000000
45	17.222	0	39.573	4490500000
63.6	16.273	0	23.736	688180000
55.9	17.04	0	188.5	2560500000
49.2	14.839	0	32.863	1783000000
15.8	16.445	0	4.5911	233690000
40	15.524	0	99.042	2397600000
27.6	17.718	0	13.409	2810300000
37.2	16.085	0	17.435	3117900000
33.4	31.231	0	27.781	1947000000
25.2	13.373	0	8.2635	887950000
28.9	9.1413	0	6.0343	230530000
21.7	15.807	0	7.0097	500240000
30	15.069	0	14.301	729310000
18.4	13.742	0	11.438	1107700000
37.4	13.015	0	13.773	658870000
42.3	17.951	0	61.399	6612600000
25	9.4771	0	6.3668	3198300000
17.4	7.8409	0.006379	1.5744	205490000
19.6	6.6767	0	7.0277	384140000
50.6	26.674	0	25.646	1703400000
32.2	29.885	0	29.191	4152900000
38.4	29.597	0	45.992	3749500000
42.6	22.889	0	48.31	1808700000

10.8	28.68	0	15.941	660160000
2.2	83.693	0.0070764	1.5306	104500000
45.4	22.127	0	37.959	1681200000
41.3	24.205	0	72.018	3362800000
32.5	22.591	0	24.401	2944800000
57.6	32.838	0	201.05	7070500000
6.2	33.566	0.00042481	3.0487	27657000
3.6	33.279	0.0064199	1.6368	188430000
44	23.764	0	76.964	4990300000
11.4	172.88	0	160.18	3774400000
62.8	31.55	0	221.06	30402000000
6.6	39.254	0	6.5236	138440000
16.8	55.249	0	25.566	1224600000
2.3	83.571	0.006739	1.565	341640000
13.2	22.239	0	3.8465	153350000
11	25.428	0	20.679	1151700000
2.1	126.61	0	6.3483	90428000
3.7	38.403	0	64.614	3119400000
31.6	28.152	0	68.98	940030000
2.9	80.376	0.0070396	1.4927	116860000
12.1	50.213	0	24.529	478490000
0.4	565.03	0.0084404	1.4106	210970000
16	10.505	0	6.8091	112510000
64.3	11.083	0	285.76	18640000000
46.9	11.158	0	8.0499	218690000
42.6	11.721	0	46.715	74807000000
18.3	10.812	0.0067466	1.569	431970000
33.7	10.051	0	35.914	4202900000
3.7	48.234	0.00041982	2.9188	77391000
11.6	66.943	0	37.575	465120000
22.3	38.62	0	18.452	832240000
2.1	111.84	0	3.6972	346340000
15.6	51.863	0	27.204	875510000
30.3	22.371	0	25.065	1045500000
15.7	22.382	0	5.0502	190880000
28.5	58.388	0	35.603	1028400000
6.8	38.028	0	5.8412	166240000
13.9	30.191	0	19.252	179630000
10.9	54.043	0	34.232	359770000
13.3	47.129	0	28.002	392620000
22.1	72.322	0	21.815	842090000

22.2	9.2833	0	13.02	235690000
40.6	15.236	0	17.319	687190000
5.8	50.964	0	8.4169	191360000
7	46.325	0.0031546	2.1289	366420000
12.7	46.6	0	5.5592	181350000
11.3	108.98	0	21.56	1392800000
44.9	72.585	0	308.82	7536000000
31.6	31.814	0	39.304	2712000000
17.2	18.382	0	9.5022	761710000
20.8	17.014	0	7.7867	304960000
6.7	20.626	0	9.7257	205390000
18.6	35.565	0	36.407	480990000
18.6	24.74	0	11.908	1045800000
28.8	86.161	0	79.983	2429200000
1.7	86.436	0.00043668	3.3559	70927000
6.1	110.78	0	10.088	240940000
27.2	129.56	0	142.51	3571800000
0.7	108.64	0.0070606	1.5086	1118200000
18.1	52.264	0	27.798	659370000
59.3	52.513	0	170.82	7430700000
20	16.377	0	3.8379	98612000
4.2	74.22	0	11.774	297910000
10.8	22.292	0.00041667	2.8272	52352000
9.2	42.906	0.00041719	2.8416	133930000
5.8	42.705	0	3.6083	139190000
7.5	48.964	0	13.918	74399000
29.8	42.747	0	52.908	1041000000
17	50.549	0	117.08	5875500000
20	49.812	0	28.634	1489200000
20	25.678	0	20.417	380230000
5.3	46.002	0	19.696	1024500000
19.4	45.974	0	46.437	3948800000
5.3	45.823	0	323.31	39329000000
16.9	45.998	0	95.703	3618000000
18.2	45.891	0	115.4	3686800000
19.9	46.879	0	206.65	7868300000
13.4	46.717	0	17.778	305380000
3	44.769	0.0020032	2.333	23723000
11.9	42.574	0	3.7487	118670000
55.3	42.598	0	131.48	7647000000
34.6	52.003	0	183.8	15143000000

21.8	54.496	0	16.265	733380000
49.1	44.207	0	140.12	9034100000
24.2	46.233	0	83.502	2765300000
1.6	54.971	0.0070685	1.5193	91158000
23.2	55.584	0	52.813	610330000
19.5	32.105	0	22.02	520890000
4.9	40.506	0	9.0585	63656000
13.5	59.656	0	26.188	561520000
4.6	88.544	0	6.0925	178000000
3.6	49.911	0	8.7399	50571000
7.2	145.81	0	13.297	422500000
5.5	125.31	0	16.023	195280000
5.4	44.355	0.0035184	2.0117	228250000
3.2	27.706	0.0027712	2.2145	1057300000
25.6	75.441	0	45.703	1611700000
34.1	35.412	0	30.464	1131800000
32.3	35.649	0	32.112	572570000
54.8	35.406	0	191.71	8386800000
17.1	43.286	0	27.709	878410000
26.2	34.872	0	56.658	923140000
18	32.133	0	21.519	1657800000
21.3	49.735	0	111.19	3595500000
6.5	32.081	0	16.777	293120000
3	63.676	0.00041684	2.8313	85075000
7.6	34.194	0	7.6222	2809100000
71.1	12.811	0	99.986	5848400000
57	10.477	0	31.498	969570000
1.6	60.323	0.0042455	1.8428	13571000000
9.2	41.518	0.0004329	3.2536	201580000
11.5	40.855	0	18.863	478970000
11.3	42.197	0	21.084	540850000
2.2	119.03	0.0023857	2.2534	230040000
18.6	55.42	0	17.072	337830000
1.1	72.512	0.0070501	1.4974	370330000
12.3	26.518	0	8.8036	34856000
25.8	18.672	0	24.472	1136200000
1.6	127.53	0.0004207	2.9341	125800000
6	58.482	0	13.881	152480000
33.1	33.931	0	44.857	1843300000
11.1	31.715	0	35.607	205630000
34.4	34.155	0	68.129	1347200000

24.1	74.569	0	77.065	2404200000
43.5	33.026	0	44.97	992750000
21.3	52.901	0	20.795	786520000
34.5	39.632	0	45.171	4549300000
25.5	32.904	0	305.74	34535000000
12.3	35.24	0	5.0664	140890000
27.9	32.931	0	64.147	5987200000
6.4	33.689	0	47.714	128990000
2.9	71.275	0.0053496	1.7262	86426000
2.8	50.076	0.00042141	2.9601	46048000
3.7	53.984	0	6.2635	33188000
9.3	58.336	0	5.6434	166460000
11.8	79.923	0	15.588	644820000
32.9	94.233	0	323.31	11007000000
3.5	116.51	0	4.2163	285510000
2.6	167.73	0	8.8323	324930000
38.7	41.864	0	111.19	7385800000
2.3	180.25	0	4.1103	202380000
3.9	121.63	0	10.329	295630000
7	121.37	0	28.224	260250000
3.5	143.23	0	9.4516	209340000
1	141.55	0	4.6093	28922000
15.9	11.542	0.00041632	2.8208	55728000
21	49.763	0	68.99	2200600000
2	89.876	0	17.196	106270000
4.9	49.857	0.00042319	2.9956	68481000
2.2	51.599	0	3.445	54352000
8.1	37.548	0	5.7266	239090000
43.1	13.159	0	24.667	561030000
23.6	102.09	0	83.157	2494500000
6.6	244.54	0	82.827	742930000
21.7	19.79	0	7.9322	500640000
18.8	31.835	0	11.91	315330000
14.2	25.323	0	22.202	286550000
16.8	13.281	0	11.439	1087700000
15.1	13.916	0	5.4933	335840000
12	10.803	0	6.5466	747840000
24.4	9.7251	0	8.3614	349870000
9.2	8.496	0.0038835	1.9336	225920000
17.5	53.664	0	54.911	851360000
32	58.081	0	69.845	2514600000

23.3	56.381	0	33.157	2413500000
18.2	19.116	0.0016234	2.5217	289760000
4.9	52.797	0	4.1111	91504000
15	67.903	0	45.613	1939600000
7.5	58.47	0	34.054	426470000
16.7	18.757	0	4.2815	475090000
5.3	51.777	0	6.9992	50704000
16.6	46.797	0	11.563	208560000
4.7	46.648	0.0070843	1.5376	173130000
21	66.545	0	27.499	560610000
31.8	15.942	0	21.586	12157000000
67.6	24.603	0	158.93	5253200000
57.4	27.392	0	230.38	32378000000
22	82.86	0	106.18	4091600000
46.6	69.476	0	170.68	7595900000
10.8	82.348	0	24.397	1319700000
7.3	38.249	0	7.1171	349600000
26.5	23.501	0	29.108	4312000000
2.3	125.35	0	4.3428	88221000
3.7	72.286	0	6.6255	153820000
8.4	24.977	0	4.9719	122270000
8.6	90.82	0	12.382	608570000
32.6	27.883	0	59.208	3732200000
23	279.86	0	289.85	3680600000
44.9	282.34	0	323.31	23995000000
22.7	245.25	0	250.88	3092800000
45.4	274.22	0	323.31	23630000000
44.3	20.296	0	60.702	1869900000
22.8	33.995	0	7.0426	586630000
12.7	12.51	0	7.0909	92351000
12.1	55.72	0	17.872	215870000
20.8	42.097	0	21.824	446190000
1.3	101.1	0	4.0408	144830000
2.7	99.438	0	4.0547	478350000
25.5	21.807	0	9.5416	296450000
15.3	22.222	0	10.973	259100000
10.9	25.476	0	18.372	451560000
4.7	39.025	0.00043706	3.3701	539100000
26.1	17.89	0	7.6676	285330000
24.6	47.756	0	38.138	1099100000
9.9	17.319	0	18.865	171580000

4.2	23.858	0.0035019	1.95	87485000
8	32.065	0	7.0147	626190000
14	18.936	0	7.7465	148340000
12.7	41.655	0	26.187	1846900000
4.7	46.127	0.0084497	1.4186	158810000
16.6	83.125	0	42.285	771100000
11.3	54.748	0	8.6692	228570000
3.4	77.566	0	12.063	276480000
33.7	62.581	0	116.56	4170300000
16.9	47.953	0	55.893	1332500000
4.5	60.319	0	12.253	84227000
38.7	31.375	0	47.422	2388800000
25.8	38.384	0	23.292	539110000
4.9	81.792	0	17.097	35800000
2.3	38.442	0.0067315	1.5511	110560000
8	66.59	0	18.78	251810000
1	80.597	0.0067139	1.5394	67360000
3.3	93.245	0	9.44	183130000
20.8	31.195	0	47.201	513590000
5.5	37.08	0	53.675	217650000
5.4	29.82	0	6.5567	157170000
17.5	61.678	0	37.548	1283500000
41.9	50.113	0	91.286	3229300000
34.7	36.154	0	117.96	6668000000
21.6	41.349	0	37.15	1270500000
17	38.158	0	8.3715	172310000
1.6	100.92	0.0031533	2.1215	118630000
9.8	84.67	0	12.161	332400000
23.2	78.178	0	93.867	2615700000
5.5	60.755	0	12.009	115450000
16.4	30.381	0	39.535	340300000
20	90.641	0	55.416	2715400000
4.3	243.16	0	28.752	523750000
7.1	42.23	0	6.6962	72747000
18.7	62.672	0	29.325	1419900000
2.8	1009.7	0	98.491	854580000
0.8	782.72	0	5.7768	293790000
2.2	140.87	0	4.2882	242340000
23.1	96.249	0	48.095	1594500000
90.5	22.576	0	323.31	3.8534E+11
7	22.47	0.0020024	2.3317	1413100000

26.7	37.387	0	28.413	2503200000
15.6	46.62	0	17.331	607180000
38.2	44.547	0	27.665	1578600000
12.9	83.355	0	16.811	532190000
1.9	132.01	0	8.8923	57030000
1.3	133.32	0	7.2747	79122000
7.3	33.88	0	4.9917	167480000
28.6	12.473	0	5.4259	411140000
28	13.17	0	32.377	1207000000
3.3	47.585	0	4.5338	53498000
41.7	60.448	0	120.91	4335500000
43.5	41.772	0	65.661	4441600000
53.2	76.723	0	323.31	31420000000
76.1	50.1	0	323.31	50878000000
55.5	74.596	0	323.31	17133000000
60.3	77.06	0	323.31	34021000000
9.4	55.992	0	7.8645	57203000
14.3	129.65	0	85.168	2857300000
6.3	38.884	0	4.5401	128260000
31.5	18.08	0	34.034	1407500000
26.3	10.458	0	14.926	834670000
6	51.091	0	10.883	144860000
2.8	39.776	0.0094891	1.3698	83882000
26.1	24.182	0	18.336	305110000
65	52.664	0	323.31	24251000000
4	194.74	0	8.9206	475980000
69.2	67.63	0	323.31	29674000000
63.1	269.82	0	323.31	2.5261E+11
4.6	253.62	0	48.32	683910000
12.2	21.175	0	8.2538	111210000
22.4	24.911	0	21.41	1346100000
20.4	22.705	0	16.957	900230000
7.2	27.127	0	14.94	261980000
24.6	11.642	0.0057099	1.6934	308160000
15	6.775	0.0042357	1.8213	41614000
42.2	44.783	0	174.19	4736800000
11.4	40.466	0	6.9576	106830000
32.1	39.502	0	78.161	1281000000
14.5	42.65	0	82.95	3707000000
7.6	75.167	0	7.4938	276790000
31.8	5.0256	0	3.5393	85570000

77.3	5.0526	0	52.644	4761400000
5.2	104.2	0	6.2859	100380000
9	31.395	0.00041771	2.8466	322780000
9.2	33.942	0	4.4741	38486000
3.9	37.131	0.0016162	2.4662	82245000
12.1	221.88	0	136.05	1704000000
11.6	22.96	0	5.497	55017000
9.2	101.31	0	27.135	866470000
3.2	100.46	0	4.7209	148460000
10.2	104.17	0	21.196	449840000
18.4	149.5	0	93.948	3748400000
10.8	54.325	0	13.685	162560000
13.4	48.407	0	21.785	479910000
22.5	15.537	0	10.498	255300000
15.5	34.28	0.00042017	2.9239	183420000
8.8	67.589	0	19.511	535880000
1.6	172.79	0	4.4088	2700900000
6.1	181.91	0	23.611	515170000
10.2	58.415	0	6.9968	257130000
2.4	54.495	0.0087751	1.3837	76808000
8.6	37.817	0	3.5574	254330000
7.5	43.813	0	4.4912	74761000
21.1	20.059	0	4.4812	44983000
29.1	24.043	0	20.441	1050200000
71.2	32.191	0	142.26	20785000000
9.9	32.708	0	205.77	34287000000
24.2	29.02	0	32.482	13179000000
39.5	28.467	0	218.78	2838000000
15.3	61.341	0	106.42	984550000
7.3	23.574	0	3.6956	24166000
52.8	18.965	0	116.89	5532300000
1.2	273.99	0	14.939	190300000
6.3	19.556	0	4.4361	17219000
48.3	19.462	0	42.153	3136600000
3.8	80.208	0	5.1679	129910000
8.6	16.441	0.0024	2.3206	41435000
15	20.302	0	4.6133	175310000
12	17.936	0	29.428	210650000
1.9	57.136	0.00041494	2.785	72432000
16.4	88.846	0	59.008	1228400000
15.8	69.912	0	34.696	886570000

1	288.71	0	4.131	105280000
15.2	62.566	0	28.536	4983100000
9.6	14.141	0.0035088	1.981	194350000
9.9	49.895	0	12.363	141070000
19.7	26.201	0	26.421	410350000
23.4	32.926	0	15.356	470620000
10.5	26.053	0	21.888	180600000
4.6	26.738	0	6.5462	158480000
38.5	18.841	0	105.95	1660200000
16.2	33.466	0	9.5156	405600000
0.6	267.46	0	3.5214	54128000
14.2	52.223	0	11.549	377110000
4.1	74.042	0.00041736	2.8442	110230000
1	3906.4	0	64.577	1209900000
3.1	50.135	0	18.864	1836200000
0	50.151	0	323.31	90416000000
5.3	49.909	0	41.359	5392100000
10	49.924	0	12.964	509080000
18.9	49.953	0	80.406	4299900000
24.7	50.418	0	45.348	1767000000
11.5	49.585	0	44.232	317010000
2.7	49.83	0	323.31	1.4471E+11
16.2	49.67	0	141.53	13081000000
30.3	49.508	0	58.67	2715100000
3.7	40.079	0	4.7589	466460000
10.4	39.311	0	18.501	215260000
55.2	11.675	0	46.957	6932900000
12.7	18.255	0	5.5928	212530000
26.4	46.415	0	47.06	2389500000
13.5	32.237	0	13.101	639390000
17.4	54.544	0	26.303	861460000
18.4	27.815	0	8.5657	287180000
7.2	53.516	0	13.159	532020000
16.8	56.613	0	15.758	441550000
47.7	117.81	0	323.31	19595000000
4.2	70.568	0	4.9195	273630000
3.8	44.325	0.0020105	2.387	112920000
14.9	44.789	0	16.936	586990000
1.8	107.24	0.00082713	2.7629	113730000
42.9	16.735	0	33.054	1212100000
13.9	18.007	0	3.9617	209290000

24.5	22.406	0	5.3236	316020000
41.6	17.861	0	31.769	3009700000
48	17.138	0	50.65	4297700000
18.6	16.367	0	6.8114	923000000
2.5	123.97	0.0035266	2.0428	9192400000
1.4	118.2	0	4.4024	73242000
1.5	133.32	0	4.2716	18848000
12.3	8.5468	0.0042438	1.8412	28720000
5.2	58.677	0	44.639	456480000
2.4	67.35	0.0004223	2.9799	68278000
1.6	570.29	0	15.972	382260000
5.4	33.572	0	37.792	439560000
6.9	43.994	0	4.3072	202680000
71.7	24.838	0	135.05	4838800000
13	26.151	0	5.1249	166870000
80.8	33.247	0	133.65	7665300000
28.7	19.481	0	10.675	1206200000
11.7	34.481	0	11.804	551730000
58.8	9.1175	0	17.609	1017000000
21.3	176.43	0	85.832	2443900000
21.5	56.979	0	51.975	1256100000
5.1	60.007	0	9.3279	69876000
4.6	52.292	0.0045959	1.7318	35535000
32.2	103.45	0	144.37	3498500000
7.5	122.66	0	16.815	651720000
37.5	7.4454	0	15.736	1168100000
21.4	6.5386	0	3.9431	1061400000
45	13.527	0	28.778	2250500000
55.6	52.851	0	236.4	8741800000
60.9	48.234	0	264.83	15694000000
46	29.367	0	113.28	3846900000
20.2	10.435	0	43.99	761640000
68.3	9.7681	0	80.737	3354600000
9.5	40.691	0	14.77	148590000
17.2	6.3814	0.00043309	3.2651	49469000
12.2	100.19	0	24.783	540440000
11.2	56.001	0	11.037	624230000
1.6	109.22	0	4.7716	33802000
1.3	102.14	0.0035308	2.0559	1262900000
11.2	108.34	0	5.88	262170000
32.8	95.832	0	185.02	2850300000

3.5	127.99	0	7.4873	181520000
1.4	88.047	0.0004363	3.3443	43175000
39	27.855	0	42.478	1134100000
17.3	26.946	0	8.2551	643610000
13.1	140.21	0	78.856	1520600000
6.7	72.26	0	13.643	157450000
27.5	39.666	0	82.623	3559000000
44.8	43.096	0	117.22	7339700000
3.1	45.817	0.0094856	1.3619	21983000
22.4	22.435	0	21.634	249450000
20.9	74.176	0	138.91	7515400000
72.5	116.72	0	323.31	2.2172E+11
53.3	89.321	0	323.31	18044000000
58.7	30.755	0	82.719	9663400000
39.3	31.732	0	44.275	4284400000
15.5	30.752	0	20.006	984960000
78.3	53.687	0	323.31	5.8226E+11
8.1	17.768	0	9.7368	173980000
11.9	19.778	0	3.5183	63237000
29.1	17.488	0	17.438	547530000
3.9	39.124	0	6.0696	153630000
19	25.452	0	9.2219	163380000
31.9	20.495	0	29.81	1138400000
3	48.439	0.0016116	2.4304	24020000
4.9	43.735	0.00042626	3.1031	172700000
4.7	65.052	0.0035047	1.9686	46048000
7.6	48.906	0.00082508	2.7324	69868000
9.7	49.419	0	22.941	972760000
4.5	33.913	0.00042301	2.9929	120710000
15.3	54.848	0	37.769	1596200000
35.7	44.708	0	78.127	1958000000
25.2	87.142	0	50.787	1275400000
4.6	32.459	0.0067189	1.5433	4875200000
4.4	213.42	0	7.335	171310000
13.8	309.27	0	158.37	4041900000
16.6	53.64	0	15.661	761930000
13	28.032	0	4.6056	232780000
70.6	66.406	0	323.31	17981000000
1.1	102.31	0.0035074	1.9765	164450000
6.6	33.772	0	48.245	305760000
0.8	100.58	0.0087912	1.3966	7026700000

31.1	27.095	0	54.028	4280900000
10.3	69.59	0	4.4144	291010000
16.2	123.09	0	50.209	1387800000
2	43.838	0.0070816	1.5347	95912000
15.7	59.105	0	19.983	546540000
9.6	35.73	0	4.138	71591000
5.5	60.629	0.0084466	1.4151	129410000
11.1	22.314	0	8.1242	220150000
36.5	27.854	0	312.47	7099300000
52.5	29.174	0	168.24	10016000000
39.3	28.302	0	239.61	9825900000
37.8	28.211	0	98.604	2233700000
29.2	27.7	0	323.31	15575000000
53.1	27.771	0	323.31	32705000000
18.3	32.841	0	17.268	566550000
1.3	131.6	0.0016188	2.4999	30880000
5.3	36.384	0	9.5057	16417000
3.3	57.232	0.0070527	1.5028	284820000
2.1	88.062	0	9.5345	71610000
59	60.545	0	323.31	33207000000

MS/MS count	Majority protein IDs	Protein names
4	P22315	Ferrochelatase, mitochondrial
5	Q8BWU5	Probable tRNA N6-adenosine threonylcarbamoyltran
10	Q8VHQ9	Acyl-coenzyme A thioesterase 11
6	Q9R0E1	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3
2	Q64191	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase
14	Q8C3W1	Uncharacterized protein C1orf198 homolog
7	Q9DBS2	Tumor protein p63-regulated gene 1-like protein
1	Q8BFP9	[Pyruvate dehydrogenase (acetyl-transferring)] kinas
8	Q9CWZ7	Gamma-soluble NSF attachment protein
2	Q8R146-2	Acylamino-acid-releasing enzyme
2	Q3UPH1	Protein PRRC1
20	Q91VU0	Protein FAM3C
47	Q60605-2	Myosin light polypeptide 6
112	P08207	Protein S100-A10
6	P51660	Peroxisomal multifunctional enzyme type 2
18	Q3UPL5	Uncharacterized protein C11orf96 homolog
49	Q33DR3-3	Decaprenyl-diphosphate synthase subunit 2
64	Q9ET54-3	Palladin
511	Q80X19-2	Collagen alpha-1(XIV) chain
112	P31001	Desmin
12	Q80W54	CAAX prenyl protease 1 homolog
16	Q9JJH1	Ribonuclease 4
55	P07214	SPARC
26	P30412	Peptidyl-prolyl cis-trans isomerase C
38	Q9R1T4-2	Septin-6
34	Q61398	Procollagen C-endopeptidase enhancer 1
29	Q6P9J9	Anoctamin-6
10	Q05D44	Eukaryotic translation initiation factor 5B
153	Q8CI51	PDZ and LIM domain protein 5
9	Q9EPW0	Type I inositol 3,4-bisphosphate 4-phosphatase
113	O08532-3	Voltage-dependent calcium channel subunit alpha-2/
40	Q9ESD7-3	Dysferlin
15	Q80SZ7	Guanine nucleotide-binding protein G(I)/G(S)/G(O) su
17	Q6PER3	Microtubule-associated protein RP/EB family membe
41	Q922F4	Tubulin beta-6 chain
30	A2AJI0-2	MAP7 domain-containing protein 1
46	O70373	Xin actin-binding repeat-containing protein 1

45	Q8BFY6	Peflin
51	Q6PIE5	Sodium/potassium-transporting ATPase subunit alph
582	Q8C6K9	Collagen alpha-6(VI) chain
1618	Q62009-3	Periostin
35	D3Z7P3-2	Glutaminase kidney isoform, mitochondrial
33	Q8VCF0	Mitochondrial antiviral-signaling protein
158	Q9QZZ6	Dermatopontin
351	O35206	Collagen alpha-1(XV) chain
148	Q80UG5-3	Septin-9
6	Q9DBZ1	Inhibitor of nuclear factor kappa-B kinase-interacting
287	Q9DAW9	Calponin-3
124	P28301	Protein-lysine 6-oxidase
51	O35855	Branched-chain-amino-acid aminotransferase, mitoc
118	Q8BMK4	Cytoskeleton-associated protein 4
328	Q91YE8	Synaptopodin-2
449	Q921U8	Smoothelin
60	Q61166	Microtubule-associated protein RP/EB family membe
61	Q9QYC0-2	Alpha-adducin
51	P26883	Peptidyl-prolyl cis-trans isomerase FKBP1A
282	Q640N1	Adipocyte enhancer-binding protein 1
997	Q08091	Calponin-1
17	P47753	F-actin-capping protein subunit alpha-1
17	Q9DAS9	Guanine nucleotide-binding protein G(I)/G(S)/G(O) s
366	P54320	Elastin
93	Q9R087	Glypican-6
337	P19324	Serpin H1
423	Q8VHX6	Filamin-C
39	P56135	ATP synthase subunit f, mitochondrial
960	Q02788	Collagen alpha-2(VI) chain
1030	P28653	Biglycan
1299	Q04857	Collagen alpha-1(VI) chain
860	Q9WVA4	Transgelin-2
318	O55222	Integrin-linked protein kinase
50	O08599	Syntaxin-binding protein 1
384	Q3TJD7	PDZ and LIM domain protein 7
31	Q9QZS0	Collagen alpha-3(IV) chain
291	Q99K41	EMILIN-1
153	Q8R2Y2-2	Cell surface glycoprotein MUC18
380	P09470	Angiotensin-converting enzyme
95	Q3TZZ7	Extended synaptotagmin-2
1489	Q7TPR4	Alpha-actinin-1

457	Q62188	Dihydropyrimidinase-related protein 3
172	Q9WTR5	Cadherin-13
98	Q05BC3-2	Echinoderm microtubule-associated protein-like 1
548	P07356	Annexin A2
388	Q8VHY0	Chondroitin sulfate proteoglycan 4
572	P39061-2	Collagen alpha-1(XVIII) chain
45	P62192	26S protease regulatory subunit 4
437	O54724	Polymerase I and transcript release factor
37	Q9Z1Y4	Thyroid receptor-interacting protein 6
184	P62737	Actin, aortic smooth muscle
142	P42208	Septin-2
372	P62962	Profilin-1
425	Q8CIB5	Fermitin family homolog 2
93	Q9Z2W0	Aspartyl aminopeptidase
127	P97429	Annexin A4
79	Q64433	10 kDa heat shock protein, mitochondrial
559	P10649	Glutathione S-transferase Mu 1
164	Q9EQH3	Vacuolar protein sorting-associated protein 35
554	P48036	Annexin A5
37	O35678	Monoglyceride lipase
67	P62827	GTP-binding nuclear protein Ran
31	P84089	Enhancer of rudimentary homolog
96	Q63918	Serum deprivation-response protein
131	Q3UTY6	Thrombospondin type-1 domain-containing protein 4
263	P08074	Carbonyl reductase [NADPH] 2
37	Q8R180	ERO1-like protein alpha
53	P48758	Carbonyl reductase [NADPH] 1
337	P10107	Annexin A1
252	P70168	Importin subunit beta-1
75	Q99L20	Glutathione S-transferase theta-3
22	Q9CQM5	Thioredoxin domain-containing protein 17
55	Q99PV0	Pre-mRNA-processing-splicing factor 8
79	P54775	26S protease regulatory subunit 6B
19	Q6PDI5-2	Proteasome-associated protein ECM29 homolog
39	P27048	Small nuclear ribonucleoprotein-associated protein B
18	P47915	60S ribosomal protein L29
182	Q8VDM4	26S proteasome non-ATPase regulatory subunit 2
20	Q9D8Y0	EF-hand domain-containing protein D2
38	Q9Z1R2	Large proline-rich protein BAG6
77	Q9JLJ2	4-trimethylaminobutyraldehyde dehydrogenase
11	Q9DBD0	Inhibitor of carbonic anhydrase

62	Q9R112	Sulfide:quinone oxidoreductase, mitochondrial
68	Q60710-2	Deoxynucleoside triphosphate triphosphohydrolase
11	Q9WV80	Sorting nexin-1
121	P80317	T-complex protein 1 subunit zeta
120	P97372	Proteasome activator complex subunit 2
27	Q6PDQ2	Chromodomain-helicase-DNA-binding protein 4
74	Q9EQ06	Estradiol 17-beta-dehydrogenase 11
18	Q8R2K1-5	Fucose mutarotase
22	P84104-2	Serine/arginine-rich splicing factor 3
10	P35831	Tyrosine-protein phosphatase non-receptor type 12
62	P07309	Transthyretin
112	P01029	Complement C4-B
28	Q99JF8-2	PC4 and SFRS1-interacting protein
37	P70398	Probable ubiquitin carboxyl-terminal hydrolase FAF-
25	Q00519	Xanthine dehydrogenase/oxidase
19	P05201	Aspartate aminotransferase, cytoplasmic
16	Q9R111	Guanine deaminase
39	Q8VCR7	Alpha/beta hydrolase domain-containing protein 14
82	P29391	Ferritin light chain 1
36	Q8R164	Valacyclovir hydrolase
35	Q9R1P0	Proteasome subunit alpha type-4
35	Q8BG51	Mitochondrial Rho GTPase 1
6	Q69ZR2	E3 ubiquitin-protein ligase HECTD1
7	Q9CZU3	Superkiller viralicidic activity 2-like 2
39	Q9CQM9	Glutaredoxin-3
8	Q9CQV7	Mitochondrial import inner membrane translocase s
35	Q8QZY1	Eukaryotic translation initiation factor 3 subunit L
4	Q569Z5-2	Probable ATP-dependent RNA helicase DDX46
24	O70475	UDP-glucose 6-dehydrogenase
40	Q9ESB3	Histidine-rich glycoprotein
3	Q8R3U1	HRAS-like suppressor 3
46	P00329	Alcohol dehydrogenase 1
3	Q9DBG7	Signal recognition particle receptor subunit alpha
29	Q62086	Serum paraoxonase/arylesterase 2
45	P12023-3	Amyloid beta A4 protein
3	Q62193	Replication protein A 32 kDa subunit
33	Q03734	Serine protease inhibitor A3M
14	O89051	Integral membrane protein 2B
14	B1AXP6-2	Mitochondrial import receptor subunit TOM5 homol
8	Q5F285	Transmembrane protein 256
133	P01872	Ig mu chain C region

3	Q07797	Galectin-3-binding protein
9	Q91X52	L-xylulose reductase
14	Q61982	Neurogenic locus notch homolog protein 3
13	Q7TNF8-2	Peripheral-type benzodiazepine receptor-associated
1	P26450	Phosphatidylinositol 3-kinase regulatory subunit alph
12	Q91W69	Epsin-3
14	O54784	Death-associated protein kinase 3
4	Q9Z2T6	Keratin, type II cuticular Hb5
18	E9Q557	Desmoplakin
5	A2BIM8	Major urinary protein 1
2	Q8CIG3-2	Lysine-specific histone demethylase 1B
7	Q8K0Y2	Keratin, type I cuticular Ha3-I
12	P62818	Protein S100-A3
13	O08633	Keratin-associated protein 8-1
6	Q925H6	Keratin-associated protein 19-3
390	Q61838	Alpha-2-macroglobulin
39	Q8BGQ7	Alanine--tRNA ligase, cytoplasmic
4	Q3THG9	Alanyl-tRNA editing protein Aarsd1
44	P61922-2	4-aminobutyrate aminotransferase, mitochondrial
10	Q8K440-2	ATP-binding cassette sub-family A member 8-B
19	P70170-3	ATP-binding cassette sub-family C member 9
13	P55096	ATP-binding cassette sub-family D member 3
16	P61222	ATP-binding cassette sub-family E member 1
15	Q6P542	ATP-binding cassette sub-family F member 1
4	Q8K4F5	Alpha/beta hydrolase domain-containing protein 11
33	Q99LR1	Monoacylglycerol lipase ABHD12
34	Q9Z1Q2	Abhydrolase domain-containing protein 16A
15	Q9DBL9	1-acylglycerol-3-phosphate O-acyltransferase ABHD5
4	Q8CBW3-5	Abl interactor 1
8	Q8K4G5-3	Actin-binding LIM protein 1
46	Q4KML4	Costars family protein ABRACL
71	Q921H8	3-ketoacyl-CoA thiolase A, peroxisomal
425	Q8BWT1	3-ketoacyl-CoA thiolase, mitochondrial
84	Q5SWU9	Acetyl-CoA carboxylase 1
3	Q8K370	Acyl-CoA dehydrogenase family member 10
7	Q8JZN5	Acyl-CoA dehydrogenase family member 9, mitochon
274	P51174	Long-chain specific acyl-CoA dehydrogenase, mitoch
181	P45952	Medium-chain specific acyl-CoA dehydrogenase, mit
122	Q07417	Short-chain specific acyl-CoA dehydrogenase, mitoch
59	Q9DBL1	Short/branched chain specific acyl-CoA dehydrogena
279	P50544	Very long-chain specific acyl-CoA dehydrogenase, mit

173	Q61282	Aggrecan core protein
252	Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial
68	Q8CAY6	Acetyl-CoA acetyltransferase, cytosolic
4	Q9JIX8-3	Apoptotic chromatin condensation inducer in the nuc
277	Q91V92	ATP-citrate synthase
123	P28271	Cytoplasmic aconitate hydratase
764	Q99KI0	Aconitate hydratase, mitochondrial
34	Q9CQR4	Acyl-coenzyme A thioesterase 13
64	Q9QYR9	Acyl-coenzyme A thioesterase 2, mitochondrial
7	Q91V12-2	Cytosolic acyl coenzyme A thioester hydrolase
105	Q9R0X4	Acyl-coenzyme A thioesterase 9, mitochondrial
36	Q9D358-2	Low molecular weight phosphotyrosine protein phos
11	Q8VCW8	Acyl-CoA synthetase family member 2, mitochondrial
2	Q3URE1	Acyl-CoA synthetase family member 3, mitochondrial
289	P41216	Long-chain-fatty-acid--CoA ligase 1
8	Q8JZR0	Long-chain-fatty-acid--CoA ligase 5
84	P60710	Actin, cytoplasmic 1
4093	P68033	Actin, alpha cardiac muscle 1
1501	P63260	Actin, cytoplasmic 2
3	Q9Z2N8	Actin-like protein 6A
447	P57780	Alpha-actinin-4
25	Q9QZB7	Actin-related protein 10
39	P61164	Alpha-centractin
122	Q8R5C5	Beta-centractin
173	P61161	Actin-related protein 2
195	Q99JY9	Actin-related protein 3
15	P56376	Acylphosphatase-1
2	O35598	Disintegrin and metalloproteinase domain-containing
8	Q80T21	ADAMTS-like protein 4
45	Q60936	Atypical kinase ADCK3, mitochondrial
50	P84309	Adenylate cyclase type 5
1	P51829	Adenylate cyclase type 7
18	Q9QYB5-2	Gamma-adducin
129	P28474	Alcohol dehydrogenase class-3
11	Q64437	Alcohol dehydrogenase class 4 mu/sigma chain
19	Q60994	Adiponectin
39	P55264	Adenosine kinase
9	Q8VDL4-3	ADP-dependent glucokinase
6	Q3UYH7	Beta-adrenergic receptor kinase 2
5	Q9JKV1	Proteasomal ubiquitin receptor ADRM1
81	P54822	Adenylosuccinate lyase

2	P28650	Adenylosuccinate synthetase isozyme 1
17	Q8JZQ2	AFG3-like protein 2
2	O89020-2	Afamin
7	Q9ESW4-2	Acylglycerol kinase, mitochondrial
11	Q8CJG0	Protein argonaute-2
4	Q8K3K7	1-acyl-sn-glycerol-3-phosphate acyltransferase beta
72	A2ASQ1-3	Agrin
64	P50247	Adenosylhomocysteinase
16	Q80SW1	Putative adenosylhomocysteinase 2
6	Q8BK64	Activator of 90 kDa heat shock protein ATPase homol
102	P29699	Alpha-2-HS-glycoprotein
14	Q9Z0X1	Apoptosis-inducing factor 1, mitochondrial
1	Q8BUE4	Apoptosis-inducing factor 2
37	P31230	Aminoacyl tRNA synthase complex-interacting multif
36	Q8R010	Aminoacyl tRNA synthase complex-interacting multif
8	O08915	AH receptor-interacting protein
120	Q9R0Y5	Adenylate kinase isoenzyme 1
92	Q9WTP6-2	Adenylate kinase 2, mitochondrial
138	Q9WTP7	GTP:AMP phosphotransferase AK3, mitochondrial
39	Q9WTQ5-2	A-kinase anchor protein 12
112	Q9JII6	Alcohol dehydrogenase [NADP(+)]
141	P45376	Aldose reductase
16	P21300	Aldose reductase-related protein 1
22	P45377	Aldose reductase-related protein 2
26	Q8CG76	Aflatoxin B1 aldehyde reductase member 2
10	Q9D1F4	Proline-rich AKT1 substrate 1
10	P10518	Delta-aminolevulinic acid dehydratase
2241	P07724	Serum albumin
27	Q61490	CD166 antigen
12	Q571I9	Aldehyde dehydrogenase family 16 member A1
7	Q9Z110-2	Delta-1-pyrroline-5-carboxylate synthase
14	P24549	Retinal dehydrogenase 1
10	Q8K009	Mitochondrial 10-formyltetrahydrofolate dehydroger
551	P47738	Aldehyde dehydrogenase, mitochondrial
73	P47740	Fatty aldehyde dehydrogenase
55	Q8CHT0	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitc
5	Q8BWF0	Succinate-semialdehyde dehydrogenase, mitochondr
152	Q9EQ20	Methylmalonate-semialdehyde dehydrogenase [acyla
83	Q9DBF1-2	Alpha-aminoadipic semialdehyde dehydrogenase
421	P05064	Fructose-bisphosphate aldolase A
4	Q9DBE8	Alpha-1,3/1,6-mannosyltransferase ALG2

3	P30355	Arachidonate 5-lipoxygenase-activating protein
16	O08583-2	THO complex subunit 4
2	P53995	Anaphase-promoting complex subunit 1
129	Q02357-5	Ankyrin-1
20	Q8C8R3	Ankyrin-2
9	Q810B6	Rabankyrin-5
23	Q8BH79-2	Anoctamin-10
39	O35381	Acidic leucine-rich nuclear phosphoprotein 32 family
23	Q9EST5	Acidic leucine-rich nuclear phosphoprotein 32 family
19	P97822-2	Acidic leucine-rich nuclear phosphoprotein 32 family
343	P97449	Aminopeptidase N
139	P97384	Annexin A11
194	O35639	Annexin A3
992	P14824	Annexin A6
87	Q07076	Annexin A7
857	O70423	Membrane primary amine oxidase
4	O54754	Aldehyde oxidase 1
36	O35643	AP-1 complex subunit beta-1
14	P22892	AP-1 complex subunit gamma-1
108	P17426-2	AP-2 complex subunit alpha-1
220	P17427	AP-2 complex subunit alpha-2
275	Q9DBG3	AP-2 complex subunit beta
67	P84091	AP-2 complex subunit mu
18	P62743	AP-2 complex subunit sigma
24	Q9Z1T1	AP-3 complex subunit beta-1
4	O54774	AP-3 complex subunit delta-1
25	P28352	DNA-(apurinic or apyrimidinic site) lyase
24	O35841	Apoptosis inhibitor 5
11	Q9D7N9	Adipocyte plasma membrane-associated protein
210	Q00623	Apolipoprotein A-I
72	Q8K4Z3	NAD(P)H-hydrate epimerase
27	P09813	Apolipoprotein A-II
75	P06728	Apolipoprotein A-IV
2	P34928	Apolipoprotein C-I
3	Q05020	Apolipoprotein C-II
37	P08226	Apolipoprotein E
127	Q01339	Beta-2-glycoprotein 1
6	Q9DCZ4-2	Apolipoprotein O
27	Q78IK4	MICOS complex subunit Mic27
33	Q8K3H0	DCC-interacting protein 13-alpha
60	P08030	Adenine phosphoribosyltransferase

33	Q02013	Aquaporin-1
36	Q5XJY5	Coatomer subunit delta
132	P84078	ADP-ribosylation factor 1
15	Q8BSL7	ADP-ribosylation factor 2
51	P61750	ADP-ribosylation factor 4
15	P84084	ADP-ribosylation factor 5
3	P62331	ADP-ribosylation factor 6
3	A2A5R2	Brefeldin A-inhibited guanine nucleotide-exchange pr
97	Q5FWK3	Rho GTPase-activating protein 1
12	Q3UIA2-4	Rho GTPase-activating protein 17
1	Q811P8	Rho GTPase-activating protein 32
137	Q99PT1	Rho GDP-dissociation inhibitor 1
14	Q61599	Rho GDP-dissociation inhibitor 2
24	Q60875-5	Rho guanine nucleotide exchange factor 2
9	Q9ES28-8	Rho guanine nucleotide exchange factor 7
19	P61211	ADP-ribosylation factor-like protein 1
32	Q9WUL7	ADP-ribosylation factor-like protein 3
14	Q9JKW0	ADP-ribosylation factor-like protein 6-interacting pro
102	Q8R5J9	PRA1 family protein 3
40	Q9CQW2	ADP-ribosylation factor-like protein 8B
4	Q9D7A8	Armadillo repeat-containing protein 1
128	Q9WV32	Actin-related protein 2/3 complex subunit 1B
177	Q9CVB6	Actin-related protein 2/3 complex subunit 2
142	Q9JM76	Actin-related protein 2/3 complex subunit 3
135	P59999	Actin-related protein 2/3 complex subunit 4
17	Q9CPW4	Actin-related protein 2/3 complex subunit 5
17	Q9D898	Actin-related protein 2/3 complex subunit 5-like prot
64	Q9WV54	Acid ceramidase
21	Q91YI0	Argininosuccinate lyase
7	O54984	ATPase Asna1
67	Q8BSY0	Aspartyl/asparaginyl beta-hydroxylase
694	Q99MQ4	Asporin
13	Q8C0M9	Isoaspartyl peptidase/L-asparaginase
16	Q925I1-2	ATPase family AAA domain-containing protein 3
3	Q99J83	Autophagy protein 5
14	Q9D906	Ubiquitin-like modifier-activating enzyme ATG7
195	Q9CWJ9	Bifunctional purine biosynthesis protein PURH
14	Q6PA06	Atlastin-2
214	Q91YH5	Atlastin-3
64	O08997	Copper transport protein ATOX1
175	Q8VDN2	Sodium/potassium-transporting ATPase subunit alph

20	P14094	Sodium/potassium-transporting ATPase subunit beta
29	P97370	Sodium/potassium-transporting ATPase subunit beta
188	O55143-2	Sarcoplasmic/endoplasmic reticulum calcium ATPase
17	Q64518-3	Sarcoplasmic/endoplasmic reticulum calcium ATPase
9	G5E829	Plasma membrane calcium-transporting ATPase 1
94	Q6Q477-2	Calcium-transporting ATPase
520	Q03265	ATP synthase subunit alpha, mitochondrial
832	P56480	ATP synthase subunit beta, mitochondrial
100	Q91VR2	ATP synthase subunit gamma, mitochondrial
81	Q9CQQ7	ATP synthase F(0) complex subunit B1, mitochondrial
127	Q9DCX2	ATP synthase subunit d, mitochondrial
34	Q06185	ATP synthase subunit e, mitochondrial
7	P97450	ATP synthase-coupling factor 6, mitochondrial
74	Q9CPQ8	ATP synthase subunit g, mitochondrial
214	Q9DB20	ATP synthase subunit O, mitochondrial
6	Q9Z1G4-3	V-type proton ATPase 116 kDa subunit a isoform 1
11	P51863	V-type proton ATPase subunit d 1
49	P50516	V-type proton ATPase catalytic subunit A
7	P62814	V-type proton ATPase subunit B, brain isoform
11	P50518	V-type proton ATPase subunit E 1
11	P28658	Ataxin-10
6	Q9JLZ3	Methylglutaconyl-CoA hydratase, mitochondrial
10	Q00993	Tyrosine-protein kinase receptor UFO
13	P01887	Beta-2-microglobulin
12	Q9Z2Y2	Beta-1,4-galactosyltransferase 2
38	Q9JLV1	BAG family molecular chaperone regulator 3
9	Q8CI32	BAG family molecular chaperone regulator 5
84	O54962	Barrier-to-autointegration factor
4	Q07813	Apoptosis regulator BAX
214	Q9R069	Basal cell adhesion molecule
1	Q61140-2	Breast cancer anti-estrogen resistance protein 1
11	Q8CCN5	Breast carcinoma-amplified sequence 3 homolog
25	P50136	2-oxoisovalerate dehydrogenase subunit alpha, mitoc
14	Q6P3A8-2	2-oxoisovalerate dehydrogenase subunit beta, mitoc
7	O55028	[3-methyl-2-oxobutanoate dehydrogenase [lipoamid
26	Q8R016	Bleomycin hydrolase
17	Q9CY64	Biliverdin reductase A
70	Q923D2	Flavin reductase (NADPH)
6	P15327	Bisphosphoglycerate mutase
29	Q9Z0S1	3(2),5-bisphosphate nucleotidase 1
3	Q8K3W0-4	BRCA1-A complex subunit BRE

1	Q8K2Q7-2	BRO1 domain-containing protein BROX
1	Q64152-2	Transcription factor BTF3
8	P35991	Tyrosine-protein kinase BTK
26	O35658	Complement component 1 Q subcomponent-binding
206	P01027	Complement C3
40	P08607	C4b-binding protein
19	P06684	Complement C5
2	P06683	Complement component C9
20	P13634	Carbonic anhydrase 1
130	P00920	Carbonic anhydrase 2
304	P16015	Carbonic anhydrase 3
74	Q06138	Calcium-binding protein 39
11	Q9CXW3	Calcyclin-binding protein
11	B2RQC6-2	CAD protein
63	P0DP28	Calmodulin-3
128	P14211	Calreticulin
10	O35887	Calumenin
28	Q91YS8	Calcium/calmodulin-dependent protein kinase type 1
118	Q6PHZ2-2	Calcium/calmodulin-dependent protein kinase type II
77	Q923T9-3	Calcium/calmodulin-dependent protein kinase type II
4	P49070	Calcium signal-modulating cyclophilin ligand
265	Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1
143	P35564	Calnexin
356	P40124	Adenylyl cyclase-associated protein 1
85	Q9CYT6	Adenylyl cyclase-associated protein 2
41	P24452	Macrophage-capping protein
19	O35350	Calpain-1 catalytic subunit
253	O08529	Calpain-2 catalytic subunit
200	O88456	Calpain small subunit 1
11	Q60865	Caprin-1
83	P47754	F-actin-capping protein subunit alpha-2
95	P47757-2	F-actin-capping protein subunit beta
10	Q9CR86	Calcium-regulated heat stable protein 1
52	Q9CZ42-3	ATP-dependent (S)-NAD(P)H-hydrate dehydratase
15	Q9CZ42-2	ATP-dependent (S)-NAD(P)H-hydrate dehydratase
6	Q9WVG6-2	Histone-arginine methyltransferase CARM1
1	Q9ER72-2	Cysteine--tRNA ligase, cytoplasmic
2	O89110	Caspase-8
20	O09165	Calsequestrin-1
29	P51125-3	Calpastatin
38	P24270	Catalase

179	P49817	Caveolin-1
56	Q9WVC3	Caveolin-2
21	Q8K354	Carbonyl reductase [NADPH] 3
3	Q8CH18-3	Cell division cycle and apoptosis regulator protein 1
10	Q8VDP4	Cell cycle and apoptosis regulator protein 2
16	Q71RI9-2	Kynurenine--oxoglutarate transaminase 3
1	Q3TC33-2	Coiled-coil domain-containing protein 127
28	Q9D024-2	Coiled-coil domain-containing protein 47
34	Q8R2G6	Coiled-coil domain-containing protein 80
9	Q8C3X2	Coiled-coil domain-containing protein 90B, mitochon
7	Q8BGU5-2	Cyclin-Y
194	P80314	T-complex protein 1 subunit beta
187	P80318	T-complex protein 1 subunit gamma
117	P80315	T-complex protein 1 subunit delta
155	P80316	T-complex protein 1 subunit epsilon
131	P80313	T-complex protein 1 subunit eta
85	P42932	T-complex protein 1 subunit theta
74	Q8R422	CD109 antigen
7	O35566	CD151 antigen
7	Q2VLH6	Scavenger receptor cysteine-rich type 1 protein M13
73	O54901	OX-2 membrane glycoprotein
18	Q9JLQ0	CD2-associated protein
12	Q64314-2	Hematopoietic progenitor cell antigen CD34
91	Q08857	Platelet glycoprotein 4
13	P15379-2	CD44 antigen
53	Q61735	Leukocyte surface antigen CD47
64	P35762	CD81 antigen
96	P40240	CD9 antigen
20	Q9Z0M6-2	CD97 antigen
14	Q8VCN6	CD99 antigen
35	Q61081	Hsp90 co-chaperone Cdc37
140	P60766	Cell division control protein 42 homolog
44	Q7TT50	Serine/threonine-protein kinase MRCK beta
8	P97326	Cadherin-6
3	Q8VDP6	CDP-diacylglycerol--inositol 3-phosphatidyltransferas
2	Q69ZA1-2	Cyclin-dependent kinase 13
17	P49615	Cyclin-dependent-like kinase 5
16	Q99L43	Phosphatidate cytidylyltransferase 2
26	Q9Z0H4-2	CUGBP Elav-like family member 2
48	Q9CXS4	Centromere protein V
103	P23953	Carboxylesterase 1C

275	Q8VCT4	Carboxylesterase 1D
37	P04186	Complement factor B
4	P03953-2	Complement factor D
141	P06909	Complement factor H
7	Q61129	Complement factor I
262	P18760	Cofilin-1
32	P45591	Cofilin-2
2	Q9CRB9	MICOS complex subunit Mic19
10	Q91VN4	MICOS complex subunit Mic25
14	Q9CQ10	Charged multivesicular body protein 3
13	Q9D8B3	Charged multivesicular body protein 4b
1	Q99LL3	Carbohydrate sulfotransferase 12
4	Q9CY57-3	Chromatin target of PRMT1 protein
19	Q91WS0	CDGSH iron-sulfur domain-containing protein 1
349	Q04447	Creatine kinase B-type
51	P07310	Creatine kinase M-type
14	Q80TV8-2	CLIP-associating protein 1
2	Q99LI2	Chloride channel CLIC-like protein 1
5	P49300	C-type lectin domain family 10 member A
25	P43025	Tetranectin
103	Q9Z1Q5	Chloride intracellular channel protein 1
344	Q9QYB1	Chloride intracellular channel protein 4
13	Q99KN9-2	Clathrin interactor 1
12	Q8BXA5	Cleft lip and palate transmembrane protein 1-like prc
16	Q6IRU5-2	Clathrin light chain B
991	Q68FD5	Clathrin heavy chain 1
94	Q06890	Clusterin
37	Q8R4N0	Citrate lyase subunit beta-like protein, mitochondrial
139	P21844	Chymase
42	Q9DBP5	UMP-CMP kinase
16	P53996-2	Cellular nucleic acid-binding protein
52	Q9D1A2	Cytosolic non-specific dipeptidase
111	Q08093	Calponin-2
11	P16330-2	2,3-cyclic-nucleotide 3-phosphodiesterase
2	Q9QXT0	Protein canopy homolog 2
4	Q8BQ47	Protein canopy homolog 4
4	Q9D2R6	Cytochrome c oxidase assembly factor 3 homolog, mi
5	Q9DBL7	Bifunctional coenzyme A synthase
41	Q60847-4	Collagen alpha-1(XII) chain
716	P11087	Collagen alpha-1(I) chain
547	Q01149	Collagen alpha-2(I) chain

45	P28481-2	Collagen alpha-1(II) chain
39	P08121	Collagen alpha-1(III) chain
472	P02463	Collagen alpha-1(IV) chain
423	P08122	Collagen alpha-2(IV) chain
2	Q9QZR9	Collagen alpha-4(IV) chain
112	O88207-2	Collagen alpha-1(V) chain
93	Q3U962	Collagen alpha-2(V) chain
63	A6H584	Collagen alpha-5(VI) chain
23	Q8K297	Procollagen galactosyltransferase 1
13	Q63829	COMM domain-containing protein 3
7	Q9CQ02	COMM domain-containing protein 4
16	Q8K2Q0	COMM domain-containing protein 9
30	O88587-2	Catechol O-methyltransferase
11	Q8BIG7	Catechol O-methyltransferase domain-containing pro
131	Q8CIE6	Coatomer subunit alpha
88	Q9JIF7	Coatomer subunit beta
26	O55029	Coatomer subunit beta
48	O89079	Coatomer subunit epsilon
109	Q9QZE5	Coatomer subunit gamma-1
7	Q9QXK3-4	Coatomer subunit gamma-2
80	P61202	COP9 signalosome complex subunit 2
26	O88543	COP9 signalosome complex subunit 3
47	O88544	COP9 signalosome complex subunit 4
3	O35864	COP9 signalosome complex subunit 5
7	O88545	COP9 signalosome complex subunit 6
30	Q9CZ04	COP9 signalosome complex subunit 7a
15	P61924	Coatomer subunit zeta-1
1	Q3THF9-2	Coenzyme Q-binding protein COQ10 homolog B, mito
12	Q8R1S0	Ubiquinone biosynthesis monooxygenase COQ6, mito
26	Q8K1Z0	Ubiquinone biosynthesis protein COQ9, mitochondria
8	O89053	Coronin-1A
59	Q9WUM3	Coronin-1B
186	Q9WUM4	Coronin-1C
8	Q9CQI6	Coactosin-like protein
77	P19783	Cytochrome c oxidase subunit 4 isoform 1, mitochon
197	P12787	Cytochrome c oxidase subunit 5A, mitochondrial
95	P19536	Cytochrome c oxidase subunit 5B, mitochondrial
92	P43024	Cytochrome c oxidase subunit 6A1, mitochondrial
77	P56391	Cytochrome c oxidase subunit 6B1
37	Q9CPQ1	Cytochrome c oxidase subunit 6C
19	P56392	Cytochrome c oxidase subunit 7A1, mitochondrial

48	P48771	Cytochrome c oxidase subunit 7A2, mitochondrial
8	P17665	Cytochrome c oxidase subunit 7C, mitochondrial
75	Q61147	Ceruloplasmin
156	P15089	Mast cell carboxypeptidase A
21	Q00493	Carboxypeptidase E
69	Q8C166	Copine-1
14	P59108	Copine-2
61	Q8BT60	Copine-3
3	P36552	Oxygen-dependent coproporphyrinogen-III oxidase, r
3	Q8BFS6-4	Serine/threonine-protein phosphatase CPPED1
22	Q9WVJ3	Carboxypeptidase Q
27	Q6NVF9	Cleavage and polyadenylation specificity factor subur
18	Q8BTV2-3	Cleavage and polyadenylation specificity factor subur
30	P97742	Carnitine O-palmitoyltransferase 1, liver isoform
49	Q924X2	Carnitine O-palmitoyltransferase 1, muscle isoform
96	P52825	Carnitine O-palmitoyltransferase 2, mitochondrial
13	Q64735-2	Complement component receptor 1-like protein
55	P47934	Carnitine O-acetyltransferase
7	Q91XD7	Cysteine-rich with EGF-like domain protein 1
98	P63254	Cysteine-rich protein 1
150	Q9DCT8	Cysteine-rich protein 2
27	Q64010	Adapter molecule crk
1	P47941	Crk-like protein
44	P23927	Alpha-crystallin B chain
25	Q99KP3	Lambda-crystallin homolog
12	P47199	Quinone oxidoreductase
369	Q9CZU6	Citrate synthase, mitochondrial
71	Q9DBE0	Cysteine sulfinic acid decarboxylase
36	Q9ERK4	Exportin-2
5	P41241	Tyrosine-protein kinase CSK
20	Q8BK63-2	Casein kinase I isoform alpha
44	Q60737	Casein kinase II subunit alpha
10	P67871	Casein kinase II subunit beta
237	P97315	Cysteine and glycine-rich protein 1
219	P97314	Cysteine and glycine-rich protein 2
3	P21460	Cystatin-C
30	Q62426	Cystatin-B
11	Q8BIQ5	Cleavage stimulation factor subunit 2
25	O88712-2	C-terminal-binding protein 1
1	Q61164	Transcriptional repressor CTCF
62	P26231	Catenin alpha-1

15	Q61301-2	Catenin alpha-2
5	Q65CL1	Catenin alpha-3
17	O88327	Alpha-catulin
51	Q02248	Catenin beta-1
7	Q9CWL8	Beta-catenin-like protein 1
53	P30999-2	Catenin delta-1
59	P10605	Cathepsin B
136	P18242	Cathepsin D
15	P49935	Pro-cathepsin H
23	Q60598	Src substrate cortactin
2	Q99LJ0	CTTNBP2 N-terminal-like protein
13	Q9WTX6	Cullin-1
21	Q9JLV5	Cullin-3
24	Q3TCH7	Cullin-4A
11	Q9D5V5	Cullin-5
68	Q9CQ89	Protein CutA
2	Q9D8X1	Copper homeostasis protein cutC homolog
9	P40224-1	Stromal cell-derived factor 1
20	P56395	Cytochrome b5
12	Q9CQX2	Cytochrome b5 type B
22	Q9DB73	NADH-cytochrome b5 reductase 1
494	Q9DCN2-2	NADH-cytochrome b5 reductase 3
20	Q3TYS2	Cytochrome b-245 chaperone 1
87	Q9D0M3-2	Cytochrome c1, heme protein, mitochondrial
72	P62897	Cytochrome c, somatic
104	Q7TMB8-2	Cytoplasmic FMR1-interacting protein 1
39	Q9CX80	Cytoglobin
11	Q8BKE6	Cytochrome P450 20A1
2	P33267	Cytochrome P450 2F2
2	Q64462	Cytochrome P450 4B1
99	Q9D172	ES1 protein homolog, mitochondrial
6	Q8BPM0-2	Disheveled-associated activator of morphogenesis 1
10	P98078-3	Disabled homolog 2
94	Q62165	Dystroglycan
91	Q922B2	Aspartate--tRNA ligase, cytoplasmic
2	Q9JII5-2	DAZ-associated protein 1
69	P31786	Acyl-CoA-binding protein
29	Q62418-3	Drebrin-like protein
90	P53395	Lipoamide acyltransferase component of branched-c
951	P28654	Decorin
19	Q9DAR7	m7GpppX diphosphatase

62	O08788-2	Dynactin subunit 1
83	Q99KJ8	Dynactin subunit 2
13	Q9Z0Y1	Dynactin subunit 3
2	Q9QZB9	Dynactin subunit 5
84	Q99LD8	N(G),N(G)-dimethylarginine dimethylaminohydrolase
57	Q3U1J4	DNA damage-binding protein 1
2	Q80Y98	Phospholipase DDHD2
77	O54734	Dolichyl-diphosphooligosaccharide--protein glycosylt
3	Q80WW9	DDRGK domain-containing protein 1
119	O35215	D-dopachrome decarboxylase
90	Q91VR5	ATP-dependent RNA helicase DDX1
24	Q501J6	Probable ATP-dependent RNA helicase DDX17
6	Q9JIK5	Nucleolar RNA helicase 2
16	Q9QY15-2	ATP-dependent RNA helicase DDX25
114	Q9Z1N5	Spliceosome RNA helicase Ddx39b
112	Q62167	ATP-dependent RNA helicase DDX3X
6	Q62095	ATP-dependent RNA helicase DDX3Y
4	Q810A7	ATP-dependent RNA helicase DDX42
110	Q61656	Probable ATP-dependent RNA helicase DDX5
9	Q99MJ9	ATP-dependent RNA helicase DDX50
16	P54823	Probable ATP-dependent RNA helicase DDX6
197	Q9CQ62	2,4-dienoyl-CoA reductase, mitochondrial
29	Q7TNV0	Protein DEK
17	Q99J56	Derlin-1
23	Q9DBB8	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase
41	Q99L04	Dehydrogenase/reductase SDR family member 1
5	Q99J47-2	Dehydrogenase/reductase SDR family member 7B
14	O35286	Pre-mRNA-splicing factor ATP-dependent RNA helicas
3	Q6PGC1	ATP-dependent RNA helicase Dhx29
92	O70133	ATP-dependent RNA helicase A
11	O08808	Protein diaphanous homolog 1
4	Q9ESX5	H/ACA ribonucleoprotein complex subunit 4
224	Q8BMF4	Dihydrolipoyllysine-residue acetyltransferase compor
169	O08749	Dihydrolipoyl dehydrogenase, mitochondrial
78	Q9D2G2	Dihydrolipoyllysine-residue succinyltransferase comp
797	P11531	Dystrophin
23	P54265-4	Myotonin-protein kinase
13	P63037	DnaJ homolog subfamily A member 1
15	Q9QYJ0	DnaJ homolog subfamily A member 2
4	Q99M87-3	DnaJ homolog subfamily A member 3, mitochondrial
51	Q9D832	DnaJ homolog subfamily B member 4

10	Q9DC23	DnaJ homolog subfamily C member 10
16	Q5U458	DnaJ homolog subfamily C member 11
11	Q91YW3	DnaJ homolog subfamily C member 3
3	P39053-5	Dynamin-1
178	Q8K1M6-3	Dynamin-1-like protein
115	P39054-2	Dynamin-2
12	Q8R1A4-2	Dedicator of cytokinesis protein 7
206	P31428	Dipeptidase 1
25	Q99KK7	Dipeptidyl peptidase 3
6	Q9ET22	Dipeptidyl peptidase 2
58	Q99LT0	Protein dpy-30 homolog
350	O08553	Dihydropyrimidinase-related protein 2
9	Q9D6N5	Dr1-associated corepressor
10	Q91ZU6	Dystonin
577	Q9R0P5	Destrin
4	Q8BHA3-2	Probable D-tyrosyl-tRNA(Tyr) deacylase 2
69	Q9D2N4-2	Dystrobrevin alpha
11	Q8K4T5	Dual specificity protein phosphatase 19
70	Q9D7X3	Dual specificity protein phosphatase 3
998	Q9JHU4	Cytoplasmic dynein 1 heavy chain 1
10	O88487	Cytoplasmic dynein 1 intermediate chain 2
36	Q8R1Q8	Cytoplasmic dynein 1 light intermediate chain 1
69	P63168	Dynein light chain 1, cytoplasmic
20	P62627	Dynein light chain roadblock-type 1
6	P51807	Dynein light chain Tctex-type 1
13	P56387	Dynein light chain Tctex-type 3
51	O35459	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitoch
3	Q3TLP5-2	Enoyl-CoA hydratase domain-containing protein 2, m
113	Q8BH95	Enoyl-CoA hydratase, mitochondrial
98	P42125	Enoyl-CoA delta isomerase 1, mitochondrial
31	Q9WUR2-2	Enoyl-CoA delta isomerase 2, mitochondrial
28	Q61508	Extracellular matrix protein 1
1	Q9QZH6	Evolutionarily conserved signaling intermediate in To
514	P10126	Elongation factor 1-alpha 1
61	O70251	Elongation factor 1-beta
50	P57776	Elongation factor 1-delta
4	Q9D1M4	Eukaryotic translation elongation factor 1 epsilon-1
100	Q9D8N0	Elongation factor 1-gamma
571	P58252	Elongation factor 2
163	Q8BPB5	EGF-containing fibulin-like extracellular matrix protei
85	Q9WVJ9	EGF-containing fibulin-like extracellular matrix protei

28	Q9D4J1	EF-hand domain-containing protein D1
6	Q8BG67	Protein EFR3 homolog A
27	O08810	116 kDa U5 small nuclear ribonucleoprotein compon
19	Q01279	Epidermal growth factor receptor
14	Q99MS7-4	EH domain-binding protein 1-like protein 1
171	Q9WVK4	EH domain-containing protein 1
1041	Q8BH64	EH domain-containing protein 2
18	Q9QXY6	EH domain-containing protein 3
275	Q9EQP2	EH domain-containing protein 4
14	Q6ZWX6	Eukaryotic translation initiation factor 2 subunit 1
39	Q9Z0N1	Eukaryotic translation initiation factor 2 subunit 3, X-
98	P23116	Eukaryotic translation initiation factor 3 subunit A
23	Q8JZQ9	Eukaryotic translation initiation factor 3 subunit B
39	Q8R1B4	Eukaryotic translation initiation factor 3 subunit C
13	O70194	Eukaryotic translation initiation factor 3 subunit D
43	P60229	Eukaryotic translation initiation factor 3 subunit E
71	Q9DCH4	Eukaryotic translation initiation factor 3 subunit F
9	Q9Z1D1	Eukaryotic translation initiation factor 3 subunit G
8	Q91WK2	Eukaryotic translation initiation factor 3 subunit H
16	Q3UGC7	Eukaryotic translation initiation factor 3 subunit J-A
14	Q9DBZ5-2	Eukaryotic translation initiation factor 3 subunit K
44	Q99JX4	Eukaryotic translation initiation factor 3 subunit M
160	P60843	Eukaryotic initiation factor 4A-I
26	P10630	Eukaryotic initiation factor 4A-II
16	Q91VC3	Eukaryotic initiation factor 4A-III
27	Q8BGD9	Eukaryotic translation initiation factor 4B
21	P63073	Eukaryotic translation initiation factor 4E
49	Q6NZJ6-2	Eukaryotic translation initiation factor 4 gamma 1
19	Q62448-2	Eukaryotic translation initiation factor 4 gamma 2
13	Q9WUK2-2	Eukaryotic translation initiation factor 4H
46	P59325	Eukaryotic translation initiation factor 5
126	P63242	Eukaryotic translation initiation factor 5A-1
53	P70372	ELAV-like protein 1
17	Q9JLJ5	Elongation of very long chain fatty acids protein 1
23	Q8C7X2-2	ER membrane protein complex subunit 1
12	O70378	ER membrane protein complex subunit 8
25	O08579	Emerin
113	Q7TNG5	Echinoderm microtubule-associated protein-like 2
125	Q03173-6	Protein enabled homolog
117	Q8C522	Endonuclease domain-containing 1 protein
475	P17182	Alpha-enolase

2	P17183	Gamma-enolase
16	P21550	Beta-enolase
53	P16406	Glutamyl aminopeptidase
13	P06802-2	Ectonucleotide pyrophosphatase/phosphodiesterase
39	Q6DYE8	Ectonucleotide pyrophosphatase/phosphodiesterase
12	Q8BTJ4-2	Bis(5-adenosyl)-triphosphatase enpp4
140	P55772	Ectonucleoside triphosphate diphosphohydrolase 1
198	O55026	Ectonucleoside triphosphate diphosphohydrolase 2
12	P48193-2	Protein 4.1
24	O70318	Band 4.1-like protein 2
309	Q9D379	Epoxide hydrolase 1
23	P34914	Bifunctional epoxide hydrolase 2
14	Q80VP1	Epsin-1
4	Q8CHU3-2	Epsin-2
9	Q8R0W0	Epiplakin
116	Q8CGC7	Bifunctional glutamate/proline--tRNA ligase
12	P42567	Epidermal growth factor receptor substrate 15
3	Q99K30	Epidermal growth factor receptor kinase substrate 8-
17	Q9EQH2	Endoplasmic reticulum aminopeptidase 1
7	Q80TH2-1	Protein LAP2
15	Q9DC16	Endoplasmic reticulum-Golgi intermediate compartm
31	P57759	Endoplasmic reticulum resident protein 29
47	Q9D1Q6	Endoplasmic reticulum resident protein 44
155	Q9R0P3	S-formylglutathione hydrolase
333	Q3U7R1	Extended synaptotagmin-1
5	Q8BWY3	Eukaryotic peptide chain release factor subunit 1
290	Q99LC5	Electron transfer flavoprotein subunit alpha, mitocho
149	Q9DCW4	Electron transfer flavoprotein subunit beta
78	Q921G7	Electron transfer flavoprotein-ubiquinone oxidoredu
53	Q9DCM0	Persulfide dioxygenase ETHE1, mitochondrial
6	Q9D4H1	Exocyst complex component 2
11	A6H5Z3	Exocyst complex component 6B
114	Q8BH61	Coagulation factor XIII A chain
39	P19221	Prothrombin
28	P11404	Fatty acid-binding protein, heart
114	P04117	Fatty acid-binding protein, adipocyte
17	Q3TDN2	FAS-associated factor 2
56	P35505	Fumarylacetoacetase
28	Q9D281	Protein Noxp20
9	Q6A0A9	Constitutive coactivator of PPAR-gamma-like protein
214	Q3UW53	Protein Niban

42	Q8R1F1	Niban-like protein 1
34	Q9D6U8	Protein FAM162A
7	Q3TCJ1	BRISC complex subunit Abro1
17	Q9CYH2	Redox-regulatory protein FAM213A
18	Q9WTJ8	Protein FAM50B
9	Q3TJZ6	Protein FAM98A
6	Q80VD1	Protein FAM98B
44	Q8C0C7	Phenylalanine--tRNA ligase alpha subunit
49	Q9WUA2	Phenylalanine--tRNA ligase beta subunit
808	P19096	Fatty acid synthase
17	P62862	40S ribosomal protein S30
30	P35550	rRNA 2-O-methyltransferase fibrillarin
553	Q71FD7	Filamin-binding LIM protein 1
19	Q08879	Fibulin-1
7	Q08879-2	Fibulin-1
133	P37889-2	Fibulin-2
875	Q9WVH9	Fibulin-5
2583	Q61554	Fibrillin-1
10	Q61555	Fibrillin-2
12	Q80UW2	F-box only protein 2
14	Q8BJL1	F-box only protein 30
6	Q9QZN4	F-box only protein 6
6	Q61559	IgG receptor FcRn large subunit p51
5	Q3UQN2	F-BAR domain only protein 2
13	Q920E5	Farnesyl pyrophosphate synthase
8	Q8K1B8	Fermitin family homolog 3
2	Q9QXC1	Fetuin-B
319	E9PV24-2	Fibrinogen alpha chain
464	Q8K0E8	Fibrinogen beta chain
19	P61148	Fibroblast growth factor 1
437	Q8VCM7	Fibrinogen gamma chain
1	P12804	Fibroleukin
255	P97807-2	Fumarate hydratase, mitochondrial
425	P97447	Four and a half LIM domains protein 1
43	Q9R059	Four and a half LIM domains protein 3
54	Q6P6L0-3	Filamin A-interacting protein 1-like
62	Q9CQ92	Mitochondrial fission 1 protein
27	Q61576	Peptidyl-prolyl cis-trans isomerase FKBP10
10	P45878	Peptidyl-prolyl cis-trans isomerase FKBP2
4	Q62446	Peptidyl-prolyl cis-trans isomerase FKBP3
15	P30416	Peptidyl-prolyl cis-trans isomerase FKBP4

18	Q9Z247	Peptidyl-prolyl cis-trans isomerase FKBP9
112	Q9JJ28	Protein flightless-1 homolog
5399	Q8BTM8	Filamin-A
214	Q80X90	Filamin-B
45	O08917	Flotillin-1
59	Q60634-3	Flotillin-2
5	Q6ZPF4-2	Formin-like protein 3
69	P50285	Dimethylaniline monooxygenase [N-oxide-forming] 1
443	Q8K2I3	Dimethylaniline monooxygenase [N-oxide-forming] 2
27	P97501	Dimethylaniline monooxygenase [N-oxide-forming] 3
97	P50608	Fibromodulin
11	P35922-11	Fragile X mental retardation protein 1 homolog
1617	P11276	Fibronectin
7	Q61239	Protein farnesyltransferase/geranylgeranyltransferas
7	O35409	Glutamate carboxypeptidase 2
4	E9Q8I9	Protein furry homolog
25	Q62356	Follistatin-related protein 1
88	P09528	Ferritin heavy chain
9	Q9D6K8	FUN14 domain-containing protein 2
23	P56959	RNA-binding protein FUS
16	Q61584-2	Fragile X mental retardation syndrome-related protei
57	P97855	Ras GTPase-activating protein-binding protein 1
16	P97379-2	Ras GTPase-activating protein-binding protein 2
90	Q00612	Glucose-6-phosphate 1-dehydrogenase X
12	P70699	Lysosomal alpha-glucosidase
1	Q9DCD6	Gamma-aminobutyric acid receptor-associated prote
10	Q99KY4-2	Cyclin-G-associated kinase
28	Q9R0N0	Galactokinase
15	Q8K157	Aldose 1-epimerase
17	O35969	Guanidinoacetate N-methyltransferase
156	Q8BHN3	Neutral alpha-glucosidase AB
978	P16858	Glyceraldehyde-3-phosphate dehydrogenase
2	Q9CZD3	Glycine--tRNA ligase
20	Q64737	Trifunctional purine biosynthetic protein adenosine-
27	O55126	Protein NipSnap homolog 2
17	Q9D6Y9	1,4-alpha-glucan-branching enzyme
31	Q9Z0E6	Interferon-induced guanylate-binding protein 2
147	P21614	Vitamin D-binding protein
12	O88986	2-amino-3-ketobutyrate coenzyme A ligase, mitochor
8	Q60759	Glutaryl-CoA dehydrogenase, mitochondrial
35	E9PVA8	eIF-2-alpha kinase activator GCN1

157	P50396	Rab GDP dissociation inhibitor alpha
334	Q61598	Rab GDP dissociation inhibitor beta
2	Q9QYC7	Vitamin K-dependent gamma-carboxylase
1	Q9D7M1	Glucose-induced degradation protein 8 homolog
3	Q99JY3	GTPase IMAP family member 4
16	Q68FF6	ARF GTPase-activating protein GIT1
7	Q9JLQ2	ARF GTPase-activating protein GIT2
61	Q61543	Golgi apparatus protein 1
131	Q9CPU0	Lactoylglutathione lyase
40	Q9CPV4-2	Glyoxalase domain-containing protein 4
44	Q9QUH0	Glutaredoxin-1
11	Q9JL62	Glycolipid transfer protein
321	P26443	Glutamate dehydrogenase 1, mitochondrial
29	P15105	Glutamine synthetase
12	Q922P9	Putative oxidoreductase GLYR1
8	Q9CQI3	Glia maturation factor beta
21	Q922H4	Mannose-1-phosphate guanyltransferase alpha
29	Q8BTZ7	Mannose-1-phosphate guanyltransferase beta
4	Q3THK7	GMP synthase [glutamine-hydrolyzing]
70	P21278	Guanine nucleotide-binding protein subunit alpha-11
12	P27601	Guanine nucleotide-binding protein subunit alpha-13
12	B2RSH2	Guanine nucleotide-binding protein G(i) subunit alph
194	P08752	Guanine nucleotide-binding protein G(i) subunit alph
35	P18872-2	Guanine nucleotide-binding protein G(o) subunit alp
9	P18872	Guanine nucleotide-binding protein G(o) subunit alp
115	P21279	Guanine nucleotide-binding protein G(q) subunit alp
64	P63094-2	Guanine nucleotide-binding protein G(s) subunit alph
59	P62874	Guanine nucleotide-binding protein G(I)/G(S)/G(T) su
134	P62880	Guanine nucleotide-binding protein G(I)/G(S)/G(T) su
107	P68040	Guanine nucleotide-binding protein subunit beta-2-li
9	P29387	Guanine nucleotide-binding protein subunit beta-4
5	Q9CRC9-2	Glucosamine-6-phosphate isomerase 2
12	Q9JK38	Glucosamine 6-phosphate N-acetyltransferase
8	Q921M4-2	Golgin subfamily A member 2
16	Q99JX3-2	Golgi reassembly-stacking protein 2
7	O35166	Golgi SNAP receptor complex member 2
273	P05202	Aspartate aminotransferase, mitochondrial
11	O08742	Platelet glycoprotein V
6	P51655	Glypican-4
160	P13707	Glycerol-3-phosphate dehydrogenase [NAD(+)], cyto
39	Q3ULJ0-2	Glycerol-3-phosphate dehydrogenase 1-like protein

264	Q64521	Glycerol-3-phosphate dehydrogenase, mitochondrial
659	P06745	Glucose-6-phosphate isomerase
1	Q99P91	Transmembrane glycoprotein NMB
10	Q99LD4	COP9 signalosome complex subunit 1
208	P11352	Glutathione peroxidase 1
148	P46412	Glutathione peroxidase 3
7	O70325-2	Phospholipid hydroperoxide glutathione peroxidase,
9	Q99LJ6	Glutathione peroxidase 7
34	Q60631	Growth factor receptor-bound protein 2
94	Q91Z53	Glyoxylate reductase/hydroxypyruvate reductase
49	P28798	Granulins
13	Q99LP6	GrpE protein homolog 1, mitochondrial
1	Q2NL51	Glycogen synthase kinase-3 alpha
16	Q9WV60	Glycogen synthase kinase-3 beta
378	P13020	Gelsolin
11	P13020-2	Gelsolin
25	P47791-2	Glutathione reductase, mitochondrial
18	P51855	Glutathione synthetase
11	P30115	Glutathione S-transferase A3
74	Q9DCM2	Glutathione S-transferase kappa 1
202	P15626	Glutathione S-transferase Mu 2
32	P48774	Glutathione S-transferase Mu 5
27	Q80W21	Glutathione S-transferase Mu 7
35	O09131	Glutathione S-transferase omega-1
251	P19157	Glutathione S-transferase P 1
161	Q64471	Glutathione S-transferase theta-1
12	Q61133	Glutathione S-transferase theta-2
52	Q9WVL0	Maleylacetoacetate isomerase
2	Q9ESZ8-5	General transcription factor II-I
183	Q9ERL9	Guanylate cyclase soluble subunit alpha-3
95	O54865	Guanylate cyclase soluble subunit beta-1
21	Q8K2A1	PTB domain-containing engulfment adapter protein 1
22	Q9R062	Glycogenin-1
1	Q9Z1E4	Glycogen [starch] synthase, muscle
93	P10922	Histone H1.0
2	P14434	H-2 class II histocompatibility antigen, A-B alpha chain
31	P01899	H-2 class I histocompatibility antigen, D-B alpha chain
11	P01901	H-2 class I histocompatibility antigen, K-B alpha chain
13	P01898	H-2 class I histocompatibility antigen, Q10 alpha chain
83	Q3THW5	Histone H2A.V
211	Q9QZQ8-2	Core histone macro-H2A.1

12	Q8CCK0	Core histone macro-H2A.2
35	P84244	Histone H3.3
9	Q8CFX1	GDH/6PGL endoplasmic bifunctional protein
225	Q61425	Hydroxyacyl-coenzyme A dehydrogenase, mitochond
763	Q8BMS1	Trifunctional enzyme subunit alpha, mitochondrial
409	Q99JY0	Trifunctional enzyme subunit beta, mitochondrial
6	Q99KB8-2	Hydroxyacylglutathione hydrolase, mitochondrial
19	Q9EQ21	Hepcidin
33	Q9QUP5	Hyaluronan and proteoglycan link protein 1
16	Q61035	Histidine--tRNA ligase, cytoplasmic
1	O35387	HCLS1-associated protein X-1
668	P01942	Hemoglobin subunit alpha
1367	P02088	Hemoglobin subunit beta-1
19	P02089	Hemoglobin subunit beta-2
8	P04444	Hemoglobin subunit beta-H1
10	Q61191	Host cell factor 1
5	P70288	Histone deacetylase 2
17	P51859	Hepatoma-derived growth factor
31	Q9JMG7	Hepatoma-derived growth factor-related protein 3
27	Q3UGR5	Haloacid dehalogenase-like hydrolase domain-contai
62	Q8VDJ3	Vigilin
19	P29416	Beta-hexosaminidase subunit alpha
2	P20060	Beta-hexosaminidase subunit beta
2	Q99LI8	Hepatocyte growth factor-regulated tyrosine kinase s
137	Q99L13	3-hydroxyisobutyrate dehydrogenase, mitochondrial
88	Q8QZS1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial
2	Q9JLR9	HIG1 domain family member 1A, mitochondrial
115	P70349	Histidine triad nucleotide-binding protein 1
27	Q9D0S9	Histidine triad nucleotide-binding protein 2, mitochoi
46	Q8VD75	Huntingtin-interacting protein 1
15	P43275	Histone H1.1
48	P43276	Histone H1.5
223	P15864	Histone H1.2
9	P43277	Histone H1.3
80	P43274	Histone H1.4
44	C0HKE9	Histone H2A type 1-H
567	Q8CGP2	Histone H2B type 1-P
52	P68433	Histone H3.1
204	P84228	Histone H3.2
471	P62806	Histone H4
15	Q64522	Histone H2A type 2-B

452	Q64523	Histone H2A type 2-C
219	P17710-3	Hexokinase-1
44	O08528	Hexokinase-2
5	P22907-2	Porphobilinogen deaminase
152	P63158	High mobility group protein B1
4	P30681	High mobility group protein B2
28	P38060	Hydroxymethylglutaryl-CoA lyase, mitochondrial
16	P54869	Hydroxymethylglutaryl-CoA synthase, mitochondrial
9	P09602	Non-histone chromosomal protein HMG-17
8	Q9JL35	High mobility group nucleosome-binding domain-con
2	O70252	Heme oxygenase 2
4	Q9CX86	Heterogeneous nuclear ribonucleoprotein A0
34	P49312	Heterogeneous nuclear ribonucleoprotein A1
162	O88569-3	Heterogeneous nuclear ribonucleoproteins A2/B1
152	Q8BG05-2	Heterogeneous nuclear ribonucleoprotein A3
82	Q99020	Heterogeneous nuclear ribonucleoprotein A/B
29	Q9Z204-4	Heterogeneous nuclear ribonucleoproteins C1/C2
108	Q60668-4	Heterogeneous nuclear ribonucleoprotein D0
10	Q9Z130	Heterogeneous nuclear ribonucleoprotein D-like
41	Q9Z2X1	Heterogeneous nuclear ribonucleoprotein F
83	O35737	Heterogeneous nuclear ribonucleoprotein H
17	P70333	Heterogeneous nuclear ribonucleoprotein H2
208	P61979	Heterogeneous nuclear ribonucleoprotein K
107	Q8R081	Heterogeneous nuclear ribonucleoprotein L
12	Q921F4	Heterogeneous nuclear ribonucleoprotein L-like
107	Q9D0E1-2	Heterogeneous nuclear ribonucleoprotein M
191	Q8VEK3	Heterogeneous nuclear ribonucleoprotein U
7	Q8VDM6-2	Heterogeneous nuclear ribonucleoprotein U-like prot
36	Q00PI9	Heterogeneous nuclear ribonucleoprotein U-like prot
14	Q8BUK6	Protein Hook homolog 3
1	P23463	Homeobox protein Hox-D8
3	Q61646	Haptoglobin
134	Q3TEA8-2	Heterochromatin protein 1-binding protein 3
21	P62748	Hippocalcin-like protein 1
42	P00493	Hypoxanthine-guanine phosphoribosyltransferase
164	Q91X72	Hemopexin
5	Q9CQZ1	Heat shock factor-binding protein 1
10	P50172	Corticosteroid 11-beta-dehydrogenase isozyme 1
133	O08756	3-hydroxyacyl-CoA dehydrogenase type-2
59	O70503	Very-long-chain 3-oxoacyl-CoA reductase
15	Q2TPA8	Hydroxysteroid dehydrogenase-like protein 2

260	P07901	Heat shock protein HSP 90-alpha
551	P11499	Heat shock protein HSP 90-beta
431	P08113	Endoplasmin
23	Q8K0U4	Heat shock 70 kDa protein 12A
83	Q9CZJ2	Heat shock 70 kDa protein 12B
354	Q61696	Heat shock 70 kDa protein 1A
15	P17879	Heat shock 70 kDa protein 1B
104	P17156	Heat shock-related 70 kDa protein 2
169	Q61316	Heat shock 70 kDa protein 4
13	P48722-2	Heat shock 70 kDa protein 4L
398	P20029	78 kDa glucose-regulated protein
715	P63017	Heat shock cognate 71 kDa protein
218	P38647	Stress-70 protein, mitochondrial
353	P14602	Heat shock protein beta-1
50	Q5EBG6	Heat shock protein beta-6
39	P35385	Heat shock protein beta-7
29	Q9JK92	Heat shock protein beta-8
379	P63038	60 kDa heat shock protein, mitochondrial
3906	Q05793	Basement membrane-specific heparan sulfate protec
58	Q61699-2	Heat shock protein 105 kDa
108	Q9R118	Serine protease HTRA1
29	Q7TMY8-3	E3 ubiquitin-protein ligase HUWE1
106	Q9JKR6	Hypoxia up-regulated protein 1
15	Q9DB29	Isoamyl acetate-hydrolyzing esterase 1 homolog
17	Q8BU30	Isoleucine--tRNA ligase, cytoplasmic
88	Q8BIJ6	Isoleucine--tRNA ligase, mitochondrial
3	P13597-2	Intercellular adhesion molecule 1
15	P35330	Intercellular adhesion molecule 2
7	Q9JHR7	Insulin-degrading enzyme
133	O88844	Isocitrate dehydrogenase [NADP] cytoplasmic
315	P54071	Isocitrate dehydrogenase [NADP], mitochondrial
224	Q9D6R2	Isocitrate dehydrogenase [NAD] subunit alpha, mitoc
100	P70404	Isocitrate dehydrogenase [NAD] subunit gamma 1, m
14	Q9D8C4	Interferon-induced 35 kDa protein homolog
13	Q61249	Immunoglobulin-binding protein 1
4	P70389	Insulin-like growth factor-binding protein complex ac
14	P47880	Insulin-like growth factor-binding protein 6
190	Q61581	Insulin-like growth factor-binding protein 7
44	P01867-2	Ig gamma-2B chain C region
8	P01868	Ig gamma-1 chain C region secreted form
132	P01837	Ig kappa chain C region

3	Q9DBZ1-2	Inhibitor of nuclear factor kappa-B kinase-interacting
5	O88351	Inhibitor of nuclear factor kappa-B kinase subunit be
19	Q9CXY6	Interleukin enhancer-binding factor 2
7	Q9Z1X4-2	Interleukin enhancer-binding factor 3
4	Q8BU33-3	Acetolactate synthase-like protein
192	Q8CAQ8-3	MICOS complex subunit Mic60
52	O55023	Inositol monophosphatase 1
16	Q0GNC1-3	Inverted formin-2
37	P40936	Indolethylamine N-methyltransferase
35	P49442	Inositol polyphosphate 1-phosphatase
2	Q7TPD0	Integrator complex subunit 3
10	Q8VI75	Importin-4
94	Q8BKC5	Importin-5
54	Q9EPL8	Importin-7
5	Q91YE6	Importin-9
428	Q9JKF1	Ras GTPase-activating-like protein IQGAP1
3	Q8K3X4	Interferon regulatory factor 2-binding protein-like
3	Q64339	Ubiquitin-like protein ISG15
54	Q6GU68	Immunoglobulin superfamily containing leucine-rich
4	Q91V64	Isochorismatase domain-containing protein 1
132	P85094	Isochorismatase domain-containing protein 2A, mito
19	Q9JHU9	Inositol-3-phosphate synthase 1
3	Q8C863	E3 ubiquitin-protein ligase Itchy
26	Q3V3R4	Integrin alpha-1
33	Q9QUM0	Integrin alpha-IIb
71	Q62470	Integrin alpha-3
81	P11688	Integrin alpha-5
6	Q61739-2	Integrin alpha-6
539	A2ARA8	Integrin alpha-8
29	B8JK39	Integrin alpha-9
126	P43406	Integrin alpha-V
565	P09055	Integrin beta-1
51	O54890	Integrin beta-3
58	O70309	Integrin beta-5
16	Q9Z0T9	Integrin beta-6
84	Q61702	Inter-alpha-trypsin inhibitor heavy chain H1
25	Q61703	Inter-alpha-trypsin inhibitor heavy chain H2
58	A6X935	Inter alpha-trypsin inhibitor, heavy chain 4
26	Q9D892	Inosine triphosphate pyrophosphatase
137	P11881-8	Inositol 1,4,5-trisphosphate receptor type 1
11	P70227	Inositol 1,4,5-trisphosphate receptor type 3

66	Q9JHI5	Isovaleryl-CoA dehydrogenase, mitochondrial
16	P52332	Tyrosine-protein kinase JAK1
20	Q9ET78	Junctophilin-2
9	Q02257	Junction plakoglobin
174	Q8BX02	KN motif and ankyrin repeat domain-containing prot
39	Q99MN1	Lysine--tRNA ligase
23	Q9D3R6-3	Katanin p60 ATPase-containing subunit A-like 2
14	Q80UY2-2	E3 ubiquitin-protein ligase KCMF1
18	O88454-2	Potassium channel subfamily K member 4
50	G5E897	Protein O-glucosyltransferase 3
9	Q6GV12	3-ketodihydrosphingosine reductase
19	Q60749	KH domain-containing, RNA-binding, signal transduct
47	Q3U0V1	Far upstream element-binding protein 2
6	Q8C2E7	WASH complex subunit strumpellin
30	Q9EQW7	Kinesin-like protein KIF13A
1	P28741	Kinesin-like protein KIF3A
23	P33175	Kinesin heavy chain isoform 5A
87	Q61768	Kinesin-1 heavy chain
30	O88447	Kinesin light chain 1
8	Q9JM71	Kallikrein 1-related peptidase b27
8	P55200-2	Histone-lysine N-methyltransferase 2A
49	O08677-2	Kininogen-1
52	O35343	Importin subunit alpha-3
38	O35345	Importin subunit alpha-7
30	P32883-2	GTPase KRas
129	Q9ERE2	Keratin, type II cuticular Hb1
13	Q6IMF0	Keratin, type II cuticular Hb3
9	O08640	Keratin-associated protein 14
10	Q9QZU5	Keratin-associated protein 15-1
7	O08632	Keratin-associated protein 19-5
6	A2A591	Keratin-associated protein 3-1
37	Q9D3I6	Keratin-associated protein 7-1
1	Q61595-6	Kinectin
2	Q9CXA2	Trans-L-3-hydroxyproline dehydratase
9	Q99KR3	Beta-lactamase-like protein 2
93	Q60675	Laminin subunit alpha-2
232	P97927	Laminin subunit alpha-4
584	Q61001	Laminin subunit alpha-5
21	P02469	Laminin subunit beta-1
996	Q61292	Laminin subunit beta-2
597	P02468	Laminin subunit gamma-1

5	P11438	Lysosome-associated membrane glycoprotein 1
37	P17047-3	Lysosome-associated membrane glycoprotein 2
11	Q9CQ22	Ragulator complex protein LAMTOR1
4	Q9D1L9	Ragulator complex protein LAMTOR5
4	Q9JJK2	LanC-like protein 2
53	Q9CPY7-2	Cytosol aminopeptidase
9	Q8BMJ2	Leucine--tRNA ligase, cytoplasmic
40	Q61792	LIM and SH3 domain protein 1
27	Q61233	Plastin-2
202	Q9JKS4-3	LIM domain-binding protein 3
342	P06151	L-lactate dehydrogenase A chain
192	P16125	L-lactate dehydrogenase B chain
12	Q9Z1F6	Leukocyte cell-derived chemotaxin 1
34	Q6DVA0	LEM domain-containing protein 2
17	Q8CG70	Prolyl 3-hydroxylase 3
58	Q9Z2I0	LETM1 and EF-hand domain-containing protein 1, mit
25	Q924L1-2	LETM1 domain-containing protein 1
343	P16045	Galectin-1
22	P16110	Galectin-3
16	O89017	Legumain
2	P42703-2	Leukemia inhibitory factor receptor
25	Q3UH68-3	LIM and calponin homology domains-containing prot
152	Q99JW4	LIM and senescent cell antigen-like-containing domai
72	Q91XD2	LIM and senescent cell antigen-like-containing domai
6	Q9Z0M5	Lysosomal acid lipase/cholesteryl ester hydrolase
62	P54310	Hormone-sensitive lipase
30	Q9D0F3	Protein ERGIC-53
25	Q9DBH5	Vesicular integral-membrane protein VIP36
279	Q8VEE1	LIM and cysteine-rich domains protein 1
3	Q8C3X8	Lipase maturation factor 2
752	P48678	Prelamin-A/C
192	P14733	Lamin-B1
68	P21619	Lamin-B2
249	Q8BVA4	Leiomodin-1
49	Q8C129	Leucyl-cystinyl aminopeptidase
77	Q8CGK3	Lon protease homolog, mitochondrial
469	P97873	Lysyl oxidase homolog 1
8	Q9Z175	Lysyl oxidase homolog 3
6	P11152	Lipoprotein lipase
813	Q8BFW7	Lipoma-preferred partner homolog
277	Q91ZX7	Prolow-density lipoprotein receptor-related protein

24	P55302	Alpha-2-macroglobulin receptor-associated protein
82	Q6PB66	Leucine-rich PPR motif-containing protein, mitochon
137	Q9CXD9	Leucine-rich repeat-containing protein 17
16	Q8BGI7	Leucine-rich repeat-containing protein 39
9	Q9CRC8	Leucine-rich repeat-containing protein 40
7	Q8C031	Leucine-rich repeat-containing protein 4C
88	Q922Q8	Leucine-rich repeat-containing protein 59
17	Q3UZ39-2	Leucine-rich repeat flightless-interacting protein 1
10	P62311	U6 snRNA-associated Sm-like protein LSm3
7	P62322	U6 snRNA-associated Sm-like protein LSm5
10	Q9CQQ8	U6 snRNA-associated Sm-like protein LSm7
158	P24527	Leukotriene A-4 hydrolase
228	Q8CG19-2	Latent-transforming growth factor beta-binding prot
4	O08999	Latent-transforming growth factor beta-binding prot
27	Q61810	Latent-transforming growth factor beta-binding prot
862	Q8K4G1-2	Latent-transforming growth factor beta-binding prot
4	Q7TNC4-2	Putative RNA-binding protein Luc7-like 2
16	Q5SUF2	Luc7-like protein 3
713	P51885	Lumican
18	P70202	Latexin
18	P05533	Lymphocyte antigen 6A-2/6E-1
9	P0CW02	Lymphocyte antigen 6C1
92	P97823-2	Acyl-protein thioesterase 1
38	Q9WTL7	Acyl-protein thioesterase 2
5	Q91V16	LYR motif-containing protein 5
20	P24668	Cation-dependent mannose-6-phosphate receptor
17	Q9QXZ0	Microtubule-actin cross-linking factor 1
32	Q922B1	O-acetyl-ADP-ribose deacetylase MACROD1
39	Q91W89	Alpha-mannosidase 2C1
28	Q9CXI5	Mesencephalic astrocyte-derived neurotrophic facto
19	Q64133	Amine oxidase [flavin-containing] A
75	Q8BW75	Amine oxidase [flavin-containing] B
58	Q9QYR6	Microtubule-associated protein 1A
208	P14873	Microtubule-associated protein 1B
16	Q91VR7	Microtubule-associated proteins 1A/1B light chain 3
25	Q9CQV6	Microtubule-associated proteins 1A/1B light chain 3
22	Q8C052	Microtubule-associated protein 1S
38	P31938	Dual specificity mitogen-activated protein kinase kina
7	O09110-2	Dual specificity mitogen-activated protein kinase kina
2	P47809	Dual specificity mitogen-activated protein kinase kina
10	E9Q3S4	Mitogen-activated protein kinase kinase kinase 19

108	P27546-3	Microtubule-associated protein 4
12	Q7TSJ2-3	Microtubule-associated protein 6
42	P63085	Mitogen-activated protein kinase 1
2	P47811-4	Mitogen-activated protein kinase 14
14	Q63844	Mitogen-activated protein kinase 3
14	Q8R001-2	Microtubule-associated protein RP/EB family membe
4	Q68FL6	Methionine--tRNA ligase, cytoplasmic
9	Q7TQJ1	MARVEL domain-containing protein 1
2	Q3THS6	S-adenosylmethionine synthase isoform type-2
106	Q8K310	Matrin-3
44	P04247	Myoglobin
2	Q9Z2E1-2	Methyl-CpG-binding domain protein 2
13	P39039	Mannose-binding protein A
10	P41317	Mannose-binding protein C
38	Q9JKP5	Muscleblind-like protein 1
4	Q8CHK3	Lysophospholipid acyltransferase 7
16	P04370-4	Myelin basic protein
33	Q99MR8	Methylcrotonoyl-CoA carboxylase subunit alpha, mit
37	Q3ULD5	Methylcrotonoyl-CoA carboxylase beta chain, mitoch
6	Q9D1I5	Methylmalonyl-CoA epimerase, mitochondrial
15	Q8K5B2	Multiple coagulation factor deficiency protein 2 hom
11	P21843	Mast cell protease 3
85	P21812	Mast cell protease 4
16	Q3UMR5-2	Calcium uniporter protein, mitochondrial
187	P14152	Malate dehydrogenase, cytoplasmic
356	P08249	Malate dehydrogenase, mitochondrial
21	Q9D967	Magnesium-dependent phosphatase 1
167	P06801	NADP-dependent malic enzyme
43	Q9Z2D6	Methyl-CpG-binding protein 2
44	Q9DCS3	Trans-2-enoyl-CoA reductase, mitochondrial
8	Q80V70	Multiple epidermal growth factor-like domains prote
8	Q91VH6	Protein MEMO1
6	O08663	Methionine aminopeptidase 2
20	P55002	Microfibrillar-associated protein 2
210	Q9D1H9	Microfibril-associated glycoprotein 4
70	Q9QZJ6	Microfibrillar-associated protein 5
341	P21956-2	Lactadherin
1	Q80U63-2	Mitofusin-2
20	P19788	Matrix Gla protein
25	Q91VS7	Microsomal glutathione S-transferase 1
9	Q9CPU4	Microsomal glutathione S-transferase 3

32	Q8VDP3-2	Protein-methionine sulfoxide oxidase MICAL1
14	Q8BML1	Protein-methionine sulfoxide oxidase MICAL2
9	Q8BGT6-2	MICAL-like protein 1
117	P34884	Macrophage migration inhibitory factor
16	Q7TNS2	MICOS complex subunit Mic10
12	Q6ZQI3	Malectin
7	Q8C7H1	Methylmalonic aciduria type A homolog, mitochondr
1	Q8K273	Membrane magnesium transporter 1
4	Q9D071-2	MMS19 nucleotide excision repair protein homolog
1	Q61884	Meiosis-specific nuclear structural protein 1
7	Q80UM7	Mannosyl-oligosaccharide glucosidase
21	P56379	6.8 kDa mitochondrial proteolipid
33	P63030	Mitochondrial pyruvate carrier 1
86	Q9D023	Mitochondrial pyruvate carrier 2
13	P70290	55 kDa erythrocyte membrane protein
7	Q99J99	3-mercaptopyruvate sulfurtransferase
32	P27573	Myelin protein P0
42	Q61830	Macrophage mannose receptor 1
31	Q64449	C-type mannose receptor 2
4	Q8VCJ6	Mas-related G-protein coupled receptor member F
3	Q9CQT1	Methylthioribose-1-phosphate isomerase
1	Q9DB15	39S ribosomal protein L12, mitochondrial
20	Q9CQX8	28S ribosomal protein S36, mitochondrial
33	Q9WUX5-2	Protein MRVI1
620	P26041	Moesin
13	Q9D6Y7-3	Mitochondrial peptide methionine sulfoxide reducta
31	Q8BU85	Methionine-R-sulfoxide reductase B3, mitochondrial
78	Q9CQ65	S-methyl-5-thioadenosine phosphorylase
39	Q922Q1	Mitochondrial amidoxime reducing component 2
16	P03930	ATP synthase protein 8
115	Q791V5	Mitochondrial carrier homolog 2
115	P00405	Cytochrome c oxidase subunit 2
3	Q9CWE0	Mitochondrial fission regulator 1-like
51	Q922D8	C-1-tetrahydrofolate synthase, cytoplasmic
14	Q3V3R1	Monofunctional C1-tetrahydrofolate synthase, mitoc
1	P03911	NADH-ubiquinone oxidoreductase chain 4
26	P03921	NADH-ubiquinone oxidoreductase chain 5
2	Q9JLN9	Serine/threonine-protein kinase mTOR
99	P62774	Myotrophin
7	P47802	Metaxin-1
39	O88441	Metaxin-2

234	P28665	Murinoglobulin-1
16	P16332	Methylmalonyl-CoA mutase, mitochondrial
107	Q9EQK5	Major vault protein
24	O35682	Myeloid-associated differentiation marker
50	Q7TPV4	Myb-binding protein 1A
13	Q9EQS3	C-Myc-binding protein
11	P22366-2	Myeloid differentiation primary response protein My
3	Q9JK81	UPF0160 protein MYG1, mitochondrial
681	Q61879	Myosin-10
4868	O08638	Myosin-11
73	O08638-2	Myosin-11
30	Q6URW6-2	Myosin-14
140	Q5SX39	Myosin-4
369	Q8VDD5	Myosin-9
59	P05977	Myosin light chain 1/3, skeletal muscle isoform
60	Q3THE2	Myosin regulatory light chain 12B
437	Q60605	Myosin light polypeptide 6
471	Q9CQ19	Myosin regulatory light polypeptide 9
659	Q6PDN3-3	Myosin light chain kinase, smooth muscle
2	Q9JMH9-5	Unconventional myosin-XVIIIa
1	O88329	Unconventional myosin-Ia
534	Q9WTI7	Unconventional myosin-Ic
64	Q5SYD0	Unconventional myosin-Id
8	Q9QY06-3	Unconventional myosin-IXb
200	Q69ZN7	Myoferlin
21	Q8BR90	UPF0600 protein C5orf51 homolog
3	P01786	Ig heavy chain V region MOPC 47A
32	Q91V76	Ester hydrolase C11orf54 homolog
66	P01864	Ig gamma-2A chain C region secreted form
14	P01878	Ig alpha chain C region
27	P03987-2	Ig gamma-3 chain C region
13	P01668	Ig kappa chain V-III region PC 7210
7	Q6SKR2	
5	Q80UM3	N-alpha-acetyltransferase 15, NatA auxiliary subunit
31	Q9CZR2	N-acetylated-alpha-linked acidic dipeptidase 2
31	Q60817	Nascent polypeptide-associated complex subunit alpl
17	Q8VBW6	NEDD8-activating enzyme E1 regulatory subunit
27	Q9QWR8	Alpha-N-acetylgalactosaminidase
32	Q99KQ4	Nicotinamide phosphoribosyltransferase
64	P28656	Nucleosome assembly protein 1-like 1
47	Q78ZA7	Nucleosome assembly protein 1-like 4

29	Q9DB05	Alpha-soluble NSF attachment protein
13	Q8CC86	Nicotinate phosphoribosyltransferase
26	Q8BP47	Asparagine--tRNA ligase, cytoplasmic
25	Q91X97	Neurocalcin-delta
56	P13595-3	Neural cell adhesion molecule 1
2	Q8BLF1	Neutral cholesterol ester hydrolase 1
36	P28660-2	Nck-associated protein 1
76	P09405	Nucleolin
21	Q8VCM8	Nicalin
46	Q62433	Protein NDRG1
112	Q9QYG0-2	Protein NDRG2
3	O35683	NADH dehydrogenase [ubiquinone] 1 alpha subcomp
111	Q99LC3	NADH dehydrogenase [ubiquinone] 1 alpha subcomp
10	Q9D8B4	NADH dehydrogenase [ubiquinone] 1 alpha subcomp
50	Q7TMF3	NADH dehydrogenase [ubiquinone] 1 alpha subcomp
34	Q9ERS2	NADH dehydrogenase [ubiquinone] 1 alpha subcomp
13	Q9CQ75	NADH dehydrogenase [ubiquinone] 1 alpha subcomp
20	Q9CQ91	NADH dehydrogenase [ubiquinone] 1 alpha subcomp
40	Q62425	Cytochrome c oxidase subunit NDUFA4
15	Q9CPP6	NADH dehydrogenase [ubiquinone] 1 alpha subcomp
38	Q9CQZ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomp
85	Q9DCJ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomp
86	Q9DC69	NADH dehydrogenase [ubiquinone] 1 alpha subcomp
8	Q9D1H6	NADH dehydrogenase [ubiquinone] 1 alpha subcomp
1	Q9CWG8-2	NADH dehydrogenase [ubiquinone] complex I, assem
49	P0DN34	NADH dehydrogenase [ubiquinone] 1 beta subcompl
32	Q9DCS9	NADH dehydrogenase [ubiquinone] 1 beta subcompl
16	Q9CQZ6	NADH dehydrogenase [ubiquinone] 1 beta subcompl
18	Q9CQC7	NADH dehydrogenase [ubiquinone] 1 beta subcompl
15	Q9CQH3	NADH dehydrogenase [ubiquinone] 1 beta subcompl
5	Q3UIU2	NADH dehydrogenase [ubiquinone] 1 beta subcompl
19	Q9CR61	NADH dehydrogenase [ubiquinone] 1 beta subcompl
38	Q9CQJ8	NADH dehydrogenase [ubiquinone] 1 beta subcompl
34	Q9CQ54	NADH dehydrogenase [ubiquinone] 1 subunit C2
130	Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit, m
96	Q91WD5	NADH dehydrogenase [ubiquinone] iron-sulfur protei
83	Q9DCT2	NADH dehydrogenase [ubiquinone] iron-sulfur protei
29	Q9CXZ1	NADH dehydrogenase [ubiquinone] iron-sulfur protei
40	Q99LY9	NADH dehydrogenase [ubiquinone] iron-sulfur protei
27	P52503	NADH dehydrogenase [ubiquinone] iron-sulfur protei
10	Q9DC70	NADH dehydrogenase [ubiquinone] iron-sulfur protei

51	Q8K3J1	NADH dehydrogenase [ubiquinone] iron-sulfur protei
88	Q91YT0	NADH dehydrogenase [ubiquinone] flavoprotein 1, m
23	Q9D6J6	NADH dehydrogenase [ubiquinone] flavoprotein 2, m
1	Q8BK30	NADH dehydrogenase [ubiquinone] flavoprotein 3, m
11	Q9DC07	LIM zinc-binding domain-containing Nebulette
114	P46935	E3 ubiquitin-protein ligase NEDD4
40	P29595	NEDD8
11	P08553	Neurofilament medium polypeptide
27	Q922L6	Negative elongation factor D
23	Q6P5H2-2	Nestin
17	Q7TPW1	Nexilin
5	P97863-3	Nuclear factor 1 B-type
7	P70255-2	Nuclear factor 1 C-type
11	P70257-2	Nuclear factor 1 X-type
7	Q9QZ23	NFU1 iron-sulfur cluster scaffold homolog, mitochon
10	Q8CHT1-2	Ephexin-1
13	Q9D0T1	NHP2-like protein 1
251	P10493	Nidogen-1
110	O88322	Nidogen-2
30	Q9EQ80	NIF3-like protein 1
7	O70131	Ninjurin-1
46	Q8VDK1-2	Nitrilase homolog 1
84	Q9JHW2	Omega-amidase NIT2
8	Q3TL44	NLR family member X1
28	P15532	Nucleoside diphosphate kinase A
280	Q01768	Nucleoside diphosphate kinase B
2	Q9WV85	Nucleoside diphosphate kinase 3
3	Q8K2T1	NmrA-like family domain-containing protein 1
18	O70310	Glycylpeptide N-tetradecanoyltransferase 1
177	Q61941	NAD(P) transhydrogenase, mitochondrial
56	Q99K48	Non-POU domain-containing octamer-binding protei
21	Q6DFW4	Nucleolar protein 58
27	Q64299	Protein NOV homolog
9	Q6NSR8	Probable aminopeptidase NPEPL1
71	Q11011	Puromycin-sensitive aminopeptidase
73	Q61937	Nucleophosmin
341	Q91V88-4	Nephronectin
15	Q91V88-3	Nephronectin
53	P97300-3	Neuroplastin
49	Q64669	NAD(P)H dehydrogenase [quinone] 1
21	Q9JI75	Ribosyldihydronicotinamide dehydrogenase [quinone

48	P46460	Vesicle-fusing ATPase
20	Q9CZ44	NSFL1 cofactor p47
41	Q9JM14	5(3)-deoxyribonucleotidase, cytosolic type
8	Q61503	5-nucleotidase
67	O09118	Netrin-1
40	Q02819	Nucleobindin-1
17	P81117	Nucleobindin-2
24	O35685	Nuclear migration protein nudC
15	P0C028	Diphosphoinositol polyphosphate phosphohydrolase
9	Q6P3D0	U8 snoRNA-decapping enzyme
12	Q3U2V3	8-oxo-dGDP phosphatase NUDT18
52	Q9CQF3	Cleavage and polyadenylation specificity factor subur
16	Q8CH40	Nucleoside diphosphate-linked moiety X motif 6
2	Q99P30-5	Peroxisomal coenzyme A diphosphatase NUDT7
18	E9Q7G0	Nuclear mitotic apparatus protein 1
3	Q8R0G9	Nuclear pore complex protein Nup133
9	Q99P88	Nuclear pore complex protein Nup155
1	Q9Z0W3-2	Nuclear pore complex protein Nup160
10	Q8BJ71	Nuclear pore complex protein Nup93
75	P61971	Nuclear transport factor 2
10	Q5DTZ0	Protein NYNRIN
200	P29758	Ornithine aminotransferase, mitochondrial
17	Q9CRD0-3	OCIA domain-containing protein 1
613	Q60597	2-oxoglutarate dehydrogenase, mitochondrial
461	Q62000	Mimecan
76	Q9CZ30	Obg-like ATPase 1
5	O35103	Osteomodulin
48	P58281	Dynamin-like 120 kDa protein, mitochondrial
19	Q60590	Alpha-1-acid glycoprotein 1
28	Q3B7Z2-2	Oxysterol-binding protein 1
6	Q8CI95	Oxysterol-binding protein-related protein 11
15	Q9DBS9	Oxysterol-binding protein-related protein 3
11	A2A8Z1-2	Oxysterol-binding protein-related protein 9
1	Q78XF5	Oligosaccharyltransferase complex subunit OSTC
36	Q62422	Osteoclast-stimulating factor 1
85	Q7TQI3	Ubiquitin thioesterase OTUB1
285	Q9D0K2	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, m
22	Q6P9R2	Serine/threonine-protein kinase OSR1
285	P09103	Protein disulfide-isomerase
34	P50580-2	Proliferation-associated protein 2G4
87	P29341	Polyadenylate-binding protein 1

5	Q8CCS6-2	Polyadenylate-binding protein 2
36	Q9WVE8	Protein kinase C and casein kinase substrate in neuro
23	P63005	Platelet-activating factor acetylhydrolase IB subunit a
61	Q61206	Platelet-activating factor acetylhydrolase IB subunit b
41	Q9DCL9	Multifunctional protein ADE2
38	Q8CIN4	Serine/threonine-protein kinase PAK 2
2	Q9Z0P4	Paralemmin-1
3	Q8C0L6	Peroxisomal N(1)-acetyl-spermine/spermidine oxidas
4	Q9EPX2	Papilin
16	O88428	Bifunctional 3-phosphoadenosine 5-phosphosulfate s
231	Q99LX0	Protein deglycase DJ-1
6	Q8BZ20	Poly [ADP-ribose] polymerase 12
18	Q3ULW8-2	
165	Q9EPC1	Alpha-parvin
9	Q9ES46	Beta-parvin
35	Q925B0-2	PRKC apoptosis WT1 regulator protein
1	Q8BSQ9-2	Protein polybromo-1
87	Q3TVI8	Pre-B-cell leukemia transcription factor-interacting pr
207	Q05920	Pyruvate carboxylase, mitochondrial
95	P60335	Poly(rC)-binding protein 1
47	Q61990-2	Poly(rC)-binding protein 2
59	Q91ZA3	Propionyl-CoA carboxylase alpha chain, mitochondria
69	Q99MN9	Propionyl-CoA carboxylase beta chain, mitochondrial
57	Q8BH04	Phosphoenolpyruvate carboxykinase [GTP], mitochon
65	P23506	Protein-L-isoaspartate(D-aspartate) O-methyltransfer
26	Q9CQF9	Prenylcysteine oxidase
3	Q8C7K6	Prenylcysteine oxidase-like
2	P49586	Choline-phosphate cytidylyltransferase A
17	Q8VE70	Programmed cell death protein 10
31	P56812	Programmed cell death protein 5
91	P12815-2	Programmed cell death protein 6
202	Q9WU78	Programmed cell death 6-interacting protein
5	Q8BFQ8	Parkinson disease 7 domain-containing protein 1
52	Q9Z0X4	cGMP-inhibited 3,5-cyclic phosphodiesterase A
8	Q8CG03	cGMP-specific 3,5-cyclic phosphodiesterase
17	P05622	Platelet-derived growth factor receptor beta
140	P35486	Pyruvate dehydrogenase E1 component subunit alph
157	Q9D051	Pyruvate dehydrogenase E1 component subunit beta
4	Q8BKZ9	Pyruvate dehydrogenase protein X component, mitoc
452	P27773	Protein disulfide-isomerase A3
103	P08003	Protein disulfide-isomerase A4

4	Q921X9	Protein disulfide-isomerase A5
150	Q922R8	Protein disulfide-isomerase A6
5	Q9JK42	[Pyruvate dehydrogenase (acetyl-transferring)] kinas
12	Q922H2	[Pyruvate dehydrogenase (acetyl-transferring)] kinas
319	O70400	PDZ and LIM domain protein 1
218	O70209	PDZ and LIM domain protein 3
79	P70271	PDZ and LIM domain protein 4
16	Q3UV70	[Pyruvate dehydrogenase [acetyl-transferring]]-phos
7	Q6A026	Sister chromatid cohesion protein PDS5 homolog A
16	Q4VA53	Sister chromatid cohesion protein PDS5 homolog B
3	Q99K01-3	Pyridoxal-dependent decarboxylase domain-containi
56	Q8K183	Pyridoxal kinase
41	Q62048	Astrocytic phosphoprotein PEA-15
201	P70296	Phosphatidylethanolamine-binding protein 1
2	Q08481-4	Platelet endothelial cell adhesion molecule
15	Q11136	Xaa-Pro dipeptidase
5	Q8VCI5-2	Peroxisomal biogenesis factor 19
7	O09012-2	Peroxisomal targeting signal 1 receptor
81	Q9Z126	Platelet factor 4
8	O70591	Prefoldin subunit 2
31	Q9WU28	Prefoldin subunit 5
16	Q03958	Prefoldin subunit 6
57	P12382	ATP-dependent 6-phosphofructokinase, liver type
63	P47857	ATP-dependent 6-phosphofructokinase, muscle type
175	Q9WUA3	ATP-dependent 6-phosphofructokinase, platelet type
229	Q9DBJ1	Phosphoglycerate mutase 1
83	Q9DCD0	6-phosphogluconate dehydrogenase, decarboxylatin
345	P09411	Phosphoglycerate kinase 1
178	Q9CQ60	6-phosphogluconolactonase
144	Q9D0F9	Phosphoglucomutase-1
11	Q7TSV4	Phosphoglucomutase-2
5	Q9CYR6	Phosphoacetylglucosamine mutase
598	Q8BZF8	Phosphoglucomutase-like protein 5
22	Q8CHP8	Phosphoglycolate phosphatase
68	O55022	Membrane-associated progesterone receptor compo
8	Q80UU9	Membrane-associated progesterone receptor compo
124	P67778	Prohibitin
103	O35129	Prohibitin-2
9	Q61753	D-3-phosphoglycerate dehydrogenase
2	Q9DB26	Phytanoyl-CoA dioxygenase domain-containing prote
66	Q8BS03	Peptidase inhibitor 15

9	E9Q3L2	Phosphatidylinositol 4-kinase alpha
98	Q7M6Y3-2	Phosphatidylinositol-binding clathrin assembly protei
3	Q6PD26	GPI transamidase component PIG-S
11	Q9QUR7	Peptidyl-prolyl cis-trans isomerase NIMA-interacting
9	O70172	Phosphatidylinositol 5-phosphate 4-kinase type-2 alp
10	Q9D711	Pirin
48	P53810	Phosphatidylinositol transfer protein alpha isoform
2	P53811	Phosphatidylinositol transfer protein beta isoform
31	Q8K411-3	Presequence protease, mitochondrial
786	P52480	Pyruvate kinase PKM
67	P52480-2	Pyruvate kinase PKM
16	P70268	Serine/threonine-protein kinase N1
25	P47713	Cytosolic phospholipase A2
1	Q9Z1B3-2	1-phosphatidylinositol 4,5-bisphosphate phosphodies
19	P51432	1-phosphatidylinositol 4,5-bisphosphate phosphodies
156	Q8R3B1	1-phosphatidylinositol 4,5-bisphosphate phosphodies
496	Q9QXS1-2	Plectin
100	P20918	Plasminogen
185	Q8CGN5	Perilipin-1
83	Q9DBG5	Perilipin-3
235	O88492	Perilipin-4
8	Q9R1Q7	Proteolipid protein 2
464	Q99K51	Plastin-3
4	Q9JIZ9	Phospholipid scramblase 3
11	Q9DC11	Plexin domain-containing protein 2
11	B2RXS4	Plexin-B2
8	Q60953-2	Protein PML
19	Q9DC61	Mitochondrial-processing peptidase subunit alpha
5	O35691	Pinin
62	P23492	Purine nucleoside phosphorylase
30	Q7TQ62	Podocan
9	Q8VHI3	GDP-fucose protein O-fucosyltransferase 2
16	Q8BYB9	Protein O-glucosyltransferase 1
16	Q923G2	DNA-directed RNA polymerases I, II, and III subunit R
11	P52430	Serum paraoxonase/arylesterase 1
85	Q62087	Serum paraoxonase/lactonase 3
93	P37040	NADPH--cytochrome P450 reductase
18	Q62009-5	Periostin
48	Q9D819	Inorganic pyrophosphatase
12	Q91VM9	Inorganic pyrophosphatase 2, mitochondrial
440	P17742	Peptidyl-prolyl cis-trans isomerase A

147	P24369	Peptidyl-prolyl cis-trans isomerase B
39	Q9CR16	Peptidyl-prolyl cis-trans isomerase D
14	Q9R269	Periplakin
16	P36993-4	Protein phosphatase 1B
23	Q8BVQ5	Protein phosphatase methylesterase 1
14	P62137	Serine/threonine-protein phosphatase PP1-alpha cat
279	P62141	Serine/threonine-protein phosphatase PP1-beta cata
3	P63087	Serine/threonine-protein phosphatase PP1-gamma c
190	Q9DBR7-2	Protein phosphatase 1 regulatory subunit 12A
13	Q8BG95	Protein phosphatase 1 regulatory subunit 12B
9	Q3UMT1	Protein phosphatase 1 regulatory subunit 12C
76	Q91VC7	Protein phosphatase 1 regulatory subunit 14A
50	Q3UM45	Protein phosphatase 1 regulatory subunit 7
46	P63330	Serine/threonine-protein phosphatase 2A catalytic su
406	Q76MZ3	Serine/threonine-protein phosphatase 2A 65 kDa reg
35	Q6P1F6	Serine/threonine-protein phosphatase 2A 55 kDa reg
71	P58389	Serine/threonine-protein phosphatase 2A activator
6	Q6PD03	Serine/threonine-protein phosphatase 2A 56 kDa reg
23	Q60996-2	Serine/threonine-protein phosphatase 2A 56 kDa reg
2	Q9CQR6	Serine/threonine-protein phosphatase 6 catalytic su
7	Q922D4-4	Serine/threonine-protein phosphatase 6 regulatory s
42	O88531	Palmitoyl-protein thioesterase 1
23	Q9JIG8	PRA1 family protein 2
343	P35700	Peroxiredoxin-1
170	Q61171	Peroxiredoxin-2
60	P20108	Thioredoxin-dependent peroxide reductase, mitocho
77	O08807	Peroxiredoxin-4
211	P99029-2	Peroxiredoxin-5, mitochondrial
234	O08709	Peroxiredoxin-6
1022	Q9JK53	Prolargin
20	Q9QUR6	Prolyl endopeptidase
31	Q5EG47	5-AMP-activated protein kinase catalytic subunit alp
28	P05132-2	cAMP-dependent protein kinase catalytic subunit alp
22	O54950	5-AMP-activated protein kinase subunit gamma-1
40	Q9DBC7	cAMP-dependent protein kinase type I-alpha regulat
32	P12367	cAMP-dependent protein kinase type II-alpha regulat
15	P31324	cAMP-dependent protein kinase type II-beta regulat
5	P20444	Protein kinase C alpha type
21	P28867	Protein kinase C delta type
176	Q91VJ2	Protein kinase C delta-binding protein
14	O08795	Glucosidase 2 subunit beta

82	P0C605-2	cGMP-dependent protein kinase 1
2	Q9WTX2	Interferon-inducible double-stranded RNA-dependen
6	P33587	Vitamin K-dependent protein C
13	Q64695	Endothelial protein C receptor
31	Q9Z2Y8	Proline synthase co-transcribed bacterial homolog pr
20	Q99KP6	Pre-mRNA-processing factor 19
40	P15331-3	Peripherin
35	Q9D7G0	Ribose-phosphate pyrophosphokinase 1
24	Q9D0M1	Phosphoribosyl pyrophosphate synthase-associated
110	Q61207	Prosaposin
90	Q9R1P4	Proteasome subunit alpha type-1
75	P49722	Proteasome subunit alpha type-2
36	O70435	Proteasome subunit alpha type-3
55	Q9Z2U1	Proteasome subunit alpha type-5
82	Q9QUM9	Proteasome subunit alpha type-6
57	Q9Z2U0	Proteasome subunit alpha type-7
82	O09061	Proteasome subunit beta type-1
57	Q9R1P3	Proteasome subunit beta type-2
48	Q9R1P1	Proteasome subunit beta type-3
31	P99026	Proteasome subunit beta type-4
20	O55234	Proteasome subunit beta type-5
24	Q60692	Proteasome subunit beta type-6
21	P70195	Proteasome subunit beta type-7
34	P46471	26S protease regulatory subunit 7
63	O88685	26S protease regulatory subunit 6A
47	P62196	26S protease regulatory subunit 8
61	P62334	26S protease regulatory subunit 10B
57	Q3TXS7	26S proteasome non-ATPase regulatory subunit 1
90	Q8BG32	26S proteasome non-ATPase regulatory subunit 11
38	Q9D8W5	26S proteasome non-ATPase regulatory subunit 12
37	Q9WVJ2	26S proteasome non-ATPase regulatory subunit 13
45	O35593	26S proteasome non-ATPase regulatory subunit 14
33	P14685	26S proteasome non-ATPase regulatory subunit 3
7	O35226	26S proteasome non-ATPase regulatory subunit 4
59	Q8BJY1	26S proteasome non-ATPase regulatory subunit 5
13	Q99JI4	26S proteasome non-ATPase regulatory subunit 6
89	P26516	26S proteasome non-ATPase regulatory subunit 7
28	Q9CX56	26S proteasome non-ATPase regulatory subunit 8
10	Q9CR00	26S proteasome non-ATPase regulatory subunit 9
118	P97371	Proteasome activator complex subunit 1
5	Q9JK23	Proteasome assembly chaperone 1

209	P17225	Polypyrimidine tract-binding protein 1
3	Q91Z31	Polypyrimidine tract-binding protein 2
1	Q14C51	Pentatricopeptide repeat domain-containing protein
2	Q60866-2	Phosphotriesterase-related protein
10	Q8BWM0	Prostaglandin E synthase 2
42	Q9R0Q7	Prostaglandin E synthase 3
4	Q9WV91	Prostaglandin F2 receptor negative regulator
532	O35074	Prostacyclin synthase
13	Q91YR9	Prostaglandin reductase 1
9	Q8VDQ1-2	Prostaglandin reductase 2
15	P22437	Prostaglandin G/H synthase 1
16	Q9D0J8	Parathymosin
14	O70274	Protein tyrosine phosphatase type IVA 2
34	P35235-2	Tyrosine-protein phosphatase non-receptor type 11
3	Q6PB44-2	Tyrosine-protein phosphatase non-receptor type 23
2	P06800-6	Receptor-type tyrosine-protein phosphatase C
30	Q8R2Y8	Peptidyl-tRNA hydrolase 2, mitochondrial
12	Q3UEB3-3	Poly(U)-binding-splicing factor PUF60
50	P42669	Transcriptional activator protein Pur-alpha
20	Q3UQ28	Peroxidasin homolog
46	Q8VI36-2	Paxillin
302	Q8CI94	Glycogen phosphorylase, brain form
41	Q9ET01	Glycogen phosphorylase, liver form
330	Q9WUB3	Glycogen phosphorylase, muscle form
92	Q8BML9	Glutamine-tRNA ligase
49	Q8BVI4	Dihydropteridine reductase
32	Q8R404	Protein QIL1
4	Q9QYS9-8	Protein quaking
43	P61027	Ras-related protein Rab-10
43	P46638	Ras-related protein Rab-11B
12	P35283	Ras-related protein Rab-12
30	Q91V41	Ras-related protein Rab-14
35	P35293	Ras-related protein Rab-18
104	P62821	Ras-related protein Rab-1A
55	Q9D1G1	Ras-related protein Rab-1B
30	P35282	Ras-related protein Rab-21
16	Q99P58	Ras-related protein Rab-27B
13	P53994	Ras-related protein Rab-2A
11	Q64008	Ras-related protein Rab-34
20	Q6PHN9	Ras-related protein Rab-35
7	Q9CQD1	Ras-related protein Rab-5A

80	P61021	Ras-related protein Rab-5B
32	P35278	Ras-related protein Rab-5C
29	P61294	Ras-related protein Rab-6B
95	P51150	Ras-related protein Rab-7a
5	P55258	Ras-related protein Rab-8A
5	P61028	Ras-related protein Rab-8B
143	P63001	Ras-related C3 botulinum toxin substrate 1
17	P54728	UV excision repair protein RAD23 homolog B
18	P63321	Ras-related protein Ral-A
5	Q64012-2	RNA-binding protein Raly
34	P34022	Ran-specific GTPase-activating protein
16	Q9ERU9	E3 SUMO-protein ligase RanBP2
6	P46061	Ran GTPase-activating protein 1
35	P62835	Ras-related protein Rap-1A
148	Q99JI6	Ras-related protein Rap-1b
3	Q8BU31	Ras-related protein Rap-2c
15	Q9DD06	Retinoic acid receptor responder protein 2
95	Q9D0I9	Arginine--tRNA ligase, cytoplasmic
9	Q9CW46	Ribonucleoprotein PTB-binding 1
46	Q60972	Histone-binding protein RBBP4
2	Q60973	Histone-binding protein RBBP7
82	O88851	Putative hydrolase RBBP9
6	Q8C2Q3	RNA-binding protein 14
10	Q8R3C6	Probable RNA-binding protein 19
9	B2RY56	RNA-binding protein 25
40	O89086	RNA-binding protein 3
17	Q8VH51-2	RNA-binding protein 39
16	Q91VM5	RNA binding motif protein, X-linked-like-1
190	Q00915	Retinol-binding protein 1
15	Q00724	Retinol-binding protein 4
67	Q9WVB0	RNA-binding protein with multiple splicing
8	Q8VC52	RNA-binding protein with multiple splicing 2
11	Q8VE37	Regulator of chromosome condensation
9	Q8BP92	Reticulocalbin-2
41	Q8BH97	Reticulocalbin-3
11	Q9QYF1	Retinol dehydrogenase 11
7	Q9ERI6	Retinol dehydrogenase 14
29	P26043	Radixin
17	Q60870	Receptor expression-enhancing protein 5
12	Q9D8S4	Oligoribonuclease, mitochondrial
10	Q99PG4	Regulator of G-protein signaling 18

186	Q9QUI0	Transforming protein RhoA
13	P62746	Rho-related GTP-binding protein RhoB
8	Q62159	Rho-related GTP-binding protein RhoC
3	Q8R527	Rho-related GTP-binding protein RhoQ
24	Q9JJC6	RILP-like protein 1
18	Q9DCV4	Regulator of microtubule dynamics protein 1
16	Q3UJU9	Regulator of microtubule dynamics protein 3
194	Q91VI7	Ribonuclease inhibitor
46	Q8VCT3	Aminopeptidase B
110	P70335-2	Rho-associated protein kinase 1
43	P70336	Rho-associated protein kinase 2
1	Q8VEE0	Ribulose-phosphate 3-epimerase
73	Q6ZWV3	60S ribosomal protein L10
68	P53026	60S ribosomal protein L10a
16	Q9CXW4	60S ribosomal protein L11
55	P35979	60S ribosomal protein L12
100	P47963	60S ribosomal protein L13
25	P19253	60S ribosomal protein L13a
66	Q9CR57	60S ribosomal protein L14
94	Q9CZM2	60S ribosomal protein L15
62	Q9CPR4	60S ribosomal protein L17
39	P35980	60S ribosomal protein L18
32	P62717	60S ribosomal protein L18a
31	P84099	60S ribosomal protein L19
21	O09167	60S ribosomal protein L21
33	P67984	60S ribosomal protein L22
21	P62830	60S ribosomal protein L23
46	P62751	60S ribosomal protein L23a
79	Q8BP67	60S ribosomal protein L24
19	P61255	60S ribosomal protein L26
30	P61358	60S ribosomal protein L27
49	P14115	60S ribosomal protein L27a
3	P41105	60S ribosomal protein L28
105	P27659	60S ribosomal protein L3
17	P62889	60S ribosomal protein L30
16	P62900	60S ribosomal protein L31
52	P62911	60S ribosomal protein L32
9	Q9D1R9	60S ribosomal protein L34
16	Q6ZWV7	60S ribosomal protein L35
27	O55142	60S ribosomal protein L35a
17	P47964	60S ribosomal protein L36

2	P61514	60S ribosomal protein L37a
34	Q9JJI8	60S ribosomal protein L38
25	P62892	60S ribosomal protein L39
250	Q9D8E6	60S ribosomal protein L4
64	P47962	60S ribosomal protein L5
111	P47911	60S ribosomal protein L6
130	P14148	60S ribosomal protein L7
140	P12970	60S ribosomal protein L7a
33	P62918	60S ribosomal protein L8
32	P51410	60S ribosomal protein L9
130	P14869	60S acidic ribosomal protein P0
77	P47955	60S acidic ribosomal protein P1
105	P99027	60S acidic ribosomal protein P2
202	Q91YQ5	Dolichyl-diphosphooligosaccharide--protein glycosylt
104	Q9DBG6	Dolichyl-diphosphooligosaccharide--protein glycosylt
51	P63325	40S ribosomal protein S10
40	P62281	40S ribosomal protein S11
97	P63323	40S ribosomal protein S12
152	P62301	40S ribosomal protein S13
26	P62264	40S ribosomal protein S14
86	P62843	40S ribosomal protein S15
56	P62245	40S ribosomal protein S15a
3	P14131	40S ribosomal protein S16
36	P63276	40S ribosomal protein S17
51	P62270	40S ribosomal protein S18
54	Q9CZX8	40S ribosomal protein S19
85	P25444	40S ribosomal protein S2
49	P60867	40S ribosomal protein S20
1	Q9CQR2	40S ribosomal protein S21
27	P62267	40S ribosomal protein S23
42	P62849-2	40S ribosomal protein S24
40	P62852	40S ribosomal protein S25
41	P62855	40S ribosomal protein S26
54	P62983	Ubiquitin-40S ribosomal protein S27a
21	Q6ZWY3	40S ribosomal protein S27-like
1	P62858	40S ribosomal protein S28
14	P62274	40S ribosomal protein S29
72	P62908	40S ribosomal protein S3
139	P97351	40S ribosomal protein S3a
158	P62702	40S ribosomal protein S4, X isoform
78	P97461	40S ribosomal protein S5

14	P62754	40S ribosomal protein S6
12	P18654	Ribosomal protein S6 kinase alpha-3
84	P62082	40S ribosomal protein S7
75	P62242	40S ribosomal protein S8
75	Q6ZWN5	40S ribosomal protein S9
169	P14206	40S ribosomal protein SA
5	Q8K4Q0-3	Regulatory-associated protein of mTOR
16	O88667	GTP-binding protein RAD
107	P10833	Ras-related protein R-Ras
126	Q99PL5	Ribosome-binding protein 1
393	Q01730	Ras suppressor protein 1
17	Q9D7H3	RNA 3-terminal phosphate cyclase
50	Q99LF4	tRNA-splicing ligase RtcB homolog
13	Q8K0T0	Reticulon-1
3	O70622-2	Reticulon-2
13	Q9ES97-3	Reticulon-3
6	Q99P72	Reticulon-4
93	Q99P72-5	Reticulon-4
69	Q9CQE8	RNA transcription, translation ad transport factor pro
1	Q8BIJ7	RUN and FYVE domain-containing protein 1
40	P60122	RuvB-like 1
1	E9PZQ0	Ryanodine receptor 1
10	P56565	Protein S100-A1
119	P50543	Protein S100-A11
8	P97352	Protein S100-A13
97	P07091	Protein S100-A4
10	P63084	Protein S100-A5
46	P14069	Protein S100-A6
1	Q9D2C2-2	Protein SAAL1
28	Q9EP69	Phosphatidylinositide phosphatase SAC1
43	Q9R1T2	SUMO-activating enzyme subunit 1
16	Q80YR5	Scaffold attachment factor B2
41	Q8BGH2	Sorting and assembly machinery component 50 homo
59	P36536	GTP-binding protein SAR1a
7	Q9CQC9	GTP-binding protein SAR1b
62	P26638	Serine--tRNA ligase, cytoplasmic
5	Q8K021	Secretory carrier-associated membrane protein 1
5	Q8K299-3	Scavenger receptor class A member 5
21	O35114	Lysosome membrane protein 2
27	Q8R127	Saccharopine dehydrogenase-like oxidoreductase
32	Q8BRF7	Sec1 family domain-containing protein 1

14	Q78YZ6-3	Short coiled-coil protein
41	P32020-2	Non-specific lipid-transfer protein
17	Q920A5	Retinoid-inducible serine carboxypeptidase
21	Q9CZC8	Secernin-1
3	Q8VCA8	Secernin-2
38	Q66PY1	Signal peptide, CUB and EGF-like domain-containing
151	Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein
105	Q9CQA3	Succinate dehydrogenase [ubiquinone] iron-sulfur su
38	Q9CZB0	Succinate dehydrogenase cytochrome b560 subunit,
15	Q9CXV1	Succinate dehydrogenase [ubiquinone] cytochrome
17	Q9R0P6	Signal peptidase complex catalytic subunit SEC11A
9	Q9D1M0	Protein SEC13 homolog
60	O08547	Vesicle-trafficking protein SEC22b
137	Q01405	Protein transport protein Sec23A
12	Q9D662	Protein transport protein Sec23B
10	Q6NZC7	SEC23-interacting protein
162	Q3UPL0-2	Protein transport protein Sec31A
20	Q3TZ89-2	Protein transport protein Sec31B
30	P61620	Protein transport protein Sec61 subunit alpha isofor
209	P17563	Selenium-binding protein 1
4	Q8VHC3	Selenoprotein M
1	Q9DBC0	Selenoprotein O
3	P62342	Selenoprotein T
4	Q8BH69	Selenide, water dikinase 1
15	P70274	Selenoprotein P
5	Q8C1B7-3	Septin-11
38	Q9Z2Q6	Septin-5
103	O55131	Septin-7
21	Q8CHH9	Septin-8
12	Q9CY58-4	Plasminogen activator inhibitor 1 RNA-binding protei
29	P07758	Alpha-1-antitrypsin 1-1
54	P22599	Alpha-1-antitrypsin 1-2
416	Q00896	Alpha-1-antitrypsin 1-3
106	Q00897	Alpha-1-antitrypsin 1-4
101	Q00898	Alpha-1-antitrypsin 1-5
145	P07759	Serine protease inhibitor A3K
16	Q91WP6	Serine protease inhibitor A3N
3	Q06770	Corticosteroid-binding globulin
7	Q9D154	Leukocyte elastase inhibitor A
207	Q60854	Serpin B6
265	P32261	Antithrombin-III

32	P49182	Heparin cofactor 2
288	Q07235	Glia-derived nexin
56	P97298	Pigment epithelium-derived factor
17	Q61247	Alpha-2-antiplasmin
56	P97290	Plasma protease C1 inhibitor
23	Q9EQU5-2	Protein SET
5	Q8VHL1	Histone-lysine N-methyltransferase SETD7
40	Q64213-2	Splicing factor 1
7	Q8K4Z5	Splicing factor 3A subunit 1
6	Q62203	Splicing factor 3A subunit 2
21	Q99NB9	Splicing factor 3B subunit 1
11	Q921M3-2	Splicing factor 3B subunit 3
13	Q8QZY9	Splicing factor 3B subunit 4
11	O70456	14-3-3 protein sigma
110	Q8VIJ6	Splicing factor, proline- and glutamine-rich
29	Q8C4U3	Secreted frizzled-related protein 1
19	Q99JR1	Sideroflexin-1
211	Q91V61	Sideroflexin-3
22	P82350	Alpha-sarcoglycan
28	P82349	Beta-sarcoglycan
55	P82347	Delta-sarcoglycan
66	O70258	Epsilon-sarcoglycan
10	P82348	Gamma-sarcoglycan
9	Q8R0X7	Sphingosine-1-phosphate lyase 1
13	Q8BJU0-2	Small glutamine-rich tetratricopeptide repeat-contai
111	Q9JJU8	SH3 domain-binding glutamic acid-rich-like protein
12	Q91VW3	SH3 domain-binding glutamic acid-rich-like protein 3
29	Q7TSG5	SH3 domain-containing protein 21
5	Q62419	Endophilin-A2
14	Q9JK48	Endophilin-B1
11	Q8R3V5-3	Endophilin-B2
12	O89032-3	SH3 and PX domain-containing protein 2A
25	Q9CZN7-2	Serine hydroxymethyltransferase
16	Q61079	Single-minded homolog 2
2	Q8VDQ8-3	NAD-dependent protein deacetylase sirtuin-2
20	Q9WTX5	S-phase kinase-associated protein 1
3	Q924N4	Solute carrier family 12 member 6
6	P51912	Neutral amino acid transporter B(0)
84	Q8JZU2	Tricarboxylate transport protein, mitochondrial
15	Q9QZD8	Mitochondrial dicarboxylate carrier
66	Q9CR62	Mitochondrial 2-oxoglutarate/malate carrier protein

81	Q8BH59	Calcium-binding mitochondrial carrier protein Aralar1
33	Q9Z2Z6	Mitochondrial carnitine/acylcarnitine carrier protein
44	Q8BMD8	Calcium-binding mitochondrial carrier protein SCaMC
136	Q8VEM8	Phosphate carrier protein, mitochondrial
421	P48962	ADP/ATP translocase 1
14	Q8R0Y8	Mitochondrial coenzyme A transporter SLC25A42
102	P51881	ADP/ATP translocase 2
5	Q5HZI9	Solute carrier family 25 member 51
15	Q60714	Long-chain fatty acid transport protein 1
15	Q9JIM1-2	Equilibrative nucleoside transporter 1
4	P17809	Solute carrier family 2, facilitated glucose transporter
8	P10852	4F2 cell-surface antigen heavy chain
21	Q8BY89-2	Choline transporter-like protein 2
210	P04919-2	Band 3 anion transport protein
7	Q8BTY2	Sodium bicarbonate cotransporter 3
26	Q9WVB4	Slit homolog 3 protein
145	Q3URD3-4	Sarcolemmal membrane-associated protein
2	Q6DIC0	Probable global transcription activator SNF2L2
16	Q91ZW3	SWI/SNF-related matrix-associated actin-dependent
17	Q6PDG5-2	SWI/SNF complex subunit SMARCC2
25	Q9CU62	Structural maintenance of chromosomes protein 1A
8	Q9CW03	Structural maintenance of chromosomes protein 3
2	Q9DB10	Essential MCU regulator, mitochondrial
79	Q8BLY1-2	SPARC-related modular calcium-binding protein 1
15	Q6ZPR5-3	Sphingomyelin phosphodiesterase 4
2	P70158	Acid sphingomyelinase-like phosphodiesterase 3a
15	P58242	Acid sphingomyelinase-like phosphodiesterase 3b
23	Q3UKJ7-2	WD40 repeat-containing protein SMU1
14	Q9Z0F7	Gamma-synuclein
88	Q78PY7	Staphylococcal nuclease domain-containing protein 1
43	Q6P4T2	U5 small nuclear ribonucleoprotein 200 kDa helicase
20	Q62376-2	U1 small nuclear ribonucleoprotein 70 kDa
15	Q62189	U1 small nuclear ribonucleoprotein A
12	Q9CQI7	U2 small nuclear ribonucleoprotein B
16	P62315	Small nuclear ribonucleoprotein Sm D1
29	P62320	Small nuclear ribonucleoprotein Sm D3
17	P62305	Small nuclear ribonucleoprotein E
18	P62307	Small nuclear ribonucleoprotein F
12	P62309	Small nuclear ribonucleoprotein G
20	Q61234	Alpha-1-syntrophin
117	Q99L88	Beta-1-syntrophin

102	Q61235	Beta-2-syntrophin
34	O70493	Sorting nexin-12
1	Q8BVL3	Sorting nexin-17
89	Q91ZR2	Sorting nexin-18
9	Q9CWK8	Sorting nexin-2
19	O70492	Sorting nexin-3
10	Q91YJ2	Sorting nexin-4
21	Q9D8U8	Sorting nexin-5
2	Q6P8X1	Sorting nexin-6
40	Q91VH2	Sorting nexin-9
62	P08228	Superoxide dismutase [Cu-Zn]
111	P09671	Superoxide dismutase [Mn], mitochondrial
348	O09164	Extracellular superoxide dismutase [Cu-Zn]
144	Q62417-2	Sorbin and SH3 domain-containing protein 1
185	Q3UTJ2-4	Sorbin and SH3 domain-containing protein 2
33	Q9R1Z8	Vinexin
29	Q64442	Sorbitol dehydrogenase
99	Q99P68	Sclerostin
9	Q58A65-6	C-Jun-amino-terminal kinase-interacting protein 4
4	P70663	SPARC-like protein 1
4	Q9CYN2	Signal peptidase complex subunit 2
13	Q8VCC9	Spondin-1
57	Q64105	Sepiapterin reductase
173	P08032	Spectrin alpha chain, erythrocytic 1
904	P16546-2	Spectrin alpha chain, non-erythrocytic 1
106	P15508	Spectrin beta chain, erythrocytic
762	Q62261	Spectrin beta chain, non-erythrocytic 1
95	Q6P069-2	Sorcin
10	Q64674	Spermidine synthase
1	P16254	Signal recognition particle 14 kDa protein
25	P14576	Signal recognition particle 54 kDa protein
26	Q9R0M3-2	Sushi-repeat-containing protein SRPX
12	Q52KI8-2	Serine/arginine repetitive matrix protein 1
7	Q99MR6-3	Serrate RNA effector molecule homolog
10	Q6PDM2-3	Serine/arginine-rich splicing factor 1
19	Q9R0U0-3	Serine/arginine-rich splicing factor 10
18	Q62093	Serine/arginine-rich splicing factor 2
15	Q3TWW8	Serine/arginine-rich splicing factor 6
16	Q8BL97-3	Serine/arginine-rich splicing factor 7
46	P32067	Lupus La protein homolog
11	Q9CYR0	Single-stranded DNA-binding protein, mitochondrial

14	Q62147	Sarcospan
16	Q9CY50	Translocon-associated protein subunit alpha
9	Q62186	Translocon-associated protein subunit delta
57	Q99L47	Hsc70-interacting protein
8	O88829-2	Lactosylceramide alpha-2,3-sialyltransferase
23	P42227-2	Signal transducer and activator of transcription 3
10	Q8CI59	Metalloreductase STEAP3
28	P70302	Stromal interaction molecule 1
144	Q60864	Stress-induced-phosphoprotein 1
71	Q99KH8	Serine/threonine-protein kinase 24
3	Q9Z1W9	STE20/SPS1-related proline-alanine-rich protein kina
65	P54116	Erythrocyte band 7 integral membrane protein
14	Q99JB2	Stomatin-like protein 2, mitochondrial
4	Q8CDJ8	Stonin-1
9	Q9Z1Z2	Serine-threonine kinase receptor-associated protein
9	P50427	Steryl-sulfatase
7	P46978	Dolichyl-diphosphooligosaccharide--protein glycosylt
17	Q3TDQ1	Dolichyl-diphosphooligosaccharide--protein glycosylt
20	Q9ER00	Syntaxin-12
7	Q8BVI5	Syntaxin-16
11	O70439	Syntaxin-7
64	Q60770-2	Syntaxin-binding protein 3
106	Q9Z2I9	Succinyl-CoA ligase [ADP-forming] subunit beta, mito
144	Q9WUM5	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha
73	Q9Z2I8-2	Succinyl-CoA ligase [GDP-forming] subunit beta, mito
11	Q9CX34	Suppressor of G2 allele of SKP1 homolog
1	Q8K007	Extracellular sulfatase Sulf-1
14	Q9D666-5	SUN domain-containing protein 1
102	Q8BJS4-3	SUN domain-containing protein 2
1	Q8R086	Sulfite oxidase, mitochondrial
36	Q64310	Surfeit locus protein 4
102	Q9DBX3	Sushi domain-containing protein 2
30	Q8K4L3	Supervillin
3	Q9EPM5-3	Syncoilin
71	Q7TMK9-2	Heterogeneous nuclear ribonucleoprotein Q
54	Q6ZWR6-4	Nesprin-1
5	Q6ZWQ0	Nesprin-2
12	Q70IV5-2	Synemin
99	Q8CC35-2	Synaptopodin
1331	P37804	Transgelin
10	Q9R1Q8	Transgelin-3

91	Q93092	Transaldolase
14	Q9R233-2	Tapasin
57	Q921F2	TAR DNA-binding protein 43
32	Q9D0R2	Threonine--tRNA ligase, cytoplasmic
8	Q60949-2	TBC1 domain family member 1
9	Q8BYA0	Tubulin-specific chaperone D
11	P10711	Transcription elongation factor A protein 1
35	P83940	Transcription elongation factor B polypeptide 1
36	P62869	Transcription elongation factor B polypeptide 2
4	O88968	Transcobalamin-2
146	P11983	T-complex protein 1 subunit alpha
98	P47226-2	Testin
499	Q921I1	Serotransferrin
592	Q62219	Transforming growth factor beta-1-induced transcrip
339	P82198	Transforming growth factor-beta-induced protein ig-h
554	P21981	Protein-glutamine gamma-glutamyltransferase 2
6	P24529	Tyrosine 3-monooxygenase
100	P35441	Thrombospondin-1
9	Q99J36	THUMP domain-containing protein 1
26	P01831	Thy-1 membrane glycoprotein
8	P62075	Mitochondrial import inner membrane translocase su
14	O35857	Mitochondrial import inner membrane translocase su
16	Q9D880	Mitochondrial import inner membrane translocase su
16	P39876	Metalloproteinase inhibitor 3
367	Q99JR5	Tubulointerstitial nephritis antigen-like
18	P39447	Tight junction protein ZO-1
523	P40142	Transketolase
2582	P26039	Talin-1
39	Q71LX4	Talin-2
14	Q921L3	Transmembrane and coiled-coil domain-containing p
43	Q9D1D4	Transmembrane emp24 domain-containing protein 1
49	Q9R0Q3	Transmembrane emp24 domain-containing protein 2
18	Q99KF1	Transmembrane emp24 domain-containing protein 9
2	Q9CQN6	Transmembrane protein 14C
6	Q9CR64-2	Protein kish-A
144	Q9DBS1	Transmembrane protein 43
2	P49813	Tropomodulin-1
46	Q9JHJ0	Tropomodulin-3
103	Q61029-2	Lamina-associated polypeptide 2, isoforms beta/delta
16	Q61033	Lamina-associated polypeptide 2, isoforms alpha/zeta
4	Q6ZWY8	Thymosin beta-10

121	P20065-2	Thymosin beta-4
11	Q8BRH0	Transmembrane and TPR repeat-containing protein
13	Q8VBT0	Thioredoxin-related transmembrane protein 1
3	Q9D710	Thioredoxin-related transmembrane protein 2
12	Q8C0L0	Thioredoxin-related transmembrane protein 4
37	Q80YX1-2	Tenascin
6	Q921Z5	Tumor necrosis factor alpha-induced protein 8
54	Q8BFY9-2	Transportin-1
2	Q99LG2	Transportin-2
26	Q6P2B1	Transportin-3
152	Q8CGB6-2	Tensin-2
11	O88746	Target of Myb protein 1
23	Q5SRX1-3	TOM1-like protein 2
15	Q9CPQ3	Mitochondrial import receptor subunit TOM22 homo
4	Q9CYG7-2	Mitochondrial import receptor subunit TOM34
29	Q9CZW5	Mitochondrial import receptor subunit TOM70
16	Q01320	DNA topoisomerase 2-alpha
31	Q64511	DNA topoisomerase 2-beta
5	Q921T2-3	Torsin-1A-interacting protein 1
1	Q8BYU6	Torsin-1A-interacting protein 2
7	Q9ER41	Torsin-1B
3	Q9ER38	Torsin-3A
3	Q62393-2	Tumor protein D52
32	Q9CYZ2	Tumor protein D54
264	P17751	Triosephosphate isomerase
466	P58771-2	Tropomyosin alpha-1 chain
108	P21107-2	Tropomyosin alpha-3 chain
64	Q6IRU2	Tropomyosin alpha-4 chain
21	O89023	Tripeptidyl-peptidase 1
2	Q7TQD2	Tubulin polymerization-promoting protein
136	Q9CRB6	Tubulin polymerization-promoting protein family me
15	F6ZDS4	Nucleoprotein TPR
4	Q8QZZ7	EKC/KEOPS complex subunit Tprkb
55	P63028	Translationally-controlled tumor protein
4	Q9CQN1	Heat shock protein 75 kDa, mitochondrial
12	Q9CQP2	Trafficking protein particle complex subunit 2
19	O55013	Trafficking protein particle complex subunit 3
15	Q9D289	Trafficking protein particle complex subunit 6B
4	Q8BGX0-3	E3 ubiquitin-protein ligase TRIM23
43	Q62318	Transcription intermediary factor 1-beta
33	Q8C0E3	Tripartite motif-containing protein 47

1	Q0KL02-3	Triple functional domain protein
40	Q8CJ53-4	Cdc42-interacting protein 4
10	Q9DCG9	Multifunctional methyltransferase subunit TRM112-li
13	Q8K1J6	CCA tRNA nucleotidyltransferase 1, mitochondrial
23	Q62348	Translin
27	Q9QZE7	Translin-associated protein X
10	Q9DCK3	Tetraspanin-4
6	Q8BJU2	Tetraspanin-9
36	P50637	Translocator protein
32	P52196	Thiosulfate sulfurtransferase
4	Q80XJ3	Tetratricopeptide repeat protein 28
14	A3KMP2	Tetratricopeptide repeat protein 38
6	Q3UDE2	Tubulin--tyrosine ligase-like protein 12
26	A2ASS6	Titin
47	P68369	Tubulin alpha-1A chain
780	P05213	Tubulin alpha-1B chain
42	P68373	Tubulin alpha-1C chain
7	P68368	Tubulin alpha-4A chain
84	Q9CWF2	Tubulin beta-2B chain
59	Q9ERD7	Tubulin beta-3 chain
12	Q9D6F9	Tubulin beta-4A chain
1258	P68372	Tubulin beta-4B chain
186	P99024	Tubulin beta-5 chain
89	Q8BFR5	Elongation factor Tu, mitochondrial
21	Q91YR1	Twinfilin-1
19	Q9Z0P5-2	Twinfilin-2
116	P10639	Thioredoxin
3	P97493	Thioredoxin, mitochondrial
114	Q91W90	Thioredoxin domain-containing protein 5
37	Q8CDN6	Thioredoxin-like protein 1
42	Q9JMH6-2	Thioredoxin reductase 1, cytoplasmic
19	Q9D883	Splicing factor U2AF 35 kDa subunit
24	P26369	Splicing factor U2AF 65 kDa subunit
44	Q3TW96	UDP-N-acetylhexosamine pyrophosphorylase-like prc
444	Q02053	Ubiquitin-like modifier-activating enzyme 1
9	Q9Z1F9	SUMO-activating enzyme subunit 2
11	Q8C878-2	NEDD8-activating enzyme E1 catalytic subunit
9	Q8VE47	Ubiquitin-like modifier-activating enzyme 5
15	Q80X50-2	Ubiquitin-associated protein 2-like
45	P62838	Ubiquitin-conjugating enzyme E2 D2
8	P63280	SUMO-conjugating enzyme UBC9

5	P61087	Ubiquitin-conjugating enzyme E2 K
54	P68037	Ubiquitin-conjugating enzyme E2 L3
78	P61089	Ubiquitin-conjugating enzyme E2 N
50	Q9D2M8	Ubiquitin-conjugating enzyme E2 variant 2
17	Q80U95	Ubiquitin-protein ligase E3C
3	E9Q735	Ubiquitin conjugation factor E4 A
2	Q9ES00	Ubiquitin conjugation factor E4 B
11	Q9EPV8	Ubiquitin-like protein 5
33	Q8R317-2	Ubiquilin-1
1	Q9QZM0	Ubiquilin-2
15	A2AN08-3	E3 ubiquitin-protein ligase UBR4
24	Q922Y1	UBX domain-containing protein 1
1	Q99PL6-2	UBX domain-containing protein 6
103	Q9R0P9	Ubiquitin carboxyl-terminal hydrolase isozyme L1
3	Q9JKB1	Ubiquitin carboxyl-terminal hydrolase isozyme L3
136	P12242	Mitochondrial brown fat uncoupling protein 1
28	Q9CR09	Ubiquitin-fold modifier-conjugating enzyme 1
31	P70362	Ubiquitin fusion degradation protein 1 homolog
24	P61961	Ubiquitin-fold modifier 1
72	Q6P5E4	UDP-glucose:glycoprotein glucosyltransferase 1
54	Q91ZJ5	UTP--glucose-1-phosphate uridylyltransferase
8	Q62452	UDP-glucuronosyltransferase 1-9
1	P13439	Uridine 5-monophosphate synthase
111	Q99KD5	Protein unc-45 homolog A
46	Q9EPU0-2	Regulator of nonsense transcripts 1
19	Q8R1I1	Cytochrome b-c1 complex subunit 9
35	Q9CPX8	Cytochrome b-c1 complex subunit 10
44	Q9D855	Cytochrome b-c1 complex subunit 7
195	Q9CZ13	Cytochrome b-c1 complex subunit 1, mitochondrial
310	Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial
104	Q9CR68	Cytochrome b-c1 complex subunit Rieske, mitochond
17	P99028	Cytochrome b-c1 complex subunit 6, mitochondrial
78	Q9CQ69	Cytochrome b-c1 complex subunit 8
16	P70697	Uroporphyrinogen decarboxylase
4	Q78IK2	Up-regulated during skeletal muscle growth protein
19	Q9Z1Z0-2	General vesicular transport factor p115
23	Q9JMA1	Ubiquitin carboxyl-terminal hydrolase 14
1	Q8R5H1-5	Ubiquitin carboxyl-terminal hydrolase 15
16	Q8C6M1	Ubiquitin carboxyl-terminal hydrolase 20
9	P35123	Ubiquitin carboxyl-terminal hydrolase 4
120	P56399	Ubiquitin carboxyl-terminal hydrolase 5

8	Q6A4J8-3	Ubiquitin carboxyl-terminal hydrolase 7
16	Q80WQ2	Protein VAC14 homolog
55	Q9WV55	Vesicle-associated membrane protein-associated pro
34	Q9QY76	Vesicle-associated membrane protein-associated pro
48	Q9Z1Q9	Valine--tRNA ligase
12	Q9CZT5	Vasorin
79	P70460	Vasodilator-stimulated phosphoprotein
185	Q62465	Synaptic vesicle membrane protein VAT-1 homolog
1	Q80TB8	Synaptic vesicle membrane protein VAT-1 homolog-li
17	P61759	Prefoldin subunit 3
124	Q62059-4	Versican core protein
1671	Q64727	Vinculin
559	Q01853	Transitional endoplasmic reticulum ATPase
165	Q60932-2	Voltage-dependent anion-selective channel protein 1
103	Q60930	Voltage-dependent anion-selective channel protein 2
41	Q60931	Voltage-dependent anion-selective channel protein 3
2322	P20152	Vimentin
13	Q9CRC0	Vitamin K epoxide reductase complex subunit 1
12	Q6TEK5	Vitamin K epoxide reductase complex subunit 1-like
39	Q9CQ80-2	Vacuolar protein-sorting-associated protein 25
11	Q8C0E2	Vacuolar protein sorting-associated protein 26B
7	Q9D1C8	Vacuolar protein sorting-associated protein 28 homo
40	Q9QZ88	Vacuolar protein sorting-associated protein 29
6	Q8BWQ6-2	VPS35 endosomal protein-sorting factor-like
8	Q91XD6	Vacuolar protein-sorting-associated protein 36
1	P97390	Vacuolar protein sorting-associated protein 45
1	Q8VEJ9	Vacuolar protein sorting-associated protein 4A
46	P46467	Vacuolar protein sorting-associated protein 4B
13	Q9CR26	Vacuolar protein sorting-associated protein VTA1 hor
71	P29788	Vitronectin
61	Q8R2Z5	von Willebrand factor A domain-containing protein 1
82	Q99KC8	von Willebrand factor A domain-containing protein 5
23	Q3UR50-5	von Willebrand factor A domain-containing protein 5
5	Q8CC88	von Willebrand factor A domain-containing protein 8
136	Q8CIZ8	von Willebrand factor
22	P32921-2	Tryptophan--tRNA ligase, cytoplasmic
11	P97765	WW domain-binding protein 2
316	O88342	WD repeat-containing protein 1
12	Q8CGF6	WD repeat-containing protein 47
13	Q9ERF3	WD repeat-containing protein 61
19	P56695	Wolframin

87	Q9Z0G4	WNT1-inducible-signaling pathway protein 2
11	Q6P1B1	Xaa-Pro aminopeptidase 1
60	Q6P5F9	Exportin-1
13	Q3U4G3	Xyloside xylosyltransferase 1
33	Q91WQ3	Tyrosine--tRNA ligase, cytoplasmic
4	P62960	Nuclease-sensitive element-binding protein 1
7	Q04736	Tyrosine-protein kinase Yes
5	Q9CQW1	Synaptobrevin homolog YKT6
81	Q9CQV8-2	14-3-3 protein beta/alpha
169	P62259	14-3-3 protein epsilon
132	P61982	14-3-3 protein gamma
69	P68510	14-3-3 protein eta
105	P68254-2	14-3-3 protein theta
420	P63101	14-3-3 protein zeta/delta
12	Q9ESL4-3	Mitogen-activated protein kinase kinase kinase MLT
2	Q6ZPZ3-2	Zinc finger CCCH domain-containing protein 4
2	P23950	Zinc finger protein 36, C3H1 type-like 1
11	P16372	Zinc finger protein 58
4	O54692	Centromere/kinetochore protein zw10 homolog
406	Q62523	Zyxin

sferase

e isozyme 1, mitochondrial

/delta-1

ubunit gamma-5
r 3

a-2

protein

ondrial

r 1

bunit gamma-12

SAMHD1

(

3

ubunit TIM14

og

protein 1
a

ndrial
ondrial
ochondrial
ondrial
se, mitochondrial
tochondrial

cleus

phatase

g protein 10

log 1

unctional protein 1
unctional protein 2

nase

ochondrial
ial
ating], mitochondrial

member A
member B
member E

a-1

rotein 2

tein 1

ein

a-1

-1
-3
2
3

chondrial
hondrial
e]] kinase, mitochondrial

protein, mitochondrial

l subunit delta
l subunit gamma

drial

ɔ

e

tein

tochondrial

tein 1

chondrial
chondrial
l

drial

nitochondrial

nit 6
nit 7

hain alpha-keto acid dehydrogenase complex, mitochondrial

2

ransferase 48 kDa subunit

se DHX15

nent of pyruvate dehydrogenase complex, mitochondrial

onent of 2-oxoglutarate dehydrogenase complex, mitochondrial

ondrial
itochondrial

ll pathway, mitochondrial

n 1
n 2

ent

linked

1

family member 1
family member 3

like protein 2

ent protein 1

ndrial

ctase, mitochondrial

1

e type-1 subunit alpha

in 1

in

3

ndrial

a-1
a-2
a
a
a
a isoforms short
bunit beta-1
bunit beta-2
ke 1

lasmic

mitochondrial

L

n

n

rial

ning protein 2

substrate

ndrial

taining protein 5

ein 1
ein 2

glycan core protein

hondrial
itochondrial

id labile subunit

protein
a

repeat protein

chondrial

ein 2

ion-associated protein 1

tochondrial

ein 1
n protein 1
n protein 2

l

drial

ein 1
ein 2
ein 3
ein 4

ase 1
ase 3
ase 4

r 2

ochondrial
ondrial

olog

in 6

ial

se

hondrial

D88

ha

lex subunit 1
lex subunit 10, mitochondrial
lex subunit 11
lex subunit 12
lex subunit 13
lex subunit 2
lex subunit 3

lex subunit 5
lex subunit 6
lex subunit 8
lex subunit 9, mitochondrial
lex assembly factor 4
bly factor 7
ex subunit 1
ex subunit 10
ex subunit 3
ex subunit 4
ex subunit 5, mitochondrial
ex subunit 6
ex subunit 7
ex subunit 9

itochondrial
in 2, mitochondrial
in 3, mitochondrial
in 4, mitochondrial
in 5
in 6, mitochondrial
in 7, mitochondrial

in 8, mitochondrial
itochondrial
itochondrial
itochondrial

drial

n

e]

3-beta

it 5

itochondrial

ns protein 2
lpha
eta

e

ynthase 2

otein 1

l

drial
ase

a, somatic form, mitochondrial
, mitochondrial
hondrial

e isozyme 2, mitochondrial
e isozyme 3, mitochondrial

phatase 1, mitochondrial

ng protein 1

e

g

nent 1
nent 2

in 1

in

1
ha

sterase beta-1
sterase beta-3
sterase delta-1

PABC3

alytic subunit
lytic subunit
atalytic subunit

ubunit alpha isoform
ulatory subunit A alpha isoform
ulatory subunit B alpha isoform

ulatory subunit alpha isoform
ulatory subunit gamma isoform
unit
ubunit 3

ndrial

a-1
ha

ory subunit
ory subunit
ory subunit

t protein kinase activator A

otein

rotein 1

3, mitochondrial

ransferase subunit 1
ransferase subunit 2

otein

olog

protein 3
subunit, mitochondrial
bunit, mitochondrial
mitochondrial
small subunit, mitochondrial

n 1

n

ning protein alpha

L

-1

member 1

regulator of chromatin subfamily A member 5

.

se

ransferase subunit STT3A
ransferase subunit STT3B

chondrial
, mitochondrial
chondrial

t 1 protein
h3

ubunit Tim13
ubunit TIM44
ubunit TIM50

rotein 1
0

a/epsilon/gamma
a

3

olog

mber 3

ike protein

tein 1

rial

;

tein A
tein B

ke

rotein 1

log

nolog

A
B2