Supplemetal material 1

	gender	age	ethnicity
mild1	male	42	the Han nationality
mild2	female	40	the Han nationality
mild3	male	39	the Han nationality
severe1	female	45	the Han nationality
severe2	female	47	the Han nationality
severe3	male	42	the Han nationality


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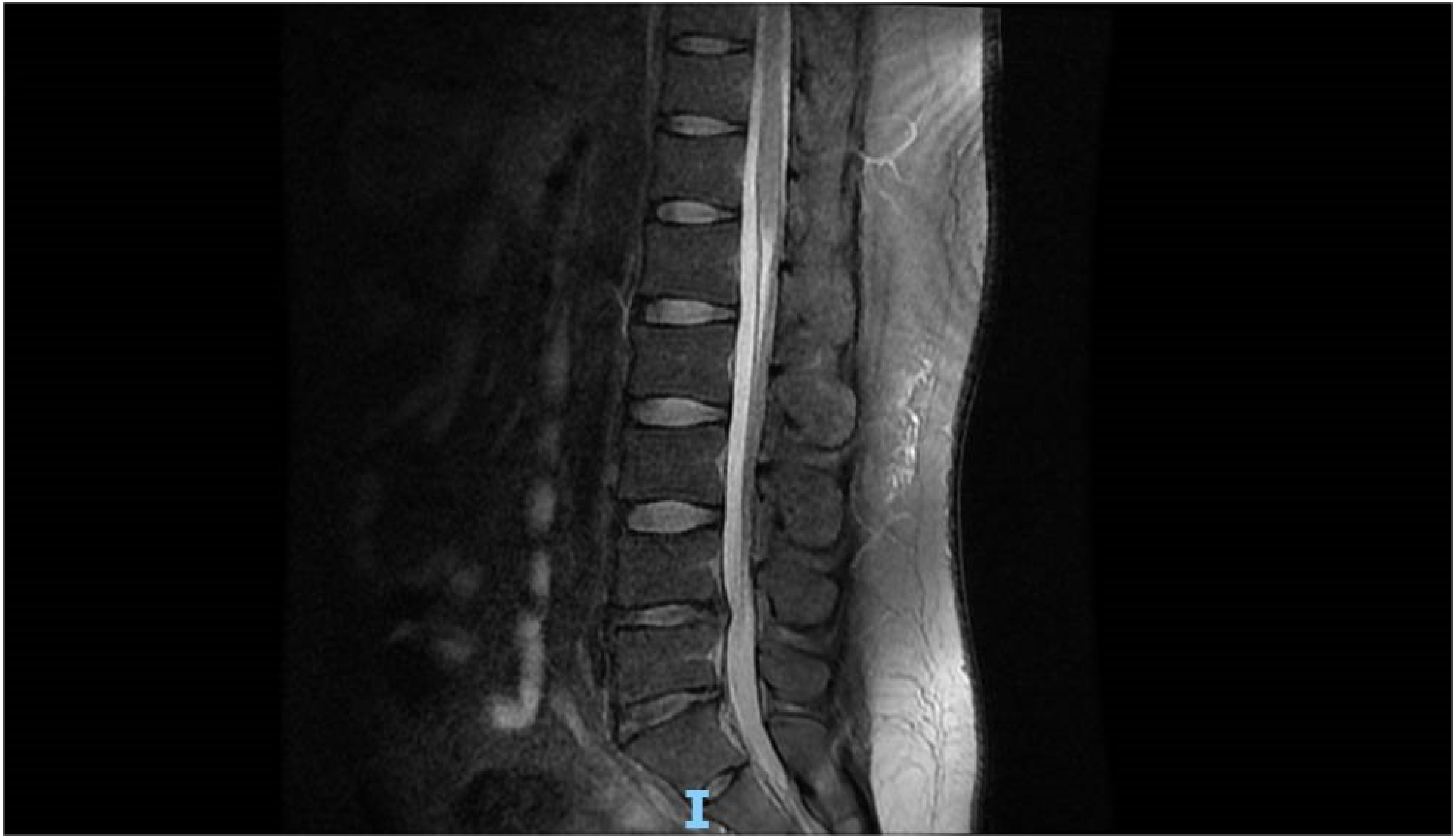

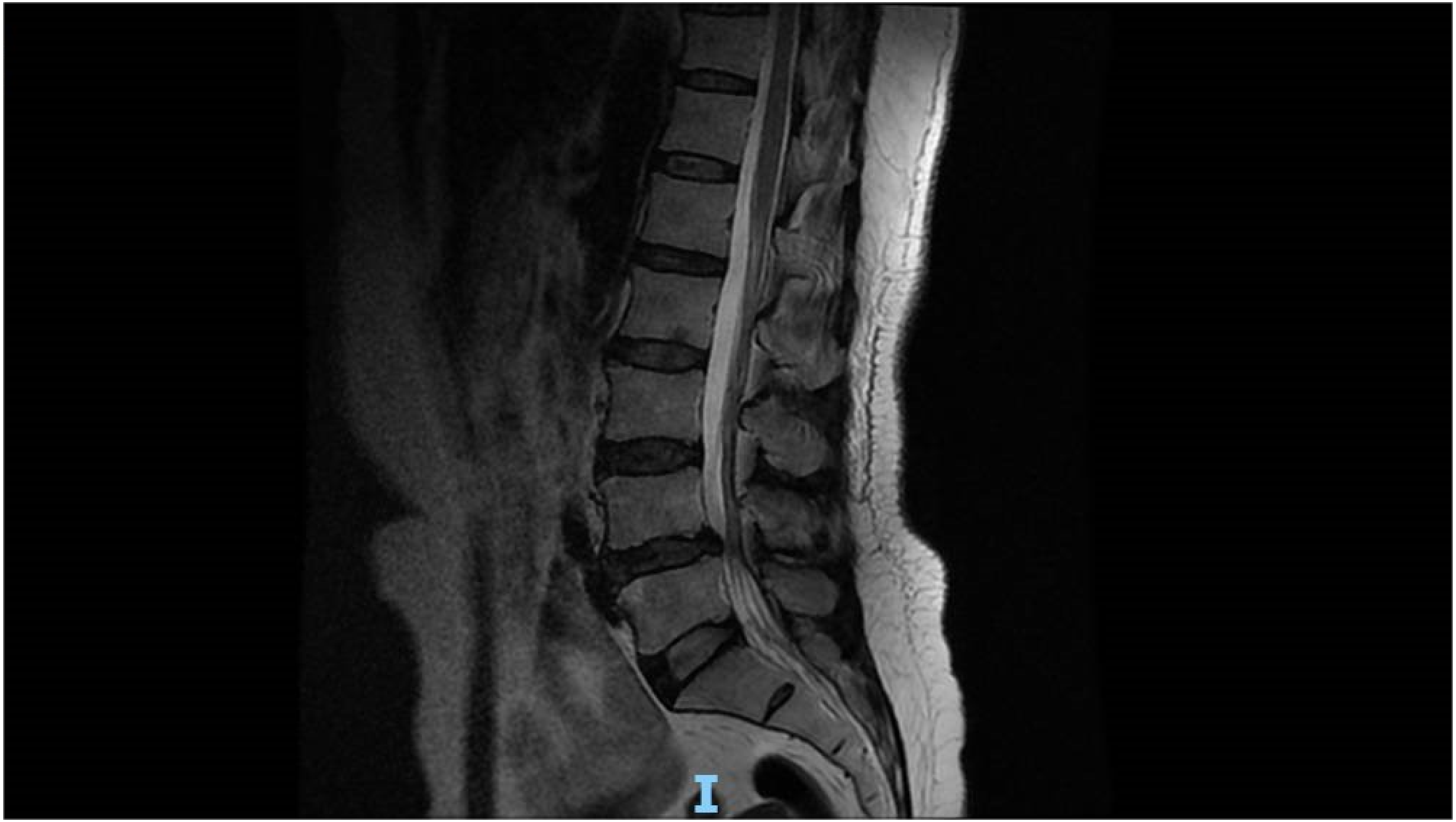
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Supplemetal material 2

Accession	Descripti	Coverage	# Peptide	# PSMs	# Unique	# AAs	MW [kDa]	calc. pI
A0A024R46	Fibronect	64	119	2847	0	2355	259	5.73
P02751	Fibronect	61	117	2720	2	2477	272.2	5.5
Q6N084	Uncharact	74	56	1378	1	1034	113.3	6.07
A0A087X1T	Aggrecan	24	50	1393	2	2473	255.4	4.13
P16112	Aggrecan	23	49	1379	1	2530	261.2	4.13
P02768	Serum alb	78	61	1115	1	609	69.3	6.28
F6KPG5	Albumin (	81	62	1025	2	585	66.5	6.04
Q53FR6	Cartilage	60	45	624	7	757	82.7	4.61
B4DN75	cDNA FLJ6	65	41	562	3	684	75.1	4.63
A6YID6	Fibronect	56	27	639	1	644	70.2	5.86
P68871	Hemoglobi	79	13	651	1	147	16	7.28
A0A384NKS	Clusterin	47	31	568	13	501	57.8	6.68
A0A1B4WRL	Beta glob	77	10	531	1	105	11.5	6.68
D9ZGF2	Collagen,	50	134	480	18	3177	343.5	6.68
P01023	Alpha-2-m	56	61	487	53	1474	163.2	6.46
B7ZW00	COL6A3 pr	54	119	457	3	2570	278	8.15
O75339	Cartilage	44	54	415	54	1184	132.5	8.41
P01024	Complemen	67	104	421	100	1663	187	6.4
Q7Z351	Uncharact	42	16	362	1	482	52.8	8.48
Q6MZQ6	Uncharact	43	16	361	1	475	52	8.06
Q4TZM4	Hemoglobi	89	9	428	1	101	11	6.52
Q3LR79	Hemoglobi	85	9	428	1	105	11.5	5.77
H0YC35	Clusterin	59	17	417	1	284	33.5	5.74
Q8IUL9	Hemoglobi	86	10	393	1	105	11.5	6.05
A0A384N66	Epididymi	47	15	393	15	338	38.4	6.61
A0A1S5UZ3	Hemoglobi	75	10	362	2	187	20.1	8.9
Q92954	Proteogly	55	63	432	34	1404	151	9.51
P02647	Apolipopr	80	33	339	33	267	30.8	5.76
B4DDQ2	Biglycan	59	18	301	10	334	37.6	7.97
P02042	Hemoglobi	79	12	312	1	147	16	8.05
Q4ZGM8	Hemoglobi	87	9	311	2	100	10.8	9.04
Q96T46	Hemoglobi	95	7	288	1	76	8.4	7.14
P07585	Decorin C	50	20	300	19	359	39.7	8.54
B4E1B2	cDNA FLJ5	72	50	267	5	678	74.8	7.12
A0A0K0K1H	Epididymi	70	47	264	2	698	77	7.21
P01009	Alpha-1-a	58	29	259	29	418	46.7	5.59
P51888	Prolargin	53	18	285	18	382	43.8	9.38
D3YTG3	Target of	22	31	236	3	1777	195.2	9.73
K7EPJ4	Cartilage	53	55	250	55	1162	126.8	8.27
Q7Z7G0	Target of	34	29	232	1	1075	118.6	9.44
Q4F786	Hemoglobi	86	8	242	1	105	11.4	6.68
B4DN21	cDNA FLJ5	75	20	237	1	306	34.5	5.64
C0JYY2	Apolipopr	37	146	237	146	4563	515.2	7.05
Q6PIL8	IGK@ prot	40	8	182	1	236	25.8	6.55
P02675	Fibrinoge	75	33	213	33	491	55.9	8.27
A0A024RAE	Heparan s	31	98	216	98	4346	463.7	6.51
A0A024RAK	Hyalurona	55	19	196	17	354	40.1	7.42
E9PEW8	Hemoglobi	86	8	193	1	104	11.3	6.37
C9JKG1	Biglycan	39	8	171	1	238	26.7	6.79
J3QSU6	Tenascin	38	60	194	2	2019	220.7	4.93

A0A024R88	Tenascin	34	61	192	3	2201	240.8	4.92
O15335	Chondroad	63	18	197	18	359	40.5	9.39
B4DI63	cDNA FLJ5	49	16	204	16	356	40.5	7.99
Q06828	Fibromodu	49	14	164	14	376	43.2	6.04
Q6N093	Uncharact	36	13	198	1	417	46	7.59
B4DMR3	cDNA FLJ5	65	26	203	26	334	37.1	9.52
P02671	Fibrinoge	38	33	198	33	866	94.9	6.01
Q8NF17	FLJ00385	40	16	189	6	509	56.1	7.59
A0A286YEY	Immunoglo	33	12	185	1	395	43.8	6.52
P12109	Collagen	43	37	175	37	1028	108.5	5.43
Q99715	Collagen	41	95	172	95	3063	332.9	5.53
P0DOX7	Immunoglo	45	7	143	1	214	23.4	7.17
A0A140TA2	Complemen	43	62	169	1	1698	187.5	7.33
A0A140TA3	Complemen	42	61	168	0	1698	187.6	7.12
P0C0L4	Complemen	41	62	166	2	1744	192.7	7.08
Q8IWM0	Apolipopr	61	6	164	1	76	9.1	8.15
A0A140VJJ	Testicula	74	28	153	3	437	49.5	6.09
Q68CN4	Uncharact	24	11	154	1	470	51.5	7.56
U3PXP0	Alpha glo	67	3	166	1	51	5.7	7.52
P07996	Thrombosp	36	44	143	1	1170	129.3	4.94
A0A024R9Q	Thrombosp	36	44	142	1	1170	129.3	4.94
Q92743	Serine pr	51	26	140	26	480	51.3	7.83
A0A2S1CVU	Beta-glob	84	5	151	1	55	6	4.81
E9M263	Hemoglobi	84	5	151	1	57	6.2	4.64
A0A024RAQ	Chondroit	12	36	134	5	3396	372.6	4.51
A0A024RAL	Chondroit	15	32	132	1	2409	264.9	4.54
P02458	Collagen	20	30	134	27	1487	141.7	6.92
S6BGD6	IgG L cha	38	7	101	1	235	24.8	7.24
D3DP16	Fibrinoge	84	26	125	1	334	37.7	6.29
P19823	Inter-alp	31	28	128	28	946	106.4	6.86
P02549	Spectrin	43	86	123	86	2419	279.8	5.05
A3KC71	Nuclear e	42	38	118	38	950	108.1	9.72
A0A0A0MTC	Gelsolin	44	30	114	28	767	84.7	5.83
A0A024R96	HCG40889,	48	52	112	2	1231	139	6.62
P06733	Alpha-eno	67	27	119	17	434	47.1	7.39
A8K5T0	cDNA FLJ7	47	51	107	1	1231	138.9	6.71
A0A384MDF	Epididymi	29	29	108	29	1019	108.5	6.21
Q9NR99	Matrix-re	21	55	120	55	2828	312	8.32
Q15582	Transform	51	26	114	26	683	74.6	7.71
V9HWB8	Pyruvate	66	31	103	3	531	57.9	7.84
Q6N092	Uncharact	34	15	83	9	519	56.4	6.93
P00747	Plasminog	54	41	114	41	810	90.5	7.24
S6BGE0	IgG H cha	30	6	78	1	300	32.2	7.85
S6C4R7	IgG L cha	32	6	87	1	212	22.5	8.24
S6BAR0	IgG L cha	31	6	86	1	216	23.1	7.69
P06727	Apolipopr	77	34	101	34	396	45.4	5.38
P04406	Glycerald	57	17	99	17	335	36	8.46
P08670	Vimentin	71	36	102	35	466	53.6	5.12
Q6GMW4	IGL@ prot	36	7	88	3	233	24.8	6.74
B4E1Z4	cDNA FLJ5	37	49	107	32	1266	140.9	7.18
P11277	Spectrin	39	75	99	3	2137	246.3	5.27

A0A5H1ZRQ	Immunoglo	58	5	79	2	106	11.3	8.29
A0A286YFJ	Immunoglo	40	11	90	5	396	43.8	6.24
A0A024R5Z	Pyruvate	60	30	95	2	531	58	7.71
A0A024R67	Spectrin	35	73	97	1	2328	267.6	5.36
P61626	Lysozyme	62	9	100	9	148	16.5	9.16
Q5FWF9	IGL@ prot	32	6	72	1	232	24.8	5.59
P01008	Antithrom	48	25	91	25	464	52.6	6.71
P00738	Haptoglob	58	25	90	14	406	45.2	6.58
B4DW52	cDNA FLJ5	59	15	87	2	347	38.6	5.35
D9ZGG2	Vitronect	34	13	91	13	478	54.3	5.8
P01031	Complemen	31	49	96	49	1676	188.2	6.52
B7Z6P1	cDNA FLJ5	52	16	98	6	343	38.6	5.38
S6AWF4	IgG L cha	29	5	71	1	180	19.8	7.09
A0A2R8Y79	Actin, cy	66	16	83	1	309	34.1	5.17
P02790	Hemopexin	45	17	77	17	462	51.6	7.02
D6RF35	Vitamin D	63	29	77	2	476	53	5.52
V9HWI6	Epididymi	66	28	76	1	474	52.9	5.54
B7Z539	cDNA FLJ5	34	18	78	11	645	72.1	7.68
A5PL27	CP protei	36	30	76	30	1065	122.1	5.72
V9HWF4	Phosphogl	76	30	81	26	417	44.6	8.1
B2R950	cDNA, FLJ	10	13	76	5	1482	163.8	6.38
A0A024RC5	Milk fat	73	21	71	1	387	43.1	8.15
P00734	Prothromb	45	24	70	24	622	70	5.9
B2RMS9	Inter-alp	35	27	73	11	930	103.3	6.98
Q08431	Lactadher	73	21	70	1	387	43.1	8.15
P08758	Annexin A	66	18	70	18	320	35.9	5.05
Q8IUX7	Adipocyte	34	32	73	32	1158	130.8	5.11
Q09666	Neuroblas	27	72	83	72	5890	628.7	6.15
P07355	Annexin A	59	24	67	24	339	38.6	7.75
O60687	Sushi rep	37	15	69	15	465	52.9	7.25
Q15063	Periostin	52	33	65	5	836	93.3	7.53
V9HWE3	Carbonic	56	11	70	11	261	28.9	7.12
A0A024R6F	Serpin pe	36	14	62	14	423	47.6	5.52
B2R6V9	cDNA, FLJ	30	18	62	3	732	83.2	6
P05154	Plasma se	33	15	61	15	406	45.6	9.26
A0A4P8J4D	IgL_IGLV3	24	3	46	1	151	16.2	5.9
Q6YHK3	CD109 ant	19	24	63	24	1445	161.6	5.85
B2R5M9	cDNA, FLJ	37	24	60	24	727	83.5	7.02
Q15113	Procollag	44	15	58	15	449	47.9	7.43
Q6VFQ6	Hemoglobi	62	3	55	1	42	4.5	8.24
A0A024RDT	Periostin	50	29	59	1	779	87	7.81
Q5XTR9	Hemoglobi	100	4	71	1	34	3.9	5.62
O00300	Tumor nec	45	20	62	20	401	46	8.29
B7Z4R8	cDNA FLJ5	55	30	75	1	853	89.5	8.91
E2RVJ0	Anion exc	25	19	53	19	912	101.9	5.22
A0A024R1N	Myosin, h	27	45	55	42	1960	226.4	5.6
V9HWK1	Triosepho	87	17	46	17	249	26.7	6.9
O00391	Sulfhydry	38	27	59	27	747	82.5	8.92
A0A1U9X7I	COL11A2 C	17	21	52	21	1736	171.7	6.39
B3KQT8	cDNA PSEC	44	15	53	15	415	45.7	8.47
P04083	Annexin A	58	18	48	18	346	38.7	7.02

Q6UVK1	Chondroit	26	44	57	44	2322	250.4	5.47
A0A024R86	Angiopoie	37	21	52	21	493	57.1	7.53
A0A384MQX	Epididymi	48	30	51	30	664	74.1	7.02
P02766	Transthyr	63	8	42	8	147	15.9	5.76
P26038	Moesin OS	52	35	59	24	577	67.8	6.4
Q14563	Semaphori	29	20	56	20	771	88.8	7.42
P04040	Catalase	53	25	50	25	527	59.7	7.39
P02760	Protein A	44	12	45	12	352	39	6.25
P35443	Thrombosp	22	14	49	10	961	105.8	4.68
A0A024R03	Complemen	33	20	52	20	559	63.2	5.52
B2R815	cDNA, FLJ	43	17	49	17	427	48.5	7.75
D9IWP9	Beta-2-gl	49	14	44	14	326	36.2	8
A0A384MDU	Collagen,	19	21	51	21	1366	129.2	8.95
P69892	Hemoglobi	78	12	49	3	147	16.1	7.2
P00338	L-lactate	43	15	48	14	332	36.7	8.27
P35527	Keratin,	47	24	44	23	623	62	5.24
D3DNU8	Kininogen	56	25	51	2	427	47.8	6.65
B4E2L8	cDNA FLJ5	29	16	49	1	626	70.3	5.34
P35625	Metallopr	53	10	52	10	211	24.1	8.72
Q07954	Prolow-de	10	41	56	41	4544	504.3	5.39
B4E1C2	Kininogen	38	25	51	2	644	71.9	6.81
P13645	Keratin,	44	23	46	21	584	58.8	5.21
B2R8I2	cDNA, FLJ	31	16	52	16	525	59.5	7.44
P09871	Complemen	34	20	47	19	688	76.6	4.96
P00739	Haptoglob	37	14	45	3	348	39	7.09
P36955	Pigment e	39	16	51	16	418	46.3	6.38
D9YZU8	Globin B1	77	11	45	2	147	16.1	7.2
S6B2A6	IgG H cha	28	6	41	1	300	32.1	7.25
Q9Y490	Talin-1 C	23	42	45	42	2541	269.6	6.07
P01871	Immunoglc	40	16	46	3	453	49.4	6.77
A0A140T9C	Tenascin-	17	42	51	42	4222	455.9	5.2
C9JF17	Apolipopr	31	7	46	7	215	24.1	5.6
P05546	Heparin c	37	17	45	17	499	57	6.9
Q7LGC8	Carbohydr	33	13	42	13	479	54.7	8.59
P02765	Alpha-2-H	39	9	41	9	367	39.3	5.72
P08582	Melanotra	46	22	38	22	738	80.2	5.94
Q6P528	ASPN prot	41	15	44	15	384	43.9	6.48
Q9UNU2	Complemen	44	12	40	2	354	38.1	8.53
A4D1W7	Inhibin,	40	19	37	19	426	47.4	8.03
P21333	Filamin-A	20	39	45	36	2647	280.6	6.06
V9HWB4	Epididymi	45	26	42	23	654	72.3	5.16
Q6FHV6	ENO2 prot	36	10	37	7	434	47.2	5.03
P35442	Thrombosp	26	24	39	21	1172	129.9	4.83
P10643	Complemen	34	24	39	3	843	93.5	6.48
A4QPB0	IQ motif	24	34	41	33	1657	189.2	6.48
H6VRF8	Keratin 1	34	24	42	19	644	66	8.12
V9HWN7	Fructose-	58	18	38	16	364	39.4	8.09
H7C0L5	Inter-alp	29	17	43	1	719	80	5.45
P08294	Extracell	37	7	36	7	240	25.8	6.61
D3DT72	Collagen,	13	19	41	18	1818	182.3	6
P32119	Peroxired	54	10	37	9	198	21.9	5.97

B2R6W1	cDNA, FLJ	32	22	37	1	843	93.5	6.48
B4DPQ0	Complemen	34	18	39	17	719	81.8	6.37
Q9NQ79	Cartilage	33	19	34	19	661	71.4	5.12
Q86TT1	Full-leng	41	14	41	1	375	41.2	6.79
Q9BYJ0	Fibroblas	47	7	36	7	223	24.6	8.87
P98066	Tumor nec	47	10	38	10	277	31.2	6.79
P13671	Complemen	23	20	32	20	934	104.7	6.76
P16157	Ankyrin-1	17	26	37	26	1881	206.1	6.01
W0UV28	Ribonucle	59	9	33	9	147	16.5	9.64
Q6MZK8	Uncharact	8	18	39	1	2060	226.3	4.44
A0A024R8S	Protein d	48	22	38	22	508	57.1	4.87
Q86Y38	Xylosyltr	22	20	39	20	959	107.5	9.22
S6C4S0	IgG H cha	16	4	37	1	275	29.4	8.16
P30043	Flavin re	61	9	38	9	206	22.1	7.65
P02649	Apolipopr	66	21	40	21	317	36.1	5.73
Q5UGI6	Serine/cy	37	12	35	12	333	37.3	8
P08254	Stromelys	36	20	40	16	477	53.9	6.16
O43854	EGF-like	34	19	40	19	480	53.7	7.28
P04003	C4b-bindi	36	19	36	19	597	67	7.3
B7ZA94	cDNA, FLJ	32	18	33	18	539	61.3	7.74
P18428	Lipopolys	27	11	36	11	481	53.4	6.7
V9HWP2	Epididymi	33	25	38	24	803	92.4	4.84
P02452	Collagen	17	22	44	7	1464	138.9	5.8
A5YM51	MYH7 prot	18	27	39	20	1934	222.9	5.8
P35908	Keratin,	32	19	31	11	639	65.4	8
V9HW22	Epididymi	37	24	34	11	646	70.9	5.52
P23142	Fibulin-1	32	17	32	7	703	77.2	5.22
A0A024R69	Actinin,	42	29	32	20	892	103	5.41
P02743	Serum amy	33	8	37	8	223	25.4	6.54
Q13217	DnaJ homo	37	19	37	19	504	57.5	6.15
A0A3B3ITK	Phosphogl	29	17	33	17	584	63.9	6.76
B3KQT9	Protein d	46	20	35	17	480	54.1	7.21
P83110	Serine pr	27	12	33	12	453	48.6	7.09
Q6IPT9	Elongatio	37	14	31	14	462	50.2	9.07
V9HWF6	Alpha-1-a	40	7	28	5	201	23.5	5.02
Q15149	Plectin O	8	38	39	38	4684	531.5	5.96
Q86UD1	Out at fi	40	8	26	8	273	30.7	6.84
Q562R1	Beta-acti	17	5	31	1	376	42	5.59
A0A384MDR	Ferritin	58	10	27	10	175	20	5.78
Q6NUR7	Ezrin OS=	31	20	32	9	586	69.2	6.27
P13929	Beta-enol	16	5	27	1	434	47	7.71
A0A0S2Z2Z	Annexin (	34	23	34	23	673	75.8	5.6
B7Z8B6	cDNA FLJ5	22	9	24	2	623	69.5	6.16
P03952	Plasma ka	39	23	33	23	638	71.3	8.22
P43652	Afamin OS	36	20	31	20	599	69	5.9
Q3SX92	C-type le	55	12	31	12	197	22.2	8.84
A0A0G2JIW	Heat shoc	36	19	31	15	642	70.1	5.66
Q92626	Peroxidas	18	21	28	21	1479	165.2	7.17
P09525	Annexin A	54	17	28	17	319	35.9	6.13
Q53GZ8	Complemen	35	22	31	5	752	83.3	7.52
B7Z1K5	Tubulin a	40	15	25	4	519	57.7	5.07

P27169	Serum par	37	9	28	9	355	39.7	5.22
B0AZL7	cDNA, FLJ	29	14	26	14	605	66	6.79
V9GYM3	Apolipopr	31	5	23	5	133	14.9	8.27
P35555	Fibrillin	11	29	32	28	2871	312.1	4.93
Q53XB4	Epididymi	54	9	26	9	147	16.8	9.03
Q5VY30	Retinol-b	67	9	27	9	199	23	6.09
B2R582	cDNA, FLJ	72	12	27	1	202	22.5	6.04
B4DLV7	Rab GDP d	51	18	25	13	449	51.1	8.18
Q15198	Platelet-	37	10	26	10	375	41.8	8.5
P68366	Tubulin a	47	16	26	5	448	49.9	5.06
A0A024R9H	Matrilin	19	14	26	14	941	104.9	6.35
Q2TUW9	Lactoferr	37	20	27	2	709	77.9	8.12
Q9Y6C2	EMILIN-1	24	19	25	19	1016	106.6	5.17
A0A087WVQ	Clathrin	17	22	25	22	1679	191.9	5.69
A0A024R96	Chitinase	40	12	22	12	383	42.6	8.46
P02008	Hemoglobi	30	4	36	3	142	15.6	8.21
P05452	Tetranect	72	12	25	1	202	22.5	5.67
A2RRP8	Matrilin	34	17	28	16	581	64	5.81
A0A024QZN	Vinculin,	23	23	29	23	1066	116.6	6.09
A0A5C2GME	IG c622_h	26	3	23	1	141	15.4	8.87
Q5EK51	Lactoferr	35	19	26	1	711	78.3	8.18
A0A024RD8	Heat shoc	22	16	27	8	724	83.2	5.03
Q9H4F8	SPARC-rel	32	15	30	15	434	48.1	8.22
Q16674	Melanoma-	35	4	26	4	131	14.5	8.79
Q6FHU2	Phosphogl	55	13	23	13	254	28.8	7.18
Q9Y240	C-type le	37	11	27	11	323	35.7	5.16
A0A024R6R	Matrix me	32	16	25	15	660	73.8	5.47
M0R0Q9	Complemen	68	5	26	1	101	11.1	4.77
A0A024RAE	Adiponect	30	7	24	1	253	26.7	8.63
Q96PD5	N-acetylm	26	9	23	9	576	62.2	7.55
P22314	Ubiquitin	20	17	24	17	1058	117.8	5.76
A0A1W2PNW	Vascular	25	20	31	20	665	74.9	9.22
A0A140VJI	Testicula	33	15	24	15	540	60.6	6.71
A0A0A0MSV	Complemen	24	7	24	1	228	24	9.16
A0A0S2Z3V	EGF conta	36	11	22	11	413	45.7	5.47
P13647	Keratin,	33	20	28	2	590	62.3	7.74
V9HWE9	Epididymi	64	11	21	11	210	23.3	5.64
Q14767	Latent-tr	11	18	25	18	1821	194.9	5.19
P05156	Complemen	28	14	22	6	583	65.7	7.5
A0A2R8Y5S	Radixin C	28	18	28	6	590	69.3	6.27
Q13228	Methaneth	37	14	23	14	472	52.4	6.37
P07357	Complemen	28	12	23	12	584	65.1	6.47
P05023	Sodium/po	23	20	25	18	1023	112.8	5.49
P31415	Calseques	18	3	16	3	396	45.1	4.16
A0A1B0GVD	Cathepsin	37	12	22	12	409	44.2	6.54
P13639	Elongatio	25	20	26	20	858	95.3	6.83
P06737	Glycogen	21	18	25	14	847	97.1	7.17
P54652	Heat shoc	27	17	25	4	639	70	5.74
Q07507	Dermatopo	42	6	22	6	201	24	4.82
B2RBH2	cDNA, FLJ	30	14	23	14	574	63.4	7.03
A0A024QYT	Serpin pe	38	12	21	12	402	45	7.2

B4E1T1	cDNA FLJ5	33	19	27	0	555	58.8	5.97
A0A087X0K	Collagen	9	11	24	11	1374	140	4.98
D3DTX7	Collagen,	22	16	24	2	885	84.7	6.24
P01033	Metallopr	40	6	23	6	207	23.2	8.1
A0A024R1T	ATP-citra	20	21	26	21	1101	120.8	7.33
B1AKG0	Complemen	30	9	23	1	271	30.8	7.81
D0PNI1	Epididymi	51	13	22	10	245	27.7	4.79
B4DJ30	cDNA FLJ6	15	16	22	16	995	112.9	6.06
P21980	Protein-g	25	15	22	15	687	77.3	5.22
Q4ZHG4	Fibronect	11	17	22	17	1894	205.4	9.32
A0A3B3IRX	Phospholi	50	7	26	7	117	13	9.06
B2ZZ86	Collagen	7	11	21	10	1838	183.5	5.06
P30041	Peroxired	46	11	23	11	224	25	6.38
Q9NT22	EMILIN-3	24	14	22	14	766	82.6	7.72
V9HW21	Epididymi	58	11	22	11	260	29.2	7.4
Q01813	ATP-depen	24	15	21	13	784	85.5	7.55
A8K491	cDNA FLJ7	30	12	21	12	486	52.8	6.7
Q99985	Semaphori	17	12	23	12	751	85.2	8.69
Q6LDQ3	Sulfated	32	4	28	1	66	7.8	5.31
E7EUC7	UTP--gluc	29	14	20	14	517	57.8	8.13
A0A0S2Z3G	Actinin a	24	17	19	10	911	104.8	5.44
K9JA46	Epididymi	22	15	21	8	732	84.6	5.02
F1T0G3	HHIP-like	22	14	19	3	782	86.7	7.58
Q2HIZ0	Thrombosp	17	14	21	12	956	104.1	4.65
A0A140G96	Alpha-cry	51	7	19	7	168	19.3	7.72
P04259	Keratin,	25	15	21	3	564	60	8
Q59F12	Protein 4	25	15	19	15	827	92.1	5.55
P07360	Complemen	58	10	18	10	202	22.3	8.31
Q05707	Collagen	13	18	19	18	1796	193.4	5.3
J3QTR3	Ubiquitin	50	6	22	6	106	12.2	10.14
P11216	Glycogen	24	18	21	14	843	96.6	6.86
A0A140VKC	Testicula	46	12	21	12	298	34.2	6.05
Q86U78	Angiotens	17	7	18	7	485	53.1	6.32
Q6FHW3	DF protei	57	10	16	10	228	24.4	7.24
Q15782	Chitinase	31	10	16	10	390	43.5	7.53
Q06830	Peroxired	51	9	21	6	199	22.1	8.13
A0A024RAA	Adiponect	25	5	15	5	245	25.8	8.41
B4DUV1	Fibulin-1	29	13	18	3	641	70.1	5.26
P0DOX2	Immunoglc	29	11	18	1	455	48.9	6.67
Q06033	Inter-alp	18	14	21	14	890	99.8	5.74
Q9UKX2	Myosin-2	10	14	22	2	1941	222.9	5.82
Q53GY0	Plastin 3	27	15	20	9	630	70.7	5.68
P04217	Alpha-1B-	29	10	16	10	495	54.2	5.86
P29401	Transketc	30	14	17	14	623	67.8	7.66
P00441	Superoxid	47	9	20	9	154	15.9	6.13
B2R4R0	Histone H	51	6	19	6	103	11.4	11.36
Q14112	Nidogen-2	11	12	19	11	1375	151.2	5.29
B2R9K6	cDNA, FLJ	31	9	19	9	345	39	6.14
Q8NFL0	UDP-GlcNA	28	10	18	10	401	46	9.03
P61204	ADP-ribos	47	7	19	4	181	20.6	7.43
Q6N091	Uncharact	24	10	17	1	500	54.1	6.34

O75462	Cytokine	33	12	20	12	422	46.3	9.11
Q6N041	Uncharact	23	10	21	0	498	54.1	7.18
V9HWC6	Peptidyl-	45	11	19	11	208	22.7	9.32
B4DK93	cDNA FLJ5	26	15	19	15	677	77.4	5.5
A0A5F9ZHM	L-lactate	35	11	19	10	341	37.4	6.25
Q5M8T4	Connectiv	36	12	22	12	349	38	7.94
V9HWC1	Epididymi	9	13	21	1	1939	223	5.74
P12259	Coagulati	9	19	20	19	2224	251.5	6.05
A0A024R8V	TIMP meta	41	8	16	8	179	20.2	7.17
P08697	Alpha-2-a	20	8	17	8	491	54.5	6.29
P09972	Fructose-	26	7	14	5	364	39.4	6.87
P67936	Tropomyos	48	16	20	1	248	28.5	4.69
Q6IAW5	CALU prot	35	10	15	2	315	37.1	4.64
Q9H3U7	SPARC-rel	28	12	19	12	446	49.6	8.46
B2RA39	cDNA, FLJ	24	13	16	12	569	64.3	7.06
A0A2R8Y5V	Tropomyos	50	16	20	1	248	28.6	4.7
A0A1U9X8Y	Chloride	54	11	18	11	240	26.8	5.26
P58215	Lysyl oxi	27	14	16	14	753	83.1	6.86
A0A384NYT	Tubulin b	27	9	18	2	442	49.4	4.89
B1AP13	Complemen	25	12	19	12	444	49.3	8.82
P55072	Transitic	21	16	18	16	806	89.3	5.26
Q59FR8	Galectin	36	9	18	9	258	27.1	8.41
P04275	von Wille	6	15	18	15	2813	309.1	5.48
Q9NRR1	Cytokine-	49	7	18	7	136	15.6	8.48
A0A0S2Z3X	Rab GDP d	35	12	16	7	447	50.6	5.14
P18085	ADP-ribos	57	9	16	6	180	20.5	7.14
Q6UXX5	Inter-alp	10	12	18	12	1313	143.1	9.01
A0A090N8Y	Protein d	27	13	17	13	645	72.9	5.07
Q16658	Fascin OS	34	13	17	13	493	54.5	7.24
P13674	Prolyl 4-	32	14	17	14	534	61	6.01
P36980	Complemen	32	8	14	5	270	30.6	6.38
Q16778	Histone H	44	7	18	2	126	13.9	10.32
Q9H2X0	Chordin C	16	12	17	12	955	102	7.75
Q5QNW6	Histone H	44	7	18	2	126	13.9	10.32
G9K389	YWHAE/FAM	30	10	17	8	384	41.3	4.97
A0A024R75	Calumenin	34	10	14	2	315	37.1	4.59
Q8N7G1	Purine nu	41	9	13	9	293	32.5	7.21
Q96RW7	Hemicenti	4	17	17	17	5635	613	6.49
P62937	Peptidyl-	63	10	20	10	165	18	7.81
P03973	Antileukc	45	8	18	8	132	14.3	8.75
B2R7N9	cDNA, FLJ	14	6	15	6	421	49.4	5.52
X6RJP6	Transgeli	73	10	16	10	187	21.1	7.81
Q6FGX9	Adenylate	48	9	17	9	194	21.6	8.63
F1T0G2	HHIP-like	20	12	15	1	665	73.7	8.09
H3BTH8	Hyalurona	19	7	16	5	422	47.7	6.68
L7RXH0	Integrin,	12	13	16	13	1048	116	5.68
B7Z4T2	2-phosphc	19	9	15	9	442	51	8.78
Q86UX2	Inter-alp	16	14	17	14	942	104.5	8.28
P06744	Glucose-6	23	12	15	12	558	63.1	8.32
Q02388	Collagen	6	13	15	13	2944	295	6.27
B4DX53	cDNA FLJ5	12	4	16	4	387	42.4	7.47

P06702	Protein S	70	7	13	7	114	13.2	6.13
Q9Y4K0	Lysyl oxi	19	11	14	11	774	86.7	6.38
Q9BY76	Angiopoie	20	7	14	7	406	45.2	8.85
P07737	Profilin-	59	7	14	7	140	15	8.27
A0A140VJR	Phosphogl	13	5	14	1	417	44.8	8.54
A0A5C2G5T	IGL c3037	64	5	12	1	109	11.9	7.96
P05109	Protein S	57	8	15	8	93	10.8	7.03
Q6LAM1	Heavy cha	29	9	13	1	321	35.9	7.59
E9PK25	Cofilin-1	47	11	15	9	204	22.7	8.34
P19021	Peptidyl-	13	10	14	10	973	108.3	6.42
A0A384MR2	Galectin	59	8	15	8	135	14.7	5.5
P25705	ATP synth	24	12	13	12	553	59.7	9.13
P21796	Voltage-d	41	9	14	8	283	30.8	8.54
A0A1I9LHJ	Sulfotran	19	7	15	7	395	44	9.98
A0A146E5L	Mesenchym	19	7	14	7	428	46	5.15
Q5TCU3	Tropomyos	37	14	18	1	284	32.8	4.68
P27348	14-3-3 pr	43	9	14	5	245	27.7	4.78
Q4W5L2	Alpha-syn	78	7	12	7	102	10.2	9.52
E7ETU9	Procollag	19	12	15	12	703	81.1	6.65
B5MDF5	GTP-bindi	23	5	12	5	233	26.2	7.01
A0A5C2G6C	IGL c3345	56	4	11	1	108	11.7	8.48
Q96IY4	Carboxype	16	7	15	7	423	48.4	7.71
Q53ET2	Dihydropy	24	10	13	7	572	62.2	6.32
E9PLD0	Ras-relat	52	7	12	2	169	18.5	5.72
P07951	Tropomyos	37	14	18	1	284	32.8	4.7
Q0QEN7	ATP synth	28	9	12	9	445	48.1	5.07
A0A5C2GRN	IG c1553_	59	6	14	2	116	12.9	8.5
Q53FA4	Cysteine-	23	9	14	4	381	42	8.31
J3KPD9	NME1-NME2	51	8	16	8	197	22.4	9.54
L0R849	Alternati	13	8	19	1	388	42.3	5.92
A0A5C2FX9	IGL c1234	47	4	11	2	108	11.7	7.97
P30044	Peroxired	48	7	11	7	214	22.1	8.7
P06732	Creatine	33	10	13	9	381	43.1	7.25
P50454	Serpin H1	29	9	13	9	418	46.4	8.69
P43026	Growth/di	19	8	13	8	501	55.4	9.79
Q10471	Polypepti	21	12	14	12	571	64.7	8.35
P19652	Alpha-1-a	33	6	12	4	201	23.6	5.11
Q14766	Latent-tr	8	12	14	4	1721	186.7	5.96
Q96D15	Reticuloc	23	6	12	6	328	37.5	4.89
D9YZV5	Tropomyos	31	12	16	5	284	32.9	4.78
Q9Y6U3	Adseverin	18	13	16	13	715	80.4	5.71
P07225	Vitamin K	14	9	14	9	676	75.1	5.67
Q5U0I6	H.sapiens	39	6	11	1	205	22.7	6.21
A0A0X9USM	GCT-A4 he	54	5	12	1	128	14.3	7.28
M1LAK4	Olfactome	38	13	15	13	406	46	6.57
A0A5C2GMV	IG c1068_	41	3	10	1	108	11.7	7.97
A1L4H1	Soluble s	13	13	13	13	1573	165.6	6.13
A0A5C2GQW	IG c31_he	63	6	10	2	118	12.7	8.46
Q6NS36	Ferritin	39	7	11	7	232	26.2	6.52
Q53G71	Calreticu	37	10	16	10	406	46.9	4.45
P16452	Erythrocy	19	13	14	13	691	77	8.09

A0A1S5UZH	Semaphori	17	9	12	9	783	86.5	8.73
B7Z8A2	cDNA FLJ5	21	9	12	9	487	54.5	5.73
A0A384NPU	Epididymi	26	8	11	8	440	48.1	5.08
V9HWC2	Epididymi	50	9	11	9	189	19.9	6.79
D9ZGF6	Frizzled-	19	6	11	6	325	36.2	8.46
P00742	Coagulati	14	7	11	7	488	54.7	5.94
A0A5C2GNE	IG c154_h	32	4	11	2	120	13.3	8.41
Q13885	Tubulin b	24	8	12	2	445	49.9	4.89
A0A0S2Z47	Creatine	22	7	11	6	405	44.9	6.11
Q6UWX4	HHIP-like	9	7	13	7	724	80.7	9.01
Q99584	Protein S	49	6	12	6	98	11.5	6.16
A0A5C2GXV	IG c1447_	39	4	11	1	124	13.6	7.12
Q6FGG5	SCRG1 prc	65	4	14	4	98	11.1	6.71
Q9UBG0	C-type ma	10	10	12	10	1479	166.6	5.83
A0A5C2GC7	IGL c3913	50	3	11	0	112	12.2	7.12
P22352	Glutathic	38	8	13	8	226	25.5	8.13
P03951	Coagulati	19	11	12	11	625	70.1	8.1
P09486	SPARC OS=	25	8	13	8	303	34.6	4.84
U5LIG7	Apolipopr	27	10	14	10	293	32.6	8.24
B7Z705	cDNA FLJ5	22	9	12	9	423	48.2	7.68
P37837	Transaldc	30	10	12	10	337	37.5	6.81
A3KPE2	Apolipopr	34	3	11	3	99	10.8	5.41
Q5T7Y6	Protein S	15	2	10	2	147	15.9	4.48
V9HWG9	Epididymi	39	10	13	10	241	27.5	6.6
Q13162	Peroxired	26	6	12	4	271	30.5	6.29
D3DSM4	Collagen,	7	8	12	8	1336	135.4	6.47
F2RM35	Serine pr	17	7	11	7	461	51.7	5.39
Q6UX71	Plexin dc	14	7	13	7	529	59.5	6.46
A0A024R32	Epididymi	41	6	10	2	193	21.8	6.1
P05164	Myeloperc	15	9	12	9	745	83.8	8.97
Q86UX7	Fermitin	19	10	12	10	667	75.9	6.98
Q13938	Calcyphos	28	7	11	7	275	30.2	6.04
A0A024R1G	Myoglobin	36	6	11	6	166	18.5	7.55
O15041	Semaphori	14	10	13	10	775	89.2	7.47
Q5T619	Zinc fing	2	1	14	1	568	62.3	8.62
P33908	Mannosyl-	13	8	11	8	653	72.9	6.47
A0A0S2Z4I	Tropomyos	39	11	15	4	248	28.9	4.75
Q59E93	Aminopept	11	10	12	10	977	110.5	5.53
P13489	Ribonucle	26	9	10	9	461	49.9	4.82
Q86VP6	Cullin-as	9	11	12	11	1230	136.3	5.78
P40925	Malate de	30	10	11	10	334	36.4	7.36
P26447	Protein S	36	4	14	4	101	11.7	6.11
A0A5C2G71	IGH c427_	45	5	9	1	121	13.4	7.12
O43866	CD5 antig	35	9	11	9	347	38.1	5.47
V9HVX6	Epididymi	30	12	14	12	501	54.8	6.92
P02461	Collagen	6	8	11	8	1466	138.5	6.61
P55058	Phospholi	16	7	11	7	493	54.7	7.01
P13497	Bone morp	10	9	12	7	986	111.2	6.9
Q99645	Epiphycan	29	7	10	7	322	36.6	4.81
P04899	Guanine n	32	9	11	8	355	40.4	5.54
Q6NUI6	Chondroad	13	9	11	9	762	82.3	8.84

A0A5C2GE7	IG c662_h	41	4	9	1	119	13	5.4
A0A5C2G5L	IGL c387C	43	3	7	2	107	11.7	5.34
C9J8S2	Retinoic	37	5	8	5	159	17.8	10.21
P02654	Apolipopr	40	7	11	7	83	9.3	8.47
Q53GN4	WD repeat	20	10	12	10	606	66.1	6.65
A0A096LPE	SAA2-SAA4	25	6	13	6	208	23.3	8.98
A0A5C2GUJ	IG c1195_	56	4	11	1	112	12.1	7.12
Q16270	Insulin-l	29	7	9	7	282	29.1	7.9
A0A5C2GZT	IG c1909_	33	2	11	1	112	12.2	8.03
O60701	UDP-glucc	23	9	11	9	494	55	7.12
P31946	14-3-3 pr	34	8	11	3	246	28.1	4.83
O43827	Angiopoie	28	9	12	9	346	40	7.85
A0A5C2GD1	IGL c483_	46	4	10	1	108	11.7	7.96
V9HWA3	Epididymi	38	7	12	7	260	29.5	7.34
A0A5C2GTX	IG c1329_	34	3	10	1	122	13.3	8.46
P61981	14-3-3 pr	30	8	11	4	247	28.3	4.89
A0A5C2GNY	IG c270_h	38	4	9	1	122	13.5	6.62
Q05DH1	Proteasom	33	6	9	6	238	26.7	8.87
Q8IZZ5	Coagulati	18	10	11	10	615	67.7	7.74
P50990	T-complex	20	10	11	10	548	59.6	5.6
B2RDW0	cDNA, FLJ	38	5	10	4	149	16.8	4.22
A0A5C2GME	IG c324_l	43	3	10	1	112	12.4	7.96
P02750	Leucine-r	18	5	9	5	347	38.2	6.95
Q8NCH0	Carbohydr	24	9	12	9	376	43	9.48
A4D2P0	Ras-relat	28	6	10	5	211	23.5	8.63
P05997	Collagen	6	7	9	5	1499	144.8	6.46
G3V2W1	Protein Z	13	7	13	7	484	55.1	7.64
A0A5C2G8Y	IGL c500_	26	4	11	1	113	12.5	7.99
B4E320	cDNA FLJ5	15	8	9	8	686	77.5	5.08
A0A5C2GS4	IG c1300_	31	3	9	1	126	13.9	7.75
A0A5C2GD6	IGH + IGL	21	2	8	1	119	13	7.96
A0A0K0K1J	Epididymi	37	5	8	5	146	15.8	8.75
Q9H173	Nucleotid	10	5	10	5	461	52.1	5.36
P05388	60S acidi	28	7	9	7	317	34.3	5.97
Q59EP1	Annexin (	22	9	9	9	510	54.9	7.27
Q8IZ52	Chondroit	12	9	10	9	775	85.4	6.93
B2R5U1	Staphyloc	11	9	10	9	885	99.6	6.96
Q9UL88	Myosin-re	24	2	8	0	131	14.1	9.63
B4DLA1	cDNA FLJ5	18	9	11	7	533	60	6.55
C9JIZ6	Prosaposi	9	5	10	5	527	58.4	5.17
B2R9K8	cDNA, FLJ	20	10	10	10	531	57.9	6.8
Q9UBX1	Cathepsin	15	8	11	8	484	53.3	8.22
Q8TB01	Similar t	18	10	11	10	560	62	5.68
A0A024R1K	Tyrosine	31	8	10	5	246	28.2	4.84
B4E3Q1	cDNA FLJ6	10	10	11	5	962	107.7	4.97
A0A5C2GWE	IG c1881_	32	3	7	1	127	13.6	5.86
Q9P2E9	Ribosome-	18	8	10	8	1410	152.4	8.6
P21926	CD9 antig	7	3	12	3	228	25.4	7.15
C9JD84	Latent-tr	8	9	10	1	1340	146.9	4.91
A0A5C2GPJ	IG c1305_	32	3	7	1	121	12.9	8.46
B4DID6	cDNA FLJ5	29	7	8	7	364	39.8	4.67

O75829	Leukocyte	15	4	8	4	334	37.1	7.56
Q9BUD6	Spondin-2	18	5	10	5	331	35.8	5.52
P24593	Insulin-l	26	7	10	7	272	30.6	8.21
A0A5C2G9W	IGH c53_h	35	3	7	1	117	13	5.41
A0A5C2GW7	IG c857_h	31	3	7	1	127	13.9	8.41
A0A024RAG	Adiponect	18	3	10	3	245	26	9.11
Q8IWU5	Extracell	8	8	11	8	870	100.4	9.17
P27824	Calnexin	15	7	10	7	592	67.5	4.6
Q8N6N5	Tubulin b	19	7	12	2	445	49.8	4.86
A0A5C2GHQ	IG c46_he	20	2	7	1	123	13.5	8.43
V9HWA6	Epididymi	48	9	11	8	165	18.5	7.85
Q53FI7	Four and	24	6	8	1	280	31.9	8.22
P30050	60S ribos	64	8	9	8	165	17.8	9.42
Q5U0C3	RAP1A, me	26	4	8	1	184	20.9	6.67
A0A5C2GCG	IGH + IGL	25	3	10	1	114	12.7	9.36
B4DWC4	Chloride	25	4	8	4	245	27.8	6.38
A0A5C2G12	IGL c33_l	24	3	10	1	112	12.2	8.91
A0A024RB8	RAP1B, me	26	4	8	1	184	20.8	5.78
A0A5C2GS3	IG c1723_	35	3	7	1	116	12.5	8.5
A0A2U8J97	Ig heavy	23	2	7	1	107	11.8	9.32
A0A024R87	Delta-ami	27	7	8	7	339	37.2	6.84
A0A5C2GXA	IG c1583_	25	2	9	1	112	12.3	6.57
A0A5C2GBW	IGH + IGL	33	2	9	1	112	12.3	7.12
E9PQH6	Rho-relat	33	5	8	1	169	19.2	5.1
A0A5C2GLN	IG c368_l	47	3	8	1	107	11.5	7.96
A8K690	cDNA FLJ7	16	9	9	9	543	62.6	6.8
A0A5C2GFM	IGH + IGL	31	2	6	1	109	12	5.06
A0A5C2GCZ	IGL c453_	31	3	7	1	109	12	8.94
A0A5C2G5V	IGL c1753	40	3	8	0	107	11.5	8.51
A0A5C2GR5	IG c1383_	43	4	9	1	122	13.5	4.77
Q53EP4	Dolichyl-	17	9	9	9	607	68.5	6.38
Q7Z406	Myosin-14	3	4	7	1	1995	227.7	5.6
V9HWH9	Protein S	34	3	7	3	105	11.7	7.12
A0A5C2GRN	IG c291_h	24	2	8	1	124	13.6	4.93
A0A140VKC	Testicula	14	8	10	5	684	73.9	6.35
A0A5C2GKF	IGH + IGL	39	3	7	2	109	12	6.57
A0A1W6IYJ	N90-VRC38	24	2	7	0	124	13.9	8.44
Q15758	Neutral a	17	7	8	7	541	56.6	5.48
Q9NS15	Latent-tr	6	7	9	7	1303	139.3	6.07
B7Z5V0	cDNA FLJ5	23	6	8	1	275	31.2	8.41
Q16715	Pyruvate	6	3	8	2	587	63.2	7.53
P04844	Dolichyl-	15	7	9	7	631	69.2	5.69
B2RCM5	cDNA, FLJ	20	7	9	7	443	49.3	4.94
I3L397	Eukaryoti	38	6	7	6	146	16	5
A0A5C2GRQ	IG c174_l	51	4	7	1	108	11.7	7.97
A0A5C2FYG	IGL c1216	31	2	7	1	108	11.8	8.5
P27918	Properdin	20	7	12	7	469	51.2	7.9
A0A5C2GCU	IGH + IGL	25	2	6	1	121	12.8	5.11
P10599	Thioredox	40	5	9	5	105	11.7	4.92
A0A024R0F	Transform	26	8	8	8	390	44.3	8.53
D3JV41	C-X-C mot	39	4	8	4	126	13.7	9

P26927	Hepatocyt	13	8	9	8	711	80.3	7.68
B4DI38	Adenylyl	17	7	8	7	452	49	8.21
A0A5C2GT2	IG c1854_	31	3	6	2	124	13.4	7.96
P60953	Cell divi	19	3	7	2	191	21.2	6.55
A0A5C2GKN	IG c369_h	32	3	6	1	117	13	7.14
A0A5C2GNX	IG c1125_	32	2	7	0	115	12.7	7.12
B3KUR3	cDNA FLJ4	32	7	9	7	242	28	5.85
Q03692	Collagen	5	3	8	3	680	66.1	9.67
O15144	Actin-rel	16	5	8	5	300	34.3	7.36
A0A5C2GV5	IG c673_l	32	2	5	1	107	11.7	6.51
A0A5C2GX3	IG c258_l	32	2	5	1	107	11.6	7.97
P11047	Laminin s	6	9	10	9	1609	177.5	5.12
A0A0X9T7	IMS-D3 hea	29	3	6	1	134	15	5.92
P55268	Laminin s	8	9	9	9	1798	195.9	6.52
A0A087X2E	Basigin (	29	5	9	5	221	23.9	5.25
Q59GA0	Thy-1 cel	27	3	7	3	145	15.9	9
A0A024QZ3	Microfibr	14	2	6	2	279	31.1	5.66
Q59FV6	ARP3 acti	22	6	8	6	369	42.2	5.87
Q53FS4	Lectin, m	11	7	9	7	510	57.5	6.81
B3KQQ9	cDNA PSEC	19	5	8	5	383	43	9.36
B4DZK8	cDNA FLJ6	21	5	8	5	280	30.8	8.25
P13798	Acylaminc	12	8	11	8	732	81.2	5.48
D9IAI1	Epididymi	35	5	7	5	187	21	7.53
A0A5C2FWN	IGL c1232	32	2	7	1	107	11.2	6.54
A0A5C2GEJ	IG c1203_	51	5	7	3	118	12.9	7.96
Q641Q3	Meteorin-	27	6	7	6	311	34.4	8.35
A0A5C2GMJ	IG c408_h	31	3	6	1	121	13.4	9.2
A0A5C2FWW	IGL c1521	24	2	5	1	120	13.4	8.81
P22626	Heterogen	17	5	8	5	353	37.4	8.95
A0A5C2GNQ	IG c294_h	35	4	10	1	129	14.5	6.62
A0A5C2GBJ	IGH + IGL	36	3	7	1	109	12	8.44
A0A5C2FSY	IGL c28_l	34	3	8	1	108	11.8	6.54
A0A5C2G6Y	IGL c148_	13	2	9	2	166	17.3	5.15
B4DUQ1	cDNA FLJ5	22	8	9	8	439	48.5	5.92
Q12841	Follistat	16	6	8	6	308	35	5.52
Q9UK22	F-box onl	17	4	10	4	296	33.3	4.37
A6XND1	Insulin-l	34	8	8	8	263	29	8.46
B2R9F2	cDNA, FLJ	15	6	8	6	405	45.1	6.04
P26572	Alpha-1,3	20	9	11	9	445	50.8	9.16
A0A494C1A	Alpha-act	12	8	8	1	858	99.7	5.67
A0A5C2GTE	IG c1109_	47	5	7	1	125	13.9	7.11
A0A5C2GRG	IG c1483_	35	4	12	1	118	13.1	8.79
P55774	C-C motif	52	3	7	3	89	9.8	8.75
K7ER74	APOC4-APC	34	6	7	4	178	20	6.64
A0A384NPH	Epididymi	18	8	8	8	558	61.6	7.3
A0A5C2GNC	IG c825_h	24	2	5	1	124	13.6	6.52
A0A5C2GHM	IG c1103_	22	2	5	1	127	14.2	8.41
P50502	Hsc70-int	17	6	8	6	369	41.3	5.27
A0A5C2GE1	IGH + IGL	27	2	5	1	125	13.9	5.1
A0A5C2GGV	IG c324_h	23	2	5	1	131	14.2	7.12
Q53RD9	Fibulin-7	15	6	9	6	439	47.3	7.62

A0A5C2G6K	IGL c3297	23	2	5	1	107	11.6	8.85
Q59GX2	Solute ca	12	6	8	6	517	57	9.47
A0A5C2G3L	IGL c3752	23	2	6	1	113	12.5	7.12
Q02985	Complemen	18	5	8	4	330	37.3	7.55
A0A5C2GKR	IGH + IGL	35	3	7	1	107	11.7	8.46
A0A024R5Z	RAB11A, m	28	6	8	6	216	24.4	6.57
A0A5C2GWZ	IG c1107_	30	3	6	1	123	13.7	7.39
A0A5C2GL6	IG c1170_	50	5	7	1	126	13.7	8.41
Q9UID7	CYR61 pro	18	6	8	1	334	37.2	8.1
A0A5C2GA9	IGH + IGL	35	3	7	0	107	11.8	7.96
Q16695	Histone H	29	5	9	5	136	15.5	11.12
A0A5C2G6E	IGL c3365	47	3	5	1	107	11.6	7.96
A0A5C2GT5	IG c1680_	50	6	9	1	125	13.5	8.78
A0A5C2G08	IGL c1365	24	2	5	1	107	11.6	8.85
Q9BVJ8	HEXA prot	20	8	8	8	409	47.1	5
A0A5C2GAA	IGH c203_	26	2	5	1	117	13	8.79
P63244	Receptor	21	6	8	6	317	35.1	7.69
A0A5C2GKG	IG c571_h	24	2	6	1	126	13.8	5.41
Q70JA7	Chondroit	8	8	8	8	882	100.2	8.75
P47755	F-actin-c	28	5	7	4	286	32.9	5.85
P07858	Cathepsin	19	5	7	5	339	37.8	6.3
P48061	Stromal c	40	4	9	4	93	10.7	9.88
A0A5C2GP2	IG c310_h	24	2	5	1	123	13.3	6
B2R7L2	Annexin C	14	7	8	7	466	50.3	6.61
A0A5C2GQV	IG c1283_	25	2	5	1	118	12.8	7.99
Q6WN34	Chordin-l	18	7	8	6	429	47.5	7.88
D0PNI2	Lysyl oxi	15	5	7	5	417	46.9	8.09
Q4VB24	Histone c	26	7	9	4	219	21.9	11.03
A0A5C2GGD	IG c695_h	40	4	7	1	122	13.6	7.94
A0A024R58	Calpain 1	11	6	7	6	713	81.8	5.82
H3BPK4	Myosin re	23	3	9	3	199	22	5.81
V9HW96	Chaperoni	17	6	6	6	535	57.5	6.46
A0A5C2GQY	IG c1134_	31	3	6	1	124	13.6	7.8
P17858	ATP-depen	10	7	8	5	780	85	7.5
B4DUF1	cDNA FLJ5	8	6	8	6	661	75.8	6.52
A0A024RAV	Branched-	15	5	7	5	386	42.9	5.3
P54578	Ubiquitin	17	7	7	7	494	56	5.3
A0A5C2GN1	IG c842_h	43	3	6	1	121	13.2	7.94
B4E2U0	6-phospho	18	8	9	3	461	50.8	8.18
A0A5C2GSF	IG c819_h	36	4	11	0	119	13.2	7.93
P21266	Glutathio	29	6	9	5	225	26.5	5.54
P40121	Macrophag	18	6	7	6	348	38.5	6.19
A0A068LKR	Ig heavy	22	2	5	1	118	12.8	6.01
A8K7Q1	cDNA FLJ7	14	6	8	6	461	53.9	5.25
B4DWB5	cDNA FLJ5	14	7	9	7	618	70	7.33
Q5U0A0	Proteasom	30	5	6	5	241	26.4	4.79
A0A140VK4	Proteasom	22	6	7	6	246	27.4	6.76
A0A024R79	Choline t	10	7	9	7	704	79.8	8.57
A0A5C2GTS	IG c717_l	31	2	5	1	108	11.8	8.48
P21246	Pleiotrop	22	3	7	3	168	18.9	9.6
O95025	Semaphori	11	9	10	9	777	89.6	7.8

P08493	Matrix Gl	23	2	6	2	103	12.3	9.67
O00462	Beta-mann	7	5	7	5	879	100.8	5.52
A0A5C2GA8	IGH c185_	29	3	7	1	120	13.4	7.12
P18084	Integrin	11	8	8	8	799	88	6.06
A0A2R8YEL	Glutamate	10	6	8	6	639	72.9	6.09
E9PRJ8	Tetraspan	21	3	6	3	209	22.5	6.15
P06703	Protein S	34	5	9	5	90	10.2	5.48
P05556	Integrin	8	7	8	7	798	88.4	5.39
Q8N2S1	Latent-tr	5	7	7	7	1624	173.3	5.43
P22061	Protein-L	33	6	7	6	227	24.6	7.21
Q6IPN0	Reticulon	15	4	6	4	343	36.9	4.81
A0A5C2G2R	IGL c288C	38	3	5	1	108	11.8	7.97
Q9UGM5	Fetuin-B	16	6	8	6	382	42	6.83
P07686	Beta-hexo	10	5	8	5	556	63.1	6.76
A0A5C2GHE	IG c56_he	39	4	7	1	119	13.3	6.77
B2R888	Monocyte	18	6	7	6	375	40	6.23
Q9HDC9	Adipocyte	13	6	8	6	416	46.5	6.16
Q6PCB0	von Wille	11	4	6	4	445	46.8	7.68
Q7Z3Z1	Myosin li	22	3	7	3	165	18.7	5
A0A0A0MRC	Voltage-d	23	5	6	5	282	30.3	7.81
Q4W4Y1	Dopamine	12	8	8	8	868	96	6.52
Q6FHJ7	Secreted	16	5	7	5	346	39.8	8.82
P18627	Lymphocyt	13	6	7	6	525	57.4	7.97
A0A5C2G08	IGL c194C	31	2	7	1	108	11.8	7.97
A0A5C2FYH	IGL c307_	39	3	5	1	109	11.8	7.96
A0A5C2GBZ	IGH + IGL	45	4	7	1	107	11.7	8.47
A0A5C2GLU	IG c316_h	22	3	6	1	127	14.2	8.19
A0A2U3TZL	CD59 glyc	27	4	6	4	120	13.3	6.25
O75874	Isocitrat	14	7	8	7	414	46.6	7.01
P20809	Interleuk	36	6	7	6	199	21.4	10.62
A0A5C2G8L	IGL c4047	36	3	5	1	113	12.6	7.93
A8K6C1	Cholester	10	4	6	4	493	54.7	6.09
P16152	Carbonyl	29	6	7	6	277	30.4	8.32
P13796	Plastin-2	12	7	7	2	627	70.2	5.43
E5RJR5	S-phase k	29	4	8	4	163	18.7	4.7
A0A0G2JLE	Glucosylc	13	7	9	7	536	59.6	7.42
A0A5C2GHX	IG c806_h	30	3	6	1	122	13.5	5.19
B4E0X1	Beta-2-mi	22	3	6	3	122	13.9	7.44
A0A024R7V	RAB2, mem	28	5	7	5	212	23.5	6.54
A0A5C2GL9	IG c96_he	24	2	6	1	125	13.8	7.93
A0A5C2GIF	IG c198_h	40	5	6	1	130	14.7	7.91
A0A5C2GX5	IG c278_l	37	3	5	1	108	11.7	8.48
A0A5C2FYE	IGL c257_	35	3	6	2	107	11.7	6.54
A0A5C2GHF	IGH + IGL	39	3	5	1	113	12.5	7.12
B4DRB0	Tetraspan	26	6	7	6	201	22.9	8.16
A0A5C2GHW	IG c507_h	25	3	6	1	127	13.9	8.46
A0A2U8J92	Ig heavy	40	4	8	1	94	10.5	8.73
P59998	Actin-rel	32	5	8	5	168	19.7	8.43
A8K8C4	cDNA FLJ7	15	4	6	4	431	47.1	4.84
Q9NZP8	Complemen	12	5	7	4	487	53.5	7.2
A0A024R6Y	Nuclear t	48	4	6	4	127	14.5	5.38

D3DV26	S100 calc	8	3	8	3	205	22.3	10.33
P23396	40S ribos	33	7	8	7	243	26.7	9.66
K9MS24	Spectrin	3	6	7	2	2364	274.2	5.55
A0A140VJF	Biliverdi	21	6	7	6	296	33.4	6.44
A0A2U8J93	Ig heavy	26	3	7	1	104	11.7	7.83
Q9UII7	E-cadheri	3	3	7	3	901	99.6	4.78
H0YJW4	Cochlin (	10	4	6	4	434	48.1	6.28
X6RFL8	Ras-relat	33	5	6	5	181	20.4	6.33
A0A5C2GR4	IG c1373_	24	2	4	1	124	13.4	7.93
Q6NZI2	Caveolae-	16	6	7	6	390	43.5	5.6
A0A3B3ITY	Calsynten	17	6	7	1	373	41.4	6.67
A8K7F6	cDNA FLJ7	23	8	8	4	406	46.1	5.48
H7BZJ3	Protein d	38	4	6	1	123	13.5	7.3
P12236	ADP/ATP t	17	5	7	1	298	32.8	9.74
Q5U043	S-(hydrox	17	5	6	5	374	39.7	7.49
A0A5C2G6T	IGH c8_he	31	3	6	1	119	13.2	8.88
A0A5C2GEI	IG c1055_	22	2	4	1	125	13.5	5.15
A0A5C2GUF	IG c1175_	32	3	6	1	107	11.8	8.5
Q76LA1	CSTB prot	24	2	6	2	98	11.1	7.56
P61020	Ras-relat	26	4	5	2	215	23.7	8.13
P04792	Heat shoc	20	5	6	5	205	22.8	6.4
A0A140VK2	Leukotrie	12	6	6	6	611	69.2	6.18
A0A5C2GL2	IG c265_h	40	4	8	1	120	13.4	7.97
A0A024R4X	NADH-cytc	19	4	5	4	291	33.2	7.58
A0A5C2GKM	IG c184_l	49	4	6	1	112	12.3	7.28
I3L145	Sex hormc	13	5	7	5	344	37.5	6.23
D3DP78	Aspartyl-	15	6	7	6	468	53.4	6.54
C9JXA5	Guanine n	16	4	6	1	251	27.5	6.76
A0A0A0MTF	Integrin-	11	5	6	5	483	54.6	7.97
A0A5C2GC9	IGL c203_	49	4	5	1	108	11.7	7.96
P51149	Ras-relat	31	6	7	6	207	23.5	6.7
P30626	Sorcin OS	31	5	7	5	198	21.7	5.59
Q9GZP4	PITH doma	19	3	5	3	211	24.2	5.74
A0A0S2Z3S	GNAS comp	13	5	6	4	380	44.2	6.29
Q6ICQ8	ARHG prot	10	2	5	1	191	21.3	8.12
A0A5C2GC7	IGH + IGL	27	2	5	1	109	11.9	9.1
P20851	C4b-bindi	21	5	6	5	252	28.3	5.14
A0N5G5	Rheumatoi	30	3	6	1	118	12.8	8.97
Q16777	Histone H	37	5	7	2	129	14	10.9
B2R6K4	cDNA, FLJ	12	4	6	1	340	37.3	6.18
Q96QV1	Hedgehog-	10	7	7	7	700	78.8	7.9
A0A5C2FYI	IGL c1226	32	2	5	1	107	11.8	7.94
A0A5C2G4F	IGL c3834	32	3	6	1	108	11.9	8.94
A0A5C2GMK	IG c83_he	26	3	6	1	121	13.4	7.91
Q04760	Lactoylgl	26	5	6	5	184	20.8	5.31
Q01995	Transgeli	31	5	6	5	201	22.6	8.84
P23526	Adenosylh	16	6	6	6	432	47.7	6.34
A0A5C2FX8	IGL c1591	40	3	6	1	111	12.2	8.88
A0A5C2GJC	IGH + IGL	39	3	6	1	112	12.4	8.51
A0A5C2GR9	IG c1244_	39	5	7	1	128	13.7	8.44
A0A5C2GM4	IG c585_h	25	2	6	1	121	13.5	4.93

A0A5C2GUV	IG c297_h	22	3	6	1	122	13.5	8.75
A0A5C2GHJ	IG c1102_	34	3	6	0	122	13.5	7.97
A0A5C2GHU	IG c477_h	25	3	6	1	122	13.1	7.11
B4DZ36	cDNA FLJ5	6	7	7	7	1156	129.7	6.87
A0A5C2GTV	IG c934_l	27	2	5	1	107	11.7	8.46
A0A5C2GQQ	IG c1745_	42	5	6	1	120	13.2	5.45
A2J1N5	Rheumatoi	32	3	6	1	94	10.4	9.13
P61026	Ras-relat	17	4	6	3	200	22.5	8.38
A0A5C2GQ8	IG c140_h	37	4	6	1	123	13.8	8.27
A5GZ70	Matrix me	54	4	7	1	71	8.1	6.67
A0A5C2GSD	IG c977_l	39	3	4	1	114	12.5	6.57
A0A5C2GLU	IG c148_h	21	3	7	0	127	14.4	7.12
K4RH61	Matrix me	5	3	5	3	582	65.9	7.97
A0A5C2GVF	IG c617_h	28	3	6	1	124	13.7	6.65
F8W6I7	Heterogen	10	3	6	2	307	33.1	9.13
A0A5C2G7K	IGL c474_	35	3	6	1	105	11.4	7.97
P39656	Dolichyl-	16	6	7	6	456	50.8	6.55
Q08257	Quinone c	14	5	6	5	329	35.2	8.44
Q14520	Hyalurona	9	6	7	6	560	62.6	6.54
A0A5C2GHW	IG c466_l	39	3	6	1	114	12.7	8.5
A0A5C2GQN	IG c1213_	42	5	7	1	120	13	8.92
P09238	Stromelys	6	3	5	1	476	54.1	5.8
P17174	Aspartate	13	5	6	5	413	46.2	7.01
A0A5C2GVI	IG c1501_	33	2	4	1	113	12.3	5.34
A0A5C2FW3	IGL c854_	24	2	5	1	106	11.7	8.44
P49908	Selenopro	12	5	8	5	381	43.2	7.87
A0A5C2G8S	IGH + IGL	21	2	5	1	126	13.7	8.85
P02741	C-reactiv	21	4	5	4	224	25	5.63
E7EUF1	Ectonucle	9	7	7	7	884	101.5	7.53
B1ALA9	Ribose-ph	19	5	7	5	285	31.4	6.86
Q14974	Importin	10	6	6	6	876	97.1	4.78
P08514	Integrin	6	6	6	6	1039	113.3	5.38
A0A024R87	Chromosom	10	6	6	6	733	82.6	6.15
A0A5C2G86	IGH + IGL	24	3	7	1	126	13.9	9.01
Q68DI0	AP comple	7	5	5	5	951	105.6	5.38
Q16775	Hydroxyac	13	4	6	4	308	33.8	8.12
A0A5C2GE4	IG c125_h	23	2	5	1	118	12.7	8.91
P22792	Carboxype	9	5	6	5	545	60.5	5.99
A0A5C2GYK	IG c1772_	33	2	4	1	112	12	7.99
P05141	ADP/ATP t	17	5	6	1	298	32.8	9.69
A0A5C2GQF	IG c1706_	21	3	10	1	123	13.5	6.04
A0A140VJJ	S-formylg	11	4	6	4	282	31.4	7.02
A0A5C2G1Y	IGL c3298	53	4	5	1	107	11.7	7.99
A0A5C2GGM	IG c55_he	34	3	6	1	124	13.6	7.97
A0A0S2Z4W	Protein k	11	5	6	5	406	45.9	4.34
P02776	Platelet	35	3	5	1	101	10.8	8.62
P08779	Keratin,	11	5	6	3	473	51.2	5.05
A0A5C2GIU	IG c231_h	37	4	5	1	121	13.2	9.07
A0A5C2GJS	IG c1285_	30	3	5	2	125	13.5	5.41
Q14847	LIM and S	23	5	6	5	261	29.7	7.05
A0A5C2GAR	IGH + IGL	24	2	4	2	125	13.5	8.47

P52895	Aldo-ketc	16	4	4	4	323	36.7	7.49
Q12797	Aspartyl/	7	6	6	6	758	85.8	5.01
A0A125QYY	IBM-B2 he	28	3	5	1	123	13.6	7.12
A0A2U8J8I	Ig heavy	31	3	5	1	101	11.4	8.46
Q6FH49	NNMT prot	17	4	5	4	264	29.6	5.74
P10253	Lysosomal	4	3	5	3	952	105.3	6
A0A5C2GA6	IGH c155_	20	3	6	0	126	13.9	8.46
Q8N428	Polypepti	8	4	5	4	558	63	9.13
E7EQG2	Eukaryoti	22	6	6	2	362	41.3	5.64
A0A5C2GXA	IG c1867_	33	2	4	1	112	12.2	7.44
Q5HYD8	Uncharact	9	4	6	4	533	60.6	5.71
Q59E85	Caveolin	23	4	5	4	217	25.1	7.91
A0A5C2GVE	IG c1534_	30	2	4	1	109	11.8	8.51
Q0ZCJ1	Immunglob	37	4	5	2	121	13.4	8.43
A0A5C2GN8	IG c776_h	25	3	6	1	123	13.4	7.97
A0A5C2GW7	IG c689_l	31	2	4	1	108	11.7	7.96
A0A5C2FX5	IGL c175_	31	3	5	1	107	11.7	8.47
P41222	Prostagla	21	3	5	3	190	21	7.8
A0A5C2G1V	IGL c2530	32	3	6	1	109	11.9	8.48
A0A5C2G8Q	IGH + IGL	19	2	5	1	118	12.9	8.85
H0YFD6	Trifuncti	8	5	5	5	792	86.3	9.1
Q09328	Alpha-1,6	9	6	6	6	741	84.5	8.12
O00292	Left-righ	15	6	7	6	366	40.9	8.56
P15169	Carboxype	15	6	6	6	458	52.3	7.34
Q9BQB4	Sclerosti	23	4	5	4	213	24	9.25
A0A0K0K1K	6-phospho	21	5	6	5	258	27.5	6.05
Q53FN7	BZW1 prot	15	5	6	5	424	48.6	6.11
Q15293	Reticuloc	18	5	5	5	331	38.9	5
Q9Y678	Coatomer	7	4	4	4	874	97.7	5.47
A0A5C2GAF	IGH + IGL	27	4	7	1	124	13.4	8.98
Q6ZS56	cDNA FLJ4	5	4	5	4	618	67	8
Q59EH3	Acid phos	30	4	4	4	165	18.7	7.88
X5D2M8	Major vau	8	5	5	5	893	99.3	5.48
F5GZS6	4F2 cell-	9	4	5	4	599	64.8	5.1
Q9Y646	Carboxype	13	5	6	5	472	51.9	6.18
A0A5C2FX4	IGL c806_	26	2	5	1	107	11.7	7.94
A0A5C2GBT	IGL c201_	32	2	5	1	107	11.6	5.96
A0A5C2G1U	IGL c3139	32	2	5	1	107	11.6	8.85
P54709	Sodium/pc	17	4	5	4	279	31.5	8.35
P49189	4-trimeth	17	7	7	7	494	53.8	5.87
P48723	Heat shoc	12	5	5	5	471	51.9	5.76
A8K2Q6	Peptidyl-	29	4	6	4	212	22.7	8.4
Q8N1C8	HSPA9 prc	7	5	6	4	681	73.8	6.37
A0A5C2GSL	IG c2_lig	33	2	3	1	112	12.1	5.96
A0A5C2GNZ	IG c685_h	31	3	5	1	122	13.6	7.94
A0A5C2GFR	IG c984_h	29	4	5	1	128	14.1	8.76
Q9NYU1	UDP-glucc	3	5	5	5	1516	174.6	6.89
H0Y8G5	Heterogen	20	4	4	4	260	29.6	9.16
A0A125U0U	MS-C1 hea	25	3	4	1	118	13.1	6.07
A0A5C2FVU	IGL c210_	33	3	4	1	108	11.6	6.01
O95747	Serine/th	8	3	4	3	527	58	6.43

A0A5C2FUL	IGL c691_	39	3	4	2	112	12.3	8.5
A0A5C2GH4	IG c421_h	41	4	6	1	120	13.1	7.99
Q9H8L6	Multimeri	5	3	4	3	949	104.3	5.86
A8K6Y1	cDNA FLJ7	15	5	6	5	367	40.9	6.4
A0A0S2Z4G	Nucleophc	15	4	5	4	265	29.4	4.61
P26641	Elongatic	9	4	5	4	437	50.1	6.67
Q6FGD7	Tubulin-s	47	5	5	5	108	12.8	5.29
A0A024R1A	Ubiquitin	31	4	4	4	154	17.9	8.51
Q68DH9	Calcium-t	5	6	6	6	1205	133.8	6.49
A0A5C2G0K	IGL c1956	43	4	5	1	107	11.6	8.5
A0A5C2GMT	IG c1332_	20	2	4	1	123	13.7	8.81
B3KNV8	Polypepti	6	4	6	4	607	69.5	6.49
A0A024R1U	RAB5C, me	17	3	4	1	216	23.5	8.41
A8K3H8	cDNA FLJ7	10	6	6	6	589	65.3	5.11
A0A384MR2	Epididymi	5	5	5	4	1114	122	5.5
A8K6A5	cDNA FLJ7	4	4	5	4	1049	114.4	5.71
P05543	Thyroxine	14	6	7	6	415	46.3	6.3
P53621	Coatomer	5	5	5	5	1224	138.3	7.66
P17655	Calpain-2	6	4	4	4	700	79.9	4.98
A0A5C2GAC	IGH + IGL	28	3	5	1	108	11.6	4.96
P54920	Alpha-sol	15	3	4	3	295	33.2	5.36
A8K7F7	cDNA FLJ7	7	3	4	3	522	58.5	6.55
Q59H77	T-complex	13	5	5	5	577	63.5	6.43
P01591	Immunoglc	23	3	5	3	159	18.1	5.24
A0A5C2FYZ	IGL c1894	31	2	3	1	108	11.8	7.96
A0A5C2GQ6	IG c510_h	12	2	5	1	128	14	9.55
P80108	Phosphati	8	6	6	6	840	92.3	6.37
A0A5C2GDZ	IG c342_h	24	2	5	1	126	13.8	5.41
A0A140VJL	Hypoxanth	17	3	4	3	218	24.6	6.68
V9H1C1	Gelsolin	35	3	6	1	69	8	5.78
Q8WWI5	Choline t	6	3	4	3	657	73.3	8.6
A0A5C2GVF	IG c1451_	22	2	5	1	127	14	6.57
Q92520	Protein F	18	3	4	3	227	24.7	8.29
Q99832	T-complex	8	4	4	4	543	59.3	7.65
Q9NZN3	EH domain	7	4	4	1	535	60.8	6.57
A0A5C2GS2	IG c171_l	22	2	4	1	111	12.3	5.99
A0A5C2GPZ	IG c943_h	25	3	6	1	120	13.2	8.46
P78328	HP47 prot	23	1	4	1	78	8.7	7.05
A0A2U8J8R	Ig heavy	32	3	6	1	98	10.8	9.45
A0A5C2GUF	IG c137_h	30	4	6	1	120	13.2	8.85
A0A5C2GPF	IG c1168_	18	2	4	1	124	13.8	9.2
A0A5C2GVM	IG c1278_	24	3	4	1	125	13.7	5.12
A0A0A0MT6	Deoxyribc	14	4	6	4	288	33.5	8.53
A0A5C2GDA	IG c887_h	32	3	6	1	120	12.8	7.97
A0A140VJN	Perilipin	13	5	5	5	433	46.9	5.44
A0A5C2GJE	IG c922_h	24	3	4	1	127	13.8	6.04
A0A5C2GPE	IG c440_h	31	3	4	1	122	13.3	8.4
P20618	Proteasom	24	4	6	4	241	26.5	8.13
V9HWE8	Epididymi	22	4	4	4	204	23.2	5.11
A8K8F9	Phosphoin	6	3	4	3	756	85.6	6.7
A0A5C2GPL	IG c520_h	20	2	4	1	123	13.5	8.46

P58546	Myotrophi	22	2	4	2	118	12.9	5.52
P17213	Bacterici	7	3	4	3	487	53.9	9.38
P16104	Histone H	22	4	5	1	143	15.1	10.74
A0A5C2FWG	IGL c526_	32	2	3	1	107	11.9	9.51
A0A024R2K	RAB5A, me	17	3	4	1	215	23.6	8.15
A0A5C2GQ9	IG c1063_	22	3	8	1	121	13.5	9.55
A0A068LKQ	Ig heavy	24	3	5	1	120	13.2	9.07
P61006	Ras-relat	9	2	4	1	207	23.7	9.07
P07942	Laminin s	3	4	4	4	1786	197.9	4.94
B4DV28	cDNA FLJ5	15	4	4	4	463	51.5	6.43
H0YJ34	Fermitin	7	4	5	4	640	73.3	6.98
C0JYZ2	Titin OS=	0	4	5	4	33423	3711.4	6.52
A0A5C2GHU	IG c340_l	37	3	4	1	107	11.5	5.01
F6WIT2	Serine/th	11	3	4	3	288	32.9	6.93
C9JSN9	Biotinida	10	2	4	2	251	28.6	6.1
A0A2U8J8Q	Ig heavy	31	3	4	2	101	10.9	9.2
Q92824	Proprotei	2	4	4	4	1860	206.8	6.1
A0A5C2GAU	IGH c345_	20	3	4	0	130	14.6	7.94
B7Z6T9	cDNA FLJ5	7	3	4	3	521	57.5	5.57
B3GQS7	Mitochond	9	5	5	5	569	60.6	6.04
B4DDU6	cDNA FLJ5	10	5	5	5	503	55.4	5.43
Q71UI9	Histone H	31	4	4	2	128	13.5	10.58
Q9UBS4	DnaJ homc	9	3	4	3	358	40.5	6.18
P05160	Coagulati	8	4	4	4	661	75.5	6.39
Q86Z22	Epididymi	12	3	5	3	226	23.8	9.06
A0A5C2GVF	IG c1561_	22	3	8	1	121	13.4	9.41
A0A024R6K	Epididymi	9	3	4	3	471	53.1	6.23
Q508I7	Anthrax t	12	5	5	5	419	46.9	6.33
P78539	Sushi rep	11	4	4	4	464	51.5	8.66
A8K0T9	F-actin-c	22	4	4	3	286	32.9	5.69
A0A5C2FZE	IGL c1045	45	3	4	1	108	11.5	6.55
A0A024RB2	HCG24991,	9	2	4	1	203	22.7	8.79
A0A5C2G32	IGL c3314	37	3	4	0	108	11.9	8.88
P30085	UMP-CMP k	24	4	4	4	196	22.2	5.57
B4DL86	6-phosphc	17	6	6	1	429	47.4	6.47
Q15404	Ras suppr	13	3	4	3	277	31.5	8.65
P02585	Troponin	28	4	5	3	160	18.1	4.2
A0A5C2GDX	IGH + IGL	20	2	4	1	119	13.1	8.84
A0A5C2GBF	IGH + IGL	20	3	5	1	127	14.2	9.47
B2R7P8	cDNA, FLJ	10	5	5	5	592	64.6	6.8
A0A172Q3A	Fibroblas	6	5	5	4	733	84.8	6.55
F6XZQ7	Glutathic	31	5	6	4	220	26.1	5.54
I4AY87	Epididymi	26	2	4	2	115	12.5	7.88
B4DVE1	cDNA FLJ5	8	4	4	4	573	64.1	5.47
A0A5C2GI5	IGH + IGL	26	3	8	2	121	13.2	8.46
A0A5C2FZQ	IGL c1145	32	3	4	1	107	11.8	8.5
P30740	Leukocyte	14	5	5	5	379	42.7	6.28
A0A5C2GT1	IG c1844_	22	3	5	2	124	13.4	9.51
Q1LZN2	NOMO3 prc	6	3	3	3	807	89.8	5.67
B4DP27	cDNA FLJ5	18	3	4	3	169	19.2	5.86
A0A5C2H01	IG c1278_	27	2	4	2	106	11.7	8.48

Q86UY0	TXNDC5 pr	9	3	4	3	360	40.3	5.83
A0A5C2G8V	IGH + IGL	15	2	4	1	123	13.6	9.07
P02533	Keratin,	8	4	5	2	472	51.5	5.16
A0A5C2GJK	IG c281_l	25	2	3	1	107	11.6	5.25
A0A5C2GY3	IG c630_l	25	2	4	1	109	11.9	8.5
A0A5C2GJV	IG c774_h	26	3	4	2	125	14	8.81
A0A5C2GES	IG c889_h	25	2	4	1	120	13.1	4.77
Q2TSD3	Protein k	9	4	5	4	672	76.7	7.05
B3KUI5	Hyaluroni	15	4	4	4	435	48.3	6.96
A0A2U8J93	Ig heavy	23	2	4	1	95	10.8	6.52
A0A5C2GVG	IG c1554_	31	3	4	1	108	11.8	8.51
O14950	Myosin re	27	4	4	4	172	19.8	4.84
A0A5C2GAS	IGH + IGL	16	2	4	1	122	13.2	8.85
B2RAZ5	UDP-Gal:b	10	4	5	4	344	40	9.07
E9PCX2	Aldo-keto	17	4	4	4	263	29.4	6.99
A0A5C2H0L	IG c1478_	14	2	4	1	111	11.7	7.84
A0A5C2GKQ	IG c85_he	32	3	4	1	120	13	7.96
Q9Y3E8	CGI-150 p	6	3	5	3	504	55	8.7
Q14315	Filamin-C	2	5	5	2	2725	290.8	5.97
A0A5C2GED	IGH + IGL	24	3	5	1	127	14.1	9.58
A2VDJ4	GNPTG pro	9	3	4	3	292	32.9	6.79
A0A5C2GBR	IGH + IGL	25	2	5	1	119	12.9	8.46
A0A5C2GXN	IG c460_l	32	3	4	1	104	11.3	8.5
A0A5C2GIV	IG c1007_	23	2	5	1	132	14.7	6.54
A0A0N9HRK	MHC class	11	3	4	3	365	40.9	6.04
A0A5C2GUN	IG c227_h	25	2	4	2	122	13.2	7.96
A0A5C2G6G	IGL c3946	29	3	4	1	108	11.6	5.99
A0A5C2G9J	IGL c495_	36	2	3	2	108	11.7	8.48
A0A5C2GF1	IG c531_h	43	4	4	1	114	12.5	8.47
Q08722	Leukocyte	11	4	4	4	323	35.2	7.21
I1W660	Dickkopf-	11	3	4	3	266	28.7	8.4
P10301	Ras-relat	11	2	3	1	218	23.5	6.93
O95450	A disinte	4	4	4	4	1211	134.7	7.15
A0A5C2G5I	IGH c200_	23	3	4	1	126	14	7.12
A0A5C2GSZ	IG c939_h	34	3	5	1	120	13.1	7.97
A0A5C2GR6	IG c1214_	15	2	4	1	121	13.2	9.13
A0A5C2G05	IGL c1184	15	2	4	1	110	11.6	6.52
A0A024QZ4	HCG198558	28	3	4	3	121	14.4	5.29
P29120	Neuroendo	5	4	5	4	753	84.1	5.99
A0A5C2GDW	IG c225_h	22	2	4	1	117	12.9	6.61
A0A5C2GMW	IG c518_h	23	3	5	1	124	13.8	8.16
A0A5C2GQE	IG c1522_	24	2	3	1	119	12.9	5.36
A0A2U8J8Z	Ig heavy	32	3	4	2	98	10.9	6.52
Q96CW1	AP-2 comp	6	3	4	3	435	49.6	9.54
B8ZWD1	Acyl-CoA-	45	3	4	3	97	11.1	8.32
P05413	Fatty aci	29	4	4	4	133	14.8	6.8
M0R0R2	40S ribos	20	4	4	4	225	25.3	9.76
P04632	Calpain s	15	3	3	3	268	28.3	5.2
A0A5C2GPS	IG c1386_	24	2	3	1	123	13.8	5.17
Q9BTY2	Plasma al	9	4	5	4	467	54	6.25
Q96HF1	Secreted	11	3	3	3	295	33.5	7.42

B4DKJ4	cDNA FLJ5	19	2	3	2	142	16.1	4.68
Q53FV0	Prohibiti	14	3	4	3	272	29.8	6.39
P10720	Platelet	38	3	4	1	104	11.5	9.1
B2R8Z8	cDNA, FLJ	7	4	4	1	623	69.6	8.76
O95631	Netrin-1	10	5	5	5	604	67.7	8.76
A0A5C2GPW	IG c620_h	36	4	6	2	122	13.3	8.85
Q9HCB6	Spondin-1	5	4	4	4	807	90.9	6.11
Q58EX2	Protein s	2	4	4	4	2172	239.2	7.06
A0A1B1CYC	Vitamin D	38	2	4	2	34	3.7	8.56
P05026	Sodium/po	13	4	4	4	303	35	8.53
Q5TDH0	Protein D	11	3	4	3	399	44.5	5.05
A0A5C2GJX	IG c121_h	30	3	4	1	123	13.6	7.96
A0A5C2GBQ	IGL c343_	24	2	3	1	113	12.3	7.93
A0A5C2G1N	IGL c2366	29	2	3	2	108	11.6	9.29
A0A5C2G9U	IGH + IGL	23	2	3	1	130	14.3	9.03
A0A5C2GDC	IGH + IGL	18	2	3	1	125	13.8	5.29
A0A5C2GXK	IG c430_l	23	4	5	3	110	11.5	7.83
K7EQL4	Troponin	8	1	6	1	210	25.3	9.66
A0A5C2GF5	IG c326_h	27	3	3	2	131	14.4	7.96
A0A5C2G28	IGL c1577	31	2	3	1	108	12	9.25
Q15365	Poly(rC)-	12	4	4	2	356	37.5	7.09
Q7Z2W2	Extracell	5	4	4	4	871	101	9.09
Q6I9T8	Serine/th	15	4	4	4	309	35.5	5.54
Q6FHZ0	Malate de	12	4	5	4	338	35.5	8.68
A0A5C2H0E	IG c1550_	45	3	3	2	107	11.6	7.96
Q7Z7H5	Transmemb	16	3	5	3	227	25.9	8.28
A0A5C2GN4	IG c283_h	18	2	4	1	122	13.6	8.43
P62280	40S ribos	26	4	4	4	158	18.4	10.3
Q6UY50	NL3 OS=Ho	15	3	4	3	218	24.6	6.79
Q6H9L7	Isthmin-2	8	4	4	4	571	63.9	4.81
A0A0S2Z51	G protein	6	4	4	4	687	77	8.44
A0A5C2G4L	IGL c3366	40	3	3	1	113	12.6	6.57
G9I6H4	BNF1 vari	15	2	4	1	136	15.3	7.64
P51991	Heterogen	8	3	4	2	378	39.6	9.01
A0A5C2GIQ	IG c88_he	31	3	6	1	123	13.3	7.99
P02778	C-X-C mot	20	2	4	2	98	10.9	9.86
A0A5C2GTZ	IG c1163_	33	2	4	2	112	12.1	7.12
Q16363	Laminin s	2	4	4	4	1823	202.4	6.28
P32969	60S ribos	15	2	3	2	192	21.9	9.95
A0A087X08	C-C motif	16	2	4	2	115	13.1	8.57
A0A024RAM	Glutaredo	31	3	3	3	106	11.8	8.09
Q7Z7M4	Superoxid	16	3	3	3	213	23.7	7.31
P49588	Alanine--	5	4	4	4	968	106.7	5.53
A0A5C2GR4	IG c359_h	20	2	3	1	123	13.6	7.11
O15145	Actin-rel	21	4	4	4	178	20.5	8.59
F8VZX2	Poly(rC)-	14	4	4	2	321	33.8	8.24
Q53R15	Uncharact	22	3	4	3	140	15.6	4.79
Q9H3Y0	Peptidase	8	2	3	2	253	28.6	9
A0A5C2GR6	IG c1688_	13	2	4	1	119	13.2	7.12
A0A5C2GNE	IG c965_h	16	2	3	1	126	14	9.06
A0A5C2GKX	IG c351_h	12	2	4	1	121	13.2	8.44

Q8N5Y3	GYG1 prot	9	3	4	3	331	37.2	5.4
A0A5C2GEI	IGH c441_	31	3	3	1	124	13.7	7.12
Q8N142	Adenylosu	9	3	3	3	457	50.2	8.59
A0A5C2FZW	IGL c2449	19	2	4	1	108	11.6	4.84
A0A494C0S	C3 and PZ	1	2	3	2	1932	211.2	6.6
A0A5C2GBE	IGL c3713	31	4	5	2	111	11.6	7.99
B4DT28	Heterogen	12	5	5	2	494	55.7	9.23
Q14DE1	GLDN prot	7	3	3	3	427	45.8	6.95
Q14651	Plastin-1	6	3	3	1	629	70.2	5.41
P50991	T-complex	7	3	3	3	539	57.9	7.83
A0A5C2GDI	IGH c31_h	36	4	4	1	120	13.1	8.43
A0A5C2GTE	IG c791_h	22	2	3	1	121	13.1	6.04
A0A5C2FWN	IGL c1222	47	3	3	1	107	11.5	8.5
O15260	Surfeit l	15	4	4	4	269	30.4	7.78
Q53GD1	Guanine n	22	1	3	1	72	8	8.97
A8K4T6	cDNA FLJ7	10	3	3	3	504	56.2	5.57
A0A5C2GLW	IG c505_h	23	3	4	1	121	13.3	8.94
A0A5C2GXM	IG c450_l	20	2	3	1	110	11.5	7.99
A0A5C2GN2	IG c263_h	25	3	3	2	125	14.1	8.41
O14792	Heparan s	11	4	5	4	307	35.8	8.84
A0A5C2GHF	IG c486_l	35	3	3	2	110	12	8.48
A0A5C2GQ5	IG c1526_	17	2	4	1	127	14.3	8.41
A0A5C2FYD	IGL c277_	25	2	3	1	106	11.5	7.12
V9HWJ1	Glutathio	8	4	4	4	474	52.4	5.92
A0A5C2GAM	IGL c482_	25	2	3	1	107	11.4	7.12
A0A5C2G9H	IGH + IGL	22	2	3	1	124	13.6	7.96
Q05DK5	ADD2 prot	3	2	3	2	709	78.8	5.63
A0A5C2GPX	IG c754_h	18	2	3	1	123	13.3	7.96
A0A140VK9	RAN bindi	13	3	3	3	201	23.3	5.29
B7Z6Z4	Myosin li	13	3	3	2	238	26.7	5.08
A0A3G1LBH	Proto-onc	12	2	3	2	188	21.5	8.12
A0A5C2GXC	IG c1247_	20	3	4	1	128	13.8	7.93
Q5T7C4	High mobi	27	3	3	3	158	18.3	9.7
B4DR61	Protein t	9	4	4	4	482	52.9	8.24
A0A5C2G6H	IGH c192_	33	3	3	1	113	12.4	8.02
I3L0A0	HCG204478	10	4	4	2	370	42.2	6.71
G3V357	Ribonucle	41	2	3	2	116	13	7.91
A8K6T3	cDNA FLJ7	3	3	3	3	896	99.9	6.15
A0A5C2GTL	IG c1056_	32	3	3	0	109	11.8	8.5
A0A1U9X79	APOM OS=H	21	3	4	3	116	13	7.75
B7Z4B2	Aminopept	6	5	5	5	825	92.8	5.4
A0A5C2GWN	IG c1232_	14	2	3	0	113	12.4	6.57
Q06210	Glutamine	6	4	4	4	699	78.8	7.11
B3KQU9	cDNA PSEC	4	2	4	1	496	53.6	7.5
A0A5C2GFM	IG c239_h	25	3	4	3	126	13.7	9.47
A0A384NPR	Epididymi	18	4	4	4	170	19.3	9.41
A0A087WUQ	Glutathio	24	3	3	3	202	21.9	6.55
F5GY37	Prohibiti	13	3	3	3	267	29.7	9.88
A0A5C2GFW	IGL c289_	21	2	4	1	107	11.5	4.65
Q86SR1	Polypepti	7	3	3	3	603	68.9	8.59
P46926	Glucosami	12	3	3	2	289	32.6	6.92

Q15043	Zinc tran	7	2	3	2	492	54.2	5.33
A0A5C2GBH	IGH + IGL	19	2	3	2	135	14.6	8
P62330	ADP-ribos	10	2	3	1	175	20.1	8.95
Q15370	Elongin-B	20	3	4	3	118	13.1	4.88
A0A5C2GGA	IG c1149_	16	2	3	1	119	13	8
Q549N0	Cofilin 2	23	3	3	1	166	18.7	7.88
A0A5C2GU7	IG c857_l	29	3	3	1	108	11.6	7.99
A0A5C2GLD	IG c345_h	16	2	4	1	122	13.3	9.17
A0A5C2GJC	IG c1142_	43	3	4	2	107	11.6	8.44
P08311	Cathepsin	9	2	3	2	255	28.8	11.19
A0A5C2G3M	IGL c3762	32	3	3	1	107	11.6	8.78
Q549J4	Erythroid	23	2	3	2	102	11.8	5
A0A5C2GY8	IG c608_l	27	2	3	1	108	11.8	8.88
B4DMH3	Coronin C	13	5	6	5	437	49.3	7.02
P63316	Troponin	7	1	3	1	161	18.4	4.18
J3KR73	Ras-relat	19	2	3	2	124	14.3	4.78
Q6IAT9	Proteasom	16	3	3	3	239	25.3	4.92
A0A5C2GLR	IG c495_h	24	2	2	1	126	13.8	6.52
P55056	Apolipopr	14	3	4	1	127	14.5	8.92
P48163	NADP-depe	8	3	3	3	572	64.1	6.13
A0A5C2GN4	IG c54_he	18	2	3	1	118	13.3	8.51
A0A5C2G1F	IGL c253_	31	4	4	3	114	12	8.47
B1AH49	3-mercapt	10	2	3	2	224	25	7.65
A0A5C2FYV	IGL c2198	15	2	3	1	110	11.4	7.96
D6RD58	Leukocyte	51	3	4	3	79	8.9	9.58
Q7RU04	Aminopept	5	3	3	3	658	73.5	6.11
A0A5C2G52	IGL c3526	15	2	3	1	110	11.4	7.11
Q9H3K6	BolA-like	41	2	2	2	86	10.1	6.52
A0A5C2GI8	IG c346_h	29	3	3	3	124	14	9.2
C9JRR0	Augurin (	13	2	4	2	142	17.1	9.79
A0A5C2GQ6	IG c864_h	21	2	2	1	126	13.5	7.96
A2VCL5	Flotillin	16	3	4	3	237	26.3	5.88
C9JD32	60S ribos	25	2	3	2	91	9.7	11.49
A0A090N8G	Glycyl-tR	4	3	4	3	685	77.5	6.24
P62318	Small nuc	15	2	3	2	126	13.9	10.32
A0A5C2G8F	IGL c3915	15	2	3	1	110	11.7	7.11
A0A4P8J54	IgG4_IGHV	15	2	3	1	134	14.7	7.75
A0A5C2GWN	IG c987_h	14	2	3	1	125	13.7	7.87
A0A5C2GDU	IG c1122_	20	2	3	1	125	13.7	8.7
A0A5C2G6L	IGH c232_	20	2	3	1	125	13.9	8.41
A0A5C2G0F	IGL c2534	34	2	2	0	108	11.7	9.25
P36959	GMP reduc	11	3	3	3	345	37.4	7.06
A0A024R7C	Brain spe	24	4	4	4	176	19	9.13
A0A5C2G24	IGL c2025	36	3	3	1	107	11.5	8.97
H0YL69	Proteasom	15	3	3	3	236	26.4	7.71
A0A5C2H0A	IG c366_l	15	2	3	1	110	11.6	7.87
P46977	Dolichyl-	3	2	3	2	705	80.5	8.07
A0A5C2FXA	IGL c1611	30	2	3	1	107	11.8	7.99
Q9NP72	Ras-relat	20	3	3	3	206	23	5.24
Q9BZM5	UL16-bind	9	2	3	2	246	27.4	7.3
W6A4U0	Tetraspan	8	2	3	2	238	25.6	7.62

O14992	HS24/P52	7	3	3	3	474	52.3	8.21
Q53HB3	Proteasom	11	3	3	3	440	49.2	6.21
A0A5C2G0E	IGL c2127	15	2	3	1	110	11.5	8.29
A0A5C2GF2	IG c450_h	24	2	3	1	127	13.9	5.15
A0A5C2FWZ	IGL c65_l	31	2	2	1	109	11.7	7.96
P55107	Growth/di	9	4	5	4	478	53.1	9.51
F5H5V4	26S prote	24	3	3	3	153	16.9	6.11
O15230	Laminin s	1	4	4	4	3695	399.5	7.02
A0A1C9J6R	B cell re	23	2	3	1	132	14.5	8.84
Q96AY3	Peptidyl-	5	3	3	3	582	64.2	5.62
A0A5C2G5G	IGL c2857	15	2	3	1	110	11.6	5.29
P80188	Neutrophi	12	2	3	2	198	22.6	8.91
P25788	Proteasom	12	3	3	3	255	28.4	5.33
A0A5C2GK8	IG c504_l	28	2	3	0	108	11.5	4.78
Q15166	Serum par	5	2	3	2	354	39.6	5.41
B4E1L0	Adenylosu	5	2	3	2	435	47.9	5.91
G3V4C1	Heterogen	7	3	3	3	292	32.2	5.08
B2R7D2	cDNA, FLJ	9	3	3	3	487	55.1	7.97
A0A5C2G11	IGL c2849	7	1	3	1	110	11.3	7.97
A0A5C2G4S	IGL c1283	36	3	4	0	107	11.6	8.91
A0A5C2GR2	IG c339_h	26	3	7	1	124	13.4	6.49
B8ZZL8	10 kDa he	18	2	3	2	101	10.7	9.58
P05387	60S acidi	14	1	2	1	115	11.7	4.54
P21781	Fibroblas	11	2	3	2	194	22.5	9.14
A2A2V4	Vascular	15	3	3	3	163	19	7.49
A0A5C2GMA	IG c1071_	35	3	3	1	107	11.9	8.92
A0A5C2FTS	IGL c381_	15	2	3	1	109	11.5	7.12
C9J3L8	Translocc	10	2	3	2	265	29.6	4.3
D3DT44	Glutamate	13	3	3	3	254	28.6	6.02
A0A494C0G	Phosphoac	6	3	3	3	501	55.4	6.42
A8KAJ7	Polypepti	6	3	3	3	559	64.2	7.74
A0A5C2H1E	IG c1930_	25	2	3	1	108	11.8	9.35
A0A2R8Y81	40S ribos	15	2	3	2	150	16.1	10.05
Q9P2E5	Chondroit	5	3	3	3	772	85.9	7.83
P04921	Glycophor	27	2	2	2	128	13.8	4.84
Q59FD4	Hexokinas	4	3	3	3	949	105.7	6.84
A8K482	Aspartate	7	3	3	3	430	47.5	9.23
A0A5C2GPI	IG c480_h	15	2	3	1	124	13.8	5.45
O43488	Aflatoxin	9	3	3	3	359	39.6	7.17
A0A5C2G67	IGL c4130	37	3	3	1	107	11.6	9.2
M0R210	40S ribos	20	3	4	3	129	14.4	10.23
A0A0S2Z4I	Phosphofr	4	3	3	2	749	81.7	7.62
Q53FU0	Carbohydr	7	3	4	3	414	48.4	9.38
A2NB44	Cold aggl	22	2	3	1	114	12.8	7.11
B4DKZ9	cDNA FLJ5	6	3	3	3	602	70.3	8.56
Q01105	Protein S	7	2	3	2	290	33.5	4.32
V9HWB5	Epididymi	9	3	3	3	289	32.6	5.86
A0A5C2GBK	IGL c23_l	35	3	3	1	107	11.4	7.97
A0A5C2GH7	IG c941_h	12	2	3	1	132	14.8	6.6
A0A5C2GTI	IG c925_l	29	2	2	1	113	12.6	8.41
J3KR23	IST1 homc	10	2	2	2	289	31.2	4.75

A0A5C2G6N	IGL c18_l	28	2	3	1	109	11.6	5.01
A0A5C2GIJ	IG c1242_	25	2	2	1	108	11.5	5.94
O14657	Torsin-1B	6	2	3	2	336	38	8.54
A0A5C2G3J	IGL c3494	27	2	2	2	107	11.7	8.29
A0A024R7W	Inositol	13	3	4	3	359	38.7	6.86
F6U1T9	Calcineur	14	2	3	2	160	18.2	4.92
P45378	Troponin	6	1	2	1	269	31.8	5.9
A4D1M6	HCG19809	6	1	2	1	225	24.9	4.82
A0A384MEE	Epididymi	11	3	3	3	406	46.9	5.26
B4DN59	cDNA FLJ5	5	2	3	2	329	36	5.9
V9HWC4	Epididymi	26	3	3	3	125	13.8	6.07
P05198	Eukaryoti	10	3	3	3	315	36.1	5.08
Q96G03	Phosphogl	5	3	3	3	612	68.2	6.73
A0A494C0L	Thymidine	14	3	3	3	289	29.7	6.92
A0A5C2GUE	IG c97_he	30	3	3	2	126	14	8.47
P55290	Cadherin-	8	4	4	4	713	78.2	4.98
V9HWB7	Epididymi	4	4	4	4	889	98.3	6.68
Q9NQW7	Xaa-Pro a	5	3	3	3	623	69.9	5.67
P47985	Cytochrom	13	2	2	2	274	29.6	8.32
Q00688	Peptidyl-	8	2	3	2	224	25.2	9.28
P24592	Insulin-l	10	2	2	2	240	25.3	7.81
P62906	60S ribos	22	4	5	4	217	24.8	9.94
A0A068LNC	Ig heavy	15	2	3	1	120	13.4	8.43
A0A5C2GLN	IG c455_h	21	3	7	1	121	13.5	9.47
Q16222	UDP-N-ace	5	2	2	2	522	58.7	6.33
P00966	Argininos	8	3	3	3	412	46.5	8.02
Q6PKX1	Myocilin	12	3	3	3	260	29.5	5.11
P14550	Aldo-ketc	14	5	5	5	325	36.6	6.79
Q96DG6	Carboxyme	7	2	3	2	245	28	7.18
A0A2U8J94	Ig heavy	17	2	3	1	103	11.4	6.57
A0A5C2GNF	IG c828_h	15	2	4	1	125	13.8	7.12
Q5JQ44	Uncharact	18	3	3	3	181	20.3	4.81
A0A5C2GRX	IG c235_l	22	3	3	1	112	11.9	6.77
A0A024R7S	Clathrin	13	3	3	3	211	23.2	4.69
A0A5C2FZ5	IGL c2202	35	2	2	1	108	11.8	9.25
A0A5C2GT4	IG c517_l	26	3	3	1	107	11.5	9.57
A0A5C2FYE	IGL c1156	26	2	2	1	108	11.8	7.28
B4DWE8	cDNA FLJ5	3	3	3	3	751	84	5.24
A0A087WUR	Inactive	7	3	3	3	416	46.5	9.04
Q04941	Proteolip	18	2	3	2	152	16.7	7.24
B4DUF7	cDNA FLJ5	8	3	3	3	435	48.9	7.42
Q9BXJ0	Complemen	10	2	3	2	243	25.3	6.54
A0A5C2GJM	IG c981_l	18	2	3	1	112	12.3	5.05
K7EL40	Septin-9	17	3	3	3	209	24	9.35
Q16706	Alpha-man	3	4	4	4	1144	131.1	7.58
A0A140VK2	Testicula	8	3	3	3	440	49.5	6.11
O00231	26S prote	10	3	3	3	422	47.4	6.48
P55327	Tumor prc	7	1	2	1	224	24.3	4.83
A0A1W6IYI	N90-VRC38	24	2	2	1	124	13.5	6.77
B3KRV7	Lipoprote	5	3	3	3	461	51.7	8.02
P13010	X-ray rep	3	2	3	2	732	82.7	5.81

A0N7I9	F5-20 (Fr	10	1	3	1	123	13.4	9.1
A0A5C2G5Q	IGL c392C	25	2	2	1	108	11.5	5.35
A0A024R71	Nicotinam	7	2	2	2	491	55.5	7.15
A0A5C2FXS	IGL c1141	52	3	3	1	107	11.4	7.96
A0A087WYT	Prostagla	12	2	3	2	164	19.1	4.55
A0A5C2GHM	IGH + IGL	18	2	3	0	125	13.7	8.43
A0A5C2H1I	IG c1778_	27	2	3	1	107	11.8	9.13
A0A346FYQ	Pro-nerve	8	3	3	3	296	32.5	9.88
A0A384NQ3	Epididymi	12	3	3	3	247	28.5	6.02
A0A494C0E	UV excisi	17	3	3	1	282	30.5	4.84
P48426	Phosphati	8	3	3	3	406	46.2	6.99
P16401	Histone H	16	4	4	1	226	22.6	10.92
E7DVW4	Epididymi	25	2	2	2	132	14.7	7.14
A0A5C2H05	IG c1450_	14	2	3	1	108	11.8	8.5
H0YGX7	Rho GDP-d	15	3	3	3	195	22.4	5.2
Q14769	Alpha-N-a	6	3	3	3	639	72	6.37
A0A5C2GED	IG c373_h	16	2	3	1	122	13.5	8.44
A0A5C2GSJ	IG c581_h	16	2	4	1	122	13.6	6.04
Q9HBA0	Transient	3	3	3	3	871	98.2	7.77
Q8NBJ4	Golgi mem	4	2	3	2	401	45.3	4.97
A0A5C2GGE	IG c1016_	13	2	3	2	137	15	8.44
P49458	Signal re	31	3	3	3	86	10.1	7.97
Q9H223	EH domain	6	3	3	1	541	61.1	6.76
B7ZLW3	Metalloen	3	3	3	1	1036	117.3	6.07
A0A5C2GJY	IG c758_l	23	2	2	1	108	11.8	7.97
B2RDN9	cDNA, FLJ	4	3	3	3	609	69.7	6.7
P62857	40S ribos	17	1	2	1	69	7.8	10.7
A0A1B0GTE	Renin rec	5	2	3	2	294	33	6.07
Q0VDC6	Peptidylp	10	1	2	1	145	15.7	9.17
E9KL48	Epididymi	5	3	3	3	558	61.4	7.8
A0A1X7SBS	Heterogen	4	4	4	4	744	81.7	5.83
P35237	Serpin B6	13	3	3	3	376	42.6	5.27
P30048	Thioredox	5	1	2	1	256	27.7	7.78
A8K9K4	cDNA FLJ7	6	2	2	2	562	62.2	7.11
A0A5C2G61	IGH c406_	13	2	3	1	123	13.4	7.12
A0A5C2G6H	IGL c2013	32	2	2	2	107	11.6	7.96
Q9UNN8	Endotheli	9	2	4	2	238	26.7	7.18
A0A024R9J	Nephrobla	8	2	2	2	357	39.1	7.72
P61160	Actin-rel	6	2	2	2	394	44.7	6.74
A0A5C2GNJ	IG c224_h	19	2	2	1	125	13.7	8.44
P35270	Sepiapter	11	2	2	2	261	28	8.05
J3KQ18	D-dopachr	20	3	3	3	132	14.2	7.3
A0A5C2GB1	IGH + IGL	13	2	3	1	128	14	9.29
Q14376	UDP-gluco	7	3	3	3	348	38.3	6.73
B3KM80	Nucleolin	7	4	4	4	536	58.5	4.67
A0A5C2GFX	IG c914_h	24	2	2	1	125	13.8	8.43
P27816	Microtubu	3	3	3	3	1152	120.9	5.43
P59665	Neutrophi	19	2	3	2	94	10.2	6.99
A0A5C2GVX	IG c1661_	12	2	3	1	122	13.2	9.55
A0A5C2FYR	IGL c785_	21	3	3	2	107	11.2	7.99
K7ESA3	Synaptic	24	2	2	2	125	13.6	9.38

A0A5C2GAD	IGH + IGL	24	2	2	2	125	13.3	9.2
A0A5C2GTH	IG c855_l	28	2	2	1	108	11.8	7.97
Q8TDX6	Chondroit	5	3	3	3	532	61.3	8.41
A4D275	Actin-rel	8	3	3	1	372	40.9	8.35
A0A5C2GEK	IGH c461_	15	2	6	1	120	13.2	9.29
A0A5C2GL8	IG c879_l	27	2	2	0	109	11.9	8.91
O15031	Plexin-B2	2	2	2	2	1838	205	6.24
A0A5C2GSR	IG c42_li	25	2	2	0	108	11.7	8.5
Q53G02	Dolichyl-	11	1	2	1	113	12.4	7.87
J3QKN1	FXYD doma	17	1	2	1	90	10.1	8.19
A0A1W2PNV	Uncharact	4	3	3	1	684	75.8	8.59
A0A024R9D	Ribosomal	32	3	3	3	115	12.8	9.63
A0A5C2GLY	IG c366_h	11	1	2	1	120	13.4	7.12
Q6FID4	SARA1 prc	6	1	2	1	198	22.3	7.03
A0A5C2GA8	IGH + IGL	17	2	2	1	121	13.6	8.81
A0A5C2GFD	IG c222_h	21	2	2	1	121	13	7.12
O60568	Multifunc	4	3	3	3	738	84.7	6.05
I1VE16	SEC22 ves	53	2	3	2	36	4.1	9.04
Q9H4B7	Tubulin b	5	2	2	1	451	50.3	5.17
P82987	ADAMTS-li	1	2	2	2	1691	188.6	7.83
Q658P3	Metallore	4	2	3	2	488	54.6	8.6
A0A5C2GX8	IG c1039_	23	2	2	2	113	12.6	8.85
C9JQL4	Dystrogly	14	1	2	1	117	12.6	5.66
A8K3Q3	cDNA FLJ7	7	3	3	3	425	48.1	8.82
Q00341	Vigilin C	2	3	3	3	1268	141.4	6.87
A0A0S2Z3D	Carbonic	13	3	3	3	459	49.7	4.72
A0A5C2GIQ	IG c885_l	12	1	2	1	110	11.6	7.99
A0A5C2GYJ	IG c800_l	23	2	2	1	108	11.7	5.06
A1MMZ0	Uncharact	4	2	2	2	563	60.7	4.68
D3DTE6	SH3 domai	19	2	2	2	113	12.7	5.25
B4DNR3	cDNA FLJ5	12	2	2	2	185	19.8	6.4
Q53F10	UV excisi	6	3	3	1	409	43.1	4.88
F4ZW63	NF45 OS=H	9	2	2	2	390	43	5.34
A0A5C2G8Z	IGL c4177	25	2	2	2	107	11.4	8.47
P39019	40S ribos	21	3	3	3	145	16.1	10.32
A0A5C2GFF	IG c500_h	22	2	2	2	123	12.9	7.08
P04271	Protein S	24	1	1	1	92	10.7	4.59
A0A5C2GBZ	IGH + IGL	23	2	2	1	108	11.7	6.55
Q5VVC8	60S ribos	13	2	2	2	167	19	9.8
O95782	AP-2 comp	3	3	3	2	977	107.5	7.03
B4E0C7	cDNA FLJ5	5	2	2	2	496	53.8	6.38
Q75MH1	40S ribos	21	2	2	2	115	13	10.98
B4DXW6	cDNA FLJ5	7	3	3	3	454	52.3	6.48
A0A5C2GI1	IGH + IGL	23	2	2	1	123	13.3	8.47
H9NKY4	IFITM3 OS	12	1	2	1	133	14.6	6.9
J3KS22	L-xylulos	13	3	3	3	223	23.8	8.21
A0A5C2GAA	IGH + IGL	15	2	6	1	123	13.7	8
B3KWI4	cDNA FLJ4	5	2	2	2	581	64.4	6.71
A0A1B0GTG	Adenylosu	11	3	3	3	377	42.5	8.09
A0A5C2G6M	IGH c307_	18	2	2	1	123	13.5	8.78
A0A5C2G7T	IGL c2483	29	2	2	1	113	12.6	6.57

A0A087WUL	26S prote	5	2	3	2	377	42.7	5.91
Q9Y663	Heparan s	5	2	2	2	406	44.9	9.5
H0YBX6	Ubiquitin	19	3	3	1	154	16.9	6.29
A0A5C2GP1	IG c38_he	24	2	2	1	124	13.6	8.16
A0A2U3TZV	Phosphoin	0	1	3	1	1685	188.6	7.84
A0A5C2G7M	IGL c3685	20	2	2	2	107	11.6	9.51
A8K4W0	40S ribos	12	4	4	4	264	29.9	9.73
F8VZG8	Ubiquitin	6	1	2	1	139	16.1	5.21
A0A5C2G1Y	IGL c353_	27	2	2	2	108	11.6	8.51
V9HW41	Epididymi	17	2	3	2	152	17.1	6.57
A0A5C2G8R	IGH c314_	22	3	3	3	127	14	8.47
P22083	Alpha-(1,	6	2	2	2	530	59	10.01
A0A5C2GMH	IG c652_h	21	2	2	1	121	13.4	8.5
B5BUB5	Autoantig	7	2	2	2	408	46.8	7.12
A0A5C2G2V	IGL c3244	12	1	2	1	113	12.4	4.88
Q5T5C7	Seryl-tRN	6	2	2	2	536	61.3	7.06
B2MUD5	Neutrophi	9	2	2	2	192	20.6	8.9
Q5JR94	40S ribos	12	2	2	2	208	24.2	10.32
B4DLB8	cDNA FLJ5	9	2	2	2	355	39.9	8.5
A8K3W7	cDNA FLJ7	5	2	2	2	429	49.9	6.6
Q96HE7	ERO1-like	6	2	2	2	468	54.4	5.68
Q14257	Reticuloc	7	2	2	2	317	36.9	4.4
Q96CG8	Collagen	7	2	2	2	243	26.2	7.99
A0A087X2I	26S prote	6	2	2	2	403	45.8	7.78
C9JA28	Transloco	8	1	2	1	174	20.1	9.44
A0A140VKA	Testis se	7	2	3	2	244	25.8	7.37
A0A5C2GNK	IG c381_l	25	2	2	1	107	11.5	8.5
A0A5C2GSG	IG c331_l	28	2	2	1	108	11.4	5.81
A0A087WWY	Apolipopr	20	2	2	2	571	62.5	5.73
P54707	Potassium	2	3	4	1	1039	115.4	6.55
A0A5C2GHE	IG c677_h	8	1	2	1	133	14.5	6.06
Q15008	26S prote	6	2	2	2	389	45.5	5.62
Q59HA3	IQ motif	1	2	2	1	1155	132.6	5.9
A0A024R99	Copine II	8	3	3	2	537	60.1	5.85
A0A140VJF	Metalloth	33	2	2	2	61	6.1	7.96
Q7L9L4	MOB kinas	5	1	2	1	216	25.1	6.73
A0A5C2G6E	IGH c217_	9	1	2	1	125	13.7	7.28
A0A4V1EJ1	IgG1_IGHV	10	2	3	1	160	17	8.47
Q15323	Keratin,	4	2	3	1	416	47.2	4.88
A0A5C2G8C	IGH c184_	17	2	2	0	120	13.1	7.14
H3BQZ9	Adenine p	15	1	1	1	153	16.6	5.59
A0A2R8Y5M	B-cell re	8	2	2	2	211	24.1	8.06
A0A5C2GHR	IGH + IGL	15	2	2	1	126	13.7	9.72
A0A5C2GMQ	IG c581_h	23	2	2	1	120	13	7.97
Q96C23	Aldose 1-	8	2	2	2	342	37.7	6.65
A0A5C2FUC	IGL c441_	32	3	3	1	107	11.7	7.96
A8K7T4	cDNA FLJ7	10	3	3	3	356	40.2	6.95
A0A5C2GX8	IG c1197_	15	2	2	1	126	14	6.52
Q9Y639	Neuroplas	5	2	2	2	398	44.4	7.99
P22413	Ectonucle	3	3	3	3	925	104.9	7.14
M0R0H5	Urokinase	24	2	2	2	152	17	5.59

A0A286YF7	D-3-phosp	9	2	2	2	276	29.7	8.02
A0A5C2GU6	IG c1045_	25	2	2	1	107	11.5	8.81
D3DP46	Signal pe	12	2	2	2	180	20.3	8.97
Q8TDQ7	Glucosami	9	2	2	1	276	31.1	6.95
P52943	Cysteine-	13	2	2	2	208	22.5	8.72
A0A0S2Z4E	Serine/th	5	3	3	3	511	57.6	6.3
A0A087WUD	Oligosacc	14	1	2	1	83	9.4	7.43
A0A5C2GJS	IG c1127_	10	1	2	1	107	11.5	8.88
A0A5C2G6C	IGH c117_	25	2	2	1	120	13.2	9.11
B4DP22	Carboxype	5	2	2	2	402	45.1	5.96
Q9UK70	Rh-null r	7	2	3	2	409	44.2	6.68
G3V4U0	Fibulin-5	5	2	2	2	453	50.8	4.77
A0A5C2G6F	IGH c590_	14	2	6	1	125	13.8	8.19
Q8TEP9	FLJ00144	8	2	2	2	255	28.4	6.18
Q9BS40	Latexin C	4	1	2	1	222	25.7	5.78
A0A5C2GT3	IG c701_h	22	2	2	1	119	13.2	8.5
A0A5C2G2E	IGL c3084	18	2	2	2	106	11.4	5.06
Q13438	Protein C	3	3	3	3	667	75.5	4.87
Q969H8	Myeloid-d	12	2	2	2	173	18.8	6.68
F8VV59	Nucleosom	9	2	2	2	327	38	4.68
A0A024RDY	Lysosomal	4	2	2	2	417	44.9	8.75
P25786	Proteasom	8	2	2	2	263	29.5	6.61
B4DN72	cDNA FLJ5	3	2	2	1	486	53.5	5.66
A0A5C2G49	IGL c3380	18	2	2	2	110	11.5	8.46
Q99727	Metallopr	9	2	2	2	224	25.5	7.8
P62851	40S ribos	7	1	2	1	125	13.7	10.11
H0YBL1	Inositol-	8	2	2	2	265	28.6	6.21
P46063	ATP-depen	3	2	2	2	649	73.4	7.88
A0A5C2GNU	IG c227_h	16	2	2	1	117	12.7	7.96
A0A3Q8BT4	Rh blood	2	1	2	1	417	45.2	8.5
A0A5C2FXE	IGL c1284	15	2	2	2	110	11.8	7.12
B7Z507	cDNA FLJ5	3	2	2	2	648	71.5	5.86
A0A024RDL	Argininos	7	2	2	2	464	51.6	6.48
P25398	40S ribos	14	2	2	2	132	14.5	7.21
A0A5C2GHI	IGH + IGL	15	2	2	1	123	13.4	9.2
A0A5C2G02	IGL c2608	21	2	2	1	112	11.7	7.12
Q8N130	Sodium-de	1	1	2	1	599	63.5	8.27
Q6XQN6	Nicotinat	6	2	2	2	538	57.5	5.68
A4D2J0	SNARE pro	8	2	2	2	198	22.4	6.92
Q13200	26S prote	3	2	2	2	908	100.1	5.2
A0A5C2FWZ	IGL c1194	29	2	2	1	107	11.4	7.97
K7EJV9	60S ribos	8	1	2	1	170	19.4	10.48
Q53R32	Uncharact	14	2	2	2	177	19.6	5.94
E7ETR0	RuvB-like	8	2	2	2	315	34.8	5.76
Q6FG43	Flotillin	7	2	2	2	379	41.7	5.29
A0A5F9UJX	45 kDa ca	5	2	2	2	341	38.7	5.11
A0A5C2GHD	IG c493_h	15	2	2	2	120	13.2	8.44
A0A5C2GBS	IGH + IGL	15	2	2	1	111	12	6.77
Q8WUJ3	Cell migr	2	2	2	2	1361	152.9	7.85
Q1HBJ4	Mitogen-a	6	2	2	2	360	41.4	6.98
G3V3E8	NPC intra	15	2	2	2	174	19.2	8.44

B2R7T8	F-actin-c	7	2	2	2	272	30.6	6
B0YIW5	Coatomer	10	4	4	4	511	57.2	6.21
Q9NZM1	Myoferlin	1	2	2	2	2061	234.6	6.18
P49755	Transmemb	8	2	2	2	219	25	7.44
A0A2R8Y84	40S ribos	11	1	2	1	131	15.2	10.9
Q5QPM7	Proteasom	5	1	2	1	263	28.9	6.44
A0A0F7T0G	IGHV2-70	23	2	2	2	91	10.3	6.57
F8W1U5	DUF3456 d	20	1	2	1	82	9.1	7.25
H3BT58	Coactosin	36	3	3	3	73	8.2	8.41
P80303	Nucleobin	6	2	2	2	420	50.2	5.12
A0A5C2GYU	IG c818_l	27	2	3	1	107	11.7	8.84
Q96M27	Protein F	7	2	2	2	445	46.7	5.83
H7C0V9	Amyloid-b	5	3	3	3	485	55.1	4.82
K7ES25	Xaa-Pro d	3	2	2	2	512	56.5	6.25
O00468	Agrin OS=	1	2	2	2	2068	217.2	6.39
A0A5C2G6C	IGH c227_	24	2	2	1	121	13.7	7.37
A0A5C2GVI	IG c1327_	19	2	2	1	110	11.5	8.29
Q9BUT1	3-hydroxy	5	1	2	1	245	26.7	7.65
A0A5C2FVL	IGL c216_	23	2	2	1	108	11.7	8.5
H7C579	Omega-ami	7	2	2	2	265	28.7	9.35
K7EJD9	Tartrate-	10	1	2	1	124	13.7	5.15
A0A384P5S	Epididymi	2	3	3	3	2452	282.1	5.34
B2R9T9	cDNA, FLJ	4	1	2	1	243	26.2	10.67
Q53GL5	Isocitrat	7	2	2	2	452	50.9	8.48
Q00577	Transcrip	6	2	2	2	322	34.9	6.44
A2J1N9	Rheumatoi	25	2	2	1	96	10.5	8.91
A0A024R5H	Barrier t	36	2	2	2	89	10.1	6.09
A0A5C2G7Y	IGH c508_	18	2	2	1	120	13.4	6.52
B2RD40	cDNA, FLJ	3	2	2	1	532	59.7	5.99
A0A5C2GGT	IG c938_h	18	2	2	1	124	13.8	5.45
A0A024RA8	Septin 7,	5	2	2	2	384	44.8	8.22
A0A5C2GS5	IG c325_l	27	2	2	2	111	11.6	6.52
A0A5C2FWW	IGL c1439	25	2	2	1	108	11.9	7.99
A0A5C2GHK	IG c672_l	17	1	2	1	107	11.5	8.88
A0A5C2GR6	IG c1832_	16	2	2	1	121	13.2	5.39
Q14914	Prostagla	8	2	2	2	329	35.8	8.29
H9KV45	Ubiquitin	8	1	2	1	141	15.9	6.29
Q96IR1	RPS4X pro	7	2	2	2	243	27.2	9.94
F8WB72	60S ribos	16	1	2	1	57	6.8	9.76
A0A5C2GJ2	IG c158_h	19	2	2	1	120	13.3	6.61
Q9NTK5	Obg-like	5	2	2	2	396	44.7	7.81
Q70UQ0	Inhibitor	9	2	2	2	350	39.3	9.17
A0A5C2GVF	IG c1297_	17	1	1	1	107	11.4	8.84
A0A5C2FTA	IGL c49_l	25	2	2	1	108	11.5	7.96
P62745	Rho-relat	27	3	4	2	196	22.1	5.24
Q5VUU6	Epididymi	5	2	2	2	407	45.8	9.76
Q00013	55 kDa er	4	2	2	2	466	52.3	7.37
Q53GF1	Matrix me	5	2	2	1	267	29.6	7.55
Q9HAB8	Phosphopa	5	2	2	2	311	34	6.71
A0A5C2GQE	IG c145_h	29	3	3	1	123	13.5	7.97
A8K6K4	cDNA FLJ7	2	1	2	1	570	65.4	8.22

P12724	Eosinophi	18	2	2	2	160	18.4	10.02
A0A5C2GCC	IGH + IGL	21	2	2	1	107	11.7	8.47
A0A5C2H3A	IG c1476_	7	1	2	1	109	11.5	7.33
P24539	ATP synth	6	2	2	2	256	28.9	9.36
P28289	Tropomodu	7	2	2	2	359	40.5	5.1
A0A5C2FUD	IGL c469_	10	1	2	1	107	11.4	8.47
A0A5C2GK9	IG c423_l	22	2	2	1	113	12.7	5.01
P21815	Bone sial	5	2	2	2	317	35.1	4.18
A0A5C2GWH	IG c1273_	15	2	2	1	108	11.3	7.85
D6R9C5	Osteopont	8	2	2	2	241	27.1	4.53
D6RFN0	COP9 sign	5	2	2	2	438	49.7	5.81
B0QZ18	Copine-1	3	2	2	2	542	59.7	6.04
O15173	Membrane-	11	2	2	1	223	23.8	4.88
E9PP21	Cysteine	20	2	2	2	160	16.9	8.91
Q03252	Lamin-B2	5	3	3	3	620	69.9	5.59
A0A5C2G7R	IGH c557_	9	1	2	1	129	14.1	7.12
A0A5C2GL7	IG c66_he	15	2	2	2	124	13.9	8.78
E7EQ64	Trypsin-1	11	2	5	2	261	28.1	7.25
O60565	Gremlin-1	16	2	2	2	184	20.7	9.39
Q05DB4	HEBP2 pro	10	2	2	2	214	24	5.38
Q92820	Gamma-glu	4	2	2	2	318	35.9	7.11
A0A2U8J8Y	Ig heavy	22	2	2	1	102	11.3	7.96
P48740	Mannan-bi	3	2	2	1	699	79.2	5.49
Q9Y230	RuvB-like	5	2	2	2	463	51.1	5.64
B3KX16	cDNA FLJ4	6	2	2	2	372	43.5	5.86
Q9BRK3	Matrix re	4	2	2	2	442	49.1	7.23
A0A0S2Z45	Serpin pe	6	2	2	2	410	46.4	4.91
Q8TAL6	Fin bud i	14	3	3	3	211	24.3	5.49
A0A5C2GFQ	IG c672_h	24	2	2	1	115	12.5	6.65
D6RJI3	Fibrillin	1	2	2	1	1473	157.6	4.93
H0YNG3	Signal pe	12	2	2	2	163	18.6	9.55
A0A024R4X	Protein k	5	2	2	2	435	50	6.43
A0A5C2GEA	IGH + IGL	19	2	2	1	123	13.4	8.81
Q14204	Cytoplasm	1	3	3	3	4646	532.1	6.4
A0A5C2GA6	IGH + IGL	21	3	3	1	125	13.8	8.84
Q9Y277	Voltage-d	6	2	2	1	283	30.6	8.66
A0A5C2G5Y	IGH c369_	20	2	2	2	122	13.4	9.36
A0A384MDU	Dynactin	6	2	2	2	401	44.2	5.21
Q8IXL6	Extracell	2	2	2	2	584	66.2	7.74
A0A5C2FVG	IGL c156_	14	2	2	1	109	11.4	8.29
P20160	Azurocidi	8	2	2	2	251	26.9	9.5
A0A5C2GA6	IGH c153_	9	1	2	1	124	13.6	8.46
P17987	T-complex	5	3	3	3	556	60.3	6.11
Q92982	Ninjurin-	13	1	1	1	152	16.3	6.28
P35606	Coatomer	4	3	3	3	906	102.4	5.27
A0A5C2FY7	IGL c1842	17	1	1	1	107	11.5	8.5
A0A5C2G81	IGH + IGL	16	1	1	1	117	12.7	7.96
O75888	Tumor nec	10	2	2	2	250	27.4	9.63
Q9UHF5	Interleuk	13	2	3	2	180	20.4	9.23
A0A384P5U	Epididymi	11	3	3	3	249	28.6	4.09
P13473	Lysosome-	4	2	2	2	410	44.9	5.63

P62070	Ras-relat	9	2	2	1	204	23.4	6.01
A0A5C2G2D	IGL c274C	18	2	2	2	107	11.9	8.97
Q8N5L9	Ribosomal	9	3	3	3	293	31.3	10.24
P62277	40S ribos	12	2	2	2	151	17.2	10.54
B2R6C4	Receptor	9	2	2	2	185	21.1	8.1
A0A5C2GTF	IG c1229_	18	2	2	0	122	13.4	8.44
Q99471	Prefoldin	12	1	1	1	154	17.3	6.33
Q9BSV4	SFPQ prot	2	2	2	2	634	68.6	8.82
F5H345	Porphobil	11	3	3	3	330	35.7	6.96
A0A5C2GHT	IG c590_h	21	2	2	1	120	13.1	7.96
A0A5C2GKF	IG c1062_	16	2	2	1	110	11.6	9.01
B3KU66	cDNA FLJ3	5	2	2	2	549	59.9	9.45
B2RAK1	cDNA, FLJ	2	2	2	2	1025	117.3	5.73
A0A0S2Z6F	Histocomp	3	1	2	1	345	38	6.86
A0A5C2G4F	IGL c4062	15	2	2	0	107	11.6	7.12
P50914	60S ribos	6	1	2	1	215	23.4	10.93
O43776	Asparagin	3	2	2	2	548	62.9	6.25
A0A5C2G83	IGH c558_	21	2	2	1	130	14.3	6.92
Q99808	Equilibra	4	2	2	2	456	50.2	8.29
Q14055	Collagen	2	1	1	1	689	65.1	9.17
A0A024R2L	40S ribos	7	2	2	2	295	32.8	4.87
A0A5C2H1W	IG c1918_	23	3	3	2	109	11.4	7.96
Q8NF20	FLJ00382	5	2	2	2	482	52.9	8.66
A0A0A0MS5	cAMP-depe	5	2	2	2	357	41.3	8.56
M0R122	Epithelia	13	1	2	1	63	7.1	4.72
A0A0U1RQK	[Protein	1	1	2	1	1967	211.7	8.4
O15427	Monocarbc	3	2	2	2	465	49.4	7.96
B7Z1R3	cDNA FLJ5	5	1	1	1	294	32.5	7.81
J3QKM9	Vesicle-a	48	1	1	1	29	3.1	7.25
H7C5W9	Sarcoplas	2	2	2	1	933	102.5	5.59
E5RGR0	Acyl-prot	7	1	2	1	197	20.8	7.06
P60827	Complemen	5	1	1	1	252	27.7	9.64
A0A5C2FVW	IGL c1218	32	2	2	1	106	11.4	8.48
P61457	Pterin-4-	16	2	2	2	104	12	6.8
O00159	Unconvent	3	3	3	3	1063	121.6	9.41
Q9GZP0	Platelet-	3	1	2	1	370	42.8	7.97
P54851	Epithelia	4	1	2	1	167	19.2	7.62
P48059	LIM and s	4	1	1	1	325	37.2	8.05
Q7Z675	Calcium-t	2	2	2	1	994	109.2	5.1
A0A5C2GJH	IG c367_l	27	2	2	1	113	12.2	8.88
Q13850	Periphera	9	2	2	2	169	18.5	8.87
Q9Y6Z7	Collectin	5	1	1	1	277	30.7	7.33
Q4G0R1	PIBF1 prc	1	1	2	1	698	83.1	5.53
A0A140VK4	Proteasom	7	2	2	2	264	29.2	5.97
P26583	High mobi	9	2	2	2	209	24	7.81
O43263	RNA editi	1	1	2	1	699	75.9	8.59
Q59HE2	Ornithine	7	1	1	1	281	30.7	4.84
Q6NXN2	Hypotheti	2	1	2	1	316	33.1	11.33
A0A5C2G57	IGL c3576	31	2	2	1	107	11.7	8.47
Q96JQ0	Protocadh	1	2	2	2	3298	346	4.94
O15127	Secretory	6	1	1	1	329	36.6	6.1

P07814	Bifunctic	2	2	2	2	1512	170.5	7.33
K7EPI2	Podocan-l	4	2	2	2	574	63.2	9.57
B4DTA2	cDNA FLJ6	6	2	2	2	271	30.2	8.72
J3QRU1	Tyrosine-	3	2	2	2	548	61.3	6.57
A0A5C2GTT	IG c182_l	16	2	2	1	113	12.1	7.37
A0A5C2G11	IGL c2812	15	2	3	1	109	11.6	7.99
B4DEN3	cDNA FLJ6	8	1	1	1	193	22.5	4.79
L0R599	Alternati	23	1	2	1	65	7.7	9.42
P24347	Stromelys	1	1	2	1	488	54.6	6.87
A8KAM5	cDNA FLJ7	3	1	1	1	313	35.3	8.85
A0A5C2GJF	IG c1141_	22	2	2	1	123	13.5	7.96
A0A5C2GXS	IG c510_l	15	2	2	1	107	11.7	7.97
H7C5I2	Uncharact	27	1	1	1	55	6.3	8.5
B4DEF0	Calseques	4	1	1	1	353	40.9	4.34
P07305	Histone H	5	1	1	1	194	20.9	10.84
Q00872	Myosin-bi	2	1	1	1	1141	128.2	6.04
E7EX73	Eukaryoti	1	2	2	2	1436	158.5	5.21
Q6EMK4	Vasorin C	4	2	3	2	673	71.7	7.39
A0A5C2GCK	IGL c323_	15	2	3	1	109	11.4	7.97
P30049	ATP synth	8	1	1	1	168	17.5	5.49
A0A5C2G68	IGH c506_	15	1	1	1	126	13.7	7.81
B3KQB4	PRA1 fami	16	2	2	2	188	21.5	9.77
A0A3B3IUC	Alpha-gal	3	2	2	2	470	53.2	5.86
Q99542	Matrix me	3	1	1	1	508	57.3	7.59
Q01459	Di-N-acet	4	1	1	1	385	43.7	6.64
Q53S24	Prothymos	13	1	1	1	110	12.1	3.79
A0A5C2G84	IGL c3795	22	1	1	1	111	12.2	7.99
Q9UN70	Protocadh	2	1	1	1	934	101	5.21
A0A5C2GE9	IGH c331_	14	2	2	1	125	14	5
G9J6Q6	GSTT2 OS=	5	1	1	1	244	27.5	6.4
A0A5C2GEH	IG c1262_	23	2	6	1	121	13.2	8.88
Q5VVQ6	Ubiquitin	5	1	1	1	348	38.3	6.11
B3KMV5	cDNA FLJ1	1	1	1	1	1104	122.8	5.85
B4E368	cDNA FLJ6	11	2	2	1	223	24.5	9.7
Q9P1F3	Costars f	16	1	1	1	81	9.1	6.29
A0A087WSZ	Immunoglc	16	1	1	1	117	12.8	7.74
Q9NR45	Sialic ac	4	1	1	1	359	40.3	6.74
B2R773	cDNA, FLJ	6	1	1	1	244	26.4	5.74
Q8TER0	Sushi, ni	1	1	1	1	1413	152.1	6.98
D6W5Y5	Cold indu	4	1	1	1	297	31.9	9.61
A0A5C2GPR	IG c1395_	13	1	1	1	120	13.1	7.88
A0A5C2FYV	IGL c1854	29	2	2	1	113	12.5	9.1
A0A5C2GKA	IG c293_h	24	2	2	2	123	13.6	5.38
C9JNV3	U6 snRNA-	21	1	1	1	77	8.3	5.24
Q5TD07	Ribosyldi	9	1	1	1	193	21.5	6.52
B3KNX7	Non-speci	3	1	1	1	522	58.2	5.49
A0A5C2FW8	IGL c1082	10	1	1	1	107	11.6	7.97
A0A5C2GMH	IG c556_h	11	1	2	1	131	14.3	8.75
D6RAR4	Hepatocyt	2	1	1	1	662	71.4	7.05
P81605	Dermcidin	10	1	1	1	110	11.3	6.54
P34820	Bone morp	4	1	1	1	402	44.7	8.41

V9HW50	All-trans	2	1	1	1	375	39.8	8.19
E9PH05	Protein F	12	1	1	1	141	15.9	9.95
B7Z2N4	cDNA FLJ5	2	1	1	1	981	109.6	6.14
B1AKP2	Tetraspan	6	1	1	1	187	20.6	7.8
Q6FHF5	Prolifera	7	1	2	1	261	28.7	4.69
P29692	Elongatic	4	1	1	1	281	31.1	5.01
A0A5C2H1Q	IG c856_l	12	1	1	1	112	12.2	5.96
I6L8B7	Fatty aci	9	1	1	1	101	11.3	6.07
O95810	Caveolae-	3	1	1	1	425	47.1	5.21
A0A5C2GHE	IG c288_l	11	1	1	1	106	11.6	8.44
A0A5C2GK5	IG c101_h	13	1	1	1	124	13.8	8.78
Q6SES1	Major pri	4	1	1	1	277	30	9
O00187	Mannan-bi	3	2	2	2	686	75.7	5.63
B4E1C4	cDNA FLJ5	3	1	1	1	421	46	7.93
A0A5C2GST	IG c1754_	7	1	1	1	130	14.2	4.54
P17050	Alpha-N-a	4	1	1	1	411	46.5	5.19
B4E324	cDNA FLJ6	3	1	1	1	480	54.2	6.98
J3QQM1	26S prote	5	1	1	1	263	29.3	6.18
B7ZB67	Serine/th	3	1	1	1	299	34.1	6.16
Q96GX3	KIAA0118	6	1	1	1	175	19.3	6.9
B4E1V6	cDNA FLJ5	3	1	1	1	273	32	5.66
O94903	Pyridoxal	3	1	1	1	275	30.3	7.5
A0A5C2G3G	IGL c3464	17	1	1	1	108	11.7	8.94
A8K865	cDNA FLJ7	6	1	1	1	259	28.5	7.99
G5E971	Collagena	3	1	1	1	489	55.8	5.97
A1KY36	Cell prol	3	2	2	2	745	73.4	9.61
A0A024R2Q	Myosin, l	10	2	2	2	195	21.9	5.1
K7EMH1	60S ribos	15	1	1	1	89	10.4	9.66
A0A5C2GLA	IG c474_h	7	1	1	1	133	14.5	10.59
Q8TAS0	ATP synth	4	1	1	1	291	32.2	9.11
A0A5C2GTG	IG c1800_	15	1	2	1	128	13.7	6.28
Q07092	Collagen	1	2	2	2	1604	157.7	7.84
E9PPH5	Acidic le	14	1	1	1	114	13.1	4.22
P48047	ATP synth	5	1	1	1	213	23.3	9.96
E9KL30	Proteasom	3	1	1	1	277	29.9	7.68
A0A5C2GHS	IG c1327_	16	1	1	1	110	11.8	8.48
Q8N6Y2	Leucine-r	2	1	1	1	441	51.8	8.24
A0A024RA9	Microfibr	5	1	1	1	183	20.8	4.97
V9HWF9	Epididymi	6	2	2	2	308	33.4	5.69
H7C2W9	60S ribos	6	1	1	1	108	12.8	11
H0Y614	Ubiquitin	19	1	1	1	81	8.7	9.47
P36578	60S ribos	5	2	2	2	427	47.7	11.06
A6PVX3	26S prote	8	1	1	1	203	21.8	7.11
A0A5C2G3Z	IGL c4011	17	1	1	1	108	11.7	8.84
B4DP31	Phosphori	5	1	1	1	282	31.2	6.95
Q5QTS3	FWP004 OS	4	1	1	1	203	23.6	11.02
Q86XS5	Angiopoie	3	1	1	1	388	44.1	6.6
Q96QK1	Vacuolar	2	1	1	1	796	91.6	5.49
A0A5C2G87	IGL c220_	14	1	1	1	107	11.7	7.28
E9PC71	Hippocalc	4	1	1	1	175	20.3	5.68
A0A5C2GPH	IG c1282_	9	1	1	1	120	13.1	7.3

A0A5C2GT6	IG c1690_	15	1	1	1	124	13.3	8.28
A0A5C2FUD	IGL c362_	7	1	1	1	110	11.6	7.24
A0A5C2GAC	IGH + IGL	8	1	1	1	118	12.8	6.58
Q9BY74	Ribosomal	9	1	1	1	142	15.6	10.04
A0A5C2GMS	IG c488_h	16	1	1	1	122	13.1	7.12
K7ERW9	Arsenical	5	1	1	1	200	21.9	4.81
J3KT73	60S ribos	19	1	1	1	64	7.6	9.99
O75106	Retina-sp	1	1	1	1	756	83.6	7.03
Q9Y5Y7	Lymphatic	2	1	1	1	322	35.2	8.28
O95373	Importin-	1	1	1	1	1038	119.4	4.82
C9JJV6	Myeloid-a	7	1	1	1	146	15.9	8.65
A2VCM6	PTMS prot	12	1	1	1	101	11.4	4.22
B7Z2B0	cDNA FLJ5	2	1	1	1	533	60	7.27
E7ENY0	Alpha-add	2	1	1	1	663	73.4	6.55
A0A5C2G61	IGH c127_	16	2	2	1	121	13.1	6.52
A0A5C2FVC	IGL c719_	15	1	1	1	106	11.3	7.99
A0A5C2GUK	IG c1191_	16	2	3	1	125	13.8	5.1
K7ELC7	60S ribos	13	2	2	2	144	16.5	10.58
P11717	Cation-in	0	1	1	1	2491	274.2	5.94
M0QZR9	ELAV-like	8	1	1	1	153	17.1	8.66
Q7Z3T9	Neuropili	2	1	1	1	931	104.7	5.22
Q9H3N1	Thioredox	3	1	1	1	280	31.8	4.98
P13224	Platelet	10	2	2	2	206	21.7	9.31
A0A5C2G5D	IGH c199_	7	1	1	1	130	14.2	7.11
P35998	26S prote	5	2	2	2	433	48.6	5.95
H3BPY5	Calcium-r	6	1	1	1	125	13.5	8.19
K7ESL0	Spermidin	11	1	1	1	119	13	6.76
P61201	COP9 sign	2	1	1	1	443	51.6	5.53
F8WF71	Exportin-	17	1	1	1	82	9.6	6.11
Q9BRW0	CD58 prot	4	1	1	1	240	27	6.09
A0A5C2GPX	IG c923_h	16	1	1	1	122	13.3	7.12
Q6ZNX5	cDNA FLJ2	5	1	1	1	165	17.7	7.52
P12645	Bone morp	2	1	1	1	472	53.3	9.58
E5RJE1	Protein F	14	1	1	1	93	10.4	4.88
E9PP73	Coatomer	2	1	1	1	485	55.4	6.43
I3L303	40S ribos	17	1	1	1	52	6	11
Q5T7F0	Neuropili	2	1	1	1	704	79	5.86
A0A5C2G73	IGL c254_	8	1	1	1	107	11.6	7.96
A0A5C2FZ4	IGL c925_	14	1	1	1	111	11.7	7.12
V9HW01	Epididymi	6	1	1	1	157	17.8	11.25
A0A5C2FVX	IGL c1079	25	2	2	1	108	11.7	6.57
Q5JTB6	Placenta-	11	1	1	1	97	10.3	4.92
Q92522	Histone H	6	1	1	1	213	22.5	10.76
A8K7R3	cDNA FLJ7	2	1	1	1	560	62.6	6.64
A0A5C2GMZ	IG c855_h	16	1	1	1	120	13	5.14
A0A5C2FY5	IGL c1106	14	1	1	1	111	11.7	5.94
A0A5C2GS9	IG c1793_	10	1	1	1	120	13.2	4.75
A0A5C2GTE	IG c617_l	17	1	1	1	109	11.8	8.53
P26373	60S ribos	5	1	1	1	211	24.2	11.65
A0A087X0X	Growth/di	3	1	1	1	353	39.3	9.91
B4DP80	NAD(P)H-h	4	1	2	1	307	33.6	8.73

A0A5C2GB4	IGH + IGL	9	1	1	1	125	13.9	8.43
Q6FHC9	STC2 prot	6	2	2	2	302	33.2	7.3
J3KRX5	60S ribos	8	1	1	1	174	20.2	10.1
P54296	Myomesin-	1	1	1	1	1465	164.8	6.19
A0A5C2GU1	IG c891_l	29	2	2	1	107	11.8	8.88
A0A345WIF	Cytochrom	4	1	1	1	227	25.5	4.82
Q86YZ3	Hornerin	2	1	1	1	2850	282.2	10.04
B3KXH8	cDNA FLJ4	4	1	1	1	395	45.6	8.15
Q32Q75	Eukaryoti	5	1	1	1	217	25.1	6.15
B3KQQ7	cDNA PSEC	3	1	1	1	415	47.1	7.2
A0A2R8Y6J	60S ribos	3	1	1	1	238	27	9.13
Q96CT6	C12orf10	4	1	1	1	322	36.3	8.06
Q96AG4	Leucine-r	3	1	1	1	307	34.9	9.57
Q9NSD9	Phenylala	2	1	1	1	589	66.1	6.84
Q3T1A9	Cellular	8	1	1	1	130	14.9	8.75
Q96FJ2	Dynein li	8	1	1	1	89	10.3	7.37
Q567U8	COPS7A pr	6	1	1	1	248	27.3	5.49
A3KFI1	Neuroblas	5	1	1	1	128	14	6.48
A0A5C2GJ1	IG c501_h	9	1	1	1	126	13.6	7.97
P05496	ATP synth	5	1	1	1	136	14.3	9.74
B2R7R4	cDNA, FLJ	1	1	1	1	671	76	8.98
Q9Y5P6	Mannose-1	7	2	2	2	360	39.8	6.61
J3KRL0	Unconvent	3	1	1	1	436	49.7	7.01
H7C2D6	Mesenceph	21	1	1	1	71	7.8	7.85
Q6N028	Uncharact	2	1	1	1	529	61.4	5.62
A0A024RDH	SEC31-lik	2	1	1	1	1181	129	7.4
A0A5C2GVW	IG c1581_	7	1	1	1	111	11.5	5.94
P20929	Nebulin C	1	1	1	1	6669	772.4	9.07
Q9Y5F9	Protocadh	1	1	1	1	930	101	5.26
A0A5C2G07	IGL c2658	14	1	1	1	111	11.6	7.11
P43034	Platelet-	5	2	2	2	410	46.6	7.37
Q6FIF1	DNAJB9 pr	6	1	1	1	223	25.5	8.27
A0A0A6YYA	Protein T	10	2	2	2	188	21.2	6.2
A0A5C2GBK	IGH + IGL	11	1	1	1	123	13.3	9.33
B7Z7Q6	cDNA FLJ5	5	2	2	2	391	43.9	6.3
O75063	Glycosami	2	1	1	1	409	46.4	6.87
A0A5C2FW9	IGL c924_	7	1	1	1	110	11.5	8.63
B4DNA0	cDNA FLJ5	3	1	1	1	430	47.4	6.84
A0A0A0MQV	Fibroblas	3	1	1	1	288	30.7	11.18
Q99747	Gamma-sol	5	1	1	1	312	34.7	5.41
A0A024R8L	WW domain	4	1	1	1	261	28.1	5.91
A0A140VK7	Testis se	3	1	1	1	314	34.3	8.85
A0A286YFL	Palmitoyl	3	1	1	1	323	35.7	8.44
B4DH43	cDNA FLJ5	2	1	1	1	830	82.7	8.56
P29373	Cellular	7	1	1	1	138	15.7	5.4
P41091	Eukaryoti	3	1	1	1	472	51.1	8.4
E9PQ80	Charged m	9	1	1	1	213	24.2	5.19
B2R4C9	cDNA, FLJ	8	1	1	1	102	11.2	9.52
B4DPZ4	cDNA FLJ6	3	1	1	1	458	52.7	6.7
A0A5C2G4C	IGL c4028	14	1	1	1	112	11.6	5.91
P37108	Signal re	6	1	1	1	136	14.6	10.04

F8VYN9	ADP-ribos	6	1	1	1	194	21.8	6.77
Q96HC4	PDZ and L	2	1	1	1	596	63.9	8.21
B4DIL7	cDNA FLJ5	4	1	1	1	212	24.3	8.88
F8VXI7	Dynein li	52	1	1	1	42	4.8	4.72
A0A5C2G84	IGL c3937	14	1	1	1	107	11.4	7.96
Q13103	Secreted	6	1	1	1	211	24.3	8.32
Q53GY9	Cation-de	5	1	1	1	277	31	5.83
Q14703	Membrane-	1	1	1	1	1052	117.7	8.75
B3KXS3	cDNA FLJ4	5	1	1	1	260	29.4	9.61
A0A024RAS	Heme binc	11	2	2	2	189	21.1	5.8
C9IZG4	Protein C	10	1	1	1	135	14.4	5.45
A0A5C2G7X	IGH + IGL	8	1	1	1	119	13.3	9.13
P00167	Cytochrom	10	1	1	1	134	15.3	4.96
K7EKQ2	Hsp90 co-	4	1	1	1	353	41.6	6.64
Q53TN4	Cytochrom	3	1	1	1	286	31.6	8.76
Q14554	Protein d	2	1	1	1	519	59.6	7.91
B3KR70	cDNA FLJ3	5	2	2	2	430	47.7	6.13
A0A1B0GVN	Uroporphy	5	1	1	1	298	33.2	7.37
O43916	Carbohydr	5	1	1	1	411	46.7	8.97
Q53H96	Pyrroline	4	1	1	1	274	28.6	7.72
P48788	Troponin	9	1	1	1	182	21.3	8.73
Q86YW5	Trem-like	5	1	1	1	311	32.7	6.05
Q5VZ73	C-C motif	8	1	1	1	124	13.6	10.05
A0A5C2GP9	IG c432_h	5	1	1	1	128	14.1	6.77
M0R1D6	DnaJ homc	13	1	1	1	91	10.3	8.19
A0A5C2H3E	IG c1526_	8	1	1	1	110	11.4	6.52
Q4VAQ1	COL8A2 pr	11	1	1	1	114	12.8	7.43
Q11201	CMP-N-ace	4	1	1	1	340	39.1	9.09
A0A5C2GR9	IG c4_lig	8	1	1	1	108	11.9	6.6
A0A5C2GCF	IGH + IGL	15	2	2	1	122	13.3	8.84
Q14427	GM2-activ	8	1	1	1	103	11.1	4.75
O76076	CCN famil	7	2	2	2	250	26.8	7.88
A0A024R7C	Dynamin 2	3	1	1	1	460	51.8	7.88
Q9UHL4	Dipeptidy	2	1	1	1	492	54.3	6.32
Q08495	Dematin C	3	1	2	1	405	45.5	8.88
A0A5C2G75	IGL c274_	7	1	1	1	109	11.7	5.31
J3KR44	Ubiquitin	4	1	1	1	272	31.4	5
Q15631	Translin	3	1	1	1	228	26.2	6.44
B2RA15	Inhibitor	3	1	1	1	280	32.7	8.05
P48556	26S prote	2	1	1	1	350	39.6	9.7
Q9Y2S6	Translati	14	1	1	1	64	7.1	9.99
A0A5C2GFF	IGH + IGL	9	1	1	1	125	13.9	6.62
A0A5C2G1A	IGL c2929	15	1	1	1	110	11.4	7.12
Q96KN2	Beta-Ala-	3	1	1	1	507	56.7	5.3
A0A2Y9CYF	Ig heavy	26	2	3	1	104	11.6	8.46
A0A5C2GDN	IG c680_h	6	1	1	1	126	14	8.98
A0A087WZ5	Tumor prc	7	1	1	1	152	16.3	4.92
A0A5C2G94	IGH + IGL	25	2	2	1	121	13	5.01
D6RE99	Histidine	9	1	1	1	78	8.6	5.39
A0A3B3ISV	ERI1 exor	4	1	1	1	315	34.7	7.47
Q6B514	Septin 6	4	2	2	2	438	50.2	6.86

O75976	Carboxype	1	1	1	1	1380	152.8	6.05
Q8IWH1	Similar t	3	1	1	1	500	56.1	8.5
Q9UM02	Prolyl en	1	1	1	1	710	80.7	5.86
A0A1B0GUE	Acid cera	3	1	1	1	330	37.4	6.79
P62081	40S ribos	4	1	1	1	194	22.1	10.1
C9JE88	Carboxype	6	1	1	1	147	16.6	6.27
P48960	CD97 anti	2	1	1	1	835	91.8	6.87
P27144	Adenylate	4	1	1	1	223	25.3	8.4
F5H608	ATP synth	9	1	1	1	81	8.9	9.36
Q6UWF9	Protein F	5	1	1	1	173	19.7	8.47
A0A077H1I	VLCAD (Fr	23	1	1	1	66	6.8	9.82
A0A5C2GJ9	IG c1326_	22	1	1	1	107	11.4	8.5
K7EL99	Tubulin-f	6	1	1	1	133	14.6	6.52
B3KPI8	cDNA FLJ3	2	1	1	1	547	62	5.25
P05106	Integrin	1	1	1	1	788	87	5.24
P30040	Endoplasm	8	2	2	2	261	29	7.31
Q8TB73	Protein N	1	1	1	1	568	64.6	8.94
A0A5C2GC7	IGL c311_	10	1	1	1	106	11.6	8.47
F5GZQ3	Trifuncti	2	1	1	1	459	49.6	9.42
A0A5C2FXI	IGL c1325	8	1	1	1	109	11.5	5.26
B2RD19	cDNA, FLJ	5	1	1	1	309	34.3	7.33
A0A5C2FX1	IGL c680_	17	1	1	1	107	11.8	8.44
P28838	Cytosol a	2	1	1	1	519	56.1	7.93
E7EM64	COP9 sign	2	1	1	1	326	36	5.73
O00571	ATP-depen	2	1	1	1	662	73.2	7.18
A0A5C2GFU	IG c675_h	16	1	1	1	121	12.9	5.11
Q5T6V7	Queuosine	5	1	1	1	200	23.3	6.3
Q9UBQ5	Eukaryoti	6	1	1	1	218	25	4.93
P36406	E3 ubiqui	2	1	1	1	574	64	6.38
Q8NBL1	Protein C	4	1	1	1	392	46.2	8.72
A0A5C2FVD	IGL c30_l	11	1	1	1	107	11.6	7.39
F8WF14	Carboxyli	2	1	1	1	562	63.4	7.84
A0A5C2G6C	IGH c400_	8	1	1	1	125	13.8	8.76
Q13098	COP9 sign	2	1	1	1	491	55.5	6.74
A0A5C2FWS	IGL c1548	7	1	1	1	111	11.6	8.31
A0A5C2FX4	IGL c1539	8	1	1	1	107	11.7	6.55
M0QYI6	NEDD8-con	10	1	1	1	114	12.9	8.82
A0A5C2GUJ	IG c187_h	7	1	1	1	127	14.1	9.13
P61086	Ubiquitin	6	1	1	1	200	22.4	5.44
Q14324	Myosin-bi	1	1	1	1	1141	128	7.52
A0A5C2GXD	IG c1623_	8	1	1	1	113	12.5	5.36
Q5U000	Cathepsin	3	1	1	1	303	33.8	7.11
A0A140VJG	Catechol	3	1	1	1	271	30	5.47
A0A5C2FVX	IGL c972_	8	1	1	1	110	11.6	6.48
B3KXK5	cDNA FLJ4	1	1	1	1	578	62.2	5.11
P25815	Protein S	11	1	1	1	95	10.4	4.88
Q7Z591	Microtubu	1	1	3	1	1439	155	6.32
P49327	Fatty aci	0	1	1	1	2511	273.3	6.44
Q9BY51	GL009 OS=	7	1	1	1	183	21.4	9.95
O43598	2'-deoxyn	10	1	1	1	174	19.1	5.05
O60844	Zymogen g	5	1	1	1	167	18.1	9.36

A0A024R89	Actin-rel	8	1	1	1	153	16.9	6.6
C9JQB3	Ras-relat	6	1	1	1	171	19.2	5
Q8IUG5	Unconvent	0	1	1	1	2567	285	6.86
P05204	Non-histc	9	1	1	1	90	9.4	9.99
A0A5C2FU5	IGL c94_l	25	2	2	1	107	11.6	8.47
B7Z4E8	Carbohydr	2	1	1	1	404	47.8	8.81
P36405	ADP-ribos	6	1	1	1	182	20.4	7.24
A0A5C2GTL	IG c83_li	8	1	1	1	110	11.4	5.19
Q9BWD1	Acetyl-Cc	9	2	2	2	397	41.3	6.92
P33947	ER lumen	4	1	1	1	212	24.4	8.72
Q9UHY7	Enolase-p	5	1	1	1	261	28.9	4.78
P40763	Signal tr	2	1	1	1	770	88	6.3
A0A024R74	NADH dehy	9	1	1	1	116	13.5	5.99
Q8IZP7	Heparan-s	3	2	2	2	471	54.8	6.83
K4DIA7	Tetraspan	4	1	1	1	230	25.6	7.24
O94919	Endonucle	2	1	1	1	500	55	5.71
Q12906	Interleuk	1	1	1	1	894	95.3	8.76
A0A0U1RQV	Rho-assoc	1	1	1	1	1137	133	5.35
B2RDE8	cDNA, FLJ	3	1	1	1	240	26.8	4.67
Q59FP8	Neogenin	1	1	1	1	1130	123.9	7.03
A0A5C2G8D	IGL c290_	15	1	1	1	110	11.6	4.96
B4DNW4	cDNA FLJ5	3	1	1	1	254	26.9	7.02
A0A5C2GIM	IG c23_li	10	1	1	1	111	11.9	6
A0A5C2GDS	IGH c121_	7	1	1	1	122	13.3	8.84
B4DEX8	S-adenosy	4	1	1	1	362	39.7	6.04
H0YGR4	Oligoribc	4	1	1	1	192	22.1	8.24
Q14165	Malectin	4	1	1	1	292	32.2	5.41
C9J177	Protein p	4	1	1	1	289	33.7	5.22
A0A5C2GBE	IGH + IGL	15	2	2	1	110	11.4	8.48
A0AVT1	Ubiquitin	1	1	1	1	1052	117.9	6.14
A0A384N6H	Epididymi	2	1	1	1	371	42.7	6.86
Q00169	Phosphati	4	1	1	1	270	31.8	6.55
A0A5C2GNH	IG c413_h	7	1	1	1	122	13.5	9.13
P46109	Crk-like	5	1	1	1	303	33.8	6.74
O43286	Beta-1,4-	2	1	1	1	388	45.1	8.15
G3V180	Dipeptidy	3	2	2	2	757	84.3	5.03
B7Z9Q5	cDNA, FLJ	4	1	1	1	252	28.2	8.32
A0A024R0L	Epididymi	4	1	1	1	231	25.7	6.84
Q9NP58	ATP-bindi	2	1	1	1	842	93.8	8.48
A0A1C7CYZ	Mitogen-a	3	1	1	1	276	30.9	7.18
P62269	40S ribos	5	1	1	1	152	17.7	10.99
O95881	Thioredox	5	1	1	1	172	19.2	5.4
Q9HB71	Calcyclin	7	2	2	2	228	26.2	8.25
Q549M8	CLE7 OS=H	4	1	1	1	244	28.1	6.65
A0A5C2FVE	IGL c40_l	17	1	1	1	109	11.9	8.5
O15263	Beta-defe	17	1	1	1	64	7	9.22
K7EP45	Vacuolar	14	1	1	1	99	11.6	9.2
Q9UFX5	Uncharact	7	1	1	1	165	17.1	8.35
Q7Z4X0	MO25-like	3	1	1	1	341	39.7	7.47
O60763	General v	2	1	1	1	962	107.8	4.91
Q597H1	Transform	4	1	1	1	394	42.8	5.82

Q59G24	Activated	10	1	1	1	134	15.1	9.38
P62310	U6 snRNA-	8	1	1	1	102	11.8	4.7
P17980	26S prote	3	1	1	1	439	49.2	5.24
A0A5C2GQF	IG c860_h	7	1	1	1	128	13.9	8.73
B4DQK8	cDNA FLJ5	4	1	1	1	359	36.7	11.37
A8K147	Multifunc	8	1	1	1	154	17.3	7.02
A0A5C2GM3	IG c345_l	15	2	2	1	110	11.4	7.94
A0A5C2GJW	IG c1105_	8	1	1	1	110	11.5	5.87
Q92734	Protein T	2	1	1	1	400	43.4	5.1
B7Z9M1	cDNA, FLJ	2	1	2	1	452	47.7	5.66
Q5IWS5	Intelecti	3	1	1	1	313	35	5.82
A0A5C2G5V	IGH c356_	16	1	1	1	119	12.8	5.39
A0A087WX3	Epidermal	3	1	1	1	232	25.4	8.44
P11586	C-1-tetra	1	1	1	1	935	101.5	7.3
Q9BXJ1	Complemen	3	1	1	1	281	31.7	6.9
A0A384NL2	Proteasom	3	1	1	1	205	22.9	6.55
O00487	26S prote	2	1	1	1	310	34.6	6.52
Q9NSN1	Uncharact	2	2	2	2	952	110.3	7.78
Q8NFW8	N-acylneu	2	1	1	1	434	48.3	7.93
K7EL62	Guanine n	5	1	1	1	236	27.4	5.35
Q53F35	Acidic (L	8	2	2	2	250	28.7	4.06
Q5JRP2	Disintegr	10	2	2	2	278	31.1	9.11
Q5NKV8	Intercell	2	1	1	1	532	57.8	7.68
A0A5C2GDX	IGH + IGL	12	1	1	1	111	12	5.96
A0A024R8I	Ubiquitin	4	1	1	1	404	45.2	4.94
B2C6G4	Fatty aci	1	1	1	1	532	58.3	9.07
A0A384ME8	S-methyl-	4	1	1	1	283	31.2	7.18
B4DSX2	cDNA FLJ6	2	1	1	1	347	36.6	6.29
A0A5C2FV2	IGL c454_	10	1	1	1	108	11.5	5.4
Q92542	Nicastrin	2	1	1	1	709	78.4	5.99
A0A1B0GVS	Alpha-cen	5	1	1	1	221	24.9	6.21
A0A5C2GPA	IG c650_h	7	1	1	1	121	13.3	7.96
E9PC52	Histone-b	2	1	1	1	416	46.9	5.07
Q9Y625	Glypican-	2	1	1	1	555	62.7	5.41
I3L4V1	RNA N6-ad	5	1	1	1	148	17.1	7.4
Q99460	26S prote	1	1	1	1	953	105.8	5.39
A0A125U0V	GCT-A2 he	9	1	1	1	126	13.8	5.45
A0A5C2GJR	IGH + IGL	6	1	1	1	112	11.7	7.97
A0A4P8J5I	IgG2_IGHV	8	1	1	1	130	14.1	8.51
P11226	Mannose-b	13	2	2	2	248	26.1	5.49
A0A140VJZ	Ubiquitin	1	1	1	1	858	95.7	5.03
A0A024R1U	Insulin-l	3	1	1	1	258	27.9	7.15
Q6P4A8	Phospholi	1	1	1	1	553	63.2	9.06
Q19UL8	Coagulati	20	1	1	1	54	6.4	5.1
B1B0D4	ADAMTS-li	1	2	2	2	1060	116.2	6.76
Q2TNB3	Cell migr	3	1	1	1	239	27.3	5.58
E9PIE3	Caveolae-	3	1	1	1	293	31.1	6.81
B0QY90	Eukaryoti	3	1	1	1	466	55.1	8.95
B4DJ06	cDNA FLJ5	1	1	1	1	629	67.9	4.91
A0A5C2FVF	IGL c584_	15	1	1	1	107	11.7	7.97
Q5D079	A4GALT pr	2	1	1	1	353	40.4	8.95

B5MDC5	cDNA FLJ5	4	1	1	1	255	29	4.94
Q8IZH2	5’-3’ exc	0	1	1	1	1706	194	7.21
Q12792	Twinfilin	2	1	1	1	350	40.3	6.96
B1AJY6	26S prote	6	1	1	1	110	11.9	5.25
Q8NDZ4	Divergent	2	1	1	1	430	49.5	8.53
A0A5C2G2U	IGL c3472	15	1	1	1	110	11.6	7.97
B4DVS2	cDNA FLJ5	1	1	1	1	800	88.8	4.97
B4DWS6	cDNA FLJ6	4	1	1	1	304	33.5	9.39
I3L4J1	Uncharact	2	1	1	1	428	48	7.53
A0A024RBC	Kit ligan	3	1	1	1	273	30.9	6.14
P53794	Sodium/my	1	1	1	1	718	79.6	7.27
Q9UDT6	CAP-Gly d	1	1	1	1	1046	115.8	6.73
B2RDT9	cDNA, FLJ	2	1	1	1	348	39.4	5.11
Q8WWX9	Selenopro	10	1	1	1	145	16.2	5.54
A4D1U3	Single-st	10	1	1	1	148	17.2	9.6
A0A5C2GGL	IG c1162_	16	1	1	1	119	13.1	8.46
B4DM33	cDNA FLJ5	3	1	1	1	238	26.6	5.29
A0A5C2GNS	IG c400_h	24	3	3	1	120	13.1	8.44
A0A5C2G5V	IGH c329_	7	1	1	1	122	13.1	8.88
O00232	26S prote	3	1	1	1	456	52.9	7.65
B4DS32	cDNA FLJ5	1	1	1	1	569	64.3	5.69
Q14696	LRP chape	13	2	2	2	234	26.1	7.78
B7Z7P8	Eukaryoti	4	2	2	2	423	47.4	5.57
R4QU15	MHC class	7	1	1	1	181	20.9	6.4
B7Z390	cDNA FLJ5	1	1	1	1	809	87.3	6.42
A0A087X0I	Myomegali	9	1	1	1	66	8.2	9.04
P29034	Protein S	19	2	2	2	98	11.1	4.78
Q02742	Beta-1,3-	2	1	1	1	428	49.8	8.41
A0A140T9V	Megakaryc	4	1	1	1	217	23.5	8.5
B2RE88	cDNA, FLJ	2	1	1	1	361	39.9	9.36
D6RA82	Annexin C	3	1	1	1	284	32.1	5.94
Q75MU2	Uncharact	8	1	1	1	156	17.1	5.31
H0YB70	Putative	4	1	1	1	186	20.7	5.36
A0A5C2GER	IGH c531_	10	1	1	1	121	13.5	7.97
B7Z7F6	cDNA FLJ5	6	1	1	1	141	15.4	9.66
P63220	40S ribos	8	1	1	1	83	9.1	8.5
A0A5C2GMF	IG c23_he	6	1	1	1	127	14.1	4.94
A0A5C2GL5	IG c783_l	15	1	1	1	107	11.7	5.78
Q6LBY7	Telo-prop	36	1	1	1	25	2.2	6.18
Q499H0	G protein	2	1	1	1	1003	110	7.34
J3QL71	Secernin-	4	1	1	1	433	47.5	5.68
C9JFR7	Cytochrom	8	1	1	1	101	11.3	9.66
Q9Y6M5	Zinc tran	2	1	1	1	507	55.3	6.48
A0A5C2H19	IG c1678_	7	1	1	1	107	11.7	9.5
A0A5C2GB6	IGH + IGL	12	1	1	1	112	12.2	6.51
A0A5C2FU5	IGL c508_	15	2	2	1	110	11.6	4.96
F2Z2K0	NSFL1 cof	3	1	1	1	274	30.2	5.1
F6IQ87	Urea tran	2	1	1	1	389	42.5	7.15
B7Z9Z3	cDNA, FLJ	1	1	1	1	826	92.7	9.39
O00743	Serine/th	4	1	1	1	305	35.1	5.69
A8K2P3	cDNA FLJ7	1	1	1	1	990	110.9	8.06

A0A5C2G9J	IGL c536_	12	1	1	1	110	11.6	8.47
A0A5F9ZH7	Adenosine	9	2	2	2	229	25.9	6.99
Q15847	Adipogene	9	1	1	1	76	7.9	5.31
O75367	Core hist	5	2	2	2	372	39.6	9.79
Q8NBY1	Serine/th	5	2	2	2	392	43.8	5.41
A0A5C2GU2	IG c7_hea	7	1	1	1	118	13.2	8.88
G3V583	Protein F	11	1	1	1	140	16.3	4.7
A0A024RBK	60S ribos	3	1	1	1	288	32.7	10.58
B4DXF3	Bleomycin	3	1	1	1	368	42.4	6.25
A0A1W2PRF	Lysosome	3	1	1	1	320	36.3	5.01
C9J3V1	Zinc fing	32	1	1	1	50	5.6	4.53
O76003	Glutaredc	7	2	2	2	335	37.4	5.39
P14735	Insulin-d	2	2	2	2	1019	117.9	6.61
A0A5C2GD5	IGH + IGL	15	1	1	1	110	11.5	6.76
O43633	Charged m	3	1	1	1	222	25.1	5.97
A0A0A0MSC	Slit homc	1	1	1	1	1393	153.7	7.39
B3KY04	cDNA FLJ4	3	1	1	1	325	35.7	5.64
E9PAL5	Collagen	0	1	1	1	2611	289.3	6.95
A0A087X26	TAR DNA-b	4	1	1	1	301	34.2	6.44
Q00532	Cyclin-de	2	1	1	1	358	41.8	8.85
B3KMK7	cDNA FLJ1	2	1	1	1	528	59.6	6.23
Q8NGA1	Olfactory	2	1	1	1	313	34.8	8.91
A0A5C2GD5	IGH + IGL	15	1	1	1	107	11.7	5.31
U3KPS2	Myeloblas	4	1	1	1	215	23.6	8.16
I3L426	Coronin (	6	1	1	1	206	22	8.81
Q3B7A7	Trifuncti	1	1	1	1	1010	107.7	6.77
Q9H444	Charged m	4	1	1	1	224	24.9	4.82
B3KRK4	cDNA FLJ3	3	1	1	1	234	26.2	4.55
O14604	Thymosin	16	1	1	1	44	5	5.36
Q7RTR0	NACHT, LR	1	1	1	1	991	113.2	6.51
B1AKZ4	Phosphopr	9	1	1	1	130	15	5.02
A0A5C2GA1	IGH + IGL	7	1	1	1	119	12.9	8.29
B7Z1G4	cDNA FLJ6	3	1	1	1	357	39	6.07
G3V560	NADH dehy	9	1	1	1	93	10.5	9.88
H3BT06	Phosphoma	9	1	1	1	90	10.4	9.44
C9JYY9	ADP-sugar	9	1	1	1	97	11.2	7.97
Q99592	Zinc fing	2	1	1	1	522	58.3	5.69
A0A0A0MSX	Isoleucyl	1	1	1	1	1242	142.2	6.09
Q9Y5C1	Angiopoie	2	1	1	1	460	53.6	6.7
Q96QB2	Sodium-in	1	1	1	1	507	55.1	7.91
O00245	EXTL2 (Fr	5	1	1	1	129	14.7	8.43
A0A5C2GM4	IG c288_h	11	2	2	1	124	13.5	9.36
A0A0S2Z4R	Tyrosine-	2	1	1	1	528	59.1	7.05
Q14D04	Ventricul	1	1	1	1	833	94.7	6.71
A2TDB8	Cysteine	4	1	1	1	194	21	8.54
A0A140TA8	MICOS com	6	1	1	1	110	12	7.96
P15529	Membrane	2	1	1	1	392	43.7	6.74
A0A5C2GUE	IG c532_l	7	1	1	1	107	11.7	7.96
A0A1B0GXE	Haloacid	5	1	1	1	131	14.6	6.8
B3KTQ1	cDNA FLJ3	3	1	1	1	350	40.8	8.03
Q9UBD9	Cardiotrc	4	1	1	1	225	25.2	8.46

B5MCT8	40S ribos	5	1	1	1	139	16.6	11.06
E9PHR9	Phospholi	5	1	1	1	239	26.2	6.09
Q53EY4	RAB31, me	6	1	1	1	195	21.7	7.06
A0A5C2GBC	IGH + IGL	9	1	1	1	118	12.8	7.97
J3QQQ9	KOW domai	8	2	2	2	107	12.7	10.78
A0A5C2G67	IGH c82_h	6	1	1	1	122	13.2	7.46
Q6VAB6	Kinase su	1	1	1	1	950	107.6	8.69
Q9UHQ9	NADH-cytc	6	2	2	2	305	34.1	9.38
J3KNF4	Copper ch	3	1	1	1	255	27.1	5.9
O95302	Peptidyl-	3	2	2	2	570	63	5.08
G3V158	2-deoxyri	5	1	1	1	230	25.1	8.16
A0A5C2GDF	IGH + IGL	8	1	1	1	130	14.3	8.69
V9HW92	Epididymi	4	1	1	1	329	36	7.02
Q9BQQ5	Ribosomal	9	1	1	1	106	12	11.46
B7ZLF2	Uncharact	7	1	1	1	96	10.1	9.69
A0A5C2G45	IGL c2715	7	1	1	1	107	11.8	8.62
A0A5C2G6I	IGL c2033	8	1	1	1	109	12	7.99
A0A0G2JS8	AP-2 comp	2	2	2	1	917	101.6	6.86
A0A087WZV	D-aminoac	4	1	1	1	223	25.3	9.04
A0A5C2GA7	IGH c163_	15	1	1	1	123	13.4	5.12
Q6GMV3	Putative	6	1	1	1	140	15.8	9.1
B4DVQ5	Eukaryoti	1	1	1	1	898	103.6	5.53
A0A384MQX	Epididymi	5	1	1	1	284	30.4	6.54
A0A5C2GBX	IGH + IGL	16	2	2	1	127	13.9	8.84
A0A5C2GXR	IG c1542_	8	1	1	1	111	11.9	8.53
P50238	Cysteine-	9	1	1	1	77	8.5	8.75
Q6IB11	PGRMC1 pr	10	2	2	1	195	21.7	4.7
Q7Z4Z1	Coatomer	3	1	1	1	307	34.4	5.2
A0A5C2FYF	IGL c1350	7	1	1	1	108	11.9	8.48
E9PFG7	2-oxoglut	1	1	1	1	873	99	7.46
A0A140T8Z	Lymphocyt	2	1	1	1	382	40.9	7.81
A0A5C2GNG	IG c718_h	14	2	2	1	125	13.4	7.96
A0A5C2G33	IGL c3010	8	1	1	1	108	11.6	7.97
E7EUT2	Piezo-typ	3	1	1	1	373	41.3	9.48
K7ERC8	3-ketodih	4	1	1	1	298	32.7	7.96
K7EM16	Vasodilat	5	1	1	1	183	20.1	7.94
Q05655	Protein k	1	1	1	1	676	77.5	7.75
A0A5C2G7J	IGL c418_	15	2	2	1	110	11.4	7.96
Q86X55	Histone-a	1	1	1	1	608	65.8	6.73
Q6N039	Transmemb	2	1	1	1	329	36.5	5.25
B4DNN3	cDNA FLJ5	1	1	1	1	725	82.2	7.78
I3L4Q9	Vesicle-f	7	1	1	1	81	8.9	9.06
A0N5T0	V-gamma-1	12	2	2	1	161	17.6	10.14
Q8IZ83	Aldehyde	1	1	1	1	802	85.1	6.79
B4E3L5	cDNA FLJ5	2	1	1	1	740	82.3	6.54
D6RCE4	Protocadh	2	1	1	1	488	53.9	7.36
Q8NHP8	Putative	1	1	1	1	589	65.4	6.8
B5BU77	Protein k	1	1	1	1	683	77.8	7.77
Q9NQH7	Xaa-Pro a	1	1	1	1	507	57	6.83
O75493	Carbonic	3	1	1	1	328	36.2	9.74
A8MUD9	60S ribos	8	2	2	2	208	24.4	10.67

O15511	Actin-rel	4	1	1	1	151	16.3	5.67
P28074	Proteasom	8	2	2	2	263	28.5	6.92
A8K122	KIAA1946,	1	1	1	1	827	92.3	8.65
A0A5C2GVX	IG c1919_	15	1	1	1	125	13.5	5.41
A0A5C2G3E	IGL c3642	14	1	1	1	111	11.6	4.94
A0A024RD4	RAB23, me	8	1	1	1	237	26.6	6.6
B4E3S9	cDNA FLJ5	2	1	1	1	549	61.5	9.16
O95180	Voltage-d	1	1	1	1	2353	259	7.37
H0YNW7	Guanine n	12	1	1	1	100	11.4	8.02
Q9Y3E7	Charged m	3	1	1	1	222	25.1	5.12
Q9Y3B5	CGI-111 p	7	1	1	1	199	22.1	7.43
A9Z1Z3	Fer-1-lik	1	1	1	1	1794	200.9	6.24
A0A5C2FUR	IGL c758_	14	1	1	1	112	11.8	7.96
H7C377	COMM doma	53	1	1	1	32	3.6	4.17
Q9UJU6	Drebrin-l	3	1	1	1	430	48.2	5.05
Q9H488	GDP-fucos	3	1	1	1	388	43.9	8.53
H3BUU9	Cadherin-	2	1	1	1	670	73.7	4.7
P05089	Arginase-	6	1	1	1	322	34.7	7.21
A0A5C2GFC	IGH + IGL	9	1	1	1	123	13.7	6.77
Q75MQ1	Uncharact	2	1	1	1	513	59.1	7.47
A0A1W2PNW	Calcium-a	1	1	1	1	1230	137	6.92
Q8TEI3	FLJ00214	4	1	1	1	322	34.6	5.08
Q14191	Werner sy	1	1	1	1	1432	162.4	6.34
A0A1B0GTF	Rho guani	4	1	1	1	263	31.5	6.54
P17813	Endoglin	2	1	1	1	658	70.5	6.61
P39023	60S ribos	2	1	1	1	403	46.1	10.18
A0A024R8F	Glutamate	1	1	1	1	1277	138.6	9.32
Q9UKA4	A-kinase	0	1	1	1	1901	210.4	5.39
G3V415	Guanine n	11	1	1	1	61	6.9	9.32
E9PCY7	Heterogen	4	1	1	1	429	47.1	6.34
Q02338	D-beta-hy	5	1	1	1	343	38.1	8.95
Q13445	Transmemb	4	1	1	1	227	25.2	4.48
Q13253	Noggin OS	5	1	1	1	232	25.8	8.85
K7EKP8	Cytosolic	3	1	1	1	279	30.8	6.99
Q13641	Trophobla	2	1	1	1	420	46	6.83
P50453	Serpin B9	3	1	1	1	376	42.4	5.86
P21741	Midkine C	11	1	1	1	143	15.6	9.79
B2R932	cDNA, FLJ	5	1	1	1	185	18.9	4.82
A0A384ME1	Elongatic	3	1	1	1	455	49.8	7.61
A4D1T9	Probable	7	1	1	1	235	26.4	8.87
Q9UKV8	Protein a	2	1	1	1	859	97.1	9.19
A0A5C2G84	IGH c587_	13	1	2	1	121	13.3	7.91
A0A1P0AYU	Sidorefle	5	1	1	1	325	36	9.09
Q6LET0	Tetraspan	6	1	1	1	267	29.6	5.24
A0A5C2GZJ	IG c136_l	7	1	1	1	109	11.8	7.96
A0A140VJZ	Ubiquitin	7	1	1	1	230	26.2	4.92
A0A5C2G1Q	IGL c2834	14	1	1	1	111	11.5	5.24
B4DMZ0	Tyrosine-	2	1	1	1	371	42.1	6.39
B3KWE1	Histidyl-	3	1	1	1	440	49.6	5.41
A0A5C2G6T	IGH c292_	6	1	1	1	127	13.8	8.16
G8JL96	Receptor-	2	1	1	1	1501	168.3	6.65

A0A5C2FYC	IGL c1889	8	1	1	1	107	11.6	8.5
A0A087WY3	Integrin	2	1	1	1	445	48.5	5.4
K7EL56	ATP-depen	9	1	1	1	108	11.9	4.5
Q7Z3L2	Uncharact	2	1	1	1	849	95.2	8.47
A0A5C2GCN	IGH + IGL	10	1	1	1	110	11.7	7.96
Q9Y3C8	Ubiquitin	6	1	1	1	167	19.4	7.4
P10644	cAMP-depe	3	1	1	1	381	43	5.35
Q8TD06	Anterior	6	1	1	1	166	19.2	7.99
H0YN88	40S ribos	7	1	1	1	136	15.9	9.91
A0A5C2G7H	IGL c3707	15	1	1	1	107	11.5	9.2
A0A024R58	Uncharact	4	1	1	1	285	33.1	9.19
A0A5C2GF8	IGH + IGL	8	1	1	1	120	12.9	6.62
Q9UFN0	Protein N	4	1	1	1	247	28.4	9.16
B7Z5N7	cDNA FLJ5	4	1	1	1	457	51.5	6.96
A8K2S1	Phospholi	2	1	1	1	749	85.2	5.38
L8EAL0	Alternati	35	1	1	1	40	4.6	8.68
B2R823	cDNA, FLJ	4	1	1	1	252	27.9	9.73
B2R736	cDNA, FLJ	3	1	1	1	547	59.5	5.43

Score Seq	# Peptide	# Razor F	Found in	Found in	Found in	Found in	Found in	Found in
9947.88	119	138	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
9376.56	117	0	High	High	High	High	High	High
5016.14	56	0	High	High	High	High	High	High
4963.08	50	50	High	High	High	High	High	High
4892.06	49	0	High	High	High	High	High	High
3934.01	61	0	High	High	High	High	High	High
3472.89	62	66	High	High	High	High	High	High
2452.59	45	40	High	High	High	High	High	High
2263.5	41	0	High	High	High	High	High	High
2239.7	27	0	High	High	High	High	High	High
2174.42	13	13	High	High	High	High	High	High
1817.33	31	20	High	High	High	High	High	High
1774.51	10	0	High	High	High	High	High	High
1669.69	134	124	High	High	High	High	High	High
1669.32	61	9	High	High	High	High	High	High
1580.55	119	0	High	High	High	High	High	High
1448.37	54	0	High	High	High	High	High	High
1426.57	104	5	High	High	High	High	High	High
1376.47	16	9	High	High	High	High	High	High
1370.78	16	0	High	High	High	High	High	High
1342.04	9	0	High	High	High	High	High	High
1339.36	9	0	High	High	High	High	High	High
1324.51	17	0	High	High	High	High	High	High
1313.13	10	0	High	High	High	High	High	High
1298.33	15	0	High	High	High	High	High	High
1295.97	10	11	High	High	High	High	High	High
1275.66	63	29	High	High	High	High	High	High
1127.78	33	0	High	High	High	High	High	High
1116.64	18	9	High	High	High	High	High	High
1085.41	12	6	High	High	High	High	High	High
1049.67	9	0	High	High	High	High	High	High
1034.31	7	0	High	High	High	High	High	High
1004.73	20	1	High	High	High	High	High	High
942.56	50	51	High	High	High	High	High	High
929.59	47	0	High	High	High	High	High	High
907.93	29	0	High	High	High	High	High	High
866.17	18	0	High	High	High	High	High	High
835.92	31	29	High	High	High	High	High	High
831.84	55	0	High	High	High	High	High	High
825.79	29	0	High	High	High	High	High	High
823.22	8	0	High	High	High	High	High	High
819.62	20	0	High	High	High	High	High	High
770.15	146	0	High	High	High	High	High	High
739.62	8	7	High	High	High	High	High	High
724.44	33	0	High	High	High	High	High	High
719.54	98	0	High	High	High	High	High	High
713.23	19	2	High	High	High	High	High	High
709.36	8	0	High	High	High	High	High	High
705.23	8	0	High	High	High	High	High	High
699.68	60	0	High	High	High	High	High	High

684.21	61	61	High	High	High	High	High	High
674.12	18	0	High	High	High	High	High	High
667.8	16	0	High	High	High	High	High	High
664.12	14	0	High	High	High	High	High	High
659.88	13	5	High	High	High	High	High	High
658.29	26	0	High	High	High	High	High	High
628.89	33	0	High	High	High	High	High	High
606.65	16	10	High	High	High	High	High	High
599.65	12	0	High	High	High	High	High	High
588.7	37	0	High	High	High	High	High	High
574.33	95	0	High	High	High	High	High	High
566.95	7	1	High	High	High	High	High	High
549.4	62	3	High	High	High	High	High	High
541.7	61	0	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
535.49	62	63	High	High	High	High	High	High
521.17	6	0	High	High	High	High	High	High
515.44	28	27	High	High	High	High	High	High
506.04	11	0	High	High	High	High	High	High
483.66	3	0	High	High	High	High	High	High
472.62	44	0	High	High	High	High	High	High
470.07	44	50	High	High	High	High	High	High
452.97	26	0	High	High	High	High	High	High
451.37	5	0	High	High	High	High	High	High
445.97	5	0	High	High	High	High	High	High
418.9	36	32	High	High	High	High	High	High
412.98	32	0	High	High	High	High	High	High
411.54	30	3	High	High	High	High	High	High
409.04	7	4	High	High	High	High	High	High
408.33	26	0	High	High	High	High	High	High
406.98	28	0	High	High	High	High	High	High
404.88	86	0	High	High	High	High	High	High
385.81	38	0	High	High	High	High	High	High
385.8	30	2	High	High	High	High	High	High
385.4	52	53	High	High	High	High	High	High
375.1	27	11	High	High	High	High	High	High
369.1	51	0	High	High	High	High	High	High
368.7	29	0	High	High	High	High	High	High
363.22	55	0	High	High	High	High	High	High
362.7	26	0	High	High	High	High	High	High
357.38	31	33	High	High	High	High	High	High
355.61	15	6	High	High	High	High	High	High
352.61	41	0	High	High	High	High	High	High
349.83	6	0	High	High	High	High	High	High
346.1	6	1	High	High	High	High	High	High
345.01	6	1	High	High	High	High	High	High
340.55	34	0	High	High	High	High	High	High
339.97	17	0	High	High	High	High	High	High
332.33	36	1	High	High	High	High	High	High
327.88	7	4	High	High	High	High	High	High
325.89	49	18	High	High	High	High	High	High
325.32	75	72	High	High	High	High	High	High

323.43	5	0	High	High	High	High	High	High
322.8	11	0	High	High	High	High	High	High
322.62	30	0	High	High	High	High	High	High
318.9	73	0	High	High	High	High	High	High
304.21	9	0	High	High	High	High	High	High
302.01	6	0	High	High	High	High	High	High
300.11	25	0	High	High	High	High	High	High
298.3	25	12	High	High	High	High	High	High
296.72	15	0	High	High	High	High	High	High
294.62	13	0	High	High	High	High	High	High
294.05	49	0	High	High	High	High	High	High
293.84	16	14	High	High	High	High	High	High
292.23	5	1	High	High	High	High	High	High
287.48	16	8	High	High	High	High	High	High
275.31	17	0	High	High	High	High	High	High
273.67	29	28	High	High	High	High	High	High
272.88	28	0	High	High	High	High	High	High
271.85	18	8	High	High	High	High	High	High
271.1	30	0	High	High	High	High	High	High
269.48	30	5	High	High	High	High	High	High
267.67	13	0	High	High	High	High	High	High
245.55	21	21	High	High	High	High	High	High
244.4	24	0	High	High	High	High	High	High
242.55	27	17	High	High	High	High	High	High
240.5	21	0	High	High	High	High	High	High
233.08	18	0	High	High	High	High	High	High
232.9	32	0	High	High	High	High	High	High
230.53	72	0	High	High	High	High	High	High
223.07	24	0	High	High	High	High	High	High
223.05	15	0	High	High	High	High	High	High
218.79	33	29	High	High	High	High	High	High
217.62	11	0	High	High	High	High	High	High
215.07	14	0	High	High	High	High	High	High
213.79	18	16	High	High	High	High	High	High
204.55	15	0	High	High	High	High	High	High
204.26	3	1	High	High	High	High	High	High
203.83	24	0	High	High	High	High	High	High
203.74	24	0	High	High	High	High	High	High
203.7	15	0	High	High	High	High	High	High
201.89	3	0	High	High	High	High	High	High
197.82	29	0	High	High	High	High	High	High
191.85	4	0	High	High	High	High	High	High
186.2	20	0	High	High	High	High	High	High
185.26	30	0	High	High	High	High	High	High
184.14	19	0	High	High	High	High	High	High
181.92	45	3	High	High	High	High	High	High
181.76	17	0	High	High	High	High	High	High
179.82	27	0	High	High	High	High	High	High
178.15	21	0	High	High	High	High	High	High
175.43	15	0	High	High	High	High	High	High
173.92	18	0	High	High	High	High	High	High

173.5	44	0	High	High	High	High	High	High
172.55	21	0	High	High	High	High	High	High
170.54	30	0	High	High	High	High	High	High
169.82	8	0	High	High	High	High	High	High
169.8	35	12	High	High	High	High	High	High
168.82	20	0	High	High	High	High	High	High
168.46	25	0	High	High	High	High	High	High
168.3	12	0	High	High	High	High	High	High
166.97	14	0	High	High	High	High	High	High
166.65	20	0	High	High	High	High	High	High
165.45	17	0	High	High	High	High	High	High
165.11	14	0	High	High	High	High	High	High
165.08	21	0	High	High	High	High	High	High
164.8	12	9	High	High	High	High	High	High
163.19	15	1	High	High	High	High	High	High
162.38	24	1	High	High	High	High	High	High
161.84	25	0	High	High	High	High	High	High
160.99	16	0	High	High	High	High	High	High
158.14	10	0	High	High	High	High	High	High
158.12	41	0	High	High	High	High	High	High
158.09	25	23	High	High	High	High	High	High
155.05	23	1	High	High	High	High	High	High
154.22	16	0	High	High	High	High	High	High
154.13	20	1	High	High	High	High	High	High
153.69	14	0	High	High	High	High	High	High
152.27	16	0	High	High	High	High	High	High
152.2	11	0	High	High	High	High	High	High
149.96	6	1	High	High	High	High	High	High
148.32	42	0	High	High	High	High	High	High
147.77	16	13	High	High	High	High	High	High
146.79	42	0	High	High	High	High	High	High
144.89	7	0	High	High	High	High	High	High
144.64	17	0	High	High	High	High	High	High
138.58	13	0	High	High	High	High	High	High
138.53	9	0	High	High	High	High	High	High
138.53	22	0	High	High	High	High	High	High
138.42	15	0	High	High	High	High	High	High
137.78	12	0	High	High	High	High	High	High
137.06	19	0	High	High	High	High	High	High
135.48	39	3	High	High	High	High	High	High
135.44	26	3	High	High	High	High	High	High
134.93	10	1	High	High	High	High	High	High
134.92	24	0	High	High	High	High	High	High
133.53	24	21	High	High	High	High	High	High
132.95	34	1	High	High	High	High	High	High
132.88	24	5	High	High	High	High	High	High
132.54	18	2	High	High	High	High	High	High
132.44	17	0	High	High	High	High	High	High
132.37	7	0	High	High	High	High	High	High
131.14	19	1	High	High	High	High	High	High
130.72	10	1	High	High	High	High	High	High

129.86	22	0	High	High	High	High	High	High
129.84	18	1	High	High	High	High	High	High
129.67	19	0	High	High	High	High	High	High
129.26	14	0	High	High	High	High	High	High
124.08	7	0	High	High	High	High	High	High
122.96	10	0	High	High	High	High	High	High
122.75	20	0	High	High	High	High	High	High
121.98	26	0	High	High	High	High	High	High
120.5	9	0	High	High	High	High	High	High
120.47	18	0	High	High	High	High	High	High
120.26	22	0	High	High	High	High	High	High
119.75	20	0	High	High	High	High	High	High
119.08	4	0	High	High	High	High	High	High
118.87	9	0	High	High	High	High	High	High
118.27	21	0	High	High	High	High	High	High
117.18	12	0	High	High	High	High	High	High
116.82	20	5	High	High	High	High	High	High
116.6	19	0	High	High	High	High	High	High
114.79	19	0	High	High	High	High	High	High
114.37	18	0	High	High	High	High	High	High
113.04	11	0	High	High	High	High	High	High
112.28	25	1	High	High	High	High	High	High
111.29	22	14	High	High	High	High	High	High
109.51	27	7	High	High	High	High	High	High
109.08	19	1	High	High	High	High	High	High
107.88	24	10	High	High	High	High	High	High
107.56	17	10	High	High	High	High	High	High
104.61	29	9	High	High	High	High	High	High
104.46	8	0	High	High	High	High	High	High
104.24	19	0	High	High	High	High	High	High
103	17	0	High	High	High	High	High	High
102.43	20	3	High	High	High	High	High	High
101.06	12	0	High	High	High	High	High	High
101	14	0	High	High	High	High	High	High
100.16	7	2	High	High	High	High	High	High
99.34	38	0	High	High	High	High	High	High
99.07	8	0	High	High	High	High	High	High
98.2	5	0	High	High	High	High	High	High
98.06	10	0	High	High	High	High	High	High
97.86	20	1	High	High	High	High	High	High
97.47	5	0	High	High	High	High	High	High
97.27	23	0	High	High	High	High	High	High
96.59	9	0	High	High	High	High	High	High
94.37	23	0	High	High	High	High	High	High
93.59	20	0	High	High	High	High	High	High
93.17	12	0	High	High	High	High	High	High
92.72	19	0	High	High	High	High	High	High
92.1	21	0	High	High	High	High	High	High
91.45	17	0	High	High	High	High	High	High
91	22	0	High	High	High	High	High	High
90.59	15	0	High	High	High	High	High	High

90.59	9	0	High	High	High	High	High	High
90.31	14	0	High	High	High	High	High	High
90.17	5	0	High	High	High	High	High	High
89.95	29	1	High	High	High	High	High	High
89.11	9	0	High	High	High	High	High	High
88.98	9	0	High	High	High	High	High	High
88.76	12	11	High	High	High	High	High	High
88.35	18	5	High	High	High	High	High	High
88.21	10	0	High	High	High	High	High	High
88.11	16	11	High	High	High	High	High	High
87.19	14	0	High	High	High	High	High	High
86.85	20	18	High	High	High	High	High	High
86.26	19	0	High	High	High	High	High	High
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85.37	12	0	High	High	High	High	High	High
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83.93	12	0	High	High	High	High	High	High
83.83	17	1	High	High	High	High	High	High
83.55	23	0	High	High	High	High	High	High
82.69	3	0	High	High	High	High	High	High
82.35	19	0	High	High	High	High	High	High
82.26	16	8	High	High	High	High	High	High
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81.11	4	0	High	High	High	High	High	High
81.06	13	0	High	High	High	High	High	High
80.98	11	0	High	High	High	High	High	High
80.9	16	1	High	High	High	High	High	High
80.42	5	0	High	High	High	High	High	High
79.6	7	0	High	High	High	High	High	High
79.58	9	0	High	High	High	High	High	High
79.4	17	0	High	High	High	High	High	High
79.39	20	0	High	High	High	High	High	High
79.26	15	0	High	High	High	High	High	High
78.88	7	7	High	High	High	High	High	High
78.74	11	0	High	High	High	High	High	High
78.48	20	16	High	High	High	High	High	High
78.47	11	0	High	High	High	High	High	High
77.71	18	0	High	High	High	High	High	High
76.77	14	8	High	High	High	High	High	High
76.72	18	0	High	High	High	High	High	High
76.42	14	0	High	High	High	High	High	High
76.39	12	0	High	High	High	High	High	High
76.09	20	2	High	High	High	High	High	High
75.72	3	0	High	High	High	High	High	High
75.69	12	0	High	High	High	High	High	High
75.69	20	0	High	High	High	High	High	High
75.55	18	4	High	High	High	High	High	High
75.08	17	0	High	High	High	High	High	High
75.07	6	0	High	High	High	High	High	High
75.03	14	0	High	High	High	High	High	High
74.94	12	0	High	High	High	High	High	High

74.84	19	1	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
73.95	11	0	High	High	High	High	High	High
73.66	16	0	High	High	High	High	High	High
73.59	6	0	High	High	High	High	High	High
73.3	21	0	High	High	High	High	High	High
72.99	9	2	High	High	High	High	High	High
72.79	13	3	High	High	High	High	High	High
72.32	16	0	High	High	High	High	High	High
72.02	15	0	High	High	High	High	High	High
71.24	17	0	High	High	High	High	High	High
71.24	7	0	High	High	High	High	High	High
71.13	11	0	High	High	High	High	High	High
69.5	11	0	High	High	High	High	High	High
68.5	14	0	High	High	High	High	High	High
68.26	11	0	High	High	High	High	High	High
66.71	15	2	High	High	High	High	High	High
66.6	12	0	High	High	High	High	High	High
66.45	12	0	High	High	High	High	High	High
66.29	4	0	High	High	High	High	High	High
65.69	14	0	High	High	High	High	High	High
64.93	17	0	High	High	High	High	High	High
64.86	15	0	High	High	High	High	High	High
64.64	14	11	High	High	High	High	High	High
64.33	14	1	High	High	High	High	High	High
64.26	7	0	High	High	High	High	High	High
64.25	15	0	High	High	High	High	High	High
63.94	15	0	High	High	High	High	High	High
63.53	10	0	High	High	High	High	High	High
63	18	0	High	High	High	High	High	High
62.99	6	0	High	High	High	High	High	High
62.98	18	0	High	High	High	High	High	High
62.85	12	0	High	High	High	High	High	High
62.49	7	0	High	High	High	High	High	High
61.5	10	0	High	High	High	High	High	High
61.26	10	0	High	High	High	High	High	High
61	9	2	High	High	High	High	High	High
60.98	5	0	High	High	High	High	High	High
60.88	13	0	High	High	High	High	High	High
60.54	11	5	High	High	High	High	High	High
59.94	14	0	High	High	High	High	High	High
59.87	14	5	High	High	High	High	High	High
59.84	15	6	High	High	High	High	High	High
59.59	10	0	High	High	High	High	High	High
59.3	14	0	High	High	High	High	High	High
58.56	9	0	High	High	High	High	High	High
57.97	6	0	High	High	High	High	High	High
57.93	12	1	High	High	High	High	High	High
57.61	9	0	High	High	High	High	High	High
57.52	10	0	High	High	High	High	High	High
57.04	7	0	High	High	High	High	High	High
56.94	10	1	High	High	High	High	High	High

56.76	12	0	High	High	High	High	High	High
56.75	10	2	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
55.92	11	0	High	High	High	High	High	High
55.72	15	0	High	High	High	High	High	High
55.69	11	0	High	High	High	High	High	High
55.54	12	0	High	High	High	High	High	High
55.49	13	0	High	High	High	High	High	High
55.48	19	0	High	High	High	High	High	High
55.18	8	0	High	High	High	High	High	High
54.9	8	0	High	High	High	High	High	High
54.46	7	0	High	High	High	High	High	High
54.36	16	15	High	High	High	High	High	High
54.35	10	0	High	High	High	High	High	High
54.17	12	0	High	High	High	High	High	High
53.85	13	1	High	High	High	High	High	High
53.73	16	0	High	High	High	High	High	High
53.58	11	0	High	High	High	High	High	High
53.49	14	0	High	High	High	High	High	High
53.3	9	7	High	High	High	High	High	High
52.98	12	0	High	High	High	High	High	High
52.97	16	0	High	High	High	High	High	High
52.95	9	0	High	High	High	High	High	High
52.9	15	0	High	High	High	High	High	High
52.76	7	0	High	High	High	High	High	High
51.99	12	0	High	High	High	High	High	High
51.79	9	3	High	High	High	High	High	High
51.72	12	0	High	High	High	High	High	High
51.69	13	0	High	High	High	High	High	High
51.33	13	0	High	High	High	High	High	High
51.32	14	0	High	High	High	High	High	High
51.1	8	0	High	High	High	High	High	High
50.93	7	7	High	High	High	High	High	High
50.7	12	0	High	High	High	High	High	High
50.65	7	0	High	High	High	High	High	High
50.54	10	0	High	High	High	High	High	High
49.87	10	8	High	High	High	High	High	High
49.51	9	0	High	High	High	High	High	High
49.5	17	0	High	High	High	High	High	High
49.44	10	0	High	High	High	High	High	High
49.2	8	0	High	High	High	High	High	High
48.86	6	0	High	High	High	High	High	High
48.61	10	0	High	High	High	High	High	High
48.49	9	0	High	High	High	High	High	High
48.31	12	0	High	High	High	High	High	High
48.29	7	0	High	High	High	High	High	High
48.13	13	0	High	High	High	High	High	High
47.73	9	0	High	High	High	High	High	High
47.71	14	0	High	High	High	High	High	High
47.36	12	0	High	High	High	High	High	High
46.82	13	0	High	High	High	High	High	High
46.76	4	0	High	High	High	High	High	High

46.33	7	0	High	High	High	High	High	High
46.27	11	0	High	High	High	High	High	High
46.03	7	0	High	High	High	High	High	High
45.71	7	0	High	High	High	High	High	High
45.7	5	0	High	High	High	High	High	High
45.68	5	4	High	High	High	High	High	High
45.54	8	0	High	High	High	High	High	High
45.51	9	0	High	High	High	High	High	High
45.48	11	2	High	High	High	High	High	High
45.14	10	0	High	High	High	High	High	High
45	8	0	High	High	High	High	High	High
44.97	12	0	High	High	High	High	High	High
44.93	9	1	High	High	High	High	High	High
44.71	7	0	High	High	High	High	High	High
44.55	7	0	High	High	High	High	High	High
44.4	14	0	High	High	High	High	High	High
43.75	9	1	High	High	High	High	High	High
43.71	7	0	High	High	High	High	High	High
43.54	12	0	High	High	High	High	High	High
43.43	5	0	High	High	High	High	High	High
43.4	4	0	High	High	High	High	High	High
43.35	7	0	High	High	High	High	High	High
43.22	10	3	High	High	High	High	High	High
43.12	7	5	High	High	High	High	High	High
43.01	14	5	High	High	High	High	High	High
42.9	9	0	High	High	High	High	High	High
42.68	6	4	High	High	High	High	High	High
41.86	9	5	High	High	High	High	High	High
41.59	8	0	High	High	High	High	High	High
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41.18	9	0	High	High	High	High	High	High
41.1	8	0	High	High	High	High	High	High
40.93	12	0	High	High	High	High	High	High
40.68	6	0	High	High	High	High	High	High
40.61	12	8	High	High	High	High	High	High
40.16	6	0	High	High	High	High	High	High
40.12	12	0	High	High	High	High	High	High
39.98	13	0	High	High	High	High	High	High
39.94	9	0	High	High	High	High	High	High
39.84	6	0	High	High	High	High	High	High
39.65	5	0	High	High	High	High	High	High
39.43	13	0	High	High	High	High	High	High
39.35	3	0	High	High	High	High	High	High
39.28	13	0	High	High	High	High	High	High
39.28	6	4	High	High	High	High	High	High
39.23	7	0	High	High	High	High	High	High
38.98	10	0	High	High	High	High	High	High
38.84	13	0	High	High	High	High	High	High

38.84	9	0	High	High	High	High	High	High
38.69	9	0	High	High	High	High	High	High
38.64	8	0	High	High	High	High	High	High
38.59	9	0	High	High	High	High	High	High
38.55	6	0	High	High	High	High	High	High
38.51	7	0	High	High	High	High	High	High
38.39	4	2	High	High	High	High	High	High
38.1	8	0	High	High	High	High	High	High
37.9	7	0	High	High	High	High	High	High
37.77	7	0	High	High	High	High	High	High
37.74	6	0	High	High	High	High	High	High
37.62	4	3	High	High	High	High	High	High
37.61	4	0	High	High	High	High	High	High
37.54	10	0	High	High	High	High	High	High
37.54	3	1	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
37.43	8	0	High	High	High	High	High	High
37.4	11	0	High	High	High	High	High	High
37.39	8	0	High	High	High	High	High	High
37.22	10	0	High	High	High	High	High	High
37.18	9	0	High	High	High	High	High	High
37.08	10	0	High	High	High	High	High	High
36.97	3	0	High	High	High	High	High	High
36.97	2	0	High	High	High	High	High	High
36.82	10	0	High	High	High	High	High	High
36.81	6	0	High	High	High	High	High	High
36.47	8	0	High	High	High	High	High	High
36.46	7	0	High	High	High	High	High	High
36.22	7	0	High	High	High	High	High	High
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36.19	9	0	High	High	High	High	High	High
36.13	10	0	High	High	High	High	High	High
36.12	7	0	High	High	High	High	High	High
36.08	6	0	High	High	High	High	High	High
35.95	10	0	High	High	High	High	High	High
35.93	1	0	High	High	High	High	High	High
35.5	8	0	High	High	High	High	High	High
35.49	11	0	High	High	High	High	High	High
35.38	10	0	High	High	High	High	High	High
35.09	9	0	High	High	High	High	High	High
35.08	11	0	High	High	High	High	High	High
35.05	10	0	High	High	High	High	High	High
35.02	4	0	High	High	High	High	High	High
35.02	5	2	High	High	High	High	High	High
34.93	9	0	High	High	High	High	High	High
34.75	12	0	High	High	High	High	High	High
34.69	8	0	High	High	High	High	High	High
34.38	7	0	High	High	High	High	High	High
34.34	9	2	High	High	High	High	High	High
34.31	7	0	High	High	High	High	High	High
34.17	9	1	High	High	High	High	High	High
34.07	9	0	High	High	High	High	High	High

33.92	4	0	High	High	High	High	High	High
33.86	3	0	High	High	High	High	High	High
33.64	5	0	High	High	High	High	High	High
33.41	7	0	High	High	High	High	High	High
33.36	10	0	High	High	High	High	High	High
33.29	6	0	High	High	High	High	High	High
33.27	4	1	High	High	High	High	High	High
33.23	7	0	High	High	High	High	High	High
32.96	2	0	High	High	High	High	High	High
32.75	9	0	High	High	High	High	High	High
32.73	8	0	High	High	High	High	High	High
32.62	9	0	High	High	High	High	High	High
32.54	4	2	High	High	High	High	High	High
32.53	7	0	High	High	High	High	High	High
32.51	3	0	High	High	High	High	High	High
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32.1	4	1	High	High	High	High	High	High
32.03	6	0	High	High	High	High	High	High
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31.97	10	0	High	High	High	High	High	High
31.94	5	1	High	High	High	High	High	High
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30.61	7	0	High	High	High	High	High	High
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30.44	9	0	High	High	High	High	High	High
30.43	2	0	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
30.42	9	2	High	High	High	High	High	High
30.06	5	0	High	High	High	High	High	High
30.01	10	0	High	High	High	High	High	High
29.97	8	0	High	High	High	High	High	High
29.89	10	0	High	High	High	High	High	High
29.89	8	0	High	High	High	High	High	High
29.83	10	5	High	High	High	High	High	High
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29.74	8	0	High	High	High	High	High	High
29.49	3	0	High	High	High	High	High	High
29.44	9	0	High	High	High	High	High	High
29.32	3	0	High	High	High	High	High	High
29.23	7	0	High	High	High	High	High	High

29.23	4	0	High	High	High	High	High	High
29.13	5	0	High	High	High	High	High	High
29.01	7	0	High	High	High	High	High	High
29.01	3	0	High	High	High	High	High	High
28.95	3	0	High	High	High	High	High	High
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28.86	7	0	High	High	High	High	High	High
28.86	2	0	High	High	High	High	High	High
28.83	9	0	High	High	High	High	High	High
28.74	6	0	High	High	High	High	High	High
28.74	8	0	High	High	High	High	High	High
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28.65	3	0	High	High	High	High	High	High
28.55	4	0	High	High	High	High	High	High
28.48	3	1	High	High	High	High	High	High
28.32	4	3	High	High	High	High	High	High
28.28	3	0	High	High	High	High	High	High
27.97	2	0	High	High	High	High	High	High
27.79	7	0	High	High	High	High	High	High
27.75	2	0	High	High	High	High	High	High
27.75	2	0	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
27.74	5	0	High	High	High	High	High	High
27.71	3	1	High	High	High	High	High	High
27.67	9	0	High	High	High	High	High	High
27.5	2	0	High	High	High	High	High	High
27.39	3	1	High	High	High	High	High	High
27.35	3	2	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
27.29	4	0	High	High	High	High	High	High
27.22	9	0	High	High	High	High	High	High
27.13	4	0	High	High	High	High	High	High
27.07	3	0	High	High	High	High	High	High
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26.85	3	2	High	High	High	High	High	High
26.71	2	0	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
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26.68	7	0	High	High	High	High	High	High
26.57	6	5	High	High	High	High	High	High
26.43	3	0	High	High	High	High	High	High
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26.11	2	0	High	High	High	High	High	High
26.1	7	0	High	High	High	High	High	High
26.09	2	0	High	High	High	High	High	High
26	5	0	High	High	High	High	High	High
25.98	8	0	High	High	High	High	High	High
25.98	4	0	High	High	High	High	High	High

25.94	8	0	High	High	High	High	High	High
25.84	7	0	High	High	High	High	High	High
25.8	3	0	High	High	High	High	High	High
25.76	3	0	High	High	High	High	High	High
25.56	3	0	High	High	High	High	High	High
25.55	2	0	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
25.47	7	0	High	High	High	High	High	High
25.4	3	0	High	High	High	High	High	High
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25.29	2	0	High	High	High	High	High	High
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24.78	7	0	High	High	High	High	High	High
24.69	5	0	High	High	High	High	High	High
24.59	5	0	High	High	High	High	High	High
24.57	8	0	High	High	High	High	High	High
24.56	5	0	High	High	High	High	High	High
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24.51	5	2	High	High	High	High	High	High
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24.07	6	0	High	High	High	High	High	High
24.03	9	0	High	High	High	High	High	High
24.01	8	0	High	High	High	High	High	High
24	5	1	High	High	High	High	High	High
23.97	4	1	High	High	High	High	High	High
23.79	3	0	High	High	High	High	High	High
23.78	6	2	High	High	High	High	High	High
23.78	8	0	High	High	High	High	High	High
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23.66	6	0	High	High	High	High	High	High
23.65	2	0	High	High	High	High	High	High
23.62	2	0	High	High	High	High	High	High
23.44	6	0	High	High	High	High	High	High

23.43	2	0	High	High	High	High	High	High
23.41	6	0	High	High	High	High	High	High
23.38	2	0	High	High	High	High	High	High
23.32	5	0	High	High	High	High	High	High
23.21	3	0	High	High	High	High	High	High
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23.08	3	1	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
23.08	5	0	High	High	High	High	High	High
23.03	3	1	High	High	High	High	High	High
22.99	6	5	High	High	High	High	High	High
22.93	2	0	High	High	High	High	High	High
22.9	8	0	High	High	High	High	High	High
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22.82	2	0	High	High	High	High	High	High
22.73	8	0	High	High	High	High	High	High
22.64	5	1	High	High	High	High	High	High
22.6	5	0	High	High	High	High	High	High
22.55	4	0	High	High	High	High	High	High
22.52	2	0	High	High	High	High	High	High
22.51	7	0	High	High	High	High	High	High
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22.16	5	0	High	High	High	High	High	High
22.05	7	0	High	High	High	High	High	High
22.01	3	1	High	High	High	High	High	High
22	8	5	High	High	High	High	High	High
21.95	4	0	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
21.94	6	1	High	High	High	High	High	High
21.93	6	0	High	High	High	High	High	High
21.82	2	0	High	High	High	High	High	High
21.81	6	0	High	High	High	High	High	High
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21.74	7	0	High	High	High	High	High	High
21.74	2	0	High	High	High	High	High	High
21.72	3	0	High	High	High	High	High	High
21.7	9	0	High	High	High	High	High	High

21.67	2	0	High	High	High	High	High	High
21.65	5	0	High	High	High	High	High	High
21.59	3	0	High	High	High	High	High	High
21.58	8	0	High	High	High	High	High	High
21.51	6	0	High	High	High	High	High	High
21.5	3	0	High	High	High	High	High	High
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21.44	7	0	High	High	High	High	High	High
21.44	7	0	High	High	High	High	High	High
21.41	6	0	High	High	High	High	High	High
21.36	4	0	High	High	High	High	High	High
21.35	3	0	High	High	High	High	High	High
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20.07	5	0	High	High	High	High	High	High
19.95	4	0	High	High	High	High	High	High
19.94	5	0	High	High	High	High	High	High
19.94	4	0	High	High	High	High	High	High

19.92	3	0	High	High	High	High	High	High
19.89	7	0	High	High	High	High	High	High
19.84	6	0	High	High	High	High	High	High
19.77	6	0	High	High	High	High	High	High
19.76	3	1	High	High	High	High	High	High
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19.34	5	0	High	High	High	High	High	High
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18.05	7	0	High	High	High	High	High	High
18.04	2	0	High	High	High	High	High	High
18.01	3	0	High	High	High	High	High	High
18	3	0	High	High	High	High	High	High
17.93	5	0	High	High	High	High	High	High
17.89	5	0	High	High	High	High	High	High
17.82	6	0	High	High	High	High	High	High
17.78	3	0	High	High	High	High	High	High
17.76	3	0	High	High	High	High	High	High
17.74	5	1	High	High	High	High	High	High
17.68	2	0	High	High	High	High	High	High

17.68	3	0	High	High	High	High	High	High
17.68	3	1	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
17.67	3	0	High	High	High	High	High	High
17.65	7	0	High	High	High	High	High	High
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17.46	3	1	High	High	High	High	High	High
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17.28	3	0	High	High	High	High	High	High
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17.09	5	0	High	High	High	High	High	High
17.09	2	0	High	High	High	High	High	High
17.06	4	0	High	High	High	High	High	High
17	7	0	High	High	High	High	High	High
16.95	5	0	High	High	High	High	High	High
16.93	6	0	High	High	High	High	High	High
16.9	6	0	High	High	High	High	High	High
16.89	6	0	High	High	High	High	High	High
16.81	3	0	High	High	High	High	High	High
16.8	5	0	High	High	High	High	High	High
16.77	4	0	High	High	High	High	High	High
16.7	2	0	High	High	High	High	High	High
16.7	5	0	High	High	High	High	High	High
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16.44	4	0	High	High	High	High	High	High
16.4	3	0	High	High	High	High	High	High
16.39	5	0	High	High	High	High	High	High
16.37	2	0	High	High	High	High	High	High

16.36	4	0	High	High	High	High	High	High
16.24	6	0	High	High	High	High	High	High
16.22	3	0	High	High	High	High	High	High
16.2	3	0	High	High	High	High	High	High
16.18	4	0	High	High	High	High	High	High
16.07	3	0	High	High	High	High	High	High
16.07	3	1	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
15.97	4	0	High	High	High	High	High	High
15.95	6	0	High	High	High	High	High	High
15.93	2	0	High	High	High	High	High	High
15.9	4	0	High	High	High	High	High	High
15.9	4	0	High	High	High	High	High	High
15.89	2	0	High	High	High	High	High	High
15.87	4	0	High	High	High	High	High	High
15.85	3	0	High	High	High	High	High	High
15.78	2	0	High	High	High	High	High	High
15.73	3	1	High	High	High	High	High	High
15.71	3	0	High	High	High	High	High	High
15.67	3	0	High	High	High	High	High	High
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15.23	4	0	High	High	High	High	High	High
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15.01	5	0	High	High	High	High	High	High
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13.09	3	0	High	High	High	High	High	High
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12.61	3	0	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
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12.28	3	0	High	High	High	High	High	High
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11.08	1	0	High	High	High	High	High	High
11.06	3	1	High	High	High	High	High	High
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10.99	4	0	High	High	High	High	High	High
10.97	4	0	High	High	High	High	High	High
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10.76	3	0	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
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10.73	2	0	High	High	High	High	High	High
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10.51	2	0	High	High	High	High	High	High

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10.43	3	0	High	High	High	High	High	High
10.39	2	0	High	High	High	High	High	High
10.37	2	0	High	High	High	High	High	High
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10.22	3	0	High	High	High	High	High	High
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9.86	3	1	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found
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9.69	4	0	High	High	High	High	High	High
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9.49	2	0	High	High	High	High	High	High
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9	3	0	High	High	High	High	High	High
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8.98	3	0	High	High	High	High	High	High
8.97	2	0	High	High	High	High	High	High
8.97	2	0	High	High	High	High	High	High

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8.61	2	0	High	High	High	High	High	High
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8.37	3	0	High	High	High	High	High	High
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# Protein	control_w	case_huan	case_hou	control_w	control_q	case_shu	Group_cas	Group_cas
1	126.8	85.5	77.4	118.3	120.3	71.8	78.23333	1
1	173.4	91.7	60.7	93.7	121.3	59.2	70.53333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	127.8	149.8	65.6	69.8	135	51.9	89.1	1
1	117.6	145.9	53.1	36	210.3	37	78.66667	1
1	94	110.4	95	116.9	60.5	123.4	109.6	1
1	91.1	99.7	105.4	117	64.6	122.2	109.1	1
1	93.1	105.8	76.6	100	157.6	67	83.13333	1
1	96.3	107.8	72.1	98.6	154.3	71	83.63333	1
1	145.4	95.9	71.7	98.3	108	80.8	82.8	1
1	118.6	125.3	64.9	94.1	97.2	99.9	96.7	1
1	119.7	91.3	114.5	78.6	108.2	87.7	97.83333	1
1	152.6	100.7	77.9	80.5	104.5	83.8	87.46667	1
1	69.7	69.8	101.8	120.1	77.1	161.4	111	1
1	132.3	178.3	63.9	55	89.5	81.1	107.7667	1
1	70.4	59.2	106.3	120.6	66.1	177.4	114.3	1
1	79.8	111.2	78.5	99.6	130.1	100.9	96.86667	1
1	83.7	79.4	127.8	123.8	75.2	110.1	105.7667	1
1	66.6	99.1	125.9	92	85.1	131.3	118.7667	1
1	89.1	87.4	109.3	97.6	120.4	96.2	97.63333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	110.9	90.2	83.3	122.3	86.5	106.7	93.4	1
1	94.2	85.8	95.9	88	159.6	76.5	86.06667	1
1	113.3	104.6	86	98.9	98.1	99	96.53333	1
1	145.6	141.5	64.6	70	122.2	56.1	87.4	1
1	120.5	130	63	87.4	102.3	96.9	96.63333	1
1	243.6	110.5	56.7	48.2	100.3	40.7	69.3	1
1	54.9	55.4	279.7	83	61.2	65.8	133.6333	1
1	72.6	119.2	97.7	98	121	91.5	102.8	1
1	116.9	127	63.6	93.1	102.2	97.1	95.9	1
1	95.9	97.9	89.9	104.5	99.5	112.3	100.0333	1
1	93.7	165.7	104.6	56.5	95.1	84.3	118.2	1
1	95.6	150.6	71	79.6	143.4	59.9	93.83333	1
1	80.1	106.1	111.2	129.2	67.9	105.4	107.5667	1
1	96.1	104.4	115.4	101.1	84.4	98.6	106.1333	1
1	115.6	106.7	91.4	103.7	107.7	74.9	91	1
1	72	114.4	97.3	90.8	149.5	75.9	95.86667	1
1	164.7	133.5	52	61.8	139.7	48.3	77.93333	1
1	74.8	94.6	85.4	102.2	158.4	84.5	88.16667	1
1	79.2	83.3	86.5	114.3	138.5	98.2	89.33333	1
1	120.9	142.5	57.1	83.1	101.8	94.4	98	1
1	98	79.4	95.4	146.7	98.2	82.3	85.7	1
1	88.4	77.1	140.9	94	63.4	136.3	118.1	1
1	69	89.7	126.4	117.9	79.2	117.9	111.3333	1
1	64.3	53.6	158.9	100.6	56.9	165.6	126.0333	1
1	86.5	86.9	98.2	120.5	103.8	104.1	96.4	1
1	114.2	133	88.9	93.3	99.2	71.4	97.76667	1
1	94.1	81.3	86.8	117.5	102.4	117.9	95.33333	1
1	72.4	79.8	144.7	122.8	123.3	57	93.83333	1
1	87.9	81.6	87.2	158.7	79	105.5	91.43333	1

1	61.4	54.3	99.9	175.8	56.4	152.1	102.1	1
1	112.4	174.3	63.4	63.8	136.7	49.4	95.7	1
1	79.8	143.5	85.6	72.8	162.7	55.6	94.9	1
1	71.9	114.8	103.9	107.6	120.4	81.3	100	1
1	46.5	91	117.6	177.6	72.5	94.8	101.1333	1
1	140.7	138.9	83.6	73.5	104.8	58.4	93.63333	1
1	60.1	52.5	160	100.8	52	174.6	129.0333	1
1	73.7	91.5	117.3	118	86.6	112.9	107.2333	1
1	74.7	92.9	116.6	134	63.5	118.3	109.2667	1
1	78.4	73.8	100.4	112.1	81.3	154.1	109.4333	1
1	63.2	57.3	95.6	150.5	61	172.4	108.4333	1
1	69.4	86.6	83.2	130.2	85.7	145	104.9333	1
1	67	69	122.2	135.5	78.7	127.6	106.2667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	76.6	75.8	122.3	128.1	76.4	120.7	106.2667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	59.1	50.3	165.6	103	51.4	170.6	128.8333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	121.5	107.2	78.8	95	104.6	92.9	92.96667	1
1	56.2	58.4	73.2	131.2	59.6	221.3	117.6333	1
1	62.3	65.5	75.3	111.4	64	221.5	120.7667	1
1	114.1	91.7	130.3	81.8	112.5	69.6	97.2	1
1	53.4	43.1	74.3	267	54.2	108.1	75.16667	1
1	105.2	83.4	93.4	123.3	115.8	78.8	85.2	1
1	123.1	158.5	56.1	61.1	148.8	52.3	88.96667	1
1	112.1	224.7	36.5	40.8	151.7	34.3	98.5	1
1	85.4	127.5	72.2	93	148.5	73.4	91.03333	1
1	66.9	98.9	117.9	120.1	76.6	119.7	112.1667	1
1	31.7	27.1	206.4	93.2	31	210.5	148	1
1	58.9	55.6	223	80.9	66	115.5	131.3667	1
1	97	109.3	71.7	80.9	86.9	154.3	111.7667	1
1	115.6	104.8	92.4	80.5	139.1	67.5	88.23333	1
1	109.4	73.1	121.2	89	115.4	91.9	95.4	1
1	69.1	69.9	130.1	134.8	68.4	127.7	109.2333	1
1	86.5	109.5	102	110.4	102.6	89	100.1667	1
1	88.3	114.1	118.8	85.9	86.4	106.5	113.1333	1
1	71.3	76	107.2	109.6	73.5	162.4	115.2	1
1	111.5	91.8	98.8	110.3	110	77.7	89.43333	1
1	110.5	60.6	91.5	140.3	78.6	118.6	90.23333	1
1	75.7	100.7	123	104.2	94.1	102.4	108.7	1
1	98.2	132.1	79.1	100.9	70.1	119.6	110.2667	1
1	61.4	52.2	161	127.3	62.2	136	116.4	1
1	65.9	90.4	111.5	117.9	100.9	113.4	105.1	1
1	67	116.3	130.5	105.1	79.4	101.8	116.2	1
1	73.5	75.3	105.1	117.4	87.9	140.9	107.1	1
1	62	61.4	173.7	122.9	70.4	109.6	114.9	1
1	80.2	97.9	105.4	113.9	80.2	122.4	108.5667	1
1	63.7	64.6	124.2	113.7	76.5	157.3	115.3667	1
1	63.8	84.9	100.4	128.8	78.2	143.9	109.7333	1
1	84	77.2	143.5	127.9	90.5	76.8	99.16667	1
1	99.9	106.1	74	82.1	87.6	150.3	110.1333	1

1	69.5	78.4	83.3	125	80.6	163.2	108.3	1
1	78.4	75.3	105	132.7	86.5	122.2	100.8333	1
1	82.2	99.7	109	94.2	122	93	100.5667	1
1	118.2	122.2	76.8	82.1	87	113.7	104.2333	1
1	128.5	126.6	55.1	53.1	141.6	95.1	92.26667	1
1	107.9	91.4	102.1	96.3	99.3	102.9	98.8	1
1	72.4	74.7	119.6	131.2	74.4	127.6	107.3	1
1	104.5	96.8	98.9	103.9	73.3	122.5	106.0667	1
1	99.3	90.9	94	102.5	89.1	124.3	103.0667	1
1	58.5	56.8	186.2	92.4	59.3	146.8	129.9333	1
1	61.5	58.5	169.9	117.6	73	119.5	115.9667	1
1	97.5	88	97.8	102.6	89.5	124.6	103.4667	1
1	61	94.6	114.7	161	75.3	93.4	100.9	1
1	87.5	94.1	100.9	100.2	81.6	135.7	110.2333	1
1	93.9	76.2	123.9	131.4	67	107.6	102.5667	1
1	89.3	89.3	107.9	138.5	74.6	100.5	99.23333	1
1	80.5	111.9	104	126	69.8	107.8	107.9	1
1	62.9	64.4	161.3	87.1	66.3	158	127.9	1
1	94.2	106.5	95.9	120.4	99.6	83.4	95.26667	1
1	77.4	105.2	109	110	93.6	104.7	106.3	1
1	109.2	92.7	162.1	69.8	79.1	87.2	114	1
1	91.5	90.8	99.7	105.1	108.5	104.4	98.3	1
1	76.8	68.1	135.3	93	66.2	160.6	121.3333	1
1	67.8	61.3	167.9	97.3	84.1	121.6	116.9333	1
1	121.8	106.7	85.6	99	96.4	90.6	94.3	1
1	122.9	117.6	92.8	90.1	82.1	94.5	101.6333	1
1	120.2	89.8	85.8	110	119.8	74.4	83.33333	1
1	83.3	80.2	103.1	112.6	83.2	137.7	107	1
1	78.8	92.2	110.8	102.5	81.6	134.1	112.3667	1
1	101.6	105.6	98.5	86.2	128.9	79.1	94.4	1
1	65.4	58.1	93.2	129.9	110.1	143.2	98.16667	1
1	124.4	129	68.5	67.6	107.6	102.9	100.1333	1
1	102.8	82.7	95.1	117.8	129.7	72	83.26667	1
1	122.8	113.7	116.6	76.9	85.1	84.8	105.0333	1
1	117.7	126	81.5	83.1	124.3	67.4	91.63333	1
1	120.8	120.4	78.4	77.6	83.8	119	105.9333	1
1	142.6	119.9	76.6	80.3	97	83.7	93.4	1
1	82.9	120.4	89.1	92.1	133.2	82.3	97.26667	1
1	84.6	91.9	106.9	97.8	104.1	114.7	104.5	1
1	119.5	104.4	74.8	106.6	109.1	85.5	88.23333	1
1	45.1	47.5	108.2	140.9	50.9	207.3	121	1
1	59.1	75.6	97.6	153.6	57.9	156.3	109.8333	1
1	123.3	200.8	74.5	63.3	83.5	54.7	110	1
1	216.4	118.4	57	49.8	103.3	55.2	76.86667	1
1	101.1	111.4	73	85	85.4	144.1	109.5	1
1	90	82.5	86.7	94.6	72	174.2	114.4667	1
1	84.9	107.2	100.6	103.3	105.5	98.5	102.1	1
1	103.5	148.2	87.2	84.5	113.3	63.2	99.53333	1
1	103.3	122	70.2	88.1	130.4	86.1	92.76667	1
1	105.9	106.8	88.9	91.6	124.7	82	92.56667	1
1	102.8	110.1	89.6	95.6	82.1	119.8	106.5	1

1	104.8	98.6	84.5	99.3	118.9	93.9	92.33333	1
1	93.6	100.9	90	113.3	105.5	96.7	95.86667	1
1	70.1	70	112.7	108	79.9	159.3	114	1
1	69.1	47.7	146	103.7	162.9	70.6	88.1	1
1	85.7	90.2	145.2	87.3	82.7	109	114.8	1
1	128	109.7	81.6	85.1	122.6	73.1	88.13333	1
1	108.1	119	83.7	90.5	100.3	98.6	100.4333	1
1	80.4	78.8	110.3	92.8	79.6	158.1	115.7333	1
1	80.4	86.8	97.8	101.4	139.1	94.5	93.03333	1
1	60.2	54.4	199.6	100.1	74.1	111.7	121.9	1
1	69.5	63.2	170.1	111.7	91.2	94.3	109.2	1
1	67.7	72.9	143.2	125.3	75	115.8	110.6333	1
1	84.7	87.4	89.7	141.7	89.1	107.5	94.86667	1
1	235	115.7	57.7	68	68.7	54.8	76.06667	1
1	85.1	103.2	110.5	107.2	97.7	96.4	103.3667	1
1	131.8	78.8	88.4	121.5	101.4	78	81.73333	1
1	87.1	88.8	128.7	124.9	57.7	112.8	110.1	1
1	134.9	129.9	87.2	71.8	99.4	76.8	97.96667	1
1	140.4	126.5	98.2	71.5	77.5	85.9	103.5333	1
1	97.9	104.3	88.9	105	93.1	110.8	101.3333	1
1	81.6	81.9	138.3	121.2	81.1	95.8	105.3333	1
1	114.4	91.4	83.6	127.1	108.3	75.2	83.4	1
1	62.5	67.2	153.5	126.9	75.7	114.2	111.6333	1
1	114	104.4	81.6	88.4	130.4	81.2	89.06667	1
1	82.5	77.1	160.8	130.8	73.3	75.5	104.4667	1
1	74.2	57.8	130.5	121.6	70.9	145	111.1	1
1	59	288.3	50	60.8	46.2	95.7	144.6667	1
1	74.8	65	101.6	125.9	108.2	124.5	97.03333	1
1	99	91.3	92.1	100.5	78.8	138.3	107.2333	1
1	93	93.6	91.2	123.3	68.9	130.1	104.9667	1
1	79.7	76.6	83.5	136.4	79.6	144.2	101.4333	1
1	157.9	105.8	67.2	80	117.7	71.4	81.46667	1
1	73.2	68.2	143.9	96.1	87.8	130.8	114.3	1
1	104	151.6	75.6	86.1	109.1	73.5	100.2333	1
1	83.9	76.6	112.8	107.1	73.8	145.7	111.7	1
1	133.7	124.8	83.1	78	107.2	73.4	93.76667	1
1	75.2	114.6	148.9	71.4	87.4	102.5	122	1
1	86.1	91.7	85.8	88	135.3	113	96.83333	1
1	145.1	104	99.9	66.1	104.4	80.6	94.83333	1
1	95.1	87.6	91.1	98.5	72.9	154.7	111.1333	1
1	79.8	91.3	105.7	113.2	95.3	114.7	103.9	1
1	95.8	123.1	93.8	97.5	98.3	91.5	102.8	1
1	85.2	90	77.2	122.5	90.5	134.5	100.5667	1
1	76.6	69.8	159.6	94	75.7	124.4	117.9333	1
1	80	85.4	112.5	110.9	79.9	131.2	109.7	1
1	119.1	79.6	91.6	126.6	105.6	77.6	82.93333	1
1	88	97.7	103.6	104.4	99.7	106.7	102.6667	1
1	72.1	72.7	126.1	141	62.9	125.3	108.0333	1
1	128.2	113.6	68.8	96.5	119	73.9	85.43333	1
1	89.5	103.5	92.7	114.4	117.4	82.5	92.9	1
1	118.8	139.9	71.8	85.4	95.1	89.1	100.2667	1

1	89.6	77	128.2	112.6	79.9	112.8	106	1
1	90.6	93.8	106.1	92.1	113.5	103.8	101.2333	1
1	115.4	73.7	94.4	127.1	104	85.4	84.5	1
1	141.9	105.8	92.5	61.1	82.3	116.2	104.8333	1
1	100.8	122.8	72.1	88.5	143.6	72.2	89.03333	1
1	167.7	110.7	71.9	78.7	113.3	57.8	80.13333	1
1	59.5	57.5	170.3	125.4	66	121.2	116.3333	1
1	95.3	105.9	71.4	86.3	90.6	150.6	109.3	1
1	102.5	114.4	64.4	81.2	142	95.5	91.43333	1
1	37.1	31.1	58.9	28.6	385.3	58.9	49.63333	1
1	66.7	91.8	115.7	104.3	112	109.6	105.7	1
1	119.5	128.3	62.1	70.7	165	54.4	81.6	1
1	100.9	104	79.9	119.1	112.6	83.5	89.13333	1
1	109.9	116.2	79.2	85.9	98	110.7	102.0333	1
1	66.7	57.2	181.1	98.3	63	133.8	124.0333	1
1	118.8	98.6	76.7	96.3	130.5	79.1	84.8	1
1	133.8	138.8	71.5	70.5	128.2	57.2	89.16667	1
1	131.8	138.5	90.7	71.1	81.4	86.6	105.2667	1
1	68.9	69.4	97	117.2	83.3	164.2	110.2	1
1	59.8	63.3	178	114.2	71.4	113.3	118.2	1
1	60.8	55.4	167.1	127.4	70.1	119.3	113.9333	1
1	65	91.1	124.8	107.5	95.7	115.9	110.6	1
1	68.3	126.7	88.8	129.1	68.3	118.8	111.4333	1
1	141.7	89.4	104.3	104.3	87.9	72.4	88.7	1
1	121.3	83.4	88	130.8	95.8	80.7	84.03333	1
1	85.7	94.5	98.3	101.1	83.2	137.1	109.9667	1
1	68.3	73.9	118.9	86.9	72.8	179.2	124	1
1	86.3	78	100.4	106.4	77.2	151.6	110	1
1	65.5	49.7	180.1	93.6	65.6	145.4	125.0667	1
1	93	108.8	94.5	92.9	102.5	108.2	103.8333	1
1	111.8	116.9	113.3	87.1	94	77.1	102.4333	1
1	77.6	91.1	115.6	94.8	116.2	104.6	103.7667	1
1	146.8	98	79.4	65.6	146.8	63.3	80.23333	1
1	73.7	82.1	128.4	106.9	85	123.8	111.4333	1
1	107.2	81.6	105.3	156.8	59.8	89.3	92.06667	1
1	82.7	73	114.4	106.7	80.7	142.4	109.9333	1
1	104.2	127.8	97	71	122.9	77.1	100.6333	1
1	107.4	107.5	92.4	87	130	75.7	91.86667	1
1	96.1	82.2	122.6	103.7	118.6	76.8	93.86667	1
1	89.5	87.3	121.3	92.9	84.5	124.5	111.0333	1
1	74.7	127.1	67.6	83.3	174.3	73	89.23333	1
1	88.4	100.3	110.3	99	79.4	122.5	111.0333	1
1	85.4	69	127.2	95.5	82.7	140.2	112.1333	1
1	72.4	66.2	165.4	113.7	71	111.4	114.3333	1
1	110.8	99.7	105.1	111.7	64.7	107.9	104.2333	1
1	102.8	157.8	52.8	61.6	161.7	63.3	91.3	1
1	92.2	103.8	101	95.8	94.8	112.4	105.7333	1
1	87.8	92.6	108.7	105.9	102.3	102.7	101.3333	1
1	105.4	110.7	104.4	95.9	86.9	96.7	103.9333	1
1	88.2	66.5	135	144.4	78.4	87.6	96.36667	1
1	77.9	80.9	109	105	78.5	148.8	112.9	1

1	77.2	71.8	162	132.3	76.7	80	104.6	1
1	71	74.8	146.5	115.6	81.8	110.3	110.5333	1
1	83.5	95.1	131.8	121.6	57.3	110.7	112.5333	1
1	78.7	83.4	100.7	114	100.8	122.4	102.1667	1
1	126	115.6	69.3	65.9	110.3	112.9	99.26667	1
1	143.6	102.3	81.7	94.8	98.1	79.5	87.83333	1
1	57.3	60.5	165.7	103.2	65.9	147.4	124.5333	1
1	102.4	106.9	93.4	96.6	100.8	99.9	100.0667	1
1	87.3	99.8	118	91	116.2	87.7	101.8333	1
1	84.7	86.2	112.7	103.8	82	130.5	109.8	1
1	72.2	89.7	83.1	105.8	152.3	96.9	89.9	1
1	88.4	89	81.2	78.3	86.9	176.2	115.4667	1
1	100.8	91.6	87.3	105.5	118.3	96.4	91.76667	1
1	91.5	88.4	103.1	104.6	86.5	125.8	105.7667	1
1	173.2	77.4	81.7	75.7	126.1	66	75.03333	1
1	138.6	74.4	74.4	111.2	94.5	107	85.26667	1
1	79.9	53.7	44.8	167.5	59.3	194.8	97.76667	1
1	96.5	161.2	99.5	62.2	108	72.8	111.1667	1
1	90.1	90.9	93	103.3	77.2	145.5	109.8	1
1	90	82.8	111.2	119.3	82	114.8	102.9333	1
1	75.8	82.7	70.9	71.3	71.6	227.7	127.1	1
1	82.6	83.2	115.2	108	89.5	121.5	106.6333	1
1	121	109.1	120.8	75.3	104.7	69	99.63333	1
1	101.8	118.2	99.4	83.1	114	83.5	100.3667	1
1	75.5	92.8	114	110.8	106	100.9	102.5667	1
1	123.5	98.3	89.7	86.4	108.1	94.1	94.03333	1
1	55.7	53.1	183.8	123.8	62.4	121.2	119.3667	1
1	117.9	120.3	97.3	86.8	104.5	73.2	96.93333	1
1	95.3	122	114	64.6	105.6	98.5	111.5	1
1	67	90.9	134	115.8	105.8	86.5	103.8	1
1	87.8	91.5	118.6	103.9	86.2	112.1	107.4	1
1	169	133	69.5	70.3	101.7	56.5	86.33333	1
1	91.4	80.4	111.9	116.7	94.4	105.2	99.16667	1
1	71.7	63.5	131.2	89	63.7	181	125.2333	1
1	70.1	61.8	131.3	107.5	106.3	123	105.3667	1
1	114.7	78.3	81.7	148.2	104.4	72.7	77.56667	1
1	82.1	99.2	120.6	101.9	103.4	92.8	104.2	1
1	86.5	88.8	76.5	108.3	154.9	84.9	83.4	1
1	88.7	84.6	127.2	130.3	70.7	98.5	103.4333	1
1	127.7	110.6	95.9	84.1	101.4	80.3	95.6	1
1	106.7	131	74	88.8	107.5	92	99	1
1	74.5	69.5	159.7	112.2	81.1	103	110.7333	1
1	100.1	94.4	101.9	102.4	95.7	105.4	100.5667	1
1	129.4	96.5	97.6	123.7	112.6	40.1	78.06667	1
1	63.8	68.6	139.2	116.2	94.6	117.6	108.4667	1
1	82.9	84.7	120.2	107.3	83.3	121.6	108.8333	1
1	80.1	104.1	106.1	101.8	105.2	102.7	104.3	1
1	77.2	83.7	165.2	101.6	91.1	81.3	110.0667	1
1	158.5	156.3	60.3	65.1	104.5	55.3	90.63333	1
1	80.2	80.6	102.3	101.6	85.5	149.8	110.9	1
1	166.5	86.6	85.1	77.1	92	92.7	88.13333	1

1	93.6	97.6	90.9	112.9	97	108.1	98.86667	1
1	68.9	62.8	82.3	133.1	62.5	190.5	111.8667	1
1	69.4	87	73.5	107.6	72.6	189.9	116.8	1
1	128.2	123.8	87.6	85	104.2	71.2	94.2	1
1	99.7	89.1	106.8	100.3	86.9	117.2	104.3667	1
1	52.4	58.1	104.2	136.1	66.8	182.4	114.9	1
1	82.2	100.4	110.7	102.5	88.5	115.7	108.9333	1
1	94.4	106.9	92.8	93.3	121.8	90.8	96.83333	1
1	103.1	93	90.7	90.7	76.2	146.3	110	1
1	85.3	105.5	86.5	130.3	112	80.5	90.83333	1
1	138.5	78.1	69.5	89.2	121.6	103.1	83.56667	1
1	67.4	72.6	112.1	154.1	100.5	93.3	92.66667	1
1	103.8	118.4	97.9	101.5	95.1	83.4	99.9	1
1	89.4	131.5	75.9	74.3	154.7	74.1	93.83333	1
1	123.6	122.8	69.5	87	93	104	98.76667	1
1	79.4	97.4	103.3	113.1	86.2	120.6	107.1	1
1	104	79.1	140.8	99.6	83.9	92.6	104.1667	1
1	83.5	99.3	101.2	95.4	126.3	94.2	98.23333	1
1	137.2	97.6	82.2	94.5	110.7	77.8	85.86667	1
1	85.4	87.6	122.2	105.4	87.7	111.8	107.2	1
1	80.5	78.8	101.1	111.4	86.2	142	107.3	1
1	67.7	88.7	99.2	107.9	124.9	111.6	99.83333	1
1	157	119.2	76.3	79.9	98.9	68.6	88.03333	1
1	82.7	87	89.9	124.2	132.5	83.8	86.9	1
1	107.2	108.4	91.8	97.9	86.6	108	102.7333	1
1	111.2	82.3	81.9	163.6	93.3	67.6	77.26667	1
1	93	106.7	73.7	80.1	88.6	158	112.8	1
1	98.1	86.1	122	105.8	93.8	94.1	100.7333	1
1	88.7	97.1	96.2	110.9	87.7	119.4	104.2333	1
1	105.3	118.8	81.2	89.2	91.9	113.6	104.5333	1
1	80.9	103.9	104.4	113.1	105.2	92.5	100.2667	1
1	92	87	100.8	141	73.2	106	97.93333	1
1	104.5	88.7	101.6	105.4	105.5	94.2	94.83333	1
1	103.6	88.9	98.6	98.1	85.2	125.7	104.4	1
1	126.8	64.1	122.6	101.1	80	105.4	97.36667	1
1	109.1	119.1	98.2	94.5	88	91	102.7667	1
1	59	59.6	130.7	86.2	52.1	212.5	134.2667	1
1	81	55.6	139.6	77.8	75.4	170.6	121.9333	1
1	127.4	103.7	68.3	124	82.3	94.3	88.76667	1
1	80.3	69.8	122.2	89.4	64.3	174.1	122.0333	1
1	126.5	94	74.7	111.8	117.2	75.8	81.5	1
1	89.3	86.7	109.6	110.9	80.8	122.6	106.3	1
1	80.3	85.5	122.6	132.8	83.4	95.4	101.1667	1
1	90.4	92.8	112.1	104.3	97.8	102.6	102.5	1
1	115.1	132.7	76.4	78.7	120.2	76.9	95.33333	1
1	72.8	83.4	109.7	87.6	81.9	164.6	119.2333	1
1	80.8	78.1	120.3	98	84.5	138.4	112.2667	1
1	109.8	103.8	88.9	99	125.8	72.7	88.46667	1
1	116.1	137.1	85	88.2	97.6	76	99.36667	1
1	97.5	93.9	114.2	85.1	90	119.2	109.1	1
1	94	109.2	91	102	94.9	108.8	103	1

1	108.6	70.8	106.8	115	113.6	85.2	87.6	1
1	68.3	95.8	108.3	125.5	68.3	133.8	112.6333	1
1	124.6	97.1	94.6	90.9	104.4	88.4	93.36667	1
1	100.8	105.1	103.2	89.9	115.1	85.9	98.06667	1
1	104.1	126.8	85.7	87	107.1	89.3	100.6	1
1	151	100	88.1	85.4	102.9	72.6	86.9	1
1	103.3	90.2	93.6	108.9	107	97	93.6	1
1	91.1	74	126.7	97.2	75.2	135.8	112.1667	1
1	173.9	117.1	87.3	74.5	76.2	71	91.8	1
1	73.8	73.6	141.8	120.5	74.7	115.7	110.3667	1
1	91.9	103.5	101.8	99.2	111.4	92.3	99.2	1
1	86.9	79.7	112	88.5	77.6	155.3	115.6667	1
1	80.5	99.7	106.2	89.3	125.7	98.6	101.5	1
1	106.3	92.5	124.4	98.7	92.3	85.8	100.9	1
1	67.8	54.7	149.3	112.3	59.7	156.2	120.0667	1
1	126	78.3	97.3	77.3	130	90.9	88.83333	1
1	82.5	91.5	104.1	98.8	90.1	133.1	109.5667	1
1	119.5	85.3	80.5	108	134.3	72.5	79.43333	1
1	82	84.9	103.9	109.6	91.3	128.2	105.6667	1
1	96.6	76.1	115.6	90.6	107.8	113.3	101.6667	1
1	84.8	104.5	94.9	104.8	99.3	111.8	103.7333	1
1	122.7	114.1	85.4	81.3	105.6	90.9	96.8	1
1	76.1	75.2	110.9	81.6	66.8	189.5	125.2	1
1	94.4	138.7	91.4	84.8	119	71.7	100.6	1
1	95.4	99	98.8	105.7	97.3	103.8	100.5333	1
1	86.8	88.2	116.2	99.4	89.6	119.8	108.0667	1
1	108.1	101.2	68.7	102.3	123.6	96.1	88.66667	1
1	82.5	92	112.4	95	117.9	100.2	101.5333	1
1	85.3	80.1	108.1	116.6	96.3	113.7	100.6333	1
1	61.6	83.6	118.6	123.6	100.8	111.7	104.6333	1
1	67.8	59.9	127	133.6	73.3	138.4	108.4333	1
1	66	78.8	110.4	94.1	82.9	167.9	119.0333	1
1	114	111.1	87	80.4	132.3	75.2	91.1	1
1	89.8	73.5	89.4	104.3	88.1	154.9	105.9333	1
1	88.3	104.4	95.2	112.2	92.7	107.2	102.2667	1
1	87.1	114.2	83.4	84.2	134.4	96.7	98.1	1
1	112.4	101.3	83	95.3	98	109.9	98.06667	1
1	99.3	82.9	97.9	121.6	107.1	91.2	90.66667	1
1	99.1	105.5	95.6	93.1	106.7	100	100.3667	1
1	111.1	174.4	59.5	61.1	97.3	96.6	110.1667	1
1	79.5	125.3	88.6	131.1	104.3	71.2	95.03333	1
1	75.4	67.3	106	120.3	62.2	168.8	114.0333	1
1	89	106.1	101.3	94.9	108.5	100.2	102.5333	1
1	289.2	52.4	83.9	64.4	53.1	57	64.43333	1
1	99.2	93	92.4	112.5	99.7	103.1	96.16667	1
1	107.6	99	111.9	86.9	91.7	102.9	104.6	1
1	98.2	141.6	88.5	82.4	116.5	72.8	100.9667	1
1	90	94.9	80.2	111.9	139.3	83.8	86.3	1
1	88.1	97.7	103.7	112.8	96.2	101.4	100.9333	1
1	96.6	76.6	85.1	124.7	94.4	122.6	94.76667	1
1	113.5	189.4	61.9	60.9	115.8	58.5	103.2667	1

1	113.7	102.9	76.4	79.2	85.8	142	107.1	1
1	83	92	93	127.5	94.2	110.2	98.4	1
1	79.5	84.1	99.5	115.8	91.7	129.4	104.3333	1
1	79.3	77.5	111.3	110	77.8	144.2	111	1
1	107.1	147.2	102.8	75.4	96.1	71.4	107.1333	1
1	85.4	96.7	115.7	110.6	93.1	98.5	103.6333	1
1	104.1	105.1	77.8	80.4	78.2	154.5	112.4667	1
1	75.9	55.7	149	171.1	46.6	101.7	102.1333	1
1	88	93.3	102.7	97.3	79.7	139	111.6667	1
1	142.5	110.3	80.9	81.7	114.4	70.2	87.13333	1
1	73.8	67.9	108.8	129.9	73.9	145.7	107.4667	1
1	75.9	80.8	107.7	104.3	90.2	141.2	109.9	1
1	77.4	81.4	107.6	102.5	80.6	150.5	113.1667	1
1	90.1	122.2	98.9	88.4	113.2	87.3	102.8	1
1	100.7	110.4	101.6	96.2	109	82	98	1
1	92.5	83.7	118.9	82.2	84.7	138	113.5333	1
1	75.8	90.9	121	104	79.4	128.9	113.6	1
1	110.3	126.7	71.3	78.3	106.8	106.6	101.5333	1
1	77.7	92.2	116.7	106	98	109.5	106.1333	1
1	96.1	110	92.2	99.1	95.7	106.9	103.0333	1
1	116.3	107.7	103.4	78.1	89.5	104.9	105.3333	1
1	85	81.6	122.1	106.4	97.7	107.1	103.6	1
1	84.5	90.2	110.3	105.7	80	129.2	109.9	1
1	81.8	94.7	108.5	95	88.7	131.3	111.5	1
1	106.4	79.6	86.3	88.7	150.2	88.7	84.86667	1
1	65.8	56	92.7	120	152.5	113.1	87.26667	1
1	81.2	110.9	95.1	117.7	99.8	95.3	100.4333	1
1	92.6	92.2	119.2	98.3	85.8	112.1	107.8333	1
1	104.4	114.5	99.8	94.9	93	93.5	102.6	1
1	137.4	105.9	76.8	104.8	115	60	80.9	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	94	103.7	103.5	93.2	100.8	104.8	104	1
1	78.9	111.6	74.2	80.4	186.8	68.2	84.66667	1
1	77.1	84.1	102.8	99.9	85.8	150.3	112.4	1
1	137	132.7	73.9	65.4	144.4	46.6	84.4	1
1	101.2	100.3	94	101.7	124.3	78.5	90.93333	1
1	91.4	83.5	113.3	151.7	62.4	97.8	98.2	1
1	67.4	57.3	102.4	161.3	70.5	141.1	100.2667	1
1	86.8	106.2	82.8	91.4	136.2	96.7	95.23333	1
1	96	87.3	94.6	96.5	88.3	137.3	106.4	1
1	101.5	95.1	116.7	94.2	111.1	81.4	97.73333	1
1	99	87.2	96.5	114.9	90.5	112	98.56667	1
1	76.5	87	109.9	92	118.8	115.8	104.2333	1
1	124.3	96.8	94.1	97.4	105.4	81.9	90.93333	1
1	79.8	79.5	107.1	119.1	86.9	127.6	104.7333	1
1	67.7	61.2	254.6	69.7	74.4	72.3	129.3667	1
1	116.2	80.6	82.7	99.6	121	99.9	87.73333	1
1	80.3	93.6	103.6	113.5	101.8	107.1	101.4333	1
1	80.4	86.3	136.1	105.3	96.2	95.7	106.0333	1
1	81.2	88.5	117.3	95.9	113.7	103.3	103.0333	1
1	97.6	108.3	72.3	85.1	100.3	136.4	105.6667	1

1	104.2	94.5	94.1	93.8	100.9	112.5	100.3667	1
1	74.1	80.8	146.7	111.7	84.1	102.6	110.0333	1
1	72.6	81.8	117.1	109.9	101.4	117.3	105.4	1
1	105.9	119.8	96.8	89.6	92.4	95.6	104.0667	1
1	115.3	116.4	72.2	65.9	169.8	60.3	82.96667	1
1	88.8	75.6	132	87.1	77.9	138.6	115.4	1
1	76.6	83.8	117.7	107.1	79.6	135.3	112.2667	1
1	60.8	98.4	103.8	87.8	89.7	159.6	120.6	1
1	105.2	109.8	90.8	84	111.3	99	99.86667	1
1	69.9	154.3	87.2	86.5	117.6	84.5	108.6667	1
1	94.8	103	96.5	107.5	92.4	105.8	101.7667	1
1	81.8	97.2	108.1	107.9	89.7	115.3	106.8667	1
1	100.1	136	108.9	77	127.7	50.2	98.36667	1
1	93.2	117.7	97.8	100.7	100.8	89.7	101.7333	1
1	94.6	114	92.7	107	96.4	95.3	100.6667	1
1	90.2	86	98.8	110.2	118.6	96.3	93.7	1
1	63.6	59.3	154.4	111.8	71.1	139.7	117.8	1
1	109.5	95.5	93.4	106.3	110.1	85.2	91.36667	1
1	82.9	114.7	128	83.8	118.2	72.3	105	1
1	87.5	109.5	109.6	92.7	110.9	89.9	103	1
1	87.5	103.9	102.2	109.5	101	95.9	100.6667	1
1	108.1	57.8	175.6	109.1	65.2	84.2	105.8667	1
1	93.9	103.5	112	91.8	123.7	75.2	96.9	1
1	110	112.9	96.4	102	103	75.8	95.03333	1
1	90.2	90.4	108.4	109.8	102.7	98.6	99.13333	1
1	68.2	78.9	93.1	108.4	73.9	177.5	116.5	1
1	87.2	75.1	136.9	94.8	80.8	125	112.3333	1
1	125.8	144.7	67.9	80	99.1	82.5	98.36667	1
1	107	109.3	99.6	90.2	90.4	103.4	104.1	1
1	99.1	102	80.6	78.4	93.6	146.3	109.6333	1
1	120.2	89.5	87.3	97.4	79	126.6	101.1333	1
1	109.1	140.5	76.6	65.3	145.9	62.6	93.23333	1
1	69.5	123.7	73.2	82.8	185.1	65.7	87.53333	1
1	88.3	113.8	80.6	88.5	98.8	130.1	108.1667	1
1	165.1	110.3	73.2	86.4	85.6	79.4	87.63333	1
1	99.9	102.8	120.2	97.7	94.2	85.2	102.7333	1
1	95.4	102.9	88.2	83.2	80.2	150.1	113.7333	1
1	81.3	79.7	114.3	112	79.8	133	109	1
1	98.8	103	94.5	100.8	93.8	109.1	102.2	1
1	90.7	99.1	93.4	102.6	94.5	119.6	104.0333	1
1	100.3	102.2	105.1	100.5	101.7	90.2	99.16667	1
1	98.4	95.6	106.5	98	91.3	110.3	104.1333	1
1	76.8	97.1	142.7	104.8	82.8	95.9	111.9	1
1	124.2	93.1	79.4	96.7	81.7	125	99.16667	1
1	114.8	107.1	77.7	92.7	112	95.7	93.5	1
1	54.6	71.3	93.8	155.8	84	140.4	101.8333	1
1	106	89.9	126	106.5	76.2	95.4	103.7667	1
1	98.7	79.9	110.8	108.7	98.5	103.4	98.03333	1
1	276.7	76.7	49.6	60.7	82.3	53.9	60.06667	1
1	103.3	100.1	107.5	91.1	85.4	112.6	106.7333	1
1	107.7	128	86	82.6	117.4	78.2	97.4	1

1	84.3	111.2	112.4	115.4	79.7	97	106.8667	1
1	61.5	84.5	145.8	98.6	77.6	132.1	120.8	1
1	75.1	108.3	87.4	90.3	123.7	115	103.5667	1
1	56.7	49.8	161.1	136.8	51.3	144.3	118.4	1
1	94.3	88.7	107.3	106.4	92.3	111.1	102.3667	1
1	61	60.3	162.2	121.3	58.2	137	119.8333	1
1	105.6	112.4	72.9	79.1	104.9	125	103.4333	1
1	124.6	120.9	69.4	80.9	121.9	82.4	90.9	1
1	122.4	95.8	96.1	105.9	96.6	83.2	91.7	1
1	87.1	80.9	112.4	114.9	85.2	119.5	104.2667	1
1	105.8	89.8	94.5	104.6	90.9	114.3	99.53333	1
1	98.3	67.5	90.4	149.2	103.6	91.1	83	1
1	76.9	97.1	115.7	116.3	95.7	98.4	103.7333	1
1	110.7	111	83.7	84.4	120.6	89.7	94.8	1
1	132.2	110.3	76.7	94.8	102.2	83.8	90.26667	1
1	98.7	98	100	98.9	99.3	105.1	101.0333	1
1	80	97.6	109.2	129.2	79.2	104.9	103.9	1
1	91.3	100.6	97.2	100	103.7	107.1	101.6333	1
1	78.3	86.3	162.5	99.5	85.8	87.5	112.1	1
1	90.6	92.5	99.5	105.7	91.8	120	104	1
1	101	100.4	103.2	96.1	86.4	112.9	105.5	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	85.7	88	104.7	153.6	74.5	93.5	95.4	1
1	89.3	109.2	97.4	88.9	110.4	104.8	103.8	1
1	92.6	108.7	99.7	90.6	86.2	122.3	110.2333	1
1	97.3	93.5	93.2	122.4	118.6	75	87.23333	1
1	68.5	71.5	156.5	111.4	72.1	119.9	115.9667	1
1	76.2	73.8	110.7	155.3	90.5	93.5	92.66667	1
1	75.7	72	100	111.6	86.5	154.2	108.7333	1
1	72.1	100.3	113.9	120.6	99.5	93.7	102.6333	1
1	73.2	84.9	117.6	111.5	94.2	118.6	107.0333	1
1	139.1	89.1	89.8	87.8	94.7	99.5	92.8	1
1	106.6	110	93	94.2	112.6	83.5	95.5	1
1	61.9	71.7	139.9	110.4	78.7	137.4	116.3333	1
1	94	116.5	93.7	95	101.8	98.9	103.0333	1
1	104	138.5	78	88.1	113.6	77.9	98.13333	1
1	76.2	78.6	111.9	108.3	84.3	140.9	110.4667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	76.8	86	110.4	114	83.7	129.1	108.5	1
1	97.6	118.1	110.3	80.4	107.3	86.3	104.9	1
1	89.6	98.8	95.8	105.4	94.2	116.2	103.6	1
1	78.8	92.6	145.2	103.6	91.8	88	108.6	1
1	65	75.1	116.2	113.2	86.3	144.1	111.8	1
1	133.8	77.9	98.8	98.8	74.3	116.5	97.73333	1
1	136.9	112.4	68.2	68.2	142.8	71.6	84.06667	1
1	72.9	119.3	102.6	109.3	102.3	93.5	105.1333	1
1	81.2	76.9	103.4	112.5	80.3	145.8	108.7	1
1	112.9	127.2	91.8	84.3	71.8	111.9	110.3	1
1	78	65.3	97.6	147.8	90.1	121.3	94.73333	1
1	73.6	99.8	96.6	151.5	73.9	104.5	100.3	1
1	149.8	109	83.1	91.6	96.8	69.7	87.26667	1

1	88.5	164.3	76.6	73.3	140.3	57	99.3	1
1	86.2	113.3	96	87	137.3	80.1	96.46667	1
1	81.1	116.7	79.6	94.9	91.4	136.3	110.8667	1
1	80.1	90.2	118.2	112.9	116.1	82.5	96.96667	1
1	86.6	88.5	133.8	97.9	72.3	121	114.4333	1
1	57.2	46.9	139.2	78.9	51.3	226.5	137.5333	1
1	120.8	90.4	109.3	94.4	103.9	81.4	93.7	1
1	83.4	88.6	100.3	99.6	103.1	125.1	104.6667	1
1	88.8	103.1	98.3	105	98.7	106.1	102.5	1
1	75.4	94.2	105.8	93.1	100.7	130.8	110.2667	1
1	78.3	82.8	129.2	102.3	85.9	121.6	111.2	1
1	75	122	98.6	86.6	130.6	87.2	102.6	1
1	97	85.3	109.2	106.9	98.9	102.7	99.06667	1
1	83.3	78.1	118	118.3	87.6	114.8	103.6333	1
1	105.6	88.8	83.1	118.1	95.1	109.2	93.7	1
1	82.9	91.5	101.1	109.7	108.9	105.9	99.5	1
1	53.1	59.8	123.1	194.1	79.2	90.7	91.2	1
1	104.7	101.1	98.9	85.4	81.9	128	109.3333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	105.1	133.2	76.8	96.7	102.5	85.8	98.6	1
1	84.2	83.6	111.6	106	94.4	120.1	105.1	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	102.2	103.3	109.9	87.4	82.3	115	109.4	1
1	103.4	98	108.5	101.8	102.2	86	97.5	1
1	94	106.5	99.1	97.4	86.7	116.4	107.3333	1
1	103.4	100.3	99.1	96.2	113.5	87.4	95.6	1
1	55	55.2	218.8	144.1	51.2	75.7	116.5667	1
1	122	97.3	109.1	93.1	91.7	86.7	97.7	1
1	87.8	96.2	86.2	149.8	94.2	85.7	89.36667	1
1	82.6	78.2	115.8	108.6	83.3	131.5	108.5	1
1	84	77.8	94.5	96.6	72.8	174.2	115.5	1
1	82.6	89.7	113	97.5	74.2	143.1	115.2667	1
1	84.4	97.2	110.3	122.5	82.9	102.9	103.4667	1
1	92.2	89.9	112.9	101.8	85.7	117.5	106.7667	1
1	90	99.7	104.6	102.6	84	119.2	107.8333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	106.7	105.8	102.7	83.9	98	102.8	103.7667	1
1	106.8	96.5	95.4	93.4	120	88	93.3	1
1	78	127.8	98.3	84.2	122	89.7	105.2667	1
1	103.7	124.1	71.8	77.5	110.7	112.1	102.6667	1
1	89.4	96.3	115.2	93.1	91.8	114.2	108.5667	1
1	86.1	92.1	108.6	104.6	109.6	98.9	99.86667	1
1	88.5	98.8	101.6	99.2	83.4	128.5	109.6333	1
1	86.3	92.6	115.5	109.5	101.6	94.6	100.9	1
1	82	87.2	102.4	119.6	83.5	125.2	104.9333	1
1	82.3	72.8	114.8	100.6	84	145.4	111	1
1	68.2	93.2	128.4	106	88.9	115.2	112.2667	1
1	109.5	105.7	88.7	96.4	93.9	105.8	100.0667	1
1	160	127.7	73.1	67.5	99.3	72.4	91.06667	1
1	115.1	109.8	77.5	85.4	75.9	136.3	107.8667	1

1	72.4	63.1	135.7	129.1	97.3	102.4	100.4	1
1	87.7	88.9	95.7	99.3	79.3	149.1	111.2333	1
1	114.9	99.1	108.5	112.4	97.4	67.8	91.8	1
1	71.2	89	121.3	112.1	87	119.5	109.9333	1
1	92.3	92.3	122.4	103.5	101.2	88.3	101	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	100.5	120.5	74.5	83.9	94.4	126.2	107.0667	1
1	80.9	79.3	134	133.7	86.8	85.3	99.53333	1
1	87.8	81.6	113.9	108.3	87.6	120.8	105.4333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	86	90	112.7	107.3	105.4	98.6	100.4333	1
1	71.1	71.7	106.9	96.3	83.3	170.7	116.4333	1
1	78	90.4	113.9	135.9	81	100.8	101.7	1
1	108.8	88.1	97.5	98.8	107.5	99.4	95	1
1	98	98.1	107.4	95.4	90.9	110.2	105.2333	1
1	119.5	97.8	107.7	89.7	103.9	81.4	95.63333	1
1	97.1	91.4	95.7	98	132.3	85.5	90.86667	1
1	85.2	80.8	113.3	104.6	89.7	126.4	106.8333	1
1	94.1	101.2	84	99.9	116.3	104.5	96.56667	1
1	161.4	113.2	81	83.4	102.3	58.7	84.3	1
1	91.2	118.5	70.5	77	123.3	119.4	102.8	1
1	111.8	112.3	83	99.1	95.6	98.2	97.83333	1
1	90.2	98.7	101.2	101.7	119.8	88.4	96.1	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	73.7	103.9	120.9	108.1	87.5	105.9	110.2333	1
1	88	107.3	97.2	89.2	123.3	95	99.83333	1
1	72.1	76.8	121	115.5	107.9	106.8	101.5333	1
1	69	58.9	107.2	94.7	102.1	168.1	111.4	1
1	67.3	77.4	118.2	109.2	83.9	144.1	113.2333	1
1	74.6	98	115.6	132.8	80.6	98.3	103.9667	1
1	81.6	84.9	118	80.7	98.8	136	112.9667	1
1	77.1	88.8	95.3	146.8	86.3	105.7	96.6	1
1	67.8	103	113.5	120.1	68.7	126.9	114.4667	1
1	146.4	85.3	84.6	86.6	79.3	117.8	95.9	1
1	158.9	108.3	76.6	84.3	103	68.9	84.6	1
1	117.7	121.8	88.4	77.8	123.4	70.9	93.7	1
1	94.3	85.6	96.5	109.5	84.7	129.4	103.8333	1
1	109.5	113.9	109.5	107	80.6	79.6	101	1
1	72.8	90.9	115.1	106.2	91.9	123	109.6667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	74.4	104.2	77	112	135.4	96.9	92.7	1
1	81.9	101.6	99.4	118.1	104.9	94.1	98.36667	1
1	103	102.7	79.1	81.1	82.1	152	111.2667	1
1	124.8	69.9	134.4	72.8	46.7	151.4	118.5667	1
1	111.7	109.1	82.5	91.8	133.8	71.2	87.6	1
1	72.6	90.7	148.9	126.7	54.1	107	115.5333	1
1	80.2	120.5	92.3	138.2	67.1	101.6	104.8	1
1	91.5	111.7	105.7	80.7	96.4	114	110.4667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	88.4	105.8	110.3	95.6	96.2	103.7	106.6	1
1	95.2	79.4	107.6	109.5	126.7	81.8	89.6	1

1	NA	NA	NA	NA	NA	NA	NA	0
1	100	116.3	87	90	81.4	125.3	109.5333	1
1	89.1	73.9	137.3	127	81.3	91.4	100.8667	1
1	75.9	72.9	104.1	139.6	77.2	130.3	102.4333	1
1	94.9	106.9	89	105.6	74.8	128.8	108.2333	1
1	102.7	93.7	109.5	92.8	97	104.3	102.5	1
1	113.5	129.8	70.2	107.7	97	81.9	93.96667	1
1	90.4	101.8	88.2	123.1	72.4	124.2	104.7333	1
1	88.1	80.2	133.3	93.3	95.6	109.6	107.7	1
1	91.8	103	86.4	110.8	88.7	119.3	102.9	1
1	69.2	81.7	107.5	96	77.6	168	119.0667	1
1	78.9	78.8	128.9	123.5	86	104	103.9	1
1	79.6	82.3	111.1	94.1	95.6	137.3	110.2333	1
1	68.1	132.2	97.9	96.7	76.7	128.3	119.4667	1
1	106.1	143.8	82.7	80.7	119.8	66.9	97.8	1
1	79.8	106.9	102.3	112.5	106	92.5	100.5667	1
1	95.6	92.2	103.3	100.7	100.8	107.5	101	1
1	103.5	96	88.2	140.1	89.8	82.4	88.86667	1
1	96.4	149.1	76.8	78	126.6	73.1	99.66667	1
1	117.1	101	88.9	98.3	95.1	99.6	96.5	1
1	90.7	85	113.1	111.6	83.6	116.1	104.7333	1
1	85.8	116.9	97	67	150.4	83	98.96667	1
1	96	98.3	91.4	131.3	91.3	91.6	93.76667	1
1	96	108.1	111.6	93.1	80.1	111	110.2333	1
1	82.3	113.4	109.7	108.6	93.4	92.6	105.2333	1
1	90.8	149.7	75.3	73.1	129.6	81.4	102.1333	1
1	85.4	103.2	95.6	99.8	112.3	103.8	100.8667	1
1	70.2	70.9	89.4	98.1	81.6	189.8	116.7	1
1	88.3	96.4	102.2	106.9	121.8	84.3	94.3	1
1	113.8	101.8	84.6	94.4	94.4	111	99.13333	1
1	134.8	88.7	62.7	110.7	153.4	49.7	67.03333	1
1	82.2	84.3	98.9	106.6	75.9	152.1	111.7667	1
1	105.9	67.1	104.3	133.3	78	111.4	94.26667	1
1	98.7	92.2	93.4	99.2	100	116.6	100.7333	1
1	76.1	99.3	116.7	116.7	82.8	108.4	108.1333	1
1	90.6	95.6	118.7	96.4	100.8	97.9	104.0667	1
1	81	99	125	100.7	73.6	120.6	114.8667	1
1	103.4	114.7	97.4	88.6	87	108.9	107	1
1	95.3	104.6	100.8	101.6	83.5	114.2	106.5333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	92.3	108.2	128.2	92.4	83.5	95.4	110.6	1
1	92.5	89	97.1	119.8	100.9	100.7	95.6	1
1	62.8	78.4	151	142.7	76	89	106.1333	1
1	113.3	91.8	86.6	108.7	126.3	73.2	83.86667	1
1	73.9	143.5	100.4	105.2	95.5	81.5	108.4667	1
1	93.2	101.7	87.7	90.8	102.7	123.9	104.4333	1
1	87.1	102.2	95.3	103.7	91.6	120.1	105.8667	1
1	97	112.6	110.5	95.8	91.5	92.5	105.2	1
1	101.4	84.6	111.7	102	95.9	104.4	100.2333	1
1	82.7	167	55.8	82.6	125.9	86	102.9333	1
1	146.1	99.3	72.2	91.8	135.4	55.3	75.6	1

1	96.6	81.6	118.9	95.1	94.6	113.2	104.5667	1
1	93.3	121.3	100.8	96.1	97.1	91.4	104.5	1
1	126.1	99.2	107	86.8	102.5	78.3	94.83333	1
1	99.3	92.4	109.4	95.7	95.1	108.1	103.3	1
1	107.3	116.3	79.8	97.5	100.4	98.7	98.26667	1
1	87.6	81.4	119.2	103.1	83.6	125.1	108.5667	1
1	103.3	108.5	94.4	88.7	87.1	118.1	107	1
1	87.8	84.7	102.5	104.2	89.4	131.4	106.2	1
1	123.4	79.9	91	112.3	88.9	104.5	91.8	1
1	85.1	90.4	87.2	98.3	85.4	153.5	110.3667	1
1	73	70.9	103.6	137.3	75.3	139.8	104.7667	1
1	85.6	89.5	103	126.5	93.7	101.6	98.03333	1
1	69.7	76.2	156.4	132.6	71.6	93.5	108.7	1
1	86.1	109.9	90.2	100.5	129.8	83.5	94.53333	1
1	81.3	93.1	106.1	130.1	86.5	102.9	100.7	1
1	85.3	80.7	145.5	108.9	77.3	102.4	109.5333	1
1	69.2	68.9	162.6	110.2	90.5	98.6	110.0333	1
1	88.4	83.2	106.2	110.4	107.9	103.9	97.76667	1
1	138.5	89.9	131.2	84.2	91.9	64.3	95.13333	1
1	65.8	70.4	105.8	103.3	81	173.6	116.6	1
1	88.4	98.3	100.4	106	86	120.9	106.5333	1
1	113.9	127.5	81.7	74.8	97.5	104.5	104.5667	1
1	106.6	102.6	99.7	87.5	110.4	93.3	98.53333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	58.2	86.2	156	114.6	80.3	104.8	115.6667	1
1	65.8	61	181.9	64.3	47.8	179.2	140.7	1
1	90.9	95.9	114.4	110.3	103.4	85	98.43333	1
1	140.5	107.5	91.9	70.8	82.7	106.6	102	1
1	94.8	111.5	99.1	98.6	112.9	83.1	97.9	1
1	110.3	77.4	73.7	90.5	82	166.1	105.7333	1
1	80.7	86.1	115.3	128.2	79.9	109.8	103.7333	1
1	93.1	73.3	160.3	72.8	65.5	135	122.8667	1
1	113.8	110	82.3	91.6	107.8	94.6	95.63333	1
1	91.2	92.9	97.1	95.2	112.6	111.1	100.3667	1
1	97.3	116.6	99.8	86.7	113.5	86.1	100.8333	1
1	127.5	98.6	85.9	105	112.5	70.4	84.96667	1
1	79.3	108.9	88.2	129.9	105.1	88.5	95.2	1
1	113.8	141.5	92.6	81.4	81.3	89.5	107.8667	1
1	92.7	97.4	93	101.5	101.6	113.7	101.3667	1
1	124.5	88.9	94.2	120	92.4	80.1	87.73333	1
1	81.3	96.5	108.4	124	77.9	111.9	105.6	1
1	90.2	64.4	77.1	97.9	78.7	191.8	111.1	1
1	92.2	95.5	110.3	99.7	98.2	104.1	103.3	1
1	75.1	66.6	120.2	147.9	100.2	90.2	92.33333	1
1	109.9	108.7	90	89.7	85.1	116.5	105.0667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	59.5	100.3	165.7	141	79.2	54.3	106.7667	1
1	71.3	88.9	124	107.4	94.6	113.9	108.9333	1
1	97.8	102.7	94.7	100.1	90.8	113.8	103.7333	1
1	98.6	90.5	130.4	106.9	93	80.6	100.5	1
1	103.1	101.2	93.3	92.2	99.2	111.1	101.8667	1

1	68.1	73.3	120.4	116.2	75.2	146.7	113.4667	1
1	91.4	84.1	104.7	92.1	100.2	127.5	105.4333	1
1	129.8	118.5	84.2	81.7	108.4	77.5	93.4	1
1	105.1	89.2	90.5	108.7	87.8	118.7	99.46667	1
1	80.8	105.1	114.9	112.6	99.3	87.3	102.4333	1
1	93.3	106	87.8	107.4	116	89.4	94.4	1
1	133.7	212.2	53.2	59.2	59.3	82.4	115.9333	1
1	115.1	104.5	103.6	85	86.9	104.9	104.3333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	73	85.5	104.9	104	96.7	136	108.8	1
1	145.9	156.3	43.6	53.2	143.6	57.4	85.76667	1
1	94.7	87.3	100.7	104.2	99.8	113.4	100.4667	1
1	93.6	103.7	91.6	107.7	94.2	109.3	101.5333	1
1	75	80.7	119.4	91.8	92.7	140.4	113.5	1
1	79.8	97.4	112.2	96.6	100.8	113.2	107.6	1
1	94	75.3	99.9	137.5	99.5	93.9	89.7	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	87.1	82.9	116.3	117.4	87.2	109.2	102.8	1
1	108.1	115.9	87.7	97.6	92.3	98.4	100.6667	1
1	119.3	112.3	102.5	77	90.6	98.3	104.3667	1
1	64.2	78.4	120.3	112.3	89.8	135.1	111.2667	1
1	88.8	105.8	109.7	98.5	101.4	95.8	103.7667	1
1	89.8	93	118.2	101.6	100.7	96.8	102.6667	1
1	67.4	87.2	120.6	104.9	87.5	132.5	113.4333	1
1	113.9	85.5	119.1	93.9	86.6	101	101.8667	1
1	64.5	71.6	160.5	104.6	84.4	114.4	115.5	1
1	92.7	90.2	105.2	104.3	97.5	110.1	101.8333	1
1	74.2	92.3	124	85.4	80.4	143.7	120	1
1	82.4	80.9	110.3	98.4	81.6	146.3	112.5	1
1	120.6	97.7	85.3	102.3	91.2	102.8	95.26667	1
1	94.8	91.8	98.6	105.4	93	116.3	102.2333	1
1	86.9	97.3	98.1	108.2	86.2	123.4	106.2667	1
1	136.4	125.6	68.7	82.3	95.5	91.5	95.26667	1
1	101.1	106.8	99.7	99.3	83.7	109.4	105.3	1
1	84.4	91.5	94.4	112.1	99	118.6	101.5	1
1	122	103.4	76.8	105	74.9	118	99.4	1
1	68.6	67.7	98.7	128.5	62.3	174.2	113.5333	1
1	91	99.7	106.9	107.6	92	102.8	103.1333	1
1	64.8	89.6	126	89.5	89	141.2	118.9333	1
1	110.3	137.8	90.8	68.6	87.3	105.2	111.2667	1
1	165.8	96.5	69.3	84.9	95.9	87.6	84.46667	1
1	104.5	86.8	125.9	97.8	107.4	77.7	96.8	1
1	70.1	93	138.4	108.4	85.8	104.4	111.9333	1
1	106.9	101.8	92.1	90.1	109.5	99.7	97.86667	1
1	97.3	113.1	103	93	102.3	91.2	102.4333	1
1	76.5	90.8	125.8	91.9	69.1	145.8	120.8	1
1	91.8	113.2	100.4	100.5	96.6	97.5	103.7	1
1	108.3	65.2	139.8	106	84.4	96.3	100.4333	1
1	62	47.7	99.4	205.5	72.5	112.9	86.66667	1
1	113.1	97.1	93	103.5	77.4	115.9	102	1
1	98.2	124.7	80.8	100.4	107.4	88.6	98.03333	1

1	91.3	77.5	104.7	161.3	72.4	92.8	91.66667	1
1	132.8	90.5	88.8	100.6	113.6	73.7	84.33333	1
1	102.4	94.2	90.5	104.9	108.3	99.6	94.76667	1
1	108.1	102.5	81.6	96	131	80.8	88.3	1
1	96.2	100.4	95.4	105.3	83.6	119.1	104.9667	1
1	79.2	78.7	89.5	119	103.3	130.4	99.53333	1
1	88.2	96.1	103.5	98.1	119.1	95	98.2	1
1	98.6	93.8	104.6	106.2	81.5	115.3	104.5667	1
1	73.9	84.4	119	94	135.7	93	98.8	1
1	198.5	136.2	38.8	79.4	48.4	98.7	91.23333	1
1	59.5	93.5	121.2	141.3	59.9	124.6	113.1	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	93.4	66.8	97.7	115.6	62.3	164.3	109.6	1
1	128	83.2	73.2	101.8	147.5	66.3	74.23333	1
1	91.7	76.6	113.6	103.4	80.9	133.7	107.9667	1
1	86.1	84.4	122.2	113.4	93.5	100.4	102.3333	1
1	77.2	93.2	122.5	100	90.4	116.7	110.8	1
1	77.3	87.9	104.5	92.5	81.4	156.4	116.2667	1
1	74.9	72.3	151.1	120.4	74	107.2	110.2	1
1	97	91	94.9	110.4	119.3	87.4	91.1	1
1	88	97.4	131.6	85.6	109.6	87.8	105.6	1
1	172.8	111.9	64.9	67.2	108.7	74.4	83.73333	1
1	100.8	114.7	83.9	97.7	110.1	92.8	97.13333	1
1	68.5	91.9	133.4	136.1	80.3	89.9	105.0667	1
1	64.4	79.4	161.6	111.4	102.1	81.2	107.4	1
1	89.9	87.9	104.7	109.4	92.1	116	102.8667	1
1	96.2	145	77.7	98.2	101.8	81	101.2333	1
1	56.8	46.6	147.2	239.3	50.6	59.5	84.43333	1
1	90.1	102	103.4	92.5	127.9	84.1	96.5	1
1	87	104.1	84.5	112.7	98.8	112.8	100.4667	1
1	92.4	102.3	84.4	99.5	95.6	125.8	104.1667	1
1	87.9	83.2	76.8	95.6	79	177.6	112.5333	1
1	81.5	83.4	103.2	110.8	83.7	137.4	108	1
1	61.1	53.6	116.4	96.3	157.1	115.6	95.2	1
1	93.5	108.7	93	97.6	110.7	96.4	99.36667	1
1	115.8	106.1	81.8	89.1	93	114.3	100.7333	1
1	76.8	80.6	136.6	97.8	85.2	123	113.4	1
1	75.1	72.6	163.6	126.4	64.5	97.8	111.3333	1
1	79	73.8	103.3	101	95.7	147.3	108.1333	1
1	94.8	92.2	101.7	91.8	81.4	138.1	110.6667	1
1	87.5	82	111.2	117.1	92.9	109.2	100.8	1
1	90.9	96.4	85.2	106.2	102.4	118.9	100.1667	1
1	101.4	108.9	101.2	111.6	82.4	94.4	101.5	1
1	74.5	84.5	106.1	131.6	88.4	114.9	101.8333	1
1	103.9	88.4	104.2	94.3	101.3	107.8	100.1333	1
1	109.4	94.3	79	87.5	81.6	148.2	107.1667	1
1	100	91.3	72.8	155.8	87.2	92.9	85.66667	1
1	95.7	90.2	125.4	88.9	92.4	107.5	107.7	1
1	90	95.9	103.3	107.8	103	99.9	99.7	1
1	106.4	107.8	83.4	93.6	106.3	102.5	97.9	1
1	91.2	118.4	122	84.7	80.6	103.2	114.5333	1

1	97.2	100	105.7	89.6	110.5	96.9	100.8667	1
1	96.9	96.1	108.7	100.1	93.3	104.9	103.2333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	93.5	139.2	100.6	72.1	103.2	91.5	110.4333	1
1	90.8	66.6	141.6	110.9	94.8	95.3	101.1667	1
1	81.2	88.3	110.3	127.8	87.7	104.8	101.1333	1
1	89	89.1	97.3	123.1	104.1	97.5	94.63333	1
1	91.8	83.1	112.2	102.2	116.6	94.2	96.5	1
1	74.3	77.1	113.4	111.7	102.9	120.6	103.7	1
1	63.7	79.2	215.4	94	72.2	75.5	123.3667	1
1	70.3	89.2	105.8	104.9	109.8	120	105	1
1	65.5	76.2	111.8	110.6	68.7	167.2	118.4	1
1	65.7	65.5	136.6	163.4	69.5	99.3	100.4667	1
1	92.9	101.2	110.3	118.2	83.6	93.9	101.8	1
1	139	95.1	87.7	97.5	103.1	77.6	86.8	1
1	114	87.8	99.7	112	90.7	95.9	94.46667	1
1	116.8	71.6	100	115.7	108.5	87.5	86.36667	1
1	80.8	74.3	111.5	89.3	81.9	162.1	115.9667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	62.9	96.2	118.5	132.3	63	127	113.9	1
1	85.2	81.8	97.9	99.8	117.9	117.4	99.03333	1
1	106.4	136.4	88.8	70.3	122.8	75.2	100.1333	1
1	81.4	124.9	90.9	88.4	84.2	130.3	115.3667	1
1	78.3	74.4	125.5	113.1	81.7	127	108.9667	1
1	111.7	175.2	67	72.4	109.6	64.1	102.1	1
1	94.1	97	112.6	100.1	92.7	103.4	104.3333	1
1	83.6	76.5	125.8	112.4	80.3	121.3	107.8667	1
1	108.6	98.4	88.6	94.2	120.6	89.6	92.2	1
1	102.6	94.3	96.7	109.4	89.3	107.7	99.56667	1
1	79.8	101.4	99.6	100	104.1	115.1	105.3667	1
1	120.9	161.4	110.4	63.2	103	41	104.2667	1
1	108.5	110.6	90.7	86.3	95.6	108.3	103.2	1
1	90.2	79.6	107.7	99.9	86.8	135.8	107.7	1
1	103.6	97	103.1	110.4	83.8	102.1	100.7333	1
1	94.9	132.2	112.1	95.3	96.3	69.2	104.5	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	99.5	93.8	110.3	93.3	85.6	117.5	107.2	1
1	89.3	108.6	93.2	105.1	106.2	97.6	99.8	1
1	131.5	112.8	88.4	96.6	102.1	68.6	89.93333	1
1	80.2	88.7	123.4	104.5	111.3	91.9	101.3333	1
1	85.2	80.6	108.7	111	80	134.6	107.9667	1
1	56.1	91.1	92.2	123.6	81.5	155.6	112.9667	1
1	92.2	85.3	102.5	105.8	112.5	101.7	96.5	1
1	77	94.3	114.4	111.8	106.3	96.2	101.6333	1
1	106.6	115.2	94.3	89.7	111.8	82.4	97.3	1
1	64.3	81.5	115.2	109	80.2	149.8	115.5	1
1	58.9	77.3	152.6	109.5	80.3	121.5	117.1333	1
1	60.5	79.5	87.4	110.1	106.2	156.4	107.7667	1
1	83.9	84.8	97.5	91.1	87.2	155.4	112.5667	1

1	64.3	109.4	117.8	152.9	78.2	77.5	101.5667	1
1	97.1	104.1	98.8	92.5	115.9	91.6	98.16667	1
1	85.3	88.5	139.4	103.7	95.5	87.6	105.1667	1
1	92.6	99	99	97.2	84.4	127.8	108.6	1
1	72.8	88.3	117.7	110.5	68.5	142.2	116.0667	1
1	75.8	69.2	130.5	120.1	78.7	125.6	108.4333	1
1	107.5	105.4	90.1	92.9	98.5	105.6	100.3667	1
1	100.7	106.2	82.8	89.5	107.3	113.5	100.8333	1
1	98	95.4	94.9	97.8	93.4	120.5	103.6	1
1	101.7	88.2	111.2	118.6	88.1	92.2	97.2	1
1	74	84.5	116.7	126.4	76.9	121.5	107.5667	1
1	104.6	95.2	83.5	122.4	102	92.3	90.33333	1
1	90.8	113.2	102.3	84.1	77.2	132.4	115.9667	1
1	109.8	89	90.8	103.5	108.3	98.6	92.8	1
1	58.3	93.4	128.6	93.2	68.5	158.1	126.7	1
1	97.3	86.1	99.2	103.1	81.8	132.6	105.9667	1
1	77.2	104.7	118.8	138.9	63.8	96.6	106.7	1
1	85.1	81	135.9	106.7	75.1	116.1	111	1
1	94	86.5	92.5	110.9	101.9	114.2	97.73333	1
1	84.4	118.6	120.3	74.8	81.8	120.2	119.7	1
1	116.5	106.6	88.1	96.9	89.5	102.4	99.03333	1
1	94.6	102.5	83.5	96.5	94.1	128.8	104.9333	1
1	92.7	95.7	100.2	104.8	100.1	106.6	100.8333	1
1	99.2	101.7	93	103.8	103	99.3	98	1
1	99.6	82.7	72.2	107.4	98.2	140	98.3	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	104.1	135.9	72.7	113.5	90.2	83.7	97.43333	1
1	79.1	85.6	95.1	129.7	107.2	103.3	94.66667	1
1	109.5	129.6	74.4	81.2	100.5	104.8	102.9333	1
1	71	57.3	153	105.8	115.9	97	102.4333	1
1	116.6	116.3	91.9	92.3	95.4	87.6	98.6	1
1	93.7	87.2	92.3	108.8	116.2	101.8	93.76667	1
1	116.5	105.5	89.6	96.9	110.7	80.8	91.96667	1
1	98.9	86.5	89.5	115.3	90.8	118.9	98.3	1
1	114.5	92.8	107.3	93.6	90.8	101	100.3667	1
1	69.7	79.8	94.5	167.2	102.3	86.5	86.93333	1
1	92.7	100.3	109.3	115.7	98.5	83.5	97.7	1
1	88.4	112.5	87.4	80.1	125	106.6	102.1667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	77.7	98.5	114	97.5	92.5	119.7	110.7333	1
1	90	109.1	116.4	100.2	84.3	100.1	108.5333	1
1	90.2	89.8	103.1	98.8	96.8	121.3	104.7333	1
1	90.5	102.1	80	80.1	147.8	99.6	93.9	1
1	94	86	100.4	110.6	95.3	113.6	100	1
1	78.9	85.3	113.7	111.2	89.4	121.5	106.8333	1
1	86.4	97.2	125.6	98.2	85.7	106.7	109.8333	1
1	64.5	98.4	98.8	119.4	123.3	95.7	97.63333	1
1	119.6	98.1	97.5	85.4	110.1	89.3	94.96667	1
1	89.9	101.9	106.9	101.5	95.4	104.4	104.4	1
1	107.2	113.9	100	93.1	105	81	98.3	1
1	96.4	94.6	86.3	118.8	101	103	94.63333	1

1	101.1	97.3	101.5	92.2	87.3	120.6	106.4667	1
1	81.8	89.6	134.6	91.7	67.8	134.4	119.5333	1
1	76.1	92.3	118.2	101	82.5	129.9	113.4667	1
1	102.5	79.1	105.8	121.9	109.2	81.5	88.8	1
1	99.6	117.9	92.3	99.2	106.7	84.3	98.16667	1
1	77.7	79.3	90	126	102.5	124.5	97.93333	1
1	86.4	94.7	101.1	105.3	91.5	121	105.6	1
1	92.2	98.3	110.2	99.4	74.7	125.3	111.2667	1
1	113.9	84.1	81.4	108.3	90.4	121.8	95.76667	1
1	98.1	98	107.6	97	104	95.2	100.2667	1
1	92.2	92.4	107.7	101.8	88.7	117.3	105.8	1
1	117.5	104.6	102.2	114	99.1	62.5	89.76667	1
1	86.3	114	93.8	104.8	88.5	112.7	106.8333	1
1	122.5	101.4	84.8	87.2	111.6	92.4	92.86667	1
1	115.1	110.1	102.8	78.6	109.7	83.6	98.83333	1
1	86.6	91.7	120	84.4	82	135.3	115.6667	1
1	95.8	88.6	108.5	107.2	94.9	105.1	100.7333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	89.4	146.5	75.9	84.3	104.6	99.3	107.2333	1
1	83.5	90	98.9	96	92.5	139.1	109.3333	1
1	85.3	110.3	93.3	101.9	92	117.3	106.9667	1
1	87.1	110.5	113.8	94.5	90.1	104.1	109.4667	1
1	114.4	96.7	104.3	87.7	105.5	91.3	97.43333	1
1	122.7	62	112.7	109.9	50.4	142.3	105.6667	1
1	102.7	95.2	105.7	81.3	94.8	120.3	107.0667	1
1	96.6	90.1	107.3	103.7	84.4	118.1	105.1667	1
1	88.9	85.2	96.1	127.1	105.2	97.5	92.93333	1
1	87.3	74.1	136.4	125.8	93.1	83.3	97.93333	1
1	94.6	103.4	103.6	95.7	89.4	113.3	106.7667	1
1	107.8	116.7	93.7	94.5	87.4	99.9	103.4333	1
1	108	92.9	66.1	101.3	177.8	53.9	70.96667	1
1	100.7	78.4	125	97.5	84.2	114.2	105.8667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	77.1	78.2	109.2	107.7	92.6	135.2	107.5333	1
1	79.1	102.2	93.2	108.2	77.6	139.7	111.7	1
1	78.4	88.5	99.9	98.5	84.4	150.4	112.9333	1
1	134.7	88	73.2	110.7	146.8	46.6	69.26667	1
1	99.7	89.2	99.2	95.6	126	90.3	92.9	1
1	79.4	63.7	117.2	136.9	89.3	113.4	98.1	1
1	113.2	98.9	99.6	93.2	94	101.2	99.9	1
1	99.8	88	95.6	118.5	112.3	85.7	89.76667	1
1	78.9	92.5	101.9	91.3	146.2	89.3	94.56667	1
1	96.9	119.7	97.7	88.5	105.4	91.8	103.0667	1
1	89.2	83.3	87.3	94.1	75.8	170.2	113.6	1
1	83.3	104.2	93.4	112.4	81.1	125.7	107.7667	1
1	60.9	80.3	118.7	112.7	122.8	104.7	101.2333	1
1	99.4	112.3	88.3	91.8	107.1	101.1	100.5667	1
1	64.7	152.1	70.4	121.1	79.7	111.9	111.4667	1
1	95.3	89.8	100.2	112.6	95.5	106.6	98.86667	1
1	90.6	79.1	105.8	107.5	99.7	117.3	100.7333	1
1	61.3	86.6	81.4	142.5	95.1	133.1	100.3667	1

1	92	73.7	106.3	103.7	112.2	112.1	97.36667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	113.4	81.7	91.8	105.3	100.6	107.2	93.56667	1
1	104.7	103.6	100.7	99.9	104.8	86.3	96.86667	1
1	127.6	107.2	85.4	92.2	108.5	79.1	90.56667	1
1	63	83.8	104.3	107.1	89.7	152.1	113.4	1
1	91.8	108.4	98.9	113.4	88.2	99.4	102.2333	1
1	113.5	106.5	96	89.6	90.9	103.5	102	1
1	113.1	102.5	95.6	82.3	125.6	81	93.03333	1
1	78.1	83.3	91.2	146.8	114.8	85.8	86.76667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	98.1	91.5	84.6	92.7	100.7	132.4	102.8333	1
1	72.4	64	102.8	141.9	94.7	124.2	97	1
1	114.6	108.2	80.3	88.1	115.1	93.7	94.06667	1
1	89.7	93.5	109.4	109.4	94.1	103.9	102.2667	1
1	75.7	83.2	61	187.2	61.4	131.3	91.83333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	118.9	118.5	88.7	88.4	104.9	80.6	95.93333	1
1	120.8	76.9	106.7	81.6	126.1	87.9	90.5	1
1	91.1	117.6	105.5	96.5	79.8	109.5	110.8667	1
1	95.1	117.2	107.1	91.1	122.6	66.9	97.06667	1
1	89.1	85.5	106.4	92.3	91.9	134.8	108.9	1
1	75.3	78.7	127.6	122.2	65.1	131.1	112.4667	1
1	93.5	114.2	91.2	121.7	90.1	89.2	98.2	1
1	118.9	96.1	83.1	87.9	100.2	113.8	97.66667	1
1	117.6	106.9	96.3	91.9	100.9	86.4	96.53333	1
1	99.8	97.8	100.8	114.6	83.1	103.8	100.8	1
1	109.4	116.8	120.4	89.2	88.9	75.4	104.2	1
1	62.1	82.6	116.5	185.6	66.8	86.3	95.13333	1
1	83.7	120.7	109.9	92	75.7	118.1	116.2333	1
1	105	142.7	100.1	65.4	101	85.9	109.5667	1
1	101	83.9	135.1	87.1	84.2	108.7	109.2333	1
1	87.4	101.5	89.4	101.7	129.3	90.6	93.83333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	92.3	85.7	118	120	96.1	87.9	97.2	1
1	82.4	83.4	99	141.8	84.1	109.2	97.2	1
1	104	130.7	96.4	89.8	77.3	101.8	109.6333	1
1	105.1	140.7	96.6	74.2	113.5	69.9	102.4	1
1	76.2	87.3	172.2	71.1	77.8	115.3	124.9333	1
1	57.8	104.4	141.2	134.6	73.2	88.9	111.5	1
1	76.7	75.9	183.8	88.9	109.4	65.3	108.3333	1
1	86.5	117.5	102.6	80	98.2	115.3	111.8	1
1	93.2	91.8	105.3	95.2	82.4	132.2	109.7667	1
1	114	94.4	129.2	73.1	121.7	67.6	97.06667	1
1	109	96.3	116.2	91.1	102.2	85.2	99.23333	1
1	70	79	114.9	109.6	85.4	141.2	111.7	1
1	103.1	121	82.4	94.2	84.8	114.6	106	1
1	81	81.3	71.9	213.9	82.8	69.1	74.1	1
1	103.8	108.7	94.9	95.5	118	79.1	94.23333	1
1	55.3	51.7	62.8	65.8	49.4	315	143.1667	1

1	97.8	100.7	113	92.8	90.4	105.3	106.3333	1
1	97.1	89	95.3	105.6	96	117	100.4333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	76.2	85.9	117.6	91	90.6	138.9	114.1333	1
1	69.2	66.3	153.7	82.4	75.9	152.6	124.2	1
1	92.1	90.3	115.4	99.2	109	94	99.9	1
1	87.3	64.9	113.3	90	80.1	164.4	114.2	1
1	93.2	99	96.3	107.5	106	98	97.76667	1
1	92.1	106	199.3	51.8	112.6	38.2	114.5	1
1	121.7	98.6	101.6	89.9	91	97.2	99.13333	1
1	98.5	123.5	76.1	94.3	98.5	109	102.8667	1
1	152.3	75.9	82.3	90.5	129.8	69.3	75.83333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	77.4	106.3	120.5	97.7	107.9	90.3	105.7	1
1	85.4	91.4	125.5	125	88.1	84.6	100.5	1
1	88.3	102.9	109.1	108.9	72.9	118	110	1
1	85	93.2	113.7	101	89.4	117.7	108.2	1
1	120.4	103.6	99.8	99.1	99.8	77.3	93.56667	1
1	72.8	97.6	102.6	145.2	81.5	100.3	100.1667	1
1	110.7	100.2	96.9	98.7	84.8	108.7	101.9333	1
1	107.2	84.3	100	110.1	76.8	121.6	101.9667	1
1	92.8	81.5	127.5	102.7	105.8	89.7	99.56667	1
1	93.7	106	99.6	96.7	95.1	108.7	104.7667	1
1	86.1	84.4	100.8	93.7	101	134	106.4	1
1	122.5	92.7	95.5	96.4	99.6	93.2	93.8	1
1	85.1	94.8	103.2	102.3	117.9	96.8	98.26667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	74.1	94	115.9	99.4	103.1	113.5	107.8	1
1	85.5	87.8	102.9	120	87	116.8	102.5	1
1	152	155.2	47.6	59.7	137.3	48.2	83.66667	1
1	163.8	86	86.9	88.2	114	61.1	78	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	92.6	180.4	39.6	40.7	199.2	47.4	89.13333	1
1	62.7	82.5	117.5	120	84.9	132.3	110.7667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	95.4	165.2	66.2	65.7	126.1	81.3	104.2333	1
1	79.6	80.3	129.8	132	88.8	89.5	99.86667	1
1	65.2	79.4	102	101.8	83	168.5	116.6333	1
1	95.2	82.5	109.4	100.7	94.3	117.9	103.2667	1
1	125.4	118.5	65.9	70.8	125.6	93.9	92.76667	1
1	100.4	105.7	91	101.7	91.9	109.2	101.9667	1
1	81.3	70.7	127.9	96.9	94	129.2	109.2667	1
1	96.8	82.1	107.3	108.7	99.5	105.5	98.3	1
1	99.3	110.8	108.4	94	87.7	99.8	106.3333	1
1	97.3	97.4	104.5	90.3	85.6	124.9	108.9333	1
1	78.2	85.1	121.4	109.5	80.8	125	110.5	1
1	122.6	91	76.2	98.2	148.8	63	76.73333	1
1	93.5	87.2	102.7	110.6	116.4	89.6	93.16667	1
1	94.2	111.2	104.9	90.2	89.9	109.7	108.6	1
1	74	88.4	116.2	66.3	91.1	164	122.8667	1
1	81.8	92.1	87.3	122.8	90.8	125.3	101.5667	1

1	108.7	92.2	86.8	118.3	91.3	102.6	93.86667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	86.8	107.9	111.8	115.9	99.3	78.3	99.33333	1
1	87.3	103.5	91.4	112.3	87.5	118	104.3	1
1	80.5	92.8	68.8	143.5	117.2	97.3	86.3	1
1	88.7	91.1	101.1	107.4	80.7	131	107.7333	1
1	78	102.3	94.5	107.4	85	132.7	109.8333	1
1	146.7	119.8	89.7	76.8	90.4	76.6	95.36667	1
1	69.8	70.4	123.9	109.7	87.2	139	111.1	1
1	110.2	99.2	93.9	94.8	100.7	101.2	98.1	1
1	105.1	106.4	95.1	93.5	97.3	102.6	101.3667	1
1	107.3	126.2	82	100.4	82.4	101.7	103.3	1
1	96.8	94.8	104.3	118.4	80.2	105.5	101.5333	1
1	87.5	85.9	101.9	119.2	84.7	120.7	102.8333	1
1	72.4	90.3	120.9	129.3	75.7	111.4	107.5333	1
1	86.9	102.9	107.1	92.3	99.8	111.1	107.0333	1
1	93.7	86.1	109.5	105.1	80.3	125.4	107	1
1	81.8	92.1	107.8	119.1	95.3	104	101.3	1
1	56.6	74.6	134.3	110.9	74.9	148.6	119.1667	1
1	103.5	126.3	69.7	88.2	143.7	68.6	88.2	1
1	130.6	103	92.7	93.6	94.1	86	93.9	1
1	94	140.4	86.6	110.3	95.2	73.4	100.1333	1
1	71.7	90.9	128.6	110.6	66.3	131.9	117.1333	1
1	82.8	136.5	113.8	107.5	86.6	72.9	107.7333	1
1	96.2	102.1	112.5	96.8	100.3	92	102.2	1
1	90.1	135.3	111	89.5	74.2	99.9	115.4	1
1	97.8	106.5	74.2	86.8	102.8	131.9	104.2	1
1	85.6	109.8	113.7	91.7	116	83.2	102.2333	1
1	123.9	113.8	82.4	82.2	100.7	97.1	97.76667	1
1	93.6	87.9	95.9	93.2	83.1	146.4	110.0667	1
1	120.5	106.5	86.3	87.9	98.3	100.5	97.76667	1
1	79.8	111.9	120.2	92.5	79.7	115.9	116	1
1	89.5	79.8	98	116.5	96.5	119.7	99.16667	1
1	72.7	67.1	119.4	108.4	73.4	159.1	115.2	1
1	64	74	130.5	142	64.3	125.1	109.8667	1
1	112.1	110.6	90	89	92.1	106.3	102.3	1
1	103.8	92.6	82.9	111	116.7	93.1	89.53333	1
1	98.5	121.9	59.5	73.2	172.7	74	85.13333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	70.9	75.2	146.5	147.6	67	92.8	104.8333	1
1	78.2	131.1	85.9	82.7	130.2	91.9	102.9667	1
1	76.4	68	126.3	147.4	74.4	107.6	100.6333	1
1	89.1	93.2	113.8	105.6	92.9	105.4	104.1333	1
1	88.3	192.3	105.8	62.2	97.4	53.9	117.3333	1
1	76.6	94.9	120.4	100.7	100.6	106.8	107.3667	1
1	62.5	72.8	132.2	63.2	61	208.4	137.8	1
1	93	97.5	92.3	101.4	94.5	121.3	103.7	1
1	97	92.6	90	103.6	107.5	109.3	97.3	1
1	82.9	98.5	81.2	109.7	98	129.7	103.1333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	107.4	112.9	89.8	102.4	101.8	85.7	96.13333	1

1	97.2	64.3	129.3	114.7	83.5	110.9	101.5	1
1	89.4	71.5	79.4	136	120.3	103.4	84.76667	1
1	94.2	95.3	107.8	94.9	73.2	134.7	112.6	1
1	101.7	116	102.1	86.3	86.3	107.7	108.6	1
1	82.4	90.3	111.9	132.7	97.9	84.8	95.66667	1
1	80.3	115.4	115.2	101	94.5	93.6	108.0667	1
1	69	105.5	76.6	104.1	110.3	134.4	105.5	1
1	57.7	73.6	178.2	76.8	81.4	132.4	128.0667	1
1	44	117.7	89.2	202.7	80.7	65.8	90.9	1
1	85.7	93	96.3	75.5	85.7	163.8	117.7	1
1	82.7	88.7	130.7	117.9	74.5	105.5	108.3	1
1	106.3	116.8	89.6	78	101.6	107.6	104.6667	1
1	114.8	91.6	105.4	97.5	91.1	99.7	98.9	1
1	86.7	80.9	104.1	103.6	86.2	138.6	107.8667	1
1	147.9	105.2	127.2	97.7	86.2	35.9	89.43333	1
1	87.3	85.6	98.5	119.3	94.3	115	99.7	1
1	102.7	83.3	72.7	149.9	113	78.3	78.1	1
1	112.4	84.9	93.6	115.4	96.7	97	91.83333	1
1	75.5	65.8	94	57.5	65.1	242.2	134	1
1	88.3	121.8	104.6	86.5	95.7	103	109.8	1
1	66.9	96.9	104.7	207.8	58.3	65.3	88.96667	1
1	78.3	98.5	120.9	111	106.1	85.2	101.5333	1
1	114.7	100.9	89.8	98.9	99.7	96	95.56667	1
1	62.6	114.4	127.6	94.2	79.6	121.6	121.2	1
1	130.7	120	74	77.5	129.3	68.4	87.46667	1
1	86.9	91.6	111.6	112.1	106	91.8	98.33333	1
1	108.1	101	77	114.2	72.5	127.2	101.7333	1
1	111	103.2	90.9	92.8	112.4	89.8	94.63333	1
1	90.3	76.7	95.8	112.8	109.6	114.7	95.73333	1
1	110.5	149.4	73.4	88.3	124.5	53.9	92.23333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	88	102	87.7	104.3	92.4	125.6	105.1	1
1	83	92.5	132.6	84.4	84.7	122.8	115.9667	1
1	73.7	67.7	120.2	128.4	82.1	127.9	105.2667	1
1	106.8	94.3	96.8	93	108.4	100.7	97.26667	1
1	88.3	103.3	42.5	161.9	59.3	144.8	96.86667	1
1	58.9	118.4	119.1	138.2	75.1	90.2	109.2333	1
1	74.7	69.6	102.5	88.5	69.4	195.3	122.4667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	73.5	80.2	128	107.6	76.9	133.8	114	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	100.8	107.4	83.6	96.6	106.1	105.4	98.8	1
1	80.2	80.9	105.8	112.9	75.2	145	110.5667	1
1	76.6	111.5	126.6	104.7	89.1	91.4	109.8333	1
1	79	95.9	90.7	112.5	93.1	128.8	105.1333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	71.7	74.8	125.6	100.1	79.1	148.6	116.3333	1
1	28.4	30.6	423.7	43.1	30.9	43.3	165.8667	1
1	88.2	98.3	98.1	105.7	97.4	112.3	102.9	1
1	181.4	112.8	79.1	70.4	80.2	76.1	89.33333	1
1	90.1	89.7	105.5	89.7	95.5	129.4	108.2	1

1	90.1	90.8	108.8	107.9	86.3	116.1	105.2333	1
1	96.5	108.4	85.1	90.1	97.3	122.6	105.3667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	121.9	108.8	85.3	84.7	108.9	90.4	94.83333	1
1	111.7	78.9	98.2	92.7	118.2	100.2	92.43333	1
1	111.9	87.1	104	105.8	101.8	89.4	93.5	1
1	123	95.3	94.9	95.9	95.9	95.1	95.1	1
1	77.6	77.1	146.9	106.9	89	102.6	108.8667	1
1	75.1	77.7	110.3	102.2	97.5	137.2	108.4	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	50.6	149.3	39.9	126.2	35.4	198.6	129.2667	1
1	81.9	101.9	99.6	98.3	101	117.3	106.2667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	46	51.4	233.4	143.2	56.1	69.8	118.2	1
1	80	82.7	128.4	123	78.4	107.5	106.2	1
1	79.5	107.9	108.2	95.8	95.1	113.5	109.8667	1
1	110.5	105.4	94.4	91.4	108.3	90	96.6	1
1	73	92	106.5	123.6	69.8	135.2	111.2333	1
1	106.7	92.3	98.7	98.2	100	104.1	98.36667	1
1	99.6	109.8	98.2	79.4	83.3	129.6	112.5333	1
1	79	84.5	112.7	110.4	96.8	116.6	104.6	1
1	130.2	91	93.5	86.8	101.5	96.9	93.8	1
1	94.9	108.8	91.8	104.4	101	99	99.86667	1
1	112.6	122.9	81.1	94.4	107.9	81.2	95.06667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	64.6	132.8	90.6	141.3	84.3	86.3	103.2333	1
1	94.6	78.8	119.9	104.2	95	107.5	102.0667	1
1	94.7	110.4	84.3	105	102.1	103.4	99.36667	1
1	100.4	106.8	105	91.6	106	90.4	100.7333	1
1	92.8	101.7	101.9	101.8	89.5	112.2	105.2667	1
1	119.5	102.6	81.6	93.4	101.4	101.4	95.2	1
1	111.8	118.6	94.2	89.1	95.1	91.2	101.3333	1
1	103.3	103.3	94	99.2	112.1	88.1	95.13333	1
1	126.1	119	58.1	70.6	96.6	129.6	102.2333	1
1	90.1	90.4	105.4	104.3	88.9	120.8	105.5333	1
1	92.7	95.4	100.7	95.4	102.4	113.4	103.1667	1
1	84	97.8	156.7	83.1	111.3	67	107.1667	1
1	94.3	111.8	92.6	102.2	99.4	99.7	101.3667	1
1	95.8	95.9	80	127.6	115.4	85.3	87.06667	1
1	65.7	78.4	127.6	109	84.7	134.4	113.4667	1
1	93.1	119.7	93	88.9	97.8	107.5	106.7333	1
1	91.4	101.3	96.9	100.1	96	114.3	104.1667	1
1	115.8	91.6	88.9	100.2	110.2	93.4	91.3	1
1	94.6	86.7	99.4	119	81	119.3	101.8	1
1	84.2	80.6	104.2	97.2	103.3	130.5	105.1	1
1	95.7	95.3	103.4	112.3	84.8	108.5	102.4	1
1	60.2	101.5	92.4	146.8	96.3	102.8	98.9	1
1	92.8	89.2	106.5	151.6	78.9	81	92.23333	1
1	107.3	112	89.1	93.4	102.7	95.4	98.83333	1
1	97.8	98.5	96.2	114.5	104.7	88.4	94.36667	1

1	90.7	74.1	94.9	128.5	118.9	92.9	87.3	1
1	115.5	101	92.3	97.1	110.5	83.6	92.3	1
1	103.1	111.5	93.5	92.3	106	93.7	99.56667	1
1	142.9	100.6	63.1	121.2	86	86.2	83.3	1
1	111.6	95.7	98.3	106.7	108.8	78.9	90.96667	1
1	102.4	93.9	110.7	95.2	96.3	101.5	102.0333	1
1	105.6	85.6	82.7	117.6	128.6	80	82.76667	1
1	61	68.3	132.5	118.3	89.1	130.8	110.5333	1
1	74.1	92.9	100.3	101.6	115.3	115.7	102.9667	1
1	87.2	88.5	92.9	100.4	82	149.1	110.1667	1
1	95.4	90.1	95.2	99.3	110.9	109.1	98.13333	1
1	77.8	90.5	108.3	112.9	84.6	125.9	108.2333	1
1	148.6	85.4	77.2	103.4	101.7	83.7	82.1	1
1	103.1	87.9	109.4	109.6	89.7	100.3	99.2	1
1	73.7	84.6	101.4	150.5	81.6	108.2	98.06667	1
1	106.6	86.3	85	113.4	80.9	127.8	99.7	1
1	95.6	92.9	116.9	110.9	91.2	92.6	100.8	1
1	113.1	110.5	96.2	86	120.4	73.9	93.53333	1
1	93.5	93.9	91.1	113.2	88.1	120.3	101.7667	1
1	137.6	100.4	90.4	81.1	88.8	101.7	97.5	1
1	83.6	80.6	99.7	128.9	91.5	115.7	98.66667	1
1	89.8	80.7	104.7	103.9	109.7	111.2	98.86667	1
1	72.3	109.3	98.5	120.7	88.1	111	106.2667	1
1	85.8	105.1	100.1	105.8	97.4	105.8	103.6667	1
1	90.2	87.2	112.4	112.4	77.3	120.5	106.7	1
1	74.8	99.2	127.6	96	93.1	109.5	112.1	1
1	121.2	89.9	93.1	101.1	107.6	87.1	90.03333	1
1	92.6	102.9	109.8	87.8	99.8	107	106.5667	1
1	90.8	87.4	94.9	114.1	109.4	103.4	95.23333	1
1	95.3	102.4	88.3	88.1	124.4	101.5	97.4	1
1	80.3	86.8	183.3	92.2	85.4	71.9	114	1
1	111.7	113.3	89.1	81	93.5	111.4	104.6	1
1	76.4	162.8	83.7	95.6	83.7	97.8	114.7667	1
1	94.3	79.7	126.7	103.6	91	104.7	103.7	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	128.5	85.4	65.1	54.7	148.2	118	89.5	1
1	57.6	90.8	72.2	127.3	114.7	137.6	100.2	1
1	112.2	81.3	114.4	99.1	87.6	105.4	100.3667	1
1	131.5	87.7	83.2	103.7	106.5	87.4	86.1	1
1	72.3	79.5	98.7	110.4	77.6	161.5	113.2333	1
1	131.1	90.1	110.7	92.3	93.1	82.8	94.53333	1
1	96.7	87.1	97.5	100	79.6	139	107.8667	1
1	79.7	91.5	144.7	93.6	74	116.6	117.6	1
1	99.4	88.2	92	112	92.7	115.8	98.66667	1
1	101.4	128.2	91.4	82.8	118.5	77.7	99.1	1
1	95.7	82.6	122	120.4	90.3	89	97.86667	1
1	96.3	98	92.2	92.7	107.4	113.5	101.2333	1
1	84.7	117.7	100.7	98	112.2	86.8	101.7333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	118.1	119.4	76.4	79.7	128	78.5	91.43333	1
1	71.9	112	102.8	97.4	97	119	111.2667	1

1	65.1	113.1	51.5	144.6	61.7	164	109.5333	1
1	67	107.1	87	139.4	81.5	117.9	104	1
1	89.3	91.4	106.6	123.1	84.2	105.5	101.1667	1
1	149.1	95.9	67.3	96.8	130.5	60.5	74.56667	1
1	106.3	86.6	98.8	83.5	108.8	116.1	100.5	1
1	110.6	97.1	91	93.1	107.3	100.9	96.33333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	120	83.1	96.5	104.1	94.6	101.8	93.8	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	121.7	92	74.9	105.9	115	90.5	85.8	1
1	108.1	103.7	72	96.6	94	125.7	100.4667	1
1	88.5	81.5	100.2	102.8	81.7	145.3	109	1
1	88.7	105.6	101.9	70	132.5	101.4	102.9667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	119.1	98.9	98.6	88.4	90.7	104.5	100.6667	1
1	113.7	129.9	100.6	76	102.8	77	102.5	1
1	90.7	93.2	100.8	114.8	105.8	94.7	96.23333	1
1	89.3	82.3	173.2	87.4	79.3	88.4	114.6333	1
1	100	107.4	114.6	79.3	84.4	114.3	112.1	1
1	95	69.8	145.4	99.6	88.2	102.1	105.7667	1
1	106.1	87	105.7	117.3	94.9	89	93.9	1
1	75.9	75.9	119	102.3	84.2	142.7	112.5333	1
1	103.1	88.9	97.8	122.9	74.4	112.9	99.86667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	91	111.7	137.3	80.9	78	101.1	116.7	1
1	82.1	80.7	104.9	111.7	105.2	115.3	100.3	1
1	53.9	90.1	117	105.3	107.4	126.3	111.1333	1
1	142.8	120.9	76.8	77.5	115.2	66.8	88.16667	1
1	98.3	102.9	85.5	93	97.9	122.4	103.6	1
1	84.9	94.5	92.5	106.8	80.5	140.9	109.3	1
1	65.3	66.9	129.5	114.8	82.3	141.2	112.5333	1
1	64.2	79	122.4	111.2	72	151.1	117.5	1
1	106.8	100.7	92.8	97	93.8	108.9	100.8	1
1	118.3	134.6	64.7	96.9	86	99.6	99.63333	1
1	94.3	99.3	96.5	89.1	86.8	134	109.9333	1
1	93.7	85.9	121.5	102.5	93.2	103.4	103.6	1
1	128.5	97.9	93	92.3	100.1	88.2	93.03333	1
1	70.9	86.8	91	103.8	95.4	152.1	109.9667	1
1	78	88.5	115.2	105.6	84.1	128.6	110.7667	1
1	69.1	77.6	113.1	108.9	130.1	101.2	97.3	1
1	91.6	102	100.5	100.2	95	110.7	104.4	1
1	107.7	130.2	78.5	101.3	80.5	101.8	103.5	1
1	78.1	76.6	86	200.3	73.7	85.3	82.63333	1
1	91.8	105.7	98.9	98	113.2	92.3	98.96667	1
1	80.2	103.6	105.2	101.4	89.5	120.1	109.6333	1
1	73.1	96	115.1	120.8	70.4	124.6	111.9	1
1	91.6	99.5	99.4	110.9	101	97.6	98.83333	1
1	51	98.8	91.4	63.5	72.1	223.3	137.8333	1
1	67.7	71.3	121.8	104.9	104.3	129.9	107.6667	1
1	83.9	100.1	152.1	92.9	76.3	94.7	115.6333	1
1	87.5	107	101.7	95.8	81.1	127	111.9	1

1	95.7	170.1	84.3	86.6	84.7	78.5	110.9667	1
1	84.9	92.3	109.4	119.3	91.5	102.7	101.4667	1
1	79.2	118.1	85.8	89.3	91.5	136.1	113.3333	1
1	81.7	106.4	103.4	102.9	82.2	123.4	111.0667	1
1	50.8	78.6	162.9	89.3	65.2	153.2	131.5667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	108.7	106.2	88.6	93.1	105.9	97.6	97.46667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	74.4	92.9	140.4	87.5	94.1	110.6	114.6333	1
1	110.3	147.4	76.1	79.6	111.2	75.4	99.63333	1
1	89.2	82.2	110.5	113.5	83.4	121.1	104.6	1
1	94	105.8	107	91.3	113.6	88.4	100.4	1
1	91.9	81.3	100.7	106.2	125.8	94.1	92.03333	1
1	62.5	69.9	128.4	109.9	90.2	139	112.4333	1
1	79.5	104.2	112.7	120.7	102.3	80.7	99.2	1
1	98.9	108.7	113.7	92.6	96.8	89.3	103.9	1
1	103.6	84.3	101.9	113.6	106.6	90	92.06667	1
1	81.8	86.3	113.2	110.1	101.2	107.3	102.2667	1
1	77.1	87.7	177.4	72.6	62.3	123	129.3667	1
1	102.1	102.8	112.2	93.3	97.4	92.3	102.4333	1
1	69	65.3	164.2	83.2	75.3	142.9	124.1333	1
1	100.9	121.7	95.5	94.3	97.9	89.6	102.2667	1
1	186.4	124.6	53.7	55.8	132	47.5	75.26667	1
1	102	101.6	92.3	104.9	131.7	67.6	87.16667	1
1	83.7	71.6	113.5	113.5	77.8	139.9	108.3333	1
1	101.1	98.7	100.8	105.2	108.5	85.7	95.06667	1
1	86.7	89.6	110.8	118.8	97.2	96.8	99.06667	1
1	94.2	98.4	108.6	98.7	99.9	100.3	102.4333	1
1	68.7	79.3	131	116.9	83.6	120.6	110.3	1
1	79.2	100.1	106.4	90	77.2	147.2	117.9	1
1	92.7	119.5	99.8	95.6	96.4	96	105.1	1
1	88.7	108	91.4	103.3	105.2	103.4	100.9333	1
1	79.4	87.2	107.9	102.8	97.1	125.7	106.9333	1
1	76.1	80.7	115.7	124.9	77	125.6	107.3333	1
1	82	94.9	105.1	101	108.7	108.3	102.7667	1
1	60.7	123	115	92.8	88.7	119.9	119.3	1
1	89	142.8	119.8	55.4	155.1	37.9	100.1667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	67.5	81.3	124.9	112.2	96.6	117.6	107.9333	1
1	85	81.2	99.8	122	104	108	96.33333	1
1	125.4	118.6	75.6	78.6	114.5	87.4	93.86667	1
1	78.9	87.1	106.2	111.2	77.1	139.6	110.9667	1
1	73.4	86.1	117.2	100	93	130.4	111.2333	1
1	74.1	83.4	205.3	89.6	74.2	73.4	120.7	1
1	122	96.2	85.7	94.6	110.2	91.3	91.06667	1
1	103	109.2	91.3	85.6	90.4	120.6	107.0333	1
1	88.4	61.5	183.2	87.8	86.2	93	112.5667	1
1	103.8	98.4	92.9	101.8	114.9	88.3	93.2	1
1	88.5	90.8	84.1	106.6	99.4	130.6	101.8333	1
1	123.4	88	83.1	111.2	94.9	99.3	90.13333	1
1	116	77.9	120.8	102.5	110.4	72.5	90.4	1

1	95.3	106.4	91	118.5	87.9	100.9	99.43333	1
1	111	119.2	70.2	110.7	75.8	113.1	100.8333	1
1	93.9	90.5	105.1	106.4	93.2	110.9	102.1667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	92	101.5	105.8	94.5	112.8	93.4	100.2333	1
1	67.1	83.7	86.2	180	69.1	114	94.63333	1
1	69.4	74.4	115.4	100.6	120	120.1	103.3	1
1	106.5	108.9	90.8	100.8	85.6	107.3	102.3333	1
1	76.8	96.9	97.7	134.7	96.1	97.8	97.46667	1
1	100.7	89.7	102.8	84.8	83	139.1	110.5333	1
1	90.7	113.9	92.1	98.2	116.6	88.5	98.16667	1
1	105	116.1	82.8	93.5	120.6	82.1	93.66667	1
1	61.1	84.1	126.9	93.5	92.4	142	117.6667	1
1	58.6	66.6	117.3	127	83.7	146.9	110.2667	1
1	72	60.6	96.5	160.4	100	110.5	89.2	1
1	93.6	97	95.7	110.8	92.9	110	100.9	1
1	109.1	93.4	74	89.4	116.1	117.9	95.1	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	88.8	83.3	116.6	123.5	84.8	103	100.9667	1
1	97.4	137.3	86.2	83.8	106.5	88.7	104.0667	1
1	76.1	89.5	102.2	99	87.7	145.4	112.3667	1
1	85.2	86.5	112.7	90.4	123.3	101.9	100.3667	1
1	124.3	78	101.2	100.7	80.4	115.3	98.16667	1
1	118.5	94	96.5	95	101.5	94.5	95	1
1	96.4	85.4	107.3	102.1	102.4	106.3	99.66667	1
1	100.4	96.8	96.1	97.8	110.1	98.8	97.23333	1
1	119.7	95	144.5	85.2	72.5	83.1	107.5333	1
1	87.4	101.1	115.3	100.4	96.1	99.6	105.3333	1
1	99.9	69.8	111	83.7	109.1	126.6	102.4667	1
1	97.2	105.6	111	92.1	74.4	119.7	112.1	1
1	70.2	79.1	148.5	69.3	149.7	83.2	103.6	1
1	145.2	88.7	89.5	83.5	117.9	75.2	84.46667	1
1	90.1	84.3	106	107.2	93.5	119	103.1	1
1	103.1	98.9	94.8	101.9	84.4	117	103.5667	1
1	39.8	61.1	151.3	136.2	111.8	99.9	104.1	1
1	116.8	129.6	87	80.3	79.6	106.7	107.7667	1
1	104.6	103.1	102.8	92.5	119.6	77.4	94.43333	1
1	72.2	111.8	115.2	111	83.1	106.6	111.2	1
1	175.2	83.9	79.3	85.8	95.9	79.9	81.03333	1
1	85.6	88.4	124.2	106.5	101.5	93.8	102.1333	1
1	100.9	112.2	95	106.5	100.3	85	97.4	1
1	59.9	75.6	107.9	115.2	76.1	165.3	116.2667	1
1	78.8	126	92.1	96.2	90.4	116.5	111.5333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	97.7	95.5	108.7	104.1	109.5	84.4	96.2	1
1	87.5	95.8	108.9	117.5	93.3	97	100.5667	1
1	84.2	80.8	118.9	95	98.8	122.3	107.3333	1
1	73.1	78.8	128.5	118.6	82.7	118.2	108.5	1
1	106	91.4	103.4	95.9	99.5	103.9	99.56667	1
1	91	95.1	86.8	99.7	98.8	128.6	103.5	1
1	228.6	77.8	71.8	61.4	62.2	98.2	82.6	1

1	68.4	76.4	126.5	137.7	84.5	106.6	103.1667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	84.2	72.8	115.4	104	114.1	109.6	99.26667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	73.3	69.9	110	116.2	98.6	131.9	103.9333	1
1	91.4	103	104.9	100.6	80.2	119.9	109.2667	1
1	65.5	79.6	126.6	106.1	81	141.1	115.7667	1
1	103.1	109.3	83.8	110.6	92	101.2	98.1	1
1	96	87.9	109.7	119.7	85	101.6	99.73333	1
1	100.9	139.3	119.5	78.2	82	80.2	113	1
1	91.5	115	57.6	72.6	85.6	177.8	116.8	1
1	80.1	66.7	119.8	115.3	91.6	126.5	104.3333	1
1	93.5	111.8	123.4	81.9	93.4	95.9	110.3667	1
1	91.5	91.1	104.2	107.6	101.1	104.6	99.96667	1
1	142	124.6	88.5	75.2	90	79.6	97.56667	1
1	119.1	86.4	91	111	101	91.5	89.63333	1
1	70.5	98.6	109.1	90	87.9	143.7	117.1333	1
1	121.3	90.4	91.1	113.2	118.6	65.4	82.3	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	130.7	82.8	85	96.3	103.7	101.5	89.76667	1
1	119.6	114.8	85.8	96.9	102.7	80.2	93.6	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	210.5	81.9	54.8	85.5	100.6	66.7	67.8	1
1	66.1	100	112.4	126.7	85.3	109.4	107.2667	1
1	127.3	122.7	87.3	72.8	115.5	74.4	94.8	1
1	69	76	104.4	111.9	106.7	132	104.1333	1
1	76	112.2	90.6	97.4	119.7	104.2	102.3333	1
1	71.1	75.3	122.9	106.6	78.5	145.5	114.5667	1
1	74.1	75.7	113.2	122.5	120.3	94.2	94.36667	1
1	59.6	58.5	32.5	299.3	51.9	98.3	63.1	1
1	95.1	89.5	90.7	125.9	87.7	111	97.06667	1
1	84.1	92	80.7	82.5	80.6	180.1	117.6	1
1	121.9	101	109.4	84.5	93.4	89.8	100.0667	1
1	86.7	97.8	101.6	105.5	104.9	103.5	100.9667	1
1	77.5	79.9	200.1	86.6	88.2	67.7	115.9	1
1	72.6	111.7	105.2	111.3	115.9	83.3	100.0667	1
1	62.6	68.9	127.7	153.6	67	120.2	105.6	1
1	93.1	90.2	86.8	115.3	113.1	101.5	92.83333	1
1	108.6	122.6	98.4	79.9	92.4	98.2	106.4	1
1	69.3	79.7	101.4	125.1	83.2	141.3	107.4667	1
1	95.2	88.8	92.7	113.1	97.6	112.6	98.03333	1
1	69.3	94.5	115.3	107.5	97.5	116	108.6	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	118.2	102.6	73.1	85.4	102.4	118.3	98	1
1	70.3	64.7	150.5	105.8	96.3	112.4	109.2	1
1	82.7	82.1	175.6	92.1	77.4	90.1	115.9333	1
1	93.4	123.8	58.9	100.1	139.6	84.2	88.96667	1
1	90.3	83.7	104.7	101.4	91	128.9	105.7667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	115	87.8	95.9	103.9	97.1	100.3	94.66667	1

1	82.5	92	124.5	107.9	81.3	111.8	109.4333	1
1	91.3	96.7	109.4	114.1	64.8	123.8	109.9667	1
1	78.7	94.7	95	89.6	110.9	131	106.9	1
1	44.7	60.3	106.9	69.2	55.8	263.1	143.4333	1
1	94.9	97.5	95.9	102.9	91.8	116.9	103.4333	1
1	107.3	99.4	86.6	110	99.8	96.9	94.3	1
1	58.2	31.9	105.6	174	111.6	118.8	85.43333	1
1	87.9	111.2	104.6	112.2	118.8	65.3	93.7	1
1	88.3	90.6	88.4	96.3	83.4	153	110.6667	1
1	95.8	90.5	117.1	101.7	107.9	87.1	98.23333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	85.5	78	131.4	109.7	80.9	114.5	107.9667	1
1	106.6	90.3	92.6	100.7	90.6	119.3	100.7333	1
1	85.6	95.9	99.7	104.1	89.3	125.5	107.0333	1
1	132.7	114.7	73.3	84.8	105.9	88.5	92.16667	1
1	53.3	54.6	155.7	109.8	80.3	146.4	118.9	1
1	104.5	90.2	93.8	111.6	99.3	100.7	94.9	1
1	91.5	102.2	105.4	105.2	105.9	89.7	99.1	1
1	110.7	99	81.4	96.7	108	104.1	94.83333	1
1	97.1	111	106.4	90.7	104.9	89.7	102.3667	1
1	82.9	75	80	117.2	81.4	163.6	106.2	1
1	106.9	97.9	91.8	106.3	96.9	100.2	96.63333	1
1	71.3	106.6	93.1	104.8	95.4	128.8	109.5	1
1	108.2	92.2	97.2	97.6	98.3	106.6	98.66667	1
1	73.8	78.2	122.2	110.7	68.5	146.6	115.6667	1
1	73.7	79.8	109	105.9	160.6	70.9	86.56667	1
1	71.5	97.6	115.4	88.3	91.2	136.1	116.3667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	122.6	107.1	79.8	95.8	99.4	95.3	94.06667	1
1	91.5	82.8	129.4	107.8	116.6	71.9	94.7	1
1	139.5	76.3	100.5	97.6	79.5	106.6	94.46667	1
1	84.6	83.7	104	103.9	110.5	113.4	100.3667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	84.6	74.8	100.7	102.1	119.9	117.9	97.8	1
1	108.9	110.5	89.9	82.2	114.4	94.1	98.16667	1
1	87.8	104.4	89.4	92.5	87	138.9	110.9	1
1	75.7	66.2	131.5	111.3	89.1	126.2	107.9667	1
1	73.4	79.7	124.3	105.7	86.8	130	111.3333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	91.5	97	97.8	105.3	100.3	108.1	100.9667	1
1	83.1	79.4	109.6	101.5	102.4	124.1	104.3667	1
1	93.4	111.6	74.5	73.4	76.2	170.8	118.9667	1
1	94.4	71.3	111.2	144.1	103.6	75.4	85.96667	1
1	117.6	109.1	81.2	107.1	98.3	86.8	92.36667	1
1	116.4	78	80.7	100.9	99	124.9	94.53333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	120.3	82.6	86.6	91.3	104.2	115	94.73333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	69.7	75.4	163	86.6	73.6	131.7	123.3667	1
1	96	86.8	108.6	104	117.7	86.8	94.06667	1

1	89.7	127.1	73.3	83.6	110.7	115.5	105.3	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	71.1	61.9	127.6	188.3	63.3	87.9	92.46667	1
1	73.9	74.3	106	96.7	87.9	161.2	113.8333	1
1	88.5	102.5	91.7	76.5	77.8	163.1	119.1	1
1	88.5	104.2	107.4	102.4	104.8	92.7	101.4333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	70.4	124	86.1	87.8	146.8	85	98.36667	1
1	129.6	62.3	88.5	117.1	89.5	113	87.93333	1
1	94.6	72.8	82	119.1	61.8	169.7	108.1667	1
1	111.4	92.3	88.5	111	105	91.9	90.9	1
1	86	113	94.9	100.5	86.2	119.4	109.1	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	117.8	91.1	87.1	115.7	101.6	86.7	88.3	1
1	77.9	74.3	109.2	123.6	104	111	98.16667	1
1	101.9	79.1	105.2	101.7	105.1	107.1	97.13333	1
1	90.8	69.2	113.9	118.1	93.4	114.7	99.26667	1
1	148.1	94.9	111.8	86	89.7	69.5	92.06667	1
1	98.3	123.8	102.1	90.5	93.5	91.8	105.9	1
1	92.6	93.4	96.7	109	119.3	88.9	93	1
1	84.1	68.4	174.2	106.9	72.1	94.4	112.3333	1
1	73.7	108.1	162.2	92.6	88.5	74.9	115.0667	1
1	117.3	82.9	92.9	92.7	84.3	130	101.9333	1
1	103.9	103.1	98.6	98.9	87.7	107.7	103.1333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	102	73.1	106.4	108.3	123.1	87.1	88.86667	1
1	143.7	119.4	75.2	77.1	114.1	70.5	88.36667	1
1	80.5	77.9	95	135.6	122.2	88.8	87.23333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	90.1	107.5	118.5	81.9	86.5	115.5	113.8333	1
1	76.1	83.1	121.6	95.3	82.4	141.5	115.4	1
1	88.7	85.8	107.8	109.1	105.7	102.8	98.8	1
1	81.7	94.6	126.8	73.8	113.6	109.5	110.3	1
1	86.6	96.3	95.3	107.2	116	98.7	96.76667	1
1	60.9	70	119.7	124.2	114.3	110.8	100.1667	1
1	77.4	88	99.9	99.2	61.9	173.6	120.5	1
1	74.6	75.6	112.1	114.6	107.6	115.5	101.0667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	83.7	106.6	109.8	105.2	107.4	87.3	101.2333	1
1	62.9	115.5	102.1	132.2	81.3	106.1	107.9	1
1	90.4	94.7	68.2	67.7	94.4	184.7	115.8667	1
1	62.9	96.3	130.1	122.1	77	111.7	112.7	1
1	96.6	92.4	88.1	110.7	96.2	115.9	98.8	1
1	131.4	99	132.1	75.5	77.3	84.8	105.3	1
1	94.4	77	106.1	110.6	85.9	125.9	103	1
1	65.5	90.8	144.2	124.1	63.1	112.3	115.7667	1
1	59.5	45.8	210.1	96.9	72.6	115.2	123.7	1
1	87.7	91.3	92	100.9	109.3	118.9	100.7333	1
1	98	105.5	76.6	76.2	174.1	69.6	83.9	1
1	101.9	132.9	95.8	82.7	93.3	93.4	107.3667	1
1	83	97	94.2	102.1	98.2	125.6	105.6	1

1	103.7	97.4	109.8	97.9	89.2	101.9	103.0333	1
1	76.9	108.1	89.6	107.2	95.8	122.4	106.7	1
1	93.5	89.8	111	93.3	93.2	119.2	106.6667	1
1	79.2	78.2	125.4	113	79.3	124.8	109.4667	1
1	72.4	79.1	103	107.3	93.9	144.4	108.8333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	76	98.8	108.5	103.8	98.6	114.3	107.2	1
1	97.4	79.1	97.4	102.2	86.2	137.6	104.7	1
1	105.2	101.6	88.7	95	95.9	113.6	101.3	1
1	116.7	82.9	95.5	105.9	93.6	105.4	94.6	1
1	104.7	96.6	77.7	111.6	86.7	122.7	99	1
1	99.9	84.3	96.7	100	102.5	116.6	99.2	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	81.2	78.2	156.2	89	68.7	126.7	120.3667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	79.1	92.5	95.9	97.1	90.9	144.5	110.9667	1
1	74.9	69.6	150.9	112.6	102.6	89.4	103.3	1
1	156.8	68.2	75.2	112.9	123.7	63.2	68.86667	1
1	71	68.4	112.9	107.8	109	130.9	104.0667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	76.5	86.4	121.4	109.1	86.3	120.3	109.3667	1
1	74.8	87.6	98.3	112.6	113.8	113	99.63333	1
1	77.6	89.5	85.6	98.4	106.9	142.1	105.7333	1
1	82.5	90.3	91.1	107.1	122.3	106.6	96	1
1	88.3	76.1	126	118.4	79.2	111.9	104.6667	1
1	104.7	121.5	95.2	91.7	116.3	70.6	95.76667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	192.8	112.2	108.5	65.2	68.2	53.1	91.26667	1
1	100.3	103.7	97.8	93.1	108.7	96.5	99.33333	1
1	104	78.5	91.6	113	105.1	107.8	92.63333	1
1	95.2	116.2	99.9	99.1	95	94.5	103.5333	1
1	107.4	96.4	79.2	105.2	115.5	96.2	90.6	1
1	106.5	69.5	113.6	124.1	82.6	103.6	95.56667	1
1	99.2	103.6	104	95.6	90	107.6	105.0667	1
1	82.7	94.3	121.6	111.1	93.1	97.2	104.3667	1
1	189.9	102.5	53.1	62.6	137	55	70.2	1
1	92.7	119.9	108.6	87.1	69.7	122	116.8333	1
1	95.4	83.3	93.2	103.5	89.7	134.9	103.8	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	87.5	99	94.4	90.7	142.8	85.6	93	1
1	84.9	85.9	121.9	92	89	126.3	111.3667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	72.5	88.8	100	137.5	90.5	110.7	99.83333	1
1	82.3	91.6	104.1	94.5	82.8	144.8	113.5	1
1	77.4	111.6	122.7	99.4	81.8	107.2	113.8333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	38.5	45.7	190.8	105.5	36	183.5	140	1
1	84.1	79.9	88.2	120.2	96.1	131.5	99.86667	1
1	93.7	130.4	81.1	81	125.8	88	99.83333	1
1	NA	NA	NA	NA	NA	NA	NA	0

1	99.6	88.7	115	93.7	90.1	112.9	105.5333	1
1	109.1	85.7	91	98.8	116	99.3	92	1
1	115	83.6	107.2	97.4	101.7	95	95.26667	1
1	89.9	92.3	103.7	99.8	94.5	119.8	105.2667	1
1	62.4	144.2	129.9	159.8	50.1	53.6	109.2333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	86.5	89.4	112.1	109.3	83.4	119.3	106.9333	1
1	155.8	88.7	116.2	74.4	89.1	75.8	93.56667	1
1	67.4	63.7	164.3	119.1	65.3	120.3	116.1	1
1	88	80.1	76.9	129.7	93.6	131.7	96.23333	1
1	100.5	94.9	103	102	94.6	104.9	100.9333	1
1	89.4	84.9	105.5	97.9	141.1	81.2	90.53333	1
1	78.2	80.2	133.9	90.6	90.6	126.4	113.5	1
1	164.8	124.9	102.8	50.6	89.8	67	98.23333	1
1	56.8	83.9	97.8	110.7	101.6	149.1	110.2667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	99.1	95.1	96.2	99.3	69.3	140.8	110.7	1
1	144.6	107.6	71.1	73.8	127.1	75.8	84.83333	1
1	95.6	127.3	94.9	80.6	119.5	82.2	101.4667	1
1	92	82.9	94.2	115	93.2	122.7	99.93333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	108.5	90	79.9	77	145.9	98.6	89.5	1
1	92.4	119.4	96.4	88.7	103.9	99.2	105	1
1	105.5	78.6	82.9	110.2	93.1	129.7	97.06667	1
1	99.4	98.3	104.8	102.8	105.2	89.4	97.5	1
1	64.9	77	129.1	90.5	112.8	125.6	110.5667	1
1	113.6	105.9	80.2	102.9	98.9	98.6	94.9	1
1	88.6	113.9	117.7	90	107.4	82.4	104.6667	1
1	101.4	99.8	91.7	122.4	81.5	103.2	98.23333	1
1	83.5	67.9	244.5	44	62.1	98	136.8	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	88.5	85.2	81.8	100.2	91.5	152.9	106.6333	1
1	133.8	100.8	97	76.2	118.3	73.9	90.56667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	87.3	100.7	105	84.9	116.3	105.8	103.8333	1
1	72.6	84.1	137.4	100.5	82.2	123.2	114.9	1
1	62.8	72.8	112.5	117.8	79.1	155	113.4333	1
1	87.8	67	89.4	119.5	120.3	115.9	90.76667	1
1	92.9	93.8	111.6	101.4	91	109.3	104.9	1
1	67.5	68.3	151.5	93.2	96.3	123.3	114.3667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	105.3	86.7	108.1	107.3	90.1	102.6	99.13333	1
1	98.3	103.2	107	101.3	86.7	103.5	104.5667	1
1	107.1	109.4	98.7	101.5	100.8	82.6	96.9	1
1	106.8	98.2	97	95.8	102.3	99.9	98.36667	1
1	75.9	165.1	106.5	107.5	76.2	68.9	113.5	1
1	105.7	90.5	94.7	114.1	118.2	76.8	87.33333	1
1	99.3	103.7	113.5	96.7	76	110.8	109.3333	1
1	118.5	98.9	87.2	98.1	116.7	80.6	88.9	1
1	141.9	110.5	100.3	79.3	89.9	78.1	96.3	1

1	67.4	137.9	111	77.6	111.3	94.8	114.5667	1
1	92.6	90.8	111.9	102.4	88.8	113.5	105.4	1
1	75.4	98.2	83.2	88.6	113.8	140.8	107.4	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	96.1	99.8	105.9	97.9	101.9	98.4	101.3667	1
1	89.2	80.6	106.4	108.4	95.6	119.7	102.2333	1
1	69.3	61.4	91.1	103.7	183.8	90.7	81.06667	1
1	79.4	95.5	88.1	108.4	102.3	126.4	103.3333	1
1	121.9	93	87.9	100.3	80.9	115.9	98.93333	1
1	64.4	87.5	97.9	121.2	85.9	143.1	109.5	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	136.8	110.9	80.6	82.1	116.2	73.4	88.3	1
1	70.1	88	94.4	108.3	81.6	157.7	113.3667	1
1	92.7	92.6	99.2	101.4	78.9	135.1	108.9667	1
1	71.7	63.3	179.2	96.1	76	113.6	118.7	1
1	99.9	90.3	160.7	78.7	84.1	86.4	112.4667	1
1	79.1	74.1	125.7	117	87.7	116.4	105.4	1
1	102.5	102.2	84.6	100.1	96.2	114.3	100.3667	1
1	65.1	83.1	106	114.8	86.4	144.6	111.2333	1
1	77.6	85.8	147.3	83.7	81	124.6	119.2333	1
1	100.7	125.3	115	85.4	85.9	87.6	109.3	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	131.8	100.5	92.3	83.1	89.8	102.4	98.4	1
1	107.1	97.8	97.8	100.4	93.6	103.3	99.63333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	105.9	87.5	108.9	109.1	86.5	102.1	99.5	1
1	106.6	93.6	95.6	96.9	136.8	70.6	86.6	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	81.1	86.2	88.5	153.9	81.4	108.9	94.53333	1
1	88.9	107.4	91.7	88.8	100.4	122.8	107.3	1
1	106.1	106.3	92.7	101.2	92.5	101.2	100.0667	1
1	95.2	129.2	74.9	85.3	133.9	81.5	95.2	1
1	100	134.8	93	76.2	90.1	105.9	111.2333	1
1	95.3	88.8	104.4	93.8	100.5	117.2	103.4667	1
1	102.6	91.8	95.2	102.1	96.2	112	99.66667	1
1	89.5	55	136.6	126.1	68	124.8	105.4667	1
1	74.4	63.4	82.8	115.4	88.6	175.4	107.2	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	96.3	98.4	107.7	104.8	103.8	89.1	98.4	1
1	73.6	81.1	125.6	112.4	73.2	134.1	113.6	1
1	86.8	92.8	107.1	109.5	80.9	122.8	107.5667	1
1	107.2	113.3	99.3	93.6	97.2	89.4	100.6667	1
1	82	101.1	106.7	114.2	95.2	100.9	102.9	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	88.2	128.4	96.9	94.7	99.8	92	105.7667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	100	131.2	41.6	74.3	120.8	132.1	101.6333	1
1	90.4	105.1	107	111.3	66.3	119.8	110.6333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	110.5	94.6	76	121.1	95	102.8	91.13333	1
1	NA	NA	NA	NA	NA	NA	NA	0

1	75.6	78.3	130	133.2	75.7	107.2	105.1667	1
1	87.9	104.6	140.7	101.8	63.5	101.5	115.6	1
1	81.3	78.5	78.1	99.5	63.6	199.1	118.5667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	70.8	66.6	221.1	85.1	70	86.4	124.7	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	100.4	85.7	117.2	88.5	81.7	126.5	109.8	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	80.6	94.5	110.8	118.6	79.4	116.1	107.1333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	82.7	95.8	99.5	105.3	68.7	148	114.4333	1
1	64.1	94.5	119.6	90.7	96.1	135	116.3667	1
1	75.5	74.3	117.7	105.6	71	155.9	115.9667	1
1	98.9	92.6	110.3	96.1	89.6	112.5	105.1333	1
1	98.3	73.2	91.3	106.2	100.9	130.2	98.23333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	93	105.3	87.9	114.6	98.4	100.8	98	1
1	58.5	69.5	140.4	107.3	74	150.3	120.0667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	80.1	88.4	117.2	108.1	71.7	134.5	113.3667	1
1	106.7	104.8	74.1	80.9	76.9	156.6	111.8333	1
1	90	82.4	108.6	106.7	97.2	115.1	102.0333	1
1	97.5	103.7	92.9	92.9	112.1	100.9	99.16667	1
1	108	100.3	107.3	96.3	80	108	105.2	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	85.8	106.8	98.6	95	92.7	121.1	108.8333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	119.2	92.4	105.7	95.1	89.6	98.1	98.73333	1
1	87.1	107.7	132.6	90.9	106.7	75.2	105.1667	1
1	93.4	149.6	71.8	106.3	73.3	105.6	109	1
1	96	95.1	66.6	62.4	72.2	207.7	123.1333	1
1	103.9	104.2	108.2	94.5	102.8	86.4	99.6	1
1	93.2	91.2	109.9	105.7	85	114.9	105.3333	1
1	58.3	73.8	129.3	99.1	89.3	150.2	117.7667	1
1	107.1	98.6	81	95	117.9	100.4	93.33333	1
1	68.7	66.5	212.6	91	82.9	78.3	119.1333	1
1	89.8	86.8	107.5	127.4	80.9	107.5	100.6	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	106.2	106.9	88.6	96	101.8	100.6	98.7	1
1	100.4	112.2	94.4	84.2	114.2	94.5	100.3667	1
1	76.5	88.3	111.3	100.9	104.1	118.8	106.1333	1
1	81.9	76.9	104.2	110.1	86.2	140.7	107.2667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	86.9	89.5	107.9	99.4	90	126.3	107.9	1
1	69.6	87.3	101.1	130.8	83.5	127.7	105.3667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	81.9	71.8	118.7	105.6	91.1	131	107.1667	1
1	114.4	102.6	88.6	93.7	135.6	65.2	85.46667	1
1	121.4	112.7	81.6	88.7	103.9	91.7	95.33333	1

1	105.6	87.6	127.5	73.3	76.1	129.8	114.9667	1
1	88.9	102.3	106	119.5	74.2	109	105.7667	1
1	73.1	73.2	114.1	115	86	138.6	108.6333	1
1	94.2	100.6	96.4	140.6	94.5	73.7	90.23333	1
1	96.4	55.8	94.6	153.3	82.2	117.6	89.33333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	93.2	95.4	106.1	90.5	89.3	125.5	109	1
1	82	93.1	81.7	118.5	95	129.7	101.5	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	64.1	88.8	109.6	109.3	133	95.1	97.83333	1
1	91.4	97.1	110.4	101.1	89.5	110.5	106	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	80.7	120.4	84.3	81.3	118.3	115	106.5667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	109.2	82.4	102.1	96.3	95.4	114.7	99.73333	1
1	199.5	80.2	69.4	98.3	94.5	58.1	69.23333	1
1	92	114.2	111.8	96.8	101.9	83.2	103.0667	1
1	80.3	97.4	133.6	82.8	68.2	137.7	122.9	1
1	107.8	126.5	74.2	97.9	102.7	91	97.23333	1
1	102	97.1	104.1	106.8	103.8	86.2	95.8	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	98.6	110.7	90.2	80.1	99.1	121.3	107.4	1
1	80.9	50.9	183.4	98.8	103.6	82.4	105.5667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	75.7	88.7	98	178.4	66.9	92.3	93	1
1	114	96.4	107.6	120	90.8	71.3	91.76667	1
1	111	91.3	100.5	102	104.4	90.7	94.16667	1
1	95.8	85.9	82.1	143.4	108.2	84.6	84.2	1
1	82.9	94.9	94.7	108.7	87.5	131.3	106.9667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	90.4	90.6	122.7	93.4	89	114	109.1	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	130.3	109.7	100.2	77.2	105.1	77.6	95.83333	1
1	77.4	96.8	62.5	124.3	103.6	135.5	98.26667	1
1	96.5	76.6	104.3	100.3	112.9	109.4	96.76667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	115	120.2	73.3	92.6	89.9	109.1	100.8667	1
1	68.8	77.1	107.7	94.3	100.5	151.7	112.1667	1
1	84.5	100.4	91.6	111.8	124.1	87.7	93.23333	1
1	86.8	77.8	94.4	118.5	92.3	130.3	100.8333	1
1	89	83.8	128.6	100.6	96.4	101.7	104.7	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	124.5	116.3	82.2	89	106.5	81.5	93.33333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	79.1	95.7	85.9	95.4	139	104.9	95.5	1
1	84	97.5	91.9	100.9	107	118.7	102.7	1
1	NA	NA	NA	NA	NA	NA	NA	0

1	121.9	99.7	101	86.6	95.1	95.6	98.76667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	110.5	67.9	102.3	112.3	69.7	137.2	102.4667	1
1	106.6	84.6	109.7	97.2	85.7	116.2	103.5	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	112.2	96.4	102.4	86.4	113.5	89	95.93333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	62.3	68.4	106.9	73.7	86.1	202.6	125.9667	1
1	92	91.8	88.5	120	98.7	109	96.43333	1
1	118.2	101	100.9	92.6	113.4	73.9	91.93333	1
1	80	97.3	93.3	158.1	75.6	95.7	95.43333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	101	129.6	88.2	82.2	102.7	96.3	104.7	1
1	76.9	88.5	94.1	95	116	129.6	104.0667	1
1	56.3	78.9	122.6	70.6	153.3	118.4	106.6333	1
1	134	112.5	80.3	84.7	107.8	80.8	91.2	1
1	70.3	99.4	133.2	77.2	95.5	124.4	119	1
1	101.3	113.6	93.1	91.7	116	84.4	97.03333	1
1	80.6	87.1	70.8	93.4	100.9	167.2	108.3667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	103.4	117.9	112.5	85.2	94.9	86.1	105.5	1
1	98.6	105	70.8	89.4	148.6	87.6	87.8	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	71.8	90.4	114	122.1	75.1	126.6	110.3333	1
1	67.7	63.8	145.8	117	101.5	104.2	104.6	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	62.3	70.5	193.3	50.8	122	101.1	121.6333	1
1	81	85.4	115.3	100.5	92.8	125	108.5667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	137.2	111.5	88.4	75.3	104.5	83.1	94.33333	1
1	144.4	169.7	72.4	50.5	79.8	83.2	108.4333	1
1	52.3	76.5	141.8	137.3	29.2	162.9	127.0667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	143.8	116.9	89	62.1	92.4	95.8	100.5667	1
1	62	81.7	121.5	98.8	95.2	140.8	114.6667	1
1	106.2	136.5	91.1	67.8	111.9	86.6	104.7333	1
1	89.2	74.6	101.9	128.6	128.3	77.3	84.6	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	105.2	96.9	94.7	79.7	128.8	94.7	95.43333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	88.5	103.7	103.5	121.9	84.6	97.8	101.6667	1
1	73.7	95.8	117.2	123.6	80.7	109	107.3333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	122.5	132.9	78.6	74.7	101.9	89.4	100.3	1
1	95.7	109.5	96	97	96.3	105.4	103.6333	1
1	267.6	56.5	70	66.2	53.2	86.4	70.96667	1

1	97.9	54.1	56.4	169.5	136.1	86	65.5	1
1	116.1	104.2	111.1	86.5	91.9	90.2	101.8333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	85.7	113.2	79.1	91.3	121.4	109.2	100.5	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	123.8	68.3	111.4	89.6	69.7	137.2	105.6333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	110.4	90	98.5	104	104.8	92.4	93.63333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	67.2	68.2	97	128.4	106.1	133	99.4	1
1	107.9	114.6	70.4	111.8	77.2	118.1	101.0333	1
1	115.4	86.4	93.1	119.1	95.9	90.1	89.86667	1
1	119.7	106.7	103.1	87.7	87.3	95.5	101.7667	1
1	129.7	162.5	72.2	64.5	117.7	53.3	96	1
1	80.4	76.1	96.3	121.4	83.6	142.1	104.8333	1
1	103.6	69.5	106.9	105	80.4	134.6	103.6667	1
1	102.9	116.2	105.7	92.7	91.5	91	104.3	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	93.9	89.2	98.8	96.4	104.6	117.1	101.7	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	80.9	107.3	122.7	91.1	94.9	103.1	111.0333	1
1	94.7	80.7	92.6	123.8	108.9	99.3	90.86667	1
1	100.5	95.9	95.8	113.9	103.4	90.5	94.06667	1
1	96.3	105.2	101.6	107.1	87.9	101.9	102.9	1
1	122.5	88.5	92.3	92.9	60.2	143.7	108.1667	1
1	91.3	95.7	107.5	102.3	102	101.3	101.5	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	69.2	79.5	110.8	138.2	79.2	123.2	104.5	1
1	114.4	90.6	91	78.1	133.3	92.5	91.36667	1
1	77.8	82.8	80.2	138.9	97.9	122.4	95.13333	1
1	103.5	81	114.8	110.8	91.8	98.1	97.96667	1
1	84.1	94.7	115.2	101.3	93.3	111.4	107.1	1
1	109.5	95.9	79	105.8	105.9	103.9	92.93333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	91.8	88.8	96.6	96.2	110.2	116.4	100.6	1
1	168.5	92.5	84.2	85.9	89.8	79.1	85.26667	1
1	127.6	109.1	47	106.9	137.1	72.3	76.13333	1
1	111.1	90.4	91.9	116.4	105.9	84.2	88.83333	1
1	64.8	80.6	107.8	92.4	164.4	89.9	92.76667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	80.8	86.2	111	114	99.4	108.7	101.9667	1
1	93.1	94	113.1	116.9	103.3	79.5	95.53333	1
1	99.6	95.9	104	78.8	91.7	130.1	110	1
1	115.9	92.4	93.7	71.8	89.7	136.4	107.5	1
1	86.8	68.9	123.8	162.2	89.7	68.5	87.06667	1
1	82.6	78.5	98.4	93.5	67.8	179.2	118.7	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	91.9	96	87.3	83.3	97.1	144.3	109.2	1
1	72.4	43	123.3	104.9	96.7	159.6	108.6333	1

1	137.2	97	91.8	90.2	90.5	93.3	94.03333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	140.9	137.3	67	96.7	91.9	66.3	90.2	1
1	43.2	92.2	78.9	110.5	143.4	131.8	100.9667	1
1	99	89	105.1	100.8	88	118.1	104.0667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	110.9	89.7	106.8	94.8	82.7	115.1	103.8667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	89.4	99	112.3	100.2	80.4	118.6	109.9667	1
1	55.8	79.5	114.5	118.8	54.1	177.3	123.7667	1
1	91.5	105.4	92.8	104.7	127.2	78.4	92.2	1
1	74.8	91.1	106.1	121.1	93.2	113.8	103.6667	1
1	78.7	90	104.7	95.9	102.6	128.1	107.6	1
1	105.4	180.8	74.1	62.7	105.2	71.8	108.9	1
1	114.4	110.9	99.1	95.6	92	88	99.33333	1
1	88	86.7	83.9	95.8	91.1	154.5	108.3667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	142.7	145.1	68.7	70.1	123.9	49.5	87.76667	1
1	83.2	92.1	116.7	105	94.4	108.6	105.8	1
1	104.4	113.4	99.6	88.1	111.8	82.7	98.56667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	90.3	101.9	101.5	115	105.4	85.8	96.4	1
1	90.9	90.5	128.8	100.8	80.6	108.5	109.2667	1
1	90.6	96.2	92.9	108.9	125.5	85.8	91.63333	1
1	100.5	82.9	91.9	125.2	98.9	100.7	91.83333	1
1	91.5	92.9	117.6	96	83.9	118.2	109.5667	1
1	94.5	110.7	103	94.4	90	107.3	107	1
1	90.2	63.7	100.8	136.1	96.7	112.6	92.36667	1
1	95.5	79.2	130.6	93.4	85.6	115.6	108.4667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	114.9	105.6	94.5	94.7	85.3	105	101.7	1
1	97.5	84.5	136	108.4	88.9	84.7	101.7333	1
1	108.4	100.9	90.2	103.7	108.9	87.8	92.96667	1
1	93.1	74.2	107	140.6	82.5	102.7	94.63333	1
1	99.6	89.6	69	126.6	116.3	98.9	85.83333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	104	92.9	90.8	109.2	95.1	107.9	97.2	1
1	73.5	76	138.6	117.5	75.3	119.1	111.2333	1
1	93.6	93.6	92.8	81.3	86.1	152.6	113	1
1	53.3	63.1	165.8	84.3	62.9	170.5	133.1333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	81.8	89.8	109	103	98.1	118.4	105.7333	1
1	69.2	81.3	110.1	101.8	97.4	140.2	110.5333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	94.3	122.8	75.2	97.5	104.7	105.3	101.1	1
1	105.2	114.2	84.3	90	96.7	109.6	102.7	1
1	98.8	104.6	98.8	85.5	85.4	126.9	110.1	1
1	108.9	88.1	113.2	94.1	76.8	118.7	106.6667	1
1	58.4	57.6	77.6	218.7	89.3	98.4	77.86667	1
1	82.5	56.5	125.8	138.2	81.3	115.7	99.33333	1

1	NA	NA	NA	NA	NA	NA	NA	0
1	94.8	108.7	112.7	95.4	94.5	94	105.1333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	79.9	82.8	131.2	97.9	104.7	103.6	105.8667	1
1	98.2	94.6	91.9	114.8	92.3	108.1	98.2	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	72	94.8	118.3	101.3	112.7	100.9	104.6667	1
1	75.8	75.7	132.1	86.6	113.9	115.9	107.9	1
1	109.6	90.6	88.2	108.4	94	109.2	96	1
1	111.9	112.4	127.3	81.7	86.8	79.8	106.5	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	88.1	95.8	92.7	112.1	103	108.4	98.96667	1
1	103.8	84.7	94.9	119.3	73.8	123.4	101	1
1	106.1	113.3	89.1	84.7	97	109.8	104.0667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	90.3	106.1	119.1	88.6	91.1	104.8	110	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	103.1	98.9	99.3	103.3	89.8	105.6	101.2667	1
1	111.4	89.5	95	101.3	101.1	101.5	95.33333	1
1	84.1	76.3	103.8	108.9	97.5	129.5	103.2	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	89.5	85.8	102.7	104	108.6	109.4	99.3	1
1	87.4	82.8	103	111.7	84	131.2	105.6667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	92.7	99.6	108.7	116.1	59.1	123.8	110.7	1
1	101.8	111.9	94.7	90.2	92.7	108.7	105.1	1
1	162.5	121.5	78.1	80.1	88.8	69	89.53333	1
1	65.7	75.4	112.9	104.9	92.7	148.4	112.2333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	81.4	85.8	116.2	101.9	79.6	135.1	112.3667	1
1	77.3	59.3	196.2	81.9	62.8	122.5	126	1
1	88.2	89.5	112.6	88.9	100.9	120	107.3667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	92.3	211.6	64.6	83.9	72.7	74.9	117.0333	1
1	73	95.9	107	108.4	88.2	127.6	110.1667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	76.8	80.3	108.2	123.7	78.1	132.9	107.1333	1
1	114.4	106.5	77.1	100.8	110	91.2	91.6	1
1	92.2	91.9	120.7	104.5	92.7	98	103.5333	1
1	89.5	88.9	98.9	89.2	92	141.5	109.7667	1
1	84.1	79.8	73.4	176.9	112.3	73.5	75.56667	1
1	165.8	120.5	89.2	68.3	91.3	64.9	91.53333	1
1	94.9	122.2	92	89	101	101	105.0667	1
1	70.2	56.2	141.8	125.9	65.3	140.6	112.8667	1
1	96.7	95.6	90.6	102.7	110.8	103.6	96.6	1
1	109.5	104.8	81	92	126.1	86.6	90.8	1
1	84.3	57	94.3	161.8	65.8	136.7	96	1
1	105	79.3	127.2	96.2	82.7	109.5	105.3333	1

1	78.9	111	91.1	102.4	125.9	90.7	97.6	1
1	137.6	190.6	96.1	53.9	64.8	57	114.5667	1
1	84	105.5	102.2	104.6	89.2	114.5	107.4	1
1	95	92	114.2	100.5	96.5	101.8	102.6667	1
1	85.5	137.9	96.1	88	115.4	77.2	103.7333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	76.2	85	136.5	122.1	75	105.1	108.8667	1
1	93.2	90.9	97.6	94.5	90.7	133	107.1667	1
1	69.5	78.4	94.2	199.3	73.3	85.3	85.96667	1
1	196.7	112.2	89.6	69.1	88.7	43.7	81.83333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	105.9	89.9	88.9	102.1	118.5	94.6	91.13333	1
1	80.3	105.1	95.8	94.5	82.9	141.4	114.1	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	79.3	66.8	71.8	251.8	69	61.2	66.6	1
1	95.9	93.6	91.2	117.2	106.2	96	93.6	1
1	101.5	99.9	101.4	104.9	76.7	115.6	105.6333	1
1	106.2	113.1	93	91.6	102.2	93.9	100	1
1	57.8	81	119.5	125.2	83.5	133	111.1667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	90.1	94.5	104.4	103.9	107.3	99.9	99.6	1
1	80.3	70.5	109.1	114	81.9	144.2	107.9333	1
1	82.9	65.4	75.4	120	73	183.4	108.0667	1
1	103.6	141.5	85.9	83	105.8	80.1	102.5	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	84.5	73.7	117.5	113.5	67.1	143.8	111.6667	1
1	107.6	132.6	75.6	72.9	90.6	120.6	109.6	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	88.5	75.8	127.7	124.2	72	111.8	105.1	1
1	98.4	87.6	110	126.5	95.7	81.8	93.13333	1
1	167.2	58.5	90	111.9	111.9	60.5	69.66667	1
1	63.3	84.1	120.3	100.1	115.2	116.8	107.0667	1
1	59.9	111.9	103.8	157.8	66.6	100	105.2333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	61	58.1	88.1	55.5	44.3	293	146.4	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	66.7	119.1	129.2	110.4	97.9	76.6	108.3	1
1	86.5	96.4	115.2	93.2	85.4	123.4	111.6667	1
1	122.3	96.4	92.8	92.5	89.6	106.4	98.53333	1
1	80.7	78.1	103.2	105.5	81.2	151.3	110.8667	1
1	82.9	101.6	105.3	120.3	99.5	90.5	99.13333	1
1	136.8	105.5	94.9	82.8	100.3	79.8	93.4	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	93.1	104.7	102.8	98.3	109.5	91.7	99.73333	1
1	NA	NA	NA	NA	NA	NA	NA	0

1	NA	NA	NA	NA	NA	NA	NA	0
1	77	80.7	99.5	97.4	163.9	81.5	87.23333	1
1	90.6	117.1	94.5	99.2	112.8	85.8	99.13333	1
1	72.7	88.2	109.4	96.1	79.3	154.2	117.2667	1
1	94.6	81.7	108.2	92.7	67.6	155.2	115.0333	1
1	78.3	137.2	69.2	120.5	84.2	110.6	105.6667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	98.8	79.5	111.5	99.1	102.3	108.7	99.9	1
1	118.1	103.7	83	102.5	89.5	103.1	96.6	1
1	64.5	99.8	116.2	91	101.3	127.2	114.4	1
1	116.8	113.8	85.8	96.2	106.6	80.8	93.46667	1
1	76.4	249.3	61.7	49.8	101.1	61.7	124.2333	1
1	141.2	91.5	95.9	75.3	120.1	76	87.8	1
1	97.1	99	94.3	120.1	95.8	93.7	95.66667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	90.4	108.4	83.7	94.6	117.9	105	99.03333	1
1	57.8	83.8	139	111.2	75.4	132.8	118.5333	1
1	55.5	49.8	80.8	87.3	42.9	283.7	138.1	1
1	75.8	79.4	132.1	110.7	84.1	117.9	109.8	1
1	70	64.1	132.6	109.9	107.8	115.6	104.1	1
1	106	116.3	66.9	78.4	139.5	93	92.06667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	133.4	116.7	59.8	74.2	103.3	112.6	96.36667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	103.2	99.4	107.9	88.1	92.9	108.4	105.2333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	146.5	133.5	66.5	62.4	84.4	106.7	102.2333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	71.2	73.1	119.7	138.3	93.4	104.4	99.06667	1
1	95	108.6	92.2	116.7	102.7	84.6	95.13333	1
1	61.4	71.8	129.8	123.8	82	131.2	110.9333	1
1	101.8	86.5	111.2	101.2	99.1	100.1	99.26667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	114.1	62.6	89.7	154.6	114	65	72.43333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	76.3	84.8	121	102.3	77.1	138.4	114.7333	1
1	98.7	96.8	112.6	90.6	81.8	119.4	109.6	1
1	97.7	123.5	83.8	82.7	126	86.3	97.86667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	91.2	88.2	91.2	124.4	104.9	100.1	93.16667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	80.4	86.7	142.2	98.8	77.5	114.4	114.4333	1
1	111.3	88.3	106.2	92.8	83.4	118	104.1667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	87.5	110.8	93.4	107.4	99	102	102.0667	1
1	114.7	112.8	74.5	78	79.8	140.3	109.2	1
1	100.7	83.5	89.1	94	106.5	126.2	99.6	1

1	NA	NA	NA	NA	NA	NA	NA	0
1	111.3	88.2	94	99.9	104.6	102	94.73333	1
1	112.7	103.5	95.6	96.6	87.8	103.9	101	1
1	84.9	89.4	92.7	105.7	110.3	117	99.7	1
1	103.6	133.6	94.5	83.8	80.3	104.1	110.7333	1
1	64.8	55.1	67.8	47.2	290.5	74.7	65.86667	1
1	111.8	194.4	70.3	73.7	77.9	71.8	112.1667	1
1	109.4	100.2	109.9	69.7	114.7	96	102.0333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	98.1	101	82.3	91.9	109	117.6	100.3	1
1	116	111.5	94	106.1	98.3	74.2	93.23333	1
1	95.6	81.9	85.8	110.7	103.4	122.6	96.76667	1
1	94.6	96.7	107.8	102.9	89.3	108.7	104.4	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	83.1	73.4	148.8	90.6	85.4	118.7	113.6333	1
1	72.9	105.7	85.1	85.5	122.1	128.8	106.5333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	117.4	110.3	81.9	90	102.8	97.5	96.56667	1
1	106	91.9	104.5	107.3	90.2	100.1	98.83333	1
1	108.7	150.5	99	73.3	72.3	96.3	115.2667	1
1	80.9	98.3	93.2	138.7	93.4	95.5	95.66667	1
1	82.2	160.6	87.4	96	86.6	87.2	111.7333	1
1	64.1	50.8	102.8	141.4	64.9	176	109.8667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	68.5	91.9	107.5	96.4	135.4	100.3	99.9	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	94.6	81	101	114.7	99.3	109.3	97.1	1
1	90.1	92.4	132.7	102.2	84.2	98.4	107.8333	1
1	106.6	88.8	93.9	107.1	98.1	105.4	96.03333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	92.6	89.8	95.6	102.8	81.1	138.1	107.8333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	104.4	118.1	87.8	103.7	94.5	91.6	99.16667	1
1	97.9	99.2	100	101.8	81.9	119.1	106.1	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	107.9	104.5	90.4	103.9	104.8	88.6	94.5	1
1	143.4	89.3	94.2	84.9	99.5	88.7	90.73333	1
1	125.9	130.8	102.4	55.8	84.8	100.2	111.1333	1
1	108.8	102	80.7	119.7	106	82.9	88.53333	1
1	117.2	111.4	78.9	115.4	83	94.1	94.8	1
1	74.1	96.9	96.5	96.5	133.6	102.3	98.56667	1
1	116.8	76.5	104	112.4	99.9	90.4	90.3	1
1	91.9	99.3	109.4	106	90	103.5	104.0667	1
1	84	130.7	94.9	99.6	105.1	85.7	103.7667	1
1	143.1	121.1	99.2	75.3	69.5	91.8	104.0333	1

1	78.3	87.1	109.8	96.7	98.7	129.4	108.7667	1
1	103.1	98.8	96.8	103.5	102.2	95.5	97.03333	1
1	20.4	13.9	263.3	128.2	11.8	162.5	146.5667	1
1	99.4	81.2	93.7	98.4	91.9	135.3	103.4	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	64.1	78.2	96.6	139.4	77.4	144.3	106.3667	1
1	134.7	90.4	86.1	113.6	88.9	86.3	87.6	1
1	95.9	88	91.5	85.8	98.6	140.3	106.6	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	81.2	76.5	123.8	96.7	120.4	101.4	100.5667	1
1	101.3	107.1	104.2	100.8	115.8	70.9	94.06667	1
1	112.1	89.7	94.8	116.9	93.3	93.3	92.6	1
1	NA	223.8	NA	183.2	NA	193.1	208.45	0.666667
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	128.9	90.3	84.1	99.3	122	75.4	83.26667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	66.4	55.2	171.2	108.4	83.1	115.7	114.0333	1
1	101.9	89.3	67.3	69.2	35.8	236.4	131	1
1	283	155.1	56.1	21.4	67.5	16.9	76.03333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	99.3	121	91.7	83.7	113.6	90.6	101.1	1
1	86.6	135.5	94.8	68.8	147.4	66.8	99.03333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	183	103.6	79.1	65.1	130.1	39.2	73.96667	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	120.9	107.1	88	93	101.3	89.7	94.93333	1
1	88.9	102.2	109.8	95.7	110.6	92.9	101.6333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	95.8	88.2	96.9	117.3	99.1	102.9	96	1
1	88.1	110.1	132.5	89.9	84.3	95.1	112.5667	1
1	125.2	96.5	87	85.7	115.3	90.3	91.26667	1
1	87.8	125.7	95.1	80	110.3	101	107.2667	1
1	89.7	76.9	110.5	114.6	94.8	113.5	100.3	1
1	97.8	89.6	81.3	109.9	113.5	107.9	92.93333	1
1	116.3	116.5	111.4	60	113.1	82.7	103.5333	1
1	48.9	52.9	83.1	104	74.5	236.6	124.2	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	95.3	85.6	86.4	91.7	125.3	115.6	95.86667	1
1	100.2	94.2	102.8	94.9	98.8	109.1	102.0333	1
1	87.1	68.3	135.3	98.1	87.9	123.2	108.9333	1
1	86.3	131.6	104.6	95.5	91.4	90.6	108.9333	1
1	73.6	74.3	221.1	96.8	69.2	65	120.1333	1

1	84.7	98.3	109.7	109.6	108.4	89.3	99.1	1
1	76	74.1	119.9	114.3	104.9	110.7	101.5667	1
1	72.9	81.1	108	107.5	77.3	153.1	114.0667	1
1	164.3	92.2	87.8	94.4	119.1	42.2	74.06667	1
1	122.2	122.9	90.4	67.4	101.4	95.7	103	1
1	95.6	111.6	95.7	102.1	98	97	101.4333	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	77.4	116.1	103.6	96.5	101.7	104.6	108.1	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	100.4	99.3	120.8	88.8	89.3	101.5	107.2	1
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	NA	NA	NA	NA	NA	NA	NA	0
1	93.8	139.6	76.2	98.7	127.5	64.2	93.33333	1
1	NA	NA	NA	NA	NA	NA	NA	0

Group_con	Group_con	Group_cas	pvalue
121.8	1	0.64231	0.000774
129.4667	1	0.544799	0.083204
NA	0	NA	NA
110.8667	1	0.803668	0.587124
121.3	1	0.64853	0.521299
90.46667	1	1.211496	0.355231
90.9	1	1.20022	0.333613
116.9	1	0.711149	0.224789
116.4	1	0.718499	0.218803
117.2333	1	0.706284	0.097746
103.3	1	0.936108	0.747447
102.1667	1	0.957586	0.784881
112.5333	1	0.777251	0.323335
88.96667	1	1.247658	0.517769
92.26667	1	1.167991	0.731103
85.7	1	1.333722	0.499378
103.1667	1	0.938934	0.737434
94.23333	1	1.122391	0.605484
81.23333	1	1.462043	0.039979
102.3667	1	0.953761	0.696943
NA	0	NA	NA
106.5667	1	0.876447	0.356273
113.9333	1	0.755413	0.302719
103.4333	1	0.93329	0.403828
112.6	1	0.776199	0.513297
103.4	1	0.934558	0.769526
130.7	1	0.530222	0.378884
66.36667	1	2.013561	0.412388
97.2	1	1.057613	0.748534
104.0667	1	0.921525	0.698031
99.96667	1	1.000667	0.99287
81.76667	1	1.445577	0.256345
106.2	1	0.883553	0.73738
92.4	1	1.164141	0.465557
93.86667	1	1.130682	0.153807
109	1	0.834862	0.140894
104.1	1	0.920909	0.766133
122.0667	1	0.638449	0.348866
111.8	1	0.788611	0.394864
110.6667	1	0.807229	0.296879
101.9333	1	0.961413	0.891301
114.3	1	0.749781	0.166452
81.93333	1	1.441416	0.184695
88.7	1	1.255167	0.289882
73.93333	1	1.704689	0.249458
103.6	1	0.930502	0.549751
102.2333	1	0.956309	0.828802
104.6667	1	0.910828	0.521358
106.1667	1	0.88383	0.713046
108.5333	1	0.842445	0.549969

97.86667	1	1.043256	0.934171
104.3	1	0.917546	0.857577
105.1	1	0.90295	0.805219
99.96667	1	1.000333	0.998575
98.86667	1	1.022927	0.95849
106.3333	1	0.880564	0.700267
70.96667	1	1.818225	0.23295
92.76667	1	1.155947	0.40016
90.73333	1	1.204262	0.471953
90.6	1	1.207873	0.508355
91.56667	1	1.184201	0.726112
95.1	1	1.1034	0.734738
93.73333	1	1.133713	0.680063
NA	0	NA	NA
93.7	1	1.134116	0.613566
NA	0	NA	NA
71.16667	1	1.810304	0.245906
NA	0	NA	NA
107.0333	1	0.868577	0.280376
82.33333	1	1.428745	0.572283
79.23333	1	1.52419	0.476662
102.8	1	0.945525	0.799358
124.8667	1	0.601975	0.53602
114.7667	1	0.742376	0.012131
111	1	0.801502	0.638728
101.5333	1	0.970125	0.96795
108.9667	1	0.835424	0.54266
87.86667	1	1.276555	0.240829
51.96667	1	2.847979	0.207183
68.6	1	1.914966	0.272735
88.26667	1	1.266239	0.388872
111.7333	1	0.789678	0.310452
104.6	1	0.912046	0.59862
90.76667	1	1.203452	0.565649
99.83333	1	1.003339	0.972951
86.86667	1	1.302379	0.001991
84.8	1	1.358491	0.340893
110.6	1	0.80862	0.027227
109.8	1	0.821797	0.468488
91.33333	1	1.190146	0.189476
89.73333	1	1.228826	0.335753
83.63333	1	1.39179	0.453301
94.9	1	1.107482	0.580625
83.83333	1	1.386083	0.081078
92.93333	1	1.152439	0.570399
85.1	1	1.350176	0.473455
91.43333	1	1.187386	0.269222
84.63333	1	1.363135	0.377495
90.26667	1	1.215657	0.502784
100.8	1	0.983796	0.95301
89.86667	1	1.225519	0.423081

91.7	1	1.181025	0.634341
99.2	1	1.016465	0.94378
99.46667	1	1.011059	0.934973
95.76667	1	1.088409	0.661627
107.7333	1	0.856436	0.676926
101.1667	1	0.976606	0.665666
92.66667	1	1.157914	0.594686
93.9	1	1.12957	0.408545
96.96667	1	1.062908	0.620794
70.06667	1	1.854424	0.207807
84.03333	1	1.380008	0.430664
96.53333	1	1.071823	0.581737
99.1	1	1.018163	0.957813
89.76667	1	1.227999	0.21768
97.43333	1	1.052686	0.836677
100.8	1	0.984458	0.941511
92.1	1	1.171553	0.414711
72.1	1	1.773925	0.162649
104.7333	1	0.909612	0.414569
93.66667	1	1.134875	0.254689
86.03333	1	1.325068	0.356825
101.7	1	0.966568	0.631
78.66667	1	1.542373	0.211043
83.06667	1	1.407705	0.349831
105.7333	1	0.891866	0.328276
98.36667	1	1.033209	0.836389
116.6667	1	0.714286	0.004245
93.03333	1	1.150125	0.510689
87.63333	1	1.282237	0.157444
105.5667	1	0.894222	0.492122
101.8	1	0.964309	0.912912
99.86667	1	1.00267	0.991771
116.7667	1	0.713103	0.030863
94.93333	1	1.10639	0.592752
108.3667	1	0.845586	0.485462
94.06667	1	1.126152	0.571444
106.6333	1	0.875899	0.594993
102.7333	1	0.946788	0.792188
95.5	1	1.094241	0.365167
111.7333	1	0.789678	0.068909
78.96667	1	1.532292	0.494296
90.2	1	1.217664	0.647767
90.03333	1	1.22177	0.704719
123.1667	1	0.624087	0.434212
90.5	1	1.209945	0.421188
85.53333	1	1.33827	0.398993
97.9	1	1.042901	0.582765
100.4333	1	0.991039	0.974702
107.2667	1	0.864823	0.502364
107.4	1	0.861887	0.287571
93.5	1	1.139037	0.294016

107.6667	1	0.857585	0.098879
104.1333	1	0.920615	0.275395
86	1	1.325581	0.376613
111.9	1	0.78731	0.587413
85.23333	1	1.346891	0.141959
111.9	1	0.787608	0.244722
99.63333	1	1.008029	0.947552
84.26667	1	1.373418	0.250669
106.9667	1	0.869741	0.470001
78.13333	1	1.560154	0.374365
90.8	1	1.202643	0.617153
89.33333	1	1.238433	0.479144
105.1667	1	0.90206	0.623252
123.9	1	0.613936	0.462893
96.66667	1	1.06931	0.426992
118.2333	1	0.691288	0.018626
89.9	1	1.224694	0.422779
102.0333	1	0.960144	0.875937
96.46667	1	1.073255	0.79226
98.66667	1	1.027027	0.73532
94.63333	1	1.113068	0.645529
116.6	1	0.715266	0.010182
88.36667	1	1.263297	0.504294
110.9333	1	0.802885	0.204187
95.53333	1	1.09351	0.801991
88.9	1	1.249719	0.520568
55.33333	1	2.614458	0.289127
102.9667	1	0.942376	0.808396
92.76667	1	1.155947	0.443663
95.06667	1	1.104137	0.648965
98.56667	1	1.029084	0.925032
118.5333	1	0.687289	0.221211
85.7	1	1.333722	0.304437
99.73333	1	1.005013	0.985914
88.26667	1	1.265483	0.351807
106.3	1	0.882095	0.607574
78	1	1.564103	0.040295
103.1333	1	0.938914	0.74519
105.2	1	0.901458	0.687112
88.83333	1	1.251032	0.391567
96.1	1	1.081165	0.545176
97.2	1	1.057613	0.612145
99.4	1	1.011737	0.958183
82.1	1	1.43646	0.252088
90.26667	1	1.215288	0.312468
117.1	1	0.708227	0.010569
97.36667	1	1.054433	0.393258
92	1	1.174275	0.624954
114.5667	1	0.745708	0.161825
107.1	1	0.867414	0.25596
99.76667	1	1.005012	0.983494

94.03333	1	1.12726	0.542558
98.73333	1	1.025321	0.778368
115.5	1	0.731602	0.025872
95.1	1	1.102348	0.718358
110.9667	1	0.802343	0.407943
119.9	1	0.668335	0.260279
83.63333	1	1.390992	0.446856
90.73333	1	1.204629	0.466104
108.5667	1	0.842186	0.497978
150.3333	1	0.330155	0.441082
94.33333	1	1.120495	0.509757
118.4	1	0.689189	0.363721
110.8667	1	0.803969	0.077524
97.93333	1	1.041865	0.775672
76	1	1.632018	0.272666
115.2	1	0.736111	0.06733
110.8333	1	0.804511	0.538896
94.76667	1	1.110798	0.697015
89.8	1	1.227171	0.553514
81.8	1	1.444988	0.382014
86.1	1	1.323268	0.509499
89.4	1	1.237136	0.260523
88.56667	1	1.258186	0.3824
111.3	1	0.796945	0.286565
115.9667	1	0.724634	0.040167
90	1	1.221852	0.246383
76	1	1.631579	0.196616
89.96667	1	1.222675	0.440687
74.9	1	1.669782	0.279071
96.13333	1	1.080097	0.244736
97.63333	1	1.049164	0.760168
96.2	1	1.078656	0.597788
119.7333	1	0.6701	0.242982
88.53333	1	1.25866	0.264457
107.9333	1	0.852996	0.611732
90.03333	1	1.221029	0.413365
99.36667	1	1.012747	0.955141
108.1333	1	0.849568	0.351674
106.1333	1	0.884422	0.483211
88.96667	1	1.248033	0.143511
110.7667	1	0.805597	0.592734
88.93333	1	1.248501	0.06123
87.86667	1	1.276176	0.336434
85.7	1	1.334111	0.420302
95.73333	1	1.088788	0.617069
108.7	1	0.839926	0.714241
94.26667	1	1.121641	0.033195
98.66667	1	1.027027	0.731903
96.06667	1	1.081888	0.305595
103.6667	1	0.929582	0.812793
87.13333	1	1.295715	0.299401

95.4	1	1.096436	0.801237
89.46667	1	1.235469	0.441356
87.46667	1	1.286585	0.30812
97.83333	1	1.044293	0.790729
100.7333	1	0.98544	0.953091
112.1667	1	0.783061	0.233168
75.46667	1	1.650177	0.237719
99.93333	1	1.001334	0.976555
98.16667	1	1.037351	0.786306
90.16667	1	1.217745	0.249484
110.1	1	0.81653	0.439601
84.53333	1	1.365931	0.36942
108.2	1	0.848121	0.048418
94.2	1	1.122788	0.394782
125	1	0.600267	0.154859
114.7667	1	0.742957	0.154553
102.2333	1	0.956309	0.943123
88.9	1	1.250469	0.493357
90.2	1	1.217295	0.369155
97.1	1	1.060076	0.720629
72.9	1	1.743484	0.343045
93.36667	1	1.142092	0.399252
100.3333	1	0.993023	0.974534
99.63333	1	1.00736	0.95918
97.43333	1	1.052686	0.70593
106	1	0.887107	0.33951
80.63333	1	1.480364	0.423749
103.0667	1	0.940492	0.725976
88.5	1	1.259887	0.17854
96.2	1	1.079002	0.738558
92.63333	1	1.15941	0.211325
113.6667	1	0.759531	0.506437
100.8333	1	0.983471	0.900123
74.8	1	1.674242	0.221507
94.63333	1	1.11342	0.691132
122.4333	1	0.633542	0.029148
95.8	1	1.087683	0.482102
116.5667	1	0.71547	0.180949
96.56667	1	1.071108	0.767
104.4	1	0.915709	0.59831
101	1	0.980198	0.916399
89.26667	1	1.240478	0.497129
99.4	1	1.011737	0.773781
121.9	1	0.640416	0.08916
91.53333	1	1.184996	0.547948
91.16667	1	1.193784	0.290615
95.7	1	1.089864	0.338773
89.96667	1	1.223416	0.519084
109.3667	1	0.828711	0.682691
89.1	1	1.244669	0.366413
111.8667	1	0.787843	0.440624

101.1667	1	0.977265	0.782063
88.16667	1	1.268809	0.631183
83.2	1	1.403846	0.434699
105.8	1	0.890359	0.591952
95.63333	1	1.091321	0.400588
85.1	1	1.350176	0.540079
91.06667	1	1.196193	0.07585
103.1667	1	0.938611	0.5827
90	1	1.222222	0.368624
109.2	1	0.831807	0.290246
116.4333	1	0.717721	0.135707
107.3333	1	0.863354	0.624694
100.1333	1	0.99767	0.983305
106.1333	1	0.884108	0.712164
101.2	1	0.975955	0.905694
92.9	1	1.152853	0.316781
95.83333	1	1.086957	0.693969
101.7333	1	0.965596	0.799945
114.1333	1	0.752336	0.110222
92.83333	1	1.154758	0.298728
92.7	1	1.157497	0.521399
100.1667	1	0.996672	0.986268
111.9333	1	0.78648	0.441877
113.1333	1	0.76812	0.165908
97.23333	1	1.056565	0.533683
122.7	1	0.62972	0.103708
87.23333	1	1.293084	0.361113
99.23333	1	1.015116	0.901955
95.76667	1	1.088409	0.473817
95.46667	1	1.094972	0.516994
99.73333	1	1.005348	0.961703
102.0667	1	0.959504	0.853486
105.1333	1	0.902029	0.051584
95.63333	1	1.09167	0.514996
102.6333	1	0.948685	0.822643
97.2	1	1.05727	0.62359
65.76667	1	2.041561	0.205719
78.06667	1	1.561913	0.271164
111.2333	1	0.798022	0.278988
78	1	1.56453	0.228388
118.5	1	0.687764	0.008187
93.66667	1	1.134875	0.411692
98.83333	1	1.023609	0.914046
97.5	1	1.051282	0.506922
104.6667	1	0.910828	0.703245
80.76667	1	1.476269	0.188669
87.76667	1	1.279149	0.258449
111.5333	1	0.793186	0.124259
100.6333	1	0.987413	0.954216
90.86667	1	1.20066	0.099498
96.96667	1	1.062221	0.406671

112.4	1	0.779359	0.080183
87.36667	1	1.289203	0.316763
106.6333	1	0.875586	0.260391
101.9333	1	0.962067	0.705289
99.4	1	1.012072	0.938258
113.1	1	0.768347	0.283259
106.4	1	0.879699	0.007497
87.83333	1	1.27704	0.297812
108.2	1	0.848429	0.668264
89.66667	1	1.230855	0.456689
100.8333	1	0.983802	0.818618
84.33333	1	1.371542	0.230317
98.5	1	1.030457	0.841216
99.1	1	1.018163	0.893115
79.93333	1	1.502085	0.334423
111.1	1	0.79958	0.279944
90.46667	1	1.211127	0.22104
120.6	1	0.658651	0.008306
94.3	1	1.120537	0.488732
98.33333	1	1.033898	0.820465
96.3	1	1.077189	0.389898
103.2	1	0.937984	0.689406
74.83333	1	1.673051	0.213029
99.4	1	1.012072	0.959733
99.46667	1	1.010724	0.779487
91.93333	1	1.175489	0.205858
111.3333	1	0.796407	0.130174
98.46667	1	1.031144	0.809969
99.4	1	1.012408	0.933364
95.33333	1	1.097552	0.681222
91.56667	1	1.184201	0.629224
81	1	1.469547	0.236421
108.9	1	0.836547	0.390657
94.06667	1	1.126152	0.665095
97.73333	1	1.046385	0.609379
101.9	1	0.962709	0.847734
101.9	1	0.962381	0.708472
109.3333	1	0.829268	0.07598
99.63333	1	1.00736	0.88752
89.83333	1	1.226345	0.611799
104.9667	1	0.905367	0.672592
85.96667	1	1.326483	0.460449
97.46667	1	1.051984	0.449526
135.5667	1	0.475289	0.410694
103.8	1	0.926461	0.242212
95.4	1	1.096436	0.277728
99.03333	1	1.019522	0.937131
113.7333	1	0.758792	0.140041
99.03333	1	1.019185	0.811931
105.2333	1	0.900538	0.575078
96.73333	1	1.06754	0.895412

92.9	1	1.152853	0.550162
101.5667	1	0.968822	0.839022
95.66667	1	1.090592	0.637924
89.03333	1	1.246724	0.373151
92.86667	1	1.153625	0.582268
96.36667	1	1.075406	0.49144
87.56667	1	1.284355	0.356813
97.86667	1	1.043597	0.930912
88.33333	1	1.264151	0.190782
112.8667	1	0.772002	0.292922
92.53333	1	1.161383	0.636242
90.13333	1	1.219305	0.363615
86.83333	1	1.303263	0.290346
97.23333	1	1.057251	0.690787
101.9667	1	0.961098	0.688346
86.46667	1	1.31303	0.170141
86.4	1	1.314815	0.135501
98.46667	1	1.031144	0.880234
93.9	1	1.13028	0.333284
96.96667	1	1.062564	0.339135
94.63333	1	1.113068	0.40078
96.36667	1	1.075061	0.61684
90.06667	1	1.220207	0.223165
88.5	1	1.259887	0.112253
115.1	1	0.73733	0.177187
112.7667	1	0.773869	0.447502
99.56667	1	1.008704	0.944816
92.23333	1	1.169136	0.152799
97.43333	1	1.053028	0.509995
119.0667	1	0.679451	0.081834
NA	0	NA	NA
96	1	1.083333	0.030721
115.3667	1	0.733892	0.466773
87.6	1	1.283105	0.298909
115.6	1	0.730104	0.432375
109.0667	1	0.833741	0.143971
101.8333	1	0.964321	0.901881
99.73333	1	1.005348	0.98979
104.8	1	0.908715	0.606885
93.6	1	1.136752	0.463764
102.2667	1	0.955671	0.710732
101.4667	1	0.971419	0.789709
95.76667	1	1.088409	0.606278
109.0333	1	0.833996	0.120479
95.26667	1	1.09937	0.634923
70.6	1	1.832389	0.40189
112.2667	1	0.781473	0.051208
98.53333	1	1.029432	0.796649
93.96667	1	1.128414	0.515139
96.93333	1	1.06293	0.652277
94.33333	1	1.120141	0.585474

99.63333	1	1.00736	0.919306
89.96667	1	1.223046	0.421138
94.63333	1	1.113772	0.545689
95.96667	1	1.084404	0.434957
117	1	0.709117	0.379986
84.6	1	1.364066	0.203369
87.76667	1	1.279149	0.244256
79.43333	1	1.518254	0.130341
100.1667	1	0.997005	0.977358
91.33333	1	1.189781	0.552606
98.23333	1	1.035969	0.551049
93.13333	1	1.147459	0.215754
101.6	1	0.968176	0.917324
98.23333	1	1.035629	0.707756
99.33333	1	1.013423	0.871662
106.3333	1	0.881191	0.245445
82.16667	1	1.433671	0.342711
108.6333	1	0.841056	0.006771
94.96667	1	1.105651	0.648959
97.03333	1	1.061491	0.57005
99.33333	1	1.013423	0.855196
94.13333	1	1.124646	0.77581
103.1333	1	0.93956	0.702042
105	1	0.905079	0.417027
100.9	1	0.982491	0.830626
83.5	1	1.39521	0.376986
87.6	1	1.282344	0.270489
101.6333	1	0.967858	0.90965
95.86667	1	1.085883	0.257562
90.36667	1	1.213205	0.396577
98.86667	1	1.022927	0.902924
106.7667	1	0.873244	0.706323
112.4667	1	0.778305	0.574225
91.86667	1	1.177431	0.33747
112.3667	1	0.779887	0.438224
97.26667	1	1.056203	0.6217
86.26667	1	1.318393	0.226625
91.03333	1	1.197364	0.393605
97.8	1	1.04499	0.403794
95.93333	1	1.084434	0.404291
100.8333	1	0.983471	0.734446
95.9	1	1.085853	0.17301
88.13333	1	1.269667	0.248217
100.8667	1	0.983146	0.930705
106.5	1	0.877934	0.303607
98.13333	1	1.037704	0.923711
96.23333	1	1.078282	0.64294
101.9667	1	0.961425	0.711562
139.9	1	0.429354	0.312858
93.26667	1	1.144389	0.103413
102.5667	1	0.949626	0.795152

93.13333	1	1.147459	0.325161
79.23333	1	1.524611	0.124786
96.36667	1	1.074715	0.686613
81.6	1	1.45098	0.453032
97.66667	1	1.048123	0.597366
80.16667	1	1.494802	0.343063
96.53333	1	1.071478	0.720292
109.1333	1	0.832926	0.433269
108.3	1	0.846722	0.127703
95.73333	1	1.089136	0.605837
100.4333	1	0.991039	0.924312
117.0333	1	0.7092	0.130358
96.3	1	1.077189	0.594247
105.2333	1	0.900855	0.486122
109.7333	1	0.8226	0.273227
98.96667	1	1.020882	0.385052
96.13333	1	1.080791	0.669301
98.33333	1	1.033559	0.519983
87.86667	1	1.275797	0.403338
96.03333	1	1.082957	0.451916
94.5	1	1.116402	0.126943
NA	0	NA	NA
104.6	1	0.912046	0.733498
96.2	1	1.079002	0.390057
89.8	1	1.227543	0.040367
112.7667	1	0.773574	0.061741
84	1	1.380556	0.320171
107.3333	1	0.863354	0.610316
91.26667	1	1.191381	0.543907
97.4	1	1.05373	0.74871
92.96667	1	1.151309	0.41978
107.2	1	0.865672	0.430025
104.4667	1	0.914167	0.396741
83.66667	1	1.390438	0.284739
96.93333	1	1.06293	0.451576
101.9	1	0.963036	0.869495
89.6	1	1.232887	0.364544
NA	0	NA	NA
91.5	1	1.185792	0.371836
95.1	1	1.103049	0.473104
96.4	1	1.074689	0.413794
91.4	1	1.188184	0.431813
88.16667	1	1.268053	0.387857
102.3	1	0.95536	0.83507
115.9667	1	0.724921	0.31573
94.83333	1	1.108612	0.487076
91.33333	1	1.190146	0.486651
89.66667	1	1.230112	0.264351
105.3	1	0.899652	0.715146
99.66667	1	1.006355	0.981746
112.7333	1	0.774098	0.309169

100.7	1	0.986097	0.972892
103.5	1	0.932045	0.735693
89.13333	1	1.243829	0.273436
103.0333	1	0.941119	0.720726
85.6	1	1.336838	0.134161
62.46667	1	2.201708	0.226184
106.3667	1	0.880915	0.324229
95.36667	1	1.097518	0.493437
97.5	1	1.051282	0.393489
89.73333	1	1.228826	0.193304
88.83333	1	1.251782	0.235135
97.4	1	1.053388	0.805727
100.9333	1	0.981506	0.821563
96.4	1	1.075035	0.69052
106.2667	1	0.881744	0.291156
100.5	1	0.99005	0.923386
108.8	1	0.838235	0.727107
90.66667	1	1.205882	0.186964
NA	0	NA	NA
NA	0	NA	NA
101.4333	1	0.972067	0.880375
94.86667	1	1.107871	0.465483
NA	0	NA	NA
90.63333	1	1.207061	0.052176
102.4667	1	0.951529	0.488503
92.7	1	1.157857	0.068892
104.3667	1	0.916001	0.248044
83.43333	1	1.397123	0.608718
102.2667	1	0.955346	0.718582
110.6	1	0.808017	0.347843
91.5	1	1.185792	0.397895
84.46667	1	1.367403	0.366844
84.76667	1	1.359811	0.145285
96.6	1	1.071084	0.637793
93.23333	1	1.145156	0.236799
92.2	1	1.169559	0.123101
NA	0	NA	NA
96.2	1	1.078656	0.323181
106.7333	1	0.874141	0.173791
94.73333	1	1.111189	0.588832
97.3	1	1.055156	0.789128
91.43333	1	1.187386	0.051485
100.1	1	0.997669	0.97966
90.36667	1	1.213205	0.141866
99.13333	1	1.017821	0.868353
95.03333	1	1.104174	0.581344
88.96667	1	1.247658	0.370085
87.7	1	1.280122	0.176685
99.93333	1	1.001334	0.986602
108.9333	1	0.835985	0.614246
92.13333	1	1.170767	0.489527

99.6	1	1.008032	0.977478
88.76667	1	1.253098	0.321993
108.2333	1	0.848168	0.289228
90.1	1	1.220126	0.279336
99	1	1.020202	0.868012
NA	0	NA	NA
92.93333	1	1.15208	0.454209
100.4667	1	0.99071	0.970918
94.56667	1	1.11491	0.477947
NA	0	NA	NA
99.56667	1	1.008704	0.931639
83.56667	1	1.393299	0.333004
98.3	1	1.034588	0.873327
105.0333	1	0.904475	0.099499
94.76667	1	1.110447	0.067517
104.3667	1	0.916321	0.490849
109.1333	1	0.832621	0.201321
93.16667	1	1.146691	0.407131
103.4333	1	0.933613	0.496772
115.7	1	0.728608	0.329737
97.16667	1	1.057976	0.803371
102.1667	1	0.957586	0.680842
103.9	1	0.924928	0.456145
NA	0	NA	NA
89.76667	1	1.227999	0.145515
100.1667	1	0.996672	0.979471
98.5	1	1.030795	0.87885
88.6	1	1.257336	0.529363
86.8	1	1.304531	0.313011
96	1	1.082986	0.702018
87.03333	1	1.29797	0.182123
103.4	1	0.934236	0.776677
85.53333	1	1.33827	0.195132
104.1	1	0.92123	0.748903
115.4	1	0.733102	0.292776
106.3	1	0.881468	0.575686
96.16667	1	1.079723	0.636511
99.03333	1	1.019859	0.896522
90.3	1	1.21447	0.229498
NA	0	NA	NA
107.2667	1	0.864201	0.49737
101.6333	1	0.967858	0.777541
88.73333	1	1.253944	0.375766
81.43333	1	1.455997	0.333747
112.4333	1	0.779128	0.207496
84.46667	1	1.367798	0.326933
95.16667	1	1.101226	0.701305
89.53333	1	1.233805	0.016367
NA	0	NA	NA
93.4	1	1.141328	0.014149
110.4667	1	0.811104	0.178977

NA	0	NA	NA
90.46667	1	1.210759	0.209139
99.13333	1	1.017485	0.944958
97.56667	1	1.04988	0.864627
91.76667	1	1.179441	0.323242
97.5	1	1.051282	0.411837
106.0667	1	0.885921	0.556106
95.3	1	1.098986	0.63115
92.33333	1	1.166426	0.378093
97.1	1	1.059732	0.647294
80.93333	1	1.47117	0.227445
96.13333	1	1.080791	0.717753
89.76667	1	1.227999	0.287153
80.5	1	1.484058	0.047249
102.2	1	0.956947	0.874288
99.43333	1	1.011398	0.921901
99.03333	1	1.019859	0.707345
111.1333	1	0.79964	0.224738
100.3333	1	0.993355	0.982464
103.5	1	0.932367	0.423193
95.3	1	1.098986	0.507913
101.0667	1	0.979222	0.941963
106.2	1	0.882925	0.387218
89.73333	1	1.228455	0.014922
94.76667	1	1.110447	0.352499
97.83333	1	1.043952	0.889698
99.16667	1	1.017143	0.84603
83.3	1	1.40096	0.426997
105.6667	1	0.892429	0.361073
100.8667	1	0.982816	0.871863
132.9667	1	0.504136	0.017381
88.23333	1	1.266717	0.357096
105.7333	1	0.891551	0.615058
99.3	1	1.014434	0.865686
91.86667	1	1.177068	0.29568
95.93333	1	1.084781	0.362398
85.1	1	1.349785	0.059347
93	1	1.150538	0.127082
93.46667	1	1.1398	0.120307
NA	0	NA	NA
89.4	1	1.237136	0.101096
104.4	1	0.915709	0.373068
93.83333	1	1.131083	0.732308
116.1	1	0.722366	0.013528
91.53333	1	1.184996	0.456169
95.56667	1	1.09278	0.470924
94.13333	1	1.124646	0.257738
94.76667	1	1.110095	0.188745
99.76667	1	1.004678	0.957986
97.06667	1	1.06044	0.879093
124.4333	1	0.607554	0.080424

95.43333	1	1.095704	0.47568
95.5	1	1.094241	0.369122
105.1333	1	0.902029	0.510571
96.7	1	1.068252	0.305247
101.7333	1	0.965924	0.767027
91.43333	1	1.187386	0.314984
93.03333	1	1.150125	0.179633
93.8	1	1.132196	0.442814
108.2	1	0.848429	0.256811
89.6	1	1.231771	0.399048
95.2	1	1.10049	0.757831
101.9333	1	0.96174	0.782635
91.3	1	1.190581	0.614914
105.4667	1	0.896334	0.509172
99.3	1	1.014099	0.934314
90.5	1	1.210313	0.421545
89.96667	1	1.223046	0.541144
102.2333	1	0.956309	0.68094
104.8667	1	0.907184	0.725514
83.36667	1	1.398641	0.360018
93.46667	1	1.1398	0.244167
95.4	1	1.096087	0.626484
101.5	1	0.970772	0.716153
NA	0	NA	NA
84.36667	1	1.371	0.303722
59.3	1	2.372681	0.113339
101.5333	1	0.969468	0.77821
98	1	1.040816	0.865243
102.1	1	0.958864	0.693104
94.26667	1	1.121641	0.733018
96.26667	1	1.077562	0.704304
77.13333	1	1.592913	0.167062
104.4	1	0.916028	0.446728
99.66667	1	1.007023	0.938815
99.16667	1	1.016807	0.894231
115	1	0.738841	0.045907
104.7667	1	0.908686	0.585124
92.16667	1	1.170344	0.476649
98.6	1	1.028059	0.71102
112.3	1	0.781241	0.086164
94.4	1	1.118644	0.511147
88.93333	1	1.24925	0.616604
96.7	1	1.068252	0.246373
107.7333	1	0.857054	0.590831
94.9	1	1.10713	0.405601
NA	0	NA	NA
93.23333	1	1.145156	0.755553
91.1	1	1.195756	0.296016
96.23333	1	1.077936	0.293269
99.5	1	1.01005	0.952412
98.16667	1	1.037691	0.574272

86.5	1	1.311753	0.361291
94.56667	1	1.11491	0.445301
106.6333	1	0.875899	0.521082
100.5333	1	0.98939	0.931073
97.56667	1	1.04988	0.711643
105.5667	1	0.894222	0.273789
84.06667	1	1.379064	0.592134
95.66667	1	1.090592	0.42384
NA	0	NA	NA
91.23333	1	1.192547	0.370599
114.2333	1	0.750802	0.57595
99.56667	1	1.009039	0.916052
98.5	1	1.030795	0.685542
86.5	1	1.312139	0.216327
92.4	1	1.164502	0.137435
110.3333	1	0.812991	0.255273
NA	0	NA	NA
97.23333	1	1.057251	0.717159
99.33333	1	1.013423	0.894503
95.63333	1	1.091321	0.542625
88.76667	1	1.253474	0.363087
96.23333	1	1.078282	0.251574
97.36667	1	1.054433	0.575819
86.6	1	1.309854	0.196994
98.13333	1	1.038043	0.783127
84.5	1	1.366864	0.332732
98.16667	1	1.037351	0.621678
80	1	1.5	0.059344
87.46667	1	1.286204	0.272432
104.7	1	0.909901	0.39993
97.73333	1	1.046044	0.614991
93.76667	1	1.13331	0.327118
104.7333	1	0.909612	0.70422
94.7	1	1.111932	0.164542
98.5	1	1.030457	0.810897
100.6333	1	0.987744	0.949516
86.46667	1	1.31303	0.515799
96.86667	1	1.064694	0.338127
81.1	1	1.466502	0.094599
88.73333	1	1.253944	0.287989
115.5333	1	0.731102	0.307204
103.2333	1	0.937682	0.691163
88.1	1	1.270526	0.246975
102.1667	1	0.957912	0.559077
97.53333	1	1.050239	0.515399
79.16667	1	1.525895	0.075162
96.3	1	1.076843	0.245347
99.56667	1	1.008704	0.971667
113.3333	1	0.764706	0.623908
98	1	1.040816	0.770027
102	1	0.961111	0.788107

108.3333	1	0.846154	0.585807
115.6667	1	0.729107	0.0437
105.2	1	0.900824	0.029511
111.7	1	0.79051	0.134088
95.03333	1	1.104525	0.35795
100.5	1	0.990381	0.962918
101.8	1	0.964637	0.723786
95.43333	1	1.095704	0.394603
101.2	1	0.976285	0.914364
108.7667	1	0.838799	0.760963
86.9	1	1.301496	0.416325
NA	0	NA	NA
90.43333	1	1.211942	0.588801
125.7667	1	0.590246	0.021775
92	1	1.173551	0.423756
97.66667	1	1.047782	0.749731
89.2	1	1.242152	0.124329
83.73333	1	1.388535	0.198386
89.76667	1	1.227627	0.49823
108.9	1	0.836547	0.059739
94.4	1	1.118644	0.505442
116.2333	1	0.72039	0.392021
102.8667	1	0.944264	0.592861
94.96667	1	1.106353	0.709182
92.63333	1	1.15941	0.655424
97.13333	1	1.059025	0.605097
98.73333	1	1.025321	0.914867
115.5667	1	0.730603	0.677348
103.5	1	0.932367	0.636499
99.5	1	1.009715	0.935308
95.83333	1	1.086957	0.530868
87.5	1	1.286095	0.489562
92	1	1.173913	0.432957
104.8333	1	0.908108	0.796274
100.6	1	0.98774	0.869549
99.3	1	1.014434	0.916415
86.6	1	1.309469	0.20938
88.66667	1	1.255639	0.532081
91.9	1	1.176641	0.508043
89.33333	1	1.238806	0.216873
99.16667	1	1.016471	0.906767
99.83333	1	1.003339	0.97712
98.46667	1	1.030806	0.766098
98.16667	1	1.037351	0.859431
99.83333	1	1.003005	0.965984
92.83333	1	1.154399	0.560834
114.3333	1	0.749271	0.26298
92.33333	1	1.166426	0.211786
100.2667	1	0.994348	0.925993
102.1	1	0.958864	0.648702
85.5	1	1.339571	0.011314

99.1	1	1.017827	0.803026
96.76667	1	1.066827	0.199928
NA	0	NA	NA
89.6	1	1.232515	0.29411
98.83333	1	1.023609	0.923062
98.9	1	1.022582	0.895739
105.4	1	0.897849	0.352636
103.5333	1	0.932067	0.561315
96.3	1	1.076843	0.695256
76.63333	1	1.60983	0.375477
95	1	1.105263	0.548753
81.6	1	1.45098	0.289978
99.53333	1	1.009377	0.981572
98.23333	1	1.036308	0.76952
113.2	1	0.766784	0.131481
105.5667	1	0.894853	0.24922
113.6667	1	0.759824	0.033957
84	1	1.380556	0.279603
NA	0	NA	NA
86.06667	1	1.323393	0.325811
100.9667	1	0.980852	0.896676
99.83333	1	1.003005	0.990695
84.66667	1	1.362598	0.069975
91.03333	1	1.196997	0.431746
97.9	1	1.042901	0.918853
95.63333	1	1.090972	0.160955
92.1	1	1.171191	0.447753
107.8	1	0.855288	0.13134
100.4333	1	0.991371	0.91001
94.63333	1	1.11342	0.297286
95.7	1	1.089516	0.836214
96.8	1	1.066116	0.516122
92.3	1	1.166847	0.408418
99.26667	1	1.014775	0.866726
95.5	1	1.094241	0.653503
NA	0	NA	NA
NA	0	NA	NA
NA	0	NA	NA
92.8	1	1.155172	0.149511
100.2	1	0.996008	0.957927
110.0667	1	0.817081	0.295806
98.66667	1	1.027027	0.863494
92.06667	1	1.172701	0.434026
87.06667	1	1.297473	0.422514
103.5	1	0.932367	0.440888
98.36667	1	1.033209	0.807607
102.7	1	0.94742	0.667857
84.5	1	1.366864	0.260327
82.9	1	1.412947	0.263126
92.26667	1	1.167991	0.623135
87.4	1	1.287948	0.313131

98.46667	1	1.031483	0.922992
101.8333	1	0.963993	0.671338
94.83333	1	1.108963	0.595216
91.4	1	1.188184	0.170392
83.93333	1	1.382844	0.192286
91.53333	1	1.184632	0.525392
99.63333	1	1.00736	0.917702
99.16667	1	1.016807	0.882871
96.4	1	1.074689	0.448775
102.8	1	0.945525	0.646769
92.43333	1	1.163722	0.503173
109.6667	1	0.823708	0.057347
84.03333	1	1.380008	0.029533
107.2	1	0.865672	0.014761
73.33333	1	1.727727	0.067041
94.06667	1	1.126506	0.478346
93.3	1	1.143623	0.606655
88.96667	1	1.247658	0.300944
102.2667	1	0.955671	0.665435
80.33333	1	1.490041	0.000175
100.9667	1	0.980852	0.853378
95.06667	1	1.103787	0.494905
99.2	1	1.016465	0.747423
102	1	0.960784	0.247542
101.7333	1	0.966252	0.879549
NA	0	NA	NA
102.6	1	0.949643	0.814626
105.3333	1	0.898734	0.529289
97.06667	1	1.06044	0.760988
97.56667	1	1.04988	0.882528
101.4333	1	0.972067	0.821375
106.2333	1	0.882648	0.188914
108.0333	1	0.85128	0.158277
101.6667	1	0.966885	0.802538
99.63333	1	1.00736	0.935957
113.0667	1	0.768868	0.418012
102.3	1	0.955034	0.676532
97.83333	1	1.044293	0.796683
NA	0	NA	NA
89.23333	1	1.240941	0.068574
91.5	1	1.186157	0.061833
95.26667	1	1.09937	0.375066
106.1333	1	0.884736	0.610589
99.96667	1	1.000333	0.997393
93.16667	1	1.146691	0.400536
90.1	1	1.219016	0.1006
102.4	1	0.953451	0.814349
105.0333	1	0.904157	0.395257
95.6	1	1.09205	0.073364
101.7667	1	0.965935	0.757695
105.4	1	0.897849	0.267259

93.53333	1	1.138275	0.191139
80.43333	1	1.486117	0.076782
86.53333	1	1.311248	0.114504
111.2	1	0.798561	0.094212
101.8333	1	0.963993	0.742726
102.0667	1	0.959504	0.842535
94.4	1	1.118644	0.313604
88.76667	1	1.253474	0.103681
104.2	1	0.919066	0.600256
99.7	1	1.005684	0.902383
94.23333	1	1.122745	0.233092
110.2	1	0.81458	0.238746
93.2	1	1.14628	0.194417
107.1	1	0.867102	0.283005
101.1333	1	0.977258	0.876162
84.33333	1	1.371542	0.07119
99.3	1	1.014434	0.85411
NA	0	NA	NA
92.76667	1	1.155947	0.540398
90.66667	1	1.205882	0.296352
93.06667	1	1.149355	0.181492
90.56667	1	1.208686	0.006095
102.5333	1	0.95026	0.58954
94.33333	1	1.120141	0.743685
92.93333	1	1.15208	0.214621
94.9	1	1.108184	0.358783
107.0667	1	0.867995	0.29465
102.0667	1	0.959504	0.865055
93.23333	1	1.145156	0.02358
96.56667	1	1.071108	0.492841
129.0333	1	0.549987	0.098231
94.13333	1	1.124646	0.47674
NA	0	NA	NA
92.46667	1	1.162942	0.465457
88.3	1	1.265006	0.249335
87.1	1	1.296594	0.264661
130.7333	1	0.529832	0.018816
107.1	1	0.867414	0.230021
101.8667	1	0.963024	0.886358
100.1333	1	0.99767	0.973382
110.2	1	0.81458	0.030965
105.4667	1	0.89665	0.631464
96.93333	1	1.063274	0.565019
86.36667	1	1.315322	0.39859
92.26667	1	1.167991	0.325791
98.8	1	1.024629	0.918051
99.43333	1	1.011398	0.897009
88.5	1	1.25951	0.472639
101.1333	1	0.977587	0.778659
99.26667	1	1.014775	0.911002
99.63333	1	1.00736	0.980851

102.6333	1	0.948685	0.712501
NA	0	NA	NA
106.4333	1	0.879111	0.196164
103.1333	1	0.939237	0.32489
109.4333	1	0.827597	0.229275
86.6	1	1.309469	0.325913
97.8	1	1.045331	0.627661
98	1	1.040816	0.657437
107	1	0.86947	0.385303
113.2333	1	0.766264	0.255974
NA	0	NA	NA
97.16667	1	1.058319	0.726538
103	1	0.941748	0.835154
105.9333	1	0.88798	0.379336
97.73333	1	1.046385	0.581757
108.1	1	0.849522	0.7352
NA	0	NA	NA
104.0667	1	0.921845	0.604972
109.5	1	0.826484	0.313965
89.13333	1	1.243829	0.023189
102.9333	1	0.943005	0.764287
91.1	1	1.19539	0.2818
87.53333	1	1.284844	0.364555
101.7667	1	0.964953	0.794808
102.3333	1	0.954397	0.731175
103.4667	1	0.93299	0.509174
99.16667	1	1.016471	0.868591
95.83333	1	1.087304	0.627657
104.8333	1	0.907472	0.827915
83.8	1	1.387033	0.004776
90.46667	1	1.211127	0.418671
90.76667	1	1.203452	0.303803
106.1333	1	0.884108	0.393845
NA	0	NA	NA
NA	0	NA	NA
102.8	1	0.945525	0.700688
102.7667	1	0.945832	0.803271
90.36667	1	1.213205	0.216689
97.6	1	1.04918	0.850327
75.03333	1	1.665038	0.117275
88.53333	1	1.259413	0.459956
91.66667	1	1.181818	0.691425
88.23333	1	1.267095	0.028955
90.26667	1	1.216027	0.194408
102.9333	1	0.943005	0.814037
100.7667	1	0.984783	0.890565
88.33333	1	1.264528	0.336157
94.03333	1	1.12726	0.411367
125.9	1	0.588562	0.305854
105.7667	1	0.890955	0.345066
56.83333	1	2.519062	0.372789

93.66667	1	1.135231	0.039275
99.56667	1	1.008704	0.927971
NA	0	NA	NA
85.93333	1	1.328161	0.155696
75.83333	1	1.637802	0.173
100.1	1	0.998002	0.983752
85.8	1	1.331002	0.38107
102.2333	1	0.956309	0.387021
85.5	1	1.339181	0.593001
100.8667	1	0.982816	0.876912
97.1	1	1.059389	0.703352
124.2	1	0.610574	0.058658
NA	0	NA	NA
94.33333	1	1.120495	0.41488
99.5	1	1.01005	0.958313
90.03333	1	1.22177	0.152301
91.8	1	1.178649	0.141309
106.4333	1	0.879111	0.298513
99.83333	1	1.003339	0.989068
98.06667	1	1.039429	0.664356
98.03333	1	1.040122	0.808292
100.4333	1	0.991371	0.955809
95.16667	1	1.100876	0.027599
93.6	1	1.136752	0.44742
106.1667	1	0.883516	0.208867
101.7667	1	0.965608	0.739162
NA	0	NA	NA
92.2	1	1.169197	0.244772
97.5	1	1.051282	0.73958
116.3333	1	0.719198	0.515237
122	1	0.639344	0.137488
NA	0	NA	NA
110.8333	1	0.804211	0.756339
89.2	1	1.241779	0.387797
NA	0	NA	NA
95.73333	1	1.088788	0.821985
100.1333	1	0.997337	0.990983
83.33333	1	1.3996	0.311252
96.73333	1	1.06754	0.579716
107.2667	1	0.864823	0.574265
98	1	1.040476	0.567008
90.73333	1	1.204262	0.403826
101.6667	1	0.966885	0.723859
93.66667	1	1.135231	0.055413
91.06667	1	1.196193	0.115592
89.5	1	1.234637	0.264985
123.2	1	0.622835	0.049686
106.8333	1	0.872075	0.178799
91.43333	1	1.187751	0.001873
77.13333	1	1.592913	0.120715
98.46667	1	1.031483	0.866106

106.1	1	0.8847	0.252712
NA	0	NA	NA
100.6667	1	0.986755	0.926207
95.7	1	1.089864	0.489536
113.7333	1	0.758792	0.247901
92.26667	1	1.16763	0.342123
90.13333	1	1.218565	0.24971
104.6333	1	0.911437	0.728934
88.9	1	1.249719	0.403769
101.9	1	0.962709	0.488496
98.63333	1	1.027712	0.596726
96.7	1	1.068252	0.678367
98.46667	1	1.031144	0.803987
97.13333	1	1.058682	0.722402
92.46667	1	1.162942	0.50389
93	1	1.150896	0.033849
93.03333	1	1.150125	0.35859
98.73333	1	1.025996	0.839585
80.8	1	1.474835	0.238447
111.8	1	0.788909	0.402662
106.1	1	0.885014	0.40802
99.83333	1	1.003005	0.989363
82.86667	1	1.413516	0.148455
92.3	1	1.167208	0.48603
97.76667	1	1.045346	0.504621
84.6	1	1.364066	0.057714
95.8	1	1.087683	0.653632
97.76667	1	1.045687	0.754635
102.2667	1	0.955997	0.780432
89.96667	1	1.223416	0.341399
102.2333	1	0.956309	0.713454
84	1	1.380952	0.002796
100.8333	1	0.983471	0.911525
84.83333	1	1.357957	0.356078
90.1	1	1.219386	0.565335
97.73333	1	1.046726	0.658437
110.5	1	0.810256	0.013724
114.8	1	0.74158	0.448115
NA	0	NA	NA
95.16667	1	1.101576	0.789613
97.03333	1	1.061147	0.799437
99.4	1	1.012408	0.968682
95.86667	1	1.086231	0.348315
82.63333	1	1.419927	0.452351
92.63333	1	1.15905	0.2474
62.23333	1	2.214247	0.126501
96.3	1	1.076843	0.470502
102.7	1	0.94742	0.470294
96.86667	1	1.064694	0.718136
NA	0	NA	NA
103.8667	1	0.925546	0.421866

98.46667	1	1.030806	0.893874
115.2333	1	0.735609	0.142423
87.43333	1	1.287838	0.138591
91.43333	1	1.187751	0.058279
104.3333	1	0.916933	0.637362
91.93333	1	1.175489	0.163655
94.46667	1	1.116796	0.628118
71.96667	1	1.779528	0.145883
109.1333	1	0.832926	0.735128
82.3	1	1.430134	0.203604
91.7	1	1.181025	0.410031
95.3	1	1.098286	0.473563
101.1333	1	0.977917	0.79721
92.16667	1	1.170344	0.425459
110.6	1	0.80862	0.560696
100.3	1	0.994018	0.965165
121.8667	1	0.640864	0.040455
108.1667	1	0.848998	0.074955
66.03333	1	2.029278	0.28384
90.16667	1	1.217745	0.041752
111	1	0.801502	0.681859
98.46667	1	1.031144	0.843544
104.4333	1	0.915097	0.217236
78.8	1	1.538071	0.012802
112.5	1	0.777481	0.354928
101.6667	1	0.967213	0.757491
98.26667	1	1.035278	0.86736
105.4	1	0.897849	0.231328
104.2333	1	0.918452	0.549705
107.7667	1	0.855861	0.64243
NA	0	NA	NA
94.9	1	1.107482	0.445832
84.03333	1	1.380008	0.057383
94.73333	1	1.111189	0.700036
102.7333	1	0.946788	0.355009
103.1667	1	0.938934	0.889592
90.73333	1	1.203894	0.515973
77.53333	1	1.579536	0.303204
NA	0	NA	NA
86	1	1.325581	0.237
NA	0	NA	NA
101.1667	1	0.976606	0.784736
89.43333	1	1.236303	0.392841
90.13333	1	1.218565	0.20535
94.86667	1	1.108222	0.541001
NA	0	NA	NA
83.63333	1	1.390992	0.234857
34.13333	1	4.859375	0.365062
97.1	1	1.059732	0.448012
110.6667	1	0.807229	0.59872
91.76667	1	1.179077	0.232519

94.76667	1	1.110447	0.356135
94.63333	1	1.11342	0.390859
NA	0	NA	NA
NA	0	NA	NA
105.1667	1	0.901743	0.472088
107.5333	1	0.859578	0.213964
106.5	1	0.877934	0.098196
104.9333	1	0.90629	0.337576
91.16667	1	1.19415	0.468112
91.6	1	1.183406	0.429346
NA	0	NA	NA
70.73333	1	1.827521	0.344532
93.73333	1	1.133713	0.199091
NA	0	NA	NA
81.76667	1	1.445577	0.60801
93.8	1	1.132196	0.563099
90.13333	1	1.218935	0.024682
103.4	1	0.934236	0.420085
88.8	1	1.252628	0.356815
101.6333	1	0.967858	0.487857
87.43333	1	1.287076	0.085765
95.4	1	1.096436	0.535802
106.1667	1	0.883516	0.390625
100.1	1	0.997669	0.969072
104.9667	1	0.905684	0.543981
NA	0	NA	NA
96.73333	1	1.067195	0.823931
97.93333	1	1.042206	0.758764
100.6	1	0.98774	0.890124
99.33333	1	1.014094	0.844076
94.7	1	1.11158	0.104684
104.7667	1	0.908686	0.405306
98.66667	1	1.027027	0.820667
104.8667	1	0.907184	0.170663
97.76667	1	1.045687	0.878615
94.43333	1	1.117543	0.332348
96.83333	1	1.065404	0.355855
92.8	1	1.154813	0.633675
98.63333	1	1.027712	0.675485
112.9333	1	0.770956	0.067254
86.46667	1	1.312259	0.280202
93.26667	1	1.144389	0.173145
95.83333	1	1.086957	0.223906
108.7333	1	0.839669	0.021335
98.2	1	1.03666	0.817548
94.9	1	1.107482	0.545788
97.6	1	1.04918	0.617169
101.1	1	0.978239	0.934953
107.7667	1	0.855861	0.544982
101.1333	1	0.977258	0.786981
105.6667	1	0.89306	0.119813

112.7	1	0.774623	0.125308
107.7	1	0.85701	0.107356
100.4667	1	0.991042	0.907557
116.7	1	0.713796	0.167794
109.0333	1	0.834301	0.044395
97.96667	1	1.041511	0.489397
117.2667	1	0.705799	0.007246
89.46667	1	1.235469	0.476225
97	1	1.061512	0.688822
89.86667	1	1.22589	0.3731
101.8667	1	0.963351	0.637863
91.76667	1	1.179441	0.329101
117.9	1	0.696353	0.082866
100.8	1	0.984127	0.860705
101.9333	1	0.962067	0.88628
100.3	1	0.994018	0.973828
99.23333	1	1.015788	0.883357
106.5	1	0.878247	0.434132
98.26667	1	1.035617	0.785549
102.5	1	0.95122	0.795464
101.3333	1	0.973684	0.884738
101.1333	1	0.977587	0.846771
93.7	1	1.134116	0.443015
96.33333	1	1.076125	0.293504
93.3	1	1.143623	0.402936
87.96667	1	1.274346	0.085649
109.9667	1	0.818733	0.031959
93.4	1	1.140971	0.030677
104.7667	1	0.909004	0.323996
102.6	1	0.949318	0.687017
85.96667	1	1.326095	0.469047
95.4	1	1.096436	0.479978
85.23333	1	1.3465	0.3028
96.3	1	1.076843	0.627242
NA	0	NA	NA
110.4667	1	0.810199	0.55236
99.86667	1	1.003338	0.991366
99.63333	1	1.00736	0.954845
113.9	1	0.755926	0.036074
86.76667	1	1.305033	0.390015
105.5	1	0.896051	0.512784
92.1	1	1.171191	0.407885
82.43333	1	1.426607	0.099061
101.3667	1	0.973364	0.806613
100.9	1	0.982161	0.926238
102.1333	1	0.958225	0.7945
98.8	1	1.024629	0.769099
98.3	1	1.034927	0.7882
NA	0	NA	NA
108.6	1	0.841928	0.445767
88.76667	1	1.253474	0.080129

90.46667	1	1.210759	0.675703
95.96667	1	1.08371	0.753649
98.86667	1	1.023264	0.869653
125.4667	1	0.594315	0.053353
99.53333	1	1.009712	0.938378
103.6667	1	0.92926	0.295175
NA	0	NA	NA
106.2333	1	0.882962	0.250775
NA	0	NA	NA
114.2	1	0.751313	0.016367
99.56667	1	1.009039	0.9583
91	1	1.197802	0.417524
97.06667	1	1.060783	0.766572
NA	0	NA	NA
99.4	1	1.012743	0.90585
97.5	1	1.051282	0.805052
103.7667	1	0.927401	0.366531
85.33333	1	1.343359	0.376764
87.9	1	1.275313	0.022044
94.26667	1	1.121994	0.631028
106.1	1	0.885014	0.236686
87.46667	1	1.286585	0.299539
100.1333	1	0.997337	0.987283
NA	0	NA	NA
83.3	1	1.40096	0.043311
99.66667	1	1.006355	0.965161
88.86667	1	1.250563	0.340294
111.8333	1	0.788376	0.400601
96.4	1	1.074689	0.541228
90.73333	1	1.204629	0.355318
87.46667	1	1.286585	0.409779
82.46667	1	1.424818	0.241576
99.2	1	1.016129	0.80525
100.4	1	0.992364	0.974219
90.06667	1	1.220577	0.18053
96.46667	1	1.073946	0.541896
106.9667	1	0.869741	0.286913
90.03333	1	1.221399	0.440406
89.23333	1	1.241315	0.210583
102.7	1	0.94742	0.807079
95.6	1	1.09205	0.095229
96.5	1	1.072539	0.70252
117.3667	1	0.704061	0.450681
101	1	0.979868	0.798198
90.36667	1	1.213205	0.075553
88.1	1	1.270148	0.265542
101.1667	1	0.976936	0.698619
62.2	1	2.21597	0.155045
92.3	1	1.166486	0.524734
84.36667	1	1.370605	0.173732
88.13333	1	1.269667	0.054063

89	1	1.246816	0.502047
98.56667	1	1.029422	0.815758
86.66667	1	1.307692	0.154103
88.93333	1	1.248876	0.077218
68.43333	1	1.922552	0.094283
NA	0	NA	NA
102.5667	1	0.950276	0.506119
NA	0	NA	NA
85.33333	1	1.343359	0.122855
100.3667	1	0.992693	0.978886
95.36667	1	1.096819	0.567177
99.63333	1	1.007695	0.937902
107.9667	1	0.852424	0.233281
87.53333	1	1.284463	0.384251
100.8333	1	0.983802	0.920036
96.1	1	1.081165	0.366593
107.9333	1	0.852996	0.056563
97.7	1	1.046742	0.715758
70.66667	1	1.83066	0.090721
97.6	1	1.049522	0.484752
75.83333	1	1.636923	0.186515
97.7	1	1.046742	0.673039
124.7333	1	0.603421	0.335592
112.8667	1	0.772298	0.137461
91.66667	1	1.181818	0.504389
104.9333	1	0.905972	0.12979
100.9	1	0.98183	0.879139
97.6	1	1.049522	0.248345
89.73333	1	1.229198	0.388266
82.13333	1	1.435471	0.079425
94.9	1	1.107482	0.238537
99.06667	1	1.018843	0.807893
93.1	1	1.148586	0.352738
92.66667	1	1.158273	0.525303
97.23333	1	1.056908	0.567966
80.73333	1	1.477704	0.020374
99.83333	1	1.003339	0.99422
NA	0	NA	NA
92.1	1	1.171915	0.44703
103.6667	1	0.92926	0.610802
106.1667	1	0.884144	0.554454
89.06667	1	1.245883	0.311561
88.8	1	1.252628	0.217848
79.3	1	1.522068	0.387272
108.9333	1	0.835985	0.103281
93	1	1.150896	0.232472
87.46667	1	1.286966	0.529187
106.8333	1	0.872387	0.052992
98.16667	1	1.037351	0.82392
109.8333	1	0.820637	0.10805
109.6333	1	0.824567	0.289697

100.5667	1	0.988731	0.917363
99.16667	1	1.016807	0.935482
97.83333	1	1.044293	0.59109
NA	0	NA	NA
99.76667	1	1.004678	0.953351
105.4	1	0.897849	0.793855
96.66667	1	1.068621	0.764506
97.63333	1	1.048139	0.610049
102.5333	1	0.950585	0.780804
89.5	1	1.235009	0.254163
101.8333	1	0.963993	0.75674
106.3667	1	0.880602	0.406201
82.33333	1	1.42915	0.157279
89.76667	1	1.22837	0.542124
110.8	1	0.805054	0.511616
99.1	1	1.018163	0.820336
104.8667	1	0.906866	0.550665
NA	0	NA	NA
99.03333	1	1.019522	0.907549
95.9	1	1.085158	0.671764
87.6	1	1.282725	0.244428
99.63333	1	1.00736	0.961138
101.8	1	0.964309	0.838488
105	1	0.904762	0.228914
100.3	1	0.993686	0.935919
102.7667	1	0.946156	0.221955
92.46667	1	1.162942	0.556338
94.63333	1	1.113068	0.164464
97.56667	1	1.050222	0.804183
87.9	1	1.275313	0.039515
96.4	1	1.074689	0.846486
115.5333	1	0.731102	0.167384
96.93333	1	1.063618	0.617004
96.46667	1	1.073601	0.479409
95.93333	1	1.085129	0.844305
92.23333	1	1.168413	0.422233
105.5667	1	0.894537	0.390589
88.76667	1	1.252722	0.130575
118.9667	1	0.681143	0.251243
97.86667	1	1.043597	0.755641
102.5667	1	0.949626	0.56215
83.73333	1	1.388535	0.352386
88.46667	1	1.260739	0.111191
NA	0	NA	NA
103.7667	1	0.92708	0.387363
99.43333	1	1.011398	0.916011
92.66667	1	1.158273	0.354041
91.46667	1	1.186224	0.453174
100.4667	1	0.991042	0.867024
96.5	1	1.072539	0.62069
117.4	1	0.703578	0.569112

96.86667	1	1.065038	0.817067
NA	0	NA	NA
100.7667	1	0.985114	0.929684
NA	0	NA	NA
96.03333	1	1.082263	0.737821
90.73333	1	1.204262	0.080397
84.2	1	1.374901	0.224829
101.9	1	0.962709	0.702618
100.2333	1	0.995012	0.968901
87.03333	1	1.298353	0.237955
83.23333	1	1.403284	0.393758
95.66667	1	1.090592	0.708359
89.6	1	1.231771	0.07886
100.0667	1	0.999001	0.988363
102.4	1	0.952799	0.853149
110.3667	1	0.812141	0.019383
82.8	1	1.414654	0.083407
117.7	1	0.699235	0.015717
NA	0	NA	NA
110.2333	1	0.814333	0.163408
106.4	1	0.879699	0.370596
NA	0	NA	NA
132.2	1	0.512859	0.184113
92.7	1	1.157138	0.469851
105.2	1	0.901141	0.660571
95.86667	1	1.086231	0.714848
97.7	1	1.047424	0.758998
85.4	1	1.34153	0.279632
105.6333	1	0.893342	0.587658
136.9333	1	0.460808	0.4262
102.9	1	0.943311	0.690465
82.4	1	1.427184	0.325519
99.93333	1	1.001334	0.992081
99.03333	1	1.019522	0.777397
84.1	1	1.378121	0.494752
99.93333	1	1.001334	0.993826
94.4	1	1.118644	0.764449
107.1667	1	0.866252	0.16094
93.63333	1	1.136347	0.332979
92.53333	1	1.161383	0.577044
101.9667	1	0.961425	0.692917
91.43333	1	1.187751	0.270507
NA	0	NA	NA
NA	0	NA	NA
102	1	0.960784	0.818073
90.8	1	1.202643	0.532876
84.06667	1	1.379064	0.351277
111.0333	1	0.801261	0.405559
94.23333	1	1.122391	0.442421
NA	0	NA	NA
105.3333	1	0.898734	0.1695

90.56667	1	1.208318	0.215426
90.06667	1	1.220947	0.288018
93.06667	1	1.148639	0.417531
56.56667	1	2.535651	0.232144
96.53333	1	1.071478	0.410526
105.7	1	0.892148	0.083307
114.6	1	0.745492	0.534975
106.3	1	0.881468	0.502875
89.33333	1	1.238806	0.377388
101.8	1	0.964964	0.741985
NA	0	NA	NA
92.03333	1	1.173126	0.428724
99.3	1	1.014434	0.897176
93	1	1.150896	0.266677
107.8	1	0.854978	0.443224
81.13333	1	1.465489	0.355161
105.1333	1	0.902663	0.095595
100.8667	1	0.982485	0.805111
105.1333	1	0.902029	0.272603
97.56667	1	1.049197	0.565066
93.83333	1	1.131794	0.710535
103.3667	1	0.93486	0.175428
90.5	1	1.209945	0.257933
101.3667	1	0.973364	0.645369
84.33333	1	1.371542	0.261973
113.4	1	0.763374	0.389904
83.66667	1	1.390837	0.061755
NA	0	NA	NA
105.9333	1	0.88798	0.361662
105.3	1	0.899335	0.608566
105.5333	1	0.895136	0.610083
99.66667	1	1.007023	0.95521
NA	0	NA	NA
NA	0	NA	NA
102.2	1	0.956947	0.798737
101.8333	1	0.963993	0.770845
89.1	1	1.244669	0.213599
92.03333	1	1.173126	0.532828
88.63333	1	1.256111	0.286127
NA	0	NA	NA
99.03333	1	1.019522	0.737931
95.66667	1	1.090941	0.583111
81	1	1.468724	0.256865
114.0333	1	0.753873	0.230086
107.6667	1	0.857895	0.20746
105.4333	1	0.896617	0.537234
NA	0	NA	NA
105.2667	1	0.899937	0.469746
NA	0	NA	NA
76.63333	1	1.60983	0.148248
105.9	1	0.888259	0.286966

94.66667	1	1.112324	0.592205
NA	0	NA	NA
107.5667	1	0.859622	0.752573
86.16667	1	1.321083	0.351243
80.93333	1	1.471582	0.165693
98.56667	1	1.029084	0.69345
NA	0	NA	NA
101.6667	1	0.967541	0.90668
112.0667	1	0.784652	0.269247
91.83333	1	1.177858	0.665541
109.1333	1	0.832926	0.001599
90.9	1	1.20022	0.106518
NA	0	NA	NA
111.7	1	0.79051	0.011381
101.8333	1	0.963993	0.847105
102.9	1	0.943959	0.560713
100.7667	1	0.985114	0.935335
107.9333	1	0.852996	0.537747
94.1	1	1.125399	0.290697
106.9667	1	0.86943	0.159603
87.7	1	1.280882	0.502052
84.93333	1	1.354788	0.312245
98.1	1	1.039076	0.836565
96.83333	1	1.06506	0.313005
NA	0	NA	NA
111.1333	1	0.79964	0.124965
111.6333	1	0.79158	0.400826
112.7667	1	0.773574	0.21459
NA	0	NA	NA
86.16667	1	1.321083	0.002403
84.6	1	1.364066	0.163108
101.1667	1	0.976606	0.809143
89.7	1	1.229654	0.249811
103.2667	1	0.937056	0.499754
99.8	1	1.003674	0.988961
79.5	1	1.515723	0.228649
98.93333	1	1.021563	0.910151
NA	0	NA	NA
98.76667	1	1.024975	0.822871
92.13333	1	1.171129	0.496504
84.16667	1	1.376634	0.43091
87.33333	1	1.290458	0.280626
101.1667	1	0.976606	0.822249
94.73333	1	1.111541	0.670859
96.96667	1	1.062221	0.724327
84.23333	1	1.374357	0.280107
76.33333	1	1.620524	0.387256
99.3	1	1.014434	0.903041
116.1	1	0.722653	0.36642
92.63333	1	1.15905	0.35013
94.43333	1	1.118249	0.390305

96.93333	1	1.06293	0.33403
93.3	1	1.143623	0.359893
93.33333	1	1.142857	0.202635
90.5	1	1.209576	0.380517
91.2	1	1.193348	0.460394
NA	0	NA	NA
92.8	1	1.155172	0.210186
95.26667	1	1.09902	0.626364
98.7	1	1.026342	0.758414
105.4	1	0.897533	0.311146
101	1	0.980198	0.90043
100.8	1	0.984127	0.873716
NA	0	NA	NA
79.63333	1	1.511511	0.157988
NA	0	NA	NA
89.03333	1	1.24635	0.280818
96.7	1	1.068252	0.81858
131.1333	1	0.525165	0.010345
95.93333	1	1.084781	0.734609
NA	0	NA	NA
90.63333	1	1.206694	0.280011
100.4	1	0.992364	0.961093
94.3	1	1.121244	0.601463
103.9667	1	0.923373	0.565997
95.3	1	1.098286	0.647811
104.2333	1	0.918772	0.631363
NA	0	NA	NA
108.7333	1	0.839362	0.724493
100.7	1	0.986428	0.799015
107.3667	1	0.862776	0.174521
96.43333	1	1.073626	0.346304
109.3667	1	0.828406	0.044768
104.4	1	0.91539	0.648736
94.93333	1	1.106742	0.026795
95.63333	1	1.091321	0.506738
129.8333	1	0.540693	0.213077
83.16667	1	1.40481	0.014061
96.2	1	1.079002	0.665469
NA	0	NA	NA
NA	0	NA	NA
107	1	0.869159	0.488007
88.63333	1	1.256487	0.154296
NA	0	NA	NA
100.1667	1	0.996672	0.987735
86.53333	1	1.311633	0.178515
86.2	1	1.320572	0.027527
NA	0	NA	NA
60	1	2.333333	0.201531
100.1333	1	0.997337	0.989583
100.1667	1	0.996672	0.987732
NA	0	NA	NA

94.46667	1	1.117149	0.280732
107.9667	1	0.852115	0.066435
104.7	1	0.909901	0.335822
94.73333	1	1.111189	0.281765
90.76667	1	1.203452	0.700473
NA	0	NA	NA
93.06667	1	1.148997	0.317769
106.4333	1	0.879111	0.666827
83.93333	1	1.383241	0.397923
103.7667	1	0.927401	0.749778
99.03333	1	1.019185	0.644022
109.4667	1	0.82704	0.345044
86.46667	1	1.312645	0.193001
101.7333	1	0.965596	0.930145
89.7	1	1.229283	0.471537
NA	0	NA	NA
89.23333	1	1.240568	0.300187
115.1667	1	0.736614	0.277994
98.56667	1	1.029422	0.876883
100.0667	1	0.998668	0.992859
NA	0	NA	NA
110.4667	1	0.810199	0.36704
95	1	1.105263	0.308063
102.9333	1	0.943005	0.749373
102.4667	1	0.951529	0.356577
89.4	1	1.236764	0.386088
105.1333	1	0.902663	0.310279
95.33333	1	1.097902	0.503689
101.7667	1	0.96528	0.788028
63.2	1	2.164557	0.257097
NA	0	NA	NA
NA	0	NA	NA
93.4	1	1.141685	0.602206
109.4333	1	0.827597	0.380335
NA	0	NA	NA
96.16667	1	1.079723	0.494633
85.1	1	1.350176	0.171556
86.56667	1	1.310358	0.403663
109.2	1	0.831197	0.357155
95.1	1	1.103049	0.202696
85.66667	1	1.335019	0.332888
NA	0	NA	NA
100.9	1	0.982491	0.843809
95.43333	1	1.095704	0.118977
103.1333	1	0.93956	0.481439
101.6333	1	0.967858	0.3785
86.53333	1	1.311633	0.417955
112.6667	1	0.775148	0.017918
90.66667	1	1.205882	0.078175
111.1	1	0.80018	0.058072
103.7	1	0.92864	0.748918

85.43333	1	1.341007	0.186097
94.6	1	1.114165	0.26607
92.6	1	1.159827	0.512286
NA	0	NA	NA
98.63333	1	1.027712	0.394886
97.73333	1	1.046044	0.742724
118.9333	1	0.681614	0.344005
96.7	1	1.068597	0.674788
101.0333	1	0.979215	0.892882
90.5	1	1.209945	0.469016
NA	0	NA	NA
111.7	1	0.79051	0.29971
86.66667	1	1.308077	0.344934
91	1	1.197436	0.289856
81.26667	1	1.460623	0.337528
87.56667	1	1.284355	0.37505
94.6	1	1.114165	0.610758
99.6	1	1.007697	0.934879
88.76667	1	1.253098	0.384084
80.76667	1	1.476269	0.099972
90.66667	1	1.205515	0.204926
NA	0	NA	NA
101.5667	1	0.968822	0.848589
100.3667	1	0.992693	0.873062
NA	0	NA	NA
100.5	1	0.99005	0.920997
113.4333	1	0.763444	0.136788
NA	0	NA	NA
105.4667	1	0.896334	0.68755
92.7	1	1.157497	0.209337
99.93333	1	1.001334	0.982198
104.8	1	0.908397	0.693336
88.76667	1	1.253098	0.187659
96.53333	1	1.071823	0.458442
100.3	1	0.993686	0.927883
94.53333	1	1.115656	0.738869
92.8	1	1.155172	0.713973
NA	0	NA	NA
101.6333	1	0.968186	0.618671
86.4	1	1.314815	0.264061
92.4	1	1.164141	0.284746
99.33333	1	1.013423	0.876308
97.13333	1	1.059369	0.57802
NA	0	NA	NA
94.23333	1	1.122391	0.386918
NA	0	NA	NA
98.36667	1	1.033209	0.925668
89.33333	1	1.238433	0.197497
NA	0	NA	NA
108.8667	1	0.83711	0.181216
NA	0	NA	NA

94.83333	1	1.108963	0.692851
84.4	1	1.369668	0.137564
81.46667	1	1.455401	0.422673
NA	0	NA	NA
75.3	1	1.656042	0.368523
NA	0	NA	NA
90.2	1	1.217295	0.220204
NA	0	NA	NA
92.86667	1	1.153625	0.378465
NA	0	NA	NA
85.56667	1	1.337359	0.220747
83.63333	1	1.391391	0.100691
84.03333	1	1.380008	0.28596
94.86667	1	1.108222	0.209632
101.8	1	0.964964	0.843854
NA	0	NA	NA
102	1	0.960784	0.655992
79.93333	1	1.502085	0.241751
NA	0	NA	NA
NA	0	NA	NA
NA	0	NA	NA
86.63333	1	1.30858	0.198709
88.16667	1	1.268431	0.411242
97.96667	1	1.041511	0.732715
100.8333	1	0.983471	0.813929
94.76667	1	1.110095	0.286131
NA	0	NA	NA
91.16667	1	1.193784	0.068418
NA	0	NA	NA
101.3	1	0.974663	0.80771
94.9	1	1.108184	0.592363
91	1	1.197802	0.503016
76.86667	1	1.601908	0.354452
100.4	1	0.992032	0.918323
94.63333	1	1.113068	0.318264
82.23333	1	1.432104	0.242013
106.6667	1	0.875	0.214995
80.86667	1	1.473207	0.463951
99.36667	1	1.012412	0.941651
NA	0	NA	NA
101.3333	1	0.974013	0.689466
99.6	1	1.007697	0.945278
93.83333	1	1.131083	0.386127
92.73333	1	1.156722	0.516666
NA	0	NA	NA
92.1	1	1.171553	0.233506
94.63333	1	1.11342	0.651063
NA	0	NA	NA
92.86667	1	1.153984	0.500091
114.5667	1	0.745999	0.148555
104.6667	1	0.910828	0.517305

85	1	1.352549	0.15566
94.2	1	1.122788	0.439318
91.36667	1	1.188982	0.49007
109.7667	1	0.822047	0.327724
110.6333	1	0.807472	0.492573
NA	0	NA	NA
NA	0	NA	NA
91	1	1.197802	0.112723
98.5	1	1.030457	0.875666
NA	0	NA	NA
102.1333	1	0.957898	0.848657
94	1	1.12766	0.103855
NA	0	NA	NA
93.43333	1	1.140564	0.477142
NA	0	NA	NA
NA	0	NA	NA
100.3	1	0.99435	0.95917
130.7667	1	0.529442	0.153298
96.9	1	1.063639	0.583711
77.1	1	1.594034	0.027945
102.8	1	0.94585	0.740486
104.2	1	0.919386	0.194323
NA	0	NA	NA
92.6	1	1.159827	0.251985
94.43333	1	1.117896	0.797288
NA	0	NA	NA
107	1	0.869159	0.716377
108.2667	1	0.847599	0.302221
105.8	1	0.890044	0.048956
115.8	1	0.727116	0.091651
93.03333	1	1.149767	0.39193
NA	0	NA	NA
90.93333	1	1.19978	0.133558
NA	0	NA	NA
NA	0	NA	NA
104.2	1	0.919706	0.667087
101.7667	1	0.965608	0.895737
103.2333	1	0.937359	0.59875
NA	0	NA	NA
NA	0	NA	NA
99.16667	1	1.017143	0.921638
87.86667	1	1.276555	0.363607
106.8	1	0.872971	0.331575
99.2	1	1.016465	0.933249
95.33333	1	1.098252	0.524629
NA	0	NA	NA
106.6667	1	0.875	0.43524
NA	0	NA	NA
104.5	1	0.913876	0.655507
97.3	1	1.055498	0.639536
NA	0	NA	NA

101.2	1	0.975955	0.832183
NA	0	NA	NA
97.5	1	1.05094	0.848431
96.5	1	1.072539	0.571526
NA	0	NA	NA
104.0333	1	0.92214	0.447975
NA	0	NA	NA
NA	0	NA	NA
74.03333	1	1.701486	0.268842
103.5667	1	0.931123	0.536616
108.0667	1	0.850709	0.24864
104.5667	1	0.912655	0.7506
NA	0	NA	NA
95.3	1	1.098636	0.546042
95.96667	1	1.084404	0.660858
93.4	1	1.141685	0.711235
108.8333	1	0.837979	0.37754
81	1	1.469136	0.039419
103	1	0.942071	0.621643
91.63333	1	1.182612	0.611022
NA	0	NA	NA
94.5	1	1.116402	0.379441
112.2	1	0.782531	0.307369
NA	0	NA	NA
NA	0	NA	NA
89.66667	1	1.230483	0.346828
95.4	1	1.096436	0.75721
NA	0	NA	NA
78.36667	1	1.552105	0.371252
91.43333	1	1.187386	0.263998
NA	0	NA	NA
NA	0	NA	NA
NA	0	NA	NA
105.6667	1	0.892744	0.599308
91.56667	1	1.184201	0.704854
72.93333	1	1.74223	0.266072
NA	0	NA	NA
NA	0	NA	NA
99.43333	1	1.011398	0.966393
85.33333	1	1.34375	0.234511
95.3	1	1.098986	0.678135
115.3667	1	0.733314	0.121669
NA	0	NA	NA
104.5667	1	0.912655	0.555023
NA	0	NA	NA
98.33333	1	1.033898	0.79485
92.66667	1	1.158273	0.431869
NA	0	NA	NA
99.7	1	1.006018	0.97918
96.33333	1	1.075779	0.143073
129	1	0.550129	0.453312

134.5	1	0.486989	0.040429
98.16667	1	1.037351	0.755268
NA	0	NA	NA
99.46667	1	1.010389	0.949885
NA	0	NA	NA
94.36667	1	1.119392	0.68218
NA	0	NA	NA
106.4	1	0.880013	0.01684
NA	0	NA	NA
100.5667	1	0.988399	0.966239
98.96667	1	1.020882	0.917979
110.1333	1	0.815981	0.053021
98.23333	1	1.035969	0.768771
103.9667	1	0.923373	0.848879
95.13333	1	1.101962	0.701521
96.33333	1	1.076125	0.73838
95.7	1	1.089864	0.351063
NA	0	NA	NA
98.3	1	1.034588	0.718854
NA	0	NA	NA
88.96667	1	1.248033	0.038705
109.1333	1	0.832621	0.142019
105.9333	1	0.88798	0.05579
97.1	1	1.059732	0.364577
91.86667	1	1.177431	0.554626
98.53333	1	1.030108	0.58271
NA	0	NA	NA
NA	0	NA	NA
95.53333	1	1.093859	0.739454
108.6	1	0.841314	0.347564
104.8667	1	0.907184	0.688585
102.0333	1	0.960144	0.735297
92.9	1	1.152853	0.151378
107.0667	1	0.867995	0.130281
NA	0	NA	NA
NA	0	NA	NA
99.4	1	1.012072	0.90948
114.7333	1	0.743173	0.33942
123.8667	1	0.614639	0.076548
111.1333	1	0.79934	0.004373
107.2	1	0.865361	0.663175
NA	0	NA	NA
98.06667	1	1.039769	0.769659
104.4333	1	0.914778	0.496924
90.03333	1	1.22177	0.170556
92.46667	1	1.162581	0.47977
112.9	1	0.771184	0.448154
81.3	1	1.460025	0.303165
NA	0	NA	NA
90.76667	1	1.203085	0.367953
91.33333	1	1.189416	0.654224

105.9667	1	0.887386	0.489361
NA	0	NA	NA
109.8333	1	0.821244	0.52527
99.03333	1	1.019522	0.956741
95.93333	1	1.084781	0.432038
NA	0	NA	NA
96.13333	1	1.080444	0.52343
NA	0	NA	NA
90	1	1.221852	0.07005
76.23333	1	1.623524	0.253419
107.8	1	0.855288	0.296906
96.36667	1	1.075752	0.652356
92.4	1	1.164502	0.313051
91.1	1	1.19539	0.669119
100.6667	1	0.986755	0.89613
91.63333	1	1.182612	0.510514
NA	0	NA	NA
112.2333	1	0.782002	0.538425
94.2	1	1.123142	0.293113
101.4333	1	0.971738	0.812333
NA	0	NA	NA
NA	0	NA	NA
103.5667	1	0.930801	0.467318
90.76667	1	1.203819	0.213148
108.3333	1	0.845846	0.188118
108.2	1	0.848737	0.175107
90.46667	1	1.211127	0.102492
92.96667	1	1.15095	0.006328
107.6667	1	0.857895	0.498102
91.5	1	1.185428	0.33668
NA	0	NA	NA
98.3	1	1.034588	0.737114
98.26667	1	1.035278	0.856963
107	1	0.868847	0.032187
105.4	1	0.897849	0.629095
114.1667	1	0.751825	0.074748
NA	0	NA	NA
102.7667	1	0.945832	0.457597
88.76667	1	1.253098	0.391816
87	1	1.298851	0.265916
66.83333	1	1.99202	0.141157
NA	0	NA	NA
94.3	1	1.121244	0.340574
89.46667	1	1.235469	0.348072
NA	0	NA	NA
98.83333	1	1.022934	0.881216
97.3	1	1.055498	0.627259
89.9	1	1.224694	0.104503
93.26667	1	1.143674	0.368063
122.1333	1	0.637555	0.430155
100.6667	1	0.986755	0.965083

NA	0	NA	NA
94.9	1	1.107833	0.146569
NA	0	NA	NA
94.16667	1	1.124248	0.501386
101.7667	1	0.964953	0.692802
NA	0	NA	NA
95.33333	1	1.097902	0.541968
92.1	1	1.171553	0.47861
104	1	0.923077	0.390539
93.46667	1	1.139444	0.482341
NA	0	NA	NA
NA	0	NA	NA
101.0667	1	0.979222	0.816693
98.96667	1	1.020546	0.913966
95.93333	1	1.084781	0.451989
NA	0	NA	NA
90	1	1.222222	0.012401
NA	0	NA	NA
98.73333	1	1.025658	0.636824
104.6	1	0.911409	0.129062
96.83333	1	1.065749	0.726276
NA	0	NA	NA
100.7	1	0.986097	0.884917
94.36667	1	1.119746	0.531645
NA	0	NA	NA
89.3	1	1.239642	0.299879
94.9	1	1.107482	0.183458
110.4667	1	0.810501	0.533387
87.76667	1	1.278769	0.366501
NA	0	NA	NA
87.63333	1	1.282237	0.198001
74	1	1.702703	0.263197
92.66667	1	1.158633	0.218034
NA	0	NA	NA
82.96667	1	1.410607	0.514705
89.86667	1	1.22589	0.216163
NA	0	NA	NA
NA	0	NA	NA
NA	0	NA	NA
92.86667	1	1.153625	0.545895
108.4	1	0.845018	0.148014
96.46667	1	1.073255	0.504167
90.23333	1	1.216476	0.293107
124.4333	1	0.607286	0.150767
108.4667	1	0.843884	0.640182
94.96667	1	1.106353	0.352069
87.13333	1	1.295333	0.495536
103.4	1	0.934236	0.289182
109.2	1	0.831502	0.205621
103.9667	1	0.923373	0.84151
94.63333	1	1.113068	0.525784

102.4	1	0.953125	0.766957
85.43333	1	1.341007	0.573358
92.6	1	1.159827	0.108813
97.33333	1	1.054795	0.46622
96.3	1	1.077189	0.73316
NA	0	NA	NA
91.1	1	1.195024	0.456253
92.8	1	1.154813	0.334633
114.0333	1	0.753873	0.548596
118.1667	1	0.692525	0.460032
NA	0	NA	NA
NA	0	NA	NA
NA	0	NA	NA
NA	0	NA	NA
NA	0	NA	NA
108.8333	1	0.837366	0.028149
85.9	1	1.328289	0.12522
NA	0	NA	NA
133.3667	1	0.499375	0.323685
106.4333	1	0.879424	0.111484
94.36667	1	1.119392	0.331259
100	1	1	1
88.83333	1	1.251407	0.423311
NA	0	NA	NA
100.4333	1	0.991703	0.896032
92.06667	1	1.172339	0.543833
91.96667	1	1.175063	0.710573
97.46667	1	1.051642	0.821322
NA	0	NA	NA
88.36667	1	1.263674	0.395771
90.36667	1	1.212837	0.3914
NA	0	NA	NA
94.9	1	1.107482	0.663492
106.8667	1	0.871491	0.352753
130.3333	1	0.534527	0.044977
92.86667	1	1.152907	0.501584
94.76667	1	1.110447	0.758347
NA	0	NA	NA
53.6	1	2.731343	0.277961
NA	0	NA	NA
91.66667	1	1.181455	0.466739
88.36667	1	1.263674	0.049381
101.4667	1	0.971091	0.806568
89.13333	1	1.243829	0.397877
100.9	1	0.982491	0.887261
106.6333	1	0.875899	0.493198
NA	0	NA	NA
NA	0	NA	NA
NA	0	NA	NA
100.3	1	0.99435	0.932786
NA	0	NA	NA

NA	0	NA	NA
112.7667	1	0.773574	0.396979
100.8667	1	0.982816	0.885994
82.7	1	1.417977	0.169679
84.96667	1	1.353864	0.26445
94.33333	1	1.120141	0.658522
NA	0	NA	NA
100.0667	1	0.998334	0.987857
103.3667	1	0.934537	0.561685
85.6	1	1.336449	0.100665
106.5333	1	0.877347	0.332635
75.76667	1	1.639683	0.492705
112.2	1	0.782531	0.296595
104.3333	1	0.916933	0.343223
NA	0	NA	NA
100.9667	1	0.980852	0.874951
81.46667	1	1.454992	0.189663
61.9	1	2.231018	0.364378
90.2	1	1.217295	0.359154
95.9	1	1.085506	0.753075
107.9667	1	0.852732	0.52239
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NA	0	NA	NA
NA	0	NA	NA
103.6333	1	0.929881	0.78621
NA	0	NA	NA
94.73333	1	1.110837	0.119981
NA	0	NA	NA
97.76667	1	1.045687	0.895182
NA	0	NA	NA
NA	0	NA	NA
100.9667	1	0.981182	0.940784
104.8	1	0.907761	0.367015
89.06667	1	1.245509	0.460849
100.7	1	0.985766	0.851695
NA	0	NA	NA
127.5667	1	0.567808	0.02643
NA	0	NA	NA
85.23333	1	1.346109	0.175581
90.36667	1	1.212837	0.080986
102.1333	1	0.958225	0.824785
NA	0	NA	NA
106.8333	1	0.872075	0.254222
NA	0	NA	NA
NA	0	NA	NA
85.56667	1	1.337359	0.17157
95.83333	1	1.086957	0.52248
NA	0	NA	NA
97.96667	1	1.041851	0.620341
90.83333	1	1.202202	0.460345
100.4	1	0.992032	0.95679

NA	0	NA	NA
105.2667	1	0.899937	0.112316
99.03333	1	1.019859	0.812777
100.3	1	0.994018	0.961545
89.23333	1	1.240941	0.194784
134.1667	1	0.490932	0.433588
87.8	1	1.277525	0.60001
97.93333	1	1.041865	0.79527
NA	0	NA	NA
NA	0	NA	NA
99.66667	1	1.006355	0.958197
106.8	1	0.872971	0.318948
103.2333	1	0.937359	0.661037
95.6	1	1.09205	0.186591
NA	0	NA	NA
86.36667	1	1.315708	0.283418
93.5	1	1.139394	0.53885
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NA	0	NA	NA
NA	0	NA	NA
103.4	1	0.933914	0.581368
101.1667	1	0.976936	0.742316
84.76667	1	1.359811	0.22566
104.3333	1	0.916933	0.648584
88.26667	1	1.265861	0.39709
90.13333	1	1.218935	0.680045
NA	0	NA	NA
NA	0	NA	NA
100.1	1	0.998002	0.992469
NA	0	NA	NA
NA	0	NA	NA
102.8667	1	0.94394	0.607552
92.16667	1	1.169982	0.314295
103.9333	1	0.92399	0.238849
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92.16667	1	1.169982	0.395235
NA	0	NA	NA
100.8667	1	0.983146	0.873881
93.86667	1	1.130327	0.241654
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NA	0	NA	NA
105.5333	1	0.895452	0.099786
109.2667	1	0.830384	0.353324
88.83333	1	1.251032	0.379598
111.5	1	0.794021	0.044615
105.2	1	0.901141	0.514172
101.4	1	0.972058	0.878891
109.7	1	0.823154	0.108392
95.96667	1	1.084404	0.237406
96.23333	1	1.078282	0.644273
95.96667	1	1.084057	0.765006

91.23333	1	1.192181	0.273926
102.9333	1	0.942681	0.004662
53.46667	1	2.741272	0.317273
96.56667	1	1.070763	0.700374
NA	0	NA	NA
NA	0	NA	NA
93.63333	1	1.135991	0.697164
112.4	1	0.779359	0.135862
93.43333	1	1.14092	0.489569
NA	0	NA	NA
NA	0	NA	NA
99.43333	1	1.011398	0.952265
105.9667	1	0.887701	0.398836
107.4333	1	0.86193	0.114042
183.2	0.333333	1.137828	NA
NA	0	NA	NA
NA	0	NA	NA
NA	0	NA	NA
116.7333	1	0.713307	0.028045
NA	0	NA	NA
NA	0	NA	NA
85.96667	1	1.326483	0.47517
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123.9667	1	0.613337	0.624402
NA	0	NA	NA
NA	0	NA	NA
98.86667	1	1.022589	0.873646
100.9333	1	0.981176	0.954139
NA	0	NA	NA
NA	0	NA	NA
NA	0	NA	NA
NA	0	NA	NA
126.0667	1	0.586727	0.251688
NA	0	NA	NA
105.0667	1	0.903553	0.380037
98.4	1	1.032859	0.70877
NA	0	NA	NA
104.0667	1	0.922486	0.366609
87.43333	1	1.287457	0.084167
108.7333	1	0.839362	0.225126
92.7	1	1.157138	0.326923
99.7	1	1.006018	0.967813
107.0667	1	0.867995	0.198536
96.46667	1	1.073255	0.754193
75.8	1	1.638522	0.458505
NA	0	NA	NA
104.1	1	0.920909	0.60101
97.96667	1	1.041511	0.426624
91.03333	1	1.196631	0.440356
91.06667	1	1.196193	0.220702
79.86667	1	1.504174	0.476174

100.9	1	0.982161	0.866279
98.4	1	1.032182	0.869782
85.9	1	1.327901	0.299553
125.9333	1	0.588142	0.116469
97	1	1.061856	0.766532
98.56667	1	1.029084	0.626028
NA	0	NA	NA
91.86667	1	1.176705	0.125642
NA	0	NA	NA
NA	0	NA	NA
92.83333	1	1.154758	0.139631
NA	0	NA	NA
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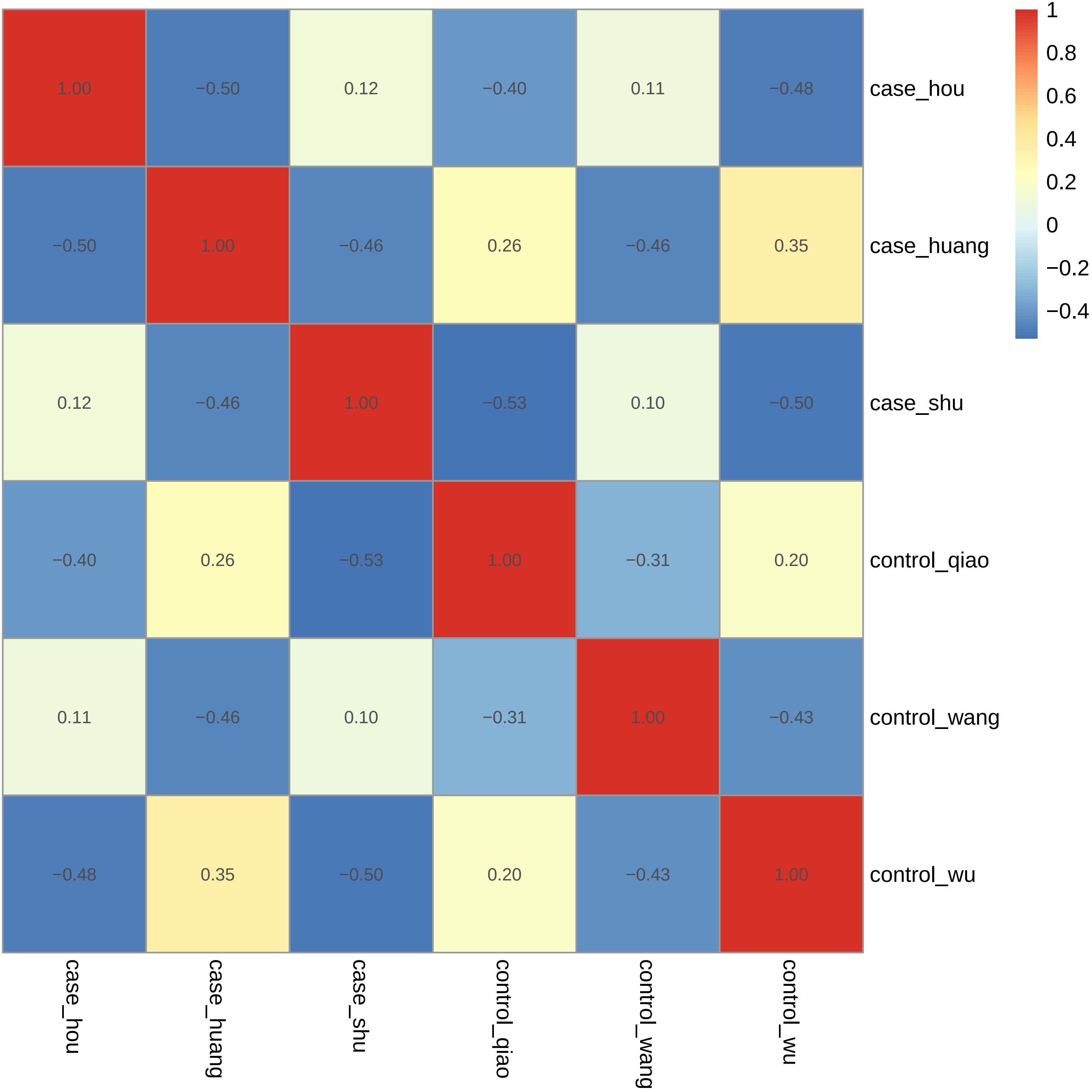
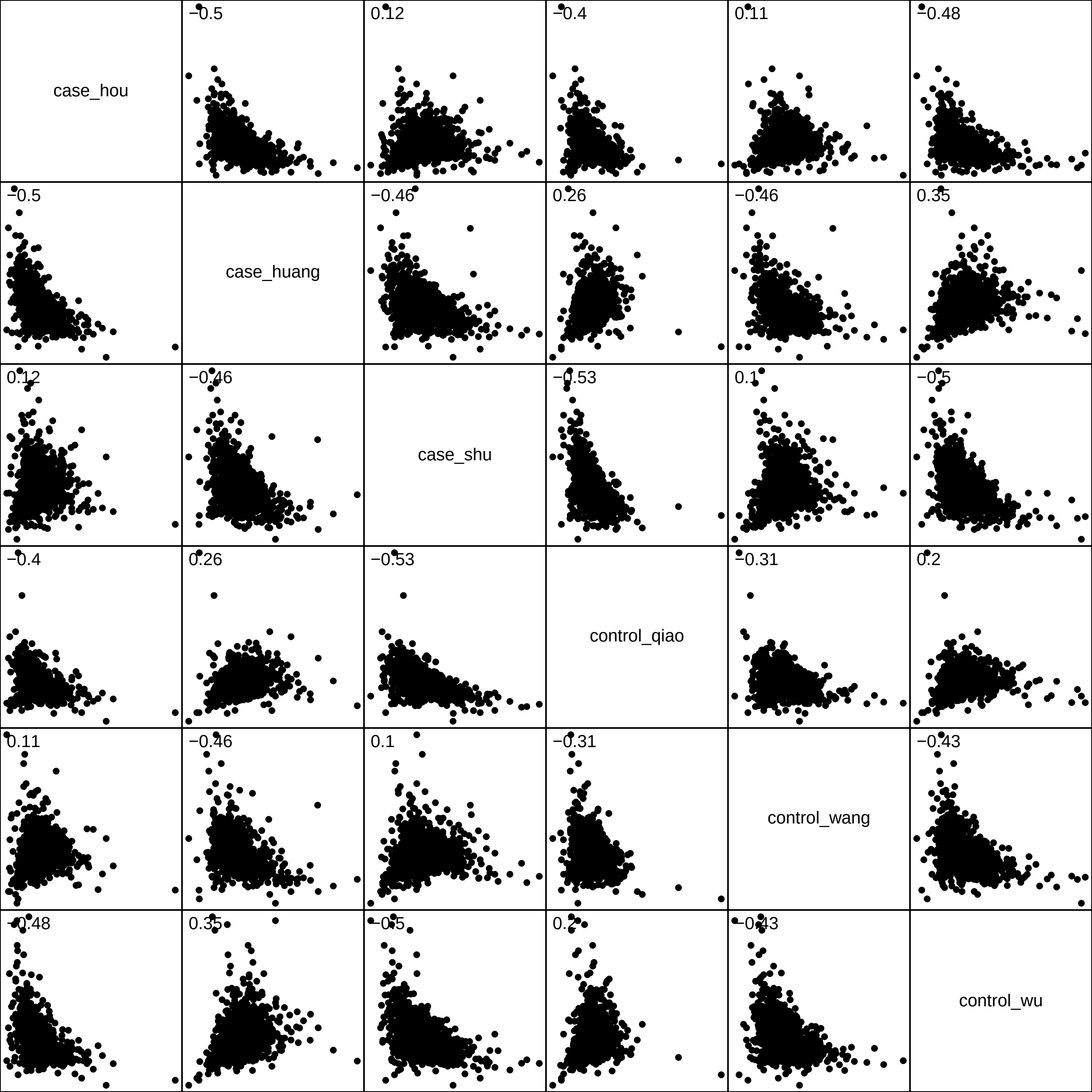


	case_hou	case_huang	case_shu	control_qiao	control_wang	control_wu
case_hou	1.00	−0.50	0.12	−0.40	0.11	−0.48
case_huang	−0.50	1.00	−0.46	0.26	−0.46	0.35
case_shu	0.12	−0.46	1.00	−0.53	0.10	−0.50
control_qiao	−0.40	0.26	−0.53	1.00	−0.31	0.20
control_wang	0.11	−0.46	0.10	−0.31	1.00	−0.43
control_wu	−0.48	0.35	−0.50	0.20	−0.43	1.00


case_hou
−0.5
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−0.4
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case_huang
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0.35
0.12
−0.46
case_shu
−0.53
0.1
−0.5
−0.4
0.26
−0.53
control_qiao
−0.31
0.2
0.11
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control_wang
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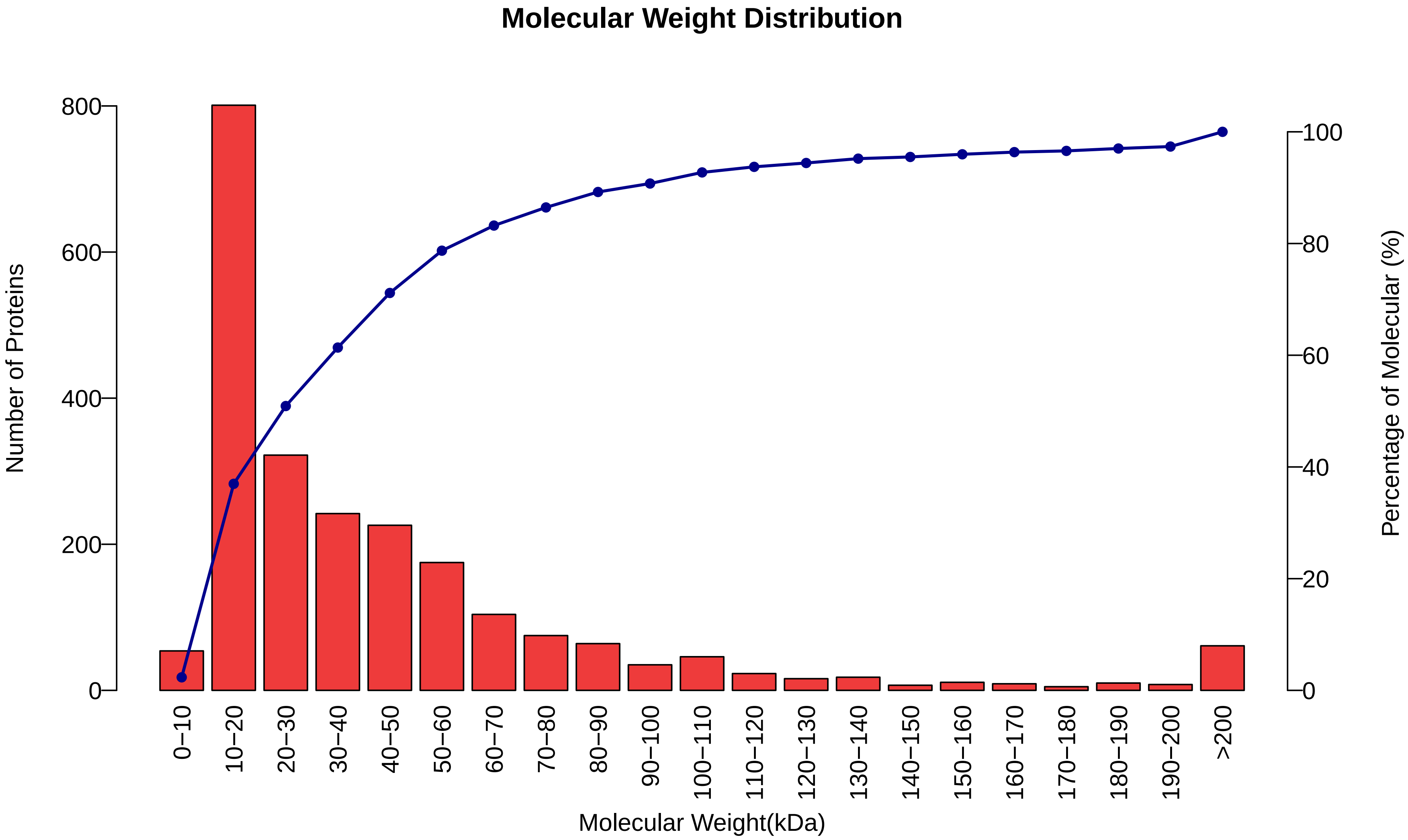
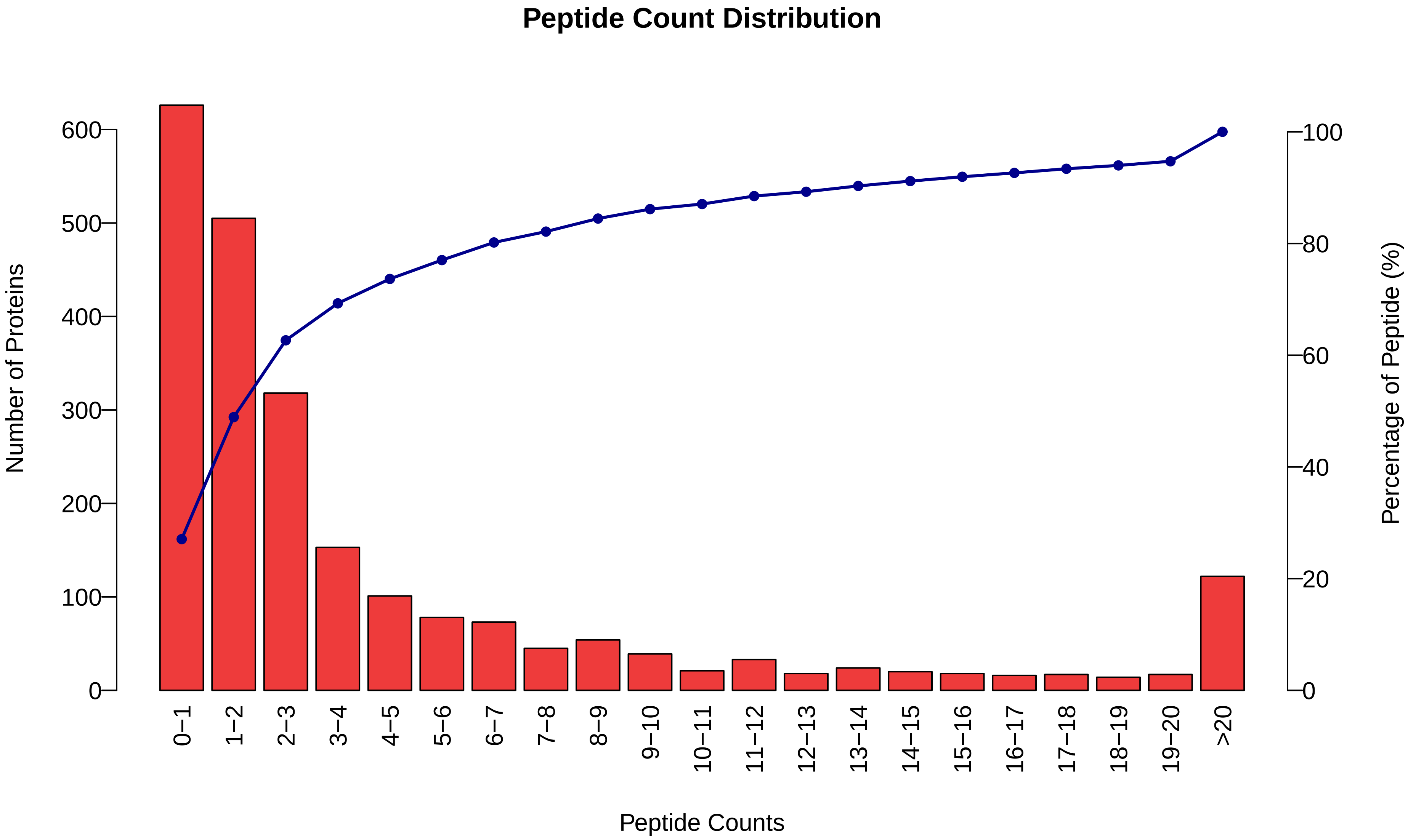
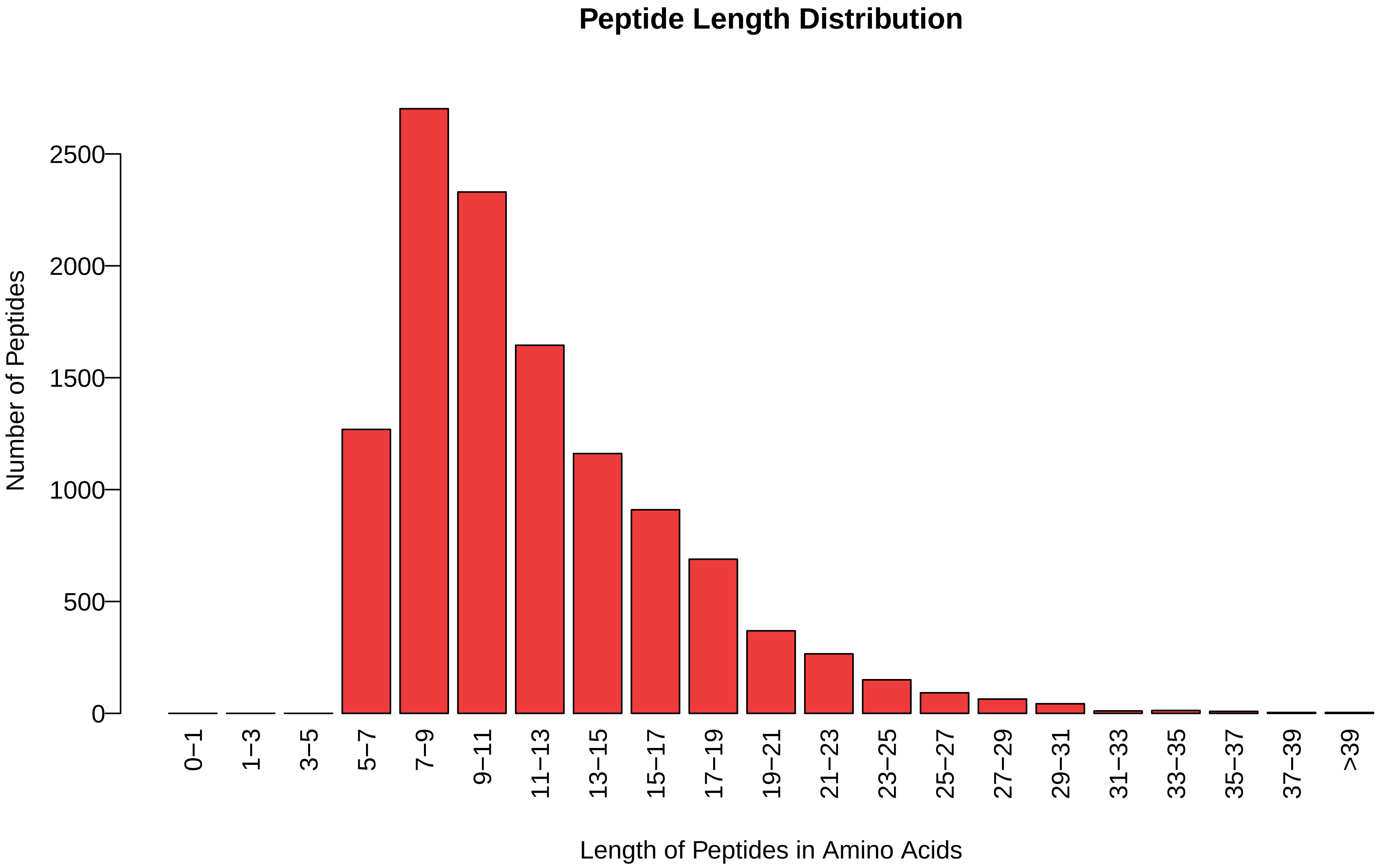
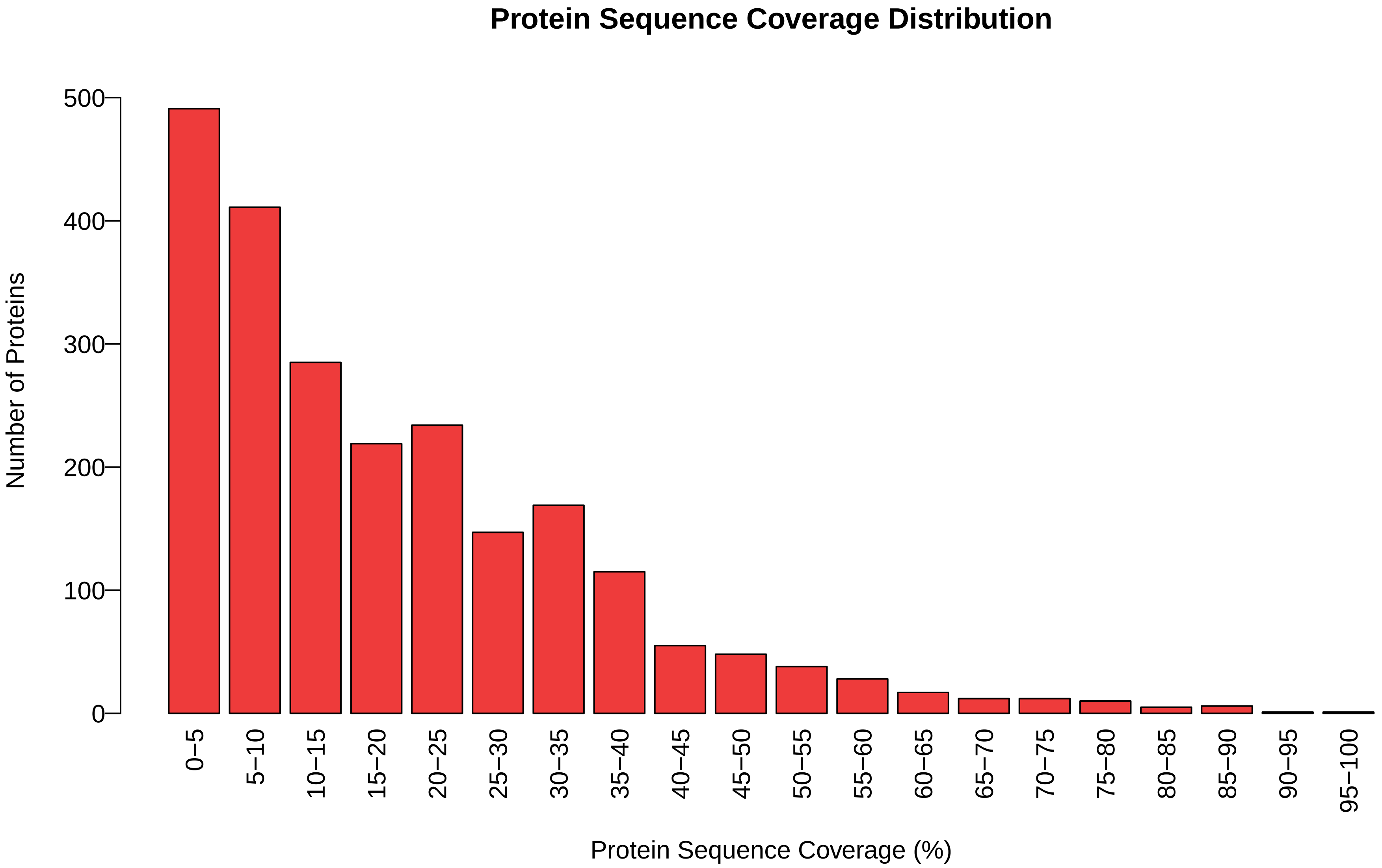
0.2
−0.43
control_wu


Molecular Weight Distribution
Number of Proteins
800
600
400
200
0
Percentage of Molecular (%)
100
80
60
40
20
0
0−10
10−20
20−30
30−40
40−50
50−60
60−70
70−80
80−90
90−100
100−110
110−120
120−130
130−140
140−150
150−160
160−170
170−180
180−190
190−200
>200
Molecular Weight(kDa)


Peptide Count Distribution
Number of Proteins
0
100
200
300
400
500
600
Percentage of Peptide (%)
0
20
40
60
80
100
0−1
1−2
2−3
3−4
4−5
5−6
6−7
7−8
8−9
9−10
10−11
11−12
12−13
13−14
14−15
15−16
16−17
17−18
18−19
19−20
>20
Peptide Counts


Peptide Length Distribution
Number of Peptides
0
500
1000
1500
2000
2500
0–1
1–3
3–5
5–7
7–9
9–11
11–13
13–15
15–17
17–19
19–21
21–23
23–25
25–27
27–29
29–31
31–33
33–35
35–37
37–39
>39
Length of Peptides in Amino Acids


Protein Sequence Coverage Distribution
Number of Proteins
500
400
300
200
100
0
0−5
5−10
10−15
15−20
20−25
25−30
30−35
35−40
40−45
45−50
50−55
55−60
60−65
65−70
70−75
75−80
80−85
85−90
90−95
95−100
Protein Sequence Coverage (%)

Supplemetal material3

We used EBI database to do GO/KEGG annotations, TermFinder to do GO enrichment of functional terms and R code to do KEGG enrichment of functional terms.

GO_ID	class	term	number	protein	label	number	protein	label
GO:00000C	biologica	reproduct	1	P54851	up	1	P35527	down
GO:00019C	biologica	cell kill	1	P54851	up	0	-	down
GO:000237	biologica	immune sy	11	A0A5C2FYV	up	4	A0A5C2GMH	down
GO:000382	molecular	catalytic	9	P05496;AC	up	10	A0A172Q3A	down
GO:000519	molecular	structura	0	-	up	7	Q9NR99;Q1	down
GO:000521	molecular	transport	3	P05496;Q9	up	2	E9M263;B7	down
GO:000548	molecular	binding	22	P05496;Q6	up	24	P60827;G3	down
GO:000562	cellular_	intracell	11	P05496;P5	up	17	D6RFN0;Q1	down
GO:000562	cellular_	cell	2	Q9HBA0;P5	up	0	-	down
GO:000815	biologica	metabolic	8	P05496;AC	up	12	A0A172Q3A	down
GO:000828	biologica	cell popu	2	P54851;A4	up	1	P35908	down
GO:000998	biologica	cellular	20	P05496;AC	up	21	G3V357;Q1	down
GO:002241	biologica	reproduct	1	P54851	up	1	P35527	down
GO:002261	biologica	biologica	2	P54851;QC	up	1	Q14324	down
GO:002305	biologica	signaling	10	A0A5C2FYV	up	4	A0A5C2GMH	down
GO:00325C	biologica	multicell	3	P54851;Q9	up	11	Q14324;Q9	down
GO:00325C	biologica	developme	2	P54851;Q9	up	8	Q9NQ79;P3	down
GO:003299	cellular_	protein-c	9	P05496;AC	up	11	D6RFN0;P6	down
GO:003802	molecular	cargo rec	0	-	up	1	P58215	down
GO:004001	biologica	locomotic	9	A0A5C2FYV	up	3	A0A5C2GMH	down
GO:005089	biologica	response	14	A0A5C2FYV	up	10	Q9NR99;AC	down
GO:005117	biologica	localizat	13	P05496;AC	up	9	A0A5C2GMH	down
GO:00517C	biologica	multi-org	6	P54851;QC	up	3	A0A5C2GMH	down
GO:006008	molecular	molecular	2	Q08722;Q9	up	0	-	down
GO:00650C	biologica	biologica	16	A0A5C2FYV	up	16	P60827;Q6	down
GO:007184	biologica	cellular	9	P05496;P5	up	9	A0A5C2GMH	down
GO:009877	molecular	molecular	1	O00487	up	0	-	down
GO:011016	cellular_	cellular	19	P05496;AC	up	29	D6RFN0;P6	down
GO:014011	molecular	transcrip	0	-	up	3	B4E3L5;Q8	down
GO:014029	molecular	small mol	1	Q9HBA0	up	0	-	down

GO-ID	description	ontology	Input num	Input all	Backgroun	Backgroun	P-Value	Corrected
GO:000588	intermedi	C	5	63	15	2002	6.20E-05	0.023572
GO:007026	cornifica	P	4	63	9	2002	9.98E-05	0.023572
GO:007025	actin-med	P	5	63	17	2002	0.000122	0.023572
GO:003142	keratiniz	P	4	63	10	2002	0.000162	0.023572
GO:003004	actin fil	P	5	63	19	2002	0.000218	0.023572
GO:004511	intermedi	C	5	63	19	2002	0.000218	0.023572
GO:003021	keratinoc	P	4	63	11	2002	0.000249	0.023572
GO:000991	epidermal	P	4	63	13	2002	0.000515	0.040864
GO:000551	calmoduli	F	3	63	6	2002	0.000556	0.040864
GO:003004	muscle fi	P	4	63	15	2002	0.000937	0.044286
GO:003327	actin-myc	P	4	63	15	2002	0.000937	0.044286
GO:004509	keratin f	C	3	63	7	2002	0.00095	0.044286
GO:003028	structura	F	2	63	2	2002	0.000975	0.044286
GO:009908	supramole	C	10	63	102	2002	0.001003	0.044286
GO:009951	supramole	C	10	63	102	2002	0.001003	0.044286
GO:000370	DNA-bindi	F	3	63	10	2002	0.003045	0.119887
GO:009908	supramole	C	10	63	118	2002	0.003079	0.119887
GO:000854	epidermis	P	4	63	21	2002	0.003565	0.13113
GO:004358	skin deve	P	4	63	22	2002	0.004256	0.148287
GO:004510	intermedi	P	2	63	4	2002	0.005615	0.16896
GO:004568	positive	P	2	63	4	2002	0.005615	0.16896
GO:000153	cornified	C	2	63	4	2002	0.005615	0.16896
GO:004589	negative	P	5	63	39	2002	0.006628	0.190779
GO:190350	negative	P	5	63	40	2002	0.007394	0.202327
GO:190267	negative	P	5	63	41	2002	0.00822	0.202327
GO:005125	negative	P	5	63	42	2002	0.009108	0.202327
GO:200104	positive	P	2	63	5	2002	0.009169	0.202327
GO:000586	troponin	C	2	63	5	2002	0.009169	0.202327
GO:003298	myosin fi	C	2	63	5	2002	0.009169	0.202327
GO:001683	carboxy-l	F	2	63	5	2002	0.009169	0.202327
GO:009951	polymeric	C	6	63	61	2002	0.010938	0.228739
GO:003002	actin fil	P	7	63	80	2002	0.011318	0.228739
GO:004593	negative	P	5	63	45	2002	0.012167	0.228739
GO:004542	regulatio	P	2	63	6	2002	0.013476	0.228739
GO:004568	regulatio	P	2	63	6	2002	0.013476	0.228739
GO:005149	regulatio	P	2	63	6	2002	0.013476	0.228739
GO:011002	regulatio	P	2	63	6	2002	0.013476	0.228739
GO:200104	regulatio	P	2	63	6	2002	0.013476	0.228739
GO:000418	metalloca	F	2	63	6	2002	0.013476	0.228739
GO:000693	muscle co	P	4	63	33	2002	0.018378	0.269185
GO:000300	skeletal	P	2	63	7	2002	0.018486	0.269185
GO:003223	regulatio	P	2	63	7	2002	0.018486	0.269185
GO:003267	regulatio	P	2	63	7	2002	0.018486	0.269185
GO:004510	intermedi	P	2	63	7	2002	0.018486	0.269185
GO:004510	intermedi	P	2	63	7	2002	0.018486	0.269185
GO:200011	negative	P	5	63	50	2002	0.018705	0.269185
GO:009743	supramole	P	7	63	90	2002	0.020783	0.292727
GO:000301	muscle sy	P	4	63	35	2002	0.022441	0.296085
GO:004687	metal ion	F	19	63	384	2002	0.022517	0.296085
GO:000012	negative	P	3	63	20	2002	0.023107	0.296085

GO:014011	transcrip	F	3	63	20	2002	0.023107	0.296085
GO:005087	multicell	P	2	63	8	2002	0.024152	0.296085
GO:005088	musculosk	P	2	63	8	2002	0.024152	0.296085
GO:001683	carbon-ca	F	2	63	8	2002	0.024152	0.296085
GO:001526	channel a	F	3	63	21	2002	0.026364	0.311661
GO:002280	passive t	F	3	63	21	2002	0.026364	0.311661
GO:001055	negative	P	5	63	56	2002	0.029195	0.339069
GO:190342	regulatic	P	2	63	9	2002	0.03043	0.341431
GO:001660	nuclear s	C	2	63	9	2002	0.03043	0.341431
GO:004316	cation bi	F	19	63	398	2002	0.031945	0.352465
GO:000821	cell deat	P	5	63	59	2002	0.035609	0.380216
GO:003132	negative	P	5	63	59	2002	0.035609	0.380216
GO:000823	metalloex	F	2	63	10	2002	0.037276	0.390308
GO:003085	epithelia	P	4	63	41	2002	0.037734	0.390308
GO:000367	DNA bindi	F	5	63	61	2002	0.040338	0.410823
GO:000418	carboxype	F	2	63	11	2002	0.04465	0.447853
GO:005508	transmemb	P	6	63	84	2002	0.045648	0.449037
GO:002289	inorganic	F	3	63	26	2002	0.046125	0.449037
GO:000697	cellular	P	3	63	27	2002	0.050756	0.451474
GO:001063	epithelia	P	2	63	12	2002	0.052513	0.451474
GO:009013	epitheliu	P	2	63	12	2002	0.052513	0.451474
GO:009752	myeloid l	P	2	63	12	2002	0.052513	0.451474
GO:000586	striated	C	2	63	12	2002	0.052513	0.451474
GO:003637	myofilame	C	2	63	12	2002	0.052513	0.451474
GO:000371	transcrip	F	2	63	12	2002	0.052513	0.451474
GO:000526	cation ch	F	2	63	12	2002	0.052513	0.451474
GO:001507	proton tr	F	2	63	12	2002	0.052513	0.451474
GO:000701	cytoskele	P	7	63	111	2002	0.056288	0.47062
GO:000989	negative	P	5	63	67	2002	0.056745	0.47062
GO:004316	proteasom	P	3	63	29	2002	0.06067	0.47062
GO:009866	inorganic	P	3	63	29	2002	0.06067	0.47062
GO:006113	regulatic	P	2	63	13	2002	0.060828	0.47062
GO:009013	tissue mi	P	2	63	13	2002	0.060828	0.47062
GO:190260	proton tr	P	2	63	13	2002	0.060828	0.47062
GO:000905	electron	F	2	63	13	2002	0.060828	0.47062
GO:000550	calcium i	F	9	63	161	2002	0.061138	0.47062
GO:000832	cation tr	F	3	63	30	2002	0.065943	0.495858
GO:000195	regulatic	P	2	63	14	2002	0.069559	0.495858
GO:001814	peptide c	P	2	63	14	2002	0.069559	0.495858
GO:002290	electron	P	2	63	14	2002	0.069559	0.495858
GO:005072	positive	P	2	63	14	2002	0.069559	0.495858
GO:190305	regulatic	P	2	63	14	2002	0.069559	0.495858
GO:190290	regulatic	P	4	63	50	2002	0.06966	0.495858
GO:009866	inorganic	P	3	63	31	2002	0.071422	0.498708
GO:000585	cytoskele	C	9	63	166	2002	0.071567	0.498708
GO:003015	regulatic	P	5	63	73	2002	0.076521	0.50565
GO:001049	proteasom	P	3	63	32	2002	0.0771	0.50565
GO:002240	regulatic	P	3	63	32	2002	0.0771	0.50565
GO:009865	cation tr	P	3	63	32	2002	0.0771	0.50565
GO:003001	sarcomere	C	3	63	32	2002	0.0771	0.50565
GO:000694	striated	P	2	63	15	2002	0.078674	0.50565

GO:003042	growth cc	C	2	63	15	2002	0.078674	0.50565
GO:004687	metal ion	F	2	63	15	2002	0.078674	0.50565
GO:00052C	structura	F	3	63	33	2002	0.082972	0.52815
GO:000269	negative	P	2	63	16	2002	0.088139	0.545311
GO:000693	regulatic	P	2	63	16	2002	0.088139	0.545311
GO:003042	site of p	C	2	63	16	2002	0.088139	0.545311
GO:000823	metallope	F	3	63	34	2002	0.089033	0.545738
GO:006042	epitheliu	P	5	63	77	2002	0.091555	0.556047
GO:000801	blood cir	P	3	63	35	2002	0.095276	0.571875
GO:00516C	proteolys	P	4	63	56	2002	0.096776	0.571875
GO:00224C	negative	P	2	63	17	2002	0.097926	0.571875
GO:000301	circulatc	P	3	63	36	2002	0.101695	0.571875
GO:00125C	programme	P	4	63	57	2002	0.101721	0.571875
GO:00015C	regulatic	P	2	63	18	2002	0.108005	0.571875
GO:005086	regulatic	P	2	63	18	2002	0.108005	0.571875
GO:000022	nuclear c	C	2	63	18	2002	0.108005	0.571875
GO:001632	apical pl	C	2	63	18	2002	0.108005	0.571875
GO:00166C	nuclear b	C	2	63	18	2002	0.108005	0.571875
GO:00483C	calcium-d	F	2	63	18	2002	0.108005	0.571875
GO:003001	myofibril	C	3	63	37	2002	0.108285	0.571875
GO:001531	inorganic	F	3	63	37	2002	0.108285	0.571875
GO:002285	transmemb	F	4	63	59	2002	0.11196	0.571875
GO:00030C	system pr	P	6	63	106	2002	0.112492	0.571875
GO:000692	movement	P	16	63	375	2002	0.114624	0.571875
GO:004329	contracti	C	3	63	38	2002	0.115038	0.571875
GO:000635	regulatic	P	7	63	132	2002	0.116755	0.571875
GO:001062	negative	P	5	63	83	2002	0.116772	0.571875
GO:000377	actin bin	F	5	63	83	2002	0.116772	0.571875
GO:004425	cellular	P	4	63	60	2002	0.117248	0.571875
GO:000628	DNA repai	P	2	63	19	2002	0.118349	0.571875
GO:001567	monovalen	P	2	63	19	2002	0.118349	0.571875
GO:190303	regulatic	P	2	63	19	2002	0.118349	0.571875
GO:190336	regulatic	P	2	63	19	2002	0.118349	0.571875
GO:015003	distal ax	C	2	63	19	2002	0.118349	0.571875
GO:000521	ion chann	F	2	63	19	2002	0.118349	0.571875
GO:001507	monovalen	F	2	63	19	2002	0.118349	0.571875
GO:19035C	regulatic	P	7	63	133	2002	0.120271	0.576953
GO:200114	regulatic	P	7	63	134	2002	0.123843	0.577062
GO:00065C	proteolys	P	8	63	161	2002	0.128119	0.577062
GO:003432	cell junc	P	2	63	20	2002	0.128931	0.577062
GO:005071	positive	P	2	63	20	2002	0.128931	0.577062
GO:009025	regulatic	P	2	63	20	2002	0.128931	0.577062
GO:004356	sequence-	F	2	63	20	2002	0.128931	0.577062
GO:000651	ubiquitin	P	3	63	40	2002	0.129011	0.577062
GO:001994	modificat	P	3	63	40	2002	0.129011	0.577062
GO:004363	modificat	P	3	63	40	2002	0.129011	0.577062
GO:004405	regulatic	P	3	63	40	2002	0.129011	0.577062
GO:003132	regulatic	P	9	63	190	2002	0.136586	0.600647
GO:200011	regulatic	P	8	63	164	2002	0.138387	0.600647
GO:000166	ameboidal	P	2	63	21	2002	0.139728	0.600647
GO:001648	protein p	P	2	63	21	2002	0.139728	0.600647

GO:003433	cell junc	P	2	63	21	2002	0.139728	0.600647
GO:200037	regulatic	P	2	63	21	2002	0.139728	0.600647
GO:000828	cell popu	P	3	63	42	2002	0.143561	0.613143
GO:007001	peptidase	F	6	63	114	2002	0.145132	0.61588
GO:000279	positive	P	2	63	22	2002	0.150715	0.61971
GO:000961	response	P	2	63	22	2002	0.150715	0.61971
GO:004887	multicell	P	2	63	22	2002	0.150715	0.61971
GO:007134	cellular	P	2	63	22	2002	0.150715	0.61971
GO:004698	protein h	F	2	63	22	2002	0.150715	0.61971
GO:004487	protein-c	F	8	63	168	2002	0.152722	0.624086
GO:007055	response	P	2	63	23	2002	0.161871	0.645714
GO:004517	apical pa	C	2	63	23	2002	0.161871	0.645714
GO:000551	collagen	F	2	63	23	2002	0.161871	0.645714
GO:000823	peptidase	F	6	63	118	2002	0.162956	0.645714
GO:003016	protein c	P	4	63	68	2002	0.163257	0.645714
GO:000521	transport	F	5	63	93	2002	0.165315	0.645714
GO:003134	positive	P	3	63	45	2002	0.166353	0.645714
GO:001507	ion trans	F	3	63	45	2002	0.166353	0.645714
GO:000988	regulatic	P	9	63	199	2002	0.167183	0.645714
GO:001055	regulatic	P	8	63	172	2002	0.167769	0.645714
GO:005125	regulatic	P	7	63	146	2002	0.170859	0.653807
GO:003422	ion trans	P	3	63	46	2002	0.174181	0.66269
GO:004316	ion bindi	F	24	63	639	2002	0.17525	0.662945
GO:000809	cytoskele	F	6	63	121	2002	0.176931	0.665501
GO:001990	protein k	F	3	63	47	2002	0.182115	0.68113
GO:003003	actin cyt	P	4	63	72	2002	0.188434	0.700805
GO:000701	actin fil	P	3	63	48	2002	0.190147	0.703224
GO:001678	hydrolase	F	13	63	319	2002	0.191726	0.705126
GO:000681	cation tr	P	3	63	49	2002	0.19827	0.725166
GO:190136	heterocyc	F	17	63	441	2002	0.206248	0.735551
GO:000823	serine-ty	F	3	63	50	2002	0.20648	0.735551
GO:001682	hydrolase	F	3	63	50	2002	0.20648	0.735551
GO:001717	serine hy	F	3	63	50	2002	0.20648	0.735551
GO:005149	positive	P	2	63	27	2002	0.207777	0.735551
GO:000823	exopeptid	F	2	63	27	2002	0.207777	0.735551
GO:005101	actin fil	F	3	63	51	2002	0.214768	0.748954
GO:004698	protein d	F	4	63	76	2002	0.214799	0.748954
GO:001921	regulatic	P	7	63	156	2002	0.215331	0.748954
GO:000625	DNA metab	P	2	63	28	2002	0.219482	0.748954
GO:005160	protein m	P	2	63	28	2002	0.219482	0.748954
GO:190290	positive	P	2	63	28	2002	0.219482	0.748954
GO:190353	positive	P	2	63	28	2002	0.219482	0.748954
GO:001562	actin cyt	C	4	63	77	2002	0.221552	0.75214
GO:009715	organic c	F	17	63	447	2002	0.223695	0.75554
GO:000916	nucleotid	P	2	63	29	2002	0.231246	0.761616
GO:007121	cellular	P	2	63	29	2002	0.231246	0.761616
GO:010400	cellular	P	2	63	29	2002	0.231246	0.761616
GO:190129	nucleosid	P	2	63	29	2002	0.231246	0.761616
GO:001682	lyase act	F	2	63	29	2002	0.231246	0.761616
GO:005122	regulatic	P	3	63	54	2002	0.240047	0.786688
GO:000699	organelle	P	9	63	218	2002	0.241439	0.787352

GO:00199C	kinase bi	F	3	63	55	2002	0.248591	0.80351
GO:00071€	negative	P	2	63	31	2002	0.25489	0.80351
GO:00165€	protein u	P	2	63	31	2002	0.25489	0.80351
GO:004217	regulatic	P	2	63	31	2002	0.25489	0.80351
GO:00512Z	positive	P	2	63	31	2002	0.25489	0.80351
GO:00200З	heme binc	F	2	63	31	2002	0.25489	0.80351
GO:00469C	tetrapyrr	F	2	63	31	2002	0.25489	0.80351
GO:00026S	regulatic	P	11	63	280	2002	0.258282	0.810345
GO:00098Ɛ	tissue de	P	7	63	166	2002	0.263712	0.821319
GO:00900Ɛ	regulatic	P	3	63	57	2002	0.265821	0.821319
GO:00507Z	regulatic	P	2	63	32	2002	0.266743	0.821319
GO:005104	positive	P	2	63	32	2002	0.266743	0.821319
GO:00300C	metal ion	P	2	63	33	2002	0.278599	0.842157
GO:003244	protein m	P	2	63	33	2002	0.278599	0.842157
GO:00005C	proteason	C	2	63	33	2002	0.278599	0.842157
GO:19053€	endopepti	C	2	63	33	2002	0.278599	0.842157
GO:00058Ɛ	integral	C	3	63	59	2002	0.283203	0.849873
GO:00380S	Fc recept	P	10	63	257	2002	0.283719	0.849873
GO:005124	regulatic	P	6	63	142	2002	0.286514	0.854379
GO:00063Ƽ	regulatic	P	4	63	88	2002	0.298998	0.880977
GO:00442€	cellular	P	4	63	88	2002	0.298998	0.880977
GO:00702C	regulatic	P	3	63	61	2002	0.300694	0.880977
GO:00507C	regulatic	P	2	63	35	2002	0.302275	0.880977
GO:19053€	peptidase	C	2	63	35	2002	0.302275	0.880977
GO:00026S	regulatic	P	6	63	145	2002	0.303418	0.880977
GO:00514S	regulatic	P	3	63	62	2002	0.309468	0.889686
GO:00432Z	non-membr	C	11	63	293	2002	0.310449	0.889686
GO:00432З	intracell	C	11	63	293	2002	0.310449	0.889686
GO:001081	regulatic	P	2	63	36	2002	0.314074	0.892347
GO:00510Ƽ	negative	P	2	63	36	2002	0.314074	0.892347
GO:00060S	generatic	P	3	63	63	2002	0.318253	0.900357
GO:00027S	regulatic	P	2	63	37	2002	0.325833	0.9047
GO:00199C	protein c	F	2	63	37	2002	0.325833	0.9047
GO:001647	cell migr	P	12	63	327	2002	0.326848	0.9047
GO:003134	regulatic	P	3	63	64	2002	0.327046	0.9047
GO:00321C	positive	P	3	63	64	2002	0.327046	0.9047
GO:00051S	structura	F	7	63	179	2002	0.330806	0.9047
GO:00509C	leukocyte	P	10	63	269	2002	0.335567	0.9047
GO:19049Ƽ	positive	P	2	63	38	2002	0.337544	0.9047
GO:00335Ƽ	cellular	P	5	63	122	2002	0.337975	0.9047
GO:00903C	nucleic a	P	4	63	94	2002	0.34275	0.9047
GO:00508€	regulatic	P	6	63	152	2002	0.343574	0.9047
GO:000367	nucleic a	F	8	63	212	2002	0.348382	0.9047
GO:00024З	Fc recept	P	9	63	242	2002	0.34899	0.9047
GO:00024З	immune re	P	9	63	242	2002	0.34899	0.9047
GO:00380S	Fc-gamma	P	9	63	242	2002	0.34899	0.9047
GO:00380S	Fc-gamma	P	9	63	242	2002	0.34899	0.9047
GO:19037C	regulatic	P	2	63	39	2002	0.349198	0.9047
GO:00304Z	axon	C	2	63	39	2002	0.349198	0.9047
GO:004887	cell moti	P	12	63	333	2002	0.351188	0.9047
GO:005167	localizat	P	12	63	333	2002	0.351188	0.9047

GO:004858	positive	P	17	63	486	2002	0.3517	0.9047
GO:000998	cell surf	C	8	63	213	2002	0.353362	0.9047
GO:001943	aromatic	P	3	63	67	2002	0.353422	0.9047
GO:003122	intrinsic	C	3	63	67	2002	0.353422	0.9047
GO:005117	negative	P	6	63	154	2002	0.35518	0.9047
GO:000582	cytosol	C	15	63	427	2002	0.360621	0.9047
GO:002268	negative	P	2	63	40	2002	0.360787	0.9047
GO:001081	regulatic	P	2	63	40	2002	0.360787	0.9047
GO:008013	regulatic	P	2	63	40	2002	0.360787	0.9047
GO:009040	organophc	P	2	63	40	2002	0.360787	0.9047
GO:200014	positive	P	3	63	68	2002	0.362199	0.904815
GO:004691	transitic	F	4	63	97	2002	0.364764	0.907797
GO:003809	Fc-epsilc	P	9	63	246	2002	0.367825	0.910742
GO:000563	nucleus	C	13	63	368	2002	0.36945	0.910742
GO:001813	heterocyc	P	3	63	69	2002	0.370962	0.910742
GO:007064	protein m	P	2	63	41	2002	0.372303	0.910742
GO:004648	heterocyc	P	7	63	187	2002	0.373531	0.910742
GO:000268	positive	P	14	63	400	2002	0.374713	0.910742
GO:005077	regulatic	P	14	63	401	2002	0.378593	0.910742
GO:200014	regulatic	P	4	63	99	2002	0.379443	0.910742
GO:005127	positive	P	3	63	70	2002	0.379705	0.910742
GO:009859	plasma me	C	3	63	70	2002	0.379705	0.910742
GO:011005	regulatic	P	2	63	42	2002	0.38374	0.913799
GO:000569	chromosom	C	2	63	42	2002	0.38374	0.913799
GO:190156	organonit	P	4	63	100	2002	0.386776	0.914449
GO:001711	nucleosid	F	4	63	100	2002	0.386776	0.914449
GO:000690	phagocytc	P	11	63	312	2002	0.391167	0.921539
GO:000242	immune re	P	11	63	313	2002	0.395505	0.925173
GO:000276	immune re	P	11	63	313	2002	0.395505	0.925173
GO:001064	positive	P	5	63	132	2002	0.402429	0.931054
GO:005125	positive	P	5	63	132	2002	0.402429	0.931054
GO:004001	positive	P	3	63	73	2002	0.405788	0.931054
GO:004578	positive	P	2	63	44	2002	0.406351	0.931054
GO:000425	serine-ty	F	2	63	44	2002	0.406351	0.931054
GO:002305	positive	P	5	63	133	2002	0.408876	0.931054
GO:000269	positive	P	5	63	134	2002	0.415317	0.931054
GO:005127	regulatic	P	4	63	104	2002	0.416007	0.931054
GO:000672	cellular	P	7	63	195	2002	0.416696	0.931054
GO:000268	regulatic	P	15	63	442	2002	0.417487	0.931054
GO:005086	positive	P	5	63	135	2002	0.42175	0.931054
GO:190136	organic c	P	3	63	75	2002	0.423017	0.931054
GO:190249	catalytic	C	3	63	75	2002	0.423017	0.931054
GO:001646	pyrophosp	F	4	63	105	2002	0.423278	0.931054
GO:001681	hydrolase	F	4	63	105	2002	0.423278	0.931054
GO:001681	hydrolase	F	4	63	105	2002	0.423278	0.931054
GO:003132	negative	P	6	63	166	2002	0.425266	0.931054
GO:000687	cellular	P	2	63	46	2002	0.428575	0.931054
GO:003802	signaling	F	2	63	46	2002	0.428575	0.931054
GO:006008	molecular	F	2	63	46	2002	0.428575	0.931054
GO:000275	immune re	P	11	63	321	2002	0.430349	0.931054
GO:000276	immune re	P	11	63	321	2002	0.430349	0.931054

GO:004803	cofactor	F	3	63	76	2002	0.431574	0.931054
GO:004001	locomotic	P	12	63	353	2002	0.434466	0.931054
GO:000803	cell recc	P	5	63	137	2002	0.434585	0.931054
GO:005085	antigen r	P	5	63	137	2002	0.434585	0.931054
GO:004001	regulatic	P	4	63	107	2002	0.437762	0.932916
GO:003464	cellular	P	9	63	261	2002	0.439314	0.932916
GO:003288	regulatic	P	3	63	77	2002	0.440088	0.932916
GO:001604	cellular	P	18	63	542	2002	0.441092	0.932916
GO:000613	nucleobas	P	6	63	169	2002	0.442746	0.933296
GO:003044	regulatic	P	9	63	262	2002	0.444091	0.933296
GO:000292	regulatic	P	9	63	263	2002	0.448865	0.940345
GO:003000	cellular	P	2	63	49	2002	0.461099	0.959898
GO:003295	regulatic	P	2	63	49	2002	0.461099	0.959898
GO:009879	membrane	C	3	63	80	2002	0.465348	0.965308
GO:000225	activatic	P	12	63	361	2002	0.468102	0.965308
GO:007184	cellular	P	18	63	550	2002	0.469964	0.965308
GO:006106	muscle st	P	2	63	50	2002	0.471708	0.965308
GO:000417	endopepti	F	3	63	81	2002	0.473664	0.965308
GO:000548	binding	F	46	63	1438	2002	0.479644	0.965308
GO:001707	purine nu	F	7	63	207	2002	0.481152	0.965308
GO:000681	ion trans	P	3	63	82	2002	0.481925	0.965308
GO:004300	neuron pr	C	3	63	82	2002	0.481925	0.965308
GO:000687	cellular	P	2	63	51	2002	0.482195	0.965308
GO:004408	positive	P	2	63	51	2002	0.482195	0.965308
GO:005506	metal ion	P	2	63	51	2002	0.482195	0.965308
GO:005117	regulatic	P	11	63	333	2002	0.482654	0.965308
GO:003055	adenyl nu	F	5	63	145	2002	0.485312	0.965359
GO:001060	negative	P	6	63	177	2002	0.48888	0.965359
GO:005105	positive	P	3	63	83	2002	0.490128	0.965359
GO:014009	catalytic	F	7	63	209	2002	0.491765	0.965359
GO:190353	regulatic	P	2	63	52	2002	0.492558	0.965359
GO:000905	macromole	P	4	63	115	2002	0.494625	0.965359
GO:000828	lipid bin	F	3	63	84	2002	0.49827	0.965359
GO:190136	organic c	P	7	63	211	2002	0.502324	0.965359
GO:000181	regulatic	P	2	63	54	2002	0.512899	0.965359
GO:001063	positive	P	2	63	54	2002	0.512899	0.965359
GO:003297	regulatic	P	2	63	54	2002	0.512899	0.965359
GO:005508	cation hc	P	2	63	54	2002	0.512899	0.965359
GO:000961	response	P	6	63	182	2002	0.517177	0.965359
GO:008013	regulatic	P	4	63	119	2002	0.522218	0.965359
GO:006034	regulatic	P	2	63	55	2002	0.522873	0.965359
GO:000392	GTPase ac	F	2	63	55	2002	0.522873	0.965359
GO:001046	regulatic	P	7	63	215	2002	0.52325	0.965359
GO:000225	immune ef	P	14	63	438	2002	0.524013	0.965359
GO:000246	adaptive	P	10	63	311	2002	0.52505	0.965359
GO:009865	import in	P	11	63	343	2002	0.525726	0.965359
GO:004851	animal or	P	8	63	248	2002	0.528684	0.965359
GO:005085	B cell re	P	4	63	120	2002	0.529013	0.965359
GO:004257	immunoglc	C	4	63	120	2002	0.529013	0.965359
GO:000244	lymphocyt	P	10	63	312	2002	0.529483	0.965359
GO:004408	regulatic	P	3	63	88	2002	0.530198	0.965359

GO:00447C	multi-org	P	2	63	56	2002	0.532713	0.965359
GO:005104	regulatic	P	2	63	56	2002	0.532713	0.965359
GO:012003	regulatic	P	2	63	56	2002	0.532713	0.965359
GO:003287	regulatic	P	7	63	217	2002	0.533606	0.965359
GO:005077	positive	P	12	63	377	2002	0.534651	0.965359
GO:00508€	regulatic	P	4	63	121	2002	0.535763	0.965359
GO:005087	positive	P	4	63	121	2002	0.535763	0.965359
GO:003498	immunoglc	F	4	63	121	2002	0.535763	0.965359
GO:00226C	cellular	P	6	63	186	2002	0.539422	0.965359
GO:000675	nucleosid	P	2	63	57	2002	0.542418	0.965359
GO:000911	nucleotid	P	2	63	57	2002	0.542418	0.965359
GO:003134	regulatic	P	2	63	57	2002	0.542418	0.965359
GO:005508	cellular	P	2	63	57	2002	0.542418	0.965359
GO:009877	inorganic	P	2	63	57	2002	0.542418	0.965359
GO:000827	zinc ion	F	2	63	57	2002	0.542418	0.965359
GO:000691	phagocytc	P	4	63	122	2002	0.542467	0.965359
GO:00068S	receptor-	P	8	63	252	2002	0.548055	0.972687
GO:003465	nucleobas	P	2	63	58	2002	0.551987	0.974452
GO:003132	regulatic	P	11	63	350	2002	0.555331	0.974452
GO:000691	phagocytc	P	4	63	124	2002	0.555736	0.974452
GO:009902	plasma me	P	4	63	124	2002	0.555736	0.974452
GO:004508	innate im	P	6	63	190	2002	0.561257	0.974452
GO:006102	membrane	P	6	63	190	2002	0.561257	0.974452
GO:00455S	negative	P	2	63	59	2002	0.561418	0.974452
GO:00099€	positive	P	4	63	125	2002	0.562297	0.974452
GO:001032	membrane	P	4	63	125	2002	0.562297	0.974452
GO:003015	cell diff	P	8	63	256	2002	0.567136	0.980272
GO:000695	complemen	P	10	63	321	2002	0.56881	0.980604
GO:000695	inflammat	P	2	63	60	2002	0.570711	0.981326
GO:004408	cellular	P	6	63	194	2002	0.582635	0.991945
GO:000573	mitochond	C	3	63	95	2002	0.583344	0.991945
GO:00098S	negative	P	6	63	195	2002	0.587903	0.991945
GO:003033	regulatic	P	3	63	96	2002	0.590632	0.991945
GO:00508C	ion homec	P	2	63	63	2002	0.59775	0.991945
GO:00001€	nucleotid	F	7	63	230	2002	0.59876	0.991945
GO:19012€	nucleosid	F	7	63	230	2002	0.59876	0.991945
GO:003033	positive	P	2	63	64	2002	0.606482	0.991945
GO:00488€	cellular	P	8	63	266	2002	0.613353	0.991945
GO:003132	regulatic	P	2	63	65	2002	0.615074	0.991945
GO:000013	Golgi mem	C	2	63	65	2002	0.615074	0.991945
GO:003304	regulatic	P	3	63	100	2002	0.618983	0.991945
GO:005104	regulatic	P	4	63	134	2002	0.61899	0.991945
GO:012003	plasma me	P	2	63	66	2002	0.623525	0.991945
GO:00164S	oxidoredu	F	3	63	101	2002	0.625867	0.991945
GO:004851	positive	P	22	63	723	2002	0.626588	0.991945
GO:000225	adaptive	P	10	63	335	2002	0.627394	0.991945
GO:00068S	endocytos	P	10	63	335	2002	0.627394	0.991945
GO:004858	regulatic	P	18	63	595	2002	0.627973	0.991945
GO:003255	ribonucle	F	6	63	203	2002	0.628849	0.991945
GO:003255	purine ri	F	6	63	203	2002	0.628849	0.991945
GO:00455S	regulatic	P	4	63	136	2002	0.630978	0.991945

GO:003003	cell proj	P	2	63	67	2002	0.631836	0.991945
GO:000188	nucleosid	F	2	63	67	2002	0.631836	0.991945
GO:000188	purine nu	F	2	63	67	2002	0.631836	0.991945
GO:000552	GTP bindi	F	2	63	67	2002	0.631836	0.991945
GO:001900	guanyl nu	F	2	63	67	2002	0.631836	0.991945
GO:003254	ribonucle	F	2	63	67	2002	0.631836	0.991945
GO:003255	purine ri	F	2	63	67	2002	0.631836	0.991945
GO:003256	guanyl ri	F	2	63	67	2002	0.631836	0.991945
GO:003198	vesicle	C	17	63	564	2002	0.632162	0.991945
GO:005079	regulatic	P	6	63	204	2002	0.63381	0.991945
GO:004320	response	P	7	63	238	2002	0.636624	0.991945
GO:005170	response	P	7	63	238	2002	0.636624	0.991945
GO:001922	regulatic	P	12	63	404	2002	0.640832	0.991945
GO:000960	response	P	7	63	239	2002	0.641222	0.991945
GO:003210	regulatic	P	3	63	104	2002	0.646022	0.991945
GO:000245	humoral i	P	9	63	307	2002	0.647654	0.991945
GO:000695	complemen	P	9	63	307	2002	0.647654	0.991945
GO:000741	central n	P	2	63	69	2002	0.648038	0.991945
GO:000828	positive	P	2	63	69	2002	0.648038	0.991945
GO:001606	immunoglo	P	9	63	308	2002	0.651746	0.991945
GO:001972	B cell me	P	9	63	308	2002	0.651746	0.991945
GO:000244	leukocyte	P	12	63	407	2002	0.651923	0.991945
GO:000726	cell-cell	P	2	63	70	2002	0.65593	0.991945
GO:001631	phosphory	P	3	63	106	2002	0.65904	0.991945
GO:006500	protein-c	P	3	63	106	2002	0.65904	0.991945
GO:003255	adenyl ri	F	4	63	141	2002	0.659918	0.991945
GO:001677	transfera	F	2	63	71	2002	0.663684	0.991945
GO:001989	enzyme bi	F	4	63	142	2002	0.665526	0.991945
GO:008009	regulatic	P	10	63	345	2002	0.666832	0.991945
GO:003299	protein-c	C	20	63	672	2002	0.668102	0.991945
GO:005087	regulatic	P	2	63	72	2002	0.6713	0.991945
GO:000962	response	P	3	63	108	2002	0.671722	0.991945
GO:009854	defense r	P	6	63	212	2002	0.672147	0.991945
GO:003250	multicell	P	14	63	479	2002	0.674449	0.991945
GO:000960	response	P	9	63	314	2002	0.675772	0.991945
GO:003005	cell junc	C	3	63	109	2002	0.677936	0.991945
GO:000520	extracell	F	2	63	73	2002	0.678779	0.991945
GO:005113	positive	P	3	63	110	2002	0.684066	0.991945
GO:000989	regulatic	P	2	63	74	2002	0.686122	0.991945
GO:001060	positive	P	5	63	182	2002	0.692793	0.991945
GO:003132	positive	P	5	63	182	2002	0.692793	0.991945
GO:000695	humoral i	P	10	63	352	2002	0.693071	0.991945
GO:000193	positive	P	2	63	75	2002	0.693331	0.991945
GO:000695	defense r	P	7	63	251	2002	0.693853	0.991945
GO:003227	positive	P	3	63	112	2002	0.696072	0.991945
GO:004858	negative	P	4	63	148	2002	0.697894	0.991945
GO:001064	regulatic	P	6	63	218	2002	0.699256	0.991945
GO:000382	catalytic	F	19	63	650	2002	0.699509	0.991945
GO:005508	nucleobas	P	2	63	76	2002	0.700405	0.991945
GO:000000	reproduct	P	2	63	77	2002	0.707347	0.991945
GO:001024	response	P	2	63	77	2002	0.707347	0.991945

GO:002241	reproduct	P	2	63	77	2002	0.707347	0.991945
GO:000716	cell surf	P	13	63	456	2002	0.707462	0.991945
GO:000989	external	C	4	63	150	2002	0.70819	0.991945
GO:004232	positive	P	2	63	78	2002	0.714157	0.991945
GO:006025	regulatio	P	10	63	359	2002	0.7181	0.991945
GO:002305	regulatio	P	6	63	224	2002	0.7249	0.991945
GO:001055	positive	P	2	63	80	2002	0.727388	0.991945
GO:005511	oxidation	P	3	63	118	2002	0.730074	0.991945
GO:000551	protein b	F	27	63	919	2002	0.73206	0.991945
GO:004274	defense r	P	4	63	155	2002	0.732847	0.991945
GO:003140	positive	P	2	63	81	2002	0.733812	0.991945
GO:004322	organelle	C	30	63	1015	2002	0.733945	0.991945
GO:001602	integral	C	7	63	262	2002	0.737728	0.991945
GO:000972	response	P	2	63	82	2002	0.740109	0.991945
GO:005109	negative	P	2	63	82	2002	0.740109	0.991945
GO:004393	protein-c	P	3	63	120	2002	0.740743	0.991945
GO:000382	antigen b	F	6	63	229	2002	0.745129	0.991945
GO:005124	positive	P	3	63	121	2002	0.745954	0.991945
GO:004887	chemical	P	2	63	83	2002	0.746281	0.991945
GO:009736	carbohydr	F	8	63	299	2002	0.746581	0.991945
GO:005123	regulatio	P	7	63	265	2002	0.74894	0.991945
GO:004322	intracell	C	25	63	862	2002	0.750276	0.991945
GO:004846	cell deve	P	3	63	122	2002	0.751084	0.991945
GO:000588	plasma me	C	17	63	603	2002	0.752096	0.991945
GO:001056	positive	P	2	63	84	2002	0.75233	0.991945
GO:004593	positive	P	2	63	84	2002	0.75233	0.991945
GO:190169	response	P	2	63	84	2002	0.75233	0.991945
GO:003609	small mol	F	8	63	301	2002	0.753575	0.991945
GO:000646	cellular	P	5	63	196	2002	0.755164	0.991945
GO:003621	protein m	P	5	63	196	2002	0.755164	0.991945
GO:003141	cytoplasm	C	6	63	232	2002	0.756766	0.991945
GO:009770	intracell	C	6	63	232	2002	0.756766	0.991945
GO:009855	side of m	C	4	63	161	2002	0.760402	0.991945
GO:012002	plasma me	C	3	63	124	2002	0.761101	0.991945
GO:004341	macromole	P	5	63	198	2002	0.763282	0.991945
GO:001972	cellular	P	2	63	86	2002	0.764064	0.991945
GO:005112	regulatio	P	5	63	199	2002	0.767268	0.991945
GO:003563	purine ri	F	5	63	199	2002	0.767268	0.991945
GO:004316	anion bin	F	9	63	340	2002	0.768466	0.991945
GO:001963	organopho	P	2	63	87	2002	0.769753	0.991945
GO:200002	regulatio	P	4	63	164	2002	0.773358	0.991945
GO:000996	regulatio	P	5	63	202	2002	0.77893	0.991945
GO:004852	negative	P	9	63	344	2002	0.780992	0.991945
GO:000695	response	P	12	63	447	2002	0.781863	0.991945
GO:003122	intrinsic	C	7	63	275	2002	0.783948	0.991945
GO:000971	response	P	3	63	129	2002	0.784758	0.991945
GO:004852	positive	P	13	63	482	2002	0.785139	0.991945
GO:007134	cellular	P	2	63	90	2002	0.786121	0.991945
GO:000989	positive	P	5	63	204	2002	0.786461	0.991945
GO:003198	nuclear l	C	5	63	204	2002	0.786461	0.991945
GO:005170	multi-org	P	9	63	347	2002	0.790077	0.991945

GO:004885	anatomica	P	10	63	382	2002	0.79128	0.991945
GO:004424	cellular	P	4	63	169	2002	0.793757	0.991945
GO:003109	organelle	C	5	63	207	2002	0.797397	0.991945
GO:004299	cell proj	C	3	63	132	2002	0.798024	0.991945
GO:000228	neutrophi	P	2	63	93	2002	0.801478	0.991945
GO:001062	positive	P	2	63	93	2002	0.801478	0.991945
GO:003623	granulocy	P	2	63	93	2002	0.801478	0.991945
GO:004211	neutrophi	P	2	63	93	2002	0.801478	0.991945
GO:004308	positive	P	2	63	93	2002	0.801478	0.991945
GO:004331	neutrophi	P	2	63	93	2002	0.801478	0.991945
GO:000679	phosphate	P	4	63	171	2002	0.801507	0.991945
GO:000715	cell adhe	P	3	63	133	2002	0.802296	0.991945
GO:001046	gene expr	P	3	63	133	2002	0.802296	0.991945
GO:002261	biologica	P	3	63	133	2002	0.802296	0.991945
GO:005117	positive	P	4	63	172	2002	0.805296	0.991945
GO:014035	export fr	P	4	63	172	2002	0.805296	0.991945
GO:003019	extracell	P	2	63	94	2002	0.80638	0.991945
GO:003132	positive	P	2	63	94	2002	0.80638	0.991945
GO:004306	extracell	P	2	63	94	2002	0.80638	0.991945
GO:004329	leukocyte	P	2	63	94	2002	0.80638	0.991945
GO:004322	membrane-	C	26	63	918	2002	0.807679	0.991945
GO:004323	intracell	C	19	63	691	2002	0.80796	0.991945
GO:190170	response	P	3	63	135	2002	0.810619	0.991945
GO:000227	myeloid c	P	2	63	95	2002	0.811177	0.991945
GO:000244	neutrophi	P	2	63	95	2002	0.811177	0.991945
GO:007194	cell peri	C	17	63	627	2002	0.81282	0.991945
GO:004259	homeostat	P	3	63	136	2002	0.814671	0.991945
GO:003409	response	P	2	63	96	2002	0.815869	0.991945
GO:000565	nucleopla	C	4	63	175	2002	0.81632	0.991945
GO:000552	ATP bindi	F	3	63	137	2002	0.818651	0.991945
GO:000680	nitrogen	P	17	63	630	2002	0.819651	0.991945
GO:000814	drug bind	F	4	63	176	2002	0.819883	0.991945
GO:000989	positive	P	2	63	97	2002	0.820459	0.991945
GO:004423	cellular	P	17	63	631	2002	0.821891	0.991945
GO:004690	intracell	P	3	63	138	2002	0.82256	0.991945
GO:001619	vesicle-m	P	14	63	531	2002	0.823327	0.991945
GO:000244	myeloid l	P	2	63	98	2002	0.824949	0.991945
GO:000727	multicell	P	9	63	360	2002	0.826406	0.991945
GO:000236	leukocyte	P	2	63	99	2002	0.829339	0.991945
GO:000996	negative	P	2	63	99	2002	0.829339	0.991945
GO:004869	generatio	P	2	63	99	2002	0.829339	0.991945
GO:000226	cell acti	P	2	63	100	2002	0.833632	0.991945
GO:000695	immune re	P	13	63	502	2002	0.834754	0.991945
GO:000679	phosphoru	P	4	63	181	2002	0.836876	0.991945
GO:005164	cellular	P	4	63	181	2002	0.836876	0.991945
GO:000227	myeloid l	P	2	63	101	2002	0.837829	0.991945
GO:004873	system de	P	8	63	329	2002	0.837966	0.991945
GO:006500	biologica	P	32	63	1123	2002	0.839022	0.991945
GO:001981	immunoglo	C	6	63	257	2002	0.839354	0.991945
GO:004249	response	P	2	63	102	2002	0.841932	0.991945
GO:000681	transport	P	20	63	741	2002	0.844411	0.991945

GO:001064	negative	P	2	63	103	2002	0.845943	0.991945
GO:002305	negative	P	2	63	103	2002	0.845943	0.991945
GO:005109	positive	P	2	63	103	2002	0.845943	0.991945
GO:003016	regulatic	P	2	63	104	2002	0.849863	0.991945
GO:005078	regulatic	P	30	63	1066	2002	0.850334	0.991945
GO:000177	cell acti	P	3	63	146	2002	0.851375	0.991945
GO:000237	immune sy	P	15	63	578	2002	0.851836	0.991945
GO:003555	intracell	P	2	63	105	2002	0.853694	0.991945
GO:009858	bounding	C	3	63	147	2002	0.854682	0.991945
GO:190157	organic s	P	4	63	187	2002	0.855527	0.991945
GO:005123	establish	P	20	63	748	2002	0.857811	0.991945
GO:000573	cytoplasm	C	25	63	911	2002	0.858181	0.991945
GO:005117	localizat	P	22	63	814	2002	0.858587	0.991945
GO:000193	regulatic	P	2	63	107	2002	0.861095	0.992559
GO:007006	extracell	C	12	63	481	2002	0.863384	0.992559
GO:000651	peptide m	P	2	63	108	2002	0.864668	0.992559
GO:190356	extracell	C	12	63	483	2002	0.867358	0.992559
GO:004409	positive	P	2	63	109	2002	0.868158	0.992559
GO:004323	extracell	C	12	63	484	2002	0.869312	0.992559
GO:003250	developme	P	10	63	414	2002	0.869617	0.992559
GO:001953	protein m	P	11	63	450	2002	0.871113	0.992559
GO:001003	response	P	6	63	271	2002	0.875036	0.994629
GO:000739	nervous s	P	3	63	154	2002	0.876117	0.994629
GO:005124	negative	P	2	63	112	2002	0.878148	0.994629
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ko00190	Oxidative	2	P05496(KC	up	0	-	down	http://ww
ko00511	Other gly	0	-	up	1	A0A0G2JLE	down	http://ww
ko00600	Sphingoli	0	-	up	1	A0A0G2JLE	down	http://ww
ko00620	Pyruvate	1	P48163(KC	up	0	-	down	http://ww
ko00860	Porphyrin	1	A0A1B0GVN	up	0	-	down	http://ww
ko01100	Metabolic	4	P05496(KC	up	1	A0A0G2JLE	down	http://ww
ko01200	Carbon me	1	P48163(KC	up	0	-	down	http://ww
ko01524	Platinum	1	C9JFR7(KC	up	0	-	down	http://ww
ko03040	Spliceoso	1	G3V4C1(K1	up	0	-	down	http://ww
ko03050	Proteasom	1	O00487(KC	up	2	D6RFN0(KC	down	http://ww
ko03320	PPAR sign	1	P48163(KC	up	1	B7Z7F6(KC	down	http://ww
ko03420	Nucleotid	0	-	up	1	A0A494C0E	down	http://ww
ko04010	MAPK sign	1	A4D2P0(KC	up	0	-	down	http://ww
ko04014	Ras signa	2	A0A024R1U	up	0	-	down	http://ww
ko04015	Rap1 sign	1	A4D2P0(KC	up	0	-	down	http://ww
ko04020	Calcium s	0	-	up	1	P02585(K1	down	http://ww
ko04024	cAMP sign	1	A4D2P0(KC	up	0	-	down	http://ww
ko04062	Chemokine	1	A4D2P0(KC	up	0	-	down	http://ww
ko04066	HIF-1 sig	0	-	up	1	B4E3L5(KC	down	http://ww
ko04071	Sphingoli	1	A4D2P0(KC	up	0	-	down	http://ww
ko04115	p53 signa	1	C9JFR7(KC	up	0	-	down	http://ww
ko04141	Protein p	0	-	up	2	A0A494C0E	down	http://ww
ko04142	Lysosome	0	-	up	1	A0A0G2JLE	down	http://ww
ko04144	Endocytos	1	A0A024R1U	up	0	-	down	http://ww
ko04145	Phagosome	2	A0A024R1U	up	0	-	down	http://ww
ko04151	PI3K-Akt	1	A4D2P0(KC	up	1	A0A024R46	down	http://ww
ko04210	Apoptosis	1	C9JFR7(KC	up	0	-	down	http://ww
ko04215	Apoptosis	1	C9JFR7(KC	up	0	-	down	http://ww
ko04217	Necroptos	1	Q71UI9(K1	up	0	-	down	http://ww
ko04218	Cellular	1	Q9HBA0(KC	up	0	-	down	http://ww
ko04310	Wnt signa	1	A4D2P0(KC	up	0	-	down	http://ww
ko04350	TGF-beta	1	D6RJI3(K1	up	0	-	down	http://ww
ko04360	Axon guid	1	A4D2P0(KC	up	0	-	down	http://ww
ko04370	VEGF sign	1	A4D2P0(KC	up	0	-	down	http://ww
ko04380	Osteoclas	1	A4D2P0(KC	up	0	-	down	http://ww
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ko04520	Adherens	1	A4D2P0(KC	up	0	-	down	http://ww
ko04530	Tight jun	1	A4D2P0(KC	up	1	Q9UKX2(K1	down	http://ww
ko04610	Complemen	1	A8K5T0(KC	up	0	-	down	http://ww
ko04620	Toll-like	1	A4D2P0(KC	up	0	-	down	http://ww
ko04650	Natural k	1	A4D2P0(KC	up	0	-	down	http://ww
ko04662	B cell re	1	A4D2P0(KC	up	0	-	down	http://ww
ko04664	Fc epsilo	1	A4D2P0(KC	up	0	-	down	http://ww
ko04666	Fc gamma	1	A4D2P0(KC	up	0	-	down	http://ww
ko04670	Leukocyte	1	A4D2P0(KC	up	1	H3BPK4(K1	down	http://ww
ko04714	Thermogen	1	P05496(KC	up	0	-	down	http://ww
ko04722	Neurotrop	1	A4D2P0(KC	up	0	-	down	http://ww
ko04750	Inflammat	1	Q9HBA0(KC	up	0	-	down	http://ww
ko04810	Regulatio	1	A4D2P0(KC	up	2	A0A024R46	down	http://ww

ko04915	Estrogen	0	-	up	2	P13645(KC	down	http://ww
ko04923	Regulatic	0	-	up	1	B7Z7F6(KC	down	http://ww
ko04932	Non-alcoh	2	C9JFR7(KC	up	0	-	down	http://ww
ko04933	AGE-RAGE	1	A4D2P0(KC	up	1	A0A024R46	down	http://ww
ko04934	Cushing s	0	-	up	1	B4E3L5(KC	down	http://ww
ko04962	Vasopress	1	A0A024R1U	up	0	-	down	http://ww
ko04972	Pancreati	1	A4D2P0(KC	up	1	A0A087WUR	down	http://ww
ko04974	Protein d	0	-	up	1	A0A087WUR	down	http://ww
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ko05012	Parkinson	2	P05496(KC	up	0	-	down	http://ww
ko05014	Amyotroph	2	C9JFR7(KC	up	0	-	down	http://ww
ko05016	Huntingtc	2	P05496(KC	up	0	-	down	http://ww
ko05034	Alcoholis	1	Q71UI9(K1	up	0	-	down	http://ww
ko05100	Bacterial	1	A4D2P0(KC	up	1	A0A024R46	down	http://ww
ko05120	Epithelia	1	A4D2P0(KC	up	0	-	down	http://ww
ko05130	Pathogeni	2	C9JFR7(KC	up	1	Q9UKX2(K1	down	http://ww
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ko05132	Salmonell	3	A0A024R1U	up	1	Q9UKX2(K1	down	http://ww
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ko05135	Yersinia	1	A4D2P0(KC	up	1	A0A024R46	down	http://ww
ko05143	African t	0	-	up	1	E9M263(K1	down	http://ww
ko05144	Malaria	0	-	up	1	E9M263(K1	down	http://ww
ko05145	Toxoplasm	1	C9JFR7(KC	up	0	-	down	http://ww
ko05146	Amoebiasi	1	A0A024R1U	up	1	A0A024R46	down	http://ww
ko05150	Staphyloc	1	A8K5T0(KC	up	2	P13645(KC	down	http://ww
ko05152	Tuberculc	2	A0A024R1U	up	0	-	down	http://ww
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ko05162	Measles	1	C9JFR7(KC	up	0	-	down	http://ww
ko05163	Human cyt	2	C9JFR7(KC	up	0	-	down	http://ww
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ko05165	Human pap	0	-	up	1	A0A024R46	down	http://ww
ko05167	Kaposi sa	2	C9JFR7(KC	up	0	-	down	http://ww
ko05168	Herpes si	1	C9JFR7(KC	up	0	-	down	http://ww
ko05169	Epstein-E	3	C9JFR7(KC	up	1	D6RFN0(KC	down	http://ww
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ko05200	Pathways	2	C9JFR7(KC	up	2	B4E3L5(KC	down	http://ww
ko05203	Viral car	1	A4D2P0(KC	up	0	-	down	http://ww
ko05204	Chemical	0	-	up	1	B4E3L5(KC	down	http://ww
ko05205	Proteogly	1	A4D2P0(KC	up	1	A0A024R46	down	http://ww
ko05210	Colorecta	2	C9JFR7(KC	up	0	-	down	http://ww
ko05211	Renal cel	1	A4D2P0(KC	up	1	B4E3L5(KC	down	http://ww
ko05212	Pancreati	1	A4D2P0(KC	up	0	-	down	http://ww
ko05222	Small cel	1	C9JFR7(KC	up	1	A0A024R46	down	http://ww
ko05231	Choline m	1	A4D2P0(KC	up	0	-	down	http://ww
ko05322	Systemic	1	Q71UI9(K1	up	0	-	down	http://ww
ko05416	Viral myc	2	C9JFR7(KC	up	0	-	down	http://ww
ko05418	Fluid she	2	Q9HBA0(KC	up	0	-	down	http://ww

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ko05416	Viral myc	2	29	10	1031	0.029901	0.222239	C9JFR7(KO
ko05210	Colorecta	2	29	10	1031	0.029901	0.222239	C9JFR7(KO
ko04932	Non-alcoh	2	29	11	1031	0.035915	0.222239	C9JFR7(KO
ko05014	Amyotroph	2	29	11	1031	0.035915	0.222239	C9JFR7(KO
ko03050	Proteasom	3	29	29	1031	0.044724	0.222239	O00487(KO
ko00190	Oxidative	2	29	14	1031	0.056406	0.222239	P05496(KO
ko03320	PPAR sign	2	29	14	1031	0.056406	0.222239	P48163(KO
ko05132	Salmonell	4	29	54	1031	0.060204	0.222239	A0A024R1U
ko05222	Small cel	2	29	15	1031	0.063967	0.222239	C9JFR7(KO
ko05211	Renal cel	2	29	15	1031	0.063967	0.222239	A4D2P0(KO
ko05150	Staphyloc	3	29	34	1031	0.066672	0.222239	A8K5T0(KO
ko05167	Kaposi sa	2	29	18	1031	0.088508	0.271497	C9JFR7(KO
ko05135	Yersinia	2	29	20	1031	0.1062	0.271497	A4D2P0(KO
ko05130	Pathogeni	3	29	42	1031	0.110137	0.271497	C9JFR7(KO
ko05200	Pathways	4	29	67	1031	0.11332	0.271497	C9JFR7(KO
ko04972	Pancreati	2	29	21	1031	0.115386	0.271497	A4D2P0(KO
ko04915	Estrogen	2	29	22	1031	0.124773	0.273327	P13645(KO
ko05012	Parkinson	2	29	23	1031	0.134345	0.273327	P05496(KO
ko05170	Human imm	2	29	25	1031	0.153972	0.273327	C9JFR7(KO
ko05131	Shigellos	3	29	50	1031	0.162095	0.273327	C9JFR7(KO
ko04670	Leukocyte	2	29	26	1031	0.163996	0.273327	A4D2P0(KO
ko05418	Fluid she	2	29	26	1031	0.163996	0.273327	Q9HBA0(KO
ko05152	Tuberculo	2	29	26	1031	0.163996	0.273327	A0A024R1U
ko04933	AGE-RAGE	2	29	27	1031	0.174142	0.278627	A4D2P0(KO
ko05163	Human cyt	2	29	29	1031	0.19474	0.2996	C9JFR7(KO
ko05100	Bacterial	2	29	31	1031	0.215662	0.319499	A4D2P0(KO
ko04530	Tight jun	2	29	34	1031	0.247447	0.353495	A4D2P0(KO
ko05016	Huntingto	2	29	35	1031	0.258106	0.354057	P05496(KO
ko04014	Ras signa	2	29	36	1031	0.268781	0.354057	A0A024R1U
ko04810	Regulatio	3	29	65	1031	0.274394	0.354057	A4D2P0(KO
ko05146	Amoebiasi	2	29	39	1031	0.300816	0.37602	A0A024R1U
ko04145	Phagosome	2	29	40	1031	0.31147	0.37754	A0A024R1U
ko04510	Focal adh	3	29	72	1031	0.330088	0.388339	A4D2P0(KO
ko05010	Alzheimer	2	29	45	1031	0.364241	0.416275	P05496(KO
ko04512	ECM-recep	2	29	47	1031	0.385003	0.427781	Q08722(KO
ko04141	Protein p	2	29	56	1031	0.474743	0.509759	A0A494C0B
ko05205	Proteogly	2	29	57	1031	0.484271	0.509759	A4D2P0(KO
ko04151	PI3K-Akt	2	29	73	1031	0.622253	0.638208	A4D2P0(KO
ko01100	Metabolic	5	29	232	1031	0.817894	0.817894	P05496(KO

pathway-web
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