

S2 Table

In order to find novel Mms19-interacting proteins, we prepared protein extracts from adult flies expressing Mms19::eGFP and performed co-IP with anti-GFP antibody-coated beads. Protein complexes bound to the beads were then analyzed by Mass spectrometry. Simultaneously, we also performed co-IP and Mass spectrometry analysis for protein extracts prepared from wild type and Imp::GFP expressing flies to determine any non-specific binding to the antibody, beads or GFP. Amongst other interesting candidates, we found the Cytoplasmic Iron sulfur Assembly (CIA) proteins and some Microtubule associated proteins exclusively co-purifying with Mms19::eGFP. Tubulin on the other hand is quite abundant and was hence found in co-IPs of all extracts, although it was clearly enriched in the Mms19::eGFP extract compared to the wild type.

Abbreviations used:

PSM: Peptide Spectral Match, defines a potentially correct interpretation of a single fragment spectrum.

SpS: Spectrum Summation, counting of how many times one particular protein was identified by peptide spectral matches. Also referred to as spectrum counting.

PMSS: Protein Match Score Summation, all scores from peptide spectral matches to one particular protein are added up irrespective of whether a peptide was identified several times, with or without modifications. PMSS is sort of an extension of SpS, adding a spectral quality factor. The idea is that fragment spectra of peptides coming from high abundant proteins in the sample will result more often in good quality spectra than peptides from low abundant proteins. In the latter case there are less parent ions available for fragmentation which results in decreased fragment ion intensities or noisy spectra which will receive decreased scores.

Proteins that bound to the anti-GFP antibody coated beads from all three fly extracts are listed. These include different isoforms of α - and β tubulin that were identified in all extracts. However, the PMSS scores are higher for the tubulin isoforms immuno-precipitating from the

Mms19::eGFP extract. This indicates that tubulin was enriched in the Mms19::eGFP fraction compared to the wild-type control.

Mms19::eGFP	Imp::GFP	wild type		
PMSS	PMSS	PMSS	Accession no.	Description
3340,474185	1760,246969	3319,12355	Q9V496	Apolipoprotein-1
2338,436802	1132,387337	860,510753	Q9XTL9	Glycogen phosphorylase
1736,689022	1489,230637	1145,05171 3	P11147	Heat shock 70 kDa protein cognate 4
1580,213491	457,537864	375,495604	A0A0B4JCW4	Succinyl-CoA ligase subunit beta
1568,201598	969,73428	700,424552	Q9VQL7	CG3523, isoform A;
1525,616386	1322,298852	1071,73411 2	Q9VIE8	Aconitase, isoform B;
1477,657455	809,006151	629,803314	P02828	Heat shock protein 83
1473,730409	1241,958002	1273,76886 2	A8JNU6	Neural conserved at 73EF, isoform I;
1434,449869	1245,137804	1273,92281 8	Q8IQQ0	CG11661-PF, isoform F;
1282,669993	1448,561123	2313,61317 3	P29845	Heat shock 70 kDa protein cognate 5
1279,648707	914,950395	496,615158	O62619_ISOFORM_B	Pyruvate kinase (PK) [ISOFORM B]
1277,714693	755,526014	695,929175	Q9Y119	BcDNA.GH08860;
1239,287804	722,1279	721,908177	Q24560	Tubulin beta-1 chain
1225,117964	1046,393098	929,133523	Q9VWH4_ISOFORM_A	Probable isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial [ISOFORM A]
1200,406235	990,974693	732,275752	P15007_ISOFORM_A	Enolase [ISOFORM A]
1198,66663	528,967521	678,343753	Q7KN97	Pyruvate carboxylase
1197,459537	1217,540409	943,375413	P07764_CHAIN_0	Fructose-bisphosphate aldolase [CHAIN 0]
1152,949151	779,705487	689,007454	A8JRB8	CG5028, isoform C;
1102,200137	1232,455907	1031,94743 7	P48610	Arginine kinase (AK)
1089,122707	107,233987	43,519561	Q9VVA4	CG9674, isoform A;
1069,543996	209,117725	406,797086	P06607_CHAIN_0	Vitellogenin-3 [CHAIN 0]
1052,951539	835,027094	740,363674	P13706_ISOFORM_GPDH-1	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic (GPD-C) (GPDH-C) [ISOFORM GPDH-1]
954,803201	683,463264	808,711421	P29844_CHAIN_0	Heat shock 70 kDa protein cognate 3 [CHAIN 0]
938,084065	367,737896	568,771445	O97355_CHAIN_0	Transferrin; [CHAIN 0]
938,035475	367,494263	568,724755	Q9VWV6	Transferrin 1, isoform A;
930,259422	619,093163	965,34448	Q9V496_CHAIN_0	Apolipoprotein-1 [CHAIN 0]
928,154207	913,317461	893,912385	P10987_CHAIN_0	Actin-5C [CHAIN 0]
909,552723	895,697465	893,912385	P02572_CHAIN_0	Actin-42A [CHAIN 0]
887,944607	399,718625	396,061267	Q9VQL6	GH22259p;
843,845255	844,999776	863,219939	E1JGP0	LD04994p1;
840,187809	864,273063	861,027289	P83967_CHAIN_0	Actin, indirect flight muscle [CHAIN 0]
812,147361	564,537549	543,117976	Q9VHN7	CG8036, isoform B;

805,037722	643,554497	743,411407	P07486	Glyceraldehyde-3-phosphate dehydrogenase 1 (GAPDH I)
802,581885	209,044843	180,545791	Q7KN62	Transitional endoplasmic reticulum ATPase TER94
765,8618	458,687046	499,194471	K7WQ63	Alpha tubulin 84B;
757,785733	426,91701	297,805568	Q9VAX7	Beta-Tubulin at 97EF, isoform C;
754,068405	495,820583	470,455031	Q7KSU6	CG8036, isoform D;
730,794767	441,400858	598,304305	P54385	Glutamate dehydrogenase, mitochondrial (GDH)
709,334965	341,83072	669,872094	Q05825_CHAIN_0	ATP synthase subunit beta, mitochondrial [CHAIN 0]
696,814119	399,911808	562,813195	P54385_ISOFORM_C	Glutamate dehydrogenase, mitochondrial (GDH) [ISOFORM C]
691,824972	162,347141	336,878562	P02843_CHAIN_0	Vitellogenin-1 [CHAIN 0]
678,123474	468,11282	355,299057	Q9VD58	CG6439, isoform A;
669,720535	535,284987	566,720804	P07487	Glyceraldehyde-3-phosphate dehydrogenase 2 (GAPDH II)
660,20129	539,027804	545,207249	Q9VEB1	IP09655p;
652,071983	671,635744	693,002957	P02574_CHAIN_0	Actin, larval muscle [CHAIN 0]
630,94309	482,810202	419,917954	P13060_CHAIN_0	Elongation factor 2 (EF-2) [CHAIN 0]
628,324565	485,911971	843,455002	P35381	ATP synthase subunit alpha, mitochondrial
614,116672	470,848176	831,290782	P35381_CHAIN_0	ATP synthase subunit alpha, mitochondrial [CHAIN 0]
610,870086	393,877287	269,39954	P52029	Glucose-6-phosphate isomerase (GPI) (PGI) (PHI)
606,050144	521,318705	305,940026	P08736	Elongation factor 1-alpha 1 (EF-1-alpha-1)
603,294766	385,063748	334,06024	Q01604	Phosphoglycerate kinase
590,936461	220,995425	88,273986	X2JGG6	Heat shock protein 26, isoform B;
588,628543	593,892996	399,633664	Q8MSI2	GH15296p;
573,635995	507,635231	843,767172	Q9VGQ1	CG5214;
572,136484	60,753319	78,597035	A0A0B4LGC0	Tripeptidyl-peptidase II, isoform F;
558,556411	985,587584	186,758747	P23128	Putative ATP-dependent RNA helicase me31b
557,520077	250,898145	204,266761	O02649	60 kDa heat shock protein, mitochondrial (HSP-60)
555,583052	413,024144	302,541871	Q7M3J9	Tubulin beta-3 chain;
546,792926	479,033645	282,925741	Q9VVL7	Dihydrolipoyl dehydrogenase
537,31862	108,439634	272,981129	X2JC31	Clathrin heavy chain
532,755873	62,062701	49,279671	Q9VXQ5	GH13725p;
528,648854	423,142875	87,003597	Q9V3R1_CHAIN_0	Accessory gland protein Acp36DE [CHAIN 0]
528,374836	495,003968	318,071898	Q94522	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial (SCS-alpha)
526,378346	395,636339	548,041159	Q9VM14	Acetyltransferase component of pyruvate dehydrogenase complex
519,78102	177,046382	215,932128	A4V0N4	MIP16230p;
518,154928	141,210537	106,942113	P48605	T-complex protein 1 subunit gamma (TCP-1-gamma)
513,821774	307,239037	90,622494	X2JC82	Heat shock protein 27, isoform B;
511,673697	352,590314	190,708494	A1Z9E3	Elongation factor Tu
506,709509	102,642997	25,404171	A1Z8U4	T-complex chaperonin 5, isoform B;

506,575442	466,892152	327,933406	Q9VNW6	CG7470, isoform A;
501,015257	109,038707	28,124164	Q9VW54	26S proteasome regulatory complex subunit p97;
500,097156	248,612775	59,415885	Q9VFN5	CG2720-PA;
499,455826	204,49371	202,418377	P31409	V-type proton ATPase subunit B (V-ATPase subunit B)
499,299002	320,378922	266,190253	X2JGP4_CHAIN_0	Protein disulfide-isomerase [CHAIN 0]
493,236467	299,913378	132,525202	P92177_ISOFORM_C	14-3-3 protein epsilon [ISOFORM C]
490,747059	523,855811	545,462691	Q9W4H6	Pyruvate dehydrogenase E1 component subunit alpha
487,579736	404,516109	234,421587	P05303	Elongation factor 1-alpha 2 (EF-1-alpha-2)
485,753735	270,636798	329,457982	Q9W401	Probable citrate synthase, mitochondrial
483,094317	326,735909	444,406945	Q7K5K3	CG11876, isoform A;
478,443563	327,598144	195,987221	E8NH18	RH27654p;
475,097115	410,673406	137,761549	Q8IPE8	CG4389-PB, isoform B;
472,722423	254,694491	312,524529	A1ZBJ2	CG7461, isoform B;
465,948321	234,285165	599,268163	P09180	60S ribosomal protein L4
465,119985	441,732311	288,970031	P17336	Catalase
461,775254	51,08585	27,453759	P12613	T-complex protein 1 subunit alpha (TCP-1-alpha)
461,492939	340,683749	202,614909	A5XCL5	LD36265p;
459,509076	33,470581	76,143713	Q7K3J0	CG8258;
457,960929	177,224872	133,310715	Q9XZT5	Heatshock protein cognate 70Cb;
454,897288	306,494989	250,260489	A9J7N9	Aldehyde dehydrogenase;
450,558248	372,455095	426,599213	Q7KUB0	Isocitrate dehydrogenase [NADP]
448,713227	520,834914	305,406962	A5XD83	Phosphoglycerate mutase
448,414108	258,046023	200,263628	X2JF59	Thioredoxin peroxidase 1, isoform C;
447,219817	175,194149	422,930809	P50887	60S ribosomal protein L22
444,216349	146,984646	129,353269	Q9NJH0	Elongation factor 1-gamma (EF-1-gamma)
433,951305	425,885834	272,94356	Q9VNX4	Delta-1-Pyrroline-5-carboxylate dehydrogenase 1, isoform A;
429,986847	582,661581	604,392015	Q9VAC1	CG7920, isoform A;
419,400371	533,662129	288,301041	Q8IGE9	RH35990p;
416,661093	360,4168	348,393959	X2JJG8	Glutamine synthetase
412,761772	237,81562	180,525643	P52034_ISOFORM_C	ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) [ISOFORM C]
411,321903	180,062836	193,844885	P29310_ISOFORM_VI	14-3-3 protein zeta [ISOFORM VI]
410,921576	366,906389	195,429249	Q8IRQ5	LP02262p;
410,801167	342,888201	325,347074	P29613	Triosephosphate isomerase (TIM)
408,287645	103,482817	31,606255	E2QCF1	ATP citrate lyase, isoform F;
402,512263	197,098553	464,522727	O97118	Ribosomal protein L23a;
400,889908	138,477601	87,390673	P91938_ISOFORM_D	Thioredoxin reductase 1, mitochondrial (TrxR-1) [ISOFORM D]
395,658156	154,261196	148,273036	Q9VGZ3	Aconitate hydratase (Aconitase)
392,454396	303,861519	399,869156	Q9V3S0	Cytochrome P450 4g1

386,114722	266,751047	160,67267	Q9VSA3_CHAIN_0	Probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial (MCAD) [CHAIN 0]
385,360793	571,062967	578,346238	P22700_ISOFORM_A	Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [ISOFORM A]
384,719985	661,831717	1404,21046	Q7K569	Glycerol-3-phosphate dehydrogenase
382,87125	209,263084	156,640585	P29310_ISOFORM_C	14-3-3 protein zeta [ISOFORM C]
377,988128	83,622292	36,148282	Q9VHR8_ISOFORM_2	Dipeptidyl peptidase 3 (Dipeptidyl arylamidase III) (DPP III) [ISOFORM 2]
376,86154	175,965786	204,913621	Q9VL70	CG4600-PA;
375,526461	66,491125	85,376067	Q9V3U6	26-29kD-proteinase;
373,057487	529,183744	262,055072	Q9VAN7	GH13304p;
365,865682	188,330099	209,893887	O96827_CHAIN_0	Probable elongation factor 1-beta (EF-1-beta) [CHAIN 0]
365,08187	77,557619	183,224409	P02844_CHAIN_0	Vitellogenin-2 [CHAIN 0]
364,999627	306,034142	282,749941	P00334_CHAIN_0	Alcohol dehydrogenase [CHAIN 0]
363,550243	268,02008	94,880377	E2QCS7	CG17097;
363,468997	187,359861	118,95484	Q86BS7	CG9485, isoform C;
361,551591	362,987102	160,585902	F6J7B3	Peptidyl-prolyl cis-trans isomerase
360,290404	132,581076	144,119625	P48602	V-type proton ATPase catalytic subunit A isoform 1 (V-ATPase subunit A 1)
357,157121	40,706526	48,227221	Q0KHS7	Lipid storage droplet-2, isoform B;
355,474914	321,678411	108,376337	P08171_CHAIN_0	Esterase-6 (Est-6) (Carboxylesterase-6) [CHAIN 0]
353,072476	415,228649	153,498502	Q9VM18	Trehalose 6-phosphate phosphatase
348,339188	139,59022	102,787523	Q9V3V6	26S proteasome regulatory complex subunit p50;
348,126231	83,90927	129,382083	Q9VA91	40S ribosomal protein S7
347,915634	162,847141	177,236404	P46150_ISOFORM_C	Moesin/ezrin/radixin homolog 1 (Ezrin-moesin-radixin 1) (dMoesin) [ISOFORM C]
345,554133	185,563505	422,386765	P55830_CHAIN_0	40S ribosomal protein S3a [CHAIN 0]
342,673578	234,736602	397,002368	Q9VFAQ9	Dipeptidase B, isoform A;
342,098764	252,286264	234,082237	Q0KHZ6	CG7834, isoform A;
337,167785	176,654781	118,95484	C7LAB1	SD23689p;
336,224109	211,494772	284,699096	Q9W1H8	GH13256p;
334,783558	293,098833	271,010535	Q94523_CHAIN_0	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (FP) [CHAIN 0]
327,851055	194,958483	179,188632	P82147	Protein lethal(2)essential for life
327,127602	67,475623	94,301505	Q7KMQ0	26S proteasome regulatory complex subunit p48B;
324,970759	91,74528	145,614684	Q9NIW0	Malic enzyme
320,890206	98,831164	65,503248	A0A0B4KF46	Ubiquitin activating enzyme 1, isoform C;
320,307968	90,771667	60,156221	Q9W227	Peptidyl-prolyl cis-trans isomerase
315,935926	407,625745	234,815405	Q7K2P3	CG1648, isoform A;
314,267241	143,548773	182,151716	Q9GU68	Eukaryotic translation initiation factor 5A (eIF-5A)
311,344371	257,898529	147,95719	A1Z992	1,4-Alpha-Glucan branching enzyme;
305,33606	141,515313	157,378632	Q8T0M9	Aspartate aminotransferase

300,633722	30,643867	26,048889	Q9VL18	Probable elongation factor 1-delta (EF-1-delta)
300,236688	313,892332	252,292395	A0A077HCQ5	Alcohol dehydrogenase
299,89885	76,47389	54,983017	Q7YWB4	Aminotransferase;
295,613123	197,663046	156,667671	B7Z0X1	Serine hydroxymethyltransferase
291,417687	144,30914	139,566179	A0A0B4LJ12	Nucleoside diphosphate kinase
289,918305	128,157938	47,87112	Q9VPX7	Adenylyl cyclase-associated protein
288,405645	54,568304	67,130565	P06606	Tubulin alpha-4 chain
285,877749	46,195988	23,835301	O18413	26S protease regulatory subunit 8
285,588357	172,038383	93,591824	Q9TWZ1_CHAIN_0	Protein disulfide-isomerase [CHAIN 0]
284,931699	258,896918	147,936404	Q9VTK9	CG6084, isoform A;
283,566335	172,038383	85,734519	Q3YMU0_CHAIN_0	Protein disulfide-isomerase [CHAIN 0]
282,263141	84,798696	25,835729	Q9VAY2	Glycoprotein 93;
279,434659	109,835163	94,021805	Q9XZC3	Tat-binding protein-1;
277,169701	410,398371	103,930631	Q9VFC8_ISOFORM_B	Glycogen [starch] synthase [ISOFORM B]
276,811032	72,47457	282,773644	X2JIQ5	Ribosomal protein L17, isoform E;
276,191395	243,989913	301,209383	P61851_CHAIN_0	Superoxide dismutase [Cu-Zn] [CHAIN 0]
276,157147	104,58745	124,75633	Q7KN94	Walrus, isoform A;
275,086409	128,674623	87,015861	Q9VKW5	CG5355;
274,52847	96,329454	251,958561	P19889	60S acidic ribosomal protein P0
273,006399	135,249258	105,944508	Q9VUY9	Phosphoglucomutase (PGM)
271,876446	54,101802	40,202736	P48601	26S protease regulatory subunit 4 (P26s4)
268,880719	73,134722	133,317543	P80455	40S ribosomal protein S12
265,201003	141,302052	121,96711	P45594	Cofilin/actin-depolymerizing factor homolog
263,267754	51,99258	154,572462	Q9VFB9	DnaJ-like-2, isoform A;
263,022885	103,843547	118,889753	P41043	Glutathione S-transferase S1
262,651327	67,863472	43,219563	Q24150	Nucleosome assembly protein NAP-1;
261,888366	234,229552	79,102421	C8VV33	AT04852p;
252,192791	146,964201	262,295251	P39018_CHAIN_0	40S ribosomal protein S19a [CHAIN 0]
248,970738	437,439112	230,403015	Q7K2W6	GH04080p;
248,499425	146,11769	323,48709	P41126	60S ribosomal protein L13
248,240647	156,066696	75,49719	Q9VKI8	CG6287-PA;
244,779716	154,636223	222,734831	Q9VWG3	40S ribosomal protein S10b
243,596917	150,874607	105,65039	Q8T9D5	SD05601p;
242,99753	85,182745	71,837652	Q9VY05	CG9512, isoform A;
239,70013	216,919743	216,98886	Q95U46	GH07925p;
238,886635	139,605786	196,742536	P46223	60S ribosomal protein L7a
237,079278	61,091491	223,294051	Q9V9W2	Ribosomal protein L6, isoform A;
236,329066	61,144176	47,595579	Q9V3G7	26S proteasome non-ATPase regulatory subunit 6
231,846937	63,612444	102,951082	Q9VN25	Eukaryotic translation initiation factor 3 subunit A (eIF3a)
231,697932	162,696678	246,078838	Q9V3G1	60S ribosomal protein L8
230,301466	83,09705	80,206226	O18640	Guanine nucleotide-binding protein subunit beta-like protein

229,619243	349,423957	56,782575	A8DZ29	Eukaryotic translation initiation factor 4G, isoform B;
223,670132	163,021009	205,649765	Q8MLY8	40S ribosomal protein S8
223,474079	37,909018	123,381293	O02195	Eukaryotic translation initiation factor 3 subunit I (eIF3i)
223,321266	148,346493	74,78204	Q4V3L7	IP10537p;
222,61468	135,05619	117,60346	O16043	Anon1A4;
221,678258	102,777342	72,545258	P29413_CHAIN_0	Calreticulin [CHAIN 0]
221,417859	116,916527	287,972811	Q24208	Eukaryotic translation initiation factor 2 subunit 3 (eIF-2-gamma)
220,368593	166,83438	129,03681	Q960M4	LD45324p;
219,032305	160,831577	87,181973	E1JGZ9	Proteasome subunit alpha type
217,48371	118,382191	71,536697	Q95U34	GH11113p;
216,452366	906,30065	39,326413	M9PF14	Trailer hitch, isoform C;
215,796774	127,775587	95,343355	Q9V521	Phenoloxidase 2 (PO A3) (Pro-phenoloxidase A3)
215,700383	139,379468	70,292219	O97428	CG4944-PA, isoform A;
214,886508	37,901043	323,801622	O16797_CHAIN_0	60S ribosomal protein L3 [CHAIN 0]
212,722271	142,762307	146,316781	A0A0B4LGS4	Vacuolar H[+]-ATPase 26kD subunit, isoform C;
210,767097	77,084631	63,008036	Q9VLB7	GDP dissociation inhibitor, isoform A;
208,225792	21,991848	130,476299	O61231	60S ribosomal protein L10
205,544904	124,138905	63,190032	P46415	Alcohol dehydrogenase class-3 (FALDH) (FDH) (GSH-FDH)
203,716305	171,125212	77,74765	Q8SY61_CHAIN_0	General odorant-binding protein 56d [CHAIN 0]
203,586541	328,613844	220,055792	Q9VTC3	CG6409, isoform B;
202,311477	70,533643	108,397735	O96553_ISOFORM_A	C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [ISOFORM A]
202,013312	182,143475	118,397462	Q9VGM2	Fatty acid bindin protein, isoform B;
199,308416	72,046176	287,11272	Q5U0W4	GM06787p;
199,217577	125,989053	231,718388	Q06559	40S ribosomal protein S3
198,070351	1031,026964	36,712747	P21187	Polyadenylate-binding protein (PABP) (Poly(A)-binding protein)
197,891404	70,632436	72,562805	P14318	Muscle-specific protein 20
191,668283	55,454529	41,429208	Q7JR58	CG6543, isoform A;
188,879456	69,229343	42,714193	P22769	Proteasome subunit alpha type-7-1
187,262296	209,069945	83,626791	Q9VXI1	CG9914, isoform A;
185,503778	155,13832	188,016626	Q9VEN1_ISOFORM_2	Filamin-A (FLN-A) (ABP-280) [ISOFORM 2]
185,375775	58,01788	64,945576	A0A0B4JD95	Zipper, isoform H;
185,119879	86,773955	138,150946	Q9VJY6	60S ribosomal protein L24
184,518696	34,457488	203,357118	P41092	60S ribosomal protein L27a
184,515685	86,368691	36,170898	M9PE40	Ubiquitin carboxyl-terminal hydrolase
182,511183	33,246042	123,102052	P36241	60S ribosomal protein L19
182,07736	165,393698	181,922912	P29746	Protein bangles and beads
181,886725	107,699861	34,284156	Q8IPF5	A kinase anchor protein 200, isoform B;
179,404829	81,426256	162,137258	Q9VA83	Ferritin
178,928196	143,633478	182,302059	P41042	40S ribosomal protein S4

178,689483	224,1845	315,557749	P48604	GrpE protein homolog, mitochondrial
178,675959	215,848124	171,705591	P29843	Heat shock 70 kDa protein cognate 1
178,233795	29,978522	318,406048	Q9VKC3	CG14945, isoform B;
175,403322	118,259718	185,079211	Q9W2X6	Lethal (1) G0230, isoform A;
174,636051	116,387206	45,070103	X2JES1	Fructose-1,6-bisphosphatase, isoform C;
174,183099	100,605166	56,953425	Q9VW68	CG7433, isoform A;
174,002324	112,590414	177,38828	Q9VNB9	RE17737p;
173,597877	260,678065	92,04987	P54192_CHAIN_0	General odorant-binding protein 19d (PBPRP-2) [CHAIN 0]
173,035459	50,507001	48,770159	F3YDF6	MIP08376p;
172,4674	78,337738	34,284156	Q86BM5	A kinase anchor protein 200, isoform G;
172,227266	85,022888	112,665841	Q9V5C6	Proteasome subunit alpha type-3
170,064487	127,303691	174,782717	Q00637_CHAIN_0	Superoxide dismutase [Mn], mitochondrial [CHAIN 0]
170,032431	82,804143	116,37461	P29327	40S ribosomal protein S6
169,350332	170,444772	164,250637	Q9VG58	Major heat shock 70 kDa protein Bbb (Heat shock protein 70Bbb)
167,518232	67,409689	21,773503	Q9VZ23	GTP-binding nuclear protein Ran
165,548247	255,391852	166,913428	Q9GV29	Prophenoloxidase;
164,632246	115,359228	214,941778	Q9VHE5	RH48056p;
164,462878	100,090837	68,216371	P18053	Proteasome subunit alpha type-4
163,227322	39,24787	35,437112	Q9VJJ0	Proteasome subunit beta type
162,16335	45,273093	123,103935	P48159	60S ribosomal protein L23
161,605363	850,968145	39,326413	Q9VTZ0	GH08269p;
160,014023	79,379395	86,560143	Q9VTV3	AT17975p;
159,35522	95,871533	98,6337	P42281	Acyl-CoA-binding protein homolog (ACBP) (DBI)
159,167688	46,976243	38,240976	Q9VRP2	CG10576, isoform A;
158,607796	99,25461	126,3997	P31009	40S ribosomal protein S2
157,396033	160,04301	231,399013	Q24251	ATP synthase subunit d, mitochondrial (ATPase subunit d)
155,603356	75,423693	35,503888	Q9VXF1	Serine/threonine-protein phosphatase 2B catalytic subunit 3
155,274736	204,834245	91,185513	Q9VBP6	GH21316p;
155,22557	177,639934	117,533042	Q9VWG1	CG14207, isoform D;
153,669583	345,309674	223,767754	Q8T8R1	CCHC-type zinc finger protein CG3800
152,120741	217,102881	175,549612	Q29QY4	Alcohol dehydrogenase
149,849866	94,419347	213,445817	R9Q794	Ribosomal protein L5, isoform G;
148,453758	84,161851	39,916132	Q9VU68	Actin-interacting protein 1 (AIP1)
148,056343	174,077103	117,075586	P20432	Glutathione S-transferase 1-1
146,137809	65,692669	139,500494	Q9W237	40S ribosomal protein S16
145,999276	174,48867	176,418364	O97125	Heat shock protein 68
145,611952	58,17417	192,934029	P41094	40S ribosomal protein S18
145,138384	115,145227	114,456216	Q9VZQ8	Glutathione peroxidase
140,430146	169,401605	270,792802	O01666	ATP synthase subunit gamma, mitochondrial
139,086242	34,811645	94,179593	X2JFR6	Eukaryotic translation initiation factor 2alpha, isoform B;

138,456968	25,289949	53,986135	P20477_CHAIN_0	Glutamine synthetase 1, mitochondrial [CHAIN 0]
138,1305	32,854311	96,977125	Q9U1J0	Malic enzyme
137,562161	88,445092	106,04889	P48588	40S ribosomal protein S25
137,383057	33,969185	159,988119	X2JDU0	Ribosomal protein L9, isoform C;
135,710616	63,702258	162,56849	Q9VBH8	F102850p;
135,514329	82,565146	125,252409	Q9V9M7	RE62581p;
134,576259	78,348455	58,358699	P41093	60S ribosomal protein L18a
133,688734	87,811473	70,209556	Q9U915	Adenylate kinase
133,681824	48,102411	58,01738	Q7K485	CathD;
133,412896	126,868494	85,516972	Q95RI5	Failed axon connections
133,189864	103,062091	249,215617	O17445	60S ribosomal protein L15
132,627402	49,024923	15,63152	M9PGX2	Pretaporter, isoform D;
131,886851	96,232075	47,767708	P23779	Cystatin-like protein
131,719408	79,250374	100,956592	Q7KT11	CG9331, isoform B;
131,703256	72,076308	77,064957	D1FZD8	Odorant-binding protein 99c;
131,665841	83,695534	81,515306	Q9VFF0	CG3731, isoform A;
131,583306	118,505402	225,49882	Q7JV23	Acetyl-CoA carboxylase, isoform B;
129,930618	61,782779	23,520981	Q9I7S8	Multifunctional protein ADE2
129,226124	61,207145	55,072738	Q7KMR7	Thioredoxin-like protein TXL;
127,442176	250,885952	134,695209	Q7K084	Odorant-binding protein 44a, isoform A;
125,463207	75,77324	103,32149	P84029	Cytochrome c-2
122,456676	88,564566	105,899743	A0A0B4LFD9	Ribosomal protein S23, isoform B;
121,922952	77,73343	89,573043	O76927_ISOFORM_E	40S ribosomal protein S21 [ISOFORM E]
120,724349	78,7372	208,418505	Q9VBN5	60S ribosomal protein L27
119,955099	87,989397	38,030803	Q9VKX2	Malate dehydrogenase
119,186118	31,093236	188,383563	M9PHM6	60S ribosomal protein L18
119,112119	238,340751	93,838339	E1JHG2	Seminal fluid protein 33A3;
116,637747	67,278155	28,546481	Q9W0E4	Puromycin sensitive aminopeptidase, isoform A;
116,406575	37,510775	52,981412	Q9W4X7	Eukaryotic translation initiation factor 3 subunit G-1 (eIF3g-1) (eIF-3 RNA-binding subunit 1)
115,915908	87,61503	46,546594	Q9VLR5	RNA polymerase II transcriptional coactivator
115,526103	119,50817	117,32896	Q9VU35	CG11267-PA;
115,344294	98,931839	160,825895	Q9V8Y2_CHAIN_0	General odorant-binding protein 56a [CHAIN 0]
114,95126	77,224104	48,865698	Q9VXK0	Protein NipSnap
114,614346	66,11217	69,158644	Q9W334	40S ribosomal protein S28
114,562105	54,7434	47,930948	P35554	Flightin
114,251321	17,489347	15,956593	Q9VSL4	Glutathione S transferase O2, isoform B;
112,911351	85,919238	128,722075	Q7JYK1	RE10554p;
111,420271	111,329177	160,113166	Q24439	ATP synthase subunit O, mitochondrial (OSCP)
110,834505	153,19269	114,87988	Q9W1C9_CHAIN_0	Ejaculatory bulb-specific protein 3 [CHAIN 0]
110,788116	99,595142	88,646394	P02516	Heat shock protein 23

110,654678	87,489418	131,922169	Q8IGR0	RE44350p;
110,550864	17,254082	38,302749	Q9VGS2	Translationally-controlled tumor protein homolog (TCTP)
110,41305	69,648872	49,147198	A0APE4	CG6459 protein;
110,383961	125,976052	21,501629	Q9VFT4	AT27578p;
109,461387	96,110725	83,581975	Q9VSP9	CG5804-PA;
108,510511	46,282571	119,403327	Q03334	40S ribosomal protein S13
107,246968	60,35119	130,05053	X2JCX8	Ribosomal protein S14b, isoform B;
106,877199	102,614067	43,040377	P22465	Annexin B10
106,034367	34,739395	147,475177	X2JC35	60S ribosomal protein L36
105,012154	71,465722	93,040992	O97479	FI05212p;
104,280421	41,442518	49,819076	Q9VCR2	Aminoacylase-1
103,423238	14,694978	114,049852	Q9VLT7	CG7424-PA;
102,760644	120,51854	120,72489	Q9Y125	BcDNA.GH08312;
101,556719	109,721192	22,542724	Q9W2J5	CG44245, isoform A;
101,345299	58,841662	85,197082	Q7JX87	Peroxisredoxin 2540-2;
100,987639	114,48412	118,847063	Q9VL68	CG4598, isoform B;
100,074213	47,337077	60,468352	O62621	Coatomer subunit beta ¹ (Beta ¹ -COP)
99,635425	77,744088	68,53998	A0A0B4JD48	Cysteine proteinase-1, isoform D;
99,409876	15,991021	121,902165	Q9VNE9	60S ribosomal protein L13a
97,806001	86,416489	51,881191	Q9VQB4	CG3609, isoform B;
97,069796	36,279598	108,080647	Q9VAI9	Odorant-binding protein 99c, isoform A;
96,406823	84,290414	205,439244	X2J5G6	Ribosomal protein L7, isoform B;
96,26933	75,325672	15,527324	Q29QY5	IP15841p;
95,991168	131,286837	326,040739	Q868Z9_CHAIN_0	Papilin [CHAIN 0]
94,181141	91,728579	49,69256	P62152_CHAIN_0	Calmodulin (CaM) [CHAIN 0]
92,999281	119,65166	104,593953	Q9VJ44	CG17597, isoform B;
92,376488	55,20429	42,989228	Q7KW39_ISOFORM_A	Probable methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial (MMSDH) (Malonate-semialdehyde dehydrogenase [acylating]) [ISOFORM A]
92,089093	60,619131	232,017511	Q7JWF1	Electron transfer flavoprotein-ubiquinone oxidoreductase, isoform A;
91,690135	51,428968	34,569617	O97102	Small ubiquitin-related modifier (SUMO)
91,22479	87,631386	42,975727	P20228	Glutamate decarboxylase (GAD)
90,649248	92,453844	64,312226	Q7KRU8	Ferritin
89,524318	42,575857	35,06719	Q9XZH6	V-type proton ATPase subunit G (V-ATPase subunit G)
88,925822	37,856587	126,471807	Q24407	ATP synthase-coupling factor 6, mitochondrial (ATPase subunit F6)
88,24906	37,052433	100,03847	Q9U9Q7	Transcription factor BTF3
86,098413	58,841662	68,29978	A1Z893	CG12896;
85,354776	216,258276	188,562807	P09491	Tropomyosin-2
85,180688	131,766794	76,383532	Q6NN12	HL05792p;
84,644763	120,45756	118,933485	Q9W596	Futsch light chain LC(f)
84,506998	211,269591	162,478873	Q26365_ISOFORM_A	ADP,ATP carrier protein (ANT) [ISOFORM A]

84,02598	80,321279	27,409917	Q6NL47	HL05814p;
82,793068	60,980793	173,004507	L0CRF4	Ribosomal protein S11;
82,702144	63,745375	68,274115	Q94518	Nascent polypeptide-associated complex subunit alpha (NAC-alpha)
82,481279	98,220794	43,930289	Q9V9S8	Ferrochelatase, mitochondrial
81,308525	95,437534	98,967992	P41964_CHAIN_0	Drosomycin [CHAIN 0]
81,305383	128,270487	164,883868	P21914	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (lp)
81,066951	96,937625	131,785489	Q27869	Protein-L-isoaspartate(D-aspartate) O-methyltransferase (PIMT)
80,496723	181,31668	231,499119	Q06943	High mobility group protein Z (HMG-Z)
79,928089	86,229328	124,704784	Q9VV75	AT02348p;
79,760708	47,612203	30,408657	Q9V6U9_CHAIN_0	Probable trans-2-enoyl-CoA reductase, mitochondrial [CHAIN 0]
79,518528	77,668252	114,656929	Q9VZS5	60S ribosomal protein L28
74,524538	162,066606	154,080007	P06754_ISOFORM_D	Tropomyosin-1, isoforms 9A/A/B [ISOFORM D]
73,521429	53,075553	36,444153	Q8T3W8	AT27079p;
72,53784	22,649181	92,383613	Q9VJ28	CG10639, isoform A;
69,853536	145,347953	124,671538	Q058U3	IP16008p;
69,557749	34,552175	76,034647	Q8SYS2	RE38869p;
69,45322	96,630751	122,056972	Q9V426	LD07162p;
69,129371	68,601536	58,717393	O77134	9 kD basic protein;
68,52543	74,29161	20,119801	Q8IR95	RH08789p;
68,237555	65,978042	62,599217	Q9VN93_CHAIN_0	Putative cysteine proteinase CG12163 [CHAIN 0]
67,1989	65,056739	79,623521	Q9VD01	LP12095p;
66,91566	100,379339	76,434219	Q9U982	Drosophila dodeca-satellite protein 1;
66,024944	20,026843	38,29339	Q07171_ISOFORM_2	Gelsolin [ISOFORM 2]
64,572815	92,177733	155,173936	P53777	Muscle LIM protein 1
62,670544	45,077529	70,540288	E1JJM9	Ribosomal protein S15Aa, isoform F;
62,403852	52,971413	29,351081	P35421	Phosphoribosylformylglycinamide synthase (FGAM synthase) (FGAMS) (FGAR amidotransferase) (FGAR-AT)
61,88491	48,59762	39,658638	Q9VK99	Atila, isoform B;
61,775846	46,93396	337,908557	Q24388_CHAIN_0	Larval serum protein 2 (LSP-2) [CHAIN 0]
61,55963	81,720072	60,269769	Q9VY92	CG11151, isoform B;
61,421159	103,304491	87,700409	Q9XZS3	Translation machinery-associated protein 7 homolog
59,95915	78,424329	36,73261	O46200_CHAIN_0	Accessory gland protein Acp63F [CHAIN 0]
59,108801	43,111811	65,899578	Q9V597	60S ribosomal protein L31
58,132213	16,609637	28,787244	Q9W0J9	CG9119;
57,106468	49,063286	38,086708	Q9VTI5	CG6140, isoform A;
56,427971	54,964826	43,541736	Q9VQF7	Bacchus, isoform B;
54,868937	52,473835	60,952488	P02283_CHAIN_0	Histone H2B [CHAIN 0]
53,958156	52,378202	17,502292	M9PB52	Galactose-1-phosphate uridylyltransferase
51,503927	191,896383	360,234385	Q94920_CHAIN_0	Voltage-dependent anion-selective channel [CHAIN 0]

48,371219	162,832547	79,510373	Q9VMV9	Reticulon-like protein
47,438138	51,075777	41,540479	Q8IPM8_ISOFORM_C	Complexin [ISOFORM C]
44,4725	81,540221	187,202276	Q94516	ATP synthase subunit b, mitochondrial (ATPase subunit b)
42,685694	64,476362	61,100165	Q9W4V3	CG14419-PA;
41,14575	397,305359	49,13281	Q08473_ISOFORM_A	RNA-binding protein squid (HNRNP 40) [ISOFORM A]
41,121509	73,998559	134,174574	Q24201	Carboxylic ester hydrolase
40,378801	50,960744	77,205122	Q9VD29	RE74312p;
39,515698	43,857904	37,661499	Q8SYQ8	CG3420, isoform A;
38,541423	40,358137	42,325594	Q9V7N5_ISOFORM_A	V-type proton ATPase subunit C (V-ATPase subunit C) [ISOFORM A]
37,841728	101,170828	220,395279	P13607_ISOFORM_3	Sodium/potassium-transporting ATPase subunit alpha (Na(+)/K(+) ATPase alpha subunit) [ISOFORM 3]
37,709448	22,91279	29,58324	Q0E940	Eukaryotic translation initiation factor 3 subunit B (eIF3b)
34,99479	15,921154	61,647788	Q9W229	40S ribosomal protein S24
34,634988	62,116106	14,750294	X2JFD6	Peroxisomal multifunctional enzyme type 2, isoform B;
34,415161	50,439013	31,632846	Q94519_ISOFORM_1	Acyl carrier protein, mitochondrial (ACP) [ISOFORM 1]
32,964941	122,835312	128,601102	Q8IQW2	CG14235-PB, isoform B;
32,819429	110,918178	27,800506	P41073_ISOFORM_C	Zinc finger protein on ecdysone puffs [ISOFORM C]
27,839934	22,570223	111,21573	X2JB24	Neuropeptide-like 2, isoform B;
26,377039	51,869708	57,908242	Q9VY87	Cathepsin B1, isoform A;
26,08523	21,653926	38,198019	Q9VZ11	Transgelin
25,072566	52,523143	35,624803	Q9W306	CG9691, isoform B;
18,19336	49,998171	37,145852	M9PFX9	Limpet, isoform N;