CEP- 1 and AAK-2 (identified by overlap between gene lists in Table S3 and S4)

CEP- 1 and AAK-2 (id	Gene	Sequence	_	Enriched	
Wormbase ID	Name	Name	GO term	GOterm	Gene > Brief Description
WBGene00001538	gcy-12	F08B1.2	Kinase	Dual/tyrosine and Ser/Thr Kinase	gcy-12 encodes a membrane guanylyl cyclase; a gcy- 12::GFP reporter is expressed in the PHA neurons as well as in a number of head sensory neurons including AFD, AWC, and ASE; when expressed in COS-M6 cells, GCY-12 exhibits temperature- dependent guanylyl cyclase activity.
WBGene00002212	kin-31	B0523.1	Kinase	Dual/tyrosine and Ser/Thr Kinase	kin-31 encodes a predicted tyrosine protein kinase expressed in the nucleus and cytoplasm of bodywall muscle cells; the expression of kin-31 was experimentally verified by RT-PCR.
WBGene00010991		R03D7.5	Kinase	Dual/tyrosine and Ser/Thr Kinase	
WBGene00012172		W01B6.5	Kinase	Dual/tyrosine and Ser/Thr Kinase	
WBGene00012207		W02B12.12	Kinase	Dual/tyrosine and Ser/Thr Kinase	
WBGene00017672		F21F3.2	Kinase	Dual/tyrosine and Ser/Thr Kinase	
WBGene00017737		F23C8.8	Kinase	Dual/tyrosine and Ser/Thr Kinase	
WBGene00022634		ZC581.7	Kinase	Dual/tyrosine and Ser/Thr Kinase	
WBGene00007977	gska-3	C36B1.10	Kinase	Dual/tyrosine and Ser/Thr Kinase	
WBGene00007448		C08F8.6	Kinase	Dual/tyrosine and Ser/Thr Kinase (TTBK)	
WBGene00007563		C14A4.13	Kinase	Dual/tyrosine and Ser/Thr Kinase (TTBK)	
WBGene00007777		C27D8.1	Kinase	Dual/tyrosine and Ser/Thr Kinase (TTBK)	
WBGene00009324		F32B6.10	Kinase	Dual/tyrosine and Ser/Thr Kinase (TTBK)	

		1	T	_	
				Dual/tyrosine	
WBGene00009402		F35C11.3	Kinase	and Ser/Thr	
				Kinase (TTBK)	
				Dual/tyrosine	
WBGene00012169		W01B6.2	Kinase	and Ser/Thr	
				Kinase (TTBK)	
				Dual/tyrosine	
WBGene00012637		Y38H8A.3	Kinase	and Ser/Thr	
				Kinase (TTBK)	
				Dual/tyrosine	
WBGene00014007		ZK596.2	Kinase	and Ser/Thr	
				Kinase (TTBK)	
				Dual/tyrosine	
WBGene00016541		C39H7.1	Kinase	and Ser/Thr	
				Kinase (TTBK)	
				Dual/tyrosine	
WBGene00016963		C56C10.6	Kinase	and Ser/Thr	
				Kinase (TTBK)	
				Dual/tyrosine	
WBGene00018178		F38E1.3	Kinase	and Ser/Thr	
				Kinase (TTBK)	
				Dual/tyrosine	
WBGene00018301		F41G3.5	Kinase	and Ser/Thr	
				Kinase (TTBK)	
				Dual/tyrosine	
WBGene00019642		K11C4.1	Kinase	and Ser/Thr	
				Kinase (TTBK)	
				Dual/tyrosine	
WBGene00021639		Y47G6A.13	Kinase	and Ser/Thr	
				Kinase (TTBK)	
				Dual/tyrosine	
WBGene00022707		ZK354.6	Kinase	and Ser/Thr	
				Kinase (TTBK)	
				Dual/tyrosine	
WBGene00015634		C09D4.3	Kinase	and Ser/Thr	
				Kinase (TTBK)	
WBGene00002193	kin-5	T13H10.1	Kinase	Dual/tyrosine and Ser/Thr Kinase(FER)	kin-5 encodes a predicted protein tyrosine kinase that is most closely related to the non-receptor tyrosine kinases Fes/Fps and Fer that contain an SH2 domain and a tyrosine kinase domain (OMIM:190030, murine Fes appears to be required for hemopoietic homeostasis); as loss of kin-5 activity via large-scale RNAi screens does not result in any obvious abnormalities, the precise role of kin-5 in C. elegans development and/or behavior is not yet known.

WBGene00002204	kin-21	W08D2.8	Kinase	Dual/tyrosine and Ser/Thr Kinase(FER)	
WBGene00004962	spe-8	F53G12.6	Kinase	Dual/tyrosine and Ser/Thr Kinase(FER)	spe-8 is predicted to encode a non-receptor tyrosine kinase with a SH2 domain; spe-8 is required for hermaphrodite spermatogenesis or sperm activation but not for male-derived sperm activation (sperm activation is the morphogenesis of a round non-motile spermatid to an amoeboid crawling sperm); however, mutant hermaphrodite spe-8 spermatids can transactivate and form functional sperm during mating with males; genetic and phenotypic evidence suggests that spe-8 acts in a common pathway with spe-12, spe-19, spe-27 and spe-29.
WBGene00009160		F26E4.5	Kinase	Dual/tyrosine and Ser/Thr Kinase(FER)	F26E4.5 encodes an SH2 domain-containing tyrosine kinase related to the vertebrate FER non-receptor protein tyrosine kinase; loss of F26E4.5 activity in an RNAi-hypersensitive strain results in axon guidance defects indicating that F26E4.5 likely plays a role in regulation of axon navigation.
WBGene00010712		K09B11.5	Kinase	Dual/tyrosine and Ser/Thr Kinase(FER)	
WBGene00012010		T25B9.4	Kinase	Dual/tyrosine and Ser/Thr Kinase(FER)	
WBGene00015994		C18H7.4	Kinase	Dual/tyrosine and Ser/Thr Kinase(FER)	
WBGene00016085		C25A8.5	Kinase	Dual/tyrosine and Ser/Thr Kinase(FER)	
WBGene00016416		C34F11.5	Kinase	Dual/tyrosine and Ser/Thr Kinase(FER)	
WBGene00016954		C55C3.4	Kinase	Dual/tyrosine and Ser/Thr Kinase(FER)	

				1, . 1	
				Dual/tyrosine	
WBGene00019081		F59A3.8	Kinase	and Ser/Thr	
				Kinase(FER)	
				Dual/tyrosine	
WBGene00022780		ZK622.1	Kinase	and Ser/Thr	
				Kinase(FER)	
				Dual/tyrosine	
WBGene00018999		F57B9.8	Kinase	and Ser/Thr	
				Kinase(FER)	
				Dual/tyrosine	
WBGene00016462		C35E7.10	Kinase	and Ser/Thr	
				Kinase(FER)	
				non-receptor	
WBGene00010366		H05L14.1	Kinase	serine/threonin	
				e protein kinase	
				non-receptor	
WBGene00015629		C09B9.4	Kinase	serine/threonin	
				e protein kinase	
				non-receptor	
WBGene00007269		602610.2	Vinces	serine/threonin	
WBGene00007269		C03C10.2	Kinase	e protein kinase	
				(TTBK)	
				non-receptor	
		005040.4		serine/threonin	
WBGene00007335		C05C12.1	Kinase	e protein kinase	
				(TTBK)	
				non-receptor	
				serine/threonin	
WBGene00008423		D2045.5	Kinase	e protein kinase	
				(TTBK)	
				non-receptor	
				serine/threonin	
WBGene00011191		R10D12.10	Kinase	e protein kinase	
				(TTBK)	
				non-receptor	
				serine/threonin	
WBGene00013979		ZK507.3	Kinase	e protein kinase	
				(TTBK)	
				non-receptor	
				serine/threonin	
WBGene00017050		D2024.1	Kinase	e protein kinase	
				· ·	
				(TTBK)	
				non-receptor	
WBGene00017802		F26A1.3	Kinase	serine/threonin	
				e protein kinase	
				(TTBK)	
				non-receptor	
WBGene00018004		F33D11.7	Kinase	serine/threonin	
				e protein kinase	
				(TTBK)	
				non-receptor	
WBGene00018122	ttbk-2	F36H12.8	Kinase	serine/threonin	
				e protein kinase	
				(TTBK)	

	,		T	1	
				non-receptor	
WBGene00019086		F59A6.4	Kinase	serine/threonin	
				e protein kinase	
				(TTBK)	
				non-receptor	
WBGene00020223		T05A7.6	Kinase	serine/threonin	
				e protein kinase	
				(TTBK)	
				non-receptor	
WBGene00020580		T19D12.5	Kinase	serine/threonin	
		. 100 1110		e protein kinase	
				(TTBK)	
				non-receptor	
WBGene00022108		Y71F9AL.2	Kinase	serine/threonin	
		., 0,		e protein kinase	
				(TTBK)	
				non-receptor	
WBGene00022229		Y73B6A.2	Kinase	serine/threonin	
				e protein kinase	
				(TTBK)	
				non-receptor	
WBGene00022632		ZC581.2	Kinase	serine/threonin	
				e protein kinase	
				(TTBK)	
				non-receptor	
WBGene00022705		ZK354.2	Kinase	serine/threonin	
		2.031.2	Killuse	e protein kinase	
				(TTBK)	
WBGene00004901	snf-2	F55H12.1	transmitter sym		
WBGene00004904	snf-5	Y46G5A.30	transmitter sym		
WBGene00004906	snf-7	ZK1010.9	transmitter sym		
WBGene00004908	snf-9	C49C3.1	transmitter sym	porter	
WBGene00004909	snf-10	Y32F6A.2	transmitter sym	porter	snf-10 encodes a member of the sodium:neurotransmitter symporter family.
WBGene00018980		F56F4.3	transmitter sym	porter	
WBGene00009129		F25H5.7	Phosphatases	Dual specific	
WBGene00009492		F36H1.3	Phosphatases	Dual specific	
WBGene00009548		F38H4.4	Phosphatases	Dual specific	
WBGene00010072		F54F12.1	Phosphatases	Dual specific	
WBGene00010634		K07F5.6	Phosphatases	Dual specific	
WBGene00010869		M05B5.1	Phosphatases	Dual specific	
WBGene00011918		T22C1.8	Phosphatases	Dual specific	
WBGene00012138		T28F4.3	Phosphatases	Dual specific	
WBGene00012679		Y39B6A.18	Phosphatases	Dual specific	
WBGene00012689		Y39B6A.30	Phosphatases	Dual specific	
WBGene00013586		Y80D3A.8	Phosphatases	Dual specific	
WBGene00015026		B0207.1	Phosphatases	Dual specific	
WBGene00013020			1	Dual specific	
WBGene00015929		C17H12.3	Phosphatases	Dual specific	
		C17H12.3 F47B3.2	Phosphatases Phosphatases	Dual specific Dual specific	
WBGene00015929					
WBGene00015929 WBGene00018526		F47B3.2	Phosphatases	Dual specific	
WBGene00015929 WBGene00018526 WBGene00019586		F47B3.2 K09F6.3	Phosphatases Phosphatases	Dual specific Dual specific	
WBGene00015929 WBGene00018526 WBGene00019586 WBGene00009401		F47B3.2 K09F6.3 F35C11.2	Phosphatases Phosphatases Phosphatases	Dual specific Dual specific Dual specific	
WBGene00015929 WBGene00018526 WBGene00019586 WBGene00009401 WBGene00013304		F47B3.2 K09F6.3 F35C11.2 Y57G11C.6	Phosphatases Phosphatases Phosphatases Phosphatases	Dual specific Dual specific Dual specific Dual specific	

WBGene00022090		Y69A2AR.19	Phosphatases	Dual specific	
WBGene00022030		C15H7.3	Phosphatases	Dual specific	
**PGEHE0000\010		C1311/13	r nospiiatases	·	
WBGene00010992		R03D7.8	Phosphatases	S/Thr specific/PPP1CA	
WBGene00012741		Y40H4A.2	Phosphatases	S/Thr specific/PPP1CA	
WBGene00016010		C23G10.1	Phosphatases	S/Thr specific/PPP1CA	
WBGene00021113	gsp-3	W09C3.6	Phosphatases	S/Thr specific/PPP1CA	
WBGene00008124		C47A4.3	Phosphatases	S/Thr specific/PPP1CB	
WBGene00016398		C34D4.2	Phosphatases	S/Thr specific/PPP1CB	
WBGene00020187	gsp-4	T03F1.5	Phosphatases	S/Thr specific/PPP1CB	
WBGene00009948		F52H3.6	Phosphatases	S/Thr specific/PPP1CC	
WBGene00010265		F58G1.3	Phosphatases	S/Thr specific/PPP1CC	
WBGene00011133		R08A2.2	Phosphatases	S/Thr specific/PPP1CC	
WBGene00014158		ZK938.1	Phosphatases	S/Thr specific/PPP1CC	
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WBGene00000389	cdc-25.4	R05H5.2	Phosphatases	tyrosine specific	a homolog of dual specificity phosphatase Cdc25.
WBGene00000389 WBGene00016742	cdc-25.4	R05H5.2 C48B6.4		-	a homolog of dual specificity phosphatase Cdc25.
	cdc-25.4		Phosphatases	tyrosine specific	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742	cdc-25.4	C48B6.4	Phosphatases Phosphatases	tyrosine specific	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347	cdc-25.4	C48B6.4 F42C5.5	Phosphatases Phosphatases	tyrosine specific tyrosine specific tyrosine specific	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207	cdc-25.4	C48B6.4 F42C5.5 Y18H1A.1	Phosphatases Phosphatases Phosphatases	tyrosine specific tyrosine specific tyrosine specific tyrosine specific	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084	cdc-25.4	C48B6.4 F42C5.5 Y18H1A.1 B0244.9	Phosphatases Phosphatases Phosphatases Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific B0244.9	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00007239	cdc-25.4	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8	Phosphatases Phosphatases Phosphatases Structural/MSP Structural/MSP Structural/MSP Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific tyrosine specific 80244.9 C01G10.14 C10H11.7 C14A4.8	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00007239 WBGene00015696 WBGene00007559 WBGene00016461	cdc-25.4	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7	Phosphatases Phosphatases Phosphatases Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific tyrosine specific B0244.9 C01G10.14 C10H11.7	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00007239 WBGene00015696 WBGene00007559 WBGene00016461 WBGene00007987		C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1	Phosphatases Phosphatases Phosphatases Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00007239 WBGene00015696 WBGene00007559 WBGene00016461 WBGene00007987 WBGene0000696	col-122	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 T05A1.2	Phosphatases Phosphatases Phosphatases Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 COLlagen	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00007239 WBGene00015696 WBGene00007559 WBGene00016461 WBGene00007987 WBGene0000696 WBGene00000707	col-122 col-133	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 T05A1.2 F52B11.4	Phosphatases Phosphatases Phosphatases Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 COLlagen COLlagen	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00007239 WBGene00015696 WBGene00007559 WBGene00016461 WBGene00007987 WBGene0000696	col-122	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 T05A1.2	Phosphatases Phosphatases Phosphatases Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 COLlagen COLlagen COLlagen	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00007239 WBGene00015696 WBGene00007559 WBGene00016461 WBGene00007987 WBGene0000696 WBGene00000707	col-122 col-133	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 T05A1.2 F52B11.4	Phosphatases Phosphatases Phosphatases Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific 80244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 COLlagen COLlagen COLlagen DAF-16/FOXO	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00007239 WBGene00015696 WBGene00007559 WBGene00016461 WBGene00007987 WBGene0000696 WBGene00000707	col-122 col-133	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 T05A1.2 F52B11.4	Phosphatases Phosphatases Phosphatases Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific 80244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 COLlagen COLlagen COLlagen DAF-16/FOXO Controlled,	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00007239 WBGene00015696 WBGene00007559 WBGene00016461 WBGene00007987 WBGene0000696 WBGene00000707 WBGene00000710	col-122 col-133 col-137	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 T05A1.2 F52B11.4 Y51H4A.9	Phosphatases Phosphatases Phosphatases Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 COLlagen COLlagen COLlagen DAF-16/FOXO Controlled, germline Tumor	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00015696 WBGene00007559 WBGene00007559 WBGene00007987 WBGene00000797 WBGene0000707 WBGene0000710 WBGene000021006	col-122 col-133 col-137	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 T05A1.2 F52B11.4 Y51H4A.9	Phosphatases Phosphatases Phosphatases Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 COLlagen COLlagen COLlagen DAF-16/FOXO Controlled, germline Tumor affecting	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00015696 WBGene00015696 WBGene00007559 WBGene00016461 WBGene00007987 WBGene00000707 WBGene00000710 WBGene000021006	col-122 col-133 col-137	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 T05A1.2 F52B11.4 Y51H4A.9 W03F11.3	Phosphatases Phosphatases Phosphatases Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 COLlagen COLlagen COLlagen DAF-16/FOXO Controlled, germline Tumor affecting F21H7.5	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00015696 WBGene00007559 WBGene00016461 WBGene00007987 WBGene00000707 WBGene0000710 WBGene0000710 WBGene00009031 WBGene00009470	col-122 col-133 col-137	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 T05A1.2 F52B11.4 Y51H4A.9 W03F11.3 F21H7.5 F36D3.4	Phosphatases Phosphatases Phosphatases Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific 80244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 COLlagen COLlagen COLlagen DAF-16/FOXO Controlled, germline Tumor affecting F21H7.5 F36D3.4	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00015696 WBGene00015696 WBGene00016461 WBGene00007987 WBGene00000696 WBGene00000710 WBGene00000710 WBGene00009031 WBGene00009470 WBGene000018119	col-122 col-133 col-137	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 T05A1.2 F52B11.4 Y51H4A.9 W03F11.3 F21H7.5 F36D3.4 F36H12.3	Phosphatases Phosphatases Phosphatases Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific 80244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 COLlagen COLlagen COLlagen DAF-16/FOXO Controlled, germline Tumor affecting F21H7.5 F36D3.4 F36H12.3	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00015696 WBGene00007559 WBGene00016461 WBGene00007987 WBGene00000707 WBGene0000710 WBGene0000710 WBGene00009031 WBGene00009470	col-122 col-133 col-137	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 T05A1.2 F52B11.4 Y51H4A.9 W03F11.3 F21H7.5 F36D3.4	Phosphatases Phosphatases Phosphatases Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 COLlagen COLlagen COLlagen COLlagen DAF-16/FOXO Controlled, germline Tumor affecting F21H7.5 F36D3.4 F36H12.3 F42A9.7	a homolog of dual specificity phosphatase Cdc25.
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WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00015696 WBGene00015696 WBGene00016461 WBGene00007987 WBGene00000707 WBGene00000710 WBGene0000710 WBGene00009031 WBGene00009470 WBGene00018336	col-122 col-133 col-137 dct-9	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 T05A1.2 F52B11.4 Y51H4A.9 W03F11.3 F21H7.5 F36D3.4 F36H12.3 F42A9.7	Phosphatases Phosphatases Phosphatases Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific 80244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 COLlagen COLlagen COLlagen COLlagen TAF-16/FOXO Controlled, germline Tumor affecting F21H7.5 F36D3.4 F36H12.3 F42A9.7 F44D12.3; F44D12.5; F44D12.7;	a homolog of dual specificity phosphatase Cdc25.
WBGene00016742 WBGene00018347 WBGene00021207 WBGene00015084 WBGene00007239 WBGene00015696 WBGene00007559 WBGene0000696 WBGene0000707 WBGene0000710 WBGene0000710 WBGene00009031 WBGene00009470 WBGene00018336	col-122 col-133 col-137 dct-9	C48B6.4 F42C5.5 Y18H1A.1 B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 T05A1.2 F52B11.4 Y51H4A.9 W03F11.3 F21H7.5 F36D3.4 F36H12.3 F42A9.7	Phosphatases Phosphatases Phosphatases Structural/MSP	tyrosine specific tyrosine specific tyrosine specific tyrosine specific B0244.9 C01G10.14 C10H11.7 C14A4.8 C35E7.9 C36H8.1 COLlagen COLlagen COLlagen DAF-16/FOXO Controlled, germline Tumor affecting F21H7.5 F36D3.4 F36H12.3 F42A9.7 F44D12.3; F44D12.5;	a homolog of dual specificity phosphatase Cdc25.

WBGene00010091	ssp-35	F55C5.1	Structural/MSP	F55C5.1	
WBGene00010114		F55D12.6	Structural/MSP	F55D12.6	
WBGene00010254		F58E6.5	Structural/MSP	F58E6.5	
WBGene00019410		K05F1.9	Structural/MSP	K05F1.9	
WBGene00019431		K06A5.3	Structural/MSP	K06A5.3	
WBGene00003424	msp-3	F26G1.7	Structural/MSP	Major Sperm Protein	msp-3 encodes a protein that belongs to a family of proteins called the Major Sperm Proteins (MSPs) that is conserved in nematodes; msp-3 is similar in nucleotide sequence to the msp genes from the nematode Onchocerca volvulus; the msp gene family consists of closely related, small, basic proteins that make up 15% of sperm protein; this multigene family consists of over fifty genes, including many pseudogenes; MSPs are involved in both extracellular signaling and cytoskeletal functions during reproduction-MSP antagonizes Eph/ephrin signaling, in part, by binding VAB-1 Eph receptor tyrosine kinase on oocytes and sheath cells to promote oocyte maturation and MAPK activation; MSP proteins assemble into fibrous networks that drive movement of the C. elegans sperm; msp genes are expressed only in late primary spermatocytes.
WBGene00003431	msp-33	R05F9.8	Structural/MSP	Major Sperm Protein	msp-33 encodes a protein that belongs to a family of proteins called the Major Sperm Proteins (MSPs) that is conserved in nematodes; msp-33 has a C. briggsae homolog as predicted by the Wobble Aware Bulk Aligner (WABA); the MSP family consists of closely related, small, basic proteins that make up 15% of sperm protein; this multigene family consists of over fifty genes, including many pseudogenes; MSPs are involved in both extracellular signaling and cytoskeletal functions during reproduction-MSP antagonizes Eph/ephrin signaling, in part, by binding VAB-1 Eph receptor tyrosine kinase on oocytes and sheath cells to promote oocyte maturation and MAPK activation; MSPs assemble into fibrous networks that drive movement of the C. elegans sperm; msp genes are expressed only in late primary spermatocytes.
WBGene00003434	msp-38	K08F4.8	Structural/MSP	Major Sperm Protein	msp-38 encodes a member of the major sperm protein family; msp-38 has a C. briggsae homolog as predicted by the Wobble Bulk Aware Bulk Aligner (WABA).

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WBGene00003465	msp-78	T13F2.11	Structural/MSP	Major Sperm Protein	msp-78 encodes a protein that belongs to a family of proteins called the Major Sperm Proteins (MSPs) that is conserved in nematodes; this family consists of closely related, small, basic proteins that make up 15% of sperm protein; this multigene family consists of over fifty genes, including many pseudogenes; MSPs are involved in both extracellular signaling and cytoskeletal functions during reproduction-MSP antagonizes Eph/ephrin signaling, in part, by binding VAB-1 Eph receptor tyrosine kinase on oocytes and sheath cells to promote oocyte maturation and MAPK activation; MSPs assemble into fibrous networks that drive movement of the C. elegans sperm; msp genes are expressed only in late primary spermatocytes.
WBGene00022875		ZK1248.4	Structural/MSP	Major Sperm Protein	
WBGene00011134	ssp-33	R08A2.3	Structural/MSP	R08A2.3	
WBGene00006039	ssp-10	K07F5.9	Structural/MSP	Sperm-Specific family, class P	
WBGene00006047	ssp-19	C55C2.2	Structural/MSP	Sperm-Specific family, class P	ssp-19 encodes a member of the C. elegans sperm-specific protein (ssp) family; loss of ssp-19 function via RNAi has been reported to result in a moderate increase of fat content; in situ hybridization experiments detect ssp-19 mRNA in the spermatheca; the SSP-19 crystal structure has been determined and reveals monomer-monomer interactions between SSP-19 molecules to be strikingly different from equivalent interactions between MSP (major sperm protein) monomers.
WBGene00006048	ssp-31	ZK1225.6	Structural/MSP	Sperm-Specific family, class P	
WBGene00006049	ssp-32	F32B6.7	Structural/MSP	Sperm-Specific family, class P	
WBGene00013858	ssp-34	ZC168.6	Structural/MSP	Sperm-specific protein ZC168.6	
WBGene00009550		F38H4.6	Structural/MSP	Uncharacterized protein R05D3.5; Uncharacterized protein ZC262.1	

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		71/4007.0		Uncharacterized	
WBGene00014246		ZK1307.3	Structural/MSP	protein	
			_	ZK1307.3	
WBGene00013290		Y57G11A.2	Structural/MSP	Y57G11A.2	
WBGene00022884		ZK1248.17	Structural/MSP	ZK1248.17	
WBGene00022760		ZK546.3	Structural/MSP	ZK546.3	
WBGene00003425	msp-10	K07F5.2	Structural/MSP		msp-10 encodes a protein that belongs to a family of proteins called the Major Sperm Proteins (MSPs) that is conserved in nematodes; this family consists of closely related, small, basic proteins that make up 15% of sperm protein; this multigene family consists of over fifty genes, including many pseudogenes; MSPs are involved in both extracellular signaling and cytoskeletal functions during reproduction-MSP antagonizes Eph/ephrin signaling, in part, by binding VAB-1 Eph receptor tyrosine kinase on oocytes and sheath cells to promote oocyte maturation and MAPK activation; MSPs assemble into fibrous networks that drive movement of the C. elegans sperm; msp genes are expressed only in late primary spermatocytes.
WBGene00003429	msp-31	R05F9.13	Structural/MSP		msp-31 encodes a member of the major sperm protein family; msp-31 has a C. briggsae homolog as predicted by the Wobble Aware Bulk Aligner (WABA); expression is enriched in sperm.
WBGene00003438	msp-45	F58A6.8	Structural/MSP		msp-45 encodes a member of the major sperm protein family.

WBGene00003442	msp-49	C34F11.6	Structural/MSP	msp-49 encodes a protein that belongs to a family of proteins called the Major Sperm Proteins (MSPs) that is conserved in nematodes; this family consists of closely related, small, basic proteins that make up 15% of sperm protein; this multigene family consists of over fifty genes, including many pseudogenes; MSPs are involved in both extracellular signaling and cytoskeletal functions during reproduction-MSP antagonizes Eph/ephrin signaling, in part, by binding VAB-1 Eph receptor tyrosine kinase on oocytes and sheath cells to promote oocyte maturation and MAPK activation; MSPs assemble into fibrous networks that drive movement of the C. elegans sperm; msp genes are expressed only in late primary spermatocytes.
WBGene00003443	msp-50	C34F11.4	Structural/MSP	msp-50 encodes a protein that belongs to a family of proteins called the Major Sperm Proteins (MSPs) that is conserved in nematodes; this family consists of closely related, small, basic proteins that make up 15% of sperm protein; this multigene family consists of over fifty genes, including many pseudogenes; MSPs are involved in both extracellular signaling and cytoskeletal functions during reproduction-MSP antagonizes Eph/ephrin signaling, in part, by binding VAB-1 Eph receptor tyrosine kinase on oocytes and sheath cells to promote oocyte maturation and MAPK activation; MSPs assemble into fibrous networks that drive movement of the C. elegans sperm; msp genes are expressed only in late primary spermatocytes.

WBGene00003456	msp-63	K05F1.7	Structural/MSP	msp-63 encodes a protein that belongs to a family of proteins called the Major Sperm Proteins (MSPs) that is conserved in nematodes; this family consists of closely related, small, basic proteins that make up 15% of sperm protein; this multigene family consists of over fifty genes, including many pseudogenes; MSPs are involved in both extracellular signaling and cytoskeletal functions during reproduction-MSP antagonizes Eph/ephrin signaling, in part, by binding VAB-1 Eph receptor tyrosine kinase on oocytes and sheath cells to promote oocyte maturation and MAPK activation; MSPs assemble into fibrous networks that drive movement of the C. elegans sperm; msp genes are expressed only in late primary spermatocytes.
WBGene00003462	msp-74	F09C12.7	Structural/MSP	msp-74 encodes a protein that belongs to a family of proteins called the Major Sperm Proteins (MSPs) that is conserved in nematodes; this family consists of closely related, small, basic proteins that make up 15% of sperm protein; this multigene family consists of over fifty genes, including many pseudogenes; MSPs are involved in both extracellular signaling and cytoskeletal functions during reproduction-MSP antagonizes Eph/ephrin signaling, in part, by binding VAB-1 Eph receptor tyrosine kinase on oocytes and sheath cells to promote oocyte maturation and MAPK activation; MSPs assemble into fibrous networks that drive movement of the C. elegans sperm; msp genes are expressed only in late primary spermatocytes.

WBGene00003463	msp-76	ZK1251.6	Structural/MSP	msp-76 encodes a protein that belongs to a family of proteins called the Major Sperm Proteins (MSPs) that is conserved in nematodes; this family consists of closely related, small, basic proteins that make up 15% of sperm protein; this multigene family consists of over fifty genes, including many pseudogenes; MSPs are involved in both extracellular signaling and cytoskeletal functions during reproduction-MSP antagonizes Eph/ephrin signaling, in part, by binding VAB-1 Eph receptor tyrosine kinase on oocytes and sheath cells to promote oocyte maturation and MAPK activation; MSPs assemble into fibrous networks that drive movement of the C. elegans sperm; msp genes are expressed only in late primary spermatocytes.
WBGene00003464	msp-77	F32B6.6	Structural/MSP	msp-77 encodes a protein that belongs to a family of proteins called the Major Sperm Proteins (MSPs) that is conserved in nematodes; this family consists of closely related, small, basic proteins that make up 15% of sperm protein; this multigene family consists of over fifty genes, including many pseudogenes; MSPs are involved in both extracellular signaling and cytoskeletal functions during reproduction-MSP antagonizes Eph/ephrin signaling, in part, by binding VAB-1 Eph receptor tyrosine kinase on oocytes and sheath cells to promote oocyte maturation and MAPK activation; MSPs assemble into fibrous networks that drive movement of the C. elegans sperm; msp genes are expressed only in late primary spermatocytes.
WBGene00003466	msp-79	T13F2.10	Structural/MSP	msp-79 encodes a member of the major sperm protein family.

WBGene00003469	msp-142	K05F1.2	Structural/MSP	msp-142 encodes a protein that belongs to a family of proteins called the Major Sperm Proteins (MSPs) that is conserved in nematodes; this family consists of closely related, small, basic proteins that make up 15% of sperm protein; this multigene family consists of over fifty genes, including many pseudogenes; MSPs are involved in both extracellular signaling and cytoskeletal functions during reproduction-MSP antagonizes Eph/ephrin signaling, in part, by binding VAB-1 Eph receptor tyrosine kinase on oocytes and sheath cells to promote oocyte maturation and MAPK activation; MSPs assemble into fibrous networks that drive movement of the C. elegans sperm; msp genes are expressed only in late primary spermatocytes.
WBGene00003470	msp-152	ZK546.6	Structural/MSP	msp-152 encodes a protein that belongs to a family of proteins called the Major Sperm Proteins (MSPs) that is conserved in nematodes; this family consists of closely related, small, basic proteins that make up 15% of sperm protein; this multigene family consists of over fifty genes, including many pseudogenes; MSPs are involved in both extracellular signaling and cytoskeletal functions during reproduction-MSP antagonizes Eph/ephrin signaling, in part, by binding VAB-1 Eph receptor tyrosine kinase on oocytes and sheath cells to promote oocyte maturation and MAPK activation; MSPs assemble into fibrous networks that drive movement of the C. elegans sperm; msp genes are expressed only in late primary spermatocytes.
WBGene00000878	cyn-2	ZK520.5		cyn-2 is a predicted member of the cytosolic Cyclosporin A-binding cyclophilin family that is functional when expressed in E. coli.

WBGene00001424	fis-1	F41G3.4	fis-1 encodes a protein similar to the yeast and human Fis1 proteins involved in mitochondrial fission; fis-1 does not seem to be required for mitochondrial fission in C. elegans, but it is possible
			that it may function redundantly along with fis-2 and other genes; fis-1 expression is enriched in the germline.
WBGene00002227	klp-17	W02B12.7	klp-17 encodes a C-terminal kinesin motor protein orthologous to Drosophila NCD and Saccharomyces cerevisiae KAR3; by homology, KLP-17 is predicted to function as a minus-end directed motor; loss of klp-17 activity via RNAi results in embryonic lethality generally at the one- or two-cell stage with disorganized mitotic spindles and polyploid nuclei, suggesting that KLP-17 plays a role in chromosome segregation and germline development; in situ hybridization studies reveal that klp-17 mRNA is localized specifically to cell nuclei during early development, from the one-cell stage of embryogenesis until early larval stages; a klp-17::gfp transgene did not yield detectable GFP expression, but did result in a small percentage of morphologically abnormal males and intersexual animals that grew slowly and died upon reaching maturity, consistent with a role for klp-17 in chromosome dynamics.
WBGene00004964	spe-10	AC3.10	spe-10 encodes a DHHC-CRD family zinc-finger transmembrane protein with homologs in other eukaryotes and is predicted to be a palmitoyl transferase; spe-10 is required during spermatogenesis and thus for fertility; specifically, spe-10 is required for the proper biogenesis and functioning of specialized Golgi-derived fibrous body-membranous organelle (FB-MO) complexes during spermatid formation; spe-10 localizes to the FB-MOs of spermatids.

WBGene00004972	spe-26	R10H10.2		spe-26 encodes a Kelch motif-containing protein similar to the Drosophila proteins kelch and diablo and the Limulus (horseshoe crab) actin-bundling protein scruin; SPE-26 activity is required for several processes including embryogenesis, spermatogenesis, thermotolerance, and regulation of lifespan; SPE-26 mRNA is detected in spermatogonial cells and spermatocytes, but not in spermatids.
WBGene00005012		F26F4.2		F26F4.2 encodes a novel protein with high similarity to C. elegans F37A8.1 and C. briggsae CBG18186.
WBGene00006050	ssq-1	K07F5.11		
WBGene00006051	ssq-2	T28H11.5		
WBGene00006052	ssq-3	ZC477.1		
WBGene00006056	sss-1	F32B6.5		
WBGene00006057	sss-2	F47B8.11		
WBGene00006624	try-6	F48A9.3		
WBGene00007060	wht-6	T26A5.1		
WBGene00007080	sfxn-1.1	AH6.2		
WBGene00007081		AH6.3		
WBGene00007082	acs-10	AH10.1		
WBGene00007159		B0379.7		
WBGene00007190	rmd-3	B0491.3		
WBGene00007230		C01G10.1		
WBGene00007301		C04F12.7		
WBGene00007306		C04G2.5		
WBGene00007307		C04G2.8		
WBGene00007308		C04G2.9		
WBGene00007337		C05C12.5		

WBGene00007446	mboa-4	C08F8.4	mboa-4 encodes a putative transmembrane O-acyl transferase (MBOAT) orthologous to human MBOAT1 (OMIM:611732), and paralogous to C54G7.2 and ZK550.1; MBOA-4 has no obvious function in mass RNAi assays, and mboa-4(RNAi) animals incorporate exogenous arachidonic acid into phosphatidylcholine (PC), phosphatidylserine (PS) and phosphatidylethanolamine (PE) normally.
WBGene00007457		C08F11.10	
WBGene00007572		C14A6.8	
WBGene00007597		C15A11.2	
WBGene00007601		C15C6.2	
WBGCHCGGGG7GG1		C15C0.2	
WBGene00007631	wht-3	C16C10.12	wht-3 encodes an ATP-binding cassette (ABC) transporter; wht-3 activity is required for efficient RNA interference (RNAi) of a germline-expressed target, pop-1, as well as for normal pharyngeal and body morphology.
WBGene00007733		C25G4.6	
WBGene00007778		C27D8.2	
WBGene00007795		C28D4.8	
WBGene00007898		C33D9.3	
WBGene00007986		C36F7.5	
WBGene00007998		C38C6.5	
WBGene00008001		C38C10.3	
WBGene00008074	nkb-2	C43F9.6	
WBGene00008141		C47E8.1	
WBGene00008272		C53B4.2	
WBGene00008312		C54G4.2	
WBGene00008313		C54G4.3	
WBGene00008383		D1081.5	
WBGene00008541		F07A5.2	
WBGene00008590		F08H9.2	
WBGene00008651		F10D11.5	
WBGene00008660	clec-153	F10F2.8	
WBGene00008912		F17C8.7	
WBGene00008950	wht-5	F19B6.4	
WBGene00009028		F21H7.2	
WBGene00009043		F22B5.5	
WBGene00009075		F23B2.7	
WBGene00009143 WBGene00009149		F26A3.5	
		F26D2.10	
WBGene00009185	<u> </u>	F27C8.5	

WBGene00009313 F32B1.2 WBGene00009321 F32B4.2 WBGene00009324 F32H2.7 WBGene00009344 F32H2.7 WBGene0000946 F35H8.1 WBGene0000947 F35H8.1 WBGene0000948 F35H8.1 WBGene00009463 F360.14 WBGene00009471 F360.14 WBGene00009471 F360.15 WBGene0000959 F38H4.5 WBGene0000978 F340.7.1 WBGene0000978 F440.7.8 WBGene0000978 F440.7.8 WBGene00010014 F548.2 WBGene00010025 F54C8.1 WBGene00010035 F54C8.1 WBGene00010082 F55A11.11 WBGene00010082 F55A11.11 WBGene00010082 F55A11.11 WBGene00010083 F54C8.1 WBGene00010084 F55A11.11 WBGene00010085 F56F3.4 WBGene00010087 F55A11.11 WBGene0001088 F57AB.6 WBGene00010891 F57AB.6 WBGene0001081 F55AB.6	14/0.0		522444.2	T	
MSGene00009314					
WBGene0009344					
WBGene00009446					
WBGene0009449					
WBGene0009457					
WBGene0009458					
WBGene00009451					
WBGene00009471					
MBGene00009501					
WBGene00009549					
WBGene00090885 F44D12.8					
WBGene00009708 F.4463.7 Image: Company of the company					
WBGene00010124 F5483.2 F5483.2 WBGene00010035 F54C8.1 F55A11.11 encodes a member of the histidine phosphatase superfamily orthologous to Bombyx mori edysteroid phosphatase (EPP), human STS1 (DMIM:609201) and human UBASH3A (OMIM:609736); F55A11.11 activity encodes a member of the histidine phosphatase superfamily orthologous to Bombyx mori edysteroid phosphatase (EPP), human STS1 (DMIM:609201) and human UBASH3A (OMIM:609736); F55A11.11 activity, and thus is predicted to be catalytically inactive; F55A11.11s also paralogous to C. elapogous					
WBGene00010014 F5483.2 F54C8.1 F54C8.1 F54C8.1 F54C8.1 F54C8.1 F55A11.11 encodes a member of the histidine phosphatase superfamily orthologous to Bombyx mori ecdysteroid phosphate phosphatase (EPP), human STS1 (OMIM:609301) and human UBASH3A (OMIM:605736); F55A11.11 lacks the consensus sequence for phosphatase activity, and thus is predicted to be catalytic hactive; F55A11.11 activity via large-scale RNAi results in no obvious defects. WBGene00010155 F56F3.4 F55A11.11 activity via large-scale RNAi results in no obvious defects. WBGene00010181 F57A8.6 F57A8.6 F55A11.41 activity via large-scale RNAi results in no obvious defects. WBGene00010241 F58D2.2	WBGene00009708		F44G3.7		
WBGene00010035 F54C8.1 F55A11.11 encodes a member of the histidine phosphatase superfamily orthologous to Bombyx mori ecdysteroid phosphatae (EPP), human STS1 (DMIM:609201) and human UBASH3A (OMIM:605736); F55A11.11 lacks the consensus sequence for phosphatase activity, and thus is predicted to be catalytically inactive; F55A11.11 is also paralogous to C. elegans C52E4.7, F09C12.8, F53B6.7, and T07F12.1; loss of F55A11.11 activity via large-scale RNAi results in no obvious defects. WBGene00010155 F56F3.4 S53B6.7, and T07F12.1; loss of F55A11.11 activity via large-scale RNAi results in no obvious defects. WBGene00010241 F58D2.2 S53B6.7, and T07F12.1; loss of F55A1.11 activity via large-scale RNAi results in no obvious defects. WBGene00010373 H08M01.1 S08G00.1 WBGene00010466 K01D12.7 S08G00.1 WBGene00010510 ent-3 K02E11.1 WBGene00010574 K04H4.5 S08G0.1 WBGene00010651 K08C9.2 S08G0.1 WBGene00010651 K08C9.2 S08G0.1 WBGene00010651 K08C9.2 S08G0.1 WBGene00010652 K08F8.5 S08G0.1 WBGene00010682 K09E4.1 S09G1.2 WBGene00010719 K09E4.1 S09G1.2 WBGene0001082 M08B8.3	WBGene00009714		F44G4.5		
WBGene00010082 F55A11.11 F55A11.11 encodes a member of the histidine phosphatase superfamily orthologous to Bombyx mori ecdysteroid phosphata phosphatase (EPP), human STS1 (OMIM:60930); and human UBASH3A (OMIM:60936); F55A11.11 lacks the consensus sequence for phosphatase activity, and thus is predicted to be catalytically inactive; F55A11.11 is also paralogous to C. elegans CS24A; F09C12.8, F53B6.7, and T07F12.1; loss of F55A11.11 activity via large-scale RNAi results in no obvious defects. WBGene00010155 F56F3.4 ————————————————————————————————————	WBGene00010014		F54B3.2		
WBGene00010082 F55A11.11 wphosphatase superfamily orthologous to Bombyx mori ecdysteroid phosphatase (EPP), human STS1 (OMIM:609201) and human UBASH3A (OMIM:605736); F55A11.11 lacks the consensus sequence for phosphatase activity, and thus is predicted to be catalytically inactive; F55A11.11 is also paralogus to C. elegans C52F4.7; F09C12.8, F53B6.7, and T07F12.1; loss of F55A11.11 activity via large-scale RNAi results in no obvious defects. WBGene00010155 F56F3.4 — WBGene00010241 F58D2.2 — WBGene00010242 F58D2.2 — WBGene00010373 H08M01.1 — WBGene00010466 K01012.7 — WBGene000105010 ent-3 K02E11.1 — WBGene00010510 ent-3 K02E11.1 — WBGene00010574 K07A1.5 — WBGene00010651 K08C9.2 — WBGene00010651 K08C9.2 — WBGene00010651 K08C9.2 — WBGene00010652 K08F8.5 — WBGene00010729 K08F4.5 — WBGene00010729 K08F8.5 — WBGene00010729 K09E1.1 — WBGene00010729 <td< td=""><td>WBGene00010035</td><td></td><td>F54C8.1</td><td></td><td></td></td<>	WBGene00010035		F54C8.1		
WBGene00010181 F57A8.6 WBGene00010241 F58D2.2 WBGene00010373 H08M01.1 WBGene00010466 K01D12.7 WBGene00010510 ent-3 K02E11.1 WBGene00010563 K04G2.4 WBGene00010574 K04H4.5 WBGene00010612 K07A1.5 WBGene00010650 K08C9.1 WBGene00010651 K08C9.2 WBGene00010682 K08F4.5 WBGene00010719 K09E4.1 WBGene00010728 K09G1.2 WBGene00010829 M02B1.4 WBGene00010906 M88.3	WBGene00010082		F55A11.11		phosphatase superfamily orthologous to Bombyx mori ecdysteroid phosphate phosphatase (EPP), human STS1 (OMIM:609201) and human UBASH3A (OMIM:605736); F55A11.11 lacks the consensus sequence for phosphatase activity, and thus is predicted to be catalytically inactive; F55A11.11 is also paralogous to C. elegans C52E4.7, F09C12.8, F53B6.7, and T07F12.1; loss of F55A11.11 activity
WBGene00010241 F58D2.2 WBGene00010373 H08M01.1 WBGene00010466 K01D12.7 WBGene00010486 K01H12.4 WBGene00010510 ent-3 K02E11.1 WBGene00010563 K04G2.4 WBGene00010574 K04H4.5 WBGene00010612 K07A1.5 WBGene00010650 K08C9.1 WBGene00010651 K08C9.2 WBGene00010679 K08F4.5 WBGene00010719 K09E4.1 WBGene00010728 K09G1.2 WBGene00010829 M02B1.4 WBGene00010906 M88.3	WBGene00010155		F56F3.4		
WBGene00010373 H08M01.1 WBGene00010466 K01D12.7 WBGene00010510 K01H12.4 WBGene00010503 K04G2.4 WBGene00010574 K04H4.5 WBGene00010612 K07A1.5 WBGene00010650 K08C9.1 WBGene00010651 K08C9.2 WBGene00010679 K08F4.5 WBGene00010682 K08F8.5 WBGene00010719 K09E4.1 WBGene00010728 K09G1.2 WBGene00010829 M02B1.4 WBGene00010906 M88.3					
WBGene00010466 K01D12.7 WBGene00010486 K01H12.4 WBGene00010510 ent-3 K02E11.1 WBGene00010563 K04G2.4 WBGene00010574 K04H4.5 WBGene00010612 K07A1.5 WBGene00010650 K08C9.1 WBGene00010651 K08C9.2 WBGene00010679 K08F4.5 WBGene00010719 K09E4.1 WBGene00010728 K09G1.2 WBGene00010829 M02B1.4 WBGene00010906 M88.3					
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WBGene00010574 K04H4.5 WBGene00010612 K07A1.5 WBGene00010650 K08C9.1 WBGene00010651 K08C9.2 WBGene00010679 K08F4.5 WBGene00010682 K08F8.5 WBGene00010719 K09E4.1 WBGene00010728 K09G1.2 WBGene00010829 M02B1.4 WBGene00010906 M88.3		ent-3	K02E11.1		
WBGene00010612 K07A1.5 WBGene00010650 K08C9.1 WBGene00010651 K08C9.2 WBGene00010679 K08F4.5 WBGene00010682 K08F8.5 WBGene00010719 K09E4.1 WBGene00010728 K09G1.2 WBGene00010829 M02B1.4 WBGene00010906 M88.3	WBGene00010563		K04G2.4		
WBGene00010650 K08C9.1 WBGene00010651 K08C9.2 WBGene00010679 K08F4.5 WBGene00010682 K08F8.5 WBGene00010719 K09E4.1 WBGene00010728 K09G1.2 WBGene00010829 M02B1.4 WBGene00010906 M88.3	WBGene00010574		K04H4.5		
WBGene00010651 K08C9.2 WBGene00010679 K08F4.5 WBGene00010682 K08F8.5 WBGene00010719 K09E4.1 WBGene00010728 K09G1.2 WBGene00010829 M02B1.4 WBGene00010906 M88.3	WBGene00010612		K07A1.5		
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WBGene00010682 K08F8.5 WBGene00010719 K09E4.1 WBGene00010728 K09G1.2 WBGene00010829 M02B1.4 WBGene00010906 M88.3	WBGene00010651		K08C9.2		
WBGene00010719 K09E4.1 WBGene00010728 K09G1.2 WBGene00010829 M02B1.4 WBGene00010906 M88.3	WBGene00010679		K08F4.5		
WBGene00010728 K09G1.2 WBGene00010829 M02B1.4 WBGene00010906 M88.3	WBGene00010682		K08F8.5		
WBGene00010829 M02B1.4 WBGene00010906 M88.3	WBGene00010719		K09E4.1		
WBGene00010829 M02B1.4 WBGene00010906 M88.3	WBGene00010728		K09G1.2		
WBGene00010906 M88.3 M88.3	WBGene00010829				
WBGene00011120 R07E5.15	WBGene00010906				
	WBGene00011120		R07E5.15		

WBGene00011203		R10E4.7	
WBGene00011214		R10E9.2	
WBGene00011297		R102.10	
WBGene00011322	irld-14	T01C3.5	
WBGene00011460	ttr-14	T05A10.3	
WBGene00011491		T05F1.5	
WBGene00011669		T09F5.10	
WBGene00011790		T15H9.5	
WBGene00011795		T16A9.5	
WBGene00011910		T22B3.2	alg-3 encodes an Argonaute (AGO) protein that is a member of the AGO clade of Argonaute small RNA-binding proteins; together with its paralog, alg-4, alg-3 is required for normal brood sizes at elevated temperatures, specifically for the process of spermiogenesis in which spermatids are converted to mobile ameboid sperm; alg-3/4 is also required for accumulation of male germline-specific 26G-RNAs, suggesting that alg-3/4 mediate thermotolerant fertility via a 26G-RNA-mediated pathway; a GFP::ALG-3 rescuing fusion protein is expressed in germ cells during spermatogenesis and localizes to the cytoplasm and to P granules.
WBGene00011954		T23F11.2	
WBGene00011968		T23G11.1	
WBGene00012087		T27E7.1	
WBGene00012102		T27F6.1	
WBGene00012120		T28C6.5	
WBGene00012171		W01B6.4	
WBGene00012191		W02A2.8	
WBGene00012357		W09D6.4	
WBGene00012486		Y18D10A.21	
WBGene00012547		Y37D8A.5	
WBGene00012627		Y38H6C.15	
WBGene00012636		Y38H8A.2	
WBGene00012711		Y39E4A.1	
WBGene00012720		Y39E4B.11	
WBGene00012784		Y43C5A.4	
WBGene00012809		Y43F8A.2	
WBGene00012827		Y43F8C.5	
WBGene00012912		Y46G5A.22	
WBGene00012925	wht-8	Y47D3A.11	
WBGene00013052	scrm-7	Y50E8A.9	scrm-7 encodes a putative phospholipid scramblase homologous to human PLSCR1-5, and paralogous to other C. elegans SCRMs (e.g., SCRM-1); scrm-7(RNAi) animals have no obvious phenotype.

WBGene0001305 WpSGene00013175 Y53F48.36 WBGene00013175 Y53F48.36 WBGene00013103 Y54E2A.5 WBGene00013303 Y57G11C.5 WBGene00013303 Y57G11C.5 WBGene00013479 Y66D12A.3 WBGene00013479 Y66D12A.1 WBGene00013479 Y67A6A.1 WBGene00013474 Y59E1A.2 WBGene00013474 Y59E1A.2 WBGene00013526 Y73F8A.15 WBGene00013576 Y73F8A.15 WBGene00013576 Y73F8A.20 WBGene00013564 Y105G6A.4 WBGene00013664 Y105G6A.4 WBGene00013700 Y106G6D.3 WBGene00013700 Y106G6D.3 WBGene00013700 Y106G6D.3 WBGene00013700 Y106G6D.3 WBGene00013700 WBGene00013700 Y106G6D.3 WBGene0001370 Y106G6D.3 WBGene0001370 WBGene0001370 Y106G6D.3 Y106G6D.3 WBGene0001370 Y106G6D.3 Y1				1
WBGene00013175	WBGene00013053		Y50E8A.10	
WBGene00013190	-	mpz-6		
WBGene00013429	-		Y53F4B.36	
WBGene00013437				
WBGene00013437	WBGene00013303		Y57G11C.5	
WBGene00013449	WBGene00013429		Y66D12A.3	
WBGene000135724	WBGene00013437		Y66D12A.11	
WBGene00013524	WBGene00013449		Y67A6A.1	
WBGene00013526 Y73F8A.20 WBGene00013684 Y105E8A.27 WBGene00013696 Y106G6A.4 WBGene00013700 Y106G6D.3 WBGene00013712 dlc-6 WBGene00013712 dlc-6 WBGene00013712 dlc-6 WBGene00013723 Y106G6H.13 WBGene00013723 Y106G6H.13 WBGene00013725 Y116A8C.4 encodes a neprilysin; neprilysins are thermolysin-like zinc metallopeptidases, found on the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin tachykinin, insulin, antiurretic peptides) by cleaving them; Y116A8C.4 has no clear orthologs in other organisms. WBGene00013785 ZC376.8 WBGene00013866 ZC412.5 WBGene0001416 ZK858.2 WBGene00014175 ZK892.3 WBGene00014169 ZK945.6 WBGene00014179 ZK1010.5 WBGene00014197 ZK1010.5	WBGene00013474		Y69E1A.2	
WBGene00013684	WBGene00013524		Y73F8A.15	
WBGene00013700 Y106G6A.4 WBGene00013700 Y106G6D.3 WBGene00013712 dlc-6 V106G6G.3 dlc-6 WBGene00013712 dlc-6 V106G6G.3 dlc-6 WBGene00013723 V106G6H.13 WBGene00013723 Y116A8C.4 WBGene00013785 nep-23 Y116A8C.4 encodes a neprilysin; neprilysins are thermolysin-like zinc metallopeptidases, found or the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin tachykinin, insulin, and natriuretic peptides) by cleaving them; Y116A8C.4 has no clear orthologs in other organisms. WBGene00013879 ZC376.8 WBGene00013886 ZC412.5 WBGene00014116 ZK858.2 WBGene00014117 ZK892.3 WBGene00014144 ZK930.4 WBGene00014169 ZK945.6 WBGene00014179 ZK1010.5 WBGene00014179 ZK1053.2	WBGene00013526		Y73F8A.20	
WBGene00013700 Y106G6D.3 WBGene00013712 dlc-6 WBGene00013712 dlc-6 Y106G6G.3 dlc-6 WBGene00013712 dlc-6 Y106G6G.3 dlc-6 WBGene00013723 Y106G6H.13 WBGene00013723 Y106G6H.13 WBGene00013785 nep-23 Y116A8C.4 encodes a neprilysin; neprilysins are thermolysin-like zinc metallopeptidases, found or the outer surface of animal cells, that negatively regulate small signallyse smal	WBGene00013684		Y105E8A.27	
WBGene00013712 dlc-6	WBGene00013696		Y106G6A.4	
WBGene00013712 dlc-6 Y106G6G.3 is orthologous to human DYNLL1 (OMIM:601562) and DYNLL2 (OMIM:608942), but much more divergent from them than its paralog DLC-1; DLC-6's other paralogs are DLC-2/-5; DLC-6 has no obvious function in mass RNAi assays. WBGene00013723 Y106G6H.13 Y116A8C.4 encodes a neprilysin; neprilysins are thermolysin-like zinc metallopeptidases, found or the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin tachykinin, insulin, and natriuretic peptides) by cleaving them; Y116A8C.4 has no clear orthologs is other organisms. WBGene00013879 ZC376.8 WBGene00013886 ZC412.5 ZK265.3 WBGene00014116 ZK858.2 ZK892.3 WBGene00014116 ZK858.2 WBGene00014127 ZK892.3 WBGene00014154 ZK930.4 WBGene00014169 ZK945.6 WBGene00014179 ZK1010.5 WBGene00014179 ZK1010.5 WBGene00014177 ZK1010.5 WBGene00014179 ZK1010.5 WBGene00014177 ZK10	WBGene00013700		Y106G6D.3	
WBGene00013785 nep-23 Y116A8C.4 encodes a neprilysin; neprilysins are thermolysin-like zinc metallopeptidases, found or the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin tachykinin, insulin, and natriuretic peptides) by cleaving them; Y116A8C.4 has no clear orthologs in other organisms. WBGene00013879 ZC376.8 WBGene00013886 ZC412.5 WBGene00013956 ZK265.3 WBGene00014116 ZK858.2 WBGene00014116 ZK858.2 WBGene00014116 ZK892.3 WBGene00014154 ZK930.4 WBGene00014154 ZK930.4 WBGene00014168 ZK945.6 WBGene00014169 ZK945.7 WBGene00014179 ZK1010.5 WBGene00014179 ZK1010.5 WBGene00014179 ZK1010.5 WBGene00014179 ZK1053.2	WBGene00013712	dlc-6	Y106G6G.3	divergent from them than its paralog DLC-1; DLC-6's other paralogs are DLC-2/-5; DLC-6 has no
WBGene00013785 nep-23 Y116A8C.4 encodes a neprilysin; neprilysins are thermolysin-like zinc metallopeptidases, found or the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin tachykinin, insulin, and natriuretic peptides) by cleaving them; Y116A8C.4 has no clear orthologs in other organisms. WBGene00013879 ZC376.8 WBGene00013886 ZC412.5 WBGene00013956 ZK265.3 WBGene00014116 ZK858.2 WBGene00014116 ZK858.2 WBGene00014116 ZK892.3 WBGene00014154 ZK930.4 WBGene00014154 ZK930.4 WBGene00014168 ZK945.6 WBGene00014169 ZK945.7 WBGene00014179 ZK1010.5 WBGene00014179 ZK1010.5 WBGene00014179 ZK1010.5 WBGene00014179 ZK1053.2	WBGene00013723		Y106G6H.13	
WBGene00013886 ZC412.5 WBGene00013956 ZK265.3 WBGene00014116 ZK858.2 WBGene00014127 ZK892.3 WBGene00014154 ZK930.4 WBGene00014168 ZK945.6 WBGene00014169 ZK945.7 WBGene00014179 ZK1010.5 WBGene00014197 ZK1053.2		nep-23		thermolysin-like zinc metallopeptidases, found on the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin, tachykinin, insulin, and natriuretic peptides) by cleaving them; Y116A8C.4 has no clear orthologs in
WBGene00013956 ZK265.3 WBGene00014116 ZK858.2 WBGene00014127 ZK892.3 WBGene00014154 ZK930.4 WBGene00014168 ZK945.6 WBGene00014169 ZK945.7 WBGene00014179 ZK1010.5 WBGene00014197 ZK1053.2	-		ZC376.8	
WBGene00014116 ZK858.2 WBGene00014127 ZK892.3 WBGene00014154 ZK930.4 WBGene00014168 ZK945.6 WBGene00014169 ZK945.7 WBGene00014179 ZK1010.5 WBGene00014197 ZK1053.2	-		1	
WBGene00014127 ZK892.3 WBGene00014154 ZK930.4 WBGene00014168 ZK945.6 WBGene00014169 ZK945.7 WBGene00014179 ZK1010.5 WBGene00014197 ZK1053.2				
WBGene00014154 ZK930.4 WBGene00014168 ZK945.6 WBGene00014169 ZK945.7 WBGene00014179 ZK1010.5 WBGene00014197 ZK1053.2	WBGene00014116		ZK858.2	
WBGene00014168 ZK945.6 WBGene00014169 ZK945.7 WBGene00014179 ZK1010.5 WBGene00014197 ZK1053.2	WBGene00014127		ZK892.3	
WBGene00014169 ZK945.7 WBGene00014179 ZK1010.5 WBGene00014197 ZK1053.2	WBGene00014154		ZK930.4	
WBGene00014179 ZK1010.5 WBGene00014197 ZK1053.2	WBGene00014168		ZK945.6	
WBGene00014197 ZK1053.2	WBGene00014169		ZK945.7	
	WBGene00014179		ZK1010.5	
	WBGene00014197		ZK1053.2	
, ·· · · · - · - · - · - · - · · - · · ·	WBGene00014238		ZK1225.4	
WBGene00014241 ZK1251.3	-			

### B0207.11 encodes a nematode-specific protein probably required for a normally high ovulation rate; g0207.11 has no obvious pron-mematode homologs, but does have a putative N-terminal colled-cocil domain and an SH2 motif, and is is paralogous to four other C. elegans proteins (F4264.6, F4467.10, T08611.2, and Y81634.1); B0207.11(m322) hermaphrodites show abnormal egg-laying, retaining significantly fewer eggs than wild-type (perhaps due to a lowered ovulation rate) while retaining late-stage embryos; B0207.11 has no obvious phenotype in mass RNAI experiments, possibly because of genetic redundancy with its paralogs. #### WBGene00015091 ### WBGene00015097 ### B0273.1 ### WBGene00015097 ### B0273.1 ### WBGene00015292 ### WBGene00015454 ### WBGene00015455 ### C0275.2 ### WBGene00015467 ### B0261.6 ### WBGene00015467 ### B0261.6 ### WBGene00015467 ### B0273.1 ### C05D2.3 generally resembles aromatic-Lamino-acid/L-bistidine decarboxylases; however, its predicted protein sequence lacks six residues critical for AADC function. ### WBGene00015690 ### C10611.10 ### WBGene00015690 ### WBGene00015690 ### C10611.10 ### WBGene00015690 ### WBGene00015690 ### C10611.10 ### WBGene00015690 ### C10611.10 ### WBGene00015690 ### WBGene00015690 ### C10611.10 ### WBGene00015690 ### C29F5.3 encodes a cytidine deaminase; by homology the product of C29F5.3 is predicted to function in deamination of cytidine to uridine. #### WBGene00016288 ### WBGene00016288 ### WBGene00016281 ### WBGene00					
WBGene00015094 B0261.6	WBGene00015034		B0207.11		probably required for a normally high ovulation rate; B0207.11 has no obvious non-nematode homologs, but does have a putative N-terminal coiled-coil domain and an SH2 motif, and is is paralogous to four other C. elegans proteins (F42G4.6, F44F4.10, T08G11.2, and Y81G3A.1); B0207.11(tm322) hermaphrodites show abnormal egg-laying, retaining significantly fewer eggs than wild-type (perhaps due to a lowered ovulation rate) while retaining late-stage embryos; B0207.11 has no obvious phenotype in mass RNAi experiments, possibly because of genetic
WBGene00015094 B0261.6					
WBGene00015097 B0273.1 CO2F5.2					
WBGene00015192 B0432.11 B0524.2 MGene00015241 B0524.2 MGene00015345 C02F5.2 C02F5.5 C02F5.6 C02					
WBGene00015241 B0524.2 C02F5.2 WBGene00015345 C02F5.2 C02F5.2 WBGene00015348 C02F5.5 C05D2.3 generally resembles aromatic-L-amino-acid/L-histidine decarboxylases; however, its predicted protein sequence lacks six residues critical for AADC function. WBGene00015627 C09B9.2 Foreign of the predicted protein sequence lacks six residues critical for AADC function. WBGene00015689 C10G11.9 Foreign of the predicted protein sequence lacks six residues critical for AADC function. WBGene00015690 C10G11.10 Foreign of the predicted protein sequence lacks six residues critical for AADC function. WBGene00015691 C10G11.10 Foreign of the predicted protein sequence lacks six residues critical for AADC function. WBGene00015692 C10G11.10 Foreign of the predicted protein sequence lacks six residues critical for AADC function. WBGene00015921 C10G11.10 Foreign of the predicted protein sequence lacks six residues critical for AADC function. WBGene00016937 C17L1.1 Foreign of the predicted protein sequence lacks six residues critical for AADC function. WBGene00016938 C18G11.9 Foreign of the predicted protein sequence lacks six residues critical for AADC function. WBGene00016181 C29F5.3 C29F5.3 encodes a cytidine deaminase; by					
WBGene00015345 C02F5.5 WBGene00015467 basl-1 C05D2.3 WBGene00015627 C0989.2 WBGene00015689 C10G11.9 WBGene00015690 C10G11.10 WBGene00015890 C10G11.10 WBGene00015920 C14C11.1 WBGene00015937 C17H12.12 WBGene00015944 C18A3.7 WBGene00016987 C18G1.9 WBGene00016987 C18G1.9 WBGene00015987 C18G1.9 WBGene00016054 C24D10.2 WBGene00016054 C24D10.2 WBGene00016161 C27D6.3 WBGene00016181 C28C12.11 WBGene00016212 C29F5.3 WBGene00016221 C29F5.3 WBGene00016222 C32E8.4 WBGene00016351 C33F10.1					
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WBGene00015689 C10G11.9 ————————————————————————————————————	WBGene00015627		CO9R9 2	+	
WBGene00015690 C10G11.10 WBGene00015765 C14C11.1 WBGene00015820 C16A11.7 WBGene00015937 C17H12.12 WBGene00015944 C18A3.7 WBGene00015987 C18G1.9 WBGene00016054 C24D10.2 WBGene00016058 nspd-3 C24D10.7 WBGene00016101 C27D6.3 WBGene00016181 C28C12.11 WBGene00016212 C29F5.3 C29F5.3 encodes a cytidine deaminase; by homology the product of C29F5.3 is predicted to function in deamination of cytidine to uridine. WBGene00016228 C31H1.5 WBGene00016351 C33F10.1					
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WBGene00016322 C32E8.4 WBGene00016351 C33F10.1					homology the product of C29F5.3 is predicted to
WBGene00016351 C33F10.1 C33F10.1	WBGene00016288		C31H1.5		
	WBGene00016322		C32E8.4		
WBGene00016414 C34F11.2	WBGene00016351		C33F10.1		
	WBGene00016414		C34F11.2		

WBGene00016440	gipc-1	C35D10.2	
WBGene00016512		C38C3.3	
WBGene00016612		C43G2.3	
WBGene00016707		C46E10.1	
WBGene00016752		C48E7.7	
WBGene00016807		C50D2.3	
WBGene00016825		C50E10.1	
WBGene00016843		C50F7.3	
WBGene00016996		D1005.2	
WBGene00017026		D1037.5	D1037.5 encodes a phospholipase A2.
WBGene00017058		D2062.6	
WBGene00017112		E03H12.5	
WBGene00017175	irld-3	F02C9.4	
WBGene00017215		F07F6.1	
WBGene00017279		F09C12.8	F09C12.8 encodes an ortholog, predicted to be catalytically inactive, of Bombyx mori ecdysteroid phosphate phosphatase (EPP), human STS1 (OMIM:609201) and human UBASH3A (OMIM:605736); F09C12.8 is also paralogous to C. elegans C52E4.7, F53B6.7, F55A11.11, and T07F12.1.
WBGene00017384		F11G11.4	
WBGene00017386	nspd-5	F11G11.8	
WBGene00017387	mpst-4	F11G11.9	
WBGene00017542		F17E9.5	F17E9.5 encodes a novel protein conserved amongst nematodes.
WBGene00017550	nep-6	F18A12.1	F18A12.1 encodes a neprilysin; neprilysins are thermolysin-like zinc metallopeptidases, found on the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin, tachykinin, insulin, and natriuretic peptides) by cleaving them; F18A12.1 has no clear orthologs in other organisms.

WBGene00017553	nep-8	F18A12.4	thermol the out regulate tachyk	2.4 encodes a neprilysin; neprilysins are ysin-like zinc metallopeptidases, found on er surface of animal cells, that negatively small signalling peptides (e.g., enkephalin, inin, insulin, and natriuretic peptides) by them; F18A12.4 has no clear orthologs in other organisms.
WBGene00017851		F27C1.1		
WBGene00017853		F27C1.3		
WBGene00017902		F28E10.4		
WBGene00017910		F28H1.5		
WBGene00017955		F31E8.5		
WBGene00018000		F33D11.1		
WBGene00018001		F33D11.2		
WBGene00018081		F36A4.2		
WBGene00018083		F36A4.4		
WBGene00018087		F36D4.1		
WBGene00018120		F36H12.4		
WBGene00018125	rmd-4	F36H12.11		
WBGene00018134		F37A4.4		
WBGene00018158		F37E3.3		
WBGene00018163		F38A5.6		
WBGene00018196	nep-13	F39E9.4	thermol the out regulate tachyk	0.4 encodes a neprilysin; neprilysins are ysin-like zinc metallopeptidases, found on er surface of animal cells, that negatively small signalling peptides (e.g., enkephalin, inin, insulin, and natriuretic peptides) by g them; F39E9.4 has no clear orthologs in other organisms.
WBGene00018360	irld-8	F42G8.9		
WBGene00018497		F46F5.6		
WBGene00018548	clec-79	F47C12.4		
WBGene00018563		F47D12.7		
WBGene00018792		F54C1.8		
WBGene00018926		F56A11.6		
WBGene00018930		F56B3.6		
WBGene00019024		F58A6.5		
WBGene00019084		F59A6.2		
11 = 1 = 1.1.22232333	l .		<u> </u>	

WBGene00019151 pck-3 H04M03.1 mospheneologyruvate carboxykinase (PEPCK); by phosphoenologyruvate carboxykinase (PEPCK); by similarity, the products of MM03.1 are predicted to function in gluconeogenesis.					
WBGene00019260 H34/24.1 WBGene00019406 acdh-8 K05F1.3 WBGene00019430 K06A5.2 WBGene00019561 K09C6.7 WBGene00019785 M70.3 WBGene00020105 R148.7 WBGene00020105 R148.7 WBGene00020293 nep-20 T06D4.4 regulate small signalling peptidases, found on the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin, tachykinin, insulin, and natriuretic peptides) by cleaving them; T06D4.4 has no clear orthologs in other organisms. WBGene00020353 T08B6.4 WBGene00020414 T10E9.4 WBGene00020715 nspd.4 T23B3.5 WBGene00020715 nspd.4 T23B7.1 WBGene00020905 T28H11.7 WBGene00020940 W02D7.4 WBGene00020996 WBGene00020990 W03D8.3 WBGene00021010 W03G1.2	WBGene00019151	pck-3	H04M03.1	pho	encodes proteins with similarity to sphoenolpyruvate carboxykinase (PEPCK); by arity, the products of H04M03.1 are predicted
WBGene00019406 acdh-8 K05F1.3 WBGene00019430 K06A5.2 WBGene00019561 K09C6.7 WBGene00019785 M70.3 WBGene00019810 R01H2.2 WBGene0002015 R148.7 WBGene00020293 nep-20 T06D4.4 T06D4.4 encodes a neprilysin; neprilysins are thermolysin-like zinc metallopeptidases, found on the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin, tachykinin, insulin, and natriuretic peptides) by cleaving them; T06D4.4 has no clear orthologs in other organisms. WBGene00020353 T08B6.4 WBGene00020414 T10E9.4 WBGene00020713 T23B3.5 WBGene00020713 T23B3.5 WBGene00020715 nspd-4 T23B7.1 WBGene00020905 T28H11.7 WBGene00020940 W02D7.4 WBGene00020986 W03D8.3 WBGene00020100 W03D8.9 WBGene0002010 W03G1.2	WBGene00019255		H32C10.1		
WBGene00019430 K06A5.2 WBGene00019561 K09C6.7 WBGene00019785 M70.3 WBGene00019810 R01H2.2 WBGene00020105 R148.7 T06D4.4 encodes a neprilysin; neprilysins are thermolysin-like zinc metallopeptidases, found on the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin, tachykinin, insulin, and natriuretic peptides) by cleaving them; T06D4.4 has no clear orthologs in other organisms. WBGene00020353 T08B6.4 WBGene00020414 T10E9.4 WBGene00020713 T23B3.5 WBGene00020715 nspd-4 WBGene00020905 T28H11.7 WBGene00020986 W03D8.3 WBGene00020900 W03D8.3 WBGene00020100 W03B8.9 WBGene0002010 W03G1.2	WBGene00019260		H34I24.1		
WBGene00019561 K09C6.7 WBGene00019785 M70.3 WBGene00019810 R01H2.2 WBGene00020105 R148.7 WBGene00020105 R148.7 WBGene00020293 nep-20 T06D4.4 T06D4.4 encodes a neprilysin; neprilysins are thermolysin-like zinc metallopeptidases, found on the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin, tachykinin, insulin, and natriuretic peptides) by cleaving them; T06D4.4 has no clear orthologs in other organisms. WBGene00020353 T08B6.4 WBGene00020533 T16A1.2 WBGene00020713 T23B3.5 WBGene00020715 nspd-4 T23B7.1 WBGene00020905 T28H11.7 WBGene00020940 W02D7.4 WBGene00020990 W03D8.9 WBGene00020110 W03G1.2	WBGene00019406	acdh-8	K05F1.3		
WBGene00019785 M70.3 WBGene00019810 R01H2.2 WBGene00020105 R148.7 WBGene00020293 nep-20 T06D4.4 T06D4.4 encodes a neprilysin; neprilysins are thermolysin-like zinc metallopeptidases, found on the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin, tachykinin, insulin, and natriuretic peptides) by cleaving them; T06D4.4 has no clear orthologs in other organisms. WBGene00020353 T08B6.4 WBGene00020414 T10E9.4 WBGene00020713 T23B3.5 WBGene00020715 nspd-4 T23B7.1 WBGene00020905 T28H11.7 WBGene00020940 W02D7.4 WBGene00020990 W03D8.3 WBGene00020910 W03D8.9 WBGene000201010 W03G1.2	WBGene00019430		K06A5.2		
WBGene00019810 R01H2.2 WBGene00020105 R148.7 WBGene00020293 nep-20 T06D4.4 T06D4.4 encodes a neprilysin; neprilysins are thermolysin-like zinc metallopeptidases, found on the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin, tachykinin, insulin, and natriuretic peptides) by cleaving them; T06D4.4 has no clear orthologs in other organisms. WBGene00020353 T08B6.4 WBGene00020414 T10E9.4 WBGene00020533 T16A1.2 WBGene00020713 T23B3.5 WBGene00020715 nspd-4 T23B7.1 WBGene00020905 T28H11.7 WBGene00020940 W02D7.4 WBGene00020990 W03D8.3 WBGene00020100 W0308.9 WBGene00021010 W03G1.2	WBGene00019561		K09C6.7		
WBGene00020105 R148.7 WBGene00020293 nep-20 T06D4.4 mep-20 T06D4.4 mep-20 T06D4.4 the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin, tachykinin, insulin, and natriuretic peptides) by cleaving them; T06D4.4 has no clear orthologs in other organisms. WBGene00020353 T08B6.4 WBGene00020533 T16A1.2 WBGene00020715 r23B3.5 WBGene00020715 nspd-4 T23B7.1 WBGene00020905 T28H11.7 WBGene00020940 W02D7.4 WBGene00020986 W03D8.3 WBGene00020990 W03D8.9 WBGene00021010 W03G1.2	WBGene00019785		M70.3		
### T06D4.4 encodes a neprilysin; neprilysins are thermolysin-like zinc metallopeptidases, found on the outer surface of animal cells, that negatively regulate small signalling peptides (e.g., enkephalin, tachykinin, insulin, and natriuretic peptides) by cleaving them; T06D4.4 has no clear orthologs in other organisms. ##################################	WBGene00019810		R01H2.2		
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WBGene00020414 T10E9.4 WBGene00020533 T16A1.2 WBGene00020713 T23B3.5 WBGene00020715 nspd-4 T23B7.1 WBGene00020905 T28H11.7 WBGene00020940 W02D7.4 WBGene00020996 W03D8.3 WBGene00020990 W03D8.9 WBGene00021010 W03G1.2	WBGene00020293	nep-20	T06D4.4	ther the regul tac	molysin-like zinc metallopeptidases, found on outer surface of animal cells, that negatively ate small signalling peptides (e.g., enkephalin, hykinin, insulin, and natriuretic peptides) by ving them; T06D4.4 has no clear orthologs in
WBGene00020533 T16A1.2 WBGene00020713 T23B3.5 WBGene00020715 nspd-4 T23B7.1 WBGene00020905 T28H11.7 WBGene00020940 W02D7.4 WBGene00020986 W03D8.3 WBGene00020990 W03D8.9 WBGene00021010 W03G1.2	WBGene00020353		T08B6.4		
WBGene00020713 T23B3.5 WBGene00020715 nspd-4 T23B7.1 WBGene00020905 T28H11.7 WBGene00020940 W02D7.4 WBGene00020986 W03D8.3 WBGene00020990 W03D8.9 WBGene00021010 W03G1.2			T10E9.4		
WBGene00020715 nspd-4 T23B7.1 WBGene00020905 T28H11.7 WBGene00020940 W02D7.4 WBGene00020986 W03D8.3 WBGene00020990 W03D8.9 WBGene00021010 W03G1.2			T16A1.2		
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WBGene00021388 Y38C1AA.7					
WBGene00021398 Y38C1AA.7 WBGene00021472 Y39G10AR.16					
WBGene00021472 Y39G10AR.16 WBGene00021579 clec-73 Y46C8AL.1		clec-72			
WBGene00021373 Clet-73 140C8AL.1 WBGene00021608 Y46H3D.1		CIEC-/3			
WBGene00021008 1401130.1 WBGene00021633 Y47G6A.3					
WBGene00021650 Y47G6A.26					
WBGene00021720 Y49F6B.8					
WBGene00021787 Y51H7C.9					
WBGene00021878 Y54G2A.13					
WBGene00021880 Y54G2A.15					
WBGene00021969 Y57G7A.6	WBGene00021969				
	WBGene00021996		Y59E9AL.6		
WBGene00021996 Y59E9AL.6	WBGene00022162		Y71G12B.27		

WBGene00022288		Y75B7B.1	
WBGene00022385		Y95B8A.4	
WBGene00022467		Y119C1B.1	
WBGene00022407		ZC155.2	
WBGene00022550		ZK84.2	
	+ - 40		
WBGene00022689	math-48	ZK250.6	
WBGene00022700		ZK353.4	
WBGene00022761		ZK546.4	
WBGene00022771		ZK616.1	
WBGene00022849	acs-6	ZK1127.2	
WBGene00023424		C53D6.10	
WBGene00044674		B0280.17	
WBGene00044684		T08G11.2	T08G11.2 encodes a nematode-specific sperm protein, required for a normally high ovulation rate, that interacts with EGL-32; despite not being EGL-32, and although T08G11.2 (tm336) complements egl-32 (n155), T08G11.2 can partially rescue egl-32 mutants when expressed transgenically, implying that T08G11.2 can be a nonorthologous replacement for EGL-32 function in vivo; T08G11.2 has an SH2 motif, but this motif lacks a critical arginine residue; T08G11.2 has no obvious non-nematode homologs, but is paralogous to four other C. elegans proteins (B0207.11, F42G4.6, F44F4.10, and Y81G3A.1); T08G11.2(tm336) hermaphrodites have a lowered ovulation rate (and thus a lowered rate of egg-laying), retaining significantly fewer eggs than wild-type, yet also retaining late-stage embryos; T08G11.2 has no obvious phenotype in mass RNAi experiments, possibly because of genetic redundancy with its paralogs; T08G11.2 expression is strongly enriched in spermatogenesis.
WBGene00045306		ZC250.5	
WBGene00045484		F34D10.9	