

Additional file 2. Alignment of *D. japonica* and *S. mediterranea* PIWI2

D. japonica PIWI2 [EST: Dj_CL0040_001_b2]

S. mediterranea PIWI2 [Swiss-Prot: Q2Q5Y8]

Protein Alignment

Identical rate of amino acids = 93.6%

Identical and homologous substitution rate of amino acids = 98.4%

			20		40		60		
PIWI2_DUGJA	M-----AK	LE	TNGSEN	RG	R-GNRGGLRR	TFRIVEPNLQ	PAEII	EKTGN IGRTVKLQSN 52	
PIWI2_SCHMD	MEEIPVKVAK	LE	ANGSET	RG	KMGNGRGLRG	TFRIVEPNLQ	PADITE	EKTGN IGRTVKLQSN 60	
			80		100		120		
PIWI2_DUGJA	FTKFSVLRSE	KFMMYDSVF	T	QVG	IPPVKVKL	QFIVRVCQEN	RLPGAF	CFDG RRLFTSEKWH 112	
PIWI2_SCHMD	FTKFSVLRSE	KFMMYDSVFS		QVGL	SPKVKL	QFIVRVCQEN	KLPGAF	CFDG RRLFTSEKWH 120	
			140		160		180		
PIWI2_DUGJA	GESDIQEF	TY	DD	KKMTLRLV	ATILPETEEY	YQMINVLLNN	LQIMM	GQERI GKGYFLSPNI 172	
PIWI2_SCHMD	GESDIQEF	SH	DE	KKMTLRLV	STILPETEEY	YQMINVLLNN	LQVML	GQERI GKGYFLSPNI 180	
			200		220		240		
PIWI2_DUGJA	TKDEVPRNSG	PTFFETNSFK	VLGGFG	TTLQ	RGTKPTGELT	TLLYIERINR	VLNDNS	VMKKA 232	
PIWI2_SCHMD	TKDEVPRNSG	PTFFETNSFK	VLGGFG	TTLQ	RGTKPTGELT	TLLYIERINR	VLNDNS	VMKKA 240	
			260		280		300		
PIWI2_DUGJA	YNRRSIDQLI	GRDII	TKYNN	KTYRI	SEIKE	MSVDEK	FEMS	GRTLSYAEY KDRYNIRLSQ 292	
PIWI2_SCHMD	YNRRSIDQLI	GRDII	TKYNN	KTYRI	SEIKE	MNVDEK	FEMG	GRTLSYAEY KERYNIRLTQ 300	
			320		340		360		
PIWI2_DUGJA	GDQPFVLTRV	KKPMR	RERK	PG	EEDKEKDK	EKEKEKEKEA	PQDKDM	TLNI PGELCFLCGF 352	
PIWI2_SCHMD	GDQPFVLTRV	KKPMR	RERK	KD	EEGVEK--	-----EKEKEA	PEEKDM	TLNI PGELCFLCGF 354	
			380		400		420		
PIWI2_DUGJA	SDQEKSNDL	QKSL	GSVLKR	EPRER	LDDIP	AFCNWI	KSSD	NANGMCNKWQ LKIENKPLEI 412	
PIWI2_SCHMD	SDQEKSNDL	QKNL	GSVLKR	EPRER	LDDIP	AYCNWI	KNSD	AATGMCNKWQ LKIDNKPLEI 414	
			440		460		480		
PIWI2_DUGJA	EGRELPPCDV	ISGNN	KINEK	IP	DDWKFRV	QFDIKRDRKH	EIDVVI	DRN DFQYKNFMSD 472	
PIWI2_SCHMD	EGRELPPCDV	ISGGS	KINEK	MG	DDWKFRV	QFDIKRDRKH	EIDVVI	DRN DFQYKNFMND 474	
			500		520		540		
PIWI2_DUGJA	VEQELRNMRI	DARVGK	VNTC	GPND	VERCLN	DAARSG	SGCA	KMALVFVPDD RVYAKVKSFT 532	
PIWI2_SCHMD	VEQELRNMRI	DARVGK	VNTC	GPND	VERCLN	DAARSG	SGCA	KMALVFVPDD RVYAKVKSFT 534	
			560		580		600		
PIWI2_DUGJA	MSTGLLTQCV	TTRNGT	NRND	KRRKV	VSNKT	VMQIFAK	FGY	DPWTVEIKLR PTMIVGMDTY 592	
PIWI2_SCHMD	MSTGLLTQCV	TTRNGT	NRND	KRRKV	VSSKT	VMQIFAK	FGY	DPWTVEIKLR PTMIVGMDTY 594	
			620		640		660		
PIWI2_DUGJA	HNKSSKKS	IQ	ASVFS	INSTF	TQYMSFV	NQ-	PKGRQE	FHET LGKNFNLALE DFKKRYDILP 651	
PIWI2_SCHMD	HNKSSKKS	IQ	ASVFS	INSTF	TQYMSFV	VNS	PKGRQE	FHET LGKNFNLALE DFKKRYDILP 654	
			680		700		720		
PIWI2_DUGJA	QRILVFRDGV	GDNQL	QFTKN	FEVDAM	KPLI	ENIYK	SNGFP	VPQIIYVIVK KRVGTKLFNR 711	
PIWI2_SCHMD	QRILVFRDGV	GDNQL	QFTKN	FEVDAM	KPLI	ENIYK	GNGFP	VPQIIYVIVK KRVGTKLFNR 714	
			740		760		780		
PIWI2_DUGJA	GNNPNPGTVV	DKEIV	KPNFY	EFFLVS	QRRT	KGTATPT	NYN	VLEDTRLLTK KGTMDPMAPN 771	
PIWI2_SCHMD	GNNPNPGTVV	DKEIV	KPNFY	EFFLVS	QRRT	KGTATPT	NYN	VLEDTRLLTK KGTMDPMAPN 774	
			800		820				
PIWI2_DUGJA	ELQKITYALT	HLFY	NWMTI	RVPVP	VHYAH	RLAELV	GKVH	KGN	SPAVINE RIRNRLFYL 830
PIWI2_SCHMD	ELQKITYALT	HLFY	NWMTI	RVPVP	VHYAH	RLAELV	GKVH	KGS	NPVAINE RIRNRLFYL 833

Nucleotide Alignment

Identical rate of nucleotides = 79.7%

			20		40		60	
PIWI2_DUGJA	ATG-----	-----	-----GCTAAG	TTAGAAACGA	ATGGCAGTGA	AAATAGAGGA	39	
PIWI2_SCHMD	ATGGAGGAAA	TACCAGTAAA	AGTAGCTAAA	CTTGAAGCGA	ATGGAAGTGA	AAACAAGAGGT	60	
			80		100		120	
PIWI2_DUGJA	AGA--GGAA	ATCGCGGTGG	CTTACGTAGA	ACTTTCAGAA	TCGTAGAGCC	CAATCTCAA	96	
PIWI2_SCHMD	AAAATGGGAA	ATCGTGGTGG	CCTGAGAGGA	ACATTAGAA	TTGTTGAACC	TAACCTTGCAA	120	
			140		160		180	
PIWI2_DUGJA	CCGGCTGAAA	TTATAGAAA	AACTGGAAAC	ATAGGTAGAA	CCGTCAAACT	TCAATCCAAT	156	
PIWI2_SCHMD	CTTGCTGATA	TCACTGAGAA	AACAGGAAAC	ATAGGAAGAA	CAGTTAAATT	ACAATCCAAT	180	
			200		220		240	
PIWI2_DUGJA	TTACCAAAT	TTTCTGTGT	ACGATCCGAA	AAATTCATGA	TGTATGATTC	TGTTTTTACA	216	
PIWI2_SCHMD	TTTACCAAAT	TTTCTGTTTT	CGGTTTCAGAA	AAGTTCATGA	TGTATGATTC	CGTGTTTTCT	240	
			260		280		300	
PIWI2_DUGJA	CAAGTTGGAA	TTCCACCAAAA	AGTCAAACCTC	CAATTTATTG	TTAGAGTTTG	CCAAGAAAAT	276	
PIWI2_SCHMD	CAAGTTGGTT	TGTCACCCAA	AGTAAAATTA	CAGTTTATTG	TTCGAGTCTG	CCAAGAAAAT	300	
			320		340		360	
PIWI2_DUGJA	AGGTTACCTG	GAGCTTTTTG	TTTCGATGGA	AGACGATTGT	TTACAAGTGA	GAAGTGGCAT	336	
PIWI2_SCHMD	AAATTGCCAG	GGCTTTTTTG	TTTTGATGGA	AGACGTCTAT	TTACTAGTGA	AAAATGGCAT	360	
			380		400		420	
PIWI2_DUGJA	GGCGAATCTG	ATATTCAAGA	GTTTACCTAC	GACGATAAAA	AAATGACCTT	ACGATTAGTT	396	
PIWI2_SCHMD	GGAGAATCGG	ACATTCAAGA	ATTTAGTCAT	GATGAAAAAA	AAATGACACT	AAGATTGGTA	420	
			440		460		480	
PIWI2_DUGJA	GCGACCATTTC	TTCCAGAAAC	AGAAGAATAT	TATCAAATGA	TAAACGTCTT	ATTGAACAAC	456	
PIWI2_SCHMD	TCAACTATCC	TTCCTGAAAC	TGAAGAATAT	TACCAAATGA	TCAATGTATT	ACTCAATAAT	480	
			500		520		540	
PIWI2_DUGJA	TTACAAATAA	TGATGGGCCA	AGAGCGAATT	GGAAAAGGTT	ACTTTTTAAG	TCCCAATATA	516	
PIWI2_SCHMD	TTACAAGTAA	TGTTAGGTCA	AGAAGAATT	GGTAAAGGTT	ATTTTTTAAG	CCCAATATT	540	
			560		580		600	
PIWI2_DUGJA	ACAAAAGACG	AAGTTCCCTCG	CAATAGTGGT	CCGACATTCT	TTGAAACGAA	TAGTTTTAAA	576	
PIWI2_SCHMD	ACAAAAGATG	AAGTTCCCCG	AAATTCCTGA	CCGACATTTT	TTGAAACCAA	TAGTTTTAAA	600	
			620		640		660	
PIWI2_DUGJA	GTATTAGGAG	GATTTGGTAC	GACACTACAG	AGAGGCACAA	AGCCTACTGG	GGAACCTAACG	636	
PIWI2_SCHMD	GTCTTGGGG	GCTTTGGTAC	AACTTTACAA	AGAGGCACAA	AACCAACTGG	TGAATTAACG	660	
			680		700		720	
PIWI2_DUGJA	ACATTGCTCT	ACATTGAGAG	AATCAACAGA	GTTCTAAATG	ATAATTTCAGT	CATGAAAGCC	696	
PIWI2_SCHMD	ACTCTTTTAT	ATATTGAGCG	TATTAACAGA	GTATTAACCG	ATAACTCTGT	TATGAAGGCA	720	
			740		760		780	
PIWI2_DUGJA	TATAATCGTC	GAAGTATTGA	TCAATTAATC	GGACGAGACA	TTATAACCAA	ATACAACAAC	756	
PIWI2_SCHMD	TACAACAGAA	GAAGTATTGA	TCAGTTGATA	GGCAGAGATA	TCATAACAAA	ATATAATAAC	780	
			800		820		840	
PIWI2_DUGJA	AAGACCTATA	GAAATTTCCGA	AATTAAGAA	ATGAGCGTAG	ATGAGAAATT	TGAAATGTCA	816	
PIWI2_SCHMD	AAAACITATA	GGATAAGTGA	AATTAAGAA	ATGAAACGTAG	ATGAGAAATT	TGAAATGGGT	840	
			860		880		900	
PIWI2_DUGJA	GGAAGAACAT	TATCTTATGC	CGAATATTTT	AAAGATCGAT	ATAACATTTCG	ATTATCTCAA	876	
PIWI2_SCHMD	GGTAGAACIT	TATCGTATGC	CGAATATTTT	AAGGAACGAT	ATAATATTTCG	ATTAACCTCAA	900	
			920		940		960	
PIWI2_DUGJA	GGTGACCAAC	CATTTGTATT	GACAAGAGTT	AAAAAACCAA	TGCGCCGTGA	GAGAAGAAAG	936	
PIWI2_SCHMD	GGCGATCAAC	CATTTGTCTT	AACGCGAGTG	AAGAAACCAA	TGCGTCGAGA	AAGAAAGAAA	960	
			980		1,000		1,020	
PIWI2_DUGJA	CCAGGAGAAG	AAGACAAAAG	AAAGGATAAA	GAGAAAGAAA	AAGAGAAAGA	GAAAGAAGCC	996	
PIWI2_SCHMD	AAAGACGAAG	AAGGAGTGA	AAAA-----	-----	--GAGAAAGA	AAAAGAGGCT	1002	
			1,040		1,060		1,080	
PIWI2_DUGJA	CCTCAGGATA	AAGATATGAC	ATTGAATATT	CCTGGAGAA	TGTGTTTCTT	ATGTGGATT	1056	
PIWI2_SCHMD	CCAGAAGAGA	AGGACATGAC	TCTCAATATT	CCTGGAGAG	TGTGTTTCTT	ATGTGGGTT	1062	
			1,100		1,120		1,140	
PIWI2_DUGJA	TCAGATCAAG	AAAAATCTAA	TATGGATCTC	CAAAAGAGCT	TAGGAAGTGT	ATTAATAAAGA	1116	
PIWI2_SCHMD	TCAGATCAAG	AGAAATCGAA	TATGGATCTG	CAGAAGAATT	TAGGTTGTGT	TTTAATAAAGA	1122	
			1,160		1,180		1,200	
PIWI2_DUGJA	GAGCCACGTG	AAAGACTTGA	TGACATTCTT	GCATTCTGCA	ATTGGATTAA	AAGTAGCGAT	1176	
PIWI2_SCHMD	GAGCCACGTG	AAAGATTGGA	TGATATACCA	GCTTATTGTA	ACTGGATTAA	AAATAGTGAT	1182	
			1,220		1,240		1,260	
PIWI2_DUGJA	AATGCTAATG	GAATGTGCAA	TAAGTGGCAA	TTAAAGATTG	AAAAATAACC	CCTCGAAATT	1236	
PIWI2_SCHMD	GCGGCAACTG	GAATGTGCAA	TAAATGGCAG	CTGAAAATAG	ATAACAAACC	ATTAGAAATC	1242	
			1,280		1,300		1,320	
PIWI2_DUGJA	GAGGGCAGGG	AGTTGCCGCC	ATGTGATGTT	ATTAGCGGTA	ATAATAAAAT	CAACGAGAAG	1296	
PIWI2_SCHMD	GAAGGTAGAG	AAATTAACCTCC	ATGCGATGTA	ATAAGTGGTG	GCAGCAAAAT	TAATGAAAAA	1302	

		1,340		1,360		1,380	
PIWI2_DUGJA	ATTCCTGATG	ATTGAAAATT	TGGAAGAGTT	CAGTTTGATA	TAAAAAGAGA	CCGTAAACAT	1356
PIWI2_SCHMD	ATGGGAGATG	ATTGAAAATT	TGGTCGAGTT	CAATTTGATA	TTAAGCGTGA	TCGTAAAGCAT	1362
		1,400		1,420		1,440	
PIWI2_DUGJA	GAAATGATG	TAGTTATCGT	CGATAGAAAT	GATTTCCAGT	ATAAAAATTT	CATGAGTGAC	1416
PIWI2_SCHMD	GAAATCGATG	TGGTCATCGT	TGATCGAAAT	GACTTTCAGT	ATAAAAATTT	TATGAATGAT	1422
		1,460		1,480		1,500	
PIWI2_DUGJA	GTAGAGCAAG	AATTGAGAAA	CATGCGAATT	GATGCAAGAG	TTGGTAAAGT	AAATACATGT	1476
PIWI2_SCHMD	GTGGACAAG	AATTGAGAAA	CATGAGAATT	GATGTCGAG	TTGGAAGGT	TAATACTTGT	1482
		1,520		1,540		1,560	
PIWI2_DUGJA	GGTCCAAATG	ACGTTGAAAG	ATGTCTAAAT	GATGCAGCAA	GAAGTGGGAG	TGGATGTGCC	1536
PIWI2_SCHMD	GGTCCAAATG	ATGTTGAAAG	ATGTTTGAAT	GATGCCGCTA	GAAGTGGGAG	TGGGTGTGCT	1542
		1,580		1,600		1,620	
PIWI2_DUGJA	AAAATGGCAT	TAGTTTTTGT	ACCGGATGAC	CGAGTTTATG	CTAAAGTTAA	ATCTTTCACC	1596
PIWI2_SCHMD	AAAATGGCGC	TGGTATTCGT	CCCAGATGAT	AGAGTATATG	CCAAGGTGAA	ATCATTTACC	1602
		1,640		1,660		1,680	
PIWI2_DUGJA	ATGAGTACTG	GTCTTTTAAC	ACAATGCGTG	ACAACCAGAA	ATGGGACCAA	CAGAAACGAT	1656
PIWI2_SCHMD	ATGAGTACTG	GTCTTTTAAC	CCAATGTGTA	ACAACACGTA	ATGGTACTAA	TAGAAACGAT	1662
		1,700		1,720		1,740	
PIWI2_DUGJA	AAACGCAGAA	AAGTCGTTTC	CAATAAACT	GTATGCAAAA	TATTTGCAAA	ATTTGGATAC	1716
PIWI2_SCHMD	AAACGAAGAA	AGGTGGTTTC	AAGTAAAACC	GTGATGCAAA	TATTTGCAAA	ATTCGGATAT	1722
		1,760		1,780		1,800	
PIWI2_DUGJA	GACCCATGGA	CTGTGAAAT	TAAATTACGA	CCAACATGTA	TTGTTGGCAT	GGACACCTAC	1776
PIWI2_SCHMD	GATCCATGGA	CAGTTGAAAT	TAAATTGAGA	CCAACATGTA	TTGTCGGTAT	GGATACCTAT	1782
		1,820		1,840		1,860	
PIWI2_DUGJA	CATAACAAGT	CTAGTAAAAA	GTC AATTCAA	GCATCTGTAT	TCTCGATAAA	CAGTACATTT	1836
PIWI2_SCHMD	CATAACAAGT	CCAGCAAGAA	ATCAATTCAA	GCATCTGTAT	TTTCGATCAA	CAGCACATTT	1842
		1,880		1,900		1,920	
PIWI2_DUGJA	ACGCAATATA	TGAGTTTCGT	AAATCAA--	CCTAAAGGTC	GACAAGAATT	TCATGAAACC	1893
PIWI2_SCHMD	ACACAATATA	TGAGCTTTGT	TGTTAATTCT	CCTAAAGGAC	GTCAAGGAATT	CCACGAAACT	1902
		1,940		1,960		1,980	
PIWI2_DUGJA	TTAGGTAAAA	ATTTTAATTT	GGCTTTAGAA	GATTTCAAGA	AAAGATACGA	TATTTTGCCG	1953
PIWI2_SCHMD	TTAGGCAAAA	ATTTCAATTT	AGCGTTAGAA	GATTTCAAGA	AACGTTATGA	CATATTTGCC	1962
		2,000		2,020		2,040	
PIWI2_DUGJA	CAAAGAATTT	TAGTATTTTG	AGATGGTGT	GGTGACAATC	AGTTGCAATT	TACAAAGAAT	2013
PIWI2_SCHMD	CAGCGAATTT	TAGTCTTTAG	AGATGGTGT	GGAGATAACC	AAC TTCAATT	TACTAAAAAT	2022
		2,060		2,080		2,100	
PIWI2_DUGJA	TTTGAGGTAG	ATGCTATGAA	ACCATTGATT	GAAAATATTT	ATAAAAAGTAA	CGGTTTCCCG	2073
PIWI2_SCHMD	TTTGAAGTTG	ATGCAATGAA	ACCGCTTATT	GAAAATATAT	ACAAAAGGCAA	CGGATTCCCT	2082
		2,120		2,140		2,160	
PIWI2_DUGJA	GTCCCAAAA	TTATCTACGT	CATCGTTAAG	AAAAGAGTGG	GGACTAAACT	ATTCAACCGA	2133
PIWI2_SCHMD	GTCCACAAA	TCAATTTATG	CATCGTAAAG	AAAAGAGTGG	GGACTAAAGT	TTTCAACAGA	2142
		2,180		2,200		2,220	
PIWI2_DUGJA	GGCAACAATC	CAAAATCCAGG	AACAGTTGTC	GATAAAGAAA	TAGTGAAACC	GAAC TTTTAC	2193
PIWI2_SCHMD	GGAAATAATC	CAAAATCC TGG	AACTGTTGTC	GATAAAGAAA	TTGTCAAACC	GAATTTCTAT	2202
		2,240		2,260		2,280	
PIWI2_DUGJA	GAGTTTTTCT	TGGTTTCACA	AAGAACAACG	AAAGGAACAG	CAACAACCAC	TAATTATAAT	2253
PIWI2_SCHMD	GAATTTTTCC	TAGTTTCACA	AAGAACAACG	AAAGGAAC TG	CAACTCCAAC	TAATTATAAT	2262
		2,300		2,320		2,340	
PIWI2_DUGJA	GTTTTGGAAG	CACTCGATT	GTTGACTAAA	AAAGGAACAA	TGGATCCCAT	GGCTCCTAAT	2313
PIWI2_SCHMD	GTTTTAGAAG	ATACTCGATT	GCTAACGAAA	AAAGGTACTA	TGGATCCTAT	GGCACCGAAT	2322
		2,360		2,380		2,400	
PIWI2_DUGJA	GAACTGCAAA	AAATTACTTA	CGCACTAACT	CATTTATATT	TCAATTGGAT	GGGTACAATT	2373
PIWI2_SCHMD	GAGCTGCAAA	AGATTACTTA	TGCTCTAACT	CATTTATATT	TCAATTGGAT	GGGAAC TATC	2382
		2,420		2,440		2,460	
PIWI2_DUGJA	CGTGTACCTG	TCCCTGTGCA	TTACGCACAT	CGATTGGCAG	AGTTAGTGGG	AAAAGTTCAC	2433
PIWI2_SCHMD	CGAGTTCGGG	TTCCAGTGCA	TTATGCGCAT	AGATTGGCTG	AATTAGTTGG	AAAGGTGCAT	2442
		2,480		2,500		2,520	
PIWI2_DUGJA	AAAGGAAATA	GTCC TGCTGT	AATCAATGAA	AGAATCAGGA	ACAGGCTTTT	CTATTTATAA	2493
PIWI2_SCHMD	AAGGGCTCTA	ATCCCGTTGC	CATTAATGAA	AGAATAAGAA	ATAGGCTCTT	CTATTTATAA	2502