

Program: water
Rundate: Sun Nov 18 2005 18:02:38
Align_format: srspair
Report_file: fly.water
#####

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Aligned_sequences: 2
1: Fly
2: Human
Matrix: EBLOSUM62
Gap_penalty: 10.0
Extend_penalty: 0.5

Length: 2031
Identity: 612/2031 (30.1%)
Similarity: 965/2031 (47.5%)
Gaps: 180/2031 (8.9%)
Score: 2497.0

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fly exon 4 and human Dscam homolog (exon 2), with Uniprot predicted Ig-like C2-type 1 underlined, and InterProScan predicted Fly IG PF00047.14 domain underlined

fly exon 6 and human homologous region (exon 4), with Uniprot predicted Ig-like C2-type 2 and InterProScan fly predicted IG PF00047.14 underlined

fly exon 9 and human homolog (exon 8), with Uniprot predicted Ig-like C2-type 1 underlined, and InterProScan fly predicted IG PF00047.14 underlined

fly exon 17 and human homolog (exon 26), with Human Dscam Uniprot predicted transmembrane domain underlined, and InterProScan fly predicted transmembrane domain underlined

Fly	41	FLKEPTNRIDFSNSTGAEIECKASGNPMPEIIWIRSDGTAVGDVPGLRQI	90
		:.....: ::: : :: : :	
Human	12	FVNASLQEVVFASTTGTLVPCPAAGIPPVTLRWYLATGEEIYDVP GIRHV	61
Fly	91	SSDGKLVFPPFRAEDYRQEVHAQVYACLARNQFGSIISR DVHVRAVVAQY	140
		..::....: :: :: : :..	
Human	62	HPNGTLQIFPFPSSFSTLIHDNTYYCTAENPSGKIRSQDVHIKAVLREP	111
Fly	141	YEADV NKEHVIRGNSAVIKCLIPSFVADFVEVVS WHTDEEENYFPGA EYD	190
		:..: . . : :..: :.. :	
Human	112	YTVRVEDQKTMRGNAVAVFKCIIPSSVEAYITVVSWEKD-TVSLVSGS---	157

Fly	240	GKYLVLPSGELHIREVGPEDGYKS YQCR TKHRLTGETRLSATKGRLVIT <u>E</u>	240
Human	205	-RFLITSTGALYIKDVQNEDGLYNRYCITRHRYTG ET RQS-NSARL FVSD	205
Fly	288	PVSSSPPKINALTYKPNIVESMAS--TAILCPAQGYPA SFRWYKFIEGT	288
Human	246	PANSAPSILDGF DHR--- KAMAGQRVELPCKALGHPEPDYWRLK ----	246
Fly	338	TRKQAVVLNDRVKOVSGTLIIKD AVVEDS GKYLCVVNNSVGGSVETVLT	338
Human	295	-DNMPLELSGRFQKTVTGLLIENIRPSDGSYSVCEVS NRYGTAKVIGRLY	295
Fly	388	VTAPLSAKIDPPTQTVD FGRPAVF TCQYTGNPIKTVSWMKDGKAIGHSEP	388
Human	345	VKQPLKATISPRKVKSSVG SQVSLSCSV TGTEDQELSWYRNGEILNP GKN	345
Fly	429	V-----LRIESVKKEDKGM YQC FVRNDQESAEASAECLKGGRFDP P	429
Human	393	VRITGINHENLIMDHMVKSDGGAYQCFVRKDKL SAQDYVQVVL--EDGTP	393
Fly	479	VIRQAFQEETMEPGPSVFLKC VAGGN PTPEISWELD GKKIANN DRYQVGQ	479
Human	443	KIISAFSEKVVSPAEPVSLMCNVKG TPLPTITWT LDDDPILKGGSHRISQ	443
Fly	529	YVTVNGDVVS YLNITS VHANDGGLYKCI A SKVGV A EHS A KLNVYG L PYI	529
Human	493	MITSEG N VSYLNISSSQVRDGGVYRCTAN S AGVVL Y QARINVRGPASI	493
Fly	578	RQMEKKAIVAGETLIVTCPVAGYPIDSIVWERDNRALPINRKQKVFP-NG	578
Human	543	RPMKNITAIAGRDTYIHCRVIGYPYYSIKWK NSNLLPFNH RQVAFENNG	543
Fly	628	TLIIENVERN SDQATY TCVAKNQEGYSARG SLEVQMVPPOQLPF SFGES	628
Human	593	TLKLSDVQKEVDEGEYTCNVLVQPQLSTSQSVHVTVK VPPFIQPF EFPRF	593
Fly	678	AADVGDIASANC V PKGDLPLEIRWSLNSAPIVNGENGFTLVRLNKRTSL	678
Human	639	S--IGORVEIPCVV VSGDLPTITWQKDGRPI-PGSLGVTIDNID-FTSS	639
Fly	728	LNIDSLNAFH R GVYKCIATNPAGTSEYVAELQVN V PPRWILEPTDKAFAQ	728
Human	689	LRISNL SLMHNGNY TCIARN EAAAVEHQSQLIVRV PPKFVVQPRDQDIY	689
Fly	777	GSDAKVECKADGF PKPQ VTWKKAVGDT P GEYKDLK KSDNI RV-E E GPLHV	777
Human	739	GKAVILNC SAE GYPVPTIW KFSKGAGV POFOPIALNGRIOVLSNGSLLI	739

Fly	778	DNIQKTNEGYYLCEAINGIGSGLSAVIMISVQAPPEFTEKLRNQ TARRGE	827
		 : . . : : : : : : :	
Human	740	KHVVEEDSGYYLCKVSNVDVGADVSKSMYLTVKIPAMITSYPNTT LATQGG	789
Fly	828	PAVLQCEAKGEKPIGILWNMNMRLDPKNDNRYTIREEILSTGVMSSLSI	877
		... : . . . : : : . . : : : .	
Human	790	KKEMSCTAHGEKPIIVRWEKEDRIINPEM-ARYLVSTKEVGEEVISTLQI	838
Fly	878	KRTERSDSALFTCVATNAFGSDDASINMIVQEVPEMPYALKVLDKSGRSV	927
		 : . . : : : . . : : . . : : : :	
Human	839	LPTVREDSGFFSCHAINS YGEDRGIIQLTVQEPPDPP-EIEIKDVKARTI	887
Fly	928	QLSWAQPYDGN SPLDRYIIIEFKRSRASWSEIDRV-IVPGHTTEAQVQKLS	976
		 : : : . . . :	
Human	888	TLRWTMGFDGN SPITGYDIECKNKSDSWDSAQRTKDVSPQLNSATIIDIH	937
Fly	977	PATTYNIRIVAENAIGTSQSSEAVTIITAE EAPSGKPQNIKVEPVNQTTM	1026
		: : : : . : . . : . . . : : : : :	
Human	938	PSSTYSIRMYAKNRIGKSEPSNELTITADEAAPDGPPQEVHLEPISSQSI	987
Fly	1027	RVTWKPPP RTEWNGEILGYVGYKLSNTNSSYVFETINFITEEGKEHNLE	1076
		. . : : : . . : : . . :	
Human	988	RVTWKAPKKHLQNGIIRGYQIGYREYSTGGNFQFNIIS-VDTSGDSEVYT	1036
Fly	1077	LQNLRVYTQYSVVIQAFNKIGAGPLSEEEKQFTAEGTPSQPPSDTACTTL	1126
		. . . : . : . : . . . : :	
Human	1037	LDNLNKFTQYGLVVQACNRAGTGPSSQEIIITTTLEDVPSYPPE NVQAIAT	1086
Fly	1127	TSQTIRVGWVSPPLESANGVIKTYKV VYAPS--DEWYDETKRHYKKTASS	1174
		: : : . : . . : . . : . : : : : : : : . :	
Human	1087	SPESISISWSTLSKEALNGILQGFRVIYWANLMDGELGEIKN--ITTTQP	1134
Fly	1175	DTVLHGLKKYTN YTMQVLATTAGGDGVR SVPIHCQTEPDVPEAPT DVKAL	1224
		 : : : : :	
Human	1135	SLELDGLEKYTNYSIQVLAFTTRAGDGRSEQIFTRTKEDVPGPPAGVKAA	1184
Fly	1225	VMGNAAILVSWRPPAQPNGIITQYTVYSKAEGAETETKTQKVPHYQMSFE	1274
		... : . : . : . . . : . : : : : : : : :	
Human	1185	AASASMVFVSWLPPLKLNGIIRKYTVFC SHPYPTVISEFEASPD-SFSYR	1233
Fly	1275	ATELEKNKPYEFWV TASTTIGEGQQSKSIVAMP SDQVPAKIASFDDTFTA	1324
		 : : : : : : . : . . .	
Human	1234	IPNLSRNRQYSVWVAVTSAGRGNSSEIITVEPLAKAPARILTFSGTVTT	1283
Fly	1325	TFKEDAKMPCLAVGAPQPEITW--KIKGVE--FSANDRM RVLDPDGSLLIK	1370
		: : : . . : : : : : : : :	
Human	1284	PWMKDIVLPCKAVGDPSPAVKWMKDSNGT PSLVTIDGRSIFSNGSFIIR	1333

[illegible]

Fly	1918	RNPGNGSPEPP-----PPPPRNHDMNSSSFND SKESN-----	1949
		. . : : . . :	
Human	1879	HRPGDLIHLPPYL RMDFL LNRGGP GTSRDLS LGQACLEP QKSRTLKRPTV	1928
Fly	1950	-----EISEAECD RDHGPRGNYGA VKRSPQ	1974
		. . :	
Human	1929	LEPIPM EAASSASSTREGQS WQP GAVATLPQ	1959

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