

RS5555\_Locus\_10591\_isoform\_1  
RS5527\_scaffold251-parc\_tblastn  
RS5522\_scaffold260-EXSNAP2012.13  
RS2333\_Contig1-snap.329  
RS2333\_Contig44-snap.18\_RACE  
RS5134\_Contig44-snap.18\_RACE  
RS5522\_scaffold1181-EXSNAP2012.3  
RS2333\_Contig24-snap.126  
RS5527\_scaffold\_5-parc\_aug2013-1

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RS5527\_scaffold251-parc\_tblastn  
RS5522\_scaffold260-EXSNAP2012.13  
RS2333\_Contig1-snap.329  
RS2333\_Contig44-snap.18\_RACE  
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RS5527\_scaffold\_5-parc\_aug2013-1

-----LRMSLTPTVTERKQIALLLLAGEQYDCYK-HLLNDDRAEEMNTFQVFNRI  
MSPRHCLSSSICFSPDAFDRRIISLLIVAGEQFEFVKRVVLGADSK--DTIYSAIHARQ  
MSSRLCLSSSISFSPDVFDRRIALLLIVAGEQFEFVKSVLGVDSK--DTIYSAIDLARR  
MSSRHWPSSIRYSPDAFDRRIALLLIVAGEQFEFVKSVLGDSSK--DTIYSAIDLARR  
MSSRHWPFSIRYSPDAFDRRIALLLIVAGEQFEFVKSVLGVDSK--DTIYSAIDLARR  
MSSRHWPFSIRYSPDAFDRRIALLLIVAGEQFEFVKSVLGDSSK--DTIYSAIDLARR  
MASR-TVSVVTRVSPDADERQIALLMLTGQQFDEFKLLLSNSKIHFNENVFTAANTLRR  
MASR-TNSRVTRVAPNAHERQVIALMLTGQQFDEFKILLFTNPKHHVENVFTAANTLQK  
MASR-AISCLTHVSPTAYDRQLIALLMLTGQQFDEFKLLLYNMNS--ETVFTAANTLQK  
:\* . :\*. \*\*:::\*\*\*: : \* : : . . .

YGRLSQFVQPKNRPLVLSLALNYERQLAKLGRSLGRLEVSQVSDV-----CKSDY  
CLTNADYVPESQWPLVIQIVRCFQSQFEKLKISIGEEKVDDYAGLQSNELVNSRISMDKY  
FLATADYVPESQWPFVIQIVRCYQSHFEKLKISIGEEKVDDYAGLQSSQLFNSRISMDMY  
FLATADYVPESQWPLVIQIIRCYQSQFEKLIRSIGEEKVDDYAGLQSNELFNSRISMDKY  
YLATADYVPESQWPLVIQIIRCYQSQFEKLIRSIGEEKVDDYAGLQSNELFNSRISMDKY  
YLATADYVPESQWPLVIQIIRCYQSQFEKLIRSIGEEKVDDYAGLQSNELFNSRISMDKY  
YLSRADYVPPNERCLVMEIALMYESQLKLLIAEIGESVNSIEEI--NDIYDQ--TYEKH  
YLALADCVPCKRCMVMEIALMYESQLKLLIAELGESVMSIEEI--NYVNEQ--TREYR  
YLALADYVPSNKRCLVMEIALLYESQFKLLISELGESVVESEIEI--NDVNDQ--TREKY  
: \* . . : \* : : : \* \* . : \* : : . . .

GKLNWKFRIETPPMTTIFHD--RIPMVKQSLGEIVLAKAIQCFTESNLPS-VPIPPQK  
LVKKS----VQVGFITTFPPAIRRPFQKVD-EFLVKKSVVDIISQPNLKV-IETLPIIT  
F-----VQVGFITTFPPAIRRPFQKAD-AFLIKKS-VDVLSQLNPKV-IESQPIA  
S-----VQIGDFITTFPPAIRRPFQKVD-AFLIKKS-VDLLSEPNLKV-IESQTNVA  
S-----VQIGDFITTFPPAIRRPFQKVD-AFLIKKS-VDLLSEPNLKV-IESQAIAS  
S-----VQIGDFITTFPPAIRRPFQKVE-AFLIKKS-VDLLSEPNLKV-IESQAIAS  
QNRNW----VKCKLMHTIFRTGSRKPIEKGTLSYLALKSAMLALSQPNKVMVLIDDE  
LNRNW----AVECNMHTIFRTGSRKPIEKGTLSYLTLKSAALALSQPNHEE-FELIDEQ  
LNRNW----AKECNMHTIFRTGSRKPIEKGSLSYLALESVAVFALSQPNYEE-FVLIDEQ  
: \* \* \* \* : . : : \* . .

DSNRKEDPCYGNRKRIFPSRKRRLSMVELEAPCAKRAARHEDTDEAREMSN--NDWIME  
KIQASEE-PALLSRPQMRFARPRRISMSP IYETFEKGL--KTIKEADFEENNFNDEL TN  
KIQSTEE-PVLLSRPQLRFARPRRISMSP IYETCEKGLFFKTIKVEADFEENNFNDEL TN  
KPQATEE-PALLFRPQRFARPRRISMSP IYETCEKGLFFKTIKVEADFEENNFNDEL TN  
KPQATEE-PALLSRPQRFARPRRISMSP IYETCEKGLFFKTIKVEADFEENNLYDEL TN  
KPQATEE-PALLSRPQRFARPRRISMSP IYETCEKGLFFKTIKVEADFEENNLYDEL TN  
PWNTHKKEPTLPTVPIINPPKRRYSMVSTEEFASKRLRTEADKEAMRAVAEENFYVGD  
TWSQKKEPTLPTAPIINPPKRRYSMVSTEEFVVKRLRTEADKEAMRAMAVEDNTYVHD  
AWYSHKKEPTLPTVPIINPPKRRCSMI STEEFAAKRLRTNAEKAMRALADEDN SHIHD  
: \* \* . \* \* \* \* \* . : : . .

DEA--FIDYEIDQFKDYC--RNSDVP IIERWLCSRSLR-----IHGTETHPCESRI  
NIAFQFDQHEVSEFT-FC--EKTAVPAKERFDCSSALFDWN----YTHNGGSHYCCRQSA  
NVA--FQDHEVTEFA-FC--EKINASARERFICASALFDCN----YTHNGGSHHDCRQSA  
NIA--FQDHEVTEIA-FC--EKINASARERFSCASDLFDCI----YTDNGGSHYDC----  
NVA--FKDHEVTEFA-FC--EKINASARERFSCASALFDCI----YTDNGGSHYDCRQSA  
NIA--FKDHEVTEFA-FC--EKINASARERFSCASALFDCI----YTDNGGSHYDCRQSA  
DIA--FEETIVPQFIHYCRAHTKYASNAERWACSRNLNRNHLTRNEEADESAIHEKCLEET  
DIA--FEETILPRFIHYCRADTAETSNGERHN-----  
DIA--FEETIMPRFIHYCRTDAKSDASNGERWACSRNLNRNHLTRNEEVANESEIHEKCLEEDT  
: \* \* : : : \* . . \* \*

RNDRSSEPDMSYVALKQR-PAKFSREFDPVLP SRHRSSFFH-  
MDRKA-TIENSGRIDGK-STK--REFEFVTKQIKVMYLHE  
MDRKTWKCDSH-----  
-----LCKSHFHIV-----VYLSQLKIVADCSE  
MDRKA-SSENSR I IDGK-STK--REFEFINKHMKVMYLHE  
MDRKA-SSENSR I IDGK-STK--REFEFINKHMKVMYLHE  
FNDQSYFLAIRSSQKQSK-VLS-----  
-----  
MRDRSYFLAIRSSQVKNRYNQFYREFWPIVPFENSSNLV-

Multiple sequence alignment (MUSCLE (3.8)) of *Pristionchus* and *Parapristionchus* dau-1 homologs.