

CLUSTAL 2.0.12 MULTIPLE SEQUENCE ALIGNMENT

File: C:/Program Files/ClustalX2/protein-homo/20125.ps
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Sequence alignment block 1 (residues 1-150) with accession numbers (gi|195972866|ref|NP_000412.3|) and a conservation plot below.

Sequence alignment block 2 (residues 160-300) with accession numbers and a conservation plot below.

Sequence alignment block 3 (residues 310-450) with accession numbers and a conservation plot below.

Sequence alignment block 4 (residues 460-600) with accession numbers and a conservation plot below.

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gi|195972866|ref|NP_000412.3|      GGYGGGSSS-GGHKSSS-----GGSVGESSSKGPRY----- 584
gi|114667511|ref|XP_001169499.1|  GGYGGGSSS-GGHKSSS-----GGSVGESSSKGPRY----- 577
gi|61740600|ref|NP_001013443.1|  GGYGGGSSS-GGHKSSS-----GGSVGESSSKGPRY----- 568
gi|194685481|ref|XP_001788780.1|  GGHGGGSSS-GGHKSTI-----TGSVGESSSKGPRSAEISWDINKTRVIKTIIEELAPDGRVLSMVESETKKHYV 566
gi|27805977|ref|NP_776802.1|     GGHGGGSSS-GGHKSTI-----TGSVGESSSKGPRY----- 526
gi|112983636|ref|NP_034790.2|     SSSGGQGGG-GGFKSS-----GGGQSSSKGPRY----- 561
gi|57012436|ref|NP_001008804.1|   KTIIEEVTP-EGRVLS-----SMIESETKKHFY----- 526
gi|118102987|ref|XP_001235182.1|   -SGGGRISGG-----VSSSHSYSSSSQSQSCRGGGESQGYGRKSFV----- 604
gi|118102989|ref|XP_418163.2|     HSQSGSCEPFGDAENLKLCLLEGNKILERGATMREVSSEATKILRERKASGPDSISND----- 593
.....610.....620.....630.....640.....650.....660.....670.....680.

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