<html><head><style type="text/css"></style></head><body>CLUSTAL 2.1 multiple sequence alignment

| humanARSA<br>mouseARSA<br>zebrafishARSA | -MSMGAPRSLLLALAAGLAVARPPNIVLIFADDLGYGDLGCYGHPSSTTPNLDQLAAGGL -MALGTLFLALAAGLSTASPPNILLIFADDLGYGDLGSYGHPSSTTPNLDQLAEGGL MMDLMRIIALCALIAAHCVGASPPNFVLLFADDLGYGDLGCFGHPCSLTPNLDRLAANGL *: :* :** * ***::*:*******************                     | 56                |
|---|--|-------------------|
| humanARSA<br>mouseARSA<br>zebrafishARSA | RFTDFYVPVSLCTPSRAALLTGRLPVRMGMYPGVLVPSSRGGLPLEEVTVAEVLAARGYL<br>RFTDFYVPVSLCTPSRAALLTGRLPVRSGMYPGVLGPSSQGGLPLEEVTLAEVLAARGYL<br>RFTDFYVTSPVCSPSRAALLTGRYQTRSGIYPGVLYPGSRGGLPLNETTIAEVLKTQGYS<br>******:*:******* .* *:****** ::**              | 119<br>116<br>120 |
| humanARSA<br>mouseARSA<br>zebrafishARSA | TGMAGKWHLGVGPEGAFLPPHQGFHRFLGIPYSHDQGPCQNLTCFPPATPCDGGCDQGLV TGMAGKWHLGVGPEGAFLPPHQGFHRFLGIPYSHDQGPCQNLTCFPPDIPCKGGCDQGLV TAIVGKWHLGVGLNGTYLPTRHGFDSYLGIPYSHDQGPCQNLSCFPPDVKCFGLCDQGVV *.:.******  | 179<br>176<br>180 |
| humanARSA<br>mouseARSA<br>zebrafishARSA | PIPLLANLSVEAQPPWLPGLEARYMAFAHDLMADAQRQDRPFFLYYASHHTHYPQFSGQS PIPLLANLTVEAQPPWLPGLEARYVSFSRDLMADAQRQGRPFFLYYASHHTHYPQFSGQS TVPLLFNEIIKQQPADFLQLEKAYGEFASQFISDSVKDNRPFFLYYPSHHTHYPQYAGAD .:*** * :: **. : ** * :::::*: ::.********               | 239<br>236<br>240 |
| humanARSA<br>mouseARSA<br>zebrafishARSA | FAERSGRGPFGDSLMELDAAVGTLMTAIGDLGLLEETLVIFTADNGPETMRMSRGGCSGL<br>FTKRSGRGPFGDSLMELDGAVGALMTTVGDLGLLEETLVIFTADNGPELMRMSNGGCSGL<br>YAGKSPRGPFGDALMEFDGTVGKILQTLEETGVINNTLIFFTGDSGPELMRKSRGGNAGL<br>:: :* ******:**:**:**:**:**:**:**:**           |                   |
| humanARSA<br>mouseARSA<br>zebrafishARSA | LRCGKGTTYEGGVREPALAFWPGHIAPGVTHELASSLDLLPTLAALAGAPLPNVTLDGFD LRCGKGTTFEGGVREPALVYWPGHITPGVTHELASSLDLLPTLAALTGAPLPNVTLDGVD MKCGKGTTYEGGMREPAIAHWPGFIKPGVTRALASSLDILPTFAKLAGAPLPEVQLDGVE ::*****:**:***:***:***:***:***:***:***                  | 359<br>356<br>360 |
| humanARSA<br>mouseARSA<br>zebrafishARSA | LSPLLLGTGKSPRQSLFFYPSYPDEVRGVFAVRTGKYKAHFFTQGSAHSDTTADPACHAS ISPLLLGTGKSPRKSVFFYPPYPDEIHGVFAVRNGKYKAHFFTQGSAHSDTTSDPACHAA MTDILFNLGPSKRQTMFYYPTDPSVKYGVFAVRWENFKAHYYTRGAAHSESTPDNSCSLL :: :*: * * * *:::*:*: * : * : *:*:*:*:*                 | 416               |
| humanARSA<br>mouseARSA<br>zebrafishARSA | SSLTAHEPPLLYDLSKDPGENYNLLGGVAGATPEVLQALKQLQLLKAQLDAAVTFGPSQV<br>NRLTAHEPPLLYDLSQDPGENYNVLESIEGVSPEALQALKHIQLLKAQYDAAMTFGPSQI<br>AFLKYHDPPLLFNLETDPSENYNLDGDQWDAVRKQIQAVKQQFEASMVFGESQI<br>*. *:****::*. **.**** : * :.:: *::* : * :** ******** | 476               |
| humanARSA<br>mouseARSA<br>zebrafishARSA | ARGEDPALQICCHPGCTPRPACCHCPDPHA 509 AKGEDPALQICCQPSCTPHPVCCHCPGSQS 506 SKGIDSLLEPCCIPNCRPKPECCRCNSAL- 503 ::* *. *: ** *.* *:*  |                   |
|   |  |                   |