```
Aurora B    MAQKENSYPWPYGRQTAPSG-------------------LSTLPQRVLR----KEPVTPS 37
Aurora C    ----------------------------------------MSSPRAVVQ----LGKAQPA 16
Aurora A    MDRSKENCISGPVKATAPVGGPKRVLVTQQFPCQNPLPVNSGQAQRVLCPSNSSQRIPLQ 60
                                                          .: *:

Aurora B    ALVLMSRSN---------VQPTAAPG------------------------QKVMENSSGT 64
Aurora C    GEELATAN-----------QTAQQPS-----------------------SPAM------ 35
Aurora A    AQKLVSSHKPVQNQKQKQLQATSVPHPVSRPLNNTQKSKQPLPSAPENNPEEELASKQKN 120
            .  * :             *.:  *                        .  :

Aurora B    PDILTRHFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVEHQLRR 124
Aurora C    -----RRLTVDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFKSQIEKEGLEHQLRR 90
Aurora A    EESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQLRR 180
                 *: :::*******************  *:*:**:*******:*:** *:******
                        <-----------------------------------------------

Aurora B    EIEIQAHLHHPNILRLYNYFYDRRRIYLILEYAPRGELYKELQKSCTFDEQRTATIMEEL 184
Aurora C    EIEIQAHLQHPNILRLYNYFHDARRVYLILEYAPRGELYKELQKSEKLDEQRTATIIEEL 150
Aurora A    EVEIQSHLRHPNILRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITEL 240
            *:***:**:********.**:*  *:******** * :*:****  .:******* : **
            ------------------------------------------------------------

Aurora B    ADALMYCHGKKVIHRDIKPENLLLGLKGELKIADFGWSVHAPSLRRKTMCGTLDYLPPEM 244
Aurora C    ADALTYCHDKKVIHRDIKPENLLLGFRGEVKIADFGWSVHTPSLRRKTMCGTLDYLPPEM 210
Aurora A    ANALSYCHSKRVIHRDIKPENLLLGSAGELKIADFGWSVHAPSSRRTTLCGTLDYLPPEM 300
            *:** ***.*:**************  **:**********:** **.*:***********
            ----------------------S/T Kinase----------------------------

Aurora B    IEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPASVPMGAQDLI 304
Aurora C    IEGRTYDEKVDLWCIGVLCYELLVGYPPFESASHSETYRRILKVDVRFPLSMPLGARDLI 270
Aurora A    IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPDFVTEGARDLI 360
            **** ::******.:******:*** ****: ::.***:** :*:. **  :. **:***
            ------------------------------------------------------------

Aurora B    SKLLRHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSVA--- 344
Aurora C    SRLLRYQPLERLPLAQILKHPWVQAHSRRVLPPCAQMAS---- 309
Aurora A    SRLLKHNPSQRPMLREVLEHPWITANSSKPSNCQNKESASKQS 403
            *:**:::* :*  * ::  ***: *:* :        :
            ---------------------->
```

Alignment of human Aurora A, B and C protein sequences. The three Aurora sequences are very similar in the serine/threonine kinase domain (indicated in red) but have differing C and particularly N terminal extensions. Overall each is between 58% (A to B), 61% (A to C) and 75% identical (B to C). Charged amino acids are hatched and hydrophobic amino acids are blocked out.