



389
456
 GGRPRQ HLLSLTRRAQKHRLRELKI QVKEFADKEEGGDVKSVC LTFLLALRARN EHRQADELEAIMQ *Rattus_norvegicus*
GGRPRQ HLLSLTRRAQKHRLRELKI QVKEFADKEEGGDVKA VCLTFLLALRARN EHRQADELEAIMQ *Mus_musculus*
 GGRPRQ HLLSLTRRAQKHRLRELKLQVKAFADKEEGGDVKSVC MTFLLALRARN EHRQADELEAIMQ *Homo_sapiens*
 GGRPRQ HLLSLTRRAQKHRLRELKLQVKAFADKEEGGDVKA VCLTFLLALRARN EHRQADELEAIMQ *Gallus_gallus*
 GGRPRQ HLLSLTRRAQKHRLRELKRQVKAFAEKEEGGDIKAVC MTFLLALRAKNE HKQADELEAIMQ *Columba_livia*
 GGRPRQ HLLSLTRRAQKHRLRELKHQVKAFAEKEEGGDVKSVC LTFLLALRARN EHRQADELEAIMQ *Xenosaurus_grandis*
 GGRPRQ HLLTLTRRAQKHRLRELKMQVKAFADKEEGGDVKSVC LTFLLALRARN EHRQADELEAIME *Xenopus_longipes*
 GGRPRQ HLLSLTRRAQKHRLRDLKNQVKMF AEKEEGGDVKSVC LTFLLALRAGNE HKQADELEAMMQ *Ctenopharyngodon_idella*
 GGRPRQ HLLSLTRRAQKHRLRDLKNQVKTFAEKEEGGDVKSVC LTFLLALRAGNE HKQADELEAMMQ *Danio_rerio*
 GGRPRQ HLLSLTRRAQKHRLKDLKNLVKTFADKEEGGDLKSVCLTFLLALRSANE HRQADELEAIMQ *Takifugu_rubripes*
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 R393 S398 D426 A441

Supplementary Figure 7 Several Omenn syndrome (OS) mutations map to the NBD in RAG1. Residues that are mutated in OS patients are indicated with yellow spheres in the structure of the NBD dimer (subunits in cyan and pink). Lower panel shows the sequence alignment of the NBD from ten divergent species, with (*) indicating conservation of residue identity and (:) indicating conserved substitutions. The murine NBD sequence is shown in red. Yellow triangles indicate the relevant residues in the protein sequence. Sequence alignment was generated using ClustalW.