Score	Expect	Method	Identities	Positives	Gaps
218 bits(556)	1e-77	Compositional matrix adjust.	108/154(70%)	118/154(76%)	0/154(0%)

```
Zebrafish 1    MVNKAVCVLKGTGEVTGTVYFNQEGEKKPVKVTGEITGLTPGKHGFHVHAFGDNTNGCIS  60
               M  KAVCVLKG G V G + F Q+     PVKV G I GLT G HGFHVH FGDNT GC S
Human     1    MATKAVCVLKGDGPVQGIINFEQKESNGPVKVWGSIKGLTEGLHGFHVHEFGDNTAGCTS  60
                                  T70I
Zebrafish 61   AGPHFNPHDKTHGGPTDSVRHVGDLGNVTADASGVAKIEIEDAMLTLSGQHSIIGRTMVI  120
               AGPHFNP  + HGGP D  RHVGDLGNVTAD  GVA + IED++++LSG H IIGRT+V+
Human     61   AGPHFNPLSRKHGGPKDEERHVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGRTLVV  120
                              N65S       G72S/C      H80R
                                 L67R           D76Y/V
                               ⌐                         ⌐
                                     Zinc binding loop
Zebrafish 121  HEKEDDLGKGGNEESLKTGNAGGRLACGVIGITQ     154
               HEK DDLGKGGNEES KTGNAG RLACGVIGI Q
Human     121  HEKADDLGKGGNEESTKTGNAGSRLACGVIGIAQ     154
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Supplementary Fig. 1. A Blast P of zebrafish and human SOD1, annotated to show the location of the T70I mutation in zebrafish Sod1 (in blue), and also the location of disease causing mutations in the zinc binding loop of human SOD1 (in red).