



--enable-multilib --enable-nls --enable-objc-gc=auto --enable-offload-targets=nvptx-none=/build/gcc-9-HskZEa/gcc-9-9.3.0/debian/tmp-nvptx/usr,hsa --enable-plugin  
--enable-shared --enable-threads=posix --host=x86\_64-linux-gnu --program-prefix=x86\_64-linux-gnu- --target=x86\_64-linux-gnu --with-abi=m64 --with-arch-32=i686  
--with-default-libstdcxx-abi=new --with-gcc-major-version-only --with-multilib-list=m32,m64,mx32 --with-target-system-zlib=auto --with-tune=generic --without-cuda-driver -v  
Processor Notes: CPU Microcode: 0x1

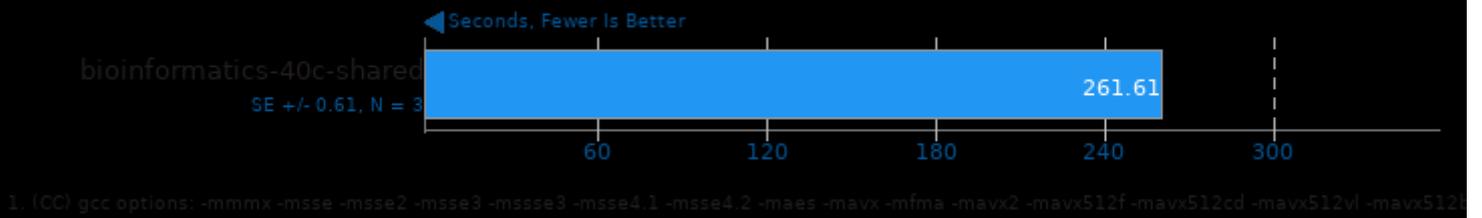
Security Notes: itlb\_multihit: Not affected + I1tf: Mitigation of PTE Inversion; VMX: flush not necessary SMT disabled + mds: Mitigation of Clear buffers; SMT Host state  
unknown + meltdown: Mitigation of PTI + spec\_store\_bypass: Mitigation of SSB disabled via prctl and seccomp + spectre\_v1: Mitigation of usercopy/swappgs barriers and  
\_\_user pointer sanitization + spectre\_v2: Mitigation of Full generic retpoline IBPB: conditional IBRS\_FW STIBP: disabled RSB filling + srbds: Not affected +  
tsx\_async\_abort: Mitigation of Clear buffers; SMT Host state unknown

**bioinformatics-40c-shared**

<b>Timed MrBayes Analysis - P.P.A (sec)</b>	261.609
Standard Deviation	0.4%
<b>QMCPACK - simple-H2O (Execution Time - sec)</b>	56.685
Standard Deviation	0.5%
<b>Timed HMMer Search - P.D.S (sec)</b>	186.492
Standard Deviation	2.2%
<b>Timed MAFFT Alignment - M.S.A - LSU RNA (sec)</b>	14.292
Standard Deviation	1.3%
<b>Himeno Benchmark - P.P.S (MFLOPS)</b>	3154
Standard Deviation	0.7%

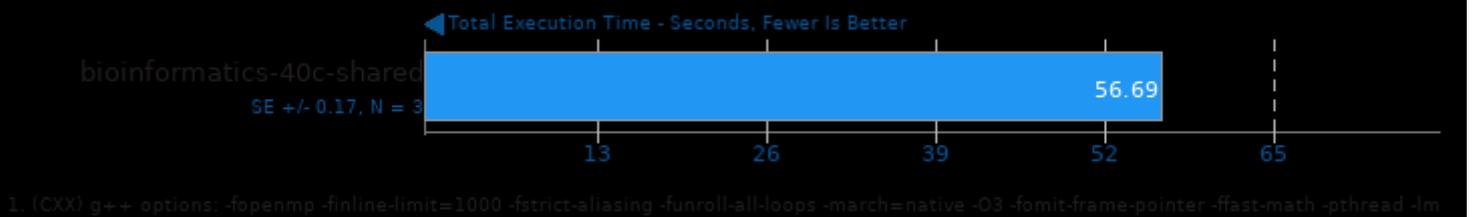
### Timed MrBayes Analysis 3.2.7

Primate Phylogeny Analysis



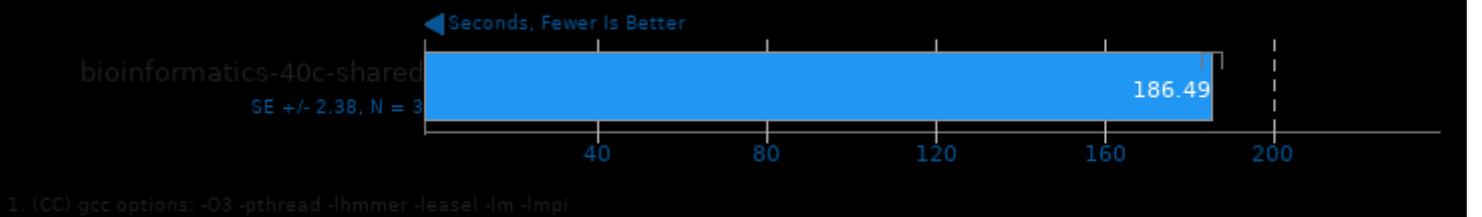
### QMCPACK 3.11

Input: simple-H2O



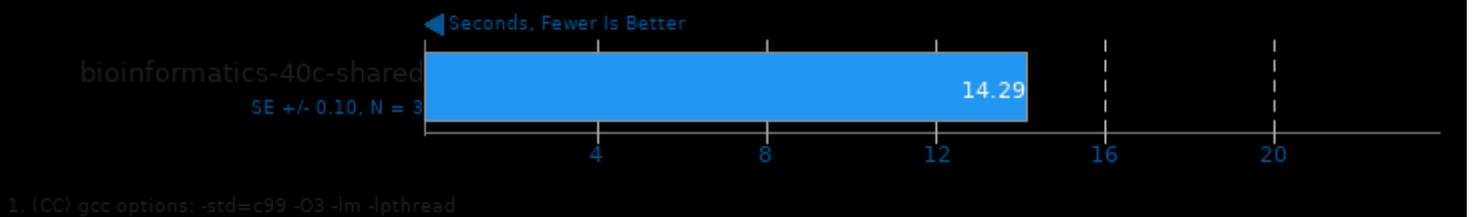
### Timed HMMer Search 3.3.2

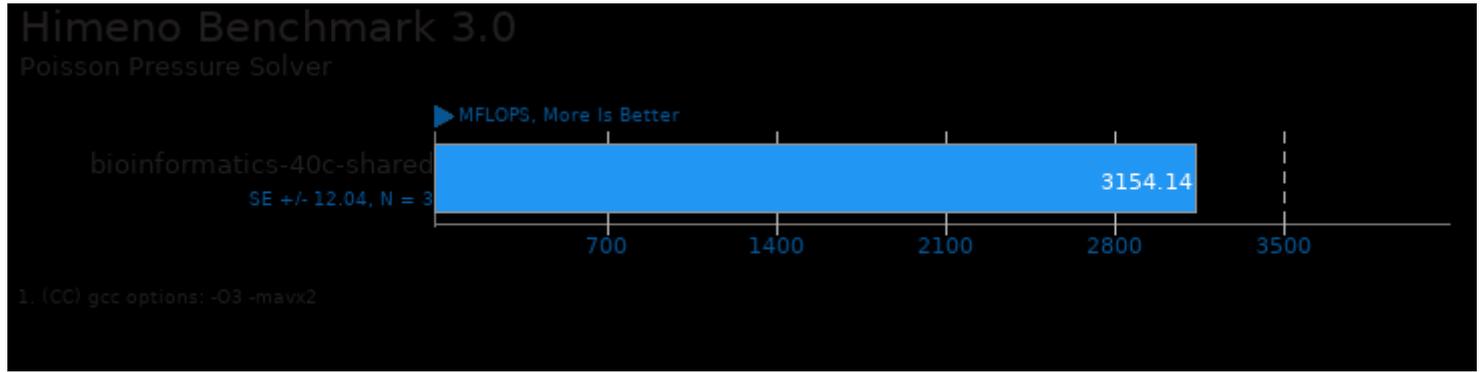
Pfam Database Search



### Timed MAFFT Alignment 7.471

Multiple Sequence Alignment - LSU RNA





*This file was automatically generated via the Phoronix Test Suite benchmarking software on Thursday, 28 March 2024 09:59.*