<div align="center">

SIM

</div>

Sim

Results of SIM with:

Sequence 1: 4rzk (90 residues)
Sequence 2: 1c3g (170 residues)

using the parameters:

Comparison matrix: BLOSUM62
Number of alignments computed: 20
Gap open penalty: 12
Gap extension penalty: 4

View these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).
LALNVIEW screenshot / Download / documentation.

20.0% identity in 10 residues overlap; Score: 22.0; Gap frequency: 0.0%

```
4rzk        59 EIDLPAEVDE
1c3g         4 QVNLPVSLED
                  **
```

20.0% identity in 15 residues overlap; Score: 22.0; Gap frequency: 0.0%

```
4rzk        59 EIDLPAEVDEKAAKA
1c3g       154 KVDYPISLNDAQKRA
                  * *         *
```

57.1% identity in 7 residues overlap; Score: 19.0; Gap frequency: 0.0%

```
4rzk        72 KANFKNG
1c3g        19 KKSFKIG
                * ** *
```

18.8% identity in 16 residues overlap; Score: 19.0; Gap frequency: 0.0%

```
4rzk        31 KEDIKVKVTNGGKKLV
1c3g       154 KVDYPISLNDAQKRAI
               * *          *
```

36.4% identity in 11 residues overlap; Score: 19.0; Gap frequency: 0.0%

```
4rzk        66 VDEKAAKANFK
1c3g        73 VIQEKSHPNFK
               *       ***
```

50.0% identity in 6 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
4rzk        72 KANFKN
1c3g        51 KITYKN
               *   **
```

30.8% identity in 13 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
4rzk        31 KEDIKVKVTNGGK
1c3g        35 KTQIDIQLKPGWK
```

```
              *    *      *  *
```

23.1% identity in 26 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
4rzk        31 KEDIKVKVTNGGKKLVITAKSEDRQY
1c3g        47 KAGTKITYKNQGDYNPQTGRRKTLQF
               *    *   * *      *      *
```

50.0% identity in 8 residues overlap; Score: 17.0; Gap frequency: 0.0%

```
4rzk        29 VNKEDIKV
1c3g         9 VSLEDLFV
               *   ** *
```

37.5% identity in 8 residues overlap; Score: 17.0; Gap frequency: 0.0%

```
4rzk         2 MISEEREP
1c3g        73 VIQEKSHP
                * *    *
```

60.0% identity in 5 residues overlap; Score: 17.0; Gap frequency: 0.0%

```
4rzk        33 DIKVK
1c3g        39 DIQLK
               **  *
```

42.9% identity in 7 residues overlap; Score: 17.0; Gap frequency: 0.0%

```
4rzk        74 NFKNGVL
1c3g        96 SFKESLL
                **   *
```

50.0% identity in 6 residues overlap; Score: 16.0; Gap frequency: 0.0%

```
4rzk        80 LEITLK
1c3g        38 IDIQLK
                 * **
```

50.0% identity in 8 residues overlap; Score: 16.0; Gap frequency: 0.0%

```
4rzk        44 KLVITAKS
1c3g        71 QFVIQEKS
                 **  **
```

75.0% identity in 4 residues overlap; Score: 16.0; Gap frequency: 0.0%

```
4rzk        85 KKKA
1c3g        18 KKKS
               ***
```

60.0% identity in 5 residues overlap; Score: 16.0; Gap frequency: 0.0%

```
4rzk        34 IKVKV
1c3g       151 VKYKV
                * **
```

33.3% identity in 12 residues overlap; Score: 16.0; Gap frequency: 0.0%

```
4rzk        59 EIDLPAEVDEKA
1c3g        37 QIDIQLKPGWKA
```

```
                         **          **


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40.0% identity in 10 residues overlap; Score: 16.0; Gap frequency: 0.0%

4rzk           7 REPLADVIEK
1c3g          67 RKTLQFVIQE
                 *   *  **


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100.0% identity in 3 residues overlap; Score: 16.0; Gap frequency: 0.0%

4rzk          42 GKK
1c3g          17 GKK
                 ***


_____

50.0% identity in 4 residues overlap; Score: 16.0; Gap frequency: 0.0%

4rzk          17 GDEI
1c3g          86 GDDL
                 **


_____
```

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