

SIM

Sim

Results of SIM with:

Sequence 1: 4fei (102 residues)

Sequence 2: 4rzk (90 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](#).

36.4% identity in 22 residues overlap; Score: 42.0; Gap frequency: 0.0%

```
4fei      7 PAADWRDAGTHLDLLDVPD
4rzk      9 PLADVIEKGDEIKVVAEVP
          *  **   *      ****
```

20.0% identity in 45 residues overlap; Score: 42.0; Gap frequency: 0.0%

```
4fei      49 GTEHLLRSEPSGRFVRELAPEPVRPASGVASLAGGVLTVRFEK
4rzk      42 GKLLVITAKSEDRQYYKEIDLPAEVDEKAAKANKGVLEITLKK
          *              *  *  *      *      ***   *
```

42.9% identity in 14 residues overlap; Score: 29.0; Gap frequency: 0.0%

```
4fei      36 EDGGQLTVSGERPG
4rzk      15 EKGDEIKVVAEVP
          *  *      *  *  **
```

44.4% identity in 9 residues overlap; Score: 19.0; Gap frequency: 0.0%

```
4fei      92 EKL RPTIDV
4rzk       5 EEREPLADV
          *   *  **
```

13.0% identity in 23 residues overlap; Score: 17.0; Gap frequency: 0.0%

```
4fei      38 GGQLTVSGERPGTEHLLRSEPS
4rzk      42 GKLLVITAKSEDRQYYKEIDLPA
          *  *              *
```

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

```
4fei      22 LDVP
4rzk      60 IDLP
          *  *
```

42.9% identity in 7 residues overlap; Score: 16.0; Gap frequency: 0.0%

```
4fei      86 VLTVRFE
4rzk      46 VITAKSE
```

* * *

26.3% identity in 19 residues overlap; Score: 15.0; Gap frequency: 0.0%

4fei	6	TPAADWRDAGTHDLLLDV
4rzk	48	TAKSEDRQYYKEIDLPAEV
		* * * * *

42.9% identity in 7 residues overlap; Score: 15.0; Gap frequency: 0.0%

4fei	37	DGGQLTV
4rzk	40	NGGKKLV
		** *

60.0% identity in 5 residues overlap; Score: 15.0; Gap frequency: 0.0%

4fei	43	VSGER
4rzk	3	ISEER
		* **

50.0% identity in 6 residues overlap; Score: 14.0; Gap frequency: 0.0%

4fei	79	VASLAG
4rzk	23	VAEVPG
		** *

60.0% identity in 5 residues overlap; Score: 14.0; Gap frequency: 0.0%

4fei	33	ALAED
4rzk	49	AKSED
		* **

60.0% identity in 5 residues overlap; Score: 14.0; Gap frequency: 0.0%

4fei	98	IDVTA
4rzk	60	IDLPA
		** *

66.7% identity in 3 residues overlap; Score: 13.0; Gap frequency: 0.0%

4fei	71	EPV
4rzk	8	EPL
		**

25.0% identity in 8 residues overlap; Score: 13.0; Gap frequency: 0.0%

4fei	40	QLTVSGER
4rzk	37	KVTNGGKK
		* *

36.4% identity in 11 residues overlap; Score: 13.0; Gap frequency: 0.0%

4fei	49	GTEHLLRSERP
4rzk	17	GDEIKVVAEVP
		* * * *

33.3% identity in 6 residues overlap; Score: 13.0; Gap frequency: 0.0%

4fei	53	LLRSER
4rzk	2	MISEER

**

75.0% identity in 4 residues overlap; Score: 13.0; Gap frequency: 0.0%

4fei 21 LLDV
4rzk 10 LADV
 * **

66.7% identity in 3 residues overlap; Score: 12.0; Gap frequency: 0.0%

4fei 100 VTA
4rzk 47 ITA
 **

25.0% identity in 4 residues overlap; Score: 12.0; Gap frequency: 0.0%

4fei 98 IDVT
4rzk 80 LEIT
 *
