

SIM

Sim

Results of SIM with:

Sequence 1: 3gt6 (103 residues)

Sequence 2: 4fei (102 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](#).

33.0% identity in 94 residues overlap; Score: 108.0; Gap frequency: 5.3%

```
3gt6      6 WVPRVDIKEEVNHFVLYADLPIDPSQIEVQMDKGILSIRGERKSESSTETERFSRIERR
4fei      5 WTPAADWRDAGTHLDLLLDVPGVDAGTLALAEDGGQLTVSGERP-----TEHLLRSERP
          * * *      * * * * *      * * *      ***      ** * **

3gt6      66 YGSFHRRFALPDSADADGITAAGRNGVLEIRIPK
4fei      60 SGRFVRELAFPEPVRPASGVASLAGGVLTVRFEK
          * * * * *      *      *** * *
```

23.8% identity in 21 residues overlap; Score: 27.0; Gap frequency: 0.0%

```
3gt6      28 IDPSQIEVQMDKGILSIRGER
4fei      73 VRPASGVASLAGGVLTVRFEK
          *      * * * *
```

66.7% identity in 6 residues overlap; Score: 22.0; Gap frequency: 0.0%

```
3gt6      98 PKRPAA
4fei      72 PVRPAS
          * ***
```

57.1% identity in 7 residues overlap; Score: 20.0; Gap frequency: 0.0%

```
3gt6      44 IRGERKS
4fei      54 LRSERPS
          * ** *
```

33.3% identity in 12 residues overlap; Score: 20.0; Gap frequency: 0.0%

```
3gt6      35 VQMDKGILSIRG
4fei      73 VRPASGVASLAG
          *      * * *
```

80.0% identity in 5 residues overlap; Score: 19.0; Gap frequency: 0.0%

```
3gt6      7 VPRVD
4fei      24 VPGVD
          ** **
```

31.2% identity in 16 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
3gt6      80 DADGITAAGRNGVLEI
4fei      28 DAGTLALAEDGGQLTV
          **      *      *      *
```

66.7% identity in 6 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
3gt6      98 PKRPAA
4fei       4 PWTCAA
          *      ***
```

16.7% identity in 18 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
3gt6      12 IKKEVNHFVLYADLPGID
4fei      34 LAEDGGQLTVSGERPGTE
          *              **
```

40.0% identity in 5 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
3gt6       8 PRVDI
4fei      96 PTIDV
          *      *
```

37.5% identity in 8 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
3gt6      37 MDKGILSI
4fei      27 VDAGTLAL
          *      *      *
```

42.9% identity in 7 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
3gt6      56 TERFSRI
4fei      88 TVRFEKL
          *      **
```

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

```
3gt6      80 DADGITA
4fei      23 DVPGVDA
          *      *      *
```

33.3% identity in 9 residues overlap; Score: 17.0; Gap frequency: 0.0%

```
3gt6      80 DADGITAAG
4fei      37 DGGQLTVSG
          *      *      *
```

33.3% identity in 15 residues overlap; Score: 16.0; Gap frequency: 0.0%

```
3gt6      47 ERKSESSTETERFSR
4fei      51 EHLLRSERPSGRFVR
          *      *      ** *
```

37.5% identity in 8 residues overlap; Score: 16.0; Gap frequency: 0.0%

```
3gt6      92 VLEIRIPK
4fei      64 VRELAFPE
          *      *      *
```

28.6% identity in 14 residues overlap; Score: 16.0; Gap frequency: 0.0%

3gt6	89	RNGVLEIRIPKRPA
4fei	47	RPGTEHLLRSERPS
		* * **

66.7% identity in 3 residues overlap; Score: 15.0; Gap frequency: 0.0%

3gt6	4	AQW
4fei	9	ADW
		* *

75.0% identity in 4 residues overlap; Score: 15.0; Gap frequency: 0.0%

3gt6	26	PGID
4fei	96	PTID
		* **

27.3% identity in 11 residues overlap; Score: 15.0; Gap frequency: 0.0%

3gt6	29	DPSQIEVQMDK
4fei	37	DGGQLTVSGER
		* * *
