

SIM

Sim

Results of SIM with:

Sequence 1: 3gt6 (103 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](#).

33.3% identity in 12 residues overlap; Score: 27.0; Gap frequency: 0.0%

```
3gt6      29 DPSQIEVQMDKG
1c3g      34 EKTQIDIQLKPG
           **  *  *
```

28.6% identity in 14 residues overlap; Score: 22.0; Gap frequency: 0.0%

```
3gt6      28 IDPSQIEVQMDKGI
1c3g     124 VQPSQTSTYPGQGM
           ***  *
```

60.0% identity in 5 residues overlap; Score: 20.0; Gap frequency: 0.0%

```
3gt6      98 PKRPA
1c3g     140 PKNPS
           ** *
```

29.4% identity in 17 residues overlap; Score: 19.0; Gap frequency: 0.0%

```
3gt6      55 ETERFSRIERRYGSFHR
1c3g      68 KTLQFVIQEKSHPNFKR
           *  *  *  *  *
```

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

```
3gt6      88 GRNGVLEIRIPKR
1c3g      65 GRRKTLQFVIQEK
           **  *  *
```

60.0% identity in 5 residues overlap; Score: 18.0; Gap frequency: 0.0%

```
3gt6      46 GERKS
1c3g      17 GK KKS
           *  **
```

75.0% identity in 4 residues overlap; Score: 17.0; Gap frequency: 0.0%

```
3gt6      88 GRNG
1c3g      25 GRKG
```

** *

75.0% identity in 4 residues overlap; Score: 17.0; Gap frequency: 0.0%

3gt6	29	DPSQ
1c3g	142	NPSQ

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

3gt6	46	GERKS
1c3g	65	GRRKT
		* **

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

3gt6	50	SESST
1c3g	127	SQTST
		* **

33.3% identity in 18 residues overlap; Score: 16.0; Gap frequency: 0.0%

3gt6	85	TAAGRNGVLEIRIPKRPA
1c3g	110	TIDGRTLPLSRVQPVQPS
		* ** * * *

40.0% identity in 5 residues overlap; Score: 15.0; Gap frequency: 0.0%

3gt6	9	RVDIK
1c3g	37	QIDIQ
		**

45.5% identity in 11 residues overlap; Score: 15.0; Gap frequency: 0.0%

3gt6	15	EVNHFVLYADL
1c3g	4	QVNLPVSLEDL
		** * **

16.7% identity in 6 residues overlap; Score: 15.0; Gap frequency: 0.0%

3gt6	93	LEIRIP
1c3g	3	VQVNLP
		*

28.6% identity in 14 residues overlap; Score: 15.0; Gap frequency: 0.0%

3gt6	88	GRNGVLEIRIPKRP
1c3g	31	GASEKTQIDIQLKP
		* * * *

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

3gt6	52	SSTET
1c3g	127	SQTST
		* * *

15.4% identity in 13 residues overlap; Score: 14.0; Gap frequency: 0.0%

3gt6	45	RGERKSESSTETE
1c3g	27	KGPHGASEKTQID

* *

50.0% identity in 4 residues overlap; Score: 14.0; Gap frequency: 0.0%

3gt6 73 FALP
1c3g 91 YTLP
 **

37.5% identity in 8 residues overlap; Score: 14.0; Gap frequency: 0.0%

3gt6 25 LPGIDPSQ
1c3g 118 LSRVQPVQ
 * * *

75.0% identity in 4 residues overlap; Score: 14.0; Gap frequency: 0.0%

3gt6 82 DGIT
1c3g 112 DGRT
 ** *
