

## SIM

## Sim

## Results of SIM with:

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

23.5% identity in 51 residues overlap; Score: 54.0; Gap frequency: 0.0%

```

3gt6      1 VVTAQWVPRVDIKEEVNHFVLYADLPGIDPSQIEVQMDKGILSIRGERKSE
4rzk      2 MISEEREPLADVIEKGDEIKVVAEVPGVNKEDIKVKVTNGGKKLVITAKSE
              *  *  *          *  **      *  *      *      ***

```

31.4% identity in 35 residues overlap; Score: 54.0; Gap frequency: 0.0%

```

3gt6      69 FHRRFALPDSADADGITAAGRNGVLEIRIPKRPAA
4rzk      56 YYKEIDLPAEVDEKAAKANFKNGVLEITLKKKASS
              **  *      *      *      *      *

```

25.0% identity in 44 residues overlap; Score: 37.0; Gap frequency: 2.3%

```

3gt6      10 VDIKEEVNHFVLYADLPG-IDPSQIEVQMDKGILSIRGERKSES
4rzk      47 ITAKSEDRQYYKEIDLPAEVDEKAAKANFKNGVLEITLKKKASS
              *  *      ***      *      *  *  *      *  *

```

30.8% identity in 13 residues overlap; Score: 24.0; Gap frequency: 0.0%

```

3gt6      5 QWVPRVDIKEEVN
4rzk      55 QYYKEIDLPAEVD
              *      *      **

```

41.7% identity in 12 residues overlap; Score: 21.0; Gap frequency: 0.0%

```

3gt6      7 VPRVDIKEEVNH
4rzk      29 VNKEDIKVKVTN
              *      ***      *

```

42.9% identity in 14 residues overlap; Score: 20.0; Gap frequency: 0.0%

```

3gt6      1 VVTAQWVPRVDIKE
4rzk      46 VITAKSEDRQYYKE
              *  **      *      **

```

23.5% identity in 17 residues overlap; Score: 17.0; Gap frequency: 0.0%

```

3gt6      84 ITAAGRNGVLEIRIPKR
4rzk      38 VTNGGKKLVITAKSEDR

```

\* \* \* \*

---

20.0% identity in 10 residues overlap; Score: 16.0; Gap frequency: 0.0%

3gt6	30	PSQIEVQMDK
4rzk	63	PAEVDEKAAK
		* * *

---

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

3gt6	94	EIRIP
4rzk	59	EIDL P
		** *

---

23.1% identity in 13 residues overlap; Score: 16.0; Gap frequency: 0.0%

3gt6	39	KGILSIRGERKSE
4rzk	21	KVVAEVPGVNKED
		* * *

---

28.6% identity in 7 residues overlap; Score: 15.0; Gap frequency: 0.0%

3gt6	33	IEVQMDK
4rzk	80	LEITLKK
		* *

---

50.0% identity in 4 residues overlap; Score: 15.0; Gap frequency: 0.0%

3gt6	63	ERRY
4rzk	53	DRQY
		* *

---

50.0% identity in 4 residues overlap; Score: 15.0; Gap frequency: 0.0%

3gt6	13	KEEV
4rzk	31	KEDI
		**

---

33.3% identity in 6 residues overlap; Score: 14.0; Gap frequency: 0.0%

3gt6	79	ADADGI
4rzk	24	AEVPGV
		* *

---

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

3gt6	94	EIRI
4rzk	19	EIKV
		**

---

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

3gt6	37	MDKG
4rzk	14	IEKG
		**

---

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

3gt6	12	IKEE
4rzk	3	ISEE

\* \*\*

---

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

3gt6	48 RKSESS
4rzk	85 KKKASS
	* **

---

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

3gt6	7 VPRVD
4rzk	26 VPGVN
	** *

---

40.0% identity in 10 residues overlap; Score: 13.0; Gap frequency: 0.0%

3gt6	10 VDIKEEVNHF
4rzk	66 VDEKAAKANF
	** * *

---