

SIM

Sim

Results of SIM with:

Sequence 1: 4fei (102 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](#).

26.2% identity in 42 residues overlap; Score: 32.0; Gap frequency: 0.0%

4fei	25	PGVDAGTLALAEDGGQLTVSGERPGTEHLLRSERPSGRFVRE
1c3g	44	PGWKAGTKITYKNQGDYNPQTGRRKTLQFVIQEKSHPNFKRD
		** *** * * *

50.0% identity in 6 residues overlap; Score: 22.0; Gap frequency: 0.0%

4fei	71	EPVRPA
1c3g	122	QPVQPS
		** *

55.6% identity in 9 residues overlap; Score: 21.0; Gap frequency: 0.0%

4fei	91	FEKLRPTID
1c3g	104	FSKTIQTID
		* * ***

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

4fei	37	DGGQLTVSGERP
1c3g	112	DGRTLPLSRVQP
		** * * *

44.4% identity in 9 residues overlap; Score: 20.0; Gap frequency: 0.0%

4fei	27	VDAGTLALA
1c3g	111	IDGRTLPLS
		* ** *

37.5% identity in 16 residues overlap; Score: 19.0; Gap frequency: 0.0%

4fei	75	PASGVASLAGGVLTVR
1c3g	94	PLSFKESLLGFSKTIQ
		* * ** * *

42.9% identity in 7 residues overlap; Score: 19.0; Gap frequency: 0.0%

4fei	70	PEPVRPA
1c3g	138	PTPKNPS

* * *

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

4fei	19	DLLLDVP
1c3g	88	DLIYTLP
		** *

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

4fei	16	THLDLLL
1c3g	36	TQIDIQL
		* * *

25.0% identity in 12 residues overlap; Score: 17.0; Gap frequency: 0.0%

4fei	67	LAFPEPVRPASG
1c3g	102	LGFSKTIQTIDG
		* * *

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

4fei	85	GVLTVRFE
1c3g	147	GNLIVKYK
		* * *

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

4fei	45	GERPGTE
1c3g	45	GWKAGTK
		* **

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

4fei	14	AGTHL
1c3g	48	AGTKI

22.2% identity in 9 residues overlap; Score: 15.0; Gap frequency: 0.0%

4fei	88	TVRFEKLRP
1c3g	115	TLPLSRVQP
		* *

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

4fei	67	LAFPE
1c3g	95	LSFKE
		* * *

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

4fei	47	RPG
1c3g	43	KPG
		**

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

4fei	1	QGGP
1c3g	135	QGMP

** *

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

4fei	37	DGGQL
1c3g	85	DGDDL
		** *

31.6% identity in 19 residues overlap; Score: 15.0; Gap frequency: 0.0%

4fei	25	PGVDAGTLALAEDGGQLTV
1c3g	133	PGQGMPTPKNPSQRGNLIV
		** * * * *

25.0% identity in 8 residues overlap; Score: 15.0; Gap frequency: 0.0%

4fei	90	RFEKLRPT
1c3g	120	RVQPVQPS
		* *
