

Module 9 ChIPSeq

Quiz template

Add questions, at least two answer alternatives and choose correct answers (at least one). Have fun creating your awesome quiz!

See an example question below (don't forget to overwrite this with your first question!)

	Question	Answer 1	Answer 2	Answer 3	Answer 4	Correct answer(s) - choose at least one
1	A Nucleosome is a complex containing DNA and	Transcription factors	Histones	Chromatin	Polymerase	2
2	A ChIPseq experiment cross-links the DNA to	DNA	Golgi Apparatus	Protein		3
3	ChIPSeq DNA fragments should be in the range	a few hundred bp	a few thousand bp	around 10kb	around 1Mb	1
4	ChIPseq reads are preferably	Longer and Single End	Longer and Paired End	Shorter and Single End	Shorter and Paired End	2
5	ChIPSeq Antibodies can be targeted against	Native protein only	Protein tags only	Native protein or Protein tags		3
6	The ChIPSeq experimental order is	pulldown, cross linking, sequencing, alignment	cross linking, pulldown, sequencing, alignment	pulldown, cross linking, alignment, sequencing	sequencing, alignment, pulldown, cross linking	2
7	The alignment of chipseq reads typically is located near	Repeat regions	Telomeres	GC - rich regions	Transcripts	4
8	Comparing Transfacs, mediators and the transcription apparatus	transcription apparatus	mediators	transfacs		1
9	Transfacs peaks typically occur around	transcription start site	Translation start	Translation stop	transcription stop	1
10	Histone modifications occur typically in Histone protein class: H1 and H2		H2 and H3	H3 and H4	H2 and H4	3
11	A commonly modified Histone residue is	Arginine	Leucine	Lysine	Methionine	3
12	The (Encode) FRIP measure should be better than		1%	5%	10%	20% 1
13	Library complexity goals (Encode) are	> 1million reads and NRF > 0.8	> 1million reads and NRF > 0.5	> 5million reads and NRF > 0.5	> 10million reads and NRF > 0.8	4
14	Nonredundant Fraction measures	Signal / Noise	Library Complexity	Shearing Efficiency	Antibody Quality	2
15						
16						