Criterion	Bacteria	Yeast	"Higher" Eukaryotes - multicellular
Cis sequences	-10, -35 elements, UP element	Only 1 upstream activating sequence (UAS)	Upstream elements, BRE, TATA/CpG island, TSS
Has Mediator? For integration of multiple signalling pathways.	No.	Yes. (up to 21 subunits)	Yes. (26 subunits)
Activator/repressor	Operons	Have activator/repressor sequences	Enhancers + super-enhancers in metazoans Activator domain -> IDRs -> LLPS
Chromatin/histone PTM's	Probably not (heterochromatin not a factor in transcription regulation) *except some preprints e.g., Hocher et al (2023) claiming to have found histone-bound chromatin in two bacterial species	Yes	Yes Regulate chromatin accessibility Pausing?
PIC structure	Only RNA Pol	RNA Pol + GTFs + activators	RNA Pol + GTFs + activators
Promoter site recognition/pol II loading	RNA Pol sigma factor used for promoter recognition Different sigma recognize different sequences	One TBP (TFIID)	TFIID Have "sharp" and "broad" promoters, core and upstream, tissue-specific TAFs and TBPs Similar to sigma factor switching in bacteria
Attenuation	Yes	No	No

	Terminator hairpin formed in mRNA if translation fast enough (occurs in high W levels)		
3D genome structure	No	Yes (TADs may be organised differently?)	Yes – topologically associated domains Looping of enhancers limited within TADs Also allows for mechaosensing – cytoskeleton can transduce forces onto the nucleus inducing changes
Promoter proximal pausing	no	no	Yes Rapid + synchronous activation Integration of signalling
Co-transcriptional RNA processing)	No introns Translation occurs co-transcriptionally Allows for attenuation	Capping, polyadenylation and splicing. Simple (usually single intron)	Capping, polyadenylation and splicing. Lengthy introns, zero length exons?
CTD	No	Require less repeats	Have more repeats (but similar function)
Number of polymerases	1	3	3 (animals), 5 (plants)
Termination	At defined points (rho-dependent or rho-independent)		Transcription continues even after end of gene. Posttranscriptional processing of mRNA instead

Transcript features	Polycistronic	Monocistronic	Monocistronic
LLPS	Y	y	y