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# STRUCTURE YOUR PARAGRAPHS AND SENTENCES FOR IMPACT WORKSHEET

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LEARNING OUTCOMES: EXPLAIN HOW TO STRUCTURE A PARAGRAPH;  
EXPLAIN THE POWER POSITIONS IN A PARAGRAPH

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BECOME THE TEACHER!

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One of the best ways to learn a topic is to teach it. Meet up with a friend or family member, and during your conversation, explain to them how to structure a paragraph. This discussion should include the four structural elements of a paragraph and an explanation of the power positions within the paragraph.

LEARNING OUTCOMES: LIST EXAMPLES OF PURPOSES OF A PARAGRAPH; DESCRIBE THE CHARACTERISTICS OF A GOOD PARAGRAPH

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FOR EACH OF THE FOLLOWING PARAGRAPHS, DETERMINE THE PURPOSE OF THE PARAGRAPH, AND CRITIQUE THE PARAGRAPH FOR THE FOUR CHARACTERISTICS OF A GOOD PARAGRAPH

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1. The finding that FnCpf1 can mediate DNA interference with crRNA alone is highly surprising given that Cas9 recognizes crRNA through the duplex structure between crRNA and tracrRNA (refs), as well as the 3' secondary structure of the tracrRNA (refs). To ensure that crRNA is indeed sufficient for forming an active complex with FnCpf1 and mediating RNA-guided DNA cleavage, we investigated whether FnCpf1 supplied only with crRNA can cleave target DNA in vitro. We purified FnCpf1 (Figure S2) and assayed its ability to cleave the same protospacer-1-containing plasmid used in the bacterial DNA interference experiments (Figure 3A). We found that FnCpf1 along with an in-vitro-transcribed mature crRNA-targeting protospacer 1 was able to efficiently cleave the target plasmid in a Mg<sup>2+</sup>- and crRNA-dependent manner (Figure 3B). Moreover, FnCpf1

was able to cleave both supercoiled and linear target DNA (Figure 3C). These results clearly demonstrate the sufficiency of FnCpf1 and crRNA for RNA-guided DNA cleavage.

2. MPC-D 102/113 can be identified as an oviraptorosaur on the basis of the laterally-everted acromion process of the scapula and by the pubis, which is mesopubic and anteriorly curved. This identity is further supported by the distinctive morphologies of the angular and the metatarsals. The skeleton contrasts with those of avimimids by being significantly larger than would be expected of *Avimimus nemegtensis*, as well as the retention of the proximal end of Metatarsal III, which is lost in avimimids. Furthermore, the preserved fragments of Metatarsals II and IV of MPC-D 102/113 indicate a deep plantar concavity on the tarsometatarsus, which is absent in both avimimids and oviraptorids. Compared to oviraptorids, the scapula is more robust and extends anteriorly to the acromion process, which changes the relative positions of the glenoid and acromion process. Whereas these are more closely placed in oviraptorids, in MPC-D 102/113, the glenoid is anterior to the acromion process. The coracoid similarly differs from those of oviraptorids in the more dorsal positions of the biceps tubercle and coracoid foramen relative to the glenoid. The pubis also contrasts with those of oviraptorids in being relatively straight distally instead of anteriorly concave, and in the presence of a distinct, enclosed medial fossa at the proximal end, a feature that is less well developed in oviraptorids.
  
3. The inDrop platform encapsulates cells into droplets with lysis buffer, reverse transcription (RT) reagents, and barcoded oligonucleotide primers (Figure 1). mRNA released from each lysed cell remains trapped in the same droplet and is barcoded during synthesis of cDNA. After barcoding, material from all cells is combined by breaking the droplets, and the cDNA library is sequenced using established methods (CEL-seq). The major challenge is to ensure that each droplet carries primers encoding a different barcode. We synthesized a library of barcoded hydrogel microspheres (BHM) that are co-encapsulated with cells (Figure 2 and S1). Each BHM carries ~109 covalently coupled, photo-releasable primers encoding one of 147,456 barcodes, and the pool size could be increased in a straightforward manner. The current pool size allows randomly labeling 3,000 cells with 99% unique labeling; many more cells can be processed by splitting a large emulsion into separate tubes.
  
4. The high frequency of AR pathway alterations in this cohort strongly implies that the vast majority of mCRPC affected individuals remain dependent on AR signaling for viability. The “second-generation” AR-directed therapies (e.g., abiraterone acetate and enzalutamide) may select for distinct phenotypes that may be indifferent to AR signaling, and prospective characterization of such cases will be of particular interest. We hypothesize that affected individuals with acquired AR mutations, including new AR mutations discovered in this cohort, will harbor differential responses to these second-generation ADT therapies. As the number of affected individuals in this cohort with AR

mutations increases, we will subsequently be able to link specific AR mutations with clinical phenotypes to determine which mutations confer selective response or resistance to subsequent AR-directed therapy.

5. While the rapamycin-FKBP12 complex directly inhibits mTORC1, mTORC2 is characterized by its insensitivity to acute rapamycin treatment. Like mTORC1, mTORC2 also contains mTOR and mLST8. Instead of Raptor, however, mTORC2 contains Rictor (rapamycin insensitive companion of mTOR), an unrelated protein that likely serves an analogous function. mTORC2 also contains DEPTOR, as well as the regulatory subunits mSin1 and Protor1/2. Although rapamycin-FKBP12 complexes do not directly bind or inhibit mTORC2, prolonged rapamycin treatment does abrogate mTORC2 signaling, likely due to the inability of rapamycin-bound mTOR to incorporate into new mTORC2 complexes.
6. However, we found an inconsistency between relative promoter unit (RPU) measurements obtained via the fluorescence and enzymatic activities of Gemini. Specifically, we observed that at high expression levels the relative promoter measurements obtained via the fluorescence activity of Gemini (Figure a) diverge from the relative promoter measurements obtained via the enzymatic activity of Gemini (Figure b). One explanation for this divergence is that the enzymatic activity of Gemini may saturate if the quantity of expressed Gemini-encoded  $\alpha$ -fragment exceeds the amount of complementing omega-fragment present within cells. Careful characterization of a functional full-length  $\beta$ -gal GFP fusion would help to consider this model.

## LEARNING OUTCOME: DETERMINE THE CORRECT SUBJECT AND VERB FOR A SENTENCE

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FOR EACH SENTENCE BELOW, IDENTIFY THE CURRENT SUBJECT AND MAIN VERB.  
THEN DETERMINE IF THE SENTENCE WOULD BE BETTER WITH A DIFFERENT SUBJECT  
AND MAIN VERB, AND RE-WRITE THE SENTENCE AS NEEDED.

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Omoe et al. used a monkey feeding test to evaluate the emetic activity of some newly discovered SEIs.

Studies have suggested several major signaling pathways and molecular targets, including oxidative stress, metabolism dysfunction, deregulated autophagy, telomere shortening, mitochondrial dysfunction, cellular calcium homeostasis, and systemic inflammation modulation of aging and lifespan in a wide range of species expanding from yeast to mammals.



Gong et al. showed that at 7 days after TBI, mGluR2/3 and mGluR5 expression was reduced in the ipsilateral hippocampus and cortex.

Each thin or thick slice was placed in a submerged recording chamber and perfused with buffer at a perfusate temperature of 35–36 °C.

## LEARNING OUTCOME: STRUCTURE SENTENCES IN CORRECT PARALLEL STRUCTURE

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EVALUATE WHETHER PARALLEL STRUCTURE AND/OR A CORRECT COMPARISON IS/ARE BEING USED IN THE FOLLOWING SENTENCES, AND IF NOT, CORRECT THE SENTENCE.

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Climate change has led to well-documented changes in marine, terrestrial and freshwater ecological communities stemming from a diversity of processes, including productivity changes, shifts in species distributions, and changes in timing of seasonal events.

We observed little evidence of menu reformulation among the top-selling items after labeling and are finding that the distribution of nutrient content for menu items was similar.

These RNA structures, as well as specific RNA sequences and motifs, govern many essential viral processes such as translation, replication, and packaging.

Two homozygous transgenic T3 lines were selected for further work, one carrying the CRIPSR/Cas9 construct and the second carried the GUS reporter construct.

The A and B transgenic lines showed elevated levels of Cas9 and sgRNA, while the C line has lower Cas9 and sgRNA levels.