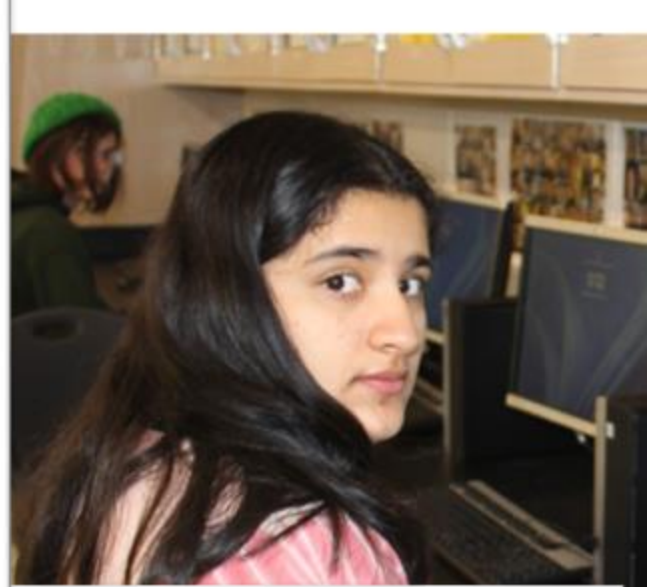
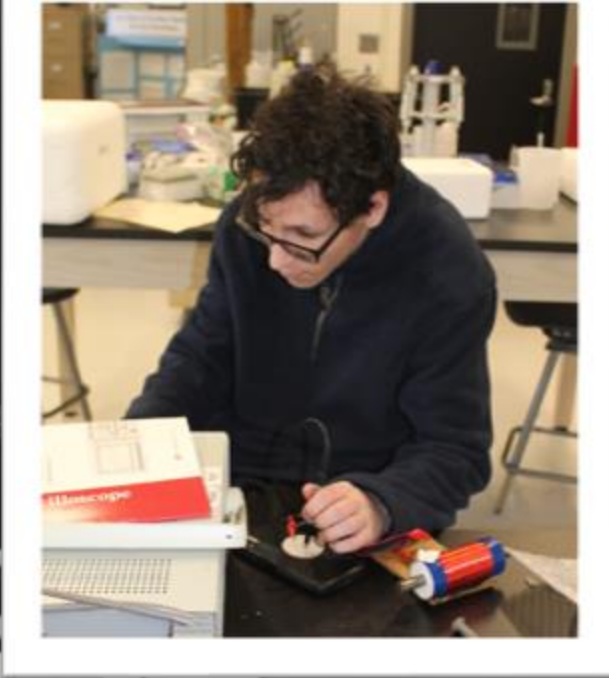
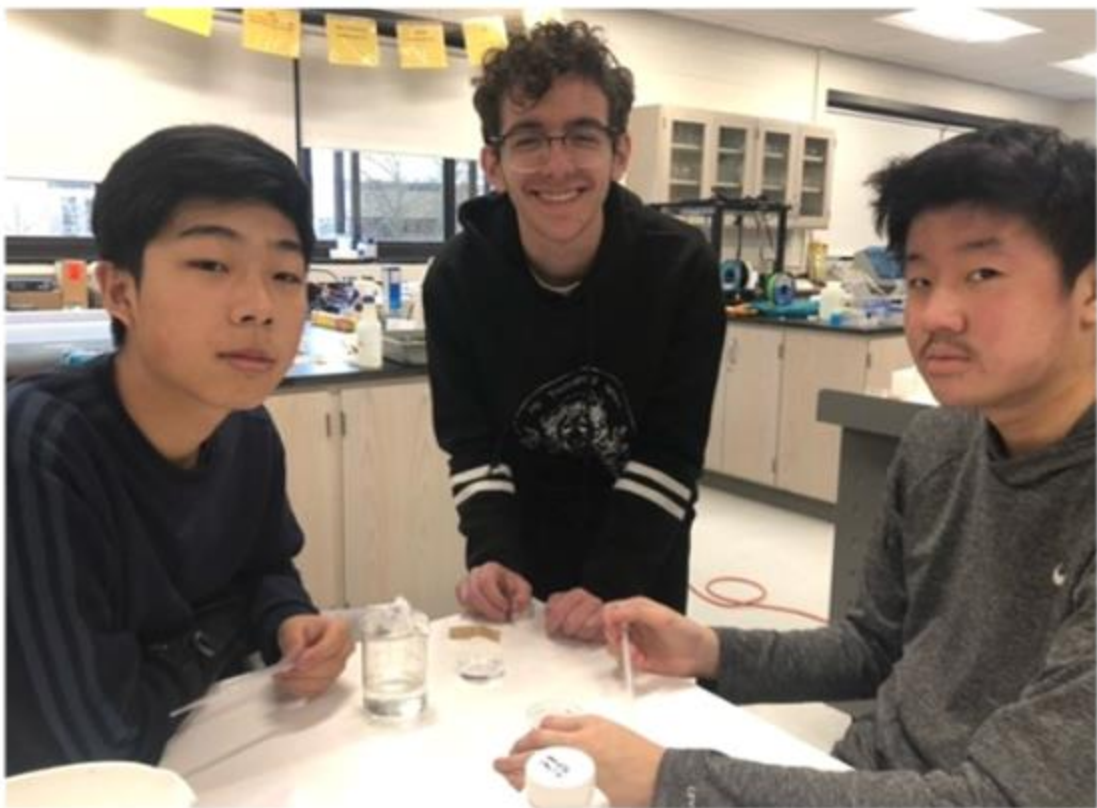
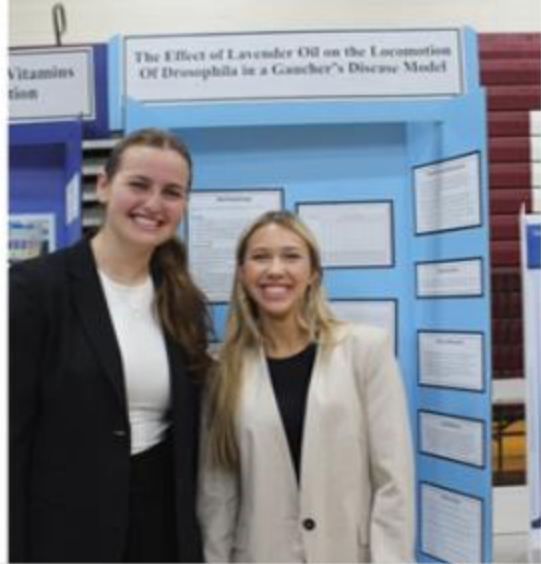
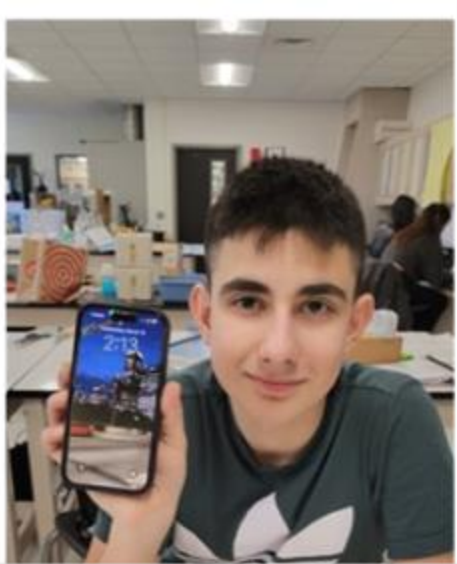




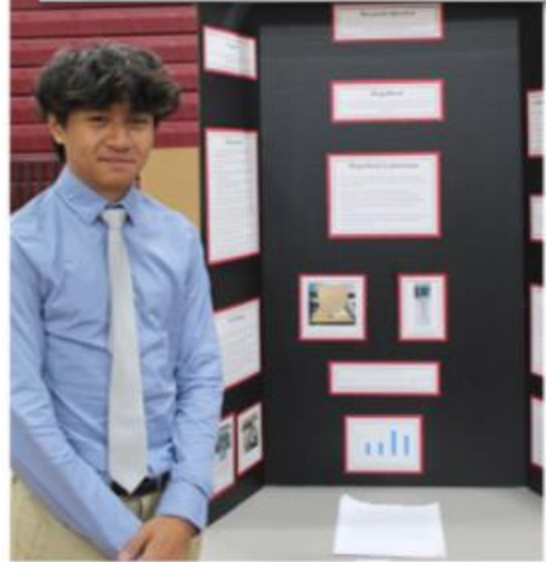
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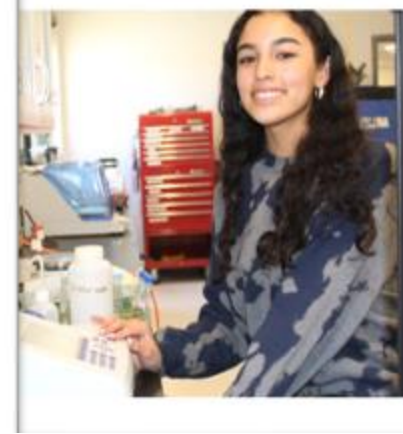
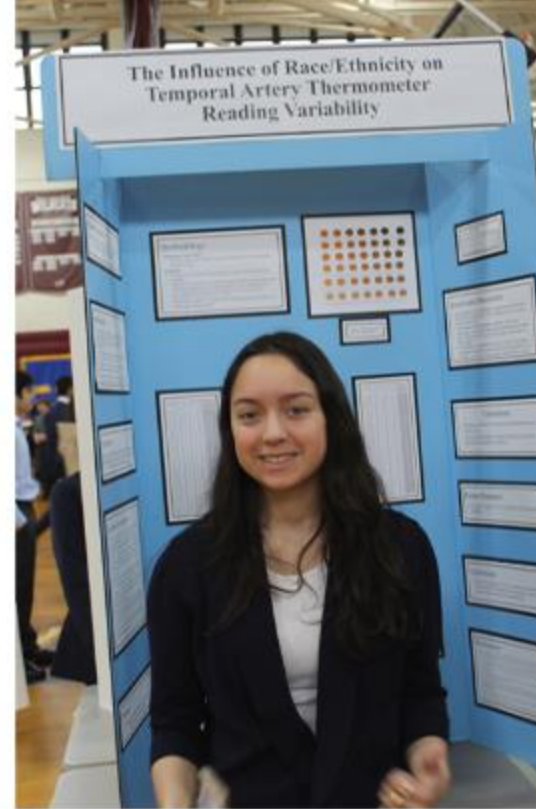
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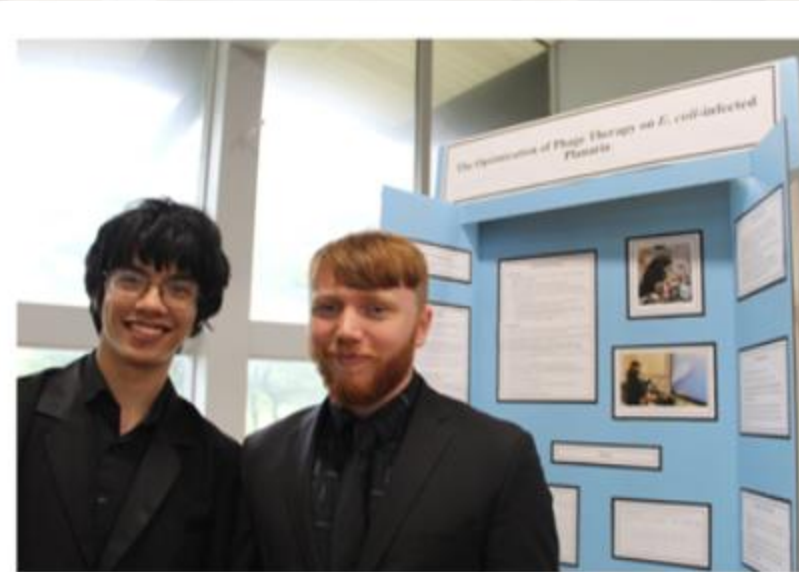
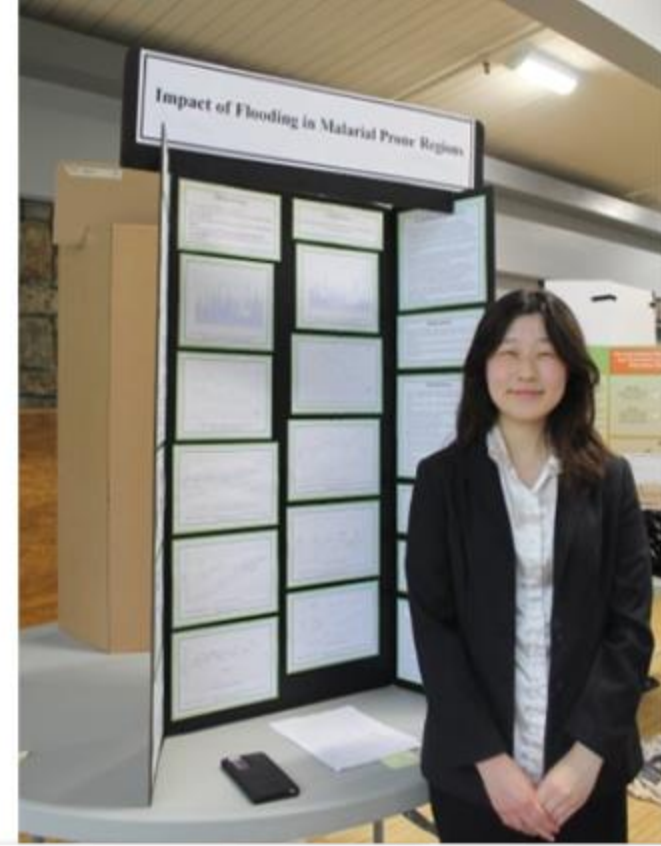
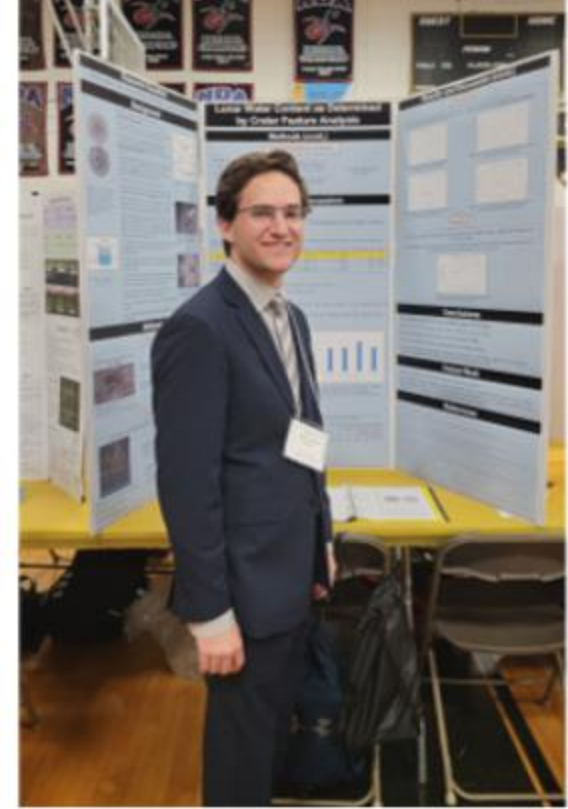


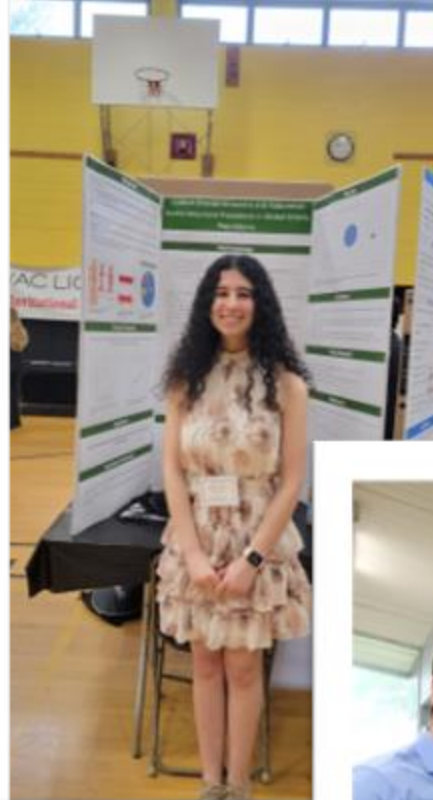
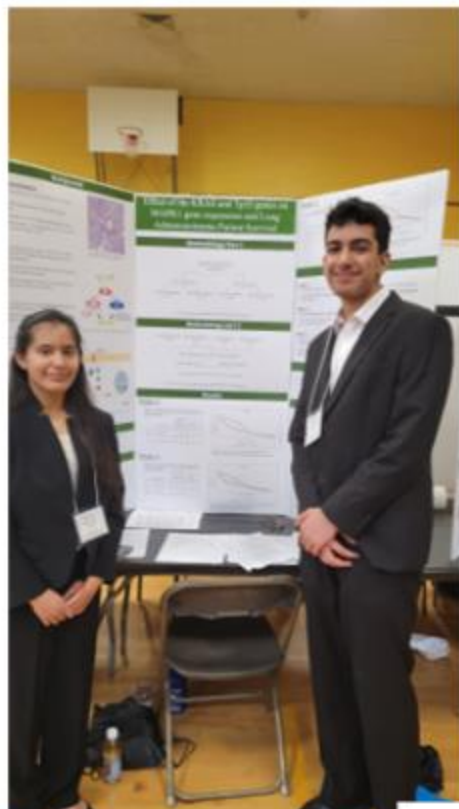
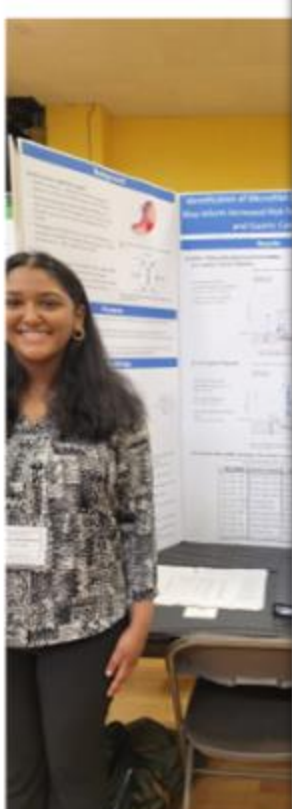


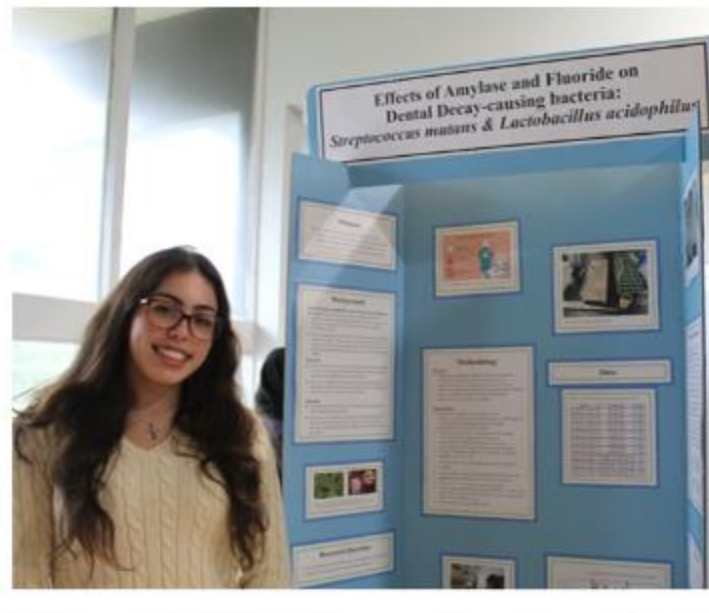
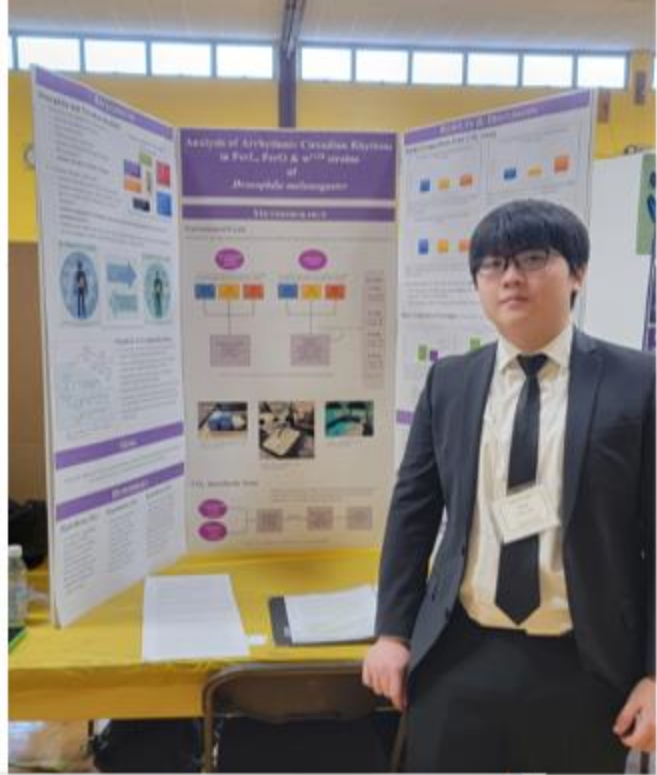
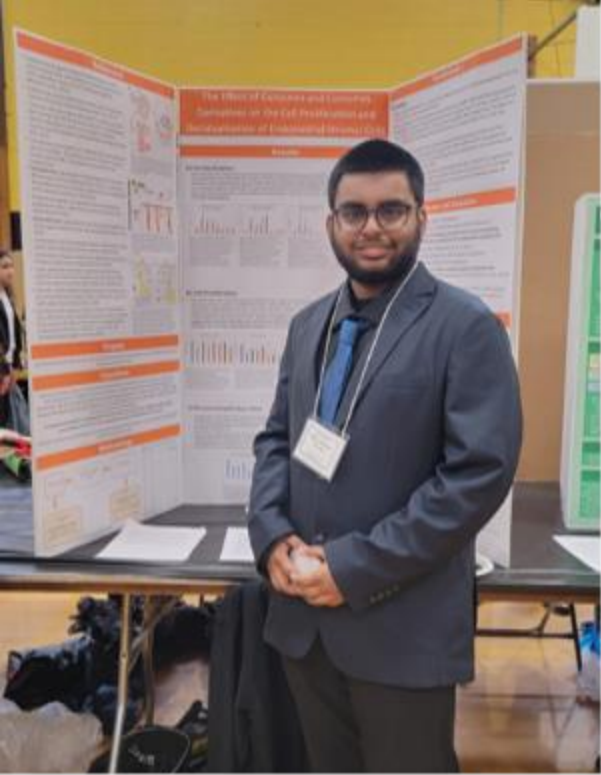


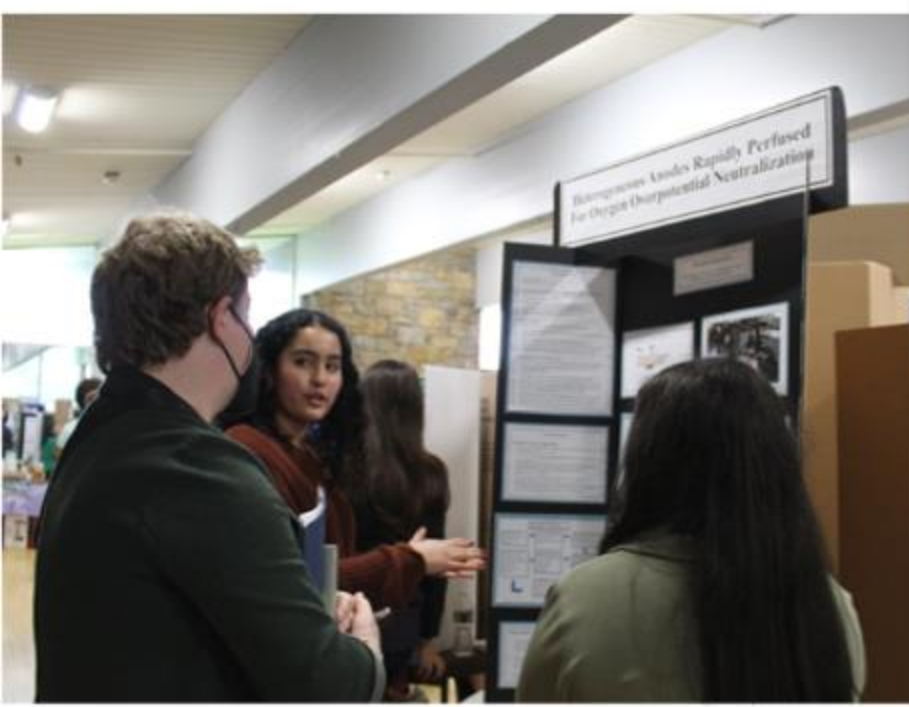


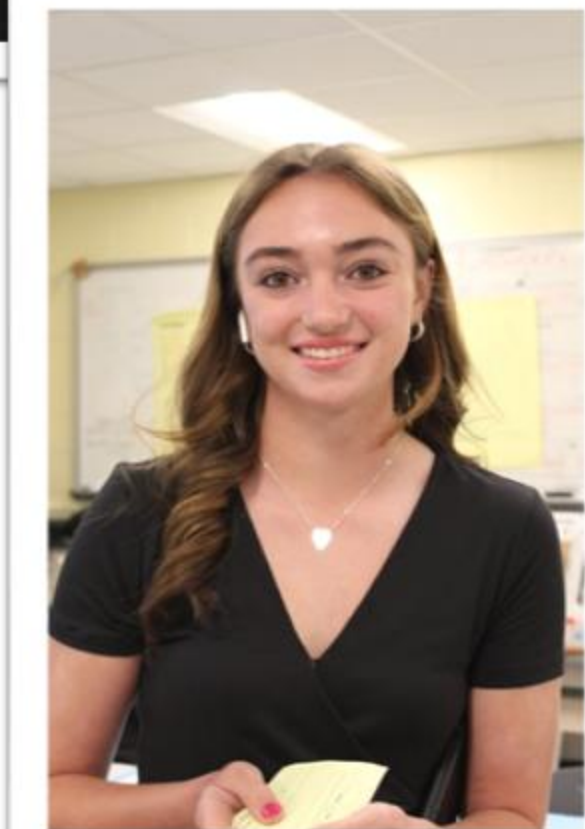
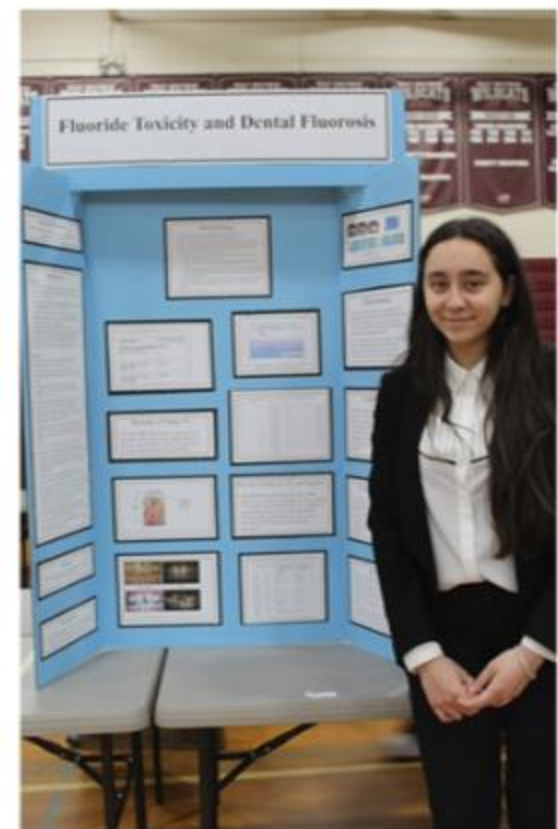


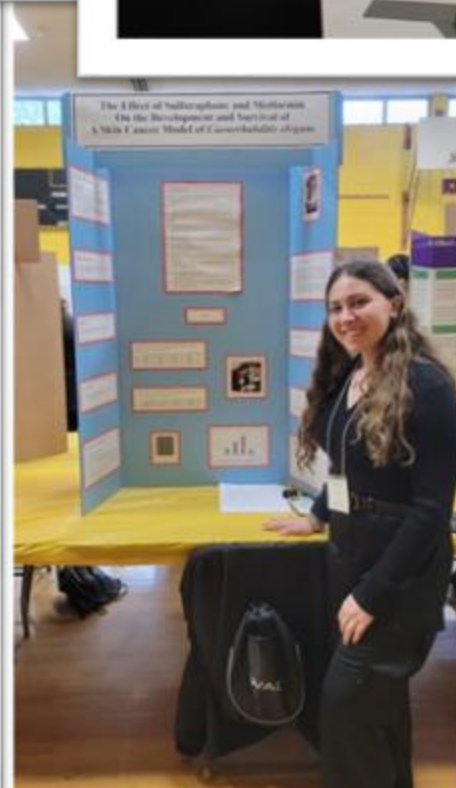
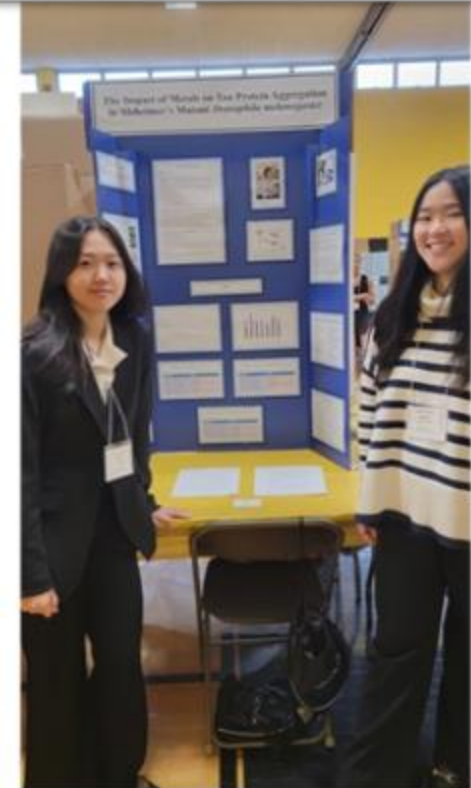


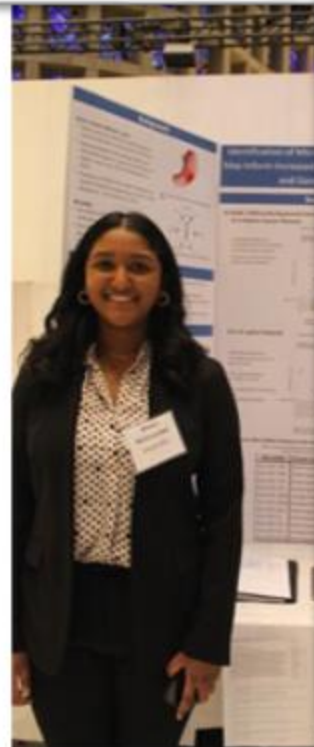
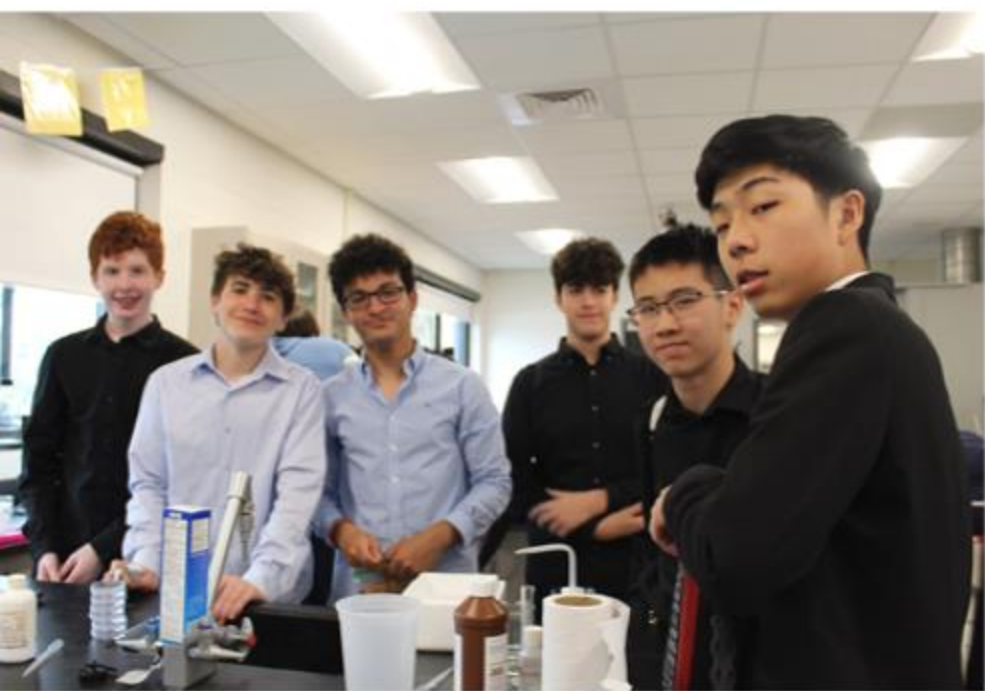


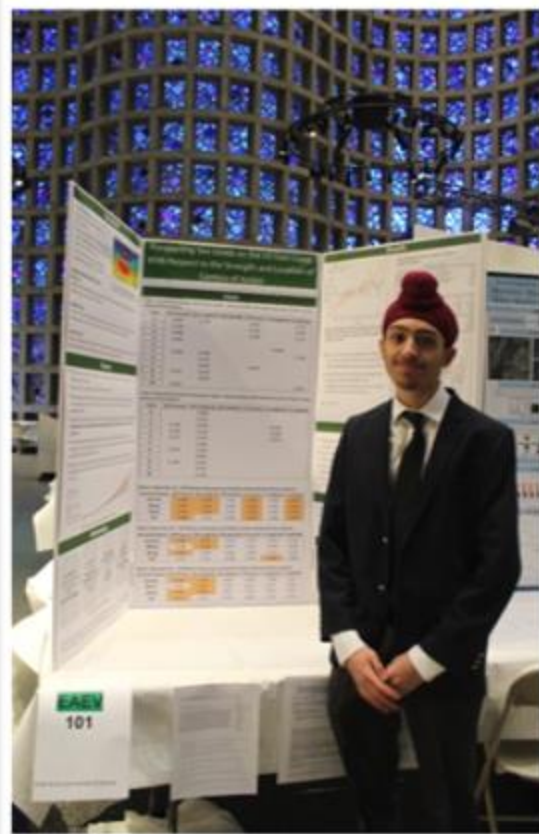
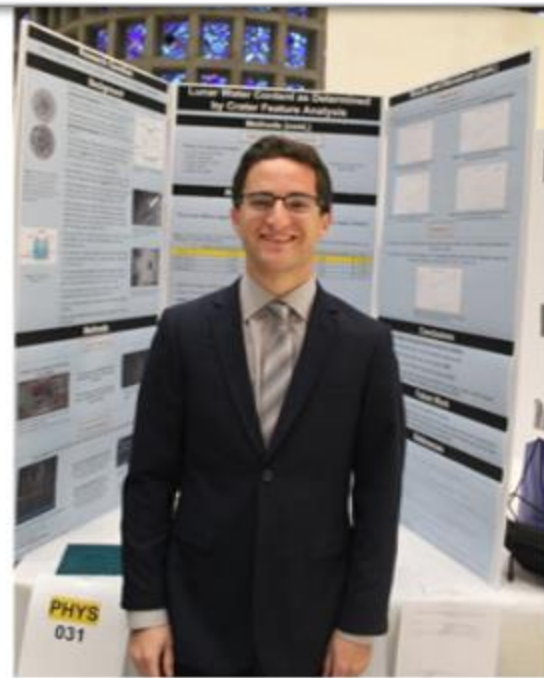
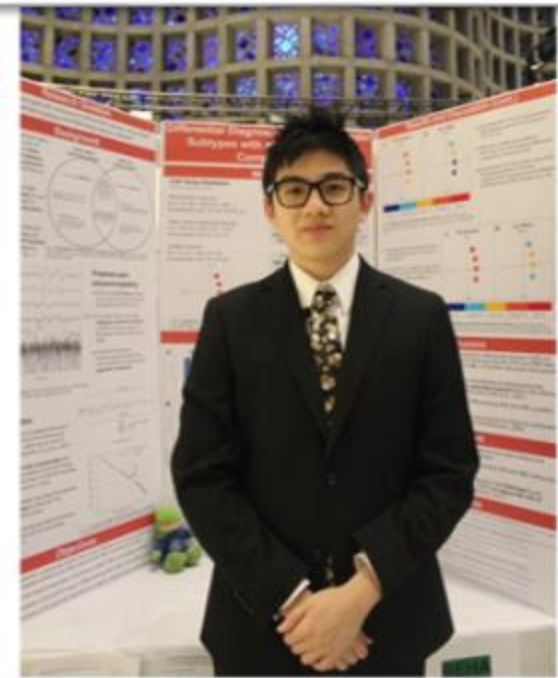


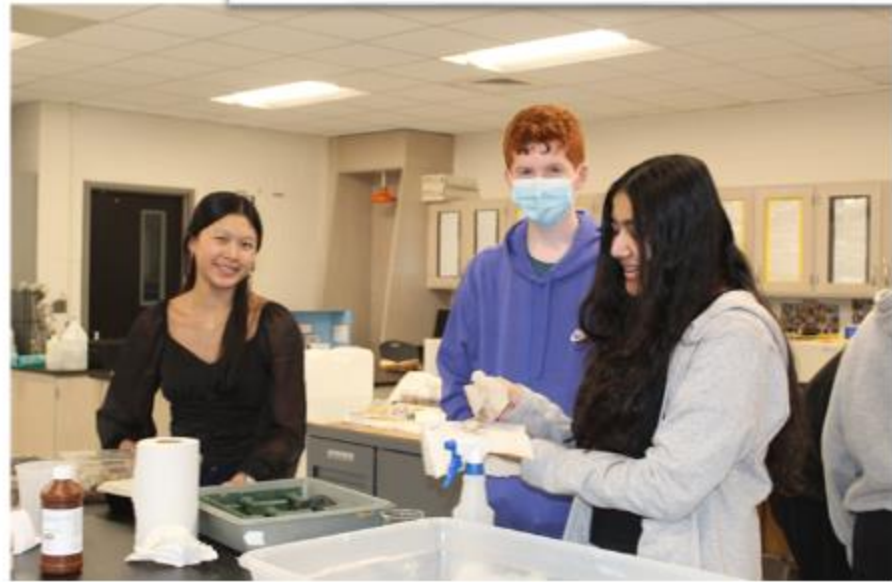
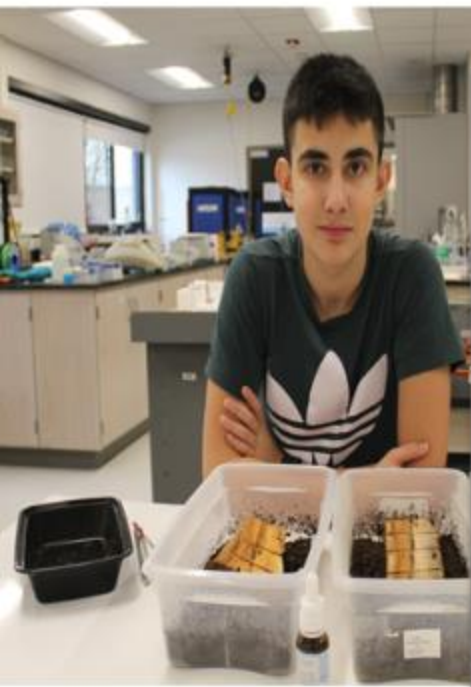
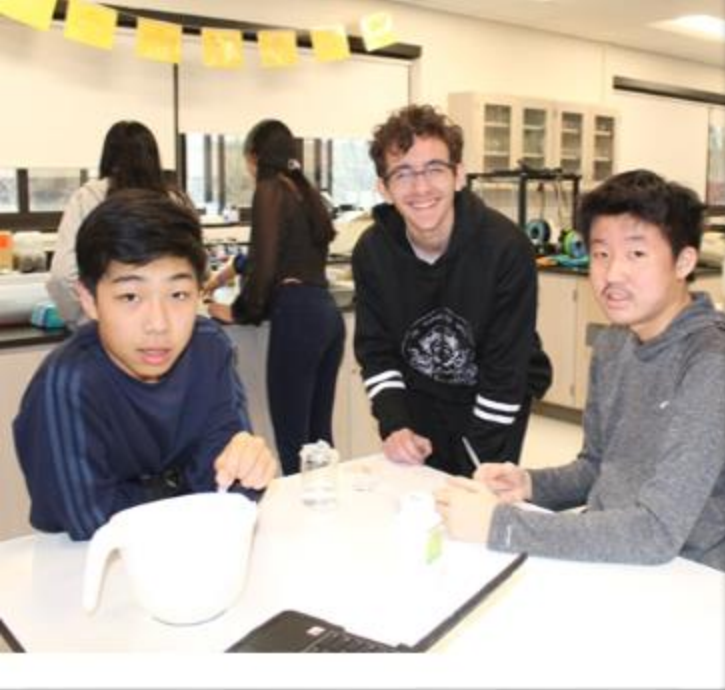


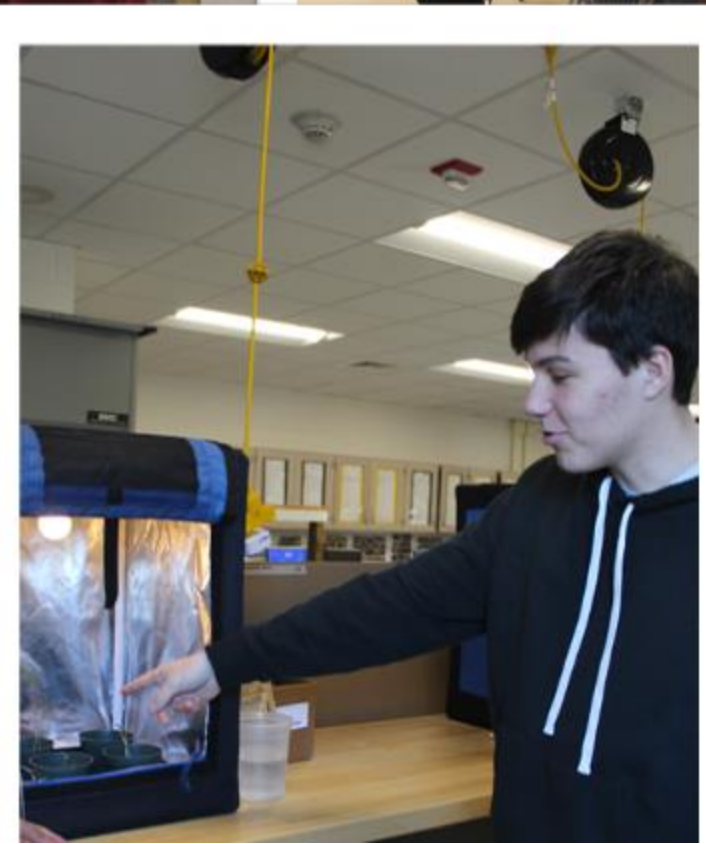


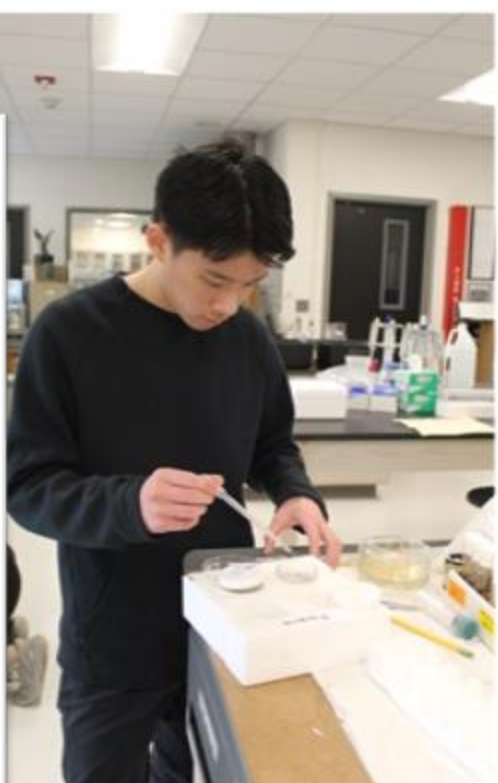
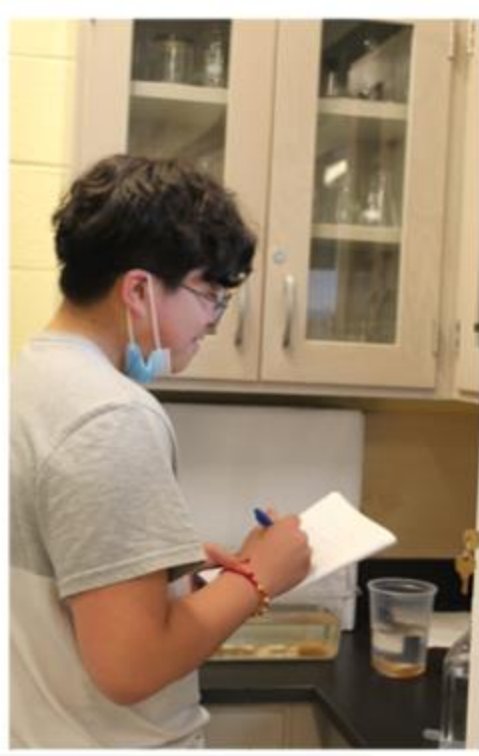
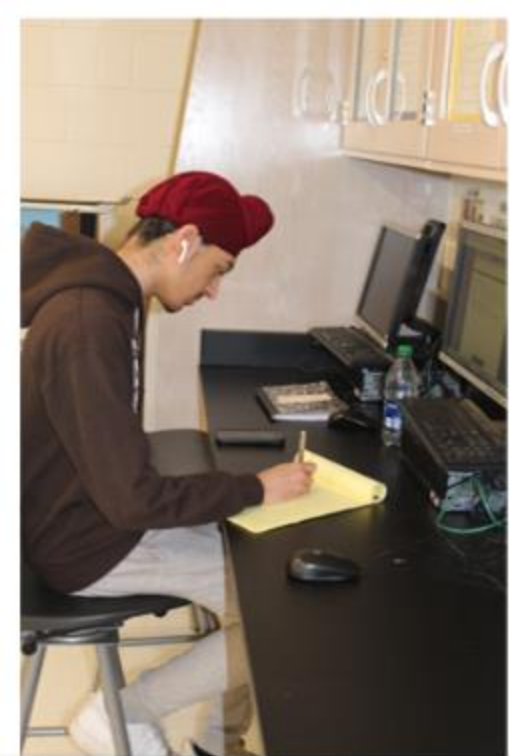






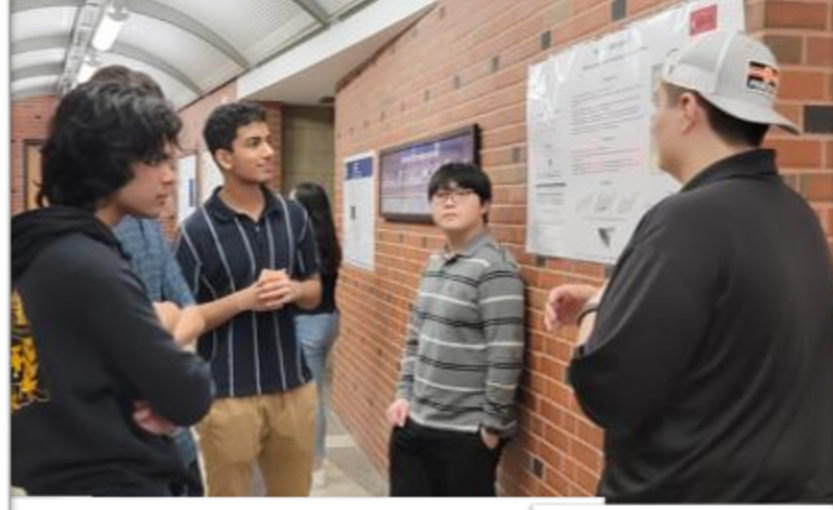




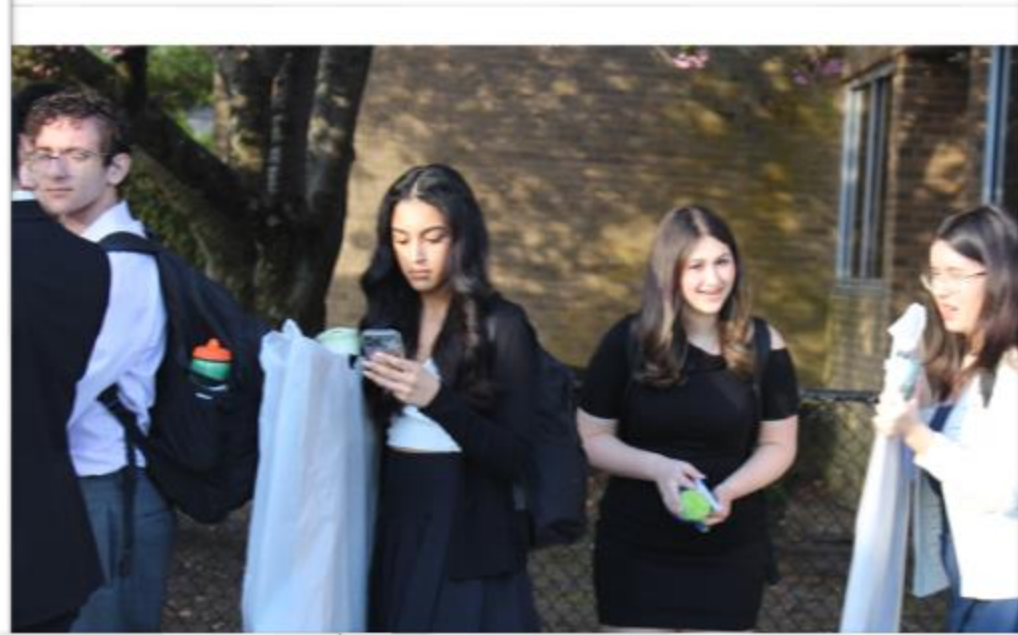


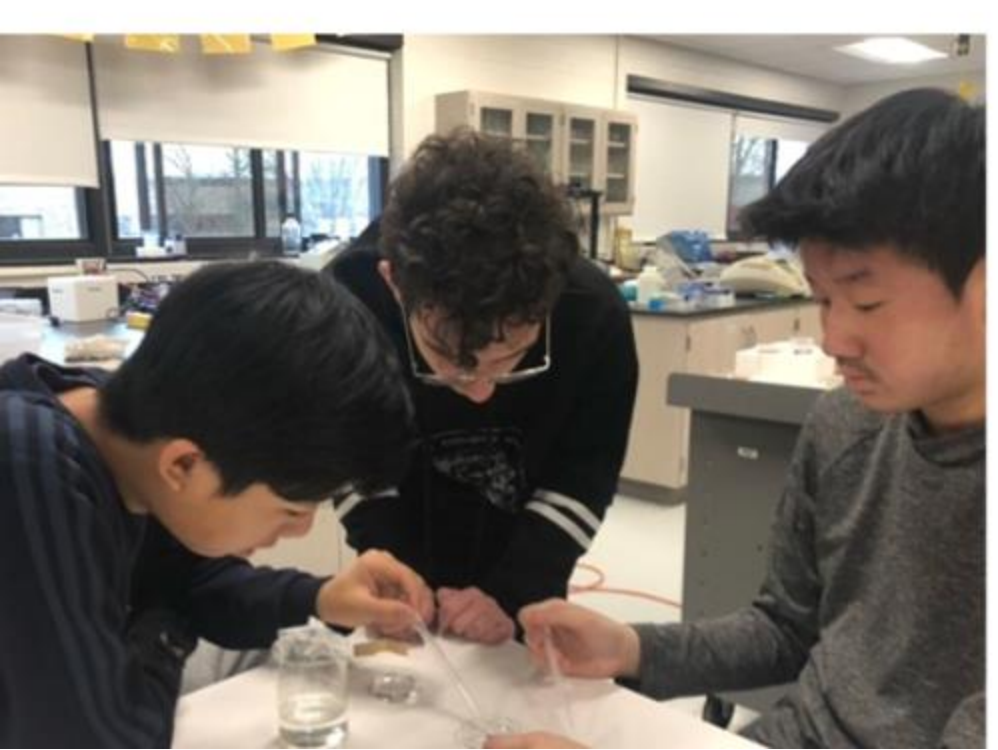
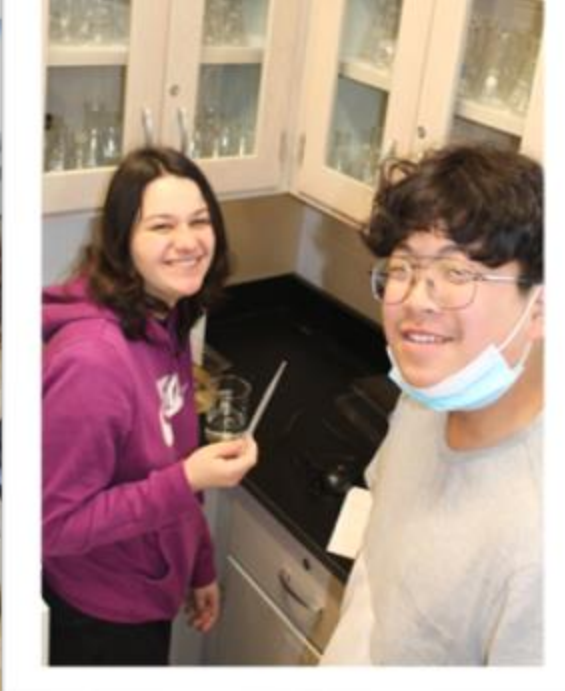












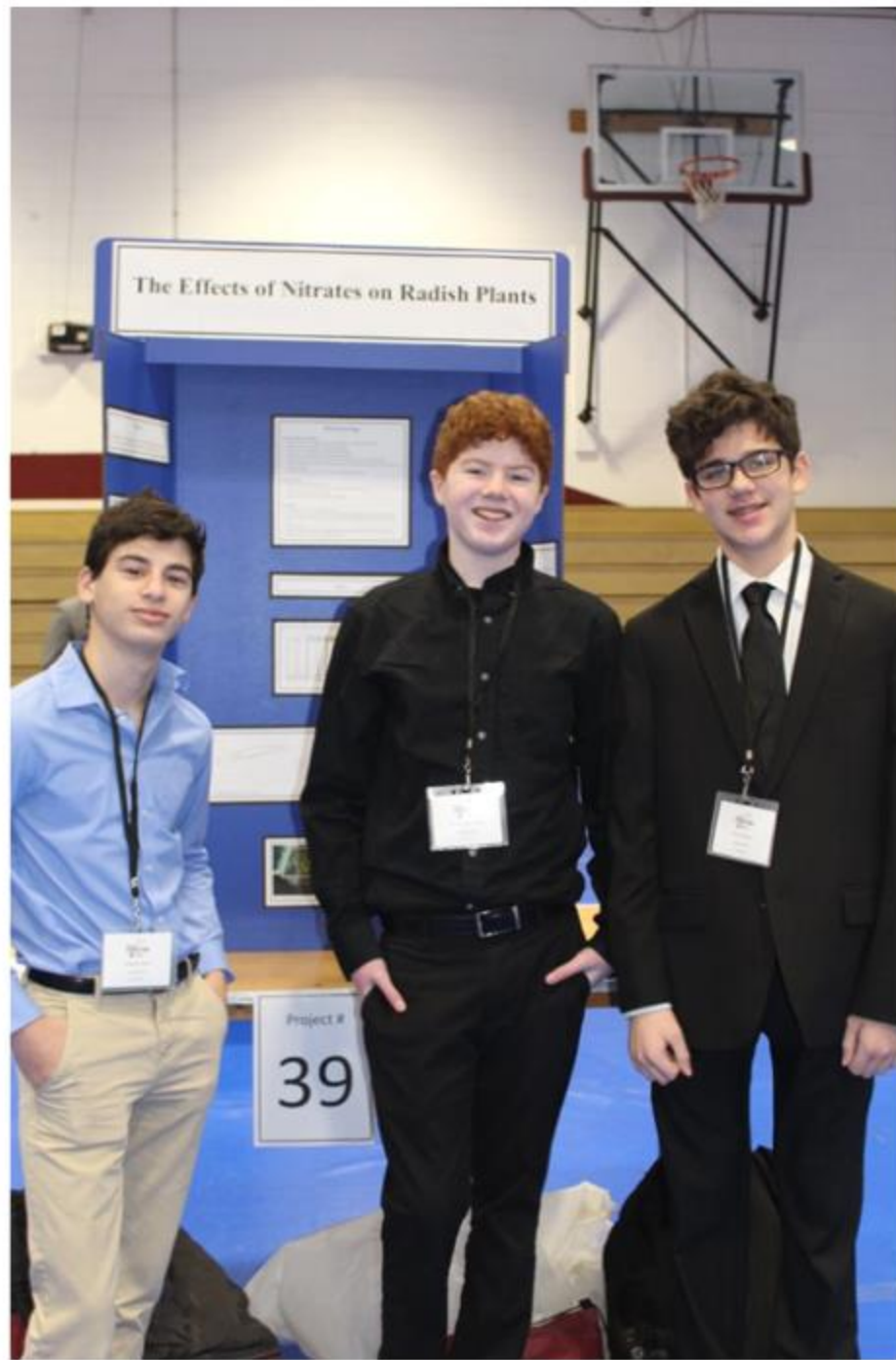


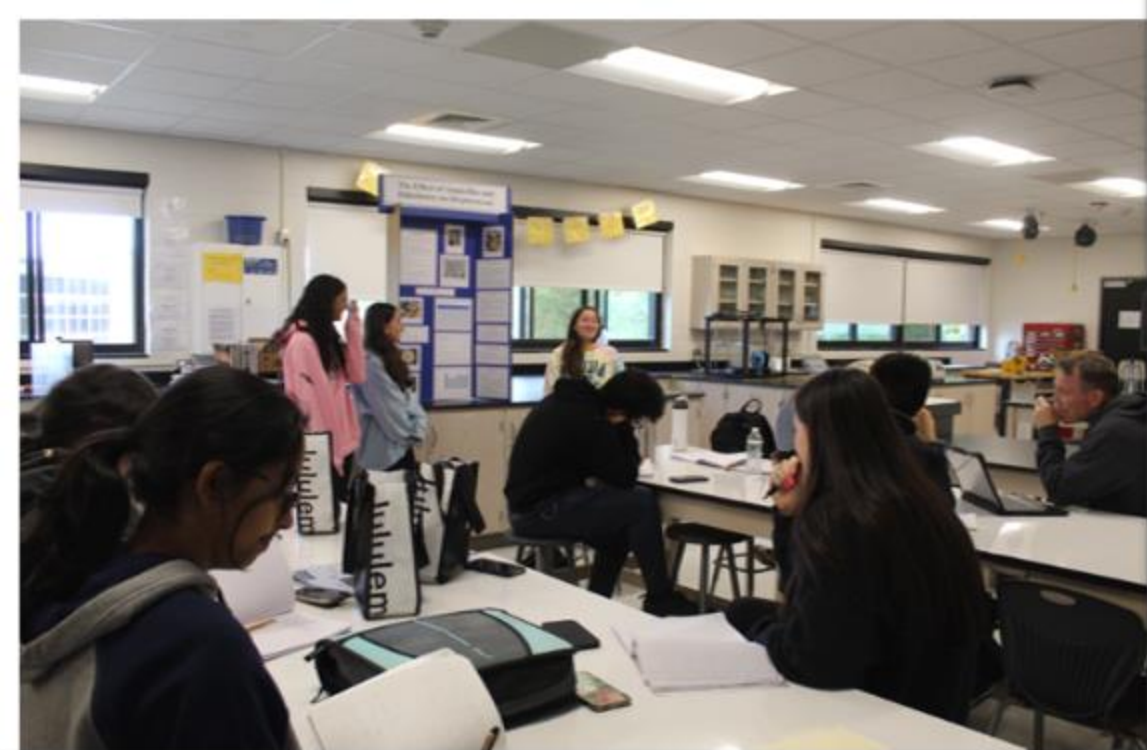




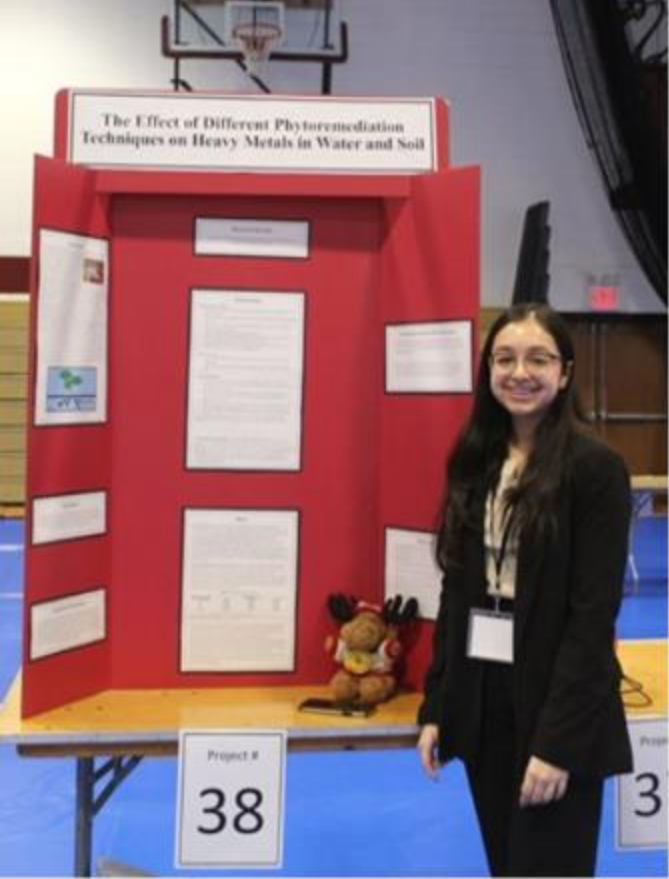


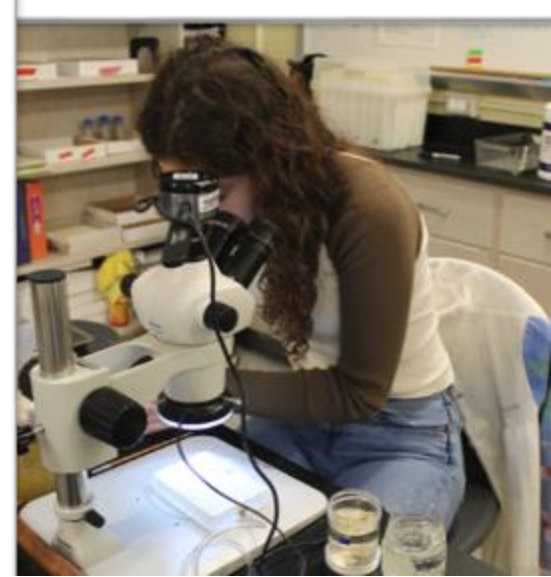
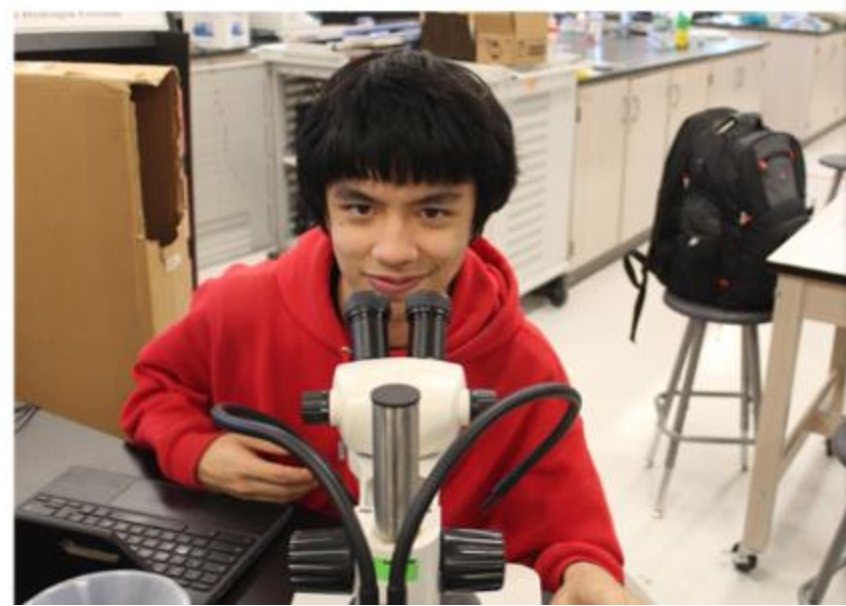
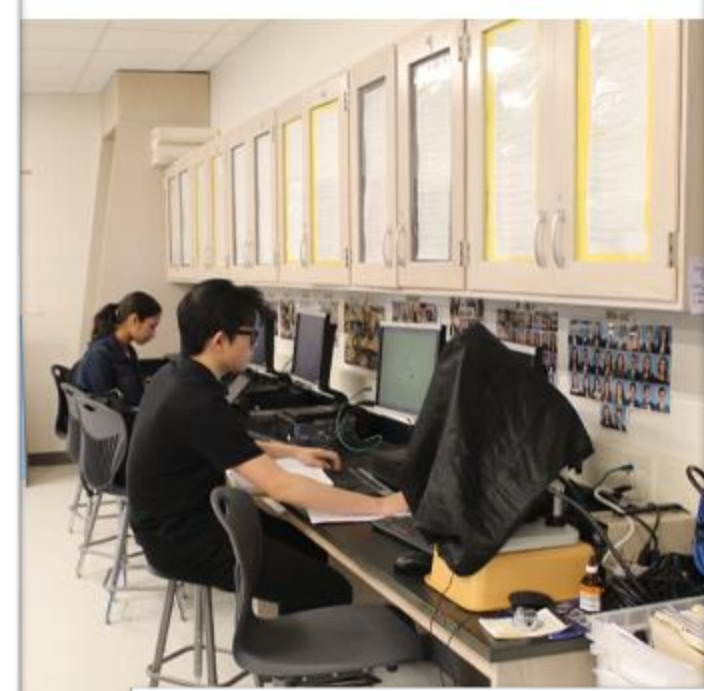
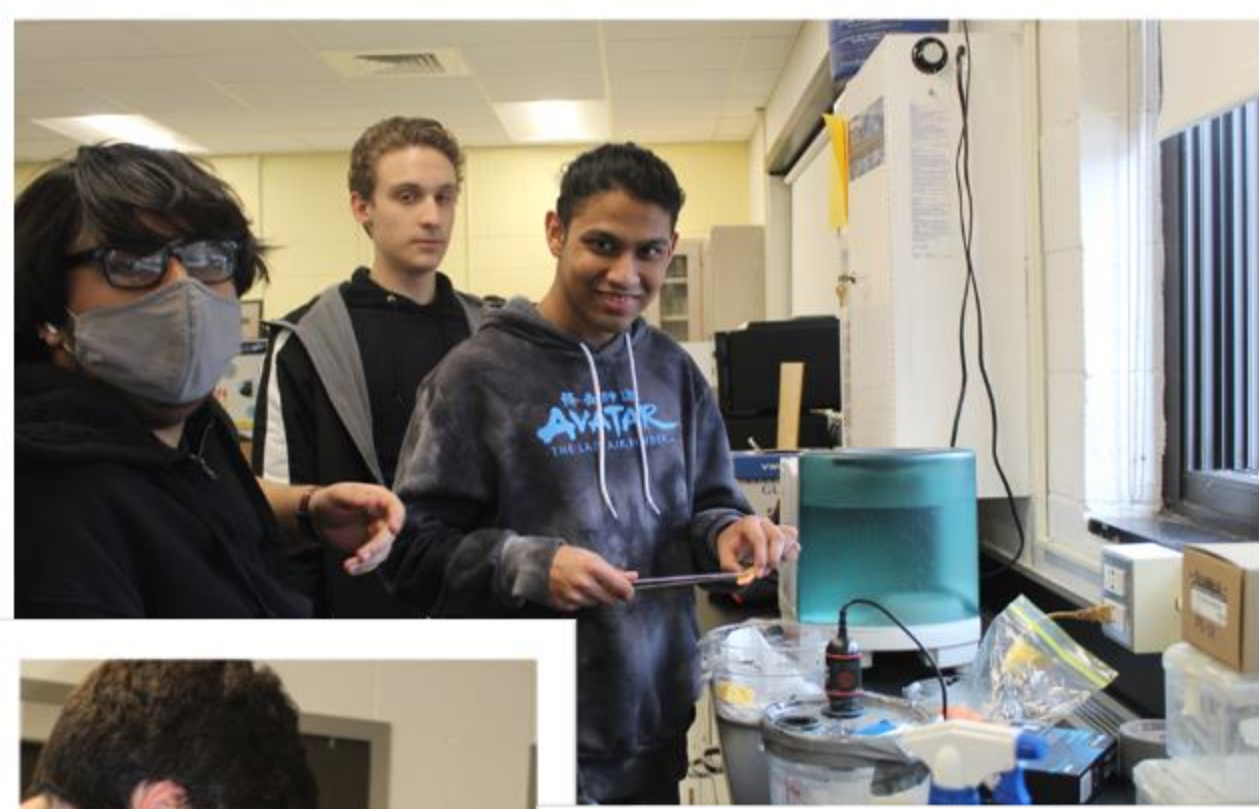


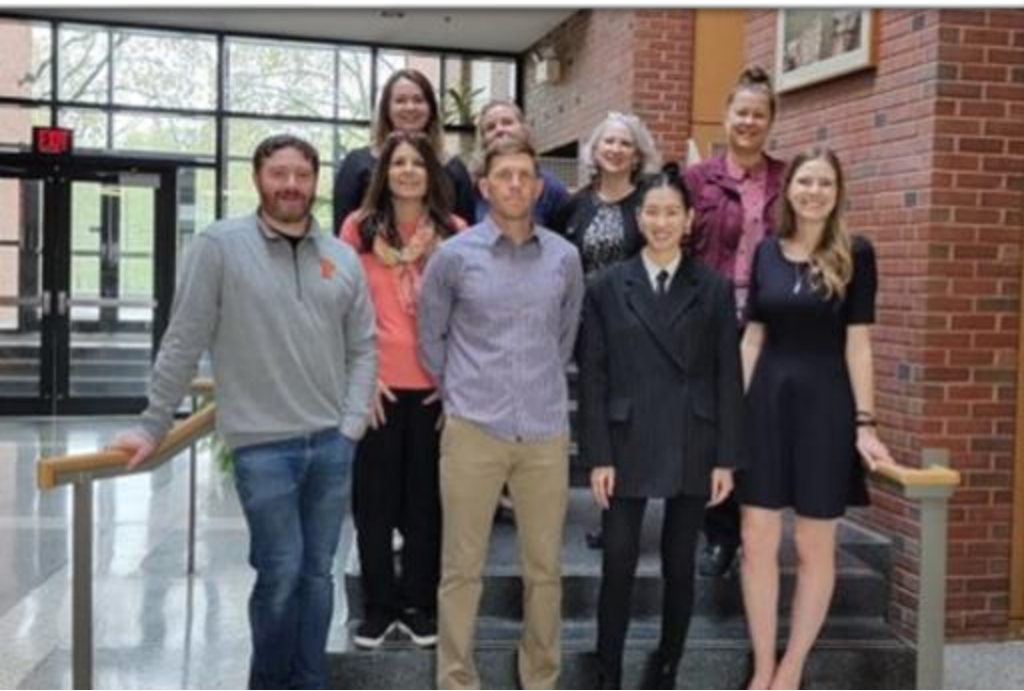










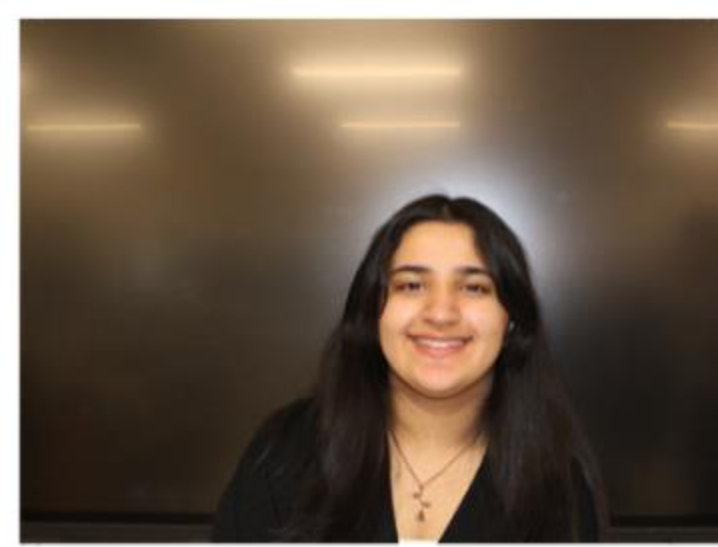


Different primers, Different enzymes

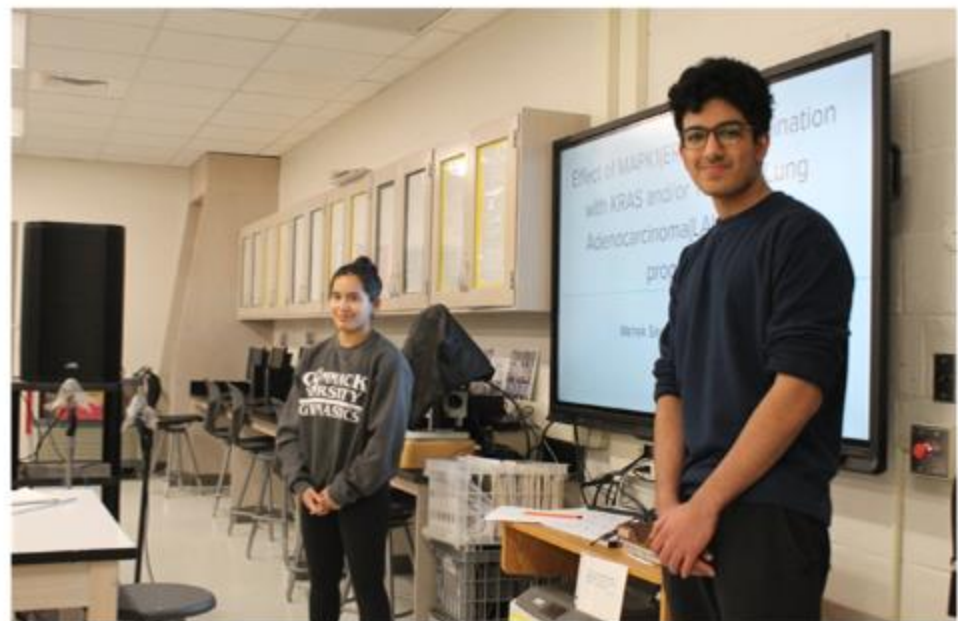
We had more success using HPAII over Sau3AI for identifying the gene, and it was more identifiable cut site, of which there was only one. Anna/Sp1 Berta was the best primer but had no success (student generated). n=15

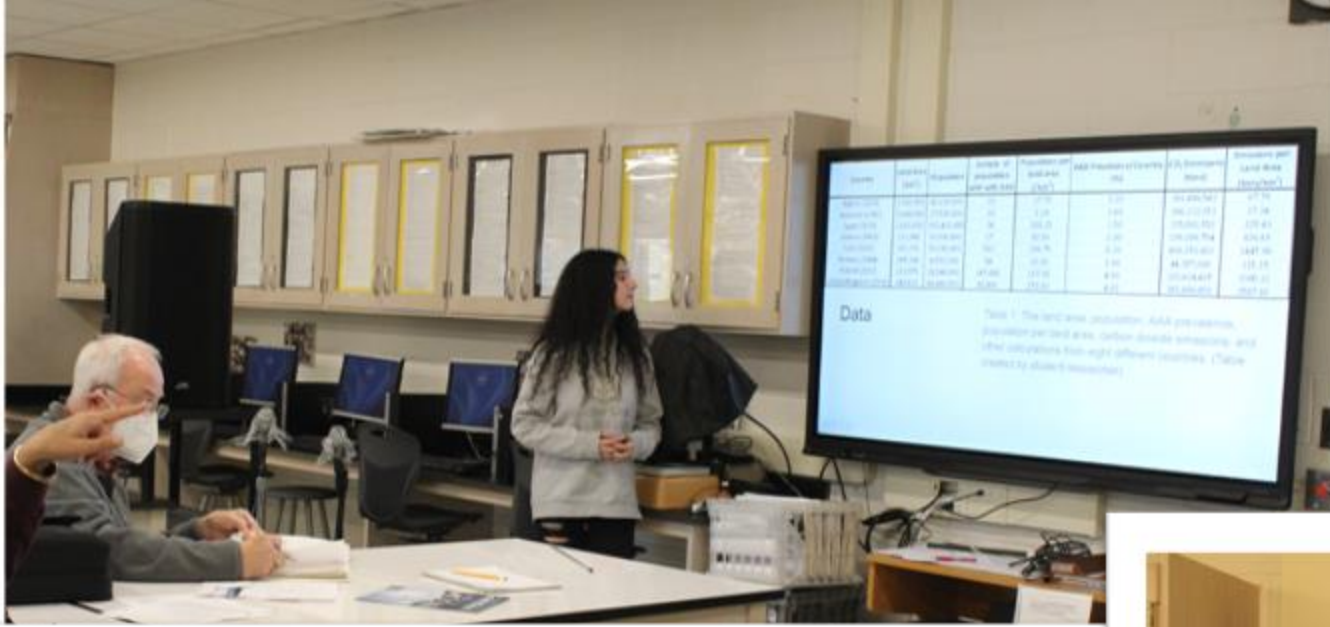
Sample run is OK (gene identified, no insertion site)	Sample run is Done (gene identified with insertion site)	Sample run is BAD
1: HPAII	1: HPAII	1: HPAII 1: Sau3AI
0	2: HPAII 1: Sau3AI (X2)	1: Sau3AI (x2)

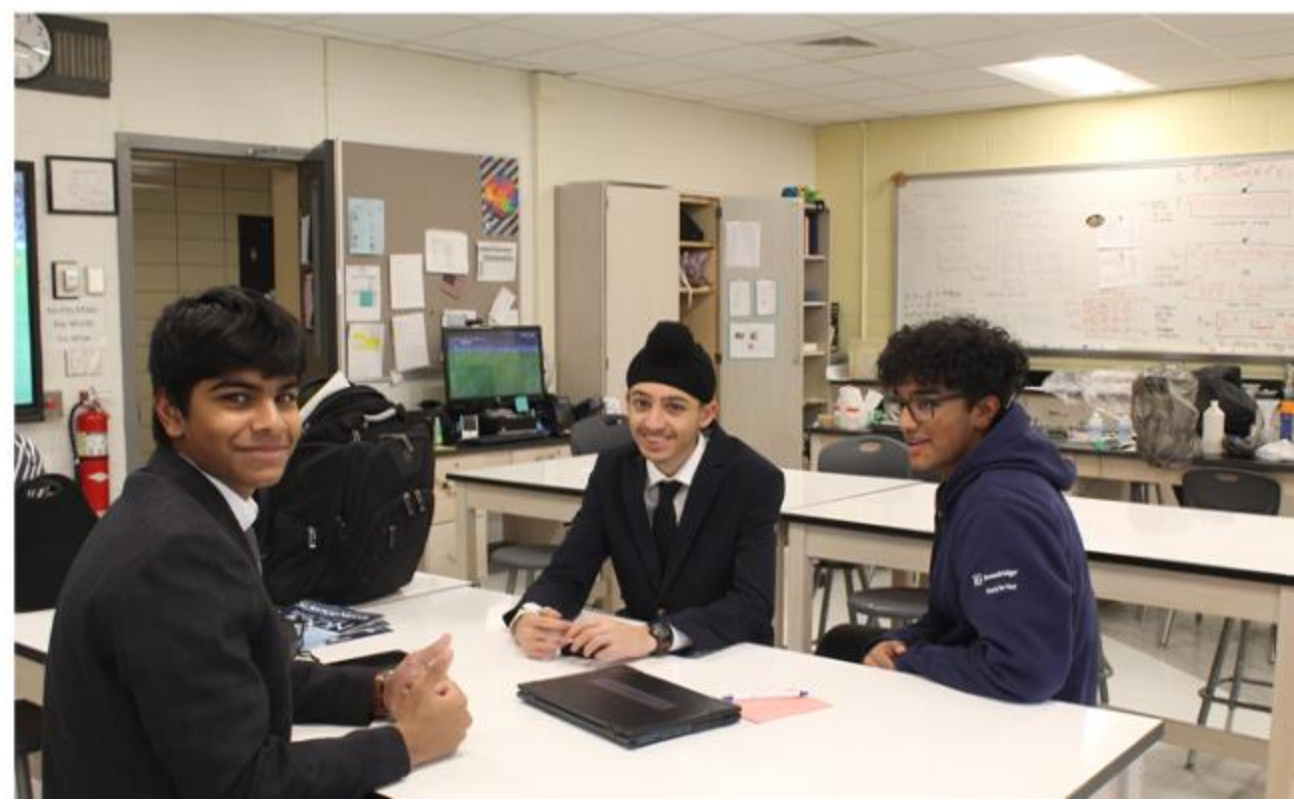


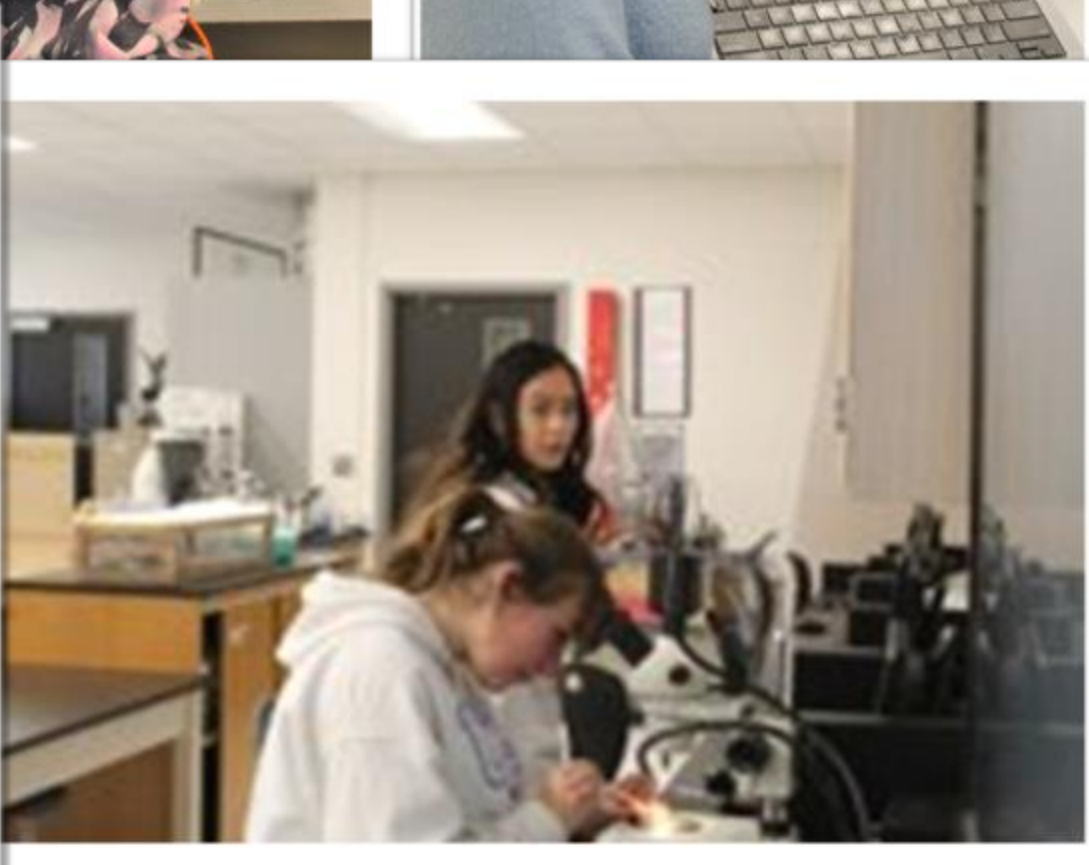
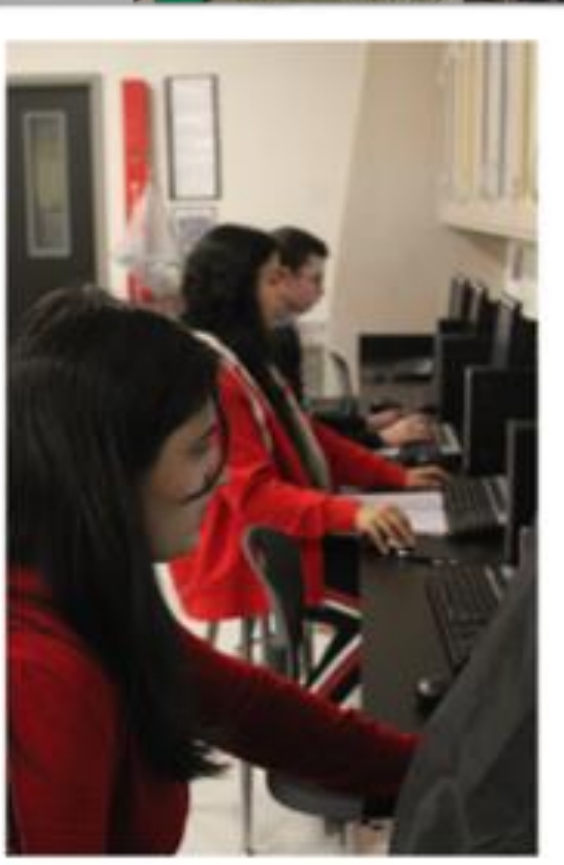
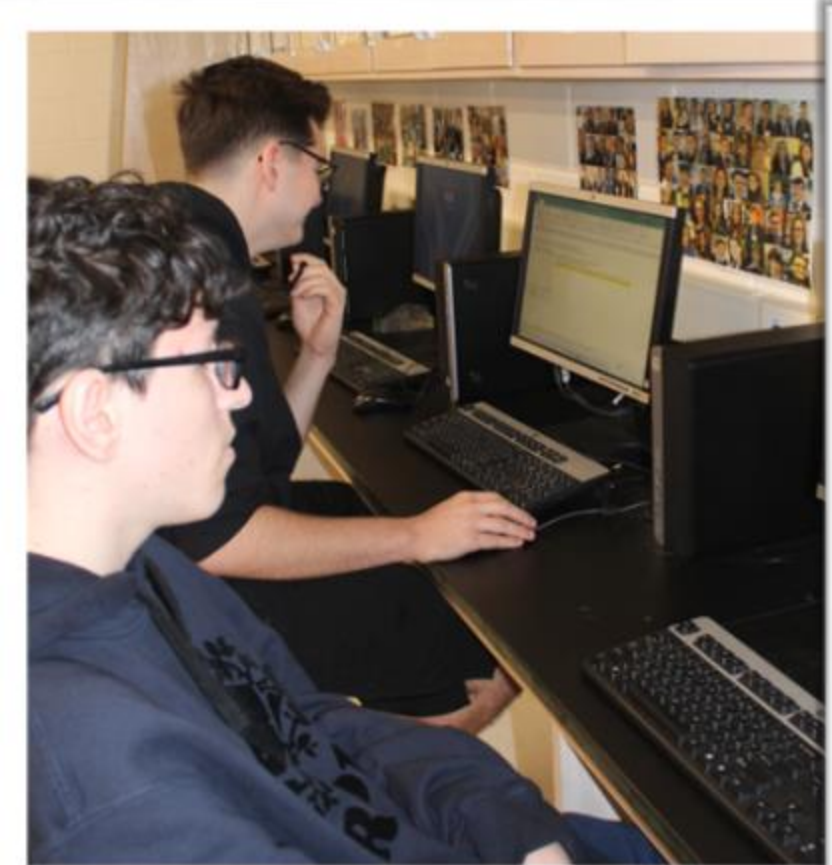




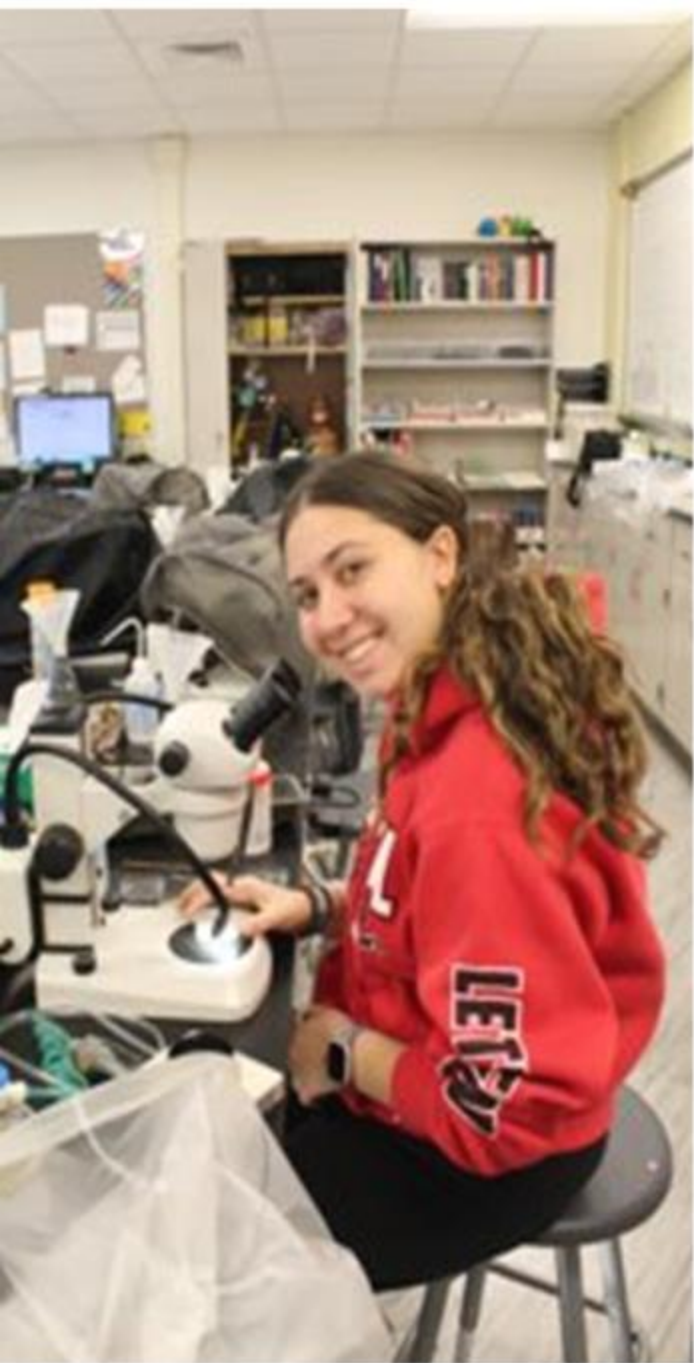




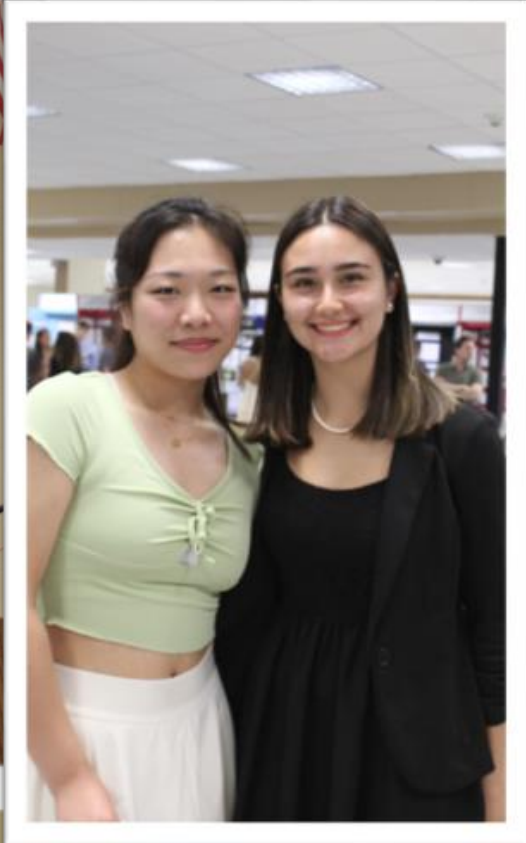












Thanks for the Memories!!!

6/8/2023