A atDNA follow-up and examples from a previous email.

FYI – For those who use multiple DNA testing, it is helpful to define the type of DNA test. Just saying DNA tests prove/indicate does not indicate what type of test(s) completed.

Y-Chromosomal DNA is often referenced as Y-DNA.
Mitochondrial DNA is referenced as mtDNA.
Autosomal DNA is cited as atDNA.

I suspect the Carpenter DNA match you cited is atDNA. These atDNA tests are all basically the same despite whether they come from FamilyTree DNA (aka Family Finder), Ancestry.com (The DNA Test – the only one they do now!) or from 23andMe or another DNA testing lab. The difference is the "add on" testing for things like medical like traits for health issues, eye color and such.

Earlier I mentioned that the following briefs are often helpful and good for review.
https://carpentercousins.com/DNATesting.pdf
https://carpentercousins.com/A-little-more-on-atDNA-and-SNP-testing.pdf - Two helpful charts on atDNA at the end of the article.

I attach those two charts. Depending on the shared size of your centimorgan (cMs) Carpenter match the related chart will help narrow down that match relationship. These charts provide a more accurate version that the DNA testing companies provide.

Let us say you have a 445 cMs match.

On the chart going right from SELF, the closest average match is a 439 for a First Cousin once removed (1C1R).

BUT … Going left from SELF, the closest match is the closest average match is a 457 Half 1C (half first cousin).

IT IS IMPORTANT to remember to look left then right (or right then left in the UK) for matches on this chart.

The other chart is to help you understanding that the randomness of recombination (egg & sperm DNA) will allow NON-MATCHES of atDNA over time. Basically some atDNA is filtered out over time.

As a reminder …
You own 100% of your atDNA but only get 50% from your parents, 25% from your grandparents and each generation back is halved. At the sixth generation in the past you are at 1.5625% and this 1% range is where you start to get random matches or matches "identical by state."

You – 100% of your atDNA Parents 50% from each <- 2 gen - most matches are 1st cousins or uncles & aunts
2GP 12.5% <- 3 gen - most matches are 2nd cousins
3GP 6.25% <- 4 gen - most matches are 3rd cousins

4GP 3.125% <- 5 gen - most matches are 4th cousins
5GP 1.5624% <- 6 gen - most matches are 5th cousins - 1% range
6GP 0.78125% <- 7 gen - most matches are 6th cousins
7GP 0.390625% <- 8 gen - most matches are 7th cousins

IF you were testing **your 5GP remains** (5 x great grandparent) and obtained a DNA sample the possibility of no detectable atDNA relationship would be **4.95%. This is a single direct line descendant match.**

BUT … If you were testing your 5th cousin and you both have the same 5GP genealogically then the probability on having no detectable atDNA relationship would be **69.80%. Why?** When you have two atDNA lines going back to your most recent common ancestor (MRCA aka 5GP) then your 5GP atDNA is halfed for each generation for two lines. **It is an exponential difference.**

AND … Since you are in the 1% range (and less than) you will start to see random matches – better known in atDNA circles as "identical by state."

This means your "matches" at the Great-Great-Great-Great-Grandparent (5GP) range (aka "Other Relationships" on chart) represent only about 30.20% of your possible atDNA ancestors. **And your best match at this range will be an average of 21 cMs and those less than 21cMs will not be as good.**

Finally the only practical way to tell if the average 21 cMs or less is a true match (identical by state), and not a random one, is to do the genealogy. This by showing a documented paper trail relationship.

The less practical way is using atDNA triangulation of many confirmed relatives - ideally one or more per generation back into time to the most recent common ancestor and a super computer like the one at GEDMATCH.com. The more valid related atDNA tests involved, the more accurate the triangulation results will be.

Why? The super computer will crunch the many cMs into various commonalty segments and using a probability routine to determine whether or not all or a portion of those specific cM segments and sequences are related to the others.

I hope you did not mind me switching into teaching mode on the above subject.

Take care and good hunting!

John R. Carpenter
La Mesa, CA USA
https://carpentercousins.com