

Supplementary data

A capsid protein fragment of a fusagra-like virus found in *Carica papaya* latex interacts with the 50S ribosomal protein L17

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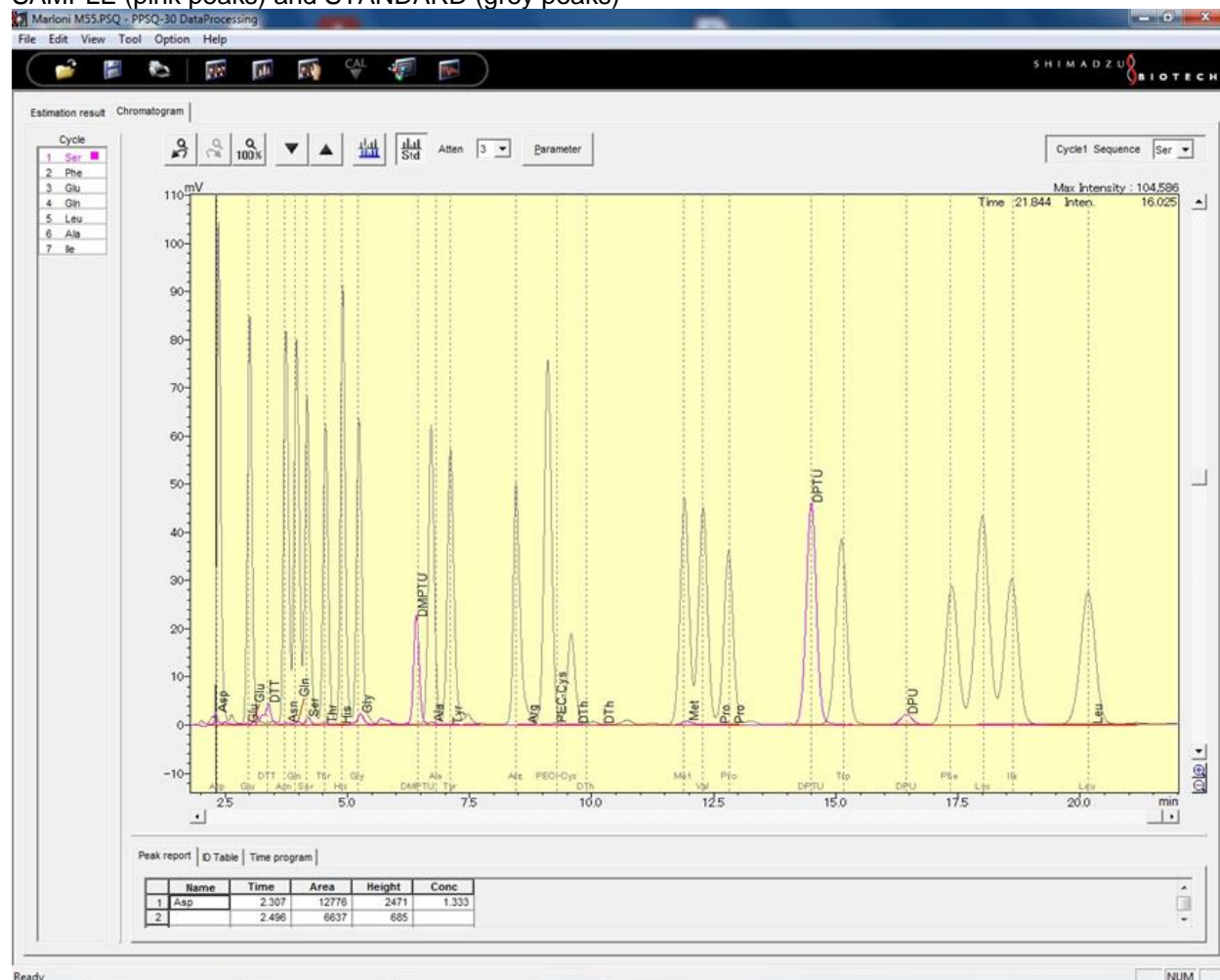
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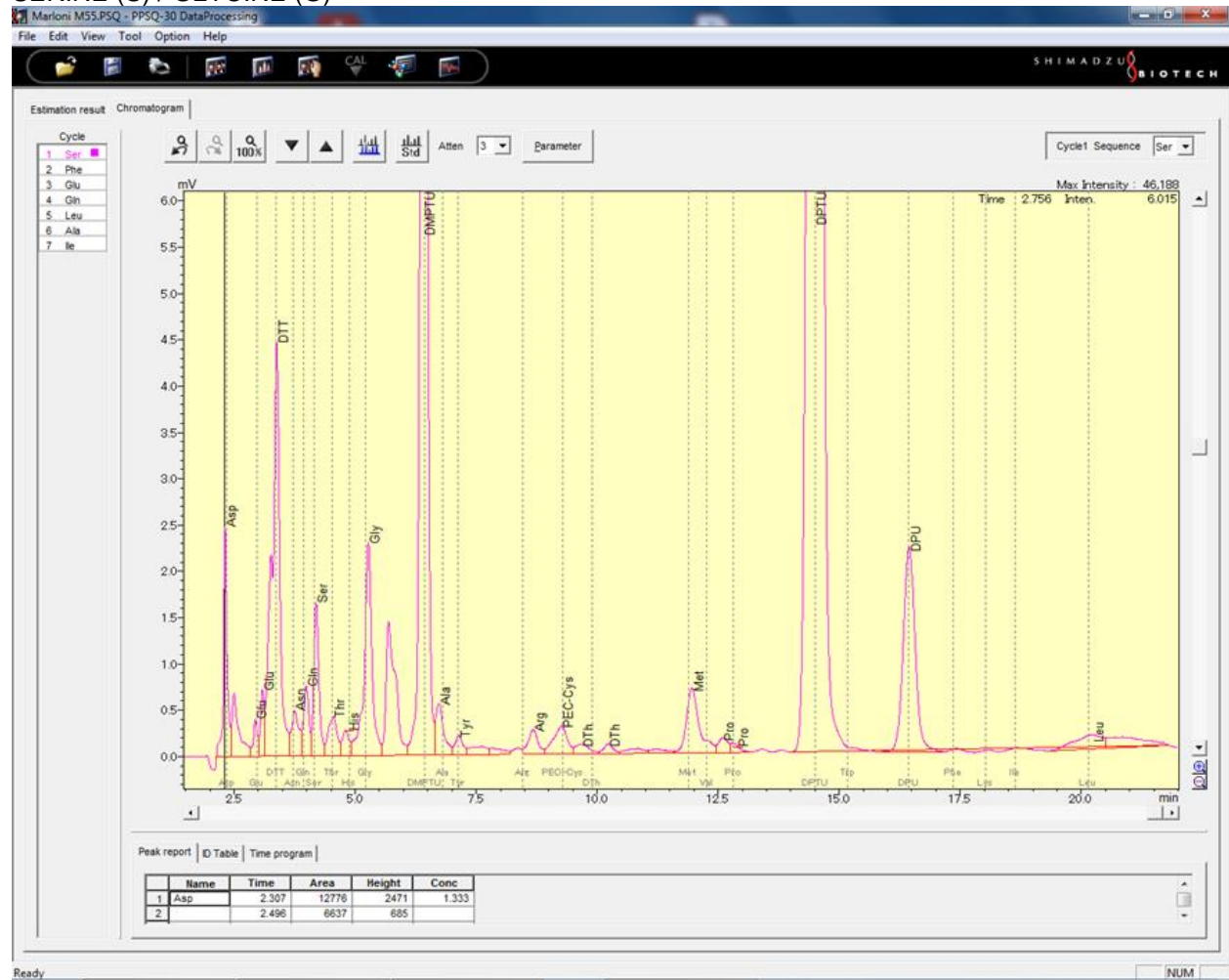
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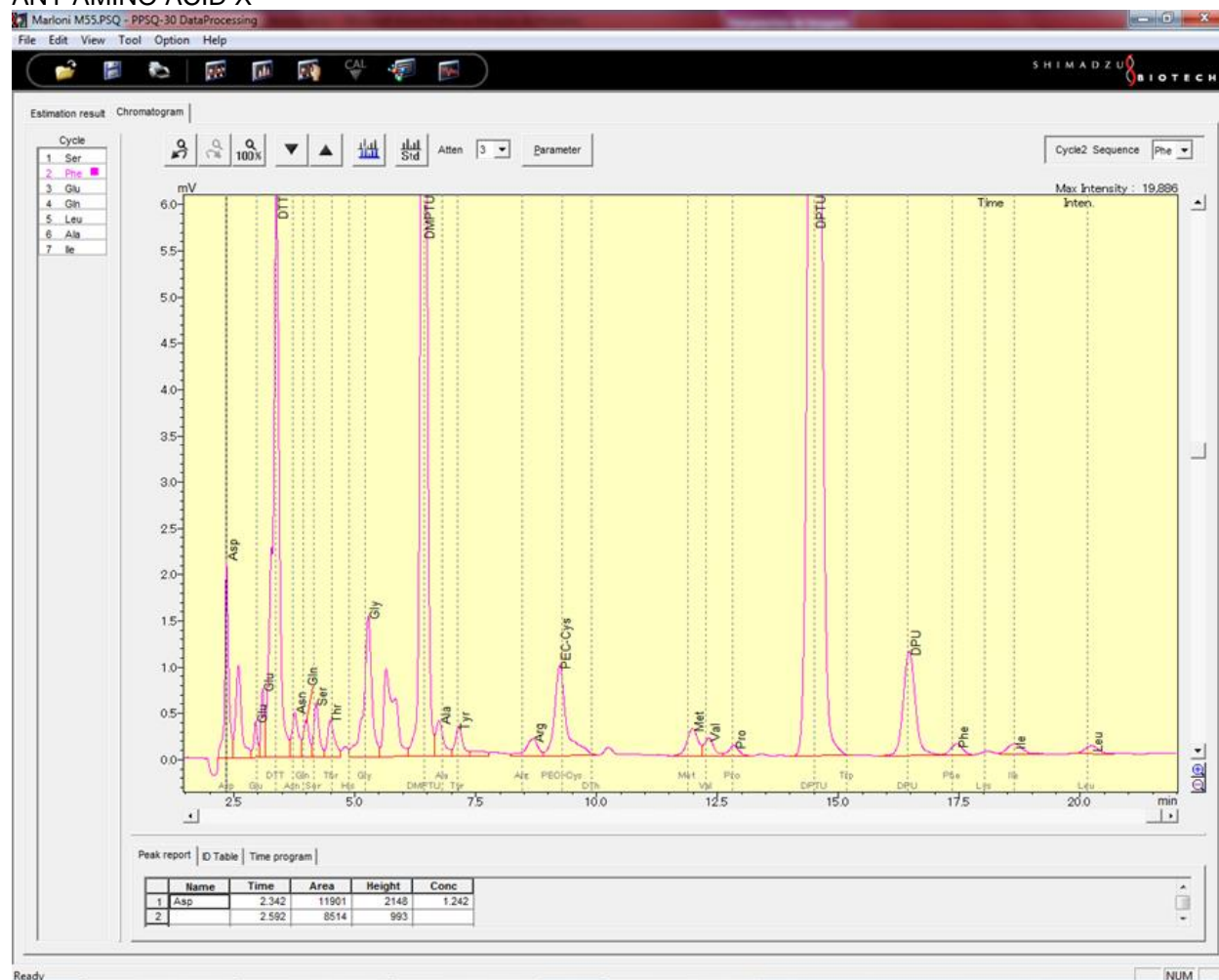
SAMPLE (pink peaks) and STANDARD (grey peaks)



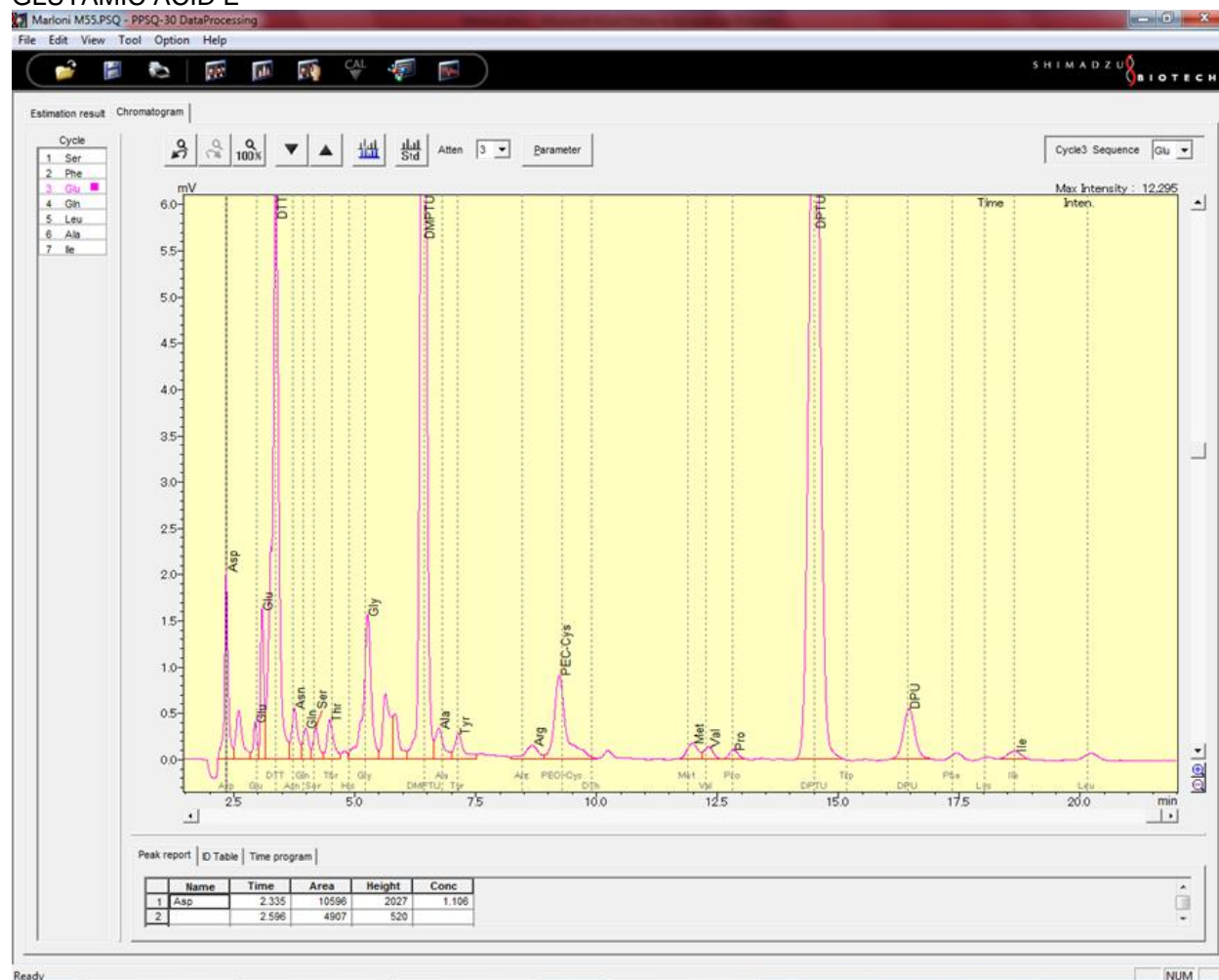
SERINE (S) / GLYCINE (G)



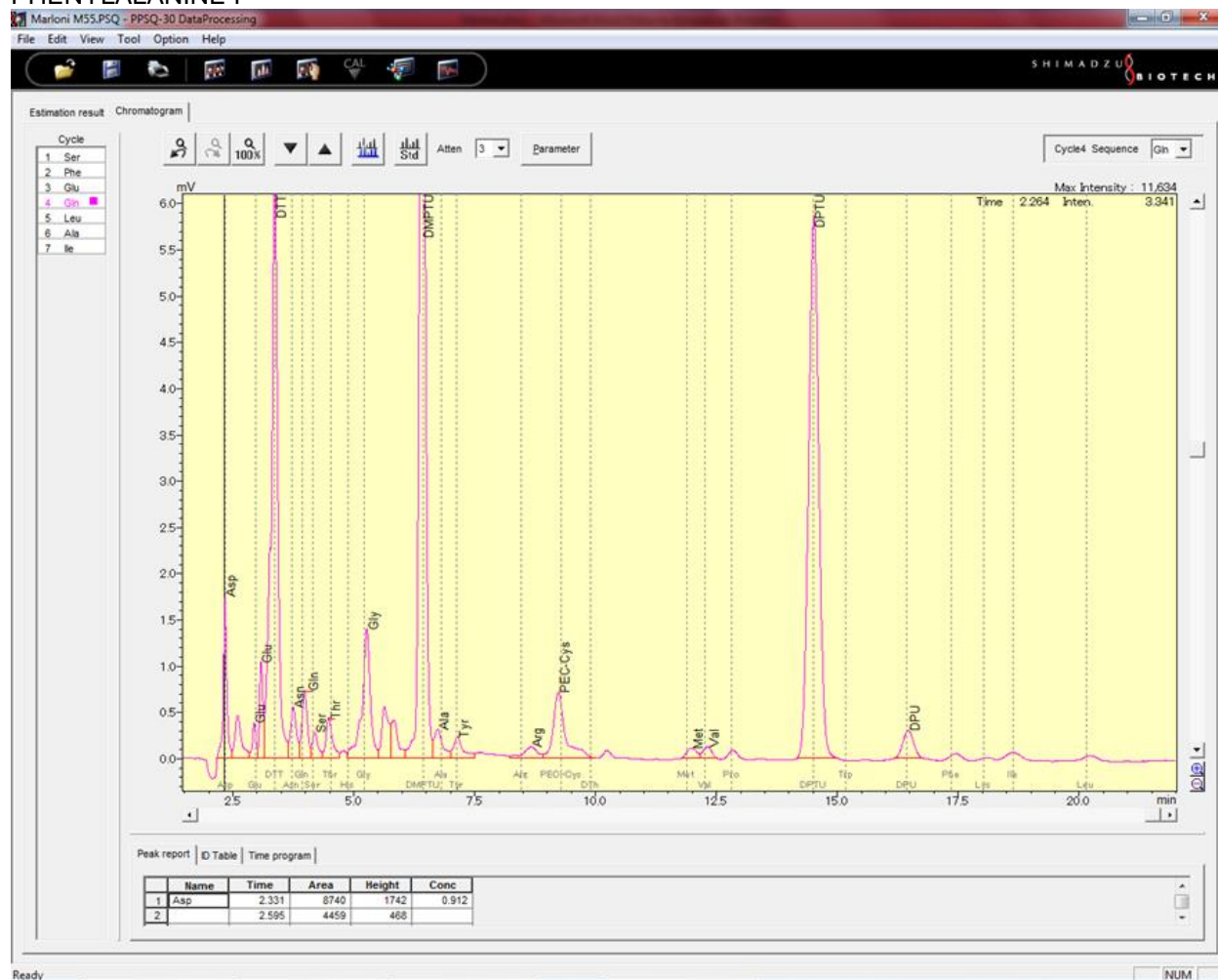
ANY AMINO ACID X



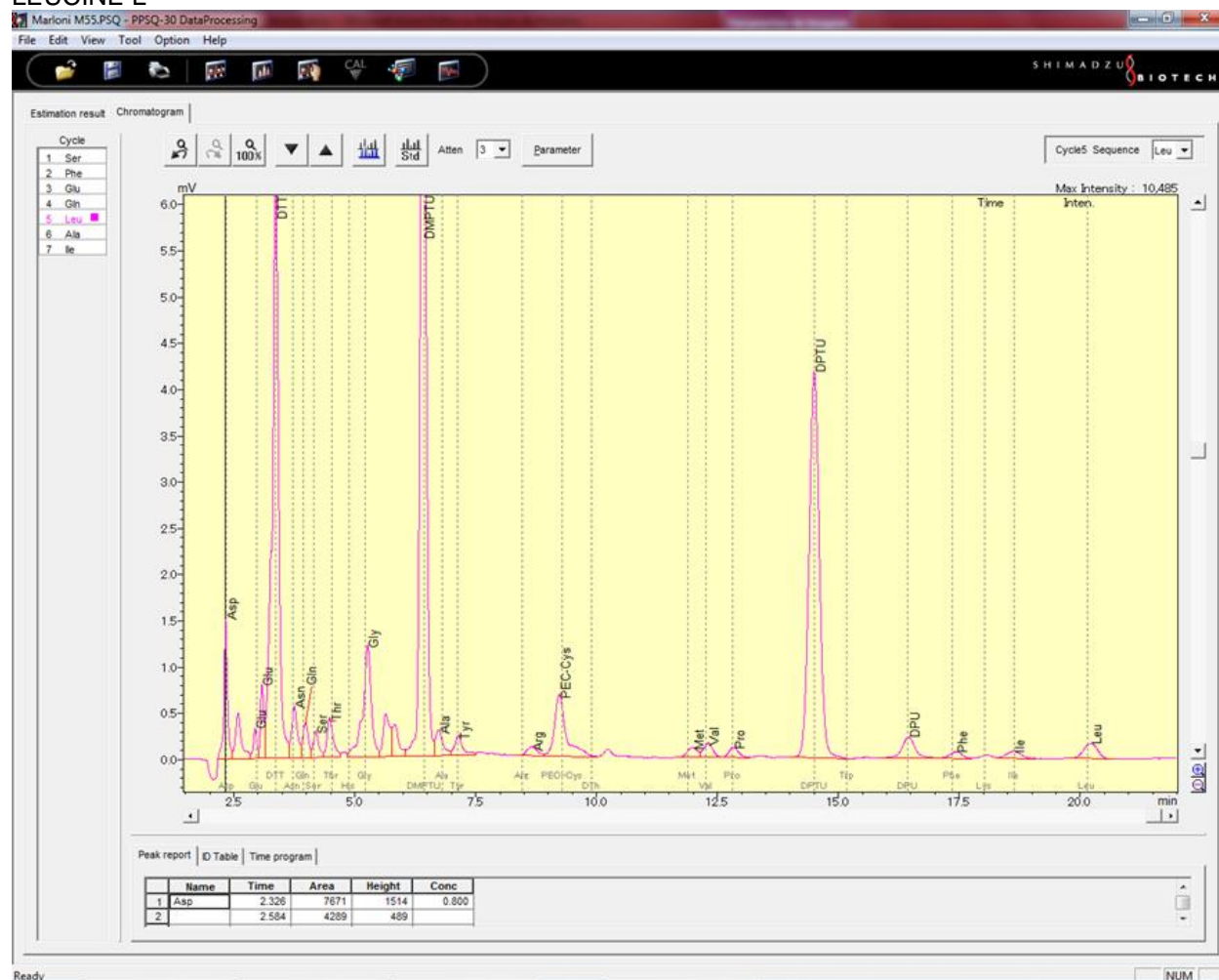
GLUTAMIC ACID E



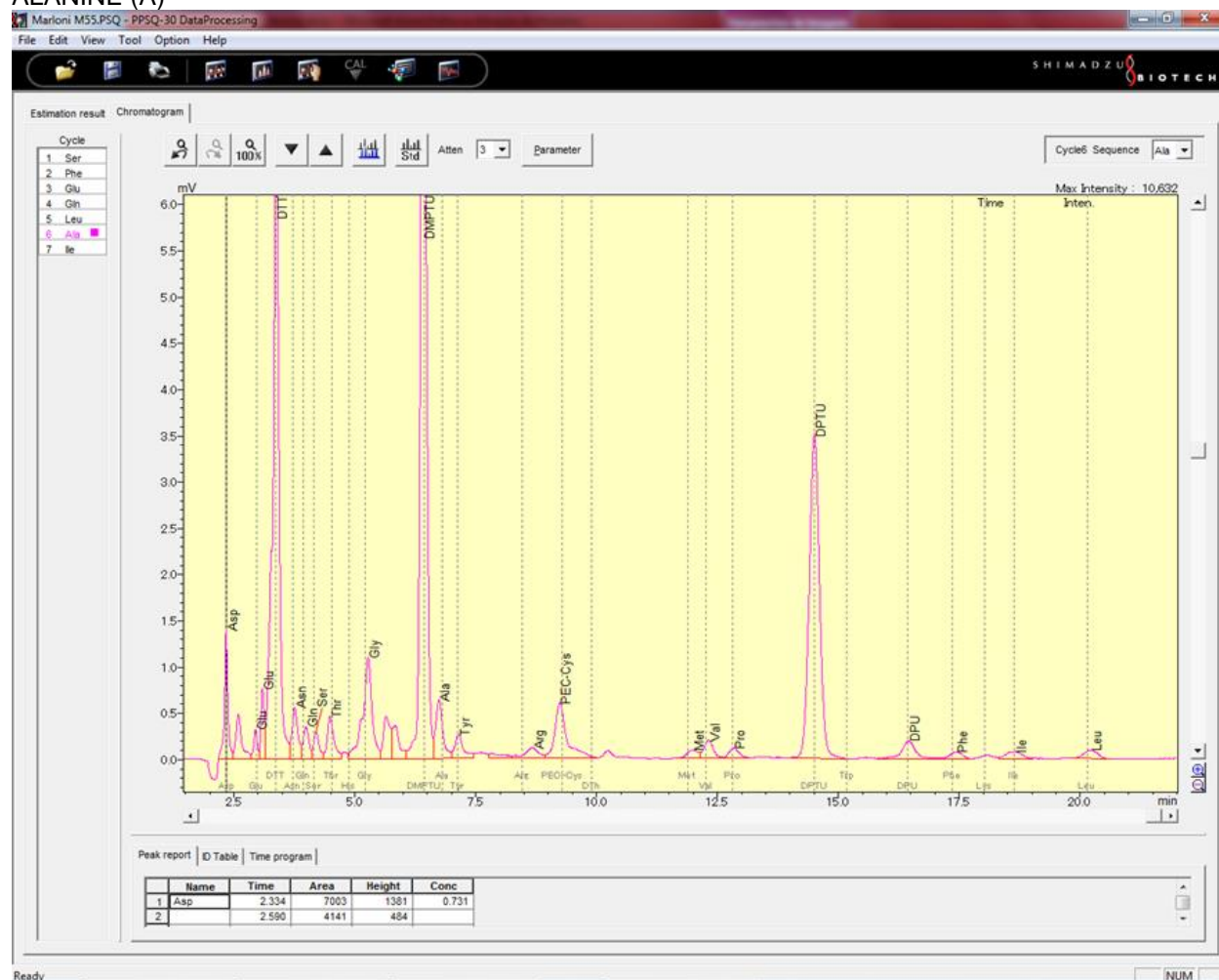
PHENYLALANINE F



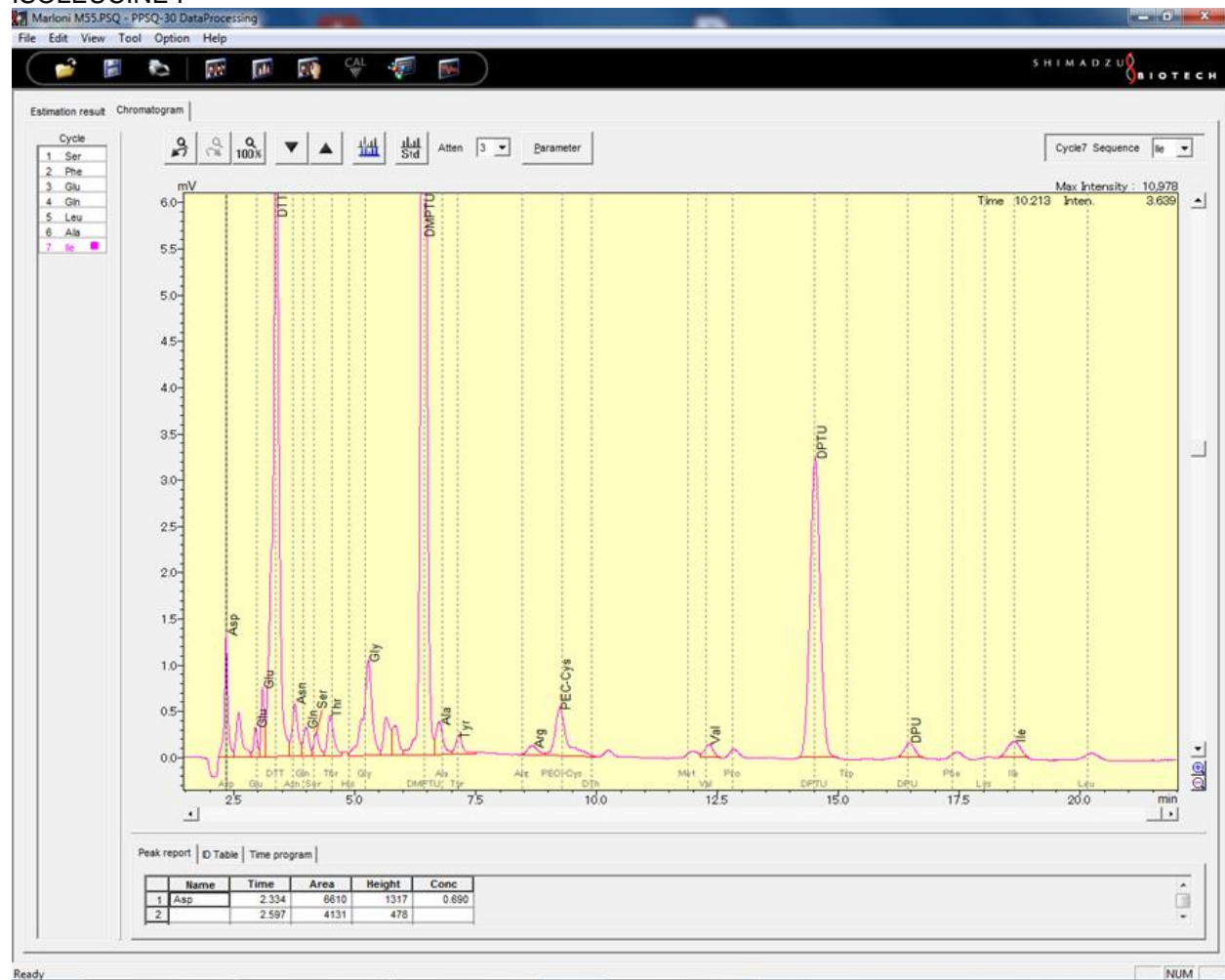
LEUCINE L



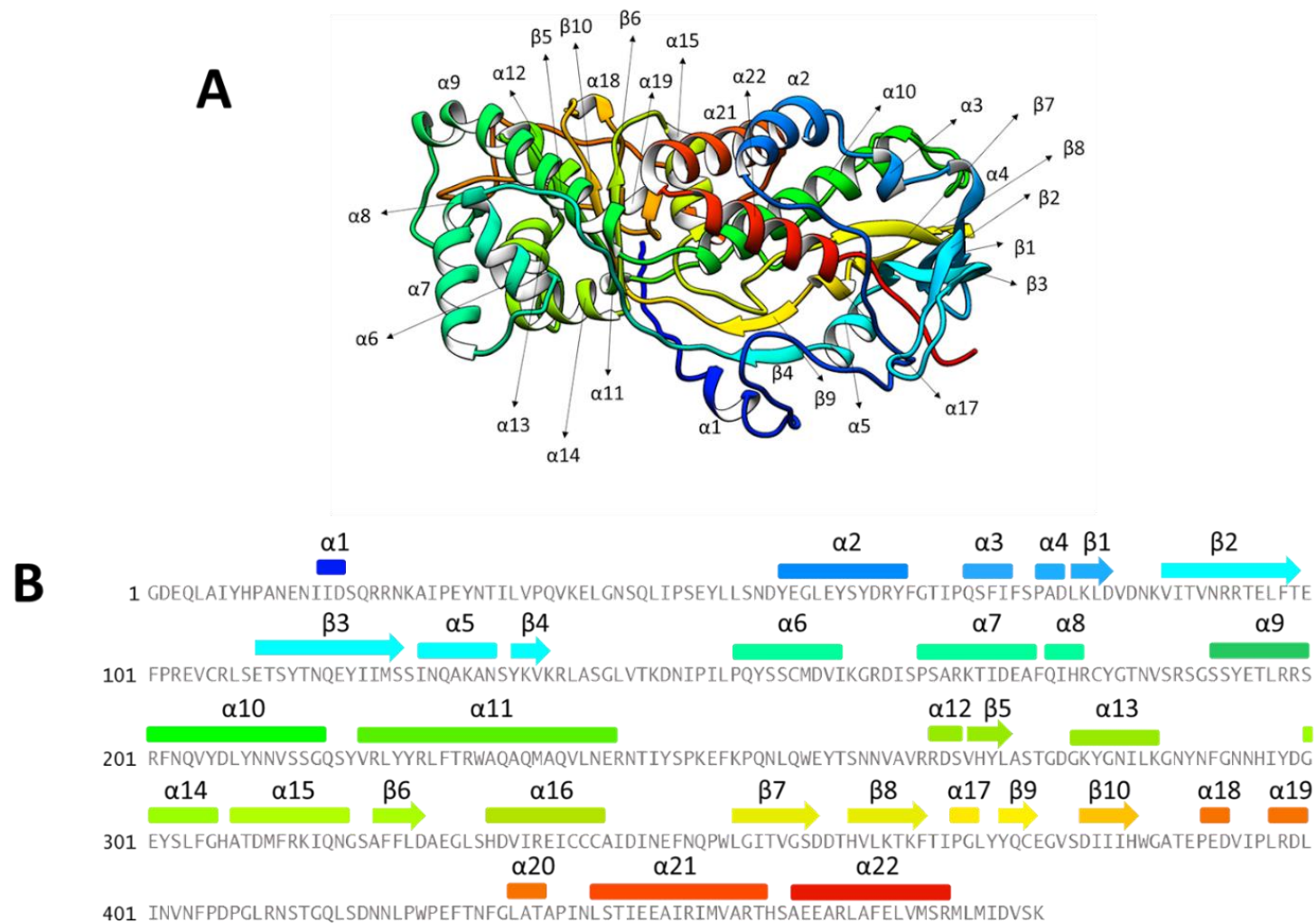
ALANINE (A)



ISOLEUCINE I

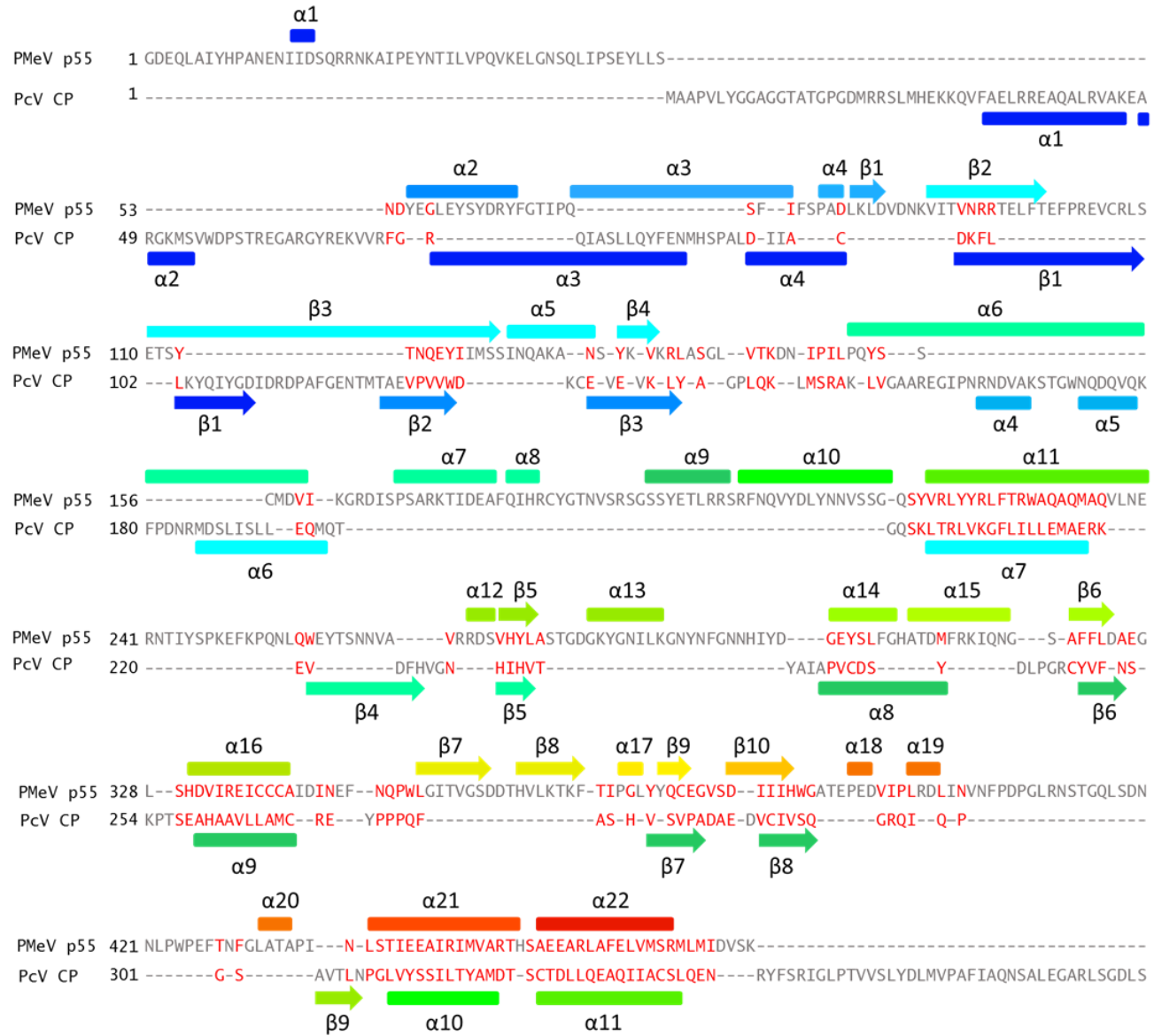


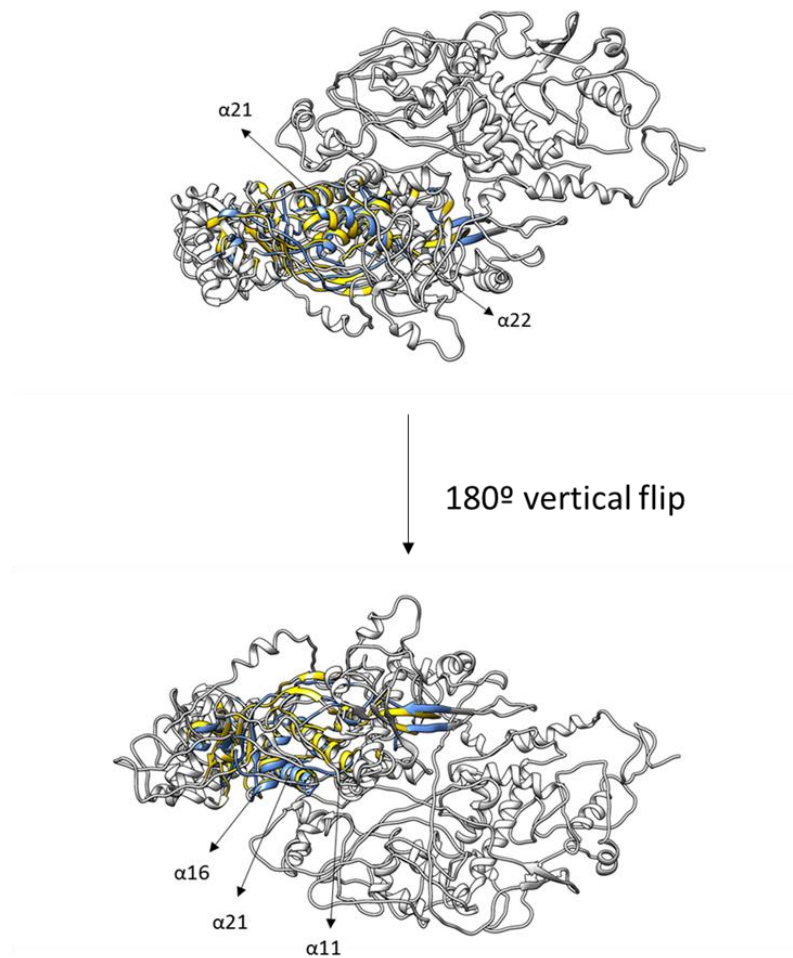
Supplementary Figure S1. N-terminal sequencing of 55kDa band. Each figure displays the chromatographic traces for each cycle ordered from N- to C- terminal.



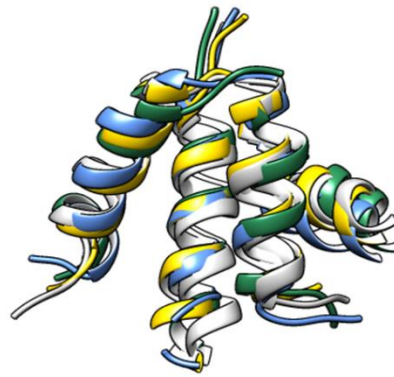
Supplementary Figure S2. Three-dimensional structure of PMeV p55 using AlphaFold. **A.** Ribbon diagram of p55 (diagram was positioned for easy visualization of secondary structures) rainbow-colored from blue (N-terminus) to red (C-terminus). **B.** Sequence of p55 and its respective secondary structures. The α -helices (rectangles) and β -strands (arrows) are rainbow-colored from blue (N-terminus) to red (C-terminus).

A



B

Supplementary Figure S3. Structural alignment of p55 and PcV capsid protein (CP) domain A. **A.** Sequence alignment of p55 and PcV CP domain A resulting from the Dali structural alignment. The α -helices (rectangles) and β -strands (arrows) are rainbow-colored from blue (N-terminus) to red (C-terminus) for each protein. Conserved residues are represented in red. **B.** Superimposed structures of p55 (yellow) and PcV CP domain A (blue). White regions indicate non superimposed regions for both domains.



— 10 Å

Supplementary Figure S4. Superimposed structures of p53 (yellow), *Penicillium chrysogenum* virus (blue), *Saccharomyces cerevisiae* virus L-A (white), Omono river virus (green) capsid proteins.

p-AD	p-BD	Yeast Growth					
		DDO	QDO	QDOXA + 3-AT			
				0 mM	1 mM	2.5 mM	5 mM
T	53						
T	Lam						
	Empty						
DNAJ heat shock family protein (AT2G22360)	ORF1 961-1200						
	ORF1 320-670						
	Empty						
Ribosomal protein L17 family protein (AT3G54210)	ORF1 961-1200						
	ORF1 320-670						
	Empty						
Sec14p-like phosphatidylinositol transfer family protein (AT1G72160)	ORF1 961-1200						
	ORF1 320-670						
	Empty						
GDSL-like Lipase/Acylhydrolase superfamily protein (AT5G45670)	ORF1 961-1200						
	ORF1 320-670						
	Empty						
Chloroplast GRX 12, GRXS12 (AT2G20270)	ORF1 961-1200						
	ORF1 320-670						
	Empty						
Chaperone protein dnaJ-like protein (AT5G06130)	ORF1 961-1200						
	ORF1 320-670						
	Empty						
GPI-anchored protein (AT3G18050)	ORF1 961-1200						
	ORF1 320-670						
	Empty						
Pyrimidin 4 (PYR4) (AT4G22930)	ORF1 961-1200						
	ORF1 320-670						
	Empty						
Pectinacetylsterase family protein (AT4G19420)	ORF1 961-1200						
	ORF1 320-670						
	Empty						
Double Clp-N motif protein (AT4G12060)	ORF1 961-1200						
	ORF1 320-670						
	Empty						
PEBP (phosphatidylethanolamine-binding protein) family protein (FT) (AT1G6548)	ORF1 961-1200						
	ORF1 320-670						
	Empty						
Clone RAFL09-89-G08 (R19778) putative cellulose synthase catalytic subunit (RSW1) (At4g32410)	ORF1 961-1200						
	ORF1 320-670						
	Empty						
mRNA for plastid protein, complete cds, clone: RAFL15-06-D14 (AT1G32580.1)	ORF1 961-1200						
	ORF1 320-670						
	Empty						
Papain family cysteine protease (AT4G16190)	ORF1 961-1200						
	ORF1 320-670						



Supplementary Figure S5. Spot plating shows the validation of genuine positives interacting with CP2 and CP4.

[illegible]

Supplementary Figure S6. Protein-protein interaction network (PPI) of *Carica papaya* differentially accumulated proteins during papaya meleira virus (PMeV) complex infection and PMeV CP2 and CP4-interacting proteins;