

Technique	Resolution	Throughput	Cost	Epitope type	Pros	Cons
crystallography	best available	low	high	linear & conformational	√ Gold standard √ interaction sites viewable	√ difficult to get crystals √ requires high quality samples √ time consuming
mutagenesis	very good	low	high	linear & conformational	√ single amide resolution √ straight-forward technique	√ labor intensive protein expression √ proper protein folding an issue √ time consuming
overlapping peptides (PepScan)	fair	high	low	linear only	√ quick results √ inexpensive to do	√ can't ID conformational epitopes √ non-specific binding false positives √ unreliable results
protease digest	poor	high	low	linear only	√ quick results √ inexpensive to do	√ can't ID conformational epitopes √ low resolution √ unreliable results
NMR	very good	low	high	linear & conformational	√ very high resolution √ complementary to crystallography approach	√ limited by size of proteins √ time consuming to make isotope-labeled proteins
antibody competition (binning)	poor	high	low	linear & conformational	√ good applicability √ inexpensive to do	√ low resolution √ need antibodies with known epitopes to start the process
electron microscopy	poor	high	low	linear & conformational	√ amount of protein needed √ quick results	√ low resolution √ use with computational modeling √ need structures to interpret data
H/D-Exchange	good	medium	mid-range	linear & conformational	√ sole source commercial provider of H/D-Exchange √ turnaround time √ expertise in the field	√ potential issues with some PTMs √ protein must be stable in H/D specific conditions

H/D-Exchange is the best choice when you need to get accurate, reliable epitope data on your antibodies within a fixed time-frame. ExSAR is the **only** commercial provider of hydrogen/deuterium exchange on a fee-for-service basis.

Typical turnaround time from receipt of sample at our laboratories to completion of project is approximately 4 to 6 weeks!

Clients typically use our H/D-Exchange data to 'narrow down the field' for their mutagenesis studies to pinpoint exact residues.