

# NISTmAb Mass Spectral Reference Libraries: *Freely Available*



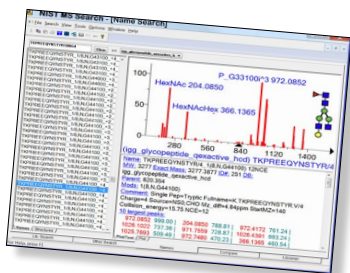
## Humanized IgG1 $\kappa$ Monoclonal Antibody

### LC-ESI-MS/MS library for detailed mAb characterization

- 3,360 peptides
- 12,608 spectra
- Extensive degradation, glycation, oxidation, and cysteine variation
- Over 20 types of analytical artifacts
- Based on 1D/2D LC-MS studies
- Multiple HCD collisional energies

### LC-ESI-MS/MS library for glycoanalysis

- 1,703 spectra
- 247 multiply charged glycopeptides
- 81 different N-glycans (NS0 and CHO)
- 20-fraction 2D-LC studies
- Energy-dependent changes in HCD fragmentation of glycoforms



### References

- J. Proteome Res. 2016, 15, 5, 1472-1486
- mAbs, 2018, 10:3, 354-369
- NIST RM 8671: <https://www.nist.gov/srm>



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## How to use libraries

- Formats: (1) ASCII text format (*MSP*) and (2) *MS Search* binary format
- Library searching with major proteomics workflows, including *Mascot* (Matrix Science) and *Proteome Discoverer* (Thermo Fisher Scientific)
- Individual spectrum search with the full-featured user-interface program: *NIST MS Search*
- Batch peptide identification with the NIST *MS PepSearch* software

## Library Downloads

Peptide.nist.gov

**Web** [chemdata.nist.gov](http://chemdata.nist.gov)

**Email** [massspec@nist.gov](mailto:massspec@nist.gov)



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