Higher-Order Structure, Stability, and Similarity Assessment of VHH Antibodies Using CD Spectroscopy

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SUMMARY

- VHH* antibodies are attracting attention as next-generation modalities
- Higher-order structure (HOS) is a critical quality attribute (CQA) responsible for VHH antibody functions
- CD spectroscopy is a suitable technique for protein HOS assessment *Variable domain of heavy chain antibodies



- Protein secondary and tertiary structure
- Wide protein concentration range
- Simple measurement/analysis procedures











Secondary structure compositions of anti-SARS-CoV-2 VHH antibodies (VHH1, VHH2, and VHH3, prepared with different sequence) were estimated from their CD spectra using BeStSel, a high-performance algorithm developed by Dr. József Kardos and Dr. András Micsonai (https://bestsel.elte.hu)⁽²⁻⁵⁾. The VHH antibodies were provided by RePHAGEN Co., Ltd (https://rephagen.com/en/).





Spectral change in anti-HSA VHH antibody (VHH4) was statistically evaluated using the JASCO qHOS program. A VHH4 at pH 7 and NaCl concentration of 200 mM was set as a reference. The CD spectral change between the reference and VHH4s under different combinations of pH and NaCl concentrations was quantified by *t*-values. The larger *t*-value is, the more spectral difference they show.

2. SIMILARITY STUDY

HEAT

CD Spectra and Similarity Test (TOST) Results





Denaturation Curve



Changes in Secondary Structure Fractions



Similarities between anti-SARS-Cov-2VHH antibodies with different sequences were statistically evaluated from their CD spectral shapes using JASCO qHOS program⁽⁷⁾. TOST (two one-sided *t*-test) was used to determine whether there was equivalence between two different VHH antibodies.





- Melting temperature (T_m) of VHH1 was calculated from the CD denaturation curve to check the thermal stability. The CD signal at 217 nm is originated from β -sheets.
- Refolding ability of VHH1 was assessed by monitoring changes in secondary structure fractions while increasing and decreasing the temperature.

1. Koch K, et al. Selection of nanobodies with broad neutralizing potential against primary HIV-1 strains using soluble subtype C gp140 envelope trimers. Sci Rep. 2017, 7(1), 8390. DOI: 10.1038/s41598-017-08273-7

- 2. Micsonai A, et al. Accurate secondary structure prediction and fold recognition for circular dichroism spectroscopy. Proc Natl Acad Sci U S A. 2015, 112(24), E3095-E3103. DOI: 10.1073/pnas.1500851112
- 3. Micsonai A, et al. BeStSel: a web server for accurate protein secondary structure prediction and fold recognition from the circular dichroism spectra. Nucleic Acids Res. 2018, 46(W1), W315-W322. DOI: 10.1093/nar/gky497
- Micsonai A, et al. BeStSel: From Secondary Structure Analysis to Protein Fold Prediction by Circular Dichroism Spectroscopy. Methods Mol Biol. 2021, 2199, 175-189. DOI: 10.1007/978-1-0716-0892-0_11

REFERENCE

- Micsonai A, et al. Disordered-Ordered Protein Binary Classification by Circular Dichroism 5. Spectroscopy. Front Mol Biosci. 2022, 9, 863141. DOI: 10.3389/fmolb.2022.863141
- 6. Micsonai A, et al. BeStSel: webserver for secondary structure and fold prediction for protein CD spectroscopy. Nucleic Acids Res. 2022, 50(W1), W90-W98. DOI: 10.1093/nar/gkac345
- 7. Oyama T, et al. Performance Comparison of Spectral Distance Calculation Methods. Appl Spectrosc. 2022, 76(12), 1482-1493. DOI: 10.1177/00037028221121687