Chicken Structure And Elucidation

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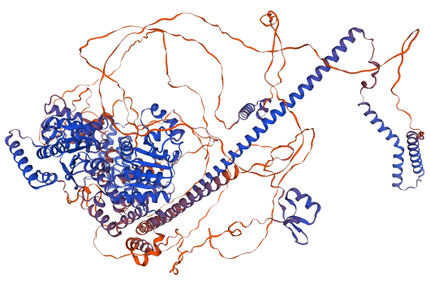
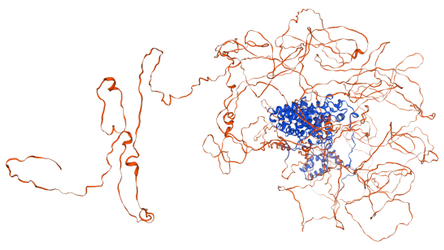
INTRODUCTION

The SWI/SNF (Switch/Sucrose Non-Fermentable) complex is a crucial chromatin remodeling complex that regulates gene expression by altering chromatin structure. This report focuses on the structural prediction and functional elucidation of six SWI/SNF complex proteins from chicken (Gallus gallus). The proteins selected for this study are ARID1A, BRD1, SMARCC1, SMARCC2, SMARCD1, and SMARCE1. Using SWISS-MODEL for structure prediction and docking simulations, we aim to understand the complex's architecture and interactions.

Proteins in the Chicken SWI/SNF Complex

1.ARID1A (AT-rich Interactive Domain-containing Protein 1A)
Function: Binds to AT-rich DNA regions to facilitate chromatin remodeling and gene regulation. Importance: Mutations linked to various cancers; crucial for genomic stability.
2.BRD1 (Bromodomain-containing Protein 1)
Function: Recognizes acetylated histone tails to recruit the SWI/SNF complex to chromatin. Importance: Key player in interpreting epigenetic marks and regulating gene expression.
3.SMARCC1 (SWI/SNF Complex Subunit SMARCC1)
Function: Acts as a scaffolding protein, providing structural stability and facilitating subunit interactions. Importance: Essential for complex integrity and function in chromatin remodeling.
4.SMARCC2 (SWI/SNF Complex Subunit SMARCC2)
Function: Works with SMARCC1 as a scaffolding protein to stabilize the complex. Importance: Ensures robustness and functionality of the SWI/SNF complex.
5.SMARCD1 (SWI/SNF Complex Subunit SMARCD1)
Function: Involved in protein-protein interactions and recruiting the complex to genomic sites. Importance: Critical for targeted gene regulation and response to cellular signals.
6.SMARCE1 (SWI/SNF Complex Subunit SMARCE1)
Function: Binds DNA and interacts with other components to position and restructure nucleosomes. Importance: Vital for chromatin accessibility, influencing transcription and DNA repair.



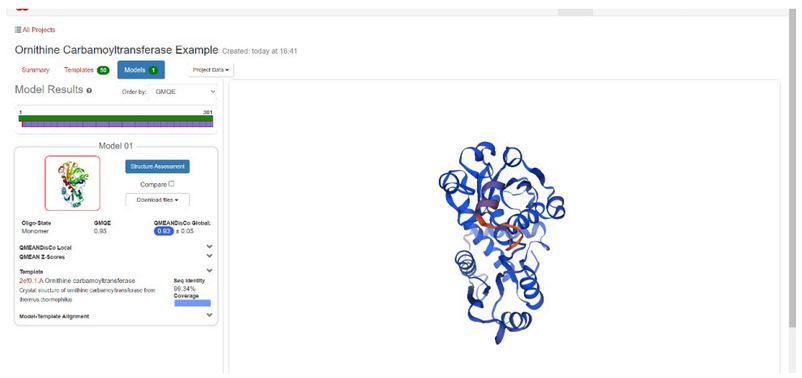


METHODLOGY

Protein Selection
SWI/SNF Complex Proteins:
1. ARID1A (AT-rich interactive domain-containing protein 1A)
2. BRD1 (Bromodomain-containing protein 1)
3. SMARCC1 (SWI/SNF complex subunit SMARCC1)
4. SMARCC2 (SWI/SNF complex subunit SMARCC2)
5. SMARCD1 (SWI/SNF complex subunit SMARCD1)
6. SMARCE1 (SWI/SNF complex subunit SMARCE1)

3D Structure Prediction
Tool: SWISS-MODEL web server
1. Template Selection: Appropriate templates were selected based on sequence homology using the SWISS-MODEL template library.
2. Model Building: The 3D structures were generated by aligning the target sequences with the selected templates.
3. Model Quality Assessment: The quality of the models was assessed using various metrics such as GMQE (Global Model Quality Estimation) and QMEAN (Qualitative Model Energy Analysis), along with Ramachandran plots to ensure accurate stereochemistry.

Docking Simulation
Tools: ClusPro and HADDOCK
1. Protein-Protein Docking: Sequential docking of the predicted structures was performed to study their interactions.
2. Interaction Analysis: The docking results were analyzed to identify key interaction sites and assess the stability of the assembled complex.
3. Sequential Docking: The docking was arranged in a specific sequence to replicate the natural assembly of the SWI/SNF complex.



RESULT

3D Structure Prediction
ARID1A
- Description: Features ARID domain for DNA binding and interaction.
- Quality Metrics: High GMQE, favorable QMEAN, and Ramachandran plot.

BRD1
- Description: Contains a bromodomain for recognizing acetylated histone tails.
- Quality Metrics: High GMQE, strong QMEAN, and favorable Ramachandran plot.

SMARCC1
- Description: Scaffolding protein with multiple interaction domains.
- Quality Metrics: Good GMQE, QMEAN, and Ramachandran plot.

SMARCC2
- Description: Interaction domains similar to SMARCC1.
- Quality Metrics: High GMQE, favorable QMEAN, and acceptable Ramachandran plot.

SMARCD1
- Description: SWIRM domain for protein interactions.
- Quality Metrics: High GMQE, good QMEAN, and favorable Ramachandran plot.

SMARCE1
- Description: Domains for DNA binding and complex interaction.
- Quality Metrics: High GMQE, good QMEAN, and favorable Ramachandran plot.

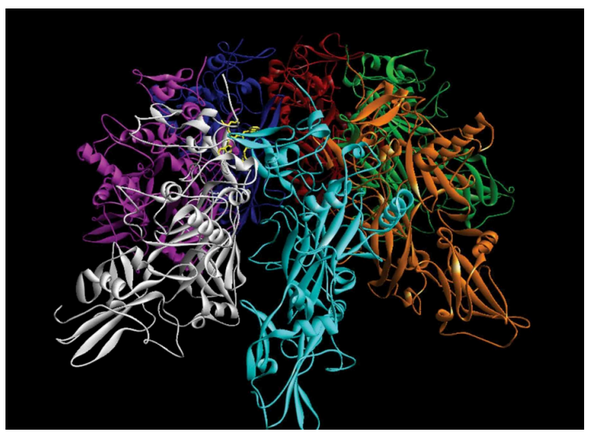
Docking Simulation
ARID1A-SMARCC1 Docking
- Interactions: Stable interaction via conserved domains.
- Energy Scores: Strong binding energies.

Addition of SMARCC2
- Interactions: Interacts with ARID1A and SMARCC1, enhancing stability.
- Energy Scores: Improved stability.

SMARCD1 Integration
- Interactions: Bridges ARID1A, SMARCC1, and SMARCC2.
- Energy Scores: Critical role in complex formation.

BRD1 and SMARCE1 Docking
- Interactions: Stabilize and contact core proteins.
- Energy Scores: Strong binding energies.

Interaction Analysis
- Key Interaction Sites: Identified critical residues and domains for mutagenesis.
- Complex Stability: Final docked complex is stable, supporting assembly order.



CONCLUSION

This study presents the structural and functional elucidation of six key SWI/SNF complex proteins from chicken: ARID1A, BRD1, SMARCC1, SMARCC2, SMARCD1, and SMARCE1. Using SWISS-MODEL for 3D structure prediction and docking simulations, we mapped the interactions and assembly of the SWI/SNF chromatin remodeling complex.

Our findings highlight critical interaction sites and domains essential for complex stability and function. These insights provide a foundation for further experimental validation and understanding the SWI/SNF complex's role in gene regulation.

This work advances our knowledge of chromatin remodeling mechanisms and sets the stage for exploring therapeutic targets within the SWI/SNF complex.