

Summary of integrative structure determination of integrative modeling of a sin3/hdac complex sub-structure (PDBDEV00000043)

| 1. Model Composition | |
|--|---|
| Entry composition | <ul style="list-style-type: none"> - SAP30L C terminal: Chain A (90 residues) - HDAC1: Chain D (369 residues) - SAP30L N terminal: Chain B (68 residues) - SIN3A: Chain C (122 residues) |
| Datasets used for modeling | <ul style="list-style-type: none"> - Comparative model, template PDB ID: Not listed - Comparative model, template PDB ID: Not listed - Comparative model, template PDB ID: Not listed - Comparative model, template PDB ID: Not listed - CX-MS data, Linker name and number of cross-links: DSSO, 12 cross-links - Experimental model, PDB ID: 2LD7 - Experimental model, PDB ID: 2N1U - Experimental model, PDB ID: 2N2H - Experimental model, PDB ID: 5IX0 - Mutagenesis data, Not listed |
| 2. Representation | |
| Atomic structural coverage | 100% |
| Number of rigid bodies, flexible units | 4, 0 |
| <i>Rigid bodies</i> | <ul style="list-style-type: none"> - A: 1-90:Comparative model/None. - B: 1-68:Comparative model/None. - C: 1-122:Comparative model/None. - D: 1-369:Comparative model/None. |
| <i>Flexible units</i> | <ul style="list-style-type: none"> - A: - - B: - - C: - - D: - |
| Resolution | <ul style="list-style-type: none"> - Rigid bodies: 1 residue per bead. - Flexible regions: N/A |
| 3. Restraints | |
| Physical principles | Information about physical principles was not provided |
| Experimental data | <ul style="list-style-type: none"> - 1 unique CrossLinkRestraint: DSSO, 12 cross-links - 16 unique DerivedDistanceRestraint: Upper Bound Distance: 2.0 |
| 4. Validation | |
| Sampling validation | - Information related to sampling validation has not been provided |
| Clustering algorithm ,clustering feature | Distance threshold-based clustering used if ensembles are deposited, Not applicable |
| Number of ensembles | 0 |

| | |
|---|---|
| <i>Number of models in ensembles</i> | Not applicable |
| <i>Model precision (uncertainty of models)</i> | Model precision can not be calculated with one structure |
| <i>Quality of data</i> | - Quality of input data has not be assessed |
| <i>Model quality: assessment of atomic segments</i> | Clashscore: 6.09, Ramachandran outliers: 0.47% , Sidechain outliers: 8.2% |
| <i>Model quality: assessment of excluded volume</i> | - Not applicable |
| <i>Fit of the model to information used to compute it</i> | - Fit of model to information used to compute it has not been determined |
| <i>Fit of the model to information not used to compute it</i> | - Fit of model to information not used to compute it has not been determined |
| 5. Methodology and Software | |
| <i>Method</i> | ? |
| <i>Name</i> | comparative modeling |
| <i>Details</i> | - Method details unspecified |
| <i>Software</i> | - HADDOCK (version None) - SWISS-MODEL (version None) - No location specified |