AUREMOL

For Windows,

Not Linux

Integrated software package for automated protein structure determination and related tasks.

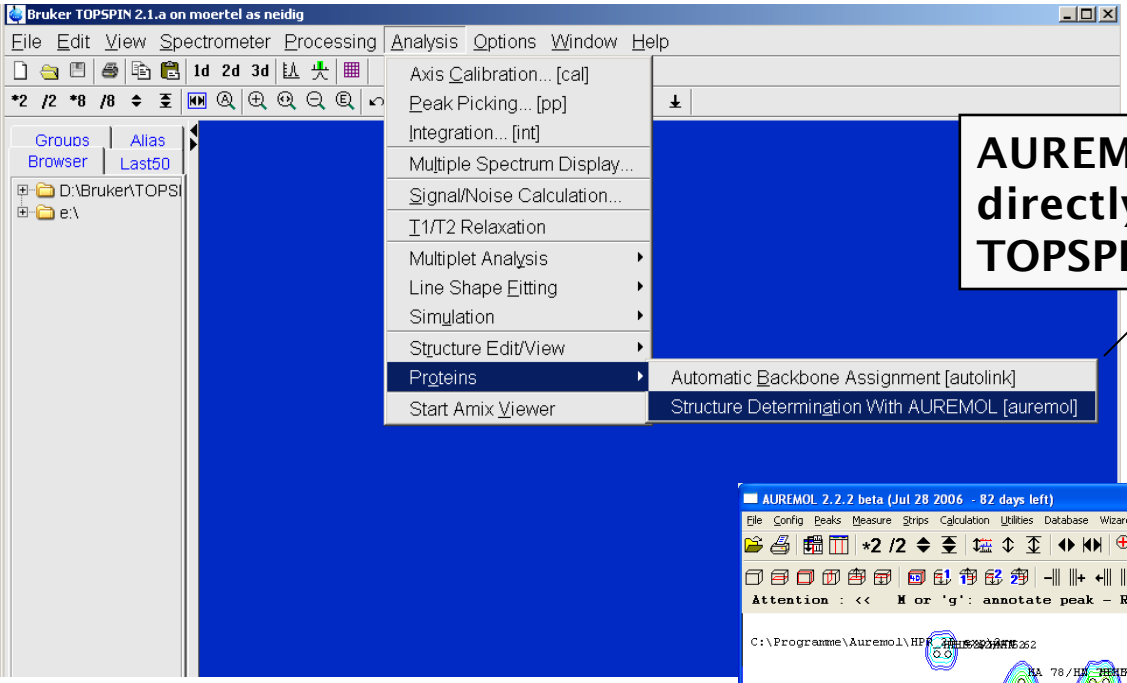
- Includes some AURELIA kernel functionality
- Has the AMIX user interface
- New top down strategy based on new class of tools

Highlights of AUREMOL !

The field of Protein structure determination by NMR is dominated by a few groups typically using some free or in-house software packages. In contrary:

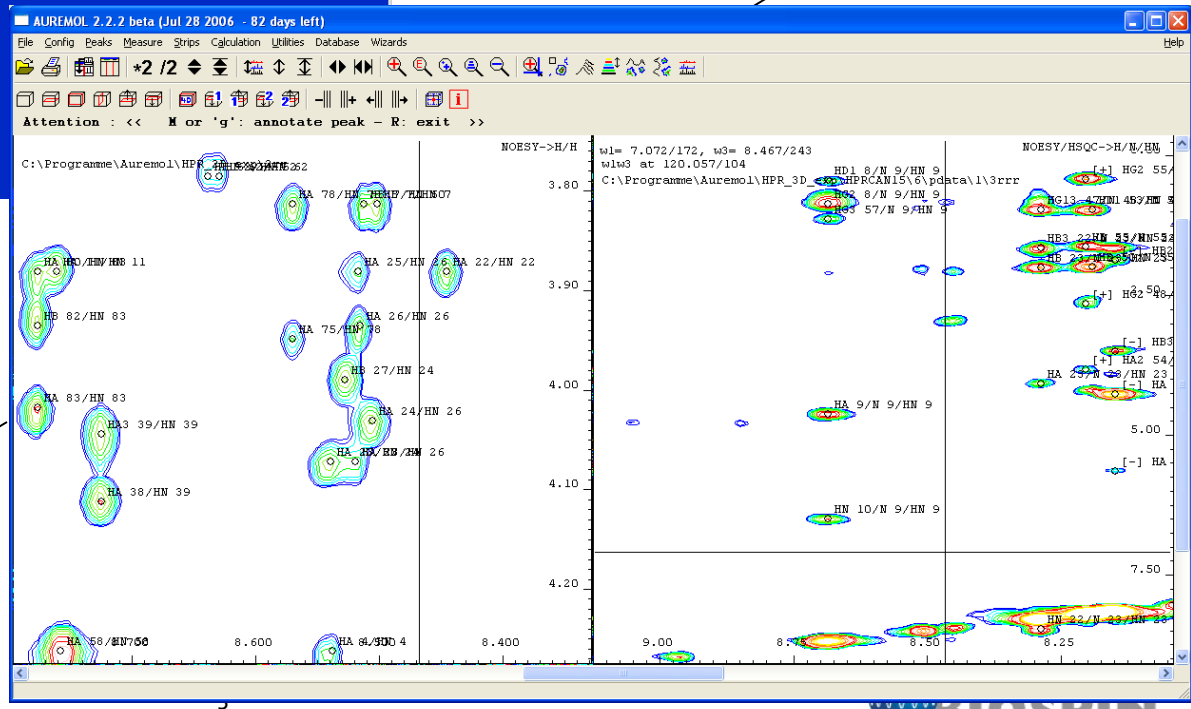
- **AUREMOL contains a number of individual qualified, published tools, some are unique**
- **AUREMOL offers all tools in a unique & integrated form (no scripting or conversions)**
- **AUREMOL fits well into the Bruker software and is suited for commercial applications**
- **AUREMOL is flexible, optimized and interfaced to external structure calculation programs**

Integration into Bruker software



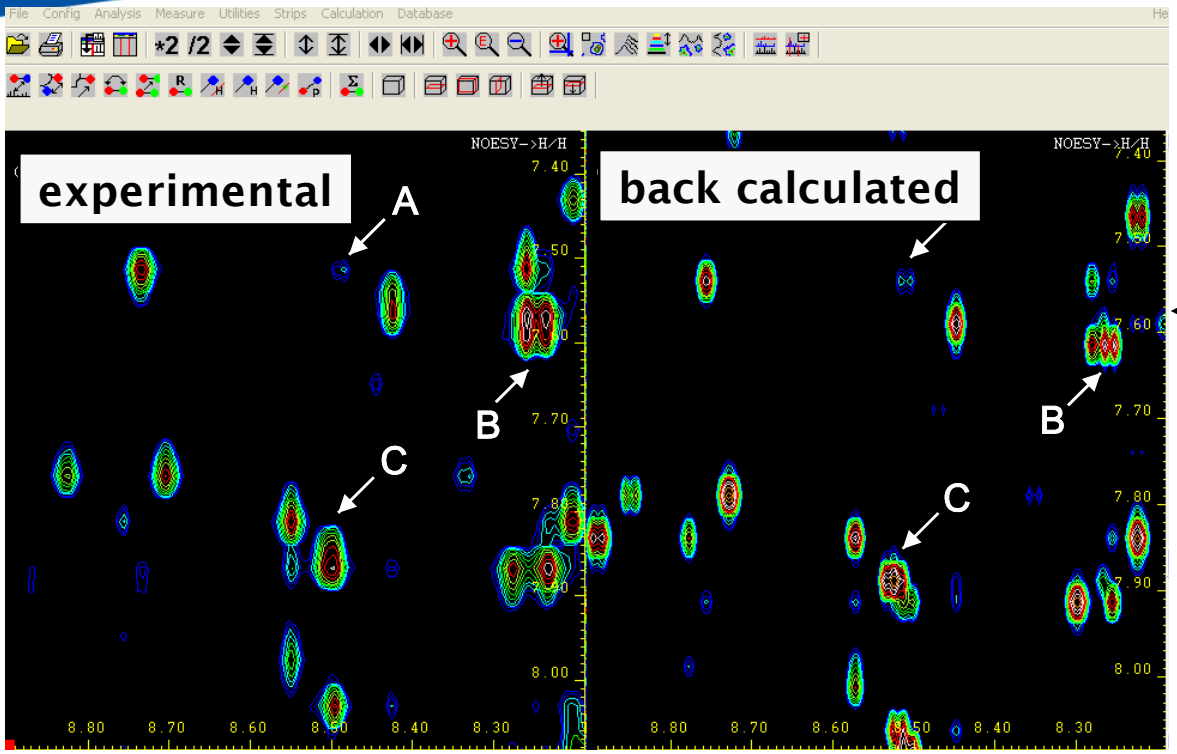
AUREMOL can be directly started from TOPSPIN 2.1

User interface from AMIX

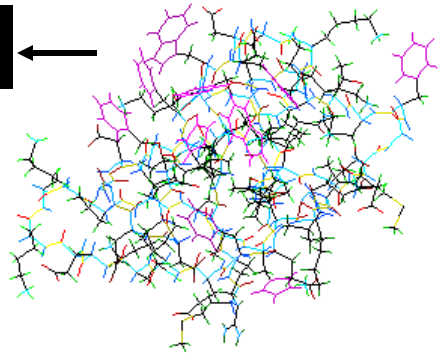


Example:
plane of 3D with manual assignments (right), 2D NOESY with automated assignment

A Key Tool: RELAX Back calculation

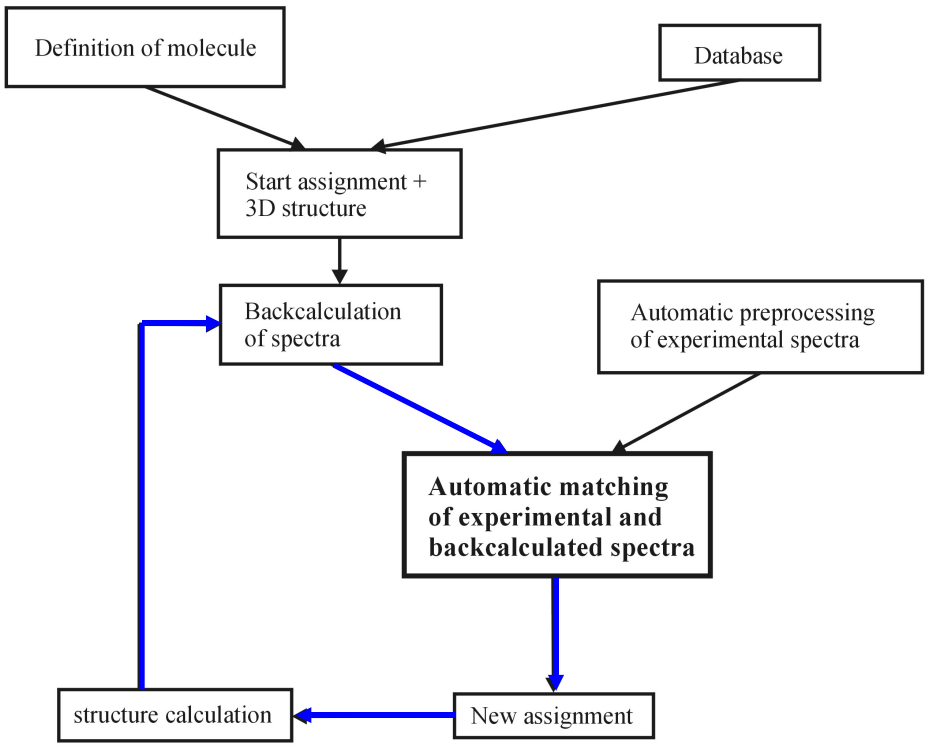


RELAX



- Back calculation of 2D NOESY / 3D ^{15}N,^{13}C HSQC
- Full relaxation matrix approach
- Various spectral density functions
- Homo- and heteronuclear dipolar relaxation
- Relaxation via chemical shift anisotropy
- Calculation of T_2 and of J-couplings

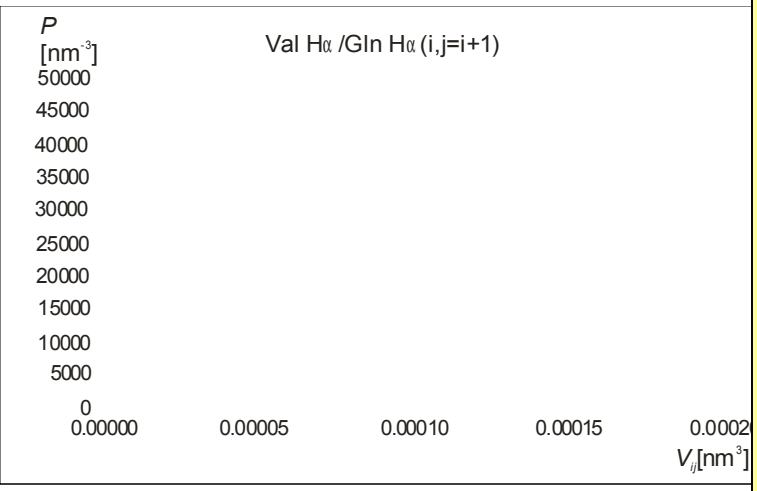
Items of structure determination

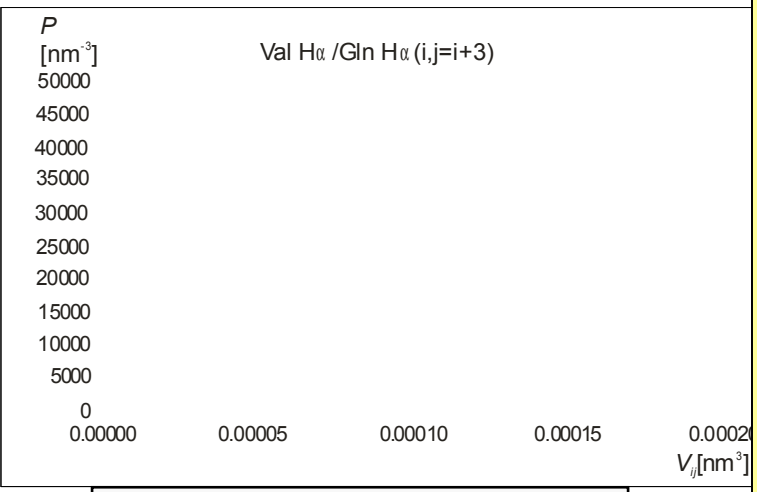


Iterative scheme for structure determination

1. Automated peak analysis (Bayes)
2. Backbone assignment
3. Side chain assignment
4. Initial structure, homology modeling (PERMOL)
5. Automated NOE assignment (KNOWNOE)
6. Distance restraints (REFINE)
7. Structure calculation (CNS, DYANA interface)
8. Back calculation (RELAX)
9. Structure validation (RFAC)

Unique: NOE Assignment with KNOWNOE



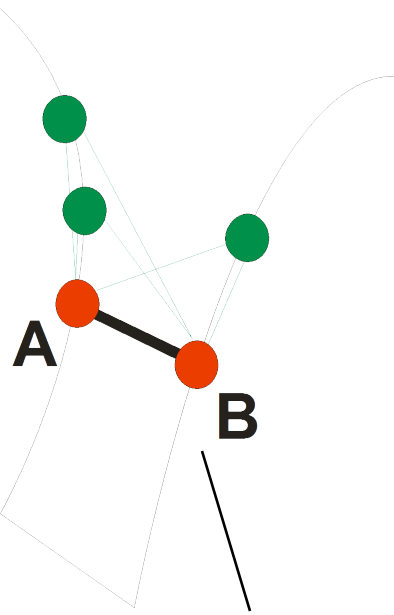


Example shows how different peak volume distributions can be.

Chemical shift degeneracy leads to ambiguous assignments.

Based on Bayesian statistics and a data base of 1000 structures and 400 000 volume-probability tables the most probable assignment is found. The data base is part of the AUREMOL installation

Important is the usage of mutual information.

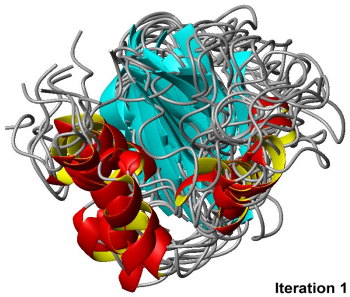


Not only pair A/B is analyzed but also neighboring pairs

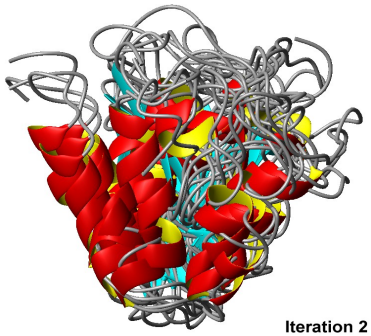
Structure determination is iterative

Iteration 0

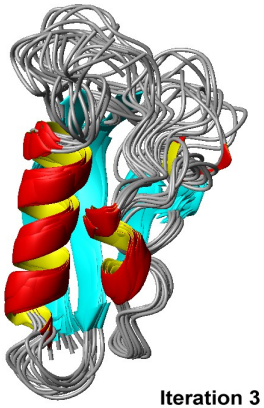
Typical structural changes occurring during iterations of side-chain assignment, KNOWNOE, REFINE, CNS, RFAC



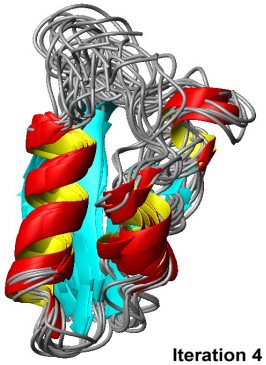
Iteration 1



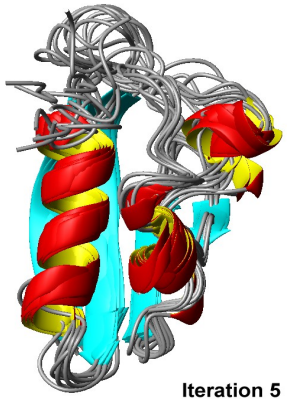
Iteration 2



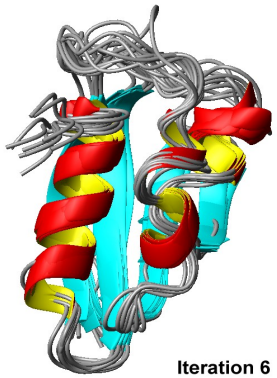
Iteration 3



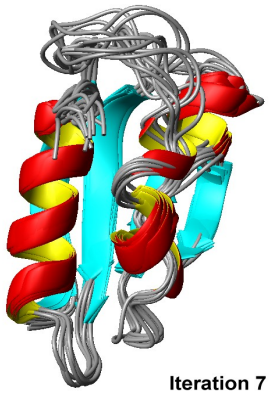
Iteration 4



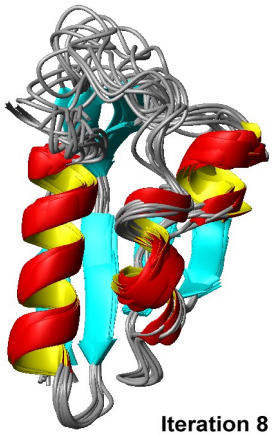
Iteration 5



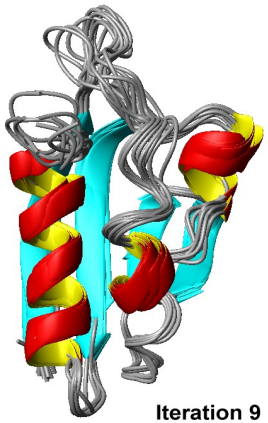
Iteration 6



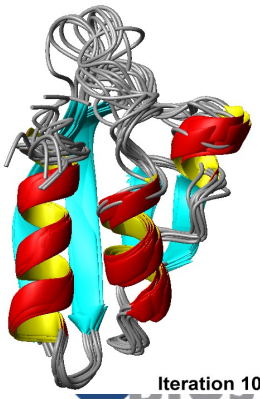
Iteration 7



Iteration 8



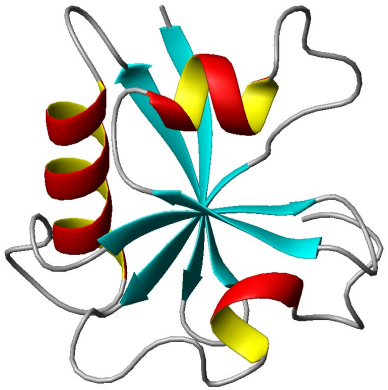
Iteration 9



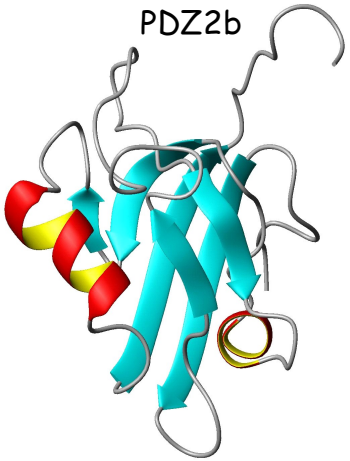
Iteration 10

Structures solved with AUREMOL

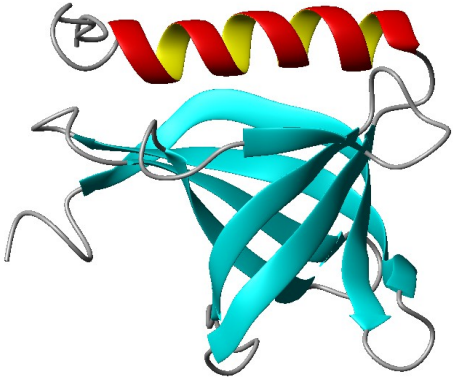
BYR2-RBD



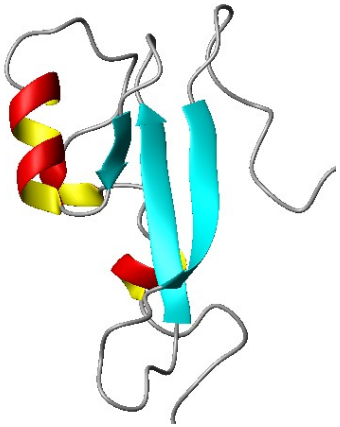
PDZ2b



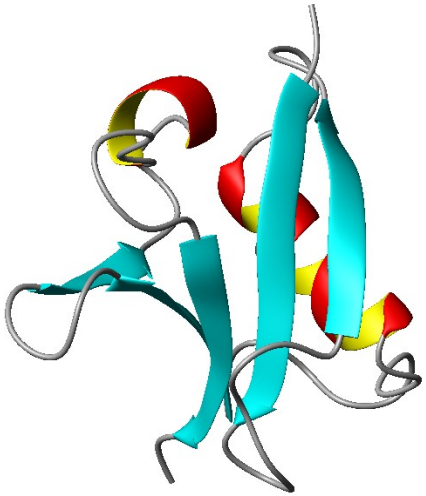
RanBP2



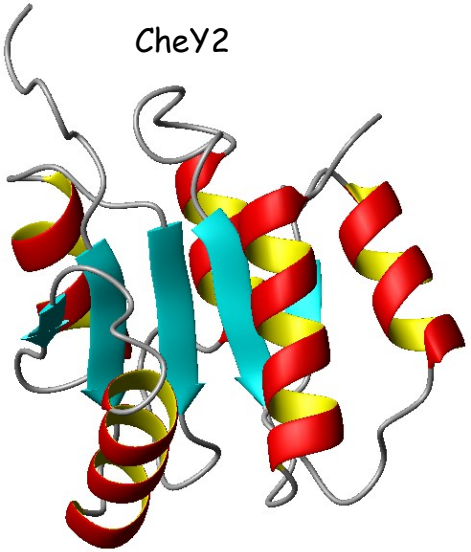
cMeCP2 MAR-E



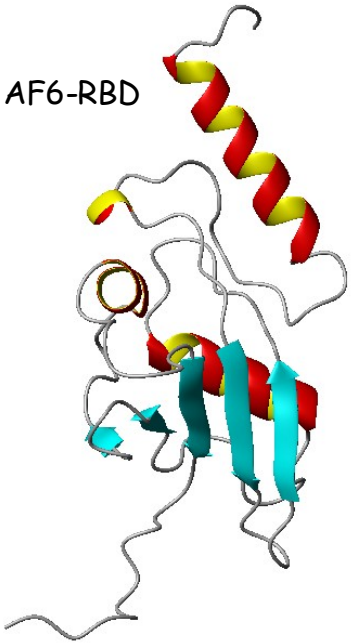
RalGDS-RBD



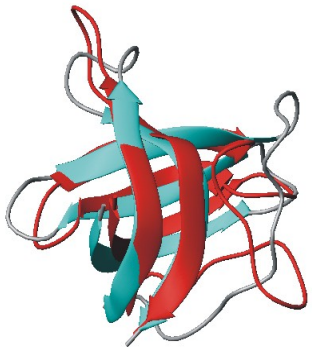
CheY2



AF6-RBD



TmCSP



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- Gronwald, W., Brunner, K., Kirchhöfer, R., Trenner, J., Neidig, K.-P. & Kalbitzer, H.R. AUREMOL-RFAC-3D, Combination of R-Factors and Their Use for Automated Quality Assessment of Protein Solution Structures. *In press* (2006).
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- Gronwald, W., Kirchhöfer, R., Görler, A., Kremer, W., Ganslmeier, B., Neidig, K.-P. & Kalbitzer, H. R. RFAC, a Program for Automated NMR R-Factor Estimation. *J. Biomol. NMR,* **17**, 137-151 (2000).
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