Control and Prediction of the Organic Solid State

A Basic Technology project of the Research Councils UK

Powder Diffraction and Crystal Structure Prediction:

A Two-Way Relationship

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cposs

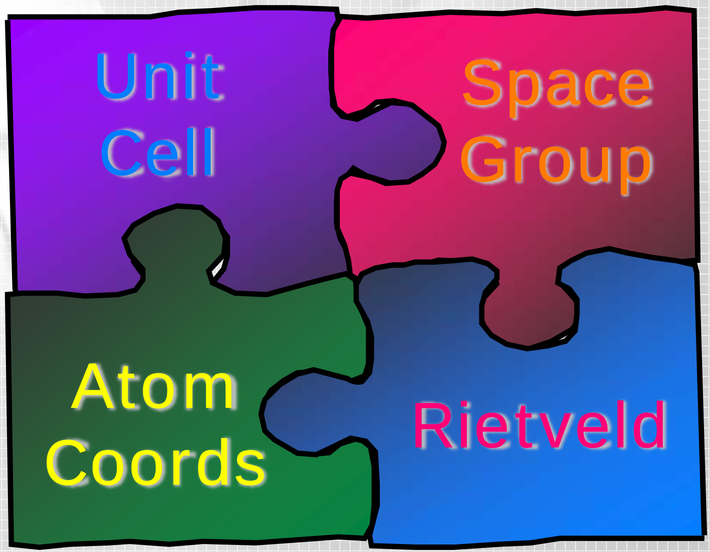
Powder Diffraction

- Fingerprinting of crystalline materials
- Identification of polymorphs & mixtures
- Characterisation of bulk

- Source of structural data

↓

Crystal Structure Determination



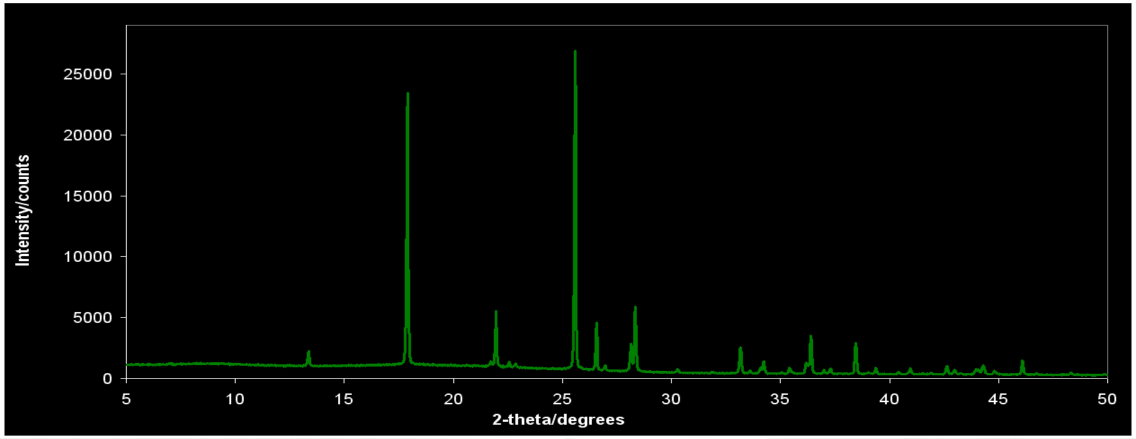
Unit Cell

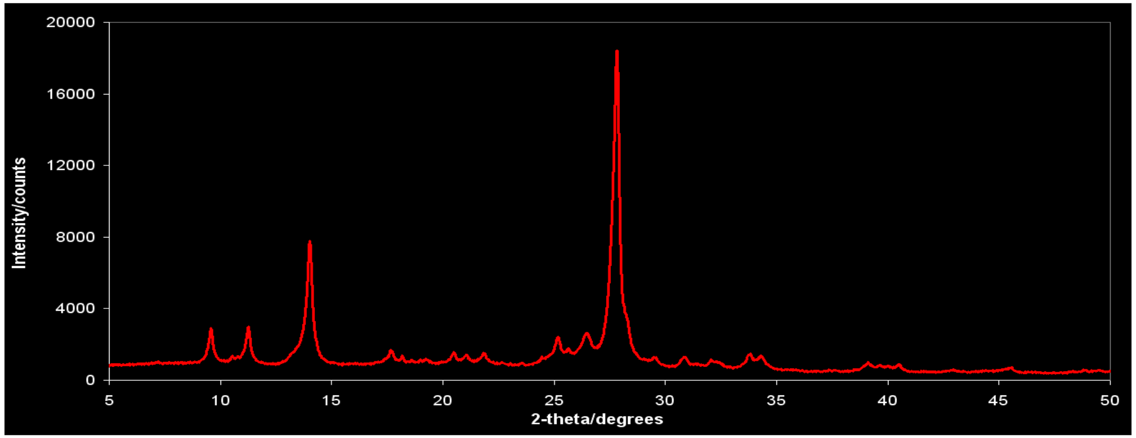
Space Group

Atom Coords

Rietveld

Powder Diffraction





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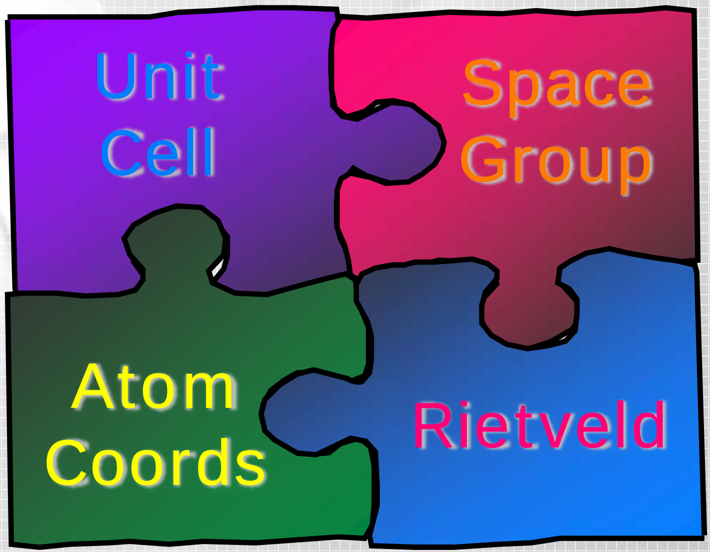

Unit Cell

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Atom Coords

Rietveld

Crystal Structure Prediction

- Prediction of crystal structure based only on molecular structure
- Ranking based primarily on lattice energy

BUT

… many more energetically feasible structures than likely polymorphs

… optimal packing at 0K

PXRD & Structure Prediction: Complementary Techniques

- PXRD simulated to identify similar theoretical structures
- PXRD data used to identify experimental polymorphs given in a prediction

… traditionally by visual comparison …

… often 50+ potential structures …

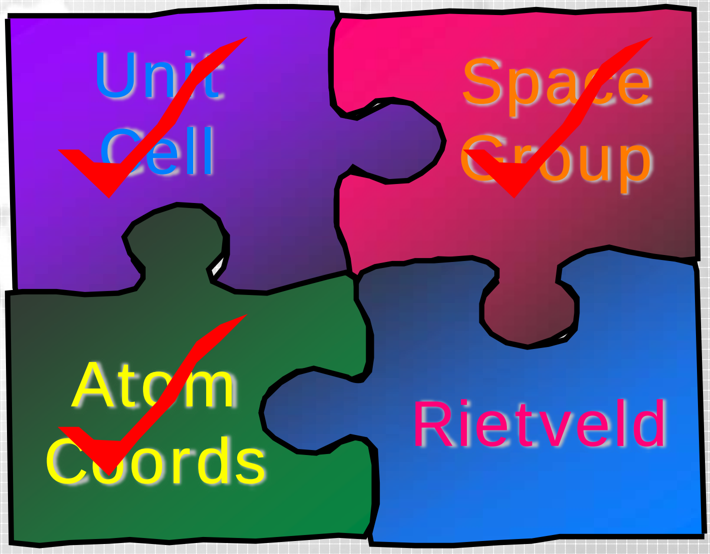
… similar motifs in structures can give rise to similar features in PXRD data …

PXRD & Structure Prediction: Complementary Techniques

- Predicted structure used as a starting point for structure determination if …

… powder data not indexed …

… of poor quality (broadening, preferred orientation)



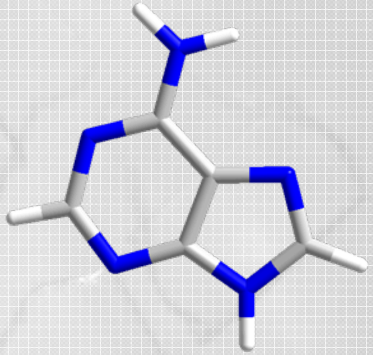
Unit Cell ✓

Space Group ✓

Atom Coords ✓

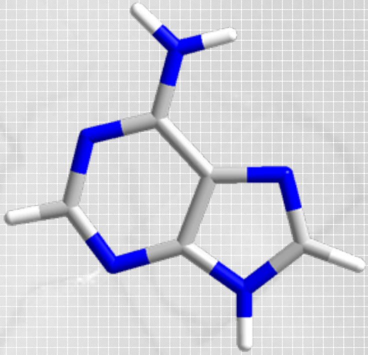
Rietveld

Adenine



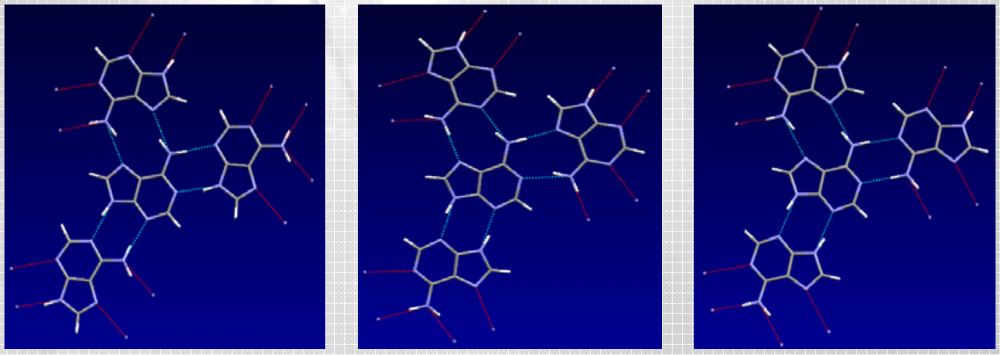
- Integral part of DNA, RNA, ATP – but crystal structure of adenine *unknown*
- PXRD data *not indexed*

Adenine

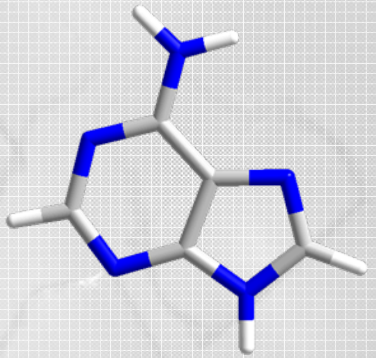


- Integral part of DNA, RNA, ATP – but crystal structure of adenine *unknown*
- PXRD data *not indexed*
- Predictions based on *ab initio* and planar molecular structures
- *33 structures* within *7 kJmol*$^{-1}$ of global *LE minimum*

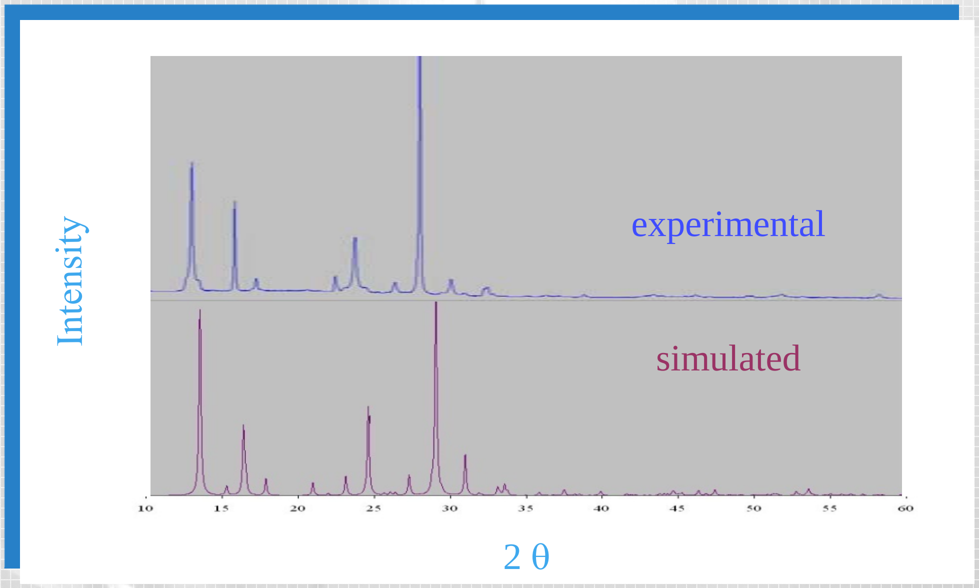
3 distinct hydrogen bond sheet motifs



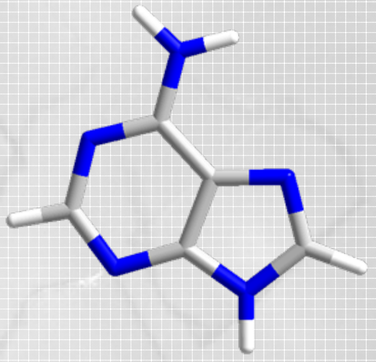
Adenine



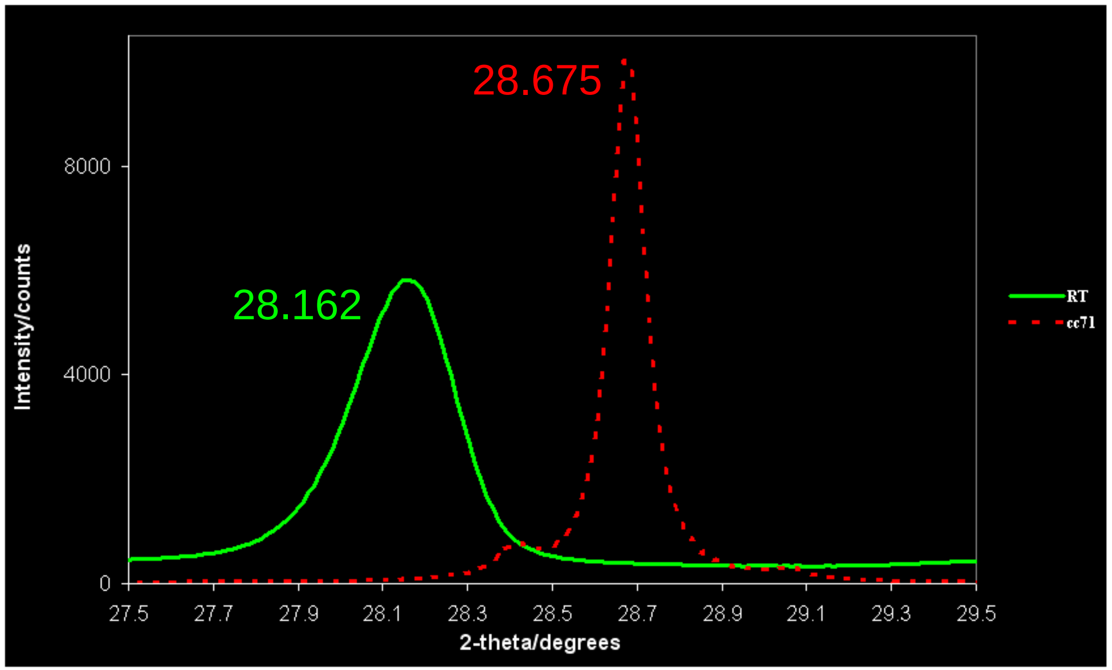
- Predicted structure identified as match to PXRD data
- cc71 ⟶ 1kJmol^{-1} *above* global LE minimum
  free energy minimum



Adenine



- Experimental *vs* simulated PXRD data from predicted structure



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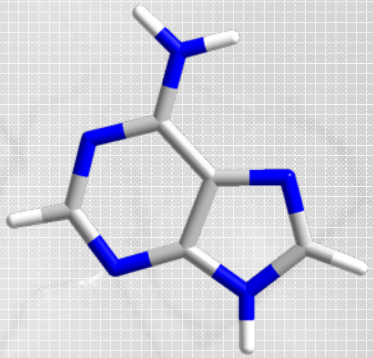
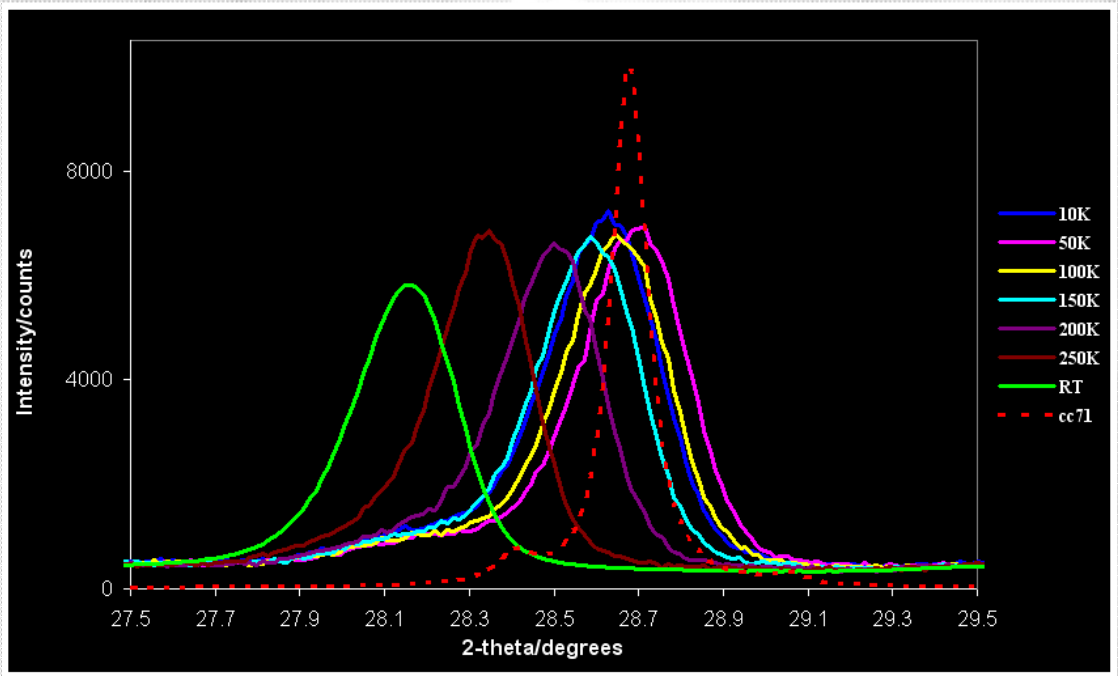


- Experimental *vs* simulated PXRD data from predicted structure (10,50,100,150,200,250K,RT)



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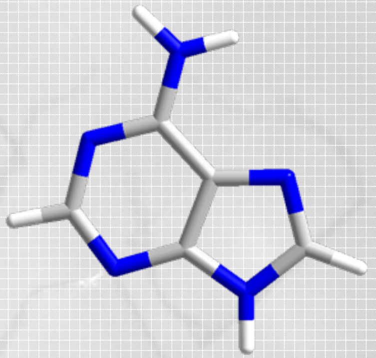

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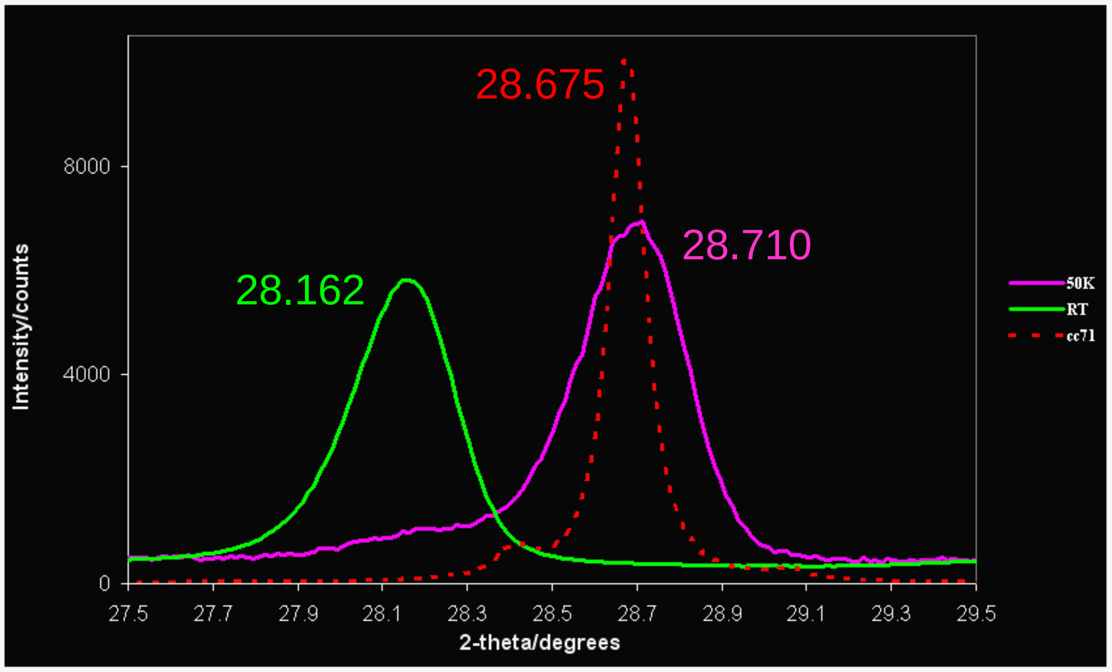
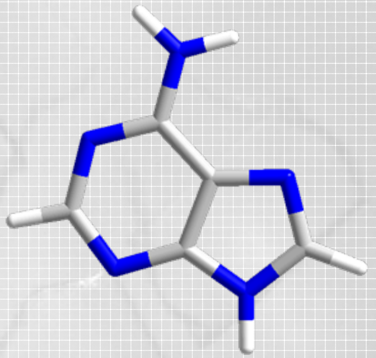
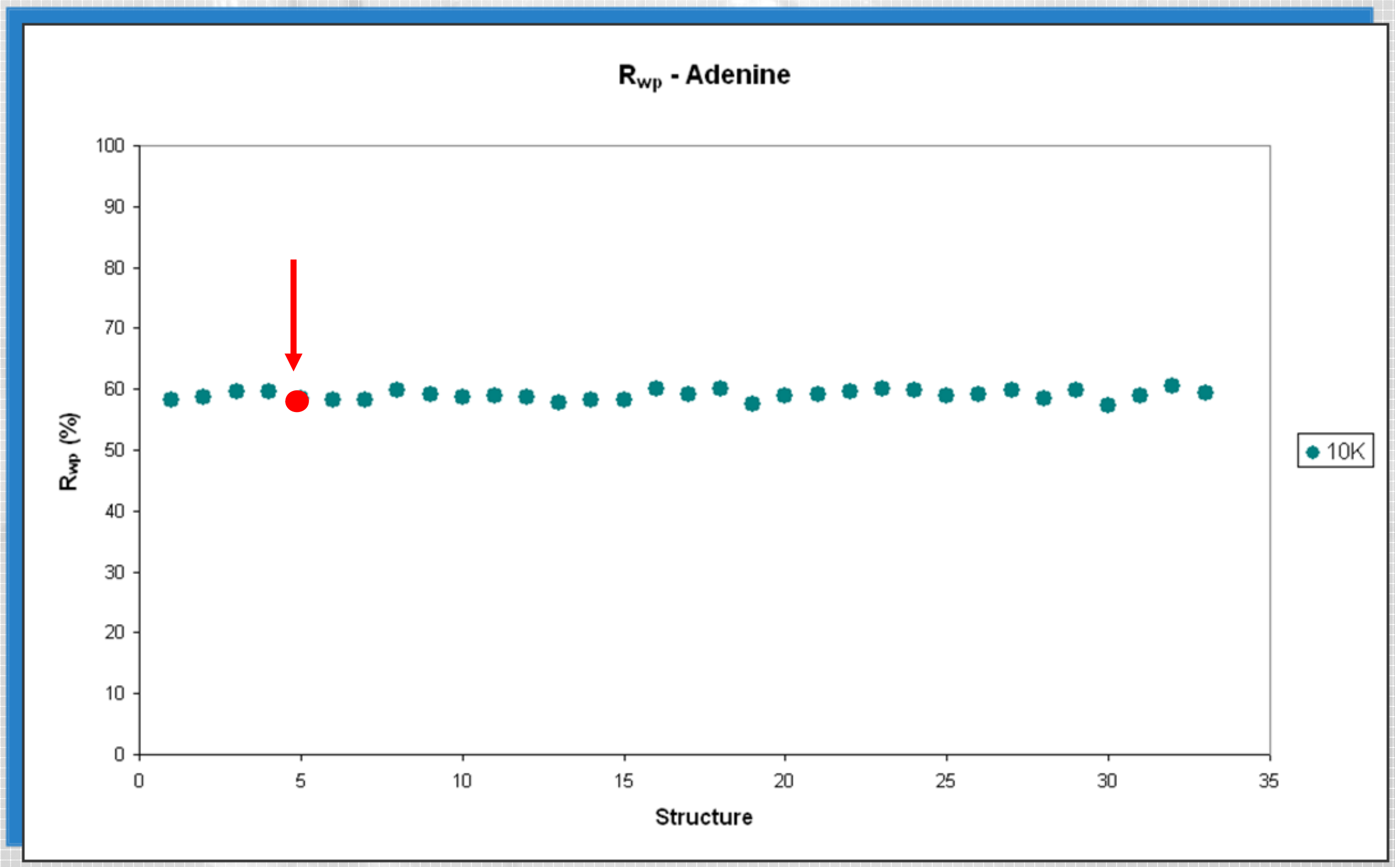


Comparison of Patterns

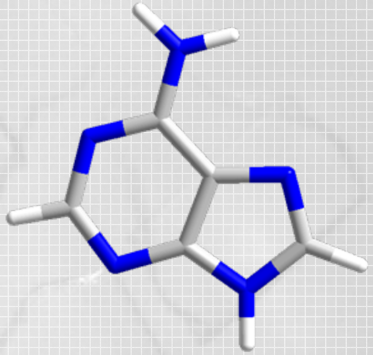
- Evaluate 3 automatic numerical methods for pattern matching of experimental and simulated PXRD:
- R_{wp} – whole profile; point-by-point comparison of diffraction data; used in direct space structure soln

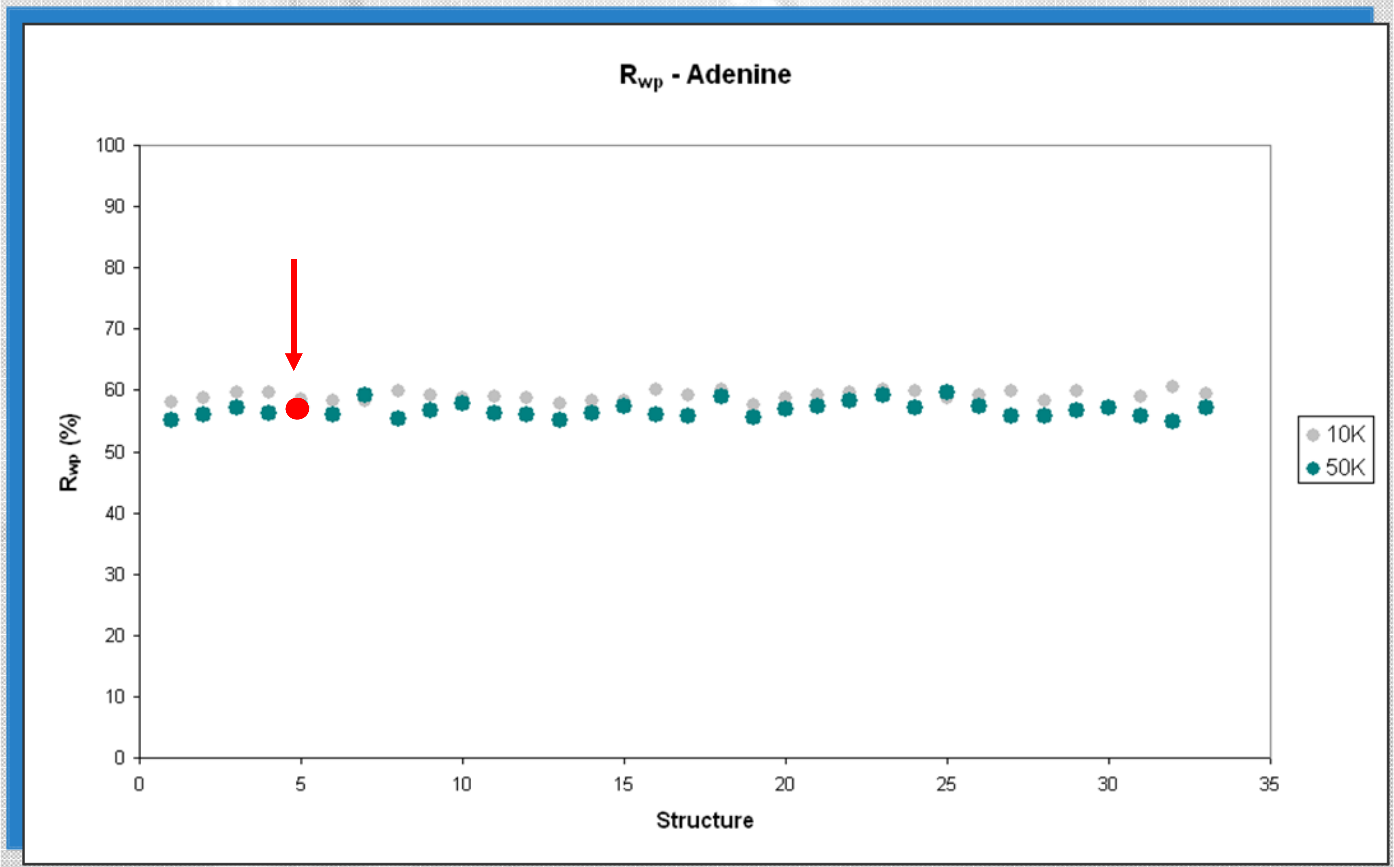
Adenine: R_{wp}



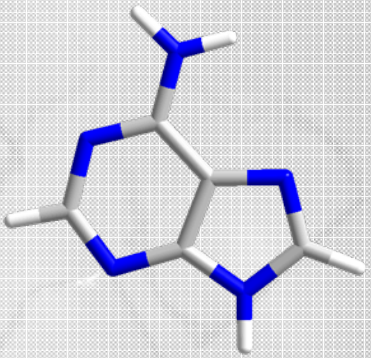

R_{wp} - Adenine
R_{wp} (%)
100
90
80
70
60
50
40
30
20
10
0
0
5
10
15
20
25
30
35
Structure
● 10K

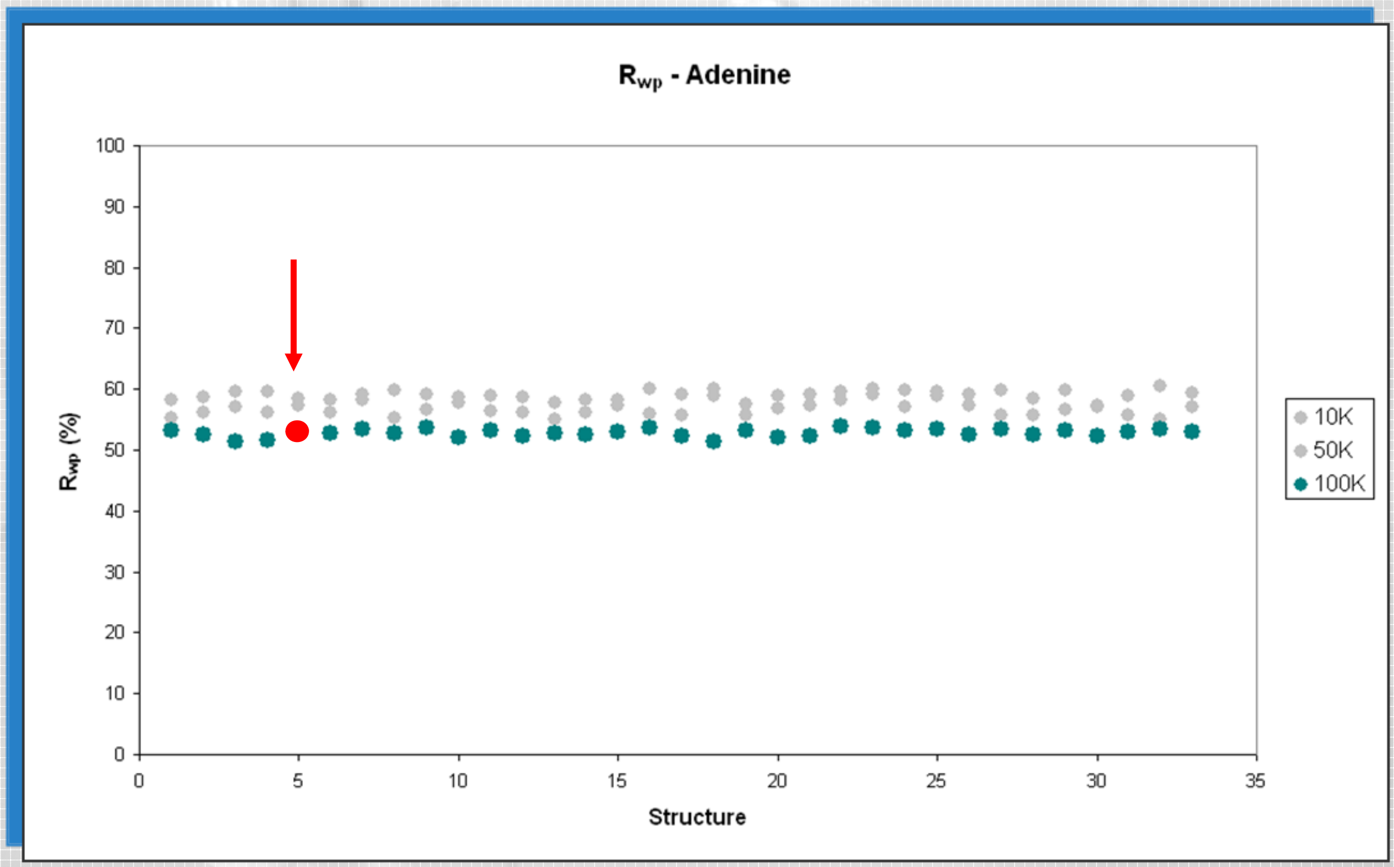
Adenine: R_{wp}




R_{wp} - Adenine
R_{wp} (%)
100
90
80
70
60
50
40
30
20
10
0
0
5
10
15
20
25
30
35
Structure
10K
50K

Adenine: R_{wp}

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R_{wp} (%)
100
90
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70
60
50
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30
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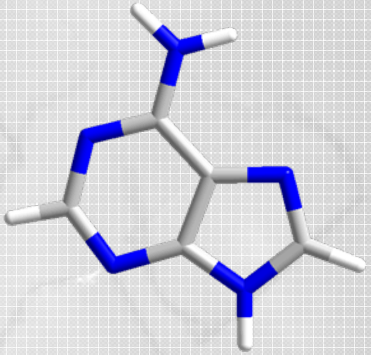
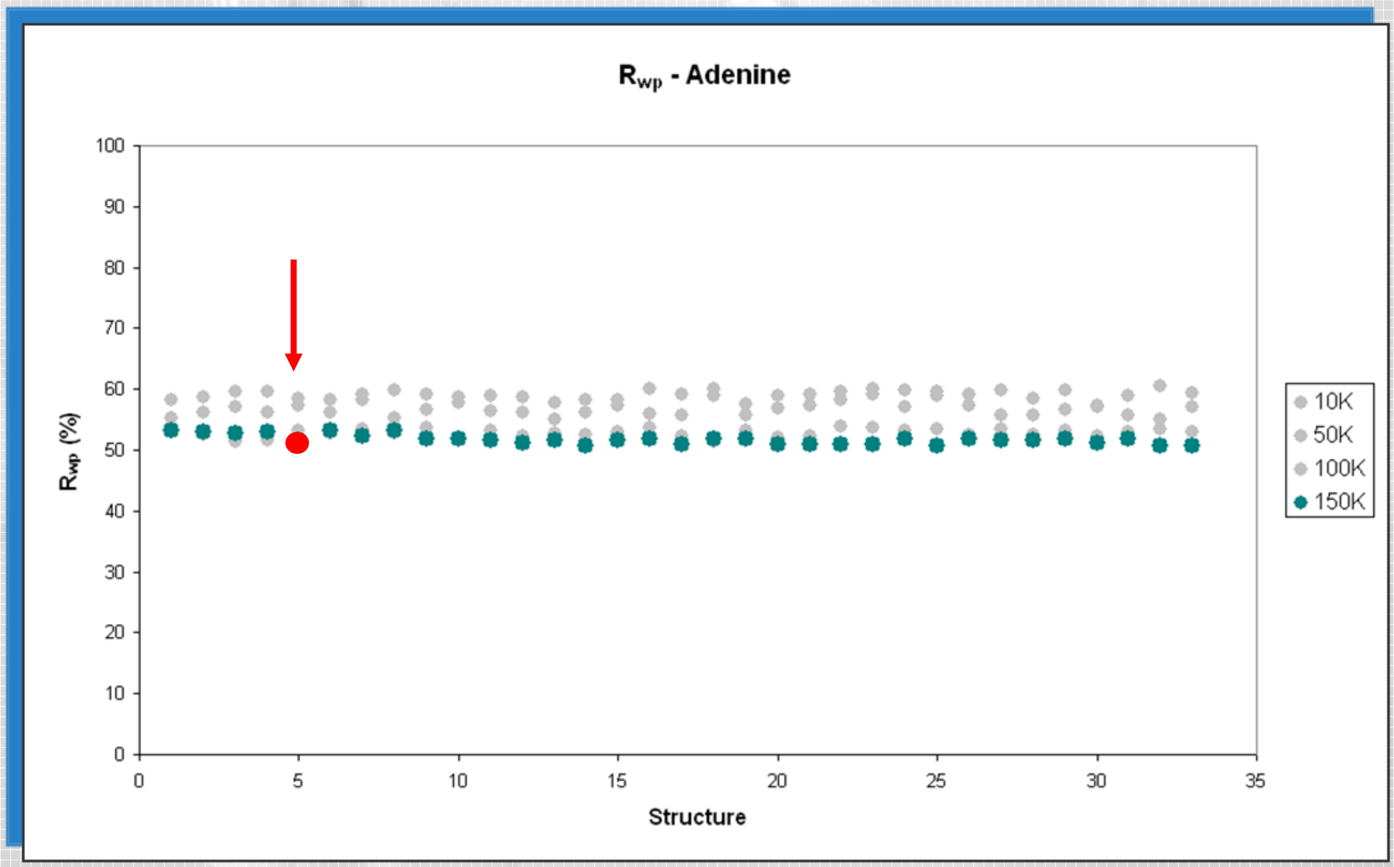
10
0
0
5
10
15
20
25
30
35
Structure
10K
50K
100K

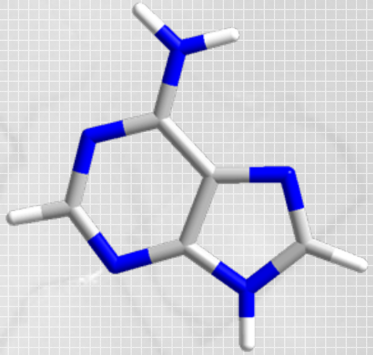
Adenine: R_{wp}

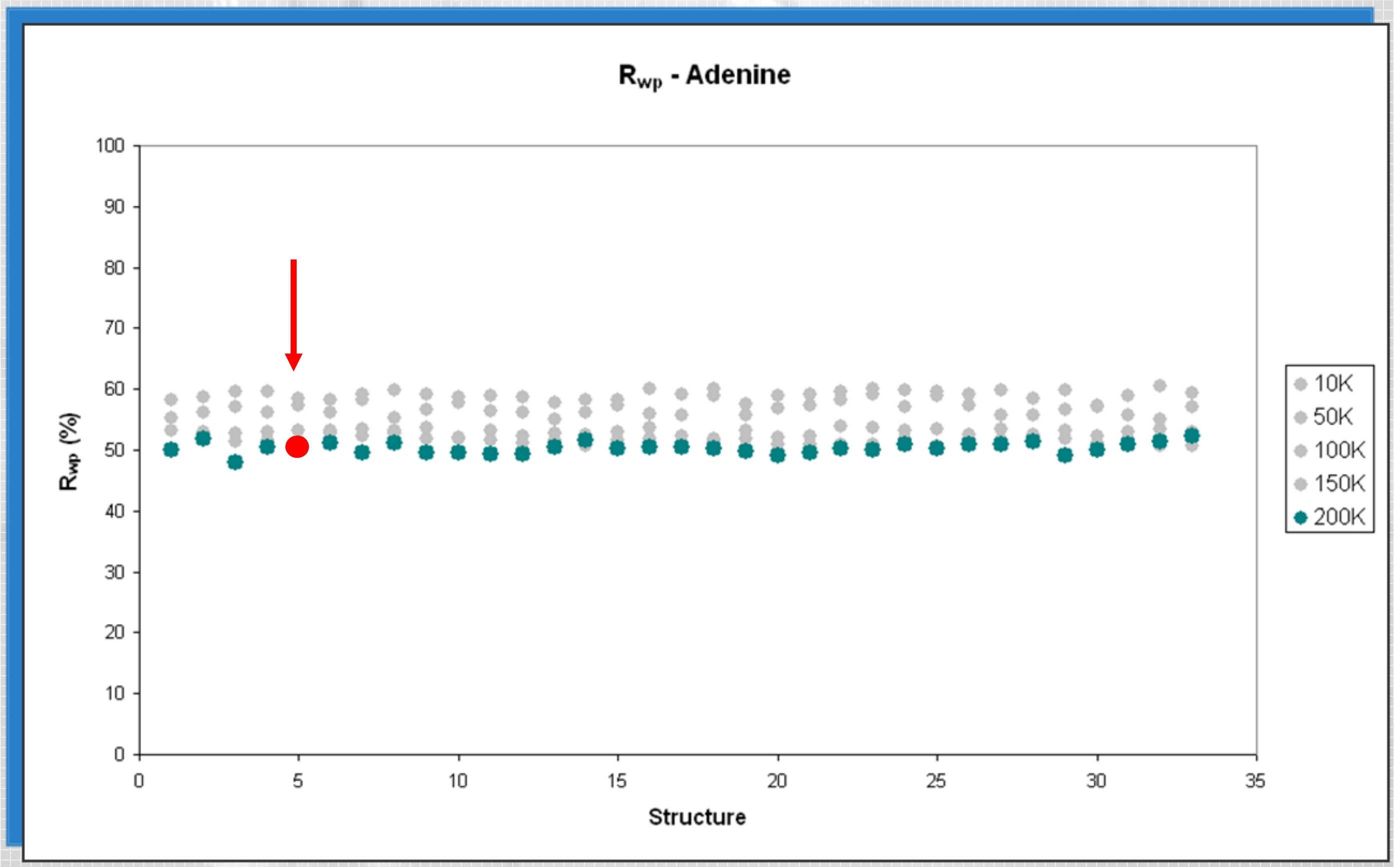




R_{wp} - Adenine
R_{wp} (%)
100
90
80
70
60
50
40
30
20
10
0
0
5
10
15
20
25
30
35
Structure
10K
50K
100K
150K

Adenine: R_{wp}

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20
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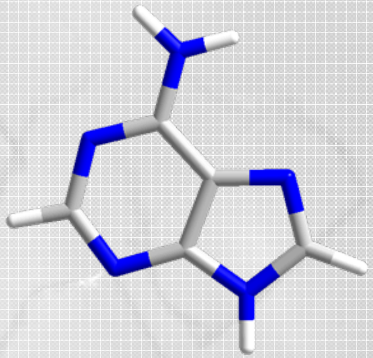
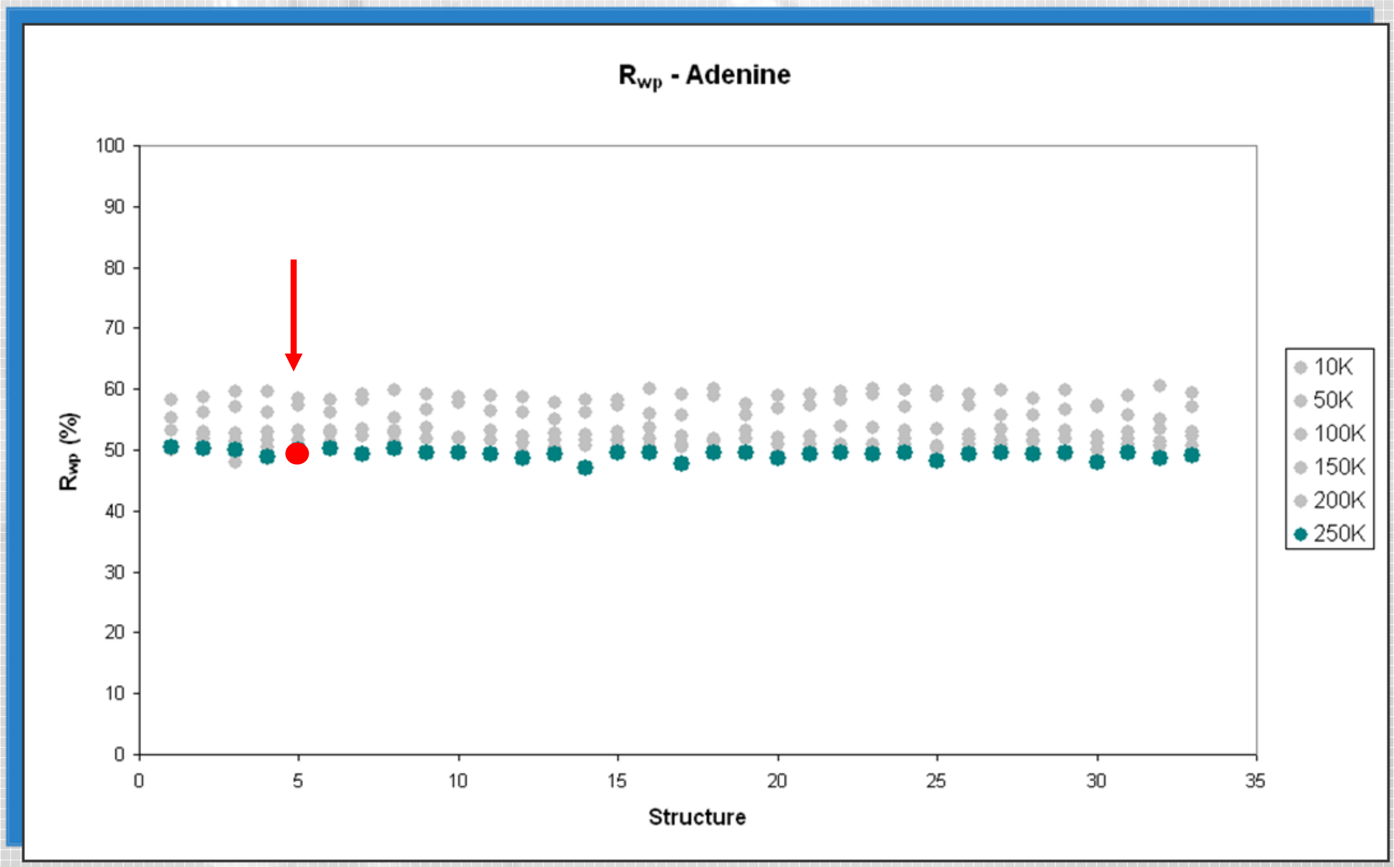
35
Structure
10K
50K
100K
150K
200K

Adenine: R_{wp}





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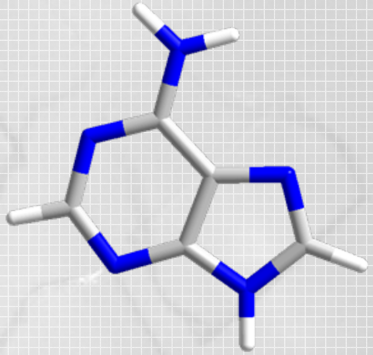
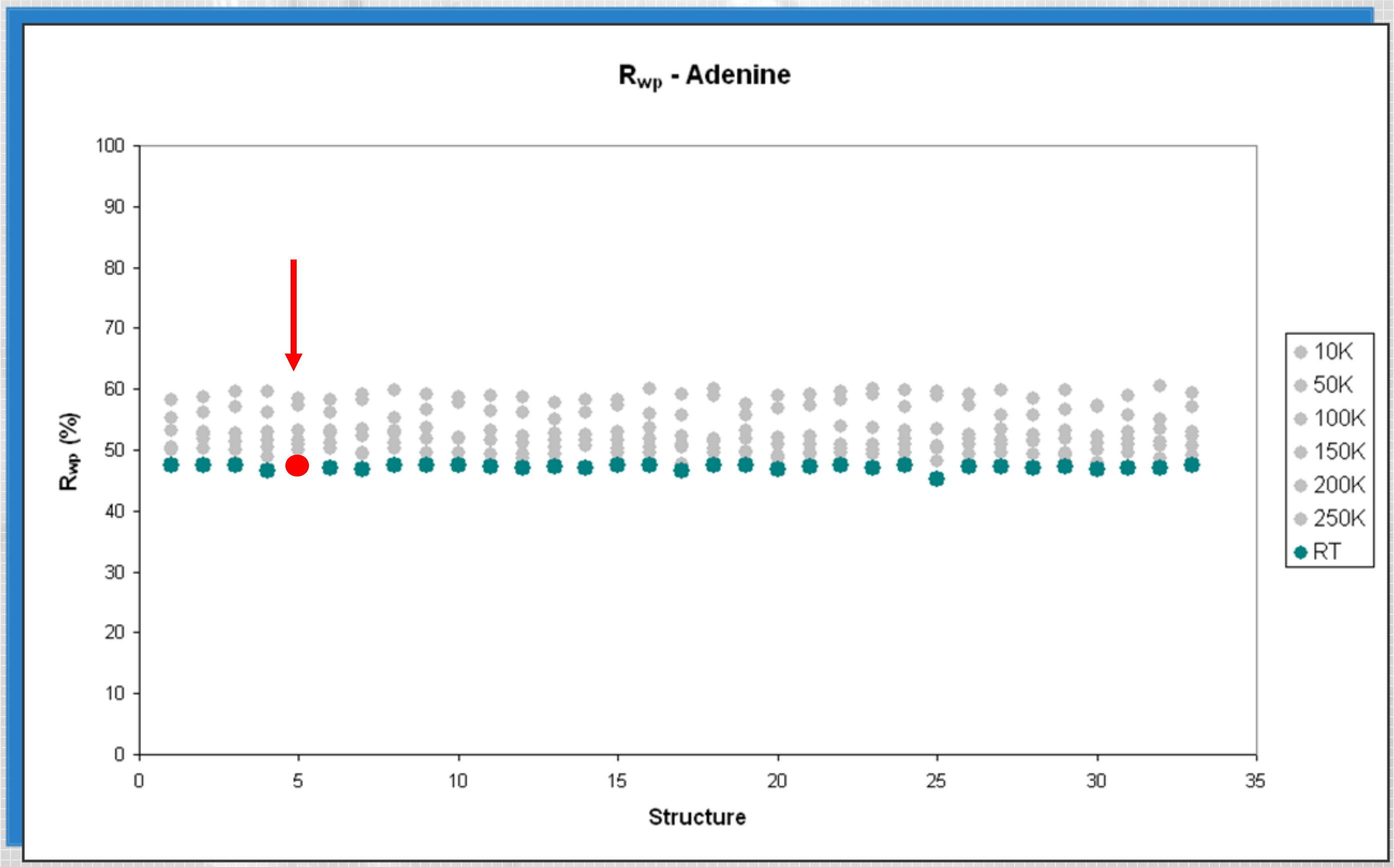
200K
250K

Adenine: R_{wp}

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250K
RT

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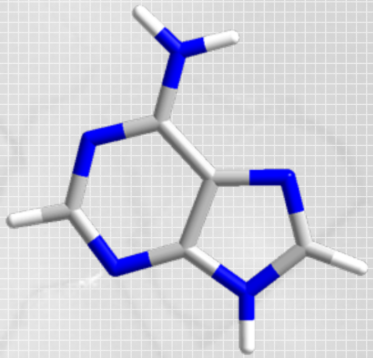
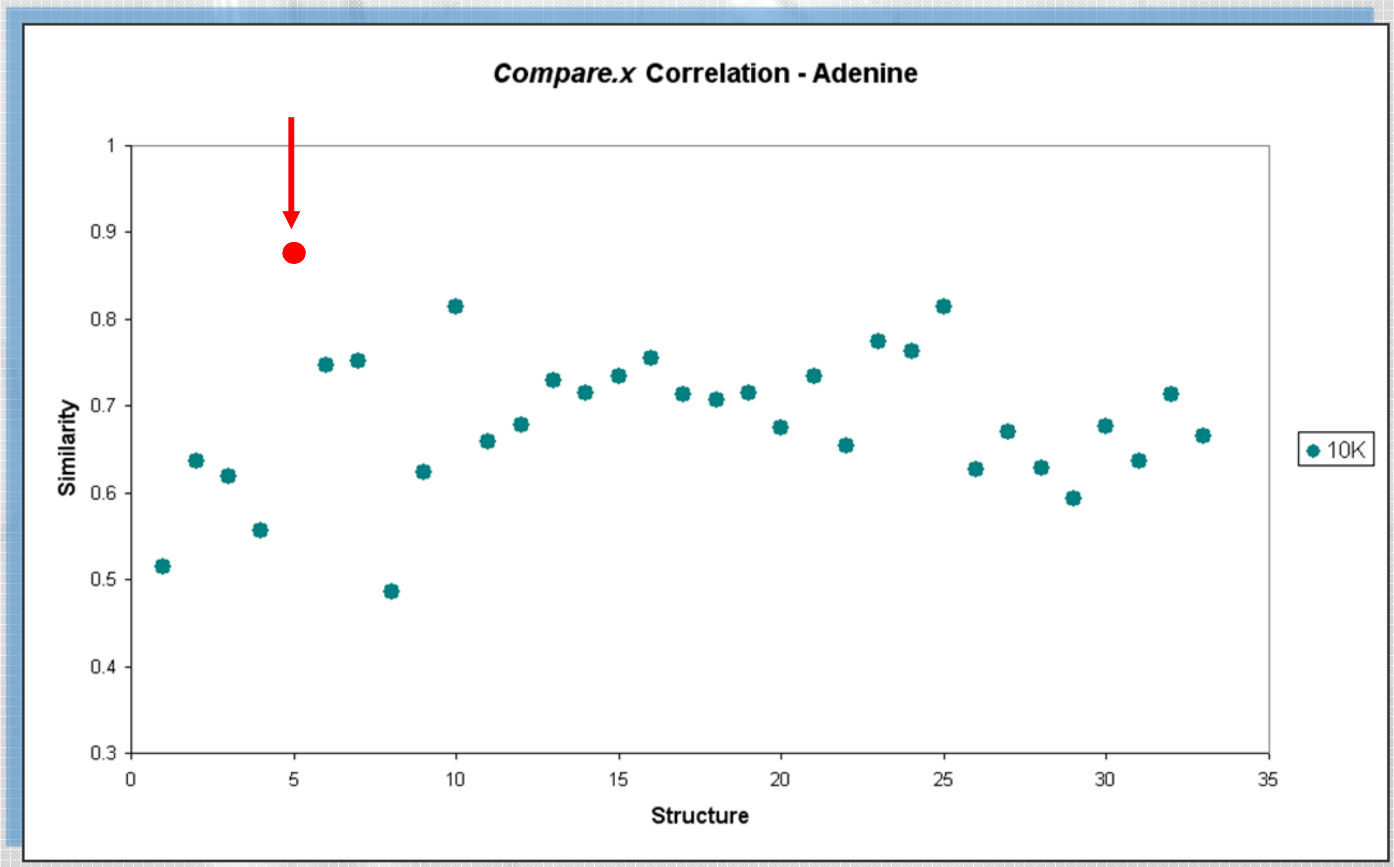
- *Compare.x* – auto and crosscorrelation; shape of weighting factor assesses neighbourhood

(De Gelder, Wehrens, Hageman, *J.Comp.Chem*, (2001) 22, 273)

Adenine: *Compare.x*





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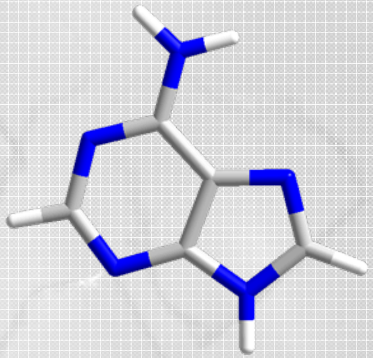

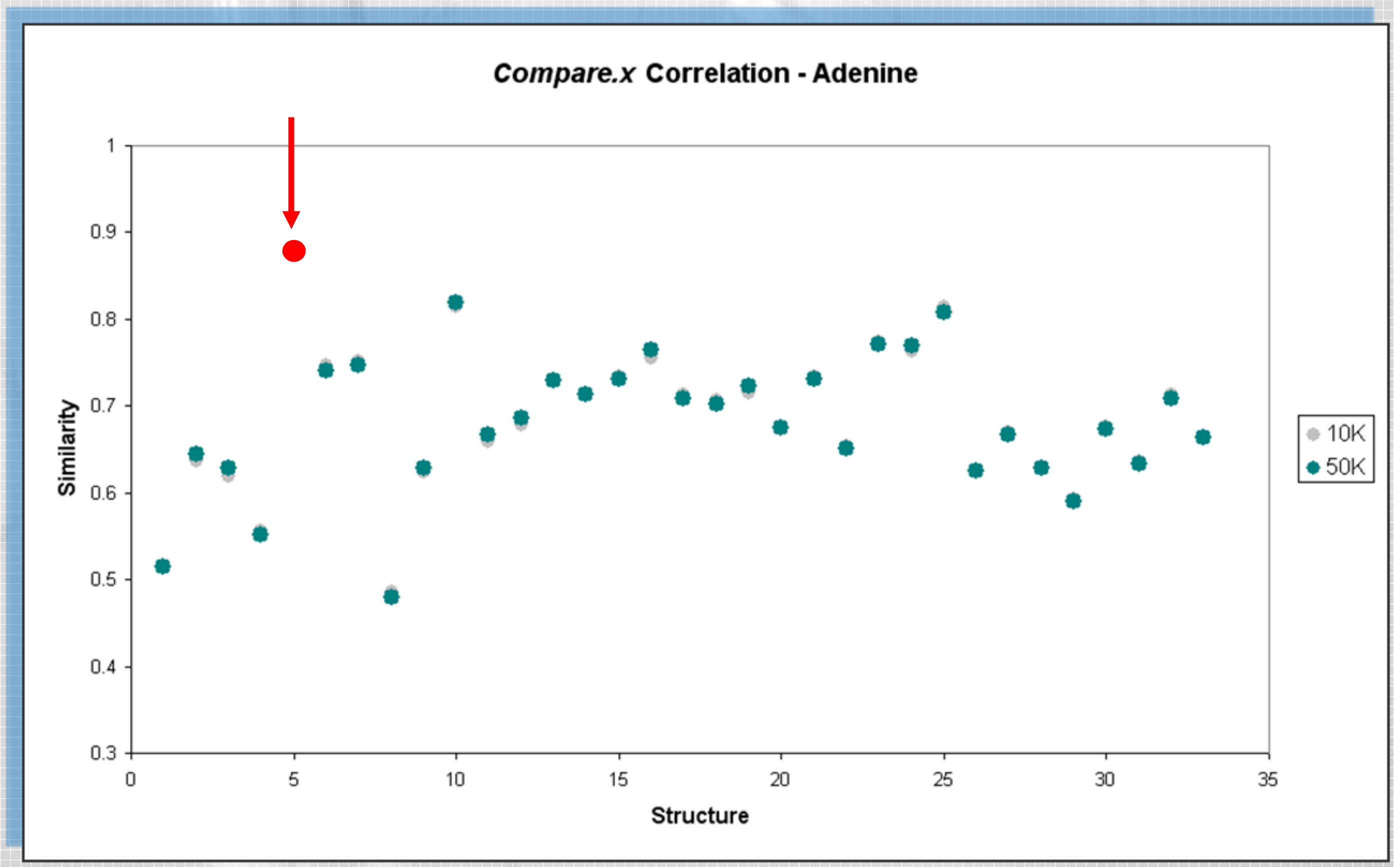

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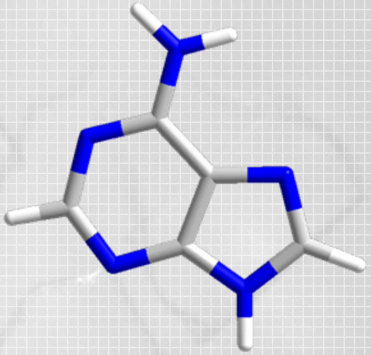

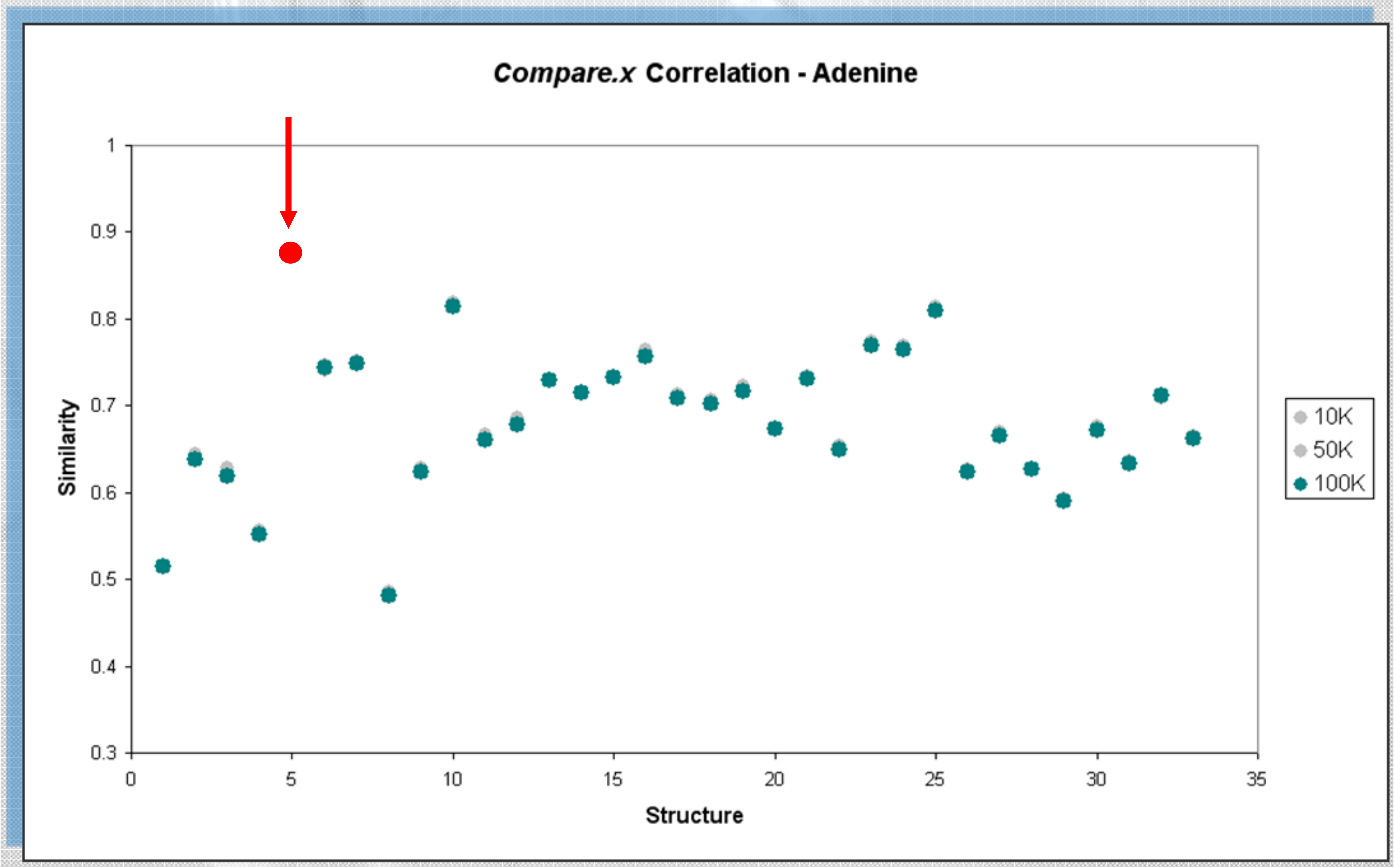

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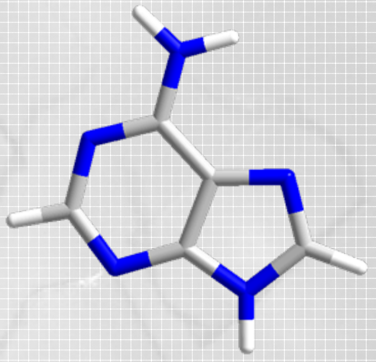

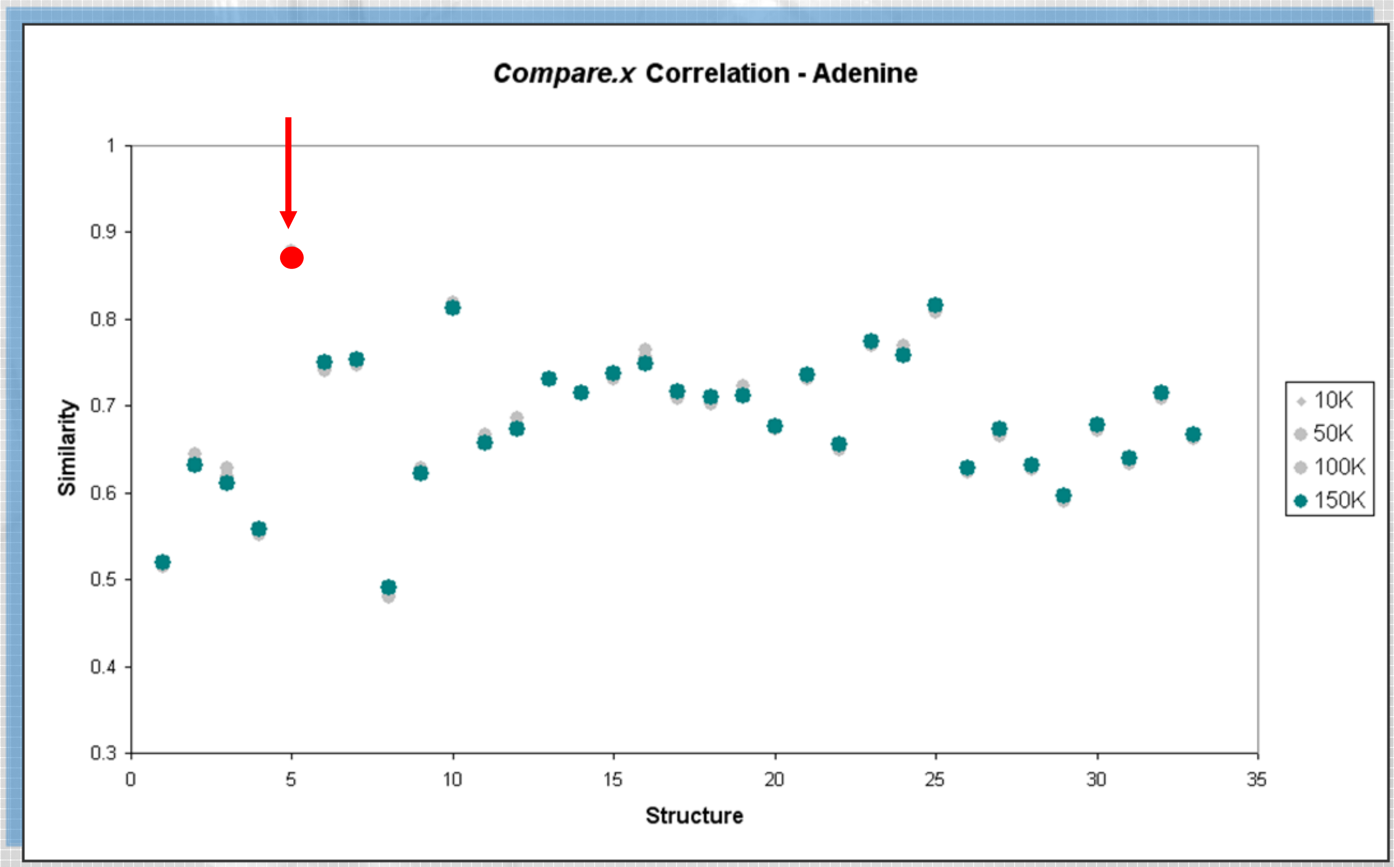

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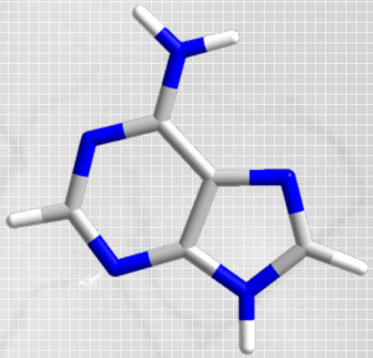

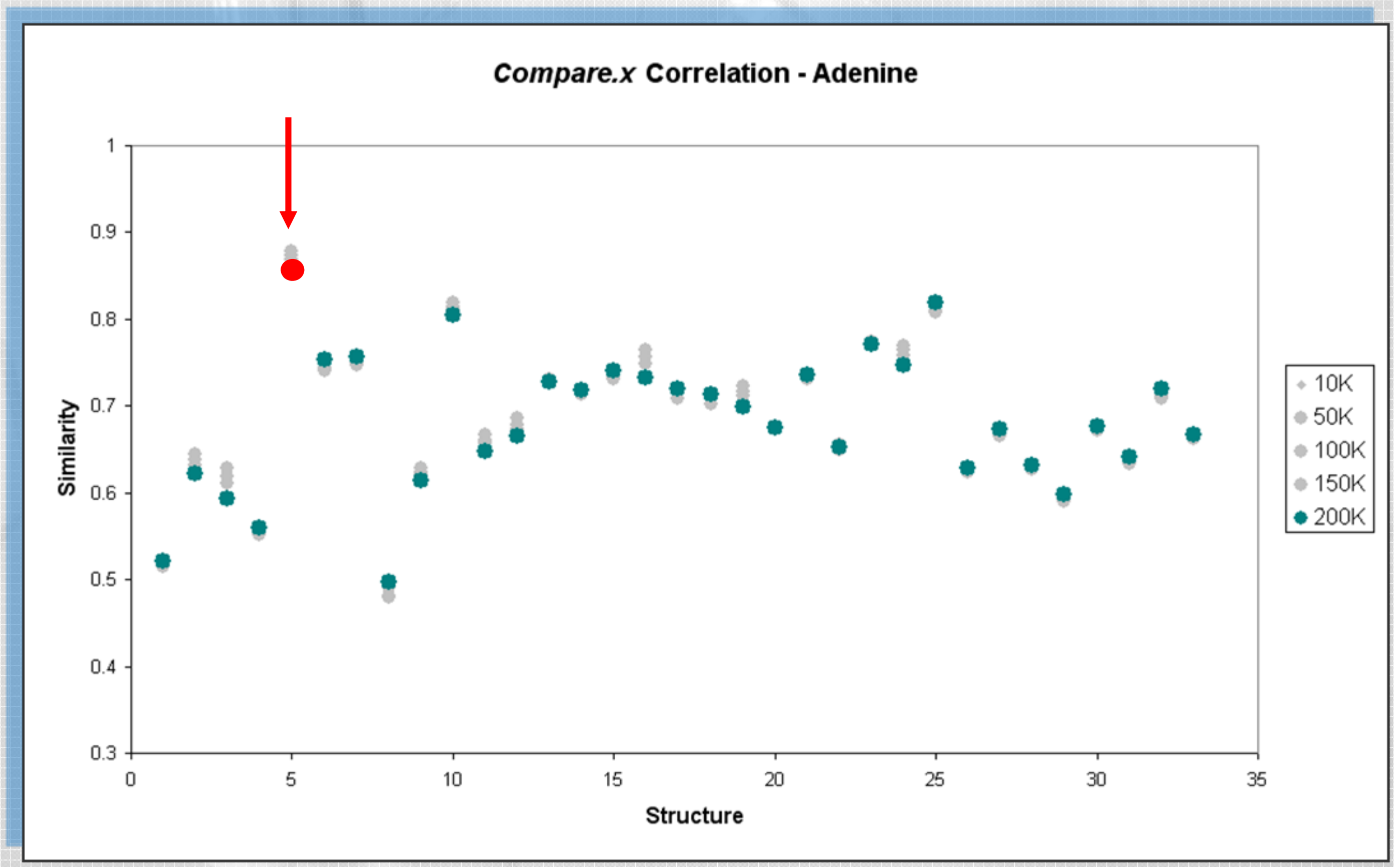

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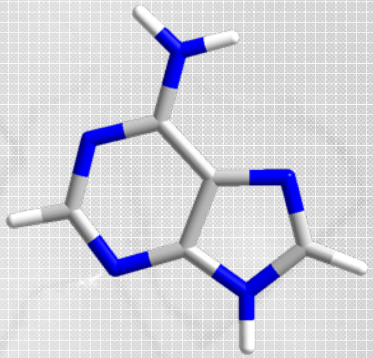

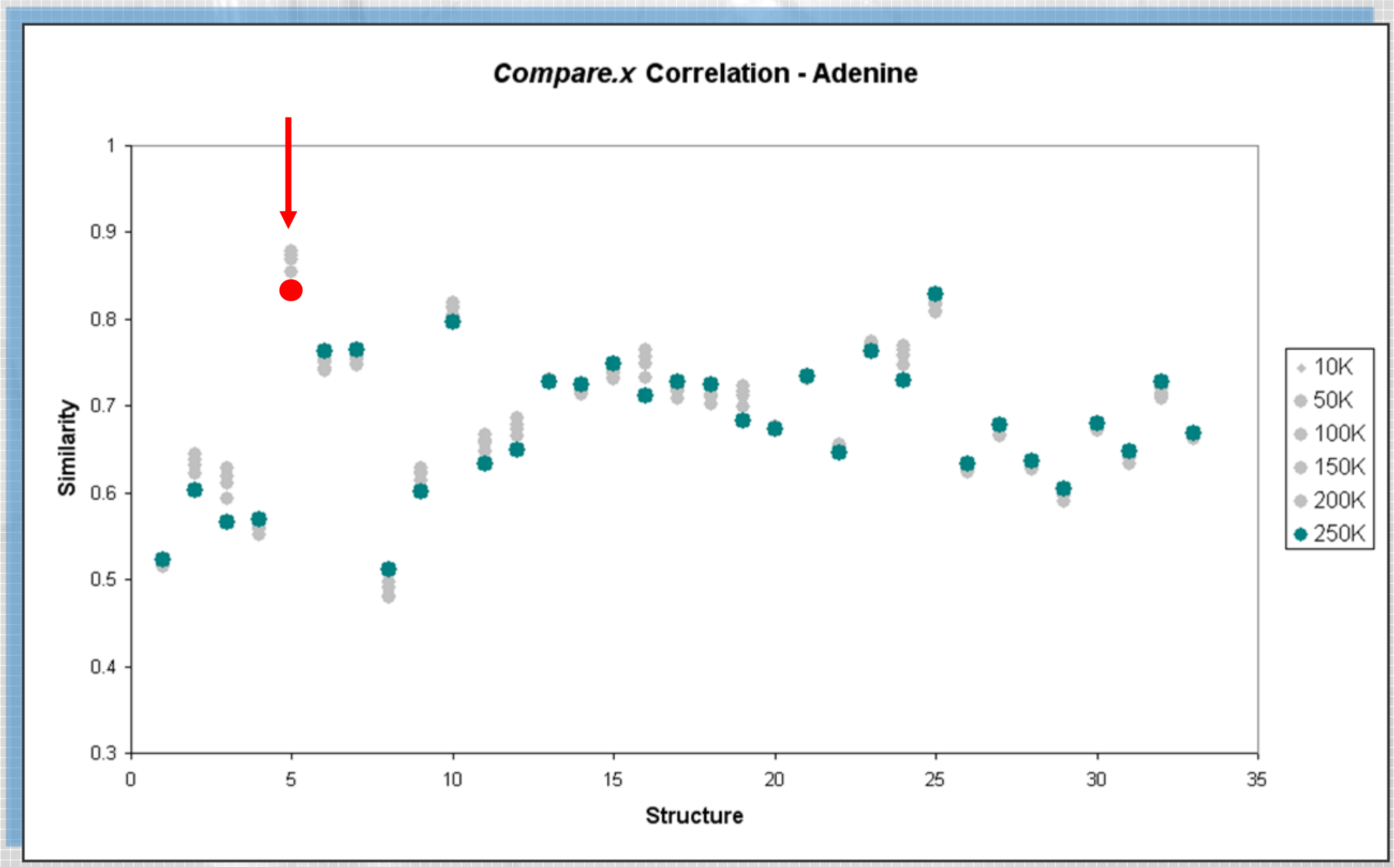

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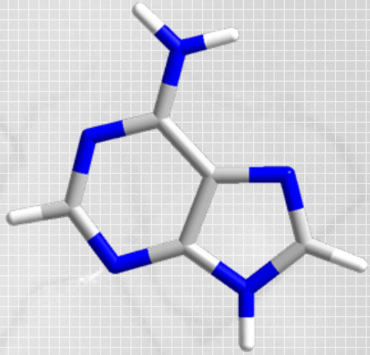

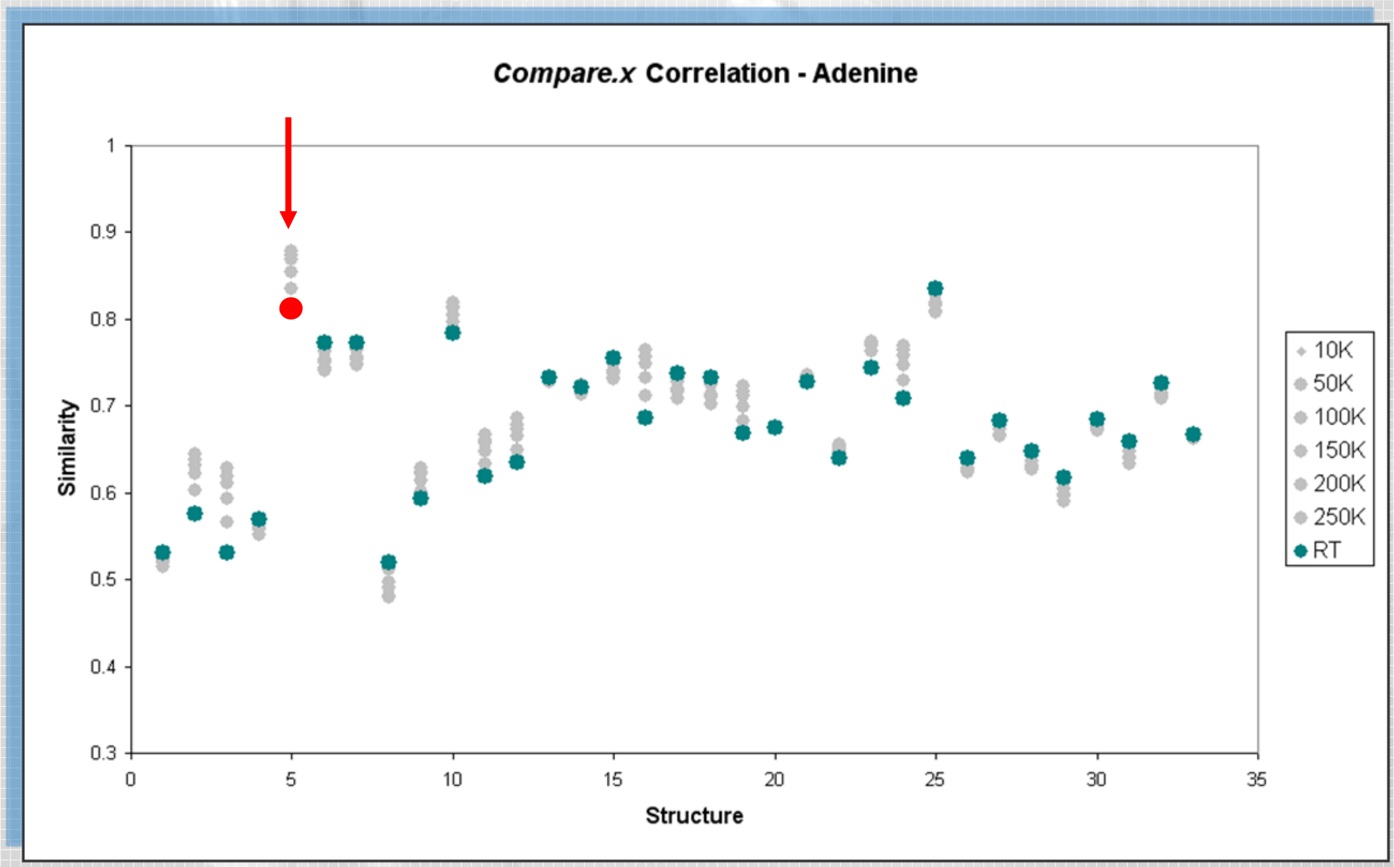

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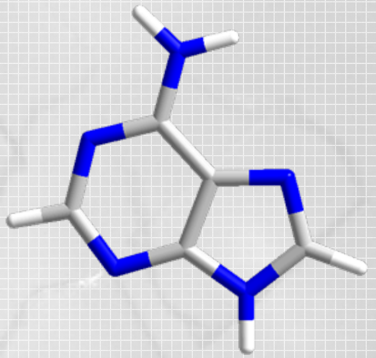
(De Gelder, Wehrens, Hageman, *J.Comp.Chem*, (2001) 22, 273)

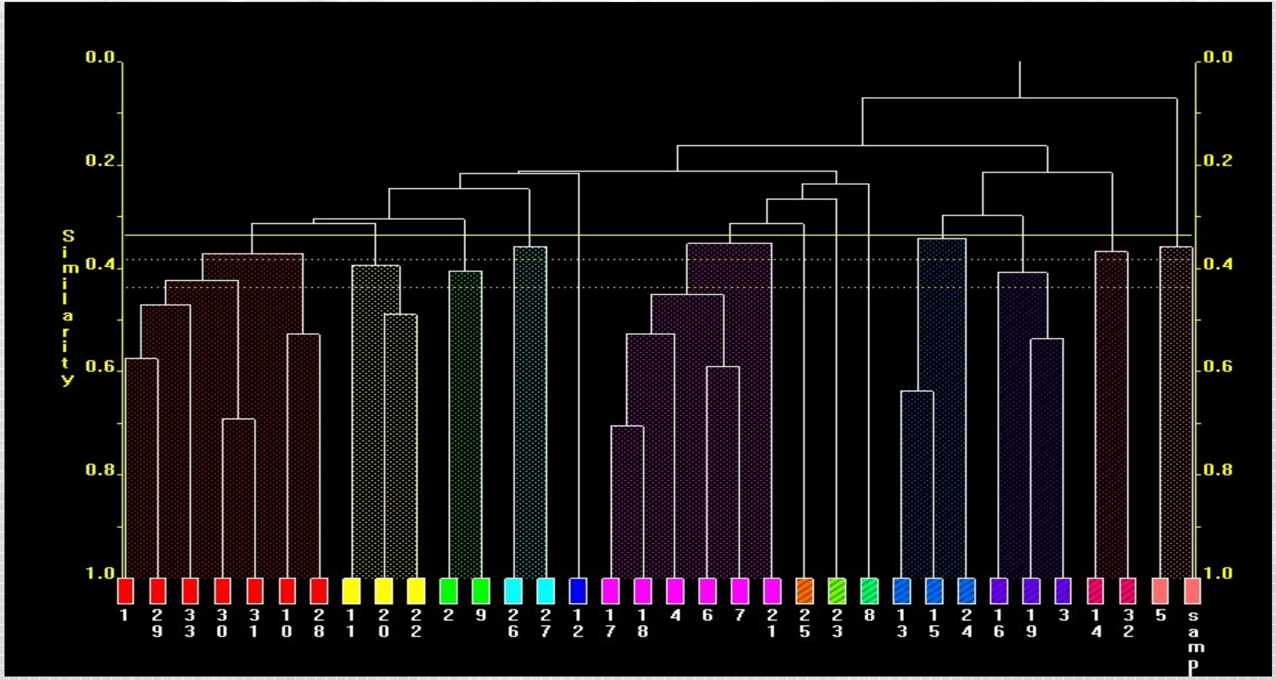
- PolySNAP – correlation; PCA highlights patterns in data reducing dimensionality; cluster analysis

(Barr, Dong, Gilmore, *J.Appl.Cryst.* (2004) 37, 658)

Adenine: PolySNAP



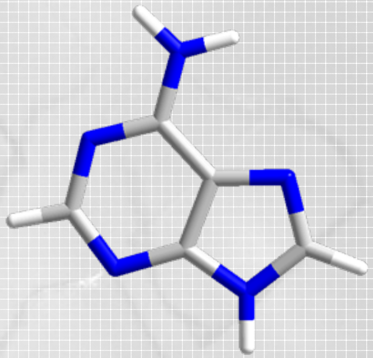
- Dendrogram for 33 predicted structures & original RT experimental data

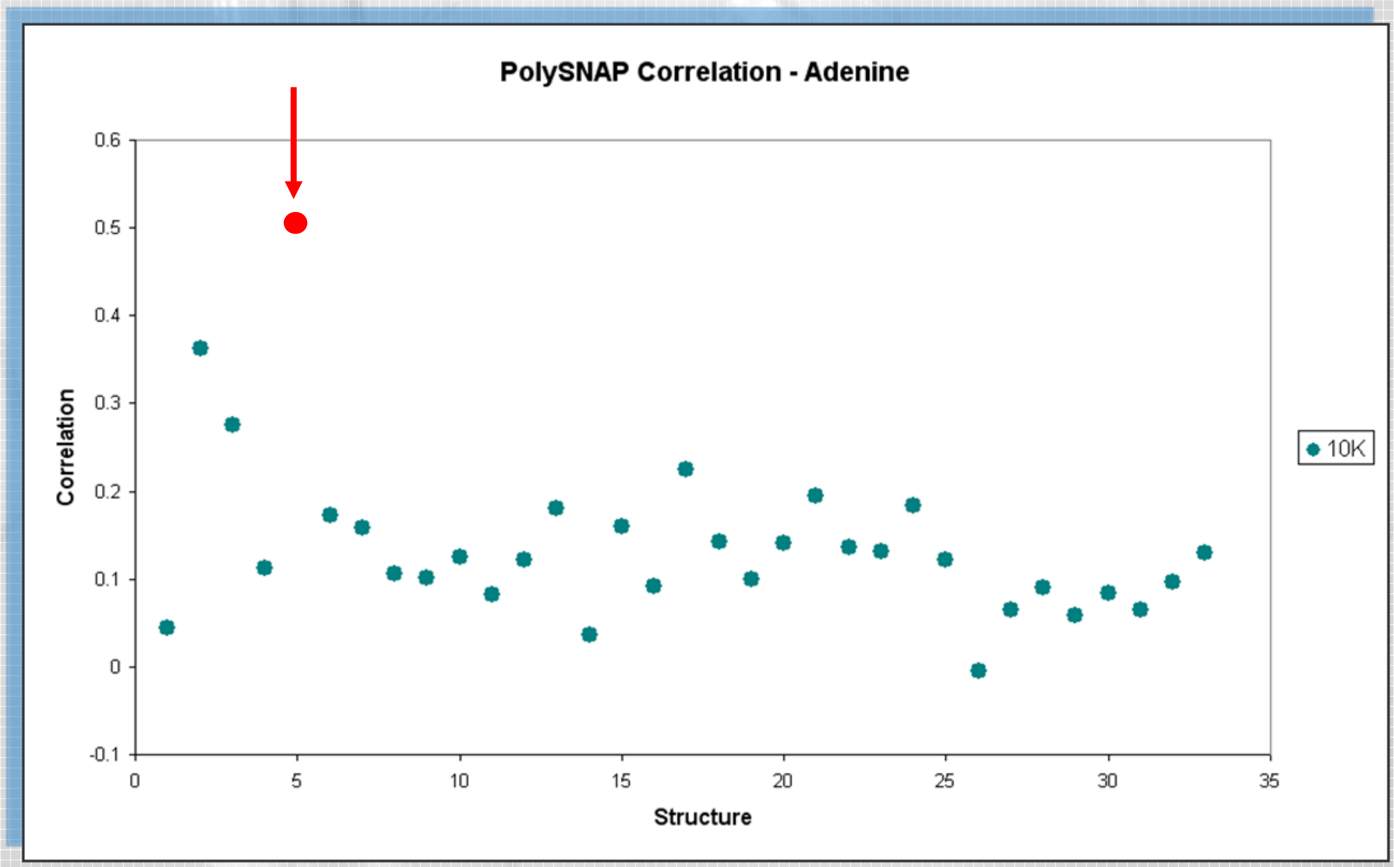


cc71

RT data

Adenine: PolySNAP





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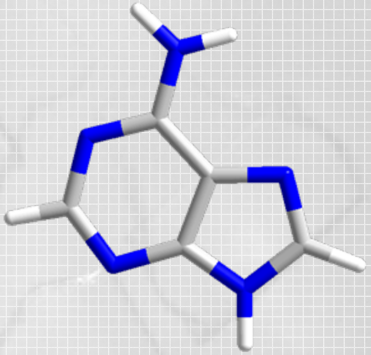

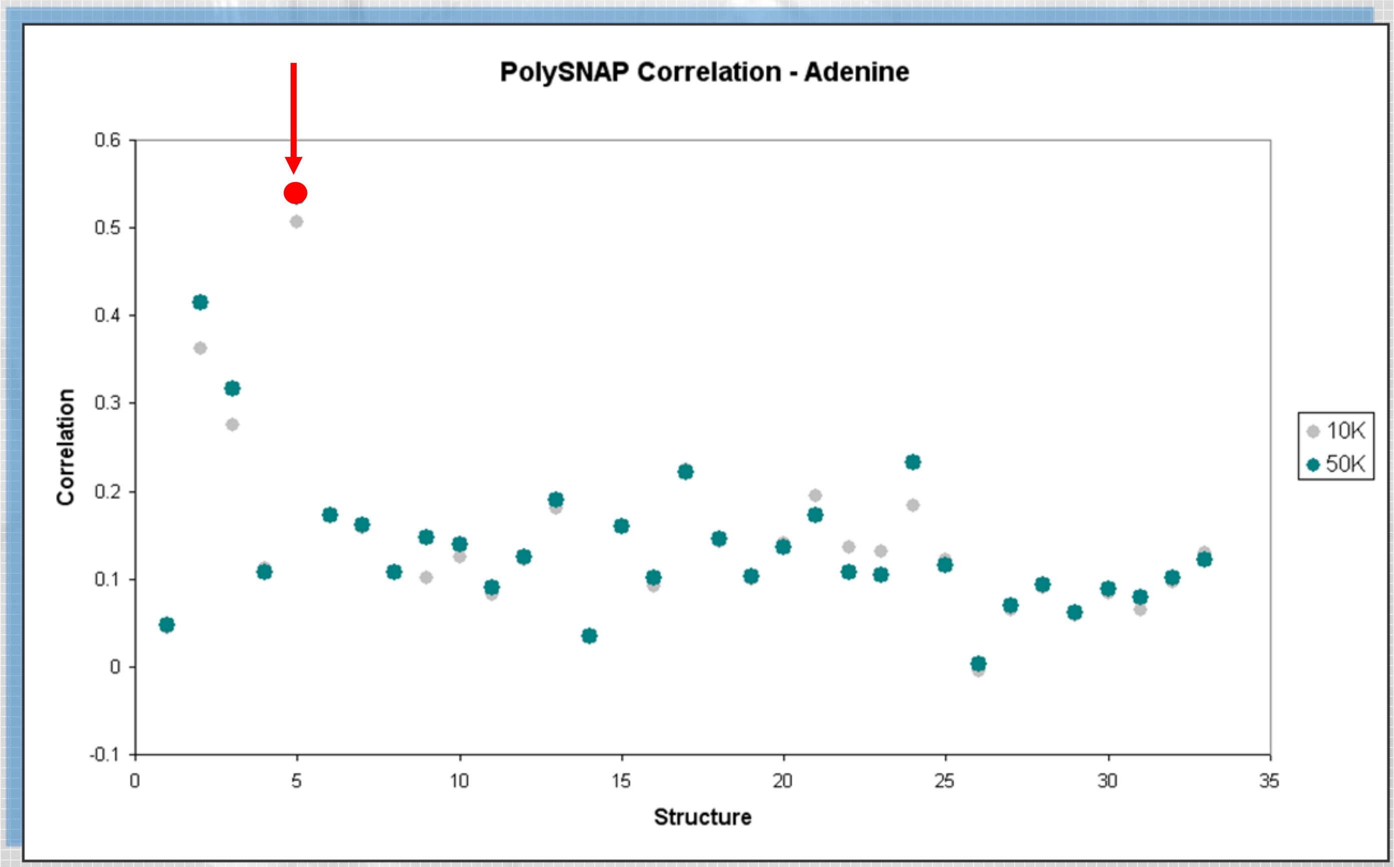

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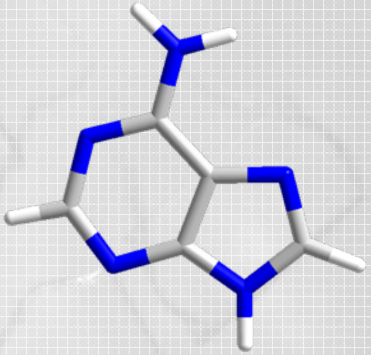

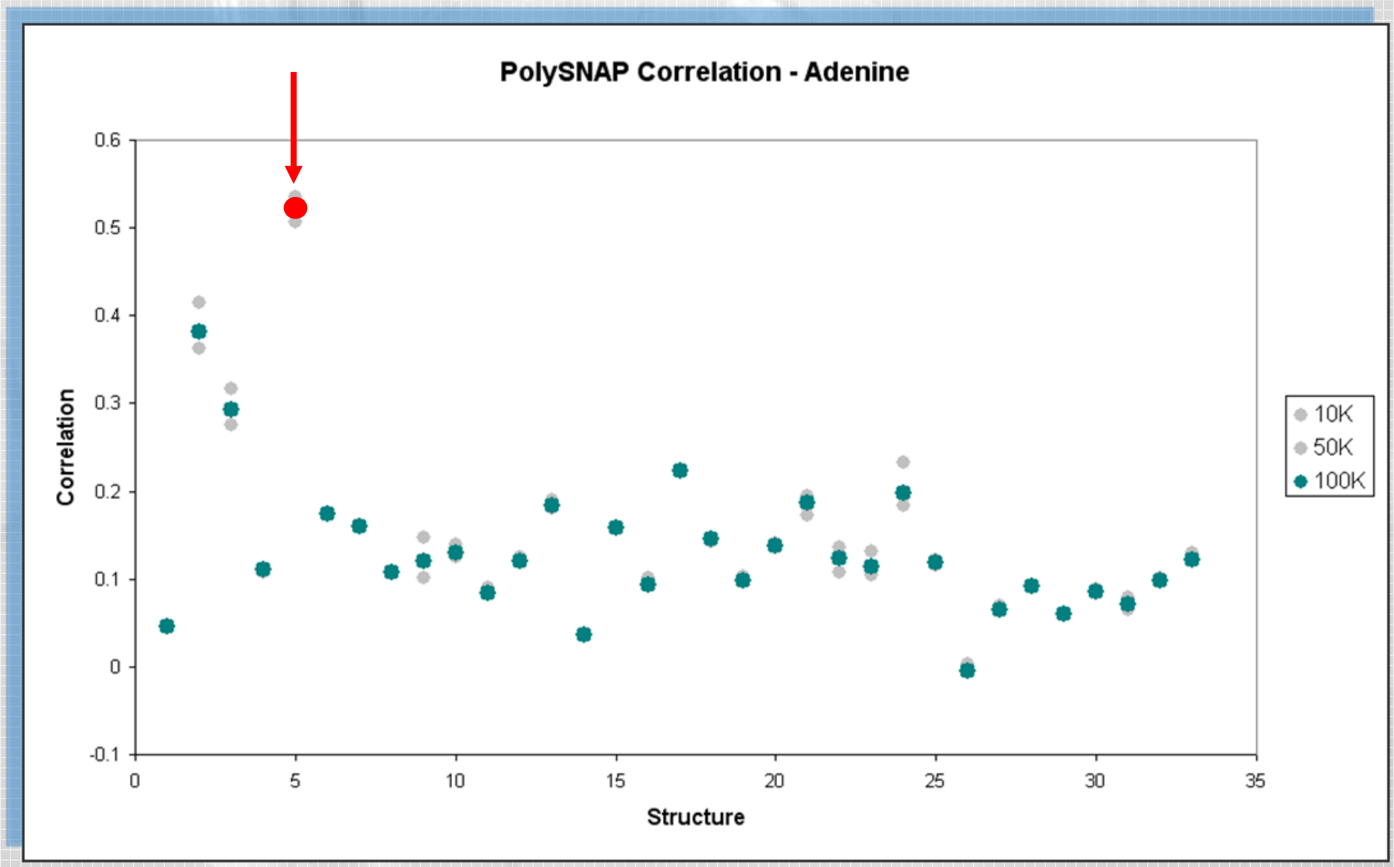

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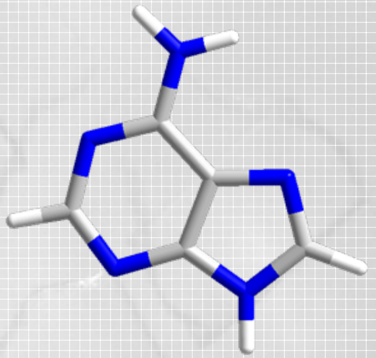

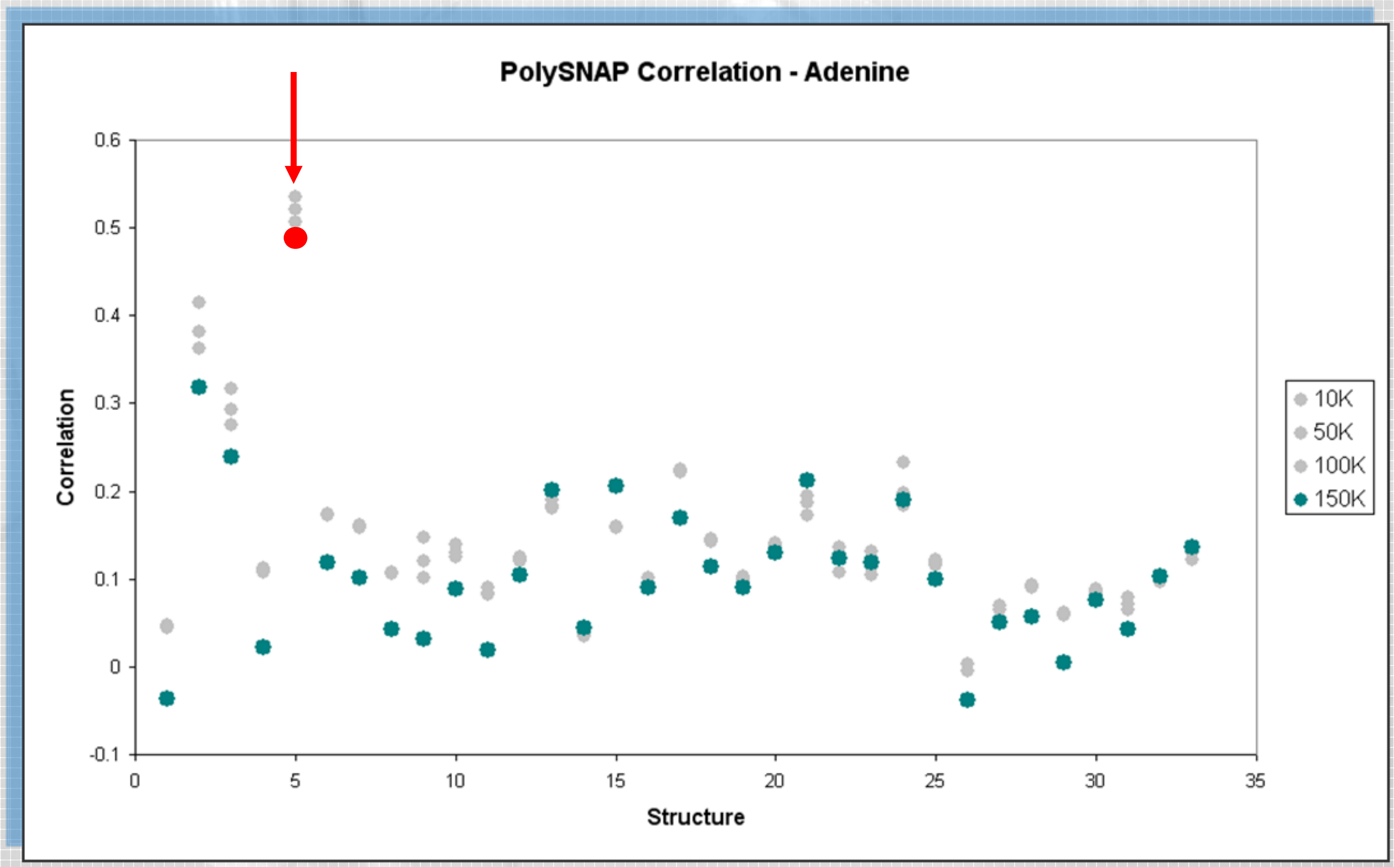

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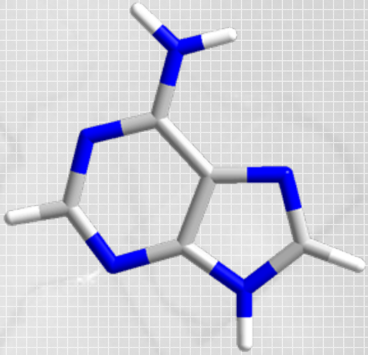

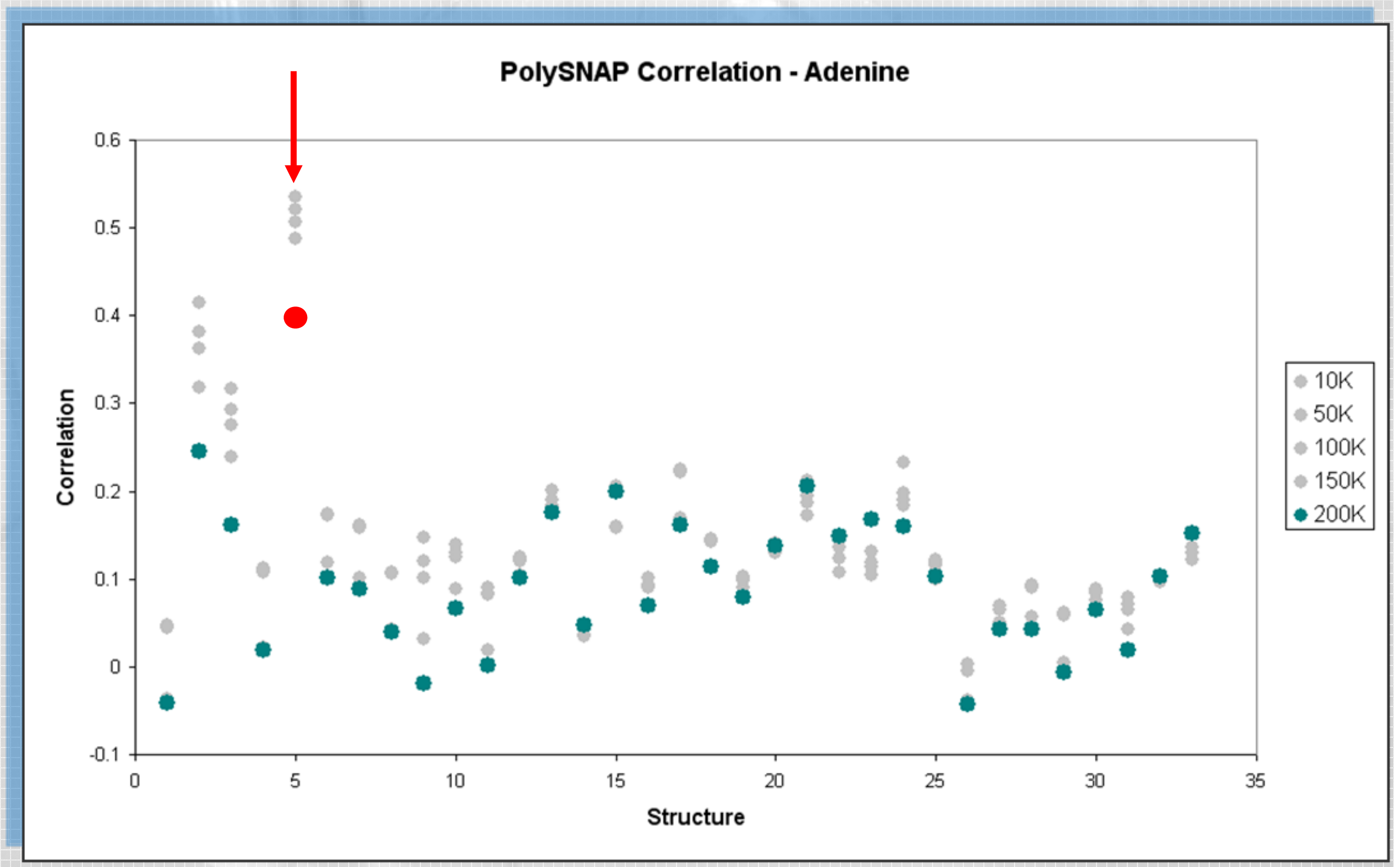

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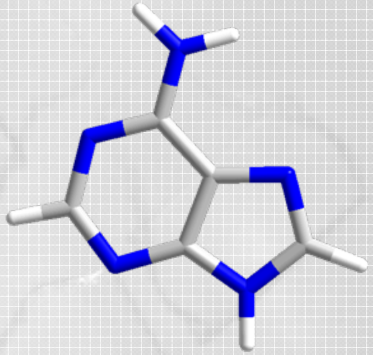
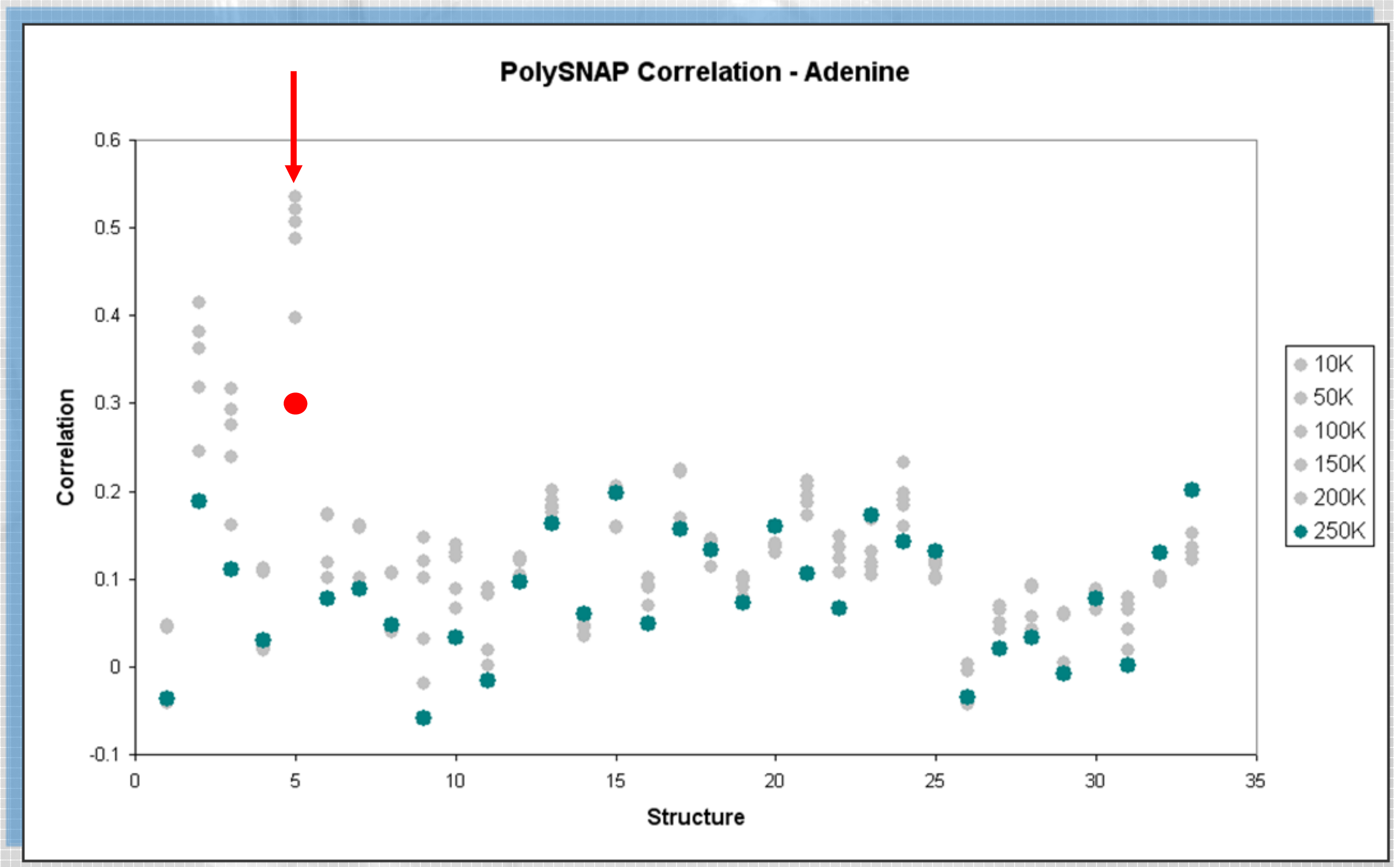
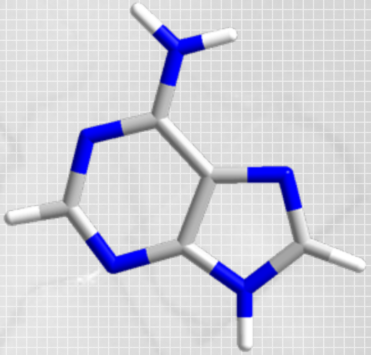
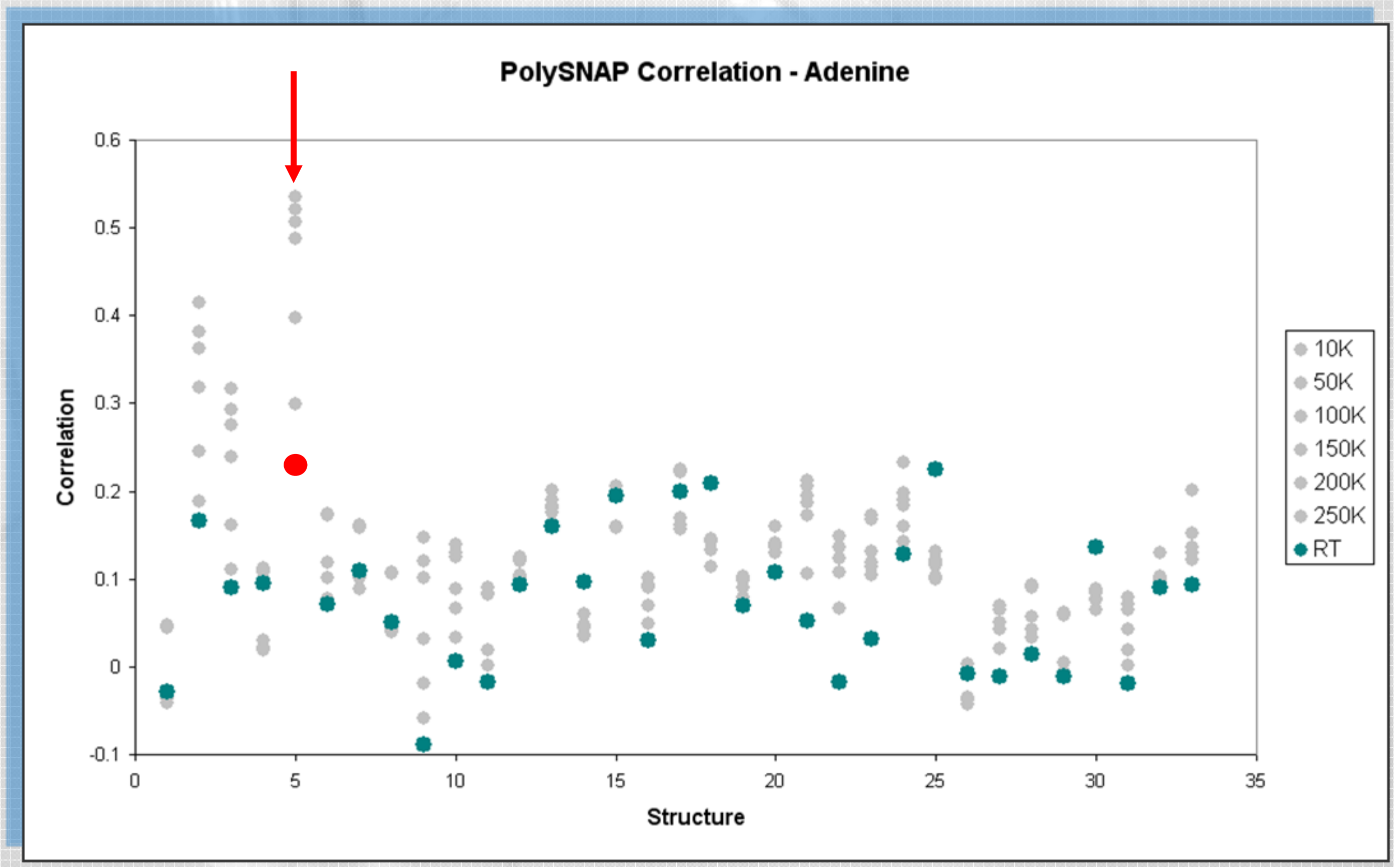


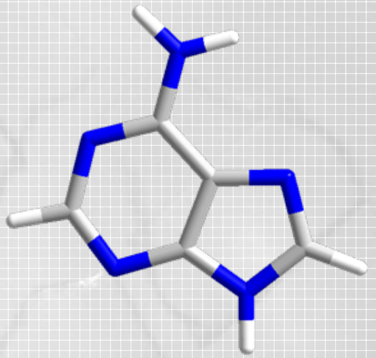


Adenine: PolySNAP





Adenine: Rietveld

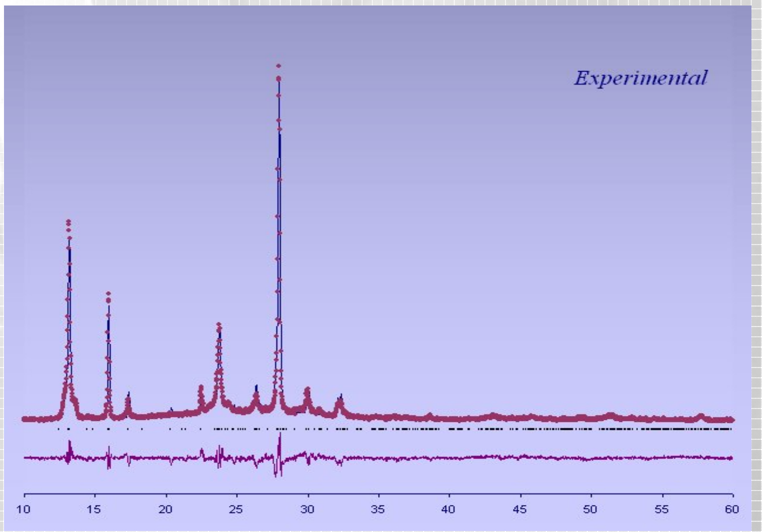


- Predicted structure (cc71) used as starting point for Rietveld refinement

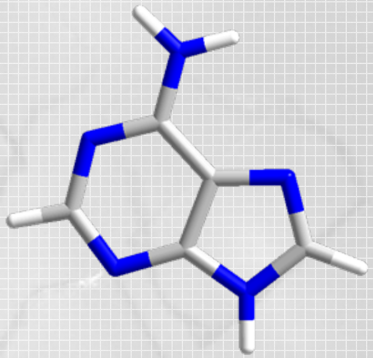
↓

Crystal Structure Determination

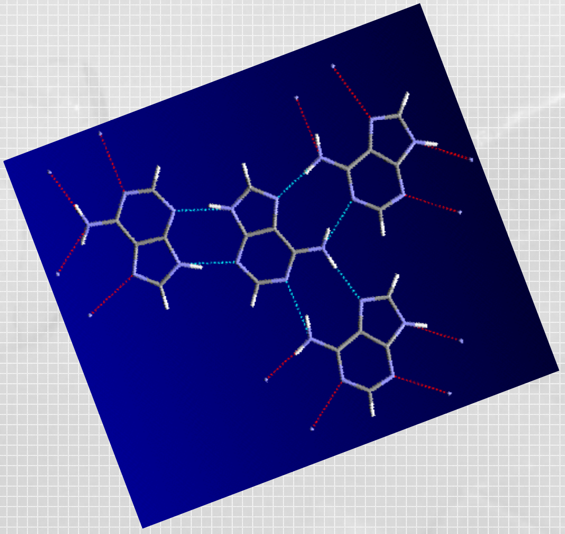
- Cell volume expansion of 5% from prediction to refinement
- Z'=2; $R_{wp} = 9.87\%$
  $R_p = 9.47\%$
  $\chi^2 = 1.77$

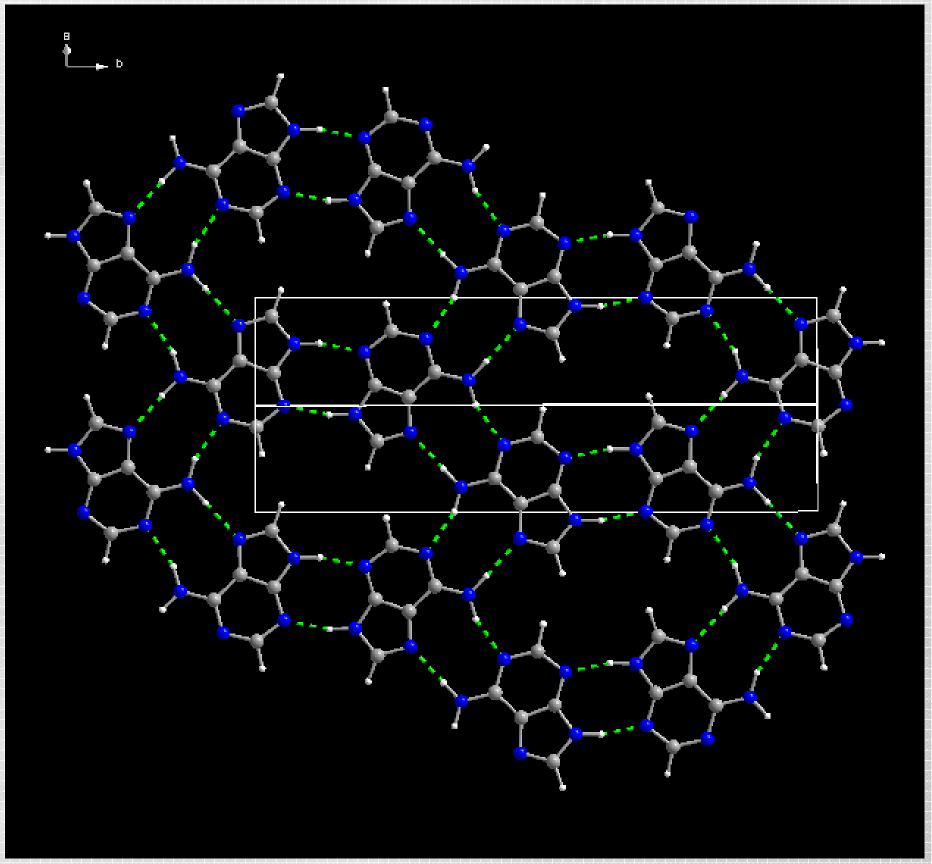


Adenine: Structure

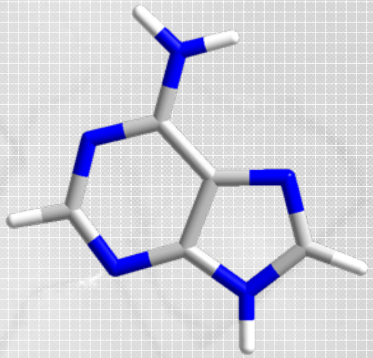


- 2D h-bonded layer network; *sheet motif (II)*



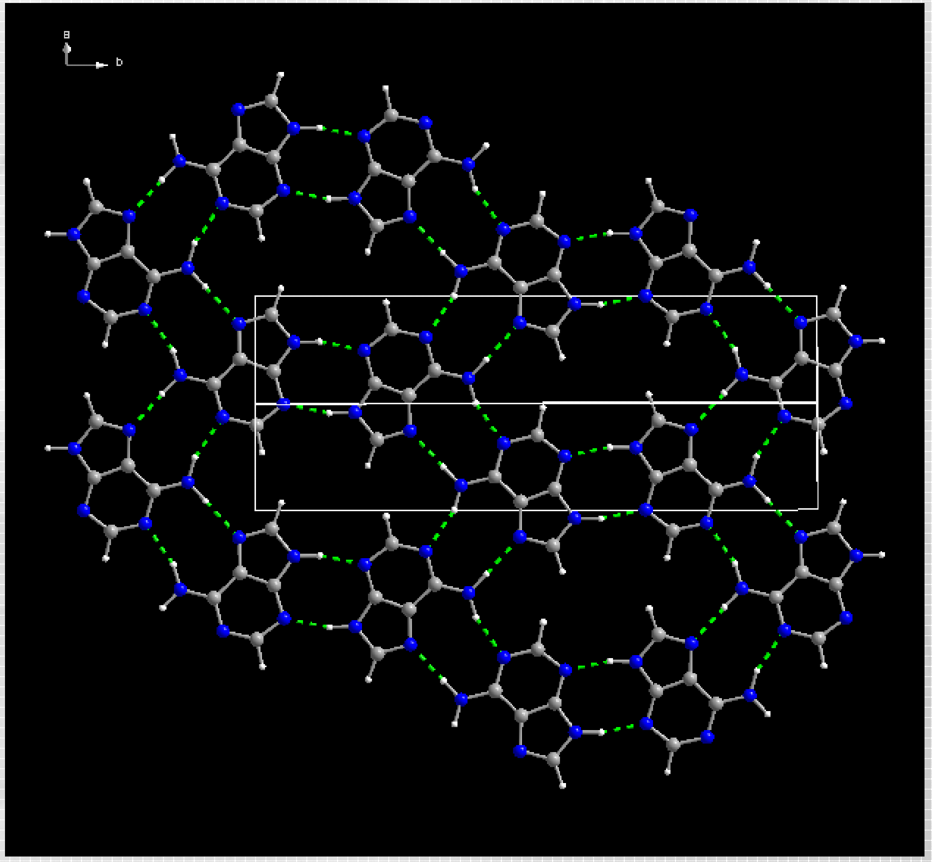


Adenine: Structure

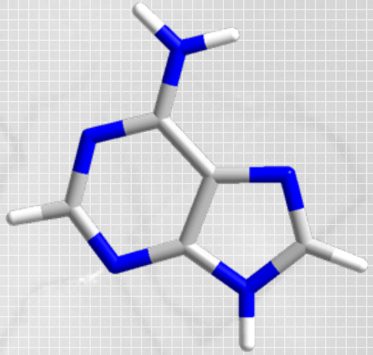


- 2D h-bonded layer network;
- All strong D/A in *NH…N* interactions;

  $R^2_2(8)$ & $R^2_2(9)$ rings
- 6-membered rings in honeycomb pattern



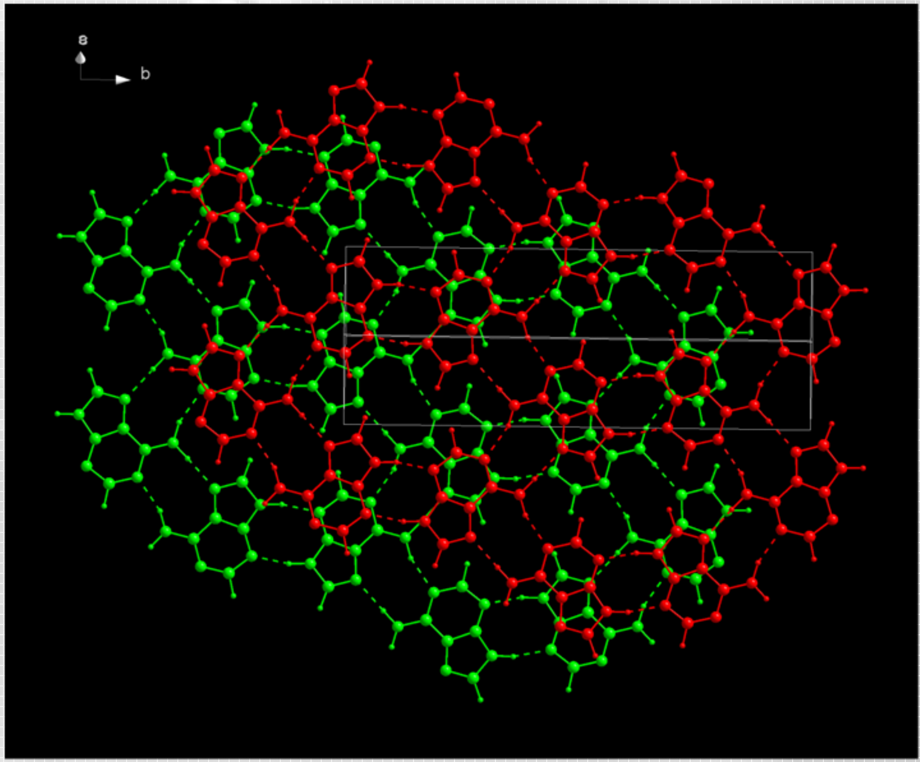
Adenine: Structure



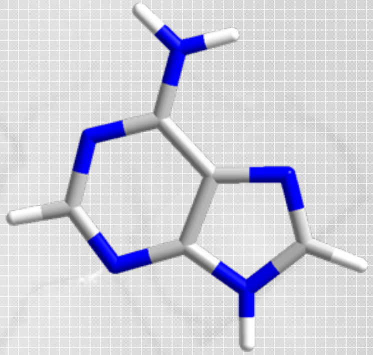
- Interlayer distance 3.11Å

- Projection over 4 layer repeat:

  ABCDABCD

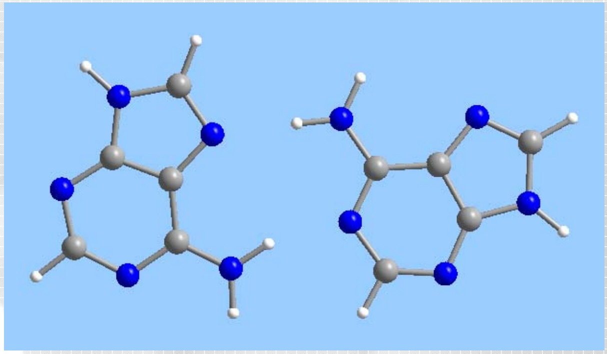


Adenine: Structure

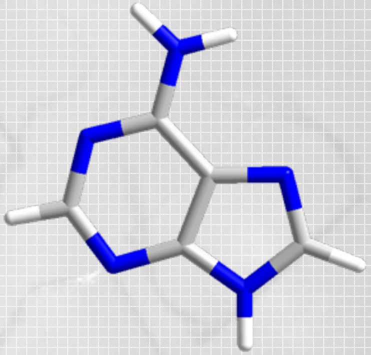


- **Prediction/PXRD**:

  a=7.668,b=22.200,c=7.624
  β=112.89
  Vol = 1196; P2_1/c; Z’=2

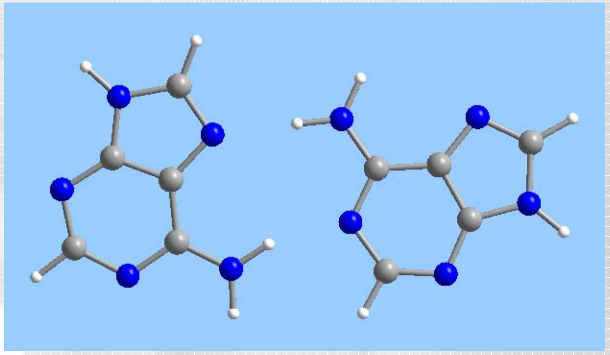


Adenine: Structure



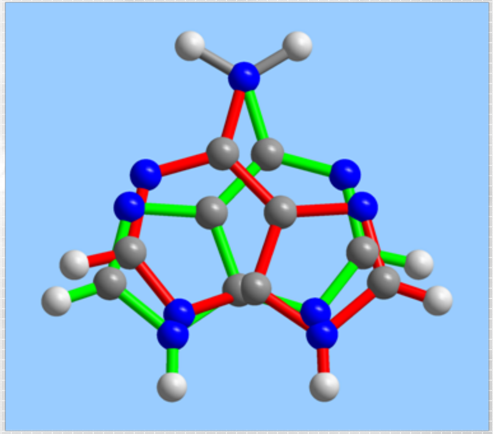
- **Prediction/PXRD**:

a=7.668,b=22.200,c=7.624
β=112.89
Vol = 1196; P2_1/c; Z'=2

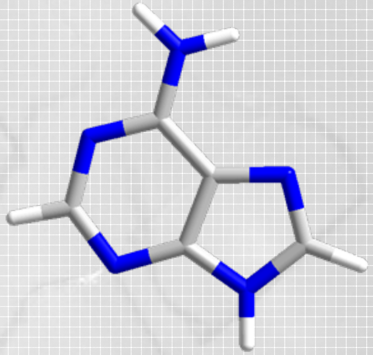


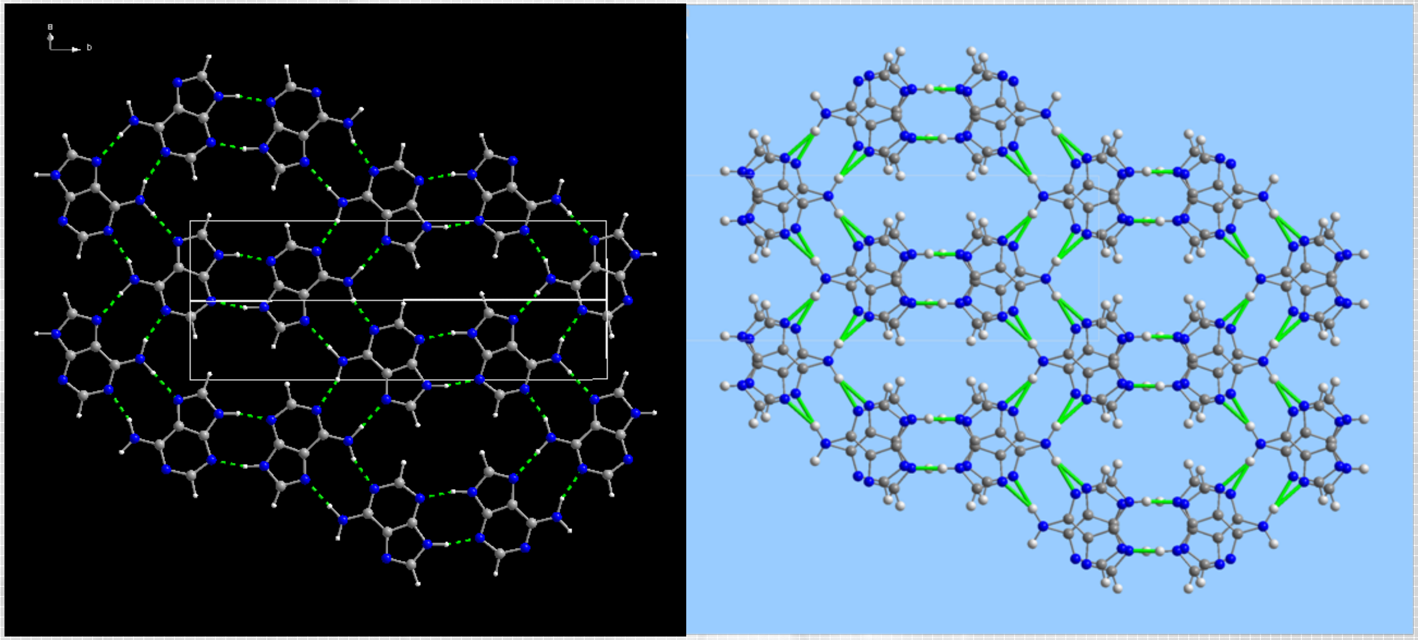
- **Single crystal**:

a=8.470,b=12.536,c=22.297
Vol = 2367; Fddd; Z=16



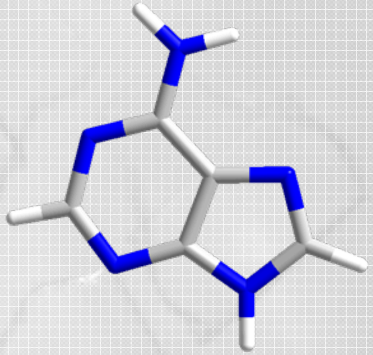
Adenine: Structure



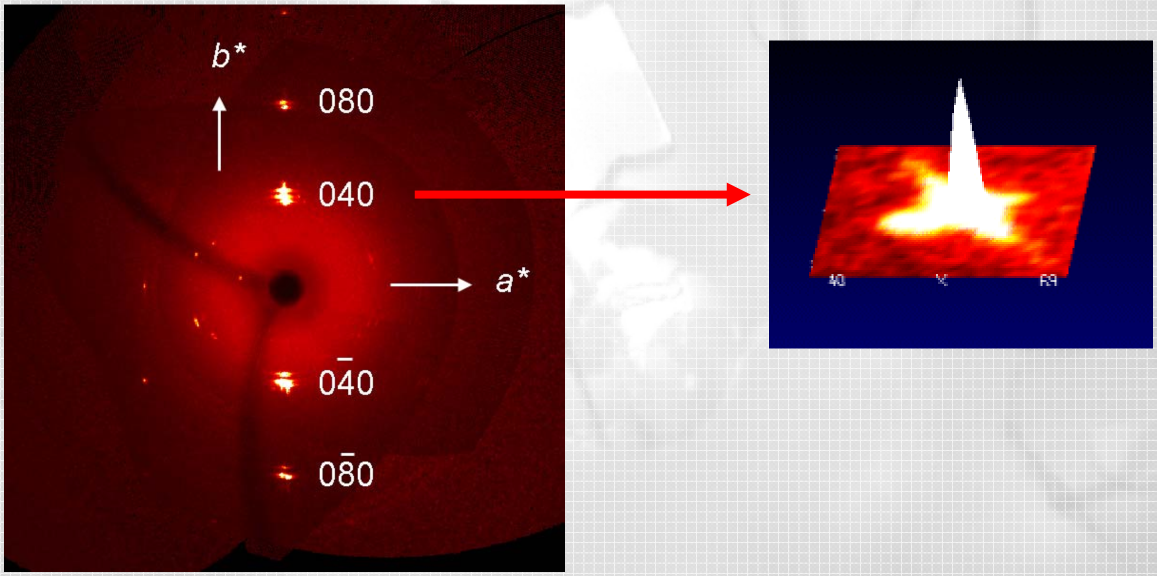


- Honeycomb pattern
- Motif comparable to ordered structure
- Interlayer distance 3.12Å
- 2 layer repeat: *ABAB*

Adenine: Disorder

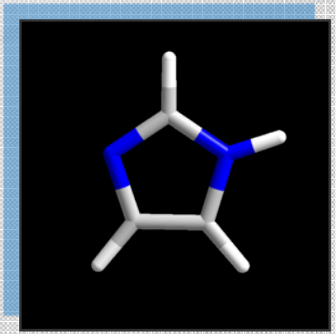


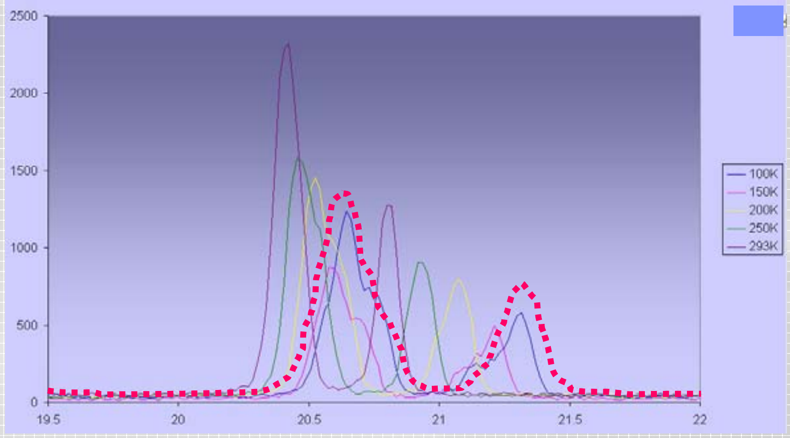
- Broadening most dramatic for 040 & 080
- Disorder in layer stacking direction



Comparison of Patterns

- Similar results for imidazole, chlorothalonil, 5-aza uracil
- Correct predicted structures identified by PolySNAP & Compare
- Matched best to low temperature data





Conclusions

- Predictions match to low temperature PXRD data
- R_{wp} is a poor discriminator; PolySNAP & *Compare.x* successfully identify predicted structure on the basis of PXRD data
- PolySNAP shows greatest discrimination
- *Compare.x* is less sensitive to different temp data
- Temperature & sample effects have a significant influence on ranking procedure

Acknowledgments

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