



# Full wwPDB NMR Structure Validation Report ⓘ

Dec 13, 2022 – 12:59 AM EST

PDB ID : 3J07  
EMDB ID : EMD-1776  
BMRB ID : 16391  
Title : Model of a 24mer alphaB-crystallin multimer  
Authors : Jehle, S.; Vollmar, B.; Bardiaux, B.; Dove, K.K.; Rajagopal, P.; Gonen, T.;  
Oschkinat, H.; Klevit, R.E.  
Deposited on : 2011-04-27  
Based on initial model : 2KLR

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : **NOT EXECUTED**  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : **NOT EXECUTED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:  
*SOLID-STATE NMR, SOLUTION SCATTERING, ELECTRON MICROSCOPY*

The reported resolution of this entry is 20.00 Å.

The overall completeness of chemical shifts assignment was not calculated.

There are no overall percentile quality scores available for this entry.

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	175	 100%
1	B	175	 100%
1	C	175	 100%
1	D	175	 100%
1	E	175	 100%
1	F	175	 100%
1	G	175	 100%
1	H	175	 100%
1	I	175	 100%
1	J	175	 100%
1	K	175	 100%
1	L	175	 100%
1	M	175	 100%
1	N	175	 100%
1	O	175	 100%
1	P	175	 100%

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Mol	Chain	Length	Quality of chain
1	Q	175	 100%
1	R	175	 100%
1	S	175	 100%
1	T	175	 100%
1	U	175	 100%
1	V	175	 100%
1	W	175	 100%
1	X	175	 100%

## 2 Ensemble composition and analysis

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

### 3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 42144 atoms, of which 8232 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Alpha-crystallin B chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	175	1756	916	343	236	259	2	0	
1	B	175	1756	916	343	236	259	2	0	
1	C	175	1756	916	343	236	259	2	0	
1	D	175	1756	916	343	236	259	2	0	
1	E	175	1756	916	343	236	259	2	0	
1	F	175	1756	916	343	236	259	2	0	
1	G	175	1756	916	343	236	259	2	0	
1	H	175	1756	916	343	236	259	2	0	
1	I	175	1756	916	343	236	259	2	0	
1	J	175	1756	916	343	236	259	2	0	
1	K	175	1756	916	343	236	259	2	0	
1	L	175	1756	916	343	236	259	2	0	
1	M	175	1756	916	343	236	259	2	0	
1	N	175	1756	916	343	236	259	2	0	
1	O	175	1756	916	343	236	259	2	0	
1	P	175	1756	916	343	236	259	2	0	
1	Q	175	1756	916	343	236	259	2	0	

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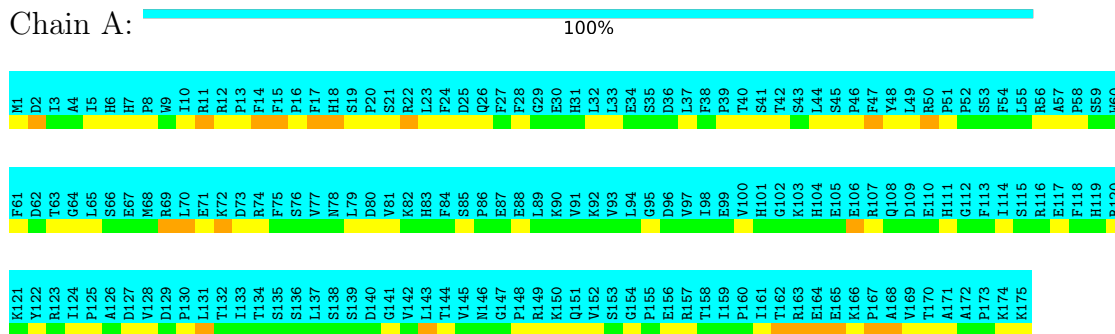
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Mol	Chain	Residues	Atoms					AltConf	Trace	
1	R	175	Total	C	H	N	O	S	0	
			1756	916	343	236	259	2		
1	S	175	Total	C	H	N	O	S	0	
			1756	916	343	236	259	2		
1	T	175	Total	C	H	N	O	S	0	
			1756	916	343	236	259	2		
1	U	175	Total	C	H	N	O	S	0	
			1756	916	343	236	259	2		
1	V	175	Total	C	H	N	O	S	0	
			1756	916	343	236	259	2		
1	W	175	Total	C	H	N	O	S	0	
			1756	916	343	236	259	2		
1	X	175	Total	C	H	N	O	S	0	
			1756	916	343	236	259	2		

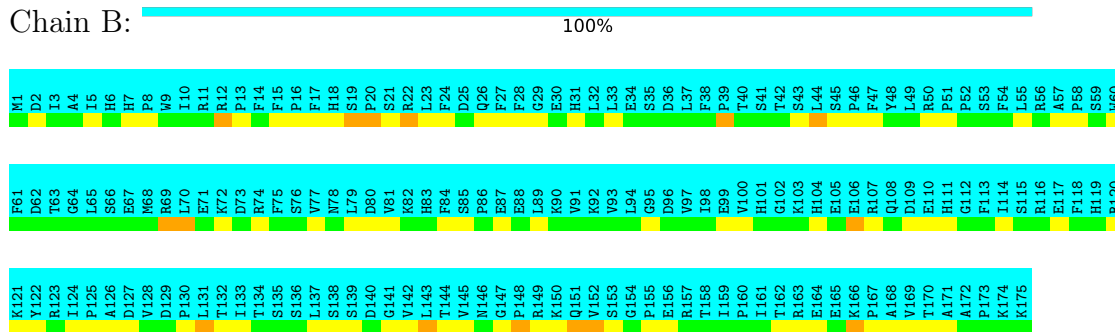
## 4 Residue-property plots

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

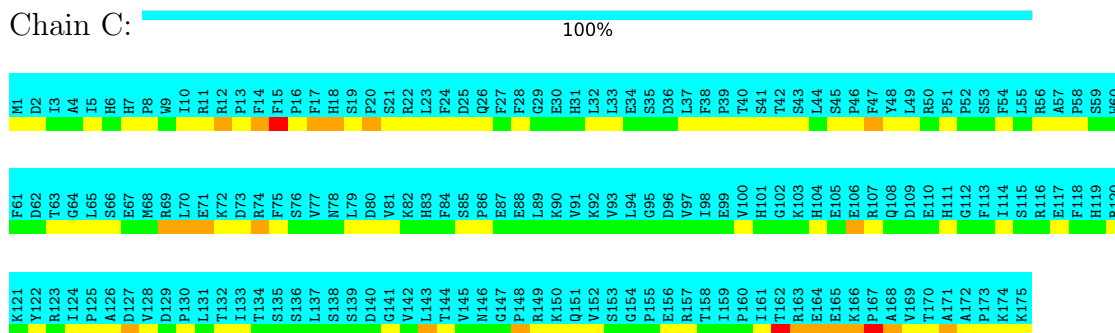
- Molecule 1: Alpha-crystallin B chain



- Molecule 1: Alpha-crystallin B chain

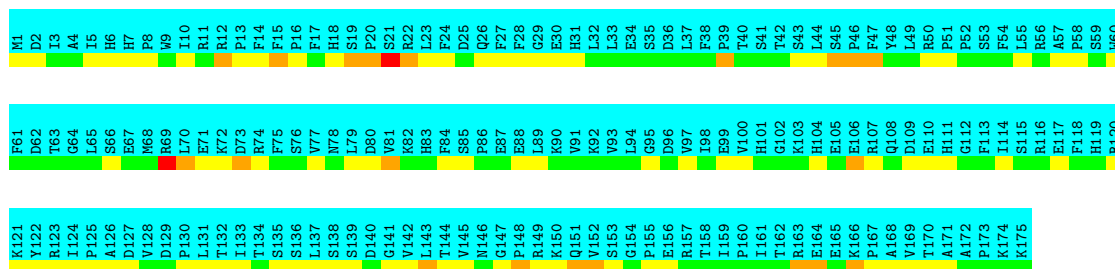


- Molecule 1: Alpha-crystallin B chain



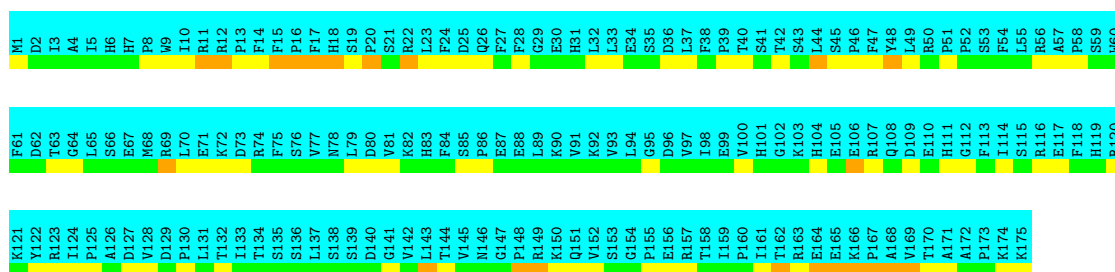
- Molecule 1: Alpha-crystallin B chain

Chain D:  100%



• Molecule 1: Alpha-crystallin B chain

Chain E:  100%



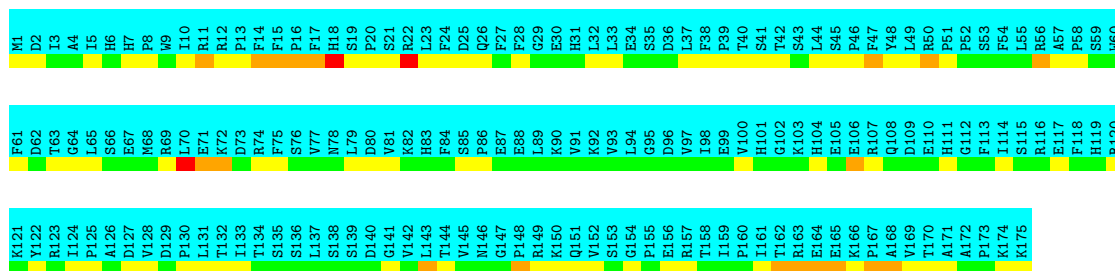
• Molecule 1: Alpha-crystallin B chain

Chain F:  100%



• Molecule 1: Alpha-crystallin B chain

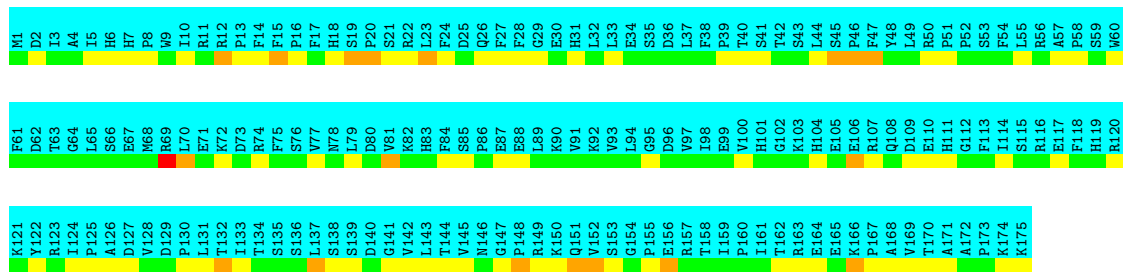
Chain G:  100%



• Molecule 1: Alpha-crystallin B chain

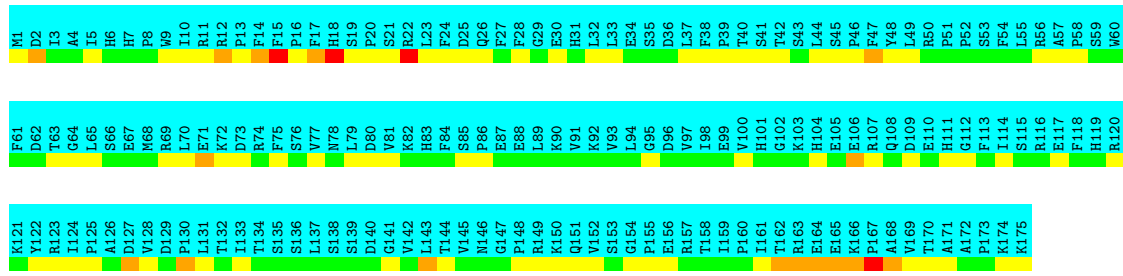


Chain H:  100%



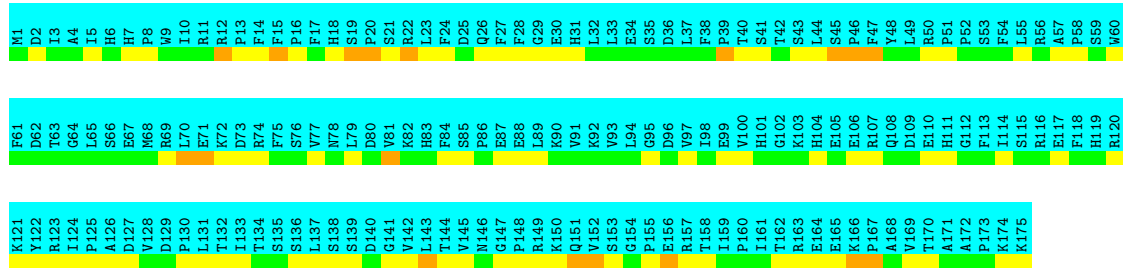
• Molecule 1: Alpha-crystallin B chain

Chain I:  100%



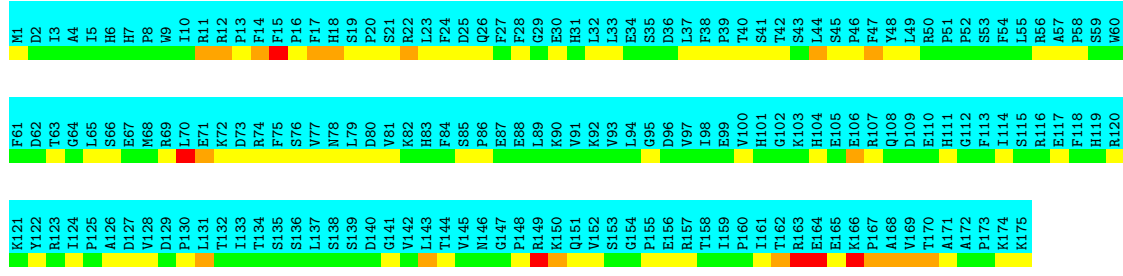
• Molecule 1: Alpha-crystallin B chain

Chain J:  100%

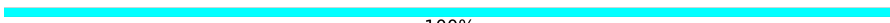


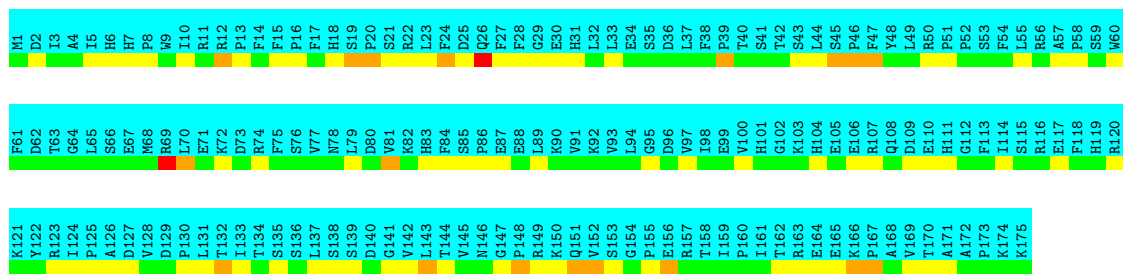
• Molecule 1: Alpha-crystallin B chain

Chain K:  100%



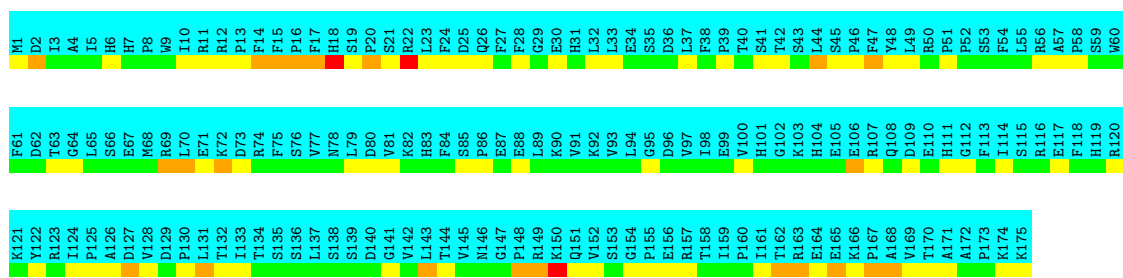
• Molecule 1: Alpha-crystallin B chain

Chain L:  100%



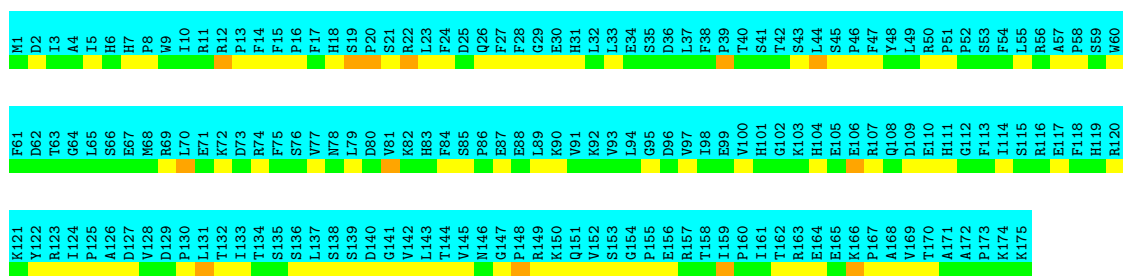
• Molecule 1: Alpha-crystallin B chain

Chain M:  100%



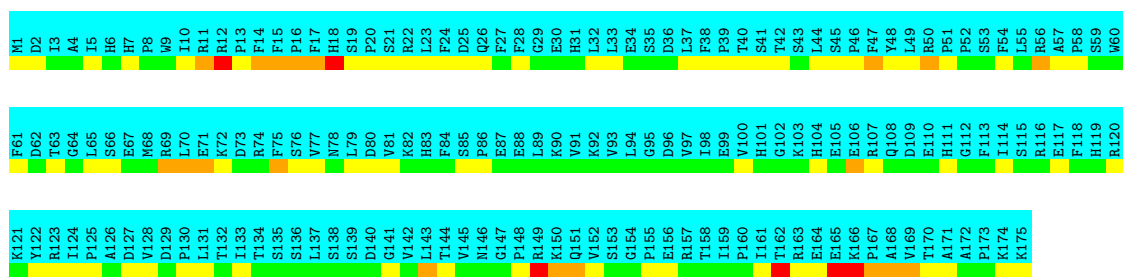
• Molecule 1: Alpha-crystallin B chain

Chain N:  100%



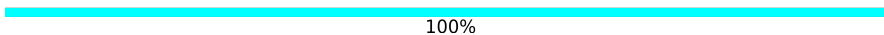
• Molecule 1: Alpha-crystallin B chain

Chain O:  100%



• Molecule 1: Alpha-crystallin B chain

Chain P:

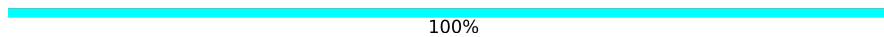


100%

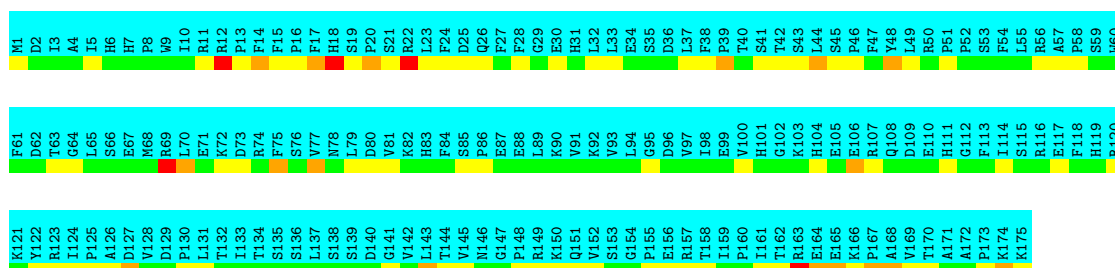


● Molecule 1: Alpha-crystallin B chain

Chain Q:

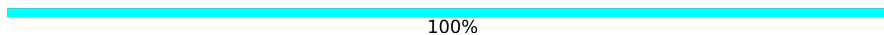


100%

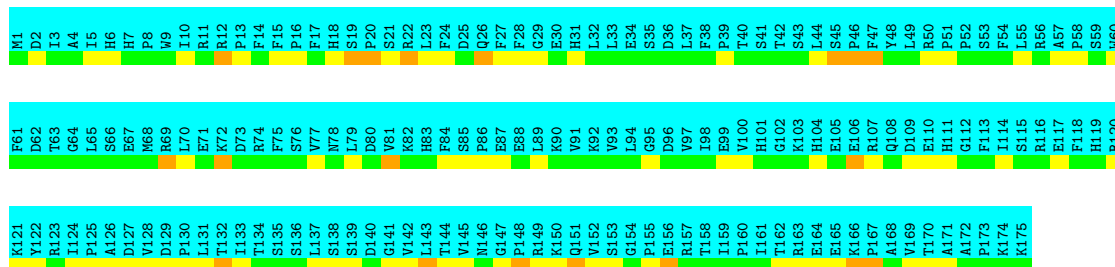


● Molecule 1: Alpha-crystallin B chain

Chain R:

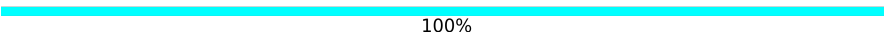


100%

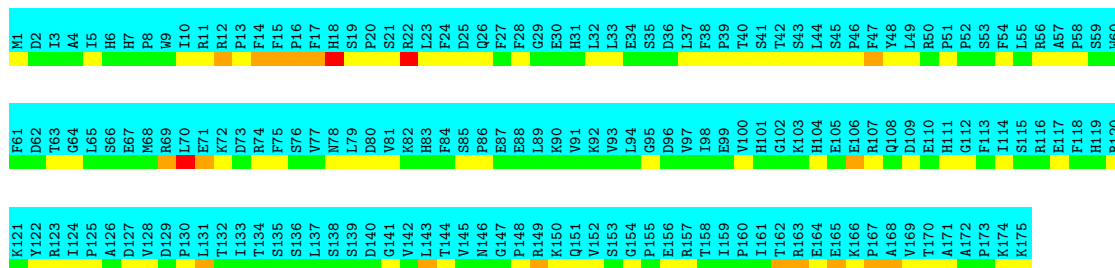


● Molecule 1: Alpha-crystallin B chain

Chain S:

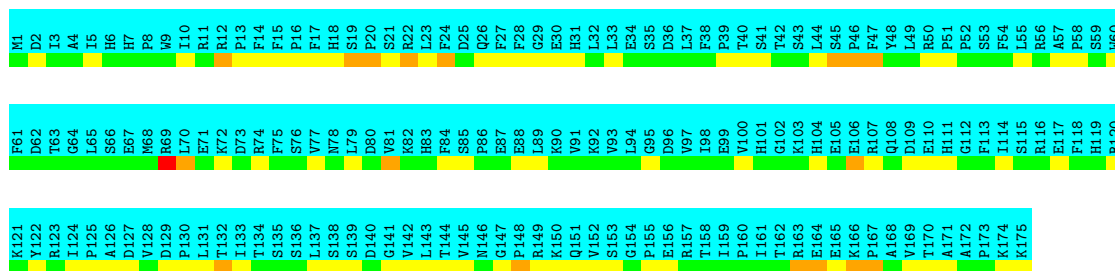


100%



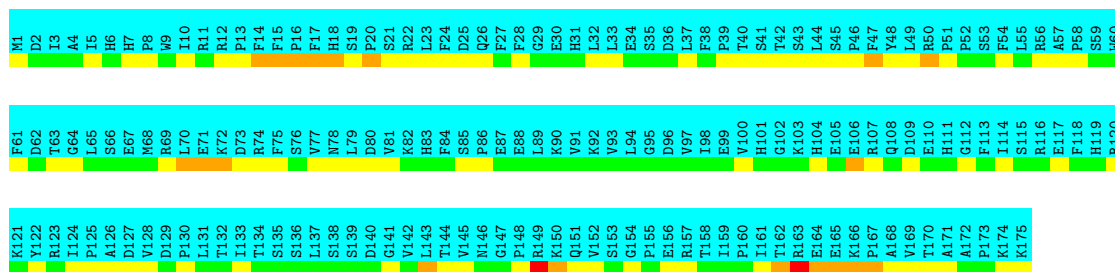
● Molecule 1: Alpha-crystallin B chain

Chain T:  100%



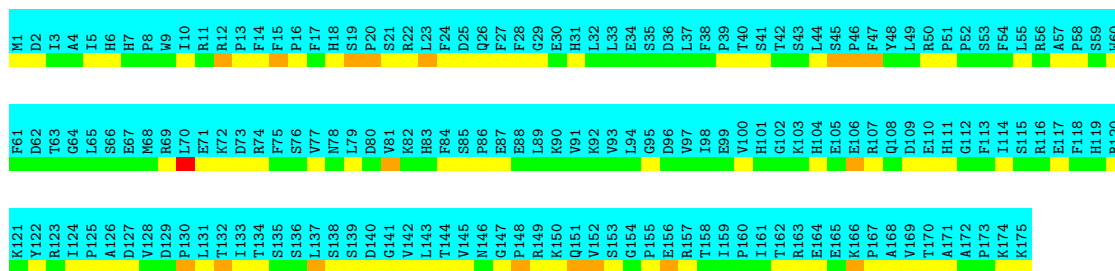
• Molecule 1: Alpha-crystallin B chain

Chain U:  100%



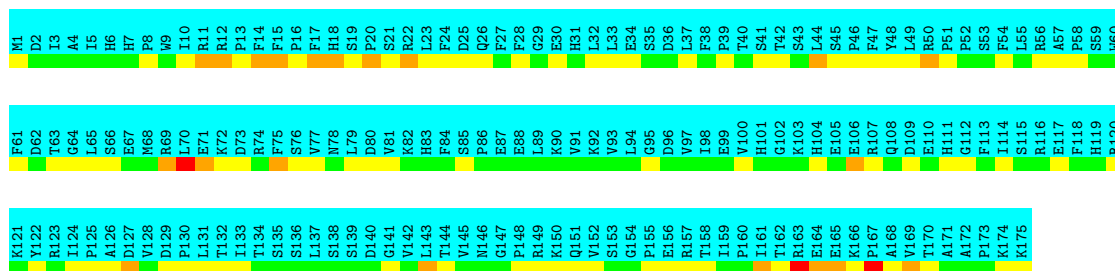
• Molecule 1: Alpha-crystallin B chain

Chain V:  100%



• Molecule 1: Alpha-crystallin B chain

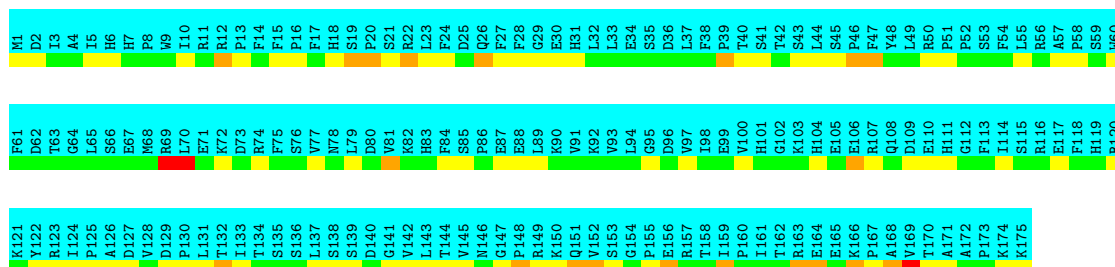
Chain W:  100%



• Molecule 1: Alpha-crystallin B chain

Chain X:

100%



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing, molecular dynamics, torsion angle dynamics*.

Of the 200 calculated structures, 1 were deposited, based on the following criterion: *structures with the lowest energy*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR NIH	structure solution	
ARIA	structure solution	2.2
ARIA	refinement	2.2
CNS	structure solution	1.2
CNS	refinement	1.2
SOLARIA	structure solution	1

No chemical shift data was provided. Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

## 6 Model quality [i](#)

### 6.1 Standard geometry [i](#)

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 6.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	0	0	0	0
1	B	0	0	0	0
1	C	0	0	0	0
1	D	0	0	0	0
1	E	0	0	0	0
1	F	0	0	0	0
1	G	0	0	0	0
1	H	0	0	0	0
1	I	0	0	0	0
1	J	0	0	0	0
1	K	0	0	0	0
1	L	0	0	0	0
1	M	0	0	0	0
1	N	0	0	0	0
1	O	0	0	0	0
1	P	0	0	0	0
1	Q	0	0	0	0
1	R	0	0	0	0
1	S	0	0	0	0
1	T	0	0	0	0
1	U	0	0	0	0
1	V	0	0	0	0
1	W	0	0	0	0
1	X	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes
All	All	0	0	0	-

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is -.

There are no clashes.

## 6.3 Torsion angles [i](#)

### 6.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	0	-	-	-	-
1	B	0	-	-	-	-
1	C	0	-	-	-	-
1	D	0	-	-	-	-
1	E	0	-	-	-	-
1	F	0	-	-	-	-
1	G	0	-	-	-	-
1	H	0	-	-	-	-
1	I	0	-	-	-	-
1	J	0	-	-	-	-
1	K	0	-	-	-	-
1	L	0	-	-	-	-
1	M	0	-	-	-	-
1	N	0	-	-	-	-
1	O	0	-	-	-	-
1	P	0	-	-	-	-
1	Q	0	-	-	-	-
1	R	0	-	-	-	-
1	S	0	-	-	-	-
1	T	0	-	-	-	-
1	U	0	-	-	-	-
1	V	0	-	-	-	-
1	W	0	-	-	-	-
1	X	0	-	-	-	-
All	All	0	-	-	-	-



There are no Ramachandran outliers.

### 6.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	0	-	-	-
1	B	0	-	-	-
1	C	0	-	-	-
1	D	0	-	-	-
1	E	0	-	-	-
1	F	0	-	-	-
1	G	0	-	-	-
1	H	0	-	-	-
1	I	0	-	-	-
1	J	0	-	-	-
1	K	0	-	-	-
1	L	0	-	-	-
1	M	0	-	-	-
1	N	0	-	-	-
1	O	0	-	-	-
1	P	0	-	-	-
1	Q	0	-	-	-
1	R	0	-	-	-
1	S	0	-	-	-
1	T	0	-	-	-
1	U	0	-	-	-
1	V	0	-	-	-
1	W	0	-	-	-
1	X	0	-	-	-
All	All	0	-	-	-

There are no protein residues with a non-rotameric sidechain to report.

### 6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 6.7 Other polymers [i](#)

There are no such molecules in this entry.

## 6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 7 Chemical shift validation

No chemical shift data were provided