



wwPDB NMR Structure Validation Summary Report ⓘ

Mar 5, 2026 – 06:40 AM UTC

PDB ID : 3J07 / pdb_00003j07
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 wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at 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>.

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

EMDB validation analysis : **NOT EXECUTED**
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **NOT EXECUTED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

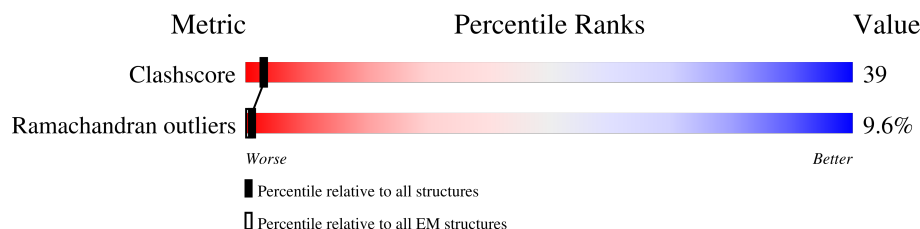
1 Overall quality at a glance ⓘ

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.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



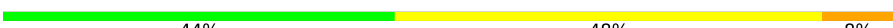
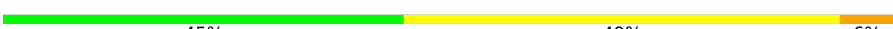
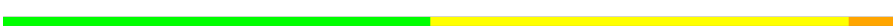
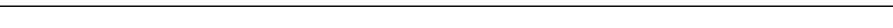
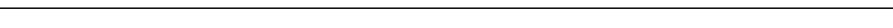
Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583

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 ≥ 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	46% 48% 6%
1	B	175	47% 47% 6%
1	C	175	43% 49% 7% .
1	D	175	42% 49% 10%
1	E	175	46% 47% 7%
1	F	175	44% 49% 7%
1	G	175	47% 50% .
1	H	175	47% 51% .
1	I	175	43% 49% 7%

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Mol	Chain	Length	Quality of chain
1	J	175	 42%50%8%
1	K	175	 46%47%7%
1	L	175	 46%44%10%
1	M	175	 44%48%8%
1	N	175	 45%49%6%
1	O	175	 48%47%5%
1	P	175	 45%54%. .
1	Q	175	 49%50%. .
1	R	175	 50%48%. .
1	S	175	 47%51%. .
1	T	175	 47%49%5%
1	U	175	 44%49%7%
1	V	175	 46%47%7%
1	W	175	 42%53%6%
1	X	175	 44%46%10%. .

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

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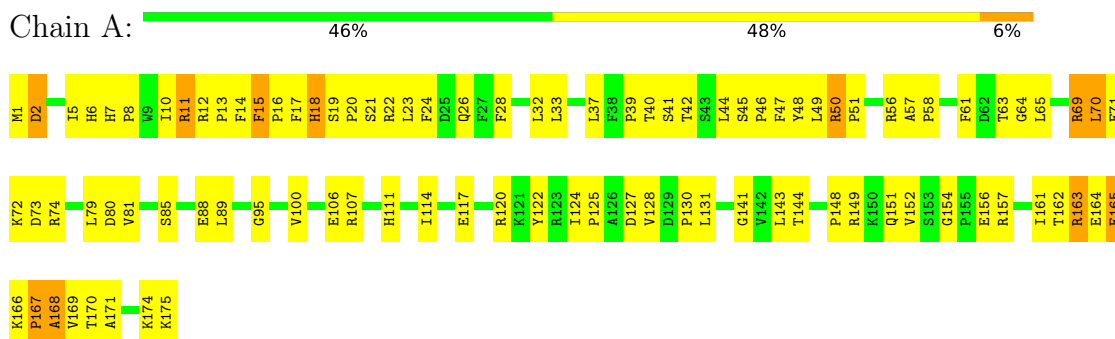
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Mol	Chain	Residues	Atoms						AltConf	Trace
1	R	175	Total	C	H	N	O	S	0	
			1756	916	343	236	259	2		
1	S	175	Total	C	H	N	O	S	0	
			1756	916	343	236	259	2		
1	T	175	Total	C	H	N	O	S	0	
			1756	916	343	236	259	2		
1	U	175	Total	C	H	N	O	S	0	
			1756	916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

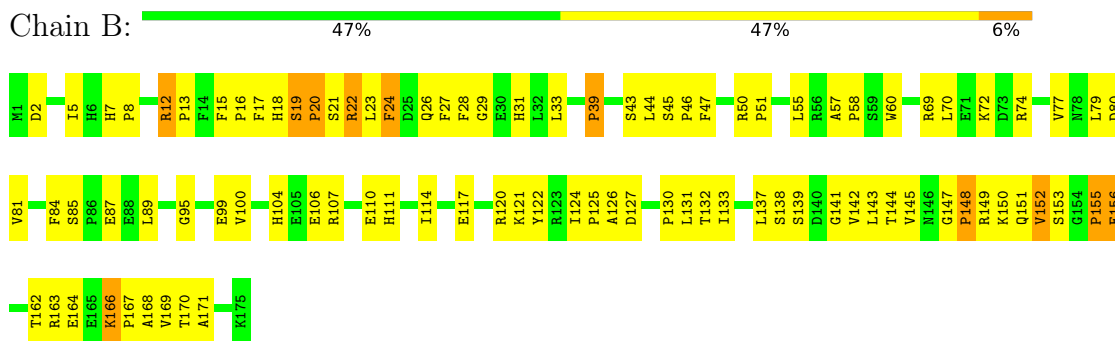
4 Residue-property plots

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

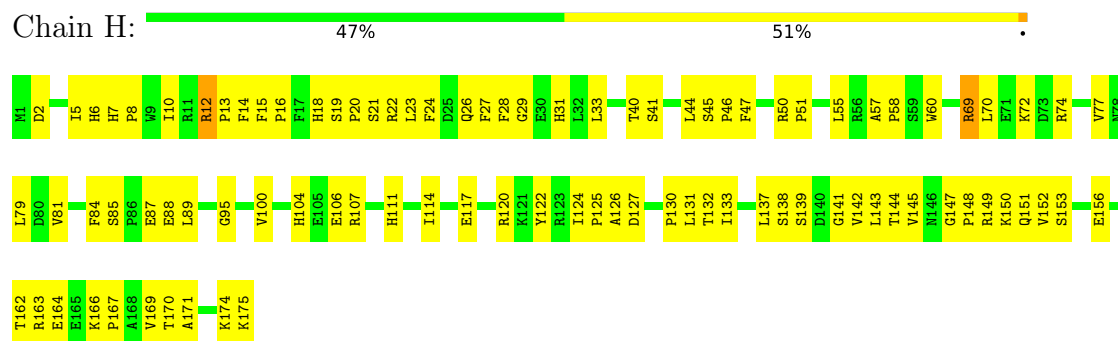


• Molecule 1: Alpha-crystallin B chain

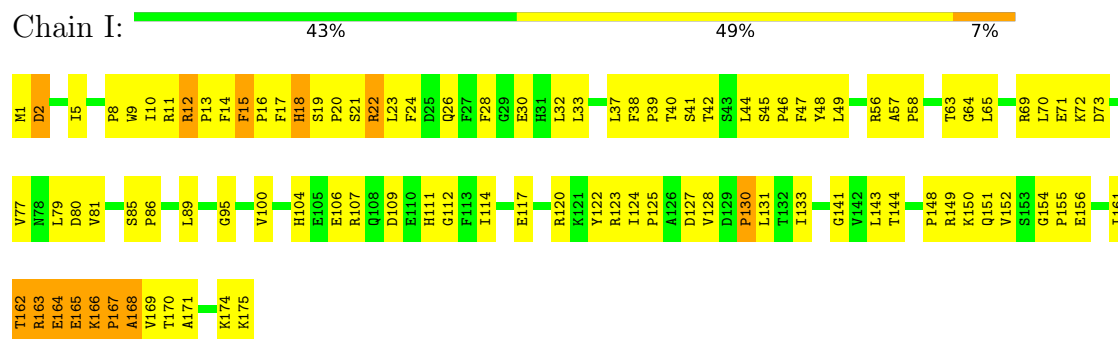


• Molecule 1: Alpha-crystallin B chain

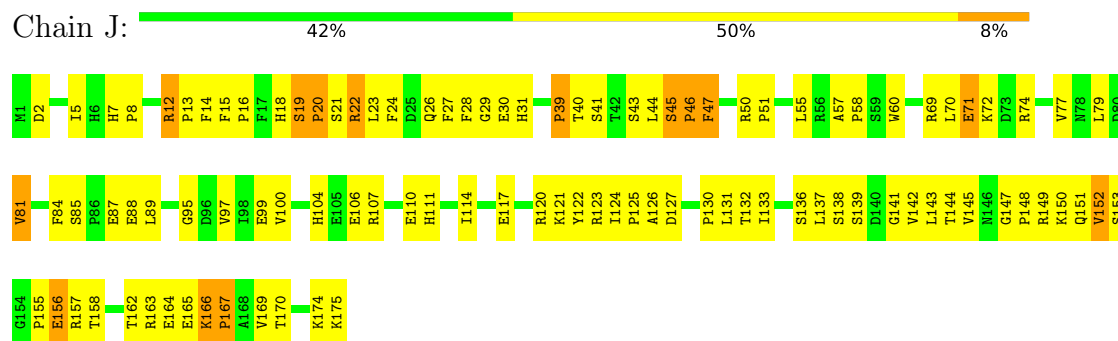




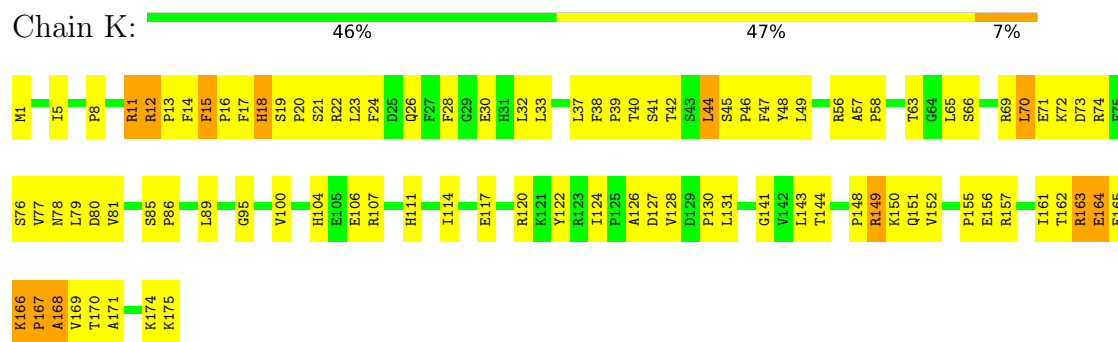
- Molecule 1: Alpha-crystallin B chain



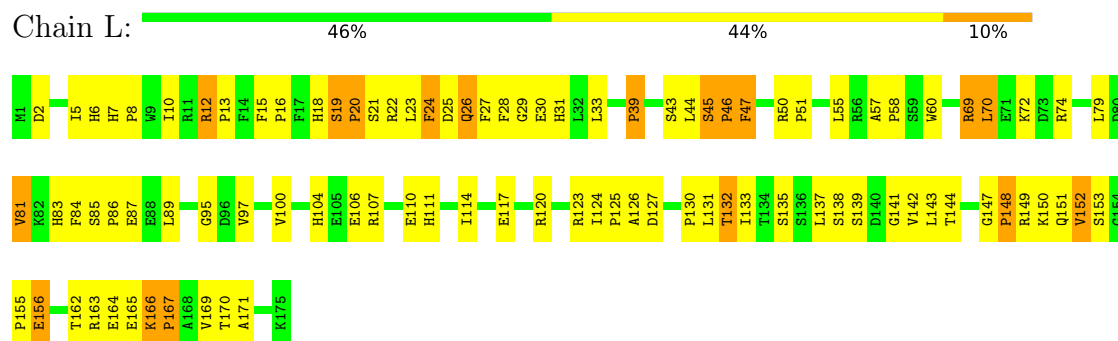
- Molecule 1: Alpha-crystallin B chain



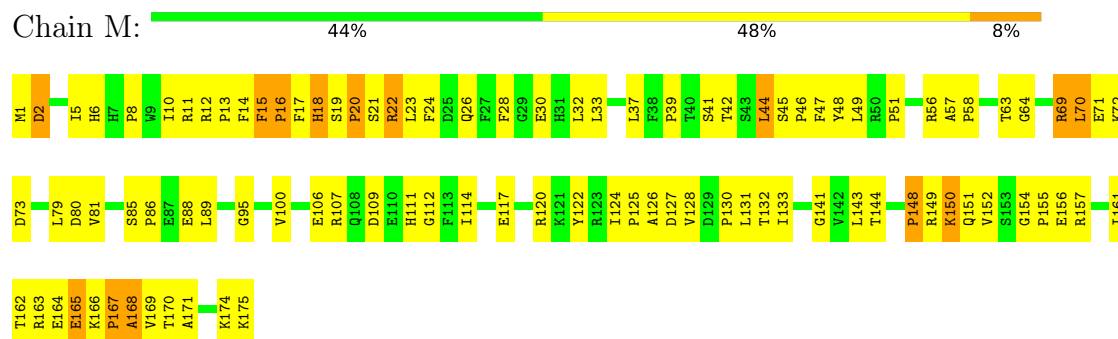
- Molecule 1: Alpha-crystallin B chain



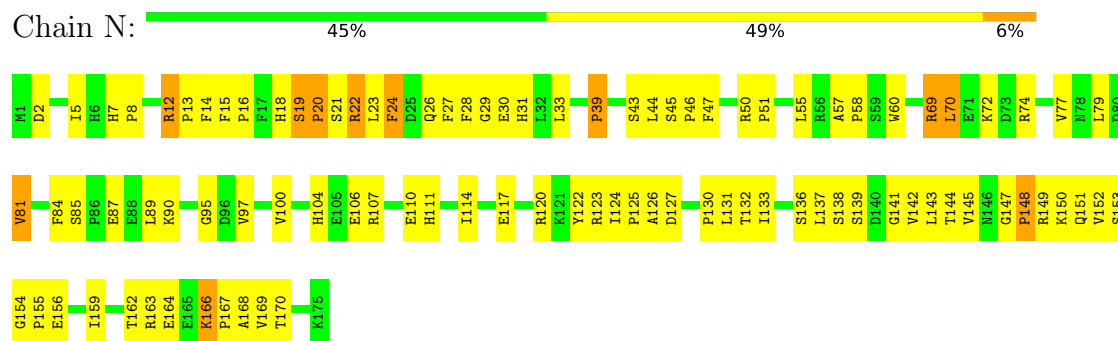
- Molecule 1: Alpha-crystallin B chain



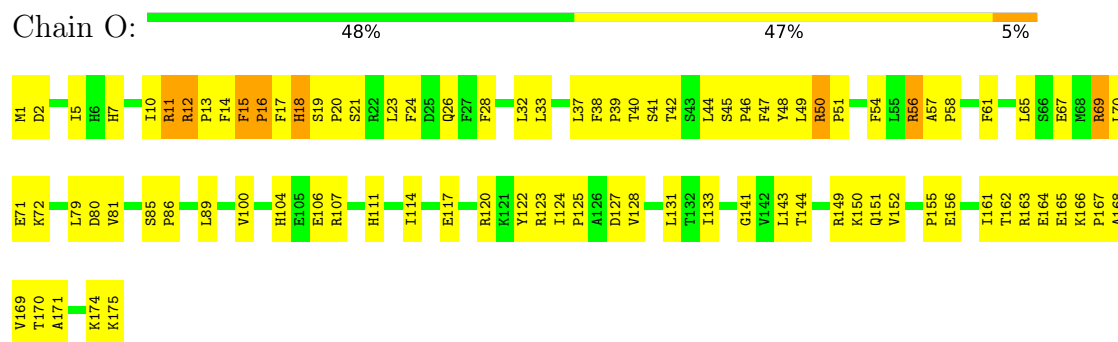
- Molecule 1: Alpha-crystallin B chain



- Molecule 1: Alpha-crystallin B chain



- Molecule 1: Alpha-crystallin B chain



- Molecule 1: Alpha-crystallin B chain



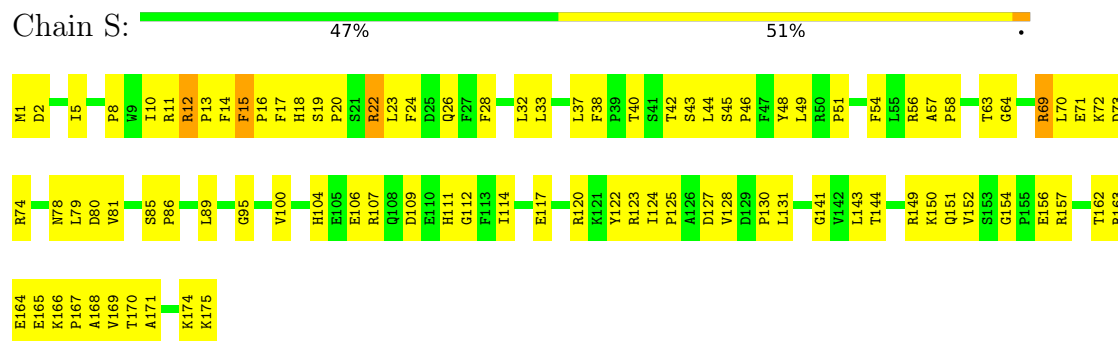
- Molecule 1: Alpha-crystallin B chain



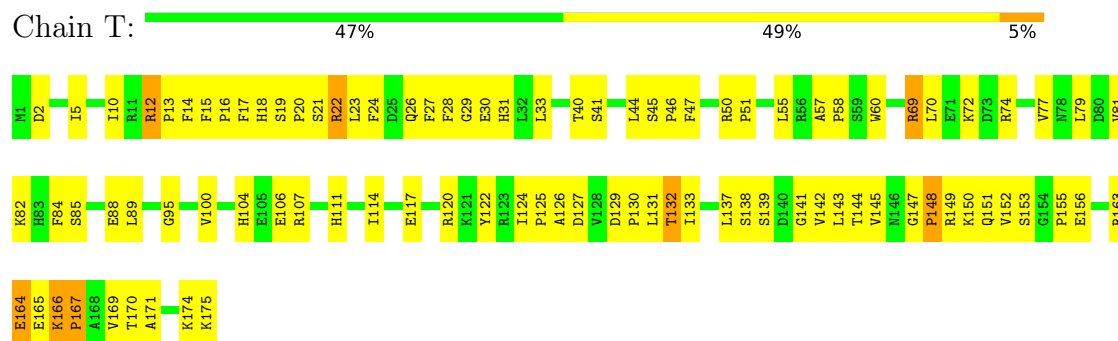
- Molecule 1: Alpha-crystallin B chain



- Molecule 1: Alpha-crystallin B chain



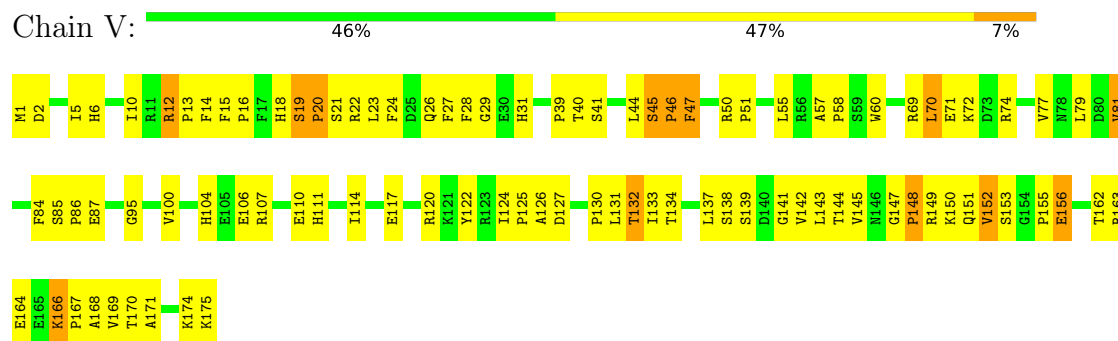
- Molecule 1: Alpha-crystallin B chain



- Molecule 1: Alpha-crystallin B chain



- Molecule 1: Alpha-crystallin B chain



- Molecule 1: Alpha-crystallin B chain



- Molecule 1: Alpha-crystallin B chain

P155 E156	I159	R163 E164 E185	P166 A168 V169	A171	K174 K175	V81	F84 S85 P86	E87 E88 L89	G95 D96 V97	V100	H104 E106 R107	E110 H111	I114	E117	R120 K121	Y122 R123 I124 P125 A126 D127 V128	D129 P130 L131 T132 I133	L137 S138 S139	D140 G141 V142 L143 T144 V145	N146 G147 P148	R149 K150 Q151	V152 S153 C154	M1 D2	I15 H6	T10 R11 R12 F14 F15 F17	S19 P20 S21 R22 L23 F24 D25 Q26 F27 G29 E30 H31	P39 T40 S41 T42 S43 L44 S45 P46 F47	R50 P51	L55 R56 A57 P58 S59 W60	R69 L70 K71 E72 D73 R74	V77 N78 L79 S80
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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

6.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.35	0/1458 (0.0%)	0.78	1/1973 (0.1%)
1	B	0.42	0/1458 (0.0%)	0.80	1/1973 (0.1%)
1	C	0.38	0/1458 (0.0%)	0.81	1/1973 (0.1%)
1	D	0.43	0/1458 (0.0%)	0.78	0/1973 (0.0%)
1	E	0.37	0/1458 (0.0%)	0.79	1/1973 (0.1%)
1	F	0.43	0/1458 (0.0%)	0.79	0/1973 (0.0%)
1	G	0.35	0/1458 (0.0%)	0.80	1/1973 (0.1%)
1	H	0.44	0/1458 (0.0%)	0.78	0/1973 (0.0%)
1	I	0.37	0/1458 (0.0%)	0.81	0/1973 (0.0%)
1	J	0.42	0/1458 (0.0%)	0.78	0/1973 (0.0%)
1	K	0.37	0/1458 (0.0%)	0.78	0/1973 (0.0%)
1	L	0.43	0/1458 (0.0%)	0.78	0/1973 (0.0%)
1	M	0.37	0/1458 (0.0%)	0.78	1/1973 (0.1%)
1	N	0.41	0/1458 (0.0%)	0.78	1/1973 (0.1%)
1	O	0.37	0/1458 (0.0%)	0.79	1/1973 (0.1%)
1	P	0.43	0/1458 (0.0%)	0.78	0/1973 (0.0%)
1	Q	0.36	0/1458 (0.0%)	0.79	0/1973 (0.0%)
1	R	0.43	0/1458 (0.0%)	0.80	1/1973 (0.1%)
1	S	0.36	0/1458 (0.0%)	0.78	1/1973 (0.1%)
1	T	0.43	0/1458 (0.0%)	0.78	0/1973 (0.0%)
1	U	0.37	0/1458 (0.0%)	0.77	1/1973 (0.1%)
1	V	0.43	0/1458 (0.0%)	0.77	0/1973 (0.0%)
1	W	0.36	0/1458 (0.0%)	0.79	0/1973 (0.0%)
1	X	0.43	0/1458 (0.0%)	0.78	0/1973 (0.0%)
All	All	0.40	0/34992 (0.0%)	0.79	11/47352 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	1	4

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Mol	Chain	Chirality	Planarity
1	B	0	4
1	C	0	2
1	D	0	4
1	E	0	3
1	F	0	4
1	G	1	5
1	H	1	3
1	I	1	3
1	J	0	4
1	K	2	3
1	L	0	3
1	M	0	3
1	N	0	4
1	O	0	5
1	P	0	3
1	Q	2	3
1	R	0	4
1	S	0	4
1	T	0	4
1	U	0	1
1	V	0	3
1	W	2	5
1	X	0	4
All	All	10	85

There are no bond-length outliers.

5 of 11 angle outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	15	PHE	CA-CB-CG	8.06	121.86	113.80
1	E	15	PHE	CA-CB-CG	7.72	121.52	113.80
1	A	15	PHE	CA-CB-CG	7.71	121.51	113.80
1	O	15	PHE	CA-CB-CG	7.20	121.00	113.80
1	S	15	PHE	CA-CB-CG	6.83	120.63	113.80

5 of 10 chiral outliers are listed below.

Mol	Chain	Res	Type	Atoms
1	A	162	THR	CB
1	G	162	THR	CB
1	H	42	THR	CB
1	I	162	THR	CB

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Mol	Chain	Res	Type	Atoms
1	K	3	ILE	CB

5 of 85 planar outliers are listed below.

Mol	Chain	Res	Type	Group
1	A	11	ARG	Sidechain
1	A	22	ARG	Sidechain
1	A	50	ARG	Sidechain
1	A	69	ARG	Sidechain
1	B	12	ARG	Sidechain

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	1413	343	1375	200
1	B	1413	343	1375	105
1	C	1413	343	1375	196
1	D	1413	343	1375	127
1	E	1413	343	1375	206
1	F	1413	343	1375	126
1	G	1413	343	1375	209
1	H	1413	343	1375	127
1	I	1413	343	1375	189
1	J	1413	343	1375	116
1	K	1413	343	1375	195
1	L	1413	343	1375	121
1	M	1413	343	1375	189
1	N	1413	343	1375	111
1	O	1413	343	1375	193
1	P	1413	343	1375	120
1	Q	1413	343	1375	199
1	R	1413	343	1375	120
1	S	1413	343	1375	201
1	T	1413	343	1375	107
1	U	1413	343	1375	193
1	V	1413	343	1375	119

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Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	W	1413	343	1375	204
1	X	1413	343	1375	131
All	All	33912	8232	33000	2606

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 39.

5 of 2606 clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:B:26:GLN:HB2	1:C:163:ARG:HB3	1.09	1.23
1:T:26:GLN:HB2	1:U:163:ARG:HB3	1.04	1.27
1:J:26:GLN:HB3	1:K:163:ARG:HB3	1.03	1.25
1:W:15:PHE:HB3	1:W:16:PRO:HD3	0.98	1.36
1:C:15:PHE:HB3	1:C:16:PRO:CD	0.96	1.90

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	173/175 (99%)	115 (66%)	45 (26%)	13 (8%)	1	15
1	B	173/175 (99%)	122 (71%)	36 (21%)	15 (9%)	1	12
1	C	173/175 (99%)	119 (69%)	36 (21%)	18 (10%)	1	9
1	D	173/175 (99%)	121 (70%)	31 (18%)	21 (12%)	1	7
1	E	173/175 (99%)	120 (69%)	40 (23%)	13 (8%)	1	15
1	F	125/175 (71%)	91 (73%)	23 (18%)	11 (9%)	1	12
1	G	0	-	-	-	-	-
1	H	6/175 (3%)	4 (67%)	2 (33%)	0 (0%)	100	100
1	I	173/175 (99%)	120 (69%)	35 (20%)	18 (10%)	1	9
1	J	173/175 (99%)	124 (72%)	32 (18%)	17 (10%)	1	10
1	K	173/175 (99%)	117 (68%)	38 (22%)	18 (10%)	1	9
1	L	173/175 (99%)	120 (69%)	35 (20%)	18 (10%)	1	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	M	173/175 (99%)	116 (67%)	42 (24%)	15 (9%)	1	12
1	N	173/175 (99%)	120 (69%)	37 (21%)	16 (9%)	1	11
1	O	52/175 (30%)	33 (63%)	13 (25%)	6 (12%)	1	7
1	P	0	-	-	-	-	-
1	Q	0	-	-	-	-	-
1	R	0	-	-	-	-	-
1	S	0	-	-	-	-	-
1	T	44/175 (25%)	22 (50%)	14 (32%)	8 (18%)	0	3
1	U	173/175 (99%)	116 (67%)	41 (24%)	16 (9%)	1	11
1	V	173/175 (99%)	118 (68%)	39 (23%)	16 (9%)	1	11
1	W	173/175 (99%)	117 (68%)	42 (24%)	14 (8%)	1	13
1	X	173/175 (99%)	120 (69%)	34 (20%)	19 (11%)	1	8
All	All	2822/4200 (67%)	1935 (69%)	615 (22%)	272 (10%)	1	10

5 of 272 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	2	ASP
1	A	18	HIS
1	A	21	SER
1	A	39	PRO
1	A	41	SER

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	-	-	-

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
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 oligosaccharides 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 ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided