Full wwPDB NMR Structure Validation Report (i)

Jun 12, 2024 – 02:28 PM EDT

PDB ID	:	1AQ5
Title	:	HIGH-RESOLUTION SOLUTION NMR STRUCTURE OF THE TRIMERIC COILED-COIL DOMAIN OF CHICKEN CARTILAGE MATRIX PROTEIN, 20 STRUCTURES
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Deposited on	:	1997-08-07

This is a Full wwPDB NMR Structure Validation 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 (i) 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 (i)) were used in the production of this report:

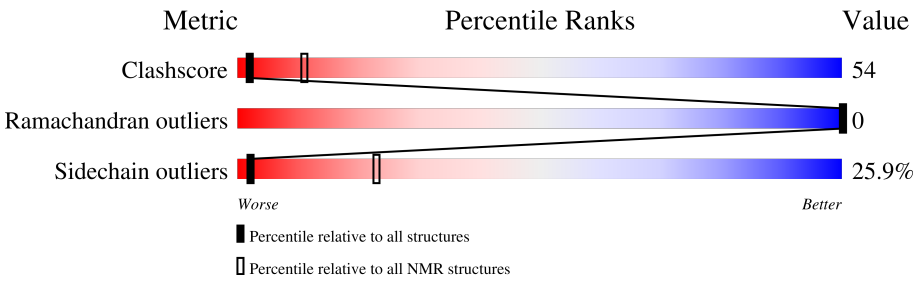
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	47	26% 38% 15% 21%
1	B	47	26% 36% 17% 21%
1	C	47	26% 34% 15% 26%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 4 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	**Residue range (total)**	**Backbone RMSD (Å)**	**Medoid model**
1	A:10-A:46, B:10-B:46, C:9-C:43 (109)	0.26	4

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 4 single-model clusters were found.

Cluster number	Models
1	1, 2, 4, 6, 9, 12, 13, 16, 18
2	5, 10, 14, 19
3	7, 8, 15
Single-model clusters	3; 11; 17; 20

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2292 atoms, of which 1167 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CARTILAGE MATRIX PROTEIN.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	47	764	234	389	63	75	3	0
1	B	47	764	234	389	63	75	3	0
1	C	47	764	234	389	63	75	3	0

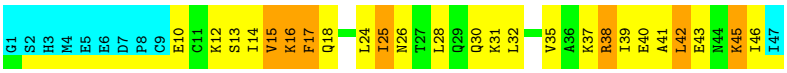
4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

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.

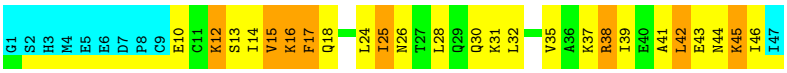
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A: 26% 38% 15% 21%



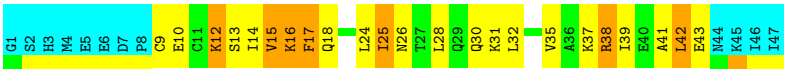
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 26% 36% 17% 21%



• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain C: 26% 34% 15% 26%



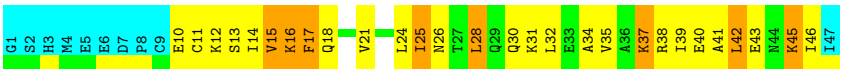
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A: 19% 43% 17% 21%



• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 23% 38% 17% 21%

G1 S2 H3 M4 E5 E6 D7 P8 C9 E10 C11 K12 S13 I14 V15 K16 F17 Q18 V21 I25 N26 T27 L28 Q29 Q30 K31 L32 E33 A34 V35 A36 K37 R38 I39 E40 A41 L42 E43 N44 K45 I46 I47

- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain C: 26% 32% 17% 26%

G1 S2 H3 M4 E5 E6 D7 P8 C9 E10 C11 K12 S13 I14 V15 K16 F17 Q18 V21 I25 N26 T27 L28 K31 L32 E33 A34 V35 A36 K37 R38 I39 E40 A41 L42 E43 N44 K45 I46 I47

4.2.2 Score per residue for model 2

- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A: 28% 34% 15% • 21%

G1 S2 H3 M4 E5 E6 D7 P8 C9 E10 C11 K12 S13 I14 V15 K16 F17 Q18 T19 L24 I25 L28 Q29 Q30 K31 L32 V35 R38 I39 E40 A41 L42 E43 N44 K45 I46 I47

- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 30% 34% 13% • 21%

G1 S2 H3 M4 E5 E6 D7 P8 C9 E10 C11 K12 S13 I14 V15 K16 F17 Q18 T19 L24 I25 L28 Q29 Q30 K31 V35 R38 I39 E40 A41 L42 E43 N44 K45 I46 I47

- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain C: 28% 32% 13% • 26%

G1 S2 H3 M4 E5 E6 D7 P8 C9 E10 C11 K12 S13 I14 V15 K16 F17 Q18 T19 L24 I25 L28 Q29 L32 E33 A34 V35 R38 I39 E40 A41 L42 E43 N44 K45 I46 I47

4.2.3 Score per residue for model 3

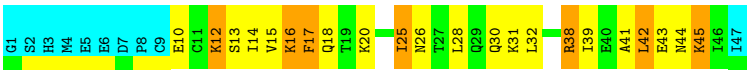
- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A: 32% 32% 15% 21%

G1 S2 H3 M4 E5 E6 D7 P8 C9 E10 C11 K12 S13 I14 V15 K16 F17 Q18 T19 K20 I25 N26 T27 L28 Q29 Q30 K31 L32 R38 I39 E40 A41 L42 E43 N44 K45 I46 I47

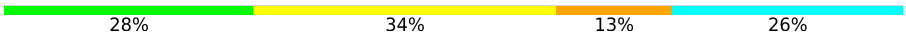
- Molecule 1: CARTILAGE MATRIX PROTEIN

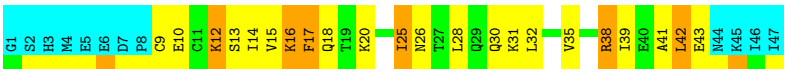
Chain B: 32% 32% 15% 21%



• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain C:

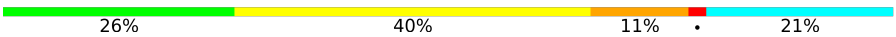


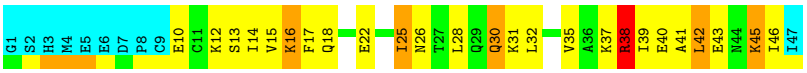


4.2.4 Score per residue for model 4 (medoid)

• Molecule 1: CARTILAGE MATRIX PROTEIN

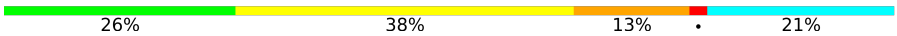
Chain A:





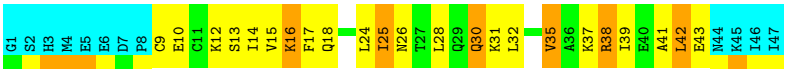
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B:



• Molecule 1: CARTILAGE MATRIX PROTEIN

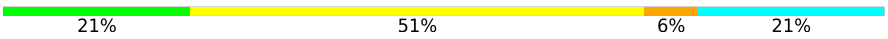
Chain C:



4.2.5 Score per residue for model 5

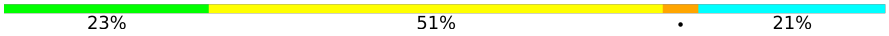
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A:



• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B:



• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain C: 17% 53% • 26%

G1 S2 H3 M4 E5 E6 D7 P8 C9 E10 C11 K12 S13 I14 V15 K16 F17 E23 L24 I25 N26 T27 L28 Q29 Q30 K31 L32 E33 A34 V35 A36 K37 R38 I39 E40 A41 L42 E43 N44 K45 I46 I47

4.2.6 Score per residue for model 6

- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A: 32% 30% 17% 21%

G1 S2 H3 M4 E5 E6 D7 P8 C9 E10 C11 K12 S13 I14 V15 K16 F17 Q18 T19 K20 I25 L28 Q29 Q30 K31 L32 V35 R38 I39 E40 A41 L42 E43 N44 K45 I46 I47

- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 30% 30% 19% 21%

G1 S2 H3 M4 E5 E6 D7 P8 C9 E10 C11 K12 S13 I14 V15 K16 F17 Q18 T19 K20 V21 E22 I25 L28 Q29 Q30 K31 L32 V35 R38 I39 E40 A41 L42 E43 N44 K45 I46 I47

- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain C: 26% 34% 15% 26%

G1 S2 H3 M4 E5 E6 D7 P8 C9 E10 C11 K12 S13 I14 V15 K16 F17 Q18 T19 K20 V21 E22 I25 L28 Q29 Q30 K31 L32 V35 R38 I39 E40 A41 L42 E43 N44 K45 I46 I47

4.2.7 Score per residue for model 7

- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A: 21% 34% 21% • 21%

G1 S2 H3 M4 E5 E6 D7 P8 C9 E10 C11 K12 S13 I14 V15 K16 F17 Q18 T19 K20 E23 L24 I25 N26 T27 L28 Q29 Q30 K31 L32 V35 A36 K37 R38 I39 E40 A41 L42 K45 I46 I47

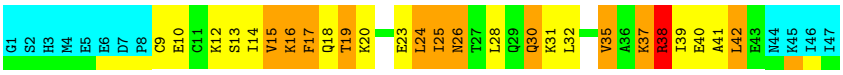
- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 19% 32% 26% • 21%

G1 S2 H3 M4 E5 E6 D7 P8 C9 E10 C11 K12 S13 I14 V15 K16 F17 Q18 T19 K20 E23 L24 I25 N26 T27 L28 Q29 Q30 K31 L32 V35 A36 K37 R38 I39 E40 A41 L42 E43 N44 K45 I46 I47

- Molecule 1: CARTILAGE MATRIX PROTEIN

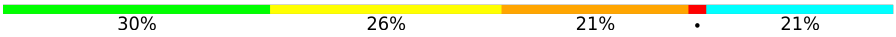
Chain C: 19% 30% 23% • 26%

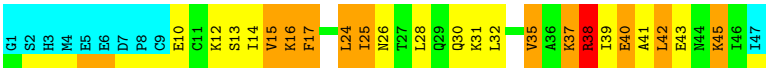


4.2.8 Score per residue for model 8

- Molecule 1: CARTILAGE MATRIX PROTEIN

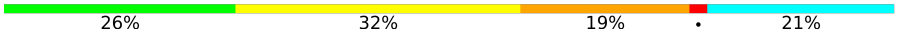
Chain A:

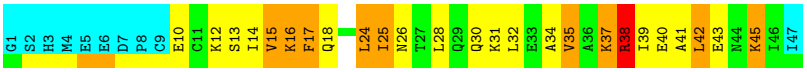




- Molecule 1: CARTILAGE MATRIX PROTEIN

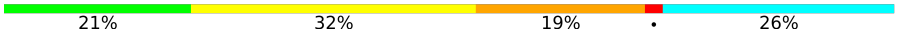
Chain B:

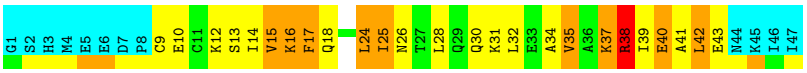




- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain C:

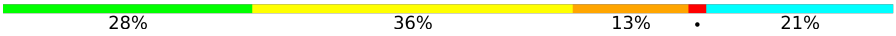


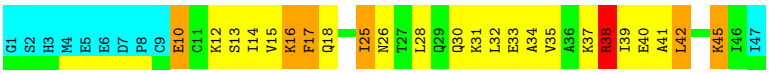


4.2.9 Score per residue for model 9

- Molecule 1: CARTILAGE MATRIX PROTEIN

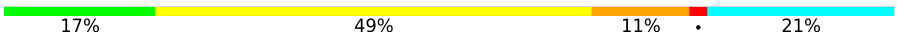
Chain A:

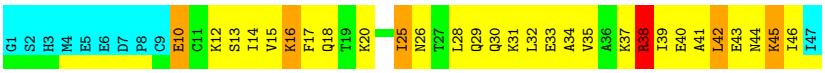




- Molecule 1: CARTILAGE MATRIX PROTEIN

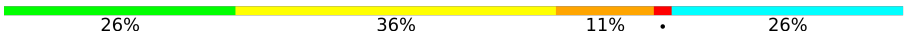
Chain B:





- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain C:



4.2.10 Score per residue for model 10

- Molecule 1: CARTILAGE MATRIX PROTEIN

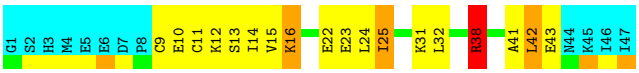
Chain A: 28% 40% 9% • 21%

- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 34% 34% 9% • 21%

- Molecule 1: CARTILAGE MATRIX PROTEIN

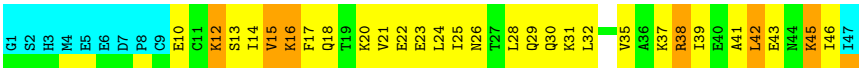
Chain C: 36% 30% 6% • 26%



4.2.11 Score per residue for model 11

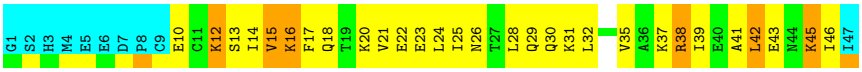
- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A: 17% 49% 13% 21%



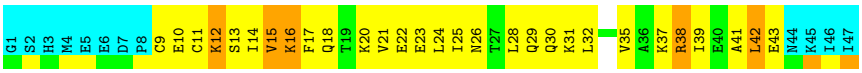
- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 17% 49% 13% 21%



- Molecule 1: CARTILAGE MATRIX PROTEIN

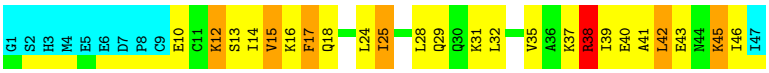
Chain C: 13% 51% 11% 26%



4.2.12 Score per residue for model 12

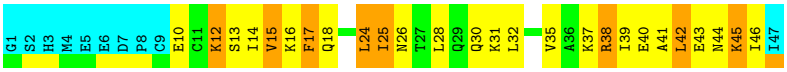
- Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A: 28% 36% 13% • 21%



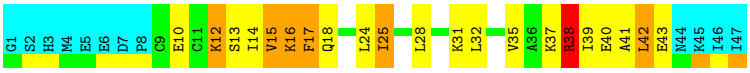
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 23% 38% 17% 21%



• Molecule 1: CARTILAGE MATRIX PROTEIN

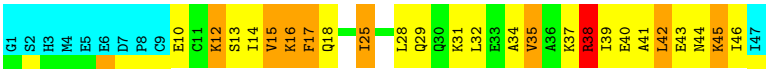
Chain C: 30% 30% 13% • 26%



4.2.13 Score per residue for model 13

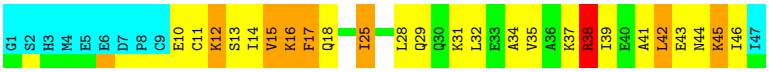
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A: 26% 34% 17% • 21%



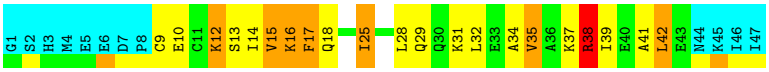
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 26% 36% 15% • 21%



• Molecule 1: CARTILAGE MATRIX PROTEIN

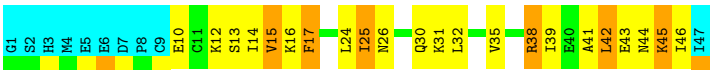
Chain C: 30% 28% 15% • 26%



4.2.14 Score per residue for model 14

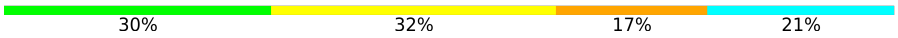
• Molecule 1: CARTILAGE MATRIX PROTEIN

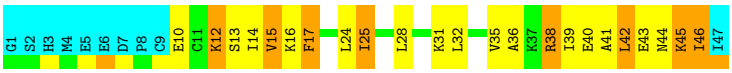
Chain A: 32% 34% 13% 21%



• Molecule 1: CARTILAGE MATRIX PROTEIN

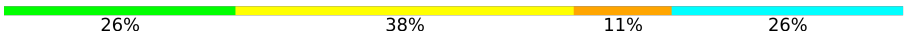
Chain B:

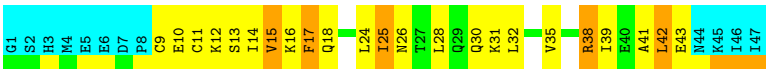




• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain C:

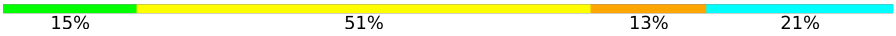




4.2.15 Score per residue for model 15

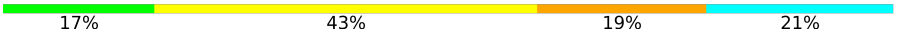
• Molecule 1: CARTILAGE MATRIX PROTEIN

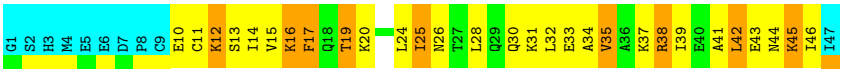
Chain A:



• Molecule 1: CARTILAGE MATRIX PROTEIN

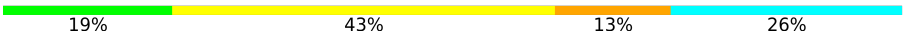
Chain B:





• Molecule 1: CARTILAGE MATRIX PROTEIN

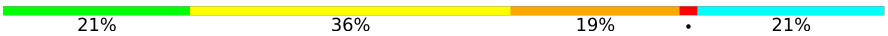
Chain C:

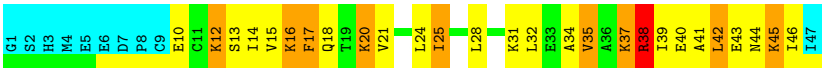


4.2.16 Score per residue for model 16

• Molecule 1: CARTILAGE MATRIX PROTEIN

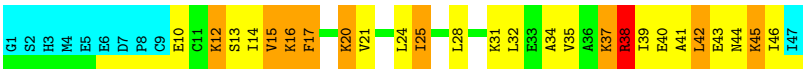
Chain A:





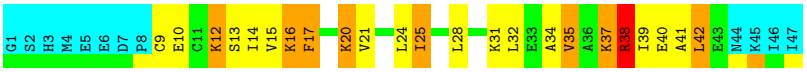
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 23% 34% 19% • 21%



• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain C: 26% 30% 17% • 26%



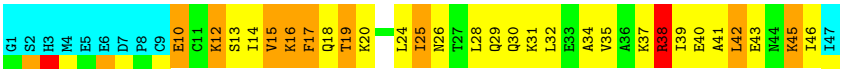
4.2.17 Score per residue for model 17

• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A: 15% 40% 21% • 21%

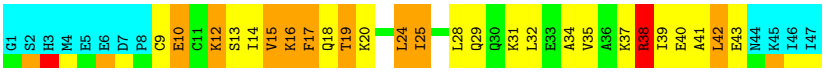
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 17% 40% 19% • 21%



• Molecule 1: CARTILAGE MATRIX PROTEIN

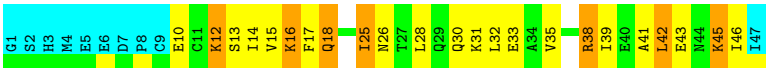
Chain C: 19% 34% 19% • 26%



4.2.18 Score per residue for model 18

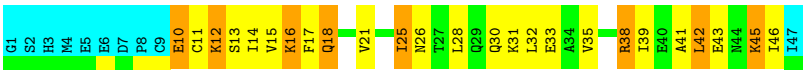
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A: 30% 34% 15% 21%



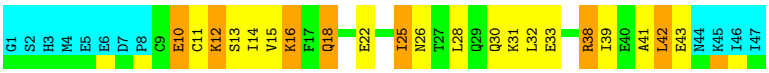
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 26% 36% 17% 21%



• Molecule 1: CARTILAGE MATRIX PROTEIN

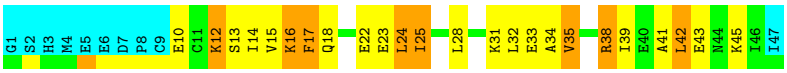
Chain C: 30% 30% 15% 26%



4.2.19 Score per residue for model 19

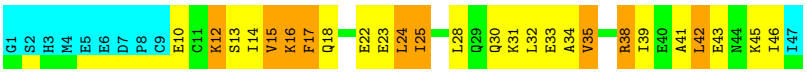
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A: 28% 34% 17% 21%



• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 23% 36% 19% 21%



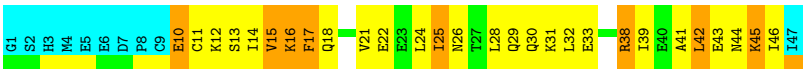
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain C: 21% 36% 17% 26%

4.2.20 Score per residue for model 20

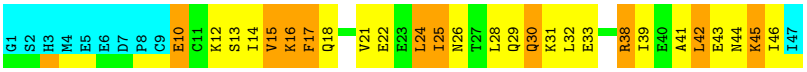
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain A: 19% 43% 17% 21%



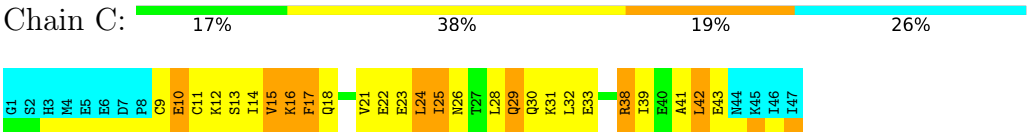
• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain B: 21% 36% 21% 21%



• Molecule 1: CARTILAGE MATRIX PROTEIN

Chain C:


17%
38%
19%
26%
G1 S2 H3 M4 E5 E6 D7 P8 C9 E10 C11 K12 S13 I14 V15 K16 F17 Q18 V21 E22 E23 L24 I25 N26 T27 L28 Q29 Q30 K31 L32 E33 R38 I39 E40 A41 L42 E43 N44 K45 I46 I47

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *DISTANCE GEOMETRY/ SIMULATED ANNEALING*.

Of the 30 calculated structures, 20 were deposited, based on the following criterion: *LOWEST ENERGY AND LEAST RESTRAINT VIOLATIONS*.

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

Software name	Classification	Version
X-PLOR	refinement	3.1
X-PLOR	structure solution	3.1

No chemical shift data was provided.

6 Model quality (i)

6.1 Standard geometry (i)

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

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	0.0±0.0	0.9±0.3
1	B	0.0±0.0	0.9±0.3
1	C	0.0±0.0	0.9±0.3
All	All	0	54

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	38	ARG	Sidechain	18
1	B	38	ARG	Sidechain	18
1	C	38	ARG	Sidechain	18

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	299	325	325	53±10
1	B	299	325	325	51±9
1	C	280	299	299	48±10
All	All	17560	18980	18980	1963

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 54.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:25:ILE:HD11	1:B:25:ILE:HD11	1.01	1.32	7	18
1:A:25:ILE:HD11	1:C:25:ILE:HD11	1.01	1.30	10	18
1:B:25:ILE:HD11	1:C:25:ILE:HD11	0.99	1.29	8	18
1:C:38:ARG:O	1:C:42:LEU:HD22	0.89	1.67	15	20
1:A:38:ARG:O	1:A:42:LEU:HD22	0.89	1.67	11	20
1:B:38:ARG:O	1:B:42:LEU:HD22	0.88	1.68	15	20
1:A:39:ILE:HD11	1:B:39:ILE:HG12	0.86	1.48	9	15
1:B:39:ILE:HD11	1:C:39:ILE:HG12	0.86	1.46	6	15
1:A:39:ILE:HG12	1:C:39:ILE:HD11	0.85	1.47	6	15
1:A:14:ILE:HG23	1:C:18:GLN:NE2	0.83	1.89	17	4
1:B:25:ILE:CD1	1:C:25:ILE:HD11	0.81	2.05	8	17
1:A:25:ILE:CD1	1:B:25:ILE:HD11	0.81	2.06	8	17
1:A:25:ILE:HD11	1:C:25:ILE:CD1	0.80	2.05	7	17
1:B:18:GLN:NE2	1:C:14:ILE:HG23	0.79	1.91	17	4
1:A:18:GLN:NE2	1:B:14:ILE:HG23	0.78	1.93	17	4
1:B:39:ILE:HD11	1:C:39:ILE:HG13	0.78	1.56	5	3
1:A:39:ILE:HG13	1:C:39:ILE:HD11	0.77	1.55	5	3
1:A:31:LYS:CB	1:C:32:LEU:HD21	0.76	2.11	3	19
1:A:28:LEU:HB3	1:B:28:LEU:HD22	0.76	1.57	19	16
1:B:28:LEU:HB3	1:C:28:LEU:HD22	0.74	1.58	15	16
1:B:32:LEU:HD21	1:C:31:LYS:CB	0.74	2.13	11	17
1:A:28:LEU:HD22	1:C:28:LEU:HB3	0.74	1.58	17	16
1:A:32:LEU:HD21	1:B:31:LYS:CB	0.74	2.13	3	17
1:A:39:ILE:HD11	1:B:39:ILE:HG13	0.73	1.58	5	3
1:A:24:LEU:HD23	1:C:25:ILE:CG2	0.73	2.14	11	2
1:A:25:ILE:HG21	1:B:24:LEU:HD23	0.72	1.59	16	7
1:A:14:ILE:HG23	1:C:18:GLN:OE1	0.71	1.84	11	1
1:A:18:GLN:OE1	1:B:14:ILE:HG23	0.70	1.86	11	1
1:B:32:LEU:HD21	1:C:31:LYS:HB2	0.70	1.63	19	13
1:A:24:LEU:HD23	1:C:25:ILE:HG21	0.70	1.64	11	7
1:A:31:LYS:HB2	1:C:32:LEU:HD21	0.69	1.63	10	14
1:B:39:ILE:HD11	1:C:39:ILE:CG1	0.69	2.18	8	6
1:A:32:LEU:HD21	1:B:31:LYS:HB2	0.69	1.63	19	14
1:A:15:VAL:HG22	1:B:14:ILE:CD1	0.68	2.19	20	4
1:A:14:ILE:CD1	1:C:15:VAL:HG22	0.67	2.18	20	6
1:B:25:ILE:CD1	1:C:25:ILE:HD12	0.67	2.19	20	2
1:B:18:GLN:OE1	1:C:14:ILE:HG23	0.66	1.90	11	1
1:A:39:ILE:HD11	1:B:39:ILE:CG1	0.66	2.21	19	5
1:A:39:ILE:HG23	1:B:42:LEU:HD21	0.66	1.68	19	3
1:A:25:ILE:HD12	1:C:25:ILE:CD1	0.65	2.21	20	2
1:A:39:ILE:CG1	1:C:39:ILE:HD11	0.65	2.21	5	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:14:ILE:HG22	1:A:18:GLN:OE1	0.65	1.91	11	1
1:B:25:ILE:HD11	1:C:25:ILE:CD1	0.65	2.21	11	1
1:A:15:VAL:HG22	1:B:14:ILE:HG12	0.65	1.67	20	15
1:B:25:ILE:HG21	1:C:24:LEU:HD23	0.64	1.68	2	7
1:A:14:ILE:HG12	1:C:15:VAL:HG22	0.64	1.68	8	16
1:B:14:ILE:HG22	1:B:18:GLN:OE1	0.64	1.93	11	1
1:A:17:PHE:CZ	1:C:22:GLU:CG	0.63	2.81	11	2
1:A:25:ILE:CD1	1:B:25:ILE:HD12	0.63	2.23	20	2
1:B:18:GLN:HE22	1:C:14:ILE:HG23	0.62	1.54	11	2
1:A:25:ILE:HD11	1:C:25:ILE:CG1	0.62	2.25	4	14
1:B:45:LYS:CD	1:B:45:LYS:N	0.61	2.63	5	19
1:A:45:LYS:CD	1:A:45:LYS:N	0.61	2.64	10	19
1:A:18:GLN:HE22	1:B:14:ILE:HG23	0.61	1.55	11	1
1:B:15:VAL:HG22	1:C:14:ILE:HG12	0.61	1.72	7	17
1:A:15:VAL:HG22	1:B:14:ILE:CG1	0.60	2.25	20	10
1:A:14:ILE:CG1	1:C:15:VAL:HG22	0.60	2.26	20	10
1:A:38:ARG:O	1:A:41:ALA:HB3	0.60	1.96	5	20
1:A:25:ILE:CG1	1:B:25:ILE:CD1	0.60	2.79	7	17
1:B:25:ILE:CG1	1:C:25:ILE:HD11	0.59	2.27	13	15
1:C:14:ILE:HG22	1:C:18:GLN:OE1	0.59	1.97	11	1
1:B:16:LYS:O	1:B:19:THR:HG22	0.59	1.97	15	4
1:B:39:ILE:HG23	1:C:42:LEU:HD21	0.59	1.72	19	3
1:A:46:ILE:HG21	1:B:42:LEU:CD1	0.59	2.27	17	1
1:B:38:ARG:O	1:B:41:ALA:HB3	0.59	1.97	5	20
1:B:15:VAL:HG22	1:C:14:ILE:CD1	0.59	2.27	20	3
1:A:25:ILE:CD1	1:C:25:ILE:CG1	0.59	2.80	7	17
1:A:25:ILE:CG1	1:B:25:ILE:HD11	0.58	2.28	15	16
1:B:25:ILE:CG1	1:C:25:ILE:CD1	0.58	2.81	8	16
1:A:31:LYS:CB	1:C:32:LEU:CD2	0.58	2.82	3	11
1:C:38:ARG:O	1:C:41:ALA:HB3	0.58	1.98	4	20
1:A:16:LYS:O	1:A:19:THR:HG22	0.58	1.99	7	4
1:A:14:ILE:HG23	1:C:18:GLN:HE22	0.58	1.56	11	1
1:B:46:ILE:HG21	1:C:42:LEU:CD1	0.58	2.29	17	1
1:A:46:ILE:HG21	1:B:42:LEU:HD12	0.58	1.75	17	4
1:A:14:ILE:CG2	1:C:18:GLN:NE2	0.58	2.67	17	1
1:A:32:LEU:CD2	1:B:31:LYS:CB	0.57	2.81	11	15
1:A:15:VAL:CG2	1:B:14:ILE:CD1	0.57	2.82	20	10
1:B:32:LEU:CD2	1:C:31:LYS:CB	0.57	2.81	11	8
1:B:46:ILE:HG21	1:C:42:LEU:HD12	0.57	1.75	17	3
1:A:39:ILE:HG23	1:B:42:LEU:CD2	0.57	2.28	19	3
1:A:14:ILE:CD1	1:C:15:VAL:CG2	0.57	2.82	20	13

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:12:LYS:O	1:A:16:LYS:CB	0.56	2.53	20	17
1:B:12:LYS:O	1:B:16:LYS:CB	0.56	2.54	17	18
1:C:16:LYS:O	1:C:19:THR:HG22	0.56	2.01	15	4
1:C:12:LYS:O	1:C:16:LYS:CB	0.56	2.54	2	17
1:B:39:ILE:HG23	1:C:42:LEU:CD2	0.55	2.32	19	2
1:B:15:VAL:HG13	1:C:14:ILE:HG12	0.55	1.78	7	5
1:A:14:ILE:CD1	1:C:15:VAL:HG21	0.55	2.32	18	1
1:B:17:PHE:CD1	1:B:17:PHE:C	0.55	2.80	7	13
1:B:22:GLU:CG	1:C:17:PHE:CZ	0.55	2.90	11	1
1:A:25:ILE:HD11	1:B:25:ILE:CD1	0.55	2.32	11	1
1:A:46:ILE:HG23	1:B:45:LYS:HG3	0.55	1.77	17	2
1:B:18:GLN:NE2	1:C:14:ILE:CG2	0.55	2.68	17	1
1:B:25:ILE:CG2	1:B:26:ASN:N	0.55	2.70	20	2
1:A:42:LEU:HD21	1:C:39:ILE:HG23	0.55	1.79	19	3
1:B:39:ILE:CD1	1:C:39:ILE:CG1	0.55	2.84	8	3
1:B:37:LYS:O	1:B:40:GLU:CG	0.54	2.56	16	4
1:C:25:ILE:CG2	1:C:26:ASN:N	0.54	2.70	20	2
1:B:45:LYS:C	1:B:46:ILE:HD13	0.54	2.23	6	2
1:B:15:VAL:CG2	1:C:14:ILE:CD1	0.54	2.85	20	8
1:B:15:VAL:HG22	1:C:14:ILE:CG1	0.54	2.32	7	7
1:B:35:VAL:HG11	1:C:35:VAL:HG11	0.54	1.80	7	12
1:C:17:PHE:CD1	1:C:17:PHE:C	0.54	2.81	2	12
1:A:25:ILE:CG2	1:A:26:ASN:N	0.54	2.70	20	2
1:A:37:LYS:O	1:A:40:GLU:CG	0.54	2.56	9	4
1:C:37:LYS:O	1:C:40:GLU:CG	0.54	2.56	9	4
1:A:17:PHE:C	1:A:17:PHE:CD1	0.54	2.81	13	8
1:A:17:PHE:CE1	1:C:22:GLU:HG2	0.54	2.38	11	1
1:C:38:ARG:O	1:C:42:LEU:CD2	0.54	2.55	6	10
1:A:18:GLN:OE1	1:B:14:ILE:CG2	0.54	2.56	11	1
1:A:21:VAL:O	1:A:25:ILE:CG1	0.54	2.55	11	1
1:A:35:VAL:HG11	1:C:35:VAL:HG11	0.54	1.80	7	13
1:B:38:ARG:O	1:B:42:LEU:CD2	0.54	2.56	6	11
1:A:39:ILE:CD1	1:B:39:ILE:CG1	0.54	2.85	19	3
1:A:17:PHE:CD1	1:C:18:GLN:CD	0.53	2.82	7	10
1:A:14:ILE:CG2	1:C:18:GLN:OE1	0.53	2.56	11	1
1:C:9:CYS:O	1:C:14:ILE:HD12	0.53	2.02	20	1
1:A:45:LYS:C	1:A:46:ILE:HD13	0.53	2.24	18	3
1:A:39:ILE:CG1	1:C:39:ILE:CD1	0.53	2.87	8	3
1:B:12:LYS:O	1:B:16:LYS:CG	0.53	2.56	13	2
1:A:15:VAL:CG2	1:B:14:ILE:HG12	0.53	2.33	20	19
1:B:18:GLN:CD	1:C:17:PHE:CD1	0.53	2.82	13	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:26:ASN:O	1:C:30:GLN:CG	0.53	2.57	11	3
1:A:14:ILE:HG23	1:C:18:GLN:CD	0.53	2.23	11	1
1:A:35:VAL:HG11	1:B:35:VAL:HG11	0.53	1.79	4	12
1:A:15:VAL:HG13	1:B:14:ILE:HG12	0.53	1.81	7	6
1:A:17:PHE:CZ	1:C:22:GLU:HG2	0.53	2.39	11	1
1:A:18:GLN:CD	1:B:17:PHE:CD1	0.53	2.82	13	6
1:A:26:ASN:O	1:A:30:GLN:CG	0.53	2.57	11	5
1:C:12:LYS:O	1:C:16:LYS:CG	0.53	2.57	13	2
1:A:38:ARG:O	1:A:42:LEU:CD2	0.53	2.57	7	11
1:B:26:ASN:O	1:B:30:GLN:CG	0.53	2.57	11	4
1:A:46:ILE:HD12	1:B:45:LYS:CB	0.53	2.34	2	2
1:A:25:ILE:CD1	1:C:25:ILE:HD11	0.53	2.33	11	1
1:C:21:VAL:O	1:C:25:ILE:CG1	0.53	2.57	11	1
1:C:25:ILE:HA	1:C:28:LEU:HD12	0.53	1.79	20	1
1:A:14:ILE:HG12	1:C:15:VAL:HG13	0.52	1.80	7	6
1:A:17:PHE:CD1	1:C:18:GLN:OE1	0.52	2.63	12	3
1:A:18:GLN:NE2	1:B:17:PHE:CD1	0.52	2.77	3	1
1:A:32:LEU:HD21	1:B:31:LYS:HB3	0.52	1.81	8	6
1:A:25:ILE:HA	1:A:28:LEU:HD12	0.52	1.80	20	1
1:A:45:LYS:N	1:A:45:LYS:HD3	0.52	2.19	12	8
1:B:32:LEU:CD2	1:C:31:LYS:HB3	0.52	2.34	8	5
1:A:31:LYS:HB2	1:C:32:LEU:CD2	0.52	2.34	11	7
1:B:21:VAL:O	1:B:25:ILE:CG1	0.52	2.57	11	1
1:A:14:ILE:HG12	1:C:15:VAL:CG2	0.52	2.33	20	20
1:B:35:VAL:HG12	1:C:35:VAL:CG2	0.52	2.34	7	6
1:B:18:GLN:OE1	1:C:14:ILE:CG2	0.52	2.57	11	1
1:B:32:LEU:CD2	1:C:31:LYS:HB2	0.52	2.34	11	7
1:A:32:LEU:CD2	1:B:31:LYS:HB2	0.52	2.34	11	9
1:A:12:LYS:O	1:A:16:LYS:CG	0.52	2.57	13	2
1:A:46:ILE:HD11	1:B:46:ILE:HD11	0.52	1.81	15	8
1:A:17:PHE:CD1	1:A:17:PHE:C	0.51	2.84	7	5
1:A:18:GLN:CD	1:B:14:ILE:HG23	0.51	2.25	11	1
1:B:25:ILE:CG2	1:C:24:LEU:HD23	0.51	2.35	2	1
1:B:25:ILE:HD12	1:C:25:ILE:HD12	0.51	1.82	20	1
1:B:45:LYS:N	1:B:45:LYS:HD3	0.51	2.20	5	10
1:B:41:ALA:O	1:B:45:LYS:CD	0.51	2.59	4	2
1:A:28:LEU:HD21	1:C:29:GLN:HB2	0.51	1.83	11	1
1:A:17:PHE:CE1	1:C:22:GLU:CG	0.51	2.93	11	1
1:B:10:GLU:CB	1:B:13:SER:HB2	0.51	2.36	8	20
1:A:17:PHE:CZ	1:C:22:GLU:HG3	0.51	2.40	11	2
1:B:34:ALA:O	1:B:38:ARG:CG	0.51	2.58	16	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:10:GLU:CB	1:C:13:SER:HB2	0.51	2.36	8	20
1:B:12:LYS:O	1:B:16:LYS:HB2	0.51	2.06	15	17
1:A:31:LYS:HB3	1:C:32:LEU:HD21	0.51	1.80	14	6
1:B:32:LEU:HD21	1:C:31:LYS:HB3	0.51	1.82	12	4
1:A:45:LYS:HD2	1:A:45:LYS:N	0.51	2.21	17	1
1:B:45:LYS:N	1:B:45:LYS:HD2	0.51	2.21	17	1
1:C:14:ILE:O	1:C:18:GLN:OE1	0.50	2.29	18	1
1:B:15:VAL:CG2	1:C:14:ILE:HG12	0.50	2.36	1	19
1:A:32:LEU:CD2	1:B:31:LYS:HB3	0.50	2.36	8	8
1:A:31:LYS:HB3	1:C:32:LEU:CD2	0.50	2.35	8	6
1:B:44:ASN:C	1:B:45:LYS:CD	0.50	2.80	20	3
1:B:25:ILE:HA	1:B:28:LEU:HD12	0.50	1.82	20	1
1:A:10:GLU:CB	1:A:13:SER:HB2	0.49	2.37	20	20
1:A:18:GLN:HB3	1:B:17:PHE:CE1	0.49	2.42	3	4
1:B:14:ILE:O	1:B:18:GLN:OE1	0.49	2.30	18	1
1:A:25:ILE:HD12	1:B:25:ILE:HD12	0.49	1.83	20	1
1:A:22:GLU:CG	1:B:17:PHE:CZ	0.49	2.95	11	1
1:A:18:GLN:NE2	1:B:14:ILE:CG2	0.49	2.72	17	1
1:A:46:ILE:CG2	1:B:45:LYS:HG3	0.49	2.38	16	2
1:B:10:GLU:HB2	1:B:14:ILE:CD1	0.49	2.37	10	10
1:A:38:ARG:HB3	1:C:39:ILE:HG21	0.49	1.83	7	5
1:A:35:VAL:CG1	1:B:35:VAL:CG2	0.49	2.90	16	8
1:B:39:ILE:CD1	1:C:39:ILE:HG12	0.49	2.36	19	2
1:A:40:GLU:HG3	1:A:41:ALA:N	0.49	2.23	7	5
1:C:12:LYS:O	1:C:16:LYS:HB2	0.49	2.08	15	19
1:B:18:GLN:CD	1:C:14:ILE:HG23	0.49	2.29	11	1
1:B:35:VAL:CG1	1:C:35:VAL:CG2	0.48	2.91	15	7
1:A:39:ILE:HG21	1:B:38:ARG:HB3	0.48	1.85	7	4
1:A:14:ILE:O	1:A:18:GLN:OE1	0.48	2.30	18	1
1:A:25:ILE:HD12	1:C:25:ILE:HD12	0.48	1.85	20	1
1:C:10:GLU:HB2	1:C:14:ILE:CD1	0.48	2.38	10	12
1:A:35:VAL:CG2	1:C:35:VAL:HG12	0.48	2.38	11	7
1:A:39:ILE:CD1	1:B:39:ILE:HG12	0.48	2.39	19	1
1:A:35:VAL:HG12	1:B:35:VAL:CG2	0.48	2.39	7	7
1:A:22:GLU:CG	1:B:17:PHE:CE1	0.48	2.97	4	1
1:A:15:VAL:CG2	1:B:14:ILE:HD11	0.48	2.38	20	1
1:A:16:LYS:CD	1:A:16:LYS:C	0.48	2.82	19	1
1:C:34:ALA:O	1:C:38:ARG:CG	0.48	2.62	16	4
1:B:39:ILE:HG21	1:C:38:ARG:HB3	0.48	1.86	6	5
1:B:18:GLN:OE1	1:C:17:PHE:CD1	0.48	2.67	12	3
1:A:44:ASN:C	1:A:45:LYS:CD	0.48	2.81	20	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:GLU:HB2	1:A:14:ILE:CD1	0.48	2.39	10	11
1:A:35:VAL:HG11	1:B:35:VAL:CG1	0.47	2.39	14	5
1:B:24:LEU:HD13	1:B:24:LEU:O	0.47	2.09	20	3
1:C:40:GLU:HG3	1:C:41:ALA:N	0.47	2.24	16	5
1:A:39:ILE:CD1	1:B:39:ILE:HG13	0.47	2.36	8	2
1:B:23:GLU:HG3	1:B:24:LEU:N	0.47	2.23	19	4
1:B:16:LYS:CD	1:B:16:LYS:C	0.47	2.83	19	3
1:B:12:LYS:O	1:B:16:LYS:CD	0.47	2.62	13	1
1:A:12:LYS:O	1:A:16:LYS:HB2	0.47	2.09	15	19
1:B:25:ILE:HD11	1:C:25:ILE:HD12	0.47	1.86	20	2
1:C:12:LYS:O	1:C:16:LYS:CD	0.47	2.63	13	1
1:A:37:LYS:O	1:A:40:GLU:HG2	0.47	2.09	7	3
1:B:35:VAL:HG11	1:C:35:VAL:CG1	0.47	2.39	14	5
1:A:46:ILE:HD13	1:A:46:ILE:N	0.47	2.24	18	1
1:B:40:GLU:HG3	1:B:41:ALA:N	0.47	2.23	1	5
1:B:39:ILE:CG2	1:C:38:ARG:HB3	0.47	2.39	6	1
1:A:46:ILE:HD12	1:B:45:LYS:HB2	0.47	1.86	2	3
1:B:44:ASN:CB	1:B:45:LYS:HD2	0.47	2.40	15	4
1:A:41:ALA:O	1:A:45:LYS:HD3	0.47	2.10	17	3
1:A:28:LEU:CB	1:B:28:LEU:HD22	0.47	2.36	19	4
1:A:39:ILE:HG13	1:C:39:ILE:CD1	0.47	2.34	5	3
1:C:16:LYS:CD	1:C:16:LYS:C	0.47	2.82	19	2
1:A:12:LYS:O	1:A:16:LYS:CD	0.47	2.63	13	1
1:A:14:ILE:HD11	1:C:15:VAL:CG2	0.47	2.40	20	1
1:B:18:GLN:OE1	1:C:14:ILE:O	0.46	2.33	4	3
1:A:35:VAL:CG1	1:C:35:VAL:HG11	0.46	2.40	14	4
1:B:34:ALA:O	1:B:38:ARG:HG3	0.46	2.10	9	6
1:C:24:LEU:HD13	1:C:24:LEU:O	0.46	2.11	17	3
1:A:23:GLU:HG3	1:A:24:LEU:N	0.46	2.25	10	5
1:A:37:LYS:O	1:A:40:GLU:HG3	0.46	2.11	8	4
1:C:37:LYS:O	1:C:40:GLU:OE2	0.46	2.33	17	1
1:A:44:ASN:CB	1:A:45:LYS:HD2	0.46	2.41	15	3
1:B:22:GLU:CG	1:C:17:PHE:CE1	0.46	2.99	4	1
1:B:16:LYS:HD3	1:B:16:LYS:N	0.46	2.26	13	1
1:A:34:ALA:O	1:A:38:ARG:CG	0.46	2.63	9	4
1:A:29:GLN:N	1:B:28:LEU:HD21	0.46	2.25	12	1
1:A:35:VAL:CG2	1:C:35:VAL:CG1	0.46	2.93	16	7
1:C:37:LYS:O	1:C:40:GLU:HG2	0.46	2.11	7	4
1:A:16:LYS:N	1:A:16:LYS:HD3	0.46	2.25	13	1
1:B:37:LYS:O	1:B:40:GLU:OE2	0.46	2.34	17	1
1:A:41:ALA:O	1:A:45:LYS:CD	0.46	2.63	4	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:41:ALA:O	1:B:45:LYS:CE	0.46	2.63	4	1
1:A:17:PHE:CE2	1:C:22:GLU:OE2	0.46	2.69	6	1
1:C:24:LEU:HD12	1:C:28:LEU:HD11	0.46	1.88	7	2
1:B:46:ILE:HD13	1:B:46:ILE:N	0.46	2.25	18	1
1:B:37:LYS:O	1:B:40:GLU:HG2	0.46	2.10	1	3
1:C:26:ASN:O	1:C:30:GLN:HG3	0.46	2.11	11	8
1:A:18:GLN:OE1	1:B:14:ILE:O	0.45	2.34	16	4
1:A:29:GLN:O	1:A:33:GLU:CG	0.45	2.65	5	1
1:C:12:LYS:O	1:C:16:LYS:HB3	0.45	2.12	8	1
1:A:28:LEU:HD22	1:C:28:LEU:CB	0.45	2.40	20	2
1:A:25:ILE:HD12	1:C:25:ILE:HD11	0.45	1.86	20	2
1:A:25:ILE:CD1	1:C:25:ILE:HG13	0.45	2.42	19	8
1:B:37:LYS:O	1:B:40:GLU:HG3	0.45	2.12	8	4
1:C:10:GLU:HG2	1:C:13:SER:CB	0.45	2.42	10	2
1:A:42:LEU:CD2	1:C:39:ILE:HG23	0.45	2.41	19	1
1:A:34:ALA:O	1:A:38:ARG:HG3	0.45	2.12	13	5
1:B:41:ALA:O	1:B:45:LYS:HD3	0.45	2.11	17	2
1:A:26:ASN:O	1:A:30:GLN:HG3	0.45	2.12	11	10
1:A:10:GLU:CB	1:A:14:ILE:HG13	0.45	2.42	20	2
1:A:44:ASN:CB	1:A:45:LYS:HD3	0.45	2.42	20	2
1:C:23:GLU:HG3	1:C:24:LEU:N	0.45	2.27	7	4
1:C:36:ALA:O	1:C:40:GLU:CG	0.45	2.65	5	1
1:B:25:ILE:HG13	1:C:25:ILE:CD1	0.45	2.41	2	5
1:A:25:ILE:HG13	1:B:25:ILE:CD1	0.45	2.41	12	7
1:A:32:LEU:HD13	1:C:32:LEU:HD13	0.45	1.89	15	3
1:B:36:ALA:O	1:B:40:GLU:CG	0.45	2.65	5	1
1:C:24:LEU:HD12	1:C:28:LEU:CD1	0.45	2.42	8	1
1:C:37:LYS:O	1:C:40:GLU:HG3	0.45	2.12	17	3
1:B:26:ASN:O	1:B:30:GLN:HG3	0.45	2.11	11	11
1:C:9:CYS:O	1:C:10:GLU:C	0.45	2.54	2	15
1:B:29:GLN:O	1:B:33:GLU:CG	0.45	2.65	5	1
1:B:17:PHE:O	1:B:20:LYS:HG3	0.45	2.12	16	1
1:A:15:VAL:CG1	1:B:14:ILE:HG12	0.45	2.42	7	5
1:B:21:VAL:O	1:B:25:ILE:HB	0.45	2.11	1	3
1:C:21:VAL:O	1:C:25:ILE:HB	0.45	2.12	1	3
1:B:22:GLU:HG2	1:C:17:PHE:CZ	0.45	2.47	11	1
1:C:12:LYS:O	1:C:16:LYS:HD3	0.45	2.12	13	1
1:A:20:LYS:HG3	1:A:21:VAL:N	0.45	2.27	16	1
1:A:13:SER:HA	1:A:16:LYS:HG2	0.44	1.89	8	1
1:B:29:GLN:HB2	1:C:28:LEU:HD21	0.44	1.89	11	1
1:A:18:GLN:OE1	1:B:17:PHE:CD1	0.44	2.70	12	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:10:GLU:CB	1:B:14:ILE:HG13	0.44	2.42	20	2
1:B:12:LYS:O	1:B:16:LYS:HD3	0.44	2.12	13	1
1:B:20:LYS:HG3	1:B:21:VAL:N	0.44	2.26	16	1
1:B:15:VAL:HG22	1:C:14:ILE:CG2	0.44	2.43	18	1
1:B:15:VAL:CG1	1:C:14:ILE:HG12	0.44	2.41	7	3
1:C:10:GLU:CB	1:C:14:ILE:HG13	0.44	2.43	20	2
1:B:35:VAL:CG1	1:C:35:VAL:HG21	0.44	2.42	15	3
1:A:14:ILE:HG12	1:C:15:VAL:CG1	0.44	2.42	7	5
1:C:34:ALA:O	1:C:38:ARG:HG3	0.44	2.12	1	4
1:C:16:LYS:HD3	1:C:16:LYS:N	0.44	2.28	13	1
1:A:14:ILE:CG2	1:C:15:VAL:HG22	0.44	2.43	18	1
1:A:17:PHE:CE1	1:C:18:GLN:HB3	0.44	2.47	2	3
1:B:12:LYS:O	1:B:16:LYS:HB3	0.44	2.12	8	2
1:A:17:PHE:O	1:A:20:LYS:HG3	0.44	2.12	16	1
1:A:15:VAL:CG2	1:B:14:ILE:CG1	0.44	2.95	20	1
1:A:28:LEU:HD21	1:C:29:GLN:N	0.44	2.28	20	1
1:A:15:VAL:HG22	1:B:14:ILE:CG2	0.44	2.43	18	1
1:B:39:ILE:O	1:B:43:GLU:HG3	0.44	2.12	3	15
1:B:20:LYS:O	1:B:24:LEU:HB2	0.44	2.13	11	1
1:C:20:LYS:HG3	1:C:21:VAL:N	0.44	2.27	16	1
1:A:24:LEU:HD13	1:A:24:LEU:O	0.44	2.13	17	1
1:A:35:VAL:HG12	1:B:35:VAL:HG22	0.44	1.90	9	2
1:A:39:ILE:O	1:A:43:GLU:HG3	0.43	2.12	19	15
1:B:39:ILE:CD1	1:C:39:ILE:HG13	0.43	2.36	5	1
1:A:42:LEU:N	1:A:42:LEU:HD13	0.43	2.28	11	2
1:A:35:VAL:CG1	1:B:35:VAL:HG21	0.43	2.43	15	2
1:B:18:GLN:HB3	1:C:17:PHE:CE1	0.43	2.48	2	2
1:A:12:LYS:O	1:A:16:LYS:HB3	0.43	2.13	8	1
1:A:12:LYS:O	1:A:16:LYS:HD3	0.43	2.13	13	1
1:C:17:PHE:O	1:C:20:LYS:HG3	0.43	2.12	16	1
1:A:25:ILE:HD11	1:B:25:ILE:HD12	0.43	1.91	20	1
1:C:20:LYS:O	1:C:24:LEU:HB2	0.43	2.14	11	1
1:C:39:ILE:O	1:C:43:GLU:HG3	0.43	2.14	20	13
1:B:42:LEU:O	1:B:46:ILE:HG12	0.43	2.13	17	8
1:B:13:SER:HA	1:B:16:LYS:HG2	0.43	1.90	8	1
1:A:25:ILE:CG2	1:B:24:LEU:HD23	0.43	2.44	11	1
1:A:25:ILE:HG21	1:B:24:LEU:CD2	0.43	2.42	5	1
1:B:44:ASN:CB	1:B:45:LYS:HD3	0.43	2.43	20	2
1:B:39:ILE:CG2	1:C:42:LEU:HD21	0.43	2.43	19	1
1:A:21:VAL:O	1:A:25:ILE:HB	0.43	2.13	1	3
1:B:28:LEU:CB	1:C:28:LEU:HD22	0.43	2.44	7	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:36:ALA:O	1:C:40:GLU:HG3	0.43	2.14	5	1
1:A:14:ILE:CG1	1:C:15:VAL:CG2	0.43	2.96	20	1
1:C:40:GLU:CD	1:C:41:ALA:N	0.42	2.72	17	1
1:A:10:GLU:O	1:A:11:CYS:C	0.42	2.57	15	4
1:A:42:LEU:O	1:A:46:ILE:HG12	0.42	2.14	20	8
1:C:10:GLU:O	1:C:11:CYS:C	0.42	2.57	10	9
1:A:24:LEU:HD12	1:A:28:LEU:HD11	0.42	1.92	7	2
1:A:37:LYS:O	1:A:40:GLU:OE2	0.42	2.36	17	1
1:A:46:ILE:HG23	1:B:45:LYS:CG	0.42	2.44	20	1
1:A:41:ALA:O	1:A:45:LYS:CE	0.42	2.67	4	1
1:A:23:GLU:CG	1:A:24:LEU:N	0.42	2.82	11	1
1:B:35:VAL:HG12	1:C:35:VAL:HG22	0.42	1.92	6	3
1:B:44:ASN:C	1:B:45:LYS:HD2	0.42	2.35	10	4
1:C:29:GLN:O	1:C:33:GLU:CG	0.42	2.68	5	1
1:B:24:LEU:HD12	1:B:28:LEU:CD1	0.42	2.44	12	2
1:A:18:GLN:NE2	1:A:18:GLN:HA	0.42	2.29	18	1
1:B:18:GLN:OE1	1:C:18:GLN:HG3	0.42	2.15	2	2
1:B:24:LEU:HD12	1:B:28:LEU:HD11	0.42	1.90	8	2
1:B:22:GLU:OE2	1:C:17:PHE:CE2	0.42	2.73	6	1
1:C:13:SER:HA	1:C:16:LYS:HG2	0.42	1.91	8	1
1:A:45:LYS:N	1:A:45:LYS:HD2	0.42	2.29	15	1
1:C:16:LYS:CD	1:C:17:PHE:N	0.42	2.83	8	1
1:B:10:GLU:HG2	1:B:13:SER:CB	0.42	2.44	10	1
1:A:36:ALA:O	1:A:40:GLU:CG	0.42	2.68	5	1
1:A:25:ILE:CD1	1:C:25:ILE:CD1	0.42	2.91	8	1
1:B:23:GLU:CG	1:B:24:LEU:N	0.42	2.83	11	1
1:B:20:LYS:CD	1:B:20:LYS:C	0.41	2.89	6	2
1:A:42:LEU:HD13	1:A:42:LEU:N	0.41	2.30	8	1
1:C:20:LYS:CD	1:C:20:LYS:C	0.41	2.88	16	1
1:A:10:GLU:HB3	1:A:13:SER:HB2	0.41	1.92	13	3
1:A:20:LYS:O	1:A:24:LEU:HB2	0.41	2.15	11	1
1:B:17:PHE:CE1	1:B:21:VAL:HG23	0.41	2.50	18	1
1:B:10:GLU:O	1:B:11:CYS:C	0.41	2.57	18	4
1:C:23:GLU:CG	1:C:24:LEU:N	0.41	2.84	11	1
1:A:39:ILE:CG2	1:B:42:LEU:HD21	0.41	2.42	19	1
1:A:39:ILE:HG12	1:C:39:ILE:CD1	0.41	2.45	8	1
1:C:19:THR:CG2	1:C:20:LYS:N	0.41	2.83	17	2
1:A:29:GLN:HB2	1:B:28:LEU:HD21	0.41	1.91	11	1
1:A:31:LYS:O	1:A:35:VAL:HG23	0.41	2.16	18	1
1:B:30:GLN:O	1:B:33:GLU:HG2	0.41	2.15	19	1
1:C:33:GLU:HG3	1:C:34:ALA:N	0.41	2.29	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:14:ILE:O	1:C:18:GLN:OE1	0.41	2.38	1	2
1:A:18:GLN:HG3	1:C:18:GLN:OE1	0.41	2.15	3	1
1:B:42:LEU:HB3	1:C:42:LEU:HG	0.41	1.93	6	1
1:C:34:ALA:O	1:C:38:ARG:HG2	0.41	2.16	8	1
1:C:16:LYS:C	1:C:16:LYS:CD	0.41	2.88	20	1
1:A:18:GLN:OE1	1:B:18:GLN:HG3	0.41	2.15	5	1
1:A:32:LEU:HD13	1:B:32:LEU:HD13	0.41	1.91	7	1
1:A:35:VAL:HG21	1:C:35:VAL:CG1	0.41	2.45	11	2
1:B:19:THR:CG2	1:B:20:LYS:N	0.41	2.83	17	1
1:A:33:GLU:HG3	1:A:34:ALA:N	0.41	2.30	19	1
1:A:36:ALA:O	1:A:40:GLU:HG3	0.41	2.16	10	1
1:B:22:GLU:HG3	1:C:17:PHE:CZ	0.41	2.51	11	1
1:C:32:LEU:HD12	1:C:32:LEU:HA	0.41	1.76	12	3
1:C:18:GLN:NE2	1:C:18:GLN:HA	0.41	2.30	18	1
1:C:16:LYS:HD3	1:C:16:LYS:O	0.41	2.16	19	1
1:A:24:LEU:O	1:A:28:LEU:HD12	0.41	2.16	1	1
1:A:20:LYS:CD	1:A:20:LYS:C	0.41	2.89	16	1
1:A:19:THR:CG2	1:A:20:LYS:N	0.41	2.83	17	1
1:C:31:LYS:O	1:C:35:VAL:HB	0.41	2.16	19	1
1:B:10:GLU:HB3	1:B:14:ILE:HG13	0.40	1.94	3	2
1:B:39:ILE:HD12	1:C:38:ARG:CB	0.40	2.45	6	1
1:A:46:ILE:CD1	1:B:46:ILE:HD11	0.40	2.46	7	1
1:B:33:GLU:HG3	1:B:34:ALA:N	0.40	2.30	19	1
1:B:45:LYS:O	1:B:46:ILE:HD13	0.40	2.16	6	1
1:B:16:LYS:HD2	1:B:17:PHE:N	0.40	2.30	7	1
1:B:42:LEU:N	1:B:42:LEU:HD13	0.40	2.30	8	1
1:A:16:LYS:HD3	1:A:16:LYS:O	0.40	2.17	19	1
1:A:44:ASN:C	1:A:45:LYS:HD2	0.40	2.36	5	1
1:A:16:LYS:HD2	1:A:17:PHE:N	0.40	2.31	7	1
1:A:14:ILE:HD13	1:C:15:VAL:CG2	0.40	2.46	18	1
1:B:18:GLN:NE2	1:B:18:GLN:HA	0.40	2.30	18	1
1:C:25:ILE:HG23	1:C:26:ASN:N	0.40	2.32	20	1
1:C:28:LEU:O	1:C:32:LEU:HB2	0.40	2.17	2	2
1:C:31:LYS:O	1:C:35:VAL:HG23	0.40	2.17	3	1
1:A:28:LEU:O	1:A:32:LEU:HB2	0.40	2.16	7	1
1:A:16:LYS:CD	1:A:17:PHE:N	0.40	2.85	8	1
1:B:34:ALA:O	1:B:38:ARG:HG2	0.40	2.17	8	1
1:A:21:VAL:O	1:A:25:ILE:CB	0.40	2.70	11	1
1:B:41:ALA:HA	1:B:44:ASN:OD1	0.40	2.16	12	1
1:A:44:ASN:HB2	1:A:45:LYS:HD2	0.40	1.94	15	1
1:B:28:LEU:O	1:B:32:LEU:HB2	0.40	2.16	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:36:ALA:O	1:B:40:GLU:HG3	0.40	2.16	14	1

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	37/47 (79%)	36±1 (97±2%)	1±1 (3±2%)	0±0 (0±0%)	100	100
1	B	37/47 (79%)	36±1 (97±2%)	1±1 (3±2%)	0±0 (0±0%)	100	100
1	C	35/47 (74%)	33±1 (95±3%)	2±1 (5±3%)	0±0 (0±0%)	100	100
All	All	2180/2820 (77%)	2107 (97%)	73 (3%)	0 (0%)	100	100

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	34/43 (79%)	25±2 (74±6%)	9±2 (26±6%)	2	23
1	B	34/43 (79%)	25±2 (74±7%)	9±2 (26±7%)	2	22
1	C	32/43 (74%)	24±2 (75±8%)	8±2 (25±8%)	2	24
All	All	2000/2580 (78%)	1481 (74%)	519 (26%)	2	23

All 72 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	42	LEU	20

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Mol	Chain	Res	Type	Models (Total)
1	B	42	LEU	20
1	C	42	LEU	20
1	A	25	ILE	19
1	A	45	LYS	19
1	B	25	ILE	19
1	C	25	ILE	19
1	B	45	LYS	18
1	C	16	LYS	18
1	A	17	PHE	17
1	B	16	LYS	17
1	A	16	LYS	16
1	B	17	PHE	16
1	C	17	PHE	16
1	B	15	VAL	12
1	B	12	LYS	11
1	A	15	VAL	10
1	C	15	VAL	10
1	A	38	ARG	10
1	C	12	LYS	10
1	A	37	LYS	9
1	B	37	LYS	9
1	C	35	VAL	9
1	C	37	LYS	9
1	B	38	ARG	9
1	C	38	ARG	9
1	A	12	LYS	9
1	B	35	VAL	7
1	A	35	VAL	6
1	B	29	GLN	6
1	C	29	GLN	6
1	B	20	LYS	6
1	A	24	LEU	6
1	B	24	LEU	6
1	C	24	LEU	6
1	A	29	GLN	5
1	C	33	GLU	5
1	A	20	LYS	5
1	C	20	LYS	5
1	A	19	THR	4
1	B	19	THR	4
1	C	19	THR	4
1	A	10	GLU	4

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Mol	Chain	Res	Type	Models (Total)
1	A	33	GLU	4
1	B	10	GLU	4
1	B	33	GLU	4
1	C	10	GLU	4
1	A	40	GLU	3
1	C	30	GLN	3
1	A	22	GLU	3
1	B	22	GLU	3
1	C	22	GLU	3
1	A	30	GLN	2
1	B	30	GLN	2
1	B	46	ILE	2
1	A	28	LEU	1
1	B	28	LEU	1
1	C	28	LEU	1
1	A	31	LYS	1
1	B	26	ASN	1
1	B	31	LYS	1
1	C	26	ASN	1
1	C	31	LYS	1
1	C	40	GLU	1
1	A	44	ASN	1
1	A	46	ILE	1
1	B	44	ASN	1
1	A	23	GLU	1
1	A	18	GLN	1
1	B	18	GLN	1
1	C	18	GLN	1
1	C	23	GLU	1

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 (i)

No chemical shift data were provided