



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 08:37 AM UTC

PDB ID : 1SOU / pdb_00001sou
Title : NMR structure of Aquifex aeolicus 5,10-methenyltetrahydrofolate synthetase:
Northeast Structural Genomics Consortium Target QR46
Authors : Cort, J.R.; Chiang, Y.; Acton, T.; Wu, M.; Montelione, G.T.; Kennedy, M.A.;
Northeast Structural Genomics Consortium (NESG)
Deposited on : 2004-03-15

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 ⓘ 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:

MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
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)	:	2.49

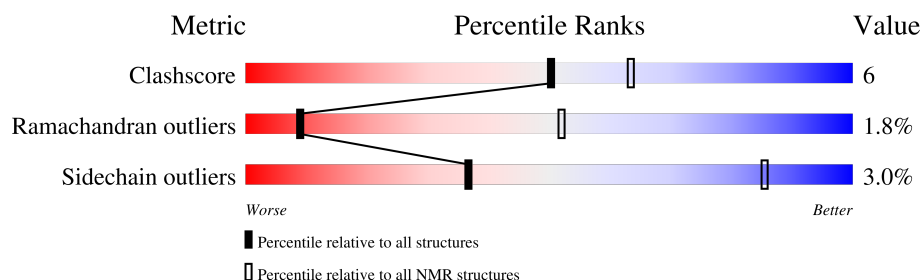
1 Overall quality at a glance

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	194	

2 Ensemble composition and analysis

This entry contains 20 models. Model 13 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *combination of factors*.

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:2-A:129, A:136-A:181 (174)	1.17	13

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. No single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3214 atoms, of which 1638 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called 5,10-methenyltetrahydrofolate synthetase.

Mol	Chain	Residues	Atoms						Trace
1	A	194	Total	C	H	N	O	S	0
			3214	1011	1638	284	277	4	

There are 8 discrepancies between the modelled and reference sequences:

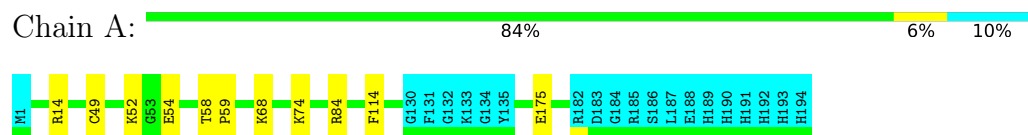
Chain	Residue	Modelled	Actual	Comment	Reference
A	187	LEU	-	cloning artifact	UNP O67621
A	188	GLU	-	cloning artifact	UNP O67621
A	189	HIS	-	expression tag	UNP O67621
A	190	HIS	-	expression tag	UNP O67621
A	191	HIS	-	expression tag	UNP O67621
A	192	HIS	-	expression tag	UNP O67621
A	193	HIS	-	expression tag	UNP O67621
A	194	HIS	-	expression tag	UNP O67621

4 Residue-property plots

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: 5,10-methenyltetrahydrofolate synthetase

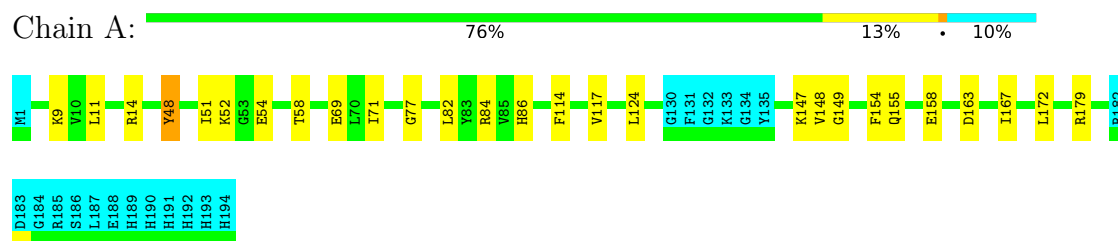


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

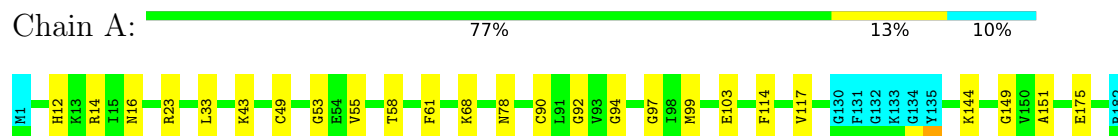
4.2.1 Score per residue for model 1

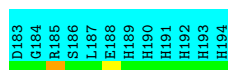
- Molecule 1: 5,10-methenyltetrahydrofolate synthetase



4.2.2 Score per residue for model 2

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase

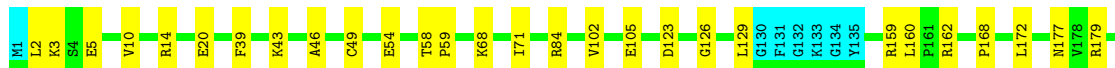




4.2.3 Score per residue for model 3

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase

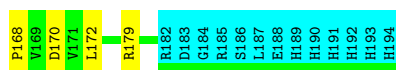
Chain A: 75% 14% 10%



4.2.4 Score per residue for model 4

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase

Chain A: 72% 16% 10%



4.2.5 Score per residue for model 5

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase

Chain A: 73% 15% 10%



4.2.6 Score per residue for model 6

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase

Chain A: 75% 15% 10%



4.2.7 Score per residue for model 7

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase

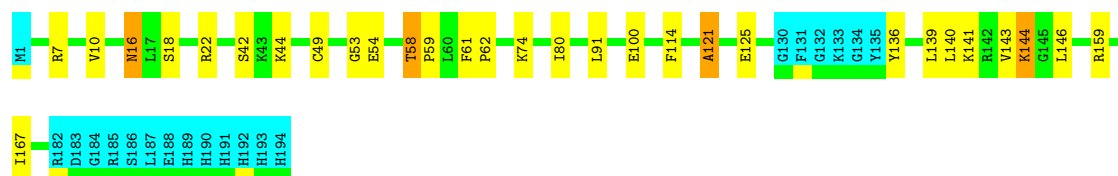
Chain A: 72% 18% 10%



4.2.8 Score per residue for model 8

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase

Chain A: 74% 13% 10%



4.2.9 Score per residue for model 9

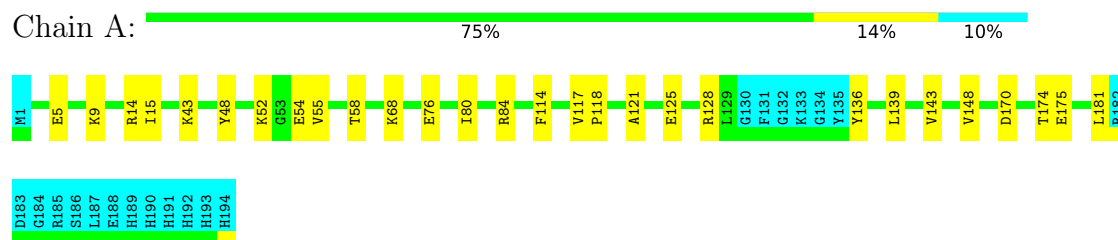
- Molecule 1: 5,10-methenyltetrahydrofolate synthetase

Chain A: 66% 21% 10%



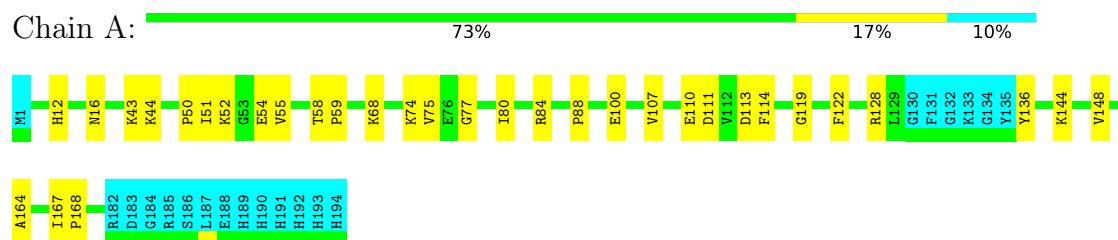
4.2.10 Score per residue for model 10

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase



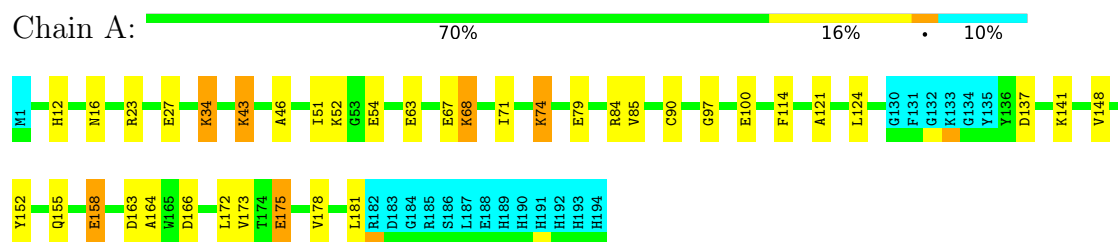
4.2.11 Score per residue for model 11

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase



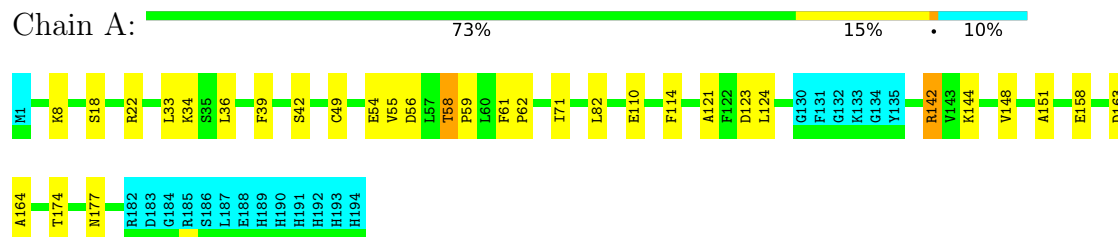
4.2.12 Score per residue for model 12

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase



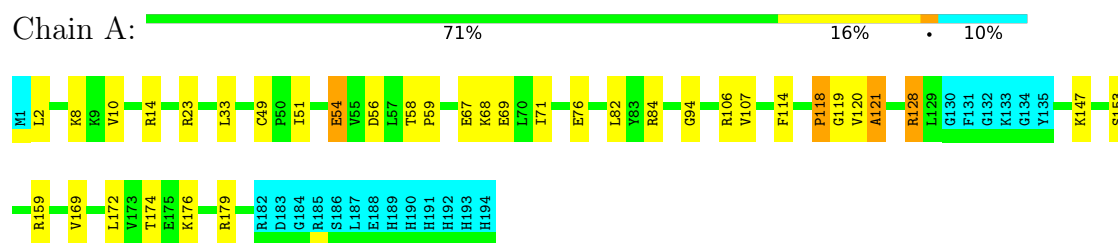
4.2.13 Score per residue for model 13 (medoid)

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase



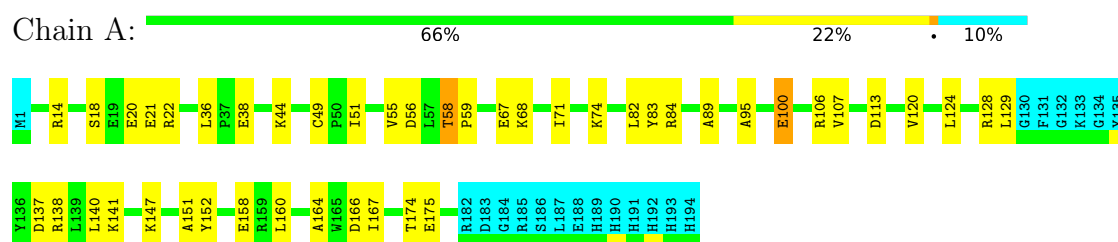
4.2.14 Score per residue for model 14

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase



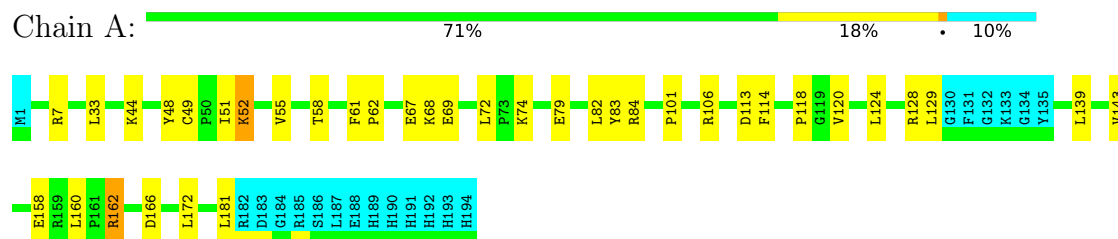
4.2.15 Score per residue for model 15

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase



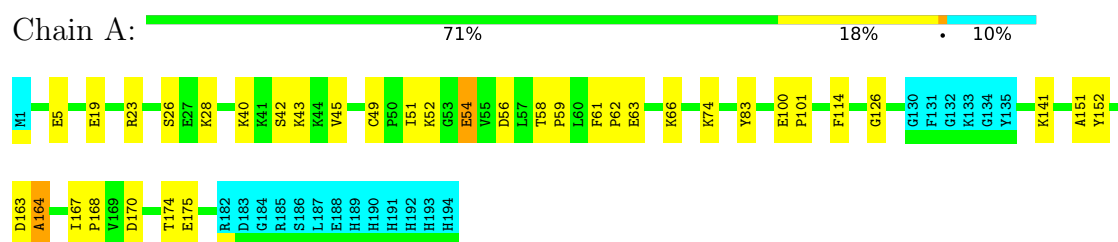
4.2.16 Score per residue for model 16

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase



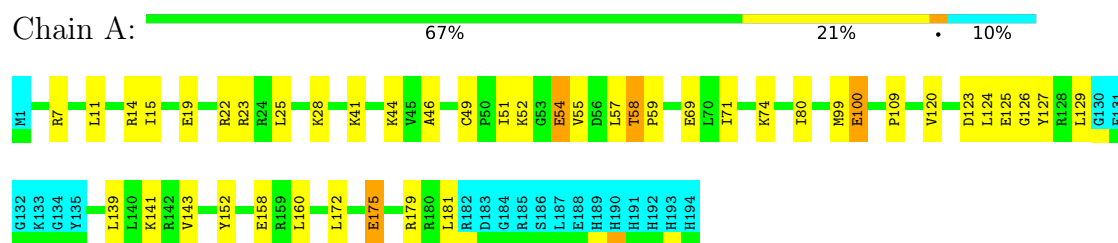
4.2.17 Score per residue for model 17

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase



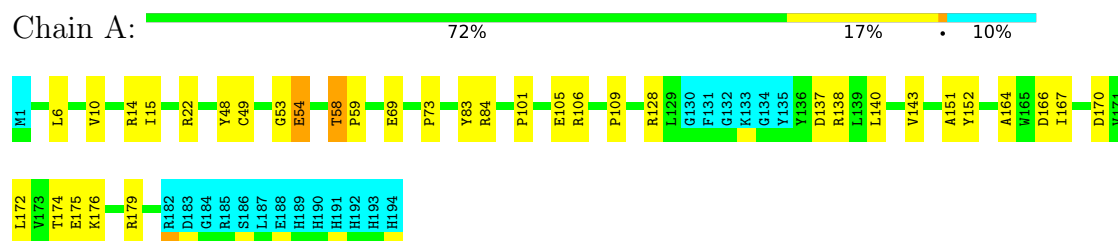
4.2.18 Score per residue for model 18

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase



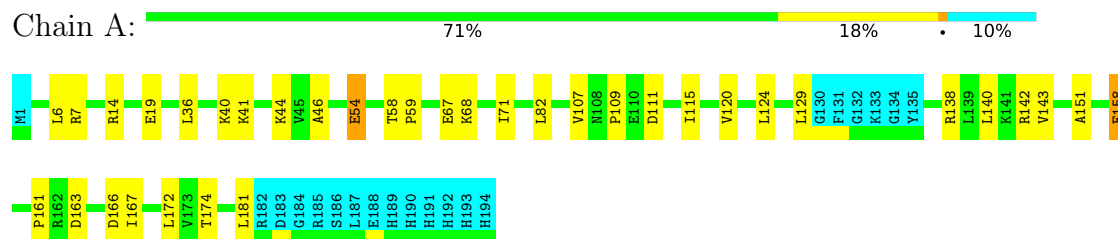
4.2.19 Score per residue for model 19

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase



4.2.20 Score per residue for model 20

- Molecule 1: 5,10-methenyltetrahydrofolate synthetase



5 Refinement protocol and experimental data overview

The models were refined using the following method: *MOLECULAR DYNAMICS, SIMULATED ANNEALING*.

Of the 29 calculated structures, 20 were deposited, based on the following criterion: *structures with acceptable covalent geometry, structures with favorable non-bond energy, structures with the least restraint violations, structures with the lowest energy*.

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

Software name	Classification	Version
NIH-XPLOR	refinement	2.0.4
CNS	refinement	1.1

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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

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	1406	1484	1482	16±4
All	All	28120	29680	29640	324

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 6.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:90:CYS:HB3	1:A:103:GLU:HB2	0.82	1.51	2	1
1:A:44:LYS:HB2	1:A:113:ASP:HB3	0.81	1.51	15	2
1:A:163:ASP:HB3	1:A:166:ASP:HB2	0.75	1.57	20	1
1:A:67:GLU:HG3	1:A:68:LYS:HD2	0.74	1.59	14	1
1:A:124:LEU:HG	1:A:158:GLU:HA	0.74	1.56	7	8
1:A:123:ASP:HB2	1:A:159:ARG:HA	0.68	1.64	9	2
1:A:72:LEU:HB2	1:A:101:PRO:HG3	0.67	1.67	16	2
1:A:74:LYS:HB2	1:A:81:SER:HB2	0.67	1.63	7	1
1:A:48:TYR:HB2	1:A:117:VAL:HG12	0.67	1.66	7	3
1:A:137:ASP:HA	1:A:140:LEU:HB2	0.67	1.66	15	1
1:A:67:GLU:HG3	1:A:68:LYS:HG3	0.66	1.68	16	2
1:A:172:LEU:HB3	1:A:179:ARG:HB2	0.66	1.67	3	4
1:A:50:PRO:HB3	1:A:54:GLU:HB2	0.66	1.68	11	1
1:A:147:LYS:HD3	1:A:167:ILE:HD11	0.66	1.68	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:175:GLU:HG3	1:A:176:LYS:HD2	0.66	1.67	19	1
1:A:14:ARG:HD3	1:A:54:GLU:HA	0.65	1.67	19	1
1:A:51:ILE:HG13	1:A:52:LYS:HD3	0.64	1.69	9	1
1:A:162:ARG:HD3	1:A:162:ARG:H	0.64	1.51	3	1
1:A:137:ASP:O	1:A:141:LYS:HG2	0.64	1.93	12	1
1:A:123:ASP:CB	1:A:159:ARG:HA	0.64	2.23	9	2
1:A:129:LEU:HB2	1:A:160:LEU:HD13	0.63	1.69	16	3
1:A:74:LYS:HG3	1:A:100:GLU:HB2	0.62	1.70	17	2
1:A:51:ILE:HG13	1:A:52:LYS:H	0.62	1.53	12	2
1:A:69:GLU:HG3	1:A:84:ARG:HB2	0.62	1.72	19	1
1:A:14:ARG:HD3	1:A:54:GLU:HG2	0.61	1.72	14	1
1:A:84:ARG:HB3	1:A:105:GLU:HG3	0.61	1.72	3	1
1:A:33:LEU:HD12	1:A:36:LEU:HD12	0.61	1.72	13	1
1:A:74:LYS:HD2	1:A:83:TYR:CE2	0.61	2.30	15	1
1:A:74:LYS:HD3	1:A:83:TYR:HE2	0.60	1.56	16	1
1:A:44:LYS:HA	1:A:69:GLU:HB2	0.59	1.74	18	1
1:A:167:ILE:HD12	1:A:168:PRO:HD2	0.59	1.73	11	3
1:A:140:LEU:HB2	1:A:167:ILE:HD13	0.58	1.74	20	2
1:A:15:ILE:HA	1:A:22:ARG:NH1	0.57	2.14	7	1
1:A:74:LYS:HD2	1:A:83:TYR:HE2	0.57	1.59	4	2
1:A:124:LEU:HA	1:A:179:ARG:HH22	0.57	1.57	7	1
1:A:129:LEU:HD13	1:A:160:LEU:HB3	0.57	1.76	3	2
1:A:172:LEU:HB3	1:A:179:ARG:HB3	0.57	1.76	14	2
1:A:58:THR:HB	1:A:59:PRO:HD3	0.57	1.76	9	3
1:A:50:PRO:HG3	1:A:57:LEU:HB2	0.56	1.75	9	1
1:A:45:VAL:HA	1:A:114:PHE:O	0.56	2.00	17	1
1:A:33:LEU:HD11	1:A:114:PHE:HZ	0.56	1.60	2	3
1:A:123:ASP:OD2	1:A:159:ARG:HA	0.56	1.98	3	1
1:A:174:THR:HB	1:A:175:GLU:OE1	0.55	2.01	6	1
1:A:36:LEU:HD21	1:A:178:VAL:HG21	0.55	1.76	9	2
1:A:42:SER:HB3	1:A:114:PHE:HB2	0.55	1.78	8	1
1:A:95:ALA:H	1:A:100:GLU:HG3	0.54	1.63	15	1
1:A:110:GLU:HG3	1:A:144:LYS:HD3	0.54	1.79	11	1
1:A:48:TYR:HB3	1:A:118:PRO:HD2	0.54	1.80	16	1
1:A:34:LYS:HE2	1:A:63:GLU:HG2	0.54	1.79	12	1
1:A:71:ILE:CG2	1:A:82:LEU:HB3	0.53	2.34	1	5
1:A:119:GLY:HA3	1:A:122:PHE:CE2	0.53	2.38	11	1
1:A:87:SER:HB2	1:A:90:CYS:SG	0.53	2.44	9	1
1:A:22:ARG:HH12	1:A:56:ASP:HB2	0.53	1.64	15	1
1:A:14:ARG:HD3	1:A:54:GLU:OE1	0.53	2.04	4	1
1:A:124:LEU:HA	1:A:179:ARG:NH2	0.53	2.19	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:147:LYS:HG2	1:A:170:ASP:OD2	0.52	2.04	4	1
1:A:122:PHE:CE2	1:A:128:ARG:HB3	0.52	2.39	4	1
1:A:109:PRO:HB3	1:A:143:VAL:HG22	0.52	1.80	19	1
1:A:110:GLU:HG3	1:A:144:LYS:HE3	0.52	1.81	13	1
1:A:125:GLU:O	1:A:181:LEU:HD11	0.52	2.05	10	2
1:A:46:ALA:HB2	1:A:71:ILE:HB	0.52	1.81	12	2
1:A:23:ARG:HH21	1:A:56:ASP:HB2	0.51	1.65	14	1
1:A:14:ARG:HD2	1:A:54:GLU:OE2	0.51	2.05	6	1
1:A:74:LYS:HD3	1:A:101:PRO:O	0.51	2.05	6	1
1:A:58:THR:HA	1:A:61:PHE:CD1	0.51	2.41	2	2
1:A:40:LYS:N	1:A:40:LYS:HD2	0.51	2.21	17	1
1:A:58:THR:N	1:A:59:PRO:HD2	0.51	2.20	19	8
1:A:42:SER:O	1:A:43:LYS:HD2	0.51	2.06	17	1
1:A:74:LYS:HG3	1:A:100:GLU:CB	0.51	2.36	18	1
1:A:75:VAL:HG12	1:A:77:GLY:H	0.51	1.66	11	1
1:A:74:LYS:HG2	1:A:100:GLU:HB2	0.51	1.83	12	1
1:A:151:ALA:O	1:A:174:THR:HA	0.51	2.06	17	5
1:A:7:ARG:HG2	1:A:120:VAL:HG11	0.51	1.83	16	1
1:A:11:LEU:HD12	1:A:14:ARG:HD3	0.50	1.84	1	1
1:A:43:LYS:HA	1:A:68:LYS:HD2	0.50	1.82	2	1
1:A:63:GLU:HA	1:A:66:LYS:NZ	0.50	2.21	17	1
1:A:171:VAL:HG22	1:A:180:ARG:HG2	0.50	1.83	5	1
1:A:82:LEU:HD11	1:A:139:LEU:HD11	0.50	1.82	16	1
1:A:18:SER:O	1:A:22:ARG:HG3	0.50	2.07	13	2
1:A:54:GLU:HG3	1:A:55:VAL:H	0.50	1.66	9	1
1:A:28:LYS:HD2	1:A:175:GLU:HB2	0.50	1.83	7	2
1:A:16:ASN:C	1:A:16:ASN:HD22	0.50	2.15	8	1
1:A:69:GLU:OE1	1:A:84:ARG:HD2	0.50	2.07	14	1
1:A:80:ILE:HD11	1:A:136:TYR:HD1	0.49	1.66	11	3
1:A:61:PHE:HB2	1:A:62:PRO:HD3	0.49	1.84	9	4
1:A:10:VAL:HG13	1:A:155:GLN:NE2	0.49	2.22	6	1
1:A:141:LYS:HG3	1:A:167:ILE:HB	0.49	1.84	17	1
1:A:47:LEU:HD23	1:A:57:LEU:HB3	0.49	1.82	9	1
1:A:74:LYS:HG3	1:A:100:GLU:OE1	0.49	2.08	15	1
1:A:137:ASP:O	1:A:141:LYS:HD3	0.49	2.07	15	1
1:A:94:GLY:HA3	1:A:100:GLU:OE2	0.49	2.08	6	1
1:A:54:GLU:OE1	1:A:54:GLU:HA	0.48	2.08	4	1
1:A:108:ASN:OD1	1:A:109:PRO:HD2	0.48	2.08	5	1
1:A:67:GLU:HB2	1:A:68:LYS:HD2	0.48	1.85	12	1
1:A:51:ILE:HG13	1:A:52:LYS:N	0.48	2.22	18	3
1:A:12:HIS:O	1:A:16:ASN:HB2	0.48	2.09	9	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:137:ASP:O	1:A:138:ARG:HB3	0.48	2.08	19	1
1:A:128:ARG:HB3	1:A:166:ASP:OD2	0.48	2.08	16	1
1:A:74:LYS:HG2	1:A:100:GLU:OE1	0.48	2.09	11	1
1:A:83:TYR:HB2	1:A:101:PRO:HG2	0.48	1.86	17	1
1:A:139:LEU:O	1:A:143:VAL:HG23	0.48	2.09	8	5
1:A:108:ASN:ND2	1:A:110:GLU:HB3	0.48	2.23	9	1
1:A:39:PHE:CZ	1:A:68:LYS:HE2	0.48	2.44	3	1
1:A:55:VAL:HG12	1:A:57:LEU:HG	0.48	1.85	18	1
1:A:20:GLU:CD	1:A:20:GLU:H	0.47	2.16	3	1
1:A:69:GLU:OE2	1:A:84:ARG:HD2	0.47	2.10	16	1
1:A:14:ARG:HH11	1:A:120:VAL:HA	0.47	1.68	18	1
1:A:43:LYS:O	1:A:68:LYS:HB3	0.47	2.09	11	2
1:A:84:ARG:HB2	1:A:107:VAL:CG2	0.47	2.39	15	2
1:A:14:ARG:NH1	1:A:120:VAL:HA	0.47	2.24	18	2
1:A:175:GLU:O	1:A:176:LYS:HG2	0.47	2.09	9	1
1:A:18:SER:HB2	1:A:21:GLU:HB3	0.47	1.84	15	1
1:A:80:ILE:HG13	1:A:139:LEU:HD13	0.47	1.86	18	1
1:A:114:PHE:CZ	1:A:148:VAL:HG21	0.47	2.44	10	3
1:A:6:LEU:O	1:A:10:VAL:HG23	0.47	2.10	19	1
1:A:162:ARG:HD2	1:A:162:ARG:C	0.47	2.34	16	1
1:A:63:GLU:HA	1:A:66:LYS:HZ3	0.46	1.71	17	1
1:A:74:LYS:HD3	1:A:83:TYR:CE2	0.46	2.43	16	1
1:A:43:LYS:O	1:A:68:LYS:HB2	0.46	2.11	12	1
1:A:51:ILE:HG13	1:A:52:LYS:HG2	0.46	1.86	11	2
1:A:74:LYS:HE2	1:A:100:GLU:HB3	0.46	1.87	8	1
1:A:92:GLY:O	1:A:99:MET:HA	0.46	2.11	2	1
1:A:166:ASP:O	1:A:168:PRO:HD3	0.46	2.11	4	1
1:A:52:LYS:N	1:A:52:LYS:HD3	0.46	2.25	16	1
1:A:48:TYR:HA	1:A:73:PRO:HG3	0.46	1.88	19	1
1:A:48:TYR:HD2	1:A:118:PRO:HD2	0.46	1.70	10	1
1:A:18:SER:HB2	1:A:21:GLU:CB	0.46	2.41	15	1
1:A:14:ARG:NH2	1:A:151:ALA:HA	0.45	2.27	2	1
1:A:61:PHE:N	1:A:62:PRO:HD2	0.45	2.25	17	3
1:A:126:GLY:O	1:A:168:PRO:HA	0.45	2.11	3	2
1:A:25:LEU:HB3	1:A:152:TYR:CE1	0.45	2.46	18	1
1:A:14:ARG:HB3	1:A:54:GLU:HB3	0.45	1.88	6	1
1:A:173:VAL:HG22	1:A:178:VAL:HG12	0.45	1.88	12	1
1:A:14:ARG:HH21	1:A:54:GLU:HG3	0.45	1.72	1	1
1:A:69:GLU:HG2	1:A:84:ARG:HD2	0.45	1.88	1	1
1:A:65:LEU:HD21	1:A:88:PRO:HA	0.45	1.89	9	1
1:A:10:VAL:HB	1:A:120:VAL:HG13	0.45	1.89	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:GLU:O	1:A:23:ARG:HG2	0.44	2.12	4	2
1:A:89:ALA:O	1:A:90:CYS:SG	0.44	2.75	5	1
1:A:85:VAL:HG13	1:A:90:CYS:SG	0.44	2.52	12	1
1:A:22:ARG:HH22	1:A:53:GLY:C	0.44	2.20	8	1
1:A:19:GLU:O	1:A:23:ARG:HB2	0.44	2.12	18	1
1:A:109:PRO:HB3	1:A:143:VAL:HA	0.44	1.88	18	1
1:A:23:ARG:O	1:A:27:GLU:HB2	0.44	2.11	12	1
1:A:152:TYR:HD1	1:A:175:GLU:HB3	0.44	1.72	15	1
1:A:20:GLU:O	1:A:24:ARG:HG2	0.44	2.13	6	1
1:A:84:ARG:HG3	1:A:107:VAL:CG2	0.44	2.43	11	1
1:A:140:LEU:HB3	1:A:167:ILE:HG21	0.44	1.87	8	2
1:A:64:VAL:HA	1:A:68:LYS:HE2	0.44	1.90	9	1
1:A:121:ALA:HA	1:A:155:GLN:O	0.44	2.11	12	1
1:A:172:LEU:HB2	1:A:181:LEU:HD21	0.44	1.90	20	1
1:A:90:CYS:CB	1:A:103:GLU:HB2	0.44	2.36	2	1
1:A:50:PRO:HG3	1:A:57:LEU:H	0.44	1.71	7	1
1:A:6:LEU:HG	1:A:129:LEU:HD21	0.44	1.89	20	1
1:A:153:SER:OG	1:A:176:LYS:HG3	0.44	2.13	14	1
1:A:163:ASP:CG	1:A:164:ALA:N	0.44	2.75	17	1
1:A:3:LYS:HD2	1:A:129:LEU:HG	0.43	1.88	3	1
1:A:84:ARG:HD3	1:A:105:GLU:OE1	0.43	2.13	6	1
1:A:58:THR:OG1	1:A:59:PRO:HD3	0.43	2.13	11	1
1:A:147:LYS:HE2	1:A:167:ILE:HD11	0.43	1.90	1	1
1:A:154:PHE:HB2	1:A:155:GLN:OE1	0.43	2.13	1	1
1:A:65:LEU:HD12	1:A:86:HIS:HA	0.43	1.90	5	1
1:A:44:LYS:HB2	1:A:113:ASP:H	0.43	1.73	16	2
1:A:11:LEU:O	1:A:15:ILE:HG12	0.43	2.14	18	1
1:A:179:ARG:HA	1:A:179:ARG:NE	0.43	2.28	1	1
1:A:69:GLU:OE2	1:A:84:ARG:HD3	0.43	2.14	9	1
1:A:51:ILE:HD12	1:A:51:ILE:O	0.43	2.12	15	1
1:A:74:LYS:HD2	1:A:101:PRO:O	0.43	2.13	5	1
1:A:84:ARG:HG3	1:A:84:ARG:O	0.43	2.13	7	1
1:A:44:LYS:HG3	1:A:111:ASP:O	0.43	2.13	20	2
1:A:22:ARG:HD2	1:A:54:GLU:HB2	0.43	1.90	18	1
1:A:128:ARG:HD3	1:A:166:ASP:OD1	0.43	2.13	15	1
1:A:84:ARG:HB3	1:A:105:GLU:HG2	0.43	1.90	4	1
1:A:15:ILE:CG2	1:A:52:LYS:HB3	0.43	2.44	10	1
1:A:138:ARG:O	1:A:142:ARG:HD3	0.43	2.13	20	1
1:A:179:ARG:HA	1:A:179:ARG:HE	0.43	1.74	1	1
1:A:141:LYS:HA	1:A:167:ILE:HG21	0.43	1.91	17	1
1:A:141:LYS:HD3	1:A:167:ILE:HG13	0.43	1.89	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:172:LEU:HB2	1:A:181:LEU:HD11	0.43	1.91	16	2
1:A:34:LYS:HD3	1:A:39:PHE:HE2	0.43	1.74	13	1
1:A:44:LYS:HD3	1:A:111:ASP:O	0.43	2.13	7	1
1:A:54:GLU:HB2	1:A:152:TYR:CE2	0.43	2.49	17	1
1:A:54:GLU:HG3	1:A:118:PRO:HB2	0.42	1.90	4	1
1:A:129:LEU:HD13	1:A:160:LEU:HD13	0.42	1.90	4	1
1:A:152:TYR:O	1:A:156:VAL:HG23	0.42	2.15	4	1
1:A:14:ARG:HG3	1:A:54:GLU:OE2	0.42	2.14	20	1
1:A:14:ARG:CZ	1:A:120:VAL:HA	0.42	2.44	5	1
1:A:121:ALA:O	1:A:128:ARG:HA	0.42	2.14	14	1
1:A:26:SER:HB3	1:A:56:ASP:HB2	0.42	1.90	17	1
1:A:14:ARG:NH1	1:A:54:GLU:HG2	0.42	2.30	10	1
1:A:8:LYS:NZ	1:A:8:LYS:HB2	0.42	2.29	14	1
1:A:30:ILE:O	1:A:34:LYS:HB2	0.42	2.15	4	1
1:A:39:PHE:HA	1:A:42:SER:OG	0.42	2.14	13	1
1:A:82:LEU:O	1:A:106:ARG:HA	0.42	2.14	15	2
1:A:40:LYS:HA	1:A:68:LYS:NZ	0.42	2.29	20	1
1:A:14:ARG:HB2	1:A:155:GLN:OE1	0.42	2.15	5	1
1:A:10:VAL:HG11	1:A:121:ALA:HB2	0.42	1.90	8	1
1:A:22:ARG:HD2	1:A:54:GLU:O	0.42	2.14	18	1
1:A:152:TYR:HB3	1:A:175:GLU:OE2	0.42	2.14	19	1
1:A:46:ALA:O	1:A:115:ILE:HA	0.42	2.14	20	1
1:A:15:ILE:HG22	1:A:53:GLY:HA3	0.42	1.92	4	1
1:A:148:VAL:HA	1:A:171:VAL:O	0.42	2.15	9	1
1:A:123:ASP:HA	1:A:157:PHE:O	0.42	2.15	5	1
1:A:5:GLU:HG3	1:A:9:LYS:HE2	0.42	1.92	10	1
1:A:144:LYS:NZ	1:A:144:LYS:HB3	0.42	2.30	8	1
1:A:46:ALA:HA	1:A:71:ILE:O	0.41	2.15	12	3
1:A:123:ASP:HB2	1:A:127:TYR:HB2	0.41	1.91	18	1
1:A:152:TYR:HD1	1:A:175:GLU:HG3	0.41	1.75	12	1
1:A:15:ILE:HA	1:A:22:ARG:HH12	0.41	1.75	19	1
1:A:83:TYR:HB2	1:A:101:PRO:HB2	0.41	1.91	19	1
1:A:2:LEU:HB2	1:A:5:GLU:HB2	0.41	1.91	7	1
1:A:22:ARG:HH12	1:A:56:ASP:CG	0.41	2.23	9	1
1:A:125:GLU:HB2	1:A:159:ARG:NH1	0.41	2.31	8	1
1:A:71:ILE:HA	1:A:83:TYR:O	0.41	2.16	15	1
1:A:28:LYS:HE2	1:A:175:GLU:HB2	0.41	1.91	18	1
1:A:39:PHE:O	1:A:68:LYS:HE3	0.41	2.16	3	1
1:A:163:ASP:CG	1:A:164:ALA:H	0.41	2.24	12	1
1:A:142:ARG:HE	1:A:142:ARG:HA	0.41	1.76	13	1
1:A:147:LYS:O	1:A:169:VAL:HB	0.41	2.16	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:22:ARG:NH1	1:A:56:ASP:HB2	0.41	2.30	15	1
1:A:117:VAL:O	1:A:149:GLY:HA2	0.41	2.15	1	2
1:A:147:LYS:NZ	1:A:147:LYS:HB2	0.41	2.31	5	1
1:A:107:VAL:HG13	1:A:111:ASP:HB3	0.41	1.91	20	1
1:A:144:LYS:HD3	1:A:144:LYS:O	0.41	2.16	2	1
1:A:14:ARG:HD3	1:A:54:GLU:HB3	0.41	1.93	7	1
1:A:55:VAL:HG22	1:A:152:TYR:CZ	0.41	2.51	15	1
1:A:10:VAL:O	1:A:14:ARG:HG3	0.41	2.16	3	1
1:A:58:THR:N	1:A:59:PRO:CD	0.40	2.84	15	3
1:A:114:PHE:CE2	1:A:148:VAL:HG21	0.40	2.51	11	3
1:A:85:VAL:HG21	1:A:101:PRO:HB3	0.40	1.92	7	1
1:A:67:GLU:OE2	1:A:68:LYS:HG3	0.40	2.16	15	1
1:A:141:LYS:HE2	1:A:141:LYS:HA	0.40	1.92	5	1
1:A:118:PRO:HB2	1:A:119:GLY:H	0.40	1.59	14	1
1:A:53:GLY:O	1:A:54:GLU:HB2	0.40	2.17	4	1
1:A:51:ILE:HD12	1:A:52:LYS:N	0.40	2.32	6	1
1:A:109:PRO:CB	1:A:143:VAL:HA	0.40	2.46	20	1

6.3 Torsion angles

6.3.1 Protein backbone

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	174/194 (90%)	154±3 (88±2%)	17±3 (10±2%)	3±1 (2±1%)	9	52
All	All	3480/3880 (90%)	3072 (88%)	345 (10%)	63 (2%)	9	52

All 21 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	49	CYS	14
1	A	55	VAL	6
1	A	121	ALA	6
1	A	164	ALA	6
1	A	54	GLU	5

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Mol	Chain	Res	Type	Models (Total)
1	A	97	GLY	4
1	A	48	TYR	2
1	A	77	GLY	2
1	A	163	ASP	2
1	A	53	GLY	2
1	A	94	GLY	2
1	A	2	LEU	2
1	A	118	PRO	2
1	A	102	VAL	1
1	A	91	LEU	1
1	A	176	LYS	1
1	A	88	PRO	1
1	A	56	ASP	1
1	A	89	ALA	1
1	A	126	GLY	1
1	A	161	PRO	1

6.3.2 Protein sidechains ⓘ

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	157/173 (91%)	152±2 (97±2%)	5±2 (3±2%)	37	85
All	All	3140/3460 (91%)	3045 (97%)	95 (3%)	37	85

All 51 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	58	THR	11
1	A	175	GLU	5
1	A	128	ARG	5
1	A	54	GLU	5
1	A	174	THR	4
1	A	43	LYS	2
1	A	177	ASN	2
1	A	16	ASN	2
1	A	105	GLU	2

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Mol	Chain	Res	Type	Models (Total)
1	A	123	ASP	2
1	A	141	LYS	2
1	A	38	GLU	2
1	A	144	LYS	2
1	A	52	LYS	2
1	A	74	LYS	2
1	A	76	GLU	2
1	A	84	ARG	2
1	A	79	GLU	2
1	A	158	GLU	2
1	A	51	ILE	2
1	A	106	ARG	2
1	A	36	LEU	2
1	A	100	GLU	2
1	A	41	LYS	2
1	A	9	LYS	1
1	A	48	TYR	1
1	A	86	HIS	1
1	A	23	ARG	1
1	A	78	ASN	1
1	A	5	GLU	1
1	A	138	ARG	1
1	A	7	ARG	1
1	A	67	GLU	1
1	A	147	LYS	1
1	A	165	TRP	1
1	A	11	LEU	1
1	A	13	LYS	1
1	A	27	GLU	1
1	A	44	LYS	1
1	A	146	LEU	1
1	A	87	SER	1
1	A	34	LYS	1
1	A	68	LYS	1
1	A	166	ASP	1
1	A	8	LYS	1
1	A	142	ARG	1
1	A	159	ARG	1
1	A	20	GLU	1
1	A	162	ARG	1
1	A	99	MET	1
1	A	19	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 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 [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided