Full wwPDB NMR Structure Validation Report (i)

Feb 23, 2022 – 02:44 PM EST

PDB ID	:	1XN7
Title	:	Solution Structure of E.Coli Protein yhgG: The Northeast Structural Genomics Consortium Target ET95
Authors	:	Shen, Y.; Acton, T.; Atreya, H.S.; Ma, L.; Liu, G.; Xiao, R.; Montelione, G.T.; Szyperski, T.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2004-10-04

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

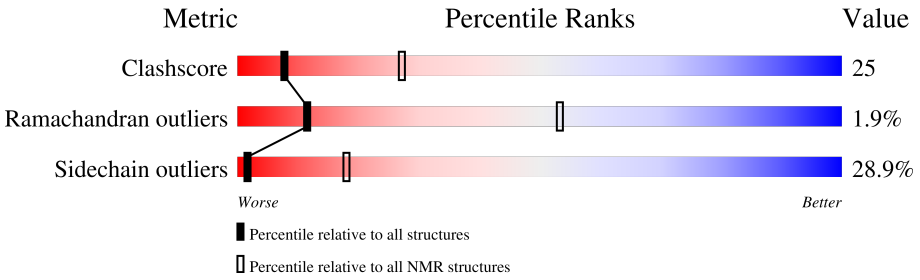
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.26
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

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	78	29% 36% 5% 29%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 1 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:4-A:51, A:72-A:78 (55)	0.18	1

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 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1102 atoms, of which 504 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Hypothetical protein yhgG.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	78	1102	368	504	110	111	9	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: Hypothetical protein yhgG

Chain A: 29% 36% 5% 29%

M1 A2 S3 L4 I5 Q6 V7 L10 L11 A12 L13 R14 G15 R16 M17 E18 Q21 I22 S23 Q24 T25 L26 N27 T28 P29 Q30 P31 M32 I33 M36 L37 Q38 R48 I49 Q50 E51 E52 P53 D54 G55 C56 L57 S58 G59 S60 C61 K62 S63 C64 P65 E66 G67 K68 A69 C70 L71

R72 E73 W74 W75 A76 L77 R78

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 (medoid)

• Molecule 1: Hypothetical protein yhgG

Chain A: 28% 35% 8% 29%

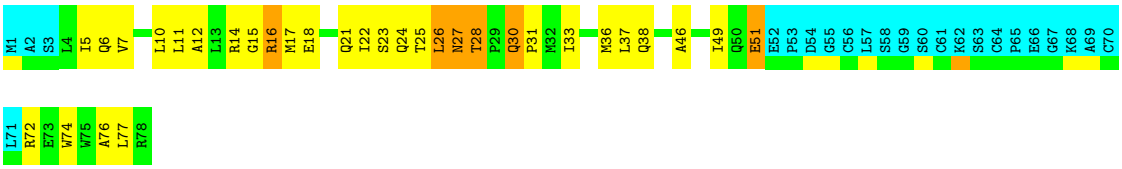
M1 A2 S3 L4 V7 L10 L11 A12 L13 R14 G15 R16 M17 E18 A19 A20 Q21 I22 S23 Q24 T25 L26 N27 T28 P29 Q30 P31 M32 I33 M36 L37 Q38 A46 V47 R48 I49 Q50 E51 E52 P53 D54 G55 C56 L57 S58 G59 S60 C61 K62 S63 C64 P65 E66 G67 K68 A69

C70 L71 R72 E73 W74 W75 A76 L77 R78

4.2.2 Score per residue for model 2

• Molecule 1: Hypothetical protein yhgG

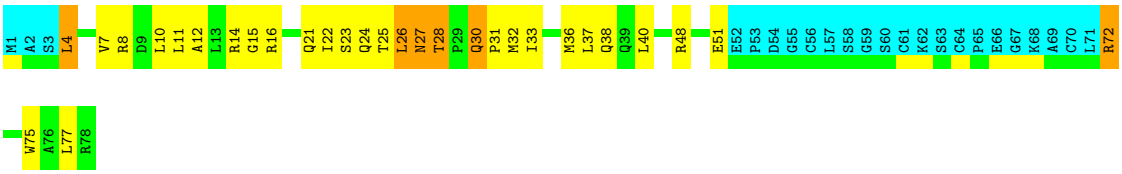
Chain A: 29% 33% 8% 29%



4.2.3 Score per residue for model 3

- Molecule 1: Hypothetical protein yhgG

Chain A: 32% 31% 8% 29%



4.2.4 Score per residue for model 4

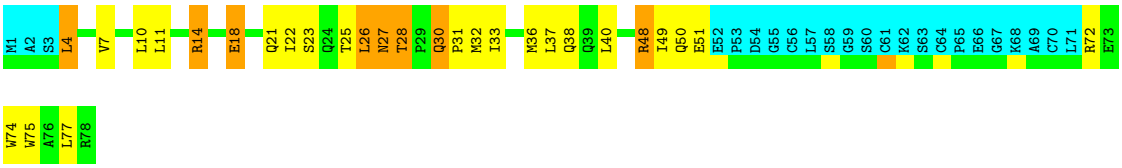
- Molecule 1: Hypothetical protein yhgG

Chain A: 32% 31% 8% 29%

4.2.5 Score per residue for model 5

- Molecule 1: Hypothetical protein yhgG

Chain A: 33% 27% 10% 29%



4.2.6 Score per residue for model 6

- Molecule 1: Hypothetical protein yhgG

Chain A: 29% 36% 5% 29%

M1 A2 S3 L4 I5 Q6 V7 L10 L11 A12 L13 R14 G15 R16 M17 E18 A19 A20 Q21 I22 S23 Q24 T25 L26 N27 T28 P29 Q30 P31 M32 M36 L37 Q38 Q39 L40 E41 K45 R48 I49 Q50 E51 E52 P53 D54 G55 C56 L57 S58 G59 S60 C61 K62 S63 C64 P65 E66

G67 K68 A69 C70 L71 R72 E73 W74 W75 A76 L77 R78

4.2.7 Score per residue for model 7

- Molecule 1: Hypothetical protein yhgG

Chain A: 35% 28% 8% 29%

M1 A2 S3 L4 I5 Q6 V7 L10 L11 R14 G15 R16 M17 E18 Q21 I22 S23 Q24 T25 L26 N27 T28 P29 Q30 P31 M32 I33 L37 Q38 Q39 L40 R48 I49 Q50 E51 E52 P53 D54 G55 C56 L57 S58 G59 S60 C61 K62 S63 C64 P65 E66 G67 K68 A69 C70 L71

R72 E73 W74 R78

4.2.8 Score per residue for model 8

- Molecule 1: Hypothetical protein yhgG

Chain A: 35% 29% 6% 29%

M1 A2 S3 L4 I5 Q6 V7 L10 L11 A12 L13 R14 G15 R16 M17 E18 I22 S23 Q24 T25 L26 N27 T28 P29 Q30 P31 M36 L37 Q38 R48 I49 E52 P53 D54 G55 C56 L57 S58 G59 S60 C61 K62 S63 C64 P65 E66 G67 K68 A69 C70 L71 R72 E73 W74 W75

A76 L77 R78

4.2.9 Score per residue for model 9

- Molecule 1: Hypothetical protein yhgG

Chain A: 33% 28% 9% 29%

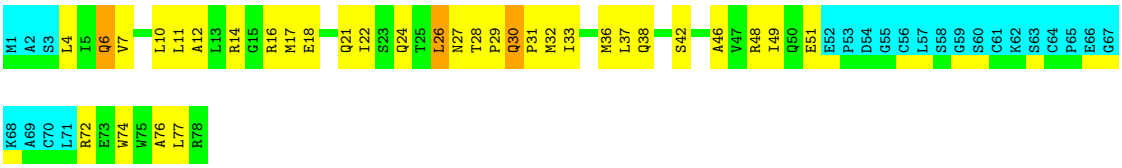
M1 A2 S3 L4 I5 Q6 V7 R8 D9 L10 L11 A12 L13 R14 G15 R16 Q21 I22 S23 Q24 T25 L26 N27 T28 P29 Q30 P31 M32 I33 M36 L37 Q38 I49 Q50 E51 E52 P53 D54 G55 C56 L57 S58 G59 S60 C61 K62 S63 C64 P65 E66 G67 K68 A69 C70 L71 R72 E73

W74 L77 R78

4.2.10 Score per residue for model 10

- Molecule 1: Hypothetical protein yhgG

Chain A: 28% 38% • 29%



4.2.11 Score per residue for model 11

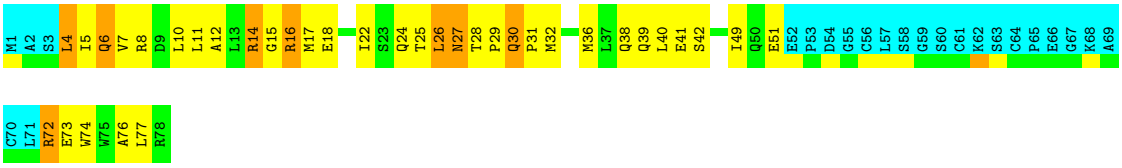
- Molecule 1: Hypothetical protein yhgG

Chain A: 27% 32% 12% 29%

4.2.12 Score per residue for model 12

- Molecule 1: Hypothetical protein yhgG

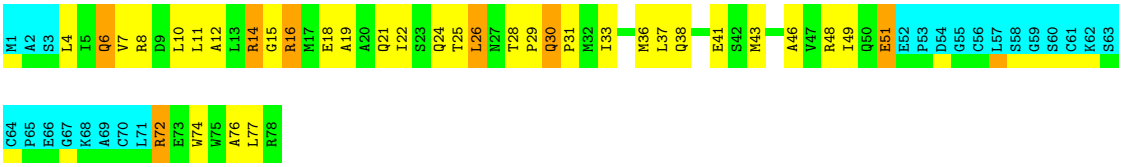
Chain A: 24% 36% 10% 29%



4.2.13 Score per residue for model 13

- Molecule 1: Hypothetical protein yhgG

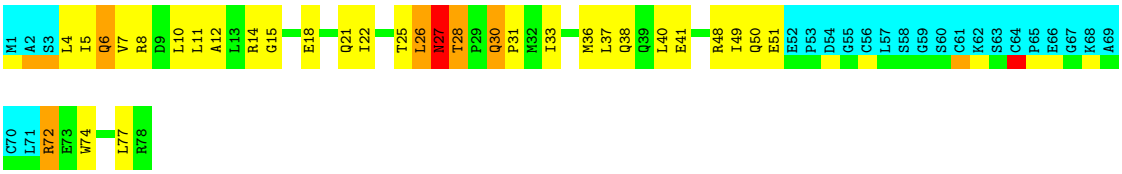
Chain A: 26% 36% 9% 29%



4.2.14 Score per residue for model 14

- Molecule 1: Hypothetical protein yhgG

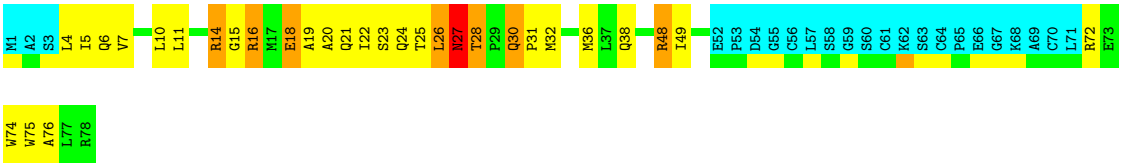
Chain A: 29% 33% 6% • 29%



4.2.15 Score per residue for model 15

- Molecule 1: Hypothetical protein yhgG

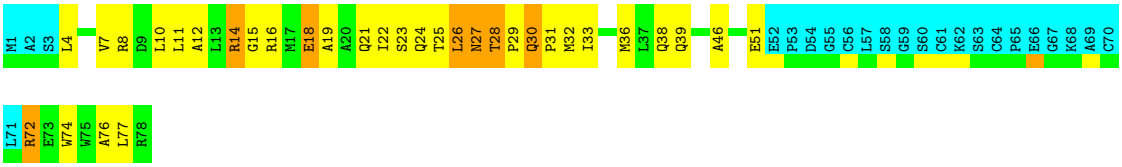
Chain A: 31% 29% 9% • 29%



4.2.16 Score per residue for model 16

- Molecule 1: Hypothetical protein yhgG

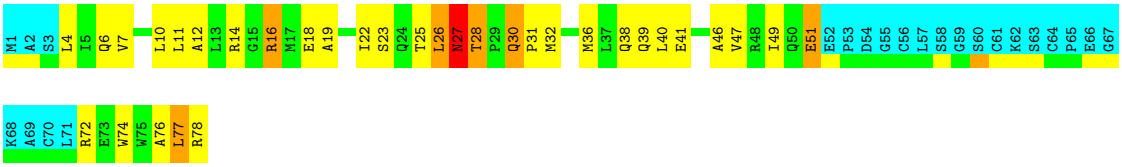
Chain A: 28% 33% 9% 29%



4.2.17 Score per residue for model 17

- Molecule 1: Hypothetical protein yhgG

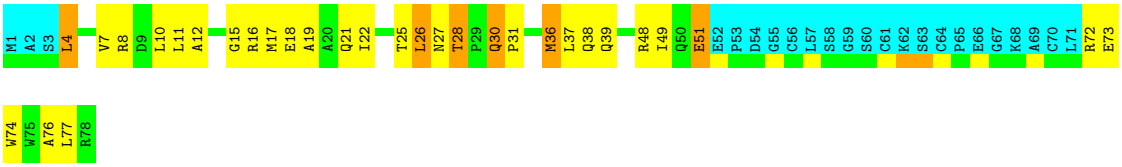
Chain A: 28% 33% 8% • 29%



4.2.18 Score per residue for model 18

- Molecule 1: Hypothetical protein yhgG

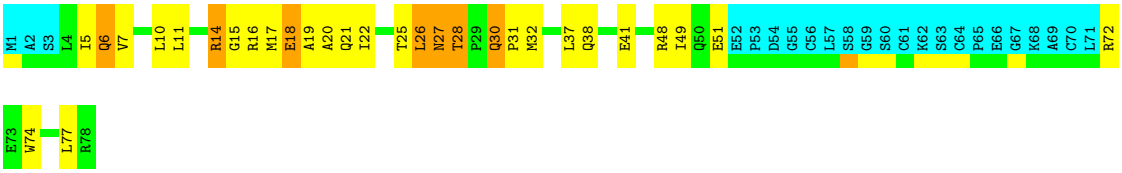
Chain A: 31% 32% 8% 29%



4.2.19 Score per residue for model 19

- Molecule 1: Hypothetical protein yhgG

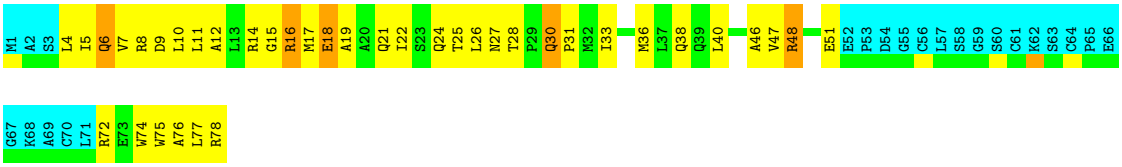
Chain A: 32% 29% 9% 29%



4.2.20 Score per residue for model 20

- Molecule 1: Hypothetical protein yhgG

Chain A: 22% 42% 6% 29%



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function,structures with the least restraint violations*.

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

Software name	Classification	Version
DYANA	structure solution	1.5
DYANA	refinement	1.5

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.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	446	388	467	23±4
All	All	8920	7760	9340	464

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 25.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:VAL:HG23	1:A:22:ILE:HG21	1.04	1.25	16	9
1:A:7:VAL:HG22	1:A:22:ILE:CG2	0.98	1.88	12	8
1:A:7:VAL:HG13	1:A:22:ILE:HG21	0.97	1.35	2	9
1:A:4:LEU:CD1	1:A:40:LEU:HD11	0.85	2.02	20	2
1:A:11:LEU:HD21	1:A:22:ILE:HD11	0.84	1.47	17	5
1:A:7:VAL:HG22	1:A:22:ILE:HG22	0.81	1.51	12	4
1:A:10:LEU:HG	1:A:25:THR:HG21	0.80	1.54	2	10
1:A:18:GLU:OE1	1:A:20:ALA:HB3	0.78	1.78	19	2
1:A:6:GLN:NE2	1:A:26:LEU:HD22	0.76	1.95	19	9
1:A:19:ALA:HA	1:A:22:ILE:HD12	0.75	1.59	13	8
1:A:12:ALA:HB2	1:A:77:LEU:CD1	0.74	2.12	4	14
1:A:6:GLN:O	1:A:10:LEU:HD23	0.69	1.87	15	3
1:A:4:LEU:HD21	1:A:40:LEU:HD21	0.68	1.65	17	1
1:A:7:VAL:CG2	1:A:22:ILE:HG21	0.68	2.14	16	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:4:LEU:HD12	1:A:40:LEU:HD21	0.67	1.67	20	1
1:A:10:LEU:CG	1:A:25:THR:HG21	0.67	2.18	14	8
1:A:4:LEU:CD2	1:A:40:LEU:HD11	0.65	2.21	11	5
1:A:12:ALA:HB2	1:A:77:LEU:HD12	0.65	1.69	13	4
1:A:7:VAL:CG1	1:A:22:ILE:HG21	0.64	2.22	17	6
1:A:18:GLU:CD	1:A:20:ALA:HB3	0.63	2.13	19	2
1:A:7:VAL:HG22	1:A:22:ILE:HG23	0.62	1.70	11	3
1:A:8:ARG:O	1:A:77:LEU:HD11	0.62	1.94	14	5
1:A:49:ILE:HD11	1:A:76:ALA:HB3	0.60	1.73	17	3
1:A:7:VAL:CG2	1:A:22:ILE:CG2	0.60	2.79	3	2
1:A:51:GLU:CD	1:A:74:TRP:CZ2	0.60	2.75	18	6
1:A:4:LEU:HD21	1:A:36:MET:HB3	0.59	1.72	1	1
1:A:12:ALA:HB2	1:A:77:LEU:HD11	0.59	1.74	12	6
1:A:11:LEU:CD2	1:A:22:ILE:HD11	0.59	2.23	17	2
1:A:4:LEU:CD1	1:A:40:LEU:HD21	0.59	2.26	20	1
1:A:7:VAL:HG21	1:A:33:ILE:HD12	0.59	1.73	7	5
1:A:4:LEU:CD2	1:A:40:LEU:HD21	0.59	2.27	17	1
1:A:46:ALA:HB1	1:A:76:ALA:O	0.59	1.97	1	6
1:A:33:ILE:HG22	1:A:37:LEU:CD1	0.58	2.28	7	5
1:A:11:LEU:HD11	1:A:37:LEU:HD21	0.58	1.75	18	4
1:A:28:THR:HG23	1:A:29:PRO:HD2	0.58	1.74	13	3
1:A:4:LEU:HD23	1:A:7:VAL:HG11	0.58	1.75	1	1
1:A:9:ASP:OD1	1:A:13:LEU:HD22	0.58	1.99	9	1
1:A:7:VAL:HG23	1:A:22:ILE:CG2	0.57	2.16	16	1
1:A:6:GLN:NE2	1:A:26:LEU:CD2	0.57	2.67	20	1
1:A:37:LEU:HD13	1:A:75:TRP:CG	0.56	2.35	5	1
1:A:16:ARG:CB	1:A:76:ALA:HB2	0.56	2.31	12	4
1:A:26:LEU:HD11	1:A:33:ILE:HD11	0.55	1.79	1	3
1:A:18:GLU:OE2	1:A:20:ALA:HB3	0.55	2.01	11	1
1:A:16:ARG:HB3	1:A:76:ALA:HB2	0.55	1.77	13	5
1:A:4:LEU:O	1:A:7:VAL:HG12	0.55	2.00	1	1
1:A:14:ARG:N	1:A:14:ARG:CD	0.55	2.70	12	12
1:A:14:ARG:CD	1:A:14:ARG:N	0.54	2.69	6	3
1:A:4:LEU:HD23	1:A:7:VAL:CG1	0.54	2.31	1	1
1:A:19:ALA:HB2	1:A:37:LEU:CD1	0.53	2.33	6	2
1:A:48:ARG:HH21	1:A:73:GLU:CD	0.53	2.06	18	1
1:A:4:LEU:HD22	1:A:36:MET:SD	0.53	2.43	9	1
1:A:26:LEU:HD23	1:A:26:LEU:N	0.53	2.19	17	5
1:A:10:LEU:CD2	1:A:25:THR:HG21	0.52	2.34	14	1
1:A:30:GLN:N	1:A:31:PRO:CD	0.52	2.72	8	20
1:A:4:LEU:HD21	1:A:40:LEU:HD11	0.52	1.80	7	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:VAL:HG13	1:A:22:ILE:CG2	0.51	2.36	17	5
1:A:11:LEU:HD22	1:A:76:ALA:HA	0.51	1.83	2	3
1:A:33:ILE:HG22	1:A:37:LEU:HD12	0.51	1.83	14	1
1:A:10:LEU:HD11	1:A:25:THR:HG21	0.50	1.83	5	2
1:A:48:ARG:HD2	1:A:75:TRP:CH2	0.50	2.42	15	2
1:A:25:THR:HB	1:A:26:LEU:HD23	0.50	1.84	7	3
1:A:4:LEU:HD12	1:A:40:LEU:HD11	0.50	1.82	14	1
1:A:11:LEU:O	1:A:15:GLY:CA	0.50	2.59	20	16
1:A:4:LEU:HD13	1:A:7:VAL:CG1	0.50	2.37	9	1
1:A:48:ARG:CD	1:A:75:TRP:CH2	0.50	2.94	20	2
1:A:26:LEU:CD1	1:A:33:ILE:HD11	0.49	2.37	20	1
1:A:7:VAL:HG22	1:A:22:ILE:HG21	0.49	1.78	11	2
1:A:18:GLU:HB3	1:A:74:TRP:CD1	0.48	2.44	11	4
1:A:18:GLU:O	1:A:22:ILE:HD12	0.48	2.08	10	1
1:A:18:GLU:HB2	1:A:74:TRP:CD1	0.48	2.43	5	6
1:A:8:ARG:HH21	1:A:40:LEU:CD2	0.48	2.22	3	1
1:A:11:LEU:HD21	1:A:22:ILE:CD1	0.48	2.38	10	1
1:A:6:GLN:HB3	1:A:26:LEU:HD13	0.47	1.87	6	1
1:A:4:LEU:O	1:A:7:VAL:CG1	0.47	2.62	1	1
1:A:8:ARG:HH21	1:A:40:LEU:HD22	0.47	1.68	3	1
1:A:37:LEU:HD13	1:A:75:TRP:CD1	0.47	2.45	5	6
1:A:47:VAL:HG11	1:A:78:ARG:HD2	0.47	1.86	11	2
1:A:23:SER:O	1:A:28:THR:N	0.46	2.48	1	12
1:A:26:LEU:O	1:A:28:THR:N	0.46	2.49	17	18
1:A:18:GLU:HG3	1:A:20:ALA:HB3	0.46	1.86	1	1
1:A:49:ILE:O	1:A:74:TRP:N	0.46	2.49	5	16
1:A:10:LEU:O	1:A:14:ARG:N	0.46	2.48	9	18
1:A:4:LEU:HD23	1:A:40:LEU:HD11	0.46	1.87	6	1
1:A:26:LEU:HD12	1:A:33:ILE:HD11	0.46	1.87	20	1
1:A:9:ASP:OD1	1:A:13:LEU:HD13	0.46	2.10	9	1
1:A:46:ALA:O	1:A:47:VAL:CG1	0.46	2.64	17	1
1:A:4:LEU:CD2	1:A:36:MET:SD	0.45	3.05	18	1
1:A:26:LEU:C	1:A:28:THR:N	0.45	2.70	4	18
1:A:18:GLU:OE2	1:A:19:ALA:N	0.45	2.50	13	1
1:A:25:THR:HG22	1:A:26:LEU:HD23	0.45	1.87	3	2
1:A:28:THR:HG21	1:A:33:ILE:HG12	0.45	1.87	16	1
1:A:22:ILE:O	1:A:26:LEU:CD2	0.45	2.65	8	2
1:A:18:GLU:OE1	1:A:21:GLN:N	0.45	2.49	11	1
1:A:11:LEU:C	1:A:77:LEU:CD1	0.45	2.86	19	1
1:A:6:GLN:NE2	1:A:26:LEU:HD23	0.45	2.26	20	1
1:A:51:GLU:HG3	1:A:74:TRP:CE2	0.44	2.47	17	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:49:ILE:HG13	1:A:76:ALA:HB2	0.44	1.90	6	2
1:A:26:LEU:HD12	1:A:33:ILE:CD1	0.44	2.42	20	1
1:A:11:LEU:CD1	1:A:37:LEU:HD21	0.44	2.43	5	1
1:A:26:LEU:O	1:A:27:ASN:C	0.44	2.55	11	17
1:A:10:LEU:CD1	1:A:25:THR:HG21	0.43	2.43	5	1
1:A:46:ALA:CB	1:A:76:ALA:O	0.43	2.67	2	1
1:A:5:ILE:O	1:A:9:ASP:N	0.43	2.49	20	1
1:A:5:ILE:HD13	1:A:5:ILE:N	0.43	2.26	12	3
1:A:28:THR:CG2	1:A:29:PRO:HD2	0.43	2.43	10	3
1:A:12:ALA:CB	1:A:77:LEU:CD1	0.43	2.94	12	1
1:A:10:LEU:HD13	1:A:14:ARG:HD3	0.43	1.90	14	1
1:A:12:ALA:CA	1:A:77:LEU:HD11	0.43	2.44	17	1
1:A:6:GLN:O	1:A:10:LEU:CD2	0.43	2.64	15	1
1:A:51:GLU:OE2	1:A:74:TRP:CZ2	0.43	2.72	7	1
1:A:48:ARG:HG2	1:A:75:TRP:CZ3	0.43	2.48	8	1
1:A:46:ALA:C	1:A:47:VAL:HG13	0.43	2.35	17	1
1:A:16:ARG:HA	1:A:76:ALA:HB2	0.42	1.91	12	1
1:A:48:ARG:HD2	1:A:75:TRP:CZ2	0.42	2.48	15	1
1:A:10:LEU:HD12	1:A:14:ARG:HG2	0.42	1.91	10	2
1:A:18:GLU:OE1	1:A:20:ALA:CB	0.42	2.68	4	1
1:A:23:SER:O	1:A:27:ASN:N	0.41	2.52	3	2
1:A:7:VAL:HA	1:A:22:ILE:CG2	0.41	2.45	16	1
1:A:30:GLN:N	1:A:31:PRO:HD2	0.41	2.30	8	2
1:A:28:THR:CG2	1:A:33:ILE:HG12	0.41	2.46	16	1
1:A:11:LEU:HB3	1:A:77:LEU:HD21	0.41	1.93	11	1
1:A:12:ALA:N	1:A:77:LEU:HD11	0.41	2.31	17	1
1:A:11:LEU:O	1:A:15:GLY:O	0.41	2.39	1	2
1:A:4:LEU:HD13	1:A:7:VAL:HG11	0.41	1.91	9	1
1:A:19:ALA:O	1:A:22:ILE:N	0.41	2.54	13	1
1:A:16:ARG:O	1:A:17:MET:SD	0.41	2.79	2	3
1:A:11:LEU:CB	1:A:77:LEU:HD21	0.41	2.46	11	1
1:A:29:PRO:O	1:A:30:GLN:C	0.41	2.59	13	2
1:A:11:LEU:O	1:A:15:GLY:C	0.41	2.59	19	2
1:A:16:ARG:CA	1:A:76:ALA:HB2	0.40	2.46	12	1
1:A:11:LEU:CD2	1:A:22:ILE:CD1	0.40	2.99	10	1
1:A:11:LEU:CB	1:A:77:LEU:HD11	0.40	2.46	19	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	54/78 (69%)	50±1 (92±1%)	3±1 (6±1%)	1±1 (2±1%)	11 53
All	All	1080/1560 (69%)	991 (92%)	68 (6%)	21 (2%)	11 53

All 2 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	27	ASN	14
1	A	72	ARG	7

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	47/65 (72%)	33±2 (71±4%)	14±2 (29±4%)	2 18
All	All	940/1300 (72%)	668 (71%)	272 (29%)	2 18

All 28 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	30	GLN	20
1	A	38	GLN	20
1	A	72	ARG	20
1	A	26	LEU	18
1	A	36	MET	18
1	A	21	GLN	17
1	A	28	THR	17
1	A	16	ARG	16

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Mol	Chain	Res	Type	Models (Total)
1	A	51	GLU	14
1	A	24	GLN	13
1	A	32	MET	13
1	A	48	ARG	13
1	A	4	LEU	13
1	A	6	GLN	12
1	A	18	GLU	10
1	A	41	GLU	8
1	A	14	ARG	8
1	A	39	GLN	4
1	A	27	ASN	4
1	A	17	MET	3
1	A	50	GLN	2
1	A	77	LEU	2
1	A	42	SER	2
1	A	45	LYS	1
1	A	8	ARG	1
1	A	73	GLU	1
1	A	43	MET	1
1	A	78	ARG	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