



Full wwPDB NMR Structure Validation Report ⓘ

Mar 6, 2026 – 02:20 PM UTC

PDB ID : 2HH8 / pdb_00002hh8
Title : Solution NMR structure of the ydfO protein from Escherichia coli. Northeast Structural Genomics target ER251.
Authors : Rossi, P.; Cort, J.R.; Ho, C.K.; Janjua, H.; Cunningham, K.; Ma, L.-C.; Xiao, R.; Liu, J.; Baran, M.; Swapna, G.V.T.; Acton, T.B.; Rost, B.; Kennedy, M.A.; Montelione, G.T.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2006-06-28

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

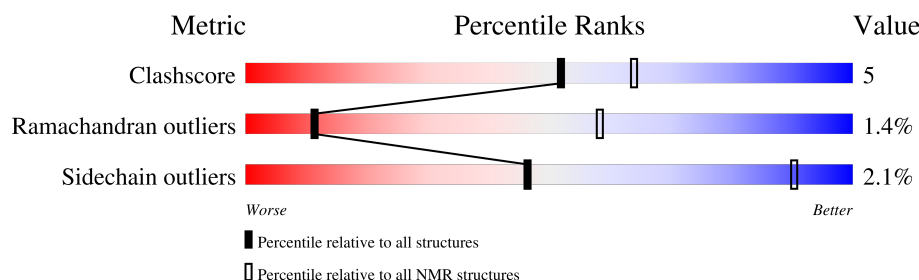
1 Overall quality at a glance

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	149	

2 Ensemble composition and analysis

This entry contains 20 models. Model 18 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:7-A:62, A:67-A:133 (123)	0.92	18

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 2 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2195 atoms, of which 1100 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Hypothetical protein ydfO.

Mol	Chain	Residues	Atoms					Trace
1	A	127	Total	C	H	N	O	0
			2195	708	1100	192	195	

There are 14 discrepancies between the modelled and reference sequences:

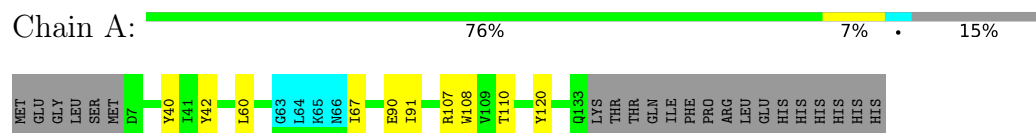
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	cloning artifact	UNP P76156
A	2	GLU	-	cloning artifact	UNP P76156
A	3	GLY	-	cloning artifact	UNP P76156
A	4	LEU	-	cloning artifact	UNP P76156
A	5	SER	-	cloning artifact	UNP P76156
A	139	PHE	LEU	cloning artifact	UNP P76156
A	142	LEU	-	cloning artifact	UNP P76156
A	143	GLU	-	cloning artifact	UNP P76156
A	144	HIS	-	expression tag	UNP P76156
A	145	HIS	-	expression tag	UNP P76156
A	146	HIS	-	expression tag	UNP P76156
A	147	HIS	-	expression tag	UNP P76156
A	148	HIS	-	expression tag	UNP P76156
A	149	HIS	-	expression tag	UNP P76156

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: Hypothetical protein ydfO

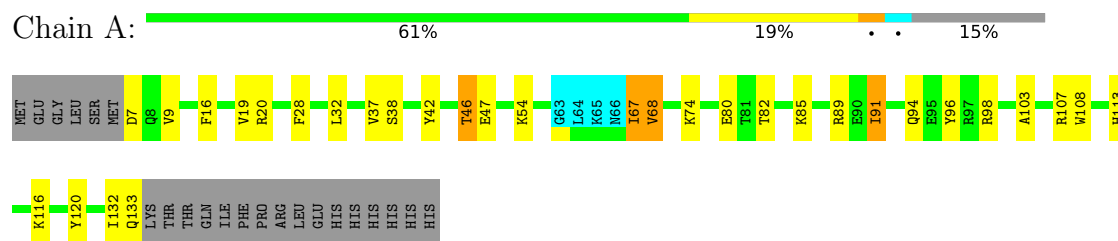


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

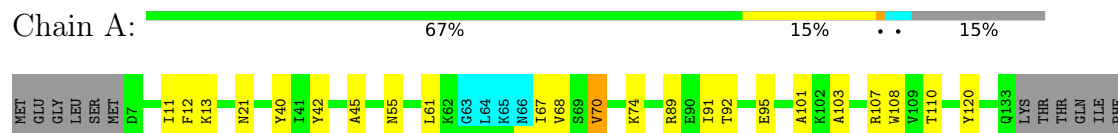
4.2.1 Score per residue for model 1

- Molecule 1: Hypothetical protein ydfO



4.2.2 Score per residue for model 2

- Molecule 1: Hypothetical protein ydfO



PRO
ARG
LEU
LEU
HIS
HIS
HIS
HIS

4.2.3 Score per residue for model 3

- Molecule 1: Hypothetical protein ydfO

Chain A: 

MET GLU GLY LEU SER MET MET D7 F12 Y40 Y41 Y42 L61 K62 G63 L64 K65 N66 K74 D75 R76 E80 T92 R107 W108 Y109 T110 R117 Y118 Y119 Y120 T121 F122 D123 N124 L127 F128 Q133 LYS THR THR GLN ILE PHE PRO ARG LEU GLU HIS HIS HIS

HIS
HIS
HIS

4.2.4 Score per residue for model 4

- Molecule 1: Hypothetical protein ydfO

Chain A: 

MET GLU GLY LEU SER MET MET D7 I11 I15 I20 F28 L32 K33 Y37 Y42 Y49 K54 L60 G63 L64 K65 N66 T82 I91 T92 F93 Q94 F95 Y96 R97 R98 R107 W108 M111 I112 H113 E114 Y120 Q133 LYS THR THR GLN

ILE
PHE
PRO
ARG
LEU
LEU
HIS
HIS
HIS
HIS

4.2.5 Score per residue for model 5

- Molecule 1: Hypothetical protein ydfO

Chain A: 

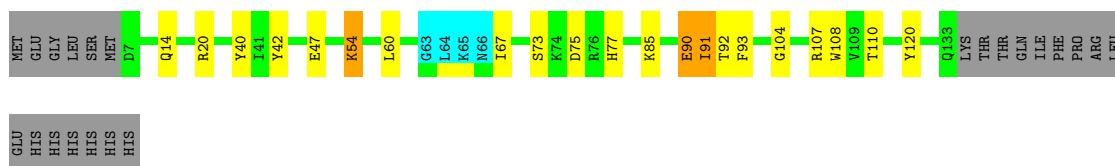
MET GLU GLY LEU SER MET MET D7 K18 V19 R20 N21 D22 L23 N24 Y25 Q26 W27 F28 L32 Y42 T46 V49 N55 L60 G63 L64 K65 N66 V70 K85 Q94 I91 R98 A101 R107 W108 Y120 T121 L127 Q133 LYS THR THR GLN

ILE
PHE
PRO
ARG
LEU
LEU
HIS
HIS
HIS
HIS

4.2.6 Score per residue for model 6

- Molecule 1: Hypothetical protein ydfO

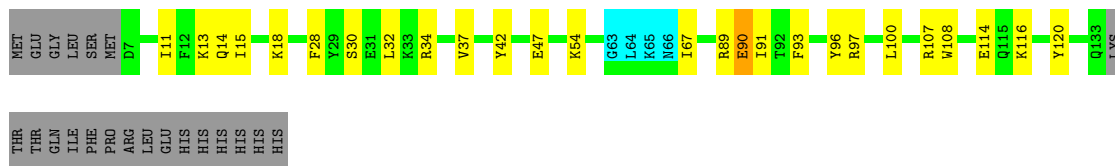
Chain A: 



4.2.7 Score per residue for model 7

- Molecule 1: Hypothetical protein ydfO

Chain A: 65% 17% • • 15%



4.2.8 Score per residue for model 8

- Molecule 1: Hypothetical protein ydfO

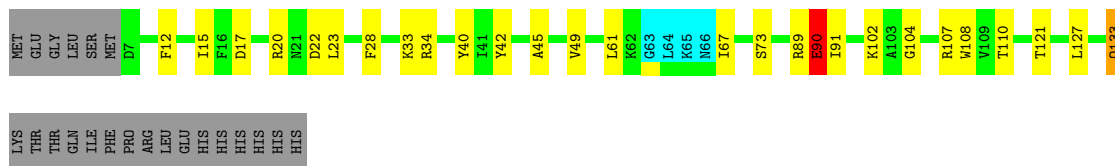
Chain A: 72% 10% • 15%



4.2.9 Score per residue for model 9

- Molecule 1: Hypothetical protein ydfO

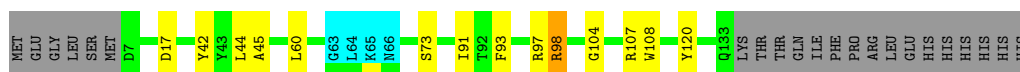
Chain A: 64% 17% • • 15%



4.2.10 Score per residue for model 10

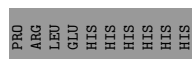
- Molecule 1: Hypothetical protein ydfO

Chain A: 73% 9% • • 15%



4.2.11 Score per residue for model 11

- Molecule 1: Hypothetical protein ydfO



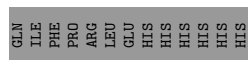
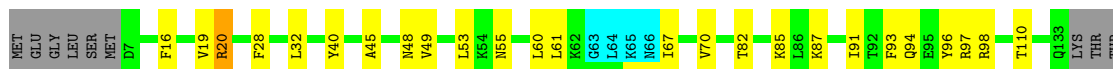
4.2.12 Score per residue for model 12

- Molecule 1: Hypothetical protein ydfO



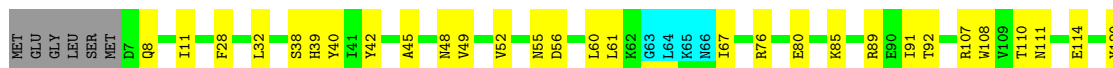
4.2.13 Score per residue for model 13

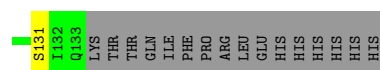
- Molecule 1: Hypothetical protein ydfO



4.2.14 Score per residue for model 14

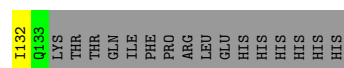
- Molecule 1: Hypothetical protein ydfO





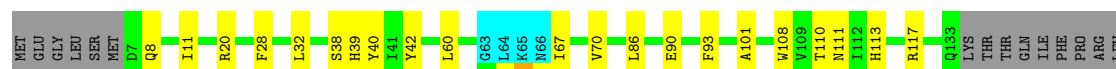
4.2.15 Score per residue for model 15

- Molecule 1: Hypothetical protein ydfO



4.2.16 Score per residue for model 16

- Molecule 1: Hypothetical protein ydfO



4.2.17 Score per residue for model 17

- Molecule 1: Hypothetical protein ydfO



4.2.18 Score per residue for model 18 (medoid)

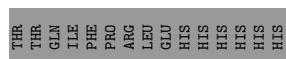
- Molecule 1: Hypothetical protein ydfO





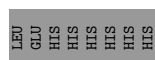
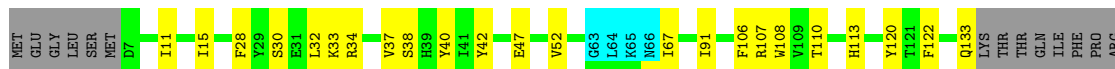
4.2.19 Score per residue for model 19

- Molecule 1: Hypothetical protein ydfO



4.2.20 Score per residue for model 20

- Molecule 1: Hypothetical protein ydfO



5 Refinement protocol and experimental data overview

The models were refined using the following method: *Noesy assignments made with iterative method using CS, 3J, Hyper (dihedral), and Dyana for simulated annealing MD. Converged structures are further refined using NIH-xplor followed by CNS in explicit water shell (Nielges) . Full lenght sequence was carried through the refinement protocol, the disordered regions and hexHIS tag are not reported. Structure based on 1885 constraints, 788 long range, 142 dihedral constraints and 114 H-bond constraints..*

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy.*

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

Software name	Classification	Version
DYANA	structure solution	1.2
X-PLOR	refinement	2.11.2
AutoStructure	structure solution	2.1.1
HYPER	structure solution	2.1
PSVS	refinement	1.3
CNS	refinement	1.1
Procheck NMR	refinement	3.51
MolProbity	refinement	3.01

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	1066	1067	1061	11±3
All	All	21320	21340	21220	229

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 5.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:107:ARG:HB3	1:A:120:TYR:HB2	0.87	1.44	20	7
1:A:107:ARG:HB2	1:A:120:TYR:HB2	0.85	1.47	5	10
1:A:42:TYR:HB3	1:A:108:TRP:HB3	0.79	1.52	7	18
1:A:18:LYS:HE2	1:A:18:LYS:HA	0.73	1.58	5	1
1:A:121:THR:HB	1:A:127:LEU:HD11	0.67	1.66	9	5
1:A:45:ALA:HA	1:A:67:ILE:O	0.64	1.92	2	4
1:A:60:LEU:H	1:A:60:LEU:HD23	0.63	1.54	13	7
1:A:40:TYR:CE1	1:A:110:THR:HB	0.63	2.29	17	8
1:A:92:THR:HB	1:A:95:GLU:OE1	0.61	1.95	2	1
1:A:38:SER:HA	1:A:113:HIS:HB2	0.61	1.72	1	2
1:A:45:ALA:HA	1:A:68:VAL:HG12	0.60	1.72	18	1
1:A:40:TYR:CE2	1:A:110:THR:HB	0.60	2.31	18	6
1:A:85:LYS:HE2	1:A:91:ILE:HG21	0.59	1.75	5	3
1:A:37:VAL:HB	1:A:54:LYS:HB2	0.57	1.75	1	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:85:LYS:HE3	1:A:91:ILE:HD13	0.57	1.77	13	1
1:A:85:LYS:HD2	1:A:91:ILE:HD13	0.56	1.78	6	1
1:A:15:ILE:HG22	1:A:28:PHE:HD1	0.56	1.61	9	1
1:A:110:THR:HG23	1:A:117:ARG:HG2	0.55	1.78	16	1
1:A:133:GLN:HA	1:A:133:GLN:HE21	0.54	1.63	9	1
1:A:70:VAL:HA	1:A:101:ALA:O	0.54	2.02	15	4
1:A:89:ARG:O	1:A:90:GLU:HB3	0.53	2.02	9	2
1:A:74:LYS:HA	1:A:103:ALA:O	0.53	2.03	2	2
1:A:22:ASP:HB3	1:A:24:ASN:OD1	0.52	2.04	5	1
1:A:15:ILE:HA	1:A:27:TRP:HZ2	0.52	1.63	19	1
1:A:16:PHE:O	1:A:20:ARG:HG3	0.52	2.05	18	3
1:A:86:LEU:O	1:A:90:GLU:HA	0.52	2.05	8	2
1:A:13:LYS:O	1:A:17:ASP:HB2	0.51	2.04	19	1
1:A:49:VAL:HB	1:A:61:LEU:HB2	0.51	1.82	9	1
1:A:19:VAL:HB	1:A:27:TRP:HE1	0.51	1.66	11	1
1:A:17:ASP:HA	1:A:20:ARG:HE	0.51	1.66	18	1
1:A:47:GLU:HG3	1:A:67:ILE:HD13	0.50	1.83	6	1
1:A:42:TYR:HB3	1:A:108:TRP:CD1	0.50	2.41	19	1
1:A:44:LEU:HD11	1:A:108:TRP:HB2	0.50	1.84	18	1
1:A:48:ASN:HA	1:A:61:LEU:O	0.50	2.06	14	3
1:A:89:ARG:HD2	1:A:90:GLU:HG2	0.49	1.84	7	1
1:A:28:PHE:O	1:A:32:LEU:HG	0.49	2.07	20	9
1:A:15:ILE:HA	1:A:27:TRP:CZ2	0.49	2.43	11	2
1:A:30:SER:O	1:A:34:ARG:HG3	0.49	2.08	7	3
1:A:123:ASP:O	1:A:124:ASN:HB3	0.49	2.08	3	1
1:A:89:ARG:CD	1:A:90:GLU:HG2	0.48	2.38	7	1
1:A:12:PHE:HB3	1:A:61:LEU:HD11	0.48	1.86	11	4
1:A:80:GLU:HG2	1:A:128:PHE:CE1	0.48	2.44	3	1
1:A:17:ASP:HA	1:A:20:ARG:HD3	0.48	1.85	9	1
1:A:20:ARG:HA	1:A:93:PHE:HB3	0.47	1.85	6	4
1:A:117:ARG:HD2	1:A:119:TYR:OH	0.47	2.09	15	1
1:A:98:ARG:HA	1:A:98:ARG:HE	0.47	1.69	10	1
1:A:16:PHE:HA	1:A:19:VAL:HG12	0.47	1.86	13	2
1:A:94:GLN:O	1:A:97:ARG:HG3	0.47	2.10	13	1
1:A:39:HIS:HB3	1:A:111:ASN:HA	0.47	1.85	14	2
1:A:115:GLN:HE21	1:A:132:ILE:HD11	0.47	1.68	15	1
1:A:44:LEU:CD2	1:A:97:ARG:HG3	0.47	2.40	19	1
1:A:7:ASP:OD2	1:A:9:VAL:HB	0.47	2.10	17	2
1:A:10:VAL:O	1:A:14:GLN:HG3	0.47	2.10	17	1
1:A:47:GLU:HB2	1:A:67:ILE:HD13	0.47	1.86	20	1
1:A:114:GLU:HB3	1:A:116:LYS:HE2	0.46	1.85	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:ASP:HA	1:A:20:ARG:NE	0.46	2.25	18	1
1:A:44:LEU:HG	1:A:108:TRP:NE1	0.46	2.26	19	1
1:A:98:ARG:O	1:A:102:LYS:HG2	0.46	2.09	12	1
1:A:72:PHE:HA	1:A:122:PHE:CZ	0.46	2.46	15	1
1:A:108:TRP:CD1	1:A:108:TRP:H	0.46	2.28	19	1
1:A:82:THR:HG22	1:A:96:TYR:CD1	0.46	2.46	4	4
1:A:12:PHE:HB2	1:A:61:LEU:HD21	0.46	1.87	8	1
1:A:85:LYS:HD3	1:A:91:ILE:HD13	0.46	1.87	1	1
1:A:10:VAL:O	1:A:14:GLN:HG2	0.46	2.11	11	1
1:A:73:SER:O	1:A:104:GLY:HA3	0.46	2.11	6	3
1:A:54:LYS:O	1:A:55:ASN:HB2	0.46	2.11	17	1
1:A:19:VAL:O	1:A:23:LEU:HD23	0.45	2.10	5	1
1:A:76:ARG:O	1:A:80:GLU:HG3	0.45	2.11	3	2
1:A:123:ASP:O	1:A:124:ASN:HB2	0.45	2.12	17	1
1:A:49:VAL:O	1:A:60:LEU:HA	0.45	2.11	4	4
1:A:108:TRP:CD1	1:A:108:TRP:C	0.45	2.95	10	1
1:A:38:SER:HB3	1:A:52:VAL:O	0.45	2.11	11	1
1:A:104:GLY:O	1:A:121:THR:HA	0.45	2.11	18	1
1:A:107:ARG:CB	1:A:120:TYR:HB2	0.45	2.42	4	1
1:A:26:GLN:HA	1:A:26:GLN:HE21	0.45	1.71	5	1
1:A:94:GLN:O	1:A:98:ARG:HG3	0.45	2.12	4	2
1:A:70:VAL:HA	1:A:101:ALA:HB1	0.45	1.89	2	1
1:A:67:ILE:HG22	1:A:68:VAL:HG23	0.44	1.89	1	1
1:A:7:ASP:HB2	1:A:10:VAL:HG23	0.44	1.89	15	1
1:A:96:TYR:O	1:A:100:LEU:HD13	0.44	2.11	7	1
1:A:11:ILE:O	1:A:15:ILE:HG13	0.44	2.13	15	5
1:A:8:GLN:HA	1:A:11:ILE:HD13	0.44	1.89	16	2
1:A:33:LYS:HD3	1:A:112:ILE:HG23	0.44	1.89	4	1
1:A:108:TRP:H	1:A:108:TRP:HD1	0.44	1.56	19	1
1:A:94:GLN:O	1:A:98:ARG:HG2	0.44	2.13	1	1
1:A:89:ARG:HG3	1:A:90:GLU:OE2	0.43	2.13	9	1
1:A:71:LYS:O	1:A:104:GLY:HA2	0.43	2.13	19	1
1:A:60:LEU:H	1:A:60:LEU:CD1	0.43	2.26	11	1
1:A:89:ARG:HA	1:A:89:ARG:NE	0.43	2.28	1	1
1:A:111:ASN:HB3	1:A:114:GLU:HB2	0.43	1.90	4	1
1:A:93:PHE:O	1:A:97:ARG:HG3	0.43	2.13	7	1
1:A:74:LYS:HB2	1:A:127:LEU:HD21	0.43	1.89	3	1
1:A:47:GLU:OE2	1:A:67:ILE:HG13	0.43	2.13	11	1
1:A:11:ILE:HD12	1:A:11:ILE:H	0.43	1.73	2	1
1:A:106:PHE:HB3	1:A:122:PHE:HA	0.43	1.90	20	1
1:A:44:LEU:HD22	1:A:97:ARG:HB3	0.43	1.91	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:38:SER:HB2	1:A:52:VAL:O	0.42	2.14	14	2
1:A:37:VAL:O	1:A:113:HIS:HB2	0.42	2.14	20	2
1:A:111:ASN:HB2	1:A:114:GLU:HB2	0.42	1.92	14	1
1:A:89:ARG:O	1:A:90:GLU:HG3	0.42	2.15	15	1
1:A:33:LYS:O	1:A:33:LYS:HD3	0.42	2.14	20	1
1:A:55:ASN:O	1:A:56:ASP:HB3	0.42	2.15	14	2
1:A:117:ARG:HD3	1:A:119:TYR:OH	0.42	2.14	3	1
1:A:75:ASP:OD1	1:A:77:HIS:HB3	0.42	2.15	6	1
1:A:20:ARG:HA	1:A:93:PHE:CB	0.41	2.45	6	1
1:A:47:GLU:HG2	1:A:67:ILE:HD13	0.41	1.91	7	1
1:A:37:VAL:HG21	1:A:54:LYS:HD3	0.41	1.90	4	1
1:A:72:PHE:HA	1:A:122:PHE:HZ	0.41	1.75	15	1
1:A:46:THR:HG23	1:A:67:ILE:HG12	0.41	1.91	1	1
1:A:45:ALA:HB3	1:A:106:PHE:CE1	0.41	2.51	19	1
1:A:114:GLU:O	1:A:116:LYS:HG3	0.41	2.15	7	1
1:A:17:ASP:HA	1:A:20:ARG:CD	0.41	2.46	11	1
1:A:23:LEU:HD11	1:A:92:THR:HA	0.41	1.92	19	1
1:A:108:TRP:C	1:A:108:TRP:CD1	0.41	2.99	5	1
1:A:45:ALA:HB2	1:A:70:VAL:HG23	0.40	1.93	13	1
1:A:20:ARG:C	1:A:20:ARG:HD2	0.40	2.41	5	1
1:A:13:LYS:HD2	1:A:13:LYS:O	0.40	2.17	7	1
1:A:93:PHE:CE2	1:A:97:ARG:HD3	0.40	2.51	10	1
1:A:22:ASP:O	1:A:23:LEU:HB2	0.40	2.17	9	1
1:A:45:ALA:O	1:A:67:ILE:HA	0.40	2.17	14	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	121/149 (81%)	109±2 (90±2%)	10±2 (9±2%)	2±1 (1±1%)	11	58
All	All	2420/2980 (81%)	2179 (90%)	206 (9%)	35 (1%)	11	58

All 11 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	91	ILE	12
1	A	68	VAL	5
1	A	55	ASN	4
1	A	90	GLU	4
1	A	67	ILE	2
1	A	54	LYS	2
1	A	53	LEU	2
1	A	70	VAL	1
1	A	45	ALA	1
1	A	132	ILE	1
1	A	46	THR	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	119/143 (83%)	116±2 (98±1%)	3±2 (2±1%)	46	90
All	All	2380/2860 (83%)	2329 (98%)	51 (2%)	46	90

All 34 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	133	GLN	5
1	A	92	THR	4
1	A	27	TRP	3
1	A	17	ASP	3
1	A	89	ARG	2
1	A	98	ARG	2
1	A	14	GLN	2
1	A	90	GLU	2
1	A	18	LYS	2
1	A	60	LEU	2
1	A	46	THR	1
1	A	80	GLU	1
1	A	116	LYS	1
1	A	132	ILE	1
1	A	13	LYS	1

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Mol	Chain	Res	Type	Models (Total)
1	A	21	ASN	1
1	A	24	ASN	1
1	A	26	GLN	1
1	A	49	VAL	1
1	A	54	LYS	1
1	A	130	GLU	1
1	A	33	LYS	1
1	A	34	ARG	1
1	A	102	LYS	1
1	A	107	ARG	1
1	A	74	LYS	1
1	A	20	ARG	1
1	A	87	LYS	1
1	A	131	SER	1
1	A	48	ASN	1
1	A	115	GLN	1
1	A	31	GLU	1
1	A	62	LYS	1
1	A	108	TRP	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry ⓘ

There are no ligands in this entry.

6.7 Other polymers ⓘ

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided