



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 08:09 PM UTC

PDB ID : 1ZHC / pdb_00001zhc
Title : Solution structure of HP1242 from Helicobacter pylori
Authors : Kang, S.J.; Park, S.J.; Jung, S.J.; Lee, B.J.
Deposited on : 2005-04-25

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

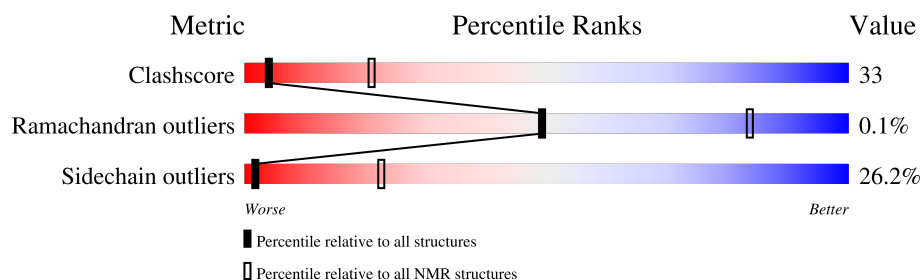
1 Overall quality at a glance

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	76	

2 Ensemble composition and analysis

This entry contains 20 models. Model 11 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:3-A:76 (74)	0.71	11

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1274 atoms, of which 634 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called hypothetical protein HP1242.

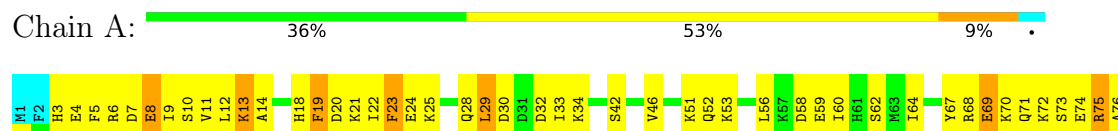
Mol	Chain	Residues	Atoms						Trace
1	A	76	Total	C	H	N	O	S	0
			1274	397	634	115	125	3	

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 HP1242

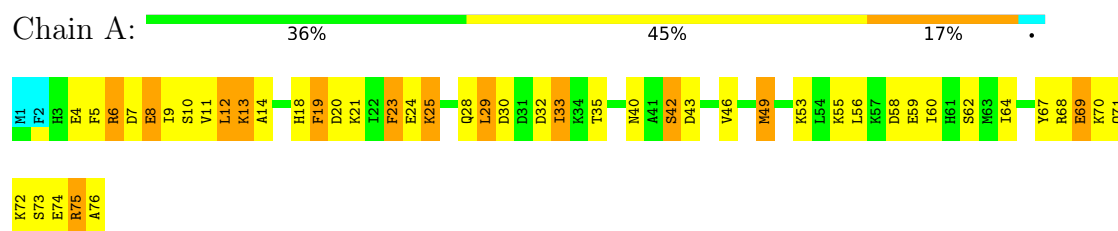


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

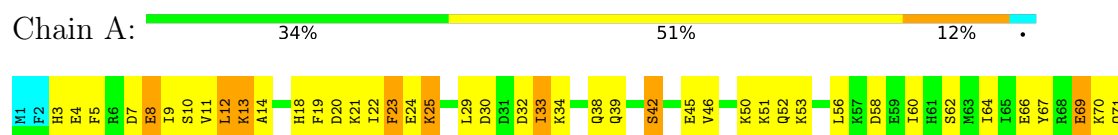
4.2.1 Score per residue for model 1

- Molecule 1: hypothetical protein HP1242



4.2.2 Score per residue for model 2

- Molecule 1: hypothetical protein HP1242

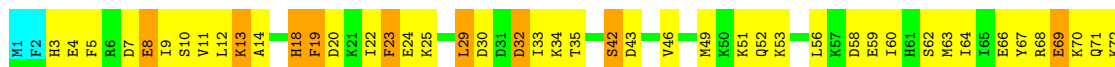


K72
S73
E74
R75
A76

4.2.3 Score per residue for model 3

- Molecule 1: hypothetical protein HP1242

Chain A: 

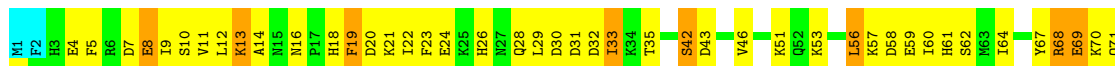


S73
E74
R75
A76

4.2.4 Score per residue for model 4

- Molecule 1: hypothetical protein HP1242

Chain A: 



K72
S73
E74
R75
A76

4.2.5 Score per residue for model 5

- Molecule 1: hypothetical protein HP1242

Chain A: 



4.2.6 Score per residue for model 6

- Molecule 1: hypothetical protein HP1242

Chain A: 

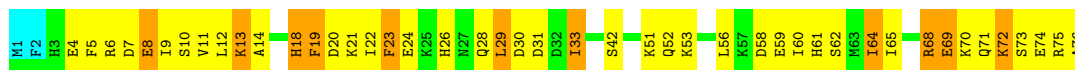


R75
A76

4.2.7 Score per residue for model 7

- Molecule 1: hypothetical protein HP1242

Chain A: 38% 45% 14%



4.2.8 Score per residue for model 8

- Molecule 1: hypothetical protein HP1242

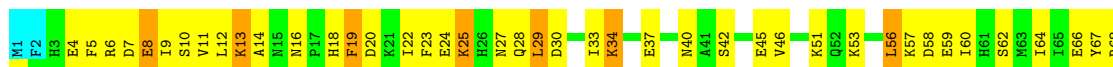
Chain A: 28% 59% 11%

K72
S73
E74
R75
A76

4.2.9 Score per residue for model 9

- Molecule 1: hypothetical protein HP1242

Chain A: 32% 54% 12%

E69
K70
Q71
K72
S73
E74
R75
A76

4.2.10 Score per residue for model 10

- Molecule 1: hypothetical protein HP1242

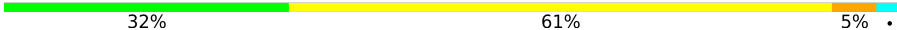
Chain A: 38% 47% 12%

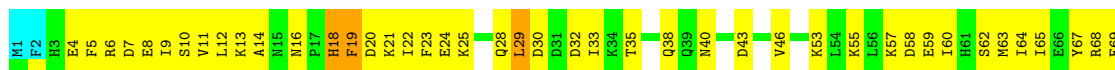


R75
A76

4.2.11 Score per residue for model 11 (medoid)

- Molecule 1: hypothetical protein HP1242

Chain A:  32% 61% 5% •



K70
Q71
K72
S73
E74
R75
A76

4.2.12 Score per residue for model 12

- Molecule 1: hypothetical protein HP1242

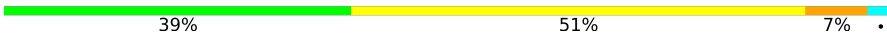
Chain A:  30% 58% 9% •

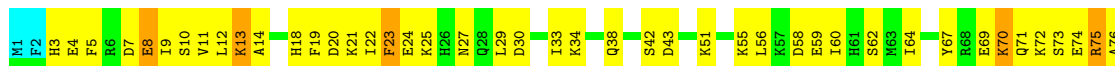


K70
Q71
K72
S73
E74
R75
A76

4.2.13 Score per residue for model 13

- Molecule 1: hypothetical protein HP1242

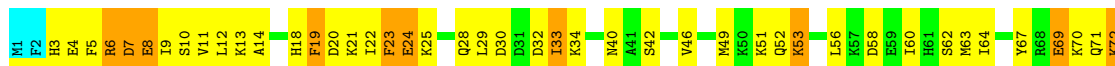
Chain A:  39% 51% 7% •



4.2.14 Score per residue for model 14

- Molecule 1: hypothetical protein HP1242

Chain A:  34% 50% 13% •

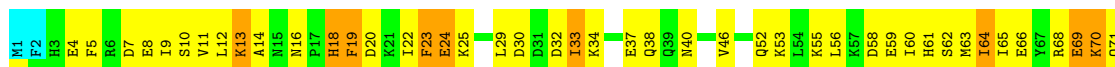


S73
E74
R75
A76

4.2.15 Score per residue for model 15

- Molecule 1: hypothetical protein HP1242

Chain A: 

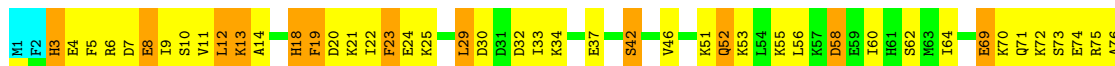


K72
S73
E74
R75
A76

4.2.16 Score per residue for model 16

- Molecule 1: hypothetical protein HP1242

Chain A: 



4.2.17 Score per residue for model 17

- Molecule 1: hypothetical protein HP1242

Chain A: 



A76

4.2.18 Score per residue for model 18

- Molecule 1: hypothetical protein HP1242

Chain A: 



K72
S73
E74
R75
A76

4.2.19 Score per residue for model 19

- Molecule 1: hypothetical protein HP1242

Chain A: 

M1 F2 H3 E4 F5 R6 D7 E8 I9 S10 V11 L12 K13 A14 H18 F19 D20 K21 I22 F23 E24 L29 D30 I33 K34 Q38 R39 N40 A41 S42 D43 A44 E45 V46 K53 L56 K57 D58 E59 I60 H61 S62 H63 I64 I65 E66 Y67 R68 E69 K70 Q71 K72 S73 E74

R75
A76

4.2.20 Score per residue for model 20

- Molecule 1: hypothetical protein HP1242

Chain A: 

M1 F2 H3 E4 F5 R6 D7 E8 I9 S10 V11 L12 K13 A14 H18 F19 D20 K21 I22 F23 E24 K25 H26 N27 Q28 L29 D30 D31 D32 I33 K34 E37 Q38 S42 E45 V46 K51 K55 D58 E59 I60 H61 S62 H63 I64 Y67 R68 E69 K70 Q71 K72 S73

E74
R75
A76

5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with acceptable covalent geometry*.

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

Software name	Classification	Version
CNS	structure solution	1.1
CNS	refinement	1.1

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.

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	621	614	609	41±5
All	All	12420	12280	12180	817

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 33.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:29:LEU:HD22	1:A:56:LEU:HD12	1.01	1.29	8	1
1:A:9:ILE:HG23	1:A:64:ILE:HD11	0.96	1.36	3	9
1:A:29:LEU:O	1:A:33:ILE:HG23	0.86	1.70	16	18
1:A:10:SER:O	1:A:14:ALA:HB3	0.84	1.72	2	20
1:A:12:LEU:HD13	1:A:67:TYR:CD1	0.83	2.09	2	8
1:A:13:LYS:HG3	1:A:60:ILE:HD12	0.82	1.48	11	6
1:A:13:LYS:CG	1:A:60:ILE:HD12	0.81	2.04	18	4
1:A:56:LEU:HD13	1:A:59:GLU:CD	0.75	2.06	4	1
1:A:29:LEU:CD2	1:A:56:LEU:HD12	0.74	2.10	8	1
1:A:13:LYS:HG2	1:A:60:ILE:HG23	0.73	1.57	3	1
1:A:33:ILE:HG22	1:A:49:MET:HB3	0.73	1.61	17	1
1:A:12:LEU:HD12	1:A:13:LYS:N	0.73	1.97	8	1
1:A:12:LEU:HD22	1:A:67:TYR:CD1	0.73	2.19	4	5
1:A:9:ILE:O	1:A:13:LYS:HB3	0.72	1.85	9	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:13:LYS:HD2	1:A:60:ILE:HD13	0.71	1.63	13	3
1:A:72:LYS:O	1:A:76:ALA:HB3	0.71	1.86	14	9
1:A:8:GLU:OE1	1:A:64:ILE:HG23	0.71	1.86	6	2
1:A:9:ILE:HG23	1:A:64:ILE:CD1	0.70	2.15	16	6
1:A:12:LEU:HD13	1:A:67:TYR:CE1	0.70	2.21	19	2
1:A:29:LEU:HD22	1:A:56:LEU:HD22	0.70	1.64	13	1
1:A:12:LEU:HD22	1:A:67:TYR:CE2	0.70	2.21	3	3
1:A:8:GLU:HG2	1:A:12:LEU:HD11	0.69	1.62	14	15
1:A:22:ILE:HG23	1:A:59:GLU:CD	0.69	2.12	8	11
1:A:64:ILE:HG23	1:A:65:ILE:HD13	0.69	1.62	7	4
1:A:12:LEU:HD22	1:A:67:TYR:CZ	0.68	2.23	12	3
1:A:19:PHE:O	1:A:23:PHE:HB3	0.68	1.89	17	8
1:A:12:LEU:HD13	1:A:67:TYR:CD2	0.68	2.24	3	1
1:A:7:ASP:O	1:A:11:VAL:HG23	0.67	1.88	8	14
1:A:12:LEU:HD22	1:A:67:TYR:CE1	0.67	2.24	18	10
1:A:61:HIS:O	1:A:64:ILE:HG22	0.66	1.91	7	4
1:A:37:GLU:OE1	1:A:46:VAL:HG11	0.65	1.91	15	3
1:A:9:ILE:O	1:A:13:LYS:HB2	0.65	1.92	19	9
1:A:29:LEU:HD13	1:A:56:LEU:HD22	0.65	1.68	10	1
1:A:26:HIS:HA	1:A:56:LEU:HD23	0.64	1.70	12	2
1:A:5:PHE:O	1:A:9:ILE:HD12	0.64	1.93	20	19
1:A:30:ASP:HA	1:A:33:ILE:CG1	0.64	2.23	1	2
1:A:56:LEU:HD23	1:A:59:GLU:OE2	0.63	1.93	9	1
1:A:29:LEU:HD22	1:A:56:LEU:CD1	0.63	2.17	8	1
1:A:13:LYS:HD3	1:A:60:ILE:HG23	0.62	1.71	10	2
1:A:25:LYS:O	1:A:29:LEU:HD23	0.62	1.94	20	3
1:A:12:LEU:HD12	1:A:64:ILE:HG12	0.62	1.71	18	2
1:A:8:GLU:HG3	1:A:12:LEU:HD11	0.62	1.70	13	3
1:A:29:LEU:HD13	1:A:56:LEU:HD11	0.61	1.72	17	1
1:A:8:GLU:O	1:A:12:LEU:HG	0.61	1.96	11	18
1:A:60:ILE:O	1:A:64:ILE:HD12	0.61	1.95	14	7
1:A:8:GLU:CG	1:A:12:LEU:HD11	0.61	2.26	1	12
1:A:9:ILE:HG22	1:A:13:LYS:CD	0.60	2.26	8	1
1:A:22:ILE:HG22	1:A:60:ILE:HG12	0.60	1.73	2	2
1:A:22:ILE:HG23	1:A:59:GLU:OE2	0.60	1.96	4	2
1:A:5:PHE:HA	1:A:9:ILE:HD13	0.59	1.73	11	1
1:A:12:LEU:HD12	1:A:64:ILE:CG1	0.59	2.28	18	4
1:A:29:LEU:HD11	1:A:49:MET:O	0.59	1.97	1	1
1:A:64:ILE:HD13	1:A:64:ILE:O	0.59	1.98	8	2
1:A:19:PHE:O	1:A:23:PHE:HB2	0.59	1.98	14	12
1:A:37:GLU:OE2	1:A:46:VAL:HG11	0.58	1.98	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:25:LYS:O	1:A:29:LEU:HD12	0.58	1.98	17	1
1:A:30:ASP:HA	1:A:33:ILE:HG12	0.58	1.75	2	4
1:A:19:PHE:CD1	1:A:19:PHE:C	0.57	2.82	10	5
1:A:22:ILE:HD12	1:A:63:MET:HE2	0.57	1.76	18	3
1:A:56:LEU:HD23	1:A:59:GLU:CD	0.57	2.24	9	1
1:A:12:LEU:HD13	1:A:67:TYR:CG	0.57	2.34	12	2
1:A:13:LYS:HG2	1:A:60:ILE:HD12	0.57	1.76	18	1
1:A:5:PHE:O	1:A:9:ILE:HB	0.57	2.00	18	20
1:A:19:PHE:O	1:A:23:PHE:CB	0.56	2.52	20	19
1:A:33:ILE:HD12	1:A:34:LYS:N	0.56	2.14	9	4
1:A:4:GLU:O	1:A:8:GLU:CB	0.56	2.53	17	20
1:A:26:HIS:HB2	1:A:56:LEU:HD12	0.56	1.77	4	1
1:A:9:ILE:HA	1:A:64:ILE:HD13	0.56	1.77	19	1
1:A:9:ILE:HG22	1:A:13:LYS:HD3	0.55	1.77	8	1
1:A:71:GLN:O	1:A:75:ARG:CB	0.55	2.55	8	17
1:A:33:ILE:HG21	1:A:53:LYS:HG3	0.55	1.77	14	1
1:A:33:ILE:HD12	1:A:33:ILE:C	0.54	2.28	9	10
1:A:29:LEU:HD13	1:A:56:LEU:HG	0.54	1.77	15	1
1:A:9:ILE:HG12	1:A:64:ILE:HG21	0.54	1.79	7	1
1:A:23:PHE:CD2	1:A:60:ILE:HD12	0.54	2.37	12	3
1:A:52:GLN:O	1:A:56:LEU:HD23	0.53	2.03	15	4
1:A:16:ASN:O	1:A:19:PHE:CD1	0.53	2.61	11	7
1:A:29:LEU:HG	1:A:56:LEU:HD12	0.53	1.80	5	1
1:A:13:LYS:HB2	1:A:60:ILE:HD12	0.53	1.80	8	1
1:A:19:PHE:CD1	1:A:20:ASP:N	0.53	2.77	17	16
1:A:58:ASP:O	1:A:62:SER:CB	0.53	2.57	19	20
1:A:70:LYS:O	1:A:74:GLU:CB	0.53	2.57	9	18
1:A:22:ILE:HG22	1:A:60:ILE:CD1	0.52	2.34	14	2
1:A:8:GLU:CD	1:A:64:ILE:HG23	0.52	2.29	9	2
1:A:12:LEU:HD22	1:A:67:TYR:CD2	0.52	2.39	17	1
1:A:56:LEU:HD13	1:A:59:GLU:OE1	0.52	2.04	15	1
1:A:30:ASP:O	1:A:33:ILE:HG13	0.51	2.05	16	12
1:A:52:GLN:O	1:A:56:LEU:HD13	0.51	2.06	12	4
1:A:4:GLU:O	1:A:8:GLU:HB2	0.51	2.06	9	14
1:A:9:ILE:HG12	1:A:64:ILE:HD13	0.51	1.83	19	2
1:A:71:GLN:O	1:A:75:ARG:HB2	0.50	2.06	11	7
1:A:19:PHE:O	1:A:23:PHE:N	0.50	2.42	4	16
1:A:29:LEU:HD23	1:A:56:LEU:CD1	0.50	2.36	5	1
1:A:9:ILE:CG2	1:A:64:ILE:HD11	0.50	2.25	13	2
1:A:8:GLU:CD	1:A:12:LEU:HD11	0.50	2.32	1	5
1:A:19:PHE:CD2	1:A:23:PHE:CD2	0.50	2.99	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:42:SER:O	1:A:46:VAL:HG23	0.50	2.06	20	6
1:A:9:ILE:CA	1:A:64:ILE:HD13	0.49	2.37	19	1
1:A:18:HIS:CG	1:A:22:ILE:HD11	0.49	2.42	16	5
1:A:64:ILE:CG2	1:A:65:ILE:HD13	0.49	2.37	15	4
1:A:40:ASN:HA	1:A:46:VAL:HG21	0.49	1.84	10	8
1:A:25:LYS:O	1:A:56:LEU:HD23	0.49	2.07	1	1
1:A:18:HIS:CD2	1:A:22:ILE:HD11	0.49	2.43	15	3
1:A:25:LYS:HB3	1:A:56:LEU:HD21	0.49	1.85	9	1
1:A:5:PHE:CA	1:A:9:ILE:HD13	0.49	2.37	11	1
1:A:37:GLU:CD	1:A:46:VAL:HG11	0.49	2.33	16	1
1:A:22:ILE:CD1	1:A:63:MET:HE2	0.49	2.37	18	1
1:A:61:HIS:HA	1:A:64:ILE:HD12	0.48	1.86	4	1
1:A:5:PHE:O	1:A:9:ILE:CG1	0.48	2.62	3	15
1:A:64:ILE:O	1:A:68:ARG:N	0.48	2.43	4	3
1:A:8:GLU:HB3	1:A:64:ILE:HD11	0.48	1.84	19	1
1:A:32:ASP:HA	1:A:35:THR:HG22	0.48	1.84	11	4
1:A:72:LYS:O	1:A:76:ALA:HA	0.48	2.09	20	11
1:A:13:LYS:HB2	1:A:60:ILE:HG23	0.47	1.85	17	1
1:A:13:LYS:CD	1:A:60:ILE:HD13	0.47	2.39	7	2
1:A:13:LYS:HD2	1:A:60:ILE:O	0.47	2.09	12	1
1:A:30:ASP:O	1:A:33:ILE:HG12	0.47	2.10	8	6
1:A:12:LEU:HD13	1:A:67:TYR:CB	0.47	2.40	11	1
1:A:12:LEU:HD13	1:A:67:TYR:HB3	0.46	1.86	20	3
1:A:13:LYS:CG	1:A:60:ILE:HG23	0.46	2.40	15	1
1:A:7:ASP:O	1:A:11:VAL:CG2	0.46	2.63	14	16
1:A:20:ASP:O	1:A:24:GLU:CB	0.46	2.63	5	14
1:A:16:ASN:O	1:A:19:PHE:HB3	0.46	2.10	9	4
1:A:3:HIS:N	1:A:3:HIS:CD2	0.46	2.84	16	1
1:A:69:GLU:O	1:A:73:SER:CB	0.46	2.64	19	19
1:A:9:ILE:HG23	1:A:64:ILE:HD13	0.46	1.86	16	1
1:A:65:ILE:HG23	1:A:68:ARG:NH2	0.46	2.25	11	1
1:A:56:LEU:O	1:A:59:GLU:HG2	0.46	2.09	15	1
1:A:12:LEU:HD22	1:A:67:TYR:CG	0.46	2.46	4	2
1:A:13:LYS:HD3	1:A:60:ILE:CD1	0.45	2.41	6	3
1:A:9:ILE:HG12	1:A:64:ILE:CD1	0.45	2.41	4	5
1:A:12:LEU:HB2	1:A:13:LYS:HE2	0.45	1.88	12	1
1:A:29:LEU:HB2	1:A:56:LEU:HD22	0.45	1.87	7	2
1:A:10:SER:O	1:A:14:ALA:CB	0.45	2.64	17	5
1:A:5:PHE:HA	1:A:9:ILE:HG13	0.45	1.89	4	3
1:A:18:HIS:CG	1:A:22:ILE:CD1	0.45	2.99	3	5
1:A:19:PHE:O	1:A:20:ASP:C	0.45	2.60	9	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:33:ILE:HG22	1:A:49:MET:CB	0.45	2.41	1	1
1:A:5:PHE:CD1	1:A:9:ILE:HD12	0.45	2.46	4	1
1:A:20:ASP:O	1:A:24:GLU:HB2	0.44	2.11	14	3
1:A:13:LYS:CD	1:A:23:PHE:CE2	0.44	3.01	18	1
1:A:57:LYS:CE	1:A:61:HIS:CD2	0.44	3.00	19	1
1:A:13:LYS:CD	1:A:63:MET:CB	0.44	2.96	3	1
1:A:29:LEU:HD22	1:A:52:GLN:CB	0.44	2.43	17	1
1:A:5:PHE:O	1:A:9:ILE:CD1	0.44	2.66	20	7
1:A:6:ARG:O	1:A:10:SER:CB	0.44	2.66	14	3
1:A:29:LEU:CB	1:A:56:LEU:HD22	0.43	2.42	12	2
1:A:70:LYS:O	1:A:74:GLU:N	0.43	2.47	16	8
1:A:18:HIS:HB2	1:A:63:MET:HE1	0.43	1.89	10	1
1:A:72:LYS:O	1:A:76:ALA:CB	0.43	2.65	7	4
1:A:13:LYS:CG	1:A:60:ILE:CD1	0.43	2.96	3	1
1:A:72:LYS:O	1:A:76:ALA:CA	0.43	2.66	16	4
1:A:13:LYS:HB3	1:A:60:ILE:HG23	0.43	1.90	12	1
1:A:53:LYS:O	1:A:57:LYS:N	0.43	2.52	8	5
1:A:19:PHE:HB2	1:A:23:PHE:HB2	0.43	1.90	8	1
1:A:13:LYS:HD3	1:A:60:ILE:HD13	0.42	1.90	1	3
1:A:4:GLU:O	1:A:8:GLU:HB3	0.42	2.14	11	3
1:A:8:GLU:HG2	1:A:64:ILE:HG23	0.42	1.91	17	1
1:A:13:LYS:O	1:A:23:PHE:CD2	0.42	2.73	19	2
1:A:9:ILE:O	1:A:13:LYS:CG	0.42	2.67	20	1
1:A:9:ILE:N	1:A:9:ILE:CD1	0.42	2.82	11	1
1:A:20:ASP:O	1:A:24:GLU:CG	0.42	2.68	6	4
1:A:4:GLU:CA	1:A:8:GLU:HB2	0.42	2.45	7	2
1:A:23:PHE:CE1	1:A:27:ASN:OD1	0.42	2.73	9	1
1:A:71:GLN:O	1:A:75:ARG:HB3	0.41	2.15	7	1
1:A:12:LEU:O	1:A:16:ASN:HB2	0.41	2.13	15	2
1:A:25:LYS:C	1:A:56:LEU:HD13	0.41	2.40	8	1
1:A:29:LEU:HD22	1:A:56:LEU:CD2	0.41	2.44	15	1
1:A:13:LYS:HD3	1:A:23:PHE:CE2	0.41	2.50	18	1
1:A:8:GLU:O	1:A:12:LEU:CG	0.41	2.68	18	3
1:A:72:LYS:HG2	1:A:76:ALA:HB3	0.41	1.92	12	1
1:A:13:LYS:HA	1:A:13:LYS:HE2	0.41	1.92	13	1
1:A:14:ALA:HB2	1:A:23:PHE:CZ	0.41	2.50	7	1
1:A:13:LYS:HG3	1:A:60:ILE:HG23	0.41	1.91	15	2
1:A:7:ASP:O	1:A:11:VAL:HB	0.41	2.16	14	1
1:A:56:LEU:O	1:A:59:GLU:CG	0.41	2.69	19	4
1:A:29:LEU:HD12	1:A:56:LEU:HG	0.41	1.91	4	1
1:A:18:HIS:HB3	1:A:22:ILE:HD12	0.41	1.93	11	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:5:PHE:HA	1:A:9:ILE:CD1	0.41	2.43	11	1
1:A:13:LYS:HG3	1:A:60:ILE:O	0.41	2.15	16	1
1:A:23:PHE:O	1:A:27:ASN:CB	0.41	2.68	18	1
1:A:57:LYS:HE3	1:A:61:HIS:CD2	0.41	2.51	19	1
1:A:23:PHE:CG	1:A:27:ASN:OD1	0.41	2.74	20	1
1:A:60:ILE:O	1:A:64:ILE:CD1	0.41	2.68	13	1
1:A:9:ILE:O	1:A:13:LYS:CB	0.41	2.68	16	1
1:A:3:HIS:CD2	1:A:7:ASP:CG	0.40	2.99	10	1
1:A:58:ASP:O	1:A:62:SER:N	0.40	2.50	10	1
1:A:9:ILE:CD1	1:A:64:ILE:HD13	0.40	2.46	11	1
1:A:3:HIS:O	1:A:7:ASP:N	0.40	2.49	8	1
1:A:13:LYS:O	1:A:19:PHE:HB2	0.40	2.16	8	1
1:A:70:LYS:O	1:A:74:GLU:CG	0.40	2.70	15	1
1:A:52:GLN:O	1:A:56:LEU:HD12	0.40	2.16	17	1
1:A:3:HIS:CG	1:A:7:ASP:OD2	0.40	2.74	8	1
1:A:12:LEU:CD1	1:A:13:LYS:N	0.40	2.79	8	1
1:A:33:ILE:CD1	1:A:34:LYS:N	0.40	2.85	9	1
1:A:13:LYS:HD3	1:A:23:PHE:CD2	0.40	2.52	18	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	73/76 (96%)	70±1 (95±1%)	3±1 (5±1%)	0±0 (0±0%)	49	83
All	All	1460/1520 (96%)	1390 (95%)	68 (5%)	2 (0%)	49	83

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	3	HIS	2

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	69/71 (97%)	51±2 (74±3%)	18±2 (26±3%)	2	22
All	All	1380/1420 (97%)	1019 (74%)	361 (26%)	2	22

All 52 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	18	HIS	19
1	A	8	GLU	18
1	A	42	SER	16
1	A	13	LYS	15
1	A	51	LYS	15
1	A	25	LYS	14
1	A	69	GLU	14
1	A	19	PHE	13
1	A	6	ARG	12
1	A	21	LYS	12
1	A	23	PHE	12
1	A	29	LEU	12
1	A	53	LYS	12
1	A	34	LYS	12
1	A	28	GLN	11
1	A	75	ARG	11
1	A	68	ARG	10
1	A	43	ASP	8
1	A	55	LYS	8
1	A	32	ASP	8
1	A	66	GLU	8
1	A	33	ILE	7
1	A	49	MET	7
1	A	3	HIS	7
1	A	38	GLN	7
1	A	31	ASP	6
1	A	72	LYS	6
1	A	12	LEU	5
1	A	45	GLU	5

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Mol	Chain	Res	Type	Models (Total)
1	A	63	MET	5
1	A	24	GLU	5
1	A	39	GLN	4
1	A	50	LYS	4
1	A	70	LYS	4
1	A	57	LYS	3
1	A	64	ILE	3
1	A	52	GLN	3
1	A	56	LEU	2
1	A	71	GLN	2
1	A	27	ASN	2
1	A	58	ASP	2
1	A	30	ASP	2
1	A	48	HIS	1
1	A	47	SER	1
1	A	74	GLU	1
1	A	54	LEU	1
1	A	7	ASP	1
1	A	4	GLU	1
1	A	16	ASN	1
1	A	20	ASP	1
1	A	5	PHE	1
1	A	61	HIS	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 [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