Full wwPDB NMR Structure Validation Report (i)

Dec 11, 2022 – 02:49 AM EST

PDB ID	:	1CPZ
Title	:	COPPER CHAPERONE OF ENTEROCOCCUS HIRAE (APO-FORM)
Authors	:	Wimmer, R.; Herrmann, T.; Solioz, M.; Wuethrich, K.
Deposited on	:	1999-05-06

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

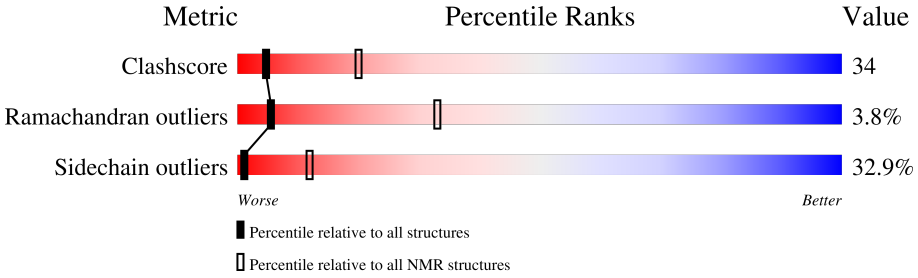
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.31.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The overall completeness of chemical shifts assignment was not calculated.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	68	31% 54% 13% •

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 3 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:2-A:68 (67)	0.31	3

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1059 atoms, of which 539 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Copper chaperone.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	68	1059	325	539	92	99	4	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	expression tag	UNP A0A1V8XBM5

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: Copper chaperone

Chain A: 31% 54% 13%

A1 Q2 E3 F4 S5 M9 S10 C11 N12 H13 C14 V15 A16 R17 I18 E19 E20 A21 V22 G23 R24 I25 V28 K29 K30 V31 K32 V33 Q34 L35 K36 K37 E38 K39 V42 K43 F44 N48 V49 Q50 A51 T52 E53 I54 C55 Q56 A57 I58 N59 E60 L61 G62 Y63 Q64 A65 E66

V67 I68

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: Copper chaperone

Chain A: 34% 54% 10%

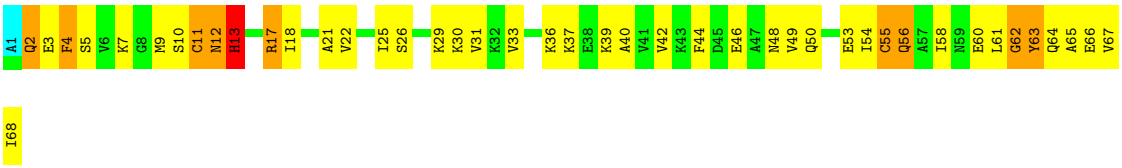
A1 Q2 E3 F4 S5 S10 C11 N12 H13 C14 V15 A16 R17 I18 A21 V22 G23 R24 I25 S26 G27 V28 K29 K30 V31 K32 L35 K36 K39 A40 V41 V42 K43 F44 D45 N48 V49 Q50 A51 T52 E53 I54 C55 Q56 A57 I58 N59 E60 L61 G62 Y63 Q64 A65 E66 V67

I68

4.2.2 Score per residue for model 2

• Molecule 1: Copper chaperone

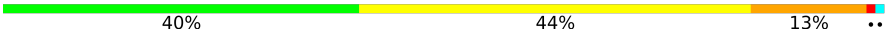
Chain A: 34% 50% 13%



4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: Copper chaperone

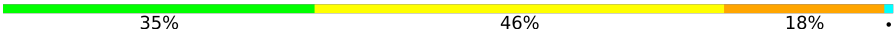
Chain A:

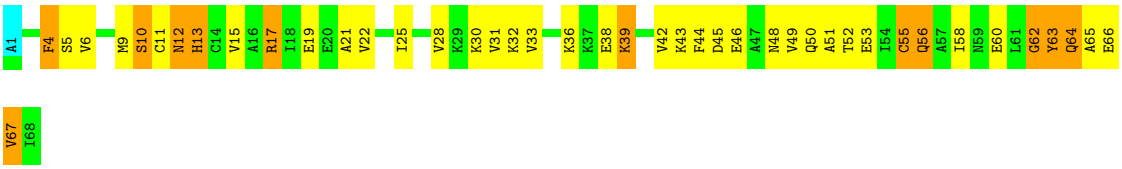


4.2.4 Score per residue for model 4

- Molecule 1: Copper chaperone

Chain A:

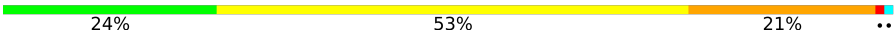


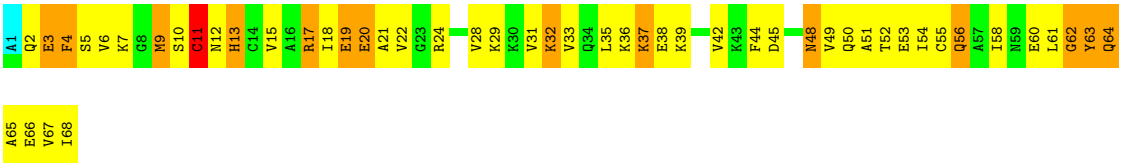


4.2.5 Score per residue for model 5

- Molecule 1: Copper chaperone

Chain A:

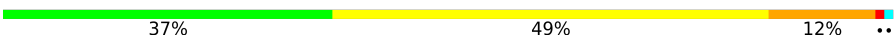




4.2.6 Score per residue for model 6

- Molecule 1: Copper chaperone

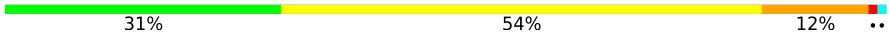
Chain A:



4.2.7 Score per residue for model 7

- Molecule 1: Copper chaperone

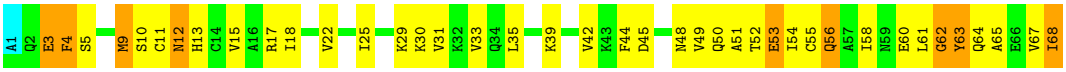
Chain A:



4.2.8 Score per residue for model 8

- Molecule 1: Copper chaperone

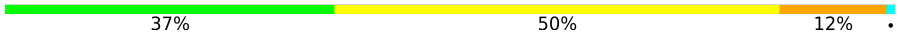
Chain A:

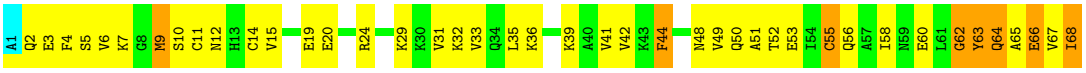


4.2.9 Score per residue for model 9

- Molecule 1: Copper chaperone

Chain A:





4.2.10 Score per residue for model 10

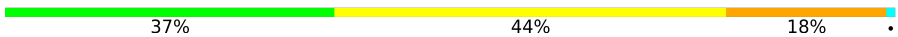
- Molecule 1: Copper chaperone

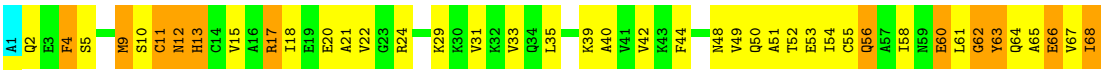
Chain A:

4.2.11 Score per residue for model 11

- Molecule 1: Copper chaperone

Chain A:

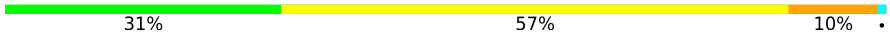




4.2.12 Score per residue for model 12

- Molecule 1: Copper chaperone

Chain A:



4.2.13 Score per residue for model 13

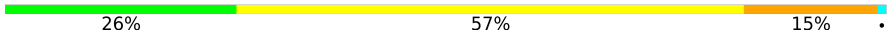
- Molecule 1: Copper chaperone

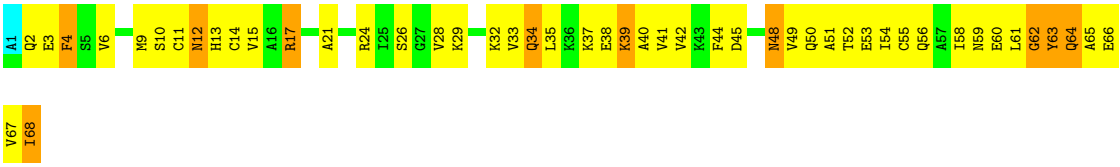
Chain A:

4.2.14 Score per residue for model 14

- Molecule 1: Copper chaperone

Chain A:

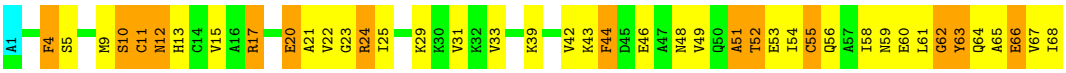




4.2.15 Score per residue for model 15

- Molecule 1: Copper chaperone

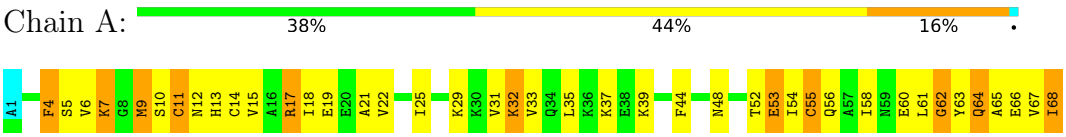
Chain A:



4.2.16 Score per residue for model 16

- Molecule 1: Copper chaperone

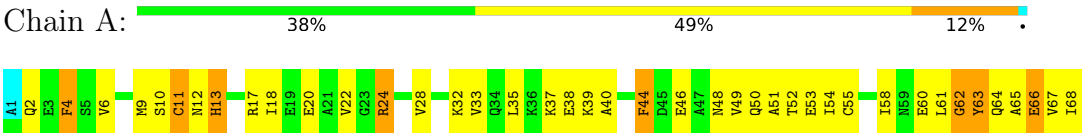
Chain A:



4.2.17 Score per residue for model 17

- Molecule 1: Copper chaperone

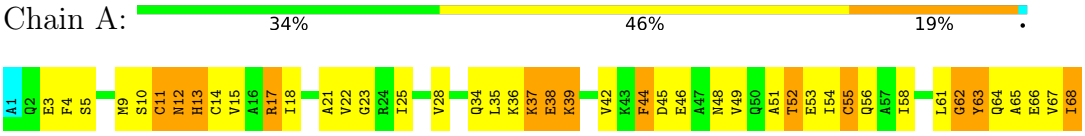
Chain A:



4.2.18 Score per residue for model 18

- Molecule 1: Copper chaperone

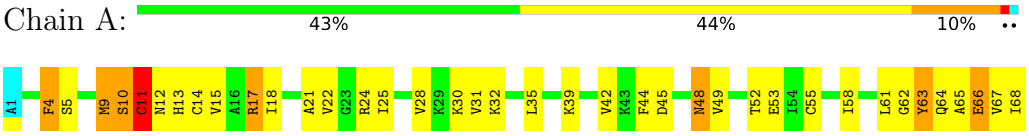
Chain A:



4.2.19 Score per residue for model 19

- Molecule 1: Copper chaperone

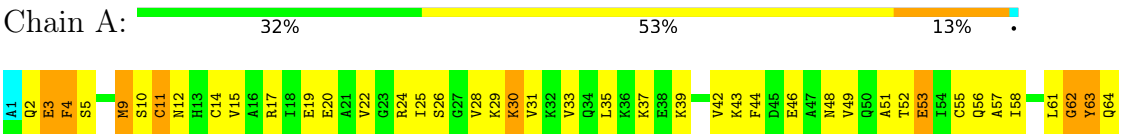
Chain A:



4.2.20 Score per residue for model 20

- Molecule 1: Copper chaperone

Chain A:



A65
E66
V67
I68

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *distance geometry*.

Of the 50 calculated structures, 20 were deposited, based on the following criterion: *LEAST RESTRAINT VIOLATION*.

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

Software name	Classification	Version
OPALp	refinement	
DYANA	structure solution	

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	515	534	534	35±6
All	All	10300	10680	10680	709

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 34.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:15:VAL:HG13	1:A:33:VAL:HG11	1.03	1.20	14	4
1:A:25:ILE:CD1	1:A:54:ILE:HG23	0.91	1.95	18	3
1:A:18:ILE:O	1:A:22:VAL:HG23	0.89	1.68	16	9
1:A:15:VAL:HG13	1:A:33:VAL:CG1	0.89	1.98	20	9
1:A:35:LEU:HD13	1:A:36:LYS:N	0.87	1.84	13	1
1:A:67:VAL:C	1:A:68:ILE:HD12	0.86	1.89	17	4
1:A:25:ILE:CG2	1:A:49:VAL:HG21	0.85	2.00	4	2
1:A:58:ILE:HG21	1:A:65:ALA:HB2	0.85	1.46	9	13
1:A:25:ILE:HD13	1:A:54:ILE:HG12	0.85	1.48	18	1
1:A:4:PHE:CZ	1:A:42:VAL:HG11	0.81	2.09	20	2
1:A:22:VAL:HG12	1:A:28:VAL:HG11	0.81	1.52	20	1
1:A:11:CYS:SG	1:A:35:LEU:HD21	0.81	2.15	16	8
1:A:3:GLU:CD	1:A:68:ILE:HD12	0.80	1.97	14	1
1:A:22:VAL:HB	1:A:31:VAL:HG21	0.80	1.53	16	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:11:CYS:SG	1:A:35:LEU:HD11	0.78	2.18	13	2
1:A:2:GLN:O	1:A:42:VAL:HG12	0.77	1.79	1	2
1:A:9:MET:CE	1:A:15:VAL:HG23	0.77	2.10	13	1
1:A:42:VAL:HG12	1:A:44:PHE:CD1	0.76	2.15	9	5
1:A:55:CYS:SG	1:A:67:VAL:HG23	0.75	2.21	12	4
1:A:23:GLY:HA2	1:A:28:VAL:HG11	0.75	1.58	18	1
1:A:22:VAL:CG2	1:A:58:ILE:HD11	0.73	2.12	18	1
1:A:5:SER:HB2	1:A:68:ILE:HD11	0.73	1.60	10	2
1:A:22:VAL:HA	1:A:25:ILE:HD12	0.73	1.60	20	2
1:A:31:VAL:HG23	1:A:42:VAL:HG22	0.71	1.61	13	5
1:A:15:VAL:HG21	1:A:35:LEU:HB2	0.71	1.60	16	1
1:A:18:ILE:HG23	1:A:58:ILE:HD12	0.70	1.62	16	2
1:A:58:ILE:CG2	1:A:65:ALA:HB2	0.69	2.17	11	17
1:A:5:SER:N	1:A:68:ILE:HD11	0.69	2.02	11	2
1:A:44:PHE:CE2	1:A:54:ILE:CD1	0.69	2.75	18	3
1:A:28:VAL:HG22	1:A:44:PHE:HB3	0.69	1.64	1	7
1:A:25:ILE:HD11	1:A:54:ILE:HG23	0.69	1.64	18	1
1:A:51:ALA:HA	1:A:54:ILE:HD12	0.68	1.66	8	2
1:A:15:VAL:HG13	1:A:33:VAL:HG12	0.68	1.64	11	5
1:A:25:ILE:HG21	1:A:54:ILE:HG12	0.68	1.64	15	1
1:A:52:THR:HA	1:A:67:VAL:HG21	0.67	1.67	18	2
1:A:4:PHE:CD1	1:A:4:PHE:N	0.66	2.63	8	10
1:A:6:VAL:HG13	1:A:64:GLN:O	0.66	1.90	14	3
1:A:25:ILE:HD11	1:A:57:ALA:CB	0.65	2.20	20	1
1:A:66:GLU:O	1:A:68:ILE:HD12	0.65	1.92	19	3
1:A:5:SER:H	1:A:68:ILE:HD11	0.63	1.53	11	2
1:A:13:HIS:CG	1:A:13:HIS:O	0.63	2.51	16	5
1:A:25:ILE:HG22	1:A:49:VAL:HG21	0.63	1.67	4	3
1:A:44:PHE:CZ	1:A:51:ALA:HB2	0.63	2.29	7	7
1:A:5:SER:HB3	1:A:68:ILE:HD13	0.62	1.71	20	3
1:A:44:PHE:C	1:A:44:PHE:CD1	0.62	2.71	17	2
1:A:42:VAL:HG12	1:A:44:PHE:HD1	0.62	1.54	9	5
1:A:67:VAL:O	1:A:68:ILE:HD12	0.62	1.93	5	2
1:A:18:ILE:HG23	1:A:58:ILE:HG12	0.62	1.72	17	2
1:A:44:PHE:CD2	1:A:49:VAL:HG13	0.62	2.29	12	1
1:A:25:ILE:HG21	1:A:49:VAL:HG11	0.61	1.72	19	2
1:A:2:GLN:OE1	1:A:51:ALA:HB2	0.61	1.95	5	1
1:A:28:VAL:CG2	1:A:42:VAL:CG1	0.61	2.78	7	1
1:A:19:GLU:HG2	1:A:31:VAL:HG22	0.61	1.71	16	2
1:A:44:PHE:CE2	1:A:54:ILE:HD12	0.61	2.30	18	3
1:A:9:MET:CE	1:A:35:LEU:HD13	0.61	2.26	11	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:SER:O	1:A:11:CYS:CB	0.61	2.49	8	18
1:A:15:VAL:HG22	1:A:33:VAL:HG11	0.60	1.71	8	2
1:A:11:CYS:SG	1:A:35:LEU:HD22	0.60	2.36	9	1
1:A:18:ILE:HG23	1:A:58:ILE:CD1	0.60	2.26	16	2
1:A:22:VAL:CG1	1:A:31:VAL:HG21	0.60	2.27	2	5
1:A:44:PHE:CD1	1:A:44:PHE:N	0.60	2.68	9	5
1:A:14:CYS:SG	1:A:63:TYR:CE1	0.60	2.94	20	1
1:A:61:LEU:CB	1:A:63:TYR:CE2	0.60	2.85	19	7
1:A:22:VAL:HG23	1:A:58:ILE:HD11	0.60	1.73	18	1
1:A:2:GLN:O	1:A:4:PHE:CE1	0.60	2.55	17	2
1:A:31:VAL:CG2	1:A:42:VAL:HG22	0.60	2.25	13	1
1:A:22:VAL:HG11	1:A:31:VAL:HG21	0.59	1.72	20	1
1:A:9:MET:HE3	1:A:15:VAL:HG23	0.59	1.74	13	1
1:A:42:VAL:HG21	1:A:54:ILE:CD1	0.59	2.27	12	1
1:A:22:VAL:CG1	1:A:28:VAL:HG11	0.59	2.27	20	1
1:A:33:VAL:HG23	1:A:40:ALA:HB2	0.59	1.75	11	2
1:A:9:MET:SD	1:A:35:LEU:HD12	0.59	2.37	7	1
1:A:44:PHE:CZ	1:A:54:ILE:CD1	0.58	2.86	5	1
1:A:22:VAL:O	1:A:25:ILE:HD12	0.58	1.99	7	2
1:A:15:VAL:CG1	1:A:33:VAL:HG11	0.58	2.13	14	2
1:A:22:VAL:HG11	1:A:31:VAL:CG2	0.58	2.28	20	1
1:A:19:GLU:CG	1:A:31:VAL:HG22	0.57	2.29	9	1
1:A:44:PHE:CD2	1:A:54:ILE:CD1	0.57	2.87	18	3
1:A:12:ASN:O	1:A:13:HIS:CG	0.57	2.57	4	3
1:A:5:SER:CB	1:A:68:ILE:HD11	0.57	2.28	10	3
1:A:15:VAL:HG22	1:A:33:VAL:HG12	0.57	1.77	5	1
1:A:4:PHE:HE1	1:A:51:ALA:HB1	0.56	1.59	12	5
1:A:12:ASN:O	1:A:13:HIS:CD2	0.56	2.59	7	3
1:A:2:GLN:NE2	1:A:67:VAL:CG1	0.56	2.69	5	2
1:A:68:ILE:HD12	1:A:68:ILE:N	0.56	2.16	17	1
1:A:4:PHE:CD1	1:A:67:VAL:HG23	0.56	2.36	7	1
1:A:44:PHE:CE1	1:A:54:ILE:CD1	0.56	2.89	2	2
1:A:22:VAL:HG13	1:A:25:ILE:CD1	0.55	2.32	7	1
1:A:4:PHE:CD2	1:A:67:VAL:HG22	0.55	2.35	10	3
1:A:35:LEU:HD13	1:A:36:LYS:H	0.55	1.60	13	1
1:A:19:GLU:OE2	1:A:31:VAL:HG13	0.55	2.02	16	1
1:A:61:LEU:HB3	1:A:63:TYR:CE2	0.55	2.37	19	1
1:A:11:CYS:SG	1:A:35:LEU:HD13	0.55	2.41	9	1
1:A:44:PHE:CZ	1:A:54:ILE:HD12	0.55	2.37	16	3
1:A:42:VAL:CG1	1:A:44:PHE:CD2	0.55	2.90	13	3
1:A:55:CYS:HA	1:A:58:ILE:HD12	0.54	1.78	1	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:25:ILE:HD13	1:A:54:ILE:CG1	0.54	2.29	18	1
1:A:25:ILE:HD13	1:A:54:ILE:HG23	0.54	1.77	7	3
1:A:18:ILE:HD11	1:A:63:TYR:CE2	0.54	2.37	16	1
1:A:12:ASN:O	1:A:13:HIS:CB	0.54	2.56	7	7
1:A:44:PHE:CD2	1:A:49:VAL:CG1	0.54	2.91	12	1
1:A:42:VAL:HG11	1:A:54:ILE:CD1	0.53	2.33	10	1
1:A:54:ILE:HG22	1:A:58:ILE:CD1	0.53	2.34	12	1
1:A:4:PHE:HD2	1:A:67:VAL:HG22	0.53	1.62	14	2
1:A:44:PHE:HZ	1:A:51:ALA:HB2	0.53	1.63	20	5
1:A:25:ILE:CD1	1:A:54:ILE:CG2	0.53	2.82	18	1
1:A:4:PHE:HZ	1:A:42:VAL:HG11	0.52	1.62	1	3
1:A:10:SER:CB	1:A:12:ASN:OD1	0.52	2.57	6	1
1:A:68:ILE:N	1:A:68:ILE:HD13	0.52	2.20	8	1
1:A:4:PHE:CE2	1:A:42:VAL:HG21	0.52	2.39	6	1
1:A:7:LYS:N	1:A:64:GLN:O	0.52	2.43	9	3
1:A:13:HIS:CD2	1:A:13:HIS:C	0.52	2.82	7	2
1:A:18:ILE:HD13	1:A:18:ILE:N	0.52	2.18	16	1
1:A:63:TYR:N	1:A:63:TYR:CD1	0.52	2.76	19	1
1:A:22:VAL:CB	1:A:31:VAL:HG21	0.52	2.32	16	1
1:A:17:ARG:O	1:A:21:ALA:CB	0.52	2.58	16	12
1:A:35:LEU:HD13	1:A:35:LEU:O	0.52	2.05	3	2
1:A:24:ARG:O	1:A:24:ARG:CG	0.51	2.58	10	4
1:A:25:ILE:HG21	1:A:54:ILE:CG1	0.51	2.35	15	1
1:A:4:PHE:HE2	1:A:42:VAL:HG21	0.51	1.65	6	1
1:A:9:MET:HE1	1:A:15:VAL:HG23	0.51	1.83	13	1
1:A:11:CYS:SG	1:A:35:LEU:CD2	0.51	2.98	9	5
1:A:3:GLU:C	1:A:4:PHE:CD1	0.51	2.84	3	9
1:A:15:VAL:HG23	1:A:35:LEU:HD13	0.51	1.82	16	1
1:A:67:VAL:C	1:A:68:ILE:HD13	0.51	2.26	9	3
1:A:2:GLN:OE1	1:A:67:VAL:CG1	0.51	2.59	2	2
1:A:42:VAL:HG12	1:A:44:PHE:CD2	0.51	2.41	15	1
1:A:22:VAL:HG13	1:A:54:ILE:HG23	0.50	1.82	5	4
1:A:23:GLY:CA	1:A:31:VAL:HG11	0.50	2.36	10	3
1:A:56:GLN:O	1:A:60:GLU:CG	0.50	2.59	6	1
1:A:34:GLN:HE22	1:A:41:VAL:HG23	0.50	1.67	14	1
1:A:17:ARG:O	1:A:21:ALA:HB2	0.50	2.06	3	9
1:A:61:LEU:HB2	1:A:63:TYR:CE2	0.50	2.41	15	15
1:A:2:GLN:OE1	1:A:51:ALA:CB	0.50	2.59	5	1
1:A:48:ASN:ND2	1:A:48:ASN:N	0.50	2.59	14	1
1:A:22:VAL:HG22	1:A:54:ILE:HG23	0.50	1.83	17	1
1:A:4:PHE:CD2	1:A:67:VAL:HG23	0.50	2.42	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:62:GLY:C	1:A:63:TYR:CD1	0.50	2.85	17	18
1:A:4:PHE:CE1	1:A:51:ALA:HB1	0.49	2.40	12	4
1:A:59:ASN:OD1	1:A:59:ASN:C	0.49	2.51	6	3
1:A:11:CYS:O	1:A:12:ASN:CB	0.49	2.61	3	6
1:A:28:VAL:HG13	1:A:42:VAL:HG13	0.49	1.84	14	2
1:A:12:ASN:ND2	1:A:12:ASN:N	0.49	2.60	18	3
1:A:38:GLU:O	1:A:39:LYS:CD	0.49	2.60	18	1
1:A:37:LYS:O	1:A:38:GLU:HB2	0.49	2.08	14	2
1:A:58:ILE:HG22	1:A:65:ALA:HB2	0.49	1.83	16	4
1:A:32:LYS:O	1:A:33:VAL:HG23	0.49	2.07	9	4
1:A:15:VAL:HG22	1:A:33:VAL:CG1	0.48	2.38	8	3
1:A:37:LYS:O	1:A:38:GLU:CB	0.48	2.61	7	2
1:A:9:MET:SD	1:A:35:LEU:CD1	0.48	3.02	12	5
1:A:15:VAL:HG13	1:A:33:VAL:CB	0.48	2.38	8	1
1:A:10:SER:CB	1:A:14:CYS:SG	0.48	3.02	3	1
1:A:44:PHE:CD2	1:A:45:ASP:N	0.48	2.81	10	3
1:A:5:SER:N	1:A:66:GLU:O	0.48	2.45	5	14
1:A:62:GLY:O	1:A:63:TYR:CD1	0.48	2.67	20	17
1:A:28:VAL:CG2	1:A:42:VAL:HG13	0.48	2.38	7	1
1:A:11:CYS:SG	1:A:35:LEU:CD1	0.48	3.02	9	2
1:A:25:ILE:HD11	1:A:57:ALA:HB3	0.48	1.86	20	1
1:A:15:VAL:HG22	1:A:33:VAL:HG13	0.47	1.86	11	1
1:A:22:VAL:HG11	1:A:42:VAL:CG2	0.47	2.39	13	3
1:A:44:PHE:HB2	1:A:49:VAL:HG11	0.47	1.85	18	1
1:A:4:PHE:C	1:A:68:ILE:CD1	0.47	2.82	2	1
1:A:44:PHE:CD1	1:A:54:ILE:CD1	0.47	2.97	2	1
1:A:44:PHE:CD2	1:A:54:ILE:HD11	0.47	2.44	5	2
1:A:25:ILE:CG2	1:A:49:VAL:HG11	0.47	2.39	19	2
1:A:9:MET:SD	1:A:35:LEU:CD2	0.47	3.02	5	1
1:A:11:CYS:O	1:A:14:CYS:SG	0.47	2.72	7	1
1:A:4:PHE:CZ	1:A:42:VAL:CG1	0.47	2.98	1	2
1:A:48:ASN:N	1:A:48:ASN:OD1	0.47	2.48	5	1
1:A:59:ASN:C	1:A:61:LEU:H	0.47	2.13	15	1
1:A:66:GLU:O	1:A:68:ILE:CD1	0.47	2.61	19	1
1:A:44:PHE:CD1	1:A:49:VAL:HG13	0.47	2.45	11	1
1:A:6:VAL:O	1:A:38:GLU:CG	0.47	2.62	12	2
1:A:6:VAL:CG1	1:A:64:GLN:O	0.47	2.61	14	1
1:A:2:GLN:O	1:A:4:PHE:CZ	0.47	2.67	17	1
1:A:26:SER:O	1:A:49:VAL:CG2	0.47	2.63	7	4
1:A:9:MET:SD	1:A:15:VAL:HG23	0.47	2.50	12	2
1:A:54:ILE:HD12	1:A:54:ILE:N	0.47	2.24	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:59:ASN:OD1	1:A:60:GLU:N	0.47	2.48	6	3
1:A:42:VAL:HG11	1:A:54:ILE:HD13	0.46	1.87	10	1
1:A:9:MET:CE	1:A:35:LEU:CD1	0.46	2.93	11	1
1:A:14:CYS:O	1:A:17:ARG:N	0.46	2.48	16	1
1:A:56:GLN:O	1:A:60:GLU:N	0.46	2.48	10	9
1:A:44:PHE:CD2	1:A:54:ILE:HD13	0.46	2.45	8	1
1:A:28:VAL:HG13	1:A:42:VAL:CG2	0.46	2.40	4	1
1:A:32:LYS:N	1:A:41:VAL:O	0.46	2.48	9	1
1:A:4:PHE:HE2	1:A:51:ALA:HB1	0.46	1.69	14	2
1:A:12:ASN:O	1:A:13:HIS:ND1	0.46	2.48	2	1
1:A:55:CYS:SG	1:A:67:VAL:N	0.46	2.88	4	2
1:A:56:GLN:O	1:A:60:GLU:CB	0.46	2.64	6	1
1:A:49:VAL:CG1	1:A:50:GLN:N	0.46	2.78	8	5
1:A:49:VAL:HG12	1:A:50:GLN:N	0.46	2.26	17	1
1:A:34:GLN:N	1:A:34:GLN:CD	0.46	2.69	3	1
1:A:42:VAL:HG11	1:A:44:PHE:CD2	0.46	2.45	18	2
1:A:30:LYS:O	1:A:43:LYS:N	0.46	2.48	20	2
1:A:2:GLN:HG3	1:A:3:GLU:N	0.46	2.26	5	1
1:A:45:ASP:O	1:A:49:VAL:HG12	0.46	2.10	18	1
1:A:13:HIS:ND1	1:A:13:HIS:C	0.46	2.70	4	3
1:A:15:VAL:HG13	1:A:33:VAL:HB	0.46	1.87	8	1
1:A:9:MET:SD	1:A:35:LEU:HD13	0.46	2.51	20	3
1:A:37:LYS:O	1:A:39:LYS:CD	0.45	2.65	13	2
1:A:38:GLU:C	1:A:39:LYS:CD	0.45	2.85	18	1
1:A:4:PHE:CE2	1:A:51:ALA:HB1	0.45	2.46	11	3
1:A:28:VAL:CG2	1:A:54:ILE:HD11	0.45	2.40	14	2
1:A:15:VAL:HA	1:A:33:VAL:HG11	0.45	1.86	11	1
1:A:12:ASN:OD1	1:A:12:ASN:N	0.45	2.49	6	1
1:A:34:GLN:NE2	1:A:41:VAL:HG23	0.45	2.26	14	1
1:A:68:ILE:N	1:A:68:ILE:CD1	0.45	2.79	17	1
1:A:4:PHE:CE2	1:A:54:ILE:HG21	0.45	2.47	6	1
1:A:22:VAL:HG12	1:A:31:VAL:HG21	0.45	1.87	6	1
1:A:54:ILE:HG22	1:A:58:ILE:HD11	0.45	1.87	12	1
1:A:20:GLU:O	1:A:24:ARG:N	0.45	2.49	15	1
1:A:14:CYS:O	1:A:15:VAL:C	0.45	2.55	18	11
1:A:5:SER:O	1:A:66:GLU:N	0.45	2.47	5	3
1:A:4:PHE:HA	1:A:66:GLU:O	0.45	2.12	9	4
1:A:44:PHE:CZ	1:A:51:ALA:N	0.45	2.85	11	1
1:A:13:HIS:O	1:A:13:HIS:CG	0.45	2.70	5	1
1:A:37:LYS:C	1:A:38:GLU:CG	0.45	2.86	5	1
1:A:22:VAL:HG13	1:A:25:ILE:HD12	0.44	1.88	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:11:CYS:O	1:A:13:HIS:N	0.44	2.50	18	2
1:A:14:CYS:SG	1:A:63:TYR:CZ	0.44	3.00	20	1
1:A:4:PHE:O	1:A:40:ALA:N	0.44	2.49	14	2
1:A:35:LEU:C	1:A:37:LYS:N	0.44	2.70	14	2
1:A:44:PHE:CE2	1:A:49:VAL:O	0.44	2.70	10	1
1:A:44:PHE:HB2	1:A:49:VAL:CG1	0.44	2.43	18	3
1:A:55:CYS:SG	1:A:65:ALA:HB1	0.44	2.53	15	1
1:A:23:GLY:CA	1:A:28:VAL:HG11	0.44	2.38	18	1
1:A:22:VAL:HG22	1:A:54:ILE:CG2	0.43	2.43	17	1
1:A:44:PHE:CE1	1:A:54:ILE:HD12	0.43	2.48	2	1
1:A:44:PHE:CD2	1:A:49:VAL:O	0.43	2.71	10	1
1:A:42:VAL:HG13	1:A:44:PHE:CD1	0.43	2.49	4	1
1:A:26:SER:O	1:A:49:VAL:HG23	0.43	2.13	20	2
1:A:6:VAL:HG11	1:A:9:MET:HE2	0.43	1.89	9	1
1:A:45:ASP:O	1:A:49:VAL:O	0.43	2.36	5	6
1:A:4:PHE:CD1	1:A:67:VAL:HG22	0.43	2.48	12	1
1:A:55:CYS:SG	1:A:66:GLU:CA	0.43	3.07	2	1
1:A:5:SER:CB	1:A:68:ILE:HD13	0.43	2.43	20	1
1:A:31:VAL:HG23	1:A:41:VAL:O	0.43	2.14	1	1
1:A:32:LYS:O	1:A:33:VAL:CG2	0.43	2.67	5	2
1:A:55:CYS:SG	1:A:67:VAL:CG2	0.43	3.07	9	4
1:A:18:ILE:O	1:A:22:VAL:N	0.42	2.48	2	2
1:A:33:VAL:HG22	1:A:40:ALA:CB	0.42	2.44	2	2
1:A:2:GLN:HG2	1:A:67:VAL:HG13	0.42	1.91	2	1
1:A:22:VAL:HG11	1:A:42:VAL:HG21	0.42	1.90	13	1
1:A:2:GLN:OE1	1:A:67:VAL:HG11	0.42	2.14	2	1
1:A:6:VAL:HA	1:A:64:GLN:O	0.42	2.15	14	4
1:A:28:VAL:HG22	1:A:54:ILE:HD11	0.42	1.90	10	1
1:A:11:CYS:C	1:A:12:ASN:CG	0.42	2.78	3	5
1:A:5:SER:O	1:A:65:ALA:HA	0.42	2.14	7	1
1:A:45:ASP:HB3	1:A:48:ASN:ND2	0.42	2.30	19	1
1:A:22:VAL:HA	1:A:25:ILE:CD1	0.42	2.45	1	1
1:A:4:PHE:CA	1:A:66:GLU:O	0.42	2.68	5	1
1:A:52:THR:CG2	1:A:53:GLU:N	0.42	2.83	16	3
1:A:6:VAL:HG11	1:A:9:MET:CE	0.42	2.44	9	1
1:A:5:SER:CA	1:A:68:ILE:HD11	0.42	2.44	2	1
1:A:22:VAL:O	1:A:25:ILE:CD1	0.42	2.66	7	1
1:A:42:VAL:CG1	1:A:44:PHE:CD1	0.42	3.03	19	1
1:A:44:PHE:CG	1:A:54:ILE:HD11	0.41	2.50	2	1
1:A:44:PHE:CE2	1:A:54:ILE:HD13	0.41	2.50	13	1
1:A:35:LEU:HD13	1:A:35:LEU:C	0.41	2.36	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:GLU:OE1	1:A:20:GLU:N	0.41	2.53	5	1
1:A:66:GLU:O	1:A:66:GLU:CG	0.41	2.68	14	1
1:A:32:LYS:HE2	1:A:33:VAL:N	0.41	2.30	16	1
1:A:44:PHE:CE1	1:A:54:ILE:HD13	0.41	2.50	5	1
1:A:54:ILE:HD12	1:A:54:ILE:H	0.41	1.74	13	1
1:A:4:PHE:CE2	1:A:42:VAL:CG2	0.41	3.02	6	1
1:A:37:LYS:HB3	1:A:39:LYS:CG	0.41	2.46	13	2
1:A:3:GLU:O	1:A:68:ILE:N	0.41	2.43	18	3
1:A:2:GLN:CG	1:A:67:VAL:HG13	0.41	2.46	2	1
1:A:38:GLU:C	1:A:39:LYS:CG	0.41	2.87	4	1
1:A:6:VAL:O	1:A:38:GLU:OE1	0.41	2.39	17	1
1:A:19:GLU:CD	1:A:20:GLU:N	0.41	2.73	20	1
1:A:22:VAL:CG1	1:A:31:VAL:CG2	0.41	2.97	2	1
1:A:44:PHE:CE2	1:A:51:ALA:HB2	0.41	2.50	9	1
1:A:48:ASN:OD1	1:A:48:ASN:N	0.41	2.54	19	1
1:A:55:CYS:SG	1:A:66:GLU:C	0.40	2.99	2	1
1:A:2:GLN:NE2	1:A:68:ILE:C	0.40	2.74	13	1
1:A:25:ILE:HG21	1:A:49:VAL:HG21	0.40	1.85	4	1
1:A:2:GLN:NE2	1:A:67:VAL:HG13	0.40	2.32	5	1
1:A:44:PHE:CZ	1:A:46:GLU:OE2	0.40	2.74	12	1
1:A:15:VAL:CG1	1:A:33:VAL:CG1	0.40	2.90	13	1
1:A:7:LYS:O	1:A:64:GLN:N	0.40	2.47	2	1
1:A:7:LYS:CB	1:A:64:GLN:HB2	0.40	2.46	16	1
1:A:58:ILE:CG2	1:A:65:ALA:CB	0.40	2.99	17	1
1:A:19:GLU:O	1:A:19:GLU:OE1	0.40	2.40	6	1
1:A:6:VAL:HG13	1:A:6:VAL:O	0.40	2.16	16	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	66/68 (97%)	53±2 (80±3%)	10±2 (16±3%)	2±1 (4±1%)	5	33
All	All	1320/1360 (97%)	1061 (80%)	209 (16%)	50 (4%)	5	33

All 8 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	62	GLY	19
1	A	11	CYS	13
1	A	12	ASN	8
1	A	13	HIS	3
1	A	26	SER	2
1	A	38	GLU	2
1	A	51	ALA	2
1	A	2	GLN	1

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	56/56 (100%)	38±2 (67±4%)	18±2 (33±4%)	1 12
All	All	1120/1120 (100%)	751 (67%)	369 (33%)	1 12

All 37 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	39	LYS	20
1	A	48	ASN	20
1	A	53	GLU	20
1	A	55	CYS	20
1	A	63	TYR	19
1	A	9	MET	19
1	A	4	PHE	18
1	A	17	ARG	18
1	A	52	THR	16
1	A	64	GLN	15
1	A	56	GLN	14
1	A	13	HIS	13
1	A	29	LYS	13
1	A	12	ASN	11
1	A	24	ARG	11
1	A	32	LYS	11

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Mol	Chain	Res	Type	Models (Total)
1	A	68	ILE	11
1	A	37	LYS	10
1	A	36	LYS	9
1	A	46	GLU	9
1	A	20	GLU	9
1	A	66	GLU	8
1	A	30	LYS	6
1	A	60	GLU	6
1	A	2	GLN	6
1	A	44	PHE	6
1	A	10	SER	5
1	A	19	GLU	5
1	A	50	GLN	3
1	A	3	GLU	3
1	A	11	CYS	3
1	A	34	GLN	3
1	A	43	LYS	3
1	A	67	VAL	2
1	A	7	LYS	2
1	A	35	LEU	1
1	A	28	VAL	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