



Full wwPDB NMR Structure Validation Report ⓘ

Mar 19, 2026 – 11:28 AM UTC

PDB ID : 1OQ3 / pdb_00001oq3
Title : A core mutation affecting the folding properties of a soluble domain of the ATPase protein CopA from Bacillus subtilis
Authors : Banci, L.; Bertini, I.; Ciofi-Baffoni, S.; Gonnelli, L.; Su, X.C.; Structural Proteomics in Europe (SPINE)
Deposited on : 2003-03-07

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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

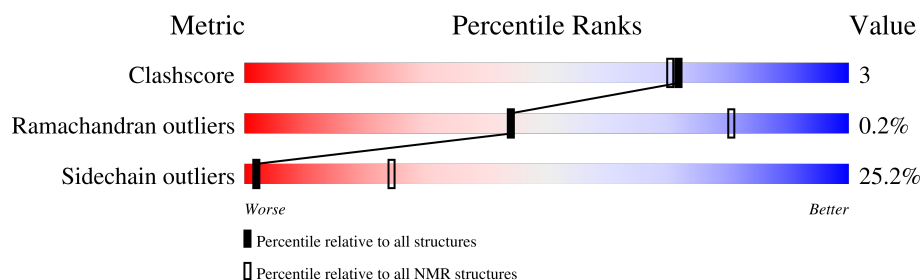
1 Overall quality at a glance

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 30 models. Model 23 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:5-A:13, A:22-A:72 (60)	0.26	23

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 3 single-model clusters were found.

Cluster number	Models
1	1, 3, 7, 8, 9, 10, 11, 12, 14, 15, 18, 19, 20, 22, 23, 24, 28
2	2, 5, 13, 16, 17, 25, 29, 30
3	6, 21
Single-model clusters	4; 26; 27

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1149 atoms, of which 582 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Potential copper-transporting ATPase.

Mol	Chain	Residues	Atoms						Trace
1	A	76	Total	C	H	N	O	S	0
			1149	350	582	98	113	6	

There are 4 discrepancies between the modelled and reference sequences:

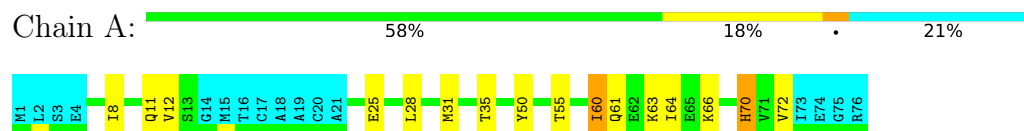
Chain	Residue	Modelled	Actual	Comment	Reference
A	46	VAL	SER	engineered mutation	UNP O32220
A	73	ILE	THR	cloning artifact	UNP O32220
A	75	GLY	LYS	cloning artifact	UNP O32220
A	76	ARG	ALA	cloning artifact	UNP O32220

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: Potential copper-transporting ATPase

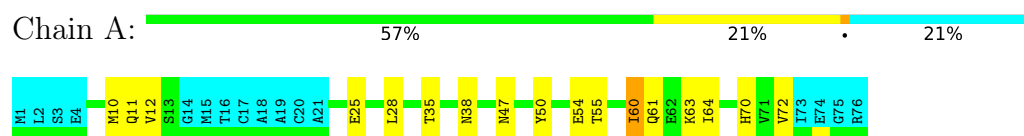


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

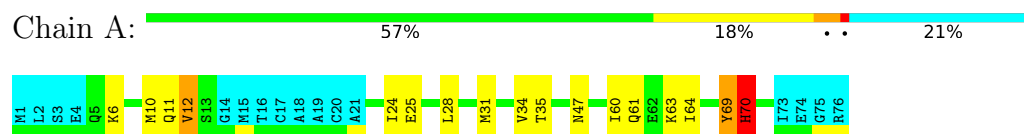
4.2.1 Score per residue for model 1

- Molecule 1: Potential copper-transporting ATPase



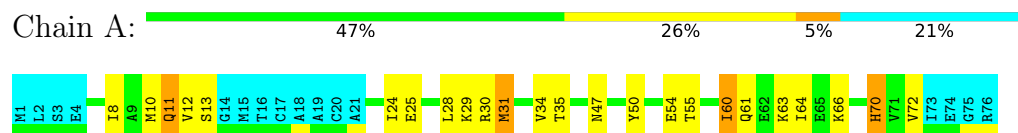
4.2.2 Score per residue for model 2

- Molecule 1: Potential copper-transporting ATPase



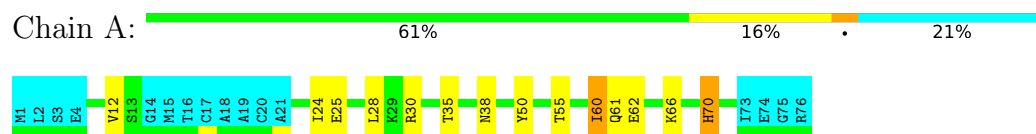
4.2.3 Score per residue for model 3

- Molecule 1: Potential copper-transporting ATPase



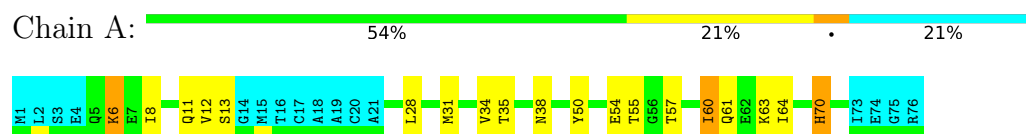
4.2.4 Score per residue for model 4

- Molecule 1: Potential copper-transporting ATPase



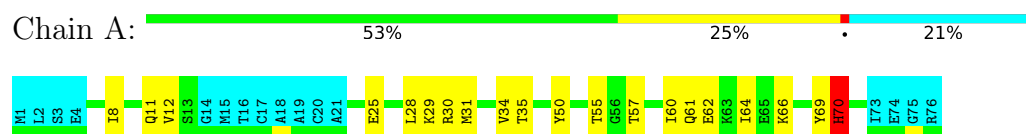
4.2.5 Score per residue for model 5

- Molecule 1: Potential copper-transporting ATPase



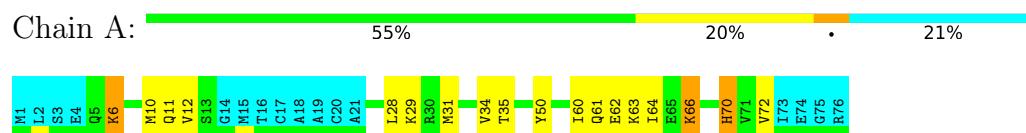
4.2.6 Score per residue for model 6

- Molecule 1: Potential copper-transporting ATPase



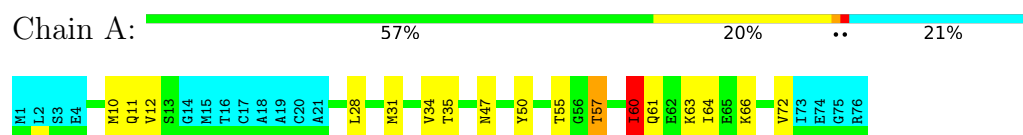
4.2.7 Score per residue for model 7

- Molecule 1: Potential copper-transporting ATPase



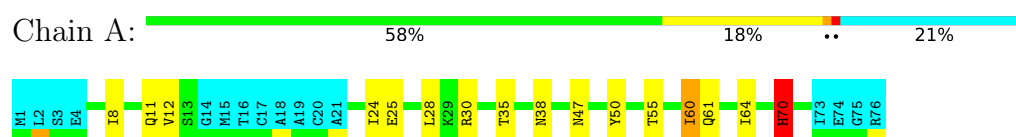
4.2.8 Score per residue for model 8

- Molecule 1: Potential copper-transporting ATPase



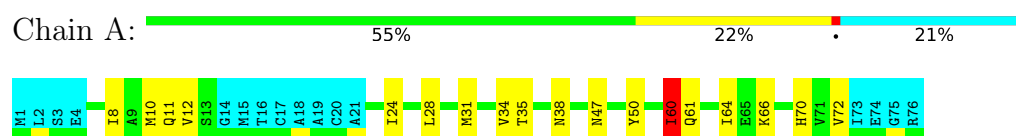
4.2.9 Score per residue for model 9

- Molecule 1: Potential copper-transporting ATPase



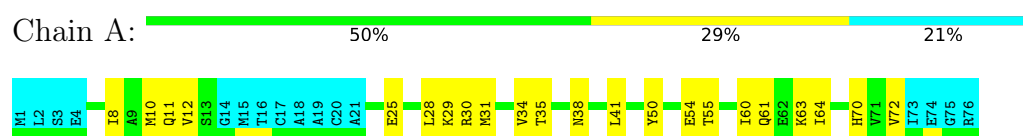
4.2.10 Score per residue for model 10

- Molecule 1: Potential copper-transporting ATPase



4.2.11 Score per residue for model 11

- Molecule 1: Potential copper-transporting ATPase



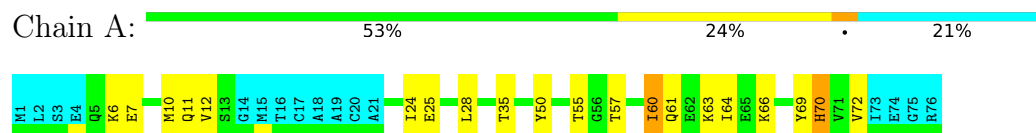
4.2.12 Score per residue for model 12

- Molecule 1: Potential copper-transporting ATPase



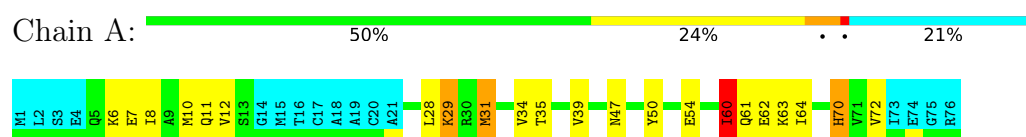
4.2.13 Score per residue for model 13

- Molecule 1: Potential copper-transporting ATPase



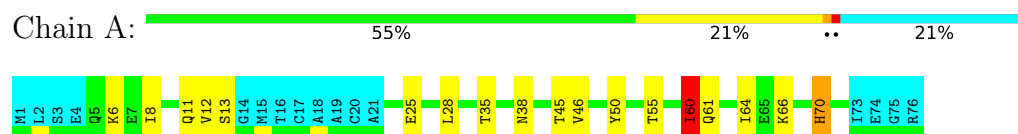
4.2.14 Score per residue for model 14

- Molecule 1: Potential copper-transporting ATPase



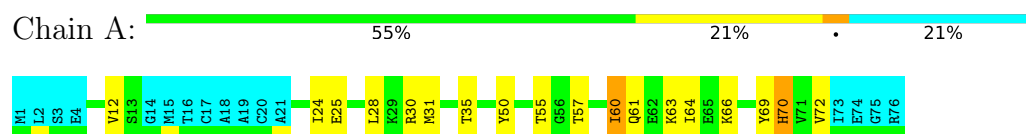
4.2.15 Score per residue for model 15

- Molecule 1: Potential copper-transporting ATPase



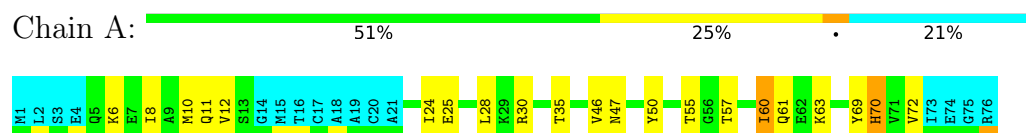
4.2.16 Score per residue for model 16

- Molecule 1: Potential copper-transporting ATPase



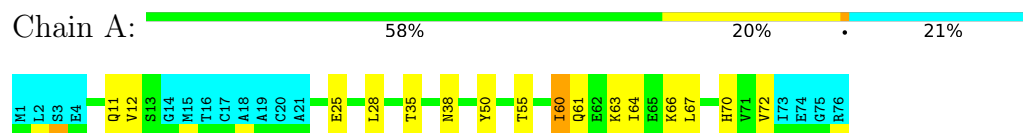
4.2.17 Score per residue for model 17

- Molecule 1: Potential copper-transporting ATPase



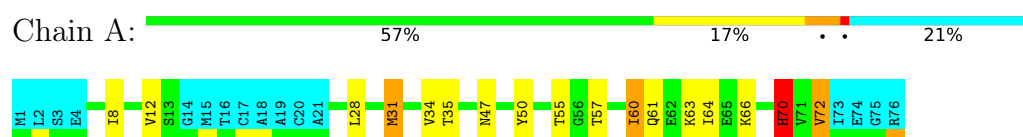
4.2.18 Score per residue for model 18

- Molecule 1: Potential copper-transporting ATPase



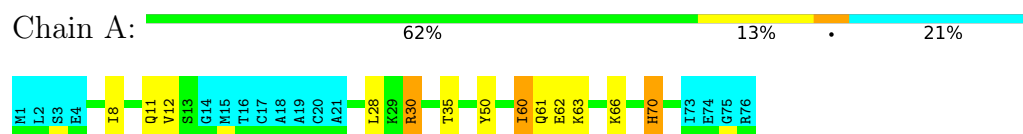
4.2.19 Score per residue for model 19

- Molecule 1: Potential copper-transporting ATPase



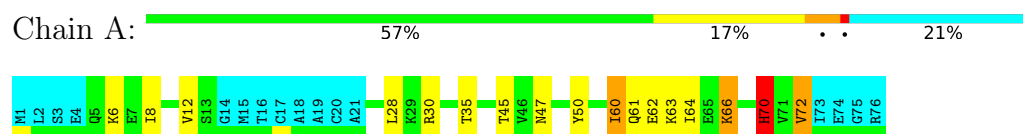
4.2.20 Score per residue for model 20

- Molecule 1: Potential copper-transporting ATPase



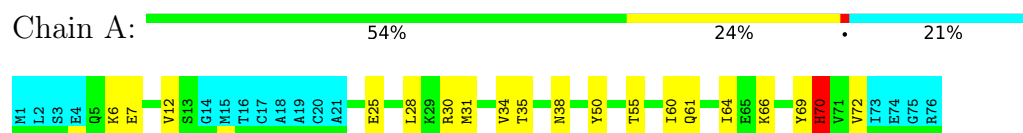
4.2.21 Score per residue for model 21

- Molecule 1: Potential copper-transporting ATPase



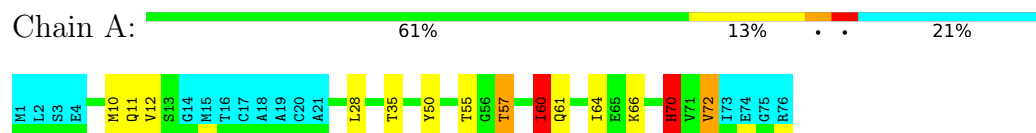
4.2.22 Score per residue for model 22

- Molecule 1: Potential copper-transporting ATPase



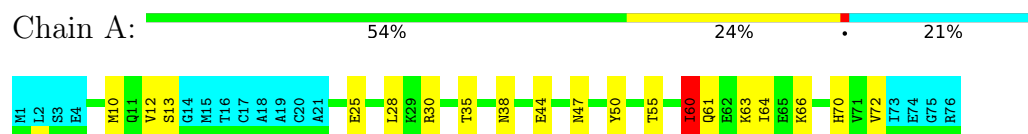
4.2.23 Score per residue for model 23 (medoid)

- Molecule 1: Potential copper-transporting ATPase



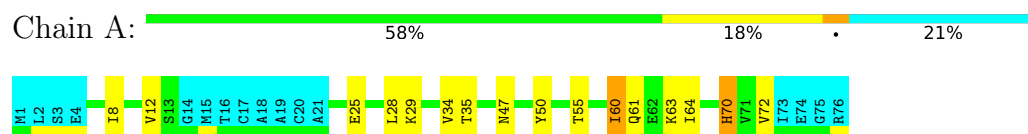
4.2.24 Score per residue for model 24

- Molecule 1: Potential copper-transporting ATPase



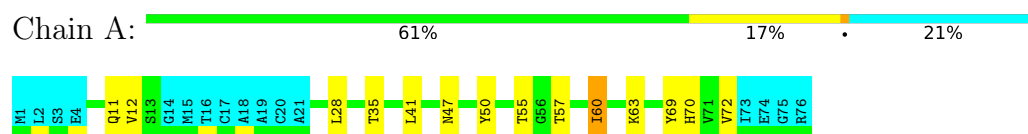
4.2.25 Score per residue for model 25

- Molecule 1: Potential copper-transporting ATPase



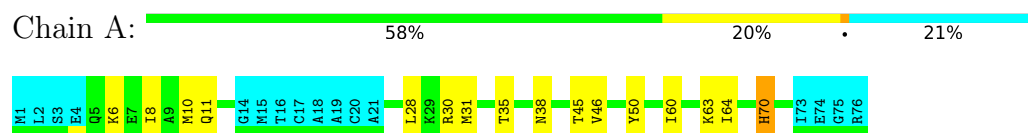
4.2.26 Score per residue for model 26

- Molecule 1: Potential copper-transporting ATPase



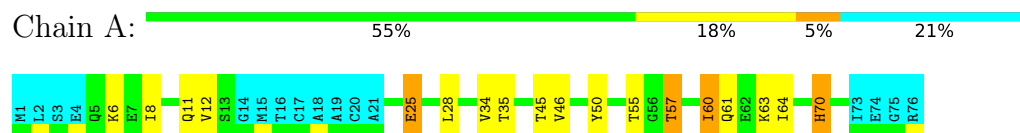
4.2.27 Score per residue for model 27

- Molecule 1: Potential copper-transporting ATPase



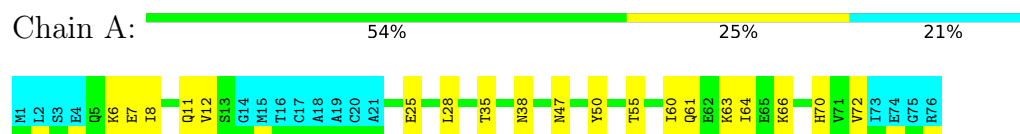
4.2.28 Score per residue for model 28

- Molecule 1: Potential copper-transporting ATPase



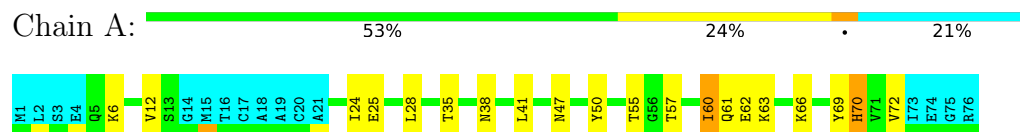
4.2.29 Score per residue for model 29

- Molecule 1: Potential copper-transporting ATPase



4.2.30 Score per residue for model 30

- Molecule 1: Potential copper-transporting ATPase



5 Refinement protocol and experimental data overview

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

Of the 300 calculated structures, 30 were deposited, based on the following criterion: *The submitted conformer models are the 30 structures with the lowest violations*.

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

Software name	Classification	Version
XEASY	structure solution	1.3
DYANA	structure solution	1.5
Amber	refinement	5.0

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.59±0.01	0±0/462 (0.0± 0.0%)	1.28±0.03	2±1/626 (0.3± 0.1%)
All	All	0.59	0/13860 (0.0%)	1.28	59/18780 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	1.6±0.6
All	All	0	47

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	70	HIS	CB-CG-CD2	-8.62	120.00	131.20	22	9
1	A	70	HIS	CA-CB-CG	7.54	121.34	113.80	16	13
1	A	55	THR	N-CA-C	6.79	119.45	108.32	9	23
1	A	6	LYS	CA-C-N	6.71	131.98	121.99	21	3
1	A	6	LYS	C-N-CA	6.71	131.98	121.99	21	3
1	A	70	HIS	CB-CA-C	5.72	120.18	109.71	6	1
1	A	60	ILE	CB-CA-C	5.55	118.75	111.81	24	7

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	50	TYR	Sidechain	29

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	70	HIS	Sidechain	7
1	A	54	GLU	Peptide	6
1	A	69	TYR	Sidechain	4
1	A	30	ARG	Sidechain	1

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	457	472	472	3±1
All	All	13710	14160	14160	95

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:28:LEU:HD11	1:A:64:ILE:HD11	0.71	1.62	16	25
1:A:28:LEU:HD22	1:A:60:ILE:HG12	0.58	1.75	17	17
1:A:70:HIS:HE1	1:A:72:VAL:HG13	0.56	1.61	19	3
1:A:28:LEU:CD1	1:A:64:ILE:HD11	0.51	2.34	16	5
1:A:28:LEU:HD22	1:A:60:ILE:HG13	0.51	1.81	25	3
1:A:29:LYS:HA	1:A:34:VAL:HG11	0.50	1.83	14	7
1:A:28:LEU:HD22	1:A:60:ILE:CG1	0.49	2.37	15	5
1:A:70:HIS:CE1	1:A:72:VAL:HG13	0.49	2.42	23	2
1:A:28:LEU:HD11	1:A:64:ILE:CD1	0.48	2.38	3	3
1:A:24:ILE:HD11	1:A:69:TYR:CD2	0.47	2.44	30	4
1:A:31:MET:O	1:A:34:VAL:HG12	0.47	2.10	14	12
1:A:12:VAL:HG11	1:A:24:ILE:HD13	0.43	1.90	2	1
1:A:25:GLU:CD	1:A:46:VAL:HG21	0.43	2.39	28	2
1:A:24:ILE:HD11	1:A:69:TYR:CE2	0.43	2.48	16	1
1:A:24:ILE:HD12	1:A:24:ILE:H	0.43	1.74	16	1
1:A:24:ILE:HD11	1:A:69:TYR:CZ	0.42	2.50	16	1
1:A:62:GLU:CD	1:A:66:LYS:HZ1	0.41	2.23	21	1
1:A:11:GLN:H	1:A:11:GLN:NE2	0.40	2.15	3	1
1:A:62:GLU:OE2	1:A:66:LYS:NZ	0.40	2.53	7	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	60/76 (79%)	54±1 (90±2%)	6±1 (10±2%)	0±0 (0±1%)	44	80
All	All	1800/2280 (79%)	1613 (90%)	184 (10%)	3 (0%)	44	80

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	57	THR	3

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	49/60 (82%)	37±2 (75±4%)	12±2 (25±4%)	2	24
All	All	1470/1800 (82%)	1100 (75%)	370 (25%)	2	24

All 27 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	35	THR	30
1	A	60	ILE	30
1	A	12	VAL	29
1	A	70	HIS	29
1	A	61	GLN	28
1	A	63	LYS	23
1	A	11	GLN	22
1	A	72	VAL	21
1	A	25	GLU	18
1	A	66	LYS	18

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Mol	Chain	Res	Type	Models (Total)
1	A	8	ILE	17
1	A	47	ASN	15
1	A	10	MET	14
1	A	38	ASN	14
1	A	30	ARG	13
1	A	57	THR	11
1	A	6	LYS	10
1	A	31	MET	5
1	A	62	GLU	5
1	A	13	SER	4
1	A	7	GLU	4
1	A	45	THR	4
1	A	46	VAL	2
1	A	29	LYS	1
1	A	67	LEU	1
1	A	44	GLU	1
1	A	34	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 oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided